

Glycopeptides detected in unfractionated and S&P pig plasma

Click the link below to view data in Mascot Peptide View OR "ATL + <- " (ATL+arrow) to go back

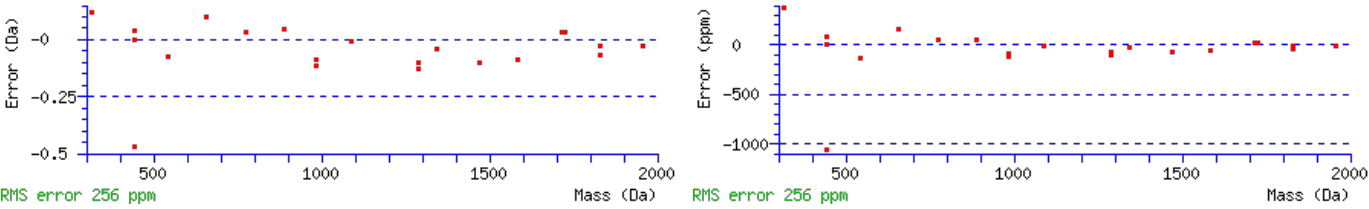
- [Spectrum_00001_F1SQX9_R.ADGTVNQIEGEATPDN#ITEPAK.L](#)
- [Spectrum_00002_F1RJS2_R.EILSVDCSASN#SSQMQLR.Q](#)
- [Spectrum_00003_I3L6Q6_K.N#GVTVSPAAGAYEN#GSSVEYR.C](#)
- [Spectrum_00004_F1SEI5_R.VN#GEN#CTTSSASSVLAN#TK.D](#)
- [Spectrum_00005_F1S8N1_R.AAPSN#SSAGGTVLTEAGOPCR.F](#)
- [Spectrum_00006_I3L5K0_K.VTVVYADN#GTVLQASTTASVYK.G](#)
- [Spectrum_00007_F1S788_R.GGSSGWGGGLTON#GSIITYR.A](#)
- [Spectrum_00008_F1RPW2_R.AVDSN#SSSPGN#ISR.A](#)
- [Spectrum_00009_F1SS24_R.DQCIVDDITYNVN#DTEHK.R](#)
- [Spectrum_00010_F1SEI5_R.VN#GEN#CTTSSASSVLANTK.D](#)
- [Spectrum_00011_F1SEI5_R.VNGEN#CTTSSASSVLAN#TK.D](#)
- [Spectrum_00012_F1SEI5_R.VNGEN#CTTSSASSVLANTK.D](#)
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- [Spectrum_00014_F1S643_K.LN#DTVDYECQQGFESR.N](#)
- [Spectrum_00015_F1S643_K.LN#DTVDYECQQ#GFESR.N](#)
- [Spectrum_00016_F1SAE9_K.LSDAALQSN#STAR.E](#)
- [Spectrum_00017_F1ST75_K.VDYESQSTDTON#ESSESK.R](#)
- [Spectrum_00018_F1RQW2_R.FSDGLDSN#SSTQFEVK.K](#)
- [Spectrum_00019_F1SN68_R.EYQTIGN#QCIYN#DSSLK.V](#)
- [Spectrum_00020_Q9XSH0_K.NSCCSVN#TSLEAHK.D](#)
- [Spectrum_00021_A8R080_K.TICGSSGN#WSSPSPICQK.L](#)
- [Spectrum_00022_F1S573_K.TASGQIESYN#DTYEIR.D](#)
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- [Spectrum_00024_F1SKB1_K.EN#LTAPGSASEVFFTR.G](#)
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- [Spectrum_00031_F1RQW2_R.FSDGLDSN#SSTQ#FEVK.K](#)
- [Spectrum_00032_F1RKY2_R.NSN#LTGISDQR.I](#)
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- [Spectrum_00240_F1SQ09_K.LHINYNN#LTESVGPLPK.S](#)
- [Spectrum_00241_I3LT35_R.SNN#ITDSLANS#R.T](#)
- [Spectrum_00242_F1S3J9_R.EGQHFEN#LSCQVSGGAPR.T](#)
- [Spectrum_00243_F1ST75_R.YKVDYESQSTDTQ#N#FSSESKR.R](#)
- [Spectrum_00244_I3LT35_R.SN#N#ITDSLANS#R.T](#)
- [Spectrum_00245_Q06AU7_K.LLVGN#KSDLTTK.K](#)
- [Spectrum_00246_F1S3Q8_K.KPCN#ASDPQ#CPPDGR.Y](#)



NCBI **BLAST** search of [ADGTVNQIEGEATPDNITEPAK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
148.7	2270.0550	-0.0074	ADGTVNQIEGEATPDNITEPAK	Deamidated N16 100.00%
22.9	2270.0550	-0.0074	ADGTVNQIEGEATPDNITEPAK	Deamidated Q7 0.00%
16.5	2270.0550	-0.0074	ADGTVNQIEGEATPDNITEPAK	Deamidated N6 0.00%
13.3	2270.0424	0.0051	HPPRGHSQSEGNPSADGGVGGLR	
9.9	2270.0525	-0.0049	SFIGEFMESLQDPDLNVRR	
6.1	2270.0484	-0.0009	ADQKDAEPQAPGIEEAQMGKR	
2.4	2269.0606	0.9869	QSLFQEEGMLSLVLNCIDR	
2.2	2270.0446	0.0029	QSLFQEEGMLSLVLNCIDR	
1.9	2269.0606	0.9869	QSLFQEEGMLSLVLNCIDR	
0.5	2269.0651	0.9825	VSKKSNGAPNGFYAEIDWER	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

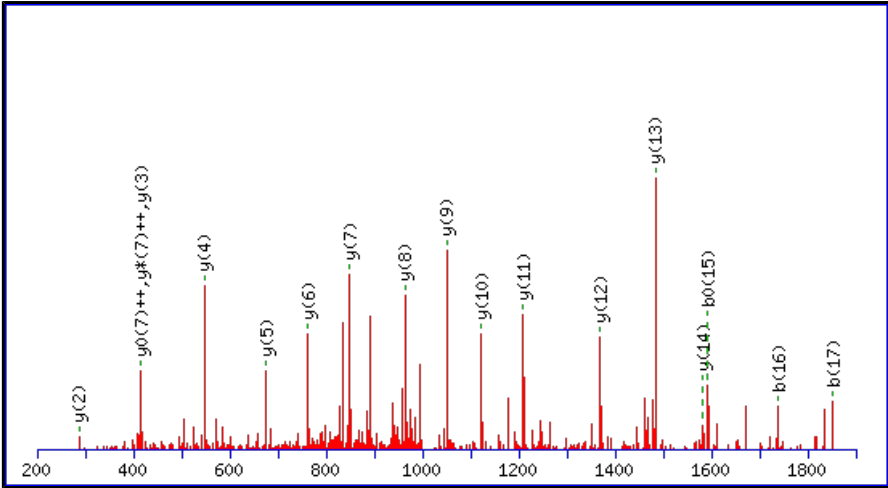
Peptide View

MS/MS Fragmentation of **EILSVDCSASNSSQMLR**
Found in **F1RJS2** in **uni_pig**, tr|F1RJS2|F1RJS2_PIG Clusterin OS=Sus scrofa GN=CLU PE=3 SV=2

Match to Query 10937: 2024.921448 from(1013.468000,2+) intensity(2249.0442) rtinseconds(1901) scans(4503) index(1565)
Title: 120325_Sunil_PigSerum_Glyco_D_14Spectrum3840_scans__4503
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

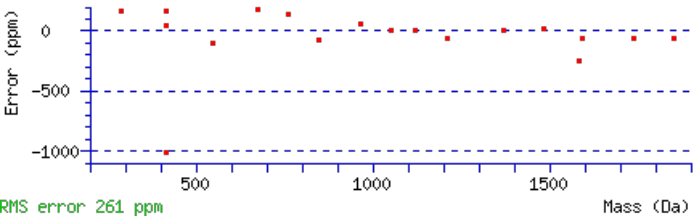
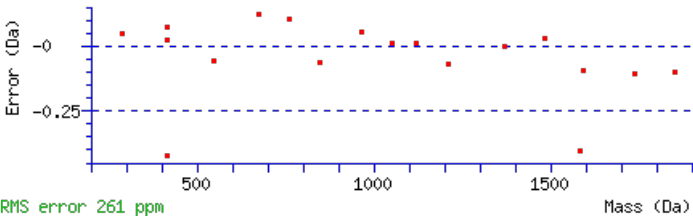
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2024.9143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Ions Score: 141 Expect: 3.7e-013
Matches : 18/174 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							18
2	243.1339	122.0706			225.1234	113.0653	I	1896.8790	948.9431	1879.8524	940.4299	1878.8684	939.9378	17
3	356.2180	178.6126			338.2074	169.6074	L	1783.7949	892.4011	1766.7684	883.8878	1765.7844	883.3958	16
4	443.2500	222.1287			425.2395	213.1234	S	1670.7109	835.8591	1653.6843	827.3458	1652.7003	826.8538	15
5	542.3184	271.6629			524.3079	262.6576	V	1583.6788	792.3431	1566.6523	783.8298	1565.6683	783.3378	14
6	657.3454	329.1763			639.3348	320.1710	D	1484.6104	742.8088	1467.5839	734.2956	1466.5999	733.8036	13
7	817.3760	409.1917			799.3655	400.1864	C	1369.5835	685.2954	1352.5569	676.7821	1351.5729	676.2901	12
8	904.4081	452.7077			886.3975	443.7024	S	1209.5528	605.2801	1192.5263	596.7668	1191.5423	596.2748	11
9	975.4452	488.2262			957.4346	479.2209	A	1122.5208	561.7640	1105.4942	553.2508	1104.5102	552.7588	10
10	1062.4772	531.7422			1044.4666	522.7370	S	1051.4837	526.2455	1034.4571	517.7322	1033.4731	517.2402	9
11	1177.5041	589.2557	1160.4776	580.7424	1159.4936	580.2504	N	964.4517	482.7295	947.4251	474.2162	946.4411	473.7242	8
12	1264.5362	632.7717	1247.5096	624.2584	1246.5256	623.7664	S	849.4247	425.2160	832.3982	416.7027	831.4141	416.2107	7
13	1351.5682	676.2877	1334.5417	667.7745	1333.5576	667.2825	S	762.3927	381.7000	745.3661	373.1867	744.3821	372.6947	6
14	1479.6268	740.3170	1462.6002	731.8038	1461.6162	731.3117	Q	675.3607	338.1840	658.3341	329.6707			5
15	1610.6673	805.8373	1593.6407	797.3240	1592.6567	796.8320	M	547.3021	274.1547	530.2755	265.6414			4
16	1738.7258	869.8666	1721.6993	861.3533	1720.7153	860.8613	Q	416.2616	208.6344	399.2350	200.1212			3
17	1851.8099	926.4086	1834.7834	917.8953	1833.7993	917.4033	L	288.2030	144.6051	271.1765	136.0919			2
18							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [EILSVDCSASNSSQMLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
141.1	2024.9143	0.0072	EILSVDCSASNSSQMLR	Deamidated N11 99.99%
97.9	2024.9143	0.0072	EILSVDCSASNSSQMLR	Deamidated Q14 0.00%
94.3	2024.9143	0.0072	EILSVDCSASNSSQMLR	Deamidated Q16 0.00%
29.5	2023.9303	0.9912	EILSVDCSASNSSQMLR	
10.5	2024.9030	0.0184	ELNESNSQMEADMLKLR	
10.5	2024.9030	0.0184	ELNESNSQMEADMLKLR	
10.5	2024.9030	0.0184	ELNESNSQMEADMLKLR	
5.9	2024.9030	0.0184	ELNESNSQMEADMLKLR	
5.9	2024.9030	0.0184	ELNESNSQMEADMLKLR	
2.9	2024.9030	0.0184	ELNESNSQMEADMLKLR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **NGVTVSPAAGAYENGSSVEYR**

Found in **I3L6Q6** in **uni_pig**, tr|I3L6Q6|I3L6Q6_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=F13B PE=4 SV=1

Match to Query 11997: 2128.946548 from(1065.480550,2+) intensity(31676.0234) rtinseconds(1777) scans(4047) index(10655)

Title: 120326 Sunil PigSerum Glyco PsetB 14Spectrum3333 scans 4047

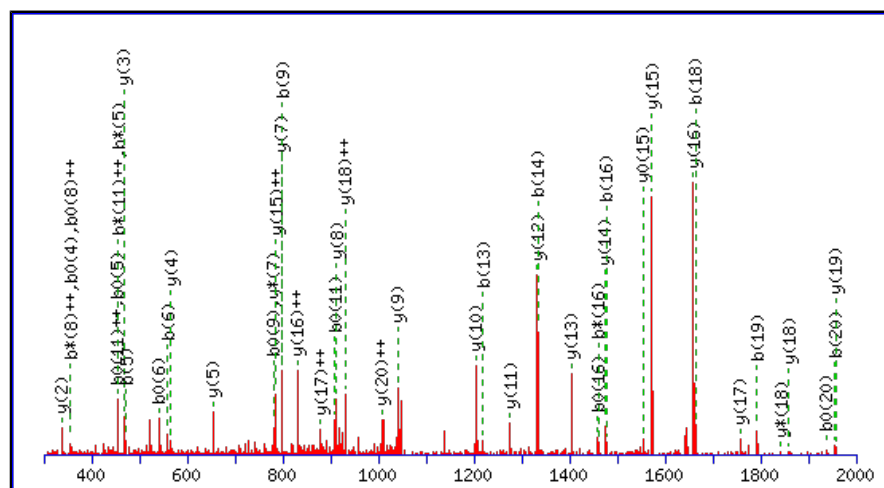
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2128.9549

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

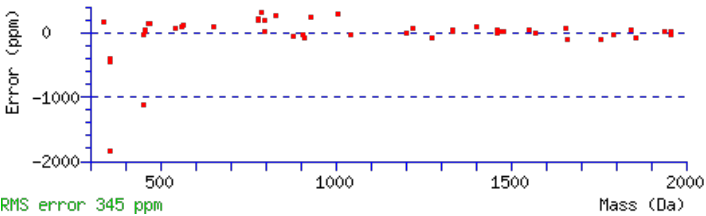
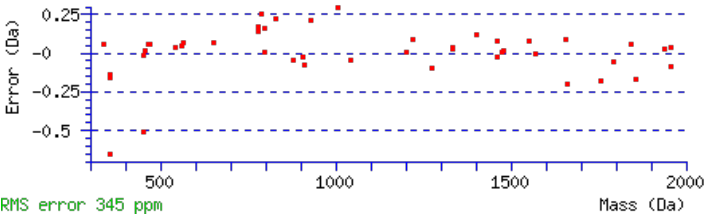
Variable modifications:

N1 : Deamidated (NQ)

N14 : Deamidated (NQ)
Ions Score: 128 Expect: 5.1e-012

Matches : 47/230 fragment ions using 68 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							21
2	173.0557	87.0315	156.0291	78.5182			G	2014.9352	1007.9713	1997.9087	999.4580	1996.9247	998.9660	20
3	272.1241	136.5657	255.0975	128.0524			V	1957.9138	979.4605	1940.8872	970.9473	1939.9032	970.4552	19
4	373.1718	187.0895	356.1452	178.5763	355.1612	178.0842	T	1858.8454	929.9263	1841.8188	921.4130	1840.8348	920.9210	18
5	472.2402	236.6237	455.2136	228.1105	454.2296	227.6185	V	1757.7977	879.4025	1740.7711	870.8892	1739.7871	870.3972	17
6	559.2722	280.1397	542.2457	271.6265	541.2617	271.1345	S	1658.7293	829.8683	1641.7027	821.3550	1640.7187	820.8630	16
7	656.3250	328.6661	639.2984	320.1529	638.3144	319.6608	P	1571.6972	786.3523	1554.6707	777.8390	1553.6867	777.3470	15
8	727.3621	364.1847	710.3355	355.6714	709.3515	355.1794	A	1474.6445	737.8259	1457.6179	729.3126	1456.6339	728.8206	14
9	798.3992	399.7032	781.3727	391.1900	780.3886	390.6980	A	1403.6074	702.3073	1386.5808	693.7940	1385.5968	693.3020	13
10	855.4207	428.2140	838.3941	419.7007	837.4101	419.2087	G	1332.5703	666.7888	1315.5437	658.2755	1314.5597	657.7835	12
11	926.4578	463.7325	909.4312	455.2193	908.4472	454.7272	A	1275.5488	638.2780	1258.5222	629.7648	1257.5382	629.2727	11
12	1089.5211	545.2642	1072.4946	536.7509	1071.5106	536.2589	Y	1204.5117	602.7595	1187.4851	594.2462	1186.5011	593.7542	10
13	1218.5637	609.7855	1201.5372	601.2722	1200.5531	600.7802	E	1041.4483	521.2278	1024.4218	512.7145	1023.4378	512.2225	9
14	1333.5907	667.2990	1316.5641	658.7857	1315.5801	658.2937	N	912.4058	456.7065	895.3792	448.1932	894.3952	447.7012	8
15	1390.6121	695.8097	1373.5856	687.2964	1372.6016	686.8044	G	797.3788	399.1930	780.3523	390.6798	779.3682	390.1878	7
16	1477.6441	739.3257	1460.6176	730.8124	1459.6336	730.3204	S	740.3573	370.6823	723.3308	362.1690	722.3468	361.6770	6
17	1564.6762	782.8417	1547.6496	774.3285	1546.6656	773.8364	S	653.3253	327.1663	636.2988	318.6530	635.3148	318.1610	5
18	1663.7446	832.3759	1646.7180	823.8627	1645.7340	823.3706	V	566.2933	283.6503	549.2667	275.1370	548.2827	274.6450	4
19	1792.7872	896.8972	1775.7606	888.3840	1774.7766	887.8919	E	467.2249	234.1161	450.1983	225.6028	449.2143	225.1108	3
20	1955.8505	978.4289	1938.8240	969.9156	1937.8399	969.4236	Y	338.1823	169.5948	321.1557	161.0815			2
21							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [NGVTVSPAAGAYENGSSVEYR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
128.3	2128.9549	-0.0083	NGVTVSPAAGAYENGSSVEYR
6.0	2128.9331	0.0135	SNQNDPAEGKNNQQMVPEK
5.7	2128.9331	0.0135	SNQNDPAEGKNNQQMVPEK
5.7	2128.9331	0.0135	SNQNDPAEGKNNQQMVPEK
1.1	2128.9458	0.0007	LCERYAMVYGYNAAYNR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNGFNCTTSSASSVLANTK**

Found in **F1SFI5** in **uni_pig**, tr|F1SFI5|F1SFI5_PIG Uncharacterized protein OS=Sus scrofa GN=HRG PE=4 SV=2

Match to Query 8895: 1959.867568 from(980.941060,2+) intensity(36203.7461) rtinseconds(1669) scans(2846) index(9085)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_17Spectrum1942_scans_2846

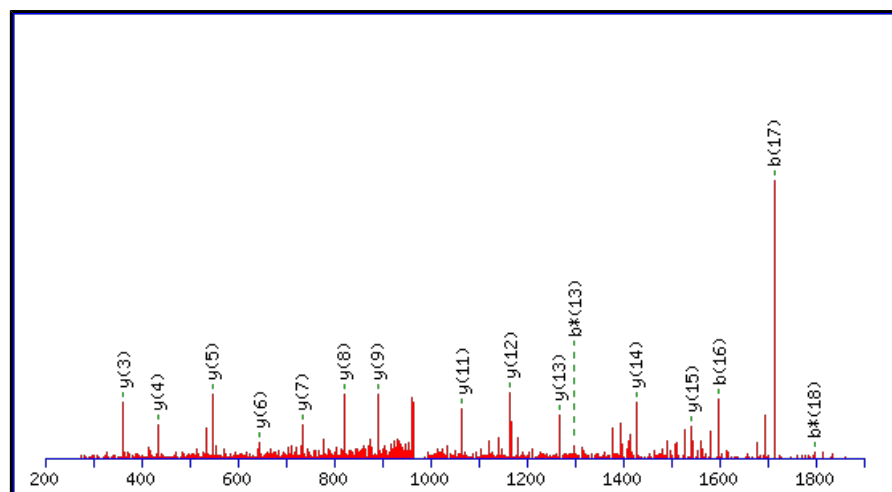
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1959.8731

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

N2 : Deamidated (NQ)

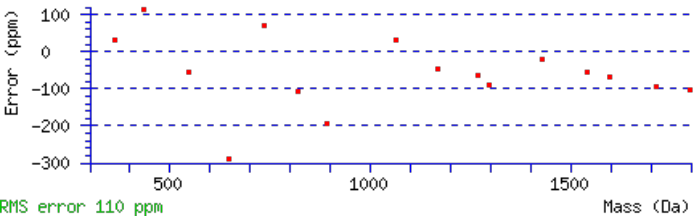
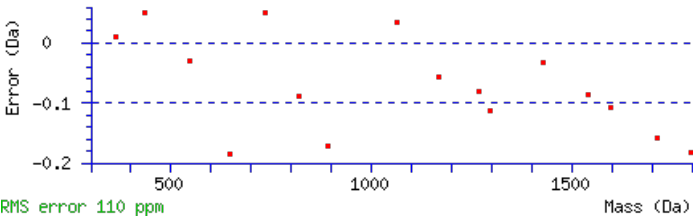
N5 : Deamidated (NQ)

N17 : Deamidated (NQ)

Ions Score: 127 Expect: 6.6e-012

Matches : 16/200 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							19
2	215.1026	108.0550	198.0761	99.5417			N	1861.8120	931.4096	1844.7855	922.8964	1843.8015	922.4044	18
3	272.1241	136.5657	255.0975	128.0524			G	1746.7851	873.8962	1729.7585	865.3829	1728.7745	864.8909	17
4	419.1925	210.0999	402.1660	201.5866			F	1689.7636	845.3854	1672.7371	836.8722	1671.7530	836.3802	16
5	534.2195	267.6134	517.1929	259.1001			N	1542.6952	771.8512	1525.6686	763.3380	1524.6846	762.8460	15
6	694.2501	347.6287	677.2236	339.1154			C	1427.6683	714.3378	1410.6417	705.8245	1409.6577	705.3325	14
7	795.2978	398.1525	778.2712	389.6393	777.2872	389.1472	T	1267.6376	634.3224	1250.6111	625.8092	1249.6270	625.3172	13
8	896.3455	448.6764	879.3189	440.1631	878.3349	439.6711	T	1166.5899	583.7986	1149.5634	575.2853	1148.5794	574.7933	12
9	983.3775	492.1924	966.3509	483.6791	965.3669	483.1871	S	1065.5422	533.2748	1048.5157	524.7615	1047.5317	524.2695	11
10	1070.4095	535.7084	1053.3830	527.1951	1052.3990	526.7031	S	978.5102	489.7587	961.4837	481.2455	960.4997	480.7535	10
11	1141.4466	571.2270	1124.4201	562.7137	1123.4361	562.2217	A	891.4782	446.2427	874.4516	437.7295	873.4676	437.2374	9
12	1228.4787	614.7430	1211.4521	606.2297	1210.4681	605.7377	S	820.4411	410.7242	803.4145	402.2109	802.4305	401.7189	8
13	1315.5107	658.2590	1298.4841	649.7457	1297.5001	649.2537	S	733.4090	367.2082	716.3825	358.6949	715.3985	358.2029	7
14	1414.5791	707.7932	1397.5526	699.2799	1396.5685	698.7879	V	646.3770	323.6921	629.3505	315.1789	628.3665	314.6869	6
15	1527.6632	764.3352	1510.6366	755.8219	1509.6526	755.3299	L	547.3086	274.1579	530.2821	265.6447	529.2980	265.1527	5
16	1598.7003	799.8538	1581.6737	791.3405	1580.6897	790.8485	A	434.2245	217.6159	417.1980	209.1026	416.2140	208.6106	4
17	1713.7272	857.3672	1696.7007	848.8540	1695.7167	848.3620	N	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
18	1814.7749	907.8911	1797.7484	899.3778	1796.7643	898.8858	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
19							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VNGENCTTSSASSVLANTK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
126.8	1959.8731	-0.0056	VNGENCTTSSASSVLANTK
6.8	1959.8779	-0.0103	VNMCTSASWRSLTTSR
0.1	1959.8751	-0.0075	QKTFYGRPNWNNEER

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

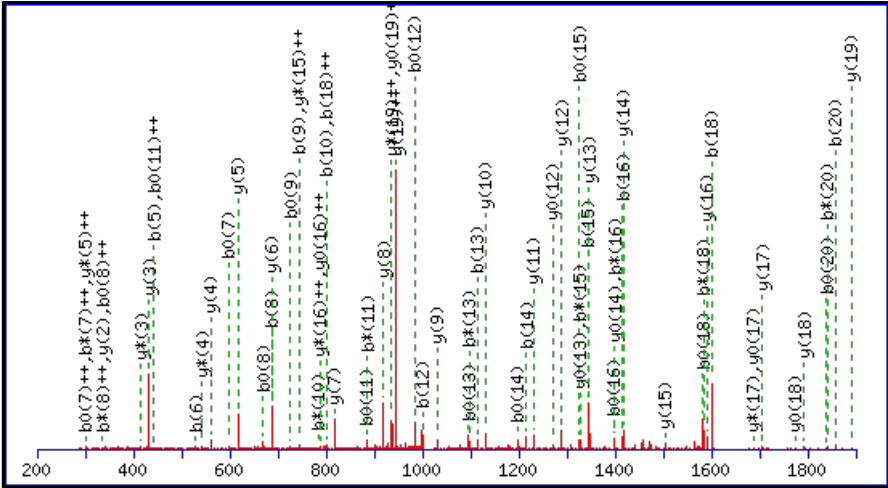
Peptide View

MS/MS Fragmentation of **AAPSNSSAGGTVLTEAGQPCR**
Found in **F1S8N1** in **uni_pig**, tr|F1S8N1|F1S8N1_PIG Uncharacterized protein OS=Sus scrofa GN=HGFAC PE=3 SV=1

Match to Query 10965: 2030.919408 from(1016.466980,2+) intensity(26674.5273) rtinseconds(1375) scans(2921) index(10608)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_14Spectrum2331_scans__2921
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

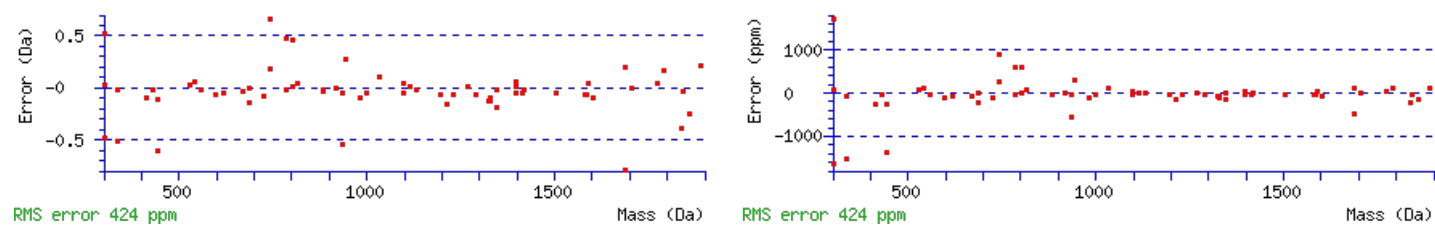
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2030.9327
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 128 Expect: 6.7e-012
Matches : 69/214 fragment ions using 97 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							21
2	143.0815	72.0444					A	1960.9029	980.9551	1943.8763	972.4418	1942.8923	971.9498	20
3	240.1343	120.5708					P	1889.8658	945.4365	1872.8392	936.9233	1871.8552	936.4312	19
4	327.1663	164.0868			309.1557	155.0815	S	1792.8130	896.9101	1775.7865	888.3969	1774.8025	887.9049	18
5	442.1932	221.6003	425.1667	213.0870	424.1827	212.5950	N	1705.7810	853.3941	1688.7544	844.8809	1687.7704	844.3889	17
6	529.2253	265.1163	512.1987	256.6030	511.2147	256.1110	S	1590.7540	795.8807	1573.7275	787.3674	1572.7435	786.8754	16
7	616.2573	308.6323	599.2307	300.1190	598.2467	299.6270	S	1503.7220	752.3646	1486.6955	743.8514	1485.7115	743.3594	15
8	687.2944	344.1508	670.2679	335.6376	669.2838	335.1456	A	1416.6900	708.8486	1399.6634	700.3354	1398.6794	699.8434	14
9	744.3159	372.6616	727.2893	364.1483	726.3053	363.6563	G	1345.6529	673.3301	1328.6263	664.8168	1327.6423	664.3248	13
10	801.3373	401.1723	784.3108	392.6590	783.3268	392.1670	G	1288.6314	644.8193	1271.6049	636.3061	1270.6208	635.8141	12
11	902.3850	451.6961	885.3585	443.1829	884.3745	442.6909	T	1231.6099	616.3086	1214.5834	607.7953	1213.5994	607.3033	11
12	1001.4534	501.2304	984.4269	492.7171	983.4429	492.2251	V	1130.5623	565.7848	1113.5357	557.2715	1112.5517	556.7795	10
13	1114.5375	557.7724	1097.5109	549.2591	1096.5269	548.7671	L	1031.4939	516.2506	1014.4673	507.7373	1013.4833	507.2453	9
14	1215.5852	608.2962	1198.5586	599.7830	1197.5746	599.2909	T	918.4098	459.7085	901.3832	451.1953	900.3992	450.7033	8
15	1344.6278	672.8175	1327.6012	664.3042	1326.6172	663.8122	E	817.3621	409.1847	800.3356	400.6714	799.3515	400.1794	7
16	1415.6649	708.3361	1398.6383	699.8228	1397.6543	699.3308	A	688.3195	344.6634	671.2930	336.1501			6
17	1472.6863	736.8468	1455.6598	728.3335	1454.6758	727.8415	G	617.2824	309.1448	600.2559	300.6316			5
18	1600.7449	800.8761	1583.7184	792.3628	1582.7344	791.8708	Q	560.2609	280.6341	543.2344	272.1208			4
19	1697.7977	849.4025	1680.7711	840.8892	1679.7871	840.3972	P	432.2024	216.6048	415.1758	208.0915			3
20	1857.8283	929.4178	1840.8018	920.9045	1839.8178	920.4125	C	335.1496	168.0784	318.1231	159.5652			2
21							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [AAPSNSSAGGTVLTEAGQPCR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
128.2	2030.9327	-0.0133	AAPSNSSAGGTVLTEAGQPCR	Deamidated N5 100.00%
62.6	2030.9327	-0.0133	AAPSNSSAGGTVLTEAGQPCR	Deamidated Q18 0.00%
7.2	2030.9149	0.0045	AACSEHQKDLEMLQAER	
3.6	2030.9392	-0.0198	TPESQEAEEKKEDINQER	
1.6	2030.9336	-0.0142	EAVTRFLMSCTECQKR	
0.8	2029.9204	0.9990	MDWGLEFDKNAGENTFLR	
0.3	2029.9116	1.0078	DWEETVQPLLQEQEQR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTVVYADNGTVLQASTTASVYK**
Found in **I3L5K0** in **uni_pig**, tr[I3L5K0]I3L5K0_PIG Uncharacterized protein OS=Sus scrofa GN=LOC100738788 PE=4 SV=1

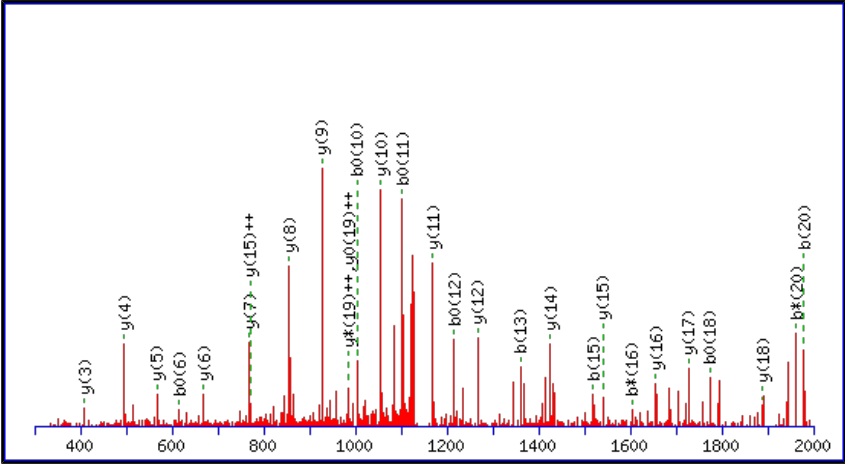
Match to Query 12676: 2287.145308 from(1144.579930,2+) intensity(13284.7334) rtinseconds(2182) scans(5165) index(10698)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_14Spectrum4331_scans_5165
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

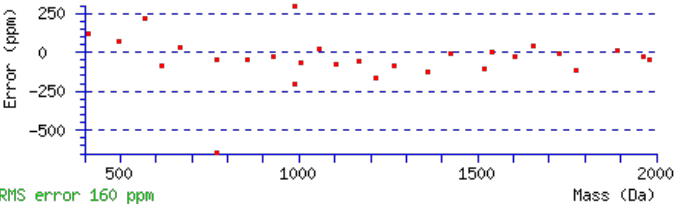
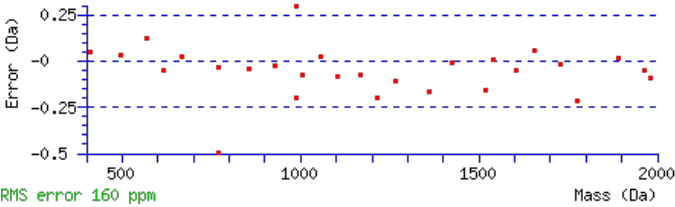
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2287.1584
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 127 Expect: 1.7e-011
Matches : 28/230 fragment ions using 34 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							22
2	201.1234	101.0653			183.1128	92.0600	T	2189.0972	1095.0522	2172.0707	1086.5390	2171.0867	1086.0470	21
3	300.1918	150.5995			282.1812	141.5942	V	2088.0495	1044.5284	2071.0230	1036.0151	2070.0390	1035.5231	20
4	399.2602	200.1337			381.2496	191.1285	V	1988.9811	994.9942	1971.9546	986.4809	1970.9706	985.9889	19
5	562.3235	281.6654			544.3130	272.6601	Y	1889.9127	945.4600	1872.8862	936.9467	1871.9022	936.4547	18
6	633.3606	317.1840			615.3501	308.1787	A	1726.8494	863.9283	1709.8228	855.4151	1708.8388	854.9230	17
7	748.3876	374.6974			730.3770	365.6921	D	1655.8123	828.4098	1638.7857	819.8965	1637.8017	819.4045	16
8	863.4145	432.2109	846.3880	423.6976	845.4040	423.2056	N	1540.7853	770.8963	1523.7588	762.3830	1522.7748	761.8910	15
9	920.4360	460.7216	903.4094	452.2084	902.4254	451.7164	G	1425.7584	713.3828	1408.7318	704.8696	1407.7478	704.3775	14
10	1021.4837	511.2455	1004.4571	502.7322	1003.4731	502.2402	T	1368.7369	684.8721	1351.7104	676.3588	1350.7264	675.8668	13
11	1120.5521	560.7797	1103.5255	552.2664	1102.5415	551.7744	V	1267.6892	634.3483	1250.6627	625.8350	1249.6787	625.3430	12
12	1233.6361	617.3217	1216.6096	608.8084	1215.6256	608.3164	L	1168.6208	584.8141	1151.5943	576.3008	1150.6103	575.8088	11
13	1361.6947	681.3510	1344.6682	672.8377	1343.6842	672.3457	Q	1055.5368	528.2720	1038.5102	519.7587	1037.5262	519.2667	10
14	1432.7318	716.8696	1415.7053	708.3563	1414.7213	707.8643	A	927.4782	464.2427	910.4516	455.7295	909.4676	455.2375	9
15	1519.7639	760.3856	1502.7373	751.8723	1501.7533	751.3803	S	856.4411	428.7242	839.4145	420.2109	838.4305	419.7189	8
16	1620.8115	810.9094	1603.7850	802.3961	1602.8010	801.9041	T	769.4090	385.2082	752.3825	376.6949	751.3985	376.2029	7
17	1721.8592	861.4333	1704.8327	852.9200	1703.8487	852.4280	T	668.3614	334.6843	651.3348	326.1710	650.3508	325.6790	6
18	1792.8963	896.9518	1775.8698	888.4385	1774.8858	887.9465	A	567.3137	284.1605	550.2871	275.6472	549.3031	275.1552	5
19	1879.9284	940.4678	1862.9018	931.9545	1861.9178	931.4625	S	496.2766	248.6419	479.2500	240.1287	478.2660	239.6366	4
20	1978.9968	990.0020	1961.9702	981.4888	1960.9862	980.9967	V	409.2445	205.1259	392.2180	196.6126			3
21	2142.0601	1071.5337	2125.0336	1063.0204	2124.0495	1062.5284	Y	310.1761	155.5917	293.1496	147.0784			2
22							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VTVVYADNGTVLQASTTASVYK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
127.3	2287.1584	-0.0131	VTVVYADNGTVLQASTTASVYK	Deamidated N8 99.94%
95.0	2287.1584	-0.0131	VTVVYADNGTVLQASTTASVYK	Deamidated Q13 0.06%
2.1	2286.1314	1.0139	CNSLPGPAQQLVQLDLQTFR	
1.8	2286.1386	1.0067	GSMQELDTLAGLRRSPAPQSR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGSSGWGGGLTQNGSIITYR**

Found in **F1S788** in **uni_pig**, tr|F1S788|F1S788_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=C8A PE=4 SV=2

Match to Query 10019: 1967.947688 from(984.981120,2+) intensity(1553.1018) rtinseconds(2273) scans(5431) index(13327)

Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum4580_scans_5431

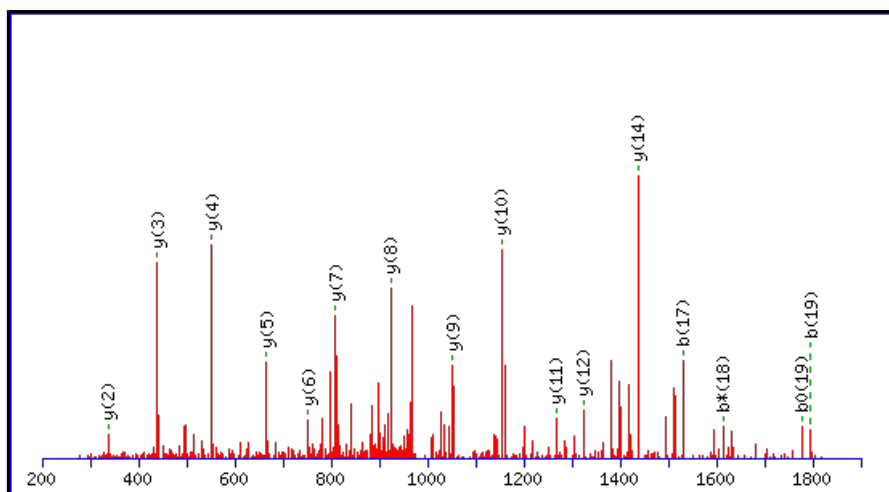
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1967.9337

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

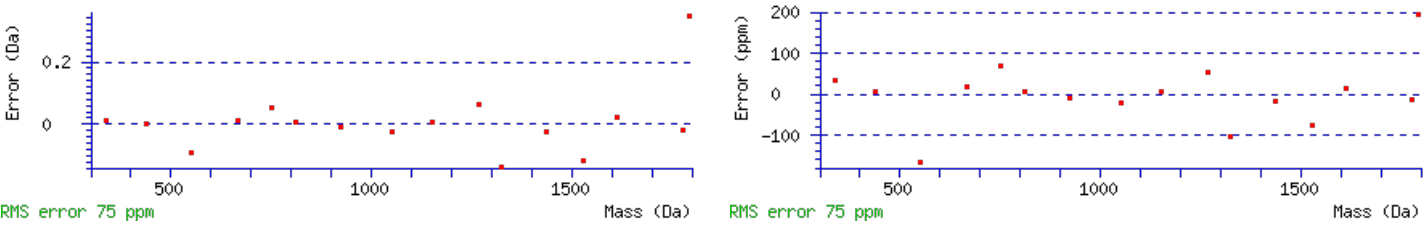
Variable modifications:

N13 : Deamidated (NQ)

Ions Score: 124 Expect: 2.8e-011

```
Matches : 16/198 fragment ions using 16 most intense peaks (help)
```

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							20
2	115.0502	58.0287					G	1911.9195	956.4634	1894.8930	947.9501	1893.9090	947.4581	19
3	202.0822	101.5448			184.0717	92.5395	S	1854.8981	927.9527	1837.8715	919.4394	1836.8875	918.9474	18
4	289.1143	145.0608			271.1037	136.0555	S	1767.8660	884.4367	1750.8395	875.9234	1749.8555	875.4314	17
5	346.1357	173.5715			328.1252	164.5662	G	1680.8340	840.9206	1663.8075	832.4074	1662.8234	831.9154	16
6	532.2150	266.6112			514.2045	257.6059	W	1623.8125	812.4099	1606.7860	803.8966	1605.8020	803.4046	15
7	589.2365	295.1219			571.2259	286.1166	G	1437.7332	719.3703	1420.7067	710.8570	1419.7227	710.3650	14
8	646.2580	323.6326			628.2474	314.6273	G	1380.7118	690.8595	1363.6852	682.3462	1362.7012	681.8542	13
9	703.2794	352.1434			685.2689	343.1381	G	1323.6903	662.3488	1306.6638	653.8355	1305.6797	653.3435	12
10	816.3635	408.6854			798.3529	399.6801	L	1266.6688	633.8381	1249.6423	625.3248	1248.6583	624.8328	11
11	917.4112	459.2092			899.4006	450.2039	T	1153.5848	577.2960	1136.5582	568.7828	1135.5742	568.2907	10
12	1045.4698	523.2385	1028.4432	514.7252	1027.4592	514.2332	Q	1052.5371	526.7722	1035.5106	518.2589	1034.5265	517.7669	9
13	1160.4967	580.7520	1143.4701	572.2387	1142.4861	571.7467	N	924.4785	462.7429	907.4520	454.2296	906.4680	453.7376	8
14	1217.5182	609.2627	1200.4916	600.7494	1199.5076	600.2574	G	809.4516	405.2294	792.4250	396.7162	791.4410	396.2241	7
15	1304.5502	652.7787	1287.5236	644.2655	1286.5396	643.7734	S	752.4301	376.7187	735.4036	368.2054	734.4196	367.7134	6
16	1417.6342	709.3208	1400.6077	700.8075	1399.6237	700.3155	I	665.3981	333.2027	648.3715	324.6894	647.3875	324.1974	5
17	1530.7183	765.8628	1513.6918	757.3495	1512.7077	756.8575	I	552.3140	276.6607	535.2875	268.1474	534.3035	267.6554	4
18	1631.7660	816.3866	1614.7394	807.8734	1613.7554	807.3814	T	439.2300	220.1186	422.2034	211.6053	421.2194	211.1133	3
19	1794.8293	897.9183	1777.8028	889.4050	1776.8188	888.9130	Y	338.1823	169.5948	321.1557	161.0815			2
20							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [GGSSGWGGGLTQNGSIITYR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
124.5	1967.9337	0.0140	GGSSGWGGGLTQNGSIITYR	Deamidated N13 99.13%
103.9	1967.9337	0.0140	GGSSGWGGGLTQNGSIITYR	Deamidated Q12 0.87%
18.6	1966.9497	0.9980	GGSSGWGGGLTQNGSIITYR	
10.5	1967.9337	0.0140	LGHLQNSWDTLQEAAAGR	
3.6	1967.9337	0.0140	LGHLQNSWDTLQEAAAGR	
3.6	1967.9337	0.0140	LGHLQNSWDTLQEAAAGR	
2.5	1967.9628	-0.0152	FAGYIEKVHYLEQQNK	
2.5	1967.9628	-0.0152	FAGYIEKVHYLEQQNK	
2.5	1967.9628	-0.0152	FAGYIEKVHYLEQQNK	
2.2	1967.9297	0.0180	NPGSVPQKGAGADLGNGSEGR	

Mascot: <http://www.matrixscience.com/>

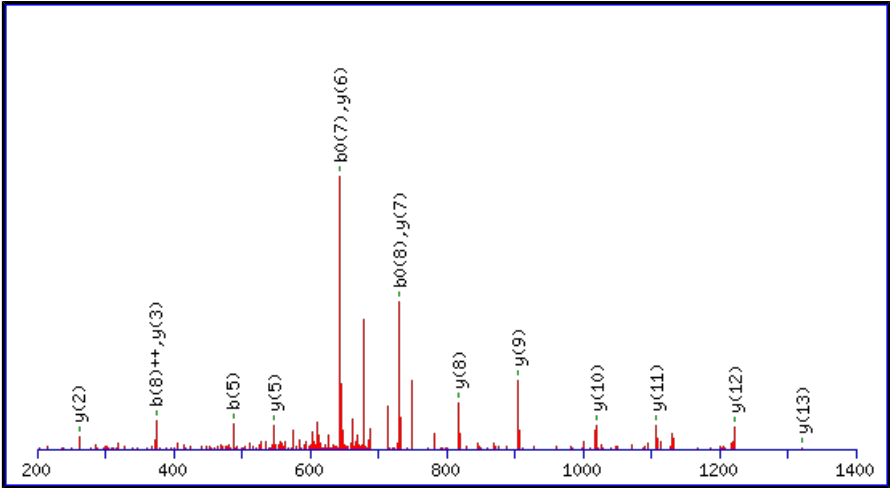
Peptide View

Found in **F1RPW2** in **uni_pig**, tr|F1RPW2|F1RPW2_PIG Coagulation factor V OS=Sus scrofa GN=F5 PE=4 SV=2

Match to Query 3415: 1391.612468 from(696.813510,2+) intensity(11589.9434) rtinseconds(873) scans(905) index(2305)
Title: 120325_Sunil_PigSerum_Glyco_D_18Spectrum357_scans_905
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

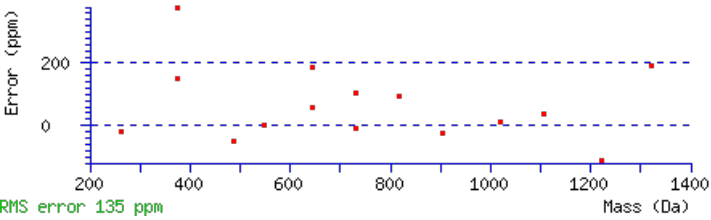
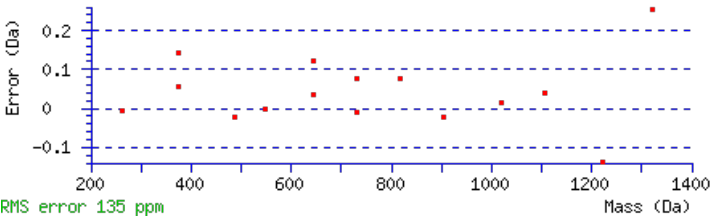
Click mouse within plot area to zoom in by factor of two about that point

Or,	to	Da
Label all possible matches		Label matches used for scoring
Show Y-axis		



Monoisotopic mass of neutral peptide Mr(calc): 1391.6164
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 N5 : Deamidated (NQ)
 N11 : Deamidated (NQ)
 Ions Score: 118 Expect: 4.1e-011
 Matches : 15/142 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							14
2	171.1128	86.0600					V	1321.5866	661.2970	1304.5601	652.7837	1303.5761	652.2917	13
3	286.1397	143.5735			268.1292	134.5682	D	1222.5182	611.7627	1205.4917	603.2495	1204.5076	602.7575	12
4	373.1718	187.0895			355.1612	178.0842	S	1107.4913	554.2493	1090.4647	545.7360	1089.4807	545.2440	11
5	488.1987	244.6030	471.1722	236.0897	470.1882	235.5977	N	1020.4592	510.7333	1003.4327	502.2200	1002.4487	501.7280	10
6	575.2307	288.1190	558.2042	279.6057	557.2202	279.1137	S	905.4323	453.2198	888.4058	444.7065	887.4217	444.2145	9
7	662.2628	331.6350	645.2362	323.1218	644.2522	322.6297	S	818.4003	409.7038	801.3737	401.1905	800.3897	400.6985	8
8	749.2948	375.1510	732.2683	366.6378	731.2842	366.1458	S	731.3682	366.1878	714.3417	357.6745	713.3577	357.1825	7
9	846.3476	423.6774	829.3210	415.1641	828.3370	414.6721	P	644.3362	322.6717	627.3097	314.1585	626.3257	313.6665	6
10	903.3690	452.1882	886.3425	443.6749	885.3585	443.1829	G	547.2835	274.1454	530.2569	265.6321	529.2729	265.1401	5
11	1018.3960	509.7016	1001.3694	501.1884	1000.3854	500.6963	N	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
12	1131.4800	566.2437	1114.4535	557.7304	1113.4695	557.2384	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
13	1218.5121	609.7597	1201.4855	601.2464	1200.5015	600.7544	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498			1

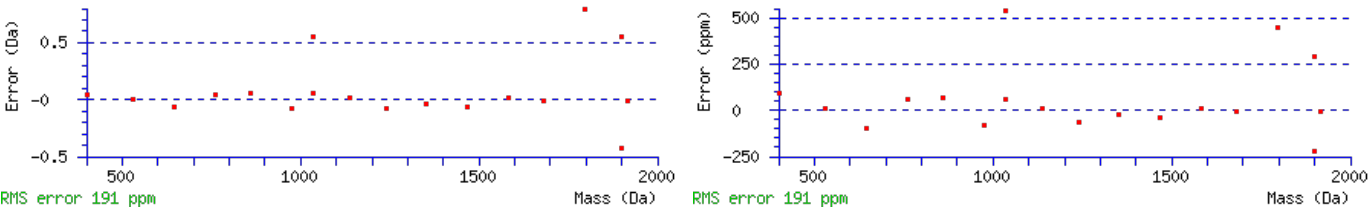


NCBI **BLAST** search of [AVDSNSSSPGNISR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
117.8	1391.6164	-0.0040	AVDSNSSSPGNISR
9.9	1389.6161	1.9964	GFPGADPSGSLNNR
9.4	1391.6180	-0.0055	SSWWMLNPEGGK
3.7	1391.6238	-0.0114	DMGIQDDELSLR
2.6	1391.6165	-0.0040	DSDAGPSTPTTSTR
2.5	1391.6238	-0.0114	CIVETENLEER

Mascot: <http://www.matrixscience.com/>

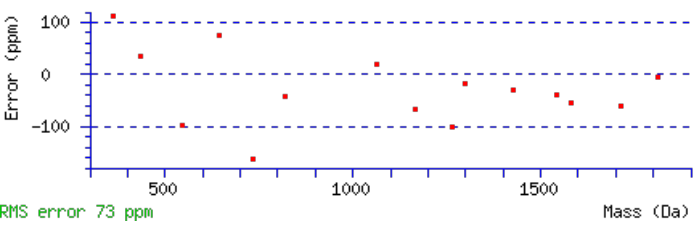
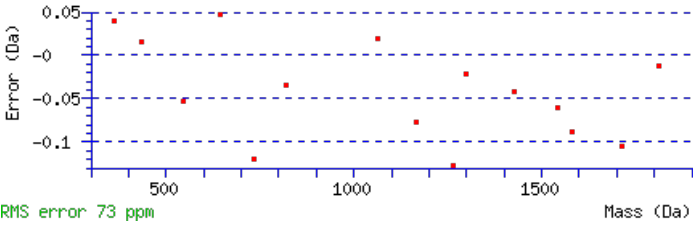


NCBI **BLAST** search of [DQCIVDDITYNVNDTFHK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
117.8	2196.9634	-0.0123	DQCIVDDITYNVNDTFHK	Deamidated N13 99.97%
82.2	2196.9634	-0.0123	DQCIVDDITYNVNDTFHK	Deamidated N11 0.03%
18.9	2196.9634	-0.0123	DQCIVDDITYNVNDTFHK	Deamidated Q2 0.00%
3.2	2194.9511	2.0001	HQVMSNQFVLTAGCAADQAK	
2.3	2194.9367	2.0144	KVMAGDMGSYTCVAENMVGK	

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [VNGFNCTTSSASSVLANTK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
113.7	1958.8891	-0.0128	VNGFNCTTSSASSVLANTK	Deamidated N2, N5 100.00%
54.2	1958.8891	-0.0128	VNGFNCTTSSASSVLANTK	Deamidated N2, N17 0.00%
54.1	1958.8891	-0.0128	VNGFNCTTSSASSVLANTK	Deamidated N5, N17 0.00%
0.7	1956.8629	2.0135	SGSMSSSNRLNRMNQAAK	
0.5	1958.8925	-0.0162	KSQECVSSDSELSTMKK	
0.3	1956.8636	2.0127	DNQCQYIWGTKASGSDK	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1SFI5** in **uni_pig**, tr|F1SFI5|F1SFI5_PIG Uncharacterized protein OS=Sus scrofa GN=HRG PE=4 SV=2

Title: 120326_Sunil_PigSerum_Glyco_DsetB_16Spectrum2278_scans__3141

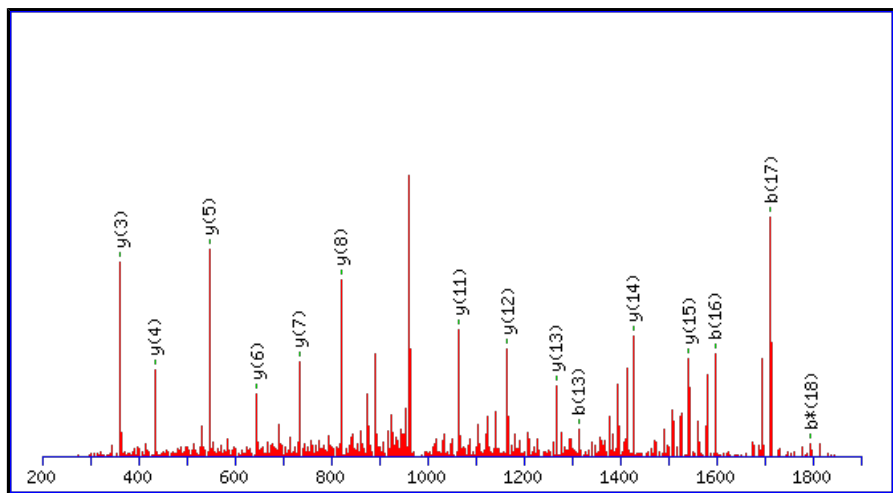
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

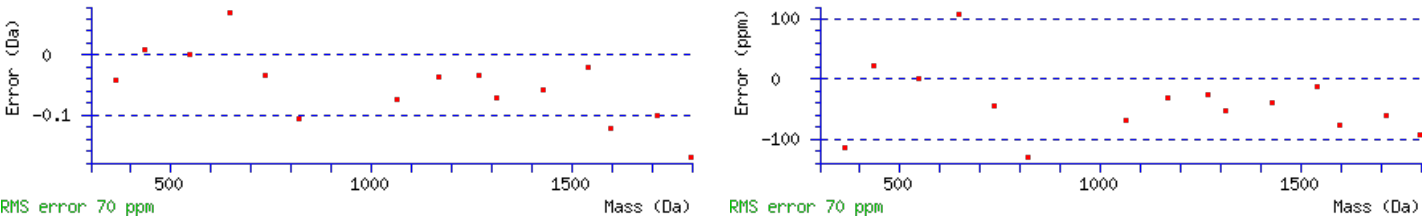
N5 : Deamidated (NQ)

N17 : Deamidated (NQ)

Ions Score: 113 Expect: 1.8e-010

Matches : 15/200 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							19
2	214.1186	107.5629	197.0921	99.0497			N	1860.8280	930.9176	1843.8015	922.4044	1842.8174	921.9124	18
3	271.1401	136.0737	254.1135	127.5604			G	1746.7851	873.8962	1729.7585	865.3829	1728.7745	864.8909	17
4	418.2085	209.6079	401.1819	201.0946			F	1689.7636	845.3854	1672.7371	836.8722	1671.7530	836.3802	16
5	533.2354	267.1214	516.2089	258.6081			N	1542.6952	771.8512	1525.6686	763.3380	1524.6846	762.8460	15
6	693.2661	347.1367	676.2395	338.6234			C	1427.6683	714.3378	1410.6417	705.8245	1409.6577	705.3325	14
7	794.3138	397.6605	777.2872	389.1472	776.3032	388.6552	T	1267.6376	634.3224	1250.6111	625.8092	1249.6270	625.3172	13
8	895.3614	448.1844	878.3349	439.6711	877.3509	439.1791	T	1166.5899	583.7986	1149.5634	575.2853	1148.5794	574.7933	12
9	982.3935	491.7004	965.3669	483.1871	964.3829	482.6951	S	1065.5422	533.2748	1048.5157	524.7615	1047.5317	524.2695	11
10	1069.4255	535.2164	1052.3990	526.7031	1051.4149	526.2111	S	978.5102	489.7587	961.4837	481.2455	960.4997	480.7535	10
11	1140.4626	570.7349	1123.4361	562.2217	1122.4521	561.7297	A	891.4782	446.2427	874.4516	437.7295	873.4676	437.2374	9
12	1227.4946	614.2510	1210.4681	605.7377	1209.4841	605.2457	S	820.4411	410.7242	803.4145	402.2109	802.4305	401.7189	8
13	1314.5267	657.7670	1297.5001	649.2537	1296.5161	648.7617	S	733.4090	367.2082	716.3825	358.6949	715.3985	358.2029	7
14	1413.5951	707.3012	1396.5685	698.7879	1395.5845	698.2959	V	646.3770	323.6921	629.3505	315.1789	628.3665	314.6869	6
15	1526.6791	763.8432	1509.6526	755.3299	1508.6686	754.8379	L	547.3086	274.1579	530.2821	265.6447	529.2980	265.1527	5
16	1597.7163	799.3618	1580.6897	790.8485	1579.7057	790.3565	A	434.2245	217.6159	417.1980	209.1026	416.2140	208.6106	4
17	1712.7432	856.8752	1695.7167	848.3620	1694.7326	847.8700	N	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
18	1813.7909	907.3991	1796.7643	898.8858	1795.7803	898.3938	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
19							K	147.1128	74.0600	130.0863	65.5468			1

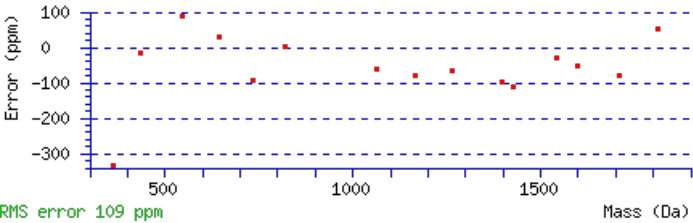
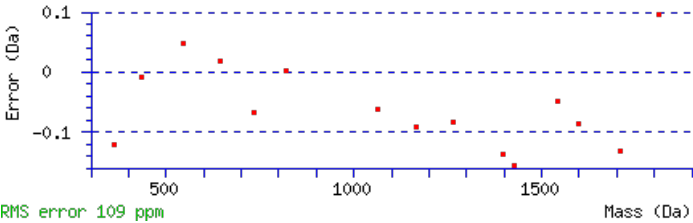


NCBI **BLAST** search of [VNGENCTTSSASSVLANTK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
113.3	1958.8891	-0.0068	VNGENCTTSSASSVLANTK	Deamidated N5, N17 98.96%
93.5	1958.8891	-0.0068	VNGENCTTSSASSVLANTK	Deamidated N2, N17 1.04%
5.3	1958.8891	-0.0068	VNGENCTTSSASSVLANTK	Deamidated N2, N5 0.00%
1.9	1958.8911	-0.0088	QKTFYGRPNWNNEFR	
1.9	1958.8911	-0.0088	QKTFYGRPNWNNEFR	
1.9	1958.8911	-0.0088	QKTFYGRPNWNNEFR	
1.9	1958.8911	-0.0088	QKTFYGRPNWNNEFR	
0.5	1956.8854	1.9970	IAAEFYGVTQGQGSWADR	

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [VNGENCTTSSASSVLANTK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
113.6	1957.9051	-0.0053	VNGENCTTSSASSVLANTK	Deamidated N5 98.98%
93.7	1957.9051	-0.0053	VNGENCTTSSASSVLANTK	Deamidated N2 1.02%
48.0	1957.9051	-0.0053	VNGENCTTSSASSVLANTK	Deamidated N17 0.00%
1.2	1957.8914	0.0084	NDFSLSLKSSQGFMHMK	

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

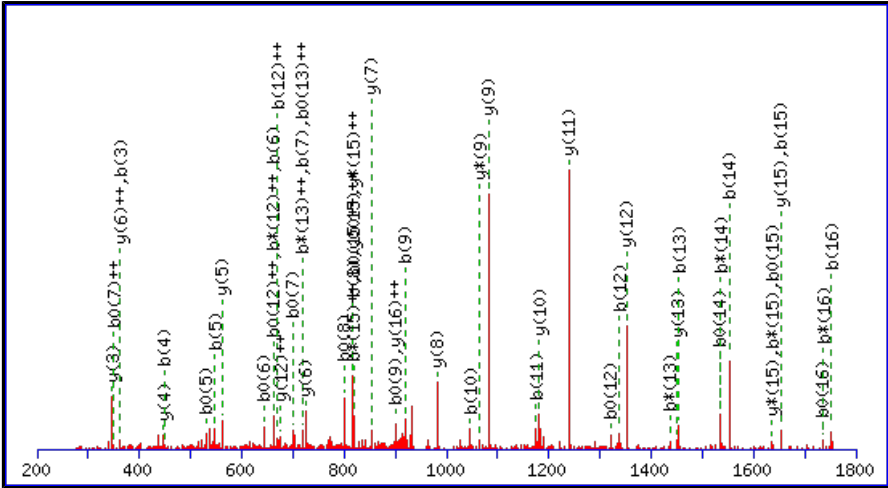
Peptide View

MS/MS Fragmentation of **VFDSVIGVTQEYNVTVK**
Found in **F1SCV8** in **uni_pig**, tr|F1SCV8|F1SCV8_PIG Uncharacterized protein (Fragment) OS=Sus scrofa PE=4 SV=2

Match to Query 7753: 1897.962368 from(949.988460,2+) intensity(53721.3398) rtinseconds(2567) scans(6339) index(3919)
Title: 120325_Sunil_PigSerum_Glyco_P_14Spectrum5369_scans__6339
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

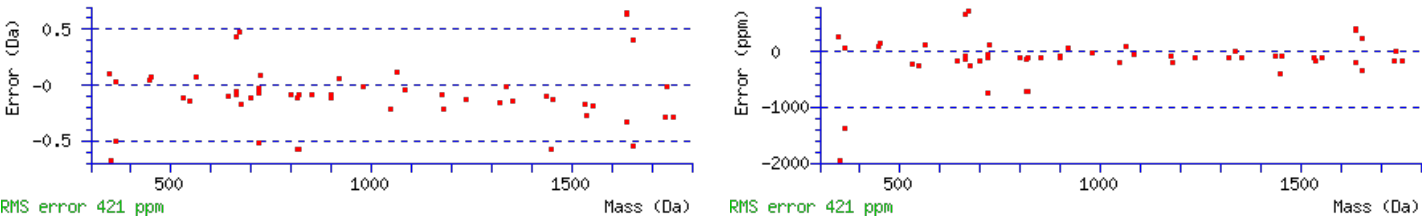
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1897.9673
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 114 Expect: 2.8e-010
Matches : 54/166 fragment ions using 60 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							17
2	247.1441	124.0757					F	1799.9062	900.4567	1782.8796	891.9435	1781.8956	891.4514	16
3	362.1710	181.5892			344.1605	172.5839	D	1652.8378	826.9225	1635.8112	818.4092	1634.8272	817.9172	15
4	449.2031	225.1052			431.1925	216.0999	S	1537.8108	769.4090	1520.7843	760.8958	1519.8003	760.4038	14
5	548.2715	274.6394			530.2609	265.6341	V	1450.7788	725.8930	1433.7522	717.3798	1432.7682	716.8878	13
6	661.3556	331.1814			643.3450	322.1761	I	1351.7104	676.3588	1334.6838	667.8456	1333.6998	667.3535	12
7	718.3770	359.6921			700.3665	350.6869	G	1238.6263	619.8168	1221.5998	611.3035	1220.6157	610.8115	11
8	817.4454	409.2264			799.4349	400.2211	V	1181.6048	591.3061	1164.5783	582.7928	1163.5943	582.3008	10
9	918.4931	459.7502			900.4825	450.7449	T	1082.5364	541.7719	1065.5099	533.2586	1064.5259	532.7666	9
10	1046.5517	523.7795	1029.5251	515.2662	1028.5411	514.7742	Q	981.4888	491.2480	964.4622	482.7347	963.4782	482.2427	8
11	1175.5943	588.3008	1158.5677	579.7875	1157.5837	579.2955	E	853.4302	427.2187	836.4036	418.7055	835.4196	418.2134	7
12	1338.6576	669.8324	1321.6311	661.3192	1320.6470	660.8272	Y	724.3876	362.6974	707.3610	354.1842	706.3770	353.6921	6
13	1453.6846	727.3459	1436.6580	718.8326	1435.6740	718.3406	N	561.3243	281.1658	544.2977	272.6525	543.3137	272.1605	5
14	1552.7530	776.8801	1535.7264	768.3668	1534.7424	767.8748	V	446.2973	223.6523	429.2708	215.1390	428.2867	214.6470	4
15	1653.8006	827.4040	1636.7741	818.8907	1635.7901	818.3987	T	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
16	1752.8691	876.9382	1735.8425	868.4249	1734.8585	867.9329	V	246.1812	123.5942	229.1547	115.0810			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VFDSVIGVTQEYNVTVK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
114.5	1897.9673	-0.0050	VFDSVIGVTQEYNVTVK	Deamidated N13 99.98%
76.9	1897.9673	-0.0050	VFDSVIGVTQEYNVTVK	Deamidated Q10 0.02%
10.2	1897.9633	-0.0009	EDGQVPLNSAALQDIISK	
7.0	1897.9633	-0.0009	EDGQVPLNSAALQDIISK	
6.8	1897.9720	-0.0096	MERDILADVNHFPVVK	
6.1	1897.9745	-0.0121	QGQGPSNKGDLLQVEVTK	
5.5	1897.9633	-0.0009	EDGQVPLNSAALQDIISK	
4.8	1897.9495	0.0128	FPYPTMSEITVLSAQAK	
2.2	1897.9455	0.0169	SMKKVQDSSAEVLANYK	
2.1	1897.9799	-0.0175	AFKVHLQLWDTAGQER	

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNDTVDYECQQGFESR**

Found in **F1S643** in **uni_pig**, tr|F1S643|F1S643_PIG Uncharacterized protein OS=Sus scrofa GN=CFH PE=4 SV=2

Match to Query 9223: 1960.804068 from(981.409310,2+) intensity(200372.0781) rtinseconds(1700) scans(3732) index(10406)

Title: 120326_Sunil_PigSerum_Glyco_PsetB_13Spectrum3076_scans__3732

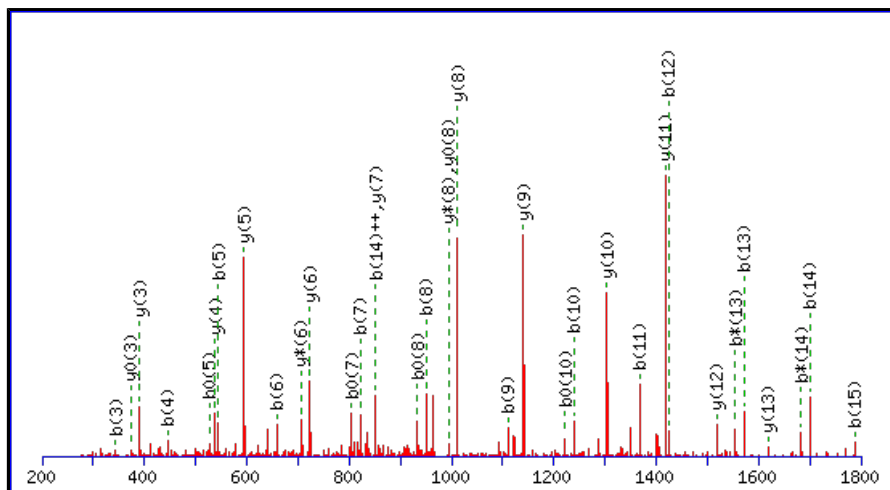
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1960.8109

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

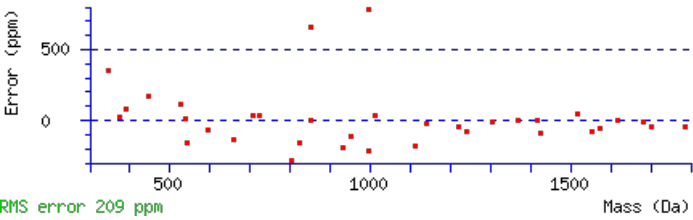
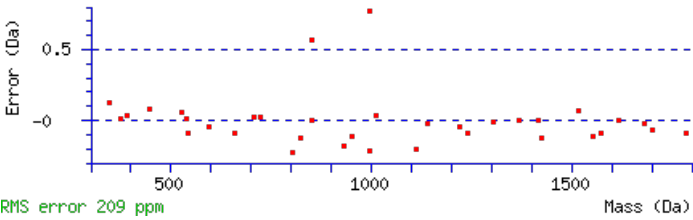
Variable modifications:

N2 : Deamidated (NQ)

Ions Score: 103 Expect: 4.2e-010

Matches : 35/172 fragment ions using 48 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							16
2	229.1183	115.0628	212.0917	106.5495			N	1848.7341	924.8707	1831.7076	916.3574	1830.7235	915.8654	15
3	344.1452	172.5763	327.1187	164.0630	326.1347	163.5710	D	1733.7072	867.3572	1716.6806	858.8439	1715.6966	858.3519	14
4	445.1929	223.1001	428.1664	214.5868	427.1823	214.0948	T	1618.6802	809.8437	1601.6537	801.3305	1600.6696	800.8385	13
5	544.2613	272.6343	527.2348	264.1210	526.2508	263.6290	V	1517.6325	759.3199	1500.6060	750.8066	1499.6220	750.3146	12
6	659.2883	330.1478	642.2617	321.6345	641.2777	321.1425	D	1418.5641	709.7857	1401.5376	701.2724	1400.5536	700.7804	11
7	822.3516	411.6794	805.3250	403.1662	804.3410	402.6742	Y	1303.5372	652.2722	1286.5106	643.7590	1285.5266	643.2669	10
8	951.3942	476.2007	934.3676	467.6875	933.3836	467.1954	E	1140.4738	570.7406	1123.4473	562.2273	1122.4633	561.7353	9
9	1111.4248	556.2161	1094.3983	547.7028	1093.4143	547.2108	C	1011.4313	506.2193	994.4047	497.7060	993.4207	497.2140	8
10	1239.4834	620.2453	1222.4569	611.7321	1221.4728	611.2401	Q	851.4006	426.2039	834.3741	417.6907	833.3900	417.1987	7
11	1367.5420	684.2746	1350.5154	675.7614	1349.5314	675.2694	Q	723.3420	362.1747	706.3155	353.6614	705.3315	353.1694	6
12	1424.5635	712.7854	1407.5369	704.2721	1406.5529	703.7801	G	595.2835	298.1454	578.2569	289.6321	577.2729	289.1401	5
13	1571.6319	786.3196	1554.6053	777.8063	1553.6213	777.3143	F	538.2620	269.6346	521.2354	261.1214	520.2514	260.6293	4
14	1700.6745	850.8409	1683.6479	842.3276	1682.6639	841.8356	E	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
15	1787.7065	894.3569	1770.6799	885.8436	1769.6959	885.3516	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
16							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LNDTVDYECQQGFESR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
103.3	1960.8109	-0.0068	LNDTVDYECQQGFESR	Deamidated N2 100.00%
57.2	1960.8109	-0.0068	LNDTVDYECQQGFESR	Deamidated Q10 0.00%
54.0	1960.8109	-0.0068	LNDTVDYECQQGFESR	Deamidated Q11 0.00%
3.5	1958.8093	1.9947	MQEMLQKMKQQMQDQ	
3.5	1959.7933	1.0107	MQEMLQKMKQQMQDQ	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNDTVDYECQQGFESR**

Found in **F1S643** in **uni_pig**, tr|F1S643|F1S643_PIG Uncharacterized protein OS=Sus scrofa GN=CFH PE=4 SV=2

Match to Query 9637: 1961.785348 from(981.899950,2+) intensity(26195.2363) rtinseconds(1733) scans(3364) index(4230)

Title: 120325_Sunil_PigSerum_Glyco_P_16Spectrum2338_scans_3364

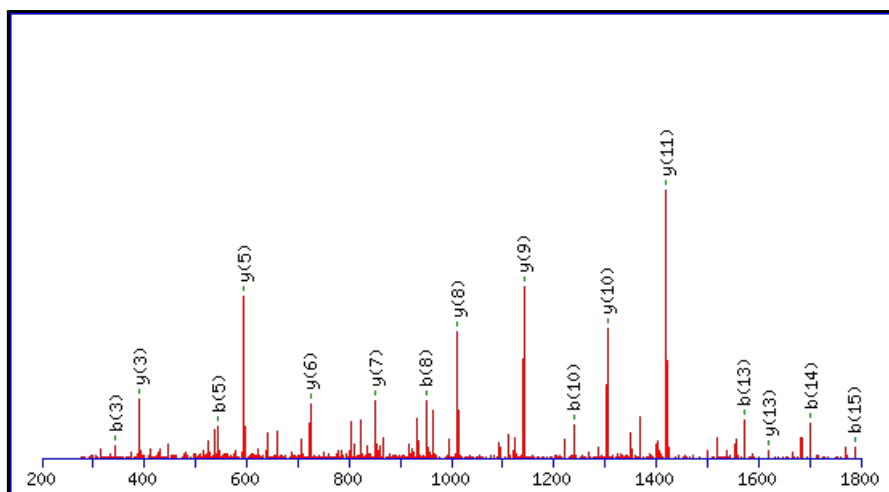
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1961.7949

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

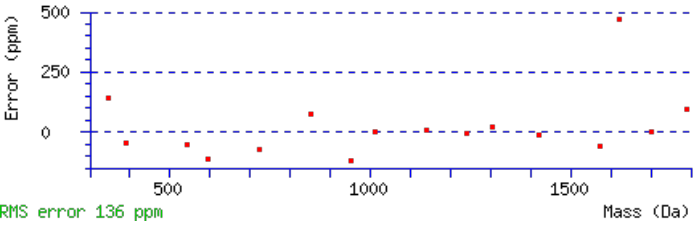
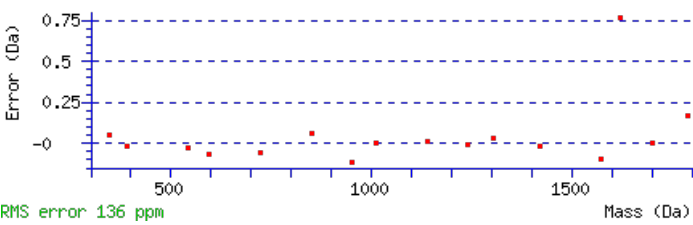
N2 : Deamidated (NQ)

Q11 : Deamidated (NQ)

Score: 97 Expect: 1.1e-009

Matches : 16/172 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							16
2	229.1183	115.0628	212.0917	106.5495			N	1849.7181	925.3627	1832.6916	916.8494	1831.7076	916.3574	15
3	344.1452	172.5763	327.1187	164.0630	326.1347	163.5710	D	1734.6912	867.8492	1717.6646	859.3360	1716.6806	858.8439	14
4	445.1929	223.1001	428.1664	214.5868	427.1823	214.0948	T	1619.6642	810.3358	1602.6377	801.8225	1601.6537	801.3305	13
5	544.2613	272.6343	527.2348	264.1210	526.2508	263.6290	V	1518.6166	759.8119	1501.5900	751.2986	1500.6060	750.8066	12
6	659.2883	330.1478	642.2617	321.6345	641.2777	321.1425	D	1419.5481	710.2777	1402.5216	701.7644	1401.5376	701.2724	11
7	822.3516	411.6794	805.3250	403.1662	804.3410	402.6742	Y	1304.5212	652.7642	1287.4946	644.2510	1286.5106	643.7590	10
8	951.3942	476.2007	934.3676	467.6875	933.3836	467.1954	E	1141.4579	571.2326	1124.4313	562.7193	1123.4473	562.2273	9
9	1111.4248	556.2161	1094.3983	547.7028	1093.4143	547.2108	C	1012.4153	506.7113	995.3887	498.1980	994.4047	497.7060	8
10	1239.4834	620.2453	1222.4569	611.7321	1221.4728	611.2401	Q	852.3846	426.6959	835.3581	418.1827	834.3741	417.6907	7
11	1368.5260	684.7666	1351.4995	676.2534	1350.5154	675.7614	Q	724.3260	362.6667	707.2995	354.1534	706.3155	353.6614	6
12	1425.5475	713.2774	1408.5209	704.7641	1407.5369	704.2721	G	595.2835	298.1454	578.2569	289.6321	577.2729	289.1401	5
13	1572.6159	786.8116	1555.5893	778.2983	1554.6053	777.8063	F	538.2620	269.6346	521.2354	261.1214	520.2514	260.6293	4
14	1701.6585	851.3329	1684.6319	842.8196	1683.6479	842.3276	E	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
15	1788.6905	894.8489	1771.6640	886.3356	1770.6799	885.8436	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
16							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LNDTVDYECQQGFESR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
96.8	1961.7949	-0.0095	LNDTVDYECQQGFESR	Deamidated N2, Q11 99.16%
76.0	1961.7949	-0.0095	LNDTVDYECQQGFESR	Deamidated N2, Q10 0.84%
40.6	1961.7949	-0.0095	LNDTVDYECQQGFESR	Deamidated Q10, Q11 0.00%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSDAALQSNSTAR**

Found in **F1SAE9** in **uni_pig**, tr|F1SAE9|F1SAE9_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=LAMB1 PE=4 SV=2

Match to Query 3051: 1333.644728 from(667.829640,2+) intensity(6639.2261) rtinseconds(1137) scans(2141) index(8592)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_15Spectrum1685_scans_2141

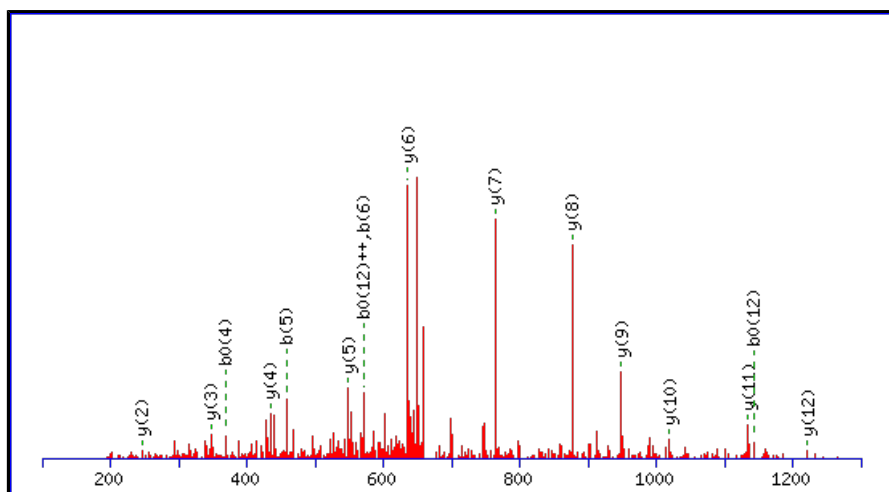
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1333.6473

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

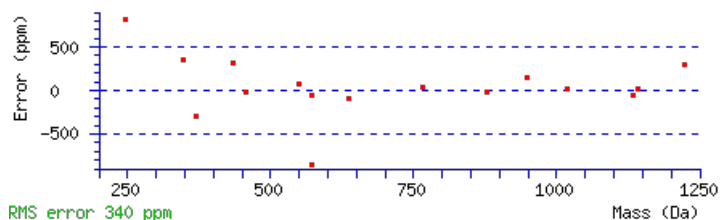
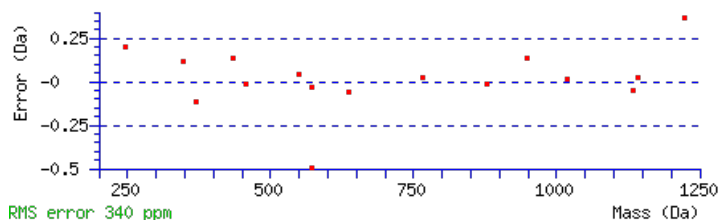
Variable modifications:

N9 : Deamidated (NQ)

Ions Score: 105 Expect: 2e-009

Matches : 16/126 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							13
2	201.1234	101.0653			183.1128	92.0600	S	1221.5706	611.2889	1204.5440	602.7757	1203.5600	602.2836	12
3	316.1503	158.5788			298.1397	149.5735	D	1134.5386	567.7729	1117.5120	559.2596	1116.5280	558.7676	11
4	387.1874	194.0974			369.1769	185.0921	A	1019.5116	510.2594	1002.4851	501.7462	1001.5010	501.2542	10
5	458.2245	229.6159			440.2140	220.6106	A	948.4745	474.7409	931.4480	466.2276	930.4639	465.7356	9
6	571.3086	286.1579			553.2980	277.1527	L	877.4374	439.2223	860.4108	430.7091	859.4268	430.2170	8
7	699.3672	350.1872	682.3406	341.6740	681.3566	341.1819	Q	764.3533	382.6803	747.3268	374.1670	746.3428	373.6750	7
8	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	S	636.2947	318.6510	619.2682	310.1377	618.2842	309.6457	6
9	901.4262	451.2167	884.3996	442.7034	883.4156	442.2114	N	549.2627	275.1350	532.2362	266.6217	531.2522	266.1297	5
10	988.4582	494.7327	971.4316	486.2195	970.4476	485.7274	S	434.2358	217.6215	417.2092	209.1082	416.2252	208.6162	4
11	1089.5059	545.2566	1072.4793	536.7433	1071.4953	536.2513	T	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
12	1160.5430	580.7751	1143.5164	572.2618	1142.5324	571.7698	A	246.1561	123.5817	229.1295	115.0684			2
13							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LSDAALQSNSTAR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
104.7	1333.6473	-0.0026	LSDAALQSNSTAR	Deamidated N9 99.96%
70.3	1333.6473	-0.0026	LSDAALQSNSTAR	Deamidated Q7 0.04%
9.3	1333.6514	-0.0066	QEEALAEFLQR	
5.4	1333.6561	-0.0114	QHMASKSLFNR	
4.5	1332.6310	1.0137	KYGSLTSYSGDR	
3.3	1333.6514	-0.0067	DDPEKLFSDLR	
0.1	1333.6409	0.0039	LQARTTDDVCR	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1ST75** in **uni_pig**, tr|F1ST75|F1ST75_PIG Insulin-like growth factor-binding protein 3 (Fragment) OS=Sus scrofa GN=IGFBP3 PE=4 SV=2

Title: 120325_Sunil_PigSerum_Glyco_D_17Spectrum1116_scans__1903

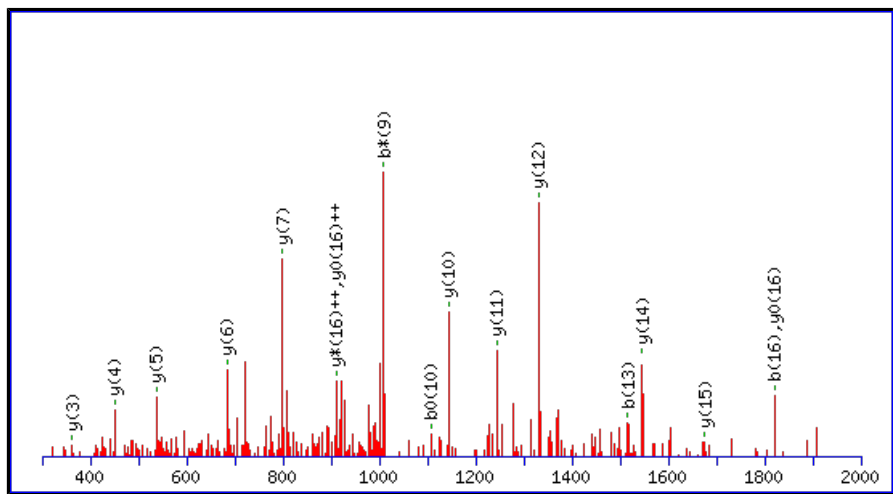
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

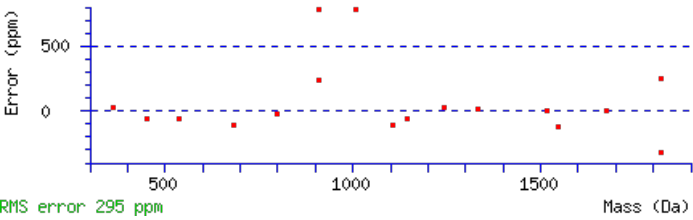
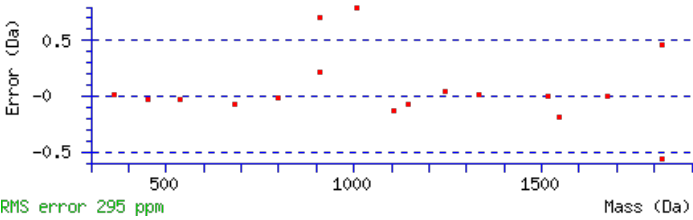
Label all possible matches Label matches used for scoring

Show Y-axis



Matches : 17/190 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							18
2	215.1026	108.0550			197.0921	99.0497	D	1953.7832	977.3952	1936.7567	968.8820	1935.7727	968.3900	17
3	378.1660	189.5866			360.1554	180.5813	Y	1838.7563	919.8818	1821.7297	911.3685	1820.7457	910.8765	16
4	507.2086	254.1079			489.1980	245.1026	E	1675.6929	838.3501	1658.6664	829.8368	1657.6824	829.3448	15
5	594.2406	297.6239			576.2300	288.6186	S	1546.6504	773.8288	1529.6238	765.3155	1528.6398	764.8235	14
6	722.2992	361.6532	705.2726	353.1399	704.2886	352.6479	Q	1459.6183	730.3128	1442.5918	721.7995	1441.6078	721.3075	13
7	809.3312	405.1692	792.3046	396.6560	791.3206	396.1640	S	1331.5597	666.2835	1314.5332	657.7702	1313.5492	657.2782	12
8	910.3789	455.6931	893.3523	447.1798	892.3683	446.6878	T	1244.5277	622.7675	1227.5012	614.2542	1226.5172	613.7622	11
9	1025.4058	513.2065	1008.3793	504.6933	1007.3952	504.2013	D	1143.4800	572.2437	1126.4535	563.7304	1125.4695	563.2384	10
10	1126.4535	563.7304	1109.4269	555.2171	1108.4429	554.7251	T	1028.4531	514.7302	1011.4265	506.2169	1010.4425	505.7249	9
11	1254.5121	627.7597	1237.4855	619.2464	1236.5015	618.7544	Q	927.4054	464.2063	910.3789	455.6931	909.3949	455.2011	8
12	1369.5390	685.2731	1352.5125	676.7599	1351.5284	676.2679	N	799.3468	400.1771	782.3203	391.6638	781.3363	391.1718	7
13	1516.6074	758.8074	1499.5809	750.2941	1498.5969	749.8021	F	684.3199	342.6636	667.2933	334.1503	666.3093	333.6583	6
14	1603.6395	802.3234	1586.6129	793.8101	1585.6289	793.3181	S	537.2515	269.1294	520.2249	260.6161	519.2409	260.1241	5
15	1690.6715	845.8394	1673.6449	837.3261	1672.6609	836.8341	S	450.2195	225.6134	433.1929	217.1001	432.2089	216.6081	4
16	1819.7141	910.3607	1802.6875	901.8474	1801.7035	901.3554	E	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
17	1906.7461	953.8767	1889.7196	945.3634	1888.7355	944.8714	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
18							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VDYESQSTDTQNFSESSESK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
93.3	2051.8443	-0.0091	VDYESQSTDTQNFSESSESK	Deamidated N12 98.38%
75.5	2051.8443	-0.0091	VDYESQSTDTQNFSESSESK	Deamidated Q11 1.62%
29.3	2051.8443	-0.0091	VDYESQSTDTQNFSESSESK	Deamidated Q6 0.00%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

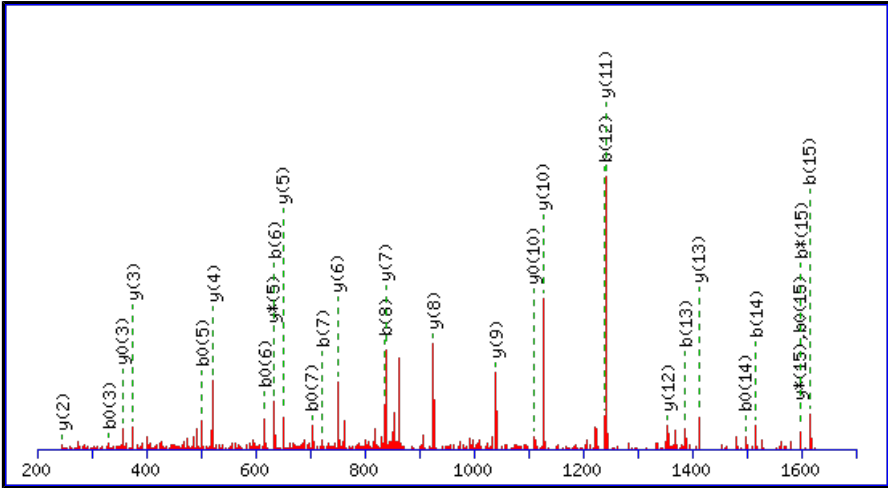
Peptide View

MS/MS Fragmentation of **FSDGLDSNSSTQFEVK**
Found in **F1RQW2** in **uni_pig**, tr|F1RQW2|F1RQW2_PIG Uncharacterized protein OS=Sus scrofa GN=C4 PE=4 SV=2

Match to Query 6046: 1760.769088 from(881.391820,2+) intensity(144063.9219) rtinseconds(1927) scans(3549) index(11658)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_03Spectrum2625_scans__3549
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

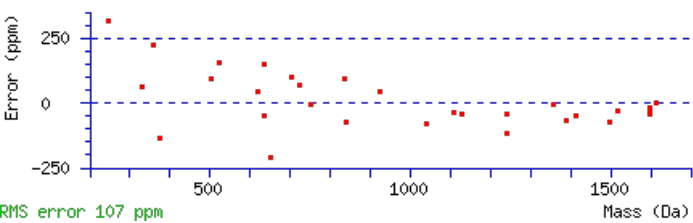
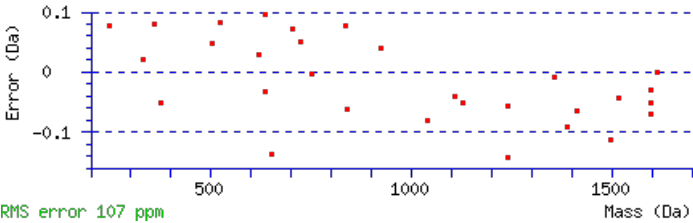
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1760.7741
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 99 Expect: 3.8e-009
Matches : 30/160 fragment ions using 42 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							16
2	235.1077	118.0575			217.0972	109.0522	S	1614.7130	807.8601	1597.6864	799.3468	1596.7024	798.8548	15
3	350.1347	175.5710			332.1241	166.5657	D	1527.6809	764.3441	1510.6544	755.8308	1509.6704	755.3388	14
4	407.1561	204.0817			389.1456	195.0764	G	1412.6540	706.8306	1395.6274	698.3174	1394.6434	697.8253	13
5	520.2402	260.6237			502.2296	251.6185	L	1355.6325	678.3199	1338.6060	669.8066	1337.6220	669.3146	12
6	635.2671	318.1372			617.2566	309.1319	D	1242.5485	621.7779	1225.5219	613.2646	1224.5379	612.7726	11
7	722.2992	361.6532			704.2886	352.6479	S	1127.5215	564.2644	1110.4950	555.7511	1109.5109	555.2591	10
8	837.3261	419.1667	820.2996	410.6534	819.3155	410.1614	N	1040.4895	520.7484	1023.4629	512.2351	1022.4789	511.7431	9
9	924.3581	462.6827	907.3316	454.1694	906.3476	453.6774	S	925.4625	463.2349	908.4360	454.7216	907.4520	454.2296	8
10	1011.3902	506.1987	994.3636	497.6854	993.3796	497.1934	S	838.4305	419.7189	821.4040	411.2056	820.4199	410.7136	7
11	1112.4378	556.7226	1095.4113	548.2093	1094.4273	547.7173	T	751.3985	376.2029	734.3719	367.6896	733.3879	367.1976	6
12	1240.4964	620.7518	1223.4699	612.2386	1222.4859	611.7466	Q	650.3508	325.6790	633.3243	317.1658	632.3402	316.6738	5
13	1387.5648	694.2861	1370.5383	685.7728	1369.5543	685.2808	F	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
14	1516.6074	758.8073	1499.5809	750.2941	1498.5969	749.8021	E	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
15	1615.6758	808.3416	1598.6493	799.8283	1597.6653	799.3363	V	246.1812	123.5942	229.1547	115.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [FSDGLDSNSSTQFEVK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
98.5	1760.7741	-0.0050	FSDGLDSNSSTQFEVK	Deamidated N8 99.96%
64.9	1760.7741	-0.0050	FSDGLDSNSSTQFEVK	Deamidated Q12 0.04%
12.0	1760.7662	0.0029	STQTQDSSFQELIMK	
5.7	1759.7644	1.0047	TLQTMQNFQKENMK	
4.6	1760.7523	0.0168	GMENSVSDAARTSEYK	
0.8	1760.7749	-0.0058	AMGIMNSFVNDIFER	
0.8	1760.7749	-0.0058	AMGIMNSFVNDIFER	

Mascot: <http://www.matrixscience.com/>

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Mascot Search Results

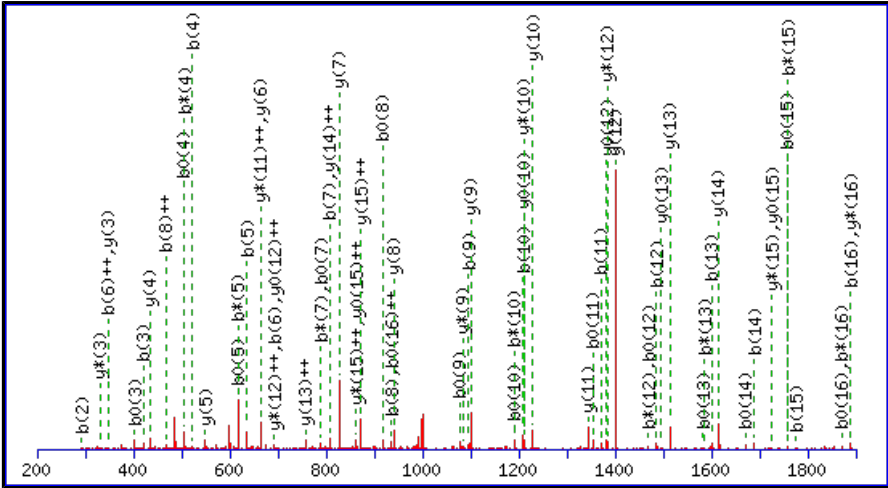
Peptide View

MS/MS Fragmentation of **EYQTIGNQCIYNDSLK**
Found in **F1SN68** in **uni_pig**, tr|F1SN68|F1SN68_PIG Alpha-1-acid glycoprotein OS=Sus scrofa GN=ORM1 PE=3 SV=1

Match to Query 11360: 2033.879868 from(1017.947210,2+) intensity(672982.6250) rtinseconds(1921) scans(4503) index(6314)
Title: 120325_Sunil_PigSerum_Glyco_S_14Spectrum3762_scans_4503
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

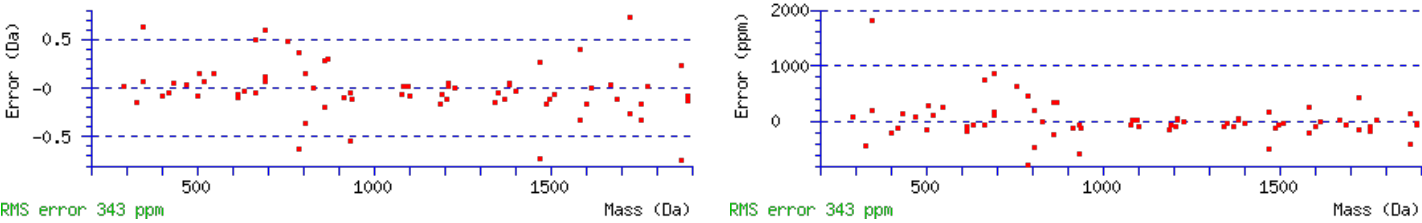
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2033.8888
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
N12 : Deamidated (NQ)
Ions Score: 97 Expect: 4.1e-009
Matches : 69/184 fragment ions using 96 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	293.1132	147.0602			275.1026	138.0550	Y	1905.8535	953.4304	1888.8269	944.9171	1887.8429	944.4251	16
3	421.1718	211.0895	404.1452	202.5763	403.1612	202.0842	Q	1742.7902	871.8987	1725.7636	863.3854	1724.7796	862.8934	15
4	522.2195	261.6134	505.1929	253.1001	504.2089	252.6081	T	1614.7316	807.8694	1597.7050	799.3562	1596.7210	798.8641	14
5	635.3035	318.1554	618.2770	309.6421	617.2930	309.1501	I	1513.6839	757.3456	1496.6574	748.8323	1495.6733	748.3403	13
6	692.3250	346.6661	675.2984	338.1529	674.3144	337.6608	G	1400.5998	700.8036	1383.5733	692.2903	1382.5893	691.7983	12
7	807.3519	404.1796	790.3254	395.6663	789.3414	395.1743	N	1343.5784	672.2928	1326.5518	663.7796	1325.5678	663.2875	11
8	935.4105	468.2089	918.3840	459.6956	917.3999	459.2036	Q	1228.5514	614.7794	1211.5249	606.2661	1210.5409	605.7741	10
9	1095.4412	548.2242	1078.4146	539.7109	1077.4306	539.2189	C	1100.4929	550.7501	1083.4663	542.2368	1082.4823	541.7448	9
10	1208.5252	604.7662	1191.4987	596.2530	1190.5147	595.7610	I	940.4622	470.7347	923.4357	462.2215	922.4516	461.7295	8
11	1371.5885	686.2979	1354.5620	677.7846	1353.5780	677.2926	Y	827.3781	414.1927	810.3516	405.6794	809.3676	405.1874	7
12	1486.6155	743.8114	1469.5889	735.2981	1468.6049	734.8061	N	664.3148	332.6610	647.2883	324.1478	646.3042	323.6558	6
13	1601.6424	801.3249	1584.6159	792.8116	1583.6319	792.3196	D	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
14	1688.6745	844.8409	1671.6479	836.3276	1670.6639	835.8356	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
15	1775.7065	888.3569	1758.6799	879.8436	1757.6959	879.3516	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
16	1888.7906	944.8989	1871.7640	936.3856	1870.7800	935.8936	L	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EYQTIGNQCIYNDSSLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
97.4	2033.8888	-0.0089	EYQTIGNQCIYNDSSLK	Deamidated N7, N12 95.62%
84.0	2033.8888	-0.0089	EYQTIGNQCIYNDSSLK	Deamidated Q8, N12 4.37%
57.8	2033.8888	-0.0089	EYQTIGNQCIYNDSSLK	Deamidated N7, Q8 0.01%
44.7	2033.8888	-0.0089	EYQTIGNQCIYNDSSLK	Deamidated Q3, N12 0.00%
16.3	2033.8888	-0.0089	EYQTIGNQCIYNDSSLK	Deamidated Q3, Q8 0.00%
13.7	2033.8888	-0.0089	EYQTIGNQCIYNDSSLK	Deamidated Q3, N7 0.00%
1.4	2033.8937	-0.0138	HNIMDFAMPYFIQVMK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSCCSVNTSLEAHK**

Found in **Q9XSH0** in **uni_pig**, tr|Q9XSH0|Q9XSH0_PIG Secreted folate binding protein OS=Sus scrofa GN=FOLR1 PE=2 SV=1

Match to Query 5145: 1606.668248 from(804.341400,2+) intensity(4936.7329) rtinseconds(971) scans(2013) index(8359)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_14Spectrum1646_scans_2013

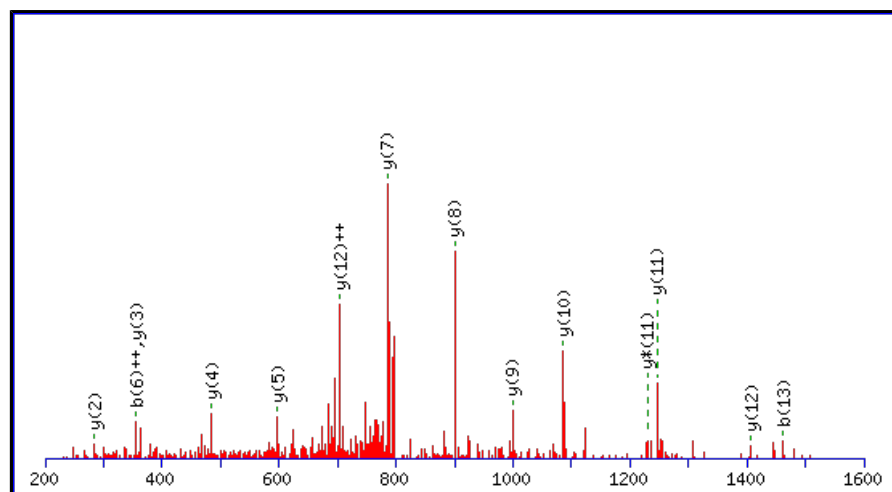
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1606.6715

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

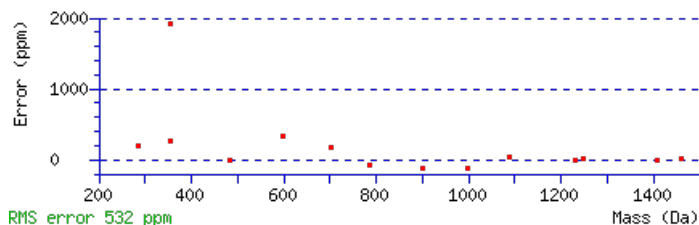
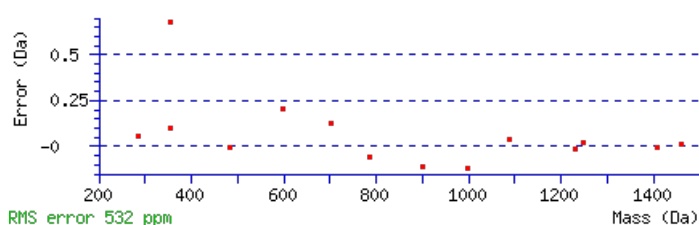
Variable modifications:

N7 : Deamidated (NQ)

Ions Score: 94 Expect: 5.2e-009

Matches : 14/148 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							14
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	S	1493.6359	747.3216	1476.6094	738.8083	1475.6253	738.3163	13
3	362.1129	181.5601	345.0863	173.0468	344.1023	172.5548	C	1406.6039	703.8056	1389.5773	695.2923	1388.5933	694.8003	12
4	522.1435	261.5754	505.1170	253.0621	504.1330	252.5701	C	1246.5732	623.7903	1229.5467	615.2770	1228.5627	614.7850	11
5	609.1756	305.0914	592.1490	296.5781	591.1650	296.0861	S	1086.5426	543.7749	1069.5160	535.2617	1068.5320	534.7696	10
6	708.2440	354.6256	691.2174	346.1123	690.2334	345.6203	V	999.5106	500.2589	982.4840	491.7456	981.5000	491.2536	9
7	823.2709	412.1391	806.2444	403.6258	805.2603	403.1338	N	900.4421	450.7247	883.4156	442.2114	882.4316	441.7194	8
8	924.3186	462.6629	907.2920	454.1497	906.3080	453.6577	T	785.4152	393.2112	768.3886	384.6980	767.4046	384.2060	7
9	1011.3506	506.1789	994.3241	497.6657	993.3401	497.1737	S	684.3675	342.6874	667.3410	334.1741	666.3570	333.6821	6
10	1124.4347	562.7210	1107.4081	554.2077	1106.4241	553.7157	L	597.3355	299.1714	580.3089	290.6581	579.3249	290.1661	5
11	1253.4773	627.2423	1236.4507	618.7290	1235.4667	618.2370	E	484.2514	242.6293	467.2249	234.1161	466.2409	233.6241	4
12	1324.5144	662.7608	1307.4878	654.2476	1306.5038	653.7556	A	355.2088	178.1081	338.1823	169.5948			3
13	1461.5733	731.2903	1444.5468	722.7770	1443.5627	722.2850	H	284.1717	142.5895	267.1452	134.0762			2
14							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [NSCCSVNTSLEAHK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
94.0	1606.6715	-0.0033	NSCCSVNTSLEAHK	Deamidated N7 100.00%
20.5	1606.6715	-0.0033	NSCCSVNTSLEAHK	Deamidated N1 0.00%
2.1	1605.6511	1.0171	EDRPGAGDMNEPMR	
0.6	1605.6738	0.9944	HCTWSLDVCAVCY	

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

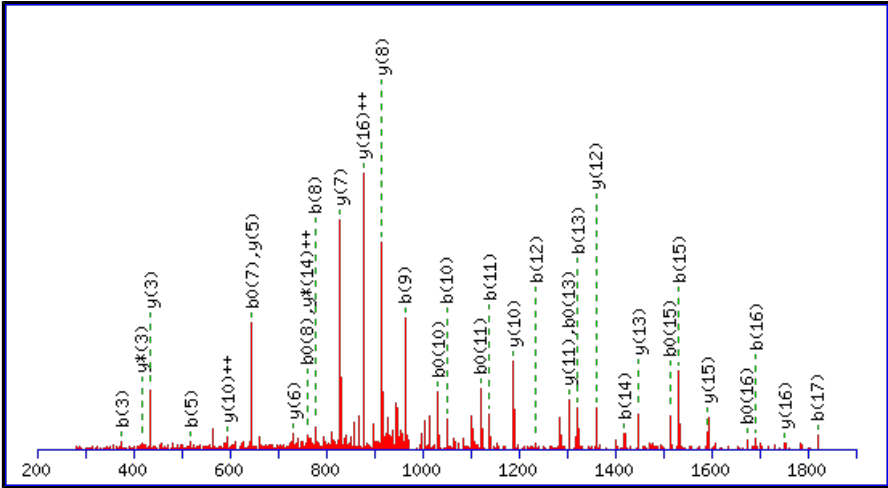
Peptide View

MS/MS Fragmentation of **TICGSSGNWSSPSPICQK**
Found in **A8R080** in **uni_pig**, tr|A8R080|A8R080_PIG L-selectin OS=Sus scrofa GN=SELL PE=2 SV=1

Match to Query 9946: 1965.849708 from(983.932130,2+) intensity(22631.3867) rtinseconds(1662) scans(3846) index(13209)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum3176_scans__3846
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

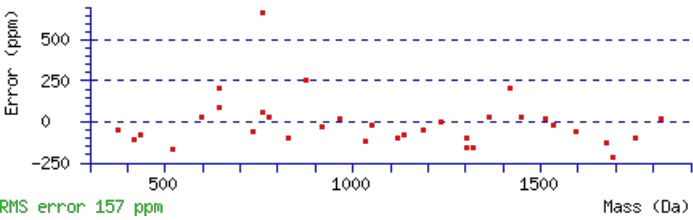
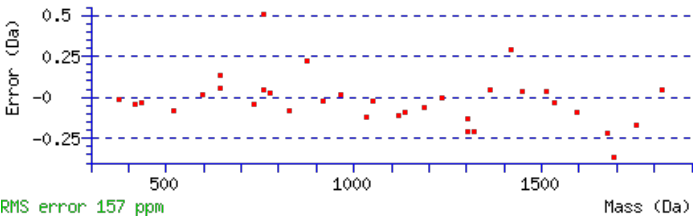
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1965.8561
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 96 Expect: 7e-009
Matches : 34/180 fragment ions using 48 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							18
2	215.1390	108.0731			197.1285	99.0679	I	1865.8157	933.4115	1848.7891	924.8982	1847.8051	924.4062	17
3	375.1697	188.0885			357.1591	179.0832	C	1752.7316	876.8694	1735.7050	868.3562	1734.7210	867.8642	16
4	432.1911	216.5992			414.1806	207.5939	G	1592.7009	796.8541	1575.6744	788.3408	1574.6904	787.8488	15
5	519.2232	260.1152			501.2126	251.1099	S	1535.6795	768.3434	1518.6529	759.8301	1517.6689	759.3381	14
6	606.2552	303.6312			588.2446	294.6259	S	1448.6475	724.8274	1431.6209	716.3141	1430.6369	715.8221	13
7	663.2767	332.1420			645.2661	323.1367	G	1361.6154	681.3114	1344.5889	672.7981	1343.6049	672.3061	12
8	778.3036	389.6554	761.2770	381.1422	760.2930	380.6502	N	1304.5940	652.8006	1287.5674	644.2873	1286.5834	643.7953	11
9	964.3829	482.6951	947.3564	474.1818	946.3723	473.6898	W	1189.5670	595.2871	1172.5405	586.7739	1171.5565	586.2819	10
10	1051.4149	526.2111	1034.3884	517.6978	1033.4044	517.2058	S	1003.4877	502.2475	986.4612	493.7342	985.4771	493.2422	9
11	1138.4470	569.7271	1121.4204	561.2138	1120.4364	560.7218	S	916.4557	458.7315	899.4291	450.2182	898.4451	449.7262	8
12	1235.4997	618.2535	1218.4732	609.7402	1217.4892	609.2482	P	829.4237	415.2155	812.3971	406.7022	811.4131	406.2102	7
13	1322.5318	661.7695	1305.5052	653.2562	1304.5212	652.7642	S	732.3709	366.6891	715.3443	358.1758	714.3603	357.6838	6
14	1419.5845	710.2959	1402.5580	701.7826	1401.5740	701.2906	P	645.3389	323.1731	628.3123	314.6598			5
15	1532.6686	766.8379	1515.6420	758.3247	1514.6580	757.8326	I	548.2861	274.6467	531.2595	266.1334			4
16	1692.6992	846.8533	1675.6727	838.3400	1674.6887	837.8480	C	435.2020	218.1047	418.1755	209.5914			3
17	1820.7578	910.8825	1803.7313	902.3693	1802.7472	901.8773	Q	275.1714	138.0893	258.1448	129.5761			2
18							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [TICGSSGNWSSPSPICQK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
95.6	1965.8561	-0.0064	TICGSSGNWSSPSPICQK	Deamidated N8 100.00%
47.4	1965.8561	-0.0064	TICGSSGNWSSPSPICQK	Deamidated Q17 0.00%
2.8	1965.8448	0.0049	MVSDINNAWGCLEQAEK	
1.7	1963.8622	1.9876	QLCTIPRDAAYYSYQN	
1.7	1963.8622	1.9876	QLCTIPRDAAYYSYQN	
1.7	1963.8622	1.9876	QLCTIPRDAAYYSYQN	
1.7	1964.8462	1.0035	QLCTIPRDAAYYSYQN	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **TASGQIESYNDTYEIR**
Found in **F1S573** in **uni_pig**, tr[F1S573]F1S573_PIG Alpha-amylase OS=Sus scrofa GN=LOC100153854 PE=3 SV=2

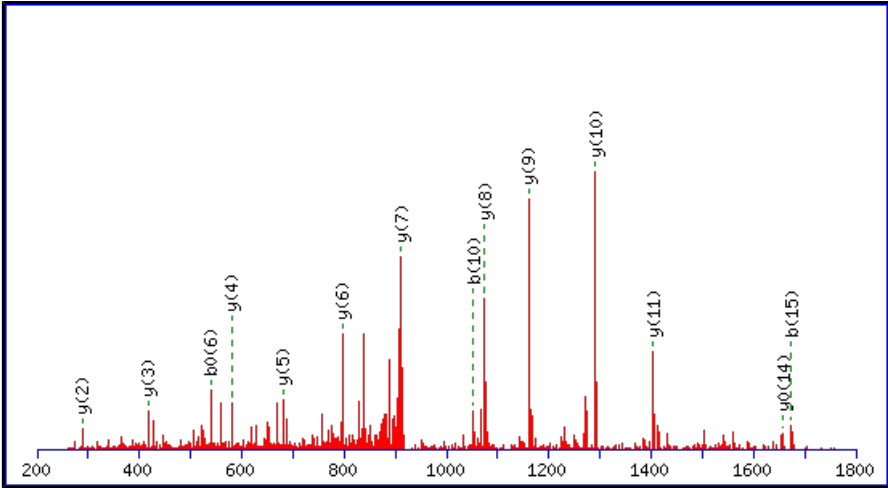
Match to Query 6910: 1846.816928 from(924.415740,2+) intensity(24815.7715) rtinseconds(1779) scans(3947) index(10418)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_13Spectrum3266_scans__3947
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

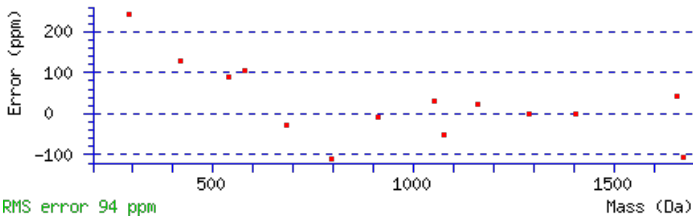
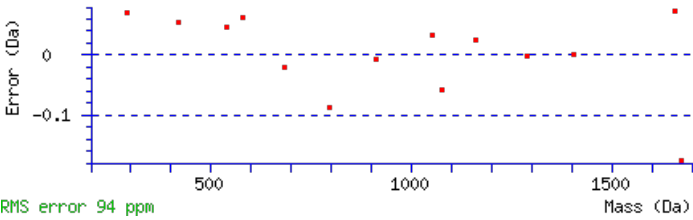
☐ Label all possible matches ☐ Label matches used for scoring

☐ Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1846.8221
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 96 Expect: 7.8e-009
Matches : 14/168 fragment ions using 15 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							16
2	173.0921	87.0497			155.0815	78.0444	A	1746.7817	873.8945	1729.7552	865.3812	1728.7711	864.8892	15
3	260.1241	130.5657			242.1135	121.5604	S	1675.7446	838.3759	1658.7180	829.8627	1657.7340	829.3706	14
4	317.1456	159.0764			299.1350	150.0711	G	1588.7126	794.8599	1571.6860	786.3466	1570.7020	785.8546	13
5	445.2041	223.1057	428.1776	214.5924	427.1936	214.1004	Q	1531.6911	766.3492	1514.6645	757.8359	1513.6805	757.3439	12
6	558.2882	279.6477	541.2617	271.1345	540.2776	270.6425	I	1403.6325	702.3199	1386.6060	693.8066	1385.6220	693.3146	11
7	687.3308	344.1690	670.3042	335.6558	669.3202	335.1638	E	1290.5485	645.7779	1273.5219	637.2646	1272.5379	636.7726	10
8	774.3628	387.6850	757.3363	379.1718	756.3523	378.6798	S	1161.5059	581.2566	1144.4793	572.7433	1143.4953	572.2513	9
9	937.4262	469.2167	920.3996	460.7034	919.4156	460.2114	Y	1074.4738	537.7406	1057.4473	529.2273	1056.4633	528.7353	8
10	1052.4531	526.7302	1035.4265	518.2169	1034.4425	517.7249	N	911.4105	456.2089	894.3840	447.6956	893.3999	447.2036	7
11	1167.4800	584.2437	1150.4535	575.7304	1149.4695	575.2384	D	796.3836	398.6954	779.3570	390.1821	778.3730	389.6901	6
12	1268.5277	634.7675	1251.5012	626.2542	1250.5172	625.7622	T	681.3566	341.1819	664.3301	332.6687	663.3461	332.1767	5
13	1431.5910	716.2992	1414.5645	707.7859	1413.5805	707.2939	Y	580.3089	290.6581	563.2824	282.1448	562.2984	281.6528	4
14	1560.6336	780.8205	1543.6071	772.3072	1542.6231	771.8152	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
15	1673.7177	837.3625	1656.6912	828.8492	1655.7071	828.3572	I	288.2030	144.6051	271.1765	136.0919			2
16							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [TASGQIESYNDTYEIR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
96.3	1846.8221	-0.0051	TASGQIESYNDTYEIR	Deamidated N10 100.00%
17.3	1846.8221	-0.0051	TASGQIESYNDTYEIR	Deamidated Q5 0.00%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **NGVTVSPAAGAYENGSSVEYR**

Found in **I3L6Q6** in **uni_pig**, tr|I3L6Q6|I3L6Q6_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=F13B PE=4 SV=1

Match to Query 12000: 2128.966408 from(1065.490480,2+) intensity(10828.6963) rtinseconds(1681) scans(3917) index(3826)

Title: 120325 Sunil PigSerum Glyco P 14Spectrum3205 scans 3917

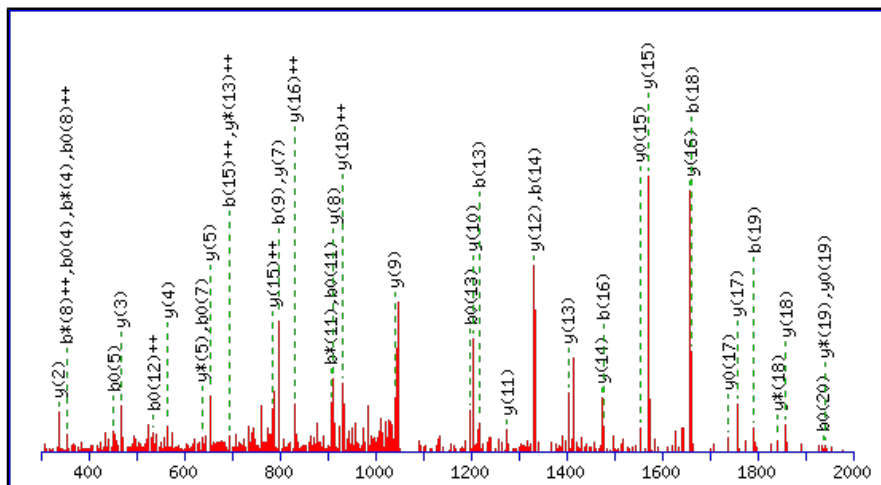
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2127.9709

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

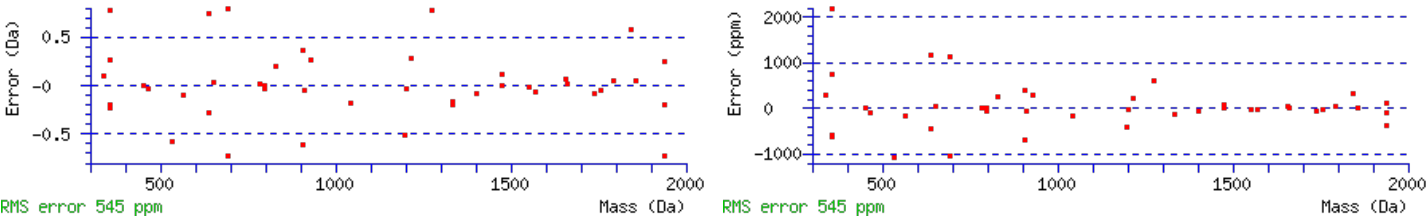
Variable modifications:

N14 : Deamidated (NQ)

Ions Score: 98 Expect: 8e-009

Matches : 44/230 fragment ions using 68 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							21
2	172.0717	86.5395	155.0451	78.0262			G	2014.9352	1007.9713	1997.9087	999.4580	1996.9247	998.9660	20
3	271.1401	136.0737	254.1135	127.5604			V	1957.9138	979.4605	1940.8872	970.9473	1939.9032	970.4552	19
4	372.1878	186.5975	355.1612	178.0842	354.1772	177.5922	T	1858.8454	929.9263	1841.8188	921.4130	1840.8348	920.9210	18
5	471.2562	236.1317	454.2296	227.6185	453.2456	227.1264	V	1757.7977	879.4025	1740.7711	870.8892	1739.7871	870.3972	17
6	558.2882	279.6477	541.2617	271.1345	540.2776	270.6425	S	1658.7293	829.8683	1641.7027	821.3550	1640.7187	820.8630	16
7	655.3410	328.1741	638.3144	319.6608	637.3304	319.1688	P	1571.6972	786.3523	1554.6707	777.8390	1553.6867	777.3470	15
8	726.3781	363.6927	709.3515	355.1794	708.3675	354.6874	A	1474.6445	737.8259	1457.6179	729.3126	1456.6339	728.8206	14
9	797.4152	399.2112	780.3886	390.6980	779.4046	390.2060	A	1403.6074	702.3073	1386.5808	693.7940	1385.5968	693.3020	13
10	854.4367	427.7220	837.4101	419.2087	836.4261	418.7167	G	1332.5703	666.7888	1315.5437	658.2755	1314.5597	657.7835	12
11	925.4738	463.2405	908.4472	454.7272	907.4632	454.2352	A	1275.5488	638.2780	1258.5222	629.7648	1257.5382	629.2727	11
12	1088.5371	544.7722	1071.5106	536.2589	1070.5265	535.7669	Y	1204.5117	602.7595	1187.4851	594.2462	1186.5011	593.7542	10
13	1217.5797	609.2935	1200.5531	600.7802	1199.5691	600.2882	E	1041.4483	521.2278	1024.4218	512.7145	1023.4378	512.2225	9
14	1332.6066	666.8070	1315.5801	658.2937	1314.5961	657.8017	N	912.4058	456.7065	895.3792	448.1932	894.3952	447.7012	8
15	1389.6281	695.3177	1372.6016	686.8044	1371.6175	686.3124	G	797.3788	399.1930	780.3523	390.6798	779.3682	390.1878	7
16	1476.6601	738.8337	1459.6336	730.3204	1458.6496	729.8284	S	740.3573	370.6823	723.3308	362.1690	722.3468	361.6770	6
17	1563.6922	782.3497	1546.6656	773.8364	1545.6816	773.3444	S	653.3253	327.1663	636.2988	318.6530	635.3148	318.1610	5
18	1662.7606	831.8839	1645.7340	823.3706	1644.7500	822.8786	V	566.2933	283.6503	549.2667	275.1370	548.2827	274.6450	4
19	1791.8032	896.4052	1774.7766	887.8919	1773.7926	887.3999	E	467.2249	234.1161	450.1983	225.6028	449.2143	225.1108	3
20	1954.8665	977.9369	1937.8399	969.4236	1936.8559	968.9316	Y	338.1823	169.5948	321.1557	161.0815			2
21							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [NGVTVSPAAGAYENGSSVEYR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
97.6	2127.9709	0.9955	NGVTVSPAAGAYENGSSVEYR	Deamidated N14 100.00%
83.8	2128.9549	0.0115	NGVTVSPAAGAYENGSSVEYR	
13.6	2127.9709	0.9955	NGVTVSPAAGAYENGSSVEYR	Deamidated N1 0.00%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of ENLTAPGSASEVFFTR

Found in **F1SKB1** in **uni_pig**, tr|F1SKB1|F1SKB1_PIG Uncharacterized protein OS=Sus scrofa GN=CP PE=4 SV=3

Match to Query 5719: 1725.816108 from(863.915330,2+) intensity(137708.8906) rtinseconds(2415) scans(5184) index(1873)

Title: 120325_Sunil_PigSerum_Glyco_D_15Spectrum4298_scans__5184

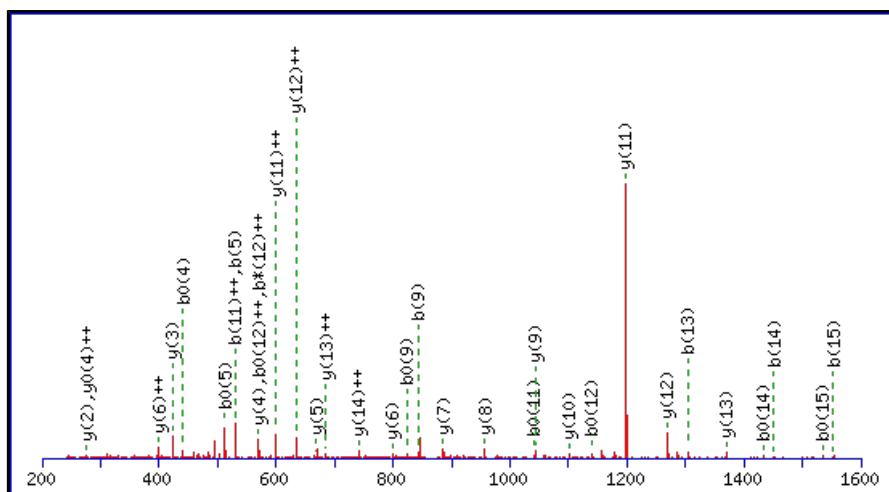
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1725.8210

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

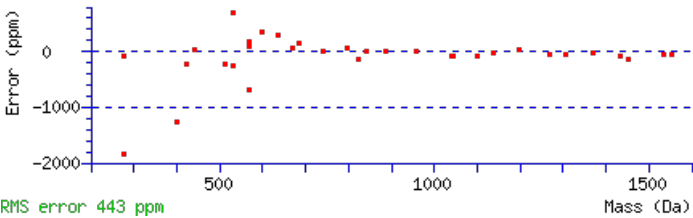
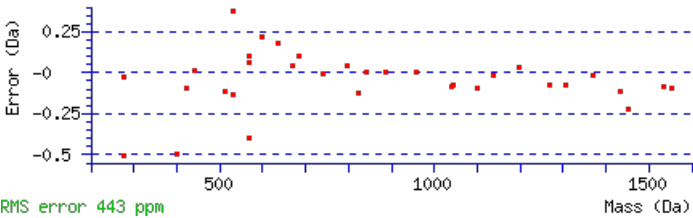
Variable modifications:

N2 : Deamidated (NQ)

Ions Score: 99 Expect: 8.9e-009

Matches : 33/176 fragment ions using 42 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	245.0768	123.0420	228.0503	114.5288	227.0662	114.0368	N	1597.7857	799.3965	1580.7591	790.8832	1579.7751	790.3912	15
3	358.1609	179.5841	341.1343	171.0708	340.1503	170.5788	L	1482.7587	741.8830	1465.7322	733.3697	1464.7482	732.8777	14
4	459.2086	230.1079	442.1820	221.5946	441.1980	221.1026	T	1369.6747	685.3410	1352.6481	676.8277	1351.6641	676.3357	13
5	530.2457	265.6265	513.2191	257.1132	512.2351	256.6212	A	1268.6270	634.8171	1251.6004	626.3039	1250.6164	625.8118	12
6	627.2984	314.1529	610.2719	305.6396	609.2879	305.1476	P	1197.5899	599.2986	1180.5633	590.7853	1179.5793	590.2933	11
7	684.3199	342.6636	667.2933	334.1503	666.3093	333.6583	G	1100.5371	550.7722	1083.5106	542.2589	1082.5265	541.7669	10
8	771.3519	386.1796	754.3254	377.6663	753.3414	377.1743	S	1043.5156	522.2615	1026.4891	513.7482	1025.5051	513.2562	9
9	842.3890	421.6982	825.3625	413.1849	824.3785	412.6929	A	956.4836	478.7454	939.4571	470.2322	938.4730	469.7402	8
10	929.4211	465.2142	912.3945	456.7009	911.4105	456.2089	S	885.4465	443.2269	868.4199	434.7136	867.4359	434.2216	7
11	1058.4637	529.7355	1041.4371	521.2222	1040.4531	520.7302	E	798.4145	399.7109	781.3879	391.1976	780.4039	390.7056	6
12	1157.5321	579.2697	1140.5055	570.7564	1139.5215	570.2644	V	669.3719	335.1896	652.3453	326.6763	651.3613	326.1843	5
13	1304.6005	652.8039	1287.5739	644.2906	1286.5899	643.7986	F	570.3035	285.6554	553.2769	277.1421	552.2929	276.6501	4
14	1451.6689	726.3381	1434.6424	717.8248	1433.6583	717.3328	F	423.2350	212.1212	406.2085	203.6079	405.2245	203.1159	3
15	1552.7166	776.8619	1535.6900	768.3487	1534.7060	767.8566	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
16							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [ENLTAPGSASEVFFTR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
98.6	1725.8210	-0.0049	ENLTAPGSASEVFFTR
11.8	1725.8104	0.0057	RHMAQEAVPQKEQR
8.1	1724.8217	0.9944	GDPGELGLTGNEGPVGQK
4.5	1724.8217	0.9945	GNAAGSAEQPASPAALSPK
3.8	1723.8046	2.0115	KQAKQNAETASAMATR
1.3	1725.8104	0.0057	SLAEQFQRMQGSSTR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

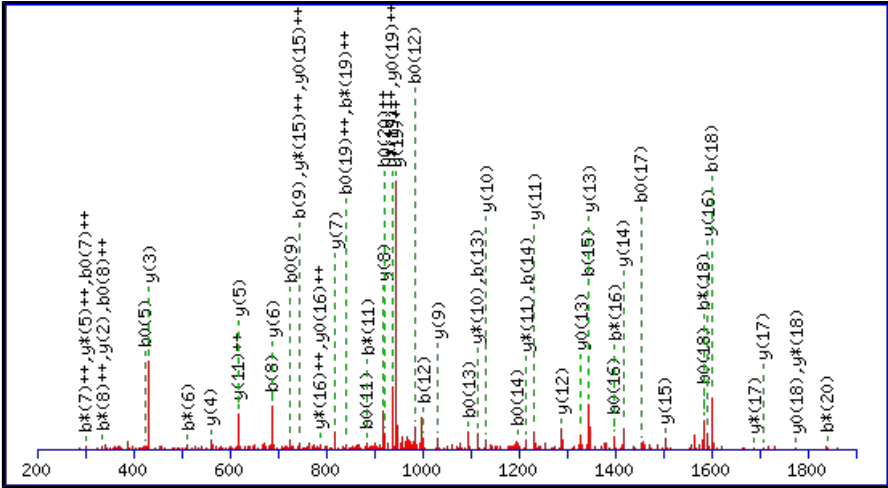
Peptide View

MS/MS Fragmentation of **AAPSNSSAGGTVLTEAGQPCR**
Found in **F1S8N1** in **uni_pig**, tr|F1S8N1|F1S8N1_PIG Uncharacterized protein OS=Sus scrofa GN=HGFAC PE=3 SV=1

Match to Query 11046: 2031.905588 from(1016.960070,2+) intensity(10936.2617) rtinseconds(1456) scans(3302) index(13183)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum2705_scans__3302
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

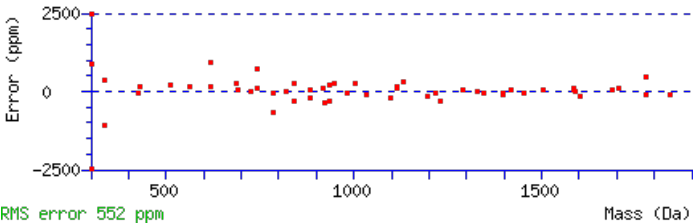
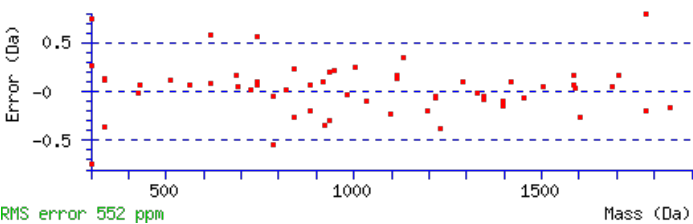
Or, to Da
Label all possible matches ☐ Label matches used for scoring ☐
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2031.9167
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Q18 : Deamidated (NQ)
Ions Score: 96 Expect: 9e-009
Matches : 59/214 fragment ions using 92 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							21
2	143.0815	72.0444					A	1961.8869	981.4471	1944.8604	972.9338	1943.8763	972.4418	20
3	240.1343	120.5708					P	1890.8498	945.9285	1873.8232	937.4153	1872.8392	936.9233	19
4	327.1663	164.0868			309.1557	155.0815	S	1793.7970	897.4022	1776.7705	888.8889	1775.7865	888.3969	18
5	442.1932	221.6003	425.1667	213.0870	424.1827	212.5950	N	1706.7650	853.8861	1689.7385	845.3729	1688.7544	844.8809	17
6	529.2253	265.1163	512.1987	256.6030	511.2147	256.1110	S	1591.7381	796.3727	1574.7115	787.8594	1573.7275	787.3674	16
7	616.2573	308.6323	599.2307	300.1190	598.2467	299.6270	S	1504.7060	752.8567	1487.6795	744.3434	1486.6955	743.8514	15
8	687.2944	344.1508	670.2679	335.6376	669.2838	335.1456	A	1417.6740	709.3406	1400.6475	700.8274	1399.6634	700.3354	14
9	744.3159	372.6616	727.2893	364.1483	726.3053	363.6563	G	1346.6369	673.8221	1329.6103	665.3088	1328.6263	664.8168	13
10	801.3373	401.1723	784.3108	392.6590	783.3268	392.1670	G	1289.6154	645.3114	1272.5889	636.7981	1271.6049	636.3061	12
11	902.3850	451.6961	885.3585	443.1829	884.3745	442.6909	T	1232.5940	616.8006	1215.5674	608.2873	1214.5834	607.7953	11
12	1001.4534	501.2304	984.4269	492.7171	983.4429	492.2251	V	1131.5463	566.2768	1114.5197	557.7635	1113.5357	557.2715	10
13	1114.5375	557.7724	1097.5109	549.2591	1096.5269	548.7671	L	1032.4779	516.7426	1015.4513	508.2293	1014.4673	507.7373	9
14	1215.5852	608.2962	1198.5586	599.7830	1197.5746	599.2909	T	919.3938	460.2005	902.3673	451.6873	901.3832	451.1953	8
15	1344.6278	672.8175	1327.6012	664.3042	1326.6172	663.8122	E	818.3461	409.6767	801.3196	401.1634	800.3356	400.6714	7
16	1415.6649	708.3361	1398.6383	699.8228	1397.6543	699.3308	A	689.3035	345.1554	672.2770	336.6421			6
17	1472.6863	736.8468	1455.6598	728.3335	1454.6758	727.8415	G	618.2664	309.6368	601.2399	301.1236			5
18	1601.7289	801.3681	1584.7024	792.8548	1583.7184	792.3628	Q	561.2450	281.1261	544.2184	272.6128			4
19	1698.7817	849.8945	1681.7552	841.3812	1680.7711	840.8892	P	432.2024	216.6048	415.1758	208.0915			3
20	1858.8124	929.9098	1841.7858	921.3965	1840.8018	920.9045	C	335.1496	168.0784	318.1231	159.5652			2

21							R	175.1190	88.0631	158.0924	79.5498			1
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NCBI **BLAST** search of [AAPSNSSAGGTVLTEAGQPCR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
96.0	2031.9167	-0.0111	AAPSNSSAGGTVLTEAGQPCR
4.5	2031.9133	-0.0077	EAEGQWGVSAEEEEQEKR
2.4	2030.8924	1.0131	EGNEKEIERIMMNYDK
1.5	2029.9084	1.9972	EGNEKEIERIMMNYDK
1.5	2029.9010	2.0045	SMQDATQDHAALEAERQK
0.7	2029.9010	2.0045	SMQDATQDHAALEAERQK
0.7	2030.8851	1.0205	SMQDATQDHAALEAERQK
0.4	2031.8989	0.0066	AACSEHQKDLEMLQAER
0.1	2030.9149	0.9907	AACSEHQKDLEMLQAER
0.1	2031.8989	0.0066	AACSEHQKDLEMLQAER

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1SFI7** in **uni_pig**, tr|F1SFI7|F1SFI7_PIG Alpha-2-HS-glycoprotein (Fragment) OS=Sus scrofa GN=AHSG PE=4 SV=2

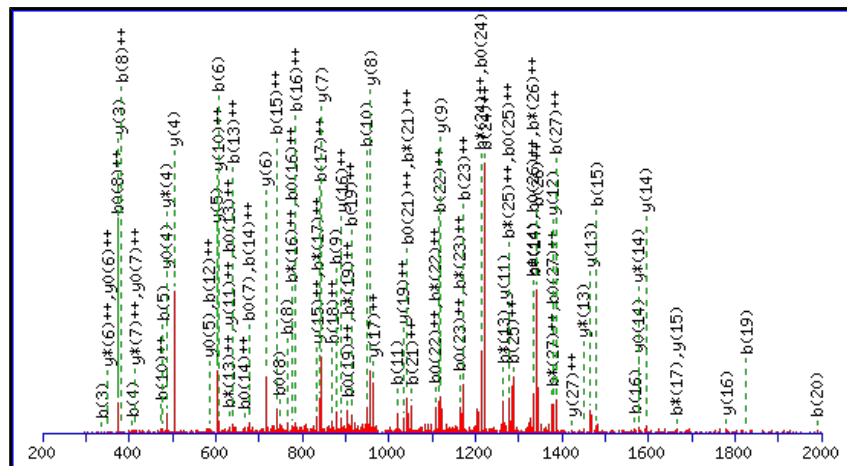
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

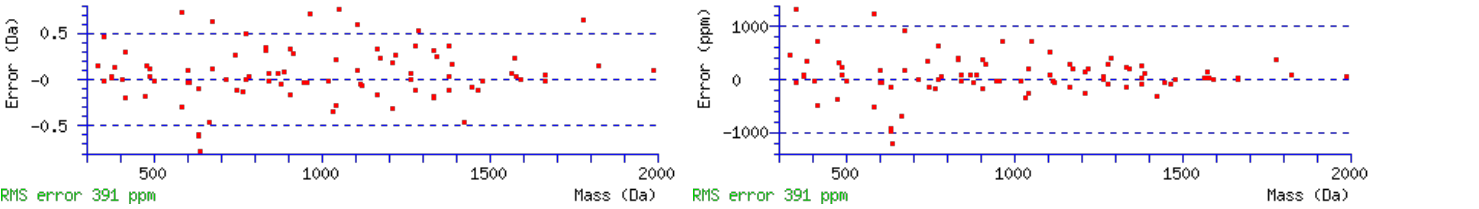
N17 : Deamidated (NQ)

Ions Score: 100 Expect: 9.8e-009

Matches : 88/288 fragment ions using 137 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							28
2	199.1441	100.0757					V	2847.4272	1424.2172	2830.4006	1415.7039	2829.4166	1415.2119	27
3	336.2030	168.6051					H	2748.3587	1374.6830	2731.3322	1366.1697	2730.3482	1365.6777	26
4	407.2401	204.1237					A	2611.2998	1306.1536	2594.2733	1297.6403	2593.2893	1297.1483	25
5	478.2772	239.6423					A	2540.2627	1270.6350	2523.2362	1262.1217	2522.2522	1261.6297	24
6	607.3198	304.1636			589.3093	295.1583	E	2469.2256	1235.1164	2452.1991	1226.6032	2451.2150	1226.1112	23
7	694.3519	347.6796			676.3413	338.6743	S	2340.1830	1170.5951	2323.1565	1162.0819	2322.1725	1161.5899	22
8	765.3890	383.1981			747.3784	374.1928	A	2253.1510	1127.0791	2236.1244	1118.5659	2235.1404	1118.0738	21
9	878.4730	439.7402			860.4625	430.7349	L	2182.1139	1091.5606	2165.0873	1083.0473	2164.1033	1082.5553	20
10	949.5102	475.2587			931.4996	466.2534	A	2069.0298	1035.0185	2052.0033	1026.5053	2051.0192	1026.0133	19
11	1020.5473	510.7773			1002.5367	501.7720	A	1997.9927	999.5000	1980.9661	990.9867	1979.9821	990.4947	18
12	1167.6157	584.3115			1149.6051	575.3062	F	1926.9556	963.9814	1909.9290	955.4682	1908.9450	954.9761	17
13	1281.6586	641.3329	1264.6321	632.8197	1263.6480	632.3277	N	1779.8872	890.4472	1762.8606	881.9339	1761.8766	881.4419	16
14	1352.6957	676.8515	1335.6692	668.3382	1334.6852	667.8462	A	1665.8442	833.4258	1648.8177	824.9125	1647.8337	824.4205	15
15	1480.7543	740.8808	1463.7278	732.3675	1462.7437	731.8755	Q	1594.8071	797.9072	1577.7806	789.3939	1576.7966	788.9019	14
16	1567.7863	784.3968	1550.7598	775.8835	1549.7758	775.3915	S	1466.7485	733.8779	1449.7220	725.3646	1448.7380	724.8726	13
17	1682.8133	841.9103	1665.7867	833.3970	1664.8027	832.9050	N	1379.7165	690.3619	1362.6900	681.8486	1361.7060	681.3566	12
18	1739.8347	870.4210	1722.8082	861.9077	1721.8242	861.4157	G	1264.6896	632.8484	1247.6630	624.3352	1246.6790	623.8431	11
19	1826.8668	913.9370	1809.8402	905.4237	1808.8562	904.9317	S	1207.6681	604.3377	1190.6416	595.8244	1189.6575	595.3324	10
20	1989.9301	995.4687	1972.9035	986.9554	1971.9195	986.4634	Y	1120.6361	560.8217	1103.6095	552.3084	1102.6255	551.8164	9
21	2103.0142	1052.0107	2085.9876	1043.4974	2085.0036	1043.0054	L	957.5728	479.2900	940.5462	470.7767	939.5622	470.2847	8
22	2231.0727	1116.0400	2214.0462	1107.5267	2213.0622	1107.0347	Q	844.4887	422.7480	827.4621	414.2347	826.4781	413.7427	7
23	2344.1568	1172.5820	2327.1303	1164.0688	2326.1462	1163.5768	L	716.4301	358.7187	699.4036	350.2054	698.4196	349.7134	6
24	2443.2252	1222.1162	2426.1987	1213.6030	2425.2147	1213.1110	V	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5

25	2572.2678	1286.6375	2555.2413	1278.1243	2554.2572	1277.6323	E	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
26	2685.3519	1343.1796	2668.3253	1334.6663	2667.3413	1334.1743	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
27	2772.3839	1386.6956	2755.3574	1378.1823	2754.3733	1377.6903	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
28							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [VVHAAESALAAFNAQSNQSYLQLVEISR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
99.5	2945.4883	-0.0085	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated N17 68.80%
94.2	2945.4883	-0.0085	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated Q15 20.35%
89.0	2945.4883	-0.0085	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated N13 6.03%
88.0	2945.4883	-0.0085	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated Q22 4.81%
79.3	2944.5042	0.9755	VVHAAESALAAFNAQSNQSYLQLVEISR	
10.7	2945.4539	0.0258	ITLEGPTEDVSAAQEQIEAMVKDLVSR	
10.3	2945.4539	0.0258	ITLEGPTEDVSAAQEQIEAMVKDLVSR	
5.6	2945.4916	-0.0119	IKTIGSTYMAAAGLSIPSGHENQVLSEK	
5.1	2943.4858	1.9939	QQLLLMLEGLVDERSRLNEALQAER	
5.0	2944.4699	1.0098	ITLEGPTEDVSAAQEQIEAMVKDLVSR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

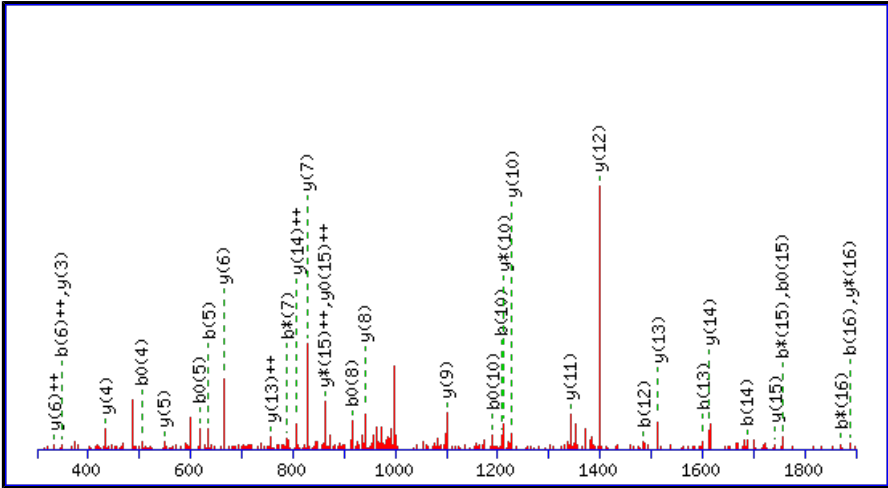
Peptide View

MS/MS Fragmentation of **EYQTIGNQCIYNDSSLK**
Found in **F1SN68** in **uni_pig**, tr|F1SN68|F1SN68_PIG Alpha-1-acid glycoprotein OS=Sus scrofa GN=ORM1 PE=3 SV=1

Match to Query 11080: 2032.892208 from(1017.453380,2+) intensity(8015.7349) rtinseconds(1840) scans(3977) index(12923)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_13Spectrum3226_scans__3977
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

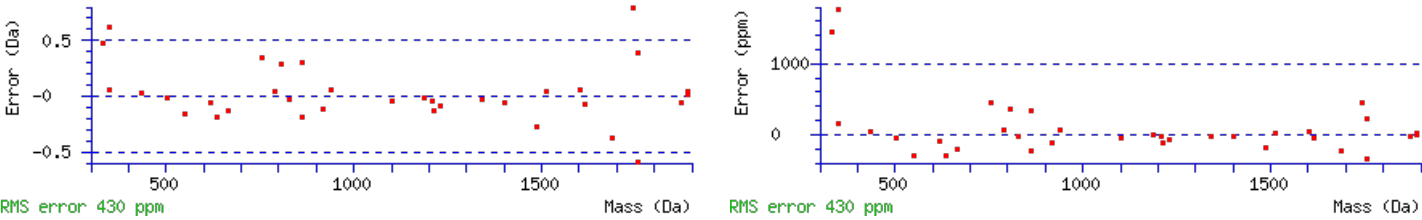
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2032.9048
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 94 Expect: 1.2e-008
Matches : 35/184 fragment ions using 48 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	293.1132	147.0602			275.1026	138.0550	Y	1904.8695	952.9384	1887.8429	944.4251	1886.8589	943.9331	16
3	421.1718	211.0895	404.1452	202.5763	403.1612	202.0842	Q	1741.8061	871.4067	1724.7796	862.8934	1723.7956	862.4014	15
4	522.2195	261.6134	505.1929	253.1001	504.2089	252.6081	T	1613.7476	807.3774	1596.7210	798.8641	1595.7370	798.3721	14
5	635.3035	318.1554	618.2770	309.6421	617.2930	309.1501	I	1512.6999	756.8536	1495.6733	748.3403	1494.6893	747.8483	13
6	692.3250	346.6661	675.2984	338.1529	674.3144	337.6608	G	1399.6158	700.3115	1382.5893	691.7983	1381.6053	691.3063	12
7	806.3679	403.6876	789.3414	395.1743	788.3573	394.6823	N	1342.5944	671.8008	1325.5678	663.2875	1324.5838	662.7955	11
8	934.4265	467.7169	917.3999	459.2036	916.4159	458.7116	Q	1228.5514	614.7794	1211.5249	606.2661	1210.5409	605.7741	10
9	1094.4571	547.7322	1077.4306	539.2189	1076.4466	538.7269	C	1100.4929	550.7501	1083.4663	542.2368	1082.4823	541.7448	9
10	1207.5412	604.2742	1190.5147	595.7610	1189.5306	595.2690	I	940.4622	470.7347	923.4357	462.2215	922.4516	461.7295	8
11	1370.6045	685.8059	1353.5780	677.2926	1352.5940	676.8006	Y	827.3781	414.1927	810.3516	405.6794	809.3676	405.1874	7
12	1485.6315	743.3194	1468.6049	734.8061	1467.6209	734.3141	N	664.3148	332.6610	647.2883	324.1478	646.3042	323.6558	6
13	1600.6584	800.8328	1583.6319	792.3196	1582.6479	791.8276	D	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
14	1687.6904	844.3489	1670.6639	835.8356	1669.6799	835.3436	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
15	1774.7225	887.8649	1757.6959	879.3516	1756.7119	878.8596	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
16	1887.8065	944.4069	1870.7800	935.8936	1869.7960	935.4016	L	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EYQTIGNQCIYNDSSLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
94.0	2032.9048	-0.0125	EYQTIGNQCIYNDSSLK	Deamidated N12 100.00%
48.3	2032.9048	-0.0125	EYQTIGNQCIYNDSSLK	Deamidated Q8 0.00%
40.6	2032.9048	-0.0125	EYQTIGNQCIYNDSSLK	Deamidated N7 0.00%
12.0	2032.9048	-0.0125	EYQTIGNQCIYNDSSLK	Deamidated Q3 0.00%
10.7	2032.8830	0.0092	MGGATSRGENSYGLDITCK	
2.1	2032.9097	-0.0175	HNIMDFAMPYFIQVMK	
1.2	2032.8758	0.0164	EDAFSGTDWMVEKMDLK	
0.8	2031.8982	0.9940	ENQKNFSLQYQCDLK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

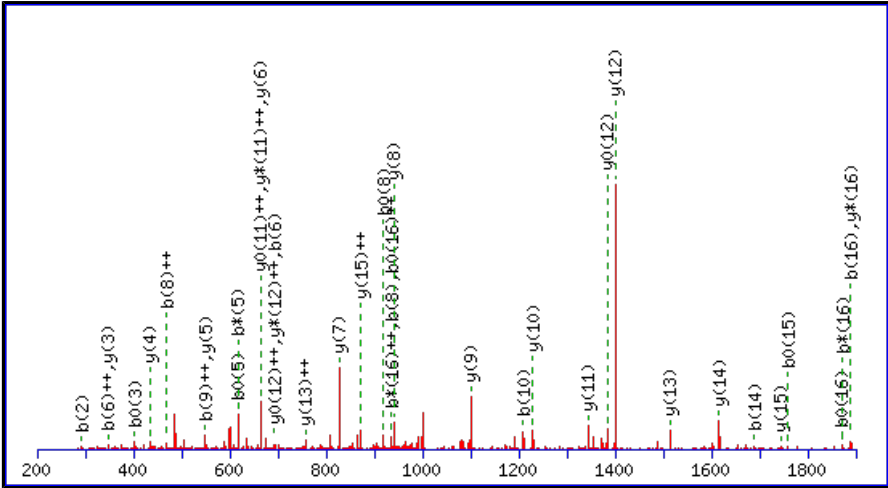
Peptide View

MS/MS Fragmentation of **EYQTIGNQCIYNDSSLK**
Found in **F1SN68** in **uni_pig**, tr|F1SN68|F1SN68_PIG Alpha-1-acid glycoprotein OS=Sus scrofa GN=ORM1 PE=3 SV=1

Match to Query 11622: 2034.864788 from(1018.439670,2+) intensity(48492.7930) rtinseconds(1976) scans(4644) index(6332)
Title: 120325_Sunil_PigSerum_Glyco_S_14Spectrum3888_scans__4644
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

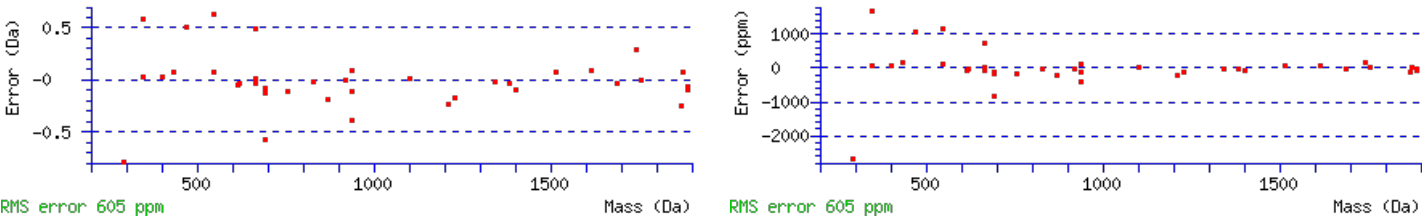
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2034.8728
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Q8 : Deamidated (NQ)
N12 : Deamidated (NQ)
Ions Score: 91 Expect: 1.4e-008
Matches : 39/184 fragment ions using 51 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	293.1132	147.0602			275.1026	138.0550	Y	1906.8375	953.9224	1889.8110	945.4091	1888.8269	944.9171	16
3	421.1718	211.0895	404.1452	202.5763	403.1612	202.0842	Q	1743.7742	872.3907	1726.7476	863.8775	1725.7636	863.3854	15
4	522.2195	261.6134	505.1929	253.1001	504.2089	252.6081	T	1615.7156	808.3614	1598.6890	799.8482	1597.7050	799.3562	14
5	635.3035	318.1554	618.2770	309.6421	617.2930	309.1501	I	1514.6679	757.8376	1497.6414	749.3243	1496.6574	748.8323	13
6	692.3250	346.6661	675.2984	338.1529	674.3144	337.6608	G	1401.5839	701.2956	1384.5573	692.7823	1383.5733	692.2903	12
7	807.3519	404.1796	790.3254	395.6663	789.3414	395.1743	N	1344.5624	672.7848	1327.5358	664.2716	1326.5518	663.7796	11
8	936.3945	468.7009	919.3680	460.1876	918.3840	459.6956	Q	1229.5354	615.2714	1212.5089	606.7581	1211.5249	606.2661	10
9	1096.4252	548.7162	1079.3986	540.2029	1078.4146	539.7109	C	1100.4929	550.7501	1083.4663	542.2368	1082.4823	541.7448	9
10	1209.5092	605.2583	1192.4827	596.7450	1191.4987	596.2530	I	940.4622	470.7347	923.4357	462.2215	922.4516	461.7295	8
11	1372.5726	686.7899	1355.5460	678.2766	1354.5620	677.7846	Y	827.3781	414.1927	810.3516	405.6794	809.3676	405.1874	7
12	1487.5995	744.3034	1470.5730	735.7901	1469.5889	735.2981	N	664.3148	332.6610	647.2883	324.1478	646.3042	323.6558	6
13	1602.6264	801.8169	1585.5999	793.3036	1584.6159	792.8116	D	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
14	1689.6585	845.3329	1672.6319	836.8196	1671.6479	836.3276	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
15	1776.6905	888.8489	1759.6640	880.3356	1758.6799	879.8436	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
16	1889.7746	945.3909	1872.7480	936.8776	1871.7640	936.3856	L	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EYQTIGNQCIYNDSSLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
90.8	2034.8728	-0.0080	EYQTIGNQCIYNDSSLK	Deamidated N7, Q8, N12 61.04%
85.9	2034.8728	-0.0080	EYQTIGNQCIYNDSSLK	Deamidated Q3, Q8, N12 19.57%
85.8	2034.8728	-0.0080	EYQTIGNQCIYNDSSLK	Deamidated Q3, N7, N12 19.39%
46.5	2034.8728	-0.0080	EYQTIGNQCIYNDSSLK	Deamidated Q3, N7, Q8 0.00%

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1S643** in **uni_pig**, tr|F1S643|F1S643_PIG Uncharacterized protein OS=Sus scrofa GN=CFH PE=4 SV=2

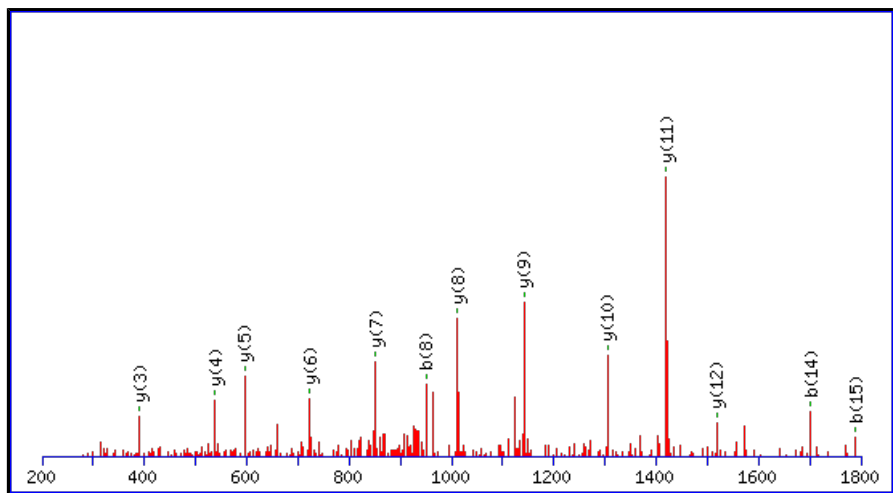
Title: 120326_Sunil_PigSerum_Glyco_SsetB_17Spectrum608_scans__1742

Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

N2 : Deamidated (NQ)

Q10 : Deamidated (NQ)

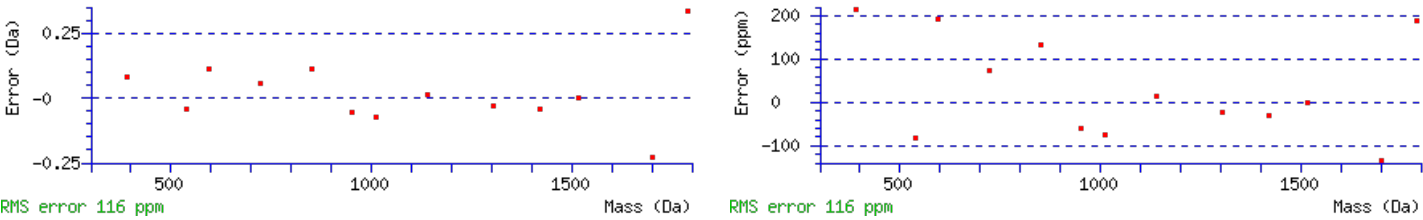
Ions Score: 86 Expect: 1.5e-008

```

Matches : 13/172 fragment ions using 16 most intense peaks  (help)

```

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							16
2	229.1183	115.0628	212.0917	106.5495			N	1849.7181	925.3627	1832.6916	916.8494	1831.7076	916.3574	15
3	344.1452	172.5763	327.1187	164.0630	326.1347	163.5710	D	1734.6912	867.8492	1717.6646	859.3360	1716.6806	858.8439	14
4	445.1929	223.1001	428.1664	214.5868	427.1823	214.0948	T	1619.6642	810.3358	1602.6377	801.8225	1601.6537	801.3305	13
5	544.2613	272.6343	527.2348	264.1210	526.2508	263.6290	V	1518.6166	759.8119	1501.5900	751.2986	1500.6060	750.8066	12
6	659.2883	330.1478	642.2617	321.6345	641.2777	321.1425	D	1419.5481	710.2777	1402.5216	701.7644	1401.5376	701.2724	11
7	822.3516	411.6794	805.3250	403.1662	804.3410	402.6742	Y	1304.5212	652.7642	1287.4946	644.2510	1286.5106	643.7590	10
8	951.3942	476.2007	934.3676	467.6875	933.3836	467.1954	E	1141.4579	571.2326	1124.4313	562.7193	1123.4473	562.2273	9
9	1111.4248	556.2161	1094.3983	547.7028	1093.4143	547.2108	C	1012.4153	506.7113	995.3887	498.1980	994.4047	497.7060	8
10	1240.4674	620.7374	1223.4409	612.2241	1222.4569	611.7321	Q	852.3846	426.6959	835.3581	418.1827	834.3741	417.6907	7
11	1368.5260	684.7666	1351.4995	676.2534	1350.5154	675.7614	Q	723.3420	362.1747	706.3155	353.6614	705.3315	353.1694	6
12	1425.5475	713.2774	1408.5209	704.7641	1407.5369	704.2721	G	595.2835	298.1454	578.2569	289.6321	577.2729	289.1401	5
13	1572.6159	786.8116	1555.5893	778.2983	1554.6053	777.8063	F	538.2620	269.6346	521.2354	261.1214	520.2514	260.6293	4
14	1701.6585	851.3329	1684.6319	842.8196	1683.6479	842.3276	E	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
15	1788.6905	894.8489	1771.6640	886.3356	1770.6799	885.8436	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
16							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LNDTVDYECQQGFESR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.8	1961.7949	-0.0055	LNDTVDYECQQGFESR	Deamidated N2, Q10 97.56%
69.8	1961.7949	-0.0055	LNDTVDYECQQGFESR	Deamidated N2, Q11 2.44%
26.9	1961.7949	-0.0055	LNDTVDYECQQGFESR	Deamidated Q10, Q11 0.00%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIPVNSPELEEPLNHSIAK**

Found in **F1SFI4** in **uni_pig**, tr|F1SFI4|F1SFI4_PIG Uncharacterized protein OS=Sus scrofa GN=KNG1 PE=4 SV=2

Match to Query 11937: 2102.046128 from(1052.030340,2+) intensity(5569.2334) rtinseconds(2132) scans(4729) index(12985)

Title: 120326_Sunil_PigSerum_Glyco_SsetB_13Spectrum3892_scans_4729

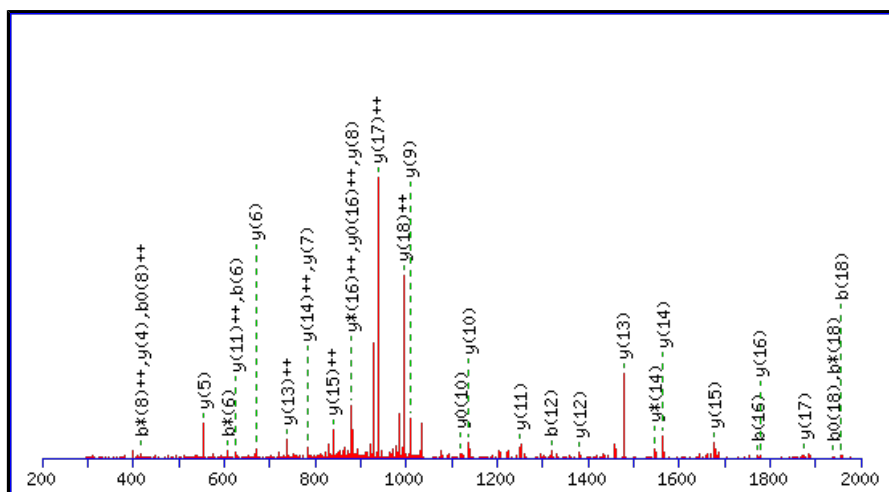
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2102.0531

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

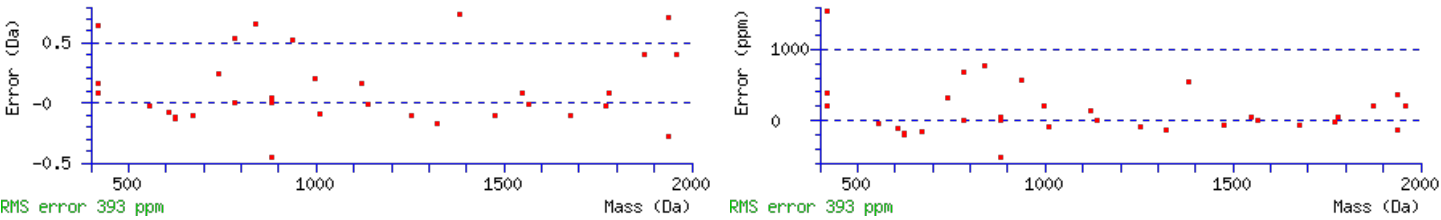
Variable modifications:

N14 : Deamidated (NQ)

Ions Score: 97 Expect: 1.7e-008

Matches : 33/202 fragment ions using 51 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							19
2	229.1183	115.0628			211.1077	106.0575	I	1988.0335	994.5204	1971.0069	986.0071	1970.0229	985.5151	18
3	326.1710	163.5892			308.1605	154.5839	P	1874.9494	937.9784	1857.9229	929.4651	1856.9389	928.9731	17
4	425.2395	213.1234			407.2289	204.1181	V	1777.8967	889.4520	1760.8701	880.9387	1759.8861	880.4467	16
5	539.2824	270.1448	522.2558	261.6316	521.2718	261.1395	N	1678.8283	839.9178	1661.8017	831.4045	1660.8177	830.9125	15
6	626.3144	313.6608	609.2879	305.1476	608.3039	304.6556	S	1564.7853	782.8963	1547.7588	774.3830	1546.7748	773.8910	14
7	723.3672	362.1872	706.3406	353.6740	705.3566	353.1819	P	1477.7533	739.3803	1460.7268	730.8670	1459.7427	730.3750	13
8	852.4098	426.7085	835.3832	418.1953	834.3992	417.7032	E	1380.7005	690.8539	1363.6740	682.3406	1362.6900	681.8486	12
9	965.4938	483.2506	948.4673	474.7373	947.4833	474.2453	L	1251.6579	626.3326	1234.6314	617.8193	1233.6474	617.3273	11
10	1094.5364	547.7719	1077.5099	539.2586	1076.5259	538.7666	E	1138.5739	569.7906	1121.5473	561.2773	1120.5633	560.7853	10
11	1223.5790	612.2931	1206.5525	603.7799	1205.5685	603.2879	E	1009.5313	505.2693	992.5047	496.7560	991.5207	496.2640	9
12	1320.6318	660.8195	1303.6052	652.3063	1302.6212	651.8142	P	880.4887	440.7480	863.4621	432.2347	862.4781	431.7427	8
13	1433.7159	717.3616	1416.6893	708.8483	1415.7053	708.3563	L	783.4359	392.2216	766.4094	383.7083	765.4254	383.2163	7
14	1548.7428	774.8750	1531.7162	766.3618	1530.7322	765.8698	N	670.3519	335.6796	653.3253	327.1663	652.3413	326.6743	6
15	1685.8017	843.4045	1668.7752	834.8912	1667.7911	834.3992	H	555.3249	278.1661	538.2984	269.6528	537.3144	269.1608	5
16	1772.8337	886.9205	1755.8072	878.4072	1754.8232	877.9152	S	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
17	1885.9178	943.4625	1868.8912	934.9493	1867.9072	934.4573	I	331.2340	166.1206	314.2074	157.6074			3
18	1956.9549	978.9811	1939.9284	970.4678	1938.9443	969.9758	A	218.1499	109.5786	201.1234	101.0653			2
19							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [DIPVNSPELEEPLNHSIAK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
97.1	2102.0531	-0.0070	DIPVNSPELEEPLNHSIAK	Deamidated N14 100.00%
29.9	2102.0531	-0.0070	DIPVNSPELEEPLNHSIAK	Deamidated N5 0.00%
5.9	2101.0514	0.9948	LEQPVGRPLSSCSYPPSVK	
5.8	2102.0275	0.0186	LPLTTTCQQMQELLPK	
4.7	2102.0435	0.0027	VVKMIISAHPNLMSCNTR	
4.6	2100.0449	2.0013	LYAYEPSDTALLLDNMKK	
1.9	2102.0354	0.0107	TLCSTYSLGTTRNPYVEK	
1.1	2102.0513	-0.0052	QQWLLRMGAGRLGAPMER	
1.1	2102.0513	-0.0052	QQWLLRMGAGRLGAPMER	
0.4	2102.0578	-0.0117	MRELQQQA AVAWHEELKR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

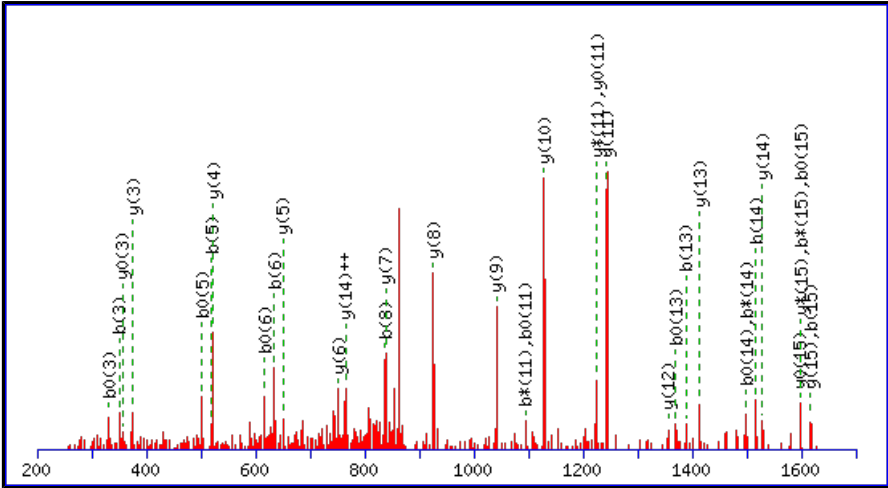
Peptide View

MS/MS Fragmentation of **FSDGLDSNSSTQFEVK**
Found in **F1RQW2** in **uni_pig**, tr|F1RQW2|F1RQW2_PIG Uncharacterized protein OS=Sus scrofa GN=C4 PE=4 SV=2

Match to Query 6175: 1761.751928 from(881.883240,2+) intensity(8439.1719) rtinseconds(1889) scans(3021) index(7341)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_03Spectrum1905_scans__3021
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

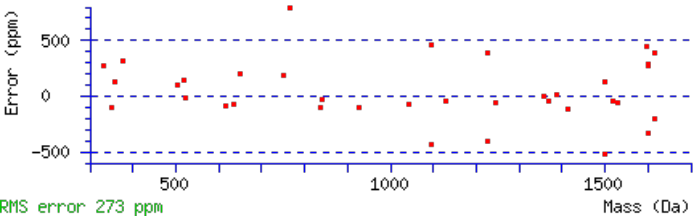
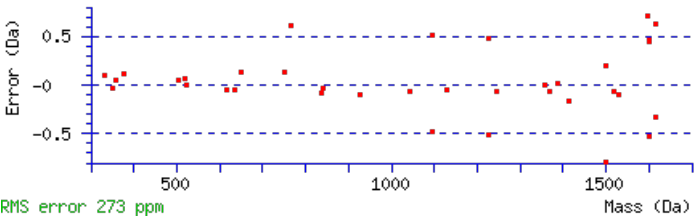
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1761.7581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Q12 : Deamidated (NQ)
Ions Score: 90 Expect: 1.9e-008
Matches : 36/160 fragment ions using 56 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							16
2	235.1077	118.0575			217.0972	109.0522	S	1615.6970	808.3521	1598.6704	799.8388	1597.6864	799.3468	15
3	350.1347	175.5710			332.1241	166.5657	D	1528.6649	764.8361	1511.6384	756.3228	1510.6544	755.8308	14
4	407.1561	204.0817			389.1456	195.0764	G	1413.6380	707.3226	1396.6114	698.8094	1395.6274	698.3174	13
5	520.2402	260.6237			502.2296	251.6185	L	1356.6165	678.8119	1339.5900	670.2986	1338.6060	669.8066	12
6	635.2671	318.1372			617.2566	309.1319	D	1243.5325	622.2699	1226.5059	613.7566	1225.5219	613.2646	11
7	722.2992	361.6532			704.2886	352.6479	S	1128.5055	564.7564	1111.4790	556.2431	1110.4950	555.7511	10
8	837.3261	419.1667	820.2996	410.6534	819.3155	410.1614	N	1041.4735	521.2404	1024.4469	512.7271	1023.4629	512.2351	9
9	924.3581	462.6827	907.3316	454.1694	906.3476	453.6774	S	926.4466	463.7269	909.4200	455.2136	908.4360	454.7216	8
10	1011.3902	506.1987	994.3636	497.6854	993.3796	497.1934	S	839.4145	420.2109	822.3880	411.6976	821.4040	411.2056	7
11	1112.4378	556.7226	1095.4113	548.2093	1094.4273	547.7173	T	752.3825	376.6949	735.3559	368.1816	734.3719	367.6896	6
12	1241.4804	621.2439	1224.4539	612.7306	1223.4699	612.2386	Q	651.3348	326.1710	634.3083	317.6578	633.3243	317.1658	5
13	1388.5488	694.7781	1371.5223	686.2648	1370.5383	685.7728	F	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
14	1517.5914	759.2994	1500.5649	750.7861	1499.5809	750.2941	E	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
15	1616.6599	808.8336	1599.6333	800.3203	1598.6493	799.8283	V	246.1812	123.5942	229.1547	115.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [FSDGLDSNSSTQFEVK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
89.9	1761.7581	-0.0062	FSDGLDSNSSTQFEVK
9.6	1760.7531	0.9988	TRMLQSDYMNMTPR
6.8	1760.7523	0.9997	GMENSVSDAARTSEYK
3.1	1761.7614	-0.0095	SLMASEEEYSTKEDK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSNLTGISDQR**

Found in **F1RKY2** in **uni_pig**, tr|F1RKY2|F1RKY2_PIG Uncharacterized protein OS=Sus scrofa GN=SERPIND1 PE=3 SV=1

Match to Query 1648: 1205.559748 from(603.787150,2+) intensity(1240.5938) rtinseconds(1042) scans(1557) index(12362)

Title: 120326 Sunil PigSerum Glyco SsetB 10Spectrum956 scans 1557

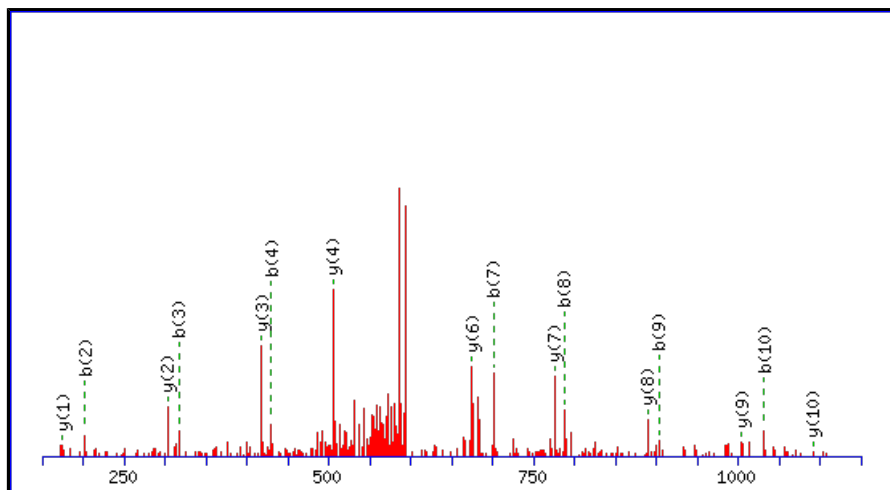
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1204.5684

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

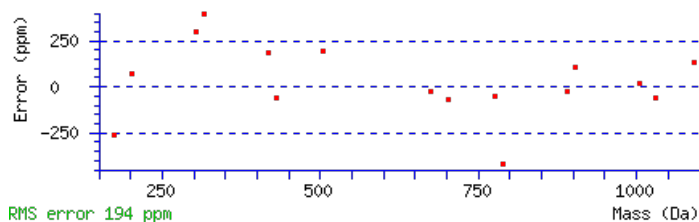
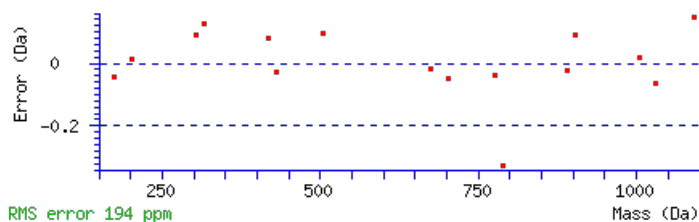
Variable modifications:

N3 : Deamidated (NQ)

Ions Score: 93 Expect: 2.2e-008

Matches : 16/114 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							11
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	S	1091.5327	546.2700	1074.5062	537.7567	1073.5222	537.2647	10
3	317.1092	159.0582	300.0826	150.5450	299.0986	150.0529	N	1004.5007	502.7540	987.4742	494.2407	986.4901	493.7487	9
4	430.1932	215.6003	413.1667	207.0870	412.1827	206.5950	L	889.4738	445.2405	872.4472	436.7272	871.4632	436.2352	8
5	531.2409	266.1241	514.2144	257.6108	513.2304	257.1188	T	776.3897	388.6985	759.3632	380.1852	758.3791	379.6932	7
6	588.2624	294.6348	571.2358	286.1216	570.2518	285.6295	G	675.3420	338.1747	658.3155	329.6614	657.3315	329.1694	6
7	701.3464	351.1769	684.3199	342.6636	683.3359	342.1716	I	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	5
8	788.3785	394.6929	771.3519	386.1796	770.3679	385.6876	S	505.2365	253.1219	488.2100	244.6086	487.2259	244.1166	4
9	903.4054	452.2063	886.3789	443.6931	885.3949	443.2011	D	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
10	1031.4640	516.2356	1014.4374	507.7224	1013.4534	507.2304	Q	303.1775	152.0924	286.1510	143.5791			2
11							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [NSNLTGISDQR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
93.0	1204.5684	0.9914	NSNLTGISDQR	Deamidated N3 99.98%
65.9	1205.5524	0.0074	NSNLTGISDQR	
55.9	1204.5684	0.9914	NSNLTGISDQR	Deamidated N1 0.02%
44.8	1205.5524	0.0074	NSNLTGISDQR	
40.0	1205.5524	0.0074	NSNLTGISDQR	
32.2	1204.5684	0.9914	NSNLTGISDQR	Deamidated Q10 0.00%
24.7	1204.5684	0.9914	SNNITDSLNR	
15.3	1204.5571	1.0026	LLTEDSENQR	
13.6	1204.5684	0.9914	SNNITDSLNR	
13.6	1205.5524	0.0074	SNNITDSLNR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVISSEFNVSAK**

Found in **F1RQW7** in **uni_pig**, tr|F1RQW7|F1RQW7_PIG Uncharacterized protein OS=Sus scrofa GN=C2 PE=3 SV=1

Match to Query 2139: 1251.632768 from(626.823660,2+) intensity(42601.2930) rtinseconds(1705) scans(3655) index(8662)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_15Spectrum3024_scans__3655

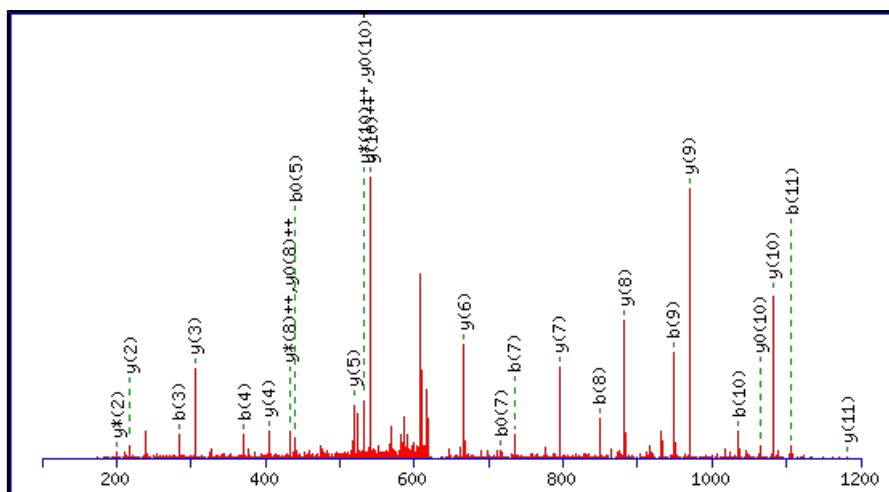
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1251.6347

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

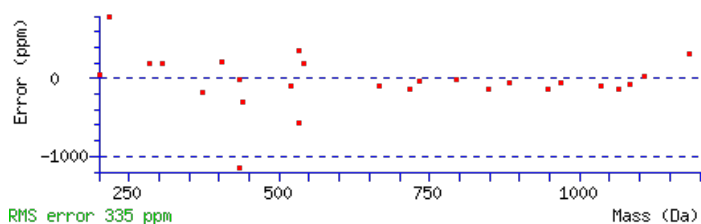
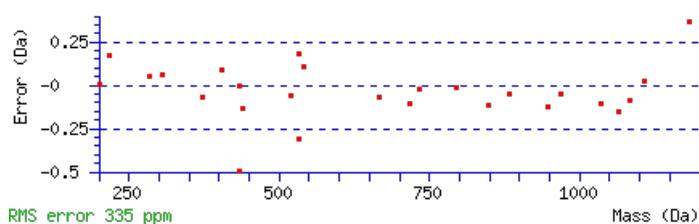
Variable modifications:

N8 : Deamidated (NQ)

Ions Score: 94 Expect: 2.4e-008

Matches : 26/108 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							12
2	171.1128	86.0600					V	1181.6048	591.3061	1164.5783	582.7928	1163.5943	582.3008	11
3	284.1969	142.6021					I	1082.5364	541.7719	1065.5099	533.2586	1064.5259	532.7666	10
4	371.2289	186.1181			353.2183	177.1128	S	969.4524	485.2298	952.4258	476.7165	951.4418	476.2245	9
5	458.2609	229.6341			440.2504	220.6288	S	882.4203	441.7138	865.3938	433.2005	864.4098	432.7085	8
6	587.3035	294.1554			569.2930	285.1501	E	795.3883	398.1978	778.3618	389.6845	777.3777	389.1925	7
7	734.3719	367.6896			716.3614	358.6843	F	666.3457	333.6765	649.3192	325.1632	648.3352	324.6712	6
8	849.3989	425.2031	832.3723	416.6898	831.3883	416.1978	N	519.2773	260.1423	502.2508	251.6290	501.2667	251.1370	5
9	948.4673	474.7373	931.4407	466.2240	930.4567	465.7320	V	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	4
10	1035.4993	518.2533	1018.4728	509.7400	1017.4888	509.2480	S	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
11	1106.5364	553.7719	1089.5099	545.2586	1088.5259	544.7666	A	218.1499	109.5786	201.1234	101.0653			2
12							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [AVISSEFNVS](#)AK

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
94.0	1251.6347	-0.0019	AVISSEFNVSAK
4.1	1251.6248	0.0080	FADNKWSVTGK
1.6	1251.6427	-0.0100	AMRVMSIERK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

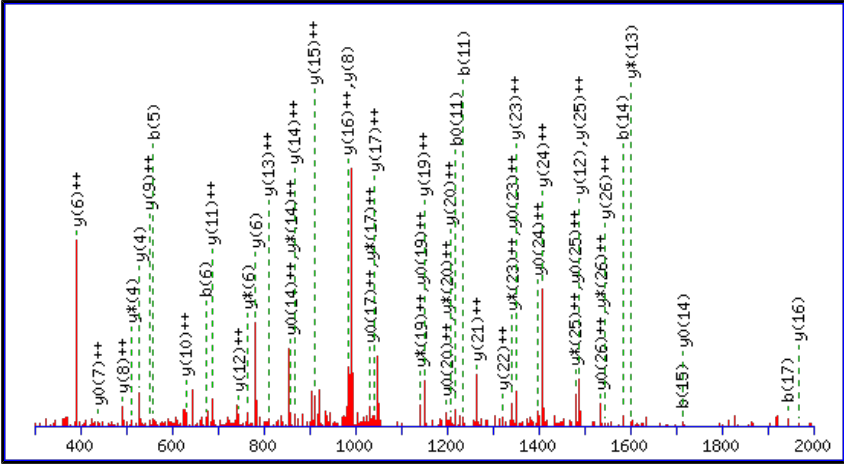
Peptide View

MS/MS Fragmentation of **LLCNGDNDCGDFSDEDDCDS DPRPPCR**
Found in **F1SMJ6** in **uni_pig**, tr|F1SMJ6|F1SMJ6_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=C9 PE=4 SV=2

Match to Query 13387: 3202.150512 from(1068.390780,3+) intensity(3563.3904) rtinseconds(1541) scans(3500) index(6228)
Title: 120325_Sunil_PigSerum_Glyco_S_14Spectrum2872_scans__3500
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

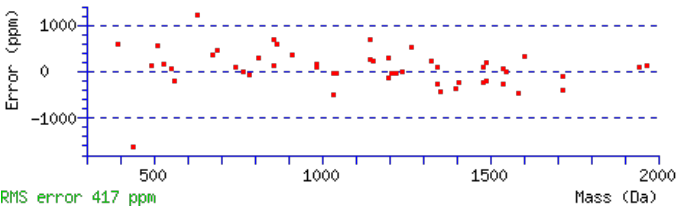
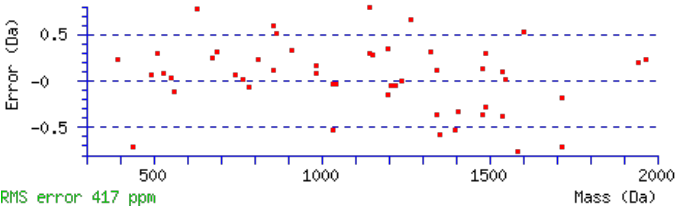
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 3202.1492
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
N7 : Deamidated (NQ)
Ions Score: 76 Expect: 2.6e-008
Matches : 51/284 fragment ions using 132 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							27
2	227.1754	114.0913					L	3090.0724	1545.5399	3073.0459	1537.0266	3072.0619	1536.5346	26
3	387.2061	194.1067					C	2976.9884	1488.9978	2959.9618	1480.4845	2958.9778	1479.9925	25
4	502.2330	251.6201	485.2064	243.1069			N	2816.9577	1408.9825	2799.9312	1400.4692	2798.9472	1399.9772	24
5	559.2545	280.1309	542.2279	271.6176			G	2701.9308	1351.4690	2684.9042	1342.9558	2683.9202	1342.4637	23
6	674.2814	337.6443	657.2549	329.1311	656.2708	328.6391	D	2644.9093	1322.9583	2627.8828	1314.4450	2626.8988	1313.9530	22
7	789.3083	395.1578	772.2818	386.6445	771.2978	386.1525	N	2529.8824	1265.4448	2512.8558	1256.9315	2511.8718	1256.4395	21
8	904.3353	452.6713	887.3087	444.1580	886.3247	443.6660	D	2414.8554	1207.9314	2397.8289	1199.4181	2396.8449	1198.9261	20
9	1064.3659	532.6866	1047.3394	524.1733	1046.3554	523.6813	C	2299.8285	1150.4179	2282.8019	1141.9046	2281.8179	1141.4126	19
10	1121.3874	561.1973	1104.3609	552.6841	1103.3768	552.1921	G	2139.7978	1070.4026	2122.7713	1061.8893	2121.7873	1061.3973	18
11	1236.4143	618.7108	1219.3878	610.1975	1218.4038	609.7055	D	2082.7764	1041.8918	2065.7498	1033.3786	2064.7658	1032.8865	17
12	1383.4828	692.2450	1366.4562	683.7317	1365.4722	683.2397	F	1967.7494	984.3784	1950.7229	975.8651	1949.7389	975.3731	16
13	1470.5148	735.7610	1453.4882	727.2478	1452.5042	726.7557	S	1820.6810	910.8441	1803.6545	902.3309	1802.6705	901.8389	15
14	1585.5417	793.2745	1568.5152	784.7612	1567.5312	784.2692	D	1733.6490	867.3281	1716.6224	858.8149	1715.6384	858.3228	14
15	1714.5843	857.7958	1697.5578	849.2825	1696.5738	848.7905	E	1618.6220	809.8147	1601.5955	801.3014	1600.6115	800.8094	13
16	1829.6113	915.3093	1812.5847	906.7960	1811.6007	906.3040	D	1489.5795	745.2934	1472.5529	736.7801	1471.5689	736.2881	12
17	1944.6382	972.8227	1927.6117	964.3095	1926.6276	963.8175	D	1374.5525	687.7799	1357.5260	679.2666	1356.5419	678.7746	11
18	2104.6689	1052.8381	2087.6423	1044.3248	2086.6583	1043.8328	C	1259.5256	630.2664	1242.4990	621.7531	1241.5150	621.2611	10
19	2219.6958	1110.3515	2202.6693	1101.8383	2201.6852	1101.3463	D	1099.4949	550.2511	1082.4684	541.7378	1081.4844	541.2458	9
20	2306.7278	1153.8676	2289.7013	1145.3543	2288.7173	1144.8623	S	984.4680	492.7376	967.4414	484.2244	966.4574	483.7323	8
21	2421.7548	1211.3810	2404.7282	1202.8677	2403.7442	1202.3757	D	897.4359	449.2216	880.4094	440.7083	879.4254	440.2163	7
22	2518.8075	1259.9074	2501.7810	1251.3941	2500.7970	1250.9021	P	782.4090	391.7081	765.3825	383.1949			6
23	2674.9086	1337.9580	2657.8821	1329.4447	2656.8981	1328.9527	R	685.3562	343.1818	668.3297	334.6685			5

24	2771.9614	1386.4843	2754.9349	1377.9711	2753.9508	1377.4791	P	529.2551	265.1312	512.2286	256.6179			4
25	2869.0142	1435.0107	2851.9876	1426.4975	2851.0036	1426.0054	P	432.2024	216.6048	415.1758	208.0915			3
26	3029.0448	1515.0260	3012.0183	1506.5128	3011.0343	1506.0208	C	335.1496	168.0784	318.1231	159.5652			2
27							R	175.1190	88.0631	158.0924	79.5498			1

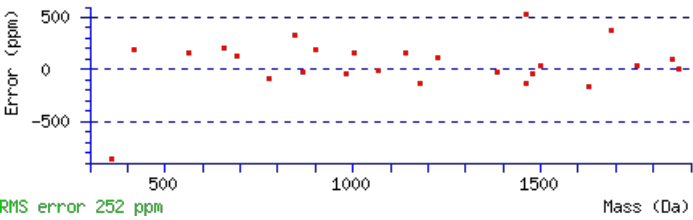
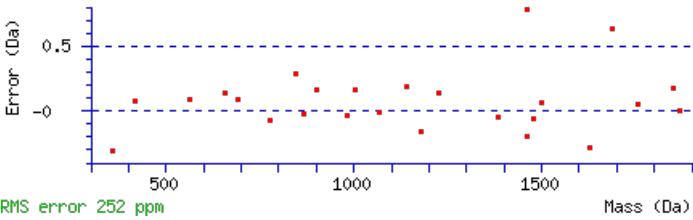


NCBI BLAST search of [LLCNGDNDCGDFSEDDCDS DPRPPCR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
75.8	3202.1492	0.0013	LLCNGDNDCGDFSEDDCDS DPRPPCR
74.7	3201.1652	0.9853	LLCNGDNDCGDFSEDDCDS DPRPPCR
65.6	3201.1652	0.9853	LLCNGDNDCGDFSEDDCDS DPRPPCR

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [EILSVDCSASNSSQMQLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
90.6	2040.9092	-0.0055	EILSVDCSASNSSQMQLR	Deamidated N11 99.98%
53.8	2040.9092	-0.0055	EILSVDCSASNSSQMQLR	Deamidated Q14 0.02%
43.0	2040.9092	-0.0055	EILSVDCSASNSSQMQLR	Deamidated Q16 0.00%
7.9	2040.8979	0.0058	ELNESNSQMEADMLKLR	
4.2	2038.9079	1.9958	DRAANKDQELIENDSYR	
4.0	2040.8979	0.0058	ELNESNSQMEADMLKLR	
3.8	2040.8979	0.0058	ELNESNSQMEADMLKLR	
3.6	2039.8953	1.0084	SSQEMERNEQEISKAQK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

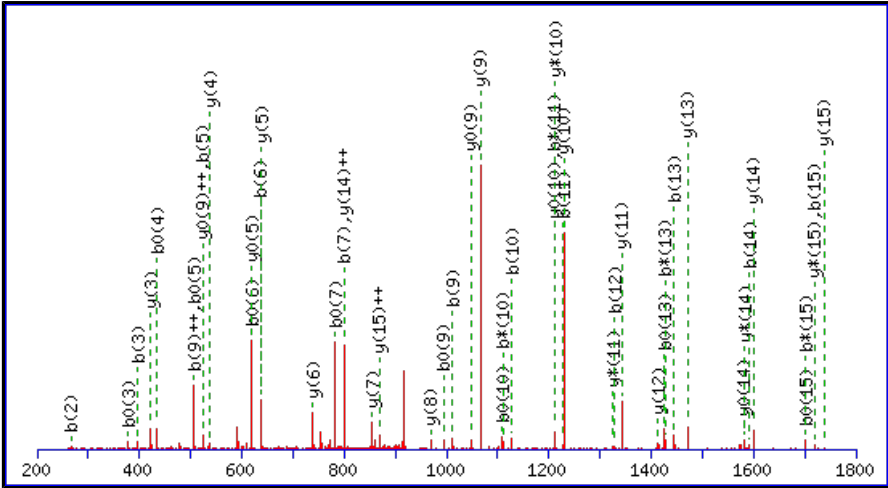
Peptide View

MS/MS Fragmentation of **EHEGAIYPDNTTDFQK**
Found in **F1SKB1** in **uni_pig**, tr|F1SKB1|F1SKB1_PIG Uncharacterized protein OS=Sus scrofa GN=CP PE=4 SV=3

Match to Query 7359: 1864.806368 from(933.410460,2+) intensity(63261.8633) rtinseconds(1451) scans(3132) index(12674)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_12Spectrum2480_scans__3132
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

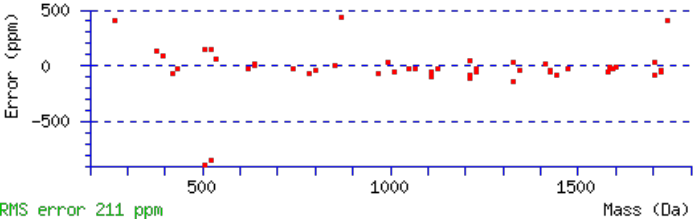
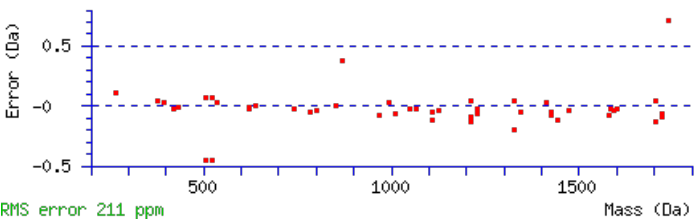
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1864.8115
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 89 Expect: 3.1e-008
Matches : 50/156 fragment ions using 75 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	267.1088	134.0580			249.0982	125.0527	H	1736.7762	868.8917	1719.7497	860.3785	1718.7657	859.8865	15
3	396.1514	198.5793			378.1408	189.5740	E	1599.7173	800.3623	1582.6908	791.8490	1581.7067	791.3570	14
4	453.1728	227.0901			435.1623	218.0848	G	1470.6747	735.8410	1453.6482	727.3277	1452.6642	726.8357	13
5	524.2100	262.6086			506.1994	253.6033	A	1413.6533	707.3303	1396.6267	698.8170	1395.6427	698.3250	12
6	637.2940	319.1506			619.2835	310.1454	I	1342.6161	671.8117	1325.5896	663.2984	1324.6056	662.8064	11
7	800.3573	400.6823			782.3468	391.6770	Y	1229.5321	615.2697	1212.5055	606.7564	1211.5215	606.2644	10
8	897.4101	449.2087			879.3995	440.2034	P	1066.4687	533.7380	1049.4422	525.2247	1048.4582	524.7327	9
9	1012.4371	506.7222			994.4265	497.7169	D	969.4160	485.2116	952.3894	476.6984	951.4054	476.2063	8
10	1127.4640	564.2356	1110.4374	555.7224	1109.4534	555.2304	N	854.3890	427.6982	837.3625	419.1849	836.3785	418.6929	7
11	1228.5117	614.7595	1211.4851	606.2462	1210.5011	605.7542	T	739.3621	370.1847	722.3355	361.6714	721.3515	361.1794	6
12	1329.5594	665.2833	1312.5328	656.7700	1311.5488	656.2780	T	638.3144	319.6608	621.2879	311.1476	620.3039	310.6556	5
13	1444.5863	722.7968	1427.5597	714.2835	1426.5757	713.7915	D	537.2667	269.1370	520.2402	260.6237	519.2562	260.1317	4
14	1591.6547	796.3310	1574.6282	787.8177	1573.6441	787.3257	F	422.2398	211.6235	405.2132	203.1103			3
15	1719.7133	860.3603	1702.6867	851.8470	1701.7027	851.3550	Q	275.1714	138.0893	258.1448	129.5761			2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EHEGAIYPDNTTDFQK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
89.1	1864.8115	-0.0052	EHEGAIYPDNTTDFQK	Deamidated N10 99.96%
55.6	1864.8115	-0.0052	EHEGAIYPDNTTDFQK	Deamidated Q15 0.04%
10.1	1864.8223	-0.0159	QMMTDEFNKQAITEK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

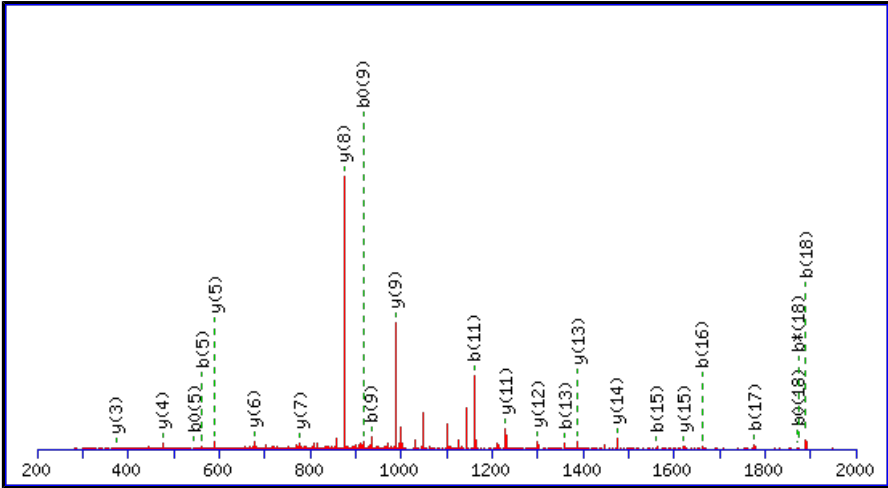
Peptide View

MS/MS Fragmentation of **VNLSFSSAQILPTSDTNLK**
Found in **I3LQ17** in **uni_pig**, tr|I3LQ17|I3LQ17_PIG Uncharacterized protein OS=Sus scrofa PE=4 SV=1

Match to Query 11716: 2035.037948 from(1018.526250,2+) intensity(18512.5195) rtinseconds(2508) scans(6040) index(10719)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_14Spectrum5111_scans__6040
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

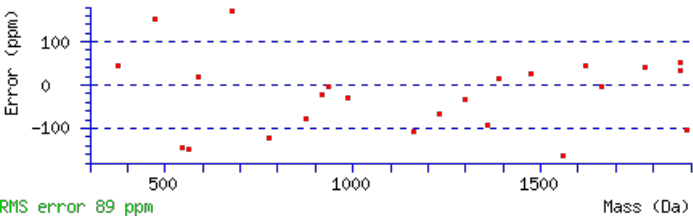
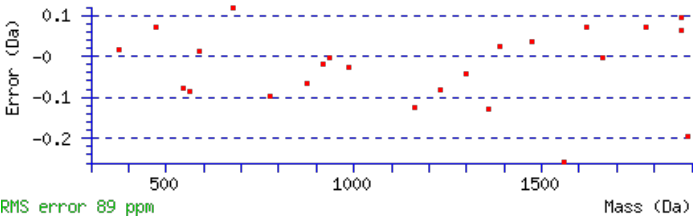
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2035.0473
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Ions Score: 94 Expect: 3.3e-008
Matches : 24/202 fragment ions using 34 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							19
2	215.1026	108.0550	198.0761	99.5417			N	1936.9862	968.9967	1919.9597	960.4835	1918.9756	959.9915	18
3	328.1867	164.5970	311.1601	156.0837			L	1821.9593	911.4833	1804.9327	902.9700	1803.9487	902.4780	17
4	415.2187	208.1130	398.1922	199.5997	397.2082	199.1077	S	1708.8752	854.9412	1691.8487	846.4280	1690.8646	845.9360	16
5	562.2871	281.6472	545.2606	273.1339	544.2766	272.6419	F	1621.8432	811.4252	1604.8166	802.9120	1603.8326	802.4199	15
6	649.3192	325.1632	632.2926	316.6499	631.3086	316.1579	S	1474.7748	737.8910	1457.7482	729.3777	1456.7642	728.8857	14
7	736.3512	368.6792	719.3246	360.1660	718.3406	359.6740	S	1387.7427	694.3750	1370.7162	685.8617	1369.7322	685.3697	13
8	807.3883	404.1978	790.3618	395.6845	789.3777	395.1925	A	1300.7107	650.8590	1283.6842	642.3457	1282.7001	641.8537	12
9	935.4469	468.2271	918.4203	459.7138	917.4363	459.2218	Q	1229.6736	615.3404	1212.6470	606.8272	1211.6630	606.3352	11
10	1048.5310	524.7691	1031.5044	516.2558	1030.5204	515.7638	I	1101.6150	551.3111	1084.5885	542.7979	1083.6045	542.3059	10
11	1161.6150	581.3111	1144.5885	572.7979	1143.6044	572.3059	L	988.5310	494.7691	971.5044	486.2558	970.5204	485.7638	9
12	1258.6678	629.8375	1241.6412	621.3243	1240.6572	620.8322	P	875.4469	438.2271	858.4203	429.7138	857.4363	429.2218	8
13	1359.7155	680.3614	1342.6889	671.8481	1341.7049	671.3561	T	778.3941	389.7007	761.3676	381.1874	760.3836	380.6954	7
14	1446.7475	723.8774	1429.7209	715.3641	1428.7369	714.8721	S	677.3464	339.1769	660.3199	330.6636	659.3359	330.1716	6
15	1561.7744	781.3909	1544.7479	772.8776	1543.7639	772.3856	D	590.3144	295.6608	573.2879	287.1476	572.3039	286.6556	5
16	1662.8221	831.9147	1645.7956	823.4014	1644.8115	822.9094	T	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
17	1776.8650	888.9362	1759.8385	880.4229	1758.8545	879.9309	N	374.2398	187.6235	357.2132	179.1103			3
18	1889.9491	945.4782	1872.9226	936.9649	1871.9385	936.4729	L	260.1969	130.6021	243.1703	122.0888			2
19							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VNLSFSSAQILPTSDTNLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
94.1	2035.0473	-0.0094	VNLSFSSAQILPTSDTNLK	Deamidated N2 99.51%
71.1	2035.0473	-0.0094	VNLSFSSAQILPTSDTNLK	Deamidated Q9 0.49%
21.6	2035.0473	-0.0094	VNLSFSSAQILPTSDTNLK	Deamidated N17 0.00%
6.7	2035.0334	0.0045	GKDNEPPGPIDNSRIAQVK	
5.9	2035.0262	0.0117	LDGEIIPHFPADQEVLNK	
5.9	2035.0262	0.0118	LDGEIIPHFPANQEVLNK	
5.9	2035.0262	0.0118	LDGEIIPHFPANQEVLNK	
1.7	2033.0285	2.0095	GTVEACANAEIEIMKKLR	
1.6	2035.0262	0.0117	LDGEIIPHFPADQEVLNK	
1.6	2035.0262	0.0118	LDGEIIPHFPANQEVLNK	

Mascot: <http://www.matrixscience.com/>

NCBI **BLAST** search of [IFFQLNNLTLEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
93.3	1623.8144	-0.0022	IFFQLNNLTLEDR	Deamidated N6, N7 99.96%
58.6	1623.8144	-0.0022	IFFQLNNLTLEDR	Deamidated Q4, N7 0.03%
46.9	1623.8144	-0.0022	IFFQLNNLTLEDR	Deamidated Q4, N6 0.00%
10.0	1623.8178	-0.0056	ENYKLDCLITDIK	
7.7	1623.8146	-0.0024	LMMILARMNEKDK	
7.2	1623.8147	-0.0025	LMLCVLVSMVASGGR	
6.8	1623.8265	-0.0143	YIHRMMQIEFIK	
6.8	1623.8265	-0.0143	YIHRMMQIEFIK	
5.7	1622.8239	0.9883	DMKSGLGGAFAVLR	
5.1	1622.8012	1.0110	SSDEINALRDYGKR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTSCATNASICGDEAR**

Found in **F1SL63** in **uni_pig**, tr|F1SL63|F1SL63_PIG Uncharacterized protein (Fragment) OS=Sus scrofa PE=4 SV=2

Match to Query 5642: 1725.722228 from(863.868390,2+) intensity(2384.4136) rtinseconds(1295) scans(1878) index(4047)

Title: 120325 Sunil PigSerum Glyco P 15Spectrum1165 scans 1878

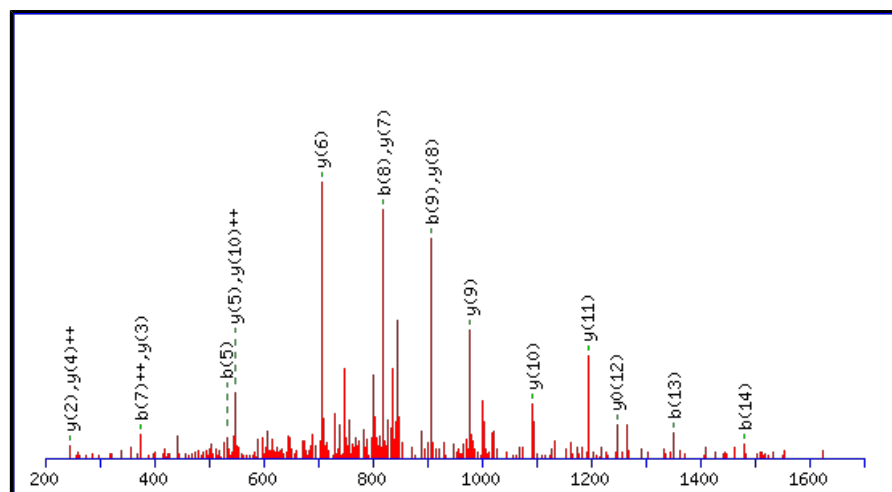
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1725.7298

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

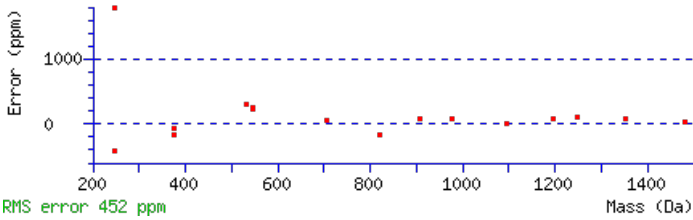
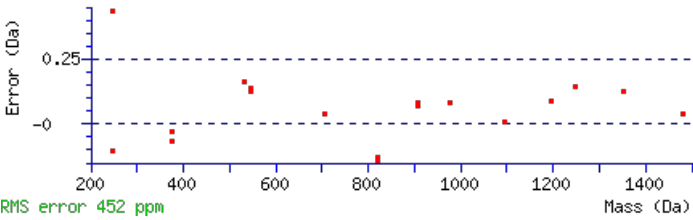
Variable modifications:

N7 : Deamidated (NQ)

Ions Score: 85 Expect: 4.5e-008

Matches : 18/162 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							16
2	215.1390	108.0731			197.1285	99.0679	T	1613.6530	807.3301	1596.6265	798.8169	1595.6424	798.3249	15
3	302.1710	151.5892			284.1605	142.5839	S	1512.6053	756.8063	1495.5788	748.2930	1494.5948	747.8010	14
4	462.2017	231.6045			444.1911	222.5992	C	1425.5733	713.2903	1408.5468	704.7770	1407.5627	704.2850	13
5	533.2388	267.1230			515.2282	258.1178	A	1265.5427	633.2750	1248.5161	624.7617	1247.5321	624.2697	12
6	634.2865	317.6469			616.2759	308.6416	T	1194.5055	597.7564	1177.4790	589.2431	1176.4950	588.7511	11
7	749.3134	375.1604	732.2869	366.6471	731.3029	366.1551	N	1093.4579	547.2326	1076.4313	538.7193	1075.4473	538.2273	10
8	820.3505	410.6789	803.3240	402.1656	802.3400	401.6736	A	978.4309	489.7191	961.4044	481.2058	960.4204	480.7138	9
9	907.3826	454.1949	890.3560	445.6817	889.3720	445.1896	S	907.3938	454.2005	890.3673	445.6873	889.3832	445.1953	8
10	1020.4666	510.7370	1003.4401	502.2237	1002.4561	501.7317	I	820.3618	410.6845	803.3352	402.1713	802.3512	401.6792	7
11	1180.4973	590.7523	1163.4707	582.2390	1162.4867	581.7470	C	707.2777	354.1425	690.2512	345.6292	689.2671	345.1372	6
12	1237.5188	619.2630	1220.4922	610.7497	1219.5082	610.2577	G	547.2471	274.1272	530.2205	265.6139	529.2365	265.1219	5
13	1352.5457	676.7765	1335.5191	668.2632	1334.5351	667.7712	D	490.2256	245.6164	473.1991	237.1032	472.2150	236.6112	4
14	1481.5883	741.2978	1464.5617	732.7845	1463.5777	732.2925	E	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
15	1552.6254	776.8163	1535.5989	768.3031	1534.6148	767.8111	A	246.1561	123.5817	229.1295	115.0684			2
16							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LTSCATNASICGDEAR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
85.2	1725.7298	-0.0076	LTSCATNASICGDEAR
3.2	1725.7298	-0.0075	INMNGINNSSGMVDAR
3.2	1725.7298	-0.0075	INMNGINNSSGMVDAR

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of IYGGILNISEITK

Found in **F1RZN7** in **uni_pig**, tr|F1RZN7|F1RZN7_PIG Uncharacterized protein OS=Sus scrofa GN=KLKB1 PE=3 SV=2

Match to Query 3658: 1420.777388 from(711.395970,2+) intensity(5262.3643) rtinseconds(2657) scans(4700) index(11326)

Title: 120326_Sunil_PigSerum_Glyco_PsetB_18Spectrum3092_scans_4700

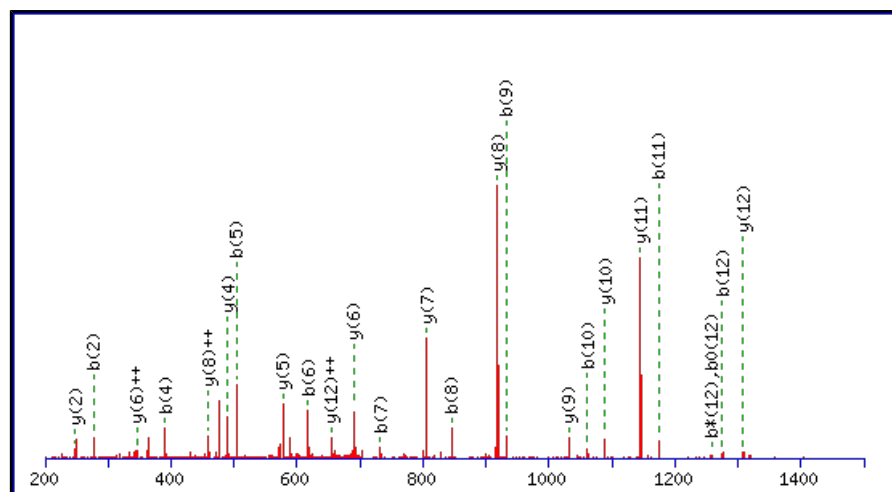
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1420.7813

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

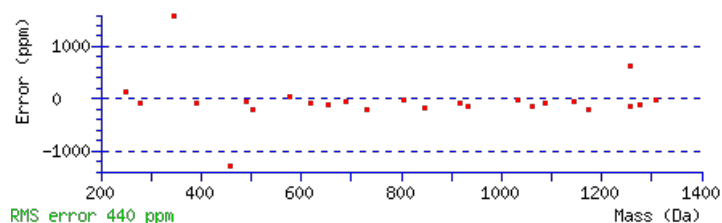
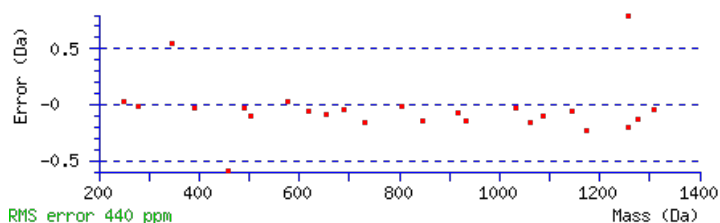
Variable modifications:

N7 : Deamidated (NQ)

Ions Score: 90 Expect: 4.5e-008

Matches : 25/114 fragment ions using 37 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							13
2	277.1547	139.0810					Y	1308.7046	654.8559	1291.6780	646.3426	1290.6940	645.8506	12
3	334.1761	167.5917					G	1145.6412	573.3243	1128.6147	564.8110	1127.6307	564.3190	11
4	391.1976	196.1024					G	1088.6198	544.8135	1071.5932	536.3002	1070.6092	535.8082	10
5	504.2817	252.6445					I	1031.5983	516.3028	1014.5718	507.7895	1013.5877	507.2975	9
6	617.3657	309.1865					L	918.5142	459.7608	901.4877	451.2475	900.5037	450.7555	8
7	732.3927	366.7000	715.3661	358.1867			N	805.4302	403.2187	788.4036	394.7055	787.4196	394.2134	7
8	845.4767	423.2420	828.4502	414.7287			I	690.4032	345.7053	673.3767	337.1920	672.3927	336.7000	6
9	932.5088	466.7580	915.4822	458.2447	914.4982	457.7527	S	577.3192	289.1632	560.2926	280.6499	559.3086	280.1579	5
10	1061.5514	531.2793	1044.5248	522.7660	1043.5408	522.2740	E	490.2871	245.6472	473.2606	237.1339	472.2766	236.6419	4
11	1174.6354	587.8213	1157.6089	579.3081	1156.6249	578.8161	I	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
12	1275.6831	638.3452	1258.6565	629.8319	1257.6725	629.3399	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
13							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [IYGGILNISEITK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
89.8	1420.7813	-0.0039	IYGGILNISEITK
10.0	1419.7651	1.0123	KLMMILAVMNEK
9.5	1420.7674	0.0100	AVRVYTINLESR
6.4	1420.7827	-0.0053	FELLTNEPRRK
6.0	1420.7748	0.0026	QYLRELNMIK
3.9	1420.7636	0.0138	IYILVTSCDPLK
3.1	1419.7829	0.9945	LIIDLAMMKNVK
2.8	1420.7782	-0.0008	VLMKKNSVDIMK
2.5	1420.7674	0.0100	QYLVLSLQSSQR
2.2	1419.7796	0.9978	GELIIFGGLMDKK

Mascot: <http://www.matrixscience.com/>

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Mascot Search Results

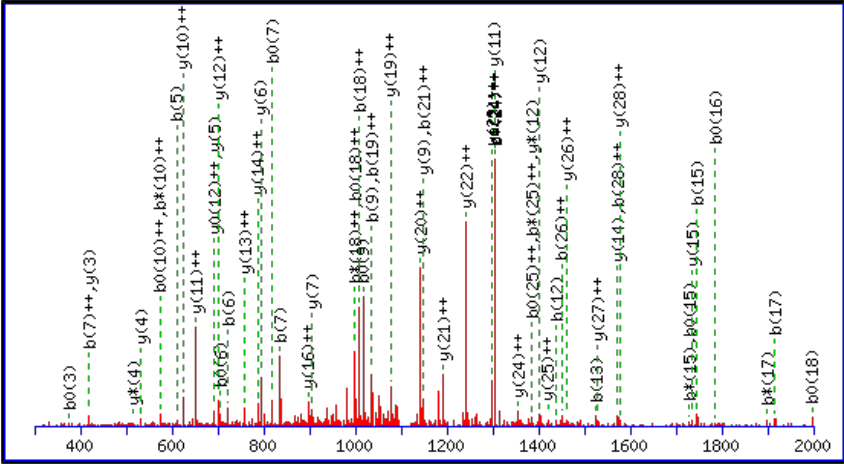
Peptide View

MS/MS Fragmentation of **YTESEIITVQCDSGYGLVGPQNITCIEDR**
Found in **F1S0J2** in **uni_pig**, tr[F1S0J2]F1S0J2_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPA PE=4 SV=2

Match to Query 13439: 3318.536292 from(1107.186040,3+) intensity(0.0000) rtinseconds(2853) scans(6787) index(3723)
Title: 120325_Sunil_PigSerum_Glyco_P_13Spectrum5808_scans_6787
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

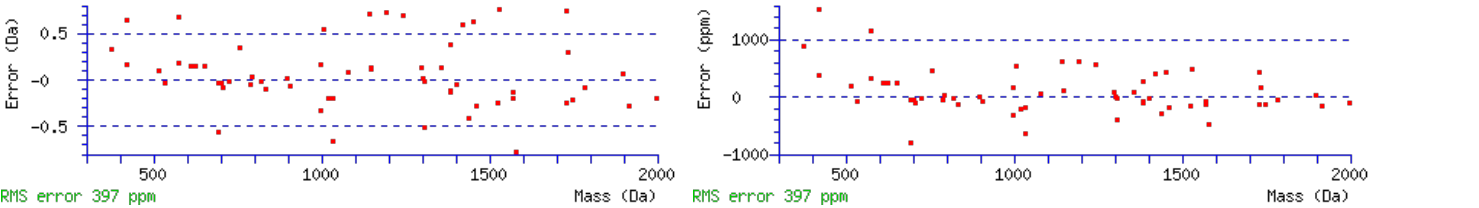
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 3317.5068
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N22 : Deamidated (NQ)
Ions Score: 91 Expect: 5.4e-008
Matches : 60/314 fragment ions using 102 most intense peaks (help)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							29
2	265.1183	133.0628			247.1077	124.0575	T	3155.4507	1578.2290	3138.4242	1569.7157	3137.4402	1569.2237	28
3	394.1609	197.5841			376.1503	188.5788	E	3054.4031	1527.7052	3037.3765	1519.1919	3036.3925	1518.6999	27
4	481.1929	241.1001			463.1823	232.0948	S	2925.3605	1463.1839	2908.3339	1454.6706	2907.3499	1454.1786	26
5	610.2355	305.6214			592.2249	296.6161	E	2838.3284	1419.6679	2821.3019	1411.1546	2820.3179	1410.6626	25
6	723.3196	362.1634			705.3090	353.1581	I	2709.2858	1355.1466	2692.2593	1346.6333	2691.2753	1346.1413	24
7	836.4036	418.7055			818.3931	409.7002	I	2596.2018	1298.6045	2579.1752	1290.0913	2578.1912	1289.5992	23
8	937.4513	469.2293			919.4407	460.2240	T	2483.1177	1242.0625	2466.0912	1233.5492	2465.1072	1233.0572	22
9	1036.5197	518.7635			1018.5092	509.7582	V	2382.0700	1191.5387	2365.0435	1183.0254	2364.0595	1182.5334	21
10	1164.5783	582.7928	1147.5517	574.2795	1146.5677	573.7875	Q	2283.0016	1142.0045	2265.9751	1133.4912	2264.9911	1132.9992	20
11	1324.6089	662.8081	1307.5824	654.2948	1306.5984	653.8028	C	2154.9430	1077.9752	2137.9165	1069.4619	2136.9325	1068.9699	19
12	1439.6359	720.3216	1422.6093	711.8083	1421.6253	711.3163	D	1994.9124	997.9598	1977.8858	989.4466	1976.9018	988.9546	18
13	1526.6679	763.8376	1509.6414	755.3243	1508.6574	754.8323	S	1879.8855	940.4464	1862.8589	931.9331	1861.8749	931.4411	17
14	1583.6894	792.3483	1566.6628	783.8351	1565.6788	783.3430	G	1792.8534	896.9304	1775.8269	888.4171	1774.8429	887.9251	16
15	1746.7527	873.8800	1729.7262	865.3667	1728.7421	864.8747	Y	1735.8320	868.4196	1718.8054	859.9063	1717.8214	859.4143	15
16	1803.7742	902.3907	1786.7476	893.8775	1785.7636	893.3854	G	1572.7686	786.8880	1555.7421	778.3747	1554.7581	777.8827	14
17	1916.8582	958.9328	1899.8317	950.4195	1898.8477	949.9275	L	1515.7472	758.3772	1498.7206	749.8639	1497.7366	749.3719	13
18	2015.9267	1008.4670	1998.9001	999.9537	1997.9161	999.4617	V	1402.6631	701.8352	1385.6366	693.3219	1384.6525	692.8299	12
19	2072.9481	1036.9777	2055.9216	1028.4644	2054.9376	1027.9724	G	1303.5947	652.3010	1286.5681	643.7877	1285.5841	643.2957	11
20	2170.0009	1085.5041	2152.9743	1076.9908	2151.9903	1076.4988	P	1246.5732	623.7903	1229.5467	615.2770	1228.5627	614.7850	10
21	2298.0595	1149.5334	2281.0329	1141.0201	2280.0489	1140.5281	Q	1149.5205	575.2639	1132.4939	566.7506	1131.5099	566.2586	9
22	2413.0864	1207.0468	2396.0599	1198.5336	2395.0758	1198.0416	N	1021.4619	511.2346	1004.4353	502.7213	1003.4513	502.2293	8
23	2526.1705	1263.5889	2509.1439	1255.0756	2508.1599	1254.5836	I	906.4349	453.7211	889.4084	445.2078	888.4244	444.7158	7
24	2627.2181	1314.1127	2610.1916	1305.5994	2609.2076	1305.1074	T	793.3509	397.1791	776.3243	388.6658	775.3403	388.1738	6

25	2787.2488	1394.1280	2770.2222	1385.6148	2769.2382	1385.1228	C	692.3032	346.6552	675.2767	338.1420	674.2926	337.6500	5
26	2900.3329	1450.6701	2883.3063	1442.1568	2882.3223	1441.6648	I	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
27	3029.3755	1515.1914	3012.3489	1506.6781	3011.3649	1506.1861	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
28	3144.4024	1572.7048	3127.3758	1564.1916	3126.3918	1563.6996	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
29							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [YTESEIITVQCDSGYGLVGPQNITCIEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

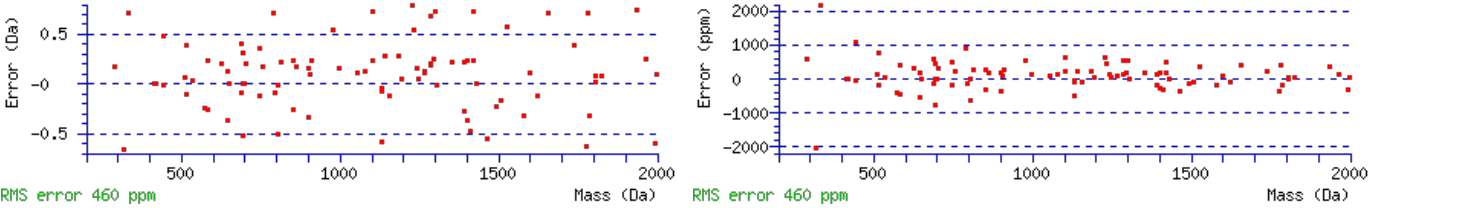
All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
90.8	3317.5068	1.0295	YTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated N22 49.71%
90.8	3317.5068	1.0295	YTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q21 49.71%
71.4	3317.5068	1.0295	YTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q10 0.57%
64.1	3316.5228	2.0135	YTESEIITVQCDSGYGLVGPQNITCIEDR	
5.7	3318.5544	-0.0181	MTLNNVTMRQGTVGMPQQQRWSIPADGR	
4.8	3318.5544	-0.0181	MTLNNVTMRQGTVGMPQQQRWSIPADGR	
4.2	3318.5544	-0.0181	MTLNNVTMRQGTVGMPQQQRWSIPADGR	
3.3	3318.5544	-0.0181	MTLNNVTMRQGTVGMPQQQRWSIPADGR	
2.4	3316.5176	2.0187	SRGFGFVTYSCVEEVDAAMCARPHKVDGR	
2.3	3318.5674	-0.0311	TYNEPKDMAVNGVSANGVNTSEKHLVVENGK	

Mascot: <http://www.matrixscience.com/>

http://mascoexp.student.main.ntu.edu.sg/mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=13715[22/Apr/15 05:58:14 PM]

25	2801.3186	1401.1629	2784.2920	1392.6497	2783.3080	1392.1576	V	1402.6631	701.8352	1385.6366	693.3219	1384.6525	692.8299	12
26	2858.3400	1429.6737	2841.3135	1421.1604	2840.3295	1420.6684	G	1303.5947	652.3010	1286.5681	643.7877	1285.5841	643.2957	11
27	2955.3928	1478.2000	2938.3663	1469.6868	2937.3822	1469.1948	P	1246.5732	623.7903	1229.5467	615.2770	1228.5627	614.7850	10
28	3083.4514	1542.2293	3066.4248	1533.7161	3065.4408	1533.2241	Q	1149.5205	575.2639	1132.4939	566.7506	1131.5099	566.2586	9
29	3198.4783	1599.7428	3181.4518	1591.2295	3180.4678	1590.7375	N	1021.4619	511.2346	1004.4353	502.7213	1003.4513	502.2293	8
30	3311.5624	1656.2848	3294.5358	1647.7716	3293.5518	1647.2796	I	906.4349	453.7211	889.4084	445.2078	888.4244	444.7158	7
31	3412.6101	1706.8087	3395.5835	1698.2954	3394.5995	1697.8034	T	793.3509	397.1791	776.3243	388.6658	775.3403	388.1738	6
32	3572.6407	1786.8240	3555.6142	1778.3107	3554.6302	1777.8187	C	692.3032	346.6552	675.2767	338.1420	674.2926	337.6500	5
33	3685.7248	1843.3660	3668.6982	1834.8528	3667.7142	1834.3608	I	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
34	3814.7674	1907.8873	3797.7408	1899.3741	3796.7568	1898.8820	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
35	3929.7943	1965.4008	3912.7678	1956.8875	3911.7838	1956.3955	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
36							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
89.4	4102.8987	-0.0215	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated N29 39.90%
89.4	4102.8987	-0.0215	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q28 39.90%
84.7	4102.8987	-0.0215	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q17 13.27%
81.8	4102.8987	-0.0215	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5 6.92%
66.9	4101.9147	0.9625	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
10.4	4102.8504	0.0268	HSGPHSPGPVMDQFTRVQDNHDPNPQSGPQRFVIR	
9.8	4100.8637	2.0136	SPAWERGENCCMPDWFEAKLYAMMVLLAVDVEGMK	
9.2	4100.8565	2.0208	DVRPAPEAQPLEKQDGEKESELEPMNGEIMDDTLK	
7.8	4100.8958	1.9815	YGELWKTGMFERMSLQDDEDEHSIEMHLPYTAK	
7.2	4101.8597	1.0176	EDGSENRPFSPSPLNNMSSTVTVKNSQEGTTKTDNPSK	

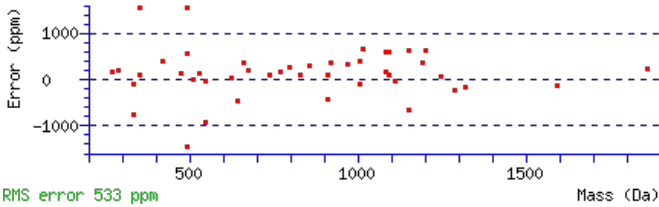
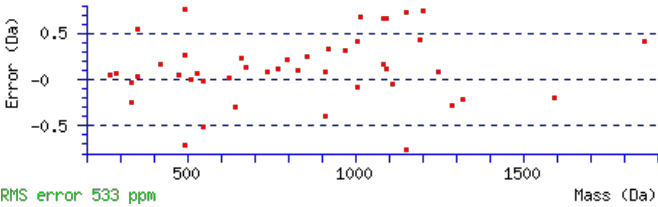
Mascot: <http://www.matrixscience.com/>

NCBI **BLAST** search of [NESCGYDTCYSWEK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
71.7	1798.6451	-0.0058	NESCGYDTCYSWEK

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [FSNCSTENGGAHYCLEEEGGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
71.5	2534.9373	-0.0075	FSNCSTENGGAHYCLEEEGGR
0.6	2533.9236	1.0061	ENSSEICTNNGECVCGQCVC

Mascot: <http://www.matrixscience.com/>

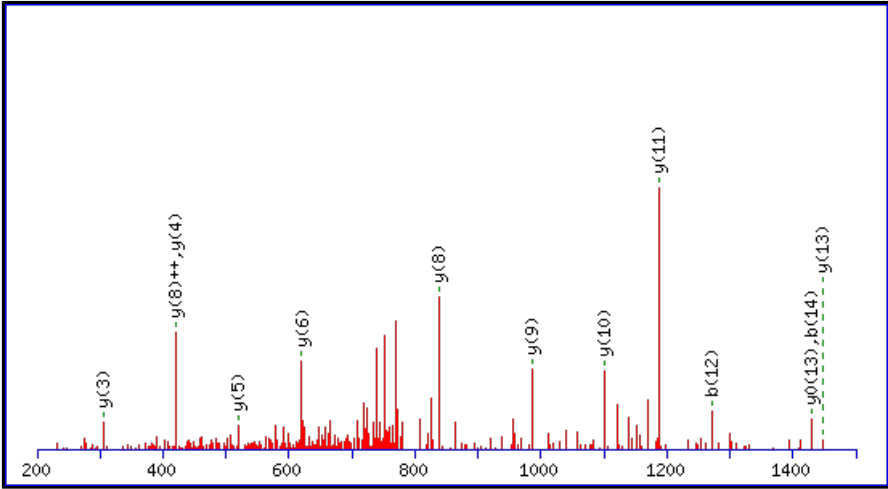
Peptide View

Found in **F1RUM4** in **uni_pig**, tr|F1RUM4|F1RUM4_PIG Inter-alpha-trypsin inhibitor heavy chain H2 OS=Sus scrofa GN=ITI2 PE=4 SV=2

Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

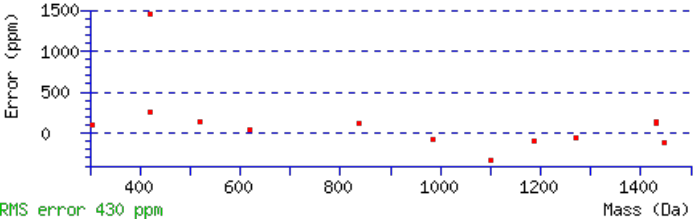
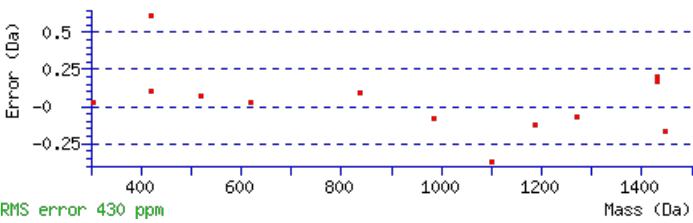
Or, _____ to _____ Da _____

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1574.7287
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
 N6 : Deamidated (NQ)
Ions Score: 87 Expect: 8.2e-008
Matches : 13/148 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							15
2	129.0659	65.0366					A	1518.7145	759.8609	1501.6879	751.3476	1500.7039	750.8556	14
3	276.1343	138.5708					F	1447.6774	724.3423	1430.6508	715.8290	1429.6668	715.3370	13
4	389.2183	195.1128					I	1300.6089	650.8081	1283.5824	642.2948	1282.5984	641.8028	12
5	476.2504	238.6288			458.2398	229.6235	S	1187.5249	594.2661	1170.4983	585.7528	1169.5143	585.2608	11
6	591.2773	296.1423	574.2508	287.6290	573.2667	287.1370	N	1100.4929	550.7501	1083.4663	542.2368	1082.4823	541.7448	10
7	738.3457	369.6765	721.3192	361.1632	720.3352	360.6712	F	985.4659	493.2366	968.4394	484.7233	967.4553	484.2313	9
8	825.3777	413.1925	808.3512	404.6792	807.3672	404.1872	S	838.3975	419.7024	821.3709	411.1891	820.3869	410.6971	8
9	956.4182	478.7128	939.3917	470.1995	938.4077	469.7075	M	751.3655	376.1864	734.3389	367.6731	733.3549	367.1811	7
10	1057.4659	529.2366	1040.4394	520.7233	1039.4553	520.2313	T	620.3250	310.6661	603.2984	302.1529	602.3144	301.6608	6
11	1156.5343	578.7708	1139.5078	570.2575	1138.5238	569.7655	V	519.2773	260.1423	502.2508	251.6290	501.2667	251.1370	5
12	1271.5613	636.2843	1254.5347	627.7710	1253.5507	627.2790	D	420.2089	210.6081	403.1823	202.0948	402.1983	201.6028	4
13	1328.5827	664.7950	1311.5562	656.2817	1310.5722	655.7897	G	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
14	1429.6304	715.3188	1412.6039	706.8056	1411.6198	706.3136	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
15							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [GAFISNESMTVDGTK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
86.8	1574.7287	-0.0060	GAFISNESMTVDGTK
11.2	1574.7287	-0.0060	CGSYLEKDFDTLK
5.2	1573.7195	1.0032	ECKDWHVSGSIQK
4.8	1574.7311	-0.0084	GEALEQNIKADEQK
3.7	1574.7246	-0.0019	KTQTHTQQNMVEK
1.1	1574.7246	-0.0019	KTQTHTQQNMVEK
1.1	1574.7246	-0.0019	KTQTHTQQNMVEK
1.1	1574.7246	-0.0019	KTQTHTQQNMVEK

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of IFFQLNNLTLEDR

Found in **F1SC20** in **uni_pig**, tr|F1SC20|F1SC20_PIG Alpha-1B-glycoprotein OS=Sus scrofa GN=A1BG PE=4 SV=1

Match to Query 5222: 1622.824888 from(812.419720,2+) intensity(11213.5684) rtinseconds(2946) scans(7329) index(3984)

Title: 120325_Sunil_PigSerum_Glyco_P_14Spectrum6243_scans__7329

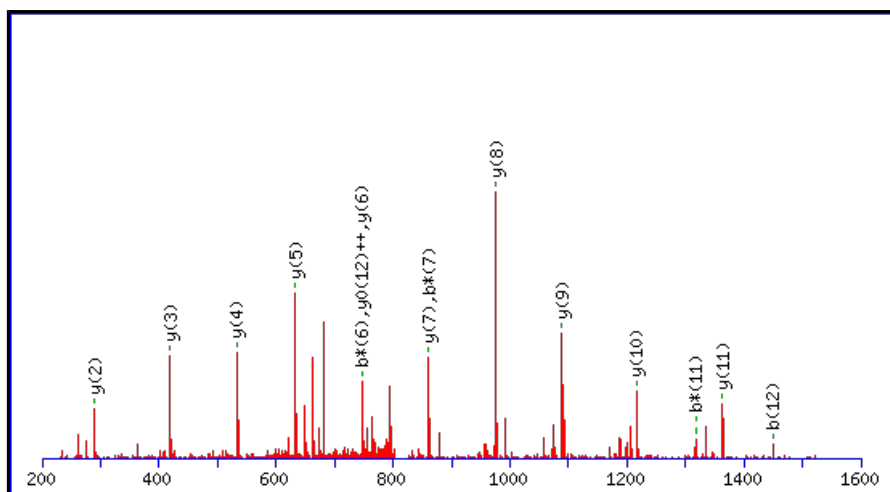
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1622.8304

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

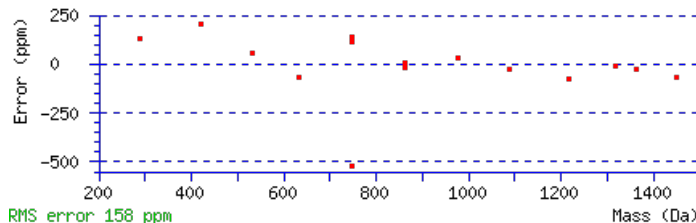
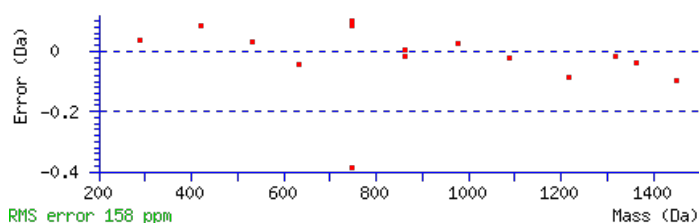
Variable modifications:

N7 : Deamidated (NQ)

Ions Score: 89 Expect: 8.7e-008

Matches : 15/120 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							13
2	261.1598	131.0835					F	1510.7536	755.8805	1493.7271	747.3672	1492.7431	746.8752	12
3	408.2282	204.6177					F	1363.6852	682.3462	1346.6587	673.8330	1345.6747	673.3410	11
4	536.2867	268.6470	519.2602	260.1337			Q	1216.6168	608.8120	1199.5903	600.2988	1198.6062	599.8068	10
5	649.3708	325.1890	632.3443	316.6758			L	1088.5582	544.7828	1071.5317	536.2695	1070.5477	535.7775	9
6	763.4137	382.2105	746.3872	373.6972			N	975.4742	488.2407	958.4476	479.7274	957.4636	479.2354	8
7	878.4407	439.7240	861.4141	431.2107			N	861.4312	431.2193	844.4047	422.7060	843.4207	422.2140	7
8	991.5247	496.2660	974.4982	487.7527			L	746.4043	373.7058	729.3777	365.1925	728.3937	364.7005	6
9	1092.5724	546.7898	1075.5459	538.2766	1074.5619	537.7846	T	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	5
10	1205.6565	603.3319	1188.6299	594.8186	1187.6459	594.3266	L	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
11	1334.6991	667.8532	1317.6725	659.3399	1316.6885	658.8479	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
12	1449.7260	725.3666	1432.6995	716.8534	1431.7155	716.3614	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
13							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [IFFQLNNLTLEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
89.5	1622.8304	-0.0055	IFFQLNNLTLEDR	Deamidated N7 98.06%
72.4	1622.8304	-0.0055	IFFQLNNLTLEDR	Deamidated N6 1.93%
41.8	1622.8304	-0.0055	IFFQLNNLTLEDR	Deamidated Q4 0.00%
7.1	1622.8264	-0.0015	GTYDILVTKDNQTR	
4.9	1622.8304	-0.0055	LTSTQVKIWFQNR	
3.5	1621.8100	1.0149	FNRDVDETISWIK	
2.5	1622.8151	0.0098	APPQPEKLQTNNVGK	
1.0	1622.8225	0.0024	MDLKVYSLLNPDSK	
0.3	1621.8311	0.9938	APPQPEKLQTNNVGK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of DGEAFEINGTEDGR

Found in **F1SFM2** in **uni_pig**, tr|F1SFM2|F1SFM2_PIG Uncharacterized protein OS=Sus scrofa GN=CHL1 PE=4 SV=2

Match to Query 4668: 1509.619188 from(755.816870,2+) intensity(5077.6582) rtinseconds(1680) scans(2696) index(2193)

Title: 120325 Sunil PigSerum Glyco D 17Spectrum1760 scans 2696

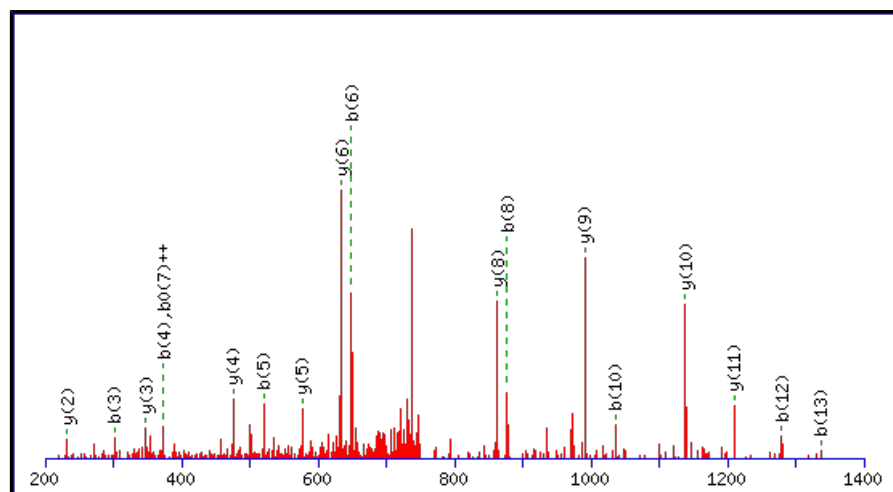
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1509.6219

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

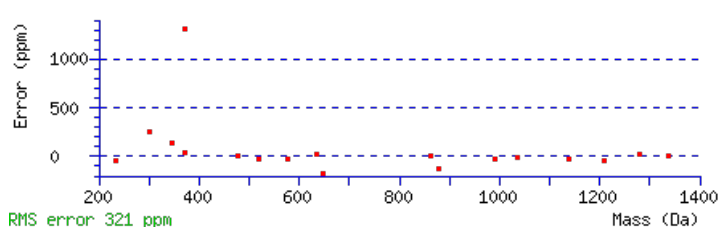
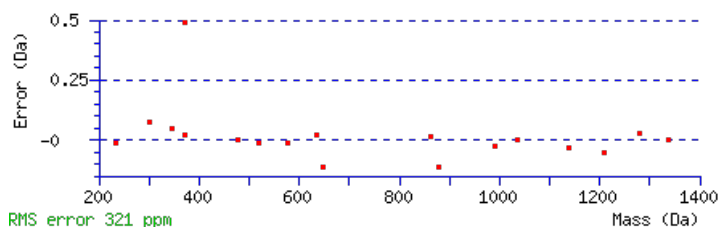
Variable modifications:

N8 : Deamidated (NQ)

Ions Score: 79 Expect: 1.4e-007

Matches : 18/138 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							14
2	173.0557	87.0315			155.0451	78.0262	G	1395.6023	698.3048	1378.5757	689.7915	1377.5917	689.2995	13
3	302.0983	151.5528			284.0877	142.5475	E	1338.5808	669.7940	1321.5543	661.2808	1320.5703	660.7888	12
4	373.1354	187.0713			355.1248	178.0661	A	1209.5382	605.2727	1192.5117	596.7595	1191.5277	596.2675	11
5	520.2038	260.6055			502.1932	251.6003	F	1138.5011	569.7542	1121.4746	561.2409	1120.4905	560.7489	10
6	649.2464	325.1268			631.2358	316.1216	E	991.4327	496.2200	974.4061	487.7067	973.4221	487.2147	9
7	762.3305	381.6689			744.3199	372.6636	I	862.3901	431.6987	845.3636	423.1854	844.3795	422.6934	8
8	877.3574	439.1823	860.3309	430.6691	859.3468	430.1771	N	749.3060	375.1567	732.2795	366.6434	731.2955	366.1514	7
9	934.3789	467.6931	917.3523	459.1798	916.3683	458.6878	G	634.2791	317.6432	617.2525	309.1299	616.2685	308.6379	6
10	1035.4265	518.2169	1018.4000	509.7036	1017.4160	509.2116	T	577.2576	289.1325	560.2311	280.6192	559.2471	280.1272	5
11	1164.4691	582.7382	1147.4426	574.2249	1146.4586	573.7329	E	476.2100	238.6086	459.1834	230.0953	458.1994	229.6033	4
12	1279.4961	640.2517	1262.4695	631.7384	1261.4855	631.2464	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
13	1336.5175	668.7624	1319.4910	660.2491	1318.5070	659.7571	G	232.1404	116.5738	215.1139	108.0606			2
14							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [DGEAFEINGTEDGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
79.0	1509.6219	-0.0027	DGEAFEINGTEDGR
11.0	1509.6228	-0.0036	TNMWTPVANMNGR
4.8	1509.6309	-0.0117	ACLGCMGAGPGRCK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSNVSCQASVSR**

Found in **F1SC57** in **uni_pig**, tr|F1SC57|F1SC57_PIG Uncharacterized protein OS=Sus scrofa GN=PLTP PE=4 SV=1

Match to Query 2513: 1293.596388 from(647.805470,2+) intensity(3727.2092) rtinseconds(825) scans(1490) index(5930)

Title: 120325_Sunil_PigSerum_Glyco_S_12Spectrum1105_scans__1490

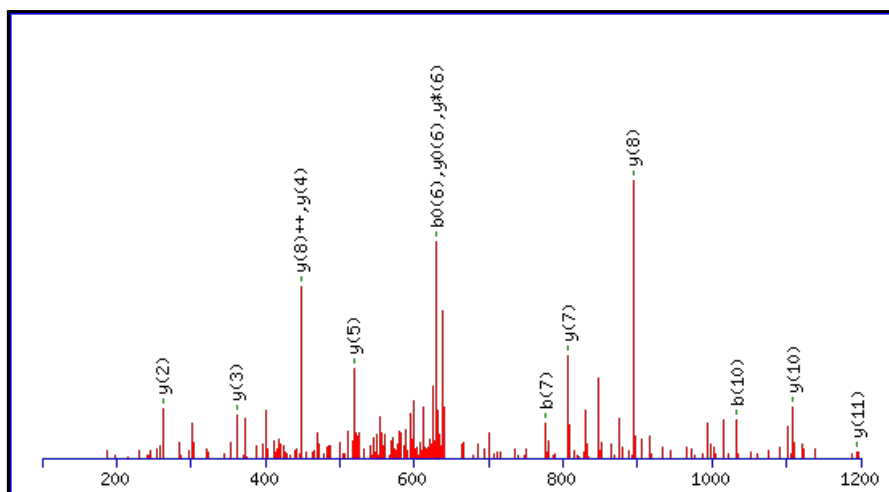
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1293.5983

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

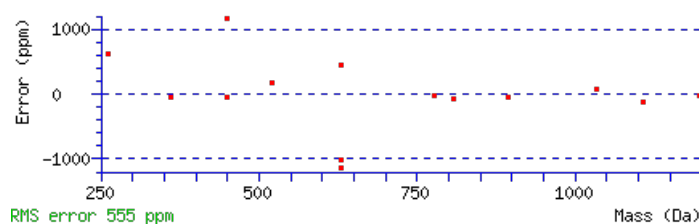
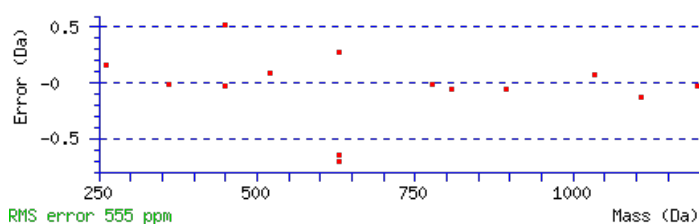
Variable modifications:

N3 : Deamidated (NQ)

Ions Score: 85 Expect: 1.4e-007

Matches : 14/124 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							12
2	187.1077	94.0575			169.0972	85.0522	S	1195.5372	598.2722	1178.5106	589.7590	1177.5266	589.2669	11
3	302.1347	151.5710	285.1081	143.0577	284.1241	142.5657	N	1108.5051	554.7562	1091.4786	546.2429	1090.4946	545.7509	10
4	401.2031	201.1052	384.1765	192.5919	383.1925	192.0999	V	993.4782	497.2427	976.4517	488.7295	975.4676	488.2375	9
5	488.2351	244.6212	471.2086	236.1079	470.2245	235.6159	S	894.4098	447.7085	877.3832	439.1953	876.3992	438.7033	8
6	648.2658	324.6365	631.2392	316.1232	630.2552	315.6312	C	807.3778	404.1925	790.3512	395.6792	789.3672	395.1872	7
7	776.3243	388.6658	759.2978	380.1525	758.3138	379.6605	Q	647.3471	324.1772	630.3206	315.6639	629.3365	315.1719	6
8	847.3614	424.1844	830.3349	415.6711	829.3509	415.1791	A	519.2885	260.1479	502.2620	251.6346	501.2780	251.1426	5
9	934.3935	467.7004	917.3669	459.1871	916.3829	458.6951	S	448.2514	224.6293	431.2249	216.1161	430.2409	215.6241	4
10	1033.4619	517.2346	1016.4353	508.7213	1015.4513	508.2293	V	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
11	1120.4939	560.7506	1103.4674	552.2373	1102.4833	551.7453	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [VSNVSCQASVSR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
84.8	1293.5983	-0.0019	VSNVSCQASVSR	Deamidated N3 99.95%
51.5	1293.5983	-0.0019	VSNVSCQASVSR	Deamidated Q7 0.05%
10.5	1293.5990	-0.0026	GQPADVFPGYSR	
8.8	1293.6023	-0.0060	WTLNGSLCGTGK	
7.7	1293.5884	0.0080	SSCLYRQHSR	
7.5	1293.5983	-0.0019	RMGESDDSilR	
5.6	1292.5957	1.0007	SVAAASGSGASGTDK	
5.5	1292.5965	0.9999	NRDMKEALCR	
5.2	1291.5892	2.0072	SSSVSQNQSPKR	
4.4	1293.5950	0.0014	GPGSESSGGLGFSR	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F2Z5E2** in **uni_pig**, tr|F2Z5E2|F2Z5E2_PIG Uncharacterized protein OS=Sus scrofa GN=SERPINC1 PE=3 SV=1

Title: 120325_Sunil_PigSerum_Glyco_D_14Spectrum3808_scans__4468

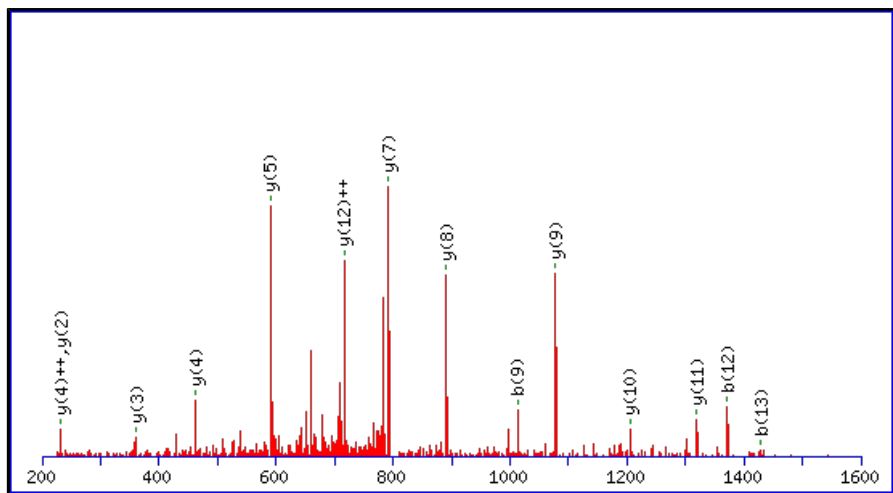
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

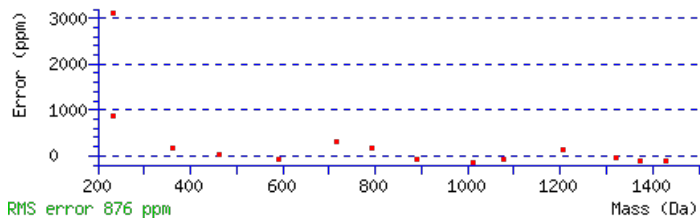
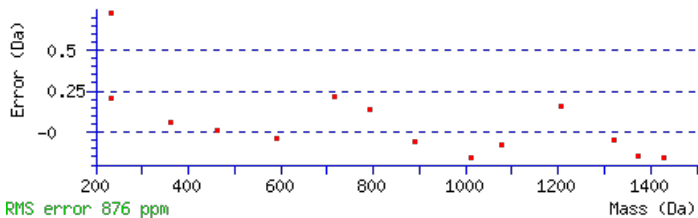
Variable modifications:

N9 : Deamidated (NQ)

Ions Score: 87 Expect: 1.4e-007

Matches : 14/132 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							14
2	171.1128	86.0600					I	1545.8020	773.4046	1528.7754	764.8914	1527.7914	764.3993	13
3	284.1969	142.6021					I	1432.7179	716.8626	1415.6914	708.3493	1414.7074	707.8573	12
4	398.2398	199.6235	381.2132	191.1103			N	1319.6339	660.3206	1302.6073	651.8073	1301.6233	651.3153	11
5	526.2984	263.6528	509.2718	255.1396			Q	1205.5909	603.2991	1188.5644	594.7858	1187.5804	594.2938	10
6	712.3777	356.6925	695.3511	348.1792			W	1077.5323	539.2698	1060.5058	530.7565	1059.5218	530.2645	9
7	811.4461	406.2267	794.4196	397.7134			V	891.4530	446.2302	874.4265	437.7169	873.4425	437.2249	8
8	898.4781	449.7427	881.4516	441.2294	880.4676	440.7374	S	792.3846	396.6959	775.3581	388.1827	774.3741	387.6907	7
9	1013.5051	507.2562	996.4785	498.7429	995.4945	498.2509	N	705.3526	353.1799	688.3260	344.6667	687.3420	344.1747	6
10	1141.6000	571.3037	1124.5735	562.7904	1123.5895	562.2984	K	590.3257	295.6665	573.2991	287.1532	572.3151	286.6612	5
11	1242.6477	621.8275	1225.6212	613.3142	1224.6371	612.8222	T	462.2307	231.6190	445.2041	223.1057	444.2201	222.6137	4
12	1371.6903	686.3488	1354.6638	677.8355	1353.6797	677.3435	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
13	1428.7118	714.8595	1411.6852	706.3462	1410.7012	705.8542	G	232.1404	116.5738	215.1139	108.0606			2
14							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [GIINQWVSNKTEGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
87.5	1601.8161	-0.0056	GIINQWVSNKTEGR	Deamidated N9 100.00%
42.1	1601.8161	-0.0056	GIINQWVSNKTEGR	Deamidated Q5 0.00%
29.3	1601.8161	-0.0056	GIINQWVSNKTEGR	Deamidated N4 0.00%
8.0	1601.8249	-0.0144	KHMQTHKVWPPGR	
3.4	1601.8049	0.0056	TLHNLVIQYASQGR	
2.0	1601.8137	-0.0032	KWVLTVAHCFEGR	
1.5	1601.8135	-0.0030	HPARSRSEHPSVR	
1.1	1599.7926	2.0179	SSGSSLALRSMFTEK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSSLCALCIGSER**

Found in **B3CL06** in **uni_pig**, tr|B3CL06|B3CL06_PIG Serotransferrin OS=Sus scrofa GN=TF PE=3 SV=1

Match to Query 4128: 1466.646588 from(734.330570,2+) intensity(25839.4316) rtinseconds(1858) scans(3255) index(9858)

Title: 120326_Sunil_PigSerum_Glyco_PsetB_09Spectrum2336_scans__3255

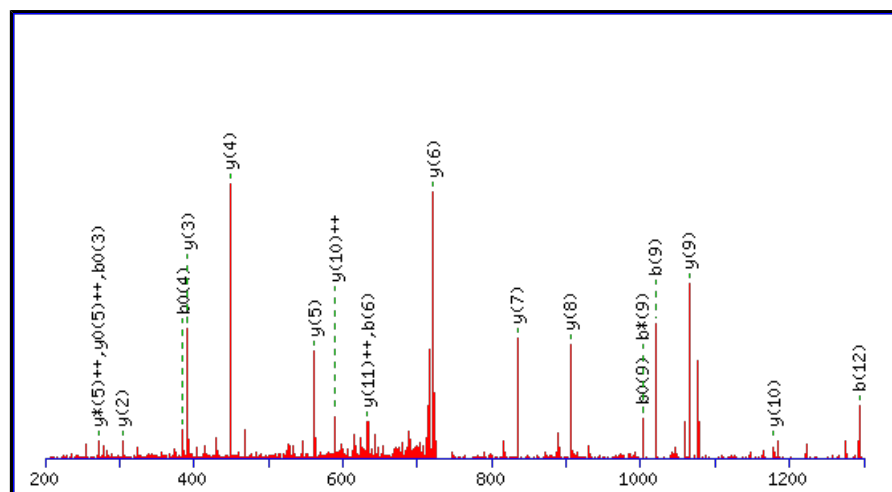
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1466.6493

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

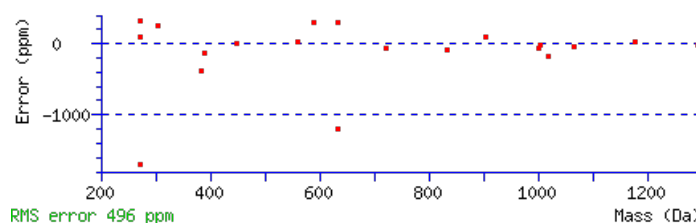
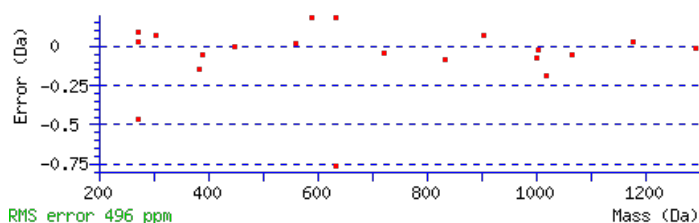
Variable modifications:

N1 : Deamidated (NQ)

Ions Score: 83 Expect: 1.5e-007

Matches : 20/140 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							13
2	203.0662	102.0368	186.0397	93.5235	185.0557	93.0315	S	1352.6297	676.8185	1335.6031	668.3052	1334.6191	667.8132	12
3	290.0983	145.5528	273.0717	137.0395	272.0877	136.5475	S	1265.5977	633.3025	1248.5711	624.7892	1247.5871	624.2972	11
4	403.1823	202.0948	386.1558	193.5815	385.1718	193.0895	L	1178.5656	589.7865	1161.5391	581.2732	1160.5551	580.7812	10
5	563.2130	282.1101	546.1864	273.5969	545.2024	273.1048	C	1065.4816	533.2444	1048.4550	524.7312	1047.4710	524.2391	9
6	634.2501	317.6287	617.2236	309.1154	616.2395	308.6234	A	905.4509	453.2291	888.4244	444.7158	887.4404	444.2238	8
7	747.3342	374.1707	730.3076	365.6574	729.3236	365.1654	L	834.4138	417.7105	817.3873	409.1973	816.4032	408.7053	7
8	907.3648	454.1860	890.3383	445.6728	889.3543	445.1808	C	721.3298	361.1685	704.3032	352.6552	703.3192	352.1632	6
9	1020.4489	510.7281	1003.4223	502.2148	1002.4383	501.7228	I	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	5
10	1077.4703	539.2388	1060.4438	530.7255	1059.4598	530.2335	G	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4
11	1164.5024	582.7548	1147.4758	574.2415	1146.4918	573.7495	S	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
12	1293.5450	647.2761	1276.5184	638.7628	1275.5344	638.2708	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
13							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [NSSLCALCIGSER](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
82.8	1466.6493	-0.0027	NSSLCALCIGSER
10.0	1466.6428	0.0038	LCDMRASALCDR
8.5	1465.6354	1.0112	SNSIQQMEQLNR
6.7	1465.6354	1.0112	SNSIQQMEQLNR
4.6	1465.6354	1.0112	SNSIQQMEQLNR
4.1	1466.6494	-0.0028	TITNNMLCAGDTR
3.2	1466.6429	0.0037	DCTVPLCRMGSR
2.1	1466.6559	-0.0093	DQTNILMDRTNK
1.3	1466.6494	-0.0028	TITNNMLCAGDTR
0.2	1465.6354	1.0112	SNSIQQMEQLNR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSNLTGISDQR**

Found in **F1RKY2** in **uni_pig**, tr|F1RKY2|F1RKY2_PIG Uncharacterized protein OS=Sus scrofa GN=SERPIND1 PE=3 SV=1

Match to Query 1635: 1205.550428 from(603.782490,2+) intensity(12986.3613) rtinseconds(1288) scans(2549) index(8603)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_15Spectrum2045_scans__2549

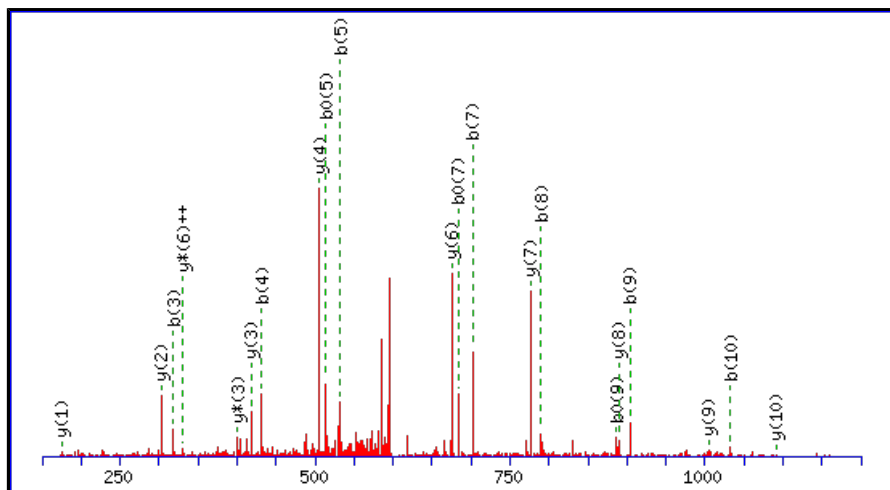
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1205.5524

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

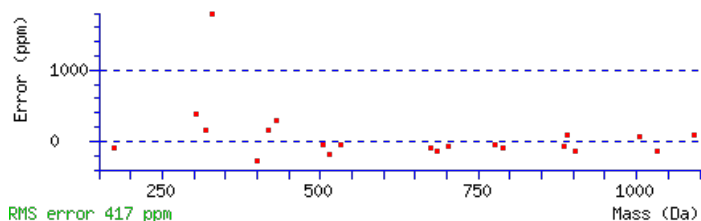
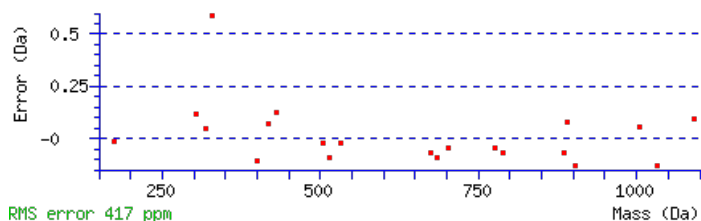
N1 : Deamidated (NQ)

N3 : Deamidated (NQ)

Ions Score: 83 Expect: 1.6e-007

Matches : 21/114 fragment ions using 30 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							11
2	203.0662	102.0368	186.0397	93.5235	185.0557	93.0315	S	1091.5327	546.2700	1074.5062	537.7567	1073.5222	537.2647	10
3	318.0932	159.5502	301.0666	151.0370	300.0826	150.5450	N	1004.5007	502.7540	987.4742	494.2407	986.4902	493.7487	9
4	431.1773	216.0923	414.1507	207.5790	413.1667	207.0870	L	889.4738	445.2405	872.4472	436.7272	871.4632	436.2352	8
5	532.2249	266.6161	515.1984	258.1028	514.2144	257.6108	T	776.3897	388.6985	759.3632	380.1852	758.3791	379.6932	7
6	589.2464	295.1268	572.2198	286.6136	571.2358	286.1216	G	675.3420	338.1747	658.3155	329.6614	657.3315	329.1694	6
7	702.3305	351.6689	685.3039	343.1556	684.3199	342.6636	I	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	5
8	789.3625	395.1849	772.3359	386.6716	771.3519	386.1796	S	505.2365	253.1219	488.2100	244.6086	487.2259	244.1166	4
9	904.3894	452.6984	887.3629	444.1851	886.3789	443.6931	D	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
10	1032.4480	516.7276	1015.4215	508.2144	1014.4374	507.7224	Q	303.1775	152.0924	286.1510	143.5791			2
11							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [NSNLTGISDOR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
83.2	1205.5524	-0.0020	NSNLTGISDQR	Deamidated N1, N3 100.00%
20.6	1205.5524	-0.0019	SNNITDSLNR	
14.3	1205.5524	-0.0020	NSNLTGISDQR	Deamidated N1, Q10 0.00%
12.4	1205.5537	-0.0033	NTRGSWSNER	
11.6	1205.5499	0.0005	ADMPAAPSQR	
11.6	1205.5524	-0.0020	QDVDTESQKR	
7.5	1205.5524	-0.0020	NSNLTGISDQR	Deamidated N3, Q10 0.00%
7.1	1203.5520	1.9984	LSDAAEEGAWR	
6.6	1205.5411	0.0093	DSNTQIEQLR	
6.1	1205.5564	-0.0060	VYELGNEPER	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

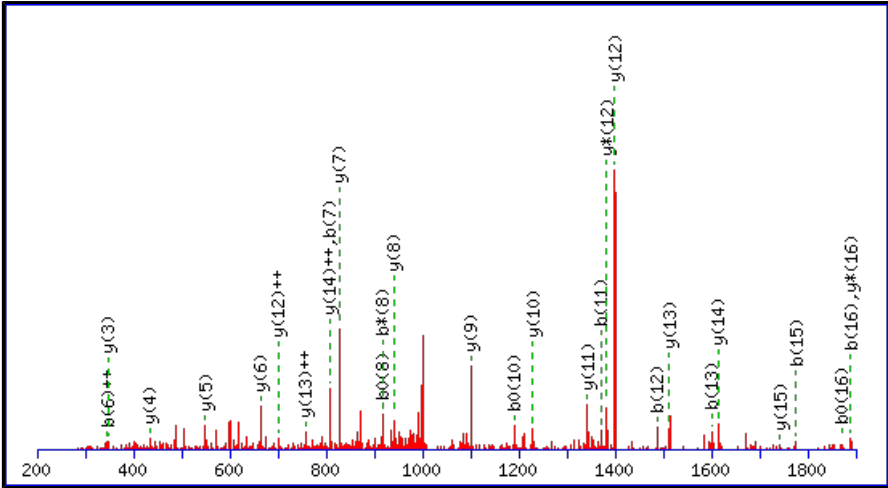
Peptide View

MS/MS Fragmentation of **EYQTIGNQCIYNDSSLK**
Found in **F1SN68** in **uni_pig**, tr|F1SN68|F1SN68_PIG Alpha-1-acid glycoprotein OS=Sus scrofa GN=ORM1 PE=3 SV=1

Match to Query 11353: 2033.879148 from(1017.946850,2+) intensity(9431.9111) rtinseconds(1861) scans(3679) index(13816)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_18Spectrum2616_scans__3679
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

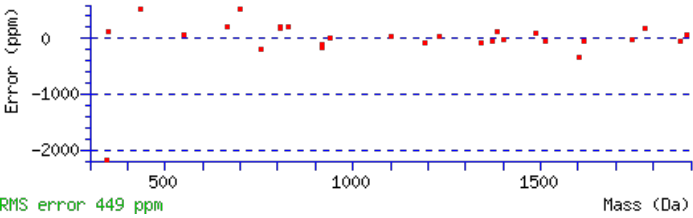
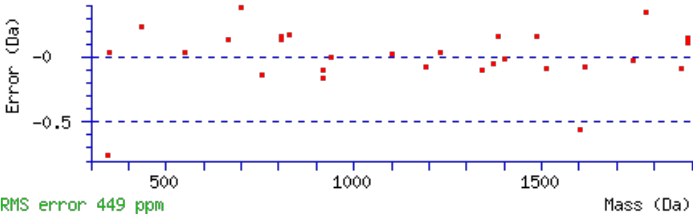
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2033.8888
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N12 : Deamidated (NQ)
Ions Score: 81 Expect: 1.8e-007
Matches : 29/184 fragment ions using 51 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	293.1132	147.0602			275.1026	138.0550	Y	1905.8535	953.4304	1888.8269	944.9171	1887.8429	944.4251	16
3	422.1558	211.5815	405.1292	203.0683	404.1452	202.5763	Q	1742.7902	871.8987	1725.7636	863.3854	1724.7796	862.8934	15
4	523.2035	262.1054	506.1769	253.5921	505.1929	253.1001	T	1613.7476	807.3774	1596.7210	798.8641	1595.7370	798.3721	14
5	636.2875	318.6474	619.2610	310.1341	618.2770	309.6421	I	1512.6999	756.8536	1495.6733	748.3403	1494.6893	747.8483	13
6	693.3090	347.1581	676.2825	338.6449	675.2984	338.1529	G	1399.6158	700.3115	1382.5893	691.7983	1381.6053	691.3063	12
7	807.3519	404.1796	790.3254	395.6663	789.3414	395.1743	N	1342.5944	671.8008	1325.5678	663.2875	1324.5838	662.7955	11
8	935.4105	468.2089	918.3840	459.6956	917.3999	459.2036	Q	1228.5514	614.7794	1211.5249	606.2661	1210.5409	605.7741	10
9	1095.4412	548.2242	1078.4146	539.7109	1077.4306	539.2189	C	1100.4929	550.7501	1083.4663	542.2368	1082.4823	541.7448	9
10	1208.5252	604.7662	1191.4987	596.2530	1190.5147	595.7610	I	940.4622	470.7347	923.4357	462.2215	922.4516	461.7295	8
11	1371.5885	686.2979	1354.5620	677.7846	1353.5780	677.2926	Y	827.3781	414.1927	810.3516	405.6794	809.3676	405.1874	7
12	1486.6155	743.8114	1469.5889	735.2981	1468.6049	734.8061	N	664.3148	332.6610	647.2883	324.1478	646.3042	323.6558	6
13	1601.6424	801.3249	1584.6159	792.8116	1583.6319	792.3196	D	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
14	1688.6745	844.8409	1671.6479	836.3276	1670.6639	835.8356	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
15	1775.7065	888.3569	1758.6799	879.8436	1757.6959	879.3516	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
16	1888.7906	944.8989	1871.7640	936.3856	1870.7800	935.8936	L	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EYQTIGNQCIYNDSSLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
81.0	2033.8888	-0.0096	EYQTIGNQCIYNDSSLK	Deamidated Q3, N12 81.31%
71.6	2033.8888	-0.0096	EYQTIGNQCIYNDSSLK	Deamidated N7, N12 9.36%
71.6	2033.8888	-0.0096	EYQTIGNQCIYNDSSLK	Deamidated Q8, N12 9.34%
32.6	2033.8888	-0.0096	EYQTIGNQCIYNDSSLK	Deamidated Q3, Q8 0.00%
30.9	2033.8888	-0.0096	EYQTIGNQCIYNDSSLK	Deamidated N7, Q8 0.00%
25.1	2033.8888	-0.0096	EYQTIGNQCIYNDSSLK	Deamidated Q3, N7 0.00%
0.9	2033.8960	-0.0169	DGSGEQPRGGGPTSSEQIMK	

Mascot: <http://www.matrixscience.com/>

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Mascot Search Results

Peptide View

MS/MS Fragmentation of **VETSDVGNYTCVVTSTVTNAR**
Found in **F1SFM5** in **uni_pig**, tr[F1SFM5]F1SFM5_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=CNTN3 PE=4 SV=2

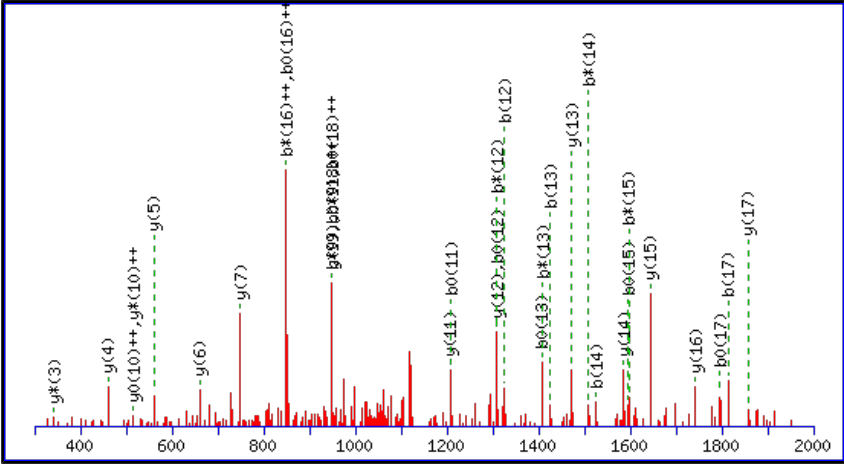
Match to Query 12667: 2274.035328 from(1138.024940,2+) intensity(1964.4222) rtinseconds(2100) scans(4945) index(8508)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_14Spectrum4238_scans_4945
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

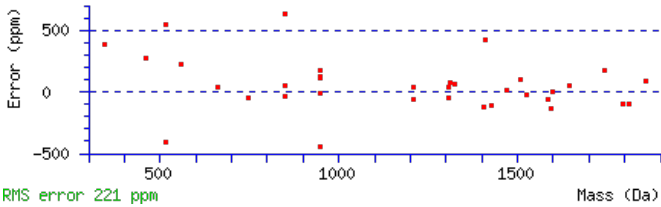
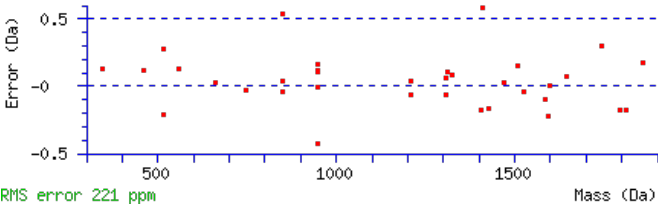
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2273.0482
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 84 Expect: 2e-007
Matches : 35/218 fragment ions using 49 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							21
2	229.1183	115.0628			211.1077	106.0575	E	2174.9870	1087.9971	2157.9605	1079.4839	2156.9765	1078.9919	20
3	330.1660	165.5866			312.1554	156.5813	T	2045.9444	1023.4759	2028.9179	1014.9626	2027.9339	1014.4706	19
4	417.1980	209.1026			399.1874	200.0974	S	1944.8967	972.9520	1927.8702	964.4387	1926.8862	963.9467	18
5	532.2249	266.6161			514.2144	257.6108	D	1857.8647	929.4360	1840.8382	920.9227	1839.8542	920.4307	17
6	631.2933	316.1503			613.2828	307.1450	V	1742.8378	871.9225	1725.8112	863.4093	1724.8272	862.9172	16
7	688.3148	344.6610			670.3042	335.6558	G	1643.7694	822.3883	1626.7428	813.8750	1625.7588	813.3830	15
8	803.3418	402.1745	786.3152	393.6612	785.3312	393.1692	N	1586.7479	793.8776	1569.7214	785.3643	1568.7373	784.8723	14
9	966.4051	483.7062	949.3785	475.1929	948.3945	474.7009	Y	1471.7210	736.3641	1454.6944	727.8508	1453.7104	727.3588	13
10	1067.4528	534.2300	1050.4262	525.7167	1049.4422	525.2247	T	1308.6576	654.8325	1291.6311	646.3192	1290.6471	645.8272	12
11	1227.4834	614.2453	1210.4569	605.7321	1209.4728	605.2401	C	1207.6099	604.3086	1190.5834	595.7953	1189.5994	595.3033	11
12	1326.5518	663.7796	1309.5253	655.2663	1308.5413	654.7743	V	1047.5793	524.2933	1030.5528	515.7800	1029.5687	515.2880	10
13	1425.6202	713.3138	1408.5937	704.8005	1407.6097	704.3085	V	948.5109	474.7591	931.4843	466.2458	930.5003	465.7538	9
14	1526.6679	763.8376	1509.6414	755.3243	1508.6574	754.8323	T	849.4425	425.2249	832.4159	416.7116	831.4319	416.2196	8
15	1613.6999	807.3536	1596.6734	798.8403	1595.6894	798.3483	S	748.3948	374.7010	731.3682	366.1878	730.3842	365.6958	7
16	1714.7476	857.8775	1697.7211	849.3642	1696.7371	848.8722	T	661.3628	331.1850	644.3362	322.6717	643.3522	322.1797	6
17	1813.8160	907.4117	1796.7895	898.8984	1795.8055	898.4064	V	560.3151	280.6612	543.2885	272.1479	542.3045	271.6559	5
18	1914.8637	957.9355	1897.8372	949.4222	1896.8532	948.9302	T	461.2467	231.1270	444.2201	222.6137	443.2361	222.1217	4
19	2028.9066	1014.9570	2011.8801	1006.4437	2010.8961	1005.9517	N	360.1990	180.6031	343.1724	172.0899			3
20	2099.9438	1050.4755	2082.9172	1041.9622	2081.9332	1041.4702	A	246.1561	123.5817	229.1295	115.0684			2
21							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [VETSDVGNYTCVVTSTVTNAR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
84.4	2273.0482	0.9871	VETSDVGNYTCVVTSTVTNAR	Deamidated N8 100.00%
42.9	2274.0322	0.0031	VETSDVGNYTCVVTSTVTNAR	
32.3	2273.0482	0.9871	VETSDVGNYTCVVTSTVTNAR	Deamidated N19 0.00%
3.5	2273.0369	0.9984	DTQDALAVVIEVANHANDTMK	
1.4	2273.0520	0.9834	DPEEGRQASGVEQSNGLGKSAR	
1.4	2273.0520	0.9834	DPEEGRQASGVEQSNGLGKSAR	
0.3	2274.0521	-0.0168	QQPTCPHELTRNYIVMNR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

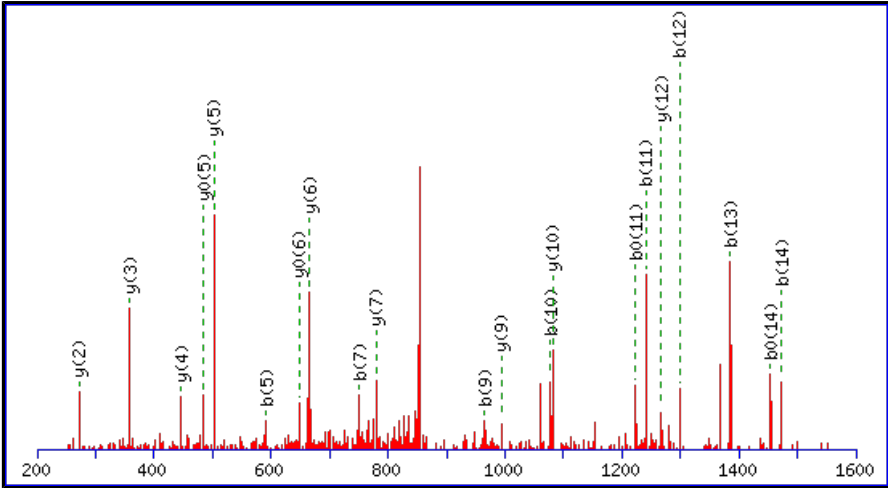
Peptide View

MS/MS Fragmentation of **DTFLNASQSLYGSSPR**
Found in **F1SJW8** in **uni_pig**, tr|F1SJW8|F1SJW8_PIG Uncharacterized protein OS=Sus scrofa GN=SERPING1 PE=3 SV=1

Match to Query 5887: 1742.806068 from(872.410310,2+) intensity(12005.4434) rtinseconds(2092) scans(4358) index(8955)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_16Spectrum3344_scans__4358
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

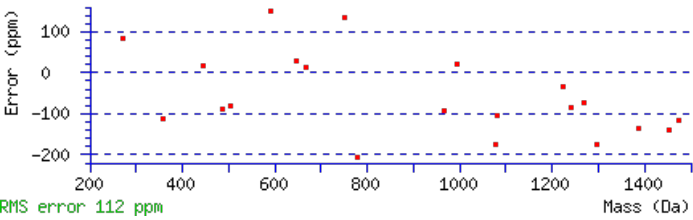
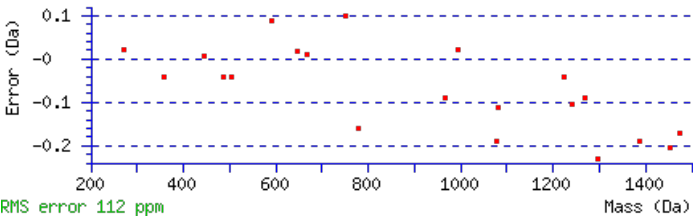
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1742.8111
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 84 Expect: 2.1e-007
Matches : 21/168 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							16
2	217.0819	109.0446			199.0713	100.0393	T	1628.7915	814.8994	1611.7649	806.3861	1610.7809	805.8941	15
3	364.1503	182.5788			346.1397	173.5735	F	1527.7438	764.3755	1510.7172	755.8623	1509.7332	755.3703	14
4	477.2344	239.1208			459.2238	230.1155	L	1380.6754	690.8413	1363.6488	682.3281	1362.6648	681.8360	13
5	592.2613	296.6343	575.2348	288.1210	574.2508	287.6290	N	1267.5913	634.2993	1250.5648	625.7860	1249.5808	625.2940	12
6	663.2984	332.1529	646.2719	323.6396	645.2879	323.1476	A	1152.5644	576.7858	1135.5378	568.2726	1134.5538	567.7805	11
7	750.3305	375.6689	733.3039	367.1556	732.3199	366.6636	S	1081.5273	541.2673	1064.5007	532.7540	1063.5167	532.2620	10
8	878.3890	439.6982	861.3625	431.1849	860.3785	430.6929	Q	994.4952	497.7513	977.4687	489.2380	976.4847	488.7460	9
9	965.4211	483.2142	948.3945	474.7009	947.4105	474.2089	S	866.4367	433.7220	849.4101	425.2087	848.4261	424.7167	8
10	1078.5051	539.7562	1061.4786	531.2429	1060.4946	530.7509	L	779.4046	390.2060	762.3781	381.6927	761.3941	381.2007	7
11	1241.5685	621.2879	1224.5419	612.7746	1223.5579	612.2826	Y	666.3206	333.6639	649.2940	325.1506	648.3100	324.6586	6
12	1298.5899	649.7986	1281.5634	641.2853	1280.5794	640.7933	G	503.2572	252.1323	486.2307	243.6190	485.2467	243.1270	5
13	1385.6220	693.3146	1368.5954	684.8013	1367.6114	684.3093	S	446.2358	223.6215	429.2092	215.1082	428.2252	214.6162	4
14	1472.6540	736.8306	1455.6274	728.3174	1454.6434	727.8253	S	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
15	1569.7067	785.3570	1552.6802	776.8437	1551.6962	776.3517	P	272.1717	136.5895	255.1452	128.0762			2
16							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [DTFLNASQSLYGSSPR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
83.7	1742.8111	-0.0051	DTFLNASQSLYGSSPR	Deamidated N5 99.98%
46.2	1742.8111	-0.0051	DTFLNASQSLYGSSPR	Deamidated Q8 0.02%
4.0	1742.8111	-0.0050	LFENYQTQSEEARK	
3.9	1742.8086	-0.0026	NHVCQYYIYDLQK	
3.6	1742.8046	0.0015	RDSNPHPSCLPTFSK	
0.5	1740.8027	2.0034	EAASHKVEDEAQRDR	

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNQNFSAVNNER**

Found in **F1SCV8** in **uni_pig**, tr|F1SCV8|F1SCV8_PIG Uncharacterized protein (Fragment) OS=Sus scrofa PE=4 SV=2

Match to Query 3991: 1455.635368 from(728.824960,2+) intensity(12713.2959) rtinseconds(1228) scans(2677) index(6187)

Title: 120325_Sunil_PigSerum_Glyco_S_14Spectrum2169_scans_2677

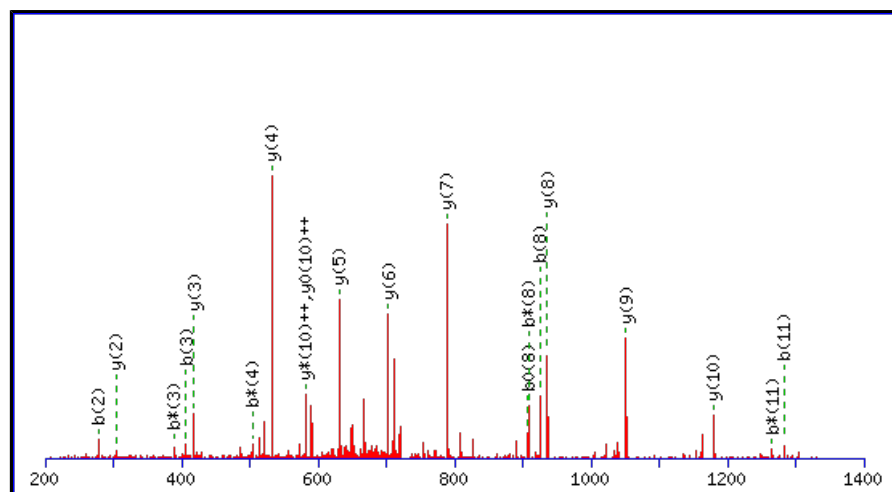
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1455.6378

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

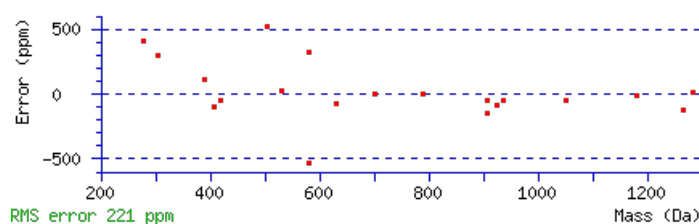
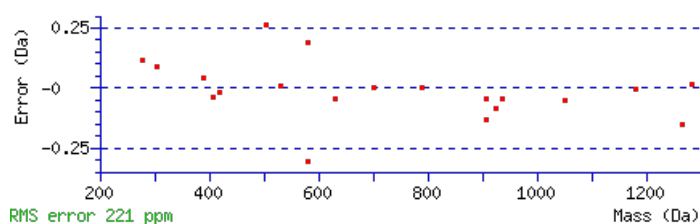
Variable modifications:

N4 : Deamidated (NQ)

Ions Score: 80 Expect: 2.7e-007

Matches : 20/118 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							12
2	278.1135	139.5604	261.0870	131.0471			N	1293.5818	647.2945	1276.5553	638.7813	1275.5713	638.2893	11
3	406.1721	203.5897	389.1456	195.0764			Q	1179.5389	590.2731	1162.5123	581.7598	1161.5283	581.2678	10
4	521.1991	261.1032	504.1725	252.5899			N	1051.4803	526.2438	1034.4538	517.7305	1033.4697	517.2385	9
5	668.2675	334.6374	651.2409	326.1241			F	936.4534	468.7303	919.4268	460.2170	918.4428	459.7250	8
6	755.2995	378.1534	738.2729	369.6401	737.2889	369.1481	S	789.3850	395.1961	772.3584	386.6828	771.3744	386.1908	7
7	826.3366	413.6719	809.3101	405.1587	808.3260	404.6667	A	702.3529	351.6801	685.3264	343.1668	684.3424	342.6748	6
8	925.4050	463.2061	908.3785	454.6929	907.3945	454.2009	V	631.3158	316.1615	614.2893	307.6483	613.3052	307.1563	5
9	1039.4480	520.2276	1022.4214	511.7143	1021.4374	511.2223	N	532.2474	266.6273	515.2209	258.1141	514.2368	257.6221	4
10	1153.4909	577.2491	1136.4643	568.7358	1135.4803	568.2438	N	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
11	1282.5335	641.7704	1265.5069	633.2571	1264.5229	632.7651	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [YNQNFSAVNNR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
79.8	1455.6378	-0.0025	YNQNFSAVNNER	Deamidated N4 99.12%
59.1	1455.6378	-0.0025	YNQNFSAVNNER	Deamidated Q3 0.84%
43.9	1455.6378	-0.0025	YNQNFSAVNNER	Deamidated N2 0.03%
36.9	1455.6378	-0.0025	YNQNFSAVNNER	Deamidated N9 0.01%
26.8	1455.6378	-0.0025	YNQNFSAVNNER	Deamidated N10 0.00%
2.2	1455.6448	-0.0094	MLDMGFEPQIMK	
1.8	1453.6368	1.9986	DQNAGEERSMQR	
1.6	1453.6242	2.0112	KMNDLDNEDSKK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNGTTYQNDIALIEMK**
Found in **F1S133** in **uni_pig**, tr|F1S133|F1S133_PIG Uncharacterized protein OS=Sus scrofa GN=CFI PE=3 SV=2

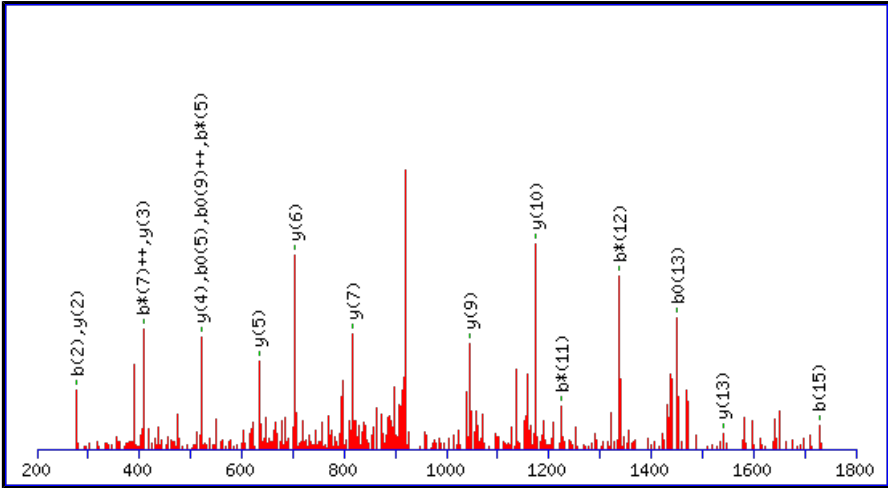
Match to Query 7518: 1873.873608 from(937.944080,2+) intensity(3746.5347) rtinseconds(2532) scans(5690) index(13023)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_13Spectrum4690_scans__5690
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

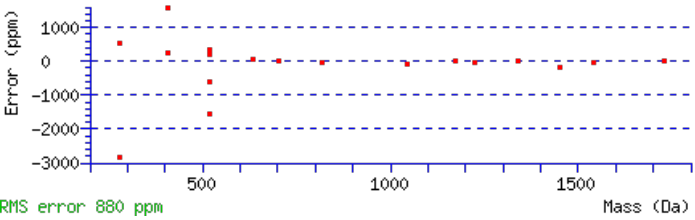
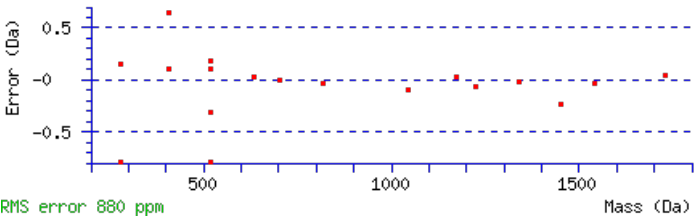
☐ Label all possible matches ☐ Label matches used for scoring

☐ Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1873.8767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Ions Score: 83 Expect: 2.8e-007
Matches : 18/168 fragment ions using 15 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							16
2	279.0975	140.0524	262.0710	131.5391			N	1711.8207	856.4140	1694.7942	847.9007	1693.8102	847.4087	15
3	336.1190	168.5631	319.0925	160.0499			G	1596.7938	798.9005	1579.7672	790.3873	1578.7832	789.8952	14
4	437.1667	219.0870	420.1401	210.5737	419.1561	210.0817	T	1539.7723	770.3898	1522.7458	761.8765	1521.7618	761.3845	13
5	538.2144	269.6108	521.1878	261.0975	520.2038	260.6055	T	1438.7246	719.8660	1421.6981	711.3527	1420.7141	710.8607	12
6	701.2777	351.1425	684.2511	342.6292	683.2671	342.1372	Y	1337.6770	669.3421	1320.6504	660.8288	1319.6664	660.3368	11
7	829.3363	415.1718	812.3097	406.6585	811.3257	406.1665	Q	1174.6136	587.8105	1157.5871	579.2972	1156.6031	578.8052	10
8	943.3792	472.1932	926.3527	463.6800	925.3686	463.1880	N	1046.5551	523.7812	1029.5285	515.2679	1028.5445	514.7759	9
9	1058.4061	529.7067	1041.3796	521.1934	1040.3956	520.7014	D	932.5121	466.7597	915.4856	458.2464	914.5016	457.7544	8
10	1171.4902	586.2487	1154.4637	577.7355	1153.4796	577.2435	I	817.4852	409.2462	800.4586	400.7330	799.4746	400.2409	7
11	1242.5273	621.7673	1225.5008	613.2540	1224.5168	612.7620	A	704.4011	352.7042	687.3746	344.1909	686.3906	343.6989	6
12	1355.6114	678.3093	1338.5848	669.7961	1337.6008	669.3040	L	633.3640	317.1856	616.3375	308.6724	615.3534	308.1804	5
13	1468.6955	734.8514	1451.6689	726.3381	1450.6849	725.8461	I	520.2799	260.6436	503.2534	252.1303	502.2694	251.6383	4
14	1597.7380	799.3727	1580.7115	790.8594	1579.7275	790.3674	E	407.1959	204.1016	390.1693	195.5883	389.1853	195.0963	3
15	1728.7785	864.8929	1711.7520	856.3796	1710.7680	855.8876	M	278.1533	139.5803	261.1267	131.0670			2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [YNGTTYQNDIALIEMK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
83.2	1873.8767	-0.0031	YNGTTYQNDIALIEMK	Deamidated N2 98.97%
61.7	1873.8767	-0.0031	YNGTTYQNDIALIEMK	Deamidated Q7 0.70%
58.5	1873.8767	-0.0031	YNGTTYQNDIALIEMK	Deamidated N8 0.34%
5.6	1871.8831	1.9905	LLQETLYMCVAIMDR	
3.2	1873.8653	0.0083	SQNDEENTQETPQVKK	
2.6	1873.8767	-0.0031	EMLDAIQQQWPELEK	
2.6	1873.8767	-0.0031	EMLDAIQQQWPELEK	
2.1	1873.8767	-0.0031	EMLDAIQQQWPELEK	
1.9	1871.8796	1.9940	TGAGMITQHTSNASPINR	
1.6	1871.8618	2.0119	FQEFSPNLWGLEFQK	

Mascot: <http://www.matrixscience.com/>

http:// MascotXP.student.main.ntu.edu.sg/Mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=4883 [22/Apr/15 05:59:24 PM]

NCBI **BLAST** search of [EENFYVNETATVK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
81.0	1543.7042	0.0131	EENFYVNETATVK	Deamidated N7 100.00%
34.1	1543.7042	0.0131	EENFYVNETATVK	Deamidated N3 0.00%
32.5	1542.7202	0.9971	EENFYVNETATVK	
13.5	1543.7228	-0.0055	KQNFYSEVMVPGK	
6.8	1542.7274	0.9899	NEKEGSESKHLQR	
4.7	1543.7262	-0.0089	GSTSGFLNIMMELK	
4.4	1543.7188	-0.0015	EEMKNHQEILK	
4.4	1543.7188	-0.0015	EEMKNHQEILK	
1.7	1542.7202	0.9971	QGSVQKVYNGLQGY	
0.7	1542.7202	0.9971	VQIFEYNENTRK	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1S3I1** in **uni_pig**, tr|F1S3I1|F1S3I1_PIG Uncharacterized protein OS=Sus scrofa GN=ANGPTL6 PE=4 SV=1

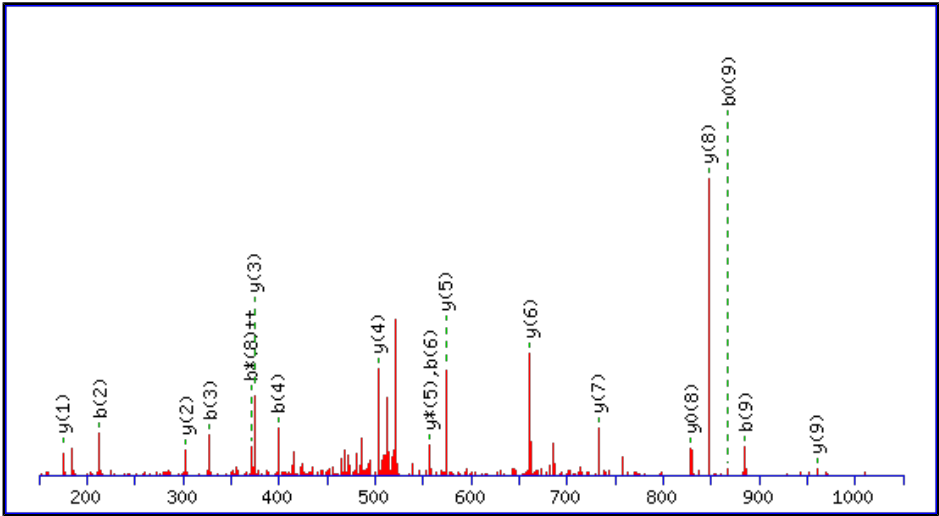
Title: 120326_Sunil_PigSerum_Glyco_PsetB_14Spectrum1048_scans__1466

W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Or, to Da

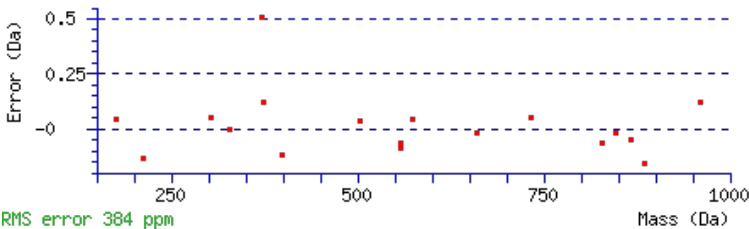
Label all possible matches Label matches used for scoring

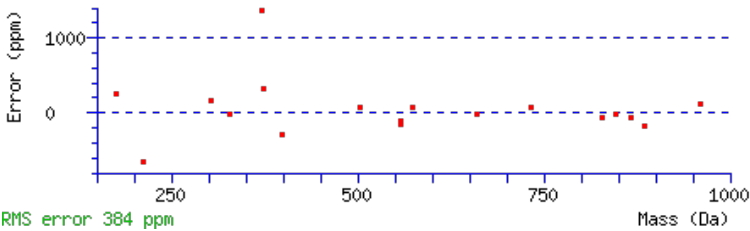
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1058.5356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
 N3 : Deamidated (NQ)
Ions Score: 81 **Expect:** 4e-007
Matches : 18/90 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							10
2	213.1598	107.0835					L	960.4745	480.7409	943.4480	472.2276	942.4639	471.7356	9
3	328.1867	164.5970	311.1601	156.0837			N	847.3904	424.1989	830.3639	415.6856	829.3799	415.1936	8
4	399.2238	200.1155	382.1973	191.6023			A	732.3635	366.6854	715.3369	358.1721	714.3529	357.6801	7
5	486.2558	243.6316	469.2293	235.1183	468.2453	234.6263	S	661.3264	331.1668	644.2998	322.6536	643.3158	322.1615	6
6	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	A	574.2944	287.6508	557.2678	279.1375	556.2838	278.6455	5
7	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	E	503.2572	252.1323	486.2307	243.6190	485.2467	243.1270	4
8	757.3727	379.1900	740.3461	370.6767	739.3621	370.1847	A	374.2146	187.6110	357.1881	179.0977			3
9	885.4312	443.2193	868.4047	434.7060	867.4207	434.2140	Q	303.1775	152.0924	286.1510	143.5791			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of [VLNASAEAAQR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
80.9	1058.5356	-0.0011	VLNASAEAAQR	Deamidated N3 100.00%
26.5	1058.5356	-0.0011	VLNASAEAAQR	Deamidated Q9 0.00%
10.7	1058.5430	-0.0085	VLPMQVQSR	
9.4	1056.5200	2.0145	SPTSSPTPQR	
9.3	1058.5396	-0.0051	LVWEQQVR	
9.3	1058.5356	-0.0011	NQEELLRR	
9.1	1056.5312	2.0033	QVAQQEAAQR	
8.5	1058.5244	0.0101	VLAELDDER	
8.5	1058.5356	-0.0011	VLEEEERQR	
8.5	1058.5365	-0.0020	VLMGNPCLR	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1SC20** in **uni_pig**, tr|F1SC20|F1SC20_PIG Alpha-1B-glycoprotein OS=Sus scrofa GN=A1BG PE=4 SV=1

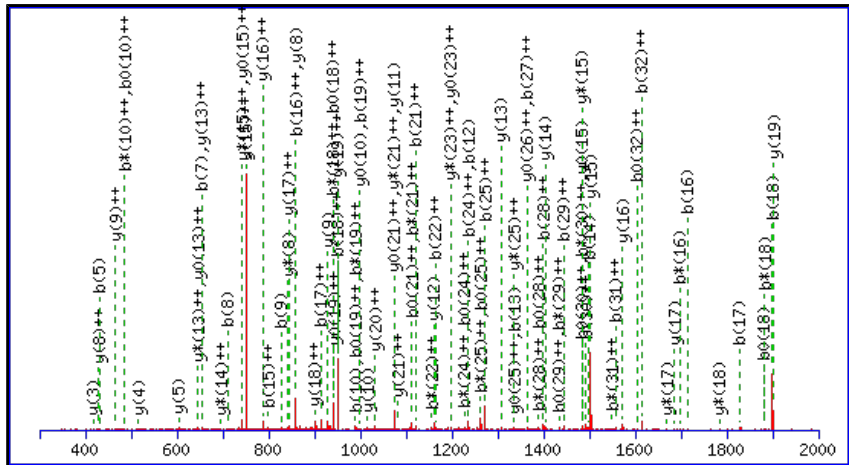
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

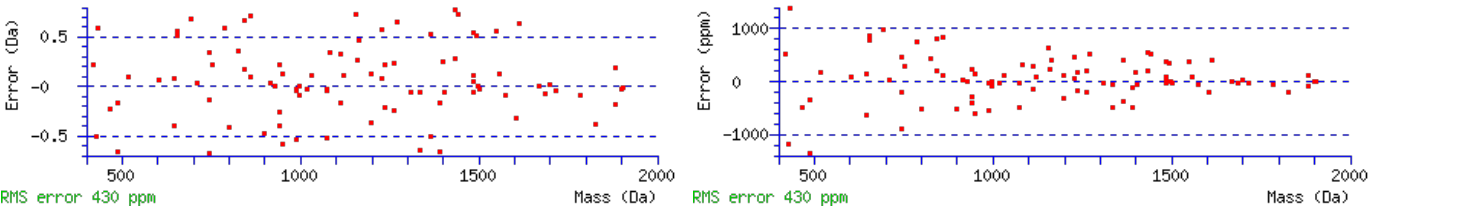
N9 : Deamidated (NQ)

Ions Score: 80 Expect: 4.1e-007

Matches : 94/364 fragment ions using 145 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							33
2	215.1026	108.0550			197.0921	99.0497	V	3284.5164	1642.7619	3267.4899	1634.2486	3266.5059	1633.7566	32
3	302.1347	151.5710			284.1241	142.5657	S	3185.4480	1593.2277	3168.4215	1584.7144	3167.4375	1584.2224	31
4	359.1561	180.0817			341.1456	171.0764	G	3098.4160	1549.7116	3081.3895	1541.1984	3080.4054	1540.7064	30
5	430.1932	215.6003			412.1827	206.5950	A	3041.3945	1521.2009	3024.3680	1512.6876	3023.3840	1512.1956	29
6	567.2522	284.1297			549.2416	275.1244	H	2970.3574	1485.6824	2953.3309	1477.1691	2952.3469	1476.6771	28
7	654.2842	327.6457			636.2736	318.6404	S	2833.2985	1417.1529	2816.2720	1408.6396	2815.2880	1408.1476	27
8	711.3056	356.1565			693.2951	347.1512	G	2746.2665	1373.6369	2729.2399	1365.1236	2728.2559	1364.6316	26
9	826.3326	413.6699	809.3060	405.1567	808.3220	404.6646	N	2689.2450	1345.1262	2672.2185	1336.6129	2671.2345	1336.1209	25
10	989.3959	495.2016	972.3694	486.6883	971.3854	486.1963	Y	2574.2181	1287.6127	2557.1915	1279.0994	2556.2075	1278.6074	24
11	1076.4279	538.7176	1059.4014	530.2043	1058.4174	529.7123	S	2411.1548	1206.0810	2394.1282	1197.5677	2393.1442	1197.0757	23
12	1236.4586	618.7329	1219.4320	610.2197	1218.4480	609.7277	C	2324.1227	1162.5650	2307.0962	1154.0517	2306.1122	1153.5597	22
13	1335.5270	668.2671	1318.5005	659.7539	1317.5164	659.2619	V	2164.0921	1082.5497	2147.0655	1074.0364	2146.0815	1073.5444	21
14	1498.5903	749.7988	1481.5638	741.2855	1480.5798	740.7935	Y	2065.0237	1033.0155	2047.9971	1024.5022	2047.0131	1024.0102	20
15	1599.6380	800.3226	1582.6115	791.8094	1581.6274	791.3174	T	1901.9603	951.4838	1884.9338	942.9705	1883.9498	942.4785	19
16	1714.6650	857.8361	1697.6384	849.3228	1696.6544	848.8308	D	1800.9127	900.9600	1783.8861	892.4467	1782.9021	891.9547	18
17	1827.7490	914.3781	1810.7225	905.8649	1809.7385	905.3729	L	1685.8857	843.4465	1668.8592	834.9332	1667.8751	834.4412	17
18	1898.7861	949.8967	1881.7596	941.3834	1880.7756	940.8914	A	1572.8016	786.9045	1555.7751	778.3912	1554.7911	777.8992	16
19	1995.8389	998.4231	1978.8124	989.9098	1977.8283	989.4178	P	1501.7645	751.3859	1484.7380	742.8726	1483.7540	742.3806	15
20	2092.8917	1046.9495	2075.8651	1038.4362	2074.8811	1037.9442	P	1404.7118	702.8595	1387.6852	694.3462	1386.7012	693.8542	14
21	2239.9601	1120.4837	2222.9335	1111.9704	2221.9495	1111.4784	F	1307.6590	654.3331	1290.6325	645.8199	1289.6484	645.3279	13
22	2326.9921	1163.9997	2309.9656	1155.4864	2308.9815	1154.9944	S	1160.5906	580.7989	1143.5640	572.2857	1142.5800	571.7937	12
23	2384.0136	1192.5104	2366.9870	1183.9971	2366.0030	1183.5051	G	1073.5586	537.2829	1056.5320	528.7696	1055.5480	528.2776	11
24	2471.0456	1236.0264	2454.0190	1227.5132	2453.0350	1227.0212	S	1016.5371	508.7722	999.5106	500.2589	998.5265	499.7669	10

25	2542.0827	1271.5450	2525.0562	1263.0317	2524.0721	1262.5397	A	929.5051	465.2562	912.4785	456.7429	911.4945	456.2509	9
26	2639.1355	1320.0714	2622.1089	1311.5581	2621.1249	1311.0661	P	858.4680	429.7376	841.4414	421.2243	840.4574	420.7323	8
27	2726.1675	1363.5874	2709.1410	1355.0741	2708.1569	1354.5821	S	761.4152	381.2112	744.3886	372.6980	743.4046	372.2060	7
28	2797.2046	1399.1059	2780.1781	1390.5927	2779.1941	1390.1007	A	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	6
29	2884.2366	1442.6220	2867.2101	1434.1087	2866.2261	1433.6167	S	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
30	2983.3051	1492.1562	2966.2785	1483.6429	2965.2945	1483.1509	V	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
31	3112.3477	1556.6775	3095.3211	1548.1642	3094.3371	1547.6722	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
32	3225.4317	1613.2195	3208.4052	1604.7062	3207.4212	1604.2142	L	288.2030	144.6051	271.1765	136.0919			2
33							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [DVSGAHSGNYSCVYTDLAPPFSGSAPSASVELR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
79.9	3398.5361	-0.0152	DVSGAHSGNYSCVYTDLAPPFSGSAPSASVELR
5.4	3396.5449	1.9760	LAEQAERYDDMASAMKAVTELNEPLSNEDR
5.1	3398.5030	0.0179	LEHPVMQDTPPRPQAQESNYENLSQMSPR
4.3	3397.5177	1.0032	EEDAASTLVTGSEYETMLTEITSMGYERER
3.9	3398.5228	-0.0019	NHMTSLNLDLQSQNVYHHGREGNRMNGSR
3.0	3398.5191	0.0018	CTNLNCSVIADVVRHDGSEPCVDVLEFGDGHR
3.0	3397.5191	1.0019	RENEDDDVHQRPLPPPTMLPMSNTFPSR
2.8	3398.5547	-0.0338	FCGATAKGLSFNSSANEMHVSFSSDFSQKK
2.4	3396.5319	1.9891	QMYGKADMNTEPNFTEEDPKFEAVEKPOS
2.4	3398.5433	-0.0224	ENSTFESINDAASHTSTMSSRHSASPVVETSAR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

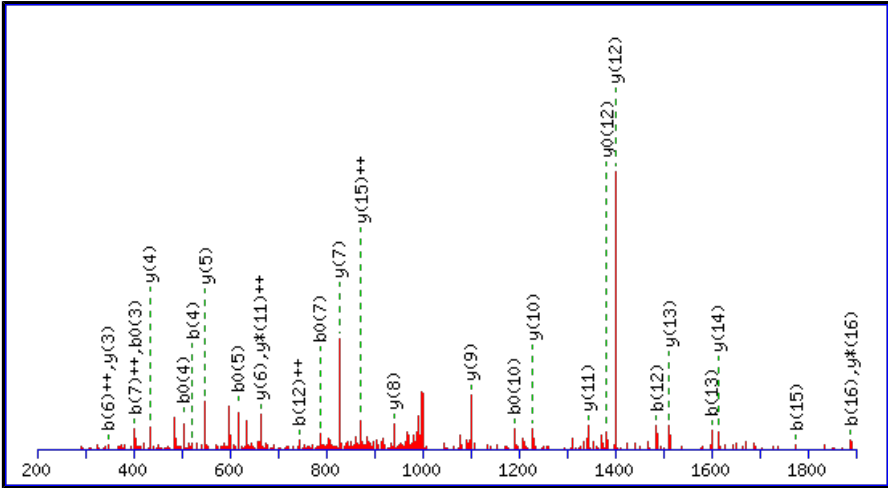
Peptide View

MS/MS Fragmentation of **EYQTIGNQCIYNDSSLK**
Found in **F1SN68** in **uni_pig**, tr|F1SN68|F1SN68_PIG Alpha-1-acid glycoprotein OS=Sus scrofa GN=ORM1 PE=3 SV=1

Match to Query 11372: 2033.880348 from(1017.947450,2+) intensity(12050.4043) rtinseconds(1812) scans(3593) index(13582)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_16Spectrum2499_scans__3593
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

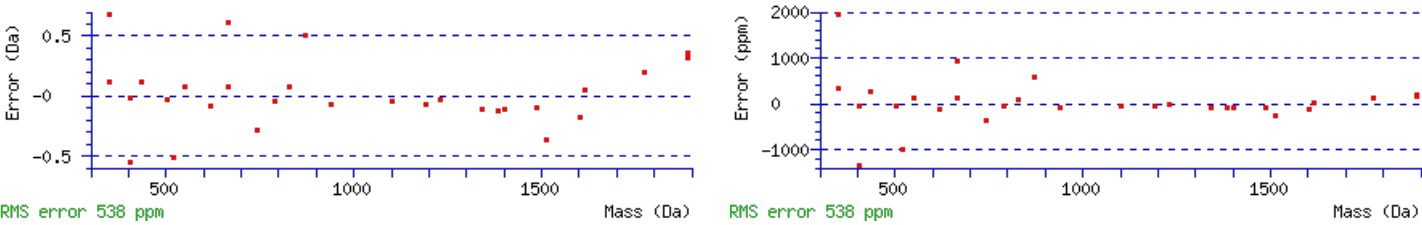
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2033.8888
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Deamidated (NQ)
N12 : Deamidated (NQ)
Ions Score: 77 Expect: 4.5e-007
Matches : 29/184 fragment ions using 48 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	293.1132	147.0602			275.1026	138.0550	Y	1905.8535	953.4304	1888.8269	944.9171	1887.8429	944.4251	16
3	421.1718	211.0895	404.1452	202.5763	403.1612	202.0842	Q	1742.7902	871.8987	1725.7636	863.3854	1724.7796	862.8934	15
4	522.2195	261.6134	505.1929	253.1001	504.2089	252.6081	T	1614.7316	807.8694	1597.7050	799.3562	1596.7210	798.8641	14
5	635.3035	318.1554	618.2770	309.6421	617.2930	309.1501	I	1513.6839	757.3456	1496.6574	748.8323	1495.6733	748.3403	13
6	692.3250	346.6661	675.2984	338.1529	674.3144	337.6608	G	1400.5998	700.8036	1383.5733	692.2903	1382.5893	691.7983	12
7	806.3679	403.6876	789.3414	395.1743	788.3573	394.6823	N	1343.5784	672.2928	1326.5518	663.7796	1325.5678	663.2875	11
8	935.4105	468.2089	918.3840	459.6956	917.3999	459.2036	Q	1229.5354	615.2714	1212.5089	606.7581	1211.5249	606.2661	10
9	1095.4412	548.2242	1078.4146	539.7109	1077.4306	539.2189	C	1100.4929	550.7501	1083.4663	542.2368	1082.4823	541.7448	9
10	1208.5252	604.7662	1191.4987	596.2530	1190.5147	595.7610	I	940.4622	470.7347	923.4357	462.2215	922.4516	461.7295	8
11	1371.5885	686.2979	1354.5620	677.7846	1353.5780	677.2926	Y	827.3781	414.1927	810.3516	405.6794	809.3676	405.1874	7
12	1486.6155	743.8114	1469.5889	735.2981	1468.6049	734.8061	N	664.3148	332.6610	647.2883	324.1478	646.3042	323.6558	6
13	1601.6424	801.3249	1584.6159	792.8116	1583.6319	792.3196	D	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
14	1688.6745	844.8409	1671.6479	836.3276	1670.6639	835.8356	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
15	1775.7065	888.3569	1758.6799	879.8436	1757.6959	879.3516	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
16	1888.7906	944.8989	1871.7640	936.3856	1870.7800	935.8936	L	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EYQTIGNQCIYNDSSLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
77.1	2033.8888	-0.0084	EYQTIGNQCIYNDSSLK	Deamidated Q8, N12 67.27%
74.0	2033.8888	-0.0084	EYQTIGNQCIYNDSSLK	Deamidated N7, N12 32.72%
38.0	2033.8888	-0.0084	EYQTIGNQCIYNDSSLK	Deamidated N7, Q8 0.01%
31.8	2033.8888	-0.0084	EYQTIGNQCIYNDSSLK	Deamidated Q3, N12 0.00%
16.0	2033.8888	-0.0084	EYQTIGNQCIYNDSSLK	Deamidated Q3, Q8 0.00%
11.9	2033.8888	-0.0084	EYQTIGNQCIYNDSSLK	Deamidated Q3, N7 0.00%
2.0	2032.8830	0.9974	MGGATSRGENSYGLDITCK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLYETEVFSTDFSNVSAAQQLNSHVER**
Found in **F1RXM6** in **uni_pig**, tr[F1RXM6]F1RXM6_PIG Thyroxine-binding globulin OS=Sus scrofa GN=SERPINA7 PE=4 SV=1

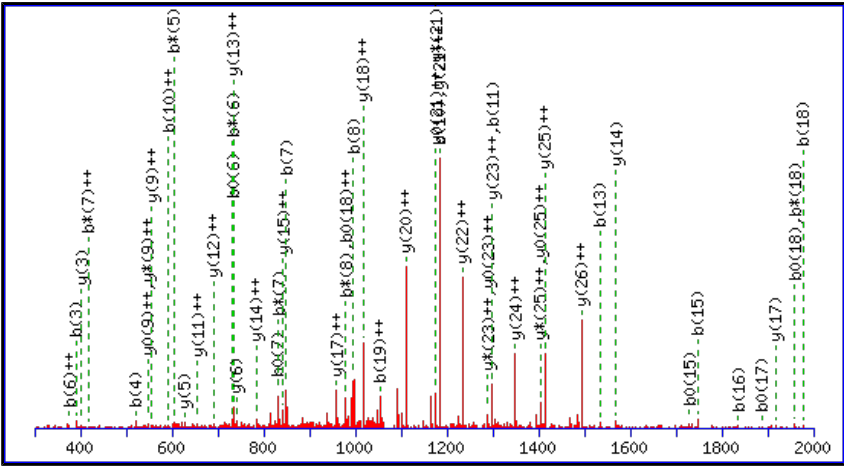
Match to Query 13402: 3215.471712 from(1072.831180,3+) intensity(0.0000) rtinseconds(2922) scans(6963) index(3727)
Title: 120325_Sunil_PigSerum_Glyco_P_13Spectrum5968_scans__6963
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

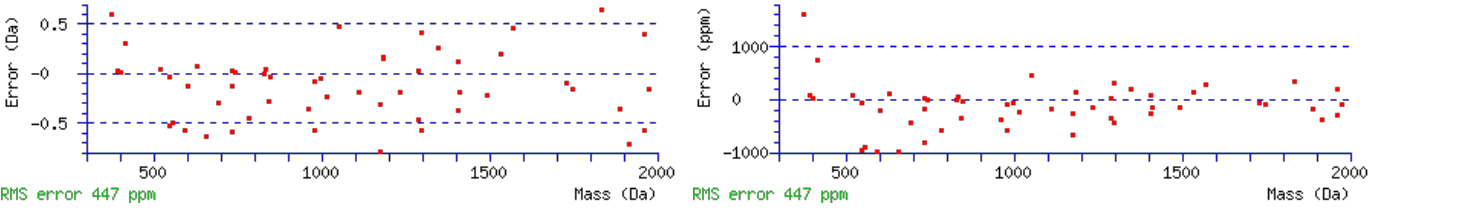
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 3215.4531
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
Q20 : Deamidated (NQ)
Ions Score: 81 Expect: 4.7e-007
Matches : 53/316 fragment ions using 85 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							28
2	228.1343	114.5708	211.1077	106.0575			L	3102.4174	1551.7124	3085.3909	1543.1991	3084.4069	1542.7071	27
3	391.1976	196.1024	374.1710	187.5892			Y	2989.3334	1495.1703	2972.3068	1486.6571	2971.3228	1486.1650	26
4	520.2402	260.6237	503.2136	252.1105	502.2296	251.6185	E	2826.2701	1413.6387	2809.2435	1405.1254	2808.2595	1404.6334	25
5	621.2879	311.1476	604.2613	302.6343	603.2773	302.1423	T	2697.2275	1349.1174	2680.2009	1340.6041	2679.2169	1340.1121	24
6	750.3305	375.6689	733.3039	367.1556	732.3199	366.6636	E	2596.1798	1298.5935	2579.1532	1290.0803	2578.1692	1289.5882	23
7	849.3989	425.2031	832.3723	416.6898	831.3883	416.1978	V	2467.1372	1234.0722	2450.1106	1225.5590	2449.1266	1225.0669	22
8	996.4673	498.7373	979.4407	490.2240	978.4567	489.7320	F	2368.0688	1184.5380	2351.0422	1176.0248	2350.0582	1175.5327	21
9	1083.4993	542.2533	1066.4728	533.7400	1065.4888	533.2480	S	2221.0004	1111.0038	2203.9738	1102.4905	2202.9898	1101.9985	20
10	1184.5470	592.7771	1167.5204	584.2639	1166.5364	583.7719	T	2133.9683	1067.4878	2116.9418	1058.9745	2115.9578	1058.4825	19
11	1299.5739	650.2906	1282.5474	641.7773	1281.5634	641.2853	D	2032.9207	1016.9640	2015.8941	1008.4507	2014.9101	1007.9587	18
12	1446.6424	723.8248	1429.6158	715.3115	1428.6318	714.8195	F	1917.8937	959.4505	1900.8672	950.9372	1899.8831	950.4452	17
13	1533.6744	767.3408	1516.6478	758.8276	1515.6638	758.3355	S	1770.8253	885.9163	1753.7987	877.4030	1752.8147	876.9110	16
14	1648.7013	824.8543	1631.6748	816.3410	1630.6908	815.8490	N	1683.7933	842.4003	1666.7667	833.8870	1665.7827	833.3950	15
15	1747.7697	874.3885	1730.7432	865.8752	1729.7592	865.3832	V	1568.7663	784.8868	1551.7398	776.3735	1550.7558	775.8815	14
16	1834.8018	917.9045	1817.7752	909.3912	1816.7912	908.8992	S	1469.6979	735.3526	1452.6714	726.8393	1451.6873	726.3473	13
17	1905.8389	953.4231	1888.8123	944.9098	1887.8283	944.4178	A	1382.6659	691.8366	1365.6393	683.3233	1364.6553	682.8313	12
18	1976.8760	988.9416	1959.8494	980.4284	1958.8654	979.9364	A	1311.6288	656.3180	1294.6022	647.8047	1293.6182	647.3127	11
19	2104.9346	1052.9709	2087.9080	1044.4576	2086.9240	1043.9656	Q	1240.5917	620.7995	1223.5651	612.2862	1222.5811	611.7942	10
20	2233.9772	1117.4922	2216.9506	1108.9789	2215.9666	1108.4869	Q	1112.5331	556.7702	1095.5065	548.2569	1094.5225	547.7649	9
21	2363.0198	1182.0135	2345.9932	1173.5002	2345.0092	1173.0082	E	983.4905	492.2489	966.4639	483.7356	965.4799	483.2436	8
22	2476.1038	1238.5555	2459.0773	1230.0423	2458.0933	1229.5503	L	854.4479	427.7276	837.4213	419.2143	836.4373	418.7223	7
23	2590.1468	1295.5770	2573.1202	1287.0637	2572.1362	1286.5717	N	741.3638	371.1856	724.3373	362.6723	723.3533	362.1803	6

24	2677.1788	1339.0930	2660.1522	1330.5798	2659.1682	1330.0877	S	627.3209	314.1641	610.2944	305.6508	609.3103	305.1588	5
25	2814.2377	1407.6225	2797.2111	1399.1092	2796.2271	1398.6172	H	540.2889	270.6481	523.2623	262.1348	522.2783	261.6428	4
26	2913.3061	1457.1567	2896.2796	1448.6434	2895.2955	1448.1514	V	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
27	3042.3487	1521.6780	3025.3221	1513.1647	3024.3381	1512.6727	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
28							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [NL YETEFVSTDFESNV SAAQQELNSHVER](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
80.8	3215.4531	0.0186	NL YETEFVSTDFESNV SAAQQELNSHVER	Deamidated N14, Q20 31.50%
80.8	3215.4531	0.0186	NL YETEFVSTDFESNV SAAQQELNSHVER	Deamidated N14, Q19 31.50%
79.5	3215.4531	0.0186	NL YETEFVSTDFESNV SAAQQELNSHVER	Deamidated N14, N23 23.57%
75.4	3214.4691	1.0027	NL YETEFVSTDFESNV SAAQQELNSHVER	
70.5	3214.4691	1.0027	NL YETEFVSTDFESNV SAAQQELNSHVER	
70.3	3215.4531	0.0186	NL YETEFVSTDFESNV SAAQQELNSHVER	Deamidated N1, Q19 2.79%
69.1	3214.4691	1.0027	NL YETEFVSTDFESNV SAAQQELNSHVER	
69.0	3215.4531	0.0186	NL YETEFVSTDFESNV SAAQQELNSHVER	Deamidated N1, N14 2.11%
69.0	3213.4850	1.9867	NL YETEFVSTDFESNV SAAQQELNSHVER	
68.9	3215.4531	0.0186	NL YETEFVSTDFESNV SAAQQELNSHVER	Deamidated N1, Q20 2.04%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **CKDGLGEYNCTCAEGFEGK**
Found in **F1RN41** in **uni_pig**, tr[F1RN41|F1RN41_PIG Uncharacterized protein OS=Sus scrofa GN=F10 PE=3 SV=1

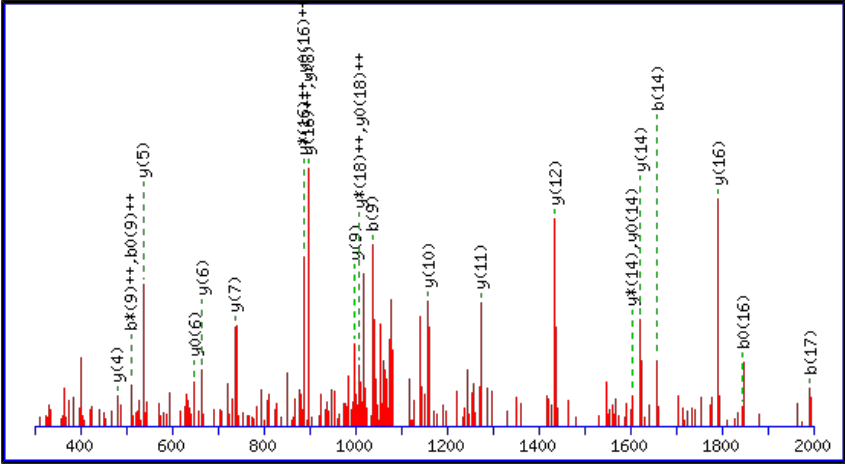
Match to Query 12172: 2194.848488 from(1098.431520,2+) intensity(0.0000) rtinseconds(1863) scans(4406) index(1551)
Title: 120325_Sunil_PigSerum_Glyco_D_14Spectrum3753_scans__4406
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

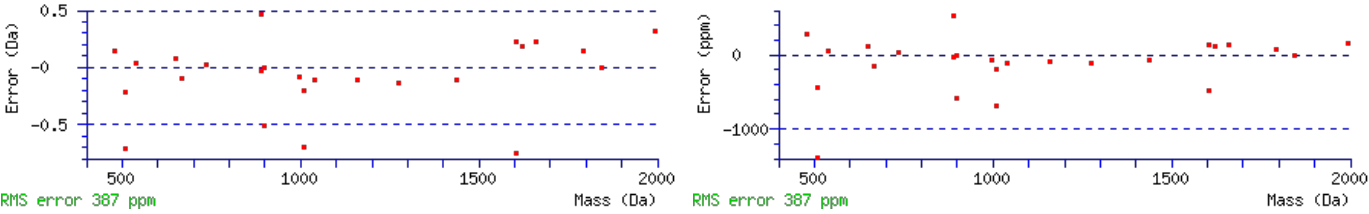
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2194.8605
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 68 Expect: 5.8e-007
Matches : 25/206 fragment ions using 34 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	161.0379	81.0226					C							19
2	289.1329	145.0701	272.1063	136.5568			K	2035.8372	1018.4222	2018.8106	1009.9090	2017.8266	1009.4169	18
3	404.1598	202.5836	387.1333	194.0703	386.1493	193.5783	D	1907.7422	954.3747	1890.7157	945.8615	1889.7317	945.3695	17
4	461.1813	231.0943	444.1547	222.5810	443.1707	222.0890	G	1792.7153	896.8613	1775.6887	888.3480	1774.7047	887.8560	16
5	574.2654	287.6363	557.2388	279.1230	556.2548	278.6310	L	1735.6938	868.3505	1718.6673	859.8373	1717.6833	859.3453	15
6	631.2868	316.1470	614.2603	307.6338	613.2763	307.1418	G	1622.6098	811.8085	1605.5832	803.2952	1604.5992	802.8032	14
7	760.3294	380.6683	743.3029	372.1551	742.3189	371.6631	E	1565.5883	783.2978	1548.5617	774.7845	1547.5777	774.2925	13
8	923.3927	462.2000	906.3662	453.6867	905.3822	453.1947	Y	1436.5457	718.7765	1419.5191	710.2632	1418.5351	709.7712	12
9	1038.4197	519.7135	1021.3931	511.2002	1020.4091	510.7082	N	1273.4824	637.2448	1256.4558	628.7315	1255.4718	628.2395	11
10	1198.4503	599.7288	1181.4238	591.2155	1180.4398	590.7235	C	1158.4554	579.7313	1141.4289	571.2181	1140.4449	570.7261	10
11	1299.4980	650.2526	1282.4715	641.7394	1281.4875	641.2474	T	998.4248	499.7160	981.3982	491.2028	980.4142	490.7107	9
12	1459.5287	730.2680	1442.5021	721.7547	1441.5181	721.2627	C	897.3771	449.1922	880.3505	440.6789	879.3665	440.1869	8
13	1530.5658	765.7865	1513.5392	757.2733	1512.5552	756.7812	A	737.3464	369.1769	720.3199	360.6636	719.3359	360.1716	7
14	1659.6084	830.3078	1642.5818	821.7945	1641.5978	821.3025	E	666.3093	333.6583	649.2828	325.1450	648.2988	324.6530	6
15	1716.6298	858.8186	1699.6033	850.3053	1698.6193	849.8133	G	537.2667	269.1370	520.2402	260.6237	519.2562	260.1317	5
16	1863.6983	932.3528	1846.6717	923.8395	1845.6877	923.3475	F	480.2453	240.6263	463.2187	232.1130	462.2347	231.6210	4
17	1992.7408	996.8741	1975.7143	988.3608	1974.7303	987.8688	E	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
18	2049.7623	1025.3848	2032.7358	1016.8715	2031.7517	1016.3795	G	204.1343	102.5708	187.1077	94.0575			2
19							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [CKDGLGEYNCTCAEGFEGK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.6	2194.8605	-0.0121	CKDGLGEYNCTCAEGFEGK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELNVTLSSMSR**

Found in **F1RQW2** in **uni_pig**, tr|F1RQW2|F1RQW2_PIG Uncharacterized protein OS=Sus scrofa GN=C4 PE=4 SV=2

Match to Query 1881: 1236.599268 from(619.306910,2+) intensity(19279.5957) rtinseconds(1946) scans(4248) index(12947)

Title: 120326 Sunil PigSerum Glyco SsetB 13Spectrum3462 scans 4248

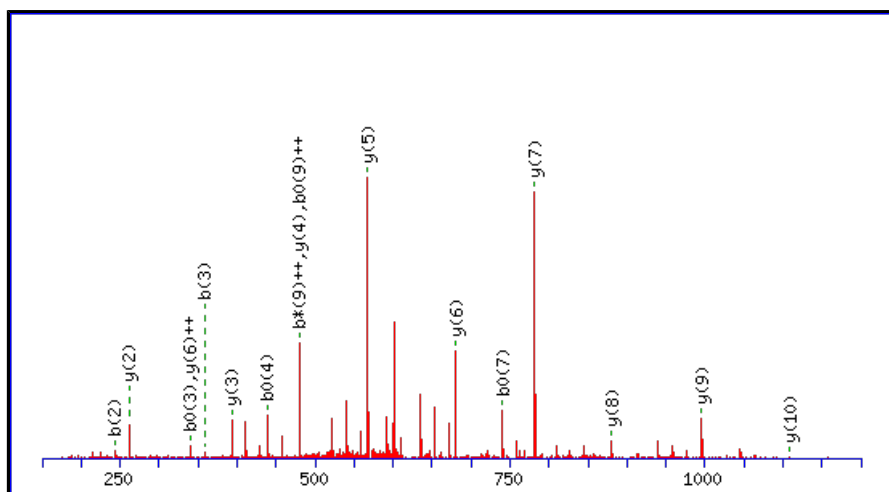
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1236.6020

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

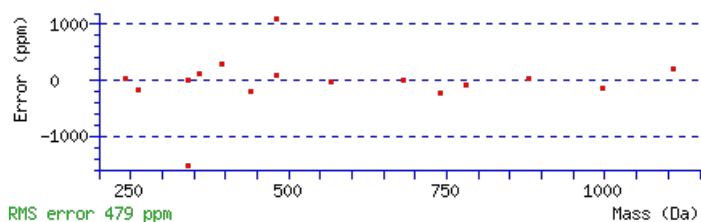
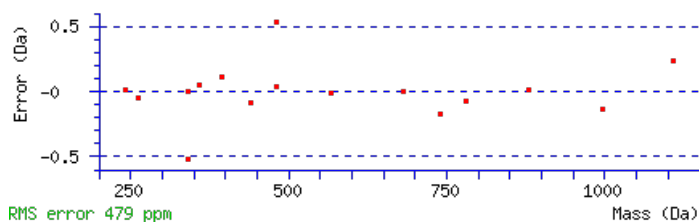
Variable modifications:

N3 : Deamidated (NQ)

Ions Score: 80 Expect: 6.1e-007

Matches : 17/114 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							11
2	243.1339	122.0706			225.1234	113.0653	L	1108.5667	554.7870	1091.5401	546.2737	1090.5561	545.7817	10
3	358.1609	179.5841	341.1343	171.0708	340.1503	170.5788	N	995.4826	498.2449	978.4561	489.7317	977.4721	489.2397	9
4	457.2293	229.1183	440.2027	220.6050	439.2187	220.1130	V	880.4557	440.7315	863.4291	432.2182	862.4451	431.7262	8
5	558.2770	279.6421	541.2504	271.1288	540.2664	270.6368	T	781.3873	391.1973	764.3607	382.6840	763.3767	382.1920	7
6	671.3610	336.1842	654.3345	327.6709	653.3505	327.1789	L	680.3396	340.6734	663.3130	332.1602	662.3290	331.6681	6
7	758.3931	379.7002	741.3665	371.1869	740.3825	370.6949	S	567.2555	284.1314	550.2290	275.6181	549.2450	275.1261	5
8	845.4251	423.2162	828.3985	414.7029	827.4145	414.2109	S	480.2235	240.6154	463.1969	232.1021	462.2129	231.6101	4
9	976.4656	488.7364	959.4390	480.2232	958.4550	479.7311	M	393.1915	197.0994	376.1649	188.5861	375.1809	188.0941	3
10	1063.4976	532.2524	1046.4711	523.7392	1045.4870	523.2472	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
11							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [ELNVTLSMSR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
80.1	1236.6020	-0.0027	ELNVTLSMSR
11.1	1236.5986	0.0007	ELDRNFSINK
10.8	1236.5986	0.0007	ELNAREDYVK
9.7	1236.5921	0.0072	KNRPAMNYDK
7.7	1236.6098	-0.0106	KQAQQIDYSR
7.7	1236.6098	-0.0106	KQAQQIDYSR
5.3	1236.6098	-0.0106	KQAQQIDYSR
3.1	1235.6080	0.9912	KNRPAMNYDK
1.0	1236.5986	0.0007	EIDEYITQAR
1.0	1236.5907	0.0085	ELDQLSEKMK

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **I3LRJ4** in **uni_pig**, tr|I3LRJ4|I3LRJ4_PIG Vitamin K-dependent protein C OS=Sus scrofa GN=PROC PE=3 SV=1

Title: 120326_Sunil_PigSerum_Glyco_PsetB_08Spectrum992_scans__1714

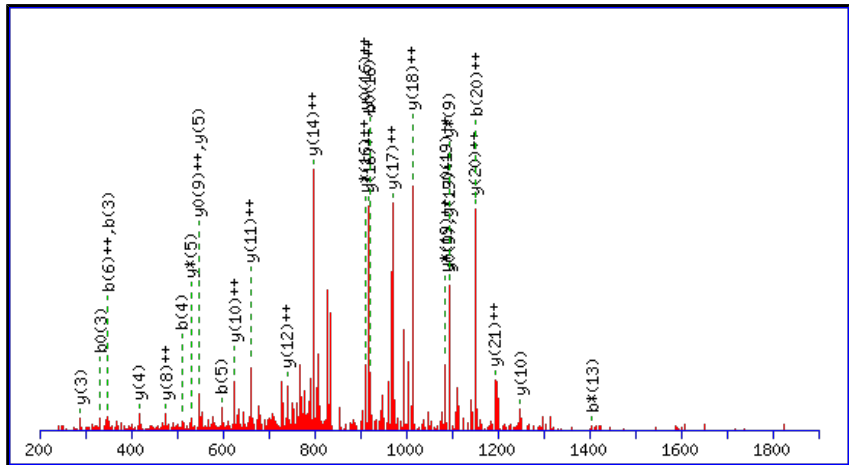
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

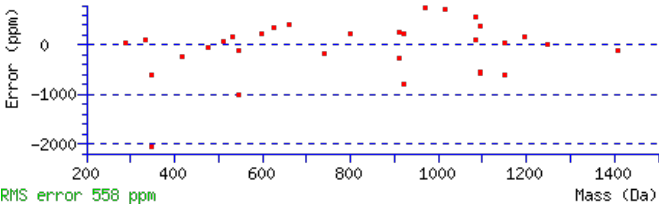
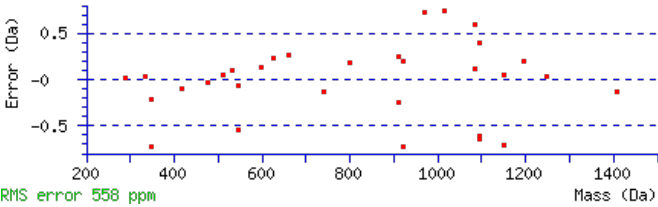
Variable modifications:

N3 : Deamidated (NQ)

Ions Score: 62 Expect: 6.1e-007

Matches : 31/240 fragment ions using 45 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							22
2	235.1077	118.0575			217.0972	109.0522	S	2387.8922	1194.4497	2370.8656	1185.9364	2369.8816	1185.4444	21
3	350.1347	175.5710	333.1081	167.0577	332.1241	166.5657	N	2300.8601	1150.9337	2283.8336	1142.4204	2282.8496	1141.9284	20
4	510.1653	255.5863	493.1388	247.0730	492.1547	246.5810	C	2185.8332	1093.4202	2168.8066	1084.9070	2167.8226	1084.4149	19
5	597.1973	299.1023	580.1708	290.5890	579.1868	290.0970	S	2025.8025	1013.4049	2008.7760	1004.8916	2007.7920	1004.3996	18
6	698.2450	349.6261	681.2185	341.1129	680.2345	340.6209	T	1938.7705	969.8889	1921.7440	961.3756	1920.7599	960.8836	17
7	827.2876	414.1474	810.2611	405.6342	809.2770	405.1422	E	1837.7228	919.3651	1820.6963	910.8518	1819.7123	910.3598	16
8	941.3305	471.1689	924.3040	462.6556	923.3200	462.1636	N	1708.6802	854.8438	1691.6537	846.3305	1690.6697	845.8385	15
9	998.3520	499.6796	981.3255	491.1664	980.3414	490.6744	G	1594.6373	797.8223	1577.6108	789.3090	1576.6267	788.8170	14
10	1055.3735	528.1904	1038.3469	519.6771	1037.3629	519.1851	G	1537.6158	769.3116	1520.5893	760.7983	1519.6053	760.3063	13
11	1215.4041	608.2057	1198.3776	599.6924	1197.3935	599.2004	C	1480.5944	740.8008	1463.5678	732.2876	1462.5838	731.7955	12
12	1286.4412	643.7243	1269.4147	635.2110	1268.4307	634.7190	A	1320.5637	660.7855	1303.5372	652.2722	1302.5532	651.7802	11
13	1423.5001	712.2537	1406.4736	703.7404	1405.4896	703.2484	H	1249.5266	625.2669	1232.5001	616.7537	1231.5160	616.2617	10
14	1586.5635	793.7854	1569.5369	785.2721	1568.5529	784.7801	Y	1112.4677	556.7375	1095.4412	548.2242	1094.4571	547.7322	9
15	1746.5941	873.8007	1729.5676	865.2874	1728.5836	864.7954	C	949.4044	475.2058	932.3778	466.6925	931.3938	466.2005	8
16	1859.6782	930.3427	1842.6516	921.8295	1841.6676	921.3374	L	789.3737	395.1905	772.3472	386.6772	771.3632	386.1852	7
17	1988.7208	994.8640	1971.6942	986.3508	1970.7102	985.8587	E	676.2897	338.6485	659.2631	330.1352	658.2791	329.6432	6
18	2117.7634	1059.3853	2100.7368	1050.8720	2099.7528	1050.3800	E	547.2471	274.1272	530.2205	265.6139	529.2365	265.1219	5
19	2246.8060	1123.9066	2229.7794	1115.3933	2228.7954	1114.9013	E	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	4
20	2303.8274	1152.4174	2286.8009	1143.9041	2285.8169	1143.4121	G	289.1619	145.0846	272.1353	136.5713			3
21	2360.8489	1180.9281	2343.8223	1172.4148	2342.8383	1171.9228	G	232.1404	116.5738	215.1139	108.0606			2
22							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [FSNCSTENGGAHYCLEEEEGGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.2	2533.9533	-0.0129	FSNCSTENGGAHYCLEEEEGGR	Deamidated N3 87.42%
53.8	2533.9533	-0.0129	FSNCSTENGGAHYCLEEEEGGR	Deamidated N8 12.58%
1.2	2533.9236	0.0167	ENSSEICTNNGECVCGQCVCR	
0.5	2532.9396	1.0007	ENSSEICTNNGECVCGQCVCR	
0.5	2533.9236	0.0167	ENSSEICTNNGECVCGQCVCR	
0.5	2532.9396	1.0007	ENSSEICTNNGECVCGQCVCR	
0.5	2533.9236	0.0167	ENSSEICTNNGECVCGQCVCR	

Mascot: <http://www.matrixscience.com/>

http:// MascotXP.student.main.ntu.edu.sg/Mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=2211 [22/Apr/15 06:00:02 PM]

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
78.3	1252.5969	-0.0032	ELNVTLSMSR
17.6	1252.5870	0.0067	MEPGPAASPGPSR
9.7	1252.5870	0.0067	KNRPAMNYDK
7.2	1251.5917	1.0020	KNKPNMNYDK
6.3	1251.5805	1.0132	LFQVPEEMSR
4.2	1250.5965	1.9972	LSSAYISDHMK
4.0	1252.5944	-0.0007	LPEVYCMVSR
3.3	1251.6017	0.9921	ALGTLGTTNEK
3.0	1251.5956	0.9981	DRQRPYSSSR
1.8	1251.5839	1.0098	MLVNIQMKNK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

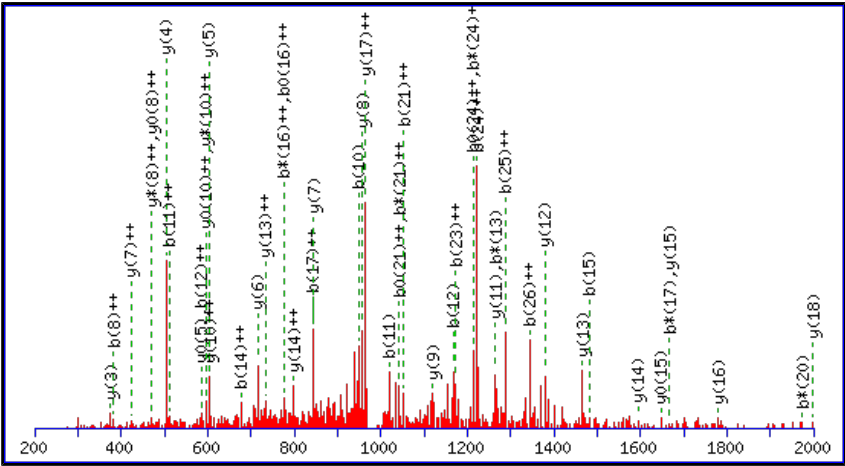
Peptide View

MS/MS Fragmentation of **VVHAAESALAAFNAQSGSYLQLVEISR**
Found in **F1SFI7** in **uni_pig**, tr[F1SFI7|F1SFI7_PIG Alpha-2-HS-glycoprotein (Fragment) OS=Sus scrofa GN=AHSG PE=4 SV=2

Match to Query 13319: 2947.465062 from(983.495630,3+) intensity(5404.5586) rtinseconds(2903) scans(6888) index(10534)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_13Spectrum5888_scans_6888
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

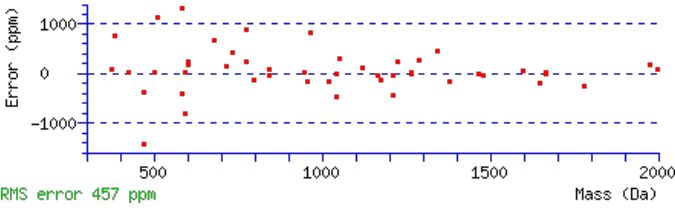
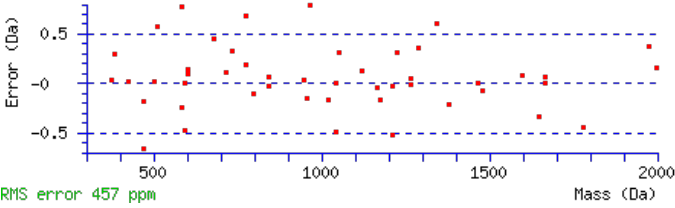
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2946.4723
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15 : Deamidated (NQ)
N17 : Deamidated (NQ)
Ions Score: 81 Expect: 6.9e-007
Matches : 48/288 fragment ions using 69 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							28
2	199.1441	100.0757					V	2848.4112	1424.7092	2831.3846	1416.1960	2830.4006	1415.7039	27
3	336.2030	168.6051					H	2749.3428	1375.1750	2732.3162	1366.6617	2731.3322	1366.1697	26
4	407.2401	204.1237					A	2612.2839	1306.6456	2595.2573	1298.1323	2594.2733	1297.6403	25
5	478.2772	239.6423					A	2541.2467	1271.1270	2524.2202	1262.6137	2523.2362	1262.1217	24
6	607.3198	304.1636			589.3093	295.1583	E	2470.2096	1235.6085	2453.1831	1227.0952	2452.1991	1226.6032	23
7	694.3519	347.6796			676.3413	338.6743	S	2341.1670	1171.0872	2324.1405	1162.5739	2323.1565	1162.0819	22
8	765.3890	383.1981			747.3784	374.1928	A	2254.1350	1127.5711	2237.1085	1119.0579	2236.1244	1118.5659	21
9	878.4730	439.7402			860.4625	430.7349	L	2183.0979	1092.0526	2166.0713	1083.5393	2165.0873	1083.0473	20
10	949.5102	475.2587			931.4996	466.2534	A	2070.0138	1035.5106	2052.9873	1026.9973	2052.0033	1026.5053	19
11	1020.5473	510.7773			1002.5367	501.7720	A	1998.9767	999.9920	1981.9502	991.4787	1980.9661	990.9867	18
12	1167.6157	584.3115			1149.6051	575.3062	F	1927.9396	964.4734	1910.9130	955.9602	1909.9290	955.4682	17
13	1281.6586	641.3329	1264.6321	632.8197	1263.6480	632.3277	N	1780.8712	890.9392	1763.8446	882.4260	1762.8606	881.9339	16
14	1352.6957	676.8515	1335.6692	668.3382	1334.6852	667.8462	A	1666.8283	833.9178	1649.8017	825.4045	1648.8177	824.9125	15
15	1481.7383	741.3728	1464.7118	732.8595	1463.7278	732.3675	Q	1595.7911	798.3992	1578.7646	789.8859	1577.7806	789.3939	14
16	1568.7703	784.8888	1551.7438	776.3755	1550.7598	775.8835	S	1466.7485	733.8779	1449.7220	725.3646	1448.7380	724.8726	13
17	1683.7973	842.4023	1666.7707	833.8890	1665.7867	833.3970	N	1379.7165	690.3619	1362.6900	681.8486	1361.7060	681.3566	12
18	1740.8188	870.9130	1723.7922	862.3997	1722.8082	861.9077	G	1264.6896	632.8484	1247.6630	624.3352	1246.6790	623.8431	11
19	1827.8508	914.4290	1810.8242	905.9158	1809.8402	905.4237	S	1207.6681	604.3377	1190.6416	595.8244	1189.6575	595.3324	10
20	1990.9141	995.9607	1973.8876	987.4474	1972.9035	986.9554	Y	1120.6361	560.8217	1103.6095	552.3084	1102.6255	551.8164	9
21	2103.9982	1052.5027	2086.9716	1043.9895	2085.9876	1043.4974	L	957.5728	479.2900	940.5462	470.7767	939.5622	470.2847	8
22	2232.0568	1116.5320	2215.0302	1108.0187	2214.0462	1107.5267	Q	844.4887	422.7480	827.4621	414.2347	826.4781	413.7427	7
23	2345.1408	1173.0740	2328.1143	1164.5608	2327.1303	1164.0688	L	716.4301	358.7187	699.4036	350.2054	698.4196	349.7134	6

24	2444.2092	1222.6083	2427.1827	1214.0950	2426.1987	1213.6030	V	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
25	2573.2518	1287.1296	2556.2253	1278.6163	2555.2413	1278.1243	E	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
26	2686.3359	1343.6716	2669.3093	1335.1583	2668.3253	1334.6663	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
27	2773.3679	1387.1876	2756.3414	1378.6743	2755.3574	1378.1823	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
28							R	175.1190	88.0631	158.0924	79.5498			1

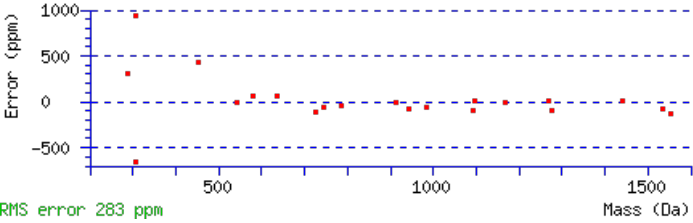
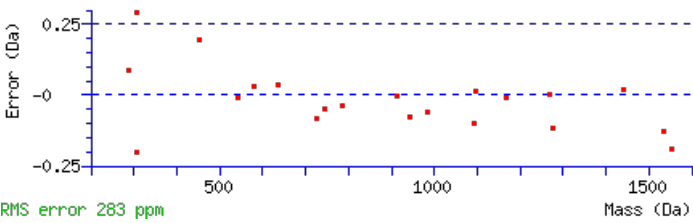


NCBI BLAST search of [VVHAAESALAAFNAQSNQSYLQLVEISR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
81.1	2946.4723	0.9928	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated Q15, N17 92.31%
70.4	2947.4563	0.0088	VVHAAESALAAFNAQSNQSYLQLVEISR	
70.2	2946.4723	0.9928	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated N13, N17 7.50%
51.4	2946.4723	0.9928	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated Q15, Q22 0.10%
50.9	2947.4563	0.0088	VVHAAESALAAFNAQSNQSYLQLVEISR	
49.2	2946.4723	0.9928	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated N13, Q15 0.06%
48.6	2947.4563	0.0088	VVHAAESALAAFNAQSNQSYLQLVEISR	
47.8	2947.4563	0.0088	VVHAAESALAAFNAQSNQSYLQLVEISR	
45.0	2946.4723	0.9928	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated N13, Q22 0.02%
37.6	2946.4723	0.9928	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated N17, Q22 0.00%

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [ELNTTALAEFGHEYIR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
79.7	1726.8413	-0.0066	ELNTTALAEFGHEYIR
4.1	1726.8204	0.0143	KHSVMMTFLSNMLR
4.1	1726.8204	0.0143	KHSVMMTFLSNMLR
0.1	1724.8403	1.9945	EKMEYSAQLQAALAR
0.1	1725.8243	1.0105	EKMEYSAQLQAALAR

Mascot: <http://www.matrixscience.com/>

Peptide View

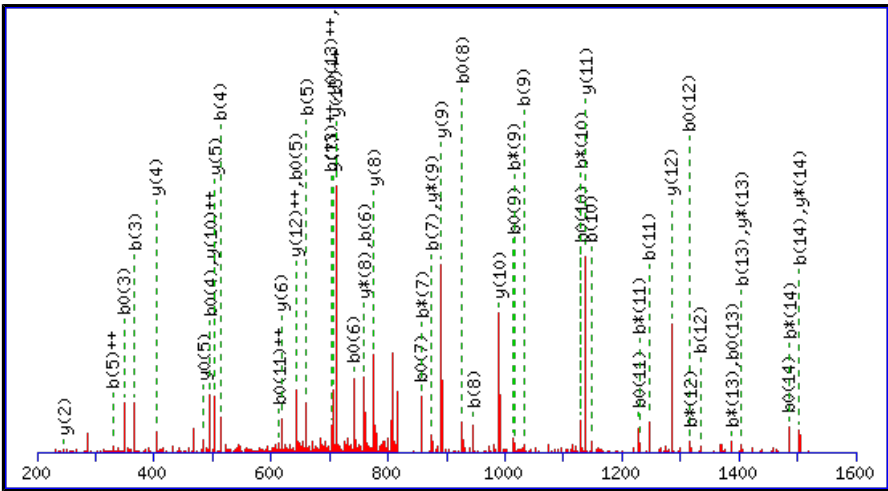
Found in **F1RK01** in **uni_pig**, tr|F1RK01|F1RK01_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=CPB2 PE=4 SV=2

Match to Query 5357: 1648.805628 from(825.410090,2+) intensity(13402.5088) rtinseconds(2133) scans(5103) index(1598)
Title: 120325_Sunil_PigSerum_Glyco_D_14Spectrum4373_scans__5103
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, to Da

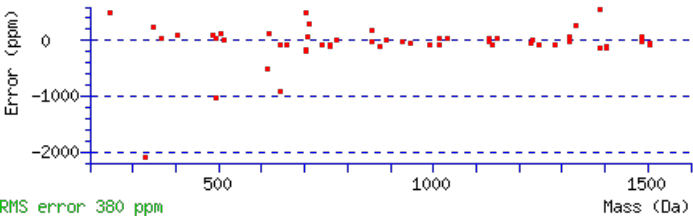
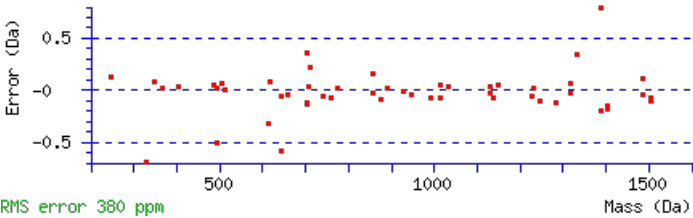
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1648.8097
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 N7 : Deamidated (NQ)
 Ions Score: 80 Expect: 8.4e-007
 Matches : 54/150 fragment ions using 78 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							15
2	229.1183	115.0628			211.1077	106.0575	V	1520.7744	760.8908	1503.7478	752.3775	1502.7638	751.8855	14
3	366.1772	183.5922			348.1666	174.5870	H	1421.7060	711.3566	1404.6794	702.8433	1403.6954	702.3513	13
4	513.2456	257.1264			495.2350	248.1212	F	1284.6470	642.8272	1267.6205	634.3139	1266.6365	633.8219	12
5	660.3140	330.6606			642.3035	321.6554	F	1137.5786	569.2930	1120.5521	560.7797	1119.5681	560.2877	11
6	759.3824	380.1949			741.3719	371.1896	V	990.5102	495.7587	973.4837	487.2455	972.4997	486.7535	10
7	874.4094	437.7083	857.3828	429.1951	856.3988	428.7030	N	891.4418	446.2245	874.4153	437.7113	873.4312	437.2193	9
8	945.4465	473.2269	928.4199	464.7136	927.4359	464.2216	A	776.4149	388.7111	759.3883	380.1978	758.4043	379.7058	8
9	1032.4785	516.7429	1015.4520	508.2296	1014.4680	507.7376	S	705.3777	353.1925	688.3512	344.6792	687.3672	344.1872	7
10	1147.5055	574.2564	1130.4789	565.7431	1129.4949	565.2511	D	618.3457	309.6765	601.3192	301.1632	600.3352	300.6712	6
11	1246.5739	623.7906	1229.5473	615.2773	1228.5633	614.7853	V	503.3188	252.1630	486.2922	243.6498	485.3082	243.1577	5
12	1333.6059	667.3066	1316.5794	658.7933	1315.5953	658.3013	S	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	4
13	1404.6430	702.8251	1387.6165	694.3119	1386.6325	693.8199	A	317.2183	159.1128	300.1918	150.5995			3
14	1503.7114	752.3594	1486.6849	743.8461	1485.7009	743.3541	V	246.1812	123.5942	229.1547	115.0810			2
15							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EVHFFVNASDVSAVK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

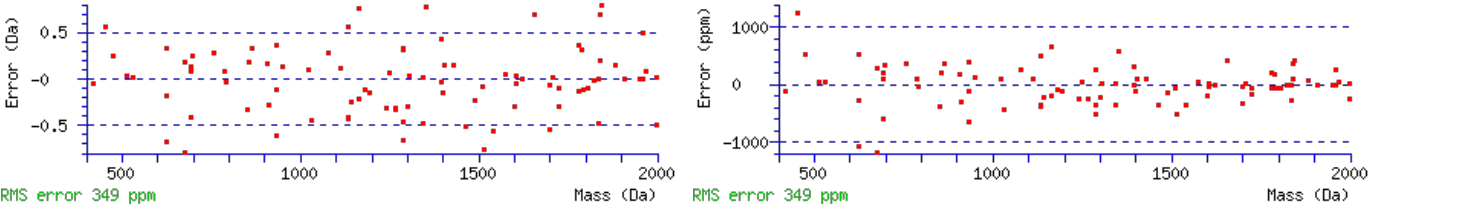
All matches to this query

Score	Mr(calc)	Delta	Sequence
79.6	1648.8097	-0.0041	EVHFFVNASDVSAVK
3.1	1648.8065	-0.0009	MAYHLQKMQDSGIK
2.6	1646.8046	2.0011	ARQRQQALETMDK
0.6	1648.7984	0.0072	YNSFYESELKIEK
0.4	1646.8012	2.0044	RKWEEETVAEQSR
0.3	1647.7960	1.0096	LMMNQLEEDLVSAR
0.2	1646.7999	2.0058	NLSTEIQENLSEIR

Mascot: <http://www.matrixscience.com/>

http:// MascotXP.student.main.ntu.edu.sg/Mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=13731 [22/Apr/15 06:00:26 PM]

24	2702.2502	1351.6287	2685.2236	1343.1154	2684.2396	1342.6234	L	1516.7312	758.8692	1499.7046	750.3560	1498.7206	749.8639	13
25	2801.3186	1401.1629	2784.2920	1392.6497	2783.3080	1392.1576	V	1403.6471	702.3272	1386.6206	693.8139	1385.6366	693.3219	12
26	2858.3400	1429.6737	2841.3135	1421.1604	2840.3295	1420.6684	G	1304.5787	652.7930	1287.5522	644.2797	1286.5681	643.7877	11
27	2955.3928	1478.2000	2938.3663	1469.6868	2937.3822	1469.1948	P	1247.5572	624.2823	1230.5307	615.7690	1229.5467	615.2770	10
28	3084.4354	1542.7213	3067.4089	1534.2081	3066.4248	1533.7161	Q	1150.5045	575.7559	1133.4779	567.2426	1132.4939	566.7506	9
29	3199.4623	1600.2348	3182.4358	1591.7215	3181.4518	1591.2295	N	1021.4619	511.2346	1004.4353	502.7213	1003.4513	502.2293	8
30	3312.5464	1656.7768	3295.5199	1648.2636	3294.5358	1647.7716	I	906.4349	453.7211	889.4084	445.2078	888.4244	444.7158	7
31	3413.5941	1707.3007	3396.5675	1698.7874	3395.5835	1698.2954	T	793.3509	397.1791	776.3243	388.6658	775.3403	388.1738	6
32	3573.6247	1787.3160	3556.5982	1778.8027	3555.6142	1778.3107	C	692.3032	346.6552	675.2767	338.1420	674.2926	337.6500	5
33	3686.7088	1843.8580	3669.6823	1835.3448	3668.6982	1834.8528	I	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
34	3815.7514	1908.3793	3798.7248	1899.8661	3797.7408	1899.3741	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
35	3930.7783	1965.8928	3913.7518	1957.3795	3912.7678	1956.8875	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
36							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
78.0	4103.8827	-0.0006	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q28, N29 49.84%
76.1	4103.8827	-0.0006	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q17, N29 32.11%
72.2	4103.8827	-0.0006	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q17, Q28 13.17%
70.0	4102.8987	0.9834	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
68.7	4102.8987	0.9834	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
66.2	4103.8827	-0.0006	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, N29 3.35%
62.8	4103.8827	-0.0006	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q28 1.50%
54.5	4102.8987	0.9834	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
49.1	4101.9147	1.9674	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
47.6	4102.8987	0.9834	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVSNAFLDKGEFYIGSK**
Found in **F1SKB1** in **uni_pig**, tr|F1SKB1|F1SKB1_PIG Uncharacterized protein OS=Sus scrofa GN=CP PE=4 SV=3

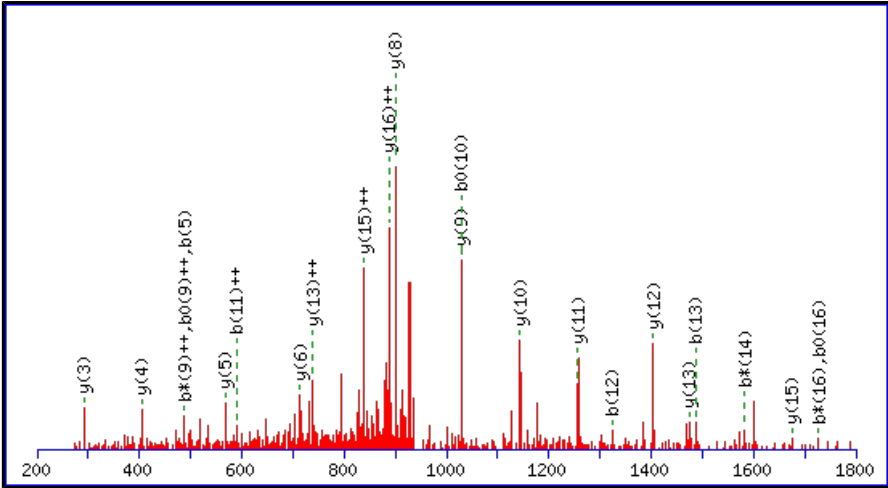
Match to Query 7606: 1888.916608 from(945.465580,2+) intensity(5503.9824) rtinseconds(2365) scans(4948) index(10284)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_12Spectrum3755_scans__4948
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

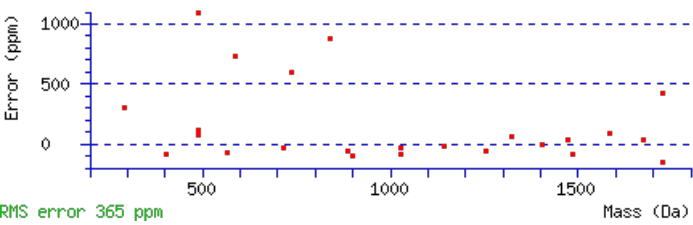
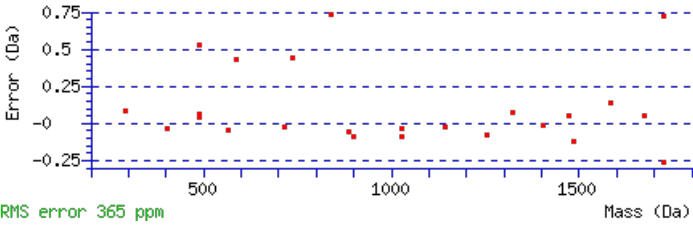
☐ Label all possible matches ☐ Label matches used for scoring

☐ Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1888.9207
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
Ions Score: 80 Expect: 9e-007
Matches : 24/186 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							17
2	215.1026	108.0550	198.0761	99.5417			V	1774.9010	887.9542	1757.8745	879.4409	1756.8905	878.9489	16
3	302.1347	151.5710	285.1081	143.0577	284.1241	142.5657	S	1675.8326	838.4199	1658.8061	829.9067	1657.8220	829.4147	15
4	416.1776	208.5924	399.1510	200.0792	398.1670	199.5871	N	1588.8006	794.9039	1571.7740	786.3907	1570.7900	785.8986	14
5	487.2147	244.1110	470.1882	235.5977	469.2041	235.1057	A	1474.7577	737.8825	1457.7311	729.3692	1456.7471	728.8772	13
6	634.2831	317.6452	617.2566	309.1319	616.2726	308.6399	F	1403.7205	702.3639	1386.6940	693.8506	1385.7100	693.3586	12
7	747.3672	374.1872	730.3406	365.6740	729.3566	365.1819	L	1256.6521	628.8297	1239.6256	620.3164	1238.6416	619.8244	11
8	862.3941	431.7007	845.3676	423.1874	844.3836	422.6954	D	1143.5681	572.2877	1126.5415	563.7744	1125.5575	563.2824	10
9	990.4891	495.7482	973.4625	487.2349	972.4785	486.7429	K	1028.5411	514.7742	1011.5146	506.2609	1010.5306	505.7689	9
10	1047.5106	524.2589	1030.4840	515.7456	1029.5000	515.2536	G	900.4462	450.7267	883.4196	442.2134	882.4356	441.7214	8
11	1176.5531	588.7802	1159.5266	580.2669	1158.5426	579.7749	E	843.4247	422.2160	826.3981	413.7027	825.4141	413.2107	7
12	1323.6216	662.3144	1306.5950	653.8011	1305.6110	653.3091	F	714.3821	357.6947	697.3556	349.1814	696.3715	348.6894	6
13	1486.6849	743.8461	1469.6583	735.3328	1468.6743	734.8408	Y	567.3137	284.1605	550.2871	275.6472	549.3031	275.1552	5
14	1599.7689	800.3881	1582.7424	791.8748	1581.7584	791.3828	I	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	4
15	1656.7904	828.8988	1639.7639	820.3856	1638.7798	819.8936	G	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
16	1743.8224	872.4149	1726.7959	863.9016	1725.8119	863.4096	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
17							K	147.1128	74.0600	130.0863	65.5468			1



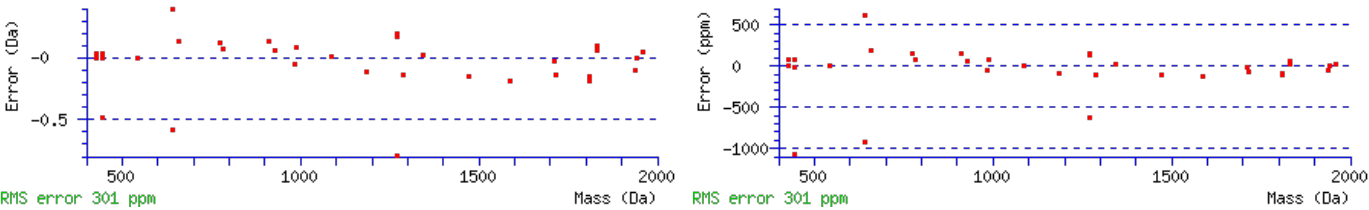
NCBI **BLAST** search of [NVSNAFLDKGEFYIGSK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
79.7	1888.9207	-0.0041	NVSNAFLDKGEFYIGSK	Deamidated N1 95.64%
66.3	1888.9207	-0.0041	NVSNAFLDKGEFYIGSK	Deamidated N4 4.36%
7.1	1887.9248	0.9918	LPNSSQLSISPVSCVNGK	
7.0	1888.9312	-0.0146	NDQKMLADLDDLNRTK	
3.5	1887.9247	0.9919	VVRNLMESLAQGAEEP	

Mascot: <http://www.matrixscience.com/>

http://mascotxp.student.main.ntu.edu.sg/mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=12623 [22/Apr/15 06:00:36 PM]



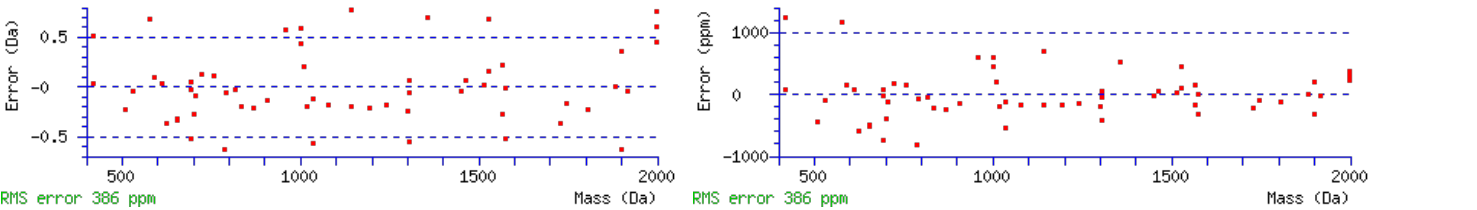
NCBI BLAST search of [ADGTVNQIEGEATPDNITEPAK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
77.7	2271.0390	-0.0069	ADGTVNQIEGEATPDNITEPAK	Deamidated N6, N16 93.88%
65.9	2271.0390	-0.0069	ADGTVNQIEGEATPDNITEPAK	Deamidated Q7, N16 6.12%
18.5	2271.0390	-0.0069	ADGTVNQIEGEATPDNITEPAK	Deamidated N6, Q7 0.00%
5.3	2271.0338	-0.0016	RSANQFYSMVQSANSIRR	
2.2	2270.0260	1.0062	VSGADNYDKTEGVDIENMALK	
1.8	2270.0446	0.9875	QSLFQEEGMLSLVLNCIDR	

Mascot: <http://www.matrixscience.com/>

24	2628.2022	1314.6047	2611.1756	1306.0914	2610.1916	1305.5994	T	793.3509	397.1791	776.3243	388.6658	775.3403	388.1738	6
25	2788.2328	1394.6200	2771.2063	1386.1068	2770.2222	1385.6148	C	692.3032	346.6552	675.2767	338.1420	674.2926	337.6500	5
26	2901.3169	1451.1621	2884.2903	1442.6488	2883.3063	1442.1568	I	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
27	3030.3595	1515.6834	3013.3329	1507.1701	3012.3489	1506.6781	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
28	3145.3864	1573.1968	3128.3599	1564.6836	3127.3758	1564.1916	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
29							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [YTESEIITVQCDSGYGLVGPQNITCIEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
77.4	3318.4908	0.0164	YTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q21, N22 98.00%
57.5	3318.4908	0.0164	YTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q10, N22 1.00%
57.5	3318.4908	0.0164	YTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q10, Q21 1.00%
50.0	3317.5068	1.0004	YTESEIITVQCDSGYGLVGPQNITCIEDR	
50.0	3317.5068	1.0004	YTESEIITVQCDSGYGLVGPQNITCIEDR	
34.6	3317.5068	1.0004	YTESEIITVQCDSGYGLVGPQNITCIEDR	
31.0	3316.5228	1.9844	YTESEIITVQCDSGYGLVGPQNITCIEDR	
8.1	3318.4980	0.0092	MGRVIPSDLNLMADNSQPENEKEASGGDSPK	
4.2	3316.5187	1.9884	AVLASMDNENMHTPDIGGQGTSEAIQDIIR	
3.7	3318.4980	0.0092	MGRVIPSDLNLMADNSQPENEKEASGGDSPK	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1S0J2** in **uni_pig**, tr|F1S0J2|F1S0J2_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPA PE=4 SV=2

Title: 120325_Sunil_PigSerum_Glyco_P_13Spectrum5757_scans__6728

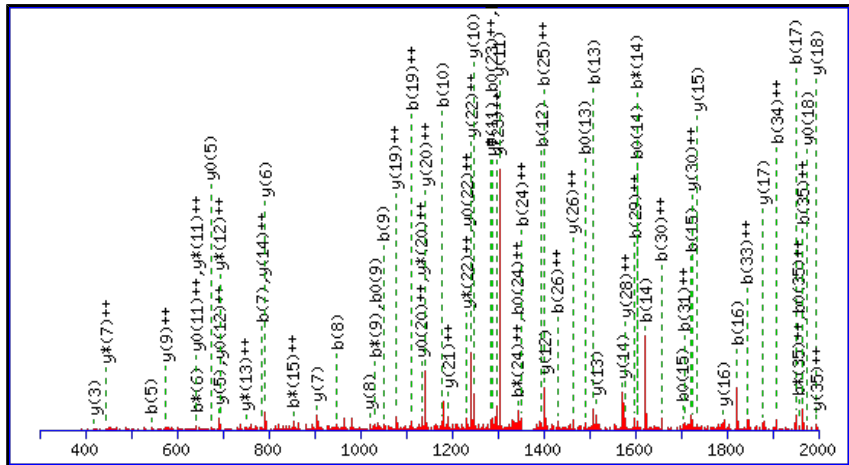
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

Q17 : Deamidated (NQ)

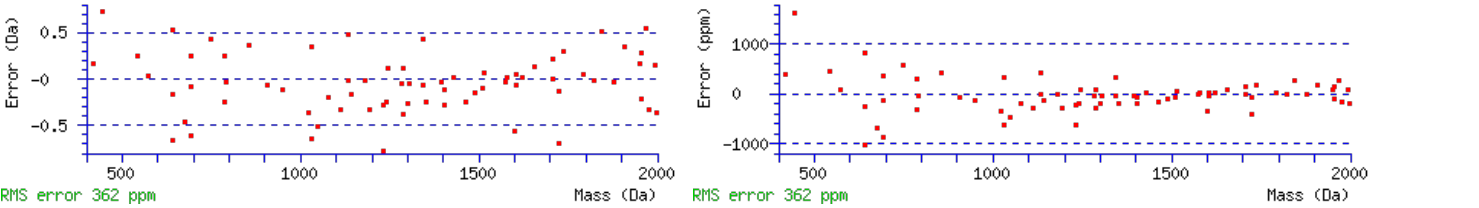
N29 : Deamidated (NQ)

Ions Score: 77 Expect: 1e-006

Matches : 74/408 fragment ions using 133 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							36
2	201.1234	101.0653			183.1128	92.0600	S	3991.8060	1996.4066	3974.7794	1987.8933	3973.7954	1987.4013	35
3	300.1918	150.5995			282.1812	141.5942	V	3904.7739	1952.8906	3887.7474	1944.3773	3886.7634	1943.8853	34
4	415.2187	208.1130			397.2082	199.1077	D	3805.7055	1903.3564	3788.6790	1894.8431	3787.6949	1894.3511	33
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	Q	3690.6786	1845.8429	3673.6520	1837.3296	3672.6680	1836.8376	32
6	658.3042	329.6558	641.2777	321.1425	640.2937	320.6505	D	3562.6200	1781.8136	3545.5934	1773.3004	3544.6094	1772.8084	31
7	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	K	3447.5930	1724.3002	3430.5665	1715.7869	3429.5825	1715.2949	30
8	949.4625	475.2349	932.4360	466.7216	931.4520	466.2296	Y	3319.4981	1660.2527	3302.4715	1651.7394	3301.4875	1651.2474	29
9	1050.5102	525.7587	1033.4837	517.2455	1032.4997	516.7535	T	3156.4348	1578.7210	3139.4082	1570.2077	3138.4242	1569.7157	28
10	1179.5528	590.2800	1162.5263	581.7668	1161.5422	581.2748	E	3055.3871	1528.1972	3038.3605	1519.6839	3037.3765	1519.1919	27
11	1266.5848	633.7961	1249.5583	625.2828	1248.5743	624.7908	S	2926.3445	1463.6759	2909.3179	1455.1626	2908.3339	1454.6706	26
12	1395.6274	698.3174	1378.6009	689.8041	1377.6169	689.3121	E	2839.3125	1420.1599	2822.2859	1411.6466	2821.3019	1411.1546	25
13	1508.7115	754.8594	1491.6849	746.3461	1490.7009	745.8541	I	2710.2699	1355.6386	2693.2433	1347.1253	2692.2593	1346.6333	24
14	1621.7956	811.4014	1604.7690	802.8881	1603.7850	802.3961	I	2597.1858	1299.0965	2580.1592	1290.5833	2579.1752	1290.0913	23
15	1722.8432	861.9253	1705.8167	853.4120	1704.8327	852.9200	T	2484.1017	1242.5545	2467.0752	1234.0412	2466.0912	1233.5492	22
16	1821.9117	911.4595	1804.8851	902.9462	1803.9011	902.4542	V	2383.0541	1192.0307	2366.0275	1183.5174	2365.0435	1183.0254	21
17	1950.9542	975.9808	1933.9277	967.4675	1932.9437	966.9755	Q	2283.9856	1142.4965	2266.9591	1133.9832	2265.9751	1133.4912	20
18	2110.9849	1055.9961	2093.9583	1047.4828	2092.9743	1046.9908	C	2154.9430	1077.9752	2137.9165	1069.4619	2136.9325	1068.9699	19
19	2226.0118	1113.5096	2208.9853	1104.9963	2208.0013	1104.5043	D	1994.9124	997.9598	1977.8858	989.4466	1976.9018	988.9546	18
20	2313.0439	1157.0256	2296.0173	1148.5123	2295.0333	1148.0203	S	1879.8855	940.4464	1862.8589	931.9331	1861.8749	931.4411	17
21	2370.0653	1185.5363	2353.0388	1177.0230	2352.0548	1176.5310	G	1792.8534	896.9304	1775.8269	888.4171	1774.8429	887.9251	16
22	2533.1287	1267.0680	2516.1021	1258.5547	2515.1181	1258.0627	Y	1735.8320	868.4196	1718.8054	859.9063	1717.8214	859.4143	15
23	2590.1501	1295.5787	2573.1236	1287.0654	2572.1396	1286.5734	G	1572.7686	786.8880	1555.7421	778.3747	1554.7581	777.8827	14

24	2703.2342	1352.1207	2686.2076	1343.6075	2685.2236	1343.1154	L	1515.7472	758.3772	1498.7206	749.8639	1497.7366	749.3719	13
25	2802.3026	1401.6549	2785.2761	1393.1417	2784.2920	1392.6497	V	1402.6631	701.8352	1385.6366	693.3219	1384.6525	692.8299	12
26	2859.3241	1430.1657	2842.2975	1421.6524	2841.3135	1421.1604	G	1303.5947	652.3010	1286.5681	643.7877	1285.5841	643.2957	11
27	2956.3768	1478.6921	2939.3503	1470.1788	2938.3663	1469.6868	P	1246.5732	623.7903	1229.5467	615.2770	1228.5627	614.7850	10
28	3084.4354	1542.7213	3067.4089	1534.2081	3066.4248	1533.7161	Q	1149.5205	575.2639	1132.4939	566.7506	1131.5099	566.2586	9
29	3199.4623	1600.2348	3182.4358	1591.7215	3181.4518	1591.2295	N	1021.4619	511.2346	1004.4353	502.7213	1003.4513	502.2293	8
30	3312.5464	1656.7768	3295.5199	1648.2636	3294.5358	1647.7716	I	906.4349	453.7211	889.4084	445.2078	888.4244	444.7158	7
31	3413.5941	1707.3007	3396.5675	1698.7874	3395.5835	1698.2954	T	793.3509	397.1791	776.3243	388.6658	775.3403	388.1738	6
32	3573.6247	1787.3160	3556.5982	1778.8027	3555.6142	1778.3107	C	692.3032	346.6552	675.2767	338.1420	674.2926	337.6500	5
33	3686.7088	1843.8580	3669.6823	1835.3448	3668.6982	1834.8528	I	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
34	3815.7514	1908.3793	3798.7248	1899.8661	3797.7408	1899.3741	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
35	3930.7783	1965.8928	3913.7518	1957.3795	3912.7678	1956.8875	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
36							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
77.4	4103.8827	0.0119	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q17, N29 45.52%
77.4	4103.8827	0.0119	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q17, Q28 45.52%
71.1	4102.8987	0.9960	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
71.1	4102.8987	0.9960	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
69.0	4103.8827	0.0119	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q28, N29 6.53%
61.7	4103.8827	0.0119	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, N29 1.21%
61.7	4103.8827	0.0119	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q28 1.21%
38.0	4103.8827	0.0119	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q17 0.01%
36.9	4102.8987	0.9960	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
36.4	4101.9147	1.9800	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

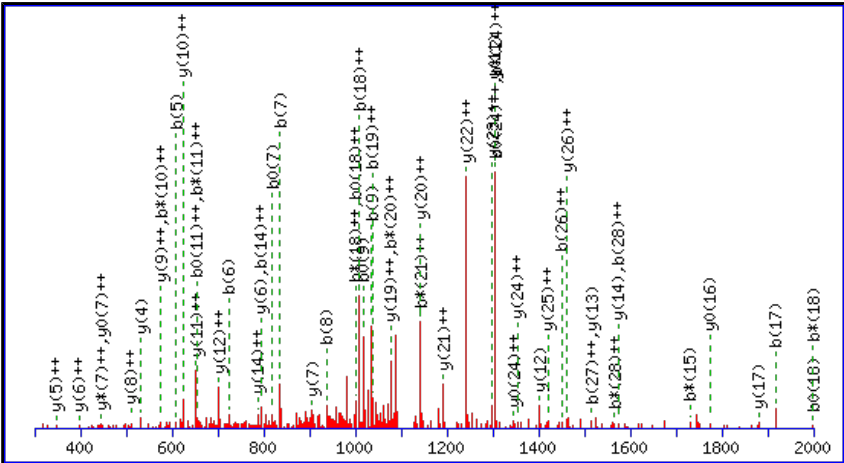
Peptide View

MS/MS Fragmentation of **YTESEIITVQCDSGYGLVGPNITCIEDR**
Found in **F1S0J2** in **uni_pig**, tr[F1S0J2]F1S0J2_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPA PE=4 SV=2

Match to Query 13427: 3318.498552 from(1107.173460,3+) intensity(0.0000) rtinseconds(2822) scans(5658) index(10151)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_11Spectrum4259_scans_5658
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

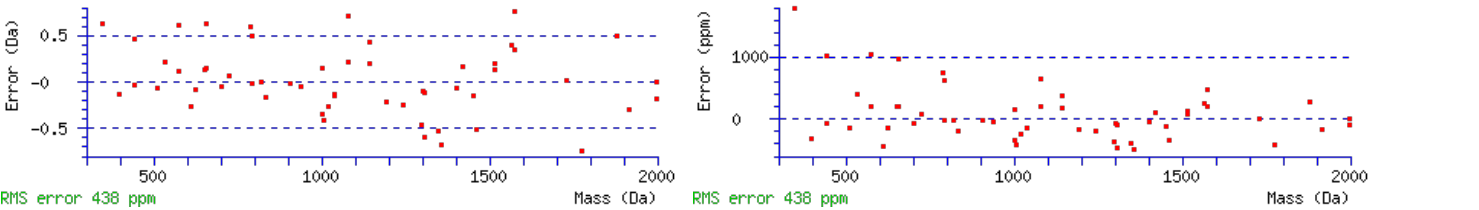
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 3318.4908
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Deamidated (NQ)
N22 : Deamidated (NQ)
Ions Score: 77 Expect: 1.1e-006
Matches : 55/314 fragment ions using 97 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							29
2	265.1183	133.0628			247.1077	124.0575	T	3156.4348	1578.7210	3139.4082	1570.2077	3138.4242	1569.7157	28
3	394.1609	197.5841			376.1503	188.5788	E	3055.3871	1528.1972	3038.3605	1519.6839	3037.3765	1519.1919	27
4	481.1929	241.1001			463.1823	232.0948	S	2926.3445	1463.6759	2909.3179	1455.1626	2908.3339	1454.6706	26
5	610.2355	305.6214			592.2249	296.6161	E	2839.3125	1420.1599	2822.2859	1411.6466	2821.3019	1411.1546	25
6	723.3196	362.1634			705.3090	353.1581	I	2710.2699	1355.6386	2693.2433	1347.1253	2692.2593	1346.6333	24
7	836.4036	418.7055			818.3931	409.7002	I	2597.1858	1299.0965	2580.1592	1290.5833	2579.1752	1290.0913	23
8	937.4513	469.2293			919.4407	460.2240	T	2484.1017	1242.5545	2467.0752	1234.0412	2466.0912	1233.5492	22
9	1036.5197	518.7635			1018.5092	509.7582	V	2383.0541	1192.0307	2366.0275	1183.5174	2365.0435	1183.0254	21
10	1165.5623	583.2848	1148.5358	574.7715	1147.5517	574.2795	Q	2283.9856	1142.4965	2266.9591	1133.9832	2265.9751	1133.4912	20
11	1325.5930	663.3001	1308.5664	654.7868	1307.5824	654.2948	C	2154.9430	1077.9752	2137.9165	1069.4619	2136.9325	1068.9699	19
12	1440.6199	720.8136	1423.5934	712.3003	1422.6093	711.8083	D	1994.9124	997.9598	1977.8859	989.4466	1976.9018	988.9546	18
13	1527.6519	764.3296	1510.6254	755.8163	1509.6414	755.3243	S	1879.8855	940.4464	1862.8589	931.9331	1861.8749	931.4411	17
14	1584.6734	792.8403	1567.6468	784.3271	1566.6628	783.8351	G	1792.8534	896.9304	1775.8269	888.4171	1774.8429	887.9251	16
15	1747.7367	874.3720	1730.7102	865.8587	1729.7262	865.3667	Y	1735.8320	868.4196	1718.8054	859.9063	1717.8214	859.4143	15
16	1804.7582	902.8827	1787.7316	894.3695	1786.7476	893.8775	G	1572.7686	786.8880	1555.7421	778.3747	1554.7581	777.8827	14
17	1917.8423	959.4248	1900.8157	950.9115	1899.8317	950.4195	L	1515.7472	758.3772	1498.7206	749.8639	1497.7366	749.3719	13
18	2016.9107	1008.9590	1999.8841	1000.4457	1998.9001	999.9537	V	1402.6631	701.8352	1385.6366	693.3219	1384.6525	692.8299	12
19	2073.9321	1037.4697	2056.9056	1028.9564	2055.9216	1028.4644	G	1303.5947	652.3010	1286.5681	643.7877	1285.5841	643.2957	11
20	2170.9849	1085.9961	2153.9583	1077.4828	2152.9743	1076.9908	P	1246.5732	623.7903	1229.5467	615.2770	1228.5627	614.7850	10
21	2299.0435	1150.0254	2282.0169	1141.5121	2281.0329	1141.0201	Q	1149.5205	575.2639	1132.4939	566.7506	1131.5099	566.2586	9
22	2414.0704	1207.5388	2397.0439	1199.0256	2396.0599	1198.5336	N	1021.4619	511.2346	1004.4353	502.7213	1003.4513	502.2293	8
23	2527.1545	1264.0809	2510.1279	1255.5676	2509.1439	1255.0756	I	906.4349	453.7211	889.4084	445.2078	888.4244	444.7158	7

24	2628.2022	1314.6047	2611.1756	1306.0914	2610.1916	1305.5994	T	793.3509	397.1791	776.3243	388.6658	775.3403	388.1738	6
25	2788.2328	1394.6200	2771.2063	1386.1068	2770.2222	1385.6148	C	692.3032	346.6552	675.2767	338.1420	674.2926	337.6500	5
26	2901.3169	1451.1621	2884.2903	1442.6488	2883.3063	1442.1568	I	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
27	3030.3595	1515.6834	3013.3329	1507.1701	3012.3489	1506.6781	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
28	3145.3864	1573.1968	3128.3599	1564.6836	3127.3758	1564.1916	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
29							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [YTESEIITVQCDSGYGLVGPQNITCIEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
76.6	3318.4908	0.0078	YTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q10, N22 34.61%
76.6	3318.4908	0.0078	YTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q10, Q21 34.61%
76.1	3318.4908	0.0078	YTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q21, N22 30.78%
75.4	3317.5068	0.9918	YTESEIITVQCDSGYGLVGPQNITCIEDR	
75.4	3317.5068	0.9918	YTESEIITVQCDSGYGLVGPQNITCIEDR	
60.8	3317.5068	0.9918	YTESEIITVQCDSGYGLVGPQNITCIEDR	
54.3	3316.5228	1.9758	YTESEIITVQCDSGYGLVGPQNITCIEDR	
12.1	3318.4987	-0.0001	MEDVYQTLVAHGQALDSGWGGLGATPEDLDR	
9.6	3317.5027	0.9958	AVLASMDNENMHTPDIGGQGTSEAIQDIIR	
7.4	3318.4980	0.0006	MGRVIPSDLNLMADNSQPENEKEASGGDSPK	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1SQX9** in **uni_pig**, tr|F1SQX9|F1SQX9_PIG Uncharacterized protein OS=Sus scrofa GN=APOD PE=4 SV=3

Title: 120325_Sunil_PigSerum_Glyco_S_16Spectrum2352_scans__3456

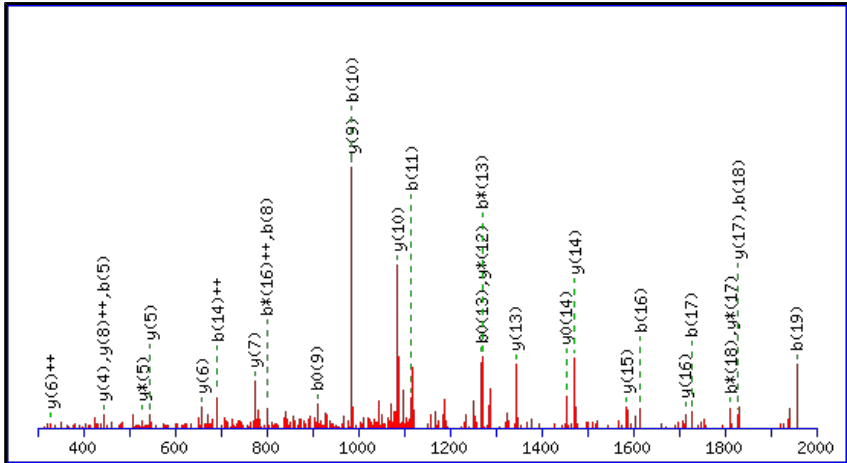
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2271.0390

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

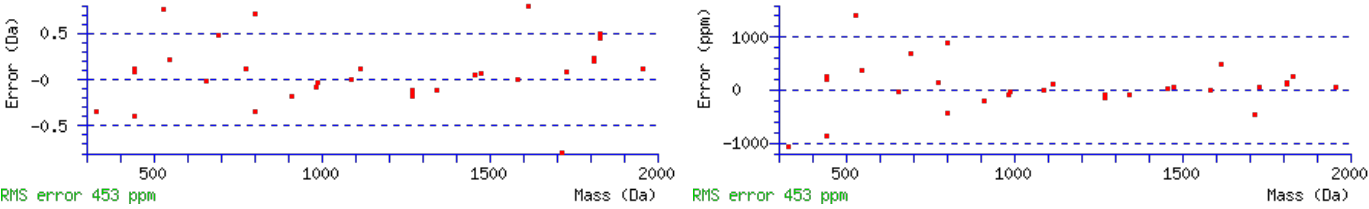
Q7 : Deamidated (NQ)

N16 : Deamidated (NQ)
 Taxa Score: 77.5 Percent:

Ions Score: 77 Expect: 1.3e-006
Matches : 31/234 fragment ions u

Matches : 31/234 Fragment Ions using 34 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							22
2	187.0713	94.0393			169.0608	85.0340	D	2201.0092	1101.0082	2183.9826	1092.4950	2182.9986	1092.0030	21
3	244.0928	122.5500			226.0822	113.5448	G	2085.9823	1043.4948	2068.9557	1034.9815	2067.9717	1034.4895	20
4	345.1405	173.0739			327.1299	164.0686	T	2028.9608	1014.9840	2011.9342	1006.4708	2010.9502	1005.9788	19
5	444.2089	222.6081			426.1983	213.6028	V	1927.9131	964.4602	1910.8866	955.9469	1909.9025	955.4549	18
6	558.2518	279.6295	541.2253	271.1163	540.2413	270.6243	N	1828.8447	914.9260	1811.8181	906.4127	1810.8341	905.9207	17
7	687.2944	344.1508	670.2679	335.6376	669.2838	335.1456	Q	1714.8018	857.9045	1697.7752	849.3912	1696.7912	848.8992	16
8	800.3785	400.6929	783.3519	392.1796	782.3679	391.6876	I	1585.7592	793.3832	1568.7326	784.8700	1567.7486	784.3779	15
9	929.4211	465.2142	912.3945	456.7009	911.4105	456.2089	E	1472.6751	736.8412	1455.6486	728.3279	1454.6645	727.8359	14
10	986.4425	493.7249	969.4160	485.2116	968.4320	484.7196	G	1343.6325	672.3199	1326.6060	663.8066	1325.6220	663.3146	13
11	1115.4851	558.2462	1098.4586	549.7329	1097.4746	549.2409	E	1286.6111	643.8092	1269.5845	635.2959	1268.6005	634.8039	12
12	1186.5222	593.7648	1169.4957	585.2515	1168.5117	584.7595	A	1157.5685	579.2879	1140.5419	570.7746	1139.5579	570.2826	11
13	1287.5699	644.2886	1270.5434	635.7753	1269.5594	635.2833	T	1086.5313	543.7693	1069.5048	535.2560	1068.5208	534.7640	10
14	1384.6227	692.8150	1367.5961	684.3017	1366.6121	683.8097	P	985.4837	493.2455	968.4571	484.7322	967.4731	484.2402	9
15	1499.6496	750.3285	1482.6231	741.8152	1481.6391	741.3232	D	888.4309	444.7191	871.4044	436.2058	870.4203	435.7138	8
16	1614.6766	807.8419	1597.6500	799.3286	1596.6660	798.8366	N	773.4040	387.2056	756.3774	378.6923	755.3934	378.2003	7
17	1727.7606	864.3840	1710.7341	855.8707	1709.7501	855.3787	I	658.3770	329.6921	641.3505	321.1789	640.3665	320.6869	6
18	1828.8083	914.9078	1811.7818	906.3945	1810.7977	905.9025	T	545.2930	273.1501	528.2664	264.6368	527.2824	264.1448	5
19	1957.8509	979.4291	1940.8244	970.9158	1939.8403	970.4238	E	444.2453	222.6263	427.2187	214.1130	426.2347	213.6210	4
20	2054.9037	1027.9555	2037.8771	1019.4422	2036.8931	1018.9502	P	315.2027	158.1050	298.1761	149.5917			3
21	2125.9408	1063.4740	2108.9142	1054.9608	2107.9302	1054.4687	A	218.1499	109.5786	201.1234	101.0653			2
22							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [ADGTVNQIEGEATPDNITEPAK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
76.6	2271.0390	0.9977	ADGTVNQIEGEATPDNITEPAK	Deamidated Q7, N16 50.00%
76.6	2271.0390	0.9977	ADGTVNQIEGEATPDNITEPAK	Deamidated N6, N16 50.00%
65.8	2272.0230	0.0137	ADGTVNQIEGEATPDNITEPAK	
15.7	2271.0390	0.9977	ADGTVNQIEGEATPDNITEPAK	Deamidated N6, Q7 0.00%
4.8	2270.0208	2.0158	NTVSGMQKFMGEDLNEHQR	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **I3LD86** in **uni_pig**, tr|I3LD86|I3LD86_PIG N-acetylmuramoyl-L-alanine amidase OS=Sus scrofa GN=PGLYRP2 PE=4 SV=1

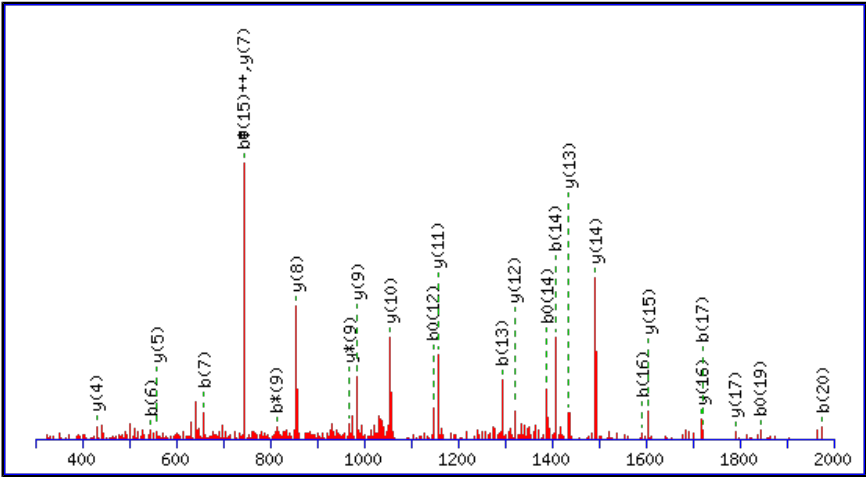
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

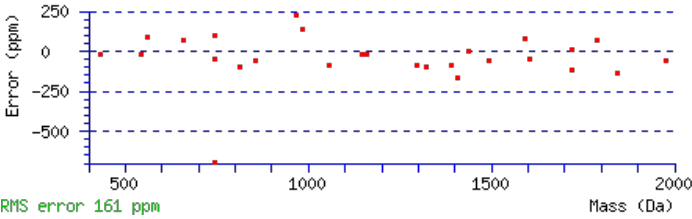
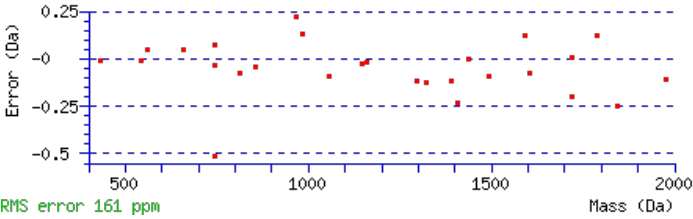
Show Y-axis



Ions Score: 78 Expect: 1.3e-006
Matches: 27/106 fragment ions:

Matches : 27/196 fragment ions using 51 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							21
2	205.0972	103.0522					F	2093.0913	1047.0493	2076.0648	1038.5360	2075.0808	1038.0440	20
3	262.1186	131.5629					G	1946.0229	973.5151	1928.9964	965.0018	1928.0124	964.5098	19
4	361.1870	181.0972					V	1889.0015	945.0044	1871.9749	936.4911	1870.9909	935.9991	18
5	432.2241	216.6157					A	1789.9331	895.4702	1772.9065	886.9569	1771.9225	886.4649	17
6	545.3082	273.1577					L	1718.8959	859.9516	1701.8694	851.4383	1700.8854	850.9463	16
7	658.3923	329.6998					I	1605.8119	803.4096	1588.7853	794.8963	1587.8013	794.4043	15
8	715.4137	358.2105					G	1492.7278	746.8675	1475.7013	738.3543	1474.7172	737.8623	14
9	830.4407	415.7240	813.4141	407.2107			N	1435.7064	718.3568	1418.6798	709.8435	1417.6958	709.3515	13
10	993.5040	497.2556	976.4775	488.7424			Y	1320.6794	660.8433	1303.6529	652.3301	1302.6688	651.8381	12
11	1094.5517	547.7795	1077.5251	539.2662	1076.5411	538.7742	T	1157.6161	579.3117	1140.5895	570.7984	1139.6055	570.3064	11
12	1165.5888	583.2980	1148.5623	574.7848	1147.5782	574.2928	A	1056.5684	528.7878	1039.5419	520.2746	1038.5578	519.7826	10
13	1294.6314	647.8193	1277.6048	639.3061	1276.6208	638.8141	E	985.5313	493.2693	968.5047	484.7560	967.5207	484.2640	9
14	1407.7155	704.3614	1390.6889	695.8481	1389.7049	695.3561	L	856.4887	428.7480	839.4621	420.2347	838.4781	419.7427	8
15	1504.7682	752.8877	1487.7417	744.3745	1486.7577	743.8825	P	743.4046	372.2060	726.3781	363.6927	725.3941	363.2007	7
16	1591.8003	796.4038	1574.7737	787.8905	1573.7897	787.3985	S	646.3519	323.6796	629.3253	315.1663	628.3413	314.6743	6
17	1720.8428	860.9251	1703.8163	852.4118	1702.8323	851.9198	E	559.3198	280.1636	542.2933	271.6503	541.3093	271.1583	5
18	1791.8800	896.4436	1774.8534	887.9303	1773.8694	887.4383	A	430.2772	215.6423	413.2507	207.1290			4
19	1862.9171	931.9622	1845.8905	923.4489	1844.9065	922.9569	A	359.2401	180.1237	342.2136	171.6104			3
20	1976.0011	988.5042	1958.9746	979.9909	1957.9906	979.4989	L	288.2030	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1



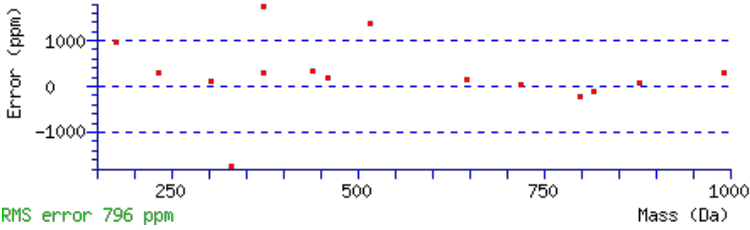
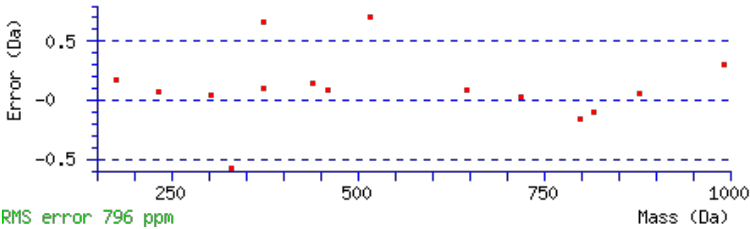
NCBI **BLAST** search of [GFGVALIGNYTAELPSEAALR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
78.1	2149.1055	-0.0026	GFGVALIGNYTAELPSEAALR
5.7	2149.0936	0.0093	VQKLKEQETTGMLQTQLR
5.7	2149.0936	0.0093	VQKLKEQETTGMLQTQLR
3.6	2148.1071	0.9958	LLQMOPIQHGEIHKHMAK
3.6	2148.1071	0.9958	LLQMOPIQHGEIHKHMAK
3.6	2147.0858	2.0171	NGYENINVSSNVLENKKPK
3.0	2147.0858	2.0171	NGYENINVSSNVLENKKPK
2.8	2149.0871	0.0158	EGLTRMSMDLKNNLLGSLR
1.6	2149.0911	0.0118	LLQMOPIQHGEIHKHMAK
1.3	2149.0976	0.0052	MLLFVEQVTSKGTGLNPNAK

Mascot: <http://www.matrixscience.com/>

http:// MascotXP.student.main.ntu.edu.sg/Mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=626 [22/Apr/15 06:00:58 PM]



NCBI **BLAST** search of [GICANASAAGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.3	1047.4767	-0.0022	GICANASAAGR
10.1	1046.4628	1.0117	QAEEEEERR
8.8	1047.4768	-0.0023	GLGQGGMDTGR
8.2	1045.4676	2.0069	QESKDEPGR
8.2	1047.4767	-0.0022	EAMEERAGR
6.4	1047.4695	0.0050	MLTYYEGR
6.4	1045.4676	2.0069	DQQVEAAQR
6.1	1047.4655	0.0090	CLGQQADVRL
5.8	1047.4767	-0.0022	EMNGNRLGR
5.1	1047.4807	-0.0062	MQAQPPGYR

Mascot: <http://www.matrixscience.com/>

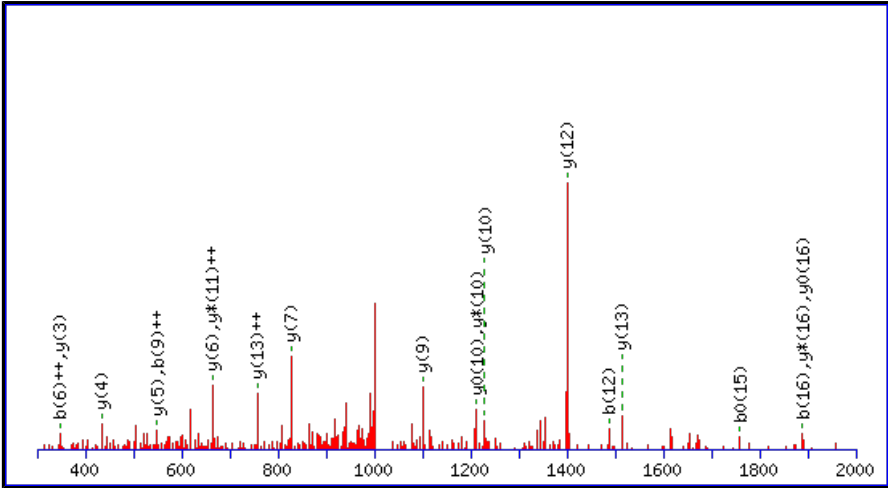
Peptide View

Match to Query 11807: 2035.880948 from(1018.947750,2+) intensity(0.0000) rtinseconds(1961) scans(3811) index(6734)
Title: 120325_Sunil_PigSerum_Glyco_S_16Spectrum2636_scans__3811
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

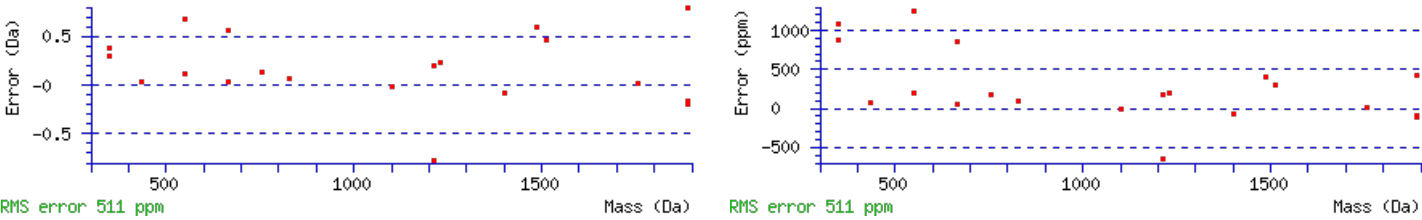
Click mouse within plot area to zoom in by factor of two about that point
Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



#	b	b ⁺⁺	b*	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	293.1132	147.0602			275.1026	138.0550	Y	1906.8375	953.9224	1889.8110	945.4091	1888.8269	944.9171	16
3	422.1558	211.5815	405.1292	203.0683	404.1452	202.5763	Q	1743.7742	872.3907	1726.7476	863.8775	1725.7636	863.3854	15
4	523.2035	262.1054	506.1769	253.5921	505.1929	253.1001	T	1614.7316	807.8694	1597.7050	799.3562	1596.7210	798.8641	14
5	636.2875	318.6474	619.2610	310.1341	618.2770	309.6421	I	1513.6839	757.3456	1496.6574	748.8323	1495.6733	748.3403	13
6	693.3090	347.1581	676.2825	338.6449	675.2984	338.1529	G	1400.5998	700.8036	1383.5733	692.2903	1382.5893	691.7983	12
7	807.3519	404.1796	790.3254	395.6663	789.3414	395.1743	N	1343.5784	672.2928	1326.5518	663.7796	1325.5678	663.2875	11
8	936.3945	468.7009	919.3680	460.1876	918.3840	459.6956	Q	1229.5354	615.2714	1212.5089	606.7581	1211.5249	606.2661	10
9	1096.4252	548.7162	1079.3986	540.2029	1078.4146	539.7109	C	1100.4929	550.7501	1083.4663	542.2368	1082.4823	541.7448	9
10	1209.5092	605.2583	1192.4827	596.7450	1191.4987	596.2530	I	940.4622	470.7347	923.4357	462.2215	922.4516	461.7295	8
11	1372.5726	686.7899	1355.5460	678.2766	1354.5620	677.7846	Y	827.3781	414.1927	810.3516	405.6794	809.3676	405.1874	7
12	1487.5995	744.3034	1470.5730	735.7901	1469.5889	735.2981	N	664.3148	332.6610	647.2883	324.1478	646.3042	323.6558	6
13	1602.6264	801.8169	1585.5999	793.3036	1584.6159	792.8116	D	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
14	1689.6585	845.3329	1672.6319	836.8196	1671.6479	836.3276	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
15	1776.6905	888.8489	1759.6640	880.3356	1758.6799	879.8436	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
16	1889.7746	945.3909	1872.7480	936.8776	1871.7640	936.3856	L	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EYQTIGNQCIYNDSSLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.0	2034.8728	1.0082	EYQTIGNQCIYNDSSLK	Deamidated Q3, Q8, N12 56.89%
70.6	2034.8728	1.0082	EYQTIGNQCIYNDSSLK	Deamidated N7, Q8, N12 41.21%
60.3	2033.8888	1.9922	EYQTIGNQCIYNDSSLK	
57.3	2034.8728	1.0082	EYQTIGNQCIYNDSSLK	Deamidated Q3, N7, N12 1.89%
47.0	2033.8888	1.9922	EYQTIGNQCIYNDSSLK	
31.6	2033.8888	1.9922	EYQTIGNQCIYNDSSLK	
23.1	2034.8728	1.0082	EYQTIGNQCIYNDSSLK	Deamidated Q3, N7, Q8 0.00%
16.6	2033.8888	1.9922	EYQTIGNQCIYNDSSLK	
9.1	2033.8888	1.9922	EYQTIGNQCIYNDSSLK	
5.4	2034.8726	1.0083	DASGRSTNSHQSTENDLK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

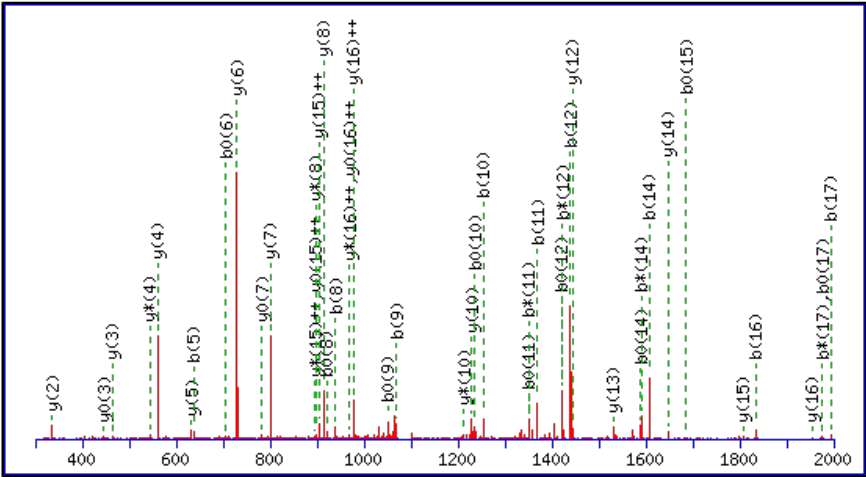
Peptide View

MS/MS Fragmentation of **TLFCNSSQEWNAPAECR**
Found in **F1S0J3** in **uni_pig**, tr|F1S0J3|F1S0J3_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPB PE=4 SV=1

Match to Query 12110: 2166.909628 from(1084.462090,2+) intensity(29580.9941) rtinseconds(2044) scans(4929) index(3872)
Title: 120325_Sunil_PigSerum_Glyco_P_14Spectrum4111_scans_4929
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

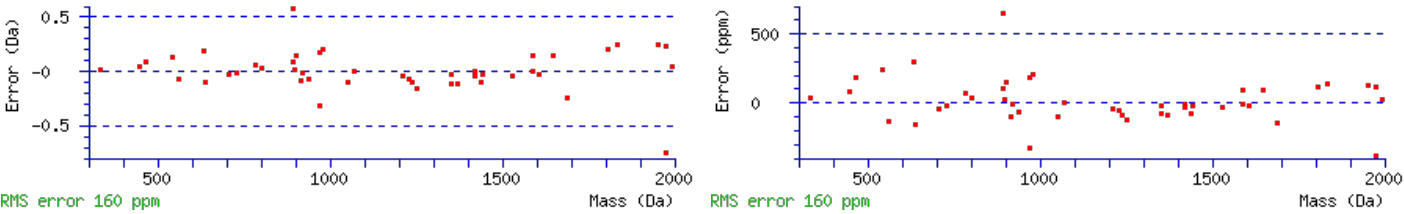
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2166.9099
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 69 Expect: 1.6e-006
Matches : 46/192 fragment ions using 85 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							18
2	215.1390	108.0731			197.1285	99.0679	L	2066.8695	1033.9384	2049.8429	1025.4251	2048.8589	1024.9331	17
3	362.2074	181.6074			344.1969	172.6021	F	1953.7854	977.3963	1936.7589	968.8831	1935.7749	968.3911	16
4	522.2381	261.6227			504.2275	252.6174	C	1806.7170	903.8621	1789.6905	895.3489	1788.7064	894.8569	15
5	637.2650	319.1362	620.2385	310.6229	619.2545	310.1309	N	1646.6864	823.8468	1629.6598	815.3335	1628.6758	814.8415	14
6	724.2971	362.6522	707.2705	354.1389	706.2865	353.6469	S	1531.6594	766.3333	1514.6329	757.8201	1513.6489	757.3281	13
7	811.3291	406.1682	794.3025	397.6549	793.3185	397.1629	S	1444.6274	722.8173	1427.6008	714.3041	1426.6168	713.8121	12
8	939.3877	470.1975	922.3611	461.6842	921.3771	461.1922	Q	1357.5954	679.3013	1340.5688	670.7880	1339.5848	670.2960	11
9	1068.4303	534.7188	1051.4037	526.2055	1050.4197	525.7135	E	1229.5368	615.2720	1212.5102	606.7588	1211.5262	606.2667	10
10	1254.5096	627.7584	1237.4830	619.2451	1236.4990	618.7531	W	1100.4942	550.7507	1083.4676	542.2375	1082.4836	541.7455	9
11	1368.5525	684.7799	1351.5259	676.2666	1350.5419	675.7746	N	914.4149	457.7111	897.3883	449.1978	896.4043	448.7058	8
12	1439.5896	720.2984	1422.5631	711.7852	1421.5790	711.2932	A	800.3720	400.6896	783.3454	392.1763	782.3614	391.6843	7
13	1536.6424	768.8248	1519.6158	760.3115	1518.6318	759.8195	P	729.3348	365.1711	712.3083	356.6578	711.3243	356.1658	6
14	1607.6795	804.3434	1590.6529	795.8301	1589.6689	795.3381	A	632.2821	316.6447	615.2555	308.1314	614.2715	307.6394	5
15	1704.7322	852.8698	1687.7057	844.3565	1686.7217	843.8645	P	561.2450	281.1261	544.2184	272.6128	543.2344	272.1208	4
16	1833.7748	917.3911	1816.7483	908.8778	1815.7643	908.3858	E	464.1922	232.5997	447.1656	224.0865	446.1816	223.5945	3
17	1993.8055	997.4064	1976.7789	988.8931	1975.7949	988.4011	C	335.1496	168.0784	318.1231	159.5652			2
18							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [TLFCNSSQEWNAPAEPCR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
69.5	2166.9099	-0.0002	TLFCNSSQEWNAPAEPCR	Deamidated N5 90.11%
59.7	2166.9099	-0.0002	TLFCNSSQEWNAPAEPCR	Deamidated Q8 9.50%
45.8	2166.9099	-0.0002	TLFCNSSQEWNAPAEPCR	Deamidated N11 0.39%
22.6	2165.9259	0.9838	TLFCNSSQEWNAPAEPCR	
0.9	2166.9099	-0.0003	EPTSPAQDSPFKNCWSCR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of EYQTIGNOCIYNDSSLK

Found in **F1SN68** in **uni_pig**, tr|F1SN68|F1SN68_PIG Alpha-1-acid glycoprotein OS=Sus scrofa GN=ORM1 PE=3 SV=1

Match to Query 11646: 2034.879688 from(1018.447120,2+) intensity(7482.6216) rtinseconds(1962) scans(3746) index(7022)

Title: 120325 Sunil PigSerum Glyco S 18Spectrum2641 scans 3746

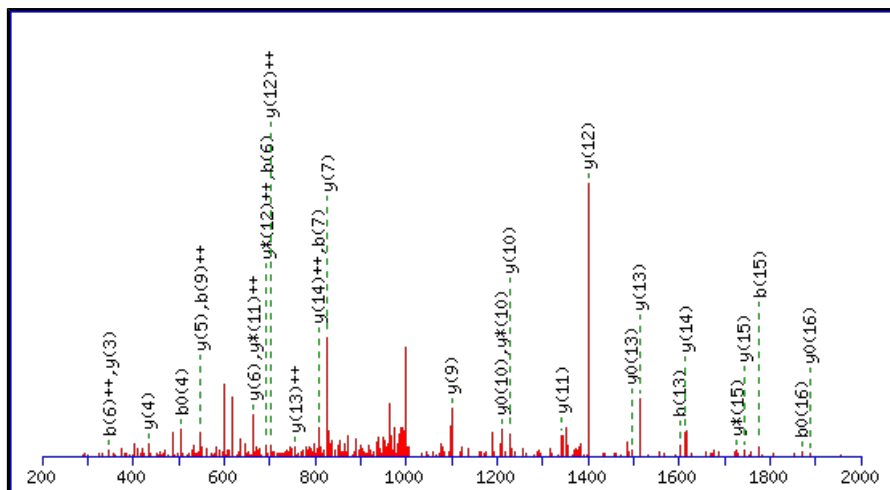
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2034.8728

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

Q3 : Deamidated (NQ)

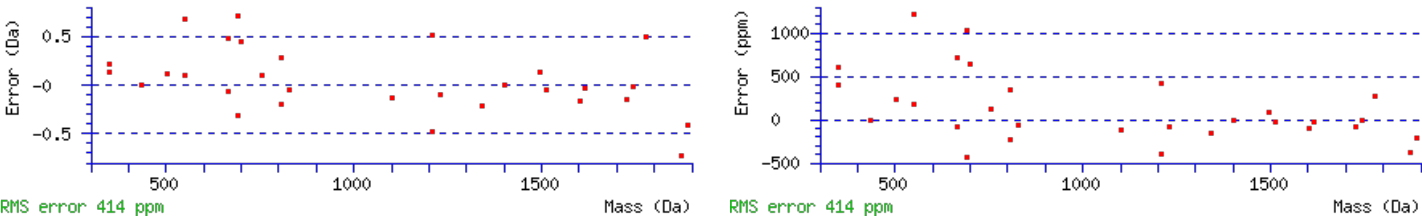
N7 : Deamidated (NQ)

N12 : Deamidated (NQ)

Ions Score: 71 Expect: 1.7e-006

Matches : 30/184 fragment ions using 49 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	293.1132	147.0602			275.1026	138.0550	Y	1906.8375	953.9224	1889.8110	945.4091	1888.8269	944.9171	16
3	422.1558	211.5815	405.1292	203.0683	404.1452	202.5763	Q	1743.7742	872.3907	1726.7476	863.8775	1725.7636	863.3854	15
4	523.2035	262.1054	506.1769	253.5921	505.1929	253.1001	T	1614.7316	807.8694	1597.7050	799.3562	1596.7210	798.8641	14
5	636.2875	318.6474	619.2610	310.1341	618.2770	309.6421	I	1513.6839	757.3456	1496.6574	748.8323	1495.6733	748.3403	13
6	693.3090	347.1581	676.2825	338.6449	675.2984	338.1529	G	1400.5998	700.8036	1383.5733	692.2903	1382.5893	691.7983	12
7	808.3359	404.6716	791.3094	396.1583	790.3254	395.6663	N	1343.5784	672.2928	1326.5518	663.7796	1325.5678	663.2875	11
8	936.3945	468.7009	919.3680	460.1876	918.3840	459.6956	Q	1228.5514	614.7794	1211.5249	606.2661	1210.5409	605.7741	10
9	1096.4252	548.7162	1079.3986	540.2029	1078.4146	539.7109	C	1100.4929	550.7501	1083.4663	542.2368	1082.4823	541.7448	9
10	1209.5092	605.2583	1192.4827	596.7450	1191.4987	596.2530	I	940.4622	470.7347	923.4357	462.2215	922.4516	461.7295	8
11	1372.5726	686.7899	1355.5460	678.2766	1354.5620	677.7846	Y	827.3781	414.1927	810.3516	405.6794	809.3676	405.1874	7
12	1487.5995	744.3034	1470.5730	735.7901	1469.5889	735.2981	N	664.3148	332.6610	647.2883	324.1478	646.3042	323.6558	6
13	1602.6264	801.8169	1585.5999	793.3036	1584.6159	792.8116	D	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
14	1689.6585	845.3329	1672.6319	836.8196	1671.6479	836.3276	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
15	1776.6905	888.8489	1759.6640	880.3356	1758.6799	879.8436	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
16	1889.7746	945.3909	1872.7480	936.8776	1871.7640	936.3856	L	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EYQTIGNQCIYNDSSLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
71.1	2034.8728	0.0069	EYQTIGNQCIYNDSSLK	Deamidated Q3, N7, N12 85.37%
63.2	2033.8888	0.9909	EYQTIGNQCIYNDSSLK	
60.8	2034.8728	0.0069	EYQTIGNQCIYNDSSLK	Deamidated N7, Q8, N12 8.12%
59.5	2034.8728	0.0069	EYQTIGNQCIYNDSSLK	Deamidated Q3, Q8, N12 5.89%
49.7	2034.8728	0.0069	EYQTIGNQCIYNDSSLK	Deamidated Q3, N7, Q8 0.63%
48.5	2033.8888	0.9909	EYQTIGNQCIYNDSSLK	
40.2	2033.8888	0.9909	EYQTIGNQCIYNDSSLK	
25.4	2033.8888	0.9909	EYQTIGNQCIYNDSSLK	
9.4	2033.8888	0.9909	EYQTIGNQCIYNDSSLK	
7.7	2033.8888	0.9909	EYQTIGNQCIYNDSSLK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

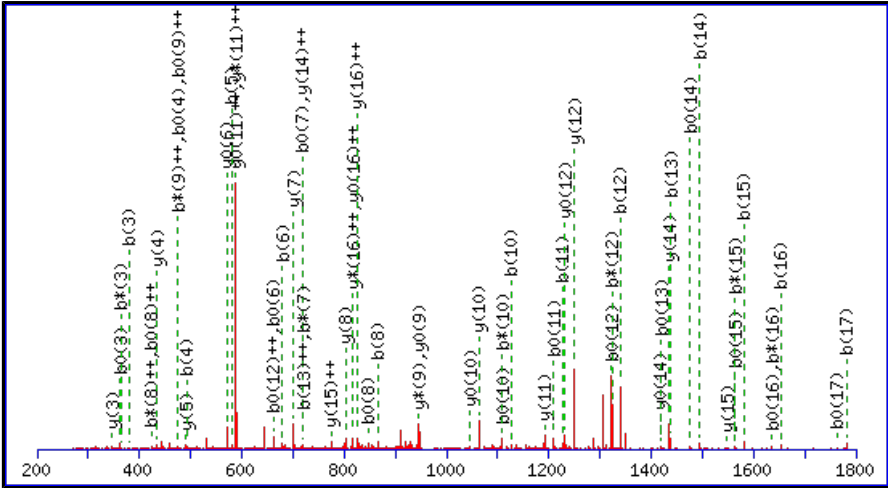
Peptide View

MS/MS Fragmentation of **NYTLSVGETCTLPGSAEK**
Found in **F1SMJ1** in **uni_pig**, tr|F1SMJ1|F1SMJ1_PIG Complement component C7 (Fragment) OS=Sus scrofa GN=C7 PE=4 SV=2

Match to Query 8091: 1926.903648 from(964.459100,2+) intensity(12294.7129) rtinseconds(2017) scans(3779) index(10083)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_11Spectrum2782_scans_3779
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

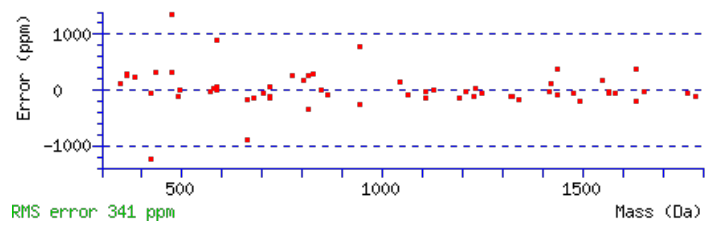
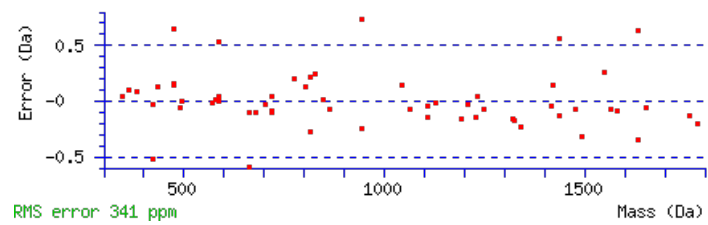
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1926.8881
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
Ions Score: 75 Expect: 1.7e-006
Matches : 62/198 fragment ions using 92 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							18
2	279.0975	140.0524	262.0710	131.5391			Y	1812.8684	906.9378	1795.8419	898.4246	1794.8578	897.9326	17
3	380.1452	190.5763	363.1187	182.0630	362.1347	181.5710	T	1649.8051	825.4062	1632.7785	816.8929	1631.7945	816.4009	16
4	493.2293	247.1183	476.2027	238.6050	475.2187	238.1130	L	1548.7574	774.8823	1531.7309	766.3691	1530.7468	765.8771	15
5	580.2613	290.6343	563.2348	282.1210	562.2508	281.6290	S	1435.6733	718.3403	1418.6468	709.8270	1417.6628	709.3350	14
6	679.3297	340.1685	662.3032	331.6552	661.3192	331.1632	V	1348.6413	674.8243	1331.6148	666.3110	1330.6307	665.8190	13
7	736.3512	368.6792	719.3246	360.1660	718.3406	359.6740	G	1249.5729	625.2901	1232.5463	616.7768	1231.5623	616.2848	12
8	865.3938	433.2005	848.3672	424.6873	847.3832	424.1953	E	1192.5514	596.7794	1175.5249	588.2661	1174.5409	587.7741	11
9	966.4415	483.7244	949.4149	475.2111	948.4309	474.7191	T	1063.5088	532.2581	1046.4823	523.7448	1045.4983	523.2528	10
10	1126.4721	563.7397	1109.4456	555.2264	1108.4616	554.7344	C	962.4612	481.7342	945.4346	473.2209	944.4506	472.7289	9
11	1227.5198	614.2635	1210.4932	605.7503	1209.5092	605.2583	T	802.4305	401.7189	785.4040	393.2056	784.4199	392.7136	8
12	1340.6039	670.8056	1323.5773	662.2923	1322.5933	661.8003	L	701.3828	351.1951	684.3563	342.6818	683.3723	342.1898	7
13	1437.6566	719.3320	1420.6301	710.8187	1419.6461	710.3267	P	588.2988	294.6530	571.2722	286.1397	570.2882	285.6477	6
14	1494.6781	747.8427	1477.6515	739.3294	1476.6675	738.8374	G	491.2460	246.1266	474.2195	237.6134	473.2354	237.1214	5
15	1581.7101	791.3587	1564.6836	782.8454	1563.6996	782.3534	S	434.2245	217.6159	417.1980	209.1026	416.2140	208.6106	4
16	1652.7472	826.8773	1635.7207	818.3640	1634.7367	817.8720	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
17	1781.7898	891.3986	1764.7633	882.8853	1763.7793	882.3933	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
18							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [NYTLVGETCTLPGSAEK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
75.5	1926.8881	0.0156	NYTLVGETCTLPGSAEK
54.3	1925.9041	0.9996	NYTLVGETCTLPGSAEK
12.4	1926.9071	-0.0035	NDHSRAWQDNLQLVTK
9.2	1926.9112	-0.0075	FQDSWRLSDGFVAAEAK
9.0	1925.8822	1.0214	DMKDQMSTSSIQALAER
7.6	1925.8928	1.0108	EDTQLMNETQKDGVAVK
7.5	1926.9147	-0.0111	KIMLCLACGQSMRAEK
6.7	1925.9081	0.9956	SLSATDIEVFWASPM EK
4.8	1925.8982	1.0055	LWDFGFCAQITPEQSK
2.5	1926.9105	-0.0069	LSDNGTYTCVVQKRER

Mascot: <http://www.matrixscience.com/>

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.9	1358.6367	-0.0040	GPSVWAGQNWTR	Deamidated N9 87.52%
64.5	1358.6367	-0.0040	GPSVWAGQNWTR	Deamidated Q8 12.48%

Mascot: <http://www.matrixscience.com/>

NCBI **BLAST** search of [LWPAVGNCSSAMR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.2	1448.6540	-0.0035	LWPAVGNCSSAMR
9.2	1448.6507	-0.0001	LWADPGAQACFGR
7.4	1447.6402	1.0104	YAENVPHNMTEK
4.3	1448.6606	-0.0100	LWQELEDMGVGR
3.5	1447.6363	1.0143	MSPINMLYFENGK
3.0	1447.6501	1.0005	AAQQTPDMAVPSSK
2.5	1448.6540	-0.0035	AYICAHPLDRMS
2.5	1448.6572	-0.0066	EAHEYYPEIPGK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

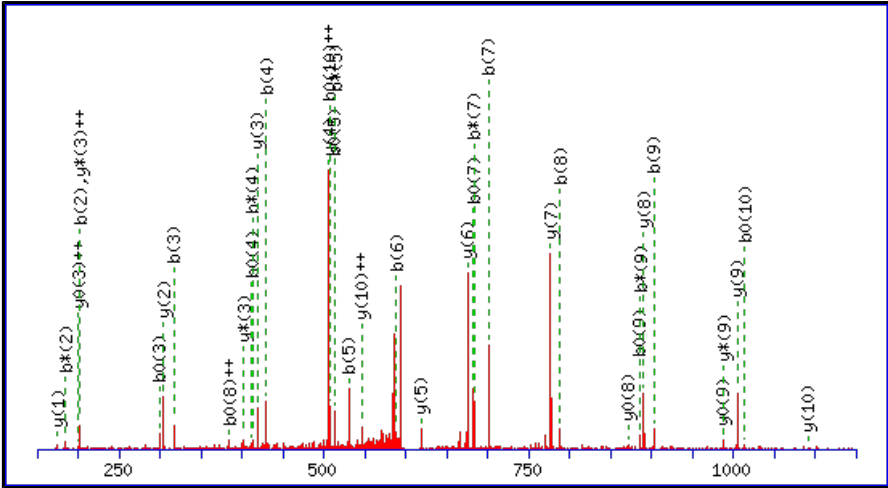
Peptide View

MS/MS Fragmentation of **NSNLTGISDQR**
Found in **F1RKY2** in **uni_pig**, tr|F1RKY2|F1RKY2_PIG Uncharacterized protein OS=Sus scrofa GN=SERPIND1 PE=3 SV=1

Match to Query 1628: 1205.550348 from(603.782450,2+) intensity(18793.7559) rtinseconds(1201) scans(1887) index(6647)
Title: 120325_Sunil_PigSerum_Glyco_S_16Spectrum1080_scans__1887
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

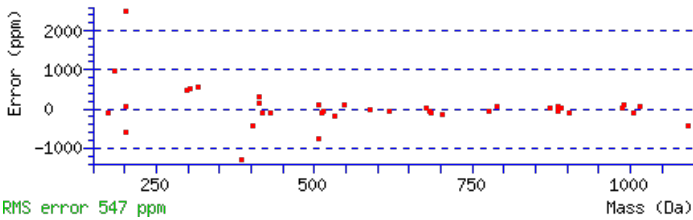
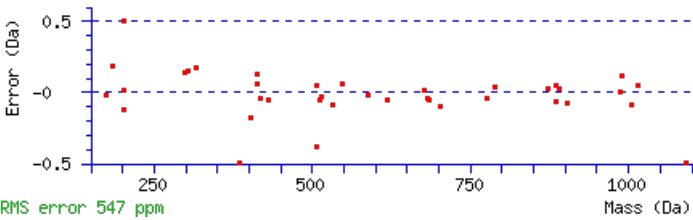
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1205.5524
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Q10 : Deamidated (NQ)
Ions Score: 72 Expect: 2e-006
Matches : 38/114 fragment ions using 70 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							11
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	S	1092.5168	546.7620	1075.4902	538.2487	1074.5062	537.7567	10
3	317.1092	159.0582	300.0826	150.5450	299.0986	150.0529	N	1005.4847	503.2460	988.4582	494.7327	987.4742	494.2407	9
4	430.1932	215.6003	413.1667	207.0870	412.1827	206.5950	L	890.4578	445.7325	873.4312	437.2193	872.4472	436.7272	8
5	531.2409	266.1241	514.2144	257.6108	513.2304	257.1188	T	777.3737	389.1905	760.3472	380.6772	759.3632	380.1852	7
6	588.2624	294.6348	571.2358	286.1216	570.2518	285.6295	G	676.3260	338.6667	659.2995	330.1534	658.3155	329.6614	6
7	701.3464	351.1769	684.3199	342.6636	683.3359	342.1716	I	619.3046	310.1559	602.2780	301.6427	601.2940	301.1506	5
8	788.3785	394.6929	771.3519	386.1796	770.3679	385.6876	S	506.2205	253.6139	489.1940	245.1006	488.2100	244.6086	4
9	903.4054	452.2063	886.3789	443.6931	885.3949	443.2011	D	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
10	1032.4480	516.7276	1015.4215	508.2144	1014.4374	507.7224	Q	304.1615	152.5844	287.1350	144.0711			2
11							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of **NSNLTGISDQR**
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.3	1205.5524	-0.0020	NSNLTGISDQR	Deamidated N3, Q10 56.75%
71.1	1205.5524	-0.0020	NSNLTGISDQR	Deamidated N1, Q10 43.25%
25.4	1205.5524	-0.0020	SNNITDSLNR	
21.5	1205.5524	-0.0020	NSNLTGISDQR	Deamidated N1, N3 0.00%
15.1	1205.5524	-0.0020	SNNITDSLNR	
14.4	1205.5411	0.0092	DSNTQIEQLR	
9.2	1205.5459	0.0045	LSGGQSGGVCER	
8.9	1205.5524	-0.0020	SLDTNEEGGRK	
8.4	1205.5425	0.0079	TWRQQDSER	
8.3	1205.5425	0.0079	TWRQQDSER	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLTFNETYQEISEVVYGAK**
Found in **F2Z5E2** in **uni_pig**, tr|F2Z5E2|F2Z5E2_PIG Uncharacterized protein OS=Sus scrofa GN=SERPINC1 PE=3 SV=1

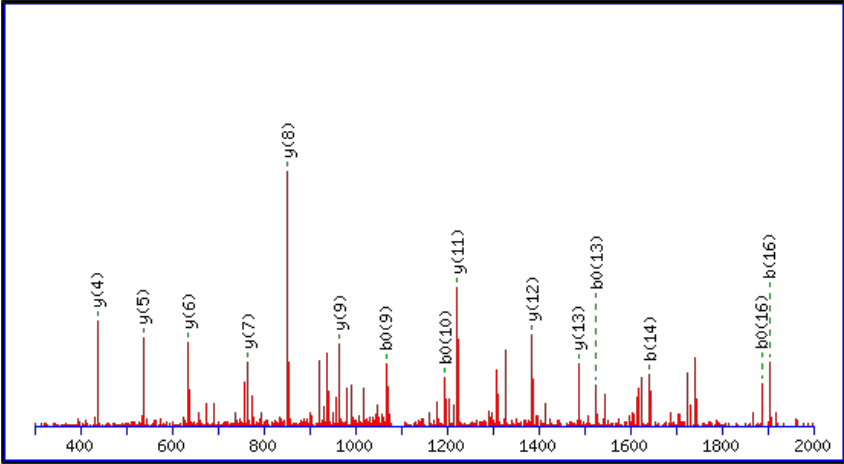
Match to Query 12124: 2178.026228 from(1090.020390,2+) intensity(47749.3750) rtinseconds(3268) scans(7990) index(10827)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_14Spectrum6814_scans_7990
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

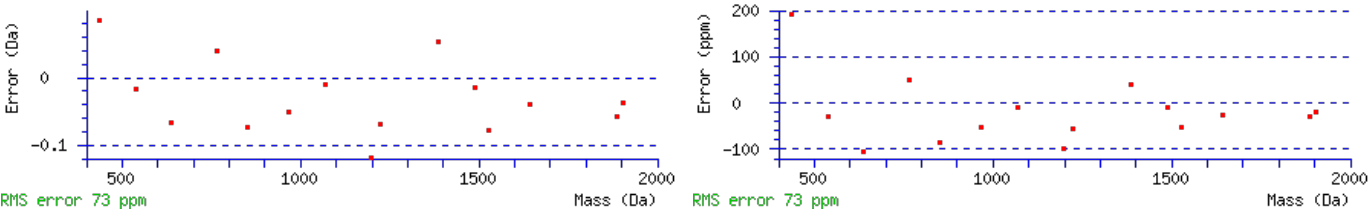
☐ Label all possible matches ☐ Label matches used for scoring

☐ Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2178.0368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 75 Expect: 2.2e-006
Matches : 15/196 fragment ions using 17 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							19
2	201.1234	101.0653			183.1128	92.0600	L	2092.0121	1046.5097	2074.9855	1037.9964	2074.0015	1037.5044	18
3	302.1710	151.5892			284.1605	142.5839	T	1978.9280	989.9677	1961.9015	981.4544	1960.9175	980.9624	17
4	449.2395	225.1234			431.2289	216.1181	F	1877.8804	939.4438	1860.8538	930.9305	1859.8698	930.4385	16
5	564.2664	282.6368	547.2399	274.1236	546.2558	273.6316	N	1730.8119	865.9096	1713.7854	857.3963	1712.8014	856.9043	15
6	693.3090	347.1581	676.2824	338.6449	675.2984	338.1529	E	1615.7850	808.3961	1598.7584	799.8829	1597.7744	799.3909	14
7	794.3567	397.6820	777.3301	389.1687	776.3461	388.6767	T	1486.7424	743.8748	1469.7159	735.3616	1468.7318	734.8696	13
8	957.4200	479.2136	940.3935	470.7004	939.4094	470.2084	Y	1385.6947	693.3510	1368.6682	684.8377	1367.6842	684.3457	12
9	1085.4786	543.2429	1068.4520	534.7297	1067.4680	534.2376	Q	1222.6314	611.8193	1205.6048	603.3061	1204.6208	602.8141	11
10	1214.5212	607.7642	1197.4946	599.2510	1196.5106	598.7589	E	1094.5728	547.7900	1077.5463	539.2768	1076.5623	538.7848	10
11	1327.6052	664.3063	1310.5787	655.7930	1309.5947	655.3010	I	965.5302	483.2688	948.5037	474.7555	947.5197	474.2635	9
12	1414.6373	707.8223	1397.6107	699.3090	1396.6267	698.8170	S	852.4462	426.7267	835.4196	418.2134	834.4356	417.7214	8
13	1543.6799	772.3436	1526.6533	763.8303	1525.6693	763.3383	E	765.4141	383.2107	748.3876	374.6974	747.4036	374.2054	7
14	1642.7483	821.8778	1625.7217	813.3645	1624.7377	812.8725	V	636.3715	318.6894	619.3450	310.1761			6
15	1741.8167	871.4120	1724.7901	862.8987	1723.8061	862.4067	V	537.3031	269.1552	520.2766	260.6419			5
16	1904.8800	952.9436	1887.8535	944.4304	1886.8695	943.9384	Y	438.2347	219.6210	421.2082	211.1077			4
17	1961.9015	981.4544	1944.8749	972.9411	1943.8909	972.4491	G	275.1714	138.0893	258.1448	129.5761			3
18	2032.9386	1016.9729	2015.9120	1008.4597	2014.9280	1007.9677	A	218.1499	109.5786	201.1234	101.0653			2
19							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [SLTFNETYQEISEVVYGAK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
75.0	2178.0368	-0.0106	SLTFNETYQEISEVVYGAK	Deamidated N5 99.84%
47.0	2178.0368	-0.0106	SLTFNETYQEISEVVYGAK	Deamidated Q9 0.16%
4.2	2176.0068	2.0194	MVINTESNVLMFQFENVK	
2.3	2176.0068	2.0194	MVINTESNVLMFQFENVK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSSTCHGEYSQNICEEFSQQTDNEGCF****TK**
Found in **I3LQ17** in **uni_pig**, tr|I3LQ17|I3LQ17_PIG Uncharacterized protein OS=Sus scrofa PE=4 SV=1

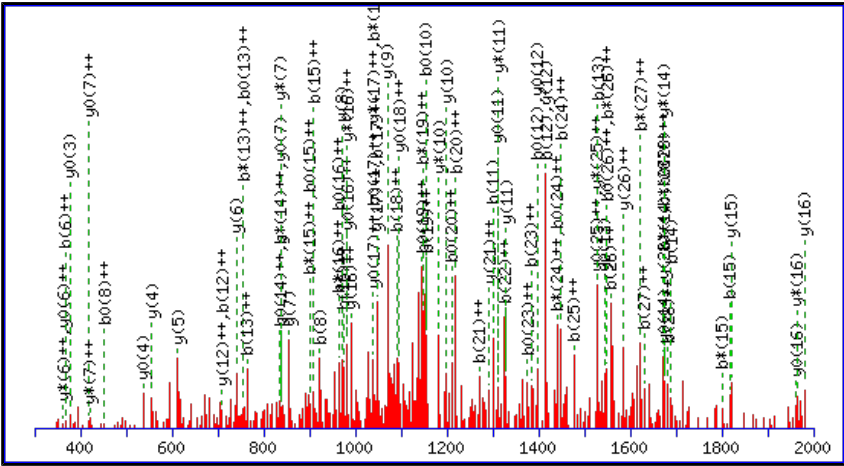
Match to Query 13500: 3507.371232 from(1170.131020,3+) intensity(2720.8403) rtinseconds(1871) scans(3606) index(7149)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_01Spectrum2789_scans_3606
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

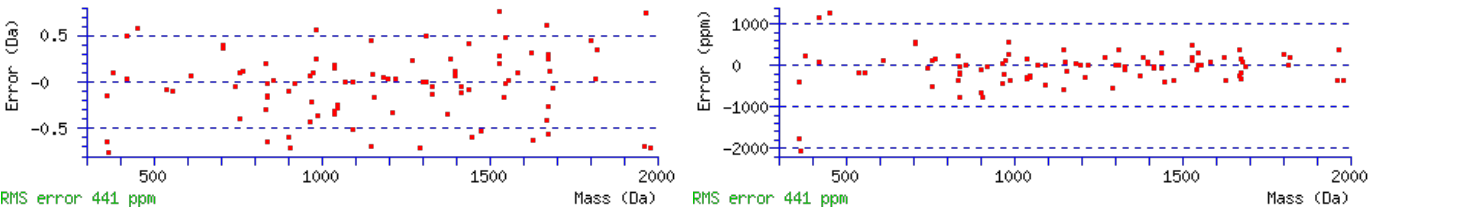
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 3507.3449
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Q19 : Deamidated (NQ)
Ions Score: 61 Expect: 2.5e-006
Matches : 92/312 fragment ions using 168 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							29
2	251.1026	126.0550			233.0921	117.0497	S	3345.2889	1673.1481	3328.2623	1664.6348	3327.2783	1664.1428	28
3	338.1347	169.5710			320.1241	160.5657	S	3258.2569	1629.6321	3241.2303	1621.1188	3240.2463	1620.6268	27
4	439.1823	220.0948			421.1718	211.0895	T	3171.2248	1586.1161	3154.1983	1577.6028	3153.2143	1577.1108	26
5	599.2130	300.1101			581.2024	291.1049	C	3070.1772	1535.5922	3053.1506	1527.0789	3052.1666	1526.5869	25
6	736.2719	368.6396			718.2613	359.6343	H	2910.1465	1455.5769	2893.1200	1447.0636	2892.1359	1446.5716	24
7	793.2934	397.1503			775.2828	388.1450	G	2773.0876	1387.0474	2756.0611	1378.5342	2755.0770	1378.0422	23
8	922.3360	461.6716			904.3254	452.6663	E	2716.0661	1358.5367	2699.0396	1350.0234	2698.0556	1349.5314	22
9	1085.3993	543.2033			1067.3887	534.1980	Y	2587.0235	1294.0154	2569.9970	1285.5021	2569.0130	1285.0101	21
10	1172.4313	586.7193			1154.4208	577.7140	S	2423.9602	1212.4837	2406.9337	1203.9705	2405.9496	1203.4785	20
11	1300.4899	650.7486	1283.4633	642.2353	1282.4793	641.7433	Q	2336.9282	1168.9677	2319.9016	1160.4545	2318.9176	1159.9624	19
12	1415.5168	708.2621	1398.4903	699.7488	1397.5063	699.2568	N	2208.8696	1104.9384	2191.8431	1096.4252	2190.8590	1095.9332	18
13	1528.6009	764.8041	1511.5744	756.2908	1510.5903	755.7988	I	2093.8427	1047.4250	2076.8161	1038.9117	2075.8321	1038.4197	17
14	1688.6315	844.8194	1671.6050	836.3061	1670.6210	835.8141	C	1980.7586	990.8829	1963.7321	982.3697	1962.7480	981.8777	16
15	1817.6741	909.3407	1800.6476	900.8274	1799.6636	900.3354	E	1820.7280	910.8676	1803.7014	902.3543	1802.7174	901.8623	15
16	1946.7167	973.8620	1929.6902	965.3487	1928.7062	964.8567	E	1691.6854	846.3463	1674.6588	837.8330	1673.6748	837.3410	14
17	2093.7851	1047.3962	2076.7586	1038.8829	2075.7746	1038.3909	F	1562.6428	781.8250	1545.6162	773.3117	1544.6322	772.8197	13
18	2180.8172	1090.9122	2163.7906	1082.3990	2162.8066	1081.9069	S	1415.5744	708.2908	1398.5478	699.7775	1397.5638	699.2855	12
19	2309.8598	1155.4335	2292.8332	1146.9202	2291.8492	1146.4282	Q	1328.5423	664.7748	1311.5158	656.2615	1310.5318	655.7695	11
20	2437.9183	1219.4628	2420.8918	1210.9495	2419.9078	1210.4575	Q	1199.4997	600.2535	1182.4732	591.7402	1181.4892	591.2482	10
21	2538.9660	1269.9867	2521.9395	1261.4734	2520.9555	1260.9814	T	1071.4412	536.2242	1054.4146	527.7109	1053.4306	527.2189	9
22	2653.9930	1327.5001	2636.9664	1318.9868	2635.9824	1318.4948	D	970.3935	485.7004	953.3669	477.1871	952.3829	476.6951	8
23	2768.0359	1384.5216	2751.0093	1376.0083	2750.0253	1375.5163	N	855.3665	428.1869	838.3400	419.6736	837.3560	419.1816	7

24	2897.0785	1449.0429	2880.0519	1440.5296	2879.0679	1440.0376	E	741.3236	371.1654	724.2971	362.6522	723.3130	362.1602	6
25	2954.1000	1477.5536	2937.0734	1469.0403	2936.0894	1468.5483	G	612.2810	306.6441	595.2545	298.1309	594.2704	297.6389	5
26	3114.1306	1557.5689	3097.1041	1549.0557	3096.1200	1548.5637	C	555.2595	278.1334	538.2330	269.6201	537.2490	269.1281	4
27	3261.1990	1631.1031	3244.1725	1622.5899	3243.1885	1622.0979	F	395.2289	198.1181	378.2023	189.6048	377.2183	189.1128	3
28	3362.2467	1681.6270	3345.2201	1673.1137	3344.2361	1672.6217	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
29							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [YSSTCHGEYSQNICEEFSQQT DNEGCF TK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
61.3	3507.3449	0.0263	YSSTCHGEYSQNICEEFSQQT DNEGCF TK	Deamidated N12, Q19 19.99%
61.3	3507.3449	0.0263	YSSTCHGEYSQNICEEFSQQT DNEGCF TK	Deamidated Q11, Q19 19.85%
59.8	3507.3449	0.0263	YSSTCHGEYSQNICEEFSQQT DNEGCF TK	Deamidated N12, Q20 14.05%
59.8	3507.3449	0.0263	YSSTCHGEYSQNICEEFSQQT DNEGCF TK	Deamidated Q11, Q20 13.96%
59.8	3507.3449	0.0263	YSSTCHGEYSQNICEEFSQQT DNEGCF TK	Deamidated N12, N23 13.93%
59.7	3507.3449	0.0263	YSSTCHGEYSQNICEEFSQQT DNEGCF TK	Deamidated Q11, N23 13.83%
59.5	3506.3609	1.0103	YSSTCHGEYSQNICEEFSQQT DNEGCF TK	
59.5	3506.3609	1.0103	YSSTCHGEYSQNICEEFSQQT DNEGCF TK	
52.5	3507.3449	0.0263	YSSTCHGEYSQNICEEFSQQT DNEGCF TK	Deamidated Q11, N12 2.61%
47.1	3506.3609	1.0103	YSSTCHGEYSQNICEEFSQQT DNEGCF TK	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1S643** in **uni_pig**, tr|F1S643|F1S643_PIG Uncharacterized protein OS=Sus scrofa GN=CFH PE=4 SV=2

Title: 120326_Sunil_PigSerum_Glyco_PsetB_10Spectrum2366_scans__3355

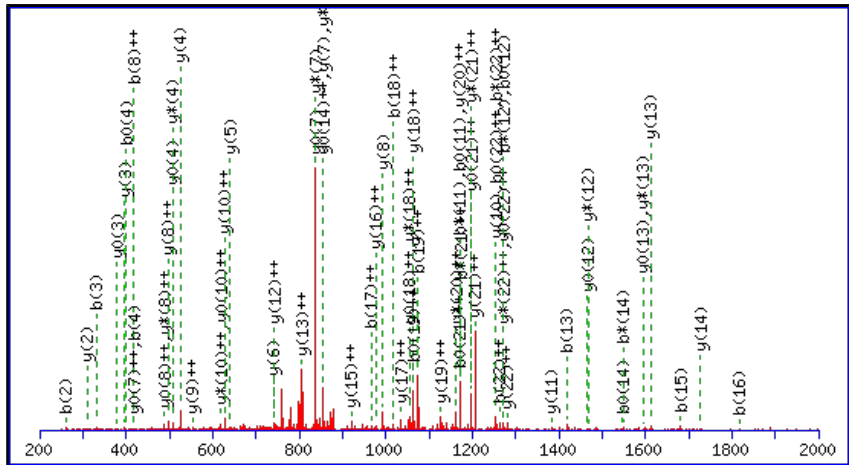
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

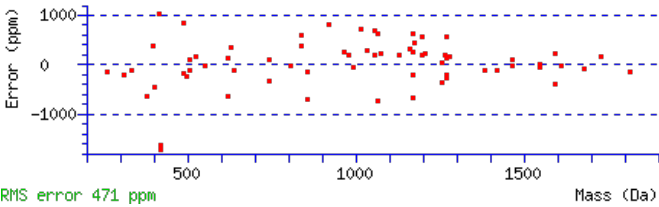
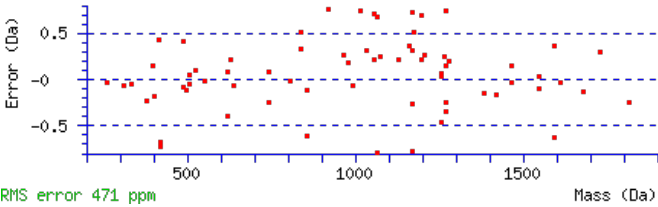
Variable modifications:

N19 : Deamidated (NQ)

Ions Score: 74 Expect: 2.9e-006

Matches : 70/242 fragment ions using 135 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							23
2	261.1598	131.0835					F	2559.1634	1280.0853	2542.1369	1271.5721	2541.1528	1271.0801	22
3	332.1969	166.6021					A	2412.0950	1206.5511	2395.0684	1198.0379	2394.0844	1197.5458	21
4	419.2289	210.1181			401.2183	201.1128	S	2341.0579	1171.0326	2324.0313	1162.5193	2323.0473	1162.0273	20
5	548.2715	274.6394			530.2609	265.6341	E	2254.0258	1127.5166	2236.9993	1119.0033	2236.0153	1118.5113	19
6	605.2930	303.1501			587.2824	294.1448	G	2124.9833	1062.9953	2107.9567	1054.4820	2106.9727	1053.9900	18
7	719.3359	360.1716	702.3093	351.6583	701.3253	351.1663	N	2067.9618	1034.4845	2050.9352	1025.9713	2049.9512	1025.4793	17
8	832.4199	416.7136	815.3934	408.2003	814.4094	407.7083	L	1953.9189	977.4631	1936.8923	968.9498	1935.9083	968.4578	16
9	945.5040	473.2556	928.4775	464.7424	927.4934	464.2504	L	1840.8348	920.9210	1823.8083	912.4078	1822.8242	911.9158	15
10	1060.5310	530.7691	1043.5044	522.2558	1042.5204	521.7638	D	1727.7507	864.3790	1710.7242	855.8657	1709.7402	855.3737	14
11	1188.6259	594.8166	1171.5994	586.3033	1170.6153	585.8113	K	1612.7238	806.8655	1595.6972	798.3523	1594.7132	797.8603	13
12	1289.6736	645.3404	1272.6470	636.8272	1271.6630	636.3352	T	1484.6288	742.8181	1467.6023	734.3048	1466.6183	733.8128	12
13	1418.7162	709.8617	1401.6896	701.3485	1400.7056	700.8564	E	1383.5812	692.2942	1366.5546	683.7809	1365.5706	683.2889	11
14	1565.7846	783.3959	1548.7581	774.8827	1547.7740	774.3907	F	1254.5386	627.7729	1237.5120	619.2596	1236.5280	618.7676	10
15	1680.8115	840.9094	1663.7850	832.3961	1662.8010	831.9041	D	1107.4701	554.2387	1090.4436	545.7254	1089.4596	545.2334	9
16	1817.8705	909.4389	1800.8439	900.9256	1799.8599	900.4336	H	992.4432	496.7252	975.4167	488.2120	974.4326	487.7200	8
17	1931.9134	966.4603	1914.8868	957.9471	1913.9028	957.4550	N	855.3843	428.1958	838.3577	419.6825	837.3737	419.1905	7
18	2032.9611	1016.9842	2015.9345	1008.4709	2014.9505	1007.9789	T	741.3414	371.1743	724.3148	362.6610	723.3308	362.1690	6
19	2147.9880	1074.4976	2130.9615	1065.9844	2129.9774	1065.4924	N	640.2937	320.6505	623.2671	312.1372	622.2831	311.6452	5
20	2276.0466	1138.5269	2259.0200	1130.0137	2258.0360	1129.5216	Q	525.2667	263.1370	508.2402	254.6237	507.2562	254.1317	4
21	2363.0786	1182.0429	2346.0521	1173.5297	2345.0680	1173.0377	S	397.2082	199.1077	380.1816	190.5944	379.1976	190.1024	3
22	2526.1419	1263.5746	2509.1154	1255.0613	2508.1314	1254.5693	Y	310.1761	155.5917	293.1496	147.0784			2
23							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [IFASEGNLLDKTEFDHNTNQSYK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.8	2671.2402	-0.0038	IFASEGNLLDKTEFDHNTNQSYK	Deamidated N19 49.29%
73.8	2671.2402	-0.0038	IFASEGNLLDKTEFDHNTNQSYK	Deamidated Q20 48.72%
59.8	2671.2402	-0.0038	IFASEGNLLDKTEFDHNTNQSYK	Deamidated N17 1.98%
35.5	2671.2402	-0.0038	IFASEGNLLDKTEFDHNTNQSYK	Deamidated N7 0.01%
25.1	2670.2561	0.9802	IFASEGNLLDKTEFDHNTNQSYK	
7.7	2671.2588	-0.0224	HYQTVLLMSSNATLNKYNEHYK	
7.3	2671.2588	-0.0224	HYQTVLLMSSNATLNKYNEHYK	
7.2	2671.2588	-0.0224	HYQTVLLMSSNATLNKYNEHYK	
2.8	2669.2207	2.0157	GPYPSSQEIPMEVFDPSQ GKYSK	
2.2	2669.2470	1.9894	SIGGRGHKISDYFEYQGGNGSSPVR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIVSNSGTR**

Found in **F1SFM2** in **uni_pig**, tr|F1SFM2|F1SFM2_PIG Uncharacterized protein OS=Sus scrofa GN=CHL1 PE=4 SV=2

Match to Query 1679: 1207.617608 from(604.816080,2+) intensity(10991.2422) rtinseconds(1422) scans(3210) index(13174)

Title: 120326 Sunil PigSerum Glyco SsetB 14Spectrum2629 scans 3210

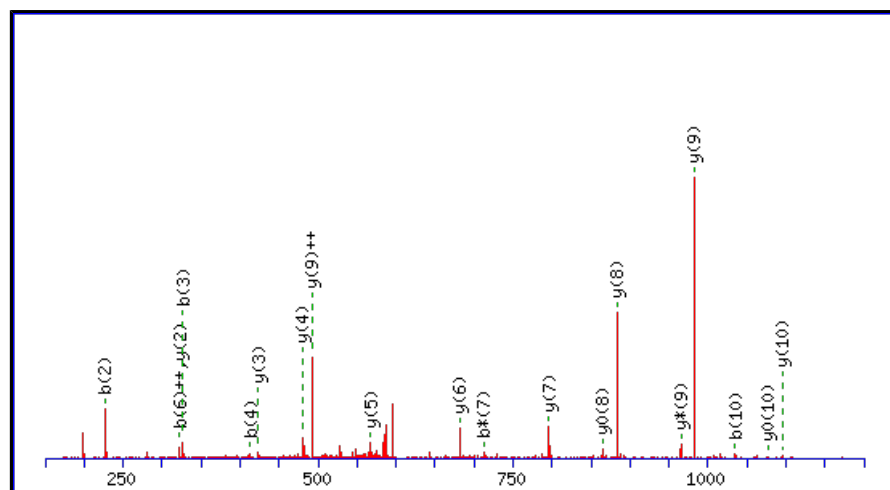
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1207.6197

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

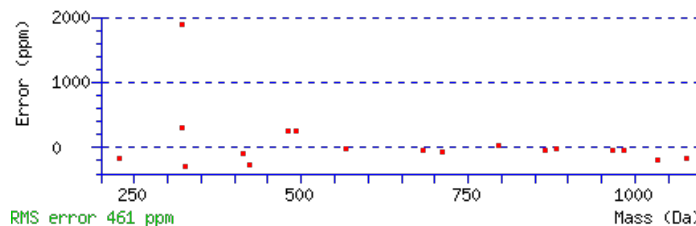
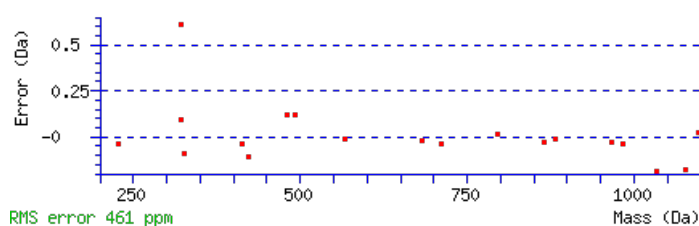
Variable modifications:

N5 : Deamidated (NQ)

Ions Score: 74 Expect: 2.9e-006

Matches : 19/102 fragment ions using 30 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							11
2	227.1754	114.0913					I	1095.5429	548.2751	1078.5164	539.7618	1077.5323	539.2698	10
3	326.2438	163.6255					V	982.4588	491.7331	965.4323	483.2198	964.4483	482.7278	9
4	413.2758	207.1416			395.2653	198.1363	S	883.3904	442.1989	866.3639	433.6856	865.3799	433.1936	8
5	528.3028	264.6550	511.2762	256.1418	510.2922	255.6497	N	796.3584	398.6828	779.3319	390.1696	778.3478	389.6776	7
6	642.3457	321.6765	625.3192	313.1632	624.3352	312.6712	N	681.3315	341.1694	664.3049	332.6561	663.3209	332.1641	6
7	729.3777	365.1925	712.3512	356.6792	711.3672	356.1872	S	567.2885	284.1479	550.2620	275.6346	549.2780	275.1426	5
8	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	G	480.2565	240.6319	463.2300	232.1186	462.2459	231.6266	4
9	887.4469	444.2271	870.4203	435.7138	869.4363	435.2218	T	423.2350	212.1212	406.2085	203.6079	405.2245	203.1159	3
10	1034.5153	517.7613	1017.4888	509.2480	1016.5047	508.7560	F	322.1874	161.5973	305.1608	153.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of **IIVSNNSGTFR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.7	1207.6197	-0.0021	IIVSNNSGTER	Deamidated N5 50.63%
73.6	1207.6197	-0.0021	IIVSNNSGTER	Deamidated N6 49.37%
1.6	1207.6084	0.0092	LLEKQYQER	
0.8	1207.6084	0.0092	LLNNQSQYVK	
0.8	1207.6084	0.0092	LLNNQSQYVK	
0.2	1207.6197	-0.0021	LLNNQSQYTK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLYLASNQSNK**

Found in **F1S1G8** in **uni_pig**, tr|F1S1G8|F1S1G8_PIG Amine oxidase OS=Sus scrofa GN=AOC3 PE=3 SV=2

Match to Query 2580: 1300.626108 from(651.320330,2+) intensity(11433.1279) rtinseconds(1472) scans(2252) index(9830)

Title: 120326 Sunil PigSerum Glyco PsetB 09Spectrum1455 scans 2252

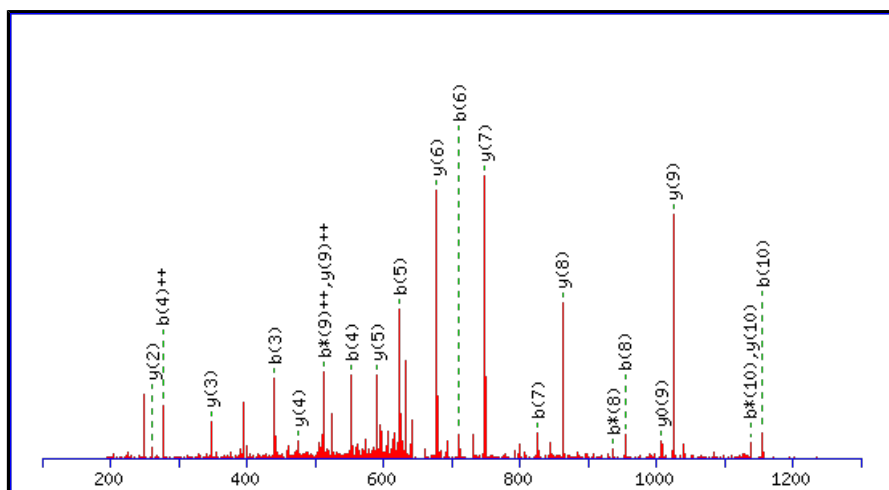
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1300.6299

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

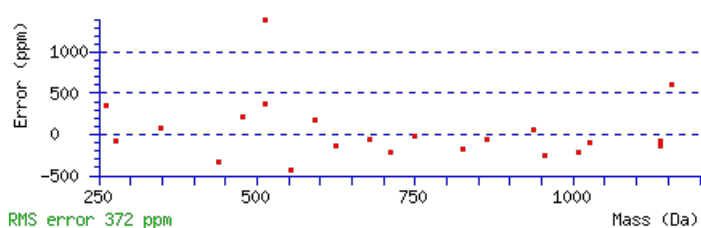
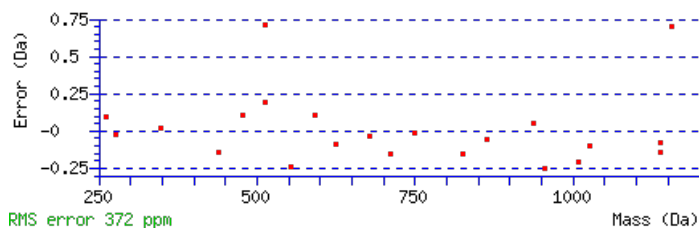
Variable modifications:

N7 : Deamidated (NQ)

Ions Score: 72 Expect: 3e-006

Matches : 23/94 fragment ions using 32 most intense peaks ([help](#))

#	b	b⁺⁺	b*	b^{*++}	b⁰	b⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							11
2	277.1547	139.0810					L	1138.5739	569.7906	1121.5473	561.2773	1120.5633	560.7853	10
3	440.2180	220.6126					Y	1025.4898	513.2485	1008.4633	504.7353	1007.4793	504.2433	9
4	553.3021	277.1547					L	862.4265	431.7169	845.3999	423.2036	844.4159	422.7116	8
5	624.3392	312.6732					A	749.3424	375.1748	732.3159	366.6616	731.3319	366.1696	7
6	711.3712	356.1892			693.3606	347.1840	S	678.3053	339.6563	661.2788	331.1430	660.2947	330.6510	6
7	826.3981	413.7027	809.3716	405.1894	808.3876	404.6974	N	591.2733	296.1403	574.2467	287.6270	573.2627	287.1350	5
8	954.4567	477.7320	937.4302	469.2187	936.4462	468.7267	Q	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
9	1041.4888	521.2480	1024.4622	512.7347	1023.4782	512.2427	S	348.1878	174.5975	331.1612	166.0842	330.1772	165.5922	3
10	1155.5317	578.2695	1138.5051	569.7562	1137.5211	569.2642	N	261.1557	131.0815	244.1292	122.5682			2
11							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [YLYLASNOSNK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
71.5	1300.6299	-0.0038	YLYLASNQS NK	Deamidated N7 97.08%
55.9	1300.6299	-0.0038	YLYLASNQS NK	Deamidated Q8 2.69%
45.2	1300.6299	-0.0038	YLYLASNQS NK	Deamidated N10 0.23%
12.4	1300.6373	-0.0112	MESFFLAETV K	
11.3	1300.6259	0.0002	QPETNPGTTVTR	
7.3	1300.6259	0.0002	QPETNPGTTVTR	
5.6	1300.6155	0.0106	MKQTGQVYAM K	
4.8	1300.6155	0.0106	MKQTGQVYAM K	
4.0	1299.6281	0.9980	FQKGCQEYL K	
3.5	1299.6162	1.0099	MMSLSQSRSI K	

Mascot: <http://www.matrixscience.com/>

MASCOT SCIENCE Mascot Search Results

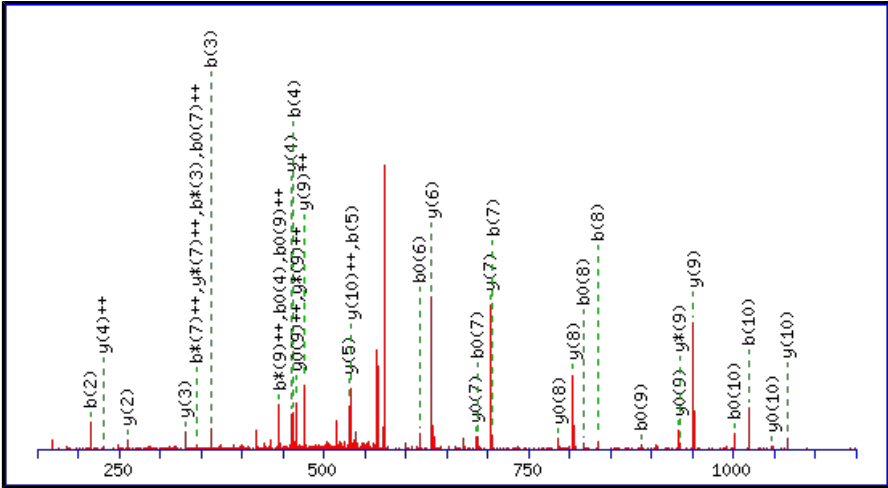
Peptide View

MS/MS Fragmentation of **VNFTATAEALK**
Found in **I3LQ17** in **uni_pig**, tr|I3LQ17|I3LQ17_PIG Uncharacterized protein OS=Sus scrofa PE=4 SV=1

Match to Query 1280: 1164.600208 from(583.307380,2+) intensity(9274.0010) rtinseconds(1810) scans(3191) index(9622)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_06Spectrum2322_scans__3191
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

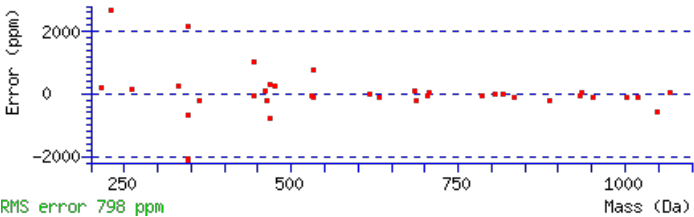
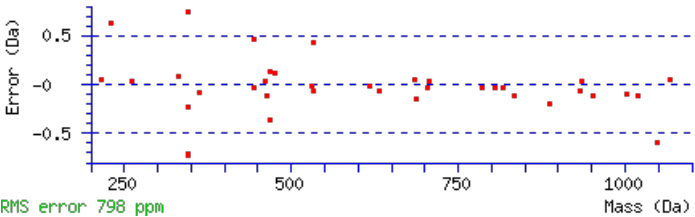
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1164.6026
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Ions Score: 73 Expect: 3.1e-006
Matches : 38/106 fragment ions using 48 most intense peaks (help)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							11
2	215.1026	108.0550	198.0761	99.5417			N	1066.5415	533.7744	1049.5150	525.2611	1048.5310	524.7691	10
3	362.1710	181.5892	345.1445	173.0759			F	951.5146	476.2609	934.4880	467.7477	933.5040	467.2556	9
4	463.2187	232.1130	446.1922	223.5997	445.2082	223.1077	T	804.4462	402.7267	787.4196	394.2134	786.4356	393.7214	8
5	534.2558	267.6316	517.2293	259.1183	516.2453	258.6263	A	703.3985	352.2029	686.3719	343.6896	685.3879	343.1976	7
6	635.3035	318.1554	618.2770	309.6421	617.2930	309.1501	T	632.3614	316.6843	615.3348	308.1710	614.3508	307.6790	6
7	706.3406	353.6740	689.3141	345.1607	688.3301	344.6687	A	531.3137	266.1605	514.2871	257.6472	513.3031	257.1552	5
8	835.3832	418.1953	818.3567	409.6820	817.3727	409.1900	E	460.2766	230.6419	443.2500	222.1287	442.2660	221.6366	4
9	906.4203	453.7138	889.3938	445.2005	888.4098	444.7085	A	331.2340	166.1206	314.2074	157.6074			3
10	1019.5044	510.2558	1002.4779	501.7426	1001.4938	501.2506	L	260.1969	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1

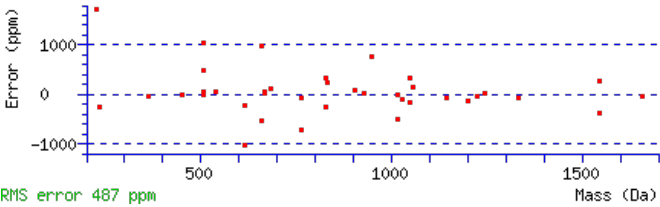
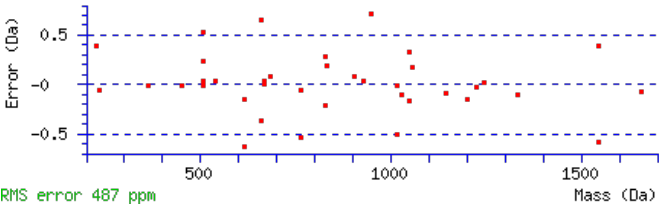


NCBI BLAST search of **VNFTATAEALK**
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.9	1164.6026	-0.0024	VNFTATAEALK
9.0	1164.6027	-0.0025	VAVEDTGLSEK
9.0	1164.5887	0.0115	GESGFERGISQK
6.4	1163.5968	1.0034	GRAMSLSDALK
5.2	1164.6074	-0.0072	NCGIYGVRVK
4.7	1162.5942	2.0060	NPKSTTGRSSK
4.6	1162.5903	2.0099	LTQLCSEALK
3.9	1164.5887	0.0115	EGADKANHVPK
3.9	1163.5975	1.0027	TLKSWWEK
3.6	1162.5942	2.0060	KTEGSSNQGKK

Mascot: <http://www.matrixscience.com/>



NCBI BLAST search of [YKVDYESQSTDQTQNFSESSESK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
68.3	2343.0026	0.9956	YKVDYESQSTDQTQNFSESSESK	Deamidated N14 50.00%
68.3	2343.0026	0.9956	YKVDYESQSTDQTQNFSESSESK	Deamidated Q13 50.00%
58.5	2343.9866	0.0116	YKVDYESQSTDQTQNFSESSESK	
50.6	2343.9866	0.0116	YKVDYESQSTDQTQNFSESSESK	
37.6	2343.9866	0.0116	YKVDYESQSTDQTQNFSESSESK	
27.7	2343.0026	0.9956	YKVDYESQSTDQTQNFSESSESK	Deamidated Q8 0.00%
3.4	2341.9851	2.0131	GNHNNFQSQDMCQRFCKR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of FGNWSAQPSCK

Found in **A0A096P6N1** in **uni_pig**, tr|A0A096P6N1|A0A096P6N1_PIG Uncharacterized protein OS=Sus scrofa GN=LOC100522100 PE=4 SV=1

Match to Query 2411: 1281.542868 from(641.778710,2+) intensity(51199.4492) rtinseconds(1461) scans(3299) index(3810)

Title: 120325 Sunil PigSerum Glyco P 14Spectrum2648 scans 3299

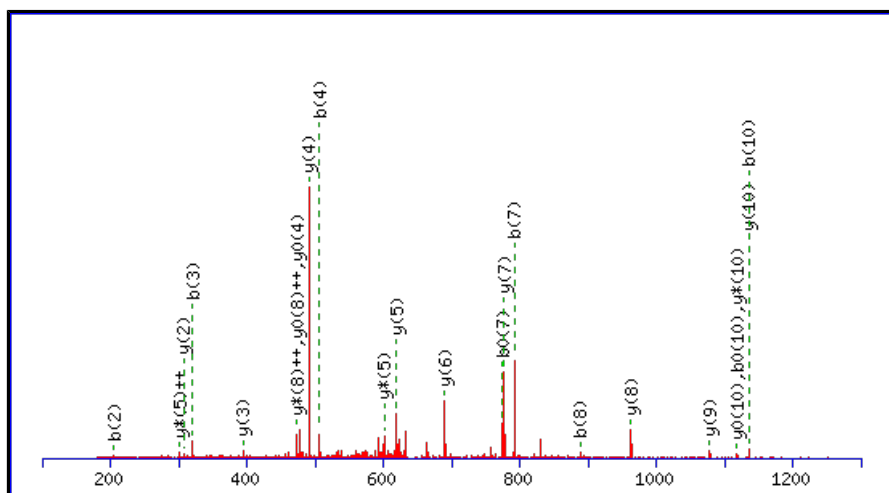
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1281.5448

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

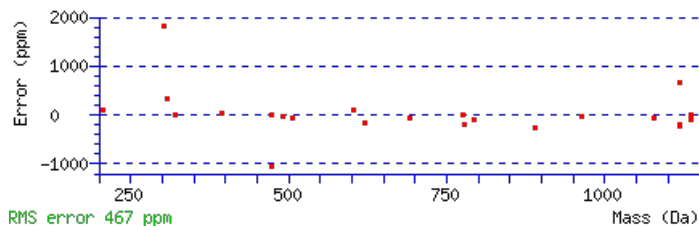
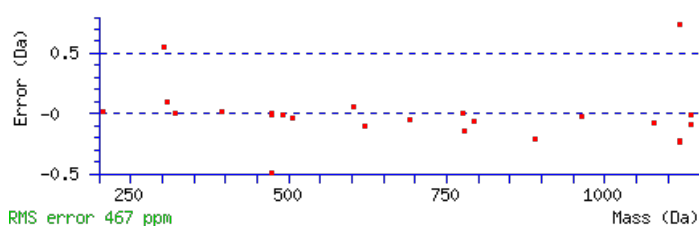
Variable modifications:

N3 : Deamidated (NQ)

Ions Score: 67 Expect: 3.3e-006

Matches : 24/104 fragment ions using 33 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							11
2	205.0972	103.0522					G	1135.4837	568.2455	1118.4571	559.7322	1117.4731	559.2402	10
3	320.1241	160.5657	303.0975	152.0524			N	1078.4622	539.7347	1061.4357	531.2215	1060.4517	530.7295	9
4	506.2034	253.6053	489.1769	245.0921			W	963.4353	482.2213	946.4087	473.7080	945.4247	473.2160	8
5	593.2354	297.1214	576.2089	288.6081	575.2249	288.1161	S	777.3560	389.1816	760.3294	380.6683	759.3454	380.1763	7
6	664.2726	332.6399	647.2460	324.1266	646.2620	323.6346	A	690.3239	345.6656	673.2974	337.1523	672.3134	336.6603	6
7	792.3311	396.6692	775.3046	388.1559	774.3206	387.6639	Q	619.2868	310.1470	602.2603	301.6338	601.2763	301.1418	5
8	889.3839	445.1956	872.3573	436.6823	871.3733	436.1903	P	491.2282	246.1178	474.2017	237.6045	473.2177	237.1125	4
9	976.4159	488.7116	959.3894	480.1983	958.4054	479.7063	S	394.1755	197.5914	377.1489	189.0781	376.1649	188.5861	3
10	1136.4466	568.7269	1119.4200	560.2136	1118.4360	559.7216	C	307.1435	154.0754	290.1169	145.5621			2
11							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [FGNWSAOPSK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
67.4	1281.5448	-0.0019	FGNWSAQPSCK	Deamidated N3 99.95%
34.4	1281.5448	-0.0019	FGNWSAQPSCK	Deamidated Q7 0.05%
21.9	1281.5361	0.0068	GFDDDELDTGDAK	
8.5	1280.5480	0.9948	GSSSGNASGAETGAK	
8.3	1281.5547	-0.0118	GFNDGLEELCK	
1.2	1281.5394	0.0034	NSVQMTEQDTK	
0.1	1281.5513	-0.0084	DDPYWSENKK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **VG**TN**VT**LSCQSPR

Found in **F1S798** in **uni_pig**, tr|F1S798|F1S798_PIG Uncharacterized protein OS=Sus scrofa GN=LOC100522817 PE=4 SV=2

Match to Query 3574: 1419.677908 from(710.846230,2+) intensity(704.5465) rtinseconds(1304) scans(2256) index(1711)

Title: 120325_Sunil_PigSerum_Glyco_D_15Spectrum1692_scans__2256

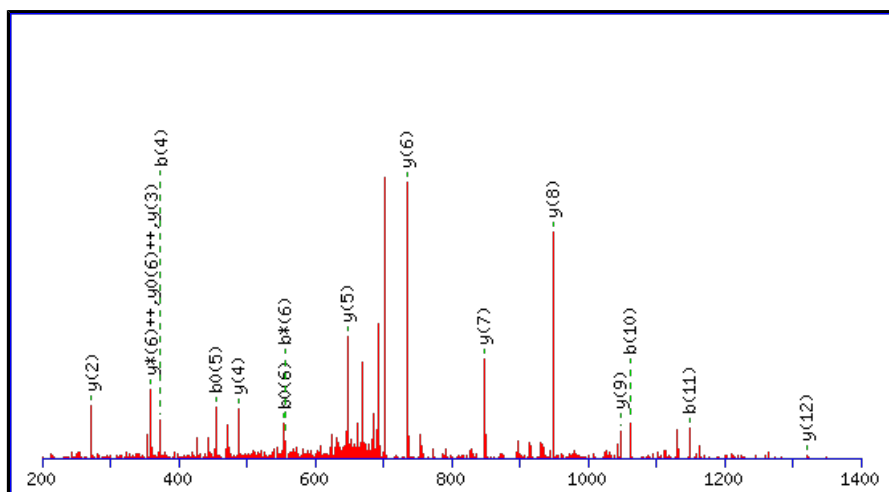
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1418.6824

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

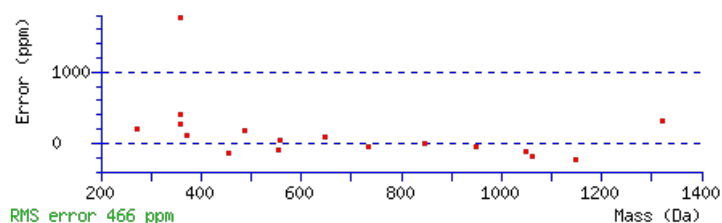
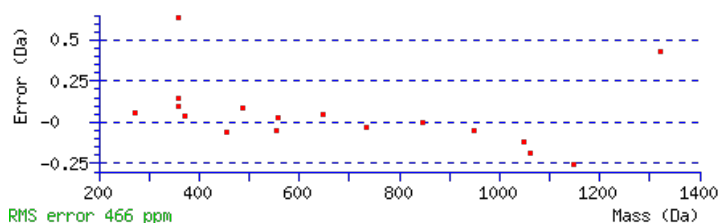
Variable modifications:

N4 : Deamidated (NQ)

Ions Score: 73 Expect: 3.3e-006

Matches : 17/130 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							13
2	157.0972	79.0522					G	1320.6212	660.8143	1303.5947	652.3010	1302.6107	651.8090	12
3	258.1448	129.5761			240.1343	120.5708	T	1263.5998	632.3035	1246.5732	623.7903	1245.5892	623.2982	11
4	373.1718	187.0895	356.1452	178.5763	355.1612	178.0842	N	1162.5521	581.7797	1145.5256	573.2664	1144.5415	572.7744	10
5	472.2402	236.6237	455.2136	228.1105	454.2296	227.6185	V	1047.5252	524.2662	1030.4986	515.7529	1029.5146	515.2609	9
6	573.2879	287.1476	556.2613	278.6343	555.2773	278.1423	T	948.4567	474.7320	931.4302	466.2187	930.4462	465.7267	8
7	686.3719	343.6896	669.3454	335.1763	668.3614	334.6843	L	847.4091	424.2082	830.3825	415.6949	829.3985	415.2029	7
8	773.4040	387.2056	756.3774	378.6923	755.3934	378.2003	S	734.3250	367.6661	717.2985	359.1529	716.3144	358.6609	6
9	933.4346	467.2209	916.4081	458.7077	915.4240	458.2157	C	647.2930	324.1501	630.2664	315.6368	629.2824	315.1448	5
10	1061.4932	531.2502	1044.4666	522.7370	1043.4826	522.2449	Q	487.2623	244.1348	470.2358	235.6215	469.2518	235.1295	4
11	1148.5252	574.7662	1131.4987	566.2530	1130.5147	565.7610	S	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
12	1245.5780	623.2926	1228.5514	614.7794	1227.5674	614.2873	P	272.1717	136.5895	255.1452	128.0762			2
13							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [VGTVNVTLSQCSPR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.7	1418.6824	0.9955	VGTVNVTLSQCSPR	Deamidated N4 99.59%
52.7	1419.6664	0.0115	VGTVNVTLSQCSPR	
48.9	1418.6824	0.9955	VGTVNVTLSQCSPR	Deamidated Q10 0.41%
23.3	1419.6817	-0.0037	WAIITLSGDMGPR	
14.5	1418.6824	0.9956	TDIREGEMLSPR	
10.4	1419.6663	0.0116	NNEMVELQRIR	
8.9	1418.6823	0.9956	NNEMVELQRIR	
8.9	1418.6823	0.9956	NNEMVELQRIR	
8.3	1419.6776	0.0003	ELRSVMNTSNPR	
8.2	1419.6915	-0.0136	LQDLTDVQIMAR	

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNITINDLPKG**

Found in **F1RQW2** in **uni_pig**, tr|F1RQW2|F1RQW2_PIG Uncharacterized protein OS=Sus scrofa GN=C4 PE=4 SV=2

Match to Query 1516: 1197.658628 from(599.836590,2+) intensity(17037.9375) rtinseconds(2122) scans(5040) index(13311)

Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum4235_scans__5040

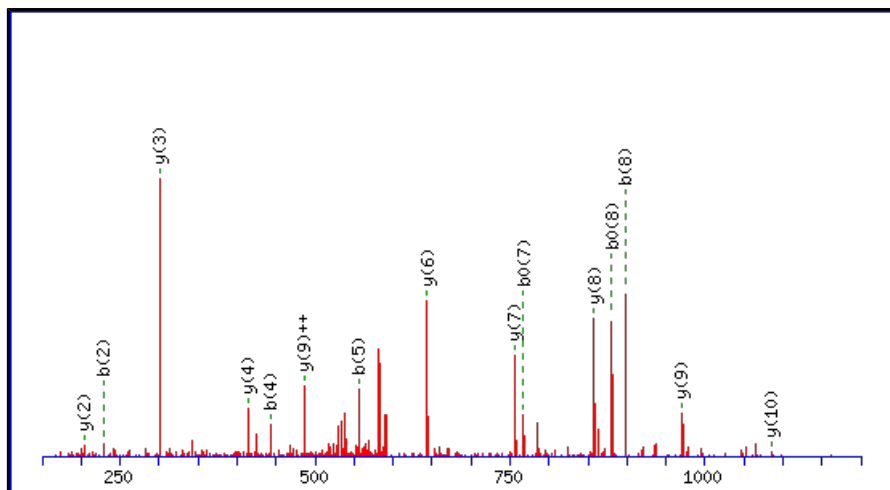
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1197.6605

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

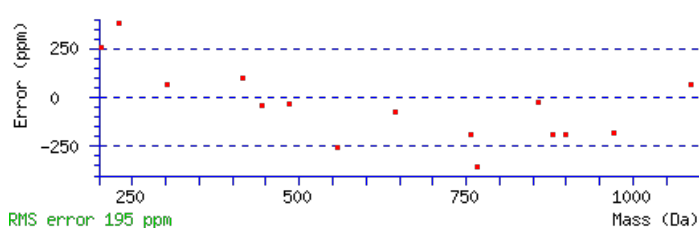
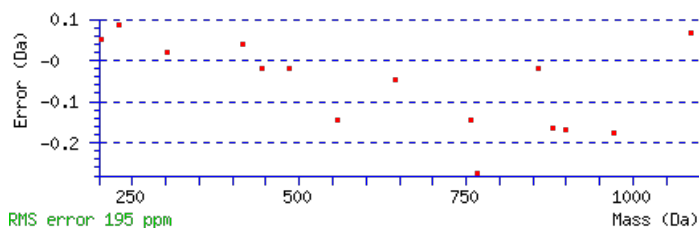
Variable modifications:

N2 : Deamidated (NQ)

Ions Score: 69 Expect: 4.4e-006

```
Matches : 15/104 fragment ions using 20 most intense peaks (help)
```

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							11
2	229.1183	115.0628	212.0917	106.5495			N	1085.5837	543.2955	1068.5572	534.7822	1067.5732	534.2902	10
3	342.2023	171.6048	325.1758	163.0915			I	970.5568	485.7820	953.5302	477.2688	952.5462	476.7767	9
4	443.2500	222.1287	426.2235	213.6154	425.2395	213.1234	T	857.4727	429.2400	840.4462	420.7267	839.4621	420.2347	8
5	556.3341	278.6707	539.3075	270.1574	538.3235	269.6654	I	756.4250	378.7162	739.3985	370.2029	738.4145	369.7109	7
6	670.3770	335.6921	653.3505	327.1789	652.3665	326.6869	N	643.3410	322.1741	626.3144	313.6608	625.3304	313.1688	6
7	785.4040	393.2056	768.3774	384.6923	767.3934	384.2003	D	529.2980	265.1527	512.2715	256.6394	511.2875	256.1474	5
8	898.4880	449.7477	881.4615	441.2344	880.4775	440.7424	L	414.2711	207.6392	397.2445	199.1259			4
9	995.5408	498.2740	978.5142	489.7608	977.5302	489.2687	P	301.1870	151.0972	284.1605	142.5839			3
10	1052.5623	526.7848	1035.5357	518.2715	1034.5517	517.7795	G	204.1343	102.5708	187.1077	94.0575			2
11							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [LNITINDLPGK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
69.5	1197.6605	-0.0018	L N I T I N D L P G K	Deamidated N2 99.59%
45.6	1197.6605	-0.0018	L N I T I N D L P G K	Deamidated N6 0.41%
10.8	1197.6605	-0.0018	L S V D A N L Q I P K	
10.1	1197.6605	-0.0018	L S V D A N L Q I P K	
5.5	1195.6488	2.0098	E A I Q S L I F F K	
3.7	1195.6495	2.0091	M A P L L A P G R D R	
3.1	1196.6626	0.9961	V L S I S T E R H R	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAFISNFSMTVDG**TK

Found in **F1RUM4** in **uni_pig**, tr|F1RUM4|F1RUM4_PIG Inter-alpha-trypsin inhibitor heavy chain H2 OS=Sus scrofa GN=ITI2 PE=4 SV=2

Match to Query 5091: 1591.721088 from(796.867820,2+) intensity(4893.8560) rtinseconds(2269) scans(5403) index(6367)

Title: 120325 Sunil PigSerum Glyco S 14Spectrum4555 scans 5403

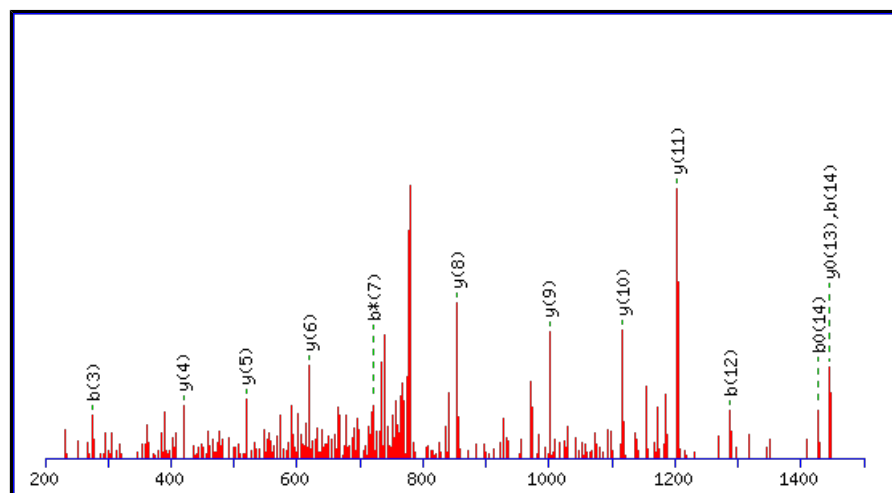
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1590.7236

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

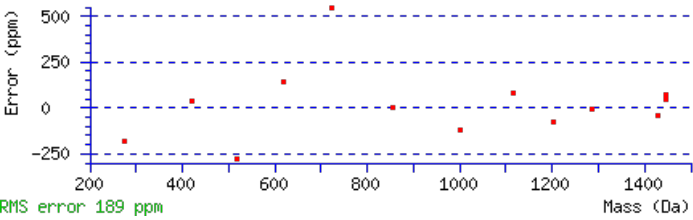
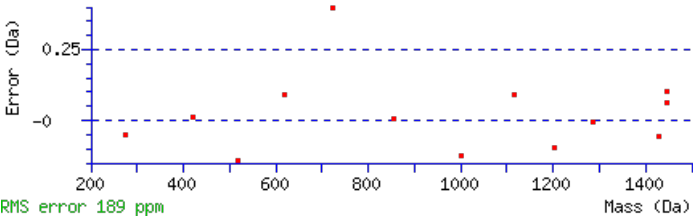
N6 : Deamidated (NQ)

M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 69 Expect: 4.9e-006

Matches : 13/232 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							15
2	129.0659	65.0366					A	1534.7094	767.8583	1517.6828	759.3451	1516.6988	758.8530	14
3	276.1343	138.5708					F	1463.6723	732.3398	1446.6457	723.8265	1445.6617	723.3345	13
4	389.2183	195.1128					I	1316.6039	658.8056	1299.5773	650.2923	1298.5933	649.8003	12
5	476.2504	238.6288			458.2398	229.6235	S	1203.5198	602.2635	1186.4932	593.7503	1185.5092	593.2583	11
6	591.2773	296.1423	574.2508	287.6290	573.2667	287.1370	N	1116.4878	558.7475	1099.4612	550.2342	1098.4772	549.7422	10
7	738.3457	369.6765	721.3192	361.1632	720.3352	360.6712	F	1001.4608	501.2341	984.4343	492.7208	983.4503	492.2288	9
8	825.3777	413.1925	808.3512	404.6792	807.3672	404.1872	S	854.3924	427.6998	837.3659	419.1866	836.3818	418.6946	8
9	972.4131	486.7102	955.3866	478.1969	954.4026	477.7049	M	767.3604	384.1838	750.3338	375.6706	749.3498	375.1785	7
10	1073.4608	537.2340	1056.4343	528.7208	1055.4503	528.2288	T	620.3250	310.6661	603.2984	302.1529	602.3144	301.6608	6
11	1172.5292	586.7683	1155.5027	578.2550	1154.5187	577.7630	V	519.2773	260.1423	502.2508	251.6290	501.2667	251.1370	5
12	1287.5562	644.2817	1270.5296	635.7685	1269.5456	635.2764	D	420.2089	210.6081	403.1823	202.0948	402.1983	201.6028	4
13	1344.5776	672.7925	1327.5511	664.2792	1326.5671	663.7872	G	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
14	1445.6253	723.3163	1428.5988	714.8030	1427.6148	714.3110	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
15							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [GAFISNESMTVDGTK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.8	1590.7236	0.9975	GAFISNESMTVDGTK
10.3	1590.7057	1.0154	CEKQPGTGGGSGSGGAK
6.6	1590.7316	0.9895	AAMALKMGDLDMHR
6.0	1591.7314	-0.0103	MNTNPSRGPYHER
5.0	1591.7260	-0.0049	GEQGSSGRLGCQLDK
4.3	1591.7148	0.0063	KPENSECDATAKNK
4.0	1591.7287	-0.0076	LDCIQNLESEIEK
3.5	1590.7300	0.9910	DIPNENELQFQIK
2.2	1591.7260	-0.0049	MQAQLEREERER
1.0	1590.7202	1.0009	ASESTDYGITESWK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNASTTDSNSTVEQSALIR**

Found in **F1SAE9** in **uni_pig**, tr|F1SAE9|F1SAE9_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=LAMB1 PE=4 SV=2

Match to Query 10725: 1994.942428 from(998.478490,2+) intensity(4808.8535) rtinseconds(1576) scans(3311) index(8634)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_15Spectrum2715_scans_3311

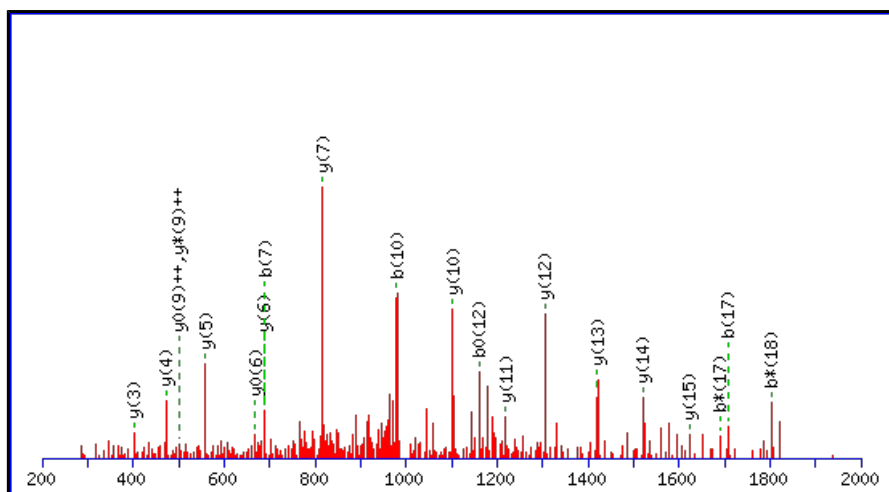
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1993.9440

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

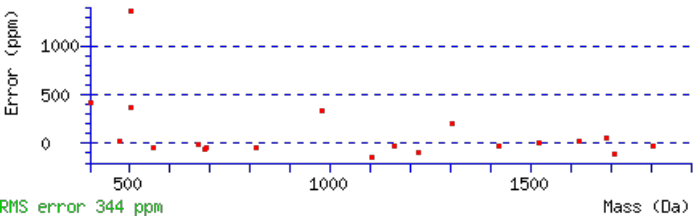
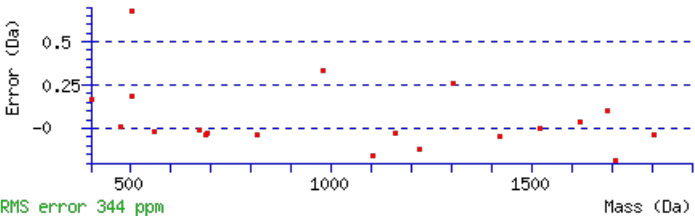
N2 : Deamidated (NQ)

N9 : Deamidated (NQ')

Ions Score: 71 Expect: 4.9e-006

Matches : 20/200 fragment ions using 33 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							19
2	215.1026	108.0550	198.0761	99.5417			N	1895.8829	948.4451	1878.8563	939.9318	1877.8723	939.4398	18
3	286.1397	143.5735	269.1132	135.0602			A	1780.8559	890.9316	1763.8294	882.4183	1762.8454	881.9263	17
4	373.1718	187.0895	356.1452	178.5763	355.1612	178.0842	S	1709.8188	855.4130	1692.7923	846.8998	1691.8082	846.4078	16
5	474.2195	237.6134	457.1929	229.1001	456.2089	228.6081	T	1622.7868	811.8970	1605.7602	803.3838	1604.7762	802.8917	15
6	575.2671	288.1372	558.2406	279.6239	557.2566	279.1319	T	1521.7391	761.3732	1504.7126	752.8599	1503.7285	752.3679	14
7	690.2941	345.6507	673.2675	337.1374	672.2835	336.6454	D	1420.6914	710.8494	1403.6649	702.3361	1402.6809	701.8441	13
8	777.3261	389.1667	760.2996	380.6534	759.3155	380.1614	S	1305.6645	653.3359	1288.6379	644.8226	1287.6539	644.3306	12
9	892.3530	446.6802	875.3265	438.1669	874.3425	437.6749	N	1218.6325	609.8199	1201.6059	601.3066	1200.6219	600.8146	11
10	979.3851	490.1962	962.3585	481.6829	961.3745	481.1909	S	1103.6055	552.3064	1086.5790	543.7931	1085.5949	543.3011	10
11	1080.4328	540.7200	1063.4062	532.2067	1062.4222	531.7147	T	1016.5735	508.7904	999.5469	500.2771	998.5629	499.7851	9
12	1179.5012	590.2542	1162.4746	581.7409	1161.4906	581.2489	V	915.5258	458.2665	898.4993	449.7533	897.5152	449.2613	8
13	1308.5438	654.7755	1291.5172	646.2622	1290.5332	645.7702	E	816.4574	408.7323	799.4308	400.2191	798.4468	399.7271	7
14	1436.6023	718.8048	1419.5758	710.2915	1418.5918	709.7995	Q	687.4148	344.2110	670.3883	335.6978	669.4042	335.2058	6
15	1523.6344	762.3208	1506.6078	753.8075	1505.6238	753.3155	S	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	5
16	1594.6715	797.8394	1577.6449	789.3261	1576.6609	788.8341	A	472.3242	236.6657	455.2976	228.1525			4
17	1707.7555	854.3814	1690.7290	845.8681	1689.7450	845.3761	L	401.2871	201.1472	384.2605	192.6339			3
18	1820.8396	910.9234	1803.8131	902.4102	1802.8290	901.9182	I	288.2030	144.6051	271.1765	136.0919			2
19							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [VNASTTDSNSTVEQSALIR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
71.3	1993.9440	0.9984	VNASTTDSNSTVEQSALIR	Deamidated N2, N9 99.56%
47.7	1993.9440	0.9984	VNASTTDSNSTVEQSALIR	Deamidated N2, Q14 0.43%
41.2	1994.9280	0.0144	VNASTTDSNSTVEQSALIR	
30.5	1993.9440	0.9984	VNASTTDSNSTVEQSALIR	Deamidated N9, Q14 0.01%
15.2	1993.9453	0.9971	YKGRSTINPSNASEAQNR	
15.2	1993.9453	0.9971	YKGRSTINPSNASQAQNR	
7.0	1993.9453	0.9971	YKGRSTINPSNASQAQNR	
6.7	1994.9293	0.0131	YKGRSTINPSNASEAQNR	
6.7	1994.9293	0.0131	YKGRSTINPSNASQAQNR	
6.0	1993.9453	0.9971	YKGRSTINPSNASEAQNR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

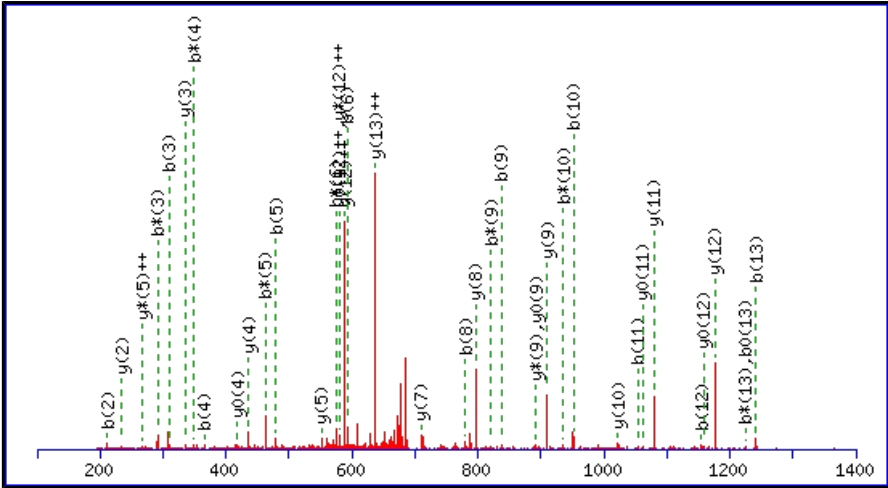
Peptide View

MS/MS Fragmentation of **NPPGLISTGNTTSK**
Found in **F1RS82** in **uni_pig**, tr|F1RS82|F1RS82_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=LOC100518580 PE=4 SV=2

Match to Query 3334: 1386.695408 from(694.354980,2+) intensity(11563.2891) rtinseconds(1279) scans(2525) index(8601)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_15Spectrum2023_scans__2525
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

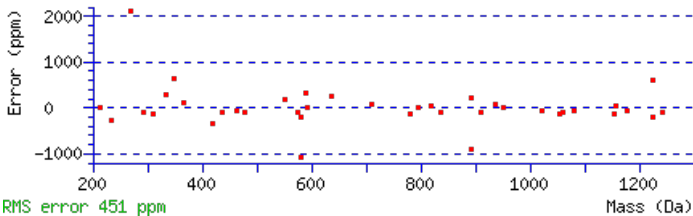
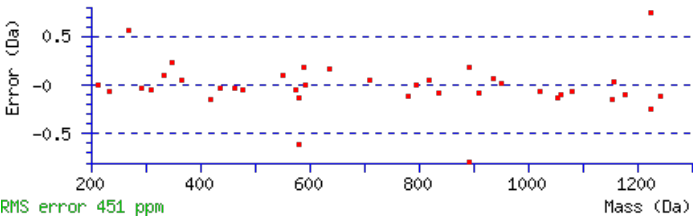
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1386.6991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 71 Expect: 5.5e-006
Matches : 39/142 fragment ions using 67 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							14
2	212.1030	106.5551	195.0764	98.0418			P	1273.6634	637.3354	1256.6369	628.8221	1255.6529	628.3301	13
3	309.1557	155.0815	292.1292	146.5682			P	1176.6107	588.8090	1159.5841	580.2957	1158.6001	579.8037	12
4	366.1772	183.5922	349.1506	175.0790			G	1079.5579	540.2826	1062.5313	531.7693	1061.5473	531.2773	11
5	479.2613	240.1343	462.2347	231.6210			L	1022.5364	511.7719	1005.5099	503.2586	1004.5259	502.7666	10
6	592.3453	296.6763	575.3188	288.1630			I	909.4524	455.2298	892.4258	446.7165	891.4418	446.2245	9
7	679.3774	340.1923	662.3508	331.6790	661.3668	331.1870	S	796.3683	398.6878	779.3418	390.1745	778.3577	389.6825	8
8	780.4250	390.7162	763.3985	382.2029	762.4145	381.7109	T	709.3363	355.1718	692.3097	346.6585	691.3257	346.1665	7
9	837.4465	419.2269	820.4199	410.7136	819.4359	410.2216	G	608.2886	304.6479	591.2620	296.1347	590.2780	295.6427	6
10	952.4734	476.7404	935.4469	468.2271	934.4629	467.7351	N	551.2671	276.1372	534.2406	267.6239	533.2566	267.1319	5
11	1053.5211	527.2642	1036.4946	518.7509	1035.5106	518.2589	T	436.2402	218.6237	419.2136	210.1105	418.2296	209.6185	4
12	1154.5688	577.7880	1137.5422	569.2748	1136.5582	568.7828	T	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
13	1241.6008	621.3040	1224.5743	612.7908	1223.5903	612.2988	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [NPPGLISTGNTTSK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
70.5	1386.6991	-0.0037	NPPGLISTGNTTSK	Deamidated N10 100.00%
8.6	1386.6991	-0.0037	NPPGLISTGNTTSK	Deamidated N1 0.00%
5.4	1386.7078	-0.0124	NSLFIRHPEMK	
3.5	1386.6891	0.0063	LPASPASPPQHQR	
2.6	1384.7020	1.9934	IQDVMEGLSKHK	
1.6	1384.6874	2.0080	FFVQDASTASALK	
0.9	1385.7013	0.9941	INMLVIESHWK	
0.7	1384.6769	2.0185	RTLLQMLDDHQ	
0.3	1385.7038	0.9916	LPTTAASTPDAVDK	
0.3	1385.7051	0.9903	LPASPASPPQHQR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

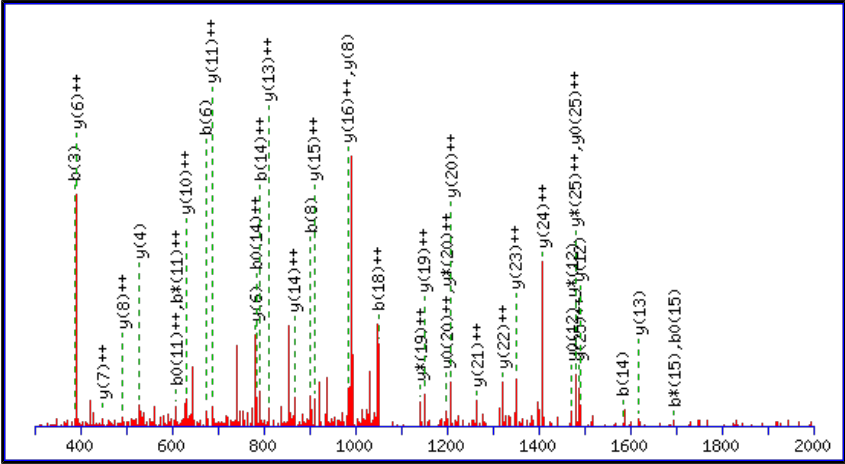
Peptide View

MS/MS Fragmentation of **LLCNGDNDCGDFSDEDDCDS DPRPPCR**
Found in **F1SMJ6** in **uni_pig**, tr|F1SMJ6|F1SMJ6_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=C9 PE=4 SV=2

Match to Query 13386: 3201.150492 from(1068.057440,3+) intensity(5664.9258) rtinseconds(1528) scans(3490) index(13195)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum2862_scans_3490
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

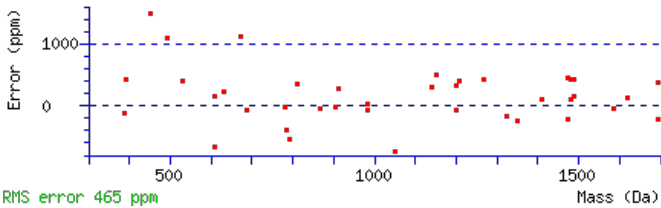
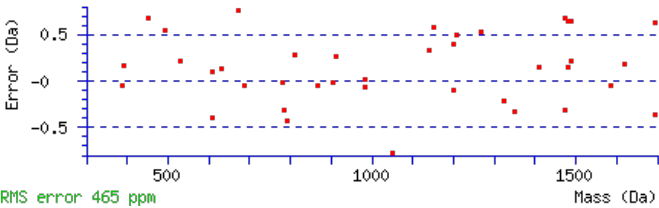
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 3201.1652
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 52 Expect: 5.6e-006
Matches : 39/284 fragment ions using 102 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							27
2	227.1754	114.0913					L	3089.0884	1545.0478	3072.0619	1536.5346	3071.0779	1536.0426	26
3	387.2061	194.1067					C	2976.0044	1488.5058	2958.9778	1479.9925	2957.9938	1479.5005	25
4	501.2490	251.1281	484.2224	242.6149			N	2815.9737	1408.4905	2798.9472	1399.9772	2797.9631	1399.4852	24
5	558.2704	279.6389	541.2439	271.1256			G	2701.9308	1351.4690	2684.9042	1342.9558	2683.9202	1342.4637	23
6	673.2974	337.1523	656.2708	328.6391	655.2868	328.1470	D	2644.9093	1322.9583	2627.8828	1314.4450	2626.8988	1313.9530	22
7	788.3243	394.6658	771.2978	386.1525	770.3138	385.6605	N	2529.8824	1265.4448	2512.8558	1256.9315	2511.8718	1256.4395	21
8	903.3513	452.1793	886.3247	443.6660	885.3407	443.1740	D	2414.8554	1207.9314	2397.8289	1199.4181	2396.8449	1198.9261	20
9	1063.3819	532.1946	1046.3554	523.6813	1045.3714	523.1893	C	2299.8285	1150.4179	2282.8019	1141.9046	2281.8179	1141.4126	19
10	1120.4034	560.7053	1103.3768	552.1921	1102.3928	551.7000	G	2139.7978	1070.4026	2122.7713	1061.8893	2121.7873	1061.3973	18
11	1235.4303	618.2188	1218.4038	609.7055	1217.4198	609.2135	D	2082.7764	1041.8918	2065.7498	1033.3786	2064.7658	1032.8865	17
12	1382.4987	691.7530	1365.4722	683.2397	1364.4882	682.7477	F	1967.7494	984.3784	1950.7229	975.8651	1949.7389	975.3731	16
13	1469.5308	735.2690	1452.5042	726.7557	1451.5202	726.2637	S	1820.6810	910.8441	1803.6545	902.3309	1802.6705	901.8389	15
14	1584.5577	792.7825	1567.5312	784.2692	1566.5471	783.7772	D	1733.6490	867.3281	1716.6224	858.8149	1715.6384	858.3228	14
15	1713.6003	857.3038	1696.5738	848.7905	1695.5897	848.2985	E	1618.6220	809.8147	1601.5955	801.3014	1600.6115	800.8094	13
16	1828.6273	914.8173	1811.6007	906.3040	1810.6167	905.8120	D	1489.5795	745.2934	1472.5529	736.7801	1471.5689	736.2881	12
17	1943.6542	972.3307	1926.6276	963.8175	1925.6436	963.3255	D	1374.5525	687.7799	1357.5260	679.2666	1356.5419	678.7746	11
18	2103.6848	1052.3461	2086.6583	1043.8328	2085.6743	1043.3408	C	1259.5256	630.2664	1242.4990	621.7531	1241.5150	621.2611	10
19	2218.7118	1109.8595	2201.6852	1101.3463	2200.7012	1100.8542	D	1099.4949	550.2511	1082.4684	541.7378	1081.4844	541.2458	9
20	2305.7438	1153.3755	2288.7173	1144.8623	2287.7332	1144.3703	S	984.4680	492.7376	967.4414	484.2244	966.4574	483.7323	8
21	2420.7708	1210.8890	2403.7442	1202.3757	2402.7602	1201.8837	D	897.4359	449.2216	880.4094	440.7083	879.4254	440.2163	7
22	2517.8235	1259.4154	2500.7970	1250.9021	2499.8130	1250.4101	P	782.4090	391.7081	765.3825	383.1949			6
23	2673.9246	1337.4660	2656.8981	1328.9527	2655.9141	1328.4607	R	685.3562	343.1818	668.3297	334.6685			5
24	2770.9774	1385.9923	2753.9508	1377.4791	2752.9668	1376.9871	P	529.2551	265.1312	512.2286	256.6179			4

25	2868.0302	1434.5187	2851.0036	1426.0054	2850.0196	1425.5134	P	432.2024	216.6048	415.1758	208.0915			3
26	3028.0608	1514.5340	3011.0343	1506.0208	3010.0502	1505.5288	C	335.1496	168.0784	318.1231	159.5652			2
27							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [LLCNGDNDCGDFSEDDCDS DPRPPCR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.5	3201.1652	-0.0147	LLCNGDNDCGDFSEDDCDS DPRPPCR	Deamidated N7 64.69%
49.9	3201.1652	-0.0147	LLCNGDNDCGDFSEDDCDS DPRPPCR	Deamidated N4 35.31%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

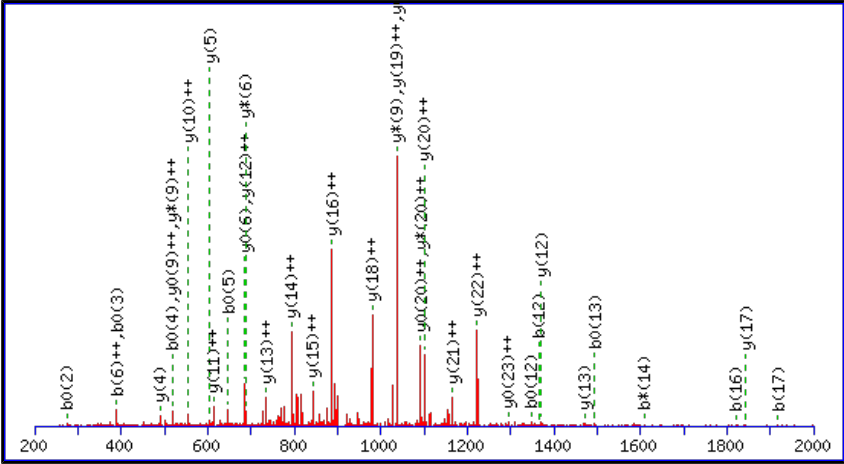
Peptide View

MS/MS Fragmentation of **EYDEQNNASVDVFLGHVNVDEITK**
Found in **F1SLV6** in **uni_pig**, tr|F1SLV6|F1SLV6_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=C1R PE=3 SV=2

Match to Query 13201: 2735.252052 from(912.757960,3+) intensity(45336.7070) rtinseconds(2644) scans(6542) index(3936)
Title: 120325_Sunil_PigSerum_Glyco_P_14Spectrum5548_scans__6542
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

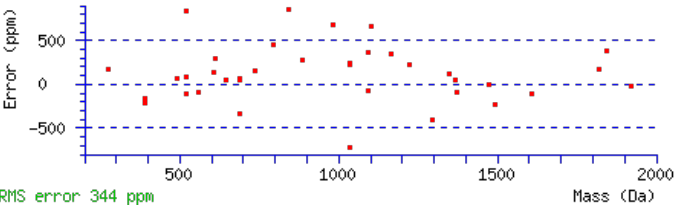
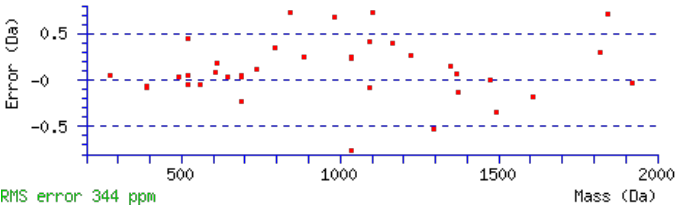
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2735.2562
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 70 Expect: 5.8e-006
Matches : 37/266 fragment ions using 52 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							24
2	293.1132	147.0602			275.1026	138.0550	Y	2607.2209	1304.1141	2590.1944	1295.6008	2589.2104	1295.1088	23
3	408.1401	204.5737			390.1296	195.5684	D	2444.1576	1222.5824	2427.1310	1214.0692	2426.1470	1213.5771	22
4	537.1827	269.0950			519.1722	260.0897	E	2329.1306	1165.0690	2312.1041	1156.5557	2311.1201	1156.0637	21
5	665.2413	333.1243	648.2148	324.6110	647.2307	324.1190	Q	2200.0881	1100.5477	2183.0615	1092.0344	2182.0775	1091.5424	20
6	779.2842	390.1458	762.2577	381.6325	761.2737	381.1405	N	2072.0295	1036.5184	2055.0029	1028.0051	2054.0189	1027.5131	19
7	894.3112	447.6592	877.2846	439.1460	876.3006	438.6539	N	1957.9865	979.4969	1940.9600	970.9836	1939.9760	970.4916	18
8	965.3483	483.1778	948.3217	474.6645	947.3377	474.1725	A	1842.9596	921.9834	1825.9331	913.4702	1824.9490	912.9782	17
9	1052.3803	526.6938	1035.3538	518.1805	1034.3698	517.6885	S	1771.9225	886.4649	1754.8959	877.9516	1753.9119	877.4596	16
10	1151.4487	576.2280	1134.4222	567.7147	1133.4382	567.2227	V	1684.8905	842.9489	1667.8639	834.4356	1666.8799	833.9436	15
11	1266.4757	633.7415	1249.4491	625.2282	1248.4651	624.7362	D	1585.8220	793.4147	1568.7955	784.9014	1567.8115	784.4094	14
12	1365.5441	683.2757	1348.5175	674.7624	1347.5335	674.2704	V	1470.7951	735.9012	1453.7686	727.3879	1452.7845	726.8959	13
13	1512.6125	756.8099	1495.5860	748.2966	1494.6019	747.8046	F	1371.7267	686.3670	1354.7001	677.8537	1353.7161	677.3617	12
14	1625.6966	813.3519	1608.6700	804.8387	1607.6860	804.3466	L	1224.6583	612.8328	1207.6317	604.3195	1206.6477	603.8275	11
15	1682.7180	841.8627	1665.6915	833.3494	1664.7075	832.8574	G	1111.5742	556.2907	1094.5477	547.7775	1093.5636	547.2855	10
16	1819.7769	910.3921	1802.7504	901.8788	1801.7664	901.3868	H	1054.5527	527.7800	1037.5262	519.2667	1036.5422	518.7747	9
17	1918.8454	959.9263	1901.8188	951.4130	1900.8348	950.9210	V	917.4938	459.2506	900.4673	450.7373	899.4833	450.2453	8
18	2032.8883	1016.9478	2015.8617	1008.4345	2014.8777	1007.9425	N	818.4254	409.7163	801.3989	401.2031	800.4149	400.7111	7
19	2131.9567	1066.4820	2114.9302	1057.9687	2113.9461	1057.4767	V	704.3825	352.6949	687.3559	344.1816	686.3719	343.6896	6
20	2246.9836	1123.9955	2229.9571	1115.4822	2228.9731	1114.9902	D	605.3141	303.1607	588.2875	294.6474	587.3035	294.1554	5
21	2376.0262	1188.5168	2358.9997	1180.0035	2358.0157	1179.5115	E	490.2871	245.6472	473.2606	237.1339	472.2766	236.6419	4
22	2489.1103	1245.0588	2472.0838	1236.5455	2471.0997	1236.0535	I	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
23	2590.1580	1295.5826	2573.1314	1287.0694	2572.1474	1286.5773	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
24							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EYDEQNNASVDVFLGHVNVDEITK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
70.3	2735.2562	-0.0042	EYDEQNNASVDVFLGHVNVDEITK	Deamidated N7 82.72%
59.2	2735.2562	-0.0042	EYDEQNNASVDVFLGHVNVDEITK	Deamidated N18 6.42%
59.2	2735.2562	-0.0042	EYDEQNNASVDVFLGHVNVDEITK	Deamidated N6 6.38%
57.7	2735.2562	-0.0042	EYDEQNNASVDVFLGHVNVDEITK	Deamidated Q5 4.48%
34.3	2734.2722	0.9798	EYDEQNNASVDVFLGHVNVDEITK	
4.2	2733.2704	1.9817	LSEEEQRLVQQAQQRNFFSMAR	
4.2	2734.2715	0.9805	KVATSVSEQRMEGNESSLPEAPSQR	
2.7	2734.2744	0.9777	YELQKHMASQHHPSAPAPLYPCR	
2.6	2734.2619	0.9902	DSLINFKEFVTGMSGMYHGDLTEK	
2.2	2735.2584	-0.0063	YELQKHMASQHHPSAPAPLYPCR	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **I3LMI9** in **uni_pig**, tr|I3LMI9|I3LMI9_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=LOC100737864 PE=4 SV=1

Title: 120326_Sunil_PigSerum_Glyco_PsetB_08Spectrum1327_scans__2102

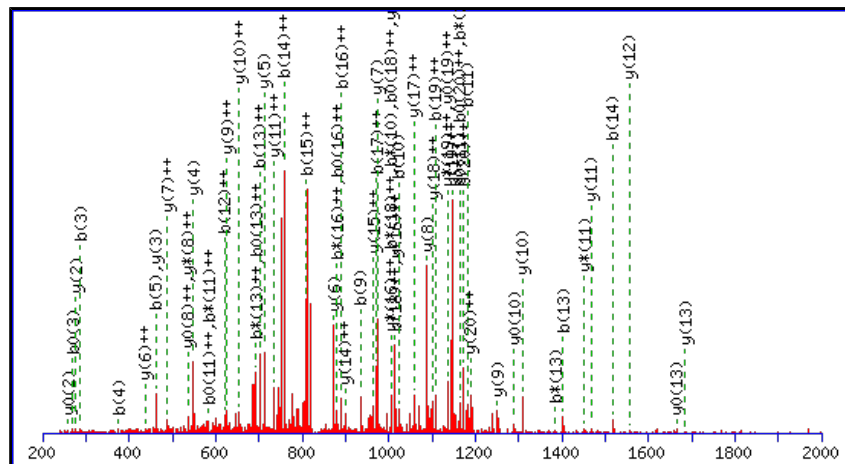
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

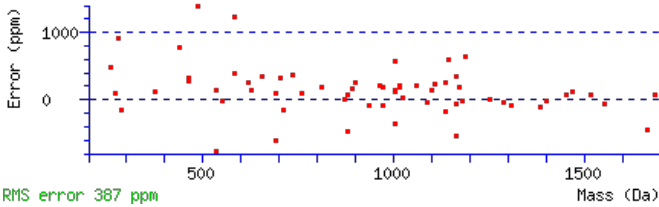
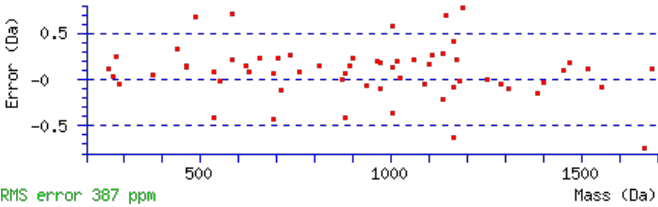
Variable modifications:

N8 : Deamidated (N0)

Ions Score: 59 Expect: 6e-006

Matches : 65/224 fragment ions using 118 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							21
2	201.1234	101.0653			183.1128	92.0600	S	2376.9231	1188.9652	2359.8965	1180.4519	2358.9125	1179.9599	20
3	288.1554	144.5813			270.1448	135.5761	S	2289.8911	1145.4492	2272.8645	1136.9359	2271.8805	1136.4439	19
4	375.1874	188.0973			357.1769	179.0921	S	2202.8590	1101.9332	2185.8325	1093.4199	2184.8485	1092.9279	18
5	462.2195	231.6134			444.2089	222.6081	S	2115.8270	1058.4171	2098.8005	1049.9039	2097.8164	1049.4119	17
6	563.2671	282.1372			545.2566	273.1319	T	2028.7950	1014.9011	2011.7684	1006.3879	2010.7844	1005.8958	16
7	691.3621	346.1847	674.3355	337.6714	673.3515	337.1794	K	1927.7473	964.3773	1910.7208	955.8640	1909.7367	955.3720	15
8	806.3890	403.6982	789.3625	395.1849	788.3785	394.6929	N	1799.6523	900.3298	1782.6258	891.8165	1781.6418	891.3245	14
9	935.4316	468.2195	918.4051	459.7062	917.4211	459.2142	E	1684.6254	842.8163	1667.5989	834.3031	1666.6148	833.8111	13
10	1022.4637	511.7355	1005.4371	503.2222	1004.4531	502.7302	S	1555.5828	778.2950	1538.5563	769.7818	1537.5722	769.2898	12
11	1182.4943	591.7508	1165.4678	583.2375	1164.4837	582.7455	C	1468.5508	734.7790	1451.5242	726.2658	1450.5402	725.7737	11
12	1239.5158	620.2615	1222.4892	611.7482	1221.5052	611.2562	G	1308.5201	654.7637	1291.4936	646.2504	1290.5096	645.7584	10
13	1402.5791	701.7932	1385.5526	693.2799	1384.5685	692.7879	Y	1251.4987	626.2530	1234.4721	617.7397	1233.4881	617.2477	9
14	1517.6060	759.3067	1500.5795	750.7934	1499.5955	750.3014	D	1088.4353	544.7213	1071.4088	536.2080	1070.4248	535.7160	8
15	1618.6537	809.8305	1601.6272	801.3172	1600.6432	800.8252	T	973.4084	487.2078	956.3818	478.6946	955.3978	478.2026	7
16	1778.6844	889.8458	1761.6578	881.3325	1760.6738	880.8405	C	872.3607	436.6840	855.3342	428.1707	854.3502	427.6787	6
17	1941.7477	971.3775	1924.7212	962.8642	1923.7371	962.3722	Y	712.3301	356.6687	695.3035	348.1554	694.3195	347.6634	5
18	2028.7797	1014.8935	2011.7532	1006.3802	2010.7692	1005.8882	S	549.2667	275.1370	532.2402	266.6237	531.2562	266.1317	4
19	2214.8590	1107.9332	2197.8325	1099.4199	2196.8485	1098.9279	W	462.2347	231.6210	445.2082	223.1077	444.2241	222.6157	3
20	2343.9016	1172.4545	2326.8751	1163.9412	2325.8911	1163.4492	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
21							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [LSSSSTKNESCGYDTCYSWEK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.6	2488.9999	-0.0065	LSSSSTKNESCGYDTCYSWEK

Mascot: <http://www.matrixscience.com/>

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Mascot Search Results

Peptide View

MS/MS Fragmentation of **FNDTEVLQR**
Found in **F1RS82** in **uni_pig**, tr|F1RS82|F1RS82_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=LOC100518580
PE=4 SV=2

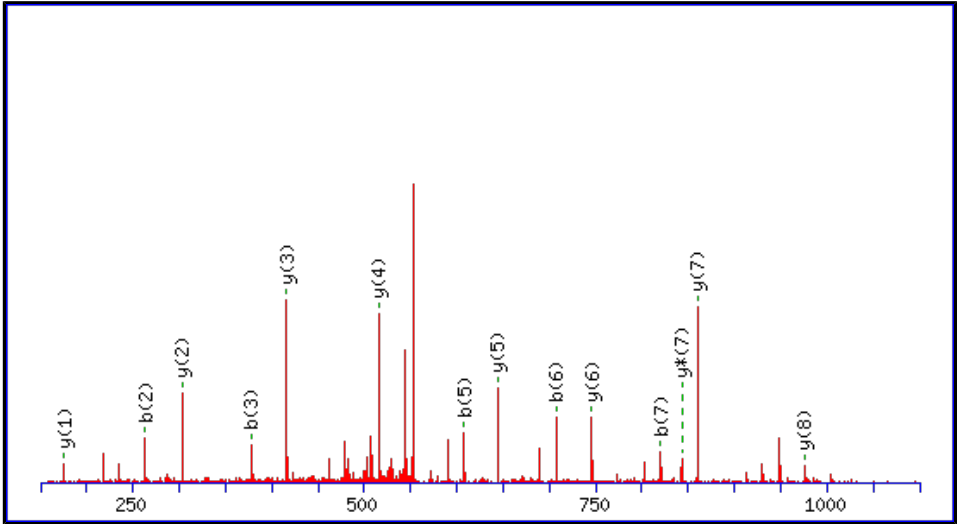
Match to Query 980: 1121.533268 from(561.773910,2+) intensity(39659.3477) rtinseconds(1512) scans(2690) index(6668)
Title: 120325_Sunil_PigSerum_Glyco_S_16Spectrum1723_scans__2690
Data file
W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

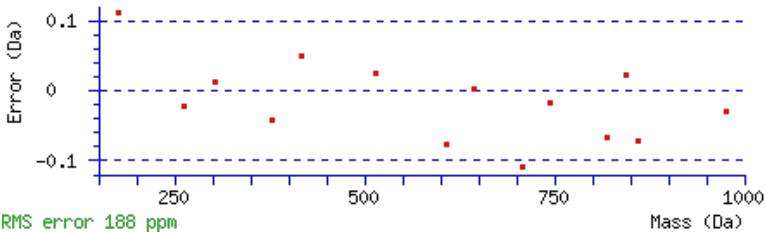
Label all possible matches Label matches used for scoring

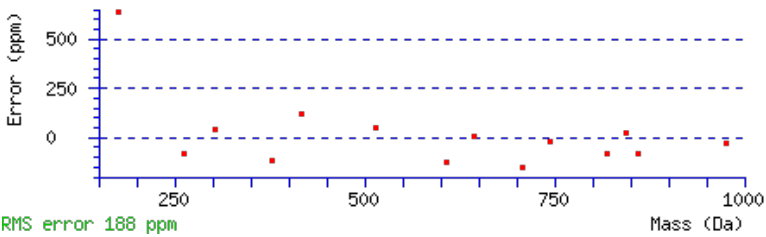
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1121.5353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Ions Score: 70 Expect: 6e-006
Matches : 14/82 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							9
2	263.1026	132.0550	246.0761	123.5417			N	975.4742	488.2407	958.4476	479.7274	957.4636	479.2354	8
3	378.1296	189.5684	361.1030	181.0552	360.1190	180.5631	D	860.4472	430.7272	843.4207	422.2140	842.4367	421.7220	7
4	479.1773	240.0923	462.1507	231.5790	461.1667	231.0870	T	745.4203	373.2138	728.3937	364.7005	727.4097	364.2085	6
5	608.2198	304.6136	591.1933	296.1003	590.2093	295.6083	E	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	5
6	707.2883	354.1478	690.2617	345.6345	689.2777	345.1425	V	515.3300	258.1686	498.3035	249.6554			4
7	820.3723	410.6898	803.3458	402.1765	802.3618	401.6845	L	416.2616	208.6344	399.2350	200.1212			3
8	948.4309	474.7191	931.4044	466.2058	930.4203	465.7138	Q	303.1775	152.0924	286.1510	143.5791			2
9							R	175.1190	88.0631	158.0924	79.5498			1



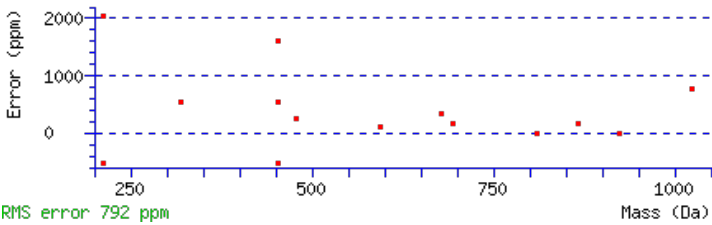


NCBI **BLAST** search of [FNDTEVLQR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
69.5	1121.5353	-0.0020	FNDTEVLQR	Deamidated N2 100.00%
19.8	1121.5353	-0.0020	FNDTEVLQR	Deamidated Q8 0.00%
18.9	1121.5386	-0.0054	METEAQLRK	
17.9	1121.5386	-0.0054	NMSVEEIKR	
10.6	1121.5387	-0.0054	ELGMITDTSR	
10.5	1121.5386	-0.0054	QNSQMIVKR	
7.7	1121.5288	0.0045	MSDAYHVKR	
7.0	1120.5335	0.9998	MYEEHLKR	
6.9	1121.5353	-0.0020	ETPTYNLQR	
6.9	1120.5248	1.0085	EKTEKEDDK	

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [LVGGDTNCSGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
64.8	1135.4928	-0.0016	LVGGDTNCSGR
12.8	1134.4903	1.0009	FNSYMVTEK
1.9	1133.4910	2.0002	QMNLQQQPK
1.9	1133.4910	2.0002	QMNLQQQPK
1.9	1133.4910	2.0002	QMNLQQQPK
1.9	1133.4910	2.0002	QMNLQQQPK
0.6	1133.4886	2.0027	GFFQLMCSK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

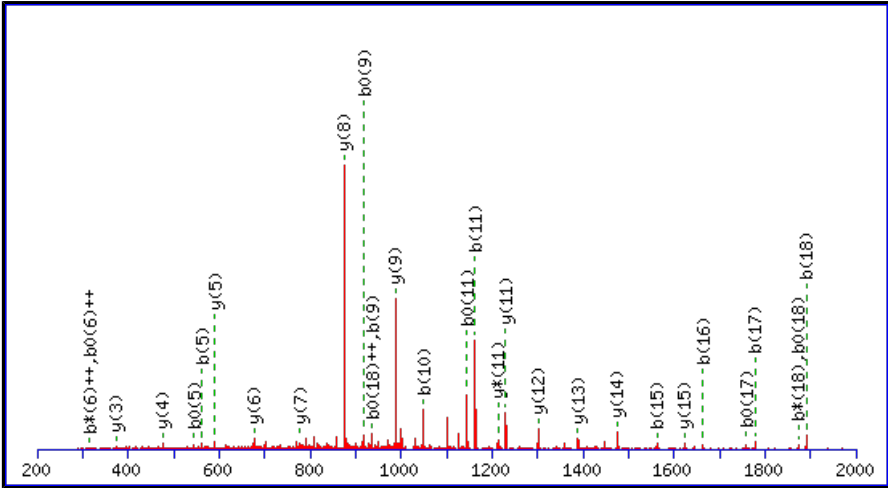
Peptide View

MS/MS Fragmentation of **VNLSFSSAQILPTSDTNLK**
Found in **I3LQ17** in **uni_pig**, tr|I3LQ17|I3LQ17_PIG Uncharacterized protein OS=Sus scrofa PE=4 SV=1

Match to Query 11816: 2036.022068 from(1019.018310,2+) intensity(52940.6172) rtinseconds(2596) scans(6417) index(3928)
Title: 120325_Sunil_PigSerum_Glyco_P_14Spectrum5438_scans_6417
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

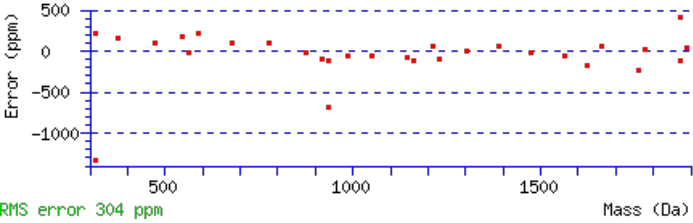
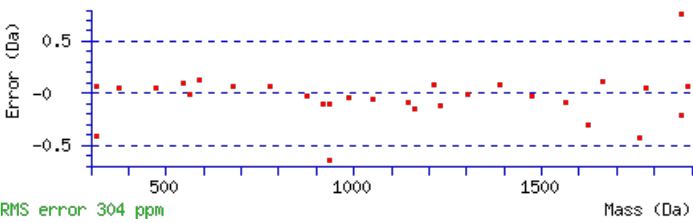
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2036.0313
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Q9 : Deamidated (NQ)
Ions Score: 71 Expect: 7.6e-006
Matches : 30/202 fragment ions using 51 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							19
2	215.1026	108.0550	198.0761	99.5417			N	1937.9702	969.4888	1920.9437	960.9755	1919.9597	960.4835	18
3	328.1867	164.5970	311.1601	156.0837			L	1822.9433	911.9753	1805.9167	903.4620	1804.9327	902.9700	17
4	415.2187	208.1130	398.1922	199.5997	397.2082	199.1077	S	1709.8592	855.4332	1692.8327	846.9200	1691.8487	846.4280	16
5	562.2871	281.6472	545.2606	273.1339	544.2766	272.6419	F	1622.8272	811.9172	1605.8006	803.4040	1604.8166	802.9120	15
6	649.3192	325.1632	632.2926	316.6499	631.3086	316.1579	S	1475.7588	738.3830	1458.7322	729.8698	1457.7482	729.3777	14
7	736.3512	368.6792	719.3246	360.1660	718.3406	359.6740	S	1388.7268	694.8670	1371.7002	686.3537	1370.7162	685.8617	13
8	807.3883	404.1978	790.3618	395.6845	789.3777	395.1925	A	1301.6947	651.3510	1284.6682	642.8377	1283.6842	642.3457	12
9	936.4309	468.7191	919.4044	460.2058	918.4203	459.7138	Q	1230.6576	615.8324	1213.6311	607.3192	1212.6470	606.8272	11
10	1049.5150	525.2611	1032.4884	516.7478	1031.5044	516.2558	I	1101.6150	551.3111	1084.5885	542.7979	1083.6045	542.3059	10
11	1162.5990	581.8032	1145.5725	573.2899	1144.5885	572.7979	L	988.5310	494.7691	971.5044	486.2558	970.5204	485.7638	9
12	1259.6518	630.3295	1242.6252	621.8163	1241.6412	621.3243	P	875.4469	438.2271	858.4203	429.7138	857.4363	429.2218	8
13	1360.6995	680.8534	1343.6729	672.3401	1342.6889	671.8481	T	778.3941	389.7007	761.3676	381.1874	760.3836	380.6954	7
14	1447.7315	724.3694	1430.7050	715.8561	1429.7209	715.3641	S	677.3464	339.1769	660.3199	330.6636	659.3359	330.1716	6
15	1562.7584	781.8829	1545.7319	773.3696	1544.7479	772.8776	D	590.3144	295.6608	573.2879	287.1476	572.3039	286.6556	5
16	1663.8061	832.4067	1646.7796	823.8934	1645.7956	823.4014	T	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
17	1777.8491	889.4282	1760.8225	880.9149	1759.8385	880.4229	N	374.2398	187.6235	357.2132	179.1103			3
18	1890.9331	945.9702	1873.9066	937.4569	1872.9225	936.9649	L	260.1969	130.6021	243.1703	122.0888			2
19							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VNLSFSSAQILPTSDTNLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
70.5	2036.0313	-0.0093	VNLSFSSAQILPTSDTNLK	Deamidated N2, Q9 80.22%
63.6	2036.0313	-0.0093	VNLSFSSAQILPTSDTNLK	Deamidated N2, N17 16.42%
56.7	2036.0313	-0.0093	VNLSFSSAQILPTSDTNLK	Deamidated Q9, N17 3.36%
10.7	2036.0270	-0.0050	HRHMFVKLIDMDHVMK	
6.0	2036.0102	0.0119	LDGEIIPHPADQEVLNK	
6.0	2036.0102	0.0119	LDGEIIPHEPANQEVLNK	
6.0	2036.0102	0.0119	LDGEIIPHEPANQEVLNK	
5.1	2035.0255	0.9966	GSQELGMSNIQELSLRKK	
4.7	2035.0109	1.0112	NNEQQELLSNKELTLDK	
4.7	2035.0109	1.0112	NNEQQELLSNKELTLDK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

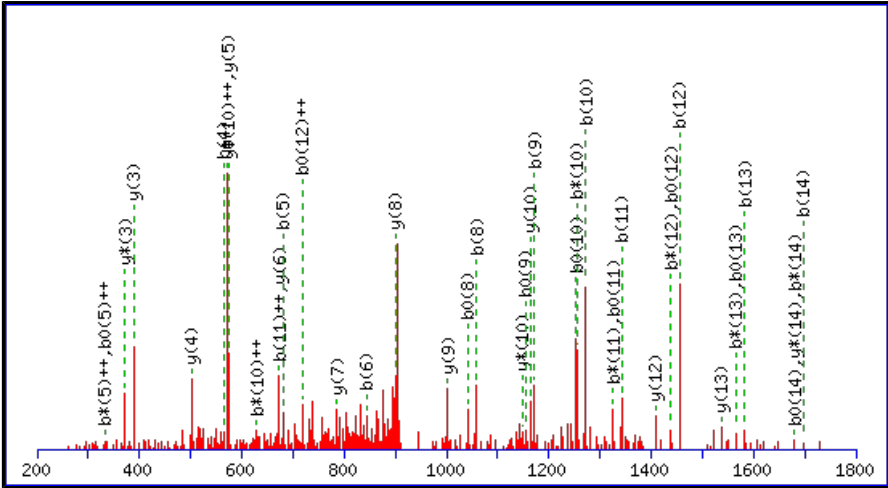
Peptide View

MS/MS Fragmentation of **FCQENYTDLVAIQNK**
Found in **A8R080** in **uni_pig**, tr|A8R080|A8R080_PIG L-selectin OS=Sus scrofa GN=SELL PE=2 SV=1

Match to Query 6889: 1842.841288 from(922.427920,2+) intensity(8984.7246) rtinseconds(1993) scans(4109) index(8950)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_16Spectrum3131_scans__4109
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

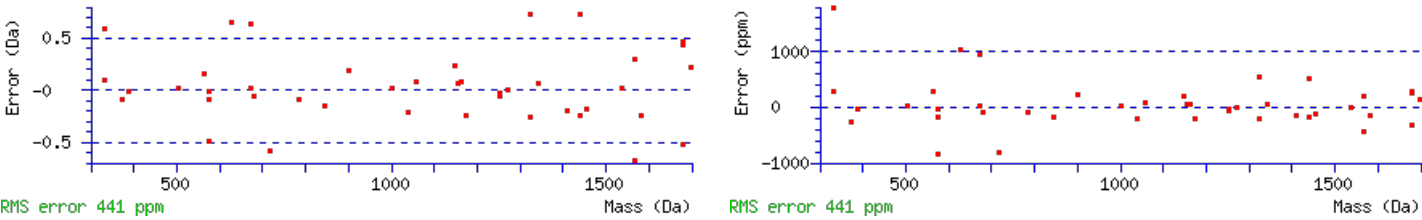
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1842.8458
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 68 Expect: 8.7e-006
Matches : 42/144 fragment ions using 60 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							15
2	308.1063	154.5568					C	1696.7847	848.8960	1679.7581	840.3827	1678.7741	839.8907	14
3	436.1649	218.5861	419.1384	210.0728			Q	1536.7540	768.8807	1519.7275	760.3674	1518.7435	759.8754	13
4	565.2075	283.1074	548.1810	274.5941	547.1969	274.1021	E	1408.6955	704.8514	1391.6689	696.3381	1390.6849	695.8461	12
5	680.2345	340.6209	663.2079	332.1076	662.2239	331.6156	N	1279.6529	640.3301	1262.6263	631.8168	1261.6423	631.3248	11
6	843.2978	422.1525	826.2712	413.6393	825.2872	413.1472	Y	1164.6259	582.8166	1147.5994	574.3033	1146.6154	573.8113	10
7	944.3455	472.6764	927.3189	464.1631	926.3349	463.6711	T	1001.5626	501.2849	984.5360	492.7717	983.5520	492.2796	9
8	1059.3724	530.1898	1042.3459	521.6766	1041.3618	521.1846	D	900.5149	450.7611	883.4884	442.2478	882.5043	441.7558	8
9	1172.4565	586.7319	1155.4299	578.2186	1154.4459	577.7266	L	785.4880	393.2476	768.4614	384.7343			7
10	1271.5249	636.2661	1254.4983	627.7528	1253.5143	627.2608	V	672.4039	336.7056	655.3774	328.1923			6
11	1342.5620	671.7846	1325.5354	663.2714	1324.5514	662.7794	A	573.3355	287.1714	556.3089	278.6581			5
12	1455.6461	728.3267	1438.6195	719.8134	1437.6355	719.3214	I	502.2984	251.6528	485.2718	243.1395			4
13	1583.7046	792.3560	1566.6781	783.8427	1565.6941	783.3507	Q	389.2143	195.1108	372.1878	186.5975			3
14	1697.7476	849.3774	1680.7210	840.8641	1679.7370	840.3721	N	261.1557	131.0815	244.1292	122.5682			2
15							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [FCQENYTDLVAIQNK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
67.7	1842.8458	-0.0045	FCQENYTDLVAIQNK	Deamidated N5 84.24%
60.4	1842.8458	-0.0045	FCQENYTDLVAIQNK	Deamidated Q3 15.72%
31.9	1842.8458	-0.0045	FCQENYTDLVAIQNK	Deamidated N14 0.02%
31.8	1842.8458	-0.0045	FCQENYTDLVAIQNK	Deamidated Q13 0.02%
1.9	1841.8465	0.9948	GDMANNSVAYGGVKNLKL	
1.9	1841.8465	0.9948	GDMANNSVAYGGVKNLKL	
1.7	1840.8261	2.0152	EQSRVVFQMGTSDAER	
1.6	1840.8189	2.0224	EEAGDAYELLAPCFQK	
0.8	1842.8346	0.0067	LFEELAMDVYDEVDR	

Mascot: <http://www.matrixscience.com/>

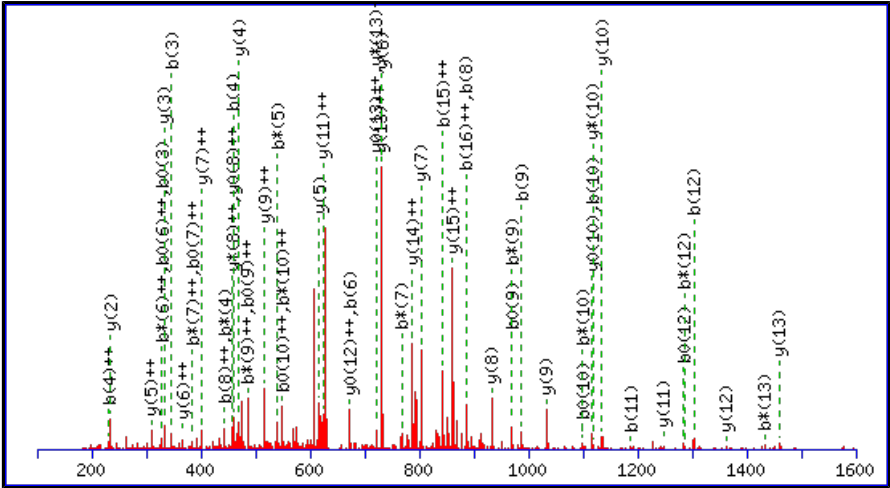


Mascot Search Results

Peptide View

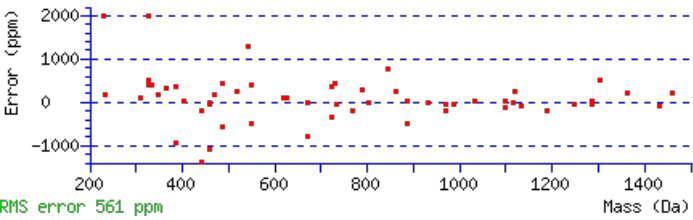
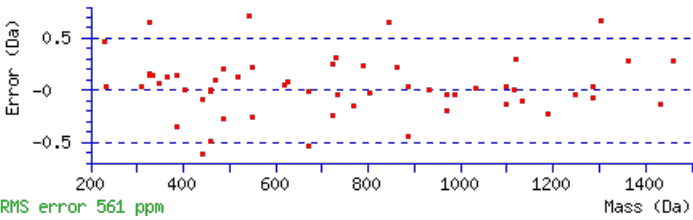
MS/MS Fragmentation of **TPFNPNLTTTEADFHVSK**
Found in **Q9GMA6** in **uni_pig**, tr|Q9GMA6|Q9GMA6_PIG Alpha-1-antichymotrypsin 2 OS=Sus scrofa GN=SERPINA3-2 PE=3 SV=1
Match to Query 7917: 1917.907482 from(640.309770,3+) intensity(128205.6797) rtinseconds(2010) scans(4785) index(1588)
Title: 120325_Sunil_PigSerum_Glyco_D_14Spectrum4092_scans__4785
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1917.9109
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 69 Expect: 8.9e-006
Matches : 58/184 fragment ions using 84 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							17
2	199.1077	100.0575			181.0972	91.0522	P	1817.8705	909.4389	1800.8439	900.9256	1799.8599	900.4336	16
3	346.1761	173.5917			328.1656	164.5864	F	1720.8177	860.9125	1703.7911	852.3992	1702.8071	851.9072	15
4	460.2191	230.6132	443.1925	222.0999	442.2085	221.6079	N	1573.7493	787.3783	1556.7227	778.8650	1555.7387	778.3730	14
5	557.2718	279.1396	540.2453	270.6263	539.2613	270.1343	P	1459.7064	730.3568	1442.6798	721.8435	1441.6958	721.3515	13
6	672.2988	336.6530	655.2722	328.1397	654.2882	327.6477	N	1362.6536	681.8304	1345.6270	673.3172	1344.6430	672.8251	12
7	785.3828	393.1951	768.3563	384.6818	767.3723	384.1898	L	1247.6266	624.3170	1230.6001	615.8037	1229.6161	615.3117	11
8	886.4305	443.7189	869.4040	435.2056	868.4199	434.7136	T	1134.5426	567.7749	1117.5160	559.2617	1116.5320	558.7696	10
9	987.4782	494.2427	970.4516	485.7295	969.4676	485.2375	T	1033.4949	517.2511	1016.4684	508.7378	1015.4843	508.2458	9
10	1116.5208	558.7640	1099.4942	550.2508	1098.5102	549.7587	E	932.4472	466.7272	915.4207	458.2140	914.4367	457.7220	8
11	1187.5579	594.2826	1170.5313	585.7693	1169.5473	585.2773	A	803.4046	402.2060	786.3781	393.6927	785.3941	393.2007	7
12	1302.5848	651.7961	1285.5583	643.2828	1284.5743	642.7908	D	732.3675	366.6874	715.3410	358.1741	714.3570	357.6821	6
13	1449.6533	725.3303	1432.6267	716.8170	1431.6427	716.3250	F	617.3406	309.1739	600.3140	300.6606	599.3300	300.1686	5
14	1586.7122	793.8597	1569.6856	785.3464	1568.7016	784.8544	H	470.2722	235.6397	453.2456	227.1264	452.2616	226.6344	4
15	1685.7806	843.3939	1668.7540	834.8807	1667.7700	834.3886	V	333.2132	167.1103	316.1867	158.5970	315.2027	158.1050	3
16	1772.8126	886.9099	1755.7861	878.3967	1754.8020	877.9047	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [TPFNPNLTTEADFHVSK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
68.9	1917.9109	-0.0034	TPFNPNLTTEADFHVSK	Deamidated N6 99.51%
45.8	1917.9109	-0.0034	TPFNPNLTTEADFHVSK	Deamidated N4 0.49%
11.0	1916.8985	1.0090	TGWIGELGAMRMPSSHR	
4.4	1915.8946	2.0129	SGLPDVAPMTKDNGPGSTR	
2.6	1915.9010	2.0064	AALQTAPESADDSPSQLSK	
0.7	1916.8976	1.0099	GQHGEYETEVQQAKRR	
0.7	1916.8976	1.0099	GQHGEYETEVQQAKRR	
0.7	1915.8887	2.0188	NESSLHTVFCATGGGAYK	

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

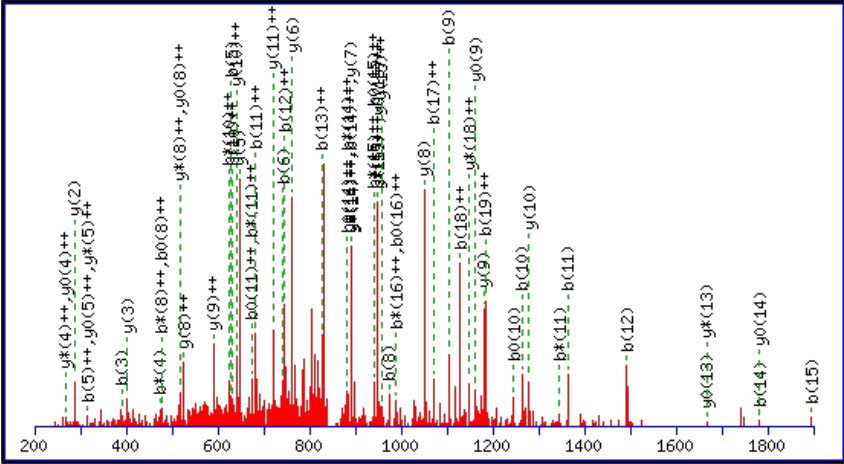
Peptide View

MS/MS Fragmentation of **NNCTHDDDMCVECEDPFDLR**
Found in **F1RN76** in **uni_pig**, tr|F1RN76|F1RN76_PIG Uncharacterized protein OS=Sus scrofa GN=CD5L PE=4 SV=2

Match to Query 13065: 2541.904572 from(848.308800,3+) intensity(9887.9981) rtinseconds(2228) scans(4371) index(10961)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_15Spectrum3307_scans_4371
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

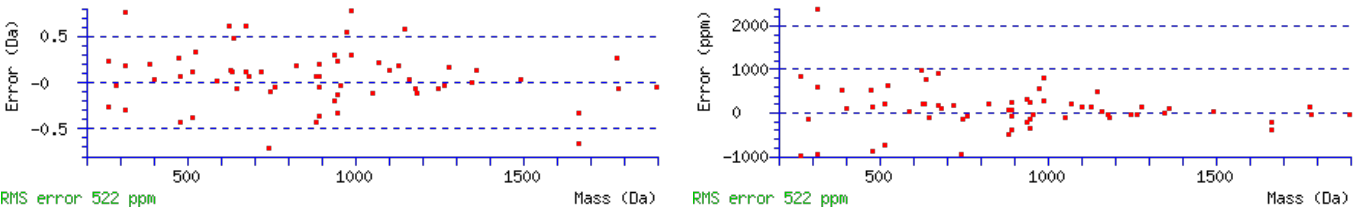
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2541.9141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Ions Score: 50 Expect: 9.5e-006
Matches : 62/218 fragment ions using 98 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							20
2	230.0771	115.5422	213.0506	107.0289			N	2428.8785	1214.9429	2411.8519	1206.4296	2410.8679	1205.9376	19
3	390.1078	195.5575	373.0812	187.0443			C	2313.8515	1157.4294	2296.8250	1148.9161	2295.8410	1148.4241	18
4	491.1555	246.0814	474.1289	237.5681	473.1449	237.0761	T	2153.8209	1077.4141	2136.7943	1068.9008	2135.8103	1068.4088	17
5	628.2144	314.6108	611.1878	306.0976	610.2038	305.6055	H	2052.7732	1026.8902	2035.7467	1018.3770	2034.7626	1017.8850	16
6	743.2413	372.1243	726.2148	363.6110	725.2308	363.1190	D	1915.7143	958.3608	1898.6877	949.8475	1897.7037	949.3555	15
7	858.2683	429.6378	841.2417	421.1245	840.2577	420.6325	D	1800.6873	900.8473	1783.6608	892.3340	1782.6768	891.8420	14
8	973.2952	487.1512	956.2687	478.6380	955.2846	478.1460	D	1685.6604	843.3338	1668.6339	834.8206	1667.6498	834.3286	13
9	1104.3357	552.6715	1087.3092	544.1582	1086.3251	543.6662	M	1570.6335	785.8204	1553.6069	777.3071	1552.6229	776.8151	12
10	1264.3663	632.6868	1247.3398	624.1735	1246.3558	623.6815	C	1439.5930	720.3001	1422.5664	711.7869	1421.5824	711.2948	11
11	1363.4348	682.2210	1346.4082	673.7077	1345.4242	673.2157	V	1279.5623	640.2848	1262.5358	631.7715	1261.5518	631.2795	10
12	1492.4774	746.7423	1475.4508	738.2290	1474.4668	737.7370	E	1180.4939	590.7506	1163.4674	582.2373	1162.4834	581.7453	9
13	1652.5080	826.7576	1635.4815	818.2444	1634.4974	817.7524	C	1051.4513	526.2293	1034.4248	517.7160	1033.4408	517.2240	8
14	1781.5506	891.2789	1764.5240	882.7657	1763.5400	882.2737	E	891.4207	446.2140	874.3941	437.7007	873.4101	437.2087	7
15	1896.5775	948.7924	1879.5510	940.2791	1878.5670	939.7871	D	762.3781	381.6927	745.3515	373.1794	744.3675	372.6874	6
16	1993.6303	997.3188	1976.6038	988.8055	1975.6197	988.3135	P	647.3511	324.1792	630.3246	315.6659	629.3406	315.1739	5
17	2140.6987	1070.8530	2123.6722	1062.3397	2122.6882	1061.8477	F	550.2984	275.6528	533.2718	267.1396	532.2878	266.6475	4
18	2255.7257	1128.3665	2238.6991	1119.8532	2237.7151	1119.3612	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
19	2368.8097	1184.9085	2351.7832	1176.3952	2350.7992	1175.9032	L	288.2030	144.6051	271.1765	136.0919			2
20							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [NNCTHDDDMCVECEDPFDLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
50.2	2541.9141	-0.0096	NNCTHDDDMCVECEDPFDLR	Deamidated N2 50.00%
50.2	2541.9141	-0.0096	NNCTHDDDMCVECEDPFDLR	Deamidated N1 50.00%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

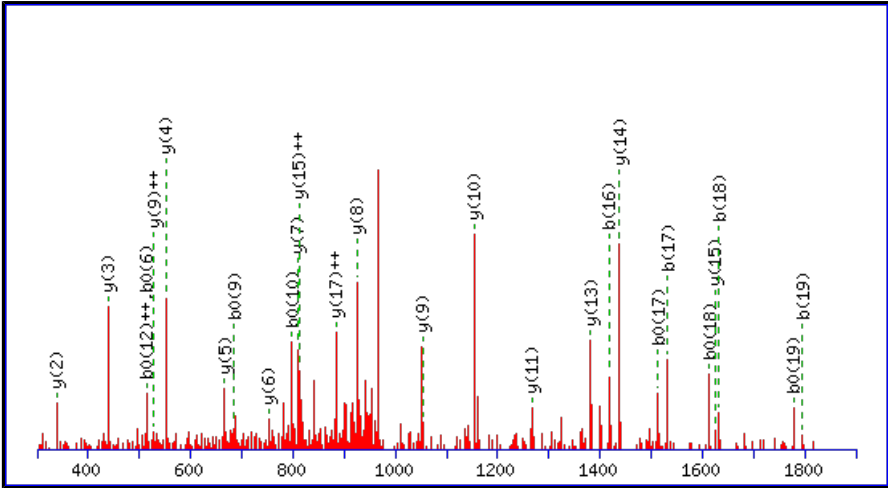
Peptide View

MS/MS Fragmentation of **GGSSGWGGGLTQNGSIITYR**
Found in **F1S788** in **uni_pig**, tr[F1S788]F1S788_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=C8A PE=4 SV=2

Match to Query 10023: 1968.927348 from(985.470950,2+) intensity(7929.7539) rtinseconds(2279) scans(4038) index(3180)
Title: 120325_Sunil_PigSerum_Glyco_P_10Spectrum2940_scans__4038
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

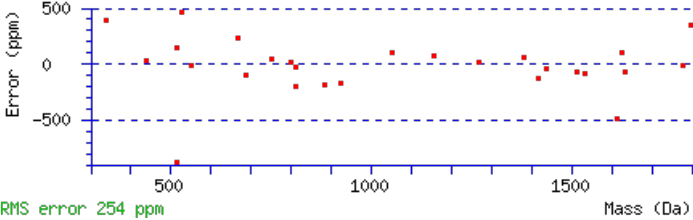
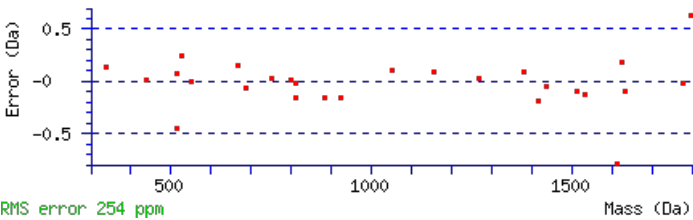
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1968.9177
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Deamidated (NQ)
N13 : Deamidated (NQ)
Ions Score: 68 Expect: 9.9e-006
Matches : 27/198 fragment ions using 61 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							20
2	115.0502	58.0287					G	1912.9035	956.9554	1895.8770	948.4421	1894.8930	947.9501	19
3	202.0822	101.5448			184.0717	92.5395	S	1855.8821	928.4447	1838.8555	919.9314	1837.8715	919.4394	18
4	289.1143	145.0608			271.1037	136.0555	S	1768.8501	884.9287	1751.8235	876.4154	1750.8395	875.9234	17
5	346.1357	173.5715			328.1252	164.5662	G	1681.8180	841.4127	1664.7915	832.8994	1663.8075	832.4074	16
6	532.2150	266.6112			514.2045	257.6059	W	1624.7966	812.9019	1607.7700	804.3886	1606.7860	803.8966	15
7	589.2365	295.1219			571.2259	286.1166	G	1438.7173	719.8623	1421.6907	711.3490	1420.7067	710.8570	14
8	646.2580	323.6326			628.2474	314.6273	G	1381.6958	691.3515	1364.6692	682.8383	1363.6852	682.3462	13
9	703.2794	352.1434			685.2689	343.1381	G	1324.6743	662.8408	1307.6478	654.3275	1306.6638	653.8355	12
10	816.3635	408.6854			798.3529	399.6801	L	1267.6529	634.3301	1250.6263	625.8168	1249.6423	625.3248	11
11	917.4112	459.2092			899.4006	450.2039	T	1154.5688	577.7880	1137.5422	569.2748	1136.5582	568.7828	10
12	1046.4538	523.7305	1029.4272	515.2172	1028.4432	514.7252	Q	1053.5211	527.2642	1036.4946	518.7509	1035.5106	518.2589	9
13	1161.4807	581.2440	1144.4542	572.7307	1143.4701	572.2387	N	924.4785	462.7429	907.4520	454.2296	906.4680	453.7376	8
14	1218.5022	609.7547	1201.4756	601.2415	1200.4916	600.7494	G	809.4516	405.2294	792.4250	396.7162	791.4410	396.2241	7
15	1305.5342	653.2707	1288.5077	644.7575	1287.5236	644.2655	S	752.4301	376.7187	735.4036	368.2054	734.4196	367.7134	6
16	1418.6183	709.8128	1401.5917	701.2995	1400.6077	700.8075	I	665.3981	333.2027	648.3715	324.6894	647.3875	324.1974	5
17	1531.7023	766.3548	1514.6758	757.8415	1513.6918	757.3495	I	552.3140	276.6607	535.2875	268.1474	534.3035	267.6554	4
18	1632.7500	816.8786	1615.7235	808.3654	1614.7394	807.8734	T	439.2300	220.1186	422.2034	211.6053	421.2194	211.1133	3
19	1795.8133	898.4103	1778.7868	889.8970	1777.8028	889.4050	Y	338.1823	169.5948	321.1557	161.0815			2
20							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [GGSSGWGGGLTQNGSIITYR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.4	1968.9177	0.0096	GGSSGWGGGLTQNGSIITYR
66.7	1967.9337	0.9936	GGSSGWGGGLTQNGSIITYR
57.5	1967.9337	0.9936	GGSSGWGGGLTQNGSIITYR
0.4	1968.9177	0.0097	LGHLQNSWDTLQEAAAGR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPSVWAGQNWTR**

Found in **F1RMN7** in **uni_pig**, tr|F1RMN7|F1RMN7_PIG Hemopexin OS=Sus scrofa GN=HPX PE=4 SV=2

Match to Query 3193: 1359.618588 from(680.816570,2+) intensity(9218.8115) rtinseconds(2083) scans(4943) index(13305)

Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum4150_scans_4943

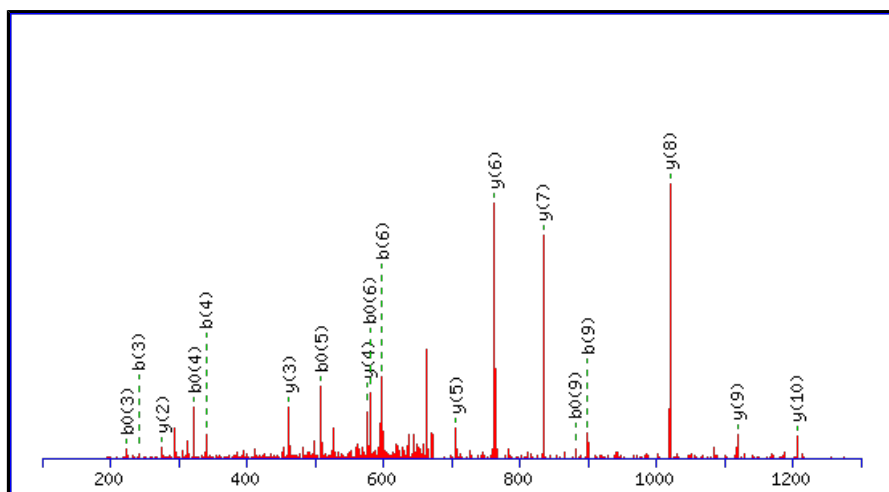
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1359.6208

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

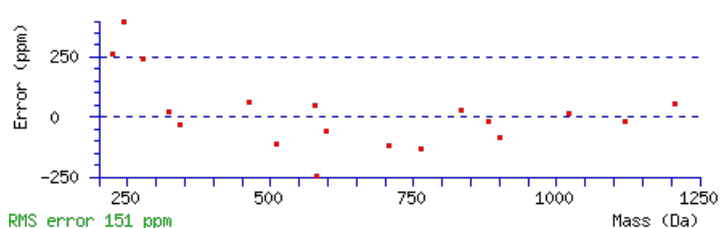
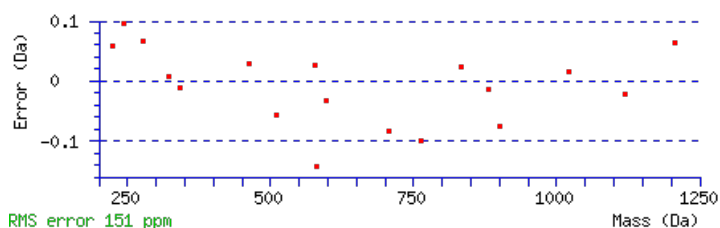
Q8 : Deamidated (NQ)

N9 : Deamidated (NQ)

Ions Score: 65 Expect: 1e-005

Matches : 18/112 fragment ions using 33 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							12
2	155.0815	78.0444					P	1303.6066	652.3069	1286.5800	643.7937	1285.5960	643.3016	11
3	242.1135	121.5604			224.1030	112.5551	S	1206.5538	603.7805	1189.5273	595.2673	1188.5432	594.7753	10
4	341.1819	171.0946			323.1714	162.0893	V	1119.5218	560.2645	1102.4952	551.7513	1101.5112	551.2592	9
5	527.2613	264.1343			509.2507	255.1290	W	1020.4534	510.7303	1003.4268	502.2170	1002.4428	501.7250	8
6	598.2984	299.6528			580.2878	290.6475	A	834.3741	417.6907	817.3475	409.1774	816.3635	408.6854	7
7	655.3198	328.1636			637.3093	319.1583	G	763.3369	382.1721	746.3104	373.6588	745.3264	373.1668	6
8	784.3624	392.6849	767.3359	384.1716	766.3519	383.6796	Q	706.3155	353.6614	689.2889	345.1481	688.3049	344.6561	5
9	899.3894	450.1983	882.3628	441.6851	881.3788	441.1930	N	577.2729	289.1401	560.2463	280.6268	559.2623	280.1348	4
10	1085.4687	543.2380	1068.4421	534.7247	1067.4581	534.2327	W	462.2459	231.6266	445.2194	223.1133	444.2354	222.6213	3
11	1186.5164	593.7618	1169.4898	585.2485	1168.5058	584.7565	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
12							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [GPSVWAGQNWTR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.0	1359.6208	-0.0022	GPSVWAGQNWTR
6.9	1359.6088	0.0097	HSKKGMDNQGQK
5.3	1359.6188	-0.0002	SSTSTNTSMLTSK
2.9	1358.6248	0.9938	HSKKGMDNQGQK

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1S643** in **uni_pig**, tr|F1S643|F1S643_PIG Uncharacterized protein OS=Sus scrofa GN=CFH PE=4 SV=2

Title: 120325_Sunil_PigSerum_Glyco_D_05Spectrum1570_scans_2700

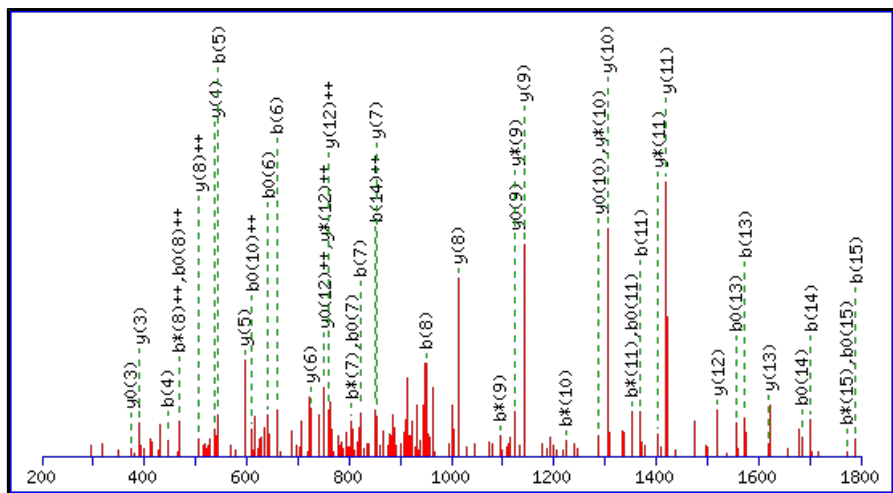
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

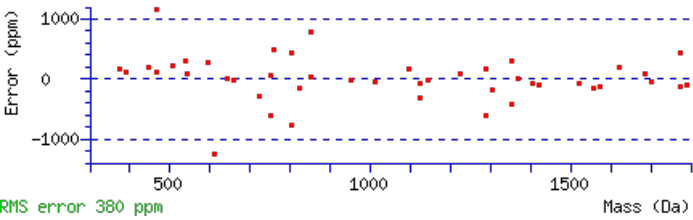
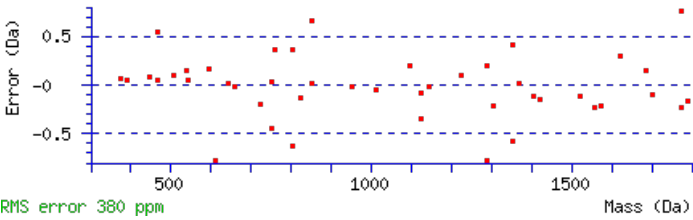
N2 : Deamidated (NQ)

Q10 : Deamidated (NQ)

Q11 : Deamidated (NQ)

Ions Score: 55 **Expect:** 1e-005
Matches : 45/172 fragment ions using 75 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							16
2	229.1183	115.0628	212.0917	106.5495			N	1850.7021	925.8547	1833.6756	917.3414	1832.6916	916.8494	15
3	344.1452	172.5763	327.1187	164.0630	326.1347	163.5710	D	1735.6752	868.3412	1718.6486	859.8280	1717.6646	859.3360	14
4	445.1929	223.1001	428.1664	214.5868	427.1823	214.0948	T	1620.6482	810.8278	1603.6217	802.3145	1602.6377	801.8225	13
5	544.2613	272.6343	527.2348	264.1210	526.2508	263.6290	V	1519.6006	760.3039	1502.5740	751.7906	1501.5900	751.2986	12
6	659.2883	330.1478	642.2617	321.6345	641.2777	321.1425	D	1420.5322	710.7697	1403.5056	702.2564	1402.5216	701.7644	11
7	822.3516	411.6794	805.3250	403.1662	804.3410	402.6742	Y	1305.5052	653.2562	1288.4787	644.7430	1287.4946	644.2510	10
8	951.3942	476.2007	934.3676	467.6875	933.3836	467.1954	E	1142.4419	571.7246	1125.4153	563.2113	1124.4313	562.7193	9
9	1111.4248	556.2161	1094.3983	547.7028	1093.4143	547.2108	C	1013.3993	507.2033	996.3727	498.6900	995.3887	498.1980	8
10	1240.4674	620.7374	1223.4409	612.2241	1222.4569	611.7321	Q	853.3686	427.1880	836.3421	418.6747	835.3581	418.1827	7
11	1369.5100	685.2586	1352.4835	676.7454	1351.4995	676.2534	Q	724.3260	362.6667	707.2995	354.1534	706.3155	353.6614	6
12	1426.5315	713.7694	1409.5049	705.2561	1408.5209	704.7641	G	595.2835	298.1454	578.2569	289.6321	577.2729	289.1401	5
13	1573.5999	787.3036	1556.5734	778.7903	1555.5893	778.2983	F	538.2620	269.6346	521.2354	261.1214	520.2514	260.6293	4
14	1702.6425	851.8249	1685.6159	843.3116	1684.6319	842.8196	E	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
15	1789.6745	895.3409	1772.6480	886.8276	1771.6640	886.3356	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
16							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LNDTVDYECQGFESR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.3	1962.7789	-0.0087	LNDTVDYECQGFESR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

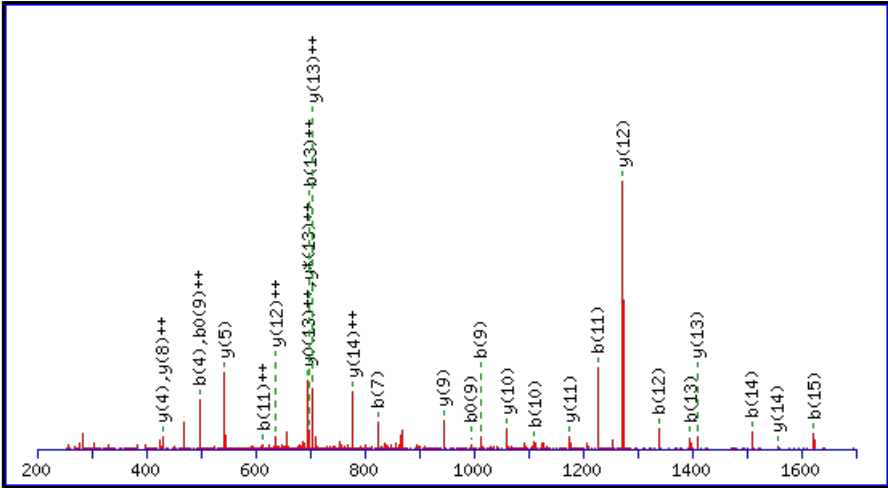
Peptide View

MS/MS Fragmentation of **VIFHPDNSTVDIGLIK**
Found in **K7GKE7** in **uni_pig**, tr[K7GKE7|K7GKE7_PIG Haptoglobin OS=Sus scrofa GN=HP PE=3 SV=1

Match to Query 6374: 1767.939548 from(884.977050,2+) intensity(40064.3633) rtinseconds(2360) scans(5287) index(13005)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_13Spectrum4362_scans__5287
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

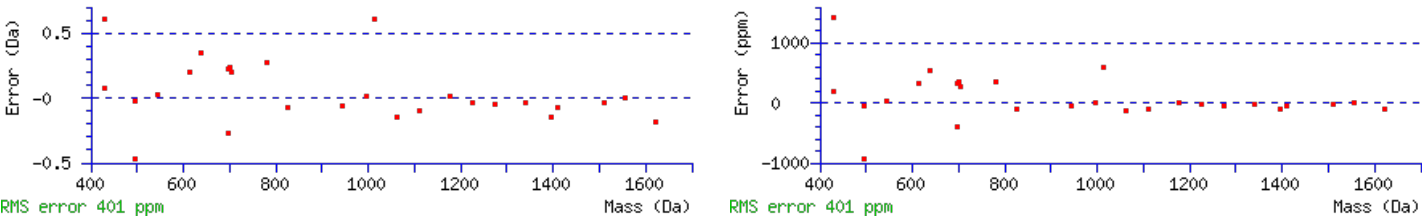
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1767.9407
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 65 Expect: 1.5e-005
Matches : 27/148 fragment ions using 43 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							16
2	213.1598	107.0835					I	1669.8796	835.4434	1652.8530	826.9301	1651.8690	826.4381	15
3	360.2282	180.6177					F	1556.7955	778.9014	1539.7690	770.3881	1538.7849	769.8961	14
4	497.2871	249.1472					H	1409.7271	705.3672	1392.7005	696.8539	1391.7165	696.3619	13
5	594.3398	297.6736					P	1272.6682	636.8377	1255.6416	628.3245	1254.6576	627.8324	12
6	709.3668	355.1870			691.3562	346.1817	D	1175.6154	588.3113	1158.5889	579.7981	1157.6048	579.3061	11
7	824.3937	412.7005	807.3672	404.1872	806.3832	403.6952	N	1060.5885	530.7979	1043.5619	522.2846	1042.5779	521.7926	10
8	911.4258	456.2165	894.3992	447.7032	893.4152	447.2112	S	945.5615	473.2844	928.5350	464.7711	927.5510	464.2791	9
9	1012.4734	506.7404	995.4469	498.2271	994.4629	497.7351	T	858.5295	429.7684	841.5029	421.2551	840.5189	420.7631	8
10	1111.5419	556.2746	1094.5153	547.7613	1093.5313	547.2693	V	757.4818	379.2445	740.4553	370.7313	739.4713	370.2393	7
11	1226.5688	613.7880	1209.5422	605.2748	1208.5582	604.7828	D	658.4134	329.7103	641.3869	321.1971	640.4028	320.7051	6
12	1339.6529	670.3301	1322.6263	661.8168	1321.6423	661.3248	I	543.3865	272.1969	526.3599	263.6836			5
13	1396.6743	698.8408	1379.6478	690.3275	1378.6638	689.8355	G	430.3024	215.6548	413.2758	207.1416			4
14	1509.7584	755.3828	1492.7318	746.8696	1491.7478	746.3775	L	373.2809	187.1441	356.2544	178.6308			3
15	1622.8424	811.9249	1605.8159	803.4116	1604.8319	802.9196	I	260.1969	130.6021	243.1703	122.0888			2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VIEHPDNSTVDIGLIK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.3	1767.9407	-0.0012	VIEHPDNSTVDIGLIK
4.1	1767.9460	-0.0065	RVIKWFDYLWTNK
2.7	1767.9479	-0.0084	ATSHTQAVLQKTVEQK
1.2	1765.9435	1.9961	GEAGTPVAAGTTAAAI PRR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **WGEVHLISNCSK**

Found in **F1S133** in **uni_pig**, tr|F1S133|F1S133_PIG Uncharacterized protein OS=Sus scrofa GN=CFI PE=3 SV=2

Match to Query 3835: 1429.662848 from(715.838700,2+) intensity(14097.1250) rtinseconds(1711) scans(3219) index(11528)

Title: 120326_Sunil_PigSerum_Glyco_SsetB_02Spectrum2413_scans__3219

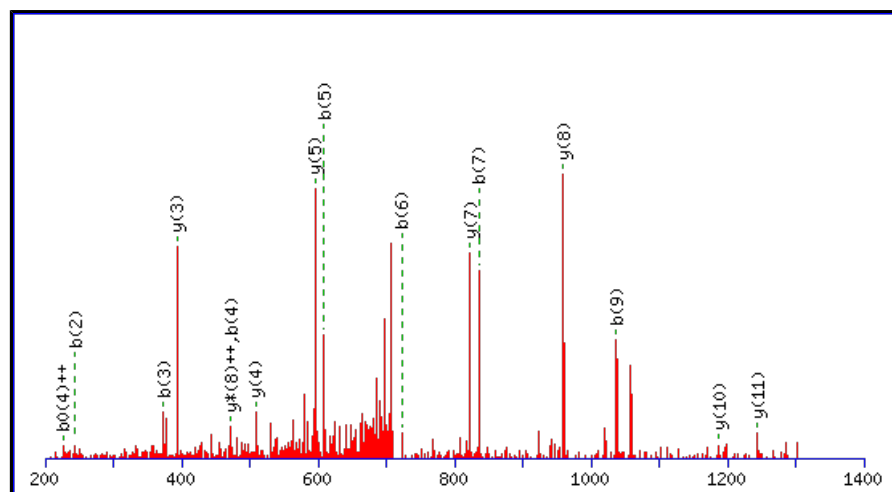
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1429.6660

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

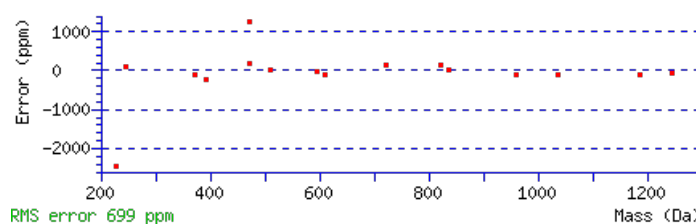
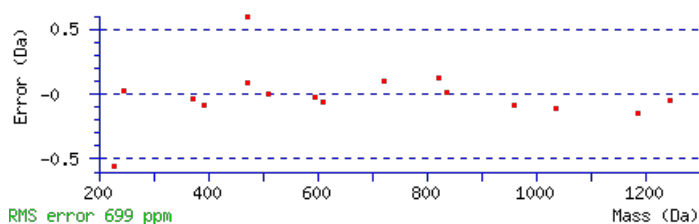
Variable modifications:

N9 : Deamidated (NQ)

Ions Score: 64 Expect: 1.5e-005

```
Matches : 16/110 fragment ions using 22 most intense peaks (help)
```

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	187.0866	94.0469					W							12
2	244.1081	122.5577					G	1244.5940	622.8006	1227.5674	614.2873	1226.5834	613.7953	11
3	373.1506	187.0790			355.1401	178.0737	E	1187.5725	594.2899	1170.5460	585.7766	1169.5619	585.2846	10
4	472.2191	236.6132			454.2085	227.6079	V	1058.5299	529.7686	1041.5034	521.2553	1040.5193	520.7633	9
5	609.2780	305.1426			591.2674	296.1373	H	959.4615	480.2344	942.4349	471.7211	941.4509	471.2291	8
6	722.3620	361.6847			704.3515	352.6794	L	822.4026	411.7049	805.3760	403.1917	804.3920	402.6996	7
7	835.4461	418.2267			817.4355	409.2214	I	709.3185	355.1629	692.2920	346.6496	691.3080	346.1576	6
8	922.4781	461.7427			904.4676	452.7374	S	596.2345	298.6209	579.2079	290.1076	578.2239	289.6156	5
9	1037.5051	519.2562	1020.4785	510.7429	1019.4945	510.2509	N	509.2024	255.1049	492.1759	246.5916	491.1919	246.0996	4
10	1197.5357	599.2715	1180.5092	590.7582	1179.5252	590.2662	C	394.1755	197.5914	377.1489	189.0781	376.1649	188.5861	3
11	1284.5677	642.7875	1267.5412	634.2742	1266.5572	633.7822	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
12							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [WGEVHLISNCSK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
64.1	1429.6660	-0.0031	WGEVHLISNCSK
8.5	1429.6685	-0.0056	GASDANTDLIGGNPK
8.4	1429.6507	0.0121	RSQPELCADPOK
6.9	1429.6620	0.0009	ACQAVQRAGDQPK
4.0	1429.6548	0.0081	DQFPSLYQMASK
2.8	1429.6685	-0.0056	ENAPGLGAQSEATGK
2.3	1429.6732	-0.0104	SSCGASGGPAAGPARK
1.9	1429.6620	0.0009	ACQAVQRAGDQPK
0.9	1429.6685	-0.0056	AQQDLSSGSSEPPK
0.3	1429.6516	0.0112	AGTNMMMVGVBHGP

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSNVSCQASVSR**

Found in **F1SC57** in **uni_pig**, tr|F1SC57|F1SC57_PIG Uncharacterized protein OS=Sus scrofa GN=PLTP PE=4 SV=1

Match to Query 2548: 1294.580328 from(648.297440,2+) intensity(3141.0649) rtinseconds(957) scans(1664) index(8583)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_15Spectrum1267_scans__1664

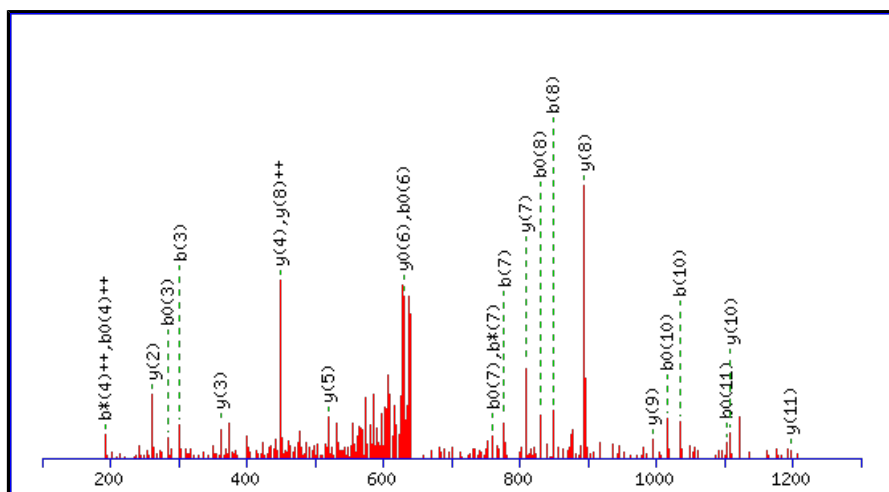
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1294.5823

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

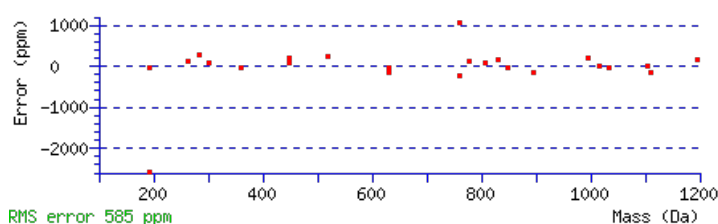
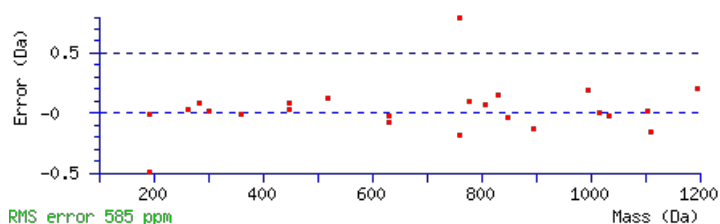
N3 : Deamidated (NQ)

Q7 : Deamidated (NQ)

Ions Score: 63 Expect: 1.6e-005

Matches : 24/124 fragment ions using 33 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							12
2	187.1077	94.0575			169.0972	85.0522	S	1196.5212	598.7642	1179.4946	590.2510	1178.5106	589.7590	11
3	302.1347	151.5710	285.1081	143.0577	284.1241	142.5657	N	1109.4892	555.2482	1092.4626	546.7349	1091.4786	546.2429	10
4	401.2031	201.1052	384.1765	192.5919	383.1925	192.0999	V	994.4622	497.7347	977.4357	489.2215	976.4517	488.7295	9
5	488.2351	244.6212	471.2086	236.1079	470.2245	235.6159	S	895.3938	448.2005	878.3673	439.6873	877.3832	439.1953	8
6	648.2658	324.6365	631.2392	316.1232	630.2552	315.6312	C	808.3618	404.6845	791.3352	396.1713	790.3512	395.6792	7
7	777.3083	389.1578	760.2818	380.6445	759.2978	380.1525	Q	648.3311	324.6692	631.3046	316.1559	630.3206	315.6639	6
8	848.3455	424.6764	831.3189	416.1631	830.3349	415.6711	A	519.2885	260.1479	502.2620	251.6346	501.2780	251.1426	5
9	935.3775	468.1924	918.3509	459.6791	917.3669	459.1871	S	448.2514	224.6293	431.2249	216.1161	430.2409	215.6241	4
10	1034.4459	517.7266	1017.4194	509.2133	1016.4353	508.7213	V	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
11	1121.4779	561.2426	1104.4514	552.7293	1103.4674	552.2373	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [VSNVSCQASVSR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.9	1294.5823	-0.0020	VSNVSCQASVSR
6.5	1294.5798	0.0005	VLCWVCSQSR
0.5	1292.5633	2.0170	FGGLAAGEDNGQR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

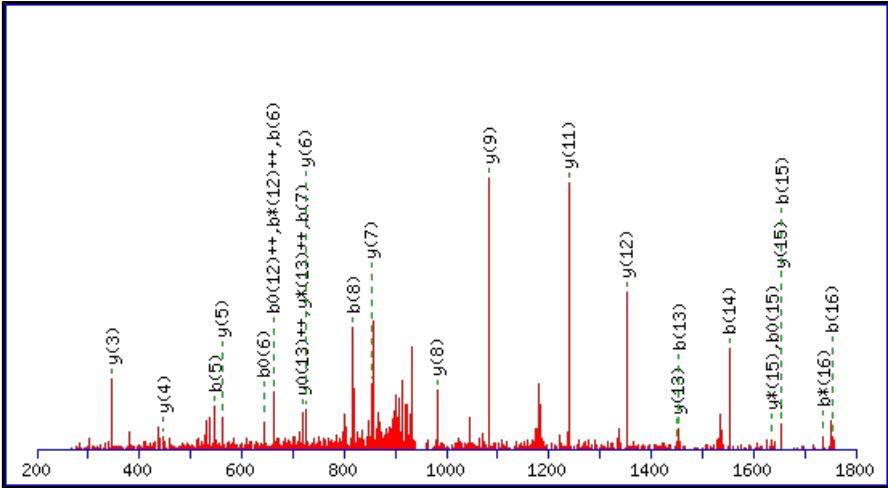
Peptide View

MS/MS Fragmentation of **VFDSVIGVTQEYNVTVK**
Found in **F1SCV8** in **uni_pig**, tr|F1SCV8|F1SCV8_PIG Uncharacterized protein (Fragment) OS=Sus scrofa PE=4 SV=2

Match to Query 7820: 1898.967148 from(950.490850,2+) intensity(9388.7275) rtinseconds(2815) scans(6836) index(10782)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_14Spectrum5811_scans__6836
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

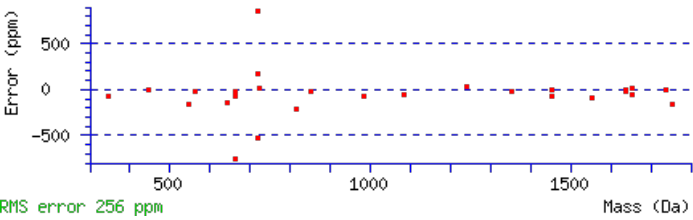
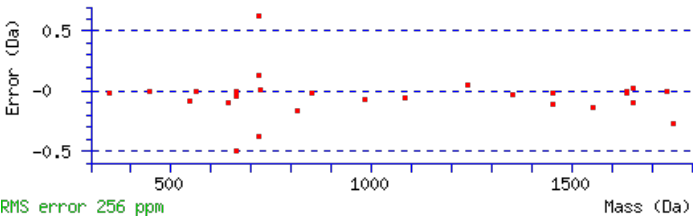
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1898.9513
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Deamidated (NQ)
N13 : Deamidated (NQ)
Ions Score: 67 Expect: 1.7e-005
Matches : 27/166 fragment ions using 45 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							17
2	247.1441	124.0757					F	1800.8902	900.9487	1783.8636	892.4355	1782.8796	891.9435	16
3	362.1710	181.5892			344.1605	172.5839	D	1653.8218	827.4145	1636.7952	818.9013	1635.8112	818.4092	15
4	449.2031	225.1052			431.1925	216.0999	S	1538.7948	769.9011	1521.7683	761.3878	1520.7843	760.8958	14
5	548.2715	274.6394			530.2609	265.6341	V	1451.7628	726.3850	1434.7363	717.8718	1433.7522	717.3798	13
6	661.3556	331.1814			643.3450	322.1761	I	1352.6944	676.8508	1335.6678	668.3376	1334.6838	667.8456	12
7	718.3770	359.6921			700.3665	350.6869	G	1239.6103	620.3088	1222.5838	611.7955	1221.5998	611.3035	11
8	817.4454	409.2264			799.4349	400.2211	V	1182.5889	591.7981	1165.5623	583.2848	1164.5783	582.7928	10
9	918.4931	459.7502			900.4825	450.7449	T	1083.5204	542.2639	1066.4939	533.7506	1065.5099	533.2586	9
10	1047.5357	524.2715	1030.5092	515.7582	1029.5251	515.2662	Q	982.4728	491.7400	965.4462	483.2267	964.4622	482.7347	8
11	1176.5783	588.7928	1159.5517	580.2795	1158.5677	579.7875	E	853.4302	427.2187	836.4036	418.7055	835.4196	418.2134	7
12	1339.6416	670.3245	1322.6151	661.8112	1321.6311	661.3192	Y	724.3876	362.6974	707.3610	354.1842	706.3770	353.6921	6
13	1454.6686	727.8379	1437.6420	719.3246	1436.6580	718.8326	N	561.3243	281.1658	544.2977	272.6525	543.3137	272.1605	5
14	1553.7370	777.3721	1536.7104	768.8589	1535.7264	768.3668	V	446.2973	223.6523	429.2708	215.1390	428.2867	214.6470	4
15	1654.7847	827.8960	1637.7581	819.3827	1636.7741	818.8907	T	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
16	1753.8531	877.4302	1736.8265	868.9169	1735.8425	868.4249	V	246.1812	123.5942	229.1547	115.0810			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VFDSVIGVTQEYNVTVK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
66.5	1898.9513	0.0158	VFDSVIGVTQEYNVTVK
60.0	1897.9673	0.9998	VFDSVIGVTQEYNVTVK
40.0	1897.9673	0.9998	VFDSVIGVTQEYNVTVK
13.2	1897.9633	1.0039	EDGQVPLNSAALQDIISK
6.9	1897.9633	1.0039	EDGQVPLNSAALQDIISK
6.5	1896.9792	1.9879	EDGQVPLNSAALQDIISK
5.3	1897.9495	1.0176	FPYPTMSEITVLSAQAK
5.2	1897.9633	1.0039	ETSQDKPPTSLALPDATK
4.8	1897.9720	0.9951	MERDILADVNHFPVVK
4.3	1897.9633	1.0039	EDGQVPLNSAALQDIISK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQNYTVNDTK**

Found in **F1SLL1** in **uni_pig**, tr|F1SLL1|F1SLL1_PIG Uncharacterized protein OS=Sus scrofa GN=IL6ST PE=4 SV=2

Match to Query 1478: 1196.553588 from(599.284070,2+) intensity(5664.6157) rtinseconds(1135) scans(1355) index(2160)

Title: 120325_Sunil_PigSerum_Glyco_D_17Spectrum667_scans__1355

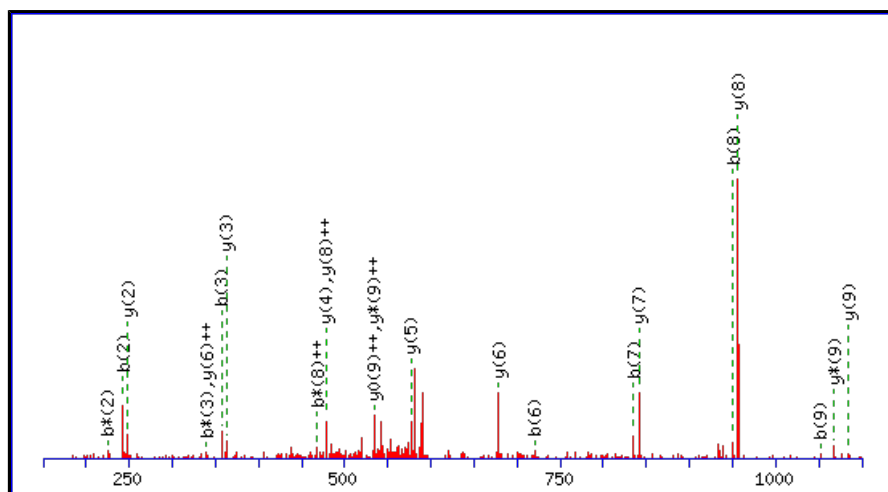
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1196.5561

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

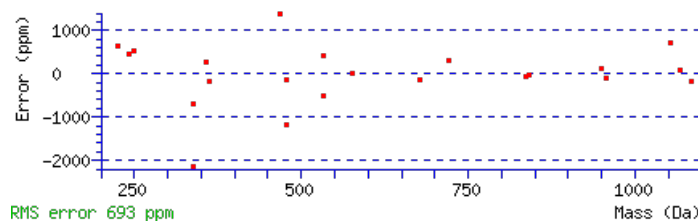
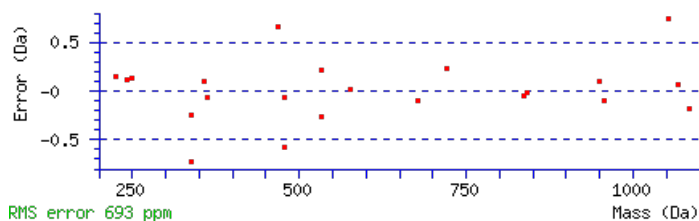
N3 : Deamidated (NQ)

N7 : Deamidated (NQ)

Ions Score: 63 Expect: 2.1e-005

Matches : 22/96 fragment ions using 30 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							10
2	242.1499	121.5786	225.1234	113.0653			Q	1084.4793	542.7433	1067.4528	534.2300	1066.4687	533.7380	9
3	357.1769	179.0921	340.1503	170.5788			N	956.4207	478.7140	939.3942	470.2007	938.4102	469.7087	8
4	520.2402	260.6237	503.2136	252.1105			Y	841.3938	421.2005	824.3672	412.6873	823.3832	412.1953	7
5	621.2879	311.1476	604.2613	302.6343	603.2773	302.1423	T	678.3305	339.6689	661.3039	331.1556	660.3199	330.6636	6
6	720.3563	360.6818	703.3297	352.1685	702.3457	351.6765	V	577.2828	289.1450	560.2562	280.6318	559.2722	280.1397	5
7	835.3832	418.1953	818.3567	409.6820	817.3727	409.1900	N	478.2144	239.6108	461.1878	231.0975	460.2038	230.6055	4
8	950.4102	475.7087	933.3836	467.1954	932.3996	466.7034	D	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
9	1051.4578	526.2326	1034.4313	517.7193	1033.4473	517.2273	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
10							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [LQNYTVNDTK](#)

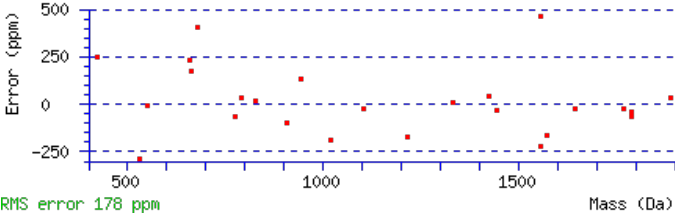
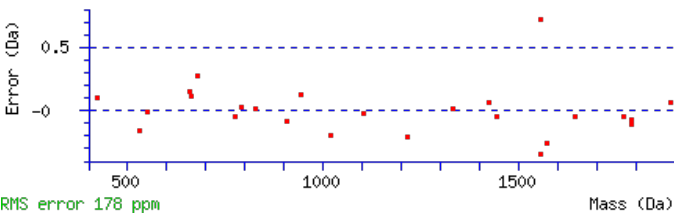
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.7	1196.5561	-0.0025	LQNYTVNDTK	Deamidated N3, N7 98.42%
44.7	1196.5561	-0.0025	LQNYTVNDTK	Deamidated Q2, N7 1.57%
19.3	1196.5561	-0.0025	LQNYTVNDTK	Deamidated Q2, N3 0.00%
6.2	1195.5391	1.0145	VMKTGGENTDK	
4.2	1195.5608	0.9928	EFEISNLQSK	

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [AQNYSIIDICDYDESTGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
57.0	2119.9004	-0.0173	AQNYSIIDICDYDESTGR	Deamidated N3 50.00%
57.0	2119.9004	-0.0173	AQNYSIIDICDYDESTGR	Deamidated Q2 50.00%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLCNGDNDCGDQSDEANCK**
Found in **F1S790** in **uni_pig**, tr[F1S790]F1S790_PIG Uncharacterized protein OS=Sus scrofa GN=C8B PE=4 SV=2

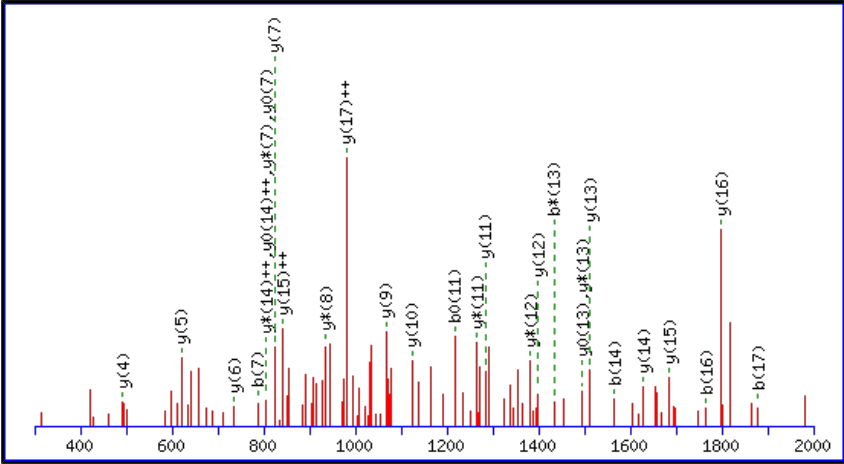
Match to Query 12159: 2184.794048 from(1093.404300,2+) intensity(2230.8577) rtinseconds(1035) scans(1892) index(12822)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_13Spectrum1404_scans_1892
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

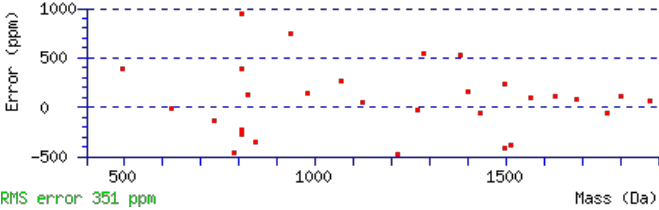
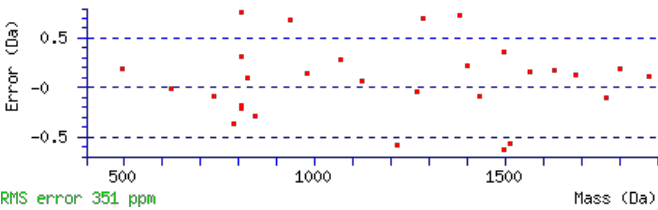
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2184.7994
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 46 Expect: 2.7e-005
Matches : 29/192 fragment ions using 69 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							19
2	227.1754	114.0913					L	2072.7226	1036.8650	2055.6961	1028.3517	2054.7121	1027.8597	18
3	387.2061	194.1067					C	1959.6386	980.3229	1942.6120	971.8096	1941.6280	971.3176	17
4	501.2490	251.1281	484.2224	242.6149			N	1799.6079	900.3076	1782.5814	891.7943	1781.5973	891.3023	16
5	558.2704	279.6389	541.2439	271.1256			G	1685.5650	843.2861	1668.5384	834.7729	1667.5544	834.2808	15
6	673.2974	337.1523	656.2708	328.6391	655.2868	328.1470	D	1628.5435	814.7754	1611.5170	806.2621	1610.5330	805.7701	14
7	788.3243	394.6658	771.2978	386.1525	770.3138	385.6605	N	1513.5166	757.2619	1496.4900	748.7487	1495.5060	748.2566	13
8	903.3513	452.1793	886.3247	443.6660	885.3407	443.1740	D	1398.4896	699.7485	1381.4631	691.2352	1380.4791	690.7432	12
9	1063.3819	532.1946	1046.3554	523.6813	1045.3714	523.1893	C	1283.4627	642.2350	1266.4361	633.7217	1265.4521	633.2297	11
10	1120.4034	560.7053	1103.3768	552.1921	1102.3928	551.7000	G	1123.4320	562.2197	1106.4055	553.7064	1105.4215	553.2144	10
11	1235.4303	618.2188	1218.4038	609.7055	1217.4198	609.2135	D	1066.4106	533.7089	1049.3840	525.1957	1048.4000	524.7036	9
12	1363.4889	682.2481	1346.4624	673.7348	1345.4783	673.2428	Q	951.3836	476.1955	934.3571	467.6822	933.3731	467.1902	8
13	1450.5209	725.7641	1433.4944	717.2508	1432.5104	716.7588	S	823.3251	412.1662	806.2985	403.6529	805.3145	403.1609	7
14	1565.5479	783.2776	1548.5213	774.7643	1547.5373	774.2723	D	736.2930	368.6502	719.2665	360.1369	718.2825	359.6449	6
15	1694.5905	847.7989	1677.5639	839.2856	1676.5799	838.7936	E	621.2661	311.1367	604.2395	302.6234	603.2555	302.1314	5
16	1765.6276	883.3174	1748.6010	874.8042	1747.6170	874.3121	A	492.2235	246.6154	475.1969	238.1021			4
17	1879.6705	940.3389	1862.6440	931.8256	1861.6599	931.3336	N	421.1864	211.0968	404.1598	202.5836			3
18	2039.7012	1020.3542	2022.6746	1011.8409	2021.6906	1011.3489	C	307.1435	154.0754	290.1169	145.5621			2
19							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [LLCNGDNDCGDSDEANCK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.8	2184.7994	-0.0054	LLCNGDNDCGDSDEANCK	Deamidated N7 46.38%
45.6	2184.7994	-0.0054	LLCNGDNDCGDSDEANCK	Deamidated Q12 44.91%
38.4	2184.7994	-0.0054	LLCNGDNDCGDSDEANCK	Deamidated N4 8.54%
21.4	2184.7994	-0.0054	LLCNGDNDCGDSDEANCK	Deamidated N17 0.17%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGQLPSSNYSNIK**

Found in **F1SM72** in **uni_pig**, tr|F1SM72|F1SM72_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=NCAM1 PE=4 SV=2

Match to Query 4745: 1535.743788 from(768.879170,2+) intensity(3250.5503) rtinseconds(1699) scans(2673) index(9220)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_18Spectrum1645_scans_2673

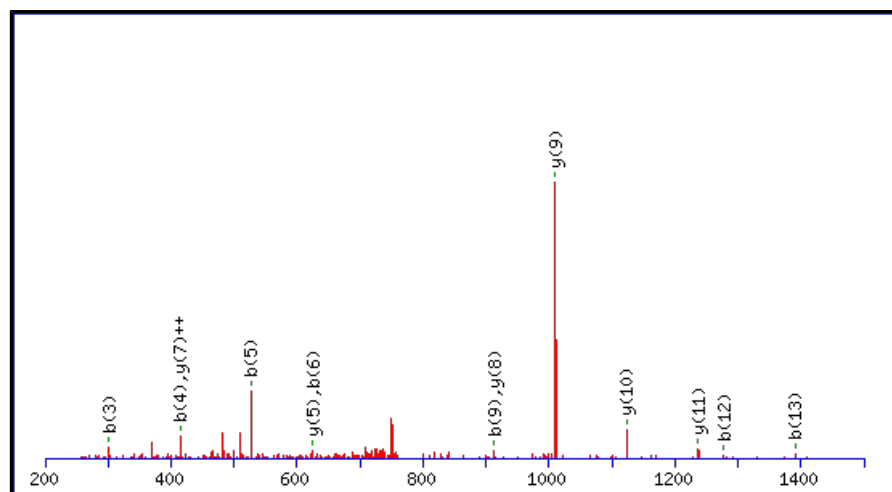
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1535.7467

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

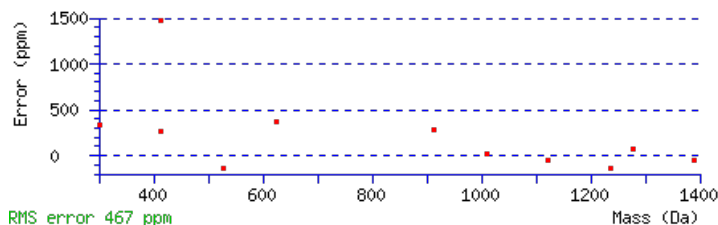
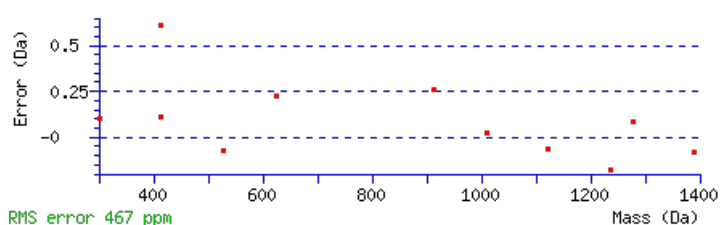
Variable modifications:

N9 : Deamidated (NQ)

Ions Score: 64 Expect: 2.8e-005

Matches : 13/146 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							14
2	173.0557	87.0315			155.0451	78.0262	G	1421.7271	711.3672	1404.7005	702.8539	1403.7165	702.3619	13
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	Q	1364.7056	682.8564	1347.6791	674.3432	1346.6951	673.8512	12
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	L	1236.6470	618.8272	1219.6205	610.3139	1218.6365	609.8219	11
5	527.2824	264.1448	510.2558	255.6316	509.2718	255.1396	L	1123.5630	562.2851	1106.5364	553.7719	1105.5524	553.2798	10
6	624.3352	312.6712	607.3086	304.1579	606.3246	303.6659	P	1010.4789	505.7431	993.4524	497.2298	992.4683	496.7378	9
7	711.3672	356.1872	694.3406	347.6740	693.3566	347.1819	S	913.4262	457.2167	896.3996	448.7034	895.4156	448.2114	8
8	798.3992	399.7032	781.3727	391.1900	780.3886	390.6980	S	826.3941	413.7007	809.3676	405.1874	808.3836	404.6954	7
9	913.4262	457.2167	896.3996	448.7034	895.4156	448.2114	N	739.3621	370.1847	722.3355	361.6714	721.3515	361.1794	6
10	1076.4895	538.7484	1059.4629	530.2351	1058.4789	529.7431	Y	624.3352	312.6712	607.3086	304.1579	606.3246	303.6659	5
11	1163.5215	582.2644	1146.4950	573.7511	1145.5109	573.2591	S	461.2718	231.1395	444.2453	222.6263	443.2613	222.1343	4
12	1277.5644	639.2859	1260.5379	630.7726	1259.5539	630.2806	N	374.2398	187.6235	357.2132	179.1103			3
13	1390.6485	695.8279	1373.6220	687.3146	1372.6379	686.8226	I	260.1969	130.6021	243.1703	122.0888			2
14							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [DGQLLPSSNYSNIK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
64.1	1535.7467	-0.0029	DGQLLPSSNYSNIK	Deamidated N9 93.43%
52.6	1535.7467	-0.0029	DGQLLPSSNYSNIK	Deamidated N12 6.57%
19.3	1535.7467	-0.0029	DGQLLPSSNYSNIK	Deamidated Q3 0.00%
12.8	1535.7436	0.0002	SNVVLERNCGMLK	
11.3	1535.7409	0.0029	LNWLSVDFNNWK	
11.3	1535.7409	0.0029	LNWLSVDFNNWK	
7.6	1535.7290	0.0148	SQWLLRNMTLGA	
4.2	1535.7290	0.0148	NSPDLGPIGGPPNGML	
1.4	1535.7436	0.0002	SNVVLERNCGMLK	
1.3	1535.7580	-0.0142	LSEVPQTNAHESK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of NANLNFTEHLK

Found in **K7GKE7** in **uni_pig**, tr|K7GKE7|K7GKE7_PIG Haptoglobin OS=Sus scrofa GN=HP PE=3 SV=1

Match to Query 2718: 1300.639108 from(651.326830,2+) intensity(27131.8594) rtinseconds(1622) scans(2686) index(8193)

Title: 120326 Sunil PigSerum Glyco DsetB 13Spectrum1782 scans 2686

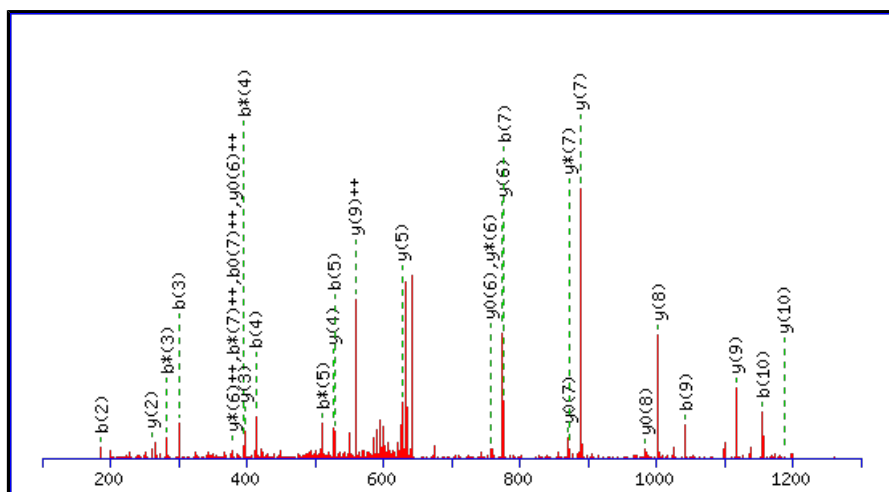
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1300.6411

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

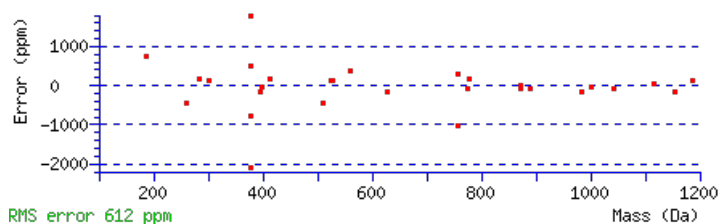
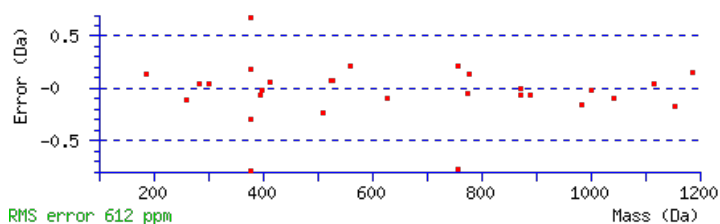
Variable modifications:

N5 : Deamidated (NQ)

Ions Score: 62 Expect: 2.8e-005

Matches : 29/102 fragment ions using 44 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							11
2	186.0873	93.5473	169.0608	85.0340			A	1187.6055	594.3064	1170.5790	585.7931	1169.5949	585.3011	10
3	300.1302	150.5688	283.1037	142.0555			N	1116.5684	558.7878	1099.5419	550.2746	1098.5578	549.7826	9
4	413.2143	207.1108	396.1878	198.5975			L	1002.5255	501.7664	985.4989	493.2531	984.5149	492.7611	8
5	528.2413	264.6243	511.2147	256.1110			N	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	7
6	675.3097	338.1585	658.2831	329.6452			F	774.4145	387.7109	757.3879	379.1976	756.4039	378.7056	6
7	776.3573	388.6823	759.3308	380.1690	758.3468	379.6770	T	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	5
8	905.3999	453.2036	888.3734	444.6903	887.3894	444.1983	E	526.2984	263.6528	509.2718	255.1396	508.2878	254.6475	4
9	1042.4588	521.7331	1025.4323	513.2198	1024.4483	512.7278	H	397.2558	199.1315	380.2292	190.6183			3
10	1155.5429	578.2751	1138.5164	569.7618	1137.5323	569.2698	L	260.1969	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [NANLNFTEHLK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.4	1300.6411	-0.0020	NANLNFTEHLK	Deamidated N5 99.87%
33.5	1300.6411	-0.0020	NANLNFTEHLK	Deamidated N3 0.13%
18.2	1300.6411	-0.0020	NANLNFTEHLK	Deamidated N1 0.00%
6.4	1300.6299	0.0092	VEEAFAFEHIK	
5.4	1300.6299	0.0092	NAVESYTYNIK	
4.2	1300.6333	0.0058	LDPSEAATPCIK	
3.1	1300.6445	-0.0054	VKANVEHMTEK	
2.3	1300.6371	0.0020	RQQQQQLDQK	
0.4	1300.6511	-0.0120	TLVVQDTNADPK	
0.4	1300.6511	-0.0120	TLVVQDTNADPK	

Mascot: <http://www.matrixscience.com/>

NCBI **BLAST** search of [AGPNGTLLVADAYK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
64.2	1389.7140	-0.0030	AGPNGTLLVADAYK
6.7	1389.7001	0.0109	QQLOFNLQNTR
5.4	1389.7140	-0.0030	QQLPVTEGNKQK
5.1	1389.7001	0.0109	QQLOFNLQNTR
3.1	1389.7099	0.0010	LTKSVTENQENK
3.0	1389.7001	0.0109	QQLOFNLQNTR
3.0	1389.7001	0.0109	QQLOFNLQNTR
2.3	1387.7096	2.0014	GISVENSWQIVR
2.3	1387.6983	2.0126	SFFNLGKSSSVSK
1.2	1389.7140	-0.0030	QQLPVTEGNKQK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENISDPTSPLR**

Found in **F1RUQ0** in **uni_pig**, tr|F1RUQ0|F1RUQ0_PIG Uncharacterized protein OS=Sus scrofa GN=IGJ PE=4 SV=1

Match to Query 1734: 1228.590508 from(615.302530,2+) intensity(311211.3125) rtinseconds(1430) scans(2297) index(4494)

Title: 120325 Sunil PigSerum Glyco P 18Spectrum1491 scans 2297

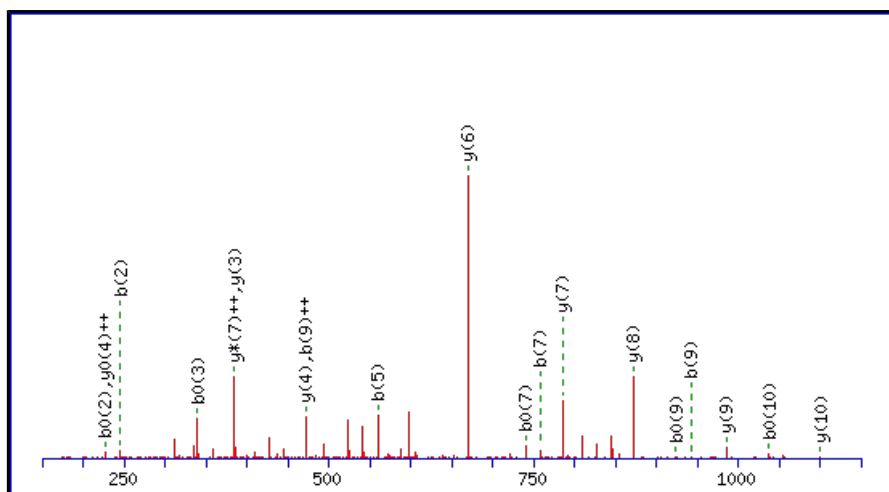
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1228.5935

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

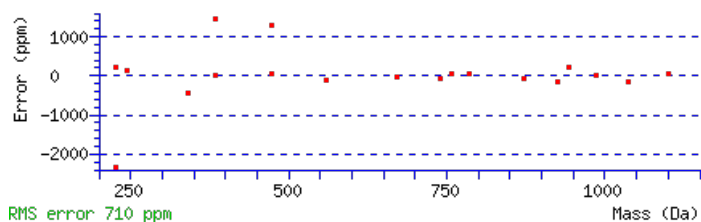
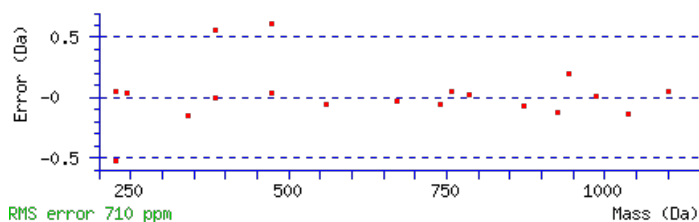
Variable modifications:

N2 : Deamidated (NQ)

Ions Score: 61 Expect: 3.1e-005

Matches : 19/112 fragment ions using 19 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							11
2	245.0768	123.0420	228.0503	114.5288	227.0662	114.0368	N	1100.5582	550.7828	1083.5317	542.2695	1082.5477	541.7775	10
3	358.1609	179.5841	341.1343	171.0708	340.1503	170.5788	I	985.5313	493.2693	968.5047	484.7560	967.5207	484.2640	9
4	445.1929	223.1001	428.1664	214.5868	427.1823	214.0948	S	872.4472	436.7272	855.4207	428.2140	854.4367	427.7220	8
5	560.2198	280.6136	543.1933	272.1003	542.2093	271.6083	D	785.4152	393.2112	768.3886	384.6980	767.4046	384.2060	7
6	657.2726	329.1399	640.2461	320.6267	639.2620	320.1347	P	670.3883	335.6978	653.3617	327.1845	652.3777	326.6925	6
7	758.3203	379.6638	741.2937	371.1505	740.3097	370.6585	T	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
8	845.3523	423.1798	828.3258	414.6665	827.3418	414.1745	S	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
9	942.4051	471.7062	925.3785	463.1929	924.3945	462.7009	P	385.2558	193.1315	368.2292	184.6183			3
10	1055.4891	528.2482	1038.4626	519.7349	1037.4786	519.2429	L	288.2030	144.6051	271.1765	136.0919			2
11							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [ENISDPTSPLR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.0	1228.5935	-0.0030	ENISDPTSPLR
7.2	1228.5836	0.0069	EQQAWAASPKNK
5.8	1228.5870	0.0035	SIAHNMTTPNK
5.8	1228.5823	0.0082	TDVEDLTPNPK
3.8	1228.5935	-0.0030	AEDEGPTIELR
3.3	1228.5935	-0.0030	QEDEGLAPLTR
2.8	1226.5891	2.0014	NVDLDLASSHR
1.6	1227.5917	0.9988	DQIQRMNPPK
1.0	1228.5935	-0.0030	ADESLEEAPLR
0.9	1226.5754	2.0151	MPPNLTGYR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGSHPVGGNLTFCEDGFTLR**
Found in **F1RQW7** in **uni_pig**, tr[F1RQW7]F1RQW7_PIG Uncharacterized protein OS=Sus scrofa GN=C2 PE=3 SV=1

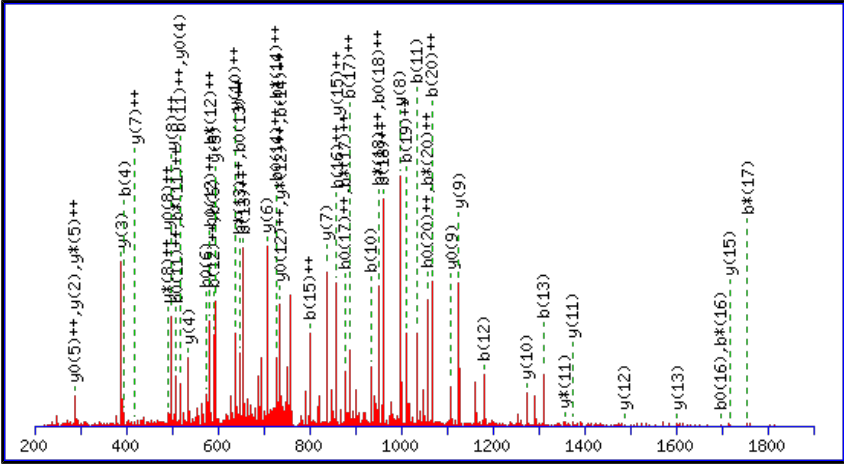
Match to Query 12688: 2306.058822 from(769.693550,3+) intensity(1577.3943) rtinseconds(2186) scans(4742) index(9307)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_01Spectrum3892_scans_4742
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

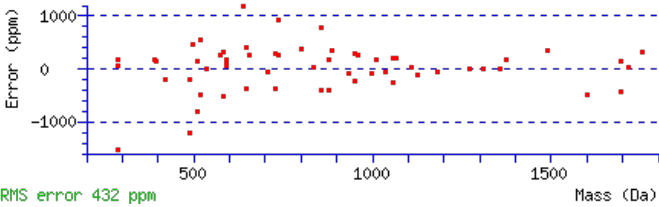
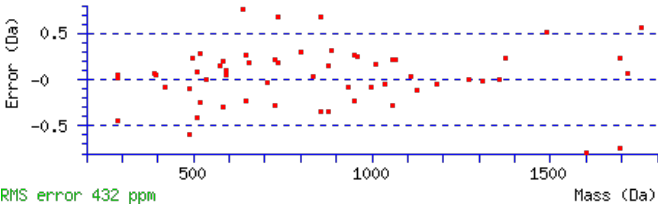
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2306.0638
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 63 Expect: 3.2e-005
Matches : 60/216 fragment ions using 94 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							21
2	171.1128	86.0600					G	2193.9870	1097.4971	2176.9604	1088.9838	2175.9764	1088.4918	20
3	258.1448	129.5761			240.1343	120.5708	S	2136.9655	1068.9864	2119.9389	1060.4731	2118.9549	1059.9811	19
4	395.2037	198.1055			377.1932	189.1002	H	2049.9335	1025.4704	2032.9069	1016.9571	2031.9229	1016.4651	18
5	492.2565	246.6319			474.2459	237.6266	P	1912.8746	956.9409	1895.8480	948.4276	1894.8640	947.9356	17
6	591.3249	296.1661			573.3144	287.1608	V	1815.8218	908.4145	1798.7952	899.9013	1797.8112	899.4093	16
7	648.3464	324.6768			630.3358	315.6715	G	1716.7534	858.8803	1699.7268	850.3671	1698.7428	849.8750	15
8	705.3679	353.1876			687.3573	344.1823	G	1659.7319	830.3696	1642.7054	821.8563	1641.7214	821.3643	14
9	820.3948	410.7010	803.3682	402.1878	802.3842	401.6958	N	1602.7105	801.8589	1585.6839	793.3456	1584.6999	792.8536	13
10	933.4789	467.2431	916.4523	458.7298	915.4683	458.2378	L	1487.6835	744.3454	1470.6570	735.8321	1469.6729	735.3401	12
11	1034.5265	517.7669	1017.5000	509.2536	1016.5160	508.7616	T	1374.5994	687.8034	1357.5729	679.2901	1356.5889	678.7981	11
12	1181.5950	591.3011	1164.5684	582.7878	1163.5844	582.2958	F	1273.5518	637.2795	1256.5252	628.7662	1255.5412	628.2742	10
13	1310.6375	655.8224	1293.6110	647.3091	1292.6270	646.8171	E	1126.4834	563.7453	1109.4568	555.2320	1108.4728	554.7400	9
14	1470.6682	735.8377	1453.6416	727.3245	1452.6576	726.8325	C	997.4408	499.2240	980.4142	490.7107	979.4302	490.2187	8
15	1599.7108	800.3590	1582.6842	791.8458	1581.7002	791.3537	E	837.4101	419.2087	820.3836	410.6954	819.3995	410.2034	7
16	1714.7377	857.8725	1697.7112	849.3592	1696.7272	848.8672	D	708.3675	354.6874	691.3410	346.1741	690.3570	345.6821	6
17	1771.7592	886.3832	1754.7326	877.8700	1753.7486	877.3780	G	593.3406	297.1739	576.3140	288.6606	575.3300	288.1686	5
18	1918.8276	959.9174	1901.8011	951.4042	1900.8170	950.9122	F	536.3191	268.6632	519.2926	260.1499	518.3085	259.6579	4
19	2019.8753	1010.4413	2002.8487	1001.9280	2001.8647	1001.4360	T	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
20	2132.9593	1066.9833	2115.9328	1058.4700	2114.9488	1057.9780	L	288.2030	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LGSHPVGGNLTFECEDGFTLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.9	2306.0638	-0.0049	LGSHPVGGNLTFECEDGFTLR
8.3	2305.0541	1.0047	FMKSKPGAAMVEMADGYAVDR
3.4	2304.0380	2.0208	RHNSSDGFDSGIGRPNGGNFGR
2.7	2305.0541	1.0047	FMKSKPGAAMVEMADGYAVDR
1.5	2306.0718	-0.0130	RSGMYTVAMAYCGSGNNKAIR
1.2	2305.0766	0.9823	CNECGKAFCQSPSLIKHLR
1.0	2304.0380	2.0208	RHNSSDGFDSGIGRPNGGNFGR
0.8	2306.0671	-0.0082	MSECEAENQGLHQLLELYK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **AINASSNITSDGVEVLGR**

Found in **F1S285** in **uni_pig**, tr|F1S285|F1S285_PIG Uncharacterized protein OS=Sus scrofa GN=COL14A1 PE=4 SV=2

Match to Query 6601: 1803.878388 from(902.946470,2+) intensity(3551.1638) rtinseconds(2090) scans(4267) index(2073)

Title: 120325_Sunil_PigSerum_Glyco_D_16Spectrum3195_scans_4267

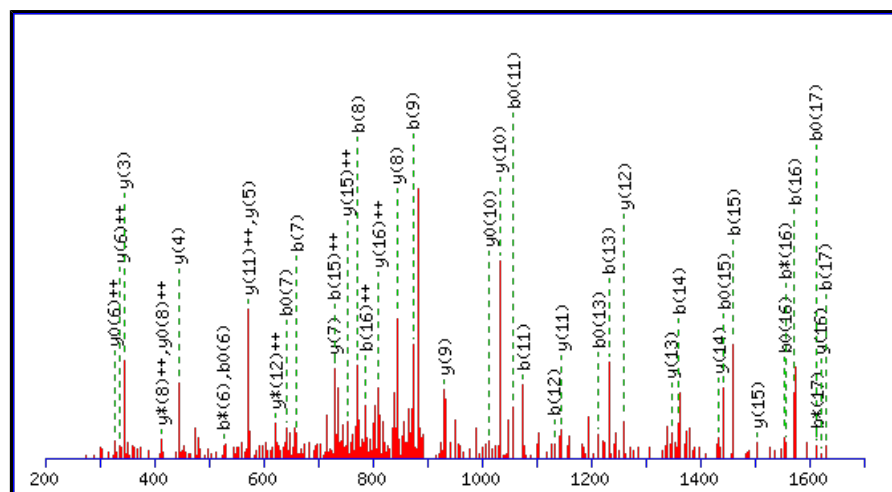
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1803.8850

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

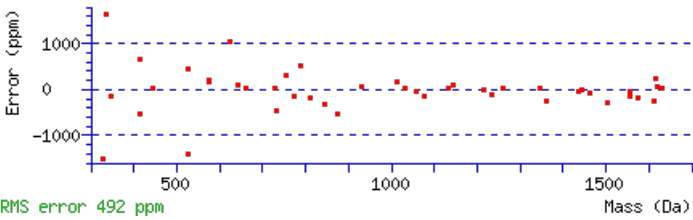
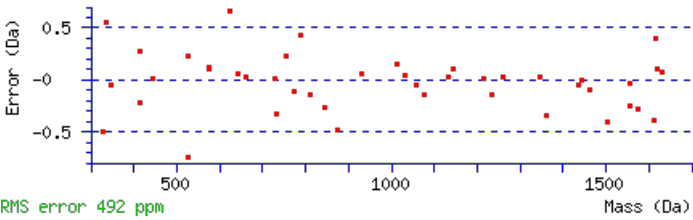
N3 : Deamidated (NQ)

N7 : Deamidated (NQ)

Ions Score: 63 Expect: 3.8e-005

Matches : 44/184 fragment ions using 98 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							18
2	185.1285	93.0679					I	1733.8552	867.4312	1716.8287	858.9180	1715.8446	858.4260	17
3	300.1554	150.5813	283.1288	142.0681			N	1620.7711	810.8892	1603.7446	802.3759	1602.7606	801.8839	16
4	371.1925	186.0999	354.1660	177.5866			A	1505.7442	753.3757	1488.7176	744.8625	1487.7336	744.3705	15
5	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	S	1434.7071	717.8572	1417.6805	709.3439	1416.6965	708.8519	14
6	545.2566	273.1319	528.2300	264.6186	527.2460	264.1266	S	1347.6751	674.3412	1330.6485	665.8279	1329.6645	665.3359	13
7	660.2835	330.6454	643.2570	322.1321	642.2729	321.6401	N	1260.6430	630.8251	1243.6165	622.3119	1242.6325	621.8199	12
8	773.3676	387.1874	756.3410	378.6742	755.3570	378.1821	I	1145.6161	573.3117	1128.5895	564.7984	1127.6055	564.3064	11
9	874.4153	437.7113	857.3887	429.1980	856.4047	428.7060	T	1032.5320	516.7696	1015.5055	508.2564	1014.5215	507.7644	10
10	961.4473	481.2273	944.4207	472.7140	943.4367	472.2220	S	931.4843	466.2458	914.4578	457.7325	913.4738	457.2405	9
11	1076.4742	538.7408	1059.4477	530.2275	1058.4637	529.7355	D	844.4523	422.7298	827.4258	414.2165	826.4417	413.7245	8
12	1133.4957	567.2515	1116.4691	558.7382	1115.4851	558.2462	G	729.4254	365.2163	712.3988	356.7030	711.4148	356.2110	7
13	1232.5641	616.7857	1215.5376	608.2724	1214.5535	607.7804	V	672.4039	336.7056	655.3774	328.1923	654.3933	327.7003	6
14	1361.6067	681.3070	1344.5801	672.7937	1343.5961	672.3017	E	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
15	1460.6751	730.8412	1443.6486	722.3279	1442.6645	721.8359	V	444.2929	222.6501	427.2663	214.1368			4
16	1573.7592	787.3832	1556.7326	778.8700	1555.7486	778.3779	L	345.2245	173.1159	328.1979	164.6026			3
17	1630.7806	815.8940	1613.7541	807.3807	1612.7701	806.8887	G	232.1404	116.5738	215.1139	108.0606			2
18							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [AINASSNITSDGVEVLGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
63.2	1803.8850	-0.0066	AINASSNITSDGVEVLGR
6.6	1802.8798	0.9986	NNIEWLKQNRDTIR
4.6	1803.8681	0.0103	MSLVMPAMAPNETLSGR
3.9	1803.8924	-0.0140	NQTDLKALDLPSCSLK
3.5	1802.8693	1.0091	TQNaNQAASERLAAMAR
3.5	1802.8693	1.0091	TQNaNQAASERLAAMAR
1.5	1801.8554	2.0230	ANASRGQVEQANRELr
1.3	1802.8873	0.9911	MVELEGLTGhIEFNSK
1.2	1802.8898	0.9886	TEQDLALGTDAEGQKVK
0.4	1803.8647	0.0136	DMAREHFEEVMAVLK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPAGEVFDIEIDTLETTCHVLDPTPLANCSVR**
Found in **F1SFI7** in **uni_pig**, tr[F1SFI7|F1SFI7_PIG Alpha-2-HS-glycoprotein (Fragment) OS=Sus scrofa GN=AHSG PE=4 SV=2

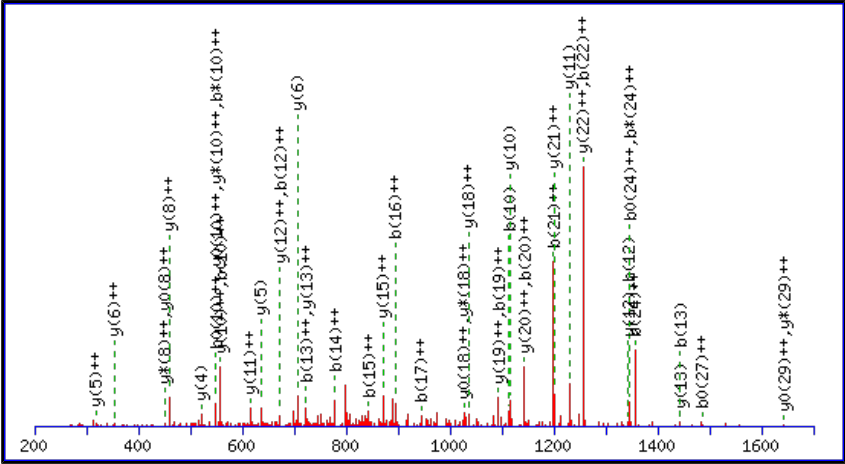
Match to Query 13548: 3625.729816 from(907.439730,4+) intensity(5577.3022) rtinseconds(3138) scans(5313) index(763)
Title: 120325_Sunil_PigSerum_Glyco_D_08Spectrum3413_scans__5313
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

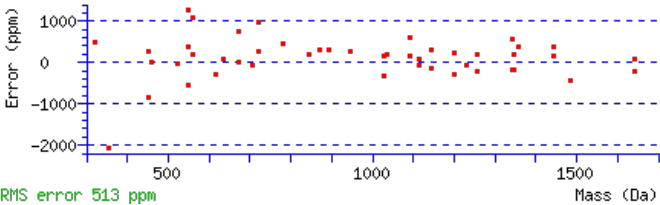
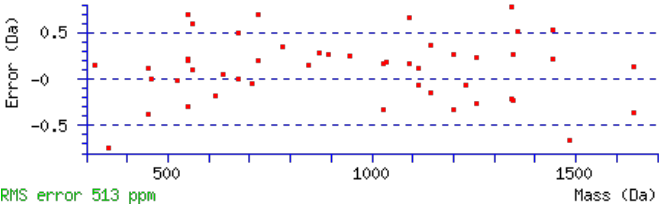
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 3625.7393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N28 : Deamidated (NQ)
Ions Score: 63 Expect: 3.8e-005
Matches : 48/360 fragment ions using 65 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							32
2	254.1612	127.5842	237.1346	119.0709			P	3470.6454	1735.8263	3453.6189	1727.3131	3452.6349	1726.8211	31
3	325.1983	163.1028	308.1717	154.5895			A	3373.5927	1687.3000	3356.5661	1678.7867	3355.5821	1678.2947	30
4	382.2197	191.6135	365.1932	183.1002			G	3302.5555	1651.7814	3285.5290	1643.2681	3284.5450	1642.7761	29
5	511.2623	256.1348	494.2358	247.6215	493.2518	247.1295	E	3245.5341	1623.2707	3228.5075	1614.7574	3227.5235	1614.2654	28
6	610.3307	305.6690	593.3042	297.1557	592.3202	296.6637	V	3116.4915	1558.7494	3099.4649	1550.2361	3098.4809	1549.7441	27
7	757.3991	379.2032	740.3726	370.6899	739.3886	370.1979	F	3017.4231	1509.2152	3000.3965	1500.7019	2999.4125	1500.2099	26
8	872.4261	436.7167	855.3995	428.2034	854.4155	427.7114	D	2870.3547	1435.6810	2853.3281	1427.1677	2852.3441	1426.6757	25
9	985.5102	493.2587	968.4836	484.7454	967.4996	484.2534	I	2755.3277	1378.1675	2738.3012	1369.6542	2737.3171	1369.1622	24
10	1114.5528	557.7800	1097.5262	549.2667	1096.5422	548.7747	E	2642.2436	1321.6255	2625.2171	1313.1122	2624.2331	1312.6202	23
11	1227.6368	614.3220	1210.6103	605.8088	1209.6262	605.3168	I	2513.2011	1257.1042	2496.1745	1248.5909	2495.1905	1248.0989	22
12	1342.6638	671.8355	1325.6372	663.3222	1324.6532	662.8302	D	2400.1170	1200.5621	2383.0904	1192.0489	2382.1064	1191.5569	21
13	1443.7114	722.3594	1426.6849	713.8461	1425.7009	713.3541	T	2285.0900	1143.0487	2268.0635	1134.5354	2267.0795	1134.0434	20
14	1556.7955	778.9014	1539.7690	770.3881	1538.7849	769.8961	L	2184.0424	1092.5248	2167.0158	1084.0115	2166.0318	1083.5195	19
15	1685.8381	843.4227	1668.8115	834.9094	1667.8275	834.4174	E	2070.9583	1035.9828	2053.9318	1027.4695	2052.9477	1026.9775	18
16	1786.8858	893.9465	1769.8592	885.4332	1768.8752	884.9412	T	1941.9157	971.4615	1924.8892	962.9482	1923.9051	962.4562	17
17	1887.9335	944.4704	1870.9069	935.9571	1869.9229	935.4651	T	1840.8680	920.9377	1823.8415	912.4244	1822.8575	911.9324	16
18	2047.9641	1024.4857	2030.9376	1015.9724	2029.9535	1015.4804	C	1739.8204	870.4138	1722.7938	861.9005	1721.8098	861.4085	15
19	2185.0230	1093.0151	2167.9965	1084.5019	2167.0124	1084.0099	H	1579.7897	790.3985	1562.7632	781.8852	1561.7791	781.3932	14
20	2284.0914	1142.5494	2267.0649	1134.0361	2266.0809	1133.5441	V	1442.7308	721.8690	1425.7042	713.3558	1424.7202	712.8638	13
21	2397.1755	1199.0914	2380.1489	1190.5781	2379.1649	1190.0861	L	1343.6624	672.3348	1326.6358	663.8216	1325.6518	663.3295	12
22	2512.2024	1256.6049	2495.1759	1248.0916	2494.1919	1247.5996	D	1230.5783	615.7928	1213.5518	607.2795	1212.5677	606.7875	11
23	2609.2552	1305.1312	2592.2286	1296.6180	2591.2446	1296.1260	P	1115.5514	558.2793	1098.5248	549.7660	1097.5408	549.2740	10
24	2710.3029	1355.6551	2693.2763	1347.1418	2692.2923	1346.6498	T	1018.4986	509.7529	1001.4721	501.2397	1000.4880	500.7477	9

25	2807.3556	1404.1815	2790.3291	1395.6682	2789.3451	1395.1762	P	917.4509	459.2291	900.4244	450.7158	899.4404	450.2238	8
26	2920.4397	1460.7235	2903.4132	1452.2102	2902.4291	1451.7182	L	820.3982	410.7027	803.3716	402.1894	802.3876	401.6974	7
27	2991.4768	1496.2420	2974.4503	1487.7288	2973.4663	1487.2368	A	707.3141	354.1607	690.2876	345.6474	689.3035	345.1554	6
28	3106.5038	1553.7555	3089.4772	1545.2422	3088.4932	1544.7502	N	636.2770	318.6421	619.2504	310.1289	618.2664	309.6368	5
29	3266.5344	1633.7708	3249.5079	1625.2576	3248.5238	1624.7656	C	521.2500	261.1287	504.2235	252.6154	503.2395	252.1234	4
30	3353.5664	1677.2869	3336.5399	1668.7736	3335.5559	1668.2816	S	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
31	3452.6349	1726.8211	3435.6083	1718.3078	3434.6243	1717.8158	V	274.1874	137.5973	257.1608	129.0840			2
32							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [RPAGEVFDIEIDTLETTCHVLDPTPLANCSVR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
63.3	3625.7393	-0.0094	RPAGEVFDIEIDTLETTCHVLDPTPLANCSVR
43.4	3624.7552	0.9746	RPAGEVFDIEIDTLETTCHVLDPTPLANCSVR
15.6	3625.7215	0.0084	VCVNDDLVAKNFACYVSPMENQNLDSLKKPR
15.6	3625.7215	0.0084	VCVNDDLVAKNFACYVSPMENQNLDSLKKPR
15.6	3625.7215	0.0084	VCVNDDLVAKNFACYVSPMENQNLDSLKKPR
14.2	3624.7027	1.0271	RADSKQNGDANAVLSDEEGAGLTQPLASVPTPEER
12.8	3625.7599	-0.0300	DVDEVAQLDMALALQDQRMLES�KVATMMSK
12.8	3625.7599	-0.0300	DVDEVAQLDMALALQDQRMLES�KVATMMSK
11.7	3624.7027	1.0271	RADSKQNGDANAVLSDEEGAGLTQPLASVPTPEER
11.7	3624.7027	1.0271	RADSKQNGDANAVLSDEEGAGLTQPLASVPTPEER

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

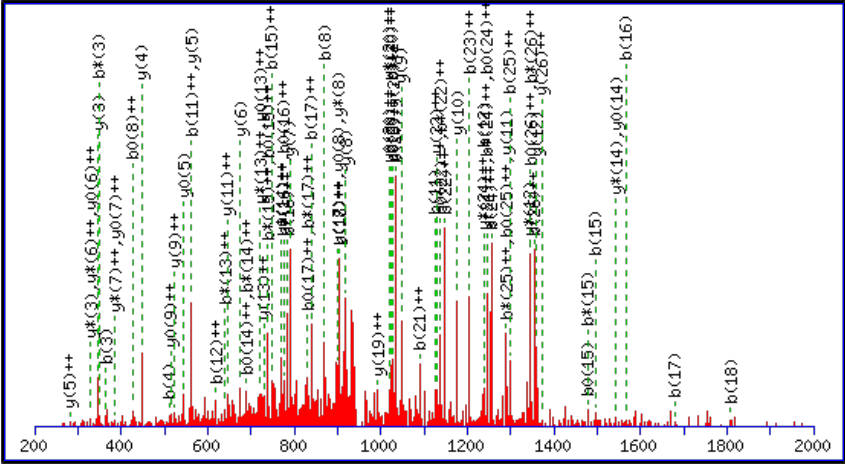
Peptide View

MS/MS Fragmentation of **NHLFSSLASPAIGTVALEQENINTSLK**
Found in **F1SCV8** in **uni_pig**, tr|F1SCV8|F1SCV8_PIG Uncharacterized protein (Fragment) OS=Sus scrofa PE=4 SV=2

Match to Query 13233: 2854.459542 from(952.493790,3+) intensity(9921.7393) rtinseconds(2894) scans(6490) index(2470)
Title: 120325_Sunil_PigSerum_Glyco_P_01Spectrum5403_scans_6490
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

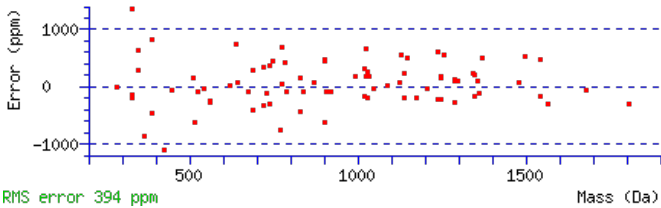
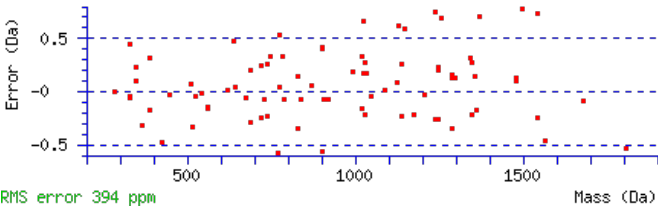
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2854.4712
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N23 : Deamidated (NQ)
Ions Score: 62 Expect: 3.9e-005
Matches : 84/300 fragment ions using 144 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							27
2	252.1091	126.5582	235.0826	118.0449			H	2741.4356	1371.2214	2724.4091	1362.7082	2723.4250	1362.2162	26
3	365.1932	183.1002	348.1666	174.5870			L	2604.3767	1302.6920	2587.3501	1294.1787	2586.3661	1293.6867	25
4	512.2616	256.6344	495.2350	248.1212			F	2491.2926	1246.1500	2474.2661	1237.6367	2473.2821	1237.1447	24
5	599.2936	300.1504	582.2671	291.6372	581.2831	291.1452	S	2344.2242	1172.6157	2327.1977	1164.1025	2326.2136	1163.6105	23
6	686.3256	343.6665	669.2991	335.1532	668.3151	334.6612	S	2257.1922	1129.0997	2240.1656	1120.5865	2239.1816	1120.0944	22
7	799.4097	400.2085	782.3832	391.6952	781.3991	391.2032	L	2170.1602	1085.5837	2153.1336	1077.0704	2152.1496	1076.5784	21
8	870.4468	435.7271	853.4203	427.2138	852.4363	426.7218	A	2057.0761	1029.0417	2040.0495	1020.5284	2039.0655	1020.0364	20
9	957.4789	479.2431	940.4523	470.7298	939.4683	470.2378	S	1986.0390	993.5231	1969.0124	985.0099	1968.0284	984.5178	19
10	1054.5316	527.7694	1037.5051	519.2562	1036.5211	518.7642	P	1899.0069	950.0071	1881.9804	941.4938	1880.9964	941.0018	18
11	1125.5687	563.2880	1108.5422	554.7747	1107.5582	554.2827	A	1801.9542	901.4807	1784.9276	892.9675	1783.9436	892.4754	17
12	1238.6528	619.8300	1221.6262	611.3168	1220.6422	610.8248	I	1730.9171	865.9622	1713.8905	857.4489	1712.9065	856.9569	16
13	1295.6743	648.3408	1278.6477	639.8275	1277.6637	639.3355	G	1617.8330	809.4201	1600.8065	800.9069	1599.8224	800.4149	15
14	1396.7219	698.8646	1379.6954	690.3513	1378.7114	689.8593	T	1560.8115	780.9094	1543.7850	772.3961	1542.8010	771.9041	14
15	1495.7904	748.3988	1478.7638	739.8855	1477.7798	739.3935	V	1459.7639	730.3856	1442.7373	721.8723	1441.7533	721.3803	13
16	1566.8275	783.9174	1549.8009	775.4041	1548.8169	774.9121	A	1360.6955	680.8514	1343.6689	672.3381	1342.6849	671.8461	12
17	1679.9115	840.4594	1662.8850	831.9461	1661.9010	831.4541	L	1289.6583	645.3328	1272.6318	636.8195	1271.6478	636.3275	11
18	1808.9541	904.9807	1791.9276	896.4674	1790.9436	895.9754	E	1176.5743	588.7908	1159.5477	580.2775	1158.5637	579.7855	10
19	1937.0127	969.0100	1919.9862	960.4967	1919.0021	960.0047	Q	1047.5317	524.2695	1030.5051	515.7562	1029.5211	515.2642	9
20	2066.0553	1033.5313	2049.0287	1025.0180	2048.0447	1024.5260	E	919.4731	460.2402	902.4466	451.7269	901.4625	451.2349	8
21	2180.0982	1090.5527	2163.0717	1082.0395	2162.0877	1081.5475	N	790.4305	395.7189	773.4040	387.2056	772.4199	386.7136	7
22	2293.1823	1147.0948	2276.1557	1138.5815	2275.1717	1138.0895	I	676.3876	338.6974	659.3610	330.1842	658.3770	329.6921	6
23	2408.2092	1204.6083	2391.1827	1196.0950	2390.1987	1195.6030	N	563.3035	282.1554	546.2770	273.6421	545.2930	273.1501	5
24	2509.2569	1255.1321	2492.2304	1246.6188	2491.2463	1246.1268	T	448.2766	224.6419	431.2500	216.1287	430.2660	215.6366	4

25	2596.2889	1298.6481	2579.2624	1290.1348	2578.2784	1289.6428	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
26	2709.3730	1355.1901	2692.3465	1346.6769	2691.3624	1346.1849	L	260.1969	130.6021	243.1703	122.0888			2
27							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [NHLFSSLASPAIGTVALEQENINTSLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.1	2854.4712	-0.0117	NHLFSSLASPAIGTVALEQENINTSLK	Deamidated N23 35.65%
62.1	2854.4712	-0.0117	NHLFSSLASPAIGTVALEQENINTSLK	Deamidated N21 35.56%
61.2	2854.4712	-0.0117	NHLFSSLASPAIGTVALEQENINTSLK	Deamidated Q19 28.77%
28.6	2854.4712	-0.0117	NHLFSSLASPAIGTVALEQENINTSLK	Deamidated N1 0.02%
13.3	2854.4712	-0.0116	AQFSQILEEHKAKVTELEQQVAQAK	
12.4	2854.4712	-0.0116	AQFSQILEEHKAKVTELEQQVAQAK	
11.2	2854.4712	-0.0116	AQFSQILEEHKAKVTELEQQVAQAK	
10.1	2854.4712	-0.0116	AQFSQILEEHKAKVTELEQQVAQAK	
8.3	2854.4721	-0.0126	MSVIVKTQSGDILLFCKGADSAVFPR	
8.2	2854.4712	-0.0116	AQFSQILEEHKAKVTELEQQVAQAK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **EHEGAIYPDNTTDFQK**

Found in **F1SKB1** in **uni_pig**, tr|F1SKB1|F1SKB1_PIG Uncharacterized protein OS=Sus scrofa GN=CP PE=4 SV=3

Match to Query 7465: 1865.788728 from(933.901640,2+) intensity(14252.9072) rtinseconds(1527) scans(3489) index(13194)

Title: 120326 Sunil PigSerum Glyco SsetB 14Spectrum2861 scans 3489

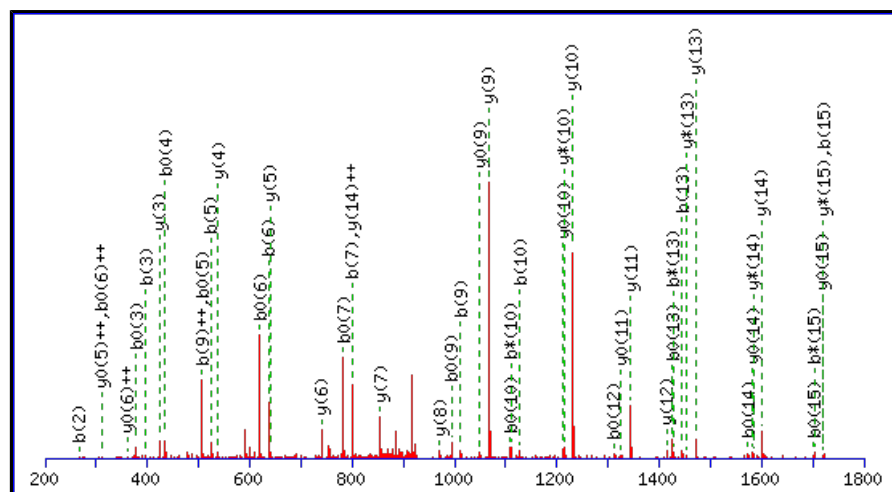
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1865.7955

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

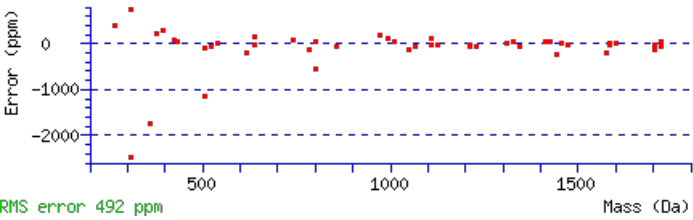
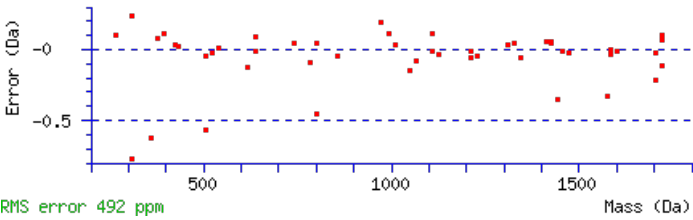
N10 : Deamidated (NQ)

Q15 : Deamidated (NQ)

Ions Score: 56 Expect: 4.3e-005

Matches : 49/156 fragment ions using 105 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	267.1088	134.0580			249.0982	125.0527	H	1737.7602	869.3838	1720.7337	860.8705	1719.7497	860.3785	15
3	396.1514	198.5793			378.1408	189.5740	E	1600.7013	800.8543	1583.6748	792.3410	1582.6908	791.8490	14
4	453.1728	227.0901			435.1623	218.0848	G	1471.6587	736.3330	1454.6322	727.8197	1453.6482	727.3277	13
5	524.2100	262.6086			506.1994	253.6033	A	1414.6373	707.8223	1397.6107	699.3090	1396.6267	698.8170	12
6	637.2940	319.1506			619.2835	310.1454	I	1343.6002	672.3037	1326.5736	663.7904	1325.5896	663.2984	11
7	800.3573	400.6823			782.3468	391.6770	Y	1230.5161	615.7617	1213.4895	607.2484	1212.5055	606.7564	10
8	897.4101	449.2087			879.3995	440.2034	P	1067.4528	534.2300	1050.4262	525.7167	1049.4422	525.2247	9
9	1012.4371	506.7222			994.4265	497.7169	D	970.4000	485.7036	953.3735	477.1904	952.3894	476.6984	8
10	1127.4640	564.2356	1110.4374	555.7224	1109.4534	555.2304	N	855.3731	428.1902	838.3465	419.6769	837.3625	419.1849	7
11	1228.5117	614.7595	1211.4851	606.2462	1210.5011	605.7542	T	740.3461	370.6767	723.3196	362.1634	722.3355	361.6714	6
12	1329.5594	665.2833	1312.5328	656.7700	1311.5488	656.2780	T	639.2984	320.1529	622.2719	311.6396	621.2879	311.1476	5
13	1444.5863	722.7968	1427.5597	714.2835	1426.5757	713.7915	D	538.2508	269.6290	521.2242	261.1157	520.2402	260.6237	4
14	1591.6547	796.3310	1574.6282	787.8177	1573.6441	787.3257	F	423.2238	212.1155	406.1973	203.6023			3
15	1720.6973	860.8523	1703.6708	852.3390	1702.6867	851.8470	Q	276.1554	138.5813	259.1288	130.0681			2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EHEGAIYPDNTTDFQK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.9	1865.7955	-0.0068	EHEGAIYPDNTTDFQK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

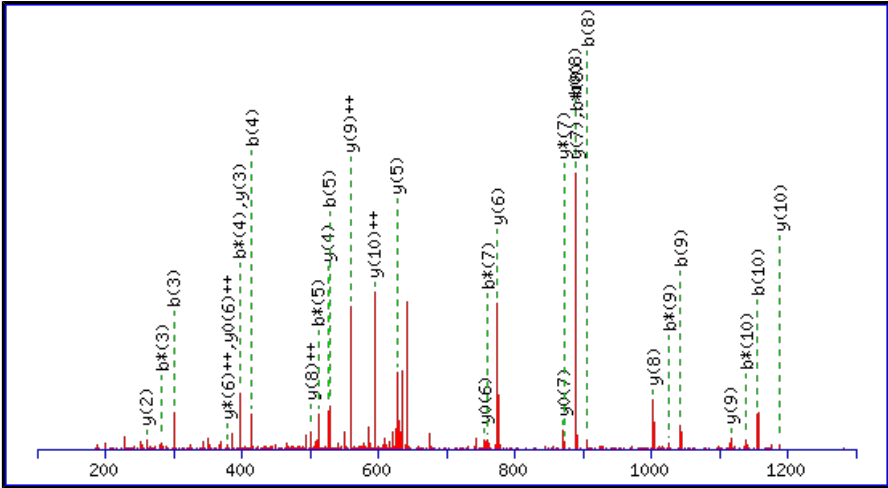
Peptide View

MS/MS Fragmentation of **NANLNFTEHLK**
Found in **K7GKE7** in **uni_pig**, tr|K7GKE7|K7GKE7_PIG Haptoglobin OS=Sus scrofa GN=HP PE=3 SV=1

Match to Query 2841: 1301.622408 from(651.818480,2+) intensity(135069.1875) rtinseconds(1810) scans(4235) index(13247)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum3519_scans__4235
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

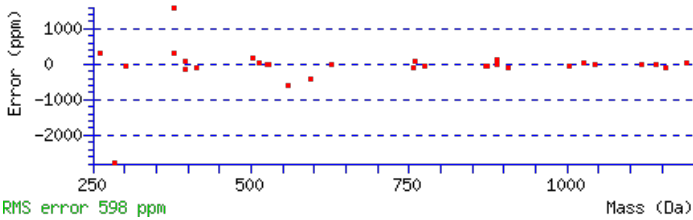
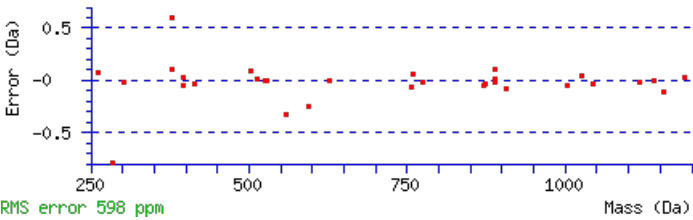
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1301.6251
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
N5 : Deamidated (NQ)
Ions Score: 59 Expect: 4.9e-005
Matches : 31/102 fragment ions using 52 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							11
2	186.0873	93.5473	169.0608	85.0340			A	1188.5895	594.7984	1171.5630	586.2851	1170.5790	585.7931	10
3	301.1143	151.0608	284.0877	142.5475			N	1117.5524	559.2798	1100.5259	550.7666	1099.5419	550.2746	9
4	414.1983	207.6028	397.1718	199.0895			L	1002.5255	501.7664	985.4989	493.2531	984.5149	492.7611	8
5	529.2253	265.1163	512.1987	256.6030			N	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	7
6	676.2937	338.6505	659.2671	330.1372			F	774.4145	387.7109	757.3879	379.1976	756.4039	378.7056	6
7	777.3414	389.1743	760.3148	380.6610	759.3308	380.1690	T	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	5
8	906.3840	453.6956	889.3574	445.1823	888.3734	444.6903	E	526.2984	263.6528	509.2718	255.1395	508.2878	254.6475	4
9	1043.4429	522.2251	1026.4163	513.7118	1025.4323	513.2198	H	397.2558	199.1315	380.2292	190.6183			3
10	1156.5269	578.7671	1139.5004	570.2538	1138.5164	569.7618	L	260.1969	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of **NANLNFTEHLK**
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.4	1301.6251	-0.0027	NANLNFTEHLK	Deamidated N3, N5 93.31%
47.6	1301.6251	-0.0027	NANLNFTEHLK	Deamidated N1, N5 6.18%
36.8	1301.6251	-0.0027	NANLNFTEHLK	Deamidated N1, N3 0.51%
11.4	1301.6139	0.0085	NAVESYTYNIK	
11.3	1301.6139	0.0085	NAVESYTYNIK	
8.5	1300.6155	1.0069	LTPTMMLYSGR	
5.8	1300.6258	0.9966	NNAQAEKNGKPK	
5.8	1300.6258	0.9966	NNAQAEKNGKPK	
5.0	1301.6099	0.0125	VSNGISEDQGPAK	
4.5	1300.6147	1.0078	LSAAEEVQGDGPK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

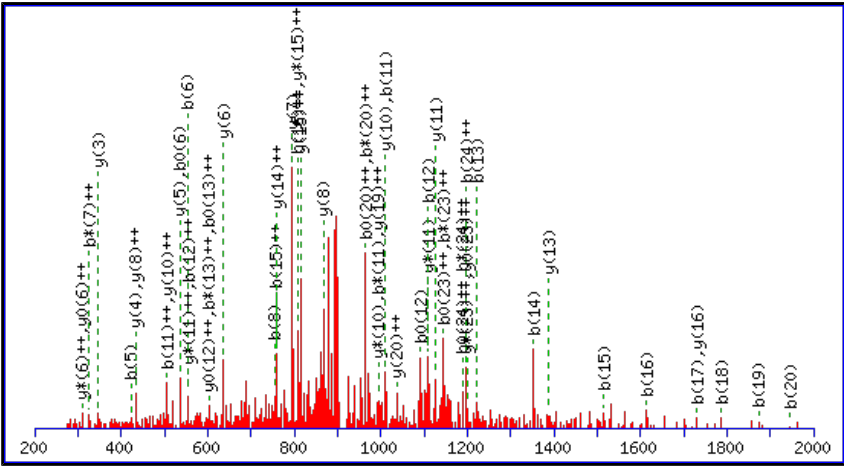
Peptide View

MS/MS Fragmentation of **AGPVVENSGLVLEYVNGSACTTSDGR**
Found in **F1SB67** in **uni_pig**, tr[F1SB67|F1SB67_PIG Uncharacterized protein OS=Sus scrofa GN=M6P/IGF2R PE=4 SV=1

Match to Query 13211: 2739.263472 from(914.095100,3+) intensity(2700.3721) rtinseconds(2711) scans(6399) index(10511)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_13Spectrum5455_scans_6399
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

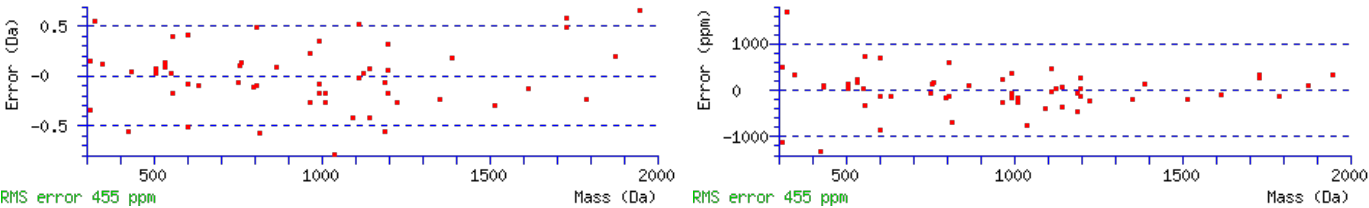
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2739.2658
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N17 : Deamidated (NQ)
Ions Score: 61 Expect: 5e-005
Matches : 55/286 fragment ions using 83 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							27
2	129.0659	65.0366					G	2669.2359	1335.1216	2652.2094	1326.6083	2651.2254	1326.1163	26
3	226.1186	113.5629					P	2612.2145	1306.6109	2595.1879	1298.0976	2594.2039	1297.6056	25
4	325.1870	163.0972					V	2515.1617	1258.0845	2498.1351	1249.5712	2497.1511	1249.0792	24
5	424.2554	212.6314					V	2416.0933	1208.5503	2399.0667	1200.0370	2398.0827	1199.5450	23
6	553.2980	277.1527			535.2875	268.1474	E	2317.0249	1159.0161	2299.9983	1150.5028	2299.0143	1150.0108	22
7	667.3410	334.1741	650.3144	325.6608	649.3304	325.1688	N	2187.9823	1094.4948	2170.9557	1085.9815	2169.9717	1085.4895	21
8	754.3730	377.6901	737.3464	369.1769	736.3624	368.6849	S	2073.9393	1037.4733	2056.9128	1028.9600	2055.9288	1028.4680	20
9	811.3945	406.2009	794.3679	397.6876	793.3839	397.1956	G	1986.9073	993.9573	1969.8808	985.4440	1968.8967	984.9520	19
10	898.4265	449.7169	881.3999	441.2036	880.4159	440.7116	S	1929.8858	965.4466	1912.8593	956.9333	1911.8753	956.4413	18
11	1011.5106	506.2589	994.4840	497.7456	993.5000	497.2536	L	1842.8538	921.9305	1825.8273	913.4173	1824.8433	912.9253	17
12	1110.5790	555.7931	1093.5524	547.2798	1092.5684	546.7878	V	1729.7698	865.3885	1712.7432	856.8752	1711.7592	856.3832	16
13	1223.6630	612.3352	1206.6365	603.8219	1205.6525	603.3299	L	1630.7013	815.8543	1613.6748	807.3410	1612.6908	806.8490	15
14	1352.7056	676.8564	1335.6791	668.3432	1334.6951	667.8512	E	1517.6173	759.3123	1500.5907	750.7990	1499.6067	750.3070	14
15	1515.7689	758.3881	1498.7424	749.8748	1497.7584	749.3828	Y	1388.5747	694.7910	1371.5481	686.2777	1370.5641	685.7857	13
16	1614.8374	807.9223	1597.8108	799.4090	1596.8268	798.9170	V	1225.5114	613.2593	1208.4848	604.7460	1207.5008	604.2540	12
17	1729.8643	865.4358	1712.8378	856.9225	1711.8537	856.4305	N	1126.4429	563.7251	1109.4164	555.2118	1108.4324	554.7198	11
18	1786.8858	893.9465	1769.8592	885.4332	1768.8752	884.9412	G	1011.4160	506.2116	994.3895	497.6984	993.4054	497.2064	10
19	1873.9178	937.4625	1856.8913	928.9493	1855.9072	928.4573	S	954.3945	477.7009	937.3680	469.1876	936.3840	468.6956	9
20	1944.9549	972.9811	1927.9284	964.4678	1926.9443	963.9758	A	867.3625	434.1849	850.3360	425.6716	849.3519	425.1796	8
21	2104.9856	1052.9964	2087.9590	1044.4831	2086.9750	1043.9911	C	796.3254	398.6663	779.2988	390.1531	778.3148	389.6611	7
22	2206.0332	1103.5203	2189.0067	1095.0070	2188.0227	1094.5150	T	636.2947	318.6510	619.2682	310.1377	618.2842	309.6457	6
23	2307.0809	1154.0441	2290.0544	1145.5308	2289.0704	1145.0388	T	535.2471	268.1272	518.2205	259.6139	517.2365	259.1219	5
24	2394.1129	1197.5601	2377.0864	1189.0468	2376.1024	1188.5548	S	434.1994	217.6033	417.1728	209.0901	416.1888	208.5980	4

25	2509.1399	1255.0736	2492.1133	1246.5603	2491.1293	1246.0683	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
26	2566.1614	1283.5843	2549.1348	1275.0710	2548.1508	1274.5790	G	232.1404	116.5738	215.1139	108.0606			2
27							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [AGPVVENSGLVLEYVNGSACTTSDGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
61.2	2739.2658	-0.0023	AGPVVENSGLVLEYVNGSACTTSDGR	Deamidated N17 99.69%
42.8	2738.2818	0.9817	AGPVVENSGLVLEYVNGSACTTSDGR	
36.2	2739.2658	-0.0023	AGPVVENSGLVLEYVNGSACTTSDGR	Deamidated N7 0.31%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANSTGTLVITDPTR**

Found in **F1SHN1** in **uni_pig**, tr|F1SHN1|F1SHN1_PIG Uncharacterized protein OS=Sus scrofa GN=LOC100521555 PE=4 SV=2

Match to Query 3887: 1445.730308 from(723.872430,2+) intensity(3553.1653) rtinseconds(1511) scans(2870) index(8866)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_16Spectrum2044_scans_2870

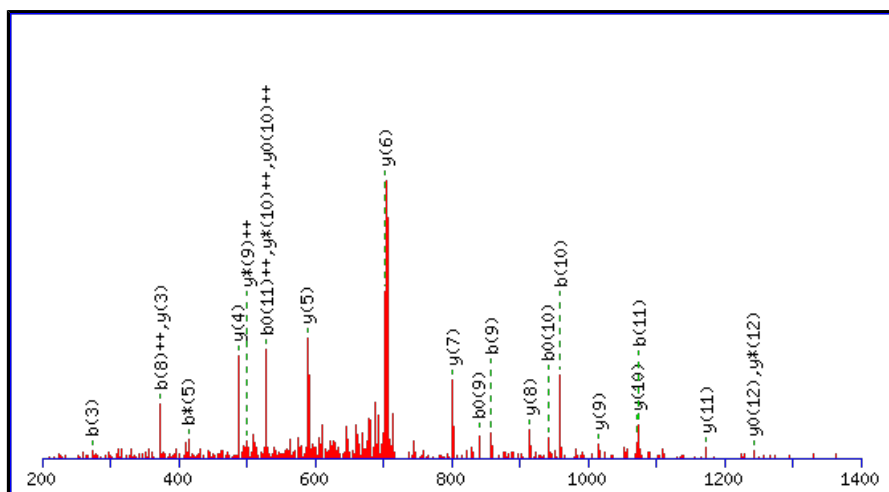
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1445.7362

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

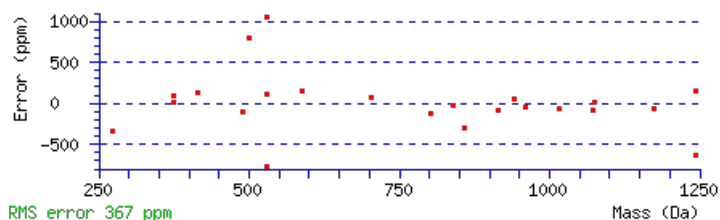
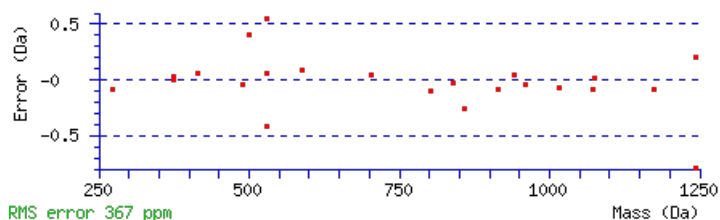
Variable modifications:

N2 : Deamidated (NQ)

Ions Score: 62 Expect: 5.2e-005

Matches : 23/148 fragment ions using 35 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							14
2	187.0713	94.0393	170.0448	85.5260			N	1375.7064	688.3568	1358.6798	679.8435	1357.6958	679.3515	13
3	274.1034	137.5553	257.0768	129.0420	256.0928	128.5500	S	1260.6794	630.8433	1243.6529	622.3301	1242.6688	621.8381	12
4	375.1510	188.0792	358.1245	179.5659	357.1405	179.0739	T	1173.6474	587.3273	1156.6208	578.8141	1155.6368	578.3220	11
5	432.1725	216.5899	415.1460	208.0766	414.1619	207.5846	G	1072.5997	536.8035	1055.5732	528.2902	1054.5891	527.7982	10
6	533.2202	267.1137	516.1936	258.6005	515.2096	258.1084	T	1015.5782	508.2928	998.5517	499.7795	997.5677	499.2875	9
7	646.3042	323.6558	629.2777	315.1425	628.2937	314.6505	L	914.5306	457.7689	897.5040	449.2556	896.5200	448.7636	8
8	745.3727	373.1900	728.3461	364.6767	727.3621	364.1847	V	801.4465	401.2269	784.4199	392.7136	783.4359	392.2216	7
9	858.4567	429.7320	841.4302	421.2187	840.4462	420.7267	I	702.3781	351.6927	685.3515	343.1794	684.3675	342.6874	6
10	959.5044	480.2558	942.4779	471.7426	941.4938	471.2506	T	589.2940	295.1506	572.2675	286.6374	571.2835	286.1454	5
11	1074.5313	537.7693	1057.5048	529.2560	1056.5208	528.7640	D	488.2463	244.6268	471.2198	236.1135	470.2358	235.6215	4
12	1171.5841	586.2957	1154.5576	577.7824	1153.5735	577.2904	P	373.2194	187.1133	356.1928	178.6001	355.2088	178.1081	3
13	1272.6318	636.8195	1255.6052	628.3063	1254.6212	627.8143	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
14							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [ANSTGTLVITDPTR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.6	1445.7362	-0.0059	ANSTGTLVITDPTR
6.2	1443.7317	1.9986	QSRLNDELQALR
4.9	1443.7358	1.9945	DKQLDAAIAWQGK
4.8	1445.7263	0.0040	LRSGGGPGEGFDVAK
3.9	1445.7436	-0.0133	LEMLQDVNDILK
3.3	1444.7205	1.0098	VCNQSLNLGRER
3.2	1445.7297	0.0006	VSSMLQRTPDQGK
3.1	1445.7337	-0.0034	MFHTLAELQTVR
3.0	1443.7205	2.0098	AEDAAVSAQLEALR
2.9	1444.7383	0.9921	DTGDSLRSRVPSRR

Mascot: <http://www.matrixscience.com/>

Peptide View

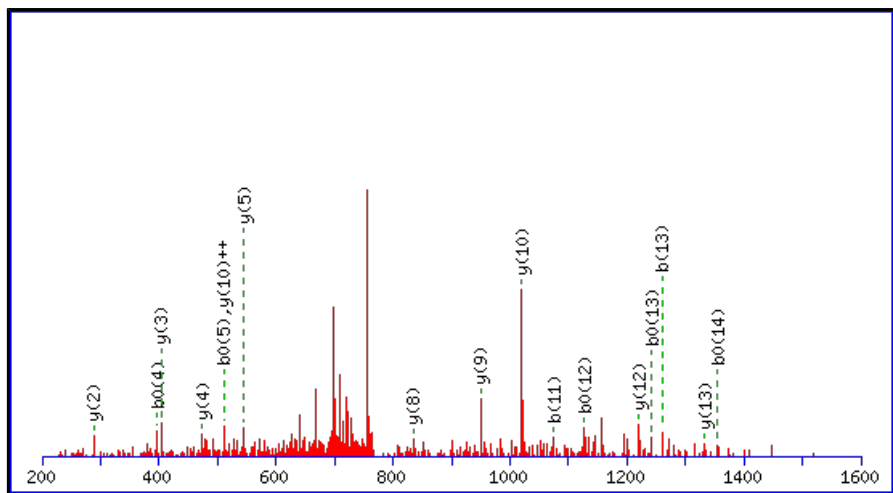
Found in **F1SQ60** in **uni_pig**, tr|F1SQ60|F1SQ60_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=HEG1 PE=4 SV=2

Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Or, to Da

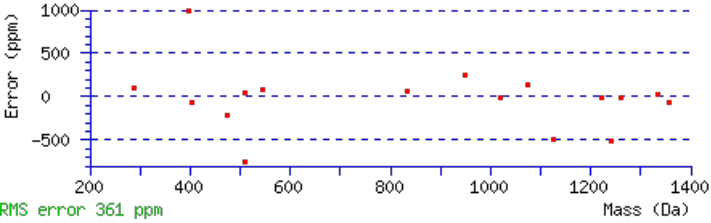
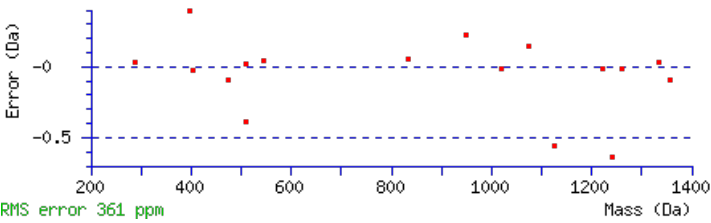
Label all possible matches Label matches used for scoring

Show Y-axis



Matches : 17/150 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							15
2	215.1390	108.0731			197.1285	99.0679	L	1446.7435	723.8754	1429.7169	715.3621	1428.7329	714.8701	14
3	328.2231	164.6152			310.2125	155.6099	L	1333.6594	667.3333	1316.6329	658.8201	1315.6488	658.3281	13
4	415.2551	208.1312			397.2445	199.1259	S	1220.5753	610.7913	1203.5488	602.2780	1202.5648	601.7860	12
5	528.3392	264.6732			510.3286	255.6679	I	1133.5433	567.2753	1116.5168	558.7620	1115.5327	558.2700	11
6	599.3763	300.1918			581.3657	291.1865	A	1020.4592	510.7333	1003.4327	502.2200	1002.4487	501.7280	10
7	714.4032	357.7053			696.3927	348.7000	D	949.4221	475.2147	932.3956	466.7014	931.4116	466.2094	9
8	829.4302	415.2187	812.4036	406.7055	811.4196	406.2134	N	834.3952	417.7012	817.3686	409.1880	816.3846	408.6959	8
9	916.4622	458.7347	899.4357	450.2215	898.4516	449.7295	S	719.3682	360.1878	702.3417	351.6745	701.3577	351.1825	7
10	1003.4942	502.2508	986.4677	493.7375	985.4837	493.2455	S	632.3362	316.6717	615.3097	308.1585	614.3256	307.6665	6
11	1074.5313	537.7693	1057.5048	529.2560	1056.5208	528.7640	A	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	5
12	1145.5685	573.2879	1128.5419	564.7746	1127.5579	564.2826	A	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
13	1260.5954	630.8013	1243.5689	622.2881	1242.5848	621.7961	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
14	1373.6795	687.3434	1356.6529	678.8301	1355.6689	678.3381	L	288.2030	144.6051	271.1765	136.0919			2
15							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [TLLSIADNSSAADLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.2	1546.7838	-0.0023	TLLSIADNSSAADLR
8.7	1546.7739	0.0076	AAGRVPDINEANIR
5.7	1545.7681	1.0134	RMAASSISNTSHRK
2.5	1546.7674	0.0141	HMSDFTERKQIR
2.2	1544.7794	2.0021	ALGASQAANRESIQK
1.8	1546.7739	0.0075	SAEGLDFEASPRLR
0.5	1546.7951	-0.0136	TLTGLARSQESDLR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

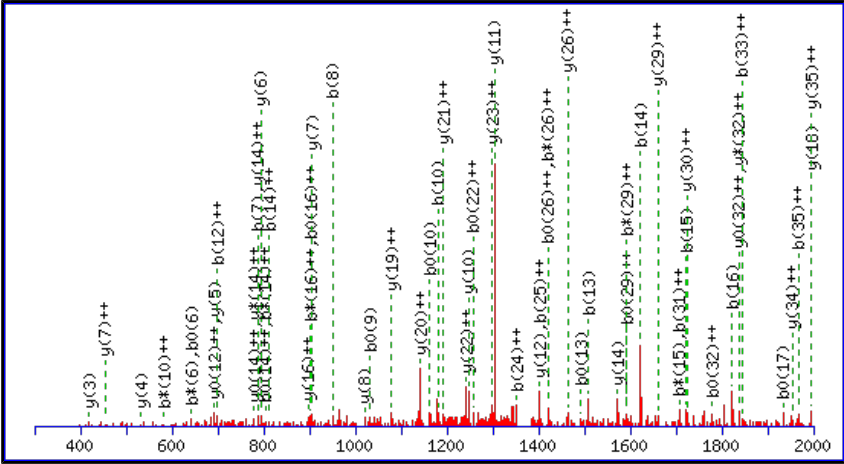
Peptide View

MS/MS Fragmentation of **LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR**
Found in **F1S0J2** in **uni_pig**, tr[F1S0J2|F1S0J2_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPA PE=4 SV=2

Match to Query 13749: 4104.870912 from(1369.297580,3+) intensity(6926.7866) rtinseconds(2825) scans(6864) index(10784)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_14Spectrum5836_scans_6864
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

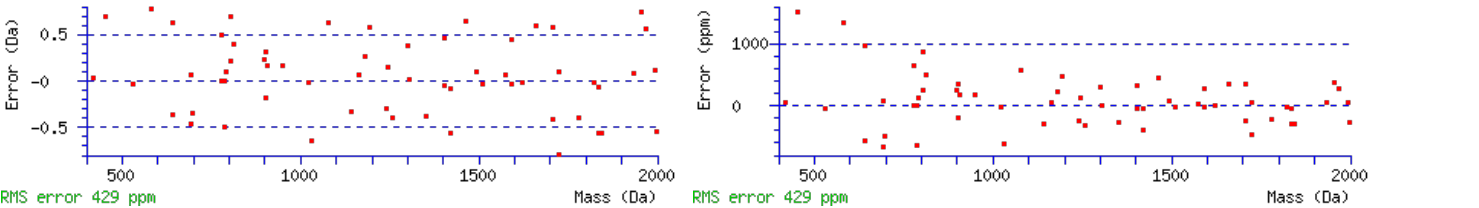
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 4104.8667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Deamidated (NQ)
Q17 : Deamidated (NQ)
N29 : Deamidated (NQ)
Ions Score: 59 Expect: 6.1e-005
Matches : 61/408 fragment ions using 112 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							36
2	201.1234	101.0653			183.1128	92.0600	S	3992.7900	1996.8986	3975.7634	1988.3853	3974.7794	1987.8933	35
3	300.1918	150.5995			282.1812	141.5942	V	3905.7579	1953.3826	3888.7314	1944.8693	3887.7474	1944.3773	34
4	415.2187	208.1130			397.2082	199.1077	D	3806.6895	1903.8484	3789.6630	1895.3351	3788.6790	1894.8431	33
5	544.2613	272.6343	527.2348	264.1210	526.2508	263.6290	Q	3691.6626	1846.3349	3674.6360	1837.8217	3673.6520	1837.3296	32
6	659.2883	330.1478	642.2617	321.6345	641.2777	321.1425	D	3562.6200	1781.8136	3545.5934	1773.3004	3544.6094	1772.8084	31
7	787.3832	394.1953	770.3567	385.6820	769.3727	385.1900	K	3447.5930	1724.3002	3430.5665	1715.7869	3429.5825	1715.2949	30
8	950.4466	475.7269	933.4200	467.2136	932.4360	466.7216	Y	3319.4981	1660.2527	3302.4715	1651.7394	3301.4875	1651.2474	29
9	1051.4942	526.2508	1034.4677	517.7375	1033.4837	517.2455	T	3156.4348	1578.7210	3139.4082	1570.2077	3138.4242	1569.7157	28
10	1180.5368	590.7721	1163.5103	582.2588	1162.5263	581.7668	E	3055.3871	1528.1972	3038.3605	1519.6839	3037.3765	1519.1919	27
11	1267.5689	634.2881	1250.5423	625.7748	1249.5583	625.2828	S	2926.3445	1463.6759	2909.3179	1455.1626	2908.3339	1454.6706	26
12	1396.6114	698.8094	1379.5849	690.2961	1378.6009	689.8041	E	2839.3125	1420.1599	2822.2859	1411.6466	2821.3019	1411.1546	25
13	1509.6955	755.3514	1492.6690	746.8381	1491.6849	746.3461	I	2710.2699	1355.6386	2693.2433	1347.1253	2692.2593	1346.6333	24
14	1622.7796	811.8934	1605.7530	803.3802	1604.7690	802.8881	I	2597.1858	1299.0965	2580.1592	1290.5833	2579.1752	1290.0913	23
15	1723.8273	862.4173	1706.8007	853.9040	1705.8167	853.4120	T	2484.1017	1242.5545	2467.0752	1234.0412	2466.0912	1233.5492	22
16	1822.8957	911.9515	1805.8691	903.4382	1804.8851	902.9462	V	2383.0541	1192.0307	2366.0275	1183.5174	2365.0435	1183.0254	21
17	1951.9383	976.4728	1934.9117	967.9595	1933.9277	967.4675	Q	2283.9856	1142.4965	2266.9591	1133.9832	2265.9751	1133.4912	20
18	2111.9689	1056.4881	2094.9424	1047.9748	2093.9583	1047.4828	C	2154.9430	1077.9752	2137.9165	1069.4619	2136.9325	1068.9699	19
19	2226.9959	1114.0016	2209.9693	1105.4883	2208.9853	1104.9963	D	1994.9124	997.9598	1977.8858	989.4466	1976.9018	988.9546	18
20	2314.0279	1157.5176	2297.0013	1149.0043	2296.0173	1148.5123	S	1879.8855	940.4464	1862.8589	931.9331	1861.8749	931.4411	17
21	2371.0493	1186.0283	2354.0228	1177.5150	2353.0388	1177.0230	G	1792.8534	896.9304	1775.8269	888.4171	1774.8429	887.9251	16
22	2534.1127	1267.5600	2517.0861	1259.0467	2516.1021	1258.5547	Y	1735.8320	868.4196	1718.8054	859.9063	1717.8214	859.4143	15
23	2591.1341	1296.0707	2574.1076	1287.5574	2573.1236	1287.0654	G	1572.7686	786.8880	1555.7421	778.3747	1554.7581	777.8827	14

24	2704.2182	1352.6127	2687.1917	1344.0995	2686.2076	1343.6075	L	1515.7472	758.3772	1498.7206	749.8639	1497.7366	749.3719	13
25	2803.2866	1402.1469	2786.2601	1393.6337	2785.2761	1393.1417	V	1402.6631	701.8352	1385.6366	693.3219	1384.6525	692.8299	12
26	2860.3081	1430.6577	2843.2815	1422.1444	2842.2975	1421.6524	G	1303.5947	652.3010	1286.5681	643.7877	1285.5841	643.2957	11
27	2957.3608	1479.1841	2940.3343	1470.6708	2939.3503	1470.1788	P	1246.5732	623.7903	1229.5467	615.2770	1228.5627	614.7850	10
28	3085.4194	1543.2133	3068.3929	1534.7001	3067.4089	1534.2081	Q	1149.5205	575.2639	1132.4939	566.7506	1131.5099	566.2586	9
29	3200.4464	1600.7268	3183.4198	1592.2135	3182.4358	1591.7215	N	1021.4619	511.2346	1004.4353	502.7213	1003.4513	502.2293	8
30	3313.5304	1657.2689	3296.5039	1648.7556	3295.5199	1648.2636	I	906.4349	453.7211	889.4084	445.2078	888.4244	444.7158	7
31	3414.5781	1707.7927	3397.5516	1699.2794	3396.5675	1698.7874	T	793.3509	397.1791	776.3243	388.6658	775.3403	388.1738	6
32	3574.6088	1787.8080	3557.5822	1779.2947	3556.5982	1778.8027	C	692.3032	346.6552	675.2767	338.1420	674.2926	337.6500	5
33	3687.6928	1844.3500	3670.6663	1835.8368	3669.6823	1835.3448	I	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
34	3816.7354	1908.8713	3799.7089	1900.3581	3798.7249	1899.8661	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
35	3931.7624	1966.3848	3914.7358	1957.8715	3913.7518	1957.3795	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
36							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.2	4104.8667	0.0042	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q17, N29 42.78%
58.3	4103.8827	0.9882	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
56.9	4104.8667	0.0042	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q28, N29 24.90%
56.1	4104.8667	0.0042	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q17, Q28, N29 21.10%
53.5	4103.8827	0.9882	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
53.4	4104.8667	0.0042	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q17, Q28 11.23%
50.7	4103.8827	0.9882	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
45.0	4103.8827	0.9882	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
43.3	4102.8987	1.9722	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
42.6	4103.8827	0.9882	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNASTTDSNSTVEQSALIR**

Found in **F1SAE9** in **uni_pig**, tr|F1SAE9|F1SAE9_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=LAMB1 PE=4 SV=2

Match to Query 10726: 1994.953228 from(998.483890,2+) intensity(0.0000) rtinseconds(1555) scans(2561) index(9059)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_17Spectrum1704_scans_2561

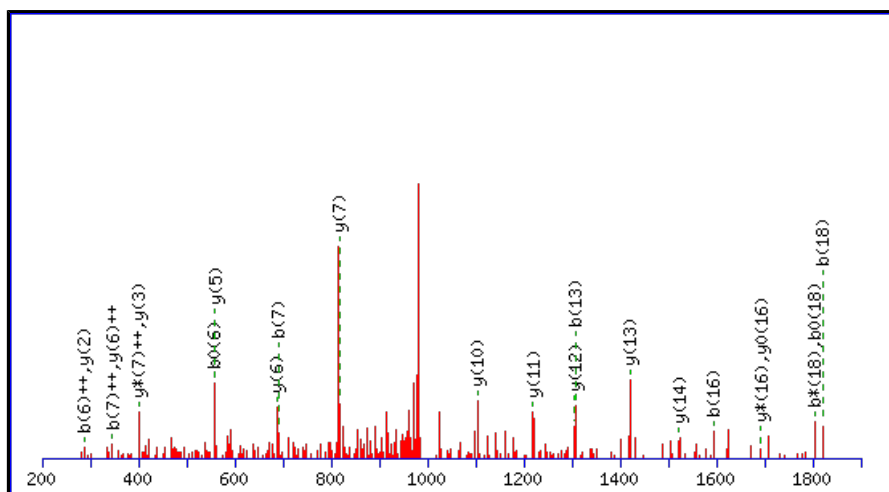
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1993.9440

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

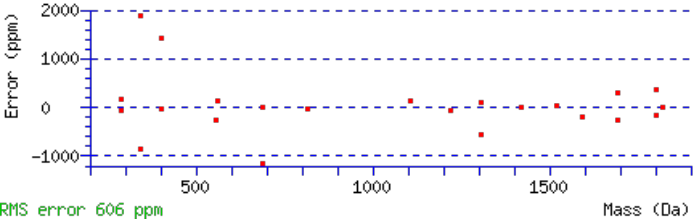
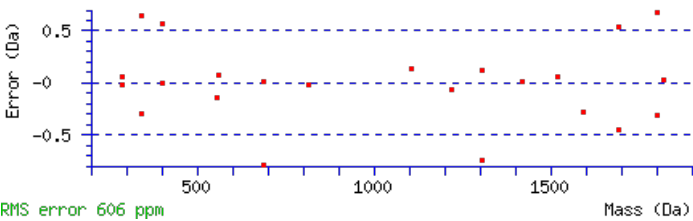
N2 : Deamidated (NQ)

Q14 : Deamidated (NQ)

Ions Score: 60 Expect: 6.6e-005

Matches : 23/200 fragment ions using 32 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							19
2	215.1026	108.0550	198.0761	99.5417			N	1895.8829	948.4451	1878.8563	939.9318	1877.8723	939.4398	18
3	286.1397	143.5735	269.1132	135.0602			A	1780.8559	890.9316	1763.8294	882.4183	1762.8454	881.9263	17
4	373.1718	187.0895	356.1452	178.5763	355.1612	178.0842	S	1709.8188	855.4130	1692.7923	846.8998	1691.8082	846.4078	16
5	474.2195	237.6134	457.1929	229.1001	456.2089	228.6081	T	1622.7868	811.8970	1605.7602	803.3838	1604.7762	802.8917	15
6	575.2671	288.1372	558.2406	279.6239	557.2566	279.1319	T	1521.7391	761.3732	1504.7126	752.8599	1503.7285	752.3679	14
7	690.2941	345.6507	673.2675	337.1374	672.2835	336.6454	D	1420.6914	710.8494	1403.6649	702.3361	1402.6809	701.8441	13
8	777.3261	389.1667	760.2996	380.6534	759.3155	380.1614	S	1305.6645	653.3359	1288.6379	644.8226	1287.6539	644.3306	12
9	891.3690	446.1882	874.3425	437.6749	873.3585	437.1829	N	1218.6325	609.8199	1201.6059	601.3066	1200.6219	600.8146	11
10	978.4011	489.7042	961.3745	481.1909	960.3905	480.6989	S	1104.5895	552.7984	1087.5630	544.2851	1086.5790	543.7931	10
11	1079.4487	540.2280	1062.4222	531.7147	1061.4382	531.2227	T	1017.5575	509.2824	1000.5310	500.7691	999.5469	500.2771	9
12	1178.5172	589.7622	1161.4906	581.2489	1160.5066	580.7569	V	916.5098	458.7585	899.4833	450.2453	898.4993	449.7533	8
13	1307.5597	654.2835	1290.5332	645.7702	1289.5492	645.2782	E	817.4414	409.2243	800.4149	400.7111	799.4308	400.2191	7
14	1436.6023	718.8048	1419.5758	710.2915	1418.5918	709.7995	Q	688.3988	344.7030	671.3723	336.1898	670.3883	335.6978	6
15	1523.6344	762.3208	1506.6078	753.8075	1505.6238	753.3155	S	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	5
16	1594.6715	797.8394	1577.6449	789.3261	1576.6609	788.8341	A	472.3242	236.6657	455.2976	228.1525			4
17	1707.7555	854.3814	1690.7290	845.8681	1689.7450	845.3761	L	401.2871	201.1472	384.2605	192.6339			3
18	1820.8396	910.9234	1803.8131	902.4102	1802.8290	901.9182	I	288.2030	144.6051	271.1765	136.0919			2
19							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [VNASTTDSNSTVEQSALIR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
60.3	1993.9440	1.0092	VNASTTDSNSTVEQSALIR	Deamidated N2, Q14 57.58%
58.7	1993.9440	1.0092	VNASTTDSNSTVEQSALIR	Deamidated N2, N9 39.93%
46.7	1993.9440	1.0092	VNASTTDSNSTVEQSALIR	Deamidated N9, Q14 2.50%
42.9	1992.9600	1.9933	VNASTTDSNSTVEQSALIR	
42.0	1992.9600	1.9933	VNASTTDSNSTVEQSALIR	
30.4	1992.9600	1.9933	VNASTTDSNSTVEQSALIR	
8.1	1993.9536	0.9996	TVSDMGLWRMQLCAVAR	
7.5	1993.9514	1.0018	EKSQEKMELTSTPSQVGV	
7.3	1993.9413	1.0119	RSSSRDQLSDSSAQAVSGR	
4.1	1993.9415	1.0117	DFVMNLVNSLDVGGDNIR	

Mascot: <http://www.matrixscience.com/>

NCBI **BLAST** search of [NTTCQDLQIEVTVK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
60.1	1648.7978	-0.0025	NTTCQDLQIEVTVK	Deamidated N1 93.15%
48.2	1648.7978	-0.0025	NTTCQDLQIEVTVK	Deamidated Q5 6.07%
39.3	1648.7978	-0.0025	NTTCQDLQIEVTVK	Deamidated Q8 0.78%
20.3	1648.7978	-0.0024	MAEERTDLEAQIVK	
12.5	1647.7992	0.9962	YPSQPQGD TVDLAKK	
12.1	1647.7951	1.0002	QSENDLNK LLESTR	
10.2	1648.8090	-0.0137	SSASRVQGDCQLVLK	
9.3	1647.7951	1.0002	QSENDLNK LLESTR	
6.9	1647.8025	0.9928	SVIDNASCEVLLAEK	
6.6	1648.7978	-0.0024	CITDTLQELVNQSK	

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEFDHNTNQSYK**

Found in **F1S643** in **uni_pig**, tr|F1S643|F1S643_PIG Uncharacterized protein OS=Sus scrofa GN=CFH PE=4 SV=2

Match to Query 4406: 1483.618268 from(742.816410,2+) intensity(4497.2007) rtinseconds(874) scans(699) index(9741)

Title: 120326_Sunil_PigSerum_Glyco_PsetB_08Spectrum157_scans_699

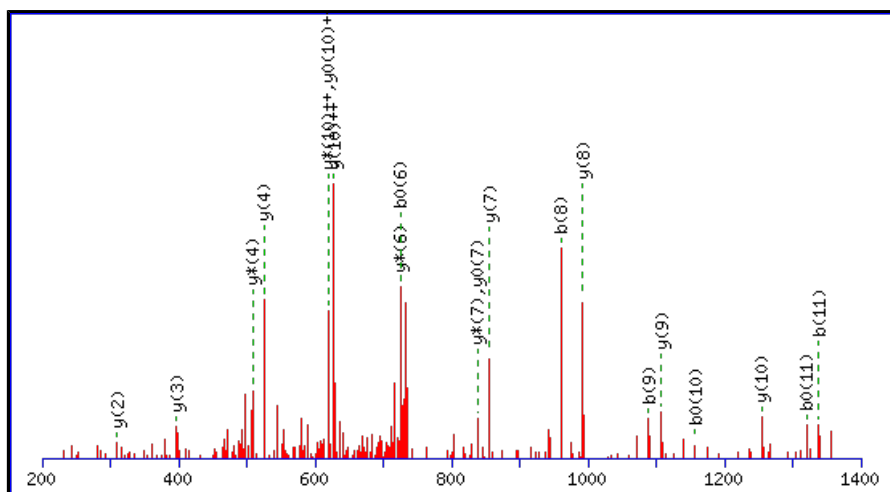
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1483.6215

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

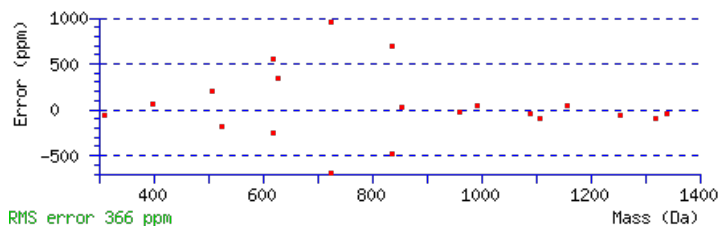
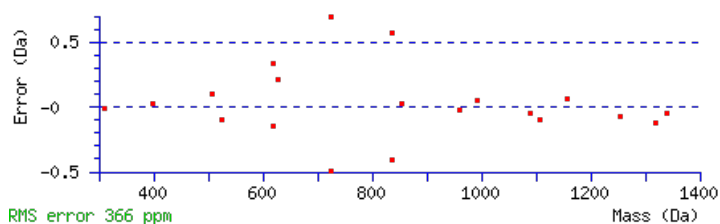
Variable modifications:

N8 : Deamidated (NQ)

Ions Score: 53 Expect: 7.2e-005

Matches : 20/118 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							12
2	231.0975	116.0524			213.0870	107.0471	E	1383.5812	692.2942	1366.5546	683.7809	1365.5706	683.2889	11
3	378.1660	189.5866			360.1554	180.5813	F	1254.5386	627.7729	1237.5120	619.2596	1236.5280	618.7676	10
4	493.1929	247.1001			475.1823	238.0948	D	1107.4701	554.2387	1090.4436	545.7254	1089.4596	545.2334	9
5	630.2518	315.6295			612.2413	306.6243	H	992.4432	496.7252	975.4167	488.2120	974.4326	487.7200	8
6	744.2947	372.6510	727.2682	364.1377	726.2842	363.6457	N	855.3843	428.1958	838.3577	419.6825	837.3737	419.1905	7
7	845.3424	423.1748	828.3159	414.6616	827.3319	414.1696	T	741.3414	371.1743	724.3148	362.6610	723.3308	362.1690	6
8	960.3694	480.6883	943.3428	472.1750	942.3588	471.6830	N	640.2937	320.6505	623.2671	312.1372	622.2831	311.6452	5
9	1088.4279	544.7176	1071.4014	536.2043	1070.4174	535.7123	Q	525.2667	263.1370	508.2402	254.6237	507.2562	254.1317	4
10	1175.4600	588.2336	1158.4334	579.7203	1157.4494	579.2283	S	397.2082	199.1077	380.1816	190.5944	379.1976	190.1024	3
11	1338.5233	669.7653	1321.4968	661.2520	1320.5127	660.7600	Y	310.1761	155.5917	293.1496	147.0784			2
12							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [TEFDHNTNQS](#)YK

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.8	1483.6215	-0.0033	TEFDHNTNQSYP	Deamidated N8 49.32%
52.8	1483.6215	-0.0033	TEFDHNTNQSYP	Deamidated N6 49.32%
37.3	1483.6215	-0.0033	TEFDHNTNQSYP	Deamidated Q9 1.36%
5.7	1483.6145	0.0037	YVQSGMMMSQYK	
5.2	1483.6145	0.0037	YVQSGMMMSQYK	
5.1	1483.6297	-0.0114	GCGRTDFQQGCAK	
4.4	1483.6145	0.0037	YVQSGMMMSQYK	
4.2	1483.6255	-0.0073	EHLSEDWNYK	
1.6	1483.6184	-0.0001	DNGGCQQLCLYR	

Mascot: <http://www.matrixscience.com/>

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.6	1202.4510	-0.0022	NYTDCTSEGR
2.5	1202.4510	-0.0022	EYNSCTDTGR

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LWPAVGNCSSAMR**

Found in **F1RMN7** in **uni_pig**, tr|F1RMN7|F1RMN7_PIG Hemopexin OS=Sus scrofa GN=HPX PE=4 SV=2

Match to Query 4052: 1464.645528 from(733.330040,2+) intensity(8783.3076) rtinseconds(1693) scans(3929) index(13213)

Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum3249_scans__3929

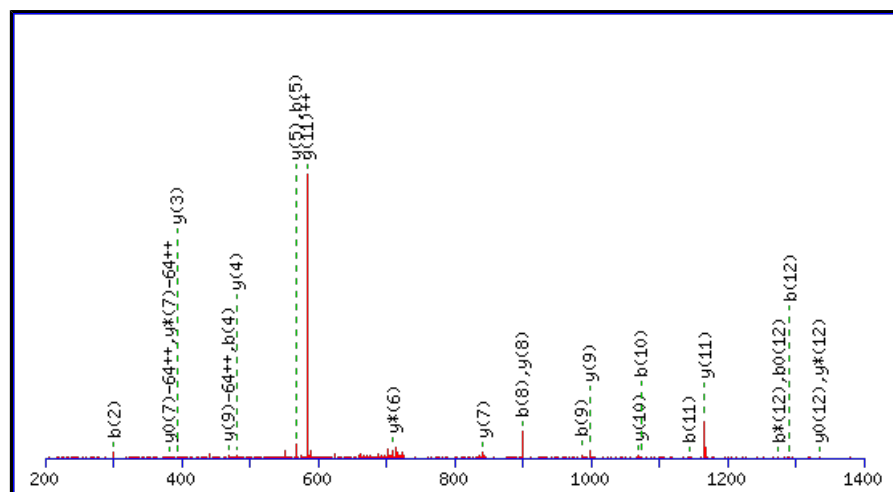
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1464.6490

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

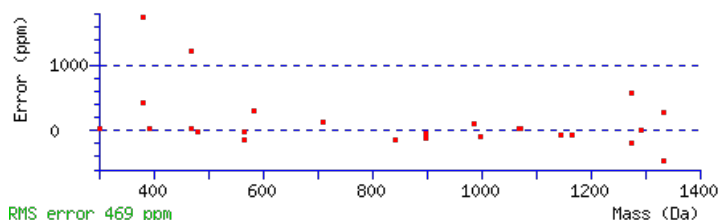
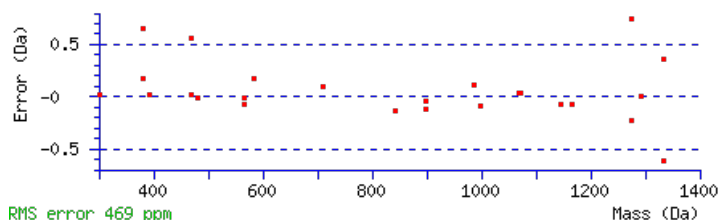
N7 : Deamidated (NQ)

M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 55 Expect: 8.5e-005

Matches : 25/178 fragment ions using 36 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							13
2	300.1707	150.5890					W	1352.5722	676.7897	1335.5456	668.2765	1334.5616	667.7844	12
3	397.2234	199.1153					P	1166.4929	583.7501	1149.4663	575.2368	1148.4823	574.7448	11
4	468.2605	234.6339					A	1069.4401	535.2237	1052.4136	526.7104	1051.4295	526.2184	10
5	567.3289	284.1681					V	998.4030	499.7051	981.3764	491.1919	980.3924	490.6999	9
6	624.3504	312.6788					G	899.3346	450.1709	882.3080	441.6577	881.3240	441.1656	8
7	739.3774	370.1923	722.3508	361.6790			N	842.3131	421.6602	825.2866	413.1469	824.3025	412.6549	7
8	899.4080	450.2076	882.3815	441.6944			C	727.2862	364.1467	710.2596	355.6334	709.2756	355.1414	6
9	986.4400	493.7237	969.4135	485.2104	968.4295	484.7184	S	567.2555	284.1314	550.2290	275.6181	549.2450	275.1261	5
10	1073.4721	537.2397	1056.4455	528.7264	1055.4615	528.2344	S	480.2235	240.6154	463.1969	232.1021	462.2129	231.6101	4
11	1144.5092	572.7582	1127.4826	564.2449	1126.4986	563.7529	A	393.1915	197.0994	376.1649	188.5861			3
12	1291.5446	646.2759	1274.5180	637.7626	1273.5340	637.2706	M	322.1544	161.5808	305.1278	153.0675			2
13							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LWPAVGNCSSAMR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.3	1464.6490	-0.0034	LWPAVGNCSSAMR
12.2	1463.6463	0.9992	WIERANMDGSQR
7.8	1462.6405	2.0050	EECECTARRPR
2.7	1464.6528	-0.0073	RCHESQDSKYR
2.3	1464.6442	0.0013	GLQEFQQEMEPK
2.1	1464.6442	0.0013	GLQEFQQEMEPK
2.0	1462.6472	1.9983	AVQMGMSAVFFNK
2.0	1463.6528	0.9927	VEATWEVSSENGR
1.9	1462.6470	1.9985	DRSGMNHSEISSK

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **O97507** in **uni_pig**, sp|O97507|FA12_PIG Coagulation factor XII OS=Sus scrofa GN=F12 PE=2 SV=1

Title: 120326_Sunil_PigSerum_Glyco_DsetB_14Spectrum1555_scans_1905

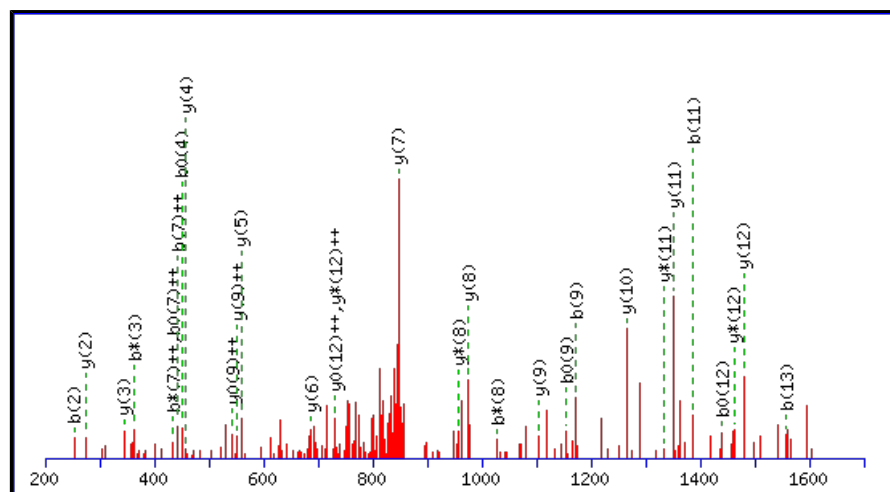
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



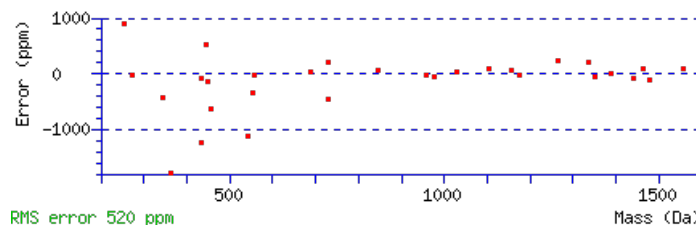
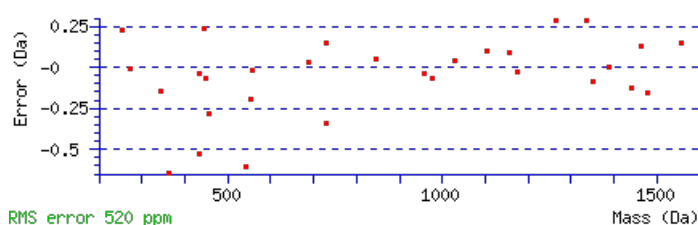
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

N2 : Deamidated (NQ)

Ions Score: 53 Expect: 9.8e-005

```
Matches : 30/140 fragment ions using 70 most intense peaks (help)
```

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	138.0662	69.5367					H							14
2	253.0931	127.0502	236.0666	118.5369			N	1594.6948	797.8510	1577.6683	789.3378	1576.6843	788.8458	13
3	381.1517	191.0795	364.1252	182.5662			Q	1479.6679	740.3376	1462.6413	731.8243	1461.6573	731.3323	12
4	468.1837	234.5955	451.1572	226.0822	450.1732	225.5902	S	1351.6093	676.3083	1334.5827	667.7950	1333.5987	667.3030	11
5	628.2144	314.6108	611.1878	306.0976	610.2038	305.6055	C	1264.5773	632.7923	1247.5507	624.2790	1246.5667	623.7870	10
6	757.2570	379.1321	740.2304	370.6189	739.2464	370.1268	E	1104.5466	552.7769	1087.5201	544.2637	1086.5361	543.7717	9
7	885.3156	443.1614	868.2890	434.6481	867.3050	434.1561	Q	975.5040	488.2557	958.4775	479.7424	957.4935	479.2504	8
8	1045.3462	523.1767	1028.3197	514.6635	1027.3356	514.1715	C	847.4454	424.2264	830.4189	415.7131	829.4349	415.2211	7
9	1173.4048	587.2060	1156.3782	578.6928	1155.3942	578.2007	Q	687.4148	344.2110	670.3883	335.6978	669.4042	335.2058	6
10	1274.4525	637.7299	1257.4259	629.2166	1256.4419	628.7246	T	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	5
11	1387.5365	694.2719	1370.5100	685.7586	1369.5260	685.2666	L	458.3085	229.6579	441.2820	221.1446			4
12	1458.5736	729.7905	1441.5471	721.2772	1440.5631	720.7852	A	345.2245	173.1159	328.1979	164.6026			3
13	1557.6421	779.3247	1540.6155	770.8114	1539.6315	770.3194	V	274.1874	137.5973	257.1608	129.0840			2
14							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [HNQSCEQCQTLAVR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.5	1730.7464	-0.0041	HNQSCEQCQTLAVR	Deamidated N2 71.39%
48.4	1730.7464	-0.0041	HNQSCEQCQTLAVR	Deamidated Q3 22.01%
42.9	1730.7464	-0.0041	HNQSCEQCQTLAVR	Deamidated Q7 6.19%
31.1	1730.7464	-0.0041	HNQSCEQCQTLAVR	Deamidated Q9 0.42%

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1S8B6** in **uni_pig**, tr|F1S8B6|F1S8B6_PIG Uncharacterized protein OS=Sus scrofa GN=ATRN PE=4 SV=1

Title: 120325_Sunil_PigSerum_Glyco_S_14Spectrum2387_scans_2931

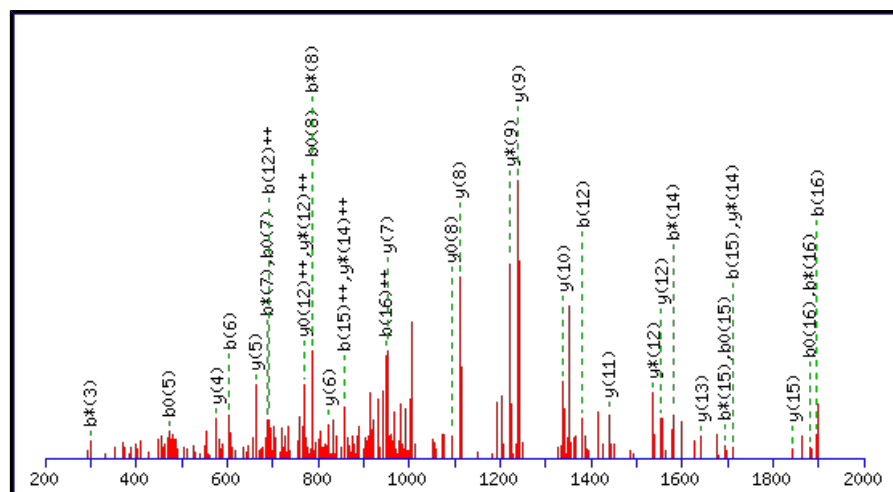
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

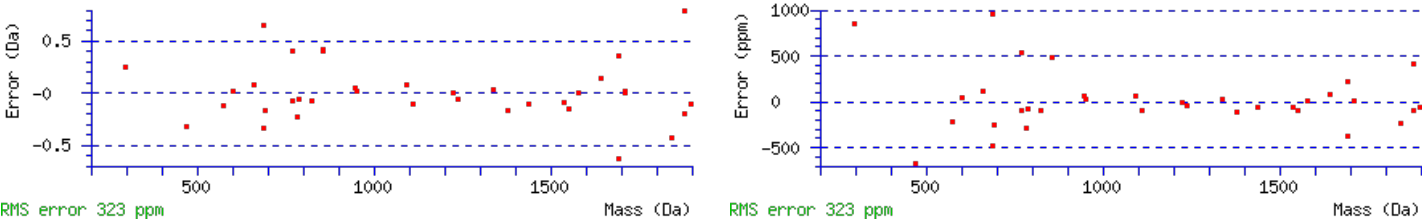
Variable modifications:

N3 : Deamidated (NQ)

Ions Score: 49 Expect: 9.9e-005

```
Matches : 36/180 fragment ions using 68 most intense peaks (help)
```

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							17
2	201.1234	101.0653			183.1128	92.0600	S	1930.7542	965.8807	1913.7276	957.3675	1912.7436	956.8754	16
3	316.1503	158.5788	299.1238	150.0655	298.1397	149.5735	N	1843.7222	922.3647	1826.6956	913.8514	1825.7116	913.3594	15
4	403.1823	202.0948	386.1558	193.5815	385.1718	193.0895	S	1728.6952	864.8512	1711.6687	856.3380	1710.6846	855.8460	14
5	490.2144	245.6108	473.1878	237.0975	472.2038	236.6055	S	1641.6632	821.3352	1624.6366	812.8220	1623.6526	812.3299	13
6	604.2573	302.6323	587.2307	294.1190	586.2467	293.6270	N	1554.6312	777.8192	1537.6046	769.3059	1536.6206	768.8139	12
7	705.3050	353.1561	688.2784	344.6429	687.2944	344.1508	T	1440.5882	720.7978	1423.5617	712.2845	1422.5777	711.7925	11
8	804.3734	402.6903	787.3468	394.1771	786.3628	393.6850	V	1339.5405	670.2739	1322.5140	661.7606	1321.5300	661.2686	10
9	932.4320	466.7196	915.4054	458.2063	914.4214	457.7143	Q	1240.4721	620.7397	1223.4456	612.2264	1222.4616	611.7344	9
10	1092.4626	546.7349	1075.4361	538.2217	1074.4520	537.7297	C	1112.4136	556.7104	1095.3870	548.1971	1094.4030	547.7051	8
11	1221.5052	611.2562	1204.4787	602.7430	1203.4946	602.2510	E	952.3829	476.6951	935.3564	468.1818	934.3723	467.6898	7
12	1381.5359	691.2716	1364.5093	682.7583	1363.5253	682.2663	C	823.3403	412.1738	806.3138	403.6605	805.3297	403.1685	6
13	1468.5679	734.7876	1451.5413	726.2743	1450.5573	725.7823	S	663.3097	332.1585	646.2831	323.6452	645.2991	323.1532	5
14	1597.6105	799.3089	1580.5839	790.7956	1579.5999	790.3036	E	576.2776	288.6425	559.2511	280.1292	558.2671	279.6372	4
15	1711.6534	856.3303	1694.6269	847.8171	1693.6428	847.3251	N	447.2350	224.1212	430.2085	215.6079			3
16	1897.7327	949.3700	1880.7062	940.8567	1879.7222	940.3647	W	333.1921	167.0997	316.1656	158.5864			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [ISNSSNTVQCECSENWK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
48.5	2042.8309	-0.0054	ISNSSNTVQCECSENWK	Deamidated N3 90.23%
38.4	2042.8309	-0.0054	ISNSSNTVQCECSENWK	Deamidated N6 8.80%
28.8	2042.8309	-0.0054	ISNSSNTVQCECSENWK	Deamidated Q9 0.96%
9.7	2042.8309	-0.0054	ISNSSNTVQCECSENWK	Deamidated N15 0.01%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNQNFSAVNNER**

Found in **F1SCV8** in **uni_pig**, tr|F1SCV8|F1SCV8_PIG Uncharacterized protein (Fragment) OS=Sus scrofa PE=4 SV=2

Match to Query 4009: 1456.625648 from(729.320100,2+) intensity(856.5191) rtinseconds(1306) scans(2587) index(12844)

Title: 120326 Sunil PigSerum Glyco SsetB 13Spectrum2011 scans 2587

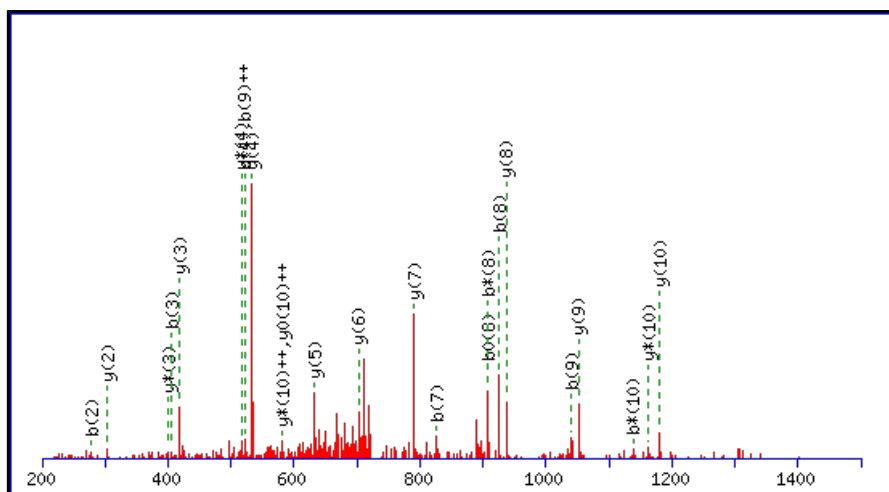
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1456.6218

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

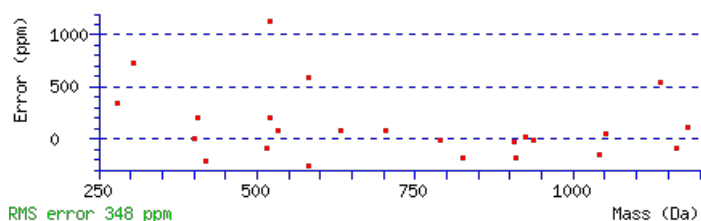
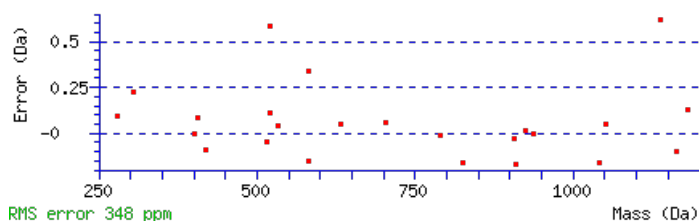
N4 : Deamidated (NQ)

N9 : Deamidated (NQ)

Ions Score: 53 Expect: 0.00011

Matches : 24/118 fragment ions using 47 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							12
2	278.1135	139.5604	261.0870	131.0471			N	1294.5658	647.7866	1277.5393	639.2733	1276.5553	638.7813	11
3	406.1721	203.5897	389.1456	195.0764			Q	1180.5229	590.7651	1163.4964	582.2518	1162.5123	581.7598	10
4	521.1991	261.1032	504.1725	252.5899			N	1052.4643	526.7358	1035.4378	518.2225	1034.4538	517.7305	9
5	668.2675	334.6374	651.2409	326.1241			F	937.4374	469.2223	920.4108	460.7091	919.4268	460.2170	8
6	755.2995	378.1534	738.2729	369.6401	737.2889	369.1481	S	790.3690	395.6881	773.3424	387.1748	772.3584	386.6828	7
7	826.3366	413.6719	809.3101	405.1587	808.3260	404.6667	A	703.3369	352.1721	686.3104	343.6588	685.3264	343.1668	6
8	925.4050	463.2061	908.3785	454.6929	907.3945	454.2009	V	632.2998	316.6536	615.2733	308.1403	614.2893	307.6483	5
9	1040.4320	520.7196	1023.4054	512.2063	1022.4214	511.7143	N	533.2314	267.1193	516.2049	258.6061	515.2209	258.1141	4
10	1154.4749	577.7411	1137.4483	569.2278	1136.4643	568.7358	N	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
11	1283.5175	642.2624	1266.4909	633.7491	1265.5069	633.2571	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [YNQNFSAVNNR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.8	1456.6218	0.0038	YNQNFSAVNNER	Deamidated N4, N9 88.47%
40.7	1456.6218	0.0038	YNQNFSAVNNER	Deamidated Q3, N9 5.36%
40.6	1456.6218	0.0038	YNQNFSAVNNER	Deamidated N4, N10 5.31%
29.9	1456.6218	0.0038	YNQNFSAVNNER	Deamidated Q3, N10 0.45%
29.0	1456.6218	0.0038	YNQNFSAVNNER	Deamidated N2, N9 0.36%
19.9	1456.6218	0.0038	YNQNFSAVNNER	Deamidated N2, N10 0.04%
13.6	1456.6218	0.0038	YNQNFSAVNNER	Deamidated N9, N10 0.01%
5.2	1455.6300	0.9957	KCENSEFSGLER	
4.3	1456.6218	0.0038	YNQNFSAVNNER	Deamidated Q3, N4 0.00%
3.3	1456.6392	-0.0135	MATTQETDGFQVK	

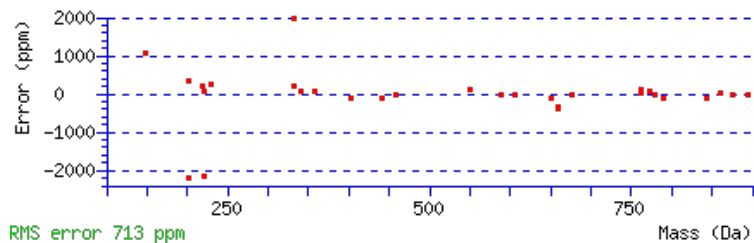
Mascot: <http://www.matrixscience.com/>

NCBI **BLAST** search of [LPENVTAWVGETLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.4	1556.8086	-0.0012	LPENVTAWVGETLK
0.9	1555.7929	1.0145	APAVDLDHKFERCK
0.2	1556.8021	0.0054	MEQKFRIVYAQK

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [LNETFAIAK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.6	1006.5335	-0.0018	LNETFAIAK
11.0	1006.5308	0.0009	VEQYRRR
8.7	1006.5335	-0.0018	EVQKEINK
8.7	1006.5335	-0.0018	VEQKLDFK
7.5	1006.5335	-0.0018	EVQYLLNK
6.2	1004.5324	1.9993	MKAAEIQAK
6.1	1004.5250	2.0067	KSSRSQSPK
6.0	1006.5335	-0.0018	LDFEKDIK
5.9	1006.5389	-0.0072	IPFAFWAR
5.1	1006.5407	-0.0090	TKKQSSNSK

Mascot: <http://www.matrixscience.com/>

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Mascot Search Results

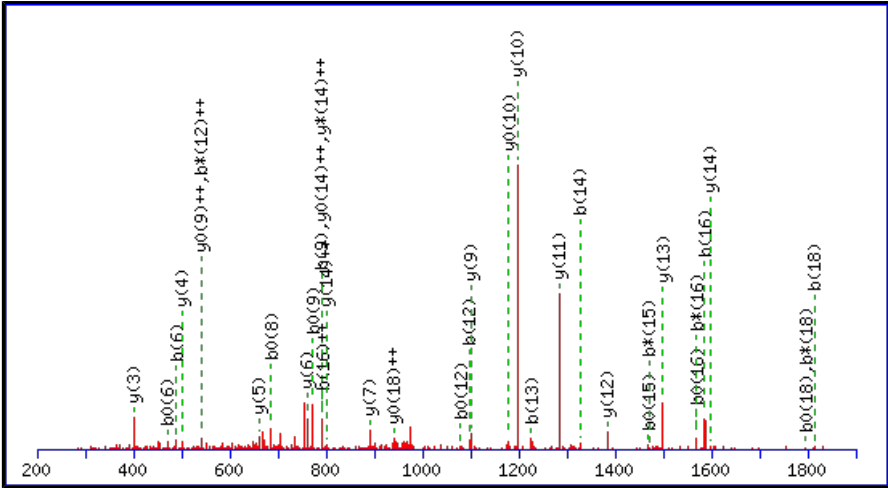
Peptide View

MS/MS Fragmentation of **SGGSTVNVSPPLETCVPER**
Found in **F1SIB1** in **uni_pig**, tr|F1SIB1|F1SIB1_PIG Prothrombin OS=Sus scrofa GN=F2 PE=3 SV=2

Match to Query 10091: 1985.932768 from(993.973660,2+) intensity(11262.6533) rtinseconds(1794) scans(4193) index(13239)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum3481_scans_4193
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

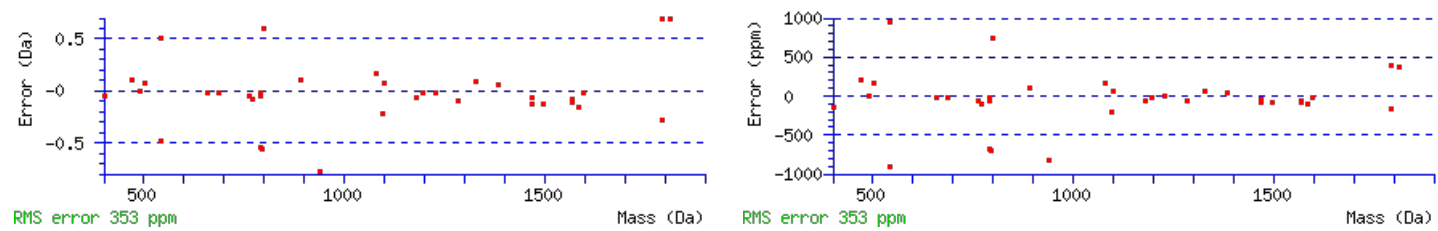
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1985.9364
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 57 Expect: 0.00013
Matches : 36/202 fragment ions using 64 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							19
2	145.0608	73.0340			127.0502	64.0287	G	1899.9117	950.4595	1882.8851	941.9462	1881.9011	941.4542	18
3	202.0822	101.5448			184.0717	92.5395	G	1842.8902	921.9487	1825.8637	913.4355	1824.8796	912.9435	17
4	289.1143	145.0608			271.1037	136.0555	S	1785.8687	893.4380	1768.8422	884.9247	1767.8582	884.4327	16
5	390.1619	195.5846			372.1514	186.5793	T	1698.8367	849.9220	1681.8102	841.4087	1680.8261	840.9167	15
6	489.2304	245.1188			471.2198	236.1135	V	1597.7890	799.3982	1580.7625	790.8849	1579.7785	790.3929	14
7	604.2573	302.6323	587.2307	294.1190	586.2467	293.6270	N	1498.7206	749.8639	1481.6941	741.3507	1480.7101	740.8587	13
8	703.3257	352.1665	686.2992	343.6532	685.3151	343.1612	V	1383.6937	692.3505	1366.6671	683.8372	1365.6831	683.3452	12
9	790.3577	395.6825	773.3312	387.1692	772.3472	386.6772	S	1284.6253	642.8163	1267.5987	634.3030	1266.6147	633.8110	11
10	887.4105	444.2089	870.3840	435.6956	869.3999	435.2036	P	1197.5932	599.3003	1180.5667	590.7870	1179.5827	590.2950	10
11	984.4633	492.7353	967.4367	484.2220	966.4527	483.7300	P	1100.5405	550.7739	1083.5139	542.2606	1082.5299	541.7686	9
12	1097.5473	549.2773	1080.5208	540.7640	1079.5368	540.2720	L	1003.4877	502.2475	986.4612	493.7342	985.4771	493.2422	8
13	1226.5899	613.7986	1209.5634	605.2853	1208.5794	604.7933	E	890.4036	445.7055	873.3771	437.1922	872.3931	436.7002	7
14	1327.6376	664.3224	1310.6111	655.8092	1309.6270	655.3172	T	761.3611	381.1842	744.3345	372.6709	743.3505	372.1789	6
15	1487.6683	744.3378	1470.6417	735.8245	1469.6577	735.3325	C	660.3134	330.6603	643.2868	322.1470	642.3028	321.6550	5
16	1586.7367	793.8720	1569.7101	785.3587	1568.7261	784.8667	V	500.2827	250.6450	483.2562	242.1317	482.2722	241.6397	4
17	1683.7894	842.3984	1666.7629	833.8851	1665.7789	833.3931	P	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
18	1812.8320	906.9196	1795.8055	898.4064	1794.8215	897.9144	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
19							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [SGGSTVNVSPPLETCVPER](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

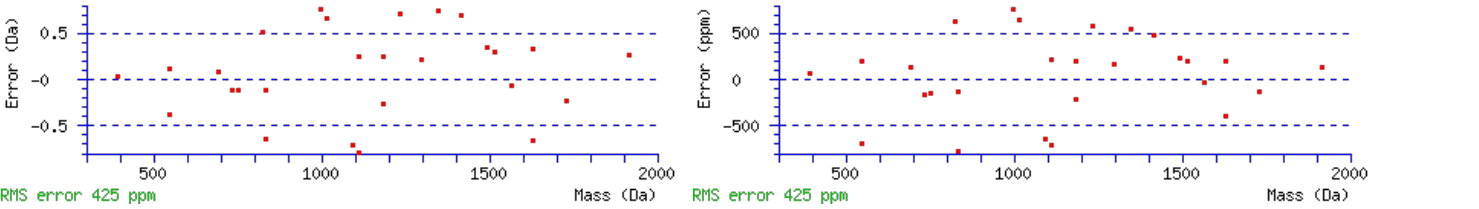
All matches to this query

Score	Mr(calc)	Delta	Sequence
56.9	1985.9364	-0.0037	SGGSTVNVSPPLETCVPER
1.9	1985.9398	-0.0070	VMMATSTKGQEESTQKAK
1.5	1985.9403	-0.0075	TLDPPGGTGQGDLSSRGR
1.2	1984.9377	0.9950	TAWGQQPDLAANEAQLLR

Mascot: <http://www.matrixscience.com/>

http://mascotxp.student.main.ntu.edu.sg/mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=13400 [22/Apr/15 06:05:29 PM]

25	2813.2537	1407.1305	2796.2271	1398.6172	2795.2431	1398.1252	H	540.2889	270.6481	523.2623	262.1348	522.2783	261.6428	4
26	2912.3221	1456.6647	2895.2955	1448.1514	2894.3115	1447.6594	V	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
27	3041.3647	1521.1860	3024.3381	1512.6727	3023.3541	1512.1807	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
28							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [NLYETEVEFSTDFSNVSAQQELNSHVER](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
54.9	3214.4691	-0.0173	NLYETEVEFSTDFSNVSAQQELNSHVER	Deamidated N14 68.14%
47.0	3214.4691	-0.0173	NLYETEVEFSTDFSNVSAQQELNSHVER	Deamidated Q19 10.97%
46.8	3214.4691	-0.0173	NLYETEVEFSTDFSNVSAQQELNSHVER	Deamidated N23 10.43%
46.8	3214.4691	-0.0173	NLYETEVEFSTDFSNVSAQQELNSHVER	Deamidated Q20 10.43%
19.8	3214.4691	-0.0173	NLYETEVEFSTDFSNVSAQQELNSHVER	Deamidated N1 0.02%
6.0	3212.4134	2.0384	IEMVNGVLMIHNVNQSDAGMYQCLAENK	
3.0	3214.4733	-0.0216	CEDNTKVFEGRPISSWTCLVDLEGLNMR	
0.7	3213.4279	1.0238	QQMEKRSMGMQRPGLMAGSGMGQGMEVER	
0.7	3213.4798	0.9719	IAQDFLNSIDQTGELLAMFEEDEIDEVK	
0.7	3213.4798	0.9719	IAQDFLNSIDQTGELLAMFEEDEIDEVK	

Mascot: <http://www.matrixscience.com/>

Peptide View

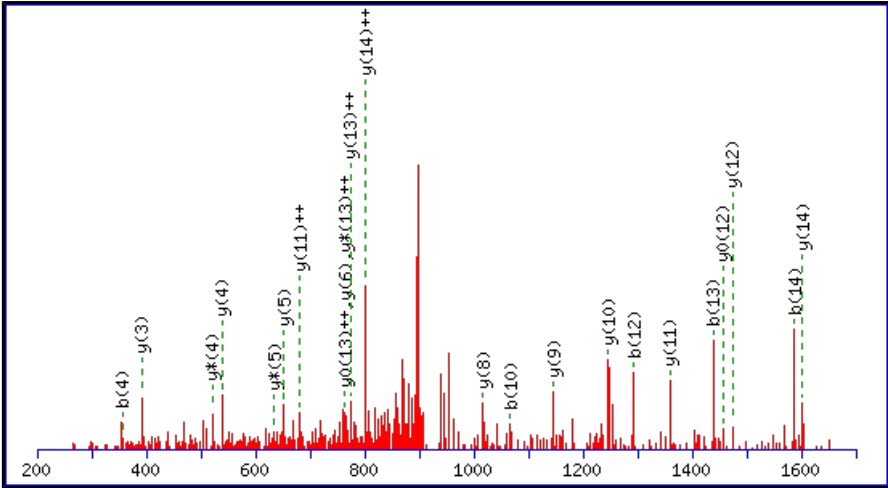
Found in **A0SEH3** in **uni_pig**, tr|A0SEH3|A0SEH3_PIG Complement component C8G OS=Sus scrofa GN=LOC100037955 PE=2 SV=1

Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Or, to Da

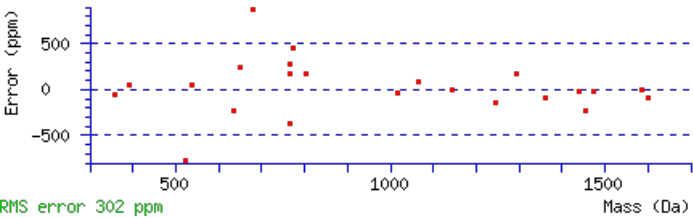
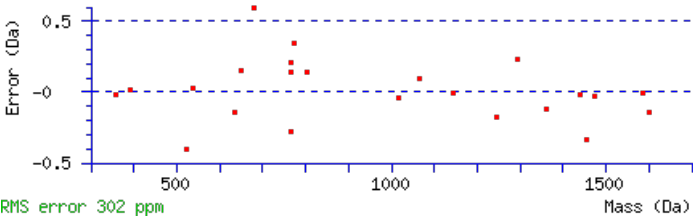
Label all possible matches Label matches used for scoring

Show Y-axis



Matches : 23/152 fragment ions using 42 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							16
2	228.1343	114.5708	211.1077	106.0575			Q	1730.8748	865.9410	1713.8483	857.4278	1712.8642	856.9358	15
3	285.1557	143.0815	268.1292	134.5682			G	1602.8162	801.9118	1585.7897	793.3985	1584.8057	792.9065	14
4	356.1928	178.6001	339.1663	170.0868			A	1545.7948	773.4010	1528.7682	764.8877	1527.7842	764.3957	13
5	471.2198	236.1135	454.1932	227.6003			N	1474.7577	737.8825	1457.7311	729.3692	1456.7471	728.8772	12
6	584.3039	292.6556	567.2773	284.1423			L	1359.7307	680.3690	1342.7042	671.8557	1341.7202	671.3637	11
7	685.3515	343.1794	668.3250	334.6661	667.3410	334.1741	T	1246.6467	623.8270	1229.6201	615.3137	1228.6361	614.8217	10
8	814.3941	407.7007	797.3676	399.1874	796.3836	398.6954	E	1145.5990	573.3031	1128.5724	564.7898	1127.5884	564.2978	9
9	929.4211	465.2142	912.3945	456.7009	911.4105	456.2089	D	1016.5564	508.7818	999.5298	500.2686	998.5458	499.7765	8
10	1066.4800	533.7436	1049.4534	525.2304	1048.4694	524.7383	H	901.5294	451.2684	884.5029	442.7551			7
11	1179.5640	590.2857	1162.5375	581.7724	1161.5535	581.2804	I	764.4705	382.7389	747.4440	374.2256			6
12	1292.6481	646.8277	1275.6216	638.3144	1274.6375	637.8224	L	651.3865	326.1969	634.3599	317.6836			5
13	1439.7165	720.3619	1422.6900	711.8486	1421.7060	711.3566	F	538.3024	269.6548	521.2758	261.1416			4
14	1586.7849	793.8961	1569.7584	785.3828	1568.7744	784.8908	F	391.2340	196.1206	374.2074	187.6074			3
15	1683.8377	842.4225	1666.8112	833.9092	1665.8271	833.4172	P	244.1656	122.5864	227.1390	114.0731			2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VQGANLTEDHILFFPK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
56.7	1828.9359	-0.0063	VQGANLTEDHILFFPK	Deamidated N5 98.99%
36.8	1828.9359	-0.0063	VQGANLTEDHILFFPK	Deamidated Q2 1.01%
1.7	1828.9148	0.0148	GVFSFSERVEPDFAPK	
1.7	1827.9366	0.9930	LLEEFRQTQQVPPNK	
1.7	1827.9366	0.9930	LLEEFRQTQQVPPNK	
1.7	1827.9366	0.9930	LLEEFRQTQQVPPNK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSCIQANYSLK**

Found in **F1SQX9** in **uni_pig**, tr|F1SQX9|F1SQX9_PIG Uncharacterized protein OS=Sus scrofa GN=APOD PE=4 SV=3

Match to Query 1937: 1240.572208 from(621.293380,2+) intensity(16594.7441) rtinseconds(1424) scans(2907) index(8615)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_15Spectrum2359_scans__2907

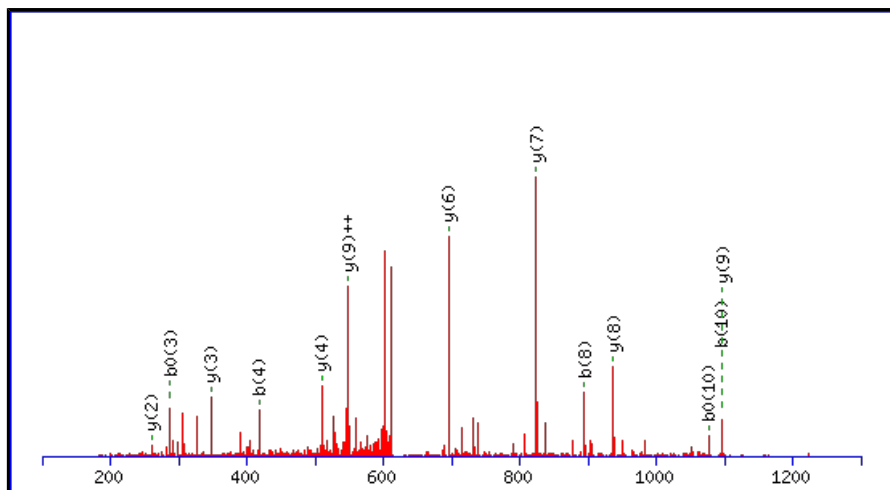
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1240.5758

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

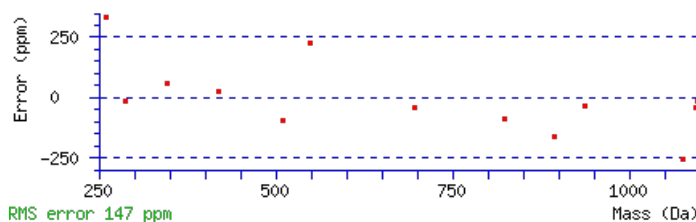
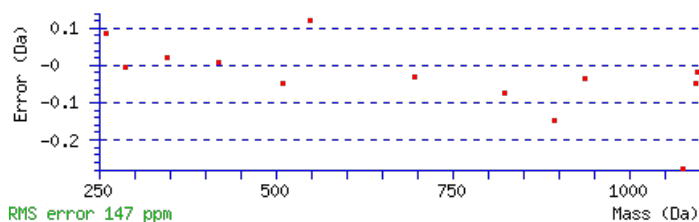
Variable modifications:

N7 : Deamidated (NQ)

Ions Score: 53 Expect: 0.00019

Matches : 13/106 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							11
2	145.0608	73.0340			127.0502	64.0287	S	1184.5616	592.7844	1167.5351	584.2712	1166.5510	583.7792	10
3	305.0914	153.0493			287.0809	144.0441	C	1097.5296	549.2684	1080.5030	540.7552	1079.5190	540.2631	9
4	418.1755	209.5914			400.1649	200.5861	I	937.4989	469.2531	920.4724	460.7398	919.4884	460.2478	8
5	546.2341	273.6207	529.2075	265.1074	528.2235	264.6154	Q	824.4149	412.7111	807.3883	404.1978	806.4043	403.7058	7
6	617.2712	309.1392	600.2446	300.6260	599.2606	300.1339	A	696.3563	348.6818	679.3297	340.1685	678.3457	339.6765	6
7	732.2981	366.6527	715.2716	358.1394	714.2876	357.6474	N	625.3192	313.1632	608.2926	304.6499	607.3086	304.1579	5
8	895.3614	448.1844	878.3349	439.6711	877.3509	439.1791	Y	510.2922	255.6498	493.2657	247.1365	492.2817	246.6445	4
9	982.3935	491.7004	965.3669	483.1871	964.3829	482.6951	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
10	1095.4775	548.2424	1078.4510	539.7291	1077.4670	539.2371	L	260.1969	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [GSCIQANYSLK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.8	1240.5758	-0.0036	GSCIQANYSLK	Deamidated N7 95.88%
39.2	1240.5758	-0.0036	GSCIQANYSLK	Deamidated Q5 4.12%
6.2	1240.5757	-0.0035	REAENMYSLK	
3.1	1240.5679	0.0043	EMTEMTGVSLK	
3.1	1240.5679	0.0043	EMTEMTGVSLK	
1.6	1240.5618	0.0104	CKENYERSR	
1.2	1239.5691	1.0031	SGAASSSSSSREK	
0.6	1240.5717	0.0005	AKMASATSSSQR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

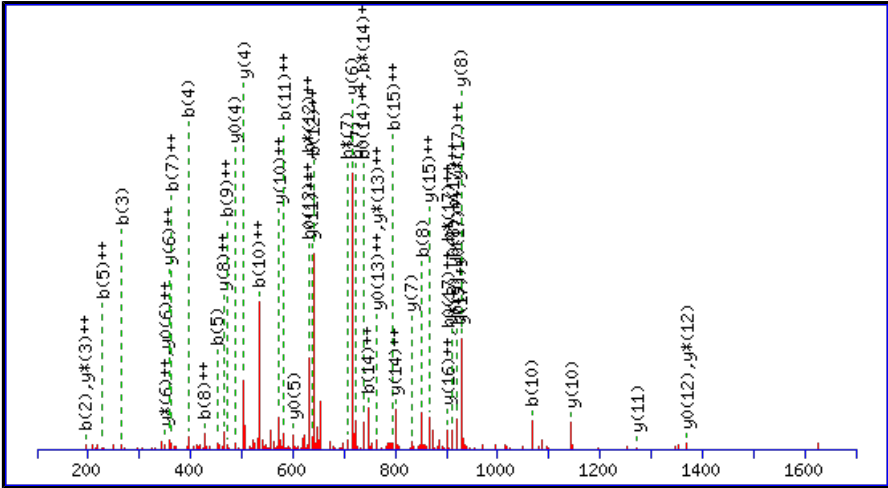
Peptide View

MS/MS Fragmentation of **HGAEGRNESKPDPDVTER**
Found in **F1RMN7** in **uni_pig**, tr|F1RMN7|F1RMN7_PIG Hemopexin OS=Sus scrofa GN=HPX PE=4 SV=2

Match to Query 10186: 1993.904532 from(665.642120,3+) intensity(5024.6646) rtinseconds(721) scans(487) index(4826)
Title: 120325_Sunil_PigSerum_Glyco_S_03Spectrum58_scans__487
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

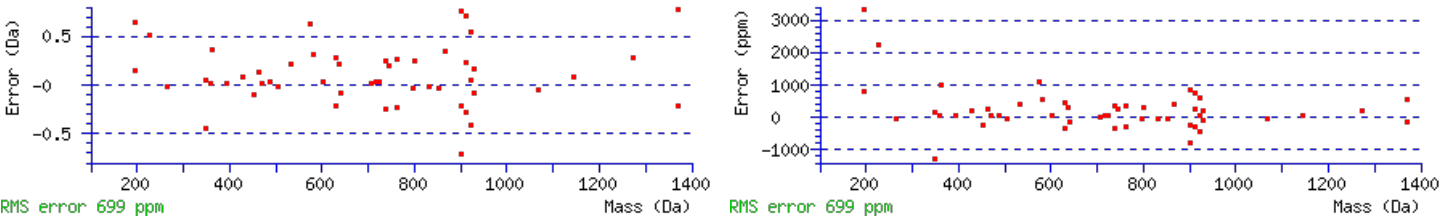
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1993.9089
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 54 Expect: 0.00019
Matches : 52/186 fragment ions using 86 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	138.0662	69.5367					H							18
2	195.0877	98.0475					G	1857.8573	929.4323	1840.8308	920.9190	1839.8468	920.4270	17
3	266.1248	133.5660					A	1800.8359	900.9216	1783.8093	892.4083	1782.8253	891.9163	16
4	395.1674	198.0873			377.1568	189.0820	E	1729.7987	865.4030	1712.7722	856.8897	1711.7882	856.3977	15
5	452.1888	226.5980			434.1783	217.5928	G	1600.7562	800.8817	1583.7296	792.3684	1582.7456	791.8764	14
6	608.2899	304.6486	591.2634	296.1353	590.2794	295.6433	R	1543.7347	772.3710	1526.7081	763.8577	1525.7241	763.3657	13
7	723.3169	362.1621	706.2903	353.6488	705.3063	353.1568	N	1387.6336	694.3204	1370.6070	685.8072	1369.6230	685.3151	12
8	852.3595	426.6834	835.3329	418.1701	834.3489	417.6781	E	1272.6066	636.8070	1255.5801	628.2937	1254.5961	627.8017	11
9	939.3915	470.1994	922.3649	461.6861	921.3809	461.1941	S	1143.5640	572.2857	1126.5375	563.7724	1125.5535	563.2804	10
10	1067.4865	534.2469	1050.4599	525.7336	1049.4759	525.2416	K	1056.5320	528.7696	1039.5055	520.2564	1038.5215	519.7644	9
11	1164.5392	582.7733	1147.5127	574.2600	1146.5287	573.7680	P	928.4371	464.7222	911.4105	456.2089	910.4265	455.7169	8
12	1279.5662	640.2867	1262.5396	631.7734	1261.5556	631.2814	D	831.3843	416.1958	814.3577	407.6825	813.3737	407.1905	7
13	1376.6189	688.8131	1359.5924	680.2998	1358.6084	679.8078	P	716.3573	358.6823	699.3308	350.1690	698.3468	349.6770	6
14	1491.6459	746.3266	1474.6193	737.8133	1473.6353	737.3213	D	619.3046	310.1559	602.2780	301.6427	601.2940	301.1506	5
15	1590.7143	795.8608	1573.6877	787.3475	1572.7037	786.8555	V	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
16	1691.7620	846.3846	1674.7354	837.8713	1673.7514	837.3793	T	405.2092	203.1082	388.1827	194.5950	387.1987	194.1030	3
17	1820.8046	910.9059	1803.7780	902.3926	1802.7940	901.9006	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
18							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [HGAEGRNESKPDVDVTER](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.6	1993.9089	-0.0044	HGAEGRNESKPDVDVTER
8.4	1993.9089	-0.0044	HSEQNNSNINTVKHDSK
8.4	1993.9089	-0.0044	HSEQNNSNINTVKHDSK
8.4	1993.9089	-0.0044	HSEQNNSNINTVKHDSK
8.4	1993.9089	-0.0044	HSEQNNSNINTVKHDSK
8.4	1993.9089	-0.0044	HSEQNNSNINTVKHDSK
8.4	1993.9089	-0.0044	HSEQNNSNINTVKHDSK
8.4	1993.9089	-0.0044	HSEQNNSNINTVKHDSK
4.3	1993.9089	-0.0044	HSEQNNSNINTVKHDSK
4.3	1993.9089	-0.0044	HSEQNNSNINTVKHDSK
4.3	1993.9089	-0.0044	HSEQNNSNINTVKHDSK

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **K7GKE7** in **uni_pig**, tr|K7GKE7|K7GKE7_PIG Haptoglobin OS=Sus scrofa GN=HP PE=3 SV=1

Title: 120325 Sunil PigSerum Glyco S 08Spectrum2357 scans 3310

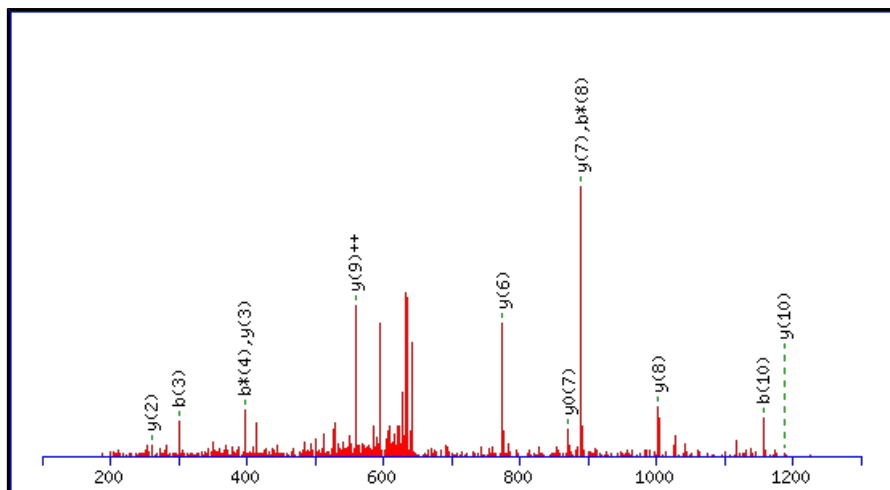
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

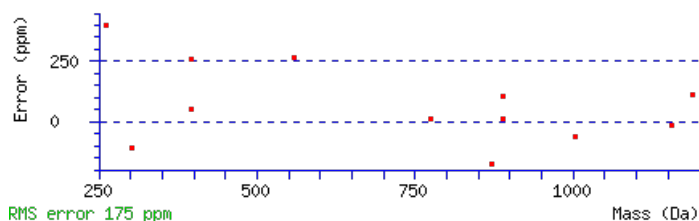
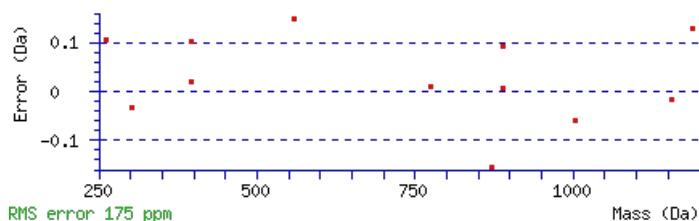
N1 : Deamidated (NQ)

N5 : Deamidated (NQ')

Ions Score: 53 Expect: 0.00019

Matches : 12/102 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							11
2	187.0713	94.0393	170.0448	85.5260			A	1187.6055	594.3064	1170.5790	585.7931	1169.5949	585.3011	10
3	301.1143	151.0608	284.0877	142.5475			N	1116.5684	558.7878	1099.5419	550.2746	1098.5578	549.7826	9
4	414.1983	207.6028	397.1718	199.0895			L	1002.5255	501.7664	985.4989	493.2531	984.5149	492.7611	8
5	529.2253	265.1163	512.1987	256.6030			N	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	7
6	676.2937	338.6505	659.2671	330.1372			F	774.4145	387.7109	757.3879	379.1976	756.4039	378.7056	6
7	777.3414	389.1743	760.3148	380.6610	759.3308	380.1690	T	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	5
8	906.3840	453.6956	889.3574	445.1823	888.3734	444.6903	E	526.2984	263.6528	509.2718	255.1395	508.2878	254.6475	4
9	1043.4429	522.2251	1026.4163	513.7118	1025.4323	513.2198	H	397.2558	199.1315	380.2292	190.6183			3
10	1156.5269	578.7671	1139.5004	570.2538	1138.5164	569.7618	L	260.1969	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1



(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.1	1301.6251	-0.0036	NANLNFTEHLK	Deamidated N1, N5 94.68%
40.4	1301.6251	-0.0036	NANLNFTEHLK	Deamidated N3, N5 5.01%
28.2	1301.6251	-0.0036	NANLNFTEHLK	Deamidated N1, N3 0.30%
6.7	1301.6139	0.0076	NAVESYTYNIK	
5.6	1301.6099	0.0116	VSNGISEDQGPAK	
5.1	1300.6259	0.9957	GSERPEEELQK	
3.9	1301.6285	-0.0070	NSPPKSCTPVSK	
3.1	1299.6129	2.0087	TYMNREETLK	
2.6	1301.6211	0.0004	RQQQQQLDQK	
1.6	1299.6095	2.0120	QDPWNLPSVR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLYLASNQSNK**

Found in **F1S1G8** in **uni_pig**, tr|F1S1G8|F1S1G8_PIG Amine oxidase OS=Sus scrofa GN=AOC3 PE=3 SV=2

Match to Query 2799: 1301.611308 from(651.812930,2+) intensity(7042.0083) rtinseconds(1599) scans(3029) index(1743)

Title: 120325_Sunil_PigSerum_Glyco_D_15Spectrum2366_scans__3029

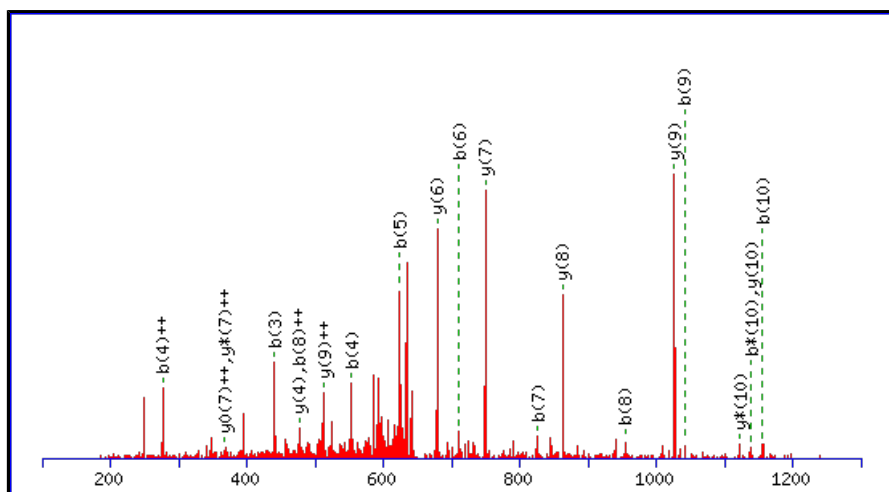
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1301.6139

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

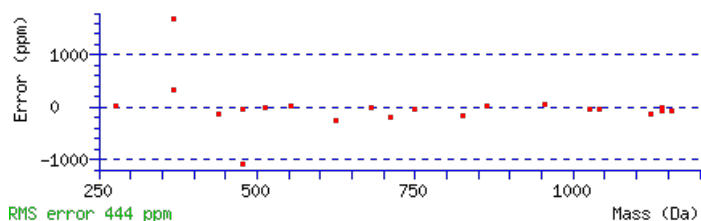
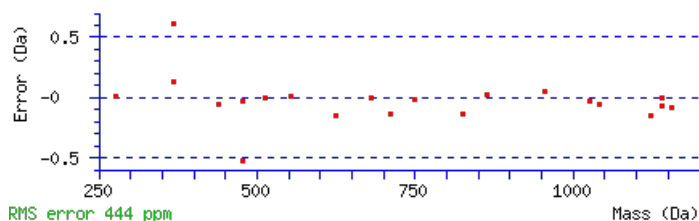
N7 : Deamidated (NQ)

N10 : Deamidated (NQ)

Ions Score: 53 Expect: 0.00019

Matches : 22/94 fragment ions using 44 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							11
2	277.1547	139.0810					L	1139.5579	570.2826	1122.5313	561.7693	1121.5473	561.2773	10
3	440.2180	220.6126					Y	1026.4738	513.7406	1009.4473	505.2273	1008.4633	504.7353	9
4	553.3021	277.1547					L	863.4105	432.2089	846.3840	423.6956	845.3999	423.2036	8
5	624.3392	312.6732					A	750.3264	375.6669	733.2999	367.1536	732.3159	366.6616	7
6	711.3712	356.1892			693.3606	347.1840	S	679.2893	340.1483	662.2628	331.6350	661.2788	331.1430	6
7	826.3981	413.7027	809.3716	405.1894	808.3876	404.6974	N	592.2573	296.6323	575.2307	288.1190	574.2467	287.6270	5
8	954.4567	477.7320	937.4302	469.2187	936.4462	468.7267	Q	477.2304	239.1188	460.2038	230.6055	459.2198	230.1135	4
9	1041.4888	521.2480	1024.4622	512.7347	1023.4782	512.2427	S	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
10	1156.5157	578.7615	1139.4891	570.2482	1138.5051	569.7562	N	262.1397	131.5735	245.1132	123.0602			2
11							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [YLYLASNOSNK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.9	1301.6139	-0.0026	YLYLASNQS NK	Deamidated N7, N10 76.44%
46.9	1301.6139	-0.0026	YLYLASNQS NK	Deamidated N7, Q8 19.42%
40.2	1301.6139	-0.0026	YLYLASNQS NK	Deamidated Q8, N10 4.14%
9.0	1301.5995	0.0118	EMFKQMLSEK	
8.8	1301.5995	0.0118	MKQTGOVYAMK	
7.3	1300.6122	0.9991	NYCGETVALFK	
3.2	1301.6220	-0.0107	RQM HETLEMK	
0.5	1301.6074	0.0039	RSNMEFLENK	
0.5	1299.6016	2.0097	EFQKESLSMGK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

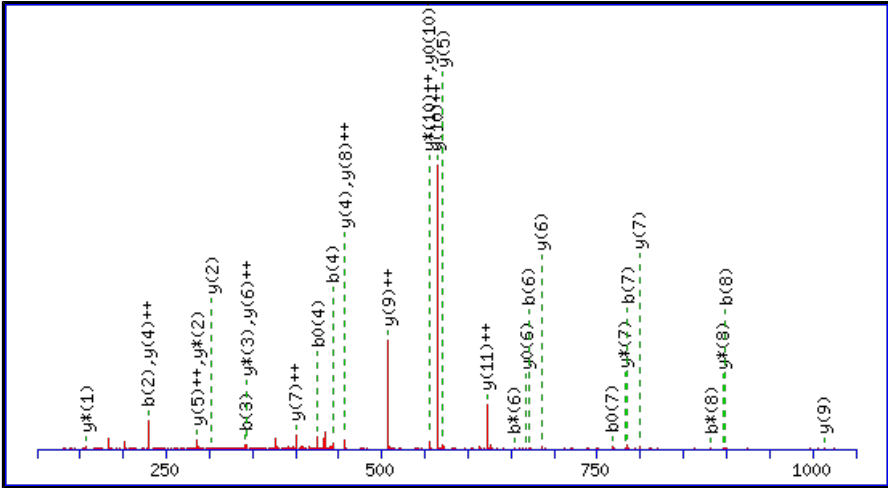
Peptide View

MS/MS Fragmentation of **LNITINDLPGKR**
Found in **F1RQW2** in **uni_pig**, tr|F1RQW2|F1RQW2_PIG Uncharacterized protein OS=Sus scrofa GN=C4 PE=4 SV=2

Match to Query 3100: 1353.759342 from(452.260390,3+) intensity(73008.1953) rtinseconds(1785) scans(4143) index(8457)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_14Spectrum3527_scans__4143
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

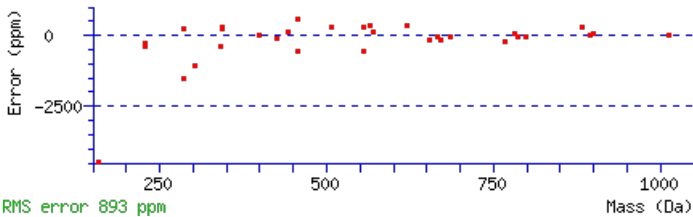
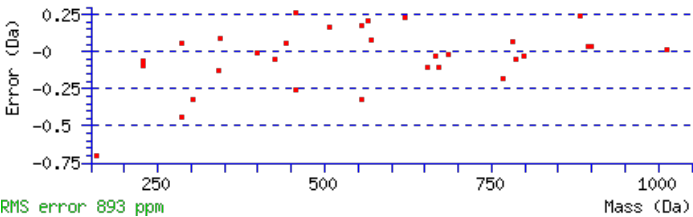
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1353.7616
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Ions Score: 52 Expect: 0.0002
Matches : 32/114 fragment ions using 44 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							12
2	229.1183	115.0628	212.0917	106.5495			N	1241.6848	621.3461	1224.6583	612.8328	1223.6743	612.3408	11
3	342.2023	171.6048	325.1758	163.0915			I	1126.6579	563.8326	1109.6313	555.3193	1108.6473	554.8273	10
4	443.2500	222.1287	426.2235	213.6154	425.2395	213.1234	T	1013.5738	507.2905	996.5473	498.7773	995.5633	498.2853	9
5	556.3341	278.6707	539.3075	270.1574	538.3235	269.6654	I	912.5261	456.7667	895.4996	448.2534	894.5156	447.7614	8
6	670.3770	335.6921	653.3505	327.1789	652.3665	326.6869	N	799.4421	400.2247	782.4155	391.7114	781.4315	391.2194	7
7	785.4040	393.2056	768.3774	384.6923	767.3934	384.2003	D	685.3991	343.2032	668.3726	334.6899	667.3886	334.1979	6
8	898.4880	449.7477	881.4615	441.2344	880.4775	440.7424	L	570.3722	285.6897	553.3457	277.1765			5
9	995.5408	498.2740	978.5142	489.7608	977.5302	489.2687	P	457.2881	229.1477	440.2616	220.6344			4
10	1052.5623	526.7848	1035.5357	518.2715	1034.5517	517.7795	G	360.2354	180.6213	343.2088	172.1081			3
11	1180.6572	590.8322	1163.6307	582.3190	1162.6466	581.8270	K	303.2139	152.1106	286.1874	143.5973			2
12							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [LNITINDLPGKR](#)

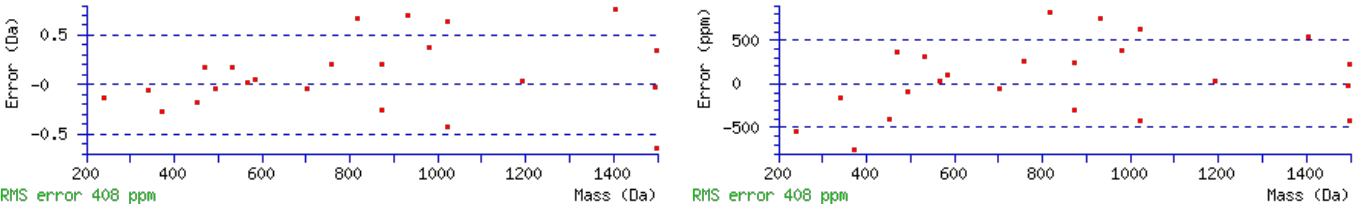
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.9	1353.7616	-0.0022	LNITINDLPGKR	Deamidated N2 64.96%
49.2	1353.7616	-0.0022	LNITINDLPGKR	Deamidated N6 35.04%
20.6	1351.7574	2.0020	NIIYMFLPITK	
13.3	1351.7500	2.0093	LLIDVHVPDGFK	
12.6	1353.7616	-0.0022	INLLQQQIQVR	
12.6	1353.7616	-0.0022	INLLQQQIQVR	
12.6	1353.7616	-0.0022	INLLQQQIQVR	
12.3	1353.7616	-0.0022	INLLQQQIQVR	
12.3	1353.7616	-0.0022	INLLQQQIQVR	
12.3	1353.7616	-0.0022	INLLQQQIQVR	

Mascot: <http://www.matrixscience.com/>

http:// MascotXP.student.main.ntu.edu.sg/Mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=12450 [22/Apr/15 06:06:11 PM]



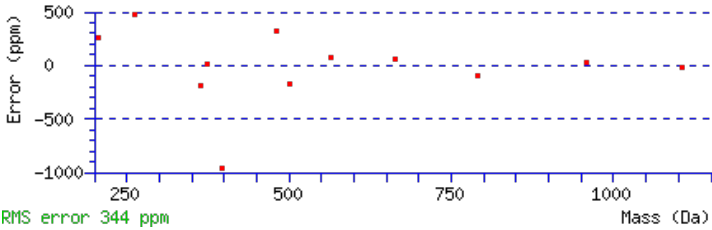
NCBI BLAST search of [VASVININPNTTNATGNCHSK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
54.3	2213.0382	-0.0058	VASVININPNTTNATGNCHSK	Deamidated N10, N13 67.70%
48.5	2213.0382	-0.0058	VASVININPNTTNATGNCHSK	Deamidated N8, N13 18.01%
42.3	2213.0382	-0.0058	VASVININPNTTNATGNCHSK	Deamidated N10, N17 4.29%
41.2	2213.0382	-0.0058	VASVININPNTTNATGNCHSK	Deamidated N8, N10 3.29%
39.3	2213.0382	-0.0058	VASVININPNTTNATGNCHSK	Deamidated N6, N13 2.14%
38.2	2213.0382	-0.0058	VASVININPNTTNATGNCHSK	Deamidated N8, N17 1.65%
38.1	2213.0382	-0.0058	VASVININPNTTNATGNCHSK	Deamidated N13, N17 1.63%
33.4	2213.0382	-0.0058	VASVININPNTTNATGNCHSK	Deamidated N6, N10 0.55%
32.3	2213.0382	-0.0058	VASVININPNTTNATGNCHSK	Deamidated N6, N17 0.43%
30.7	2213.0382	-0.0058	VASVININPNTTNATGNCHSK	Deamidated N6, N8 0.30%

Mascot: <http://www.matrixscience.com/>

http:// MascotXP.student.main.ntu.edu.sg/Mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=1261 [22/Apr/15 06:06:16 PM]



NCBI **BLAST** search of [GFPAEPNSTSR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.7	1162.5255	-0.0013	GFPAEPNSTSR
10.7	1162.5223	0.0018	CNAGVCALNGK
8.0	1162.5189	0.0052	SWVQAQGACR
6.6	1162.5354	-0.0113	QGSEVTDPTTK
4.0	1162.5329	-0.0087	GGKTEIMPQW
2.8	1160.5058	2.0183	DSEGRGSGDPGK
2.7	1162.5176	0.0065	QLQDMQDVGK
2.7	1162.5176	0.0065	QLQDMQDVGK
2.7	1162.5176	0.0065	QLQDMQDVGK
2.5	1162.5255	-0.0013	GGAGQQEPVYR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **DEGLCSANVTR**

Found in **F1SFC1** in **uni_pig**, tr|F1SFC1|F1SFC1_PIG Tissue factor pathway inhibitor OS=Sus scrofa GN=TFPI2 PE=4 SV=1

Match to Query 1698: 1221.526348 from(611.770450,2+) intensity(2254.1399) rtinseconds(1163) scans(1592) index(9030)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_17Spectrum922_scans__1592

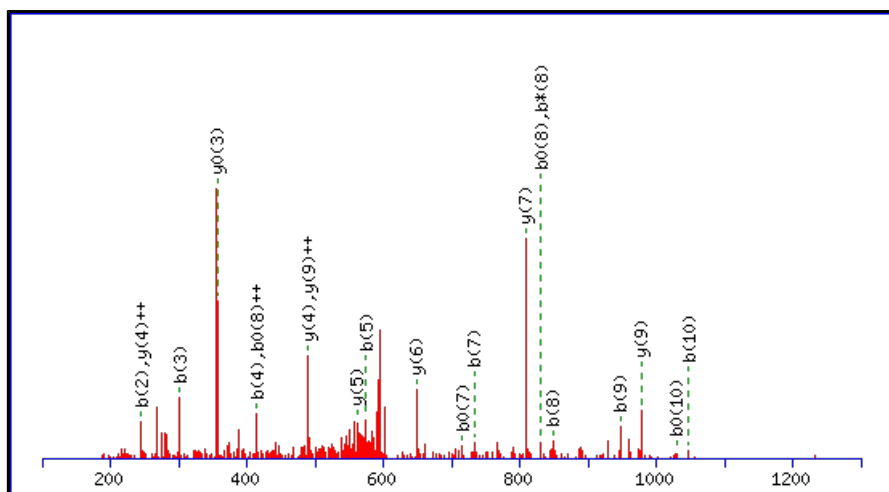
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1221.5296

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

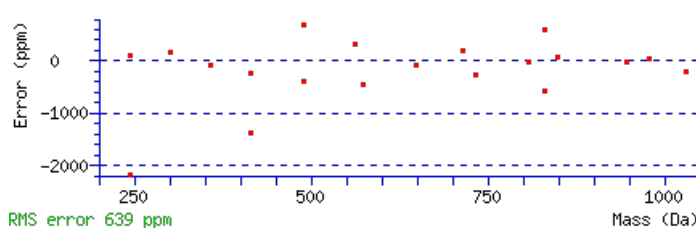
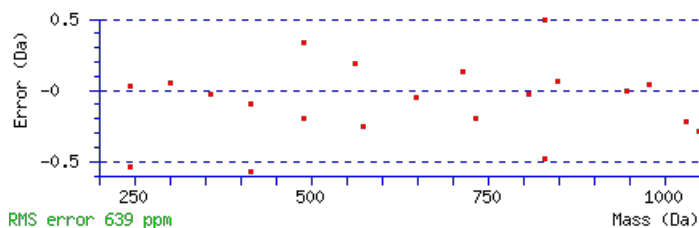
Variable modifications:

N8 : Deamidated (NQ)

Ions Score: 49 Expect: 0.00028

```
Matches : 21/104 fragment ions using 36 most intense peaks (help)
```

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							11
2	245.0768	123.0420			227.0662	114.0368	E	1107.5099	554.2586	1090.4834	545.7453	1089.4993	545.2533	10
3	302.0983	151.5528			284.0877	142.5475	G	978.4673	489.7373	961.4408	481.2240	960.4567	480.7320	9
4	415.1823	208.0948			397.1718	199.0895	L	921.4458	461.2266	904.4193	452.7133	903.4353	452.2213	8
5	575.2130	288.1101			557.2024	279.1049	C	808.3618	404.6845	791.3352	396.1713	790.3512	395.6792	7
6	662.2450	331.6261			644.2345	322.6209	S	648.3311	324.6692	631.3046	316.1559	630.3206	315.6639	6
7	733.2821	367.1447			715.2716	358.1394	A	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	5
8	848.3091	424.6582	831.2825	416.1449	830.2985	415.6529	N	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
9	947.3775	474.1924	930.3509	465.6791	929.3669	465.1871	V	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	1048.4252	524.7162	1031.3986	516.2029	1030.4146	515.7109	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
11							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [DEGLCSANVTR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.6	1221.5296	-0.0032	DEGLCSANVTR
13.2	1221.5296	-0.0032	DQGAMTDQLSR
5.7	1221.5361	-0.0097	EDTEKENTEK
5.0	1220.5156	1.0107	EDTEKEAENR
4.8	1221.5296	-0.0032	DQGAMTDQLSR
4.1	1220.5278	0.9986	AVANMQGEMDR
3.7	1221.5336	-0.0072	QQLPDMEFGR
2.5	1221.5295	-0.0032	CKNVAEENTR
0.9	1221.5360	-0.0097	NKEDSEKDEK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

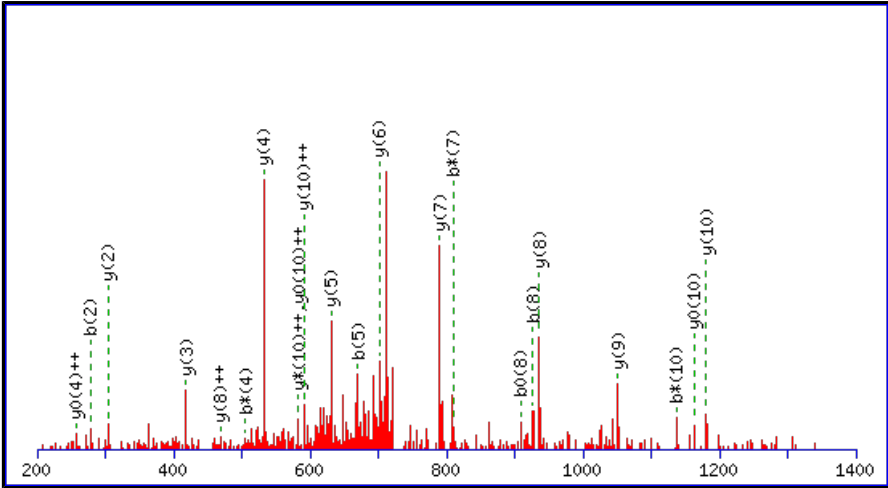
Peptide View

MS/MS Fragmentation of **YNQNFSAVNNER**
Found in **F1SCV8** in **uni_pig**, tr|F1SCV8|F1SCV8_PIG Uncharacterized protein (Fragment) OS=Sus scrofa PE=4 SV=2

Match to Query 4005: 1456.616248 from(729.315400,2+) intensity(2547.4968) rtinseconds(1405) scans(2159) index(12495)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_11Spectrum1378_scans_2159
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

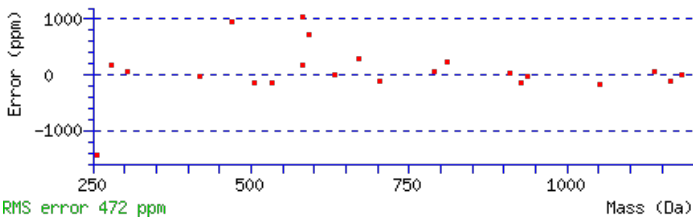
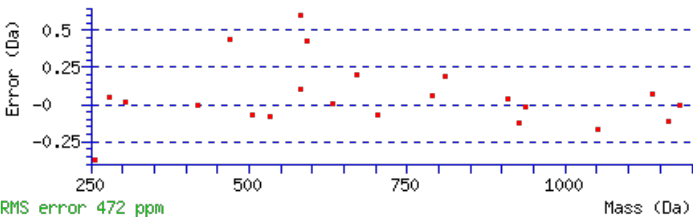
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1456.6218
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N4 : Deamidated (NQ)
Ions Score: 48 Expect: 0.00028
Matches : 22/118 fragment ions using 46 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							12
2	278.1135	139.5604	261.0870	131.0471			N	1294.5658	647.7866	1277.5393	639.2733	1276.5553	638.7813	11
3	407.1561	204.0817	390.1296	195.5684			Q	1180.5229	590.7651	1163.4964	582.2518	1162.5123	581.7598	10
4	522.1831	261.5952	505.1565	253.0819			N	1051.4803	526.2438	1034.4538	517.7305	1033.4697	517.2385	9
5	669.2515	335.1294	652.2249	326.6161			F	936.4534	468.7303	919.4268	460.2170	918.4428	459.7250	8
6	756.2835	378.6454	739.2570	370.1321	738.2729	369.6401	S	789.3850	395.1961	772.3584	386.6828	771.3744	386.1908	7
7	827.3206	414.1640	810.2941	405.6507	809.3101	405.1587	A	702.3529	351.6801	685.3264	343.1668	684.3424	342.6748	6
8	926.3890	463.6982	909.3625	455.1849	908.3785	454.6929	V	631.3158	316.1615	614.2893	307.6483	613.3052	307.1563	5
9	1040.4320	520.7196	1023.4054	512.2063	1022.4214	511.7143	N	532.2474	266.6273	515.2209	258.1141	514.2368	257.6221	4
10	1154.4749	577.7411	1137.4483	569.2278	1136.4643	568.7358	N	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
11	1283.5175	642.2624	1266.4909	633.7491	1265.5069	633.2571	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [YNQNFSAVNNER](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
48.0	1456.6218	-0.0056	YNQNFSAVNNER	Deamidated Q3, N4 96.79%
32.6	1456.6218	-0.0056	YNQNFSAVNNER	Deamidated N2, N4 2.78%
23.8	1456.6218	-0.0056	YNQNFSAVNNER	Deamidated N2, Q3 0.37%
11.3	1456.6218	-0.0056	YNQNFSAVNNER	Deamidated Q3, N9 0.02%
10.3	1456.6218	-0.0056	YNQNFSAVNNER	Deamidated N4, N9 0.02%
7.9	1456.6293	-0.0130	EFQGGGEMFQQK	
5.3	1456.6293	-0.0130	EFQGGGEMFQQK	
5.3	1456.6218	-0.0056	YNQNFSAVNNER	Deamidated Q3, N10 0.01%
5.0	1456.6218	-0.0056	YNQNFSAVNNER	Deamidated N2, N9 0.00%
4.9	1456.6218	-0.0056	YNQNFSAVNNER	Deamidated N4, N10 0.00%

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1SFM2** in **uni_pig**, tr|F1SFM2|F1SFM2_PIG Uncharacterized protein OS=Sus scrofa GN=CHL1 PE=4 SV=2

Title: 120325_Sunil_PigSerum_Glyco_S_14Spectrum2129_scans__2630

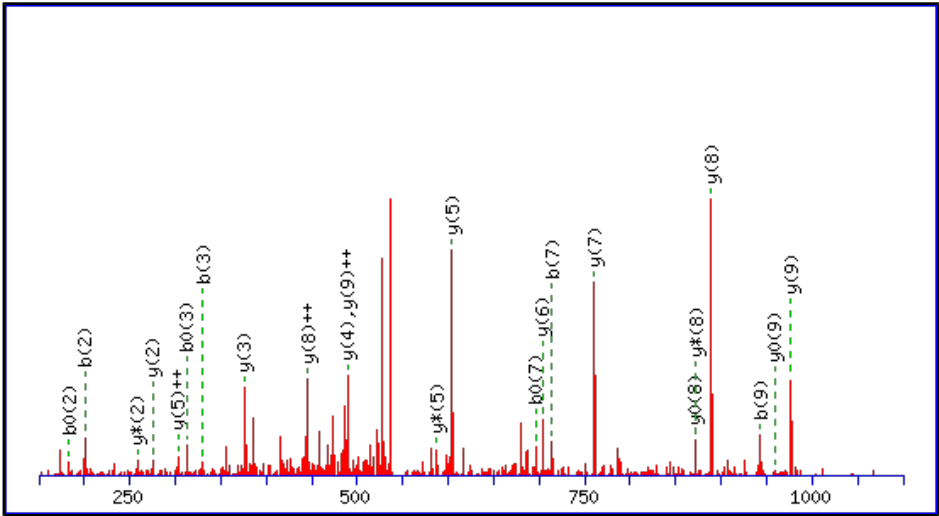
W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

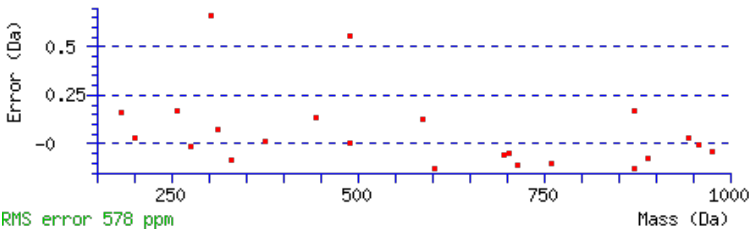
Label all possible matches Label matches used for scoring

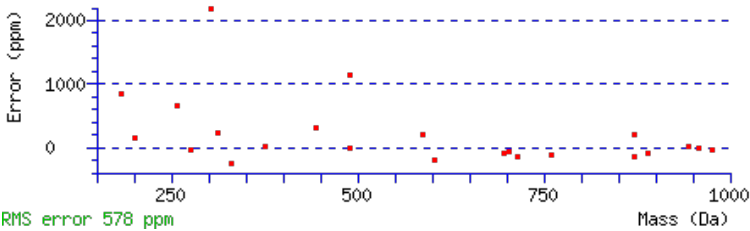
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1088.5713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 54 **Expect:** 0.0003
Matches : 23/92 fragment ions using 46 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							10
2	201.1234	101.0653			183.1128	92.0600	S	976.4946	488.7509	959.4680	480.2376	958.4840	479.7456	9
3	330.1660	165.5866			312.1554	156.5813	E	889.4625	445.2349	872.4360	436.7216	871.4520	436.2296	8
4	387.1874	194.0974			369.1769	185.0921	G	760.4199	380.7136	743.3934	372.2003	742.4094	371.7083	7
5	486.2558	243.6316			468.2453	234.6263	V	703.3985	352.2029	686.3719	343.6896	685.3879	343.1976	6
6	601.2828	301.1450	584.2562	292.6318	583.2722	292.1397	N	604.3301	302.6687	587.3035	294.1554	586.3195	293.6634	5
7	714.3668	357.6871	697.3403	349.1738	696.3563	348.6818	L	489.3031	245.1552	472.2766	236.6419	471.2926	236.1499	4
8	815.4145	408.2109	798.3880	399.6976	797.4040	399.2056	T	376.2191	188.6132	359.1925	180.0999	358.2085	179.6079	3
9	943.4731	472.2402	926.4466	463.7269	925.4625	463.2349	Q	275.1714	138.0893	258.1448	129.5761			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of [ISEGVNLTQK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
54.0	1088.5713	-0.0015	ISEGVNLTQK	Deamidated N6 99.21%
33.0	1088.5713	-0.0015	ISEGVNLTQK	Deamidated Q9 0.79%
11.2	1088.5713	-0.0015	SIGTGGIQDLK	
8.1	1086.5669	2.0029	QAEDQVLRK	
6.0	1088.5713	-0.0015	EAEKNIEKK	
2.9	1088.5713	-0.0015	EQIKTLNDK	
2.9	1088.5713	-0.0015	EQIKTLNNK	
2.8	1086.5570	2.0128	LDVRDAWGR	
2.4	1088.5713	-0.0015	SSQIDQAIVK	
2.1	1087.5621	1.0077	QAQKASEAQK	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1RN76** in **uni_pig**, tr|F1RN76|F1RN76_PIG Uncharacterized protein OS=Sus scrofa GN=CD5L PE=4 SV=2

Title: 120325_Sunil_PigSerum_Glyco_P_13Spectrum4003_scans_4768

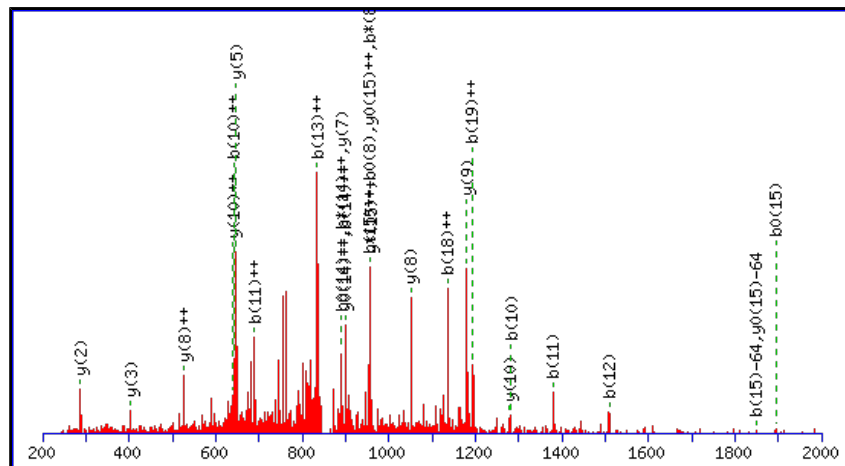
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

N1 : Deamidated (NQ)

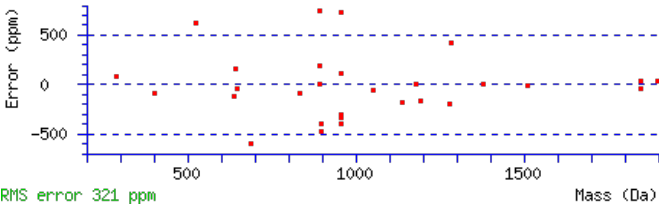
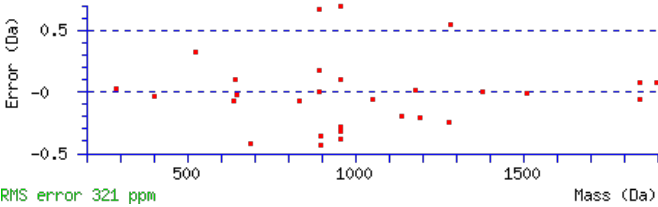
N2 : Deamidated (NQ)

M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 35 Expect: 0.00033

Matches : 29/332 fragment ions using 36 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							20
2	231.0612	116.0342	214.0346	107.5209			N	2444.8734	1222.9403	2427.8468	1214.4271	2426.8628	1213.9351	19
3	391.0918	196.0495	374.0653	187.5363			C	2329.8464	1165.4269	2312.8199	1156.9136	2311.8359	1156.4216	18
4	492.1395	246.5734	475.1129	238.0601	474.1289	237.5681	T	2169.8158	1085.4115	2152.7892	1076.8983	2151.8052	1076.4063	17
5	629.1984	315.1028	612.1719	306.5896	611.1878	306.0976	H	2068.7681	1034.8877	2051.7416	1026.3744	2050.7576	1025.8824	16
6	744.2253	372.6163	727.1988	364.1030	726.2148	363.6110	D	1931.7092	966.3582	1914.6827	957.8450	1913.6986	957.3530	15
7	859.2523	430.1298	842.2257	421.6165	841.2417	421.1245	D	1816.6823	908.8448	1799.6557	900.3315	1798.6717	899.8395	14
8	974.2792	487.6433	957.2527	479.1300	956.2687	478.6380	D	1701.6553	851.3313	1684.6288	842.8180	1683.6448	842.3260	13
9	1121.3146	561.1610	1104.2881	552.6477	1103.3041	552.1557	M	1586.6284	793.8178	1569.6018	785.3046	1568.6178	784.8125	12
10	1281.3453	641.1763	1264.3187	632.6630	1263.3347	632.1710	C	1439.5930	720.3001	1422.5664	711.7869	1421.5824	711.2948	11
11	1380.4137	690.7105	1363.3871	682.1972	1362.4031	681.7052	V	1279.5623	640.2848	1262.5358	631.7715	1261.5518	631.2795	10
12	1509.4563	755.2318	1492.4297	746.7185	1491.4457	746.2265	E	1180.4939	590.7506	1163.4674	582.2373	1162.4834	581.7453	9
13	1669.4869	835.2471	1652.4604	826.7338	1651.4764	826.2418	C	1051.4513	526.2293	1034.4248	517.7160	1033.4408	517.2240	8
14	1798.5295	899.7684	1781.5030	891.2551	1780.5190	890.7631	E	891.4207	446.2140	874.3941	437.7007	873.4101	437.2087	7
15	1913.5565	957.2819	1896.5299	948.7686	1895.5459	948.2766	D	762.3781	381.6927	745.3515	373.1794	744.3675	372.6874	6
16	2010.6092	1005.8083	1993.5827	997.2950	1992.5987	996.8030	P	647.3511	324.1792	630.3246	315.6659	629.3406	315.1739	5
17	2157.6777	1079.3425	2140.6511	1070.8292	2139.6671	1070.3372	F	550.2984	275.6528	533.2718	267.1396	532.2878	266.6475	4
18	2272.7046	1136.8559	2255.6780	1128.3427	2254.6940	1127.8507	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
19	2385.7887	1193.3980	2368.7621	1184.8847	2367.7781	1184.3927	L	288.2030	144.6051	271.1765	136.0919			2
20							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [NNCTHDDDMCVECEDPFDLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
34.8	2558.8931	1.0144	NNCTHDDDMCVECEDPFDLR	
34.8	2557.9091	1.9984	NNCTHDDDMCVECEDPFDLR	Deamidated N2 50.00%
34.8	2557.9091	1.9984	NNCTHDDDMCVECEDPFDLR	Deamidated N1 50.00%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTQGICLERNETSGCEK**

Found in **F1SF32** in **uni_pig**, tr|F1SF32|F1SF32_PIG Uncharacterized protein OS=Sus scrofa GN=CD34 PE=4 SV=1

Match to Query 10709: 1994.911968 from(998.463260,2+) intensity(0.0000) rtinseconds(1289) scans(2915) index(1466)

Title: 120325 Sunil PigSerum Glyco D 14Spectrum2442 scans 2915

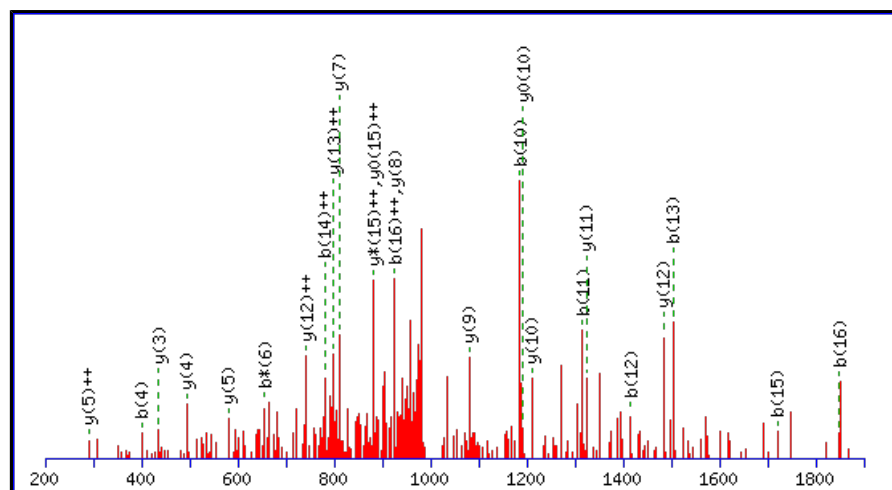
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1994.9037

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

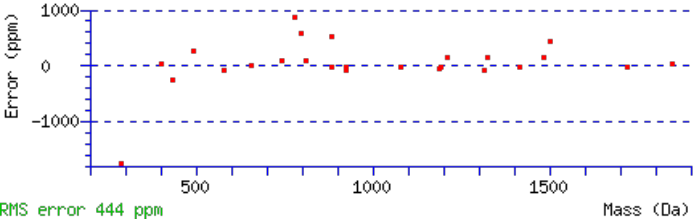
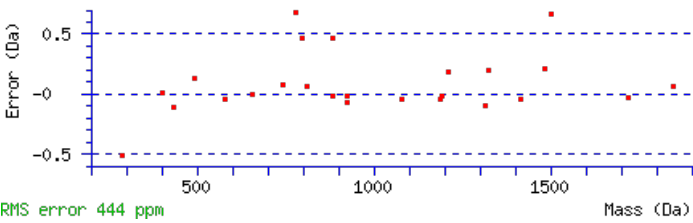
Variable modifications:

N10 : Deamidated (NQ)

Ions Score: 52 Expect: 0.00034

Matches : 25/184 fragment ions using 48 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							17
2	215.1390	108.0731			197.1285	99.0679	T	1882.8270	941.9171	1865.8004	933.4038	1864.8164	932.9118	16
3	343.1976	172.1024	326.1710	163.5892	325.1870	163.0972	Q	1781.7793	891.3933	1764.7527	882.8800	1763.7687	882.3880	15
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	G	1653.7207	827.3640	1636.6941	818.8507	1635.7101	818.3587	14
5	513.3031	257.1552	496.2766	248.6419	495.2926	248.1499	I	1596.6992	798.8533	1579.6727	790.3400	1578.6887	789.8480	13
6	673.3338	337.1705	656.3072	328.6573	655.3232	328.1652	C	1483.6152	742.3112	1466.5886	733.7979	1465.6046	733.3059	12
7	786.4178	393.7126	769.3913	385.1993	768.4073	384.7073	L	1323.5845	662.2959	1306.5580	653.7826	1305.5740	653.2906	11
8	915.4604	458.2339	898.4339	449.7206	897.4499	449.2286	E	1210.5005	605.7539	1193.4739	597.2406	1192.4899	596.7486	10
9	1071.5615	536.2844	1054.5350	527.7711	1053.5510	527.2791	R	1081.4579	541.2326	1064.4313	532.7193	1063.4473	532.2273	9
10	1186.5885	593.7979	1169.5619	585.2846	1168.5779	584.7926	N	925.3568	463.1820	908.3302	454.6687	907.3462	454.1767	8
11	1315.6311	658.3192	1298.6045	649.8059	1297.6205	649.3139	E	810.3298	405.6685	793.3033	397.1553	792.3192	396.6633	7
12	1416.6788	708.8430	1399.6522	700.3297	1398.6682	699.8377	T	681.2872	341.1472	664.2607	332.6340	663.2767	332.1420	6
13	1503.7108	752.3590	1486.6842	743.8458	1485.7002	743.3537	S	580.2395	290.6234	563.2130	282.1101	562.2290	281.6181	5
14	1560.7322	780.8698	1543.7057	772.3565	1542.7217	771.8645	G	493.2075	247.1074	476.1810	238.5941	475.1969	238.1021	4
15	1720.7629	860.8851	1703.7363	852.3718	1702.7523	851.8798	C	436.1860	218.5967	419.1595	210.0834	418.1755	209.5914	3
16	1849.8055	925.4064	1832.7789	916.8931	1831.7949	916.4011	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [LTQGICLERNETSGCEK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.8	1994.9037	0.0083	LTQGICLERNETSGCEK	Deamidated N10 99.99%
11.5	1994.9037	0.0083	LTQGICLERNETSGCEK	Deamidated Q3 0.01%
2.6	1994.9288	-0.0169	QQQLLSVQEEMRTMQK	
2.0	1994.9288	-0.0169	QQQLLSVQEEMRTMQK	
1.9	1994.9102	0.0017	QGSNSIIPNSISDTMNSTK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

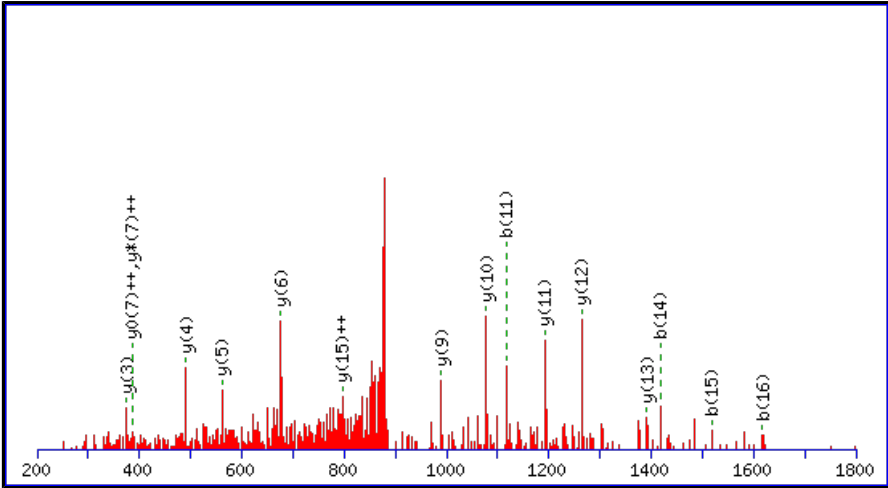
Peptide View

MS/MS Fragmentation of **SLEAQNSSNLDADTVR**
Found in **F1SIW0** in **uni_pig**, tr|F1SIW0|F1SIW0_PIG Uncharacterized protein OS=Sus scrofa GN=STAB1 PE=4 SV=1

Match to Query 6586: 1791.826768 from(896.920660,2+) intensity(4041.7813) rtinseconds(1498) scans(2517) index(10876)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_15Spectrum1735_scans__2517
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

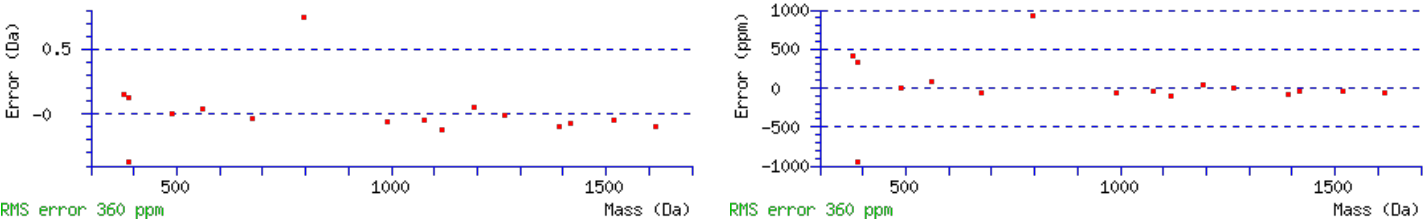
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1790.8282
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 52 Expect: 0.00035
Matches : 16/180 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							17
2	201.1234	101.0653			183.1128	92.0600	L	1704.8035	852.9054	1687.7769	844.3921	1686.7929	843.9001	16
3	330.1660	165.5866			312.1554	156.5813	E	1591.7194	796.3634	1574.6929	787.8501	1573.7089	787.3581	15
4	401.2031	201.1052			383.1925	192.0999	A	1462.6768	731.8421	1445.6503	723.3288	1444.6663	722.8368	14
5	529.2617	265.1345	512.2351	256.6212	511.2511	256.1292	Q	1391.6397	696.3235	1374.6132	687.8102	1373.6292	687.3182	13
6	600.2988	300.6530	583.2722	292.1397	582.2882	291.6477	A	1263.5811	632.2942	1246.5546	623.7809	1245.5706	623.2889	12
7	715.3257	358.1665	698.2992	349.6532	697.3151	349.1612	N	1192.5440	596.7757	1175.5175	588.2624	1174.5335	587.7704	11
8	802.3577	401.6825	785.3312	393.1692	784.3472	392.6772	S	1077.5171	539.2622	1060.4905	530.7489	1059.5065	530.2569	10
9	889.3898	445.1985	872.3632	436.6852	871.3792	436.1932	S	990.4851	495.7462	973.4585	487.2329	972.4745	486.7409	9
10	1003.4327	502.2200	986.4061	493.7067	985.4221	493.2147	N	903.4530	452.2302	886.4265	443.7169	885.4425	443.2249	8
11	1116.5168	558.7620	1099.4902	550.2487	1098.5062	549.7567	L	789.4101	395.2087	772.3836	386.6954	771.3995	386.2034	7
12	1231.5437	616.2755	1214.5172	607.7622	1213.5331	607.2702	D	676.3260	338.6667	659.2995	330.1534	658.3155	329.6614	6
13	1302.5808	651.7940	1285.5543	643.2808	1284.5702	642.7888	A	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	5
14	1417.6078	709.3075	1400.5812	700.7942	1399.5972	700.3022	D	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
15	1518.6554	759.8314	1501.6289	751.3181	1500.6449	750.8261	T	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
16	1617.7239	809.3656	1600.6973	800.8523	1599.7133	800.3603	V	274.1874	137.5973	257.1608	129.0840			2
17							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [SLEAQANSSNLDADTVR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.9	1790.8282	0.9986	SLEAQANSSNLDADTVR	Deamidated N7 86.69%
47.1	1791.8122	0.0145	SLEAQANSSNLDADTVR	
42.3	1790.8282	0.9986	SLEAQANSSNLDADTVR	Deamidated N10 9.50%
38.3	1790.8282	0.9986	SLEAQANSSNLDADTVR	Deamidated Q5 3.81%
23.0	1791.8122	0.0145	SLEAQANSSNLDADTVR	
21.9	1791.8122	0.0145	SLEAQANSSNLDADTVR	
8.2	1791.8131	0.0137	NSMDIQCEVDALLER	
4.2	1790.8217	1.0051	TNLAQMTDANGNIQQR	
3.1	1791.8210	0.0058	MRDSQEWALAETEAR	
2.6	1791.8315	-0.0048	FGDPLGYEDVIPEADR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSNTTGTALEGDQR**

Found in **I3LC14** in **uni_pig**, tr|I3LC14|I3LC14_PIG Uncharacterized protein OS=Sus scrofa GN=ADAMTSL2 PE=4 SV=1

Match to Query 4063: 1465.631148 from(733.822850,2+) intensity(1021.2267) rtinseconds(941) scans(1266) index(4485)

Title: 120325_Sunil_PigSerum_Glyco_P_18Spectrum748_scans__1266

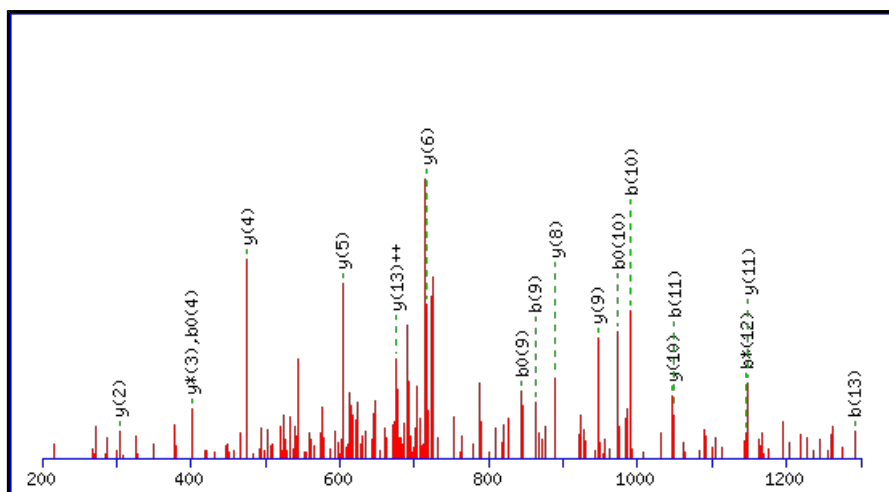
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1464.6328

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

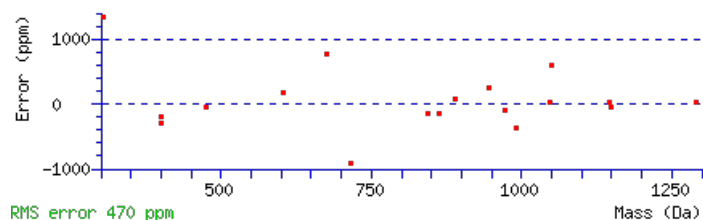
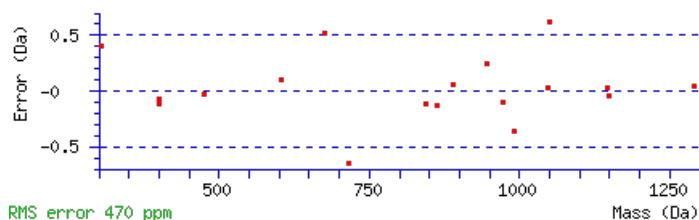
Variable modifications:

N3 : Deamidated (NQ)

Ions Score: 48 Expect: 0.00036

Matches : 18/148 fragment ions using 33 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							14
2	203.0662	102.0368			185.0557	93.0315	S	1350.6132	675.8102	1333.5866	667.2970	1332.6026	666.8049	13
3	318.0932	159.5502	301.0666	151.0370	300.0826	150.5450	N	1263.5812	632.2942	1246.5546	623.7809	1245.5706	623.2889	12
4	419.1409	210.0741	402.1143	201.5608	401.1303	201.0688	T	1148.5542	574.7807	1131.5277	566.2675	1130.5436	565.7755	11
5	520.1885	260.5979	503.1620	252.0846	502.1780	251.5926	T	1047.5065	524.2569	1030.4800	515.7436	1029.4960	515.2516	10
6	577.2100	289.1086	560.1835	280.5954	559.1994	280.1034	G	946.4589	473.7331	929.4323	465.2198	928.4483	464.7278	9
7	678.2577	339.6325	661.2311	331.1192	660.2471	330.6272	T	889.4374	445.2223	872.4108	436.7091	871.4268	436.2170	8
8	749.2948	375.1510	732.2683	366.6378	731.2842	366.1458	A	788.3897	394.6985	771.3632	386.1852	770.3791	385.6932	7
9	862.3789	431.6931	845.3523	423.1798	844.3683	422.6878	L	717.3526	359.1799	700.3260	350.6667	699.3420	350.1747	6
10	991.4215	496.2144	974.3949	487.7011	973.4109	487.2091	E	604.2685	302.6379	587.2420	294.1246	586.2580	293.6326	5
11	1048.4429	524.7251	1031.4164	516.2118	1030.4324	515.7198	G	475.2259	238.1166	458.1994	229.6033	457.2154	229.1113	4
12	1163.4699	582.2386	1146.4433	573.7253	1145.4593	573.2333	D	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
13	1291.5284	646.2679	1274.5019	637.7546	1273.5179	637.2626	Q	303.1775	152.0924	286.1510	143.5791			2
14							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [DSNTTGTALEGDQR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.5	1464.6328	0.9983	DSNTTGTALEGDQR	Deamidated N3 99.74%
21.6	1464.6328	0.9983	DSNTTGTALEGDQR	Deamidated Q13 0.26%
19.4	1465.6169	0.0143	DSNTTGTALEGDQR	
8.3	1464.6402	0.9910	AVVMNNKEEEER	
6.3	1464.6191	1.0120	DWDQVAGGCVTEK	
5.1	1464.6402	0.9910	SKMQEQQADLQR	
4.3	1464.6402	0.9910	MEEEQTSETKPR	
2.5	1464.6263	1.0049	MRDAGNDSASTAPR	
1.5	1464.6328	0.9983	SDDVASQSNKDNGK	
1.1	1464.6416	0.9896	YGPQMDGNGDRVR	

Mascot: <http://www.matrixscience.com/>

MATRIX
SCIENCE

Mascot Search Results

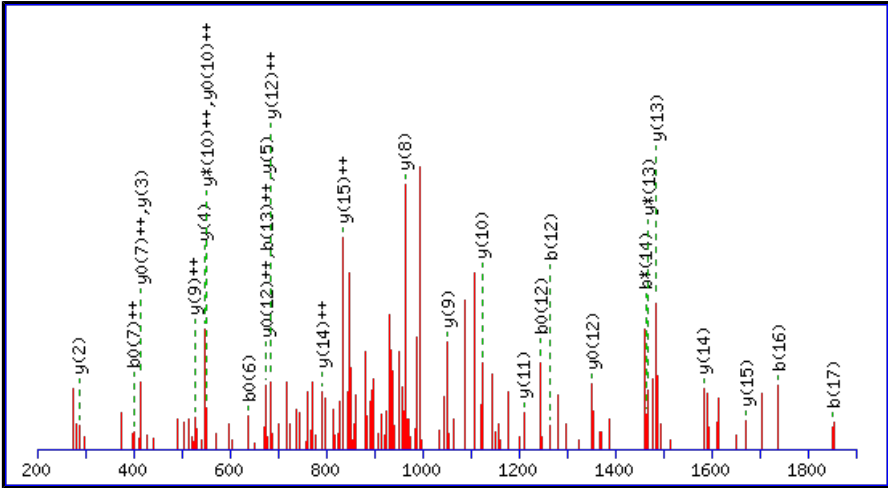
Peptide View

MS/MS Fragmentation of **EILSVDCSASNSSQMQLR**
Found in **F1RJS2** in **uni_pig**, tr|F1RJS2|F1RJS2_PIG Clusterin OS=Sus scrofa GN=CLU PE=3 SV=2

Match to Query 10957: 2026.910188 from(1014.462370,2+) intensity(2495.9228) rtinseconds(2005) scans(3214) index(853)
Title: 120325_Sunil_PigSerum_Glyco_D_09Spectrum2130_scans__3214
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

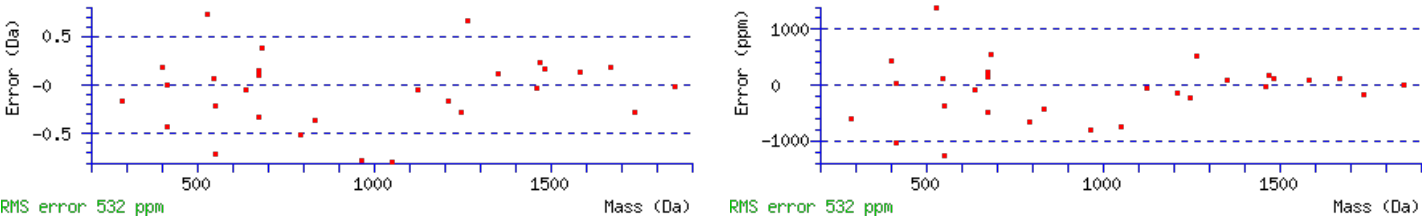
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2025.8983
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Q14 : Deamidated (NQ)
Ions Score: 50 Expect: 0.00039
Matches : 29/174 fragment ions using 60 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							18
2	243.1339	122.0706			225.1234	113.0653	I	1897.8630	949.4351	1880.8365	940.9219	1879.8524	940.4299	17
3	356.2180	178.6126			338.2074	169.6074	L	1784.7789	892.8931	1767.7524	884.3798	1766.7684	883.8878	16
4	443.2500	222.1287			425.2395	213.1234	S	1671.6949	836.3511	1654.6683	827.8378	1653.6843	827.3458	15
5	542.3184	271.6629			524.3079	262.6576	V	1584.6628	792.8351	1567.6363	784.3218	1566.6523	783.8298	14
6	657.3454	329.1763			639.3348	320.1710	D	1485.5944	743.3009	1468.5679	734.7876	1467.5839	734.2956	13
7	817.3760	409.1917			799.3655	400.1864	C	1370.5675	685.7874	1353.5409	677.2741	1352.5569	676.7821	12
8	904.4081	452.7077			886.3975	443.7024	S	1210.5368	605.7721	1193.5103	597.2588	1192.5263	596.7668	11
9	975.4452	488.2262			957.4346	479.2209	A	1123.5048	562.2560	1106.4783	553.7428	1105.4942	553.2508	10
10	1062.4772	531.7422			1044.4666	522.7370	S	1052.4677	526.7375	1035.4412	518.2242	1034.4571	517.7322	9
11	1177.5041	589.2557	1160.4776	580.7424	1159.4936	580.2504	N	965.4357	483.2215	948.4091	474.7082	947.4251	474.2162	8
12	1264.5362	632.7717	1247.5096	624.2584	1246.5256	623.7664	S	850.4087	425.7080	833.3822	417.1947	832.3982	416.7027	7
13	1351.5682	676.2877	1334.5417	667.7745	1333.5576	667.2825	S	763.3767	382.1920	746.3502	373.6787	745.3661	373.1867	6
14	1480.6108	740.8090	1463.5842	732.2958	1462.6002	731.8038	Q	676.3447	338.6760	659.3181	330.1627			5
15	1611.6513	806.3293	1594.6247	797.8160	1593.6407	797.3240	M	547.3021	274.1547	530.2755	265.6414			4
16	1739.7099	870.3586	1722.6833	861.8453	1721.6993	861.3533	Q	416.2616	208.6344	399.2350	200.1212			3
17	1852.7939	926.9006	1835.7674	918.3873	1834.7834	917.8953	L	288.2030	144.6051	271.1765	136.0919			2
18							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [EILSVDCSASNSSQMQLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.8	2025.8983	1.0119	EILSVDCSASNSSQMQLR	Deamidated N11, Q14 93.64%
37.8	2024.9143	1.9959	EILSVDCSASNSSQMQLR	
35.2	2025.8983	1.0119	EILSVDCSASNSSQMQLR	Deamidated Q14, Q16 3.22%
35.1	2025.8983	1.0119	EILSVDCSASNSSQMQLR	Deamidated N11, Q16 3.14%
16.9	2024.9143	1.9959	EILSVDCSASNSSQMQLR	
6.2	2026.9167	-0.0065	EACEGQHKLEWDLQQR	
4.4	2024.9143	1.9959	EILSVDCSASNSSQMQLR	
2.6	2024.8956	2.0146	RAMSLVSSDSEGEQNELR	
0.7	2026.9241	-0.0139	VWCTTNEGEPMRIVYR	
0.2	2026.9266	-0.0164	ALDGQKVQSMGIFSDGNSR	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1S3Q8** in **uni_pig**, tr|F1S3Q8|F1S3Q8_PIG Uncharacterized protein OS=Sus scrofa GN=VNN3 PE=4 SV=2

Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum333_scans_452

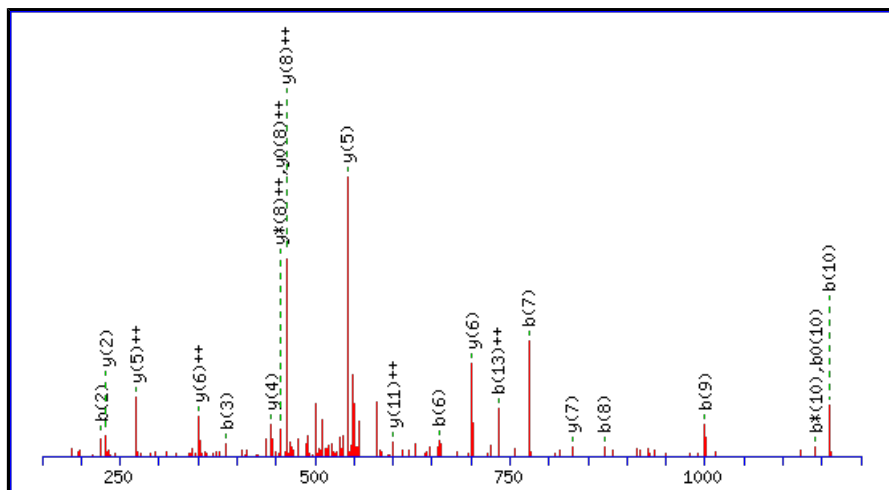
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

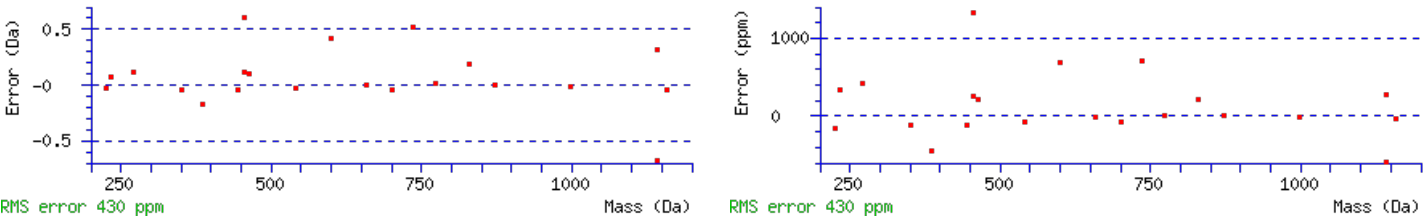
Variable modifications:

N4 : Deamidated (NQ)

Ions Score: 45 Expect: 0.0004

Matches : 21/154 fragment ions using 30 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							15
2	226.1550	113.5811	209.1285	105.0679			P	1571.6213	786.3143	1554.5948	777.8010	1553.6108	777.3090	14
3	386.1857	193.5965	369.1591	185.0832			C	1474.5686	737.7879	1457.5420	729.2746	1456.5580	728.7826	13
4	501.2126	251.1099	484.1860	242.5967			N	1314.5379	657.7726	1297.5114	649.2593	1296.5273	648.7673	12
5	572.2497	286.6285	555.2232	278.1152			A	1199.5110	600.2591	1182.4844	591.7458	1181.5004	591.2538	11
6	659.2817	330.1445	642.2552	321.6312	641.2712	321.1392	S	1128.4738	564.7406	1111.4473	556.2273	1110.4633	555.7353	10
7	774.3087	387.6580	757.2821	379.1447	756.2981	378.6527	D	1041.4418	521.2245	1024.4153	512.7113	1023.4313	512.2193	9
8	871.3614	436.1844	854.3349	427.6711	853.3509	427.1791	P	926.4149	463.7111	909.3883	455.1978	908.4043	454.7058	8
9	999.4200	500.2136	982.3935	491.7004	981.4095	491.2084	Q	829.3621	415.1847	812.3356	406.6714	811.3515	406.1794	7
10	1159.4507	580.2290	1142.4241	571.7157	1141.4401	571.2237	C	701.3035	351.1554	684.2770	342.6421	683.2930	342.1501	6
11	1256.5034	628.7554	1239.4769	620.2421	1238.4929	619.7501	P	541.2729	271.1401	524.2463	262.6268	523.2623	262.1348	5
12	1353.5562	677.2817	1336.5297	668.7685	1335.5456	668.2765	P	444.2201	222.6137	427.1936	214.1004	426.2096	213.6084	4
13	1468.5831	734.7952	1451.5566	726.2819	1450.5726	725.7899	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
14	1525.6046	763.3059	1508.5781	754.7927	1507.5940	754.3007	G	232.1404	116.5738	215.1139	108.0606			2
15							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [KPCNASDPQCPPDGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.0	1698.7090	-0.0026	KPCNASDPQCPPDGR	Deamidated N4 98.04%
28.0	1698.7090	-0.0026	KPCNASDPQCPPDGR	Deamidated Q9 1.96%
1.2	1697.7025	1.0039	MQHEKEQFEDSMK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of FGNWSAQPSCK

Found in **A0A096P6N1** in **uni_pig**, tr|A0A096P6N1|A0A096P6N1_PIG Uncharacterized protein OS=Sus scrofa GN=LOC100522100 PE=4 SV=1

Match to Query 2434: 1282.527428 from(642.270990,2+) intensity(6953.1650) rtinseconds(1682) scans(2577) index(5472)

Title: 120325 Sunil PigSerum Glyco S 09Spectrum1690 scans 2577

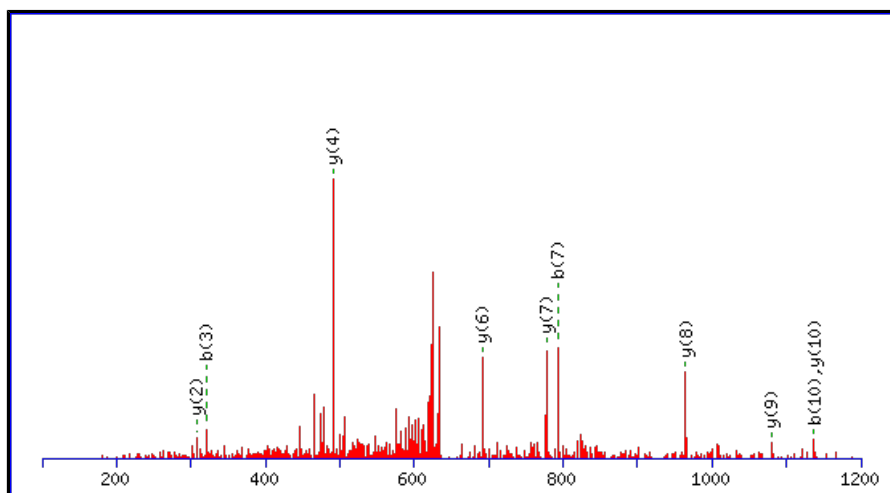
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1282.5288

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

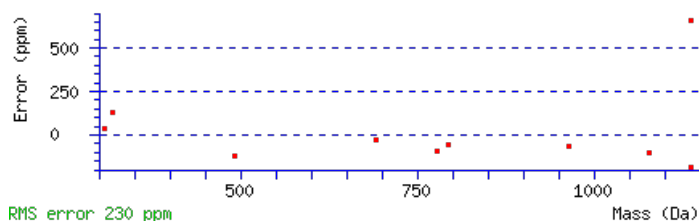
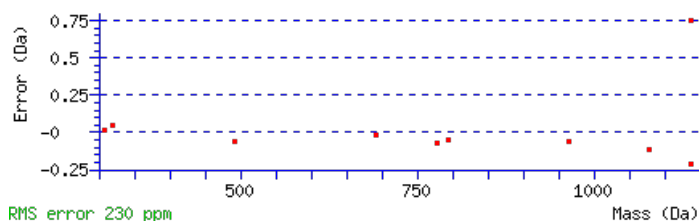
N3 : Deamidated (NQ)

Q7 : Deamidated (NQ)

Ions Score: 45 Expect: 0.00041

Matches : 10/104 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							11
2	205.0972	103.0522					G	1136.4677	568.7375	1119.4412	560.2242	1118.4571	559.7322	10
3	320.1241	160.5657	303.0975	152.0524			N	1079.4462	540.2268	1062.4197	531.7135	1061.4357	531.2215	9
4	506.2034	253.6053	489.1769	245.0921			W	964.4193	482.7133	947.3927	474.2000	946.4087	473.7080	8
5	593.2354	297.1214	576.2089	288.6081	575.2249	288.1161	S	778.3400	389.6736	761.3134	381.1604	760.3294	380.6683	7
6	664.2726	332.6399	647.2460	324.1266	646.2620	323.6346	A	691.3080	346.1576	674.2814	337.6443	673.2974	337.1523	6
7	793.3151	397.1612	776.2886	388.6479	775.3046	388.1559	Q	620.2708	310.6391	603.2443	302.1258	602.2603	301.6338	5
8	890.3679	445.6876	873.3414	437.1743	872.3573	436.6823	P	491.2282	246.1178	474.2017	237.6045	473.2177	237.1125	4
9	977.3999	489.2036	960.3734	480.6903	959.3894	480.1983	S	394.1755	197.5914	377.1489	189.0781	376.1649	188.5861	3
10	1137.4306	569.2189	1120.4040	560.7057	1119.4200	560.2136	C	307.1435	154.0754	290.1169	145.5621			2
11							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [EGNWSAQPSCK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.6	1282.5288	-0.0014	EGNWSAQPSCK
7.1	1282.5313	-0.0039	EFSNSNNLDNK
7.1	1282.5313	-0.0039	EFSNSNNLDNK
5.1	1282.5313	-0.0039	FENADLNDTSR
4.2	1282.5201	0.0073	YDDDISPSEDK
3.8	1280.5092	2.0182	CRGPDGFDDDK
3.7	1281.5361	0.9914	NFSDNQLQEGK
3.7	1281.5361	0.9914	NFSDNQLQEGK
3.7	1281.5361	0.9914	NFSDNQLQEGK
2.8	1281.5361	0.9914	NFSDNQLQEGK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

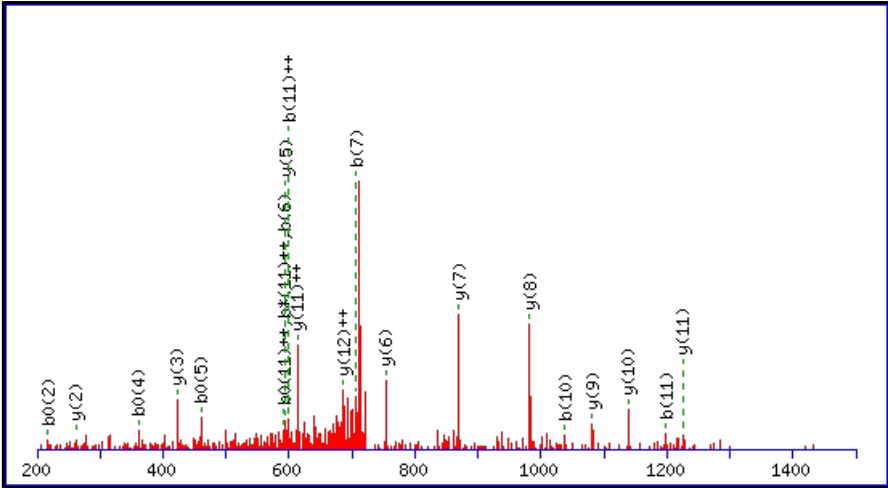
Peptide View

MS/MS Fragmentation of **SFSGVLDCGNCSR**
Found in **O77773** in **uni_pig**, tr|O77773|O77773_PIG Uncharacterized protein OS=Sus scrofa GN=CACNA2D1 PE=2 SV=1

Match to Query 4028: 1458.581728 from(730.298140,2+) intensity(1643.2797) rtinseconds(1619) scans(3469) index(5965)
Title: 120325_Sunil_PigSerum_Glyco_S_12Spectrum2757_scans__3469
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

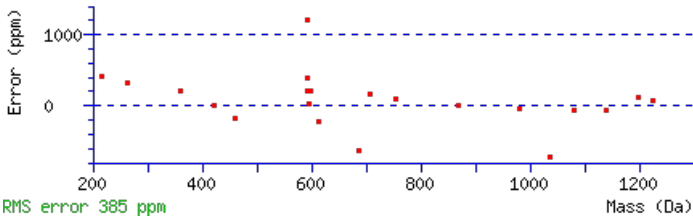
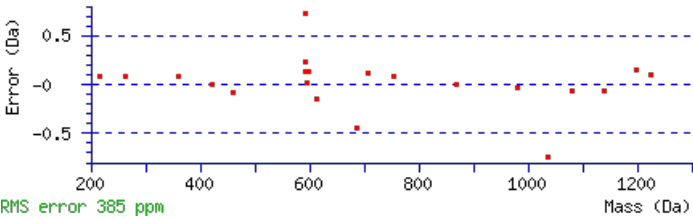
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1458.5868
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 41 Expect: 0.00043
Matches : 21/124 fragment ions using 46 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	235.1077	118.0575			217.0972	109.0522	F	1372.5620	686.7846	1355.5355	678.2714	1354.5514	677.7794	12
3	322.1397	161.5735			304.1292	152.5682	S	1225.4936	613.2504	1208.4670	604.7372	1207.4830	604.2452	11
4	379.1612	190.0842			361.1506	181.0790	G	1138.4616	569.7344	1121.4350	561.2211	1120.4510	560.7291	10
5	478.2296	239.6185			460.2191	230.6132	V	1081.4401	541.2237	1064.4136	532.7104	1063.4295	532.2184	9
6	591.3137	296.1605			573.3031	287.1552	L	982.3717	491.6895	965.3451	483.1762	964.3611	482.6842	8
7	706.3406	353.6740			688.3301	344.6687	D	869.2876	435.1475	852.2611	426.6342	851.2771	426.1422	7
8	866.3713	433.6893			848.3607	424.6840	C	754.2607	377.6340	737.2341	369.1207	736.2501	368.6287	6
9	923.3927	462.2000			905.3822	453.1947	G	594.2300	297.6187	577.2035	289.1054	576.2195	288.6134	5
10	1038.4197	519.7135	1021.3931	511.2002	1020.4091	510.7082	N	537.2086	269.1079	520.1820	260.5946	519.1980	260.1026	4
11	1198.4503	599.7288	1181.4238	591.2155	1180.4398	590.7235	C	422.1816	211.5945	405.1551	203.0812	404.1711	202.5892	3
12	1285.4824	643.2448	1268.4558	634.7315	1267.4718	634.2395	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [SFSGVLDCGNCSR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.4	1458.5868	-0.0050	SFSGVLDCGNCSR
3.3	1458.5874	-0.0057	NFCWPYEAESR
1.5	1456.5711	2.0106	DPFSAAASECSCR

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **I3LF89** in **uni_pig**, tr|I3LF89|I3LF89_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=CPN2 PE=4 SV=1

Title: 120325_Sunil_PigSerum_Glyco_P_14Spectrum1986_scans__2537

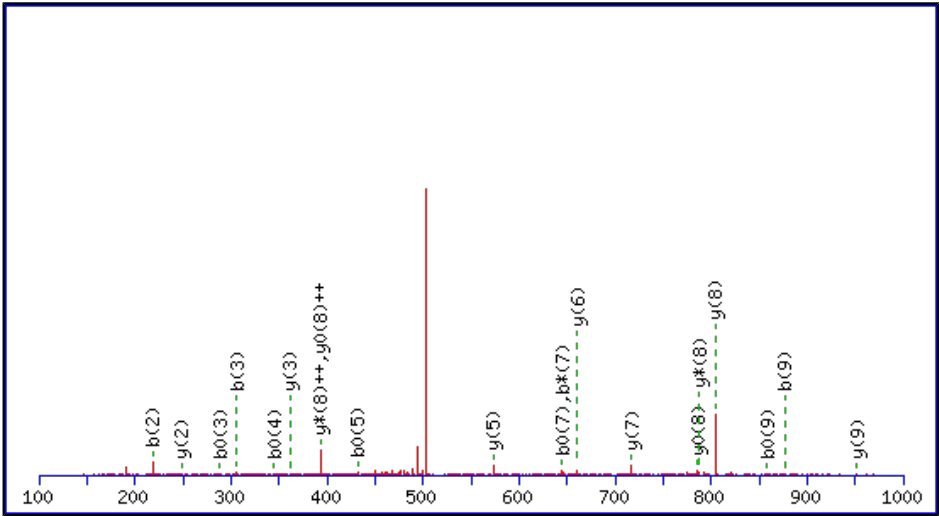
W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

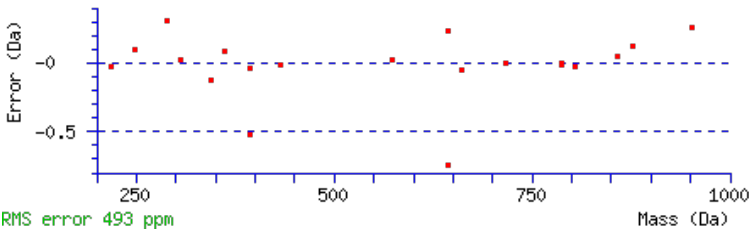
Label all possible matches Label matches used for scoring

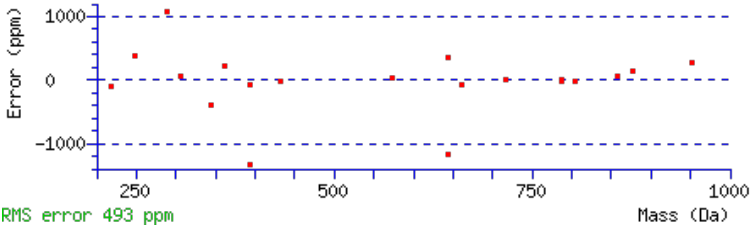
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1021.5080
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
 N7 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.00046
Matches : 20/90 fragment ions using 35 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							10
2	219.1128	110.0600					F	951.4782	476.2427	934.4516	467.7295	933.4676	467.2374	9
3	306.1448	153.5761			288.1343	144.5708	S	804.4098	402.7085	787.3832	394.1953	786.3992	393.7032	8
4	363.1663	182.0868			345.1557	173.0815	G	717.3777	359.1925	700.3512	350.6792	699.3672	350.1872	7
5	450.1983	225.6028			432.1878	216.5975	S	660.3563	330.6818	643.3297	322.1685	642.3457	321.6765	6
6	547.2511	274.1292			529.2405	265.1239	P	573.3243	287.1658	556.2977	278.6525	555.3137	278.1605	5
7	662.2780	331.6427	645.2515	323.1294	644.2675	322.6374	N	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
8	775.3621	388.1847	758.3355	379.6714	757.3515	379.1794	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
9	876.4098	438.7085	859.3832	430.1953	858.3992	429.7032	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of [AFSGSPNLTK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.8	1021.5080	-0.0018	AFSGSPNLTK
22.2	1021.5114	-0.0052	MANTVIQTK
21.2	1021.5015	0.0047	AMSNKWIR
18.4	1021.5114	-0.0052	MANTVIQTK
16.8	1020.5087	0.9975	SALTQSQSAK
15.4	1021.5080	-0.0018	AFLEETNAK
14.8	1020.5022	1.0040	GCSLTKAQR
14.7	1021.5114	-0.0051	ASMEEKLAK
14.7	1021.4975	0.0088	MASVQASRR
13.8	1021.4975	0.0087	MASTGVERR

Mascot: <http://www.matrixscience.com/>

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Mascot Search Results

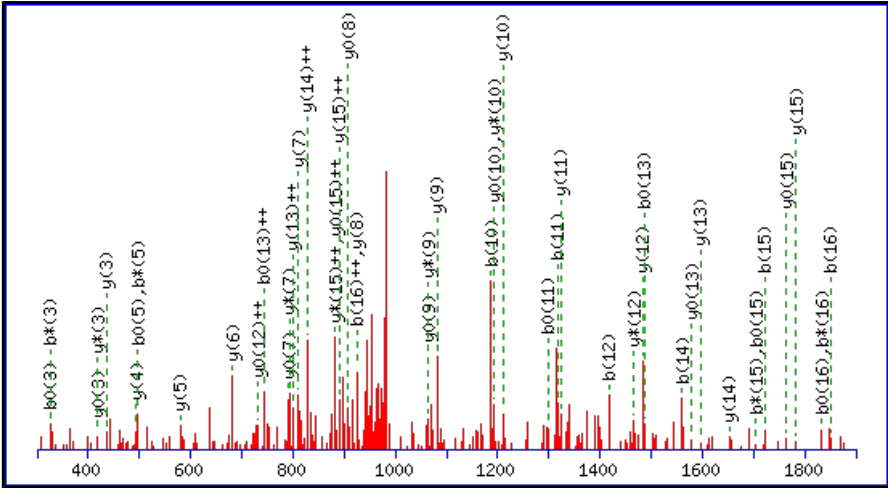
Peptide View

MS/MS Fragmentation of **LTQGICLERNETSGCEK**
Found in **F1SF32** in **uni_pig**, tr[F1SF32]F1SF32_PIG Uncharacterized protein OS=Sus scrofa GN=CD34 PE=4 SV=1

Match to Query 10727: 1995.897228 from(998.955890,2+) intensity(2936.8223) rtinseconds(1286) scans(2907) index(1465)
Title: 120325_Sunil_PigSerum_Glyco_D_14Spectrum2436_scans__2907
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

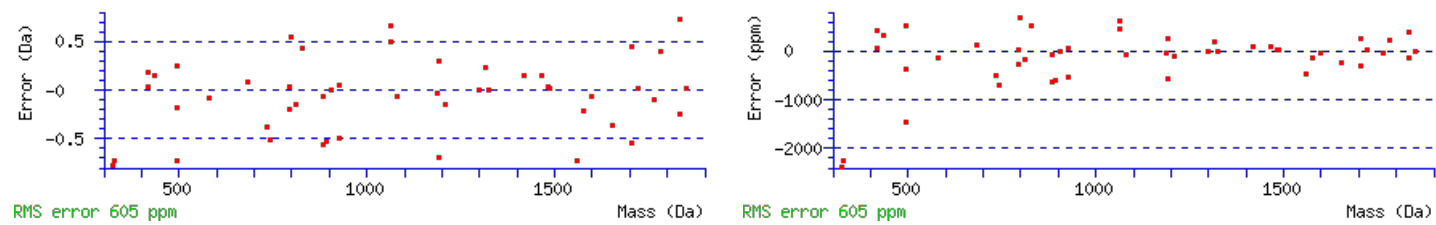
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1995.8877
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N10 : Deamidated (NQ)
Ions Score: 50 Expect: 0.00047
Matches : 49/184 fragment ions using 125 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							17
2	215.1390	108.0731			197.1285	99.0679	T	1883.8110	942.4091	1866.7844	933.8958	1865.8004	933.4038	16
3	344.1816	172.5944	327.1551	164.0812	326.1710	163.5892	Q	1782.7633	891.8853	1765.7367	883.3720	1764.7527	882.8800	15
4	401.2031	201.1052	384.1765	192.5919	383.1925	192.0999	G	1653.7207	827.3640	1636.6941	818.8507	1635.7101	818.3587	14
5	514.2871	257.6472	497.2606	249.1339	496.2766	248.6419	I	1596.6992	798.8533	1579.6727	790.3400	1578.6887	789.8480	13
6	674.3178	337.6625	657.2912	329.1493	656.3072	328.6573	C	1483.6152	742.3112	1466.5886	733.7979	1465.6046	733.3059	12
7	787.4019	394.2046	770.3753	385.6913	769.3913	385.1993	L	1323.5845	662.2959	1306.5580	653.7826	1305.5740	653.2906	11
8	916.4444	458.7259	899.4179	450.2126	898.4339	449.7206	E	1210.5005	605.7539	1193.4739	597.2406	1192.4899	596.7486	10
9	1072.5456	536.7764	1055.5190	528.2631	1054.5350	527.7711	R	1081.4579	541.2326	1064.4313	532.7193	1063.4473	532.2273	9
10	1187.5725	594.2899	1170.5460	585.7766	1169.5619	585.2846	N	925.3568	463.1820	908.3302	454.6687	907.3462	454.1767	8
11	1316.6151	658.8112	1299.5885	650.2979	1298.6045	649.8059	E	810.3298	405.6685	793.3033	397.1553	792.3192	396.6633	7
12	1417.6628	709.3350	1400.6362	700.8218	1399.6522	700.3297	T	681.2872	341.1472	664.2607	332.6340	663.2767	332.1420	6
13	1504.6948	752.8510	1487.6683	744.3378	1486.6842	743.8458	S	580.2395	290.6234	563.2130	282.1101	562.2290	281.6181	5
14	1561.7163	781.3618	1544.6897	772.8485	1543.7057	772.3565	G	493.2075	247.1074	476.1810	238.5941	475.1969	238.1021	4
15	1721.7469	861.3771	1704.7204	852.8638	1703.7363	852.3718	C	436.1860	218.5967	419.1595	210.0834	418.1755	209.5914	3
16	1850.7895	925.8984	1833.7630	917.3851	1832.7789	916.8931	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
17							K	147.1128	74.0600	130.0863	65.5468			1

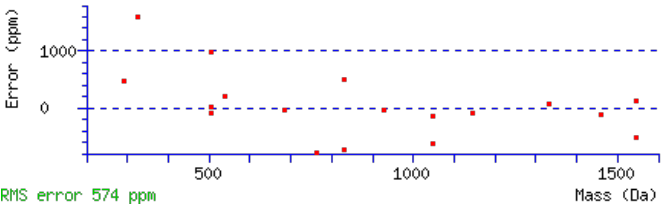
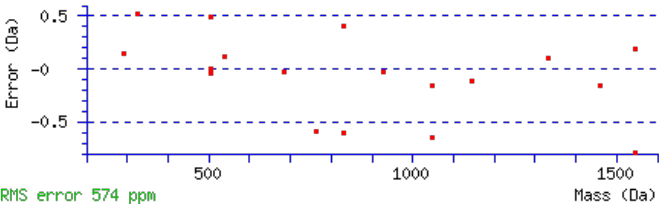


NCBI **BLAST** search of [LTQGICLERNETSGCEK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.6	1995.8877	0.0095	LTQGICLERNETSGCEK
45.7	1994.9037	0.9935	LTQGICLERNETSGCEK
12.0	1994.9037	0.9935	LTQGICLERNETSGCEK
2.9	1994.9102	0.9870	QGSNSIIPNSISDTMNSTK
2.4	1994.9102	0.9870	QGSNSIIPNSISDTMNSTK
2.4	1994.9102	0.9870	QGSNSIIPNSISDTMNSTK

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [YKVDYESQSTDTQNFSESSESK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
46.3	2343.9866	0.0081	YKVDYESQSTDTQNFSESSESK	Deamidated Q8, N14 74.04%
40.9	2343.9866	0.0081	YKVDYESQSTDTQNFSESSESK	Deamidated Q8, Q13 21.45%
37.1	2343.0026	0.9921	YKVDYESQSTDTQNFSESSESK	
35.5	2343.0026	0.9921	YKVDYESQSTDTQNFSESSESK	
34.1	2343.9866	0.0081	YKVDYESQSTDTQNFSESSESK	Deamidated Q13, N14 4.51%
17.9	2343.0026	0.9921	YKVDYESQSTDTQNFSESSESK	
3.7	2342.9716	1.0231	QYDTYGSAGFDAGAGGSGQGYWK	
1.5	2343.9922	0.0025	EKVLEYGCSHGDPYGAEMMR	
1.5	2343.9922	0.0025	EKVLEYGCSHGDPYGAEMMR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

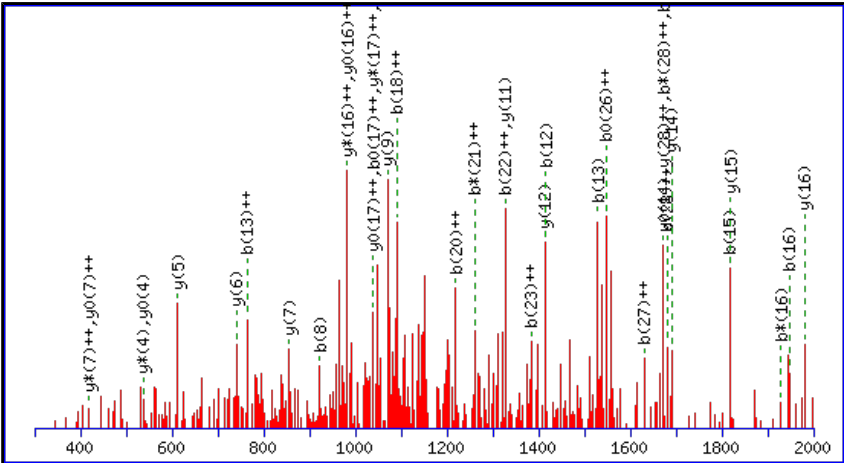
Peptide View

MS/MS Fragmentation of **Y****S****S****T****C****H****G****E****Y****S****Q****N****I****C****E****E****F****S****Q****Q****T****D****N****E****G****C****F****T****K**
Found in **I3LQ17** in **uni_pig**, tr|I3LQ17|I3LQ17_PIG Uncharacterized protein OS=Sus scrofa PE=4 SV=1

Match to Query 13496: 3506.359812 from(1169.793880,3+) intensity(6269.8164) rtinseconds(1828) scans(3712) index(9392)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_02Spectrum2917_scans_3712
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

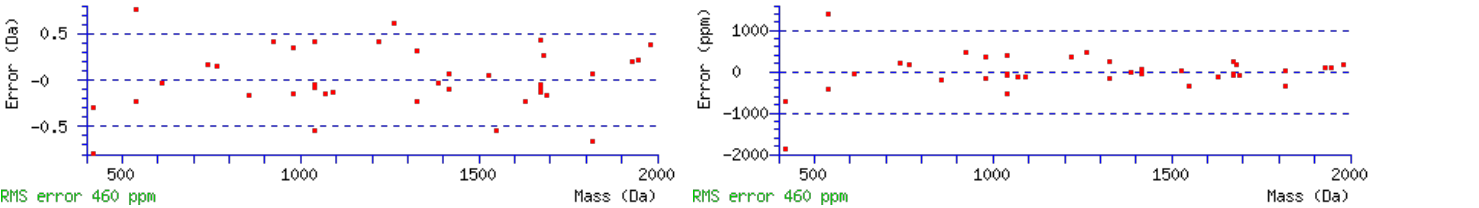
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 3506.3609
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 37 Expect: 0.00052
Matches : 38/312 fragment ions using 51 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							29
2	251.1026	126.0550			233.0921	117.0497	S	3344.3049	1672.6561	3327.2783	1664.1428	3326.2943	1663.6508	28
3	338.1347	169.5710			320.1241	160.5657	S	3257.2729	1629.1401	3240.2463	1620.6268	3239.2623	1620.1348	27
4	439.1823	220.0948			421.1718	211.0895	T	3170.2408	1585.6240	3153.2143	1577.1108	3152.2303	1576.6188	26
5	599.2130	300.1101			581.2024	291.1049	C	3069.1931	1535.1002	3052.1666	1526.5869	3051.1826	1526.0949	25
6	736.2719	368.6396			718.2613	359.6343	H	2909.1625	1455.0849	2892.1359	1446.5716	2891.1519	1446.0796	24
7	793.2934	397.1503			775.2828	388.1450	G	2772.1036	1386.5554	2755.0770	1378.0422	2754.0930	1377.5501	23
8	922.3360	461.6716			904.3254	452.6663	E	2715.0821	1358.0447	2698.0556	1349.5314	2697.0716	1349.0394	22
9	1085.3993	543.2033			1067.3887	534.1980	Y	2586.0395	1293.5234	2569.0130	1285.0101	2568.0290	1284.5181	21
10	1172.4313	586.7193			1154.4208	577.7140	S	2422.9762	1211.9917	2405.9496	1203.4785	2404.9656	1202.9865	20
11	1300.4899	650.7486	1283.4633	642.2353	1282.4793	641.7433	Q	2335.9442	1168.4757	2318.9176	1159.9624	2317.9336	1159.4704	19
12	1415.5168	708.2621	1398.4903	699.7488	1397.5063	699.2568	N	2207.8856	1104.4464	2190.8590	1095.9332	2189.8750	1095.4412	18
13	1528.6009	764.8041	1511.5744	756.2908	1510.5903	755.7988	I	2092.8586	1046.9330	2075.8321	1038.4197	2074.8481	1037.9277	17
14	1688.6315	844.8194	1671.6050	836.3061	1670.6210	835.8141	C	1979.7746	990.3909	1962.7480	981.8777	1961.7640	981.3856	16
15	1817.6741	909.3407	1800.6476	900.8274	1799.6636	900.3354	E	1819.7439	910.3756	1802.7174	901.8623	1801.7334	901.3703	15
16	1946.7167	973.8620	1929.6902	965.3487	1928.7062	964.8567	E	1690.7013	845.8543	1673.6748	837.3410	1672.6908	836.8490	14
17	2093.7851	1047.3962	2076.7586	1038.8829	2075.7746	1038.3909	F	1561.6587	781.3330	1544.6322	772.8197	1543.6482	772.3277	13
18	2180.8172	1090.9122	2163.7906	1082.3990	2162.8066	1081.9069	S	1414.5903	707.7988	1397.5638	699.2855	1396.5798	698.7935	12
19	2308.8758	1154.9415	2291.8492	1146.4282	2290.8652	1145.9362	Q	1327.5583	664.2828	1310.5318	655.7695	1309.5477	655.2775	11
20	2436.9343	1218.9708	2419.9078	1210.4575	2418.9238	1209.9655	Q	1199.4997	600.2535	1182.4732	591.7402	1181.4892	591.2482	10
21	2537.9820	1269.4946	2520.9555	1260.9814	2519.9714	1260.4894	T	1071.4412	536.2242	1054.4146	527.7109	1053.4306	527.2189	9
22	2653.0090	1327.0081	2635.9824	1318.4948	2634.9984	1318.0028	D	970.3935	485.7004	953.3669	477.1871	952.3829	476.6951	8
23	2767.0519	1384.0296	2750.0253	1375.5163	2749.0413	1375.0243	N	855.3665	428.1869	838.3400	419.6736	837.3560	419.1816	7
24	2896.0945	1448.5509	2879.0679	1440.0376	2878.0839	1439.5456	E	741.3236	371.1654	724.2971	362.6522	723.3130	362.1602	6

25	2953.1159	1477.0616	2936.0894	1468.5483	2935.1054	1468.0563	G	612.2810	306.6441	595.2545	298.1309	594.2704	297.6389	5
26	3113.1466	1557.0769	3096.1200	1548.5637	3095.1360	1548.0716	C	555.2595	278.1334	538.2330	269.6201	537.2490	269.1281	4
27	3260.2150	1630.6111	3243.1885	1622.0979	3242.2044	1621.6059	F	395.2289	198.1181	378.2023	189.6048	377.2183	189.1128	3
28	3361.2627	1681.1350	3344.2361	1672.6217	3343.2521	1672.1297	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
29							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [YSSTCHGEYSQNICEEFSQQTDNEGCFTK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
37.1	3506.3609	-0.0011	YSSTCHGEYSQNICEEFSQQTDNEGCFTK	Deamidated N12 26.92%
37.1	3506.3609	-0.0011	YSSTCHGEYSQNICEEFSQQTDNEGCFTK	Deamidated Q11 26.92%
36.8	3506.3609	-0.0011	YSSTCHGEYSQNICEEFSQQTDNEGCFTK	Deamidated Q20 25.24%
35.0	3506.3609	-0.0011	YSSTCHGEYSQNICEEFSQQTDNEGCFTK	Deamidated Q19 16.63%
30.5	3505.3769	0.9829	YSSTCHGEYSQNICEEFSQQTDNEGCFTK	
29.1	3506.3609	-0.0011	YSSTCHGEYSQNICEEFSQQTDNEGCFTK	Deamidated N23 4.30%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

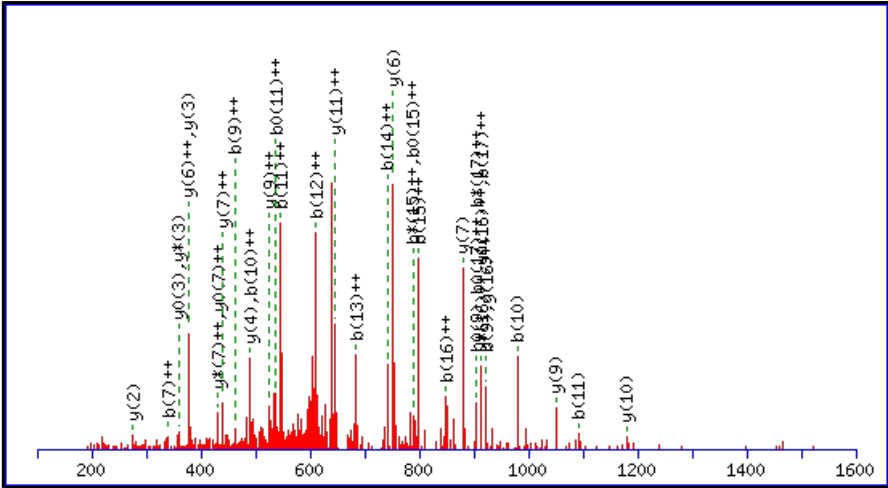
Peptide View

MS/MS Fragmentation of **GATHAEILEGLQFNLTEK**
Found in **F1SCF0** in **uni_pig**, tr|F1SCF0|F1SCF0_PIG Alpha-1-antitrypsin OS=Sus scrofa GN=SERPINA1 PE=3 SV=1

Match to Query 10034: 1970.989602 from(658.003810,3+) intensity(2687.7817) rtinseconds(2533) scans(6067) index(1641)
Title: 120325_Sunil_PigSerum_Glyco_D_14Spectrum5193_scans__6067
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

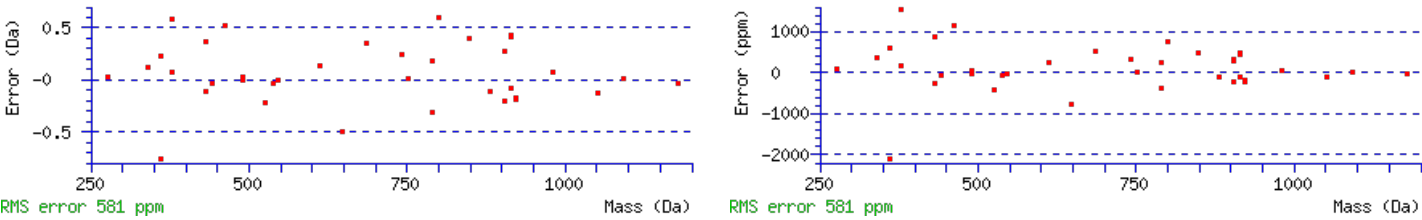
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1970.9949
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
Ions Score: 51 Expect: 0.00057
Matches : 37/176 fragment ions using 58 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							18
2	129.0659	65.0366					A	1914.9807	957.9940	1897.9542	949.4807	1896.9702	948.9887	17
3	230.1135	115.5604			212.1030	106.5551	T	1843.9436	922.4754	1826.9171	913.9622	1825.9331	913.4702	16
4	367.1724	184.0899			349.1619	175.0846	H	1742.8959	871.9516	1725.8694	863.4383	1724.8854	862.9463	15
5	438.2096	219.6084			420.1990	210.6031	A	1605.8370	803.4222	1588.8105	794.9089	1587.8265	794.4169	14
6	567.2522	284.1297			549.2416	275.1244	E	1534.7999	767.9036	1517.7734	759.3903	1516.7894	758.8983	13
7	680.3362	340.6717			662.3257	331.6665	I	1405.7573	703.3823	1388.7308	694.8690	1387.7468	694.3770	12
8	793.4203	397.2138			775.4097	388.2085	L	1292.6733	646.8403	1275.6467	638.3270	1274.6627	637.8350	11
9	922.4629	461.7351			904.4523	452.7298	E	1179.5892	590.2982	1162.5626	581.7850	1161.5786	581.2930	10
10	979.4843	490.2458			961.4738	481.2405	G	1050.5466	525.7769	1033.5201	517.2637	1032.5360	516.7717	9
11	1092.5684	546.7878			1074.5578	537.7826	L	993.5251	497.2662	976.4986	488.7529	975.5146	488.2609	8
12	1220.6270	610.8171	1203.6004	602.3039	1202.6164	601.8118	Q	880.4411	440.7242	863.4145	432.2109	862.4305	431.7189	7
13	1367.6954	684.3513	1350.6688	675.8381	1349.6848	675.3461	F	752.3825	376.6949	735.3559	368.1816	734.3719	367.6896	6
14	1482.7223	741.8648	1465.6958	733.3515	1464.7118	732.8595	N	605.3141	303.1607	588.2875	294.6474	587.3035	294.1554	5
15	1595.8064	798.4068	1578.7799	789.8936	1577.7958	789.4016	L	490.2871	245.6472	473.2606	237.1339	472.2766	236.6419	4
16	1696.8541	848.9307	1679.8275	840.4174	1678.8435	839.9254	T	377.2031	189.1052	360.1765	180.5919	359.1925	180.0999	3
17	1825.8967	913.4520	1808.8701	904.9387	1807.8861	904.4467	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
18							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [GATHAEILEGLQFNLTEK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.3	1970.9949	-0.0053	GATHAEILEGLQFNLTEK	Deamidated N14 59.55%
49.6	1970.9949	-0.0053	GATHAEILEGLQFNLTEK	Deamidated Q12 40.45%
6.0	1968.9682	2.0214	MELLIMINACKIASSSR	
5.4	1970.9917	-0.0021	LPENQAVQMRLVDVACK	
5.2	1970.9805	0.0091	EYEAMKLVNMLDKLSR	
5.0	1970.9958	-0.0062	QAEWLSSCLKKMISEK	
4.8	1970.9917	-0.0021	LPENQAVQMRLVDVACK	
4.3	1970.9917	-0.0021	LPENQAVQMRLVDVACK	
4.1	1970.9731	0.0165	MERQQQGPPSTLPTEKK	
4.1	1970.9731	0.0165	MERQQQGPPSTLPTEKK	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1RN76** in **uni_pig**, tr|F1RN76|F1RN76_PIG Uncharacterized protein OS=Sus scrofa GN=CD5L PE=4 SV=2

Title: 120326_Sunil_PigSerum_Glyco_PsetB_15Spectrum2874_scans__3861

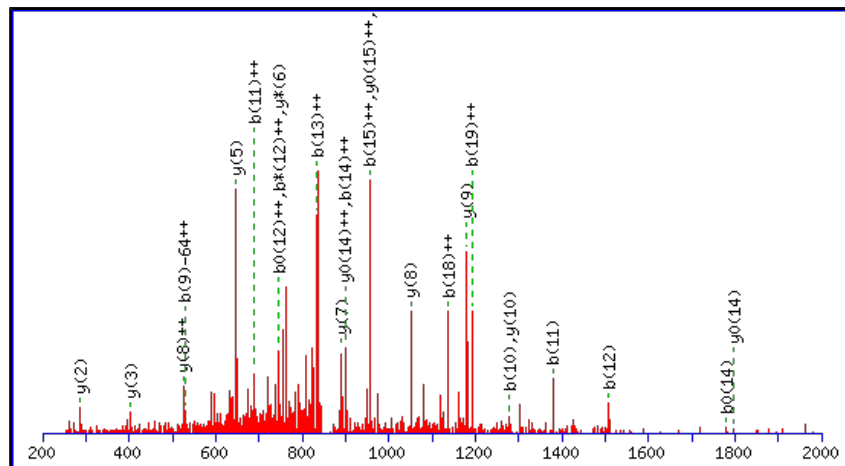
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

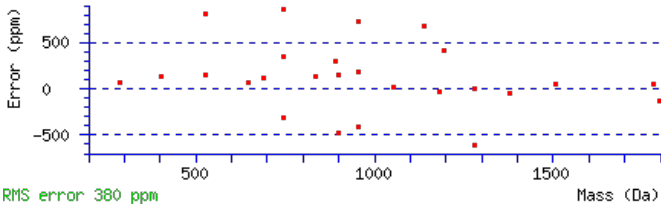
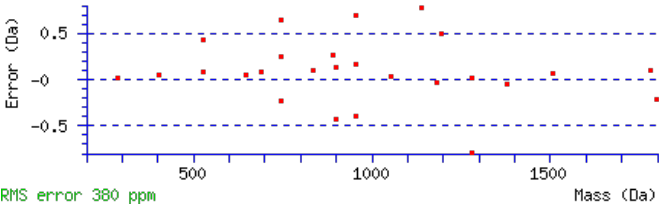
N2 : Deamidated (NQ)

M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 32 Expect: 0.00059

Matches : 26/332 fragment ions using 36 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							20
2	230.0771	115.5422	213.0506	107.0289			N	2444.8734	1222.9403	2427.8468	1214.4271	2426.8628	1213.9351	19
3	390.1078	195.5575	373.0812	187.0443			C	2329.8464	1165.4269	2312.8199	1156.9136	2311.8359	1156.4216	18
4	491.1555	246.0814	474.1289	237.5681	473.1449	237.0761	T	2169.8158	1085.4115	2152.7892	1076.8983	2151.8052	1076.4063	17
5	628.2144	314.6108	611.1878	306.0976	610.2038	305.6055	H	2068.7681	1034.8877	2051.7416	1026.3744	2050.7576	1025.8824	16
6	743.2413	372.1243	726.2148	363.6110	725.2308	363.1190	D	1931.7092	966.3582	1914.6827	957.8450	1913.6986	957.3530	15
7	858.2683	429.6378	841.2417	421.1245	840.2577	420.6325	D	1816.6823	908.8448	1799.6557	900.3315	1798.6717	899.8395	14
8	973.2952	487.1512	956.2687	478.6380	955.2846	478.1460	D	1701.6553	851.3313	1684.6288	842.8180	1683.6448	842.3260	13
9	1120.3306	560.6689	1103.3041	552.1557	1102.3200	551.6637	M	1586.6284	793.8178	1569.6018	785.3046	1568.6178	784.8125	12
10	1280.3613	640.6843	1263.3347	632.1710	1262.3507	631.6790	C	1439.5930	720.3001	1422.5664	711.7869	1421.5824	711.2948	11
11	1379.4297	690.2185	1362.4031	681.7052	1361.4191	681.2132	V	1279.5623	640.2848	1262.5358	631.7715	1261.5518	631.2795	10
12	1508.4723	754.7398	1491.4457	746.2265	1490.4617	745.7345	E	1180.4939	590.7506	1163.4674	582.2373	1162.4834	581.7453	9
13	1668.5029	834.7551	1651.4764	826.2418	1650.4924	825.7498	C	1051.4513	526.2293	1034.4248	517.7160	1033.4408	517.2240	8
14	1797.5455	899.2764	1780.5190	890.7631	1779.5349	890.2711	E	891.4207	446.2140	874.3941	437.7007	873.4101	437.2087	7
15	1912.5725	956.7899	1895.5459	948.2766	1894.5619	947.7846	D	762.3781	381.6927	745.3515	373.1794	744.3675	372.6874	6
16	2009.6252	1005.3162	1992.5987	996.8030	1991.6147	996.3110	P	647.3511	324.1792	630.3246	315.6659	629.3406	315.1739	5
17	2156.6936	1078.8505	2139.6671	1070.3372	2138.6831	1069.8452	F	550.2984	275.6528	533.2718	267.1396	532.2878	266.6475	4
18	2271.7206	1136.3639	2254.6940	1127.8507	2253.7100	1127.3586	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
19	2384.8046	1192.9060	2367.7781	1184.3927	2366.7941	1183.9007	L	288.2030	144.6051	271.1765	136.0919			2
20							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [NNCTHDDDMCVECEDPFDLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
32.3	2557.9091	-0.0191	NNCTHDDDMCVECEDPFDLR	Deamidated N2 50.00%
32.3	2557.9091	-0.0191	NNCTHDDDMCVECEDPFDLR	Deamidated N1 50.00%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPFNPNTTEADFHVSK**

Found in **Q9GMA6** in **uni_pig**, tr|Q9GMA6|Q9GMA6_PIG Alpha-1-antichymotrypsin 2 OS=Sus scrofa GN=SERPINA3-2 PE=3 SV=1

Match to Query 7957: 1918.909122 from(640.643650,3+) intensity(3984.3945) rtinseconds(2095) scans(3073) index(474)

Title: 120325_Sunil_PigSerum_Glyco_D_05Spectrum1805_scans__3073

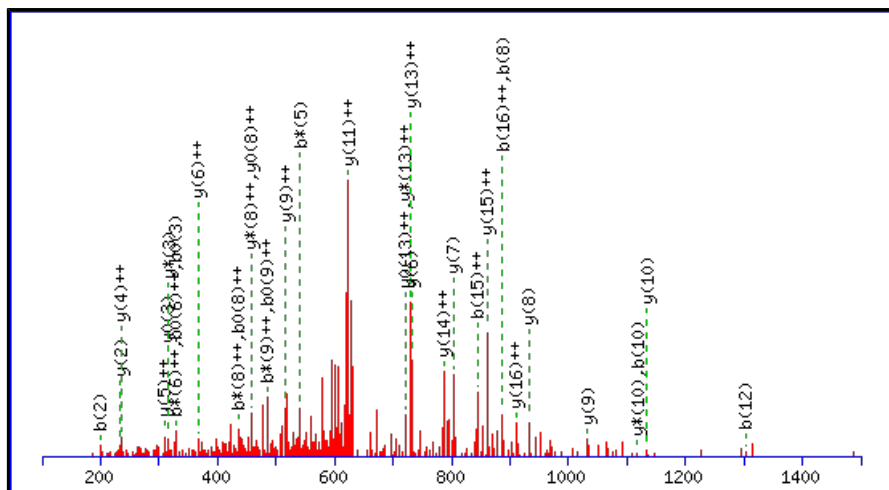
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1918.8949

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

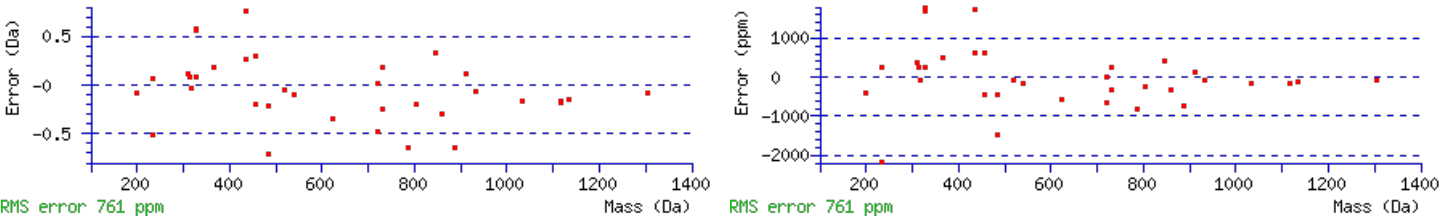
N4 : Deamidated (NQ)

N6 : Deamidated (NQ')

Ions Score: 49 Expect: 0.0008

Matches : 36/184 fragment ions using 56 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							17
2	199.1077	100.0575			181.0972	91.0522	P	1818.8545	909.9309	1801.8279	901.4176	1800.8439	900.9256	16
3	346.1761	173.5917			328.1656	164.5864	F	1721.8017	861.4045	1704.7752	852.8912	1703.7911	852.3992	15
4	461.2031	231.1052	444.1765	222.5919	443.1925	222.0999	N	1574.7333	787.8703	1557.7067	779.3570	1556.7227	778.8650	14
5	558.2558	279.6316	541.2293	271.1183	540.2453	270.6263	P	1459.7064	730.3568	1442.6798	721.8435	1441.6958	721.3515	13
6	673.2828	337.1450	656.2562	328.6318	655.2722	328.1397	N	1362.6536	681.8304	1345.6270	673.3172	1344.6430	672.8251	12
7	786.3668	393.6871	769.3403	385.1738	768.3563	384.6818	L	1247.6266	624.3170	1230.6001	615.8037	1229.6161	615.3117	11
8	887.4145	444.2109	870.3880	435.6976	869.4040	435.2056	T	1134.5426	567.7749	1117.5160	559.2617	1116.5320	558.7696	10
9	988.4622	494.7347	971.4357	486.2215	970.4516	485.7295	T	1033.4949	517.2511	1016.4684	508.7378	1015.4843	508.2458	9
10	1117.5048	559.2560	1100.4782	550.7428	1099.4942	550.2508	E	932.4472	466.7272	915.4207	458.2140	914.4367	457.7220	8
11	1188.5419	594.7746	1171.5154	586.2613	1170.5313	585.7693	A	803.4046	402.2060	786.3781	393.6927	785.3941	393.2007	7
12	1303.5689	652.2881	1286.5423	643.7748	1285.5583	643.2828	D	732.3675	366.6874	715.3410	358.1741	714.3570	357.6821	6
13	1450.6373	725.8223	1433.6107	717.3090	1432.6267	716.8170	F	617.3406	309.1739	600.3140	300.6606	599.3300	300.1686	5
14	1587.6962	794.3517	1570.6696	785.8385	1569.6856	785.3464	H	470.2722	235.6397	453.2456	227.1264	452.2616	226.6344	4
15	1686.7646	843.8859	1669.7380	835.3727	1668.7540	834.8807	V	333.2132	167.1103	316.1867	158.5970	315.2027	158.1050	3
16	1773.7966	887.4019	1756.7701	878.8887	1755.7861	878.3967	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [TPFNPNLTTTEADFHVSK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.3	1918.8949	0.0143	TPFNPNLTTTEADFHVSK
46.5	1917.9109	0.9983	TPFNPNLTTTEADFHVSK
45.2	1917.9109	0.9983	TPFNPNLTTTEADFHVSK
4.0	1918.9054	0.0037	LMQDDNRGLGQGLKDNK
3.9	1916.8985	2.0106	TGWIGELGAMRMPSSHR
3.6	1916.8851	2.0241	AALQTAPESADDSPSQLSK
3.1	1916.9210	1.9882	EEKAFHDKYFGPFFR
2.2	1918.9272	-0.0181	EALDISNSISESGGLNWK
1.2	1917.9030	1.0061	VVIWNMSPVLQEDDEK
1.1	1918.9167	-0.0075	GTKGNASSRSMTEEHISK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

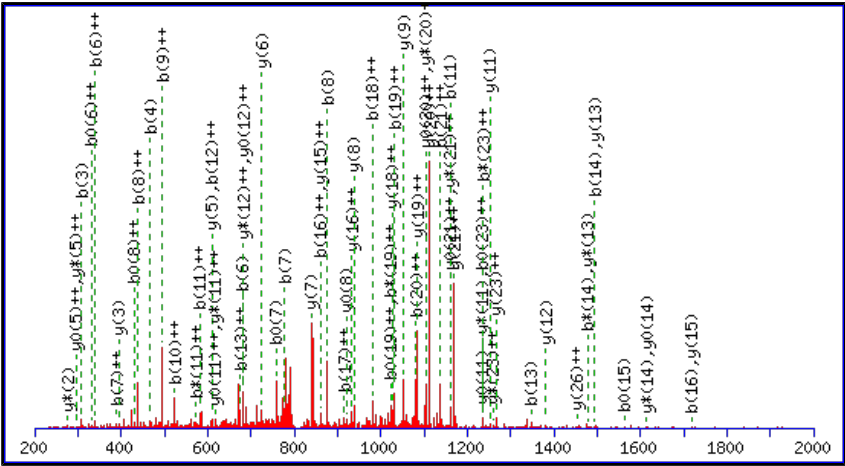
Peptide View

MS/MS Fragmentation of **LGHC PDPVLGNGEFSHLETVNVNDTITFK**
Found in **F1S0J3** in **uni_pig**, tr[F1S0J3]F1S0J3_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPB PE=4 SV=1

Match to Query 13397: 3211.523616 from(803.888180,4+) intensity(0.0000) rtinseconds(2429) scans(5375) index(9324)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_01Spectrum4456_scans_5375
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

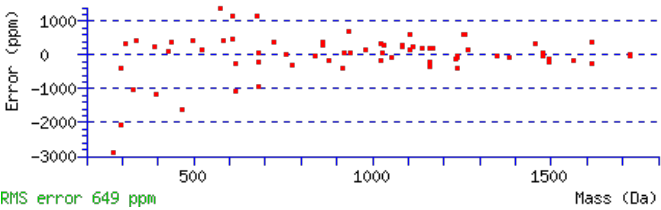
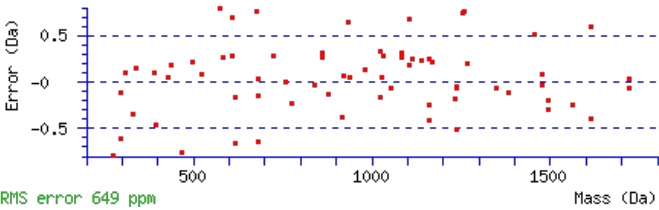
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 3211.5132
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
N23 : Deamidated (NQ)
Ions Score: 50 Expect: 0.00082
Matches : 69/302 fragment ions using 141 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							29
2	171.1128	86.0600					G	3099.4364	1550.2218	3082.4099	1541.7086	3081.4258	1541.2166	28
3	308.1717	154.5895					H	3042.4149	1521.7111	3025.3884	1513.1978	3024.4044	1512.7058	27
4	468.2024	234.6048					C	2905.3560	1453.1817	2888.3295	1444.6684	2887.3455	1444.1764	26
5	565.2551	283.1312					P	2745.3254	1373.1663	2728.2988	1364.6531	2727.3148	1364.1610	25
6	680.2821	340.6447			662.2715	331.6394	D	2648.2726	1324.6399	2631.2461	1316.1267	2630.2621	1315.6347	24
7	777.3348	389.1711			759.3243	380.1658	P	2533.2457	1267.1265	2516.2191	1258.6132	2515.2351	1258.1212	23
8	876.4033	438.7053			858.3927	429.7000	V	2436.1929	1218.6001	2419.1664	1210.0868	2418.1823	1209.5948	22
9	989.4873	495.2473			971.4767	486.2420	L	2337.1245	1169.0659	2320.0979	1160.5526	2319.1139	1160.0606	21
10	1046.5088	523.7580			1028.4982	514.7527	G	2224.0404	1112.5239	2207.0139	1104.0106	2206.0299	1103.5186	20
11	1161.5357	581.2715	1144.5092	572.7582	1143.5252	572.2662	N	2167.0190	1084.0131	2149.9924	1075.4998	2149.0084	1075.0078	19
12	1218.5572	609.7822	1201.5306	601.2690	1200.5466	600.7769	G	2051.9920	1026.4997	2034.9655	1017.9864	2033.9815	1017.4944	18
13	1347.5998	674.3035	1330.5732	665.7903	1329.5892	665.2982	E	1994.9706	997.9889	1977.9440	989.4756	1976.9600	988.9836	17
14	1494.6682	747.8377	1477.6416	739.3245	1476.6576	738.8325	F	1865.9280	933.4676	1848.9014	924.9543	1847.9174	924.4623	16
15	1581.7002	791.3537	1564.6737	782.8405	1563.6897	782.3485	S	1718.8596	859.9334	1701.8330	851.4201	1700.8490	850.9281	15
16	1718.7591	859.8832	1701.7326	851.3699	1700.7486	850.8779	H	1631.8275	816.4174	1614.8010	807.9041	1613.8170	807.4121	14
17	1831.8432	916.4252	1814.8166	907.9120	1813.8326	907.4200	L	1494.7686	747.8879	1477.7421	739.3747	1476.7581	738.8827	13
18	1960.8858	980.9465	1943.8592	972.4333	1942.8752	971.9413	E	1381.6846	691.3459	1364.6580	682.8326	1363.6740	682.3406	12
19	2061.9335	1031.4704	2044.9069	1022.9571	2043.9229	1022.4651	T	1252.6420	626.8246	1235.6154	618.3113	1234.6314	617.8193	11
20	2161.0019	1081.0046	2143.9753	1072.4913	2142.9913	1071.9993	V	1151.5943	576.3008	1134.5677	567.7875	1133.5837	567.2955	10
21	2275.0448	1138.0260	2258.0183	1129.5128	2257.0342	1129.0208	N	1052.5259	526.7666	1035.4993	518.2533	1034.5153	517.7613	9
22	2374.1132	1187.5602	2357.0867	1179.0470	2356.1027	1178.5550	V	938.4829	469.7451	921.4564	461.2318	920.4724	460.7398	8
23	2489.1402	1245.0737	2472.1136	1236.5604	2471.1296	1236.0684	N	839.4145	420.2109	822.3880	411.6976	821.4040	411.2056	7

24	2604.1671	1302.5872	2587.1406	1294.0739	2586.1565	1293.5819	D	724.3876	362.6974	707.3610	354.1842	706.3770	353.6921	6
25	2705.2148	1353.1110	2688.1882	1344.5978	2687.2042	1344.1057	T	609.3606	305.1840	592.3341	296.6707	591.3501	296.1787	5
26	2818.2989	1409.6531	2801.2723	1401.1398	2800.2883	1400.6478	I	508.3130	254.6601	491.2864	246.1468	490.3024	245.6548	4
27	2919.3465	1460.1769	2902.3200	1451.6636	2901.3360	1451.1716	T	395.2289	198.1181	378.2023	189.6048	377.2183	189.1128	3
28	3066.4149	1533.7111	3049.3884	1525.1978	3048.4044	1524.7058	F	294.1812	147.5942	277.1547	139.0810			2
29							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [LGHCPDPVLGNGEFSHLETNVNNDTITEK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.7	3211.5132	0.0104	LGHCPDPVLGNGEFSHLETNVNNDTITEK	Deamidated N11, N23 56.70%
45.8	3211.5132	0.0104	LGHCPDPVLGNGEFSHLETNVNNDTITEK	Deamidated N21, N23 23.04%
45.2	3211.5132	0.0104	LGHCPDPVLGNGEFSHLETNVNNDTITEK	Deamidated N11, N21 20.26%
43.3	3210.5292	0.9944	LGHCPDPVLGNGEFSHLETNVNNDTITEK	
36.5	3210.5292	0.9944	LGHCPDPVLGNGEFSHLETNVNNDTITEK	
30.0	3210.5292	0.9944	LGHCPDPVLGNGEFSHLETNVNNDTITEK	
15.6	3209.5452	1.9784	LGHCPDPVLGNGEFSHLETNVNNDTITEK	
10.3	3211.4965	0.0271	QSVTDYLMAYKEETQQLQEELEALEER	
7.8	3210.5255	0.9981	MAGPSLACCLLGLLALTSACYIONCPLGGK	
7.1	3209.5415	1.9821	MAGPSLACCLLGLLALTSACYIONCPLGGK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR**
Found in **F1S0J2** in **uni_pig**, tr[F1S0J2]F1S0J2_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPA PE=4 SV=2

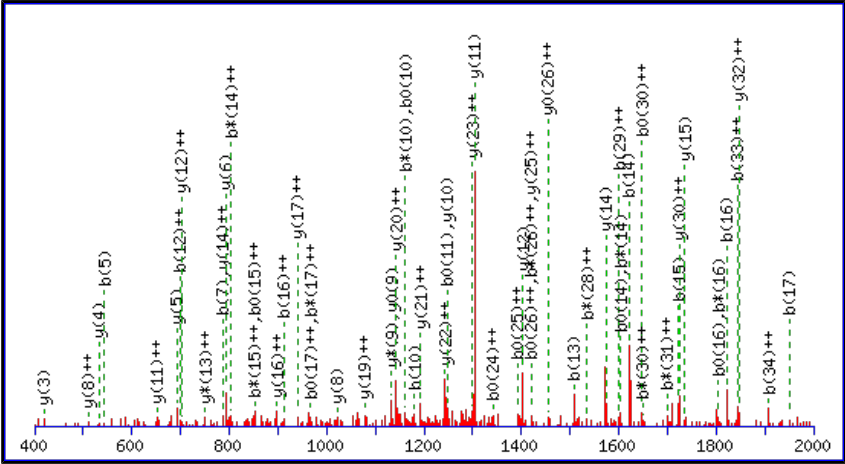
Match to Query 13757: 4104.899202 from(1369.307010,3+) intensity(0.0000) rtinseconds(2769) scans(5723) index(3514)
Title: 120325_Sunil_PigSerum_Glyco_P_12Spectrum4341_scans__5723
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

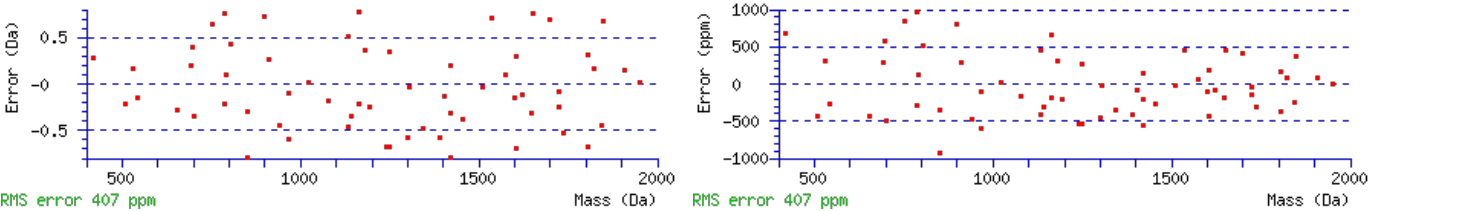
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 4104.8667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17 : Deamidated (NQ)
Q28 : Deamidated (NQ)
N29 : Deamidated (NQ)
Ions Score: 48 Expect: 0.00084
Matches : 61/408 fragment ions using 128 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							36
2	201.1234	101.0653			183.1128	92.0600	S	3992.7900	1996.8986	3975.7634	1988.3853	3974.7794	1987.8933	35
3	300.1918	150.5995			282.1812	141.5942	V	3905.7579	1953.3826	3888.7314	1944.8693	3887.7474	1944.3773	34
4	415.2187	208.1130			397.2082	199.1077	D	3806.6895	1903.8484	3789.6630	1895.3351	3788.6790	1894.8431	33
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	Q	3691.6626	1846.3349	3674.6360	1837.8217	3673.6520	1837.3296	32
6	658.3042	329.6558	641.2777	321.1425	640.2937	320.6505	D	3563.6040	1782.3056	3546.5775	1773.7924	3545.5934	1773.3004	31
7	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	K	3448.5771	1724.7922	3431.5505	1716.2789	3430.5665	1715.7869	30
8	949.4625	475.2349	932.4360	466.7216	931.4520	466.2296	Y	3320.4821	1660.7447	3303.4556	1652.2314	3302.4715	1651.7394	29
9	1050.5102	525.7587	1033.4837	517.2455	1032.4997	516.7535	T	3157.4188	1579.2130	3140.3922	1570.6997	3139.4082	1570.2077	28
10	1179.5528	590.2800	1162.5263	581.7668	1161.5422	581.2748	E	3056.3711	1528.6892	3039.3445	1520.1759	3038.3605	1519.6839	27
11	1266.5848	633.7961	1249.5583	625.2828	1248.5743	624.7908	S	2927.3285	1464.1679	2910.3020	1455.6546	2909.3179	1455.1626	26
12	1395.6274	698.3174	1378.6009	689.8041	1377.6169	689.3121	E	2840.2965	1420.6519	2823.2699	1412.1386	2822.2859	1411.6466	25
13	1508.7115	754.8594	1491.6849	746.3461	1490.7009	745.8541	I	2711.2539	1356.1306	2694.2273	1347.6173	2693.2433	1347.1253	24
14	1621.7956	811.4014	1604.7690	802.8881	1603.7850	802.3961	I	2598.1698	1299.5885	2581.1433	1291.0753	2580.1592	1290.5833	23
15	1722.8432	861.9253	1705.8167	853.4120	1704.8327	852.9200	T	2485.0858	1243.0465	2468.0592	1234.5332	2467.0752	1234.0412	22
16	1821.9117	911.4595	1804.8851	902.9462	1803.9011	902.4542	V	2384.0381	1192.5227	2367.0115	1184.0094	2366.0275	1183.5174	21
17	1950.9542	975.9808	1933.9277	967.4675	1932.9437	966.9755	Q	2284.9697	1142.9885	2267.9431	1134.4752	2266.9591	1133.9832	20
18	2110.9849	1055.9961	2093.9583	1047.4828	2092.9743	1046.9908	C	2155.9271	1078.4672	2138.9005	1069.9539	2137.9165	1069.4619	19
19	2226.0118	1113.5096	2208.9853	1104.9963	2208.0013	1104.5043	D	1995.8964	998.4518	1978.8699	989.9386	1977.8858	989.4466	18
20	2313.0439	1157.0256	2296.0173	1148.5123	2295.0333	1148.0203	S	1880.8695	940.9384	1863.8429	932.4251	1862.8589	931.9331	17
21	2370.0653	1185.5363	2353.0388	1177.0230	2352.0548	1176.5310	G	1793.8374	897.4224	1776.8109	888.9091	1775.8269	888.4171	16
22	2533.1287	1267.0680	2516.1021	1258.5547	2515.1181	1258.0627	Y	1736.8160	868.9116	1719.7894	860.3984	1718.8054	859.9063	15
23	2590.1501	1295.5787	2573.1236	1287.0654	2572.1396	1286.5734	G	1573.7527	787.3800	1556.7261	778.8667	1555.7421	778.3747	14

24	2703.2342	1352.1207	2686.2076	1343.6075	2685.2236	1343.1154	L	1516.7312	758.8692	1499.7046	750.3560	1498.7206	749.8639	13
25	2802.3026	1401.6549	2785.2761	1393.1417	2784.2920	1392.6497	V	1403.6471	702.3272	1386.6206	693.8139	1385.6366	693.3219	12
26	2859.3241	1430.1657	2842.2975	1421.6524	2841.3135	1421.1604	G	1304.5787	652.7930	1287.5522	644.2797	1286.5681	643.7877	11
27	2956.3768	1478.6921	2939.3503	1470.1788	2938.3663	1469.6868	P	1247.5572	624.2823	1230.5307	615.7690	1229.5467	615.2770	10
28	3085.4194	1543.2133	3068.3929	1534.7001	3067.4089	1534.2081	Q	1150.5045	575.7559	1133.4779	567.2426	1132.4939	566.7506	9
29	3200.4464	1600.7268	3183.4198	1592.2135	3182.4358	1591.7215	N	1021.4619	511.2346	1004.4353	502.7213	1003.4513	502.2293	8
30	3313.5304	1657.2689	3296.5039	1648.7556	3295.5199	1648.2636	I	906.4349	453.7211	889.4084	445.2078	888.4244	444.7158	7
31	3414.5781	1707.7927	3397.5516	1699.2794	3396.5675	1698.7874	T	793.3509	397.1791	776.3243	388.6658	775.3403	388.1738	6
32	3574.6088	1787.8080	3557.5822	1779.2947	3556.5982	1778.8027	C	692.3032	346.6552	675.2767	338.1420	674.2926	337.6500	5
33	3687.6928	1844.3500	3670.6663	1835.8368	3669.6823	1835.3448	I	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
34	3816.7354	1908.8713	3799.7089	1900.3581	3798.7248	1899.8661	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
35	3931.7624	1966.3848	3914.7358	1957.8715	3913.7518	1957.3795	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
36							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

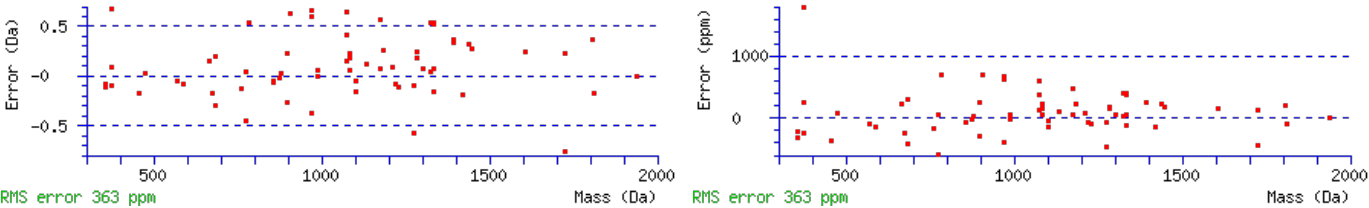
All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
48.4	4104.8667	0.0325	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q17, Q28, N29 73.39%
45.4	4103.8827	1.0165	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
42.6	4103.8827	1.0165	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
42.1	4104.8667	0.0325	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q28, N29 17.20%
41.9	4103.8827	1.0165	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
39.0	4102.8987	2.0005	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
37.7	4102.8987	2.0005	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
37.3	4104.8667	0.0325	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q17, N29 5.68%
35.4	4104.8667	0.0325	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q17, Q28 3.72%
31.8	4103.8827	1.0165	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	

Mascot: <http://www.matrixscience.com/>

http:// MascotXP.student.main.ntu.edu.sg/Mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=13356[22/Apr/15 06:08:14 PM]

25	2781.3400	1391.1736	2764.3134	1382.6604	2763.3294	1382.1683	N	374.2398	187.6235	357.2132	179.1103			3
26	2894.4241	1447.7157	2877.3975	1439.2024	2876.4135	1438.7104	L	260.1969	130.6021	243.1703	122.0888			2
27							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [IENCFVNKVNLSFSSAQILPTSDTNLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.8	3039.5223	-0.0089	IENCFVNKVNLSFSSAQILPTSDTNLK	Deamidated N10 68.01%
43.9	3039.5223	-0.0089	IENCFVNKVNLSFSSAQILPTSDTNLK	Deamidated Q17 17.36%
41.1	3039.5223	-0.0089	IENCFVNKVNLSFSSAQILPTSDTNLK	Deamidated N7 9.15%
36.4	3039.5223	-0.0089	IENCFVNKVNLSFSSAQILPTSDTNLK	Deamidated N25 3.07%
36.1	3038.5383	0.9751	IENCFVNKVNLSFSSAQILPTSDTNLK	
35.3	3039.5223	-0.0089	IENCFVNKVNLSFSSAQILPTSDTNLK	Deamidated N3 2.41%
11.9	3037.4913	2.0221	KLAMSLEQALQTNNHLQTKLDHVQEK	
11.5	3037.4913	2.0221	KLAMSLEQALQTNNHLQTKLDHVQEK	
9.3	3037.4913	2.0221	KLAMSLEQALQTNNHLQTKLDHVQEK	
8.9	3039.5117	0.0017	MERQEKANNAGHMDVDVVVIGGGISGLSAAK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

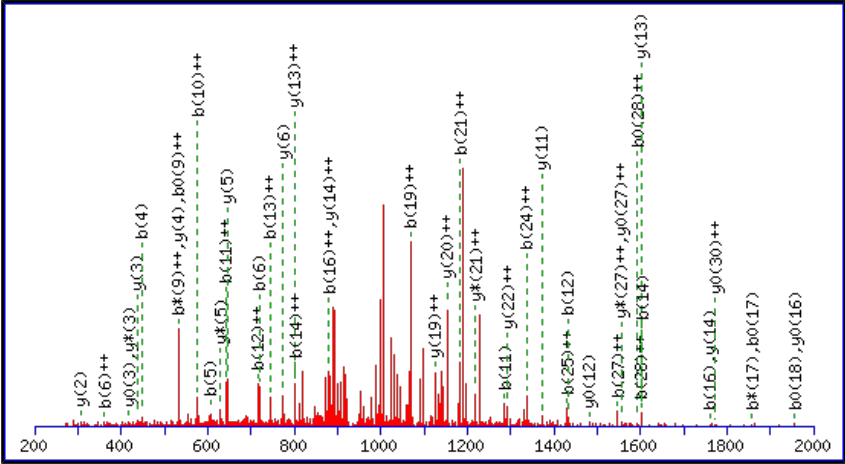
Peptide View

MS/MS Fragmentation of **AVFECLPQHAMEFGNGTITCTE**HGNWTELPECK
Found in **A0A096P6N1** in **uni_pig**, tr|A0A096P6N1|A0A096P6N1_PIG Uncharacterized protein OS=Sus scrofa GN=LOC100522100 PE=4 SV=1

Match to Query 13679: 3735.608536 from(934.909410,4+) intensity(6481.8516) rtinseconds(2624) scans(6207) index(3690)
Title: 120325_Sunil_PigSerum_Glyco_P_13Spectrum5294_scans_6207
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

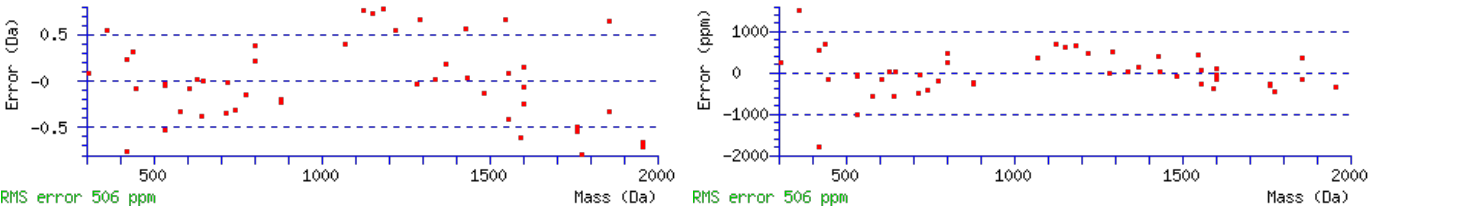
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 3735.6102
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Deamidated (NQ)
N24 : Deamidated (NQ)
Ions Score: 44 Expect: 0.0009
Matches : 48/348 fragment ions using 99 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							32
2	171.1128	86.0600					V	3665.5804	1833.2938	3648.5538	1824.7806	3647.5698	1824.2886	31
3	318.1812	159.5942					F	3566.5120	1783.7596	3549.4854	1775.2464	3548.5014	1774.7543	30
4	447.2238	224.1155			429.2132	215.1103	E	3419.4436	1710.2254	3402.4170	1701.7121	3401.4330	1701.2201	29
5	607.2545	304.1309			589.2439	295.1256	C	3290.4010	1645.7041	3273.3744	1637.1908	3272.3904	1636.6988	28
6	720.3385	360.6729			702.3280	351.6676	L	3130.3703	1565.6888	3113.3438	1557.1755	3112.3598	1556.6835	27
7	817.3913	409.1993			799.3807	400.1940	P	3017.2863	1509.1468	3000.2597	1500.6335	2999.2757	1500.1415	26
8	946.4339	473.7206	929.4073	465.2073	928.4233	464.7153	Q	2920.2335	1460.6204	2903.2069	1452.1071	2902.2229	1451.6151	25
9	1083.4928	542.2500	1066.4662	533.7368	1065.4822	533.2448	H	2791.1909	1396.0991	2774.1644	1387.5858	2773.1803	1387.0938	24
10	1154.5299	577.7686	1137.5034	569.2553	1136.5193	568.7633	A	2654.1320	1327.5696	2637.1054	1319.0564	2636.1214	1318.5643	23
11	1285.5704	643.2888	1268.5438	634.7756	1267.5598	634.2836	M	2583.0949	1292.0511	2566.0683	1283.5378	2565.0843	1283.0458	22
12	1432.6388	716.8230	1415.6123	708.3098	1414.6282	707.8178	F	2452.0544	1226.5308	2435.0278	1218.0176	2434.0438	1217.5256	21
13	1489.6603	745.3338	1472.6337	736.8205	1471.6497	736.3285	G	2304.9860	1152.9966	2287.9594	1144.4834	2286.9754	1143.9913	20
14	1603.7032	802.3552	1586.6766	793.8420	1585.6926	793.3500	N	2247.9645	1124.4859	2230.9380	1115.9726	2229.9539	1115.4806	19
15	1660.7247	830.8660	1643.6981	822.3527	1642.7141	821.8607	G	2133.9216	1067.4644	2116.8950	1058.9512	2115.9110	1058.4591	18
16	1761.7723	881.3898	1744.7458	872.8765	1743.7618	872.3845	T	2076.9001	1038.9537	2059.8736	1030.4404	2058.8896	1029.9484	17
17	1874.8564	937.9318	1857.8299	929.4186	1856.8458	928.9266	I	1975.8524	988.4299	1958.8259	979.9166	1957.8419	979.4246	16
18	1975.9041	988.4557	1958.8775	979.9424	1957.8935	979.4504	T	1862.7684	931.8878	1845.7418	923.3746	1844.7578	922.8825	15
19	2135.9347	1068.4710	2118.9082	1059.9577	2117.9242	1059.4657	C	1761.7207	881.3640	1744.6941	872.8507	1743.7101	872.3587	14
20	2236.9824	1118.9948	2219.9559	1110.4816	2218.9718	1109.9896	T	1601.6900	801.3487	1584.6635	792.8354	1583.6795	792.3434	13
21	2366.0250	1183.5161	2348.9985	1175.0029	2348.0144	1174.5109	E	1500.6424	750.8248	1483.6158	742.3115	1482.6318	741.8195	12
22	2503.0839	1252.0456	2486.0574	1243.5323	2485.0734	1243.0403	H	1371.5998	686.3035	1354.5732	677.7903	1353.5892	677.2982	11
23	2560.1054	1280.5563	2543.0788	1272.0431	2542.0948	1271.5510	G	1234.5409	617.7741	1217.5143	609.2608	1216.5303	608.7688	10

24	2675.1323	1338.0698	2658.1058	1329.5565	2657.1218	1329.0645	N	1177.5194	589.2633	1160.4929	580.7501	1159.5088	580.2581	9
25	2861.2116	1431.1095	2844.1851	1422.5962	2843.2011	1422.1042	W	1062.4925	531.7499	1045.4659	523.2366	1044.4819	522.7446	8
26	2962.2593	1481.6333	2945.2328	1473.1200	2944.2488	1472.6280	T	876.4131	438.7102	859.3866	430.1969	858.4026	429.7049	7
27	3091.3019	1546.1546	3074.2754	1537.6413	3073.2913	1537.1493	E	775.3655	388.1864	758.3389	379.6731	757.3549	379.1811	6
28	3204.3860	1602.6966	3187.3594	1594.1833	3186.3754	1593.6913	L	646.3229	323.6651	629.2963	315.1518	628.3123	314.6598	5
29	3301.4387	1651.2230	3284.4122	1642.7097	3283.4282	1642.2177	P	533.2388	267.1230	516.2123	258.6098	515.2282	258.1178	4
30	3430.4813	1715.7443	3413.4548	1707.2310	3412.4708	1706.7390	E	436.1860	218.5967	419.1595	210.0834	418.1755	209.5914	3
31	3590.5120	1795.7596	3573.4854	1787.2464	3572.5014	1786.7543	C	307.1435	154.0754	290.1169	145.5621			2
32							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [AVFECLPQHAMEFGNGTITCTEHGNWTELPECK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
44.3	3735.6102	-0.0017	AVFECLPQHAMEFGNGTITCTEHGNWTELPECK	Deamidated Q8, N24 44.80%
42.3	3735.6102	-0.0017	AVFECLPQHAMEFGNGTITCTEHGNWTELPECK	Deamidated Q8, N14 28.46%
42.1	3735.6102	-0.0017	AVFECLPQHAMEFGNGTITCTEHGNWTELPECK	Deamidated N14, N24 26.74%
39.5	3734.6262	0.9823	AVFECLPQHAMEFGNGTITCTEHGNWTELPECK	
37.9	3734.6262	0.9823	AVFECLPQHAMEFGNGTITCTEHGNWTELPECK	
36.2	3734.6262	0.9823	AVFECLPQHAMEFGNGTITCTEHGNWTELPECK	
6.7	3735.6401	-0.0316	APTFCDYCGEMLWGLVRQGLKCEGCGLNYHK	
5.1	3735.6268	-0.0183	MQVSETCTSPMLQAKMDEIGNHYMEMLKNLR	
3.2	3735.6268	-0.0183	MQVSETCTSPMLQAKMDEIGNHYMEMLKNLR	
1.5	3735.6457	-0.0372	NSTSSTSQSLFCEERVGYNWAYNTMLTKTWR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

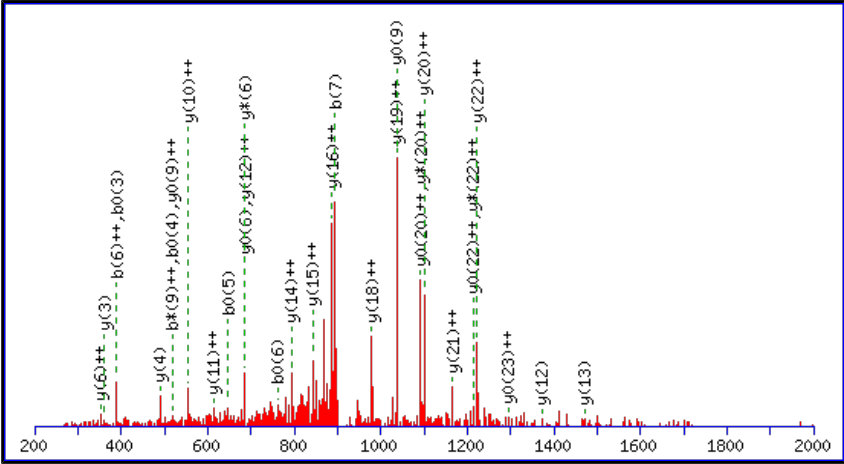
Peptide View

MS/MS Fragmentation of **EYDEQNNASVDVFLGHVNVDEITK**
Found in **F1SLV6** in **uni_pig**, tr|F1SLV6|F1SLV6_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=C1R PE=3 SV=2

Match to Query 13205: 2736.256302 from(913.092710,3+) intensity(0.0000) rtinseconds(2699) scans(5414) index(10135)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_11Spectrum4090_scans_5414
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2736.2402
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
N18 : Deamidated (NQ)
Ions Score: 48 Expect: 0.00092
Matches : 32/266 fragment ions using 62 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							24
2	293.1132	147.0602			275.1026	138.0550	Y	2608.2049	1304.6061	2591.1784	1296.0928	2590.1944	1295.6008	23
3	408.1401	204.5737			390.1296	195.5684	D	2445.1416	1223.0744	2428.1151	1214.5612	2427.1310	1214.0692	22
4	537.1827	269.0950			519.1722	260.0897	E	2330.1147	1165.5610	2313.0881	1157.0477	2312.1041	1156.5557	21
5	665.2413	333.1243	648.2148	324.6110	647.2307	324.1190	Q	2201.0721	1101.0397	2184.0455	1092.5264	2183.0615	1092.0344	20
6	779.2842	390.1458	762.2577	381.6325	761.2737	381.1405	N	2073.0135	1037.0104	2055.9869	1028.4971	2055.0029	1028.0051	19
7	894.3112	447.6592	877.2846	439.1460	876.3006	438.6539	N	1958.9706	979.9889	1941.9440	971.4756	1940.9600	970.9836	18
8	965.3483	483.1778	948.3217	474.6645	947.3377	474.1725	A	1843.9436	922.4754	1826.9171	913.9622	1825.9331	913.4702	17
9	1052.3803	526.6938	1035.3538	518.1805	1034.3698	517.6885	S	1772.9065	886.9569	1755.8800	878.4436	1754.8959	877.9516	16
10	1151.4487	576.2280	1134.4222	567.7147	1133.4382	567.2227	V	1685.8745	843.4409	1668.8479	834.9276	1667.8639	834.4356	15
11	1266.4757	633.7415	1249.4491	625.2282	1248.4651	624.7362	D	1586.8061	793.9067	1569.7795	785.3934	1568.7955	784.9014	14
12	1365.5441	683.2757	1348.5175	674.7624	1347.5335	674.2704	V	1471.7791	736.3932	1454.7526	727.8799	1453.7686	727.3879	13
13	1512.6125	756.8099	1495.5860	748.2966	1494.6019	747.8046	F	1372.7107	686.8590	1355.6842	678.3457	1354.7001	677.8537	12
14	1625.6966	813.3519	1608.6700	804.8387	1607.6860	804.3466	L	1225.6423	613.3248	1208.6157	604.8115	1207.6317	604.3195	11
15	1682.7180	841.8627	1665.6915	833.3494	1664.7075	832.8574	G	1112.5582	556.7828	1095.5317	548.2695	1094.5477	547.7775	10
16	1819.7769	910.3921	1802.7504	901.8788	1801.7664	901.3868	H	1055.5368	528.2720	1038.5102	519.7587	1037.5262	519.2667	9
17	1918.8454	959.9263	1901.8188	951.4130	1900.8348	950.9210	V	918.4779	459.7426	901.4513	451.2293	900.4673	450.7373	8
18	2033.8723	1017.4398	2016.8458	1008.9265	2015.8617	1008.4345	N	819.4094	410.2084	802.3829	401.6951	801.3989	401.2031	7
19	2132.9407	1066.9740	2115.9142	1058.4607	2114.9302	1057.9687	V	704.3825	352.6949	687.3559	344.1816	686.3719	343.6896	6
20	2247.9677	1124.4875	2230.9411	1115.9742	2229.9571	1115.4822	D	605.3141	303.1607	588.2875	294.6474	587.3035	294.1554	5
21	2377.0103	1189.0088	2359.9837	1180.4955	2358.9997	1180.0035	E	490.2871	245.6472	473.2606	237.1339	472.2766	236.6419	4
22	2490.0943	1245.5508	2473.0678	1237.0375	2472.0838	1236.5455	I	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
23	2591.1420	1296.0746	2574.1154	1287.5614	2573.1314	1287.0694	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2

24

K

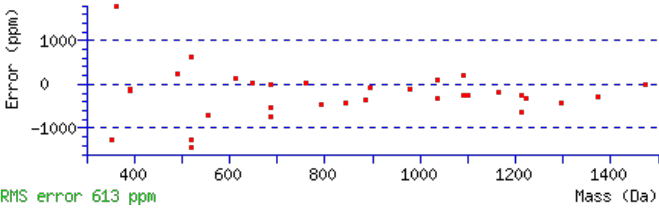
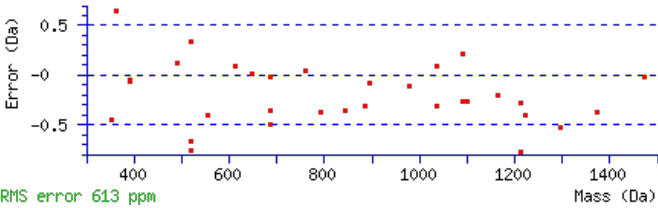
147.1128

74.0600

130.0863

65.5468

1

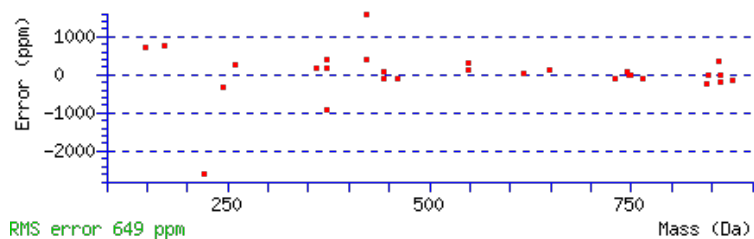


NCBI **BLAST** search of [EYDEQNNASVDVFLGHVNVDEITK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
48.4	2736.2402	0.0161	EYDEQNNASVDVFLGHVNVDEITK	Deamidated N7, N18 30.78%
47.0	2736.2402	0.0161	EYDEQNNASVDVFLGHVNVDEITK	Deamidated N6, N18 21.99%
47.0	2736.2402	0.0161	EYDEQNNASVDVFLGHVNVDEITK	Deamidated Q5, N18 21.99%
44.3	2736.2402	0.0161	EYDEQNNASVDVFLGHVNVDEITK	Deamidated N6, N7 11.78%
44.3	2736.2402	0.0161	EYDEQNNASVDVFLGHVNVDEITK	Deamidated Q5, N7 11.78%
43.4	2735.2562	1.0001	EYDEQNNASVDVFLGHVNVDEITK	
41.1	2735.2562	1.0001	EYDEQNNASVDVFLGHVNVDEITK	
35.8	2736.2402	0.0161	EYDEQNNASVDVFLGHVNVDEITK	Deamidated Q5, N6 1.67%
33.0	2735.2562	1.0001	EYDEQNNASVDVFLGHVNVDEITK	
33.0	2735.2562	1.0001	EYDEQNNASVDVFLGHVNVDEITK	

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [MLNTSSLLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.5	1006.5369	-0.0011	MLNTSSLLK
17.3	1004.5212	2.0146	EMQDKILK
15.0	1005.5382	0.9975	FENEIILK
14.5	1004.5212	2.0146	NELEKMLK
14.1	1004.5250	2.0107	KNDGSAASKK
13.2	1004.5212	2.0146	EINKLEMK
12.2	1005.5277	1.0081	MSRQLNIK
12.0	1004.5325	2.0033	KEVQTCLK
11.4	1004.5324	2.0033	ESIEMRLK
11.2	1004.5251	2.0107	KNESSSVVR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQCIVDDITYNVNDTFHK**
Found in **F1SS24** in **uni_pig**, tr[F1SS24]F1SS24_PIG Uncharacterized protein OS=Sus scrofa GN=FN1 PE=4 SV=1

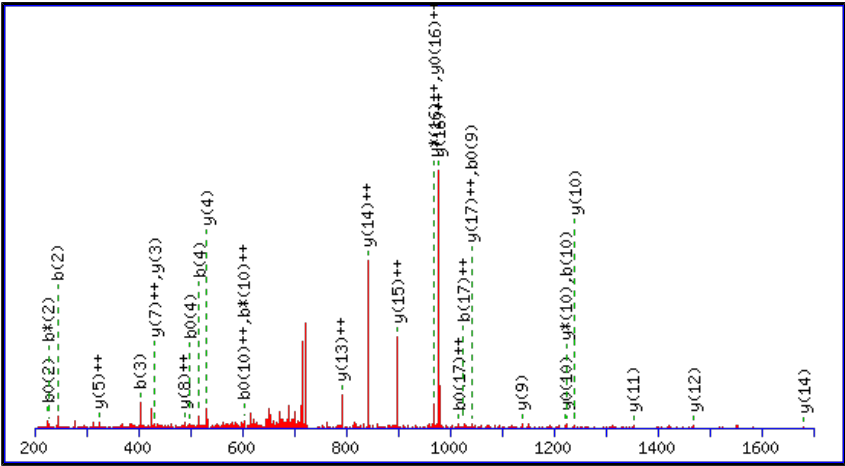
Match to Query 12361: 2197.960992 from(733.660940,3+) intensity(2923.2134) rtinseconds(2307) scans(4710) index(3465)
Title: 120325_Sunil_PigSerum_Glyco_P_12Spectrum3573_scans__4710
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

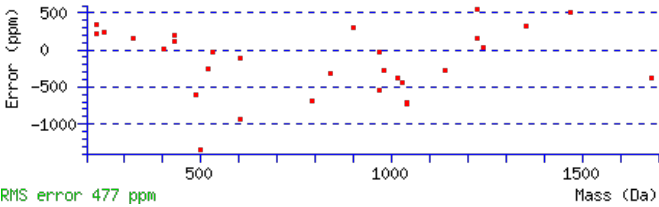
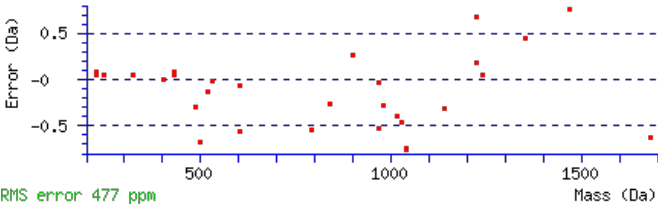
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2197.9474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
N13 : Deamidated (NQ)
Ions Score: 45 Expect: 0.0011
Matches : 31/196 fragment ions using 57 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							18
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	Q	2083.9277	1042.4675	2066.9012	1033.9542	2065.9171	1033.4622	17
3	404.1234	202.5654	387.0969	194.0521	386.1129	193.5601	C	1955.8691	978.4382	1938.8426	969.9249	1937.8586	969.4329	16
4	517.2075	259.1074	500.1810	250.5941	499.1969	250.1021	I	1795.8385	898.4229	1778.8119	889.9096	1777.8279	889.4176	15
5	616.2759	308.6416	599.2494	300.1283	598.2654	299.6363	V	1682.7544	841.8809	1665.7279	833.3676	1664.7439	832.8756	14
6	731.3029	366.1551	714.2763	357.6418	713.2923	357.1498	D	1583.6860	792.3466	1566.6595	783.8334	1565.6754	783.3414	13
7	846.3298	423.6685	829.3033	415.1553	828.3192	414.6633	D	1468.6591	734.8332	1451.6325	726.3199	1450.6485	725.8279	12
8	959.4139	480.2106	942.3873	471.6973	941.4033	471.2053	I	1353.6321	677.3197	1336.6056	668.8064	1335.6216	668.3144	11
9	1060.4616	530.7344	1043.4350	522.2211	1042.4510	521.7291	T	1240.5481	620.7777	1223.5215	612.2644	1222.5375	611.7724	10
10	1223.5249	612.2661	1206.4983	603.7528	1205.5143	603.2608	Y	1139.5004	570.2538	1122.4738	561.7406	1121.4898	561.2485	9
11	1338.5518	669.7796	1321.5253	661.2663	1320.5413	660.7743	N	976.4371	488.7222	959.4105	480.2089	958.4265	479.7169	8
12	1437.6202	719.3138	1420.5937	710.8005	1419.6097	710.3085	V	861.4101	431.2087	844.3836	422.6954	843.3995	422.2034	7
13	1552.6472	776.8272	1535.6206	768.3140	1534.6366	767.8219	N	762.3417	381.6745	745.3151	373.1612	744.3311	372.6692	6
14	1667.6741	834.3407	1650.6476	825.8274	1649.6636	825.3354	D	647.3148	324.1610	630.2882	315.6477	629.3042	315.1557	5
15	1768.7218	884.8645	1751.6953	876.3513	1750.7112	875.8593	T	532.2878	266.6475	515.2613	258.1343	514.2772	257.6423	4
16	1915.7902	958.3987	1898.7637	949.8855	1897.7797	949.3935	F	431.2401	216.1237	414.2136	207.6104			3
17	2052.8491	1026.9282	2035.8226	1018.4149	2034.8386	1017.9229	H	284.1717	142.5895	267.1452	134.0762			2
18							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [DQCIVDDITYNVNDTFHK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
44.5	2197.9474	0.0136	DQCIVDDITYNVNDTFHK	Deamidated N11, N13 98.96%
28.6	2196.9634	0.9976	DQCIVDDITYNVNDTFHK	
27.6	2196.9634	0.9976	DQCIVDDITYNVNDTFHK	
22.9	2197.9474	0.0136	DQCIVDDITYNVNDTFHK	Deamidated Q2, N13 0.69%
20.0	2197.9474	0.0136	DQCIVDDITYNVNDTFHK	Deamidated Q2, N11 0.35%
16.9	2196.9634	0.9976	DQCIVDDITYNVNDTFHK	
15.6	2197.9645	-0.0035	GSDSSSLSESESAKGSADCLPK	
8.4	2197.9545	0.0065	ENSERAEE MQDSFQRNVK	
6.6	2197.9797	-0.0187	ENAEKMSEQYDINLEDVR	
6.4	2197.9554	0.0055	AGEELDMKDQSCKPCAEGR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

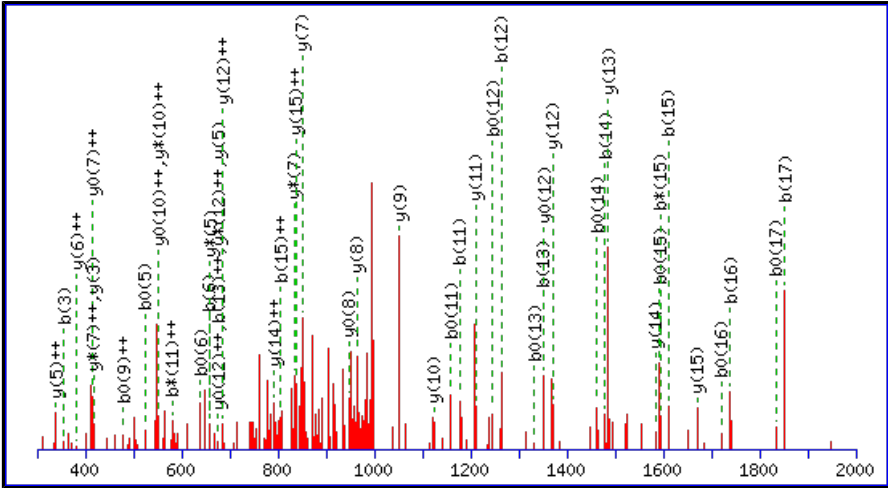
Peptide View

MS/MS Fragmentation of **EILSVDCSASNSSQMQLR**
Found in **F1RJS2** in **uni_pig**, tr|F1RJS2|F1RJS2_PIG Clusterin OS=Sus scrofa GN=CLU PE=3 SV=2

Match to Query 10943: 2025.907068 from(1013.960810,2+) intensity(1992.0930) rtinseconds(1854) scans(3240) index(8253)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_13Spectrum2232_scans__3240
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

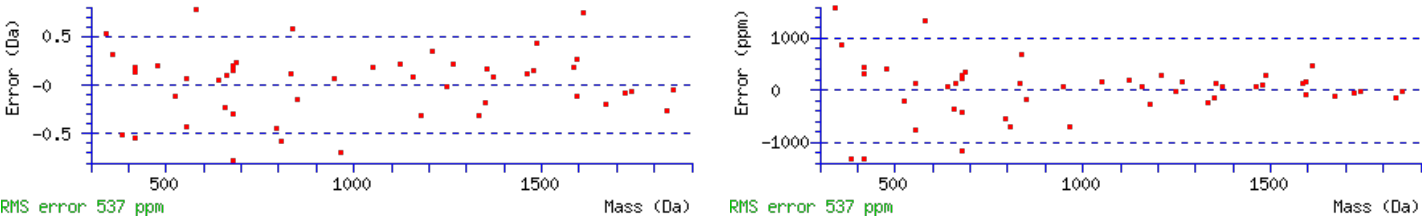
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2025.8983
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Q16 : Deamidated (NQ)
Ions Score: 45 Expect: 0.0011
Matches : 49/174 fragment ions using 117 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							18
2	243.1339	122.0706			225.1234	113.0653	I	1897.8630	949.4351	1880.8365	940.9219	1879.8524	940.4299	17
3	356.2180	178.6126			338.2074	169.6074	L	1784.7789	892.8931	1767.7524	884.3798	1766.7684	883.8878	16
4	443.2500	222.1287			425.2395	213.1234	S	1671.6949	836.3511	1654.6683	827.8378	1653.6843	827.3458	15
5	542.3184	271.6629			524.3079	262.6576	V	1584.6628	792.8351	1567.6363	784.3218	1566.6523	783.8298	14
6	657.3454	329.1763			639.3348	320.1710	D	1485.5944	743.3009	1468.5679	734.7876	1467.5839	734.2956	13
7	817.3760	409.1917			799.3655	400.1864	C	1370.5675	685.7874	1353.5409	677.2741	1352.5569	676.7821	12
8	904.4081	452.7077			886.3975	443.7024	S	1210.5368	605.7721	1193.5103	597.2588	1192.5263	596.7668	11
9	975.4452	488.2262			957.4346	479.2209	A	1123.5048	562.2560	1106.4783	553.7428	1105.4942	553.2508	10
10	1062.4772	531.7422			1044.4666	522.7370	S	1052.4677	526.7375	1035.4412	518.2242	1034.4571	517.7322	9
11	1177.5041	589.2557	1160.4776	580.7424	1159.4936	580.2504	N	965.4357	483.2215	948.4091	474.7082	947.4251	474.2162	8
12	1264.5362	632.7717	1247.5096	624.2584	1246.5256	623.7664	S	850.4087	425.7080	833.3822	417.1947	832.3982	416.7027	7
13	1351.5682	676.2877	1334.5417	667.7745	1333.5576	667.2825	S	763.3767	382.1920	746.3502	373.6787	745.3661	373.1867	6
14	1479.6268	740.3170	1462.6002	731.8038	1461.6162	731.3117	Q	676.3447	338.6760	659.3181	330.1627			5
15	1610.6673	805.8373	1593.6407	797.3240	1592.6567	796.8320	M	548.2861	274.6467	531.2595	266.1334			4
16	1739.7099	870.3586	1722.6833	861.8453	1721.6993	861.3533	Q	417.2456	209.1264	400.2191	200.6132			3
17	1852.7939	926.9006	1835.7674	918.3873	1834.7834	917.8953	L	288.2030	144.6051	271.1765	136.0919			2
18							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [EILSVDCSASNSSQMQLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.1	2025.8983	0.0088	EILSVDCSASNSSQMQLR	Deamidated N11, Q16 49.72%
45.1	2025.8983	0.0088	EILSVDCSASNSSQMQLR	Deamidated N11, Q14 49.50%
45.1	2024.9143	0.9928	EILSVDCSASNSSQMQLR	
38.2	2024.9143	0.9928	EILSVDCSASNSSQMQLR	
29.9	2024.9143	0.9928	EILSVDCSASNSSQMQLR	
27.1	2025.8983	0.0088	EILSVDCSASNSSQMQLR	Deamidated Q14, Q16 0.78%
2.2	2025.8870	0.0201	ELNESNSQMEADMLKLR	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1RN76** in **uni_pig**, tr|F1RN76|F1RN76_PIG Uncharacterized protein OS=Sus scrofa GN=CD5L PE=4 SV=2

Title: 120325_Sunil_PigSerum_Glyco_D_14Spectrum4550_scans__5306

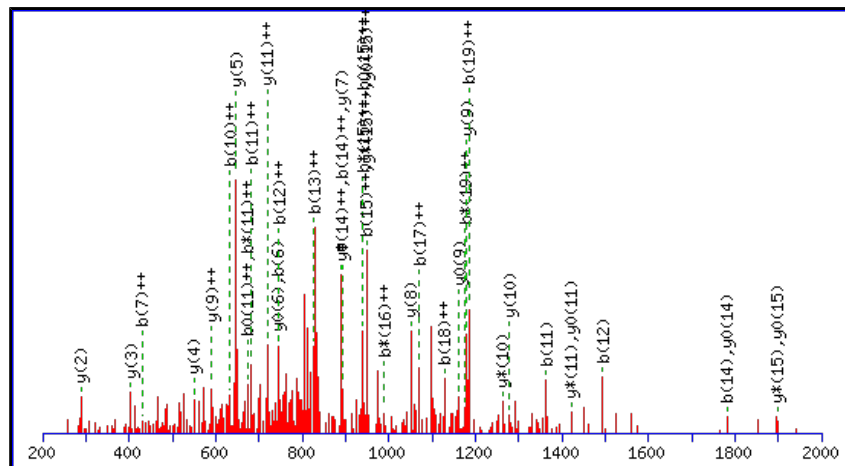
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

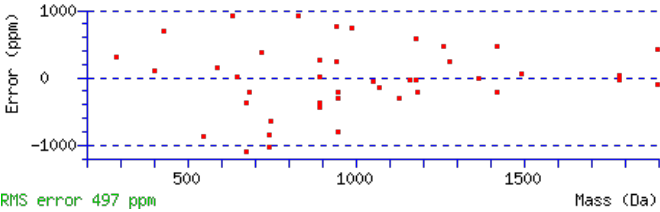
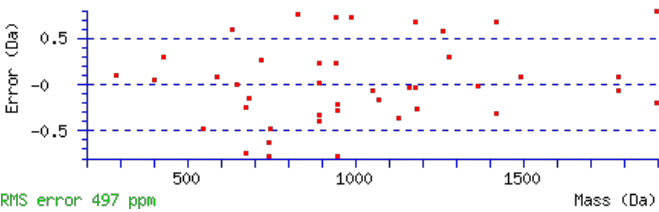
N1 : Deamidated (NQ)

N2 : Deamidated (NQ)

Ions Score: 29 Expect: 0.0013

Matches : 42/218 fragment ions using 85 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							20
2	231.0612	116.0342	214.0346	107.5209			N	2428.8785	1214.9429	2411.8519	1206.4296	2410.8679	1205.9376	19
3	391.0918	196.0495	374.0653	187.5363			C	2313.8515	1157.4294	2296.8250	1148.9161	2295.8410	1148.4241	18
4	492.1395	246.5734	475.1129	238.0601	474.1289	237.5681	T	2153.8209	1077.4141	2136.7943	1068.9008	2135.8103	1068.4088	17
5	629.1984	315.1028	612.1719	306.5896	611.1878	306.0976	H	2052.7732	1026.8902	2035.7467	1018.3770	2034.7626	1017.8850	16
6	744.2253	372.6163	727.1988	364.1030	726.2148	363.6110	D	1915.7143	958.3608	1898.6877	949.8475	1897.7037	949.3555	15
7	859.2523	430.1298	842.2257	421.6165	841.2417	421.1245	D	1800.6873	900.8473	1783.6608	892.3340	1782.6768	891.8420	14
8	974.2792	487.6433	957.2527	479.1300	956.2687	478.6380	D	1685.6604	843.3338	1668.6339	834.8206	1667.6498	834.3286	13
9	1105.3197	553.1635	1088.2932	544.6502	1087.3092	544.1582	M	1570.6335	785.8204	1553.6069	777.3071	1552.6229	776.8151	12
10	1265.3504	633.1788	1248.3238	624.6655	1247.3398	624.1735	C	1439.5930	720.3001	1422.5664	711.7869	1421.5824	711.2948	11
11	1364.4188	682.7130	1347.3922	674.1998	1346.4082	673.7077	V	1279.5623	640.2848	1262.5358	631.7715	1261.5518	631.2795	10
12	1493.4614	747.2343	1476.4348	738.7210	1475.4508	738.2290	E	1180.4939	590.7506	1163.4674	582.2373	1162.4834	581.7453	9
13	1653.4920	827.2496	1636.4655	818.7364	1635.4815	818.2444	C	1051.4513	526.2293	1034.4248	517.7160	1033.4408	517.2240	8
14	1782.5346	891.7709	1765.5081	883.2577	1764.5240	882.7657	E	891.4207	446.2140	874.3941	437.7007	873.4101	437.2087	7
15	1897.5616	949.2844	1880.5350	940.7711	1879.5510	940.2791	D	762.3781	381.6927	745.3515	373.1794	744.3675	372.6874	6
16	1994.6143	997.8108	1977.5878	989.2975	1976.6038	988.8055	P	647.3511	324.1792	630.3246	315.6659	629.3406	315.1739	5
17	2141.6827	1071.3450	2124.6562	1062.8317	2123.6722	1062.3397	F	550.2984	275.6528	533.2718	267.1396	532.2878	266.6475	4
18	2256.7097	1128.8585	2239.6831	1120.3452	2238.6991	1119.8532	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
19	2369.7937	1185.4005	2352.7672	1176.8872	2351.7832	1176.3952	L	288.2030	144.6051	271.1765	136.0919			2
20							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [NNCTHDDDMCVECEDPFDLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.8	2542.8981	2.0164	NNCTHDDDMCVECEDPFDLR

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1S0J3** in **uni_pig**, tr|F1S0J3|F1S0J3_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPB PE=4 SV=1

Title: 120325_Sunil_PigSerum_Glyco_P_01Spectrum4884_scans__5917

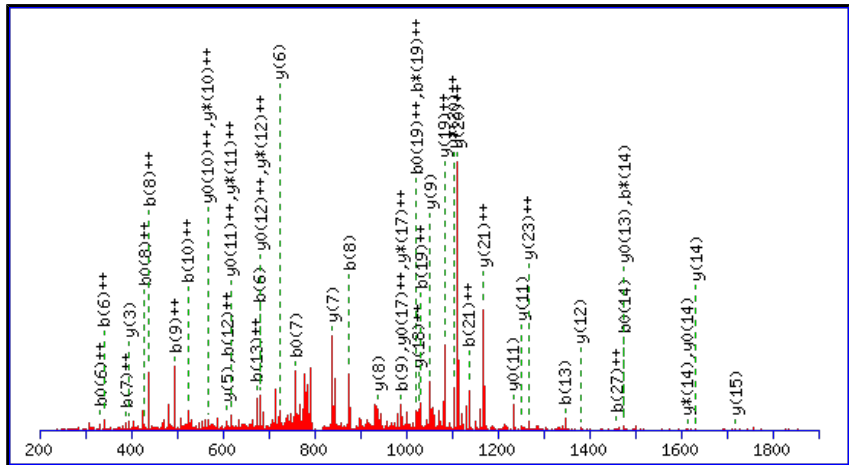
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

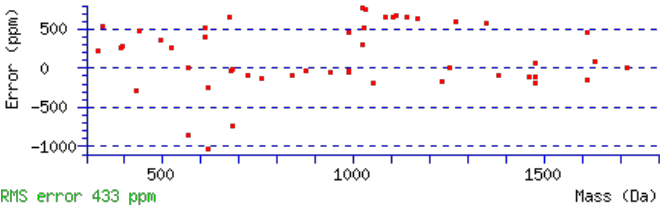
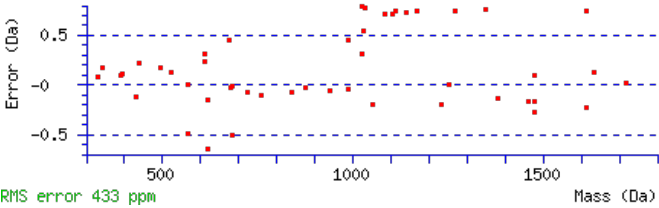
N23 : Deamidated (NQ)

Ions Score: 47 Expect: 0.0013

Matches : 49/302 fragment ions using 95 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							29
2	171.1128	86.0600					G	3098.4524	1549.7298	3081.4258	1541.2166	3080.4418	1540.7246	28
3	308.1717	154.5895					H	3041.4309	1521.2191	3024.4044	1512.7058	3023.4204	1512.2138	27
4	468.2024	234.6048					C	2904.3720	1452.6896	2887.3455	1444.1764	2886.3615	1443.6844	26
5	565.2551	283.1312					P	2744.3414	1372.6743	2727.3148	1364.1610	2726.3308	1363.6690	25
6	680.2821	340.6447			662.2715	331.6394	D	2647.2886	1324.1479	2630.2621	1315.6347	2629.2780	1315.1427	24
7	777.3348	389.1711			759.3243	380.1658	P	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	23
8	876.4033	438.7053			858.3927	429.7000	V	2435.2089	1218.1081	2418.1823	1209.5948	2417.1983	1209.1028	22
9	989.4873	495.2473			971.4767	486.2420	L	2336.1405	1168.5739	2319.1139	1160.0606	2318.1299	1159.5686	21
10	1046.5088	523.7580			1028.4982	514.7527	G	2223.0564	1112.0318	2206.0299	1103.5186	2205.0459	1103.0266	20
11	1160.5517	580.7795	1143.5252	572.2662	1142.5411	571.7742	N	2166.0350	1083.5211	2149.0084	1075.0078	2148.0244	1074.5158	19
12	1217.5732	609.2902	1200.5466	600.7769	1199.5626	600.2849	G	2051.9920	1026.4997	2034.9655	1017.9864	2033.9815	1017.4944	18
13	1346.6158	673.8115	1329.5892	665.2982	1328.6052	664.8062	E	1994.9706	997.9889	1977.9440	989.4756	1976.9600	988.9836	17
14	1493.6842	747.3457	1476.6576	738.8325	1475.6736	738.3404	F	1865.9280	933.4676	1848.9014	924.9543	1847.9174	924.4623	16
15	1580.7162	790.8617	1563.6897	782.3485	1562.7056	781.8565	S	1718.8596	859.9334	1701.8330	851.4201	1700.8490	850.9281	15
16	1717.7751	859.3912	1700.7486	850.8779	1699.7646	850.3859	H	1631.8275	816.4174	1614.8010	807.9041	1613.8170	807.4121	14
17	1830.8592	915.9332	1813.8326	907.4200	1812.8486	906.9279	L	1494.7686	747.8879	1477.7421	739.3747	1476.7581	738.8827	13
18	1959.9018	980.4545	1942.8752	971.9413	1941.8912	971.4492	E	1381.6846	691.3459	1364.6580	682.8326	1363.6740	682.3406	12
19	2060.9495	1030.9784	2043.9229	1022.4651	2042.9389	1021.9731	T	1252.6420	626.8246	1235.6154	618.3113	1234.6314	617.8193	11
20	2160.0179	1080.5126	2142.9913	1071.9993	2142.0073	1071.5073	V	1151.5943	576.3008	1134.5677	567.7875	1133.5837	567.2955	10
21	2274.0608	1137.5340	2257.0342	1129.0208	2256.0502	1128.5288	N	1052.5259	526.7666	1035.4993	518.2533	1034.5153	517.7613	9
22	2373.1292	1187.0682	2356.1027	1178.5550	2355.1186	1178.0630	V	938.4829	469.7451	921.4564	461.2318	920.4724	460.7398	8
23	2488.1561	1244.5817	2471.1296	1236.0684	2470.1456	1235.5764	N	839.4145	420.2109	822.3880	411.6976	821.4040	411.2056	7
24	2603.1831	1302.0952	2586.1565	1293.5819	2585.1725	1293.0899	D	724.3876	362.6974	707.3610	354.1842	706.3770	353.6921	6

25	2704.2308	1352.6190	2687.2042	1344.1057	2686.2202	1343.6137	T	609.3606	305.1840	592.3341	296.6707	591.3501	296.1787	5
26	2817.3148	1409.1611	2800.2883	1400.6478	2799.3043	1400.1558	I	508.3130	254.6601	491.2864	246.1468	490.3024	245.6548	4
27	2918.3625	1459.6849	2901.3360	1451.1716	2900.3519	1450.6796	T	395.2289	198.1181	378.2023	189.6048	377.2183	189.1128	3
28	3065.4309	1533.2191	3048.4044	1524.7058	3047.4204	1524.2138	F	294.1812	147.5942	277.1547	139.0810			2
29							K	147.1128	74.0600	130.0863	65.5468			1

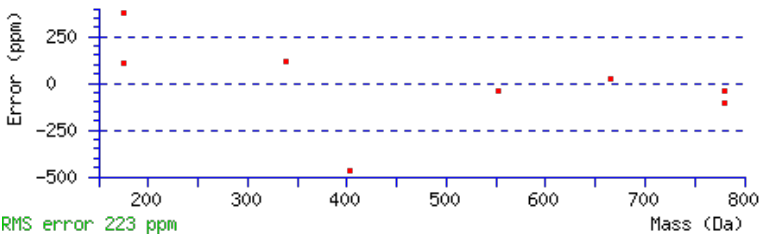


NCBI BLAST search of [LGHCDDPVLGNGEFSLHETVNVNDTITEK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.5	3210.5292	0.9763	LGHCDDPVLGNGEFSLHETVNVNDTITEK	Deamidated N23 87.33%
45.1	3211.5132	-0.0077	LGHCDDPVLGNGEFSLHETVNVNDTITEK	
39.0	3210.5292	0.9763	LGHCDDPVLGNGEFSLHETVNVNDTITEK	Deamidated N21 12.31%
36.8	3211.5132	-0.0077	LGHCDDPVLGNGEFSLHETVNVNDTITEK	
26.6	3211.5132	-0.0077	LGHCDDPVLGNGEFSLHETVNVNDTITEK	
23.6	3210.5292	0.9763	LGHCDDPVLGNGEFSLHETVNVNDTITEK	Deamidated N11 0.36%
8.6	3209.4733	2.0322	WSSRDSFSGFFGGMQSPLSLRQMSIPK	
4.4	3211.4882	0.0173	GANPNLRNCNMMAPLHVAVQRLNNEVMK	
4.4	3211.4882	0.0173	GANPNLRNCNMMAPLHVAVQRLNNEVMK	
2.9	3210.5255	0.9800	MAGPSLACCLLGLLALTSACYIQCPLGGK	

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [SSNITIYR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

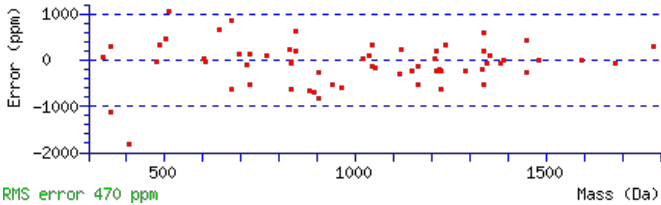
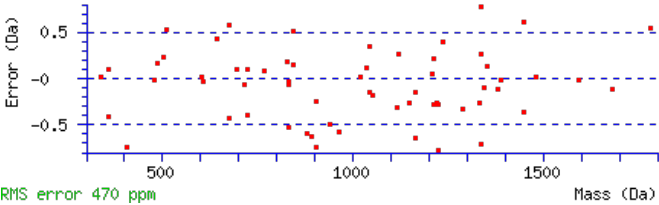
All matches to this query

Score	Mr(calc)	Delta	Sequence
44.9	953.4818	-0.0014	SSNITIYR
13.1	952.4800	1.0004	AMAQLTYR
13.1	951.4661	2.0143	TVAENVYR
12.9	952.4800	1.0004	QCITYIR
9.2	953.4818	-0.0014	STYVTEVR
9.2	953.4719	0.0085	WNLHVER
8.9	952.4800	1.0004	NKEIMYR
7.7	953.4752	0.0052	MIAEYRR
6.5	953.4719	0.0085	WNTSKYR
6.5	953.4753	0.0052	FRELMR

Mascot: <http://www.matrixscience.com/>

[http://mascotxp.student.main.ntu.edu.sg/mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=13309\[22/Apr/15 06:08:38 PM\]](http://mascotxp.student.main.ntu.edu.sg/mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=13309[22/Apr/15 06:08:38 PM])

24	2444.2092	1222.6083	2427.1827	1214.0950	2426.1987	1213.6030	V	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
25	2573.2518	1287.1296	2556.2253	1278.6163	2555.2413	1278.1243	E	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
26	2686.3359	1343.6716	2669.3093	1335.1583	2668.3253	1334.6663	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
27	2773.3679	1387.1876	2756.3414	1378.6743	2755.3574	1378.1823	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
28							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [VVHAAESALAAFNAQSNGSYLQLVEISR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
48.4	2946.4723	0.0144	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated N13, N17 47.58%
44.4	2946.4723	0.0144	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated N13, Q15 18.81%
42.9	2946.4723	0.0144	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated Q15, N17 13.41%
42.9	2946.4723	0.0144	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated N13, Q22 13.32%
37.7	2946.4723	0.0144	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated Q15, Q22 4.05%
36.8	2945.4883	0.9984	VVHAAESALAAFNAQSNGSYLQLVEISR	
36.1	2946.4723	0.0144	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated N17, Q22 2.83%
32.8	2945.4883	0.9984	VVHAAESALAAFNAQSNGSYLQLVEISR	
32.7	2945.4883	0.9984	VVHAAESALAAFNAQSNGSYLQLVEISR	
26.1	2945.4883	0.9984	VVHAAESALAAFNAQSNGSYLQLVEISR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

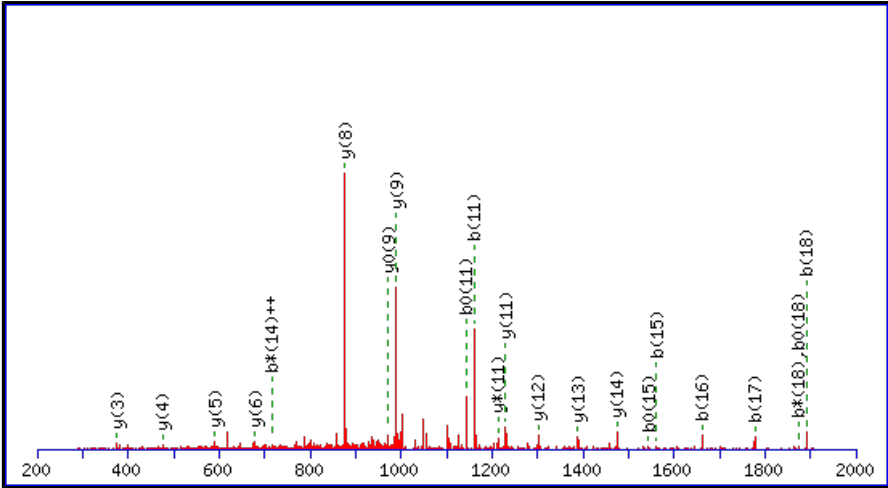
Peptide View

MS/MS Fragmentation of **VNLSFSSAQILPTSDTNLK**
Found in **I3LQ17** in **uni_pig**, tr|I3LQ17|I3LQ17_PIG Uncharacterized protein OS=Sus scrofa PE=4 SV=1

Match to Query 11817: 2036.024348 from(1019.019450,2+) intensity(10679.7139) rtinseconds(2628) scans(6192) index(10504)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_13Spectrum5272_scans__6192
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

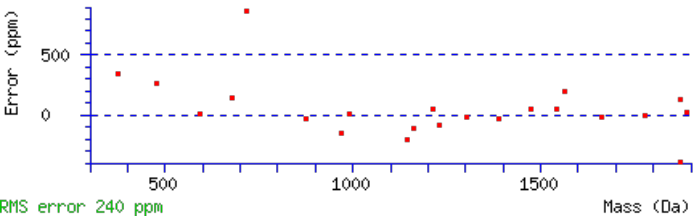
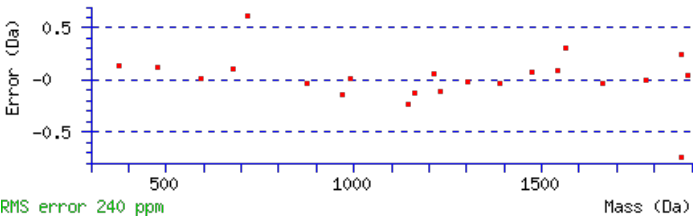
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2036.0313
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
N17 : Deamidated (NQ)
Ions Score: 48 Expect: 0.0014
Matches : 22/202 fragment ions using 51 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							19
2	215.1026	108.0550	198.0761	99.5417			N	1937.9702	969.4888	1920.9437	960.9755	1919.9597	960.4835	18
3	328.1867	164.5970	311.1601	156.0837			L	1822.9433	911.9753	1805.9167	903.4620	1804.9327	902.9700	17
4	415.2187	208.1130	398.1922	199.5997	397.2082	199.1077	S	1709.8592	855.4332	1692.8327	846.9200	1691.8487	846.4280	16
5	562.2871	281.6472	545.2606	273.1339	544.2766	272.6419	F	1622.8272	811.9172	1605.8006	803.4040	1604.8166	802.9120	15
6	649.3192	325.1632	632.2926	316.6499	631.3086	316.1579	S	1475.7588	738.3830	1458.7322	729.8698	1457.7482	729.3777	14
7	736.3512	368.6792	719.3246	360.1660	718.3406	359.6740	S	1388.7268	694.8670	1371.7002	686.3537	1370.7162	685.8617	13
8	807.3883	404.1978	790.3618	395.6845	789.3777	395.1925	A	1301.6947	651.3510	1284.6682	642.8377	1283.6842	642.3457	12
9	935.4469	468.2271	918.4203	459.7138	917.4363	459.2218	Q	1230.6576	615.8324	1213.6311	607.3192	1212.6470	606.8272	11
10	1048.5310	524.7691	1031.5044	516.2558	1030.5204	515.7638	I	1102.5990	551.8032	1085.5725	543.2899	1084.5885	542.7979	10
11	1161.6150	581.3111	1144.5885	572.7979	1143.6044	572.3059	L	989.5150	495.2611	972.4884	486.7478	971.5044	486.2558	9
12	1258.6678	629.8375	1241.6412	621.3243	1240.6572	620.8322	P	876.4309	438.7191	859.4044	430.2058	858.4203	429.7138	8
13	1359.7155	680.3614	1342.6889	671.8481	1341.7049	671.3561	T	779.3781	390.1927	762.3516	381.6794	761.3676	381.1874	7
14	1446.7475	723.8774	1429.7209	715.3641	1428.7369	714.8721	S	678.3305	339.6689	661.3039	331.1556	660.3199	330.6636	6
15	1561.7744	781.3909	1544.7479	772.8776	1543.7639	772.3856	D	591.2984	296.1529	574.2719	287.6396	573.2879	287.1476	5
16	1662.8221	831.9147	1645.7956	823.4014	1644.8115	822.9094	T	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
17	1777.8491	889.4282	1760.8225	880.9149	1759.8385	880.4229	N	375.2238	188.1155	358.1973	179.6023			3
18	1890.9331	945.9702	1873.9066	937.4569	1872.9226	936.9649	L	260.1969	130.6021	243.1703	122.0888			2
19							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VNLSESSAQILPTSDTNLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

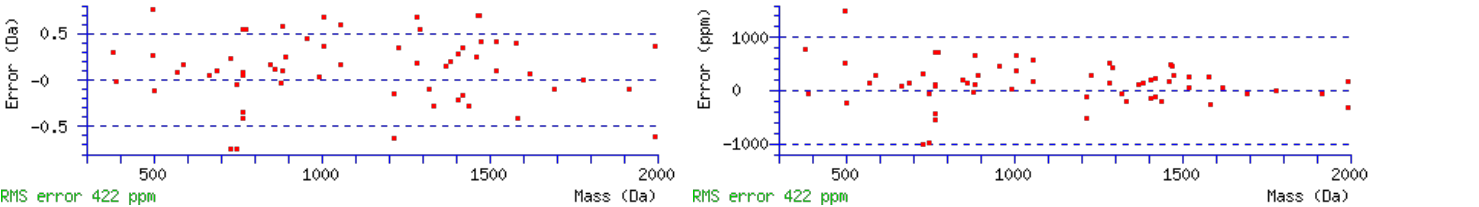
All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.8	2036.0313	-0.0070	VNLSESSAQILPTSDTNLK	Deamidated N2, N17 62.22%
45.6	2036.0313	-0.0070	VNLSESSAQILPTSDTNLK	Deamidated Q9, N17 37.49%
24.4	2036.0313	-0.0070	VNLSESSAQILPTSDTNLK	Deamidated N2, Q9 0.28%
9.4	2035.0109	1.0134	NNFQQELLSNKELTDK	
9.4	2035.0109	1.0134	NNFQQELLSNKELTDK	
9.4	2035.0109	1.0134	NNFQQELLSNKELTDK	
6.7	2036.0061	0.0182	EFLRLQQENKSNSEALK	
4.5	2035.0109	1.0134	NNFQQELLSNKELTDK	
4.5	2035.0109	1.0134	NNFQQELLSNKELTDK	
4.5	2035.0109	1.0134	NNFQQELLSNKELTDK	

Mascot: <http://www.matrixscience.com/>

[http://mascotxp.student.main.ntu.edu.sg/mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=13457\[22/Apr/15 06:08:47 PM\]](http://mascotxp.student.main.ntu.edu.sg/mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=13457[22/Apr/15 06:08:47 PM])

24	2641.1610	1321.0841	2624.1345	1312.5709	2623.1505	1312.0789	G	747.4359	374.2216	730.4094	365.7083	729.4254	365.2163	7
25	2742.2087	1371.6080	2725.1822	1363.0947	2724.1981	1362.6027	T	690.4145	345.7109	673.3879	337.1976	672.4039	336.7056	6
26	2829.2407	1415.1240	2812.2142	1406.6107	2811.2302	1406.1187	S	589.3668	295.1870	572.3402	286.6738	571.3562	286.1817	5
27	2942.3248	1471.6660	2925.2982	1463.1528	2924.3142	1462.6608	L	502.3348	251.6710	485.3082	243.1577	484.3242	242.6657	4
28	3043.3725	1522.1899	3026.3459	1513.6766	3025.3619	1513.1846	T	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
29	3156.4565	1578.7319	3139.4300	1570.2186	3138.4460	1569.7266	I	288.2030	144.6051	271.1765	136.0919			2
30							R	175.1190	88.0631	158.0924	79.5498			1

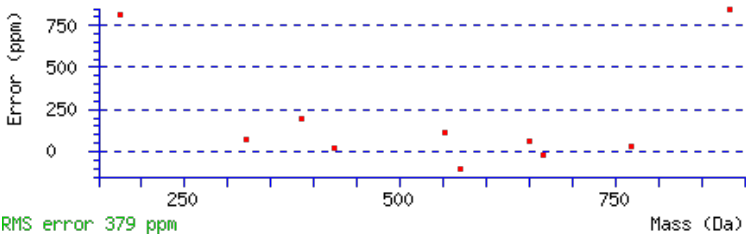


NCBI BLAST search of [YESNATTDEHGLVQFSINTTEIMGTSLTIR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.2	3329.5609	0.9877	YESNATTDEHGLVQFSINTTEIMGTSLTIR	Deamidated Q14, N18 97.12%
37.3	3330.5449	0.0037	YESNATTDEHGLVQFSINTTEIMGTSLTIR	
31.3	3329.5609	0.9877	YESNATTDEHGLVQFSINTTEIMGTSLTIR	Deamidated N4, N18 2.53%
22.8	3329.5609	0.9877	YESNATTDEHGLVQFSINTTEIMGTSLTIR	Deamidated N4, Q14 0.36%
7.2	3329.5436	1.0050	QREEKQQSTLTEWYSAQENTFKPESQR	
7.2	3329.5436	1.0050	QREEKQQSTLTEWYSAQENTFKPESQR	
6.7	3329.5436	1.0050	QREEKQQSTLTEWYSAQENTFKPESQR	
6.6	3330.5276	0.0210	QREEKQQSTLTEWYSAQENTFKPESQR	
5.6	3328.5306	2.0180	FLSGTSPHGTNQHSPQVGPTATQAMQEFLTR	
5.3	3328.5306	2.0180	FLSGTSPHGTNQHSPQVGPTATQAMQEFLTR	

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [EITNETER](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.9	1009.4716	-0.0011	EITNETER
4.7	1008.4620	1.0085	TPMDMGTIK
4.7	1009.4730	-0.0025	DDWPRGHK
4.3	1008.4620	1.0085	NEMNIMIK
4.2	1009.4725	-0.0020	KACYMPPK
2.6	1008.4658	1.0047	MSEAANSKR
1.3	1009.4716	-0.0011	IQQNTETR
0.7	1008.4764	0.9941	TEENFLK

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1SKB1** in **uni_pig**, tr|F1SKB1|F1SKB1_PIG Uncharacterized protein OS=Sus scrofa GN=CP PE=4 SV=3

Title: 120325_Sunil_PigSerum_Glyco_S_11Spectrum1776_scans__2728

Data file

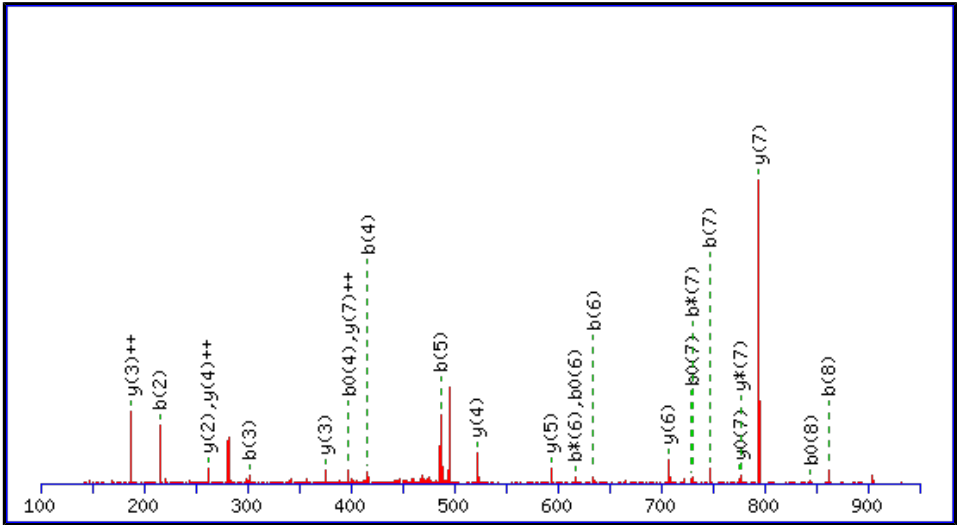
W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



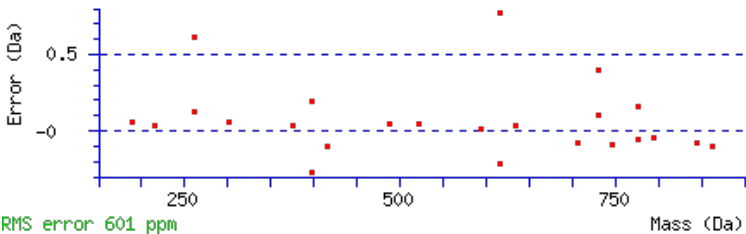
Variable modifications:

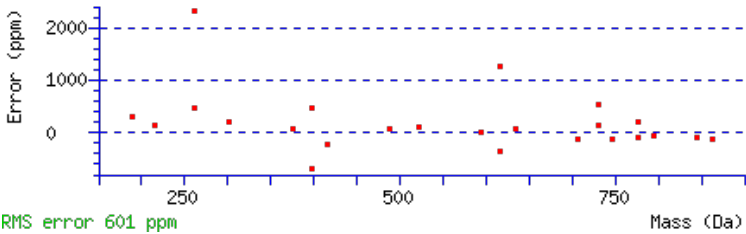
N1 : Deamidated (NQ)

Ions Score: 45 Expect: 0.0014

Matches : 24/90 fragment ions using 40 most intense peaks ([help](#))

#	b	b⁺⁺	b*	b^{*++}	b⁰	b⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							9
2	215.1026	108.0550	198.0761	99.5417			V	893.4727	447.2400	876.4462	438.7267	875.4621	438.2347	8
3	302.1347	151.5710	285.1081	143.0577	284.1241	142.5657	S	794.4043	397.7058	777.3777	389.1925	776.3937	388.7005	7
4	416.1776	208.5924	399.1510	200.0792	398.1670	199.5871	N	707.3723	354.1898	690.3457	345.6765	689.3617	345.1845	6
5	487.2147	244.1110	470.1882	235.5977	469.2041	235.1057	A	593.3293	297.1683	576.3028	288.6550	575.3188	288.1630	5
6	634.2831	317.6452	617.2566	309.1319	616.2726	308.6399	F	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
7	747.3672	374.1872	730.3406	365.6740	729.3566	365.1819	L	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
8	862.3941	431.7007	845.3676	423.1874	844.3836	422.6954	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of [NVSNAFLDK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.3	1007.4924	-0.0015	NVSNAFLDK	Deamidated N1 91.37%
35.1	1007.4924	-0.0015	NVSNAFLDK	Deamidated N4 8.63%
13.3	1007.4924	-0.0015	DVDSAFLNK	
11.4	1007.4825	0.0084	WNLFNASR	
8.7	1005.4913	1.9995	GLQNAMTVR	
7.7	1007.4892	0.0016	QGMGKKACK	
6.4	1006.4827	1.0081	VLECMLDK	
6.2	1007.4818	0.0090	ITCTSRNR	
5.9	1007.4997	-0.0089	YPILMNQK	
5.4	1007.4923	-0.0015	YNPSALTNK	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1RUC0** in **uni_pig**, tr|F1RUC0|F1RUC0_PIG Uncharacterized protein OS=Sus scrofa GN=LAMP2 PE=4 SV=2

Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum2892_scans_3523

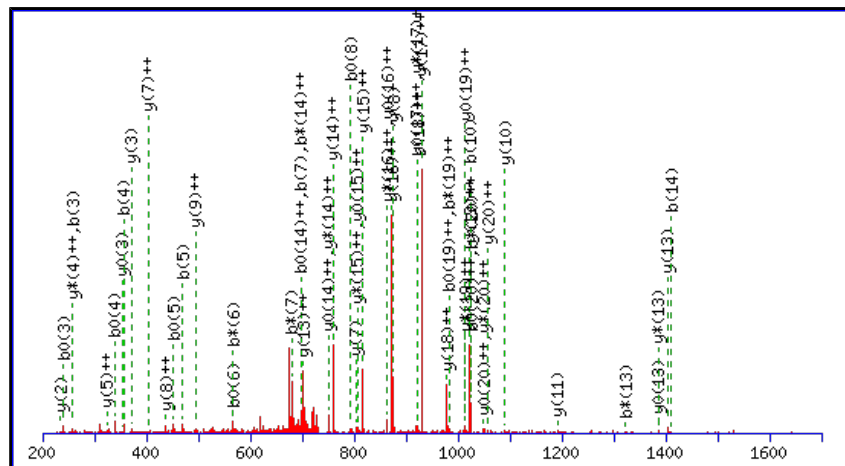
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

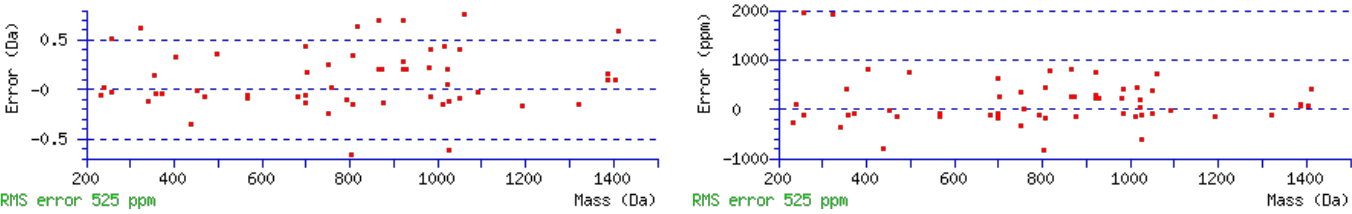
N10 : Deamidated (NQ)

N17 : Deamidated (NQ)

Ions Score: 46 Expect: 0.0015

Matches : 56/224 fragment ions using 125 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							21
2	171.1128	86.0600					A	2114.9771	1057.9922	2097.9506	1049.4789	2096.9666	1048.9869	20
3	258.1448	129.5761			240.1343	120.5708	S	2043.9400	1022.4736	2026.9135	1013.9604	2025.9294	1013.4684	19
4	357.2132	179.1103			339.2027	170.1050	V	1956.9080	978.9576	1939.8814	970.4444	1938.8974	969.9523	18
5	470.2973	235.6523			452.2867	226.6470	I	1857.8396	929.4234	1840.8130	920.9101	1839.8290	920.4181	17
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	N	1744.7555	872.8814	1727.7290	864.3681	1726.7449	863.8761	16
7	697.4243	349.2158	680.3978	340.7025	679.4137	340.2105	I	1630.7126	815.8599	1613.6860	807.3467	1612.7020	806.8546	15
8	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	N	1517.6285	759.3179	1500.6020	750.8046	1499.6179	750.3126	14
9	908.5200	454.7636	891.4934	446.2504	890.5094	445.7584	P	1403.5856	702.2964	1386.5590	693.7832	1385.5750	693.2911	13
10	1023.5469	512.2771	1006.5204	503.7638	1005.5364	503.2718	N	1306.5328	653.7700	1289.5063	645.2568	1288.5223	644.7648	12
11	1124.5946	562.8009	1107.5681	554.2877	1106.5840	553.7957	T	1191.5059	596.2566	1174.4793	587.7433	1173.4953	587.2513	11
12	1225.6423	613.3248	1208.6157	604.8115	1207.6317	604.3195	T	1090.4582	545.7327	1073.4317	537.2195	1072.4476	536.7275	10
13	1339.6852	670.3462	1322.6587	661.8330	1321.6747	661.3410	N	989.4105	495.2089	972.3840	486.6956	971.4000	486.2036	9
14	1410.7223	705.8648	1393.6958	697.3515	1392.7118	696.8595	A	875.3676	438.1874	858.3410	429.6742	857.3570	429.1822	8
15	1511.7700	756.3886	1494.7435	747.8754	1493.7594	747.3834	T	804.3305	402.6689	787.3039	394.1556	786.3199	393.6636	7
16	1568.7915	784.8994	1551.7649	776.3861	1550.7809	775.8941	G	703.2828	352.1450	686.2563	343.6318	685.2722	343.1398	6
17	1683.8184	842.4128	1666.7919	833.8996	1665.8079	833.4076	N	646.2613	323.6343	629.2348	315.1210	628.2508	314.6290	5
18	1843.8491	922.4282	1826.8225	913.9149	1825.8385	913.4229	C	531.2344	266.1208	514.2078	257.6076	513.2238	257.1156	4
19	1980.9080	990.9576	1963.8814	982.4444	1962.8974	981.9523	H	371.2037	186.1055	354.1772	177.5922	353.1932	177.1002	3
20	2067.9400	1034.4736	2050.9135	1025.9604	2049.9294	1025.4684	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
21							K	147.1128	74.0600	130.0863	65.5468			1

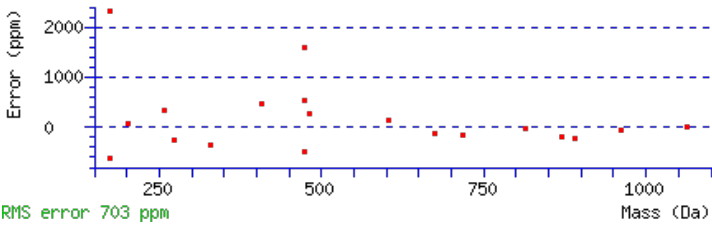


NCBI BLAST search of [VASVININPNTTNATGNCHSK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
46.3	2213.0382	-0.0031	VASVININPNTTNATGNCHSK	Deamidated N10, N17 35.91%
43.7	2213.0382	-0.0031	VASVININPNTTNATGNCHSK	Deamidated N8, N17 19.69%
42.6	2213.0382	-0.0031	VASVININPNTTNATGNCHSK	Deamidated N6, N17 15.39%
41.2	2213.0382	-0.0031	VASVININPNTTNATGNCHSK	Deamidated N13, N17 11.12%
39.9	2213.0382	-0.0031	VASVININPNTTNATGNCHSK	Deamidated N10, N13 8.13%
37.2	2213.0382	-0.0031	VASVININPNTTNATGNCHSK	Deamidated N8, N13 4.44%
36.2	2213.0382	-0.0031	VASVININPNTTNATGNCHSK	Deamidated N6, N13 3.52%
31.4	2213.0382	-0.0031	VASVININPNTTNATGNCHSK	Deamidated N8, N10 1.17%
28.1	2213.0382	-0.0031	VASVININPNTTNATGNCHSK	Deamidated N6, N10 0.54%
21.1	2213.0382	-0.0031	VASVININPNTTNATGNCHSK	Deamidated N6, N8 0.11%

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [VTFPNLTNVR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.9	1161.6030	-0.0035	VTFPNLTNVR
14.6	1161.6030	-0.0035	QAFSPETLIR
10.1	1160.6037	0.9958	AKGSELQTQAK
8.8	1161.6030	-0.0035	QSDIVFTPQK
6.9	1160.6037	0.9958	AKGSELQTQAK
6.3	1160.5859	1.0136	MAEPEKLTAR
5.9	1161.6030	-0.0035	FTAIIGPNGSGK
5.7	1161.5924	0.0071	LSTCEQLRR
5.5	1159.5842	2.0153	TPMNLPGKMR
4.5	1161.5989	0.0006	LSNEKLNSTR

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1S3J9** in **uni_pig**, tr|F1S3J9|F1S3J9_PIG Intercellular adhesion molecule 1 OS=Sus scrofa GN=ICAM-1 PE=2 SV=1

Data file

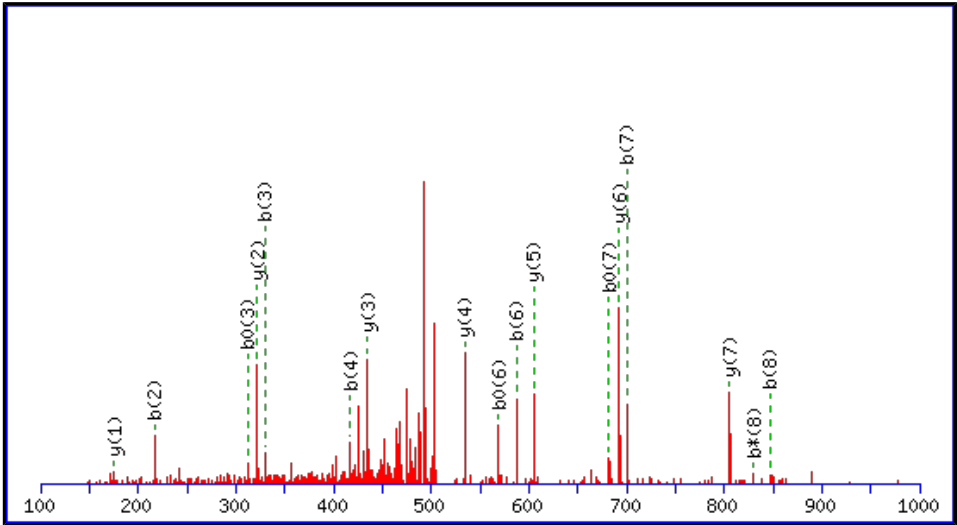
W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis

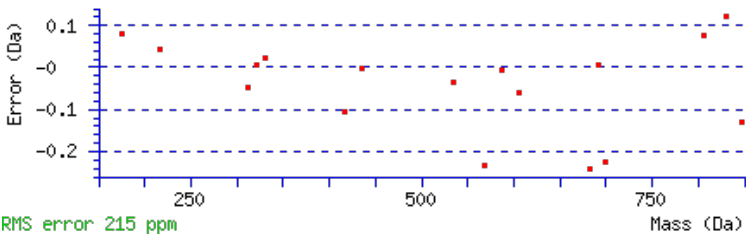


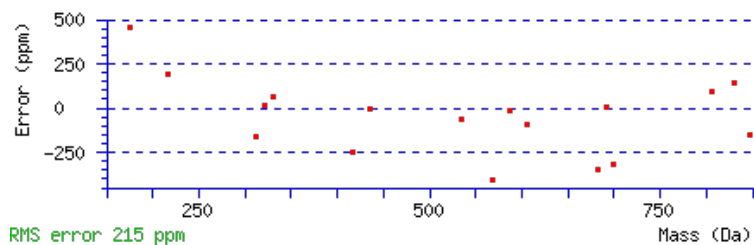
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Monoisotopic mass of neutral peptide Mr(calc): 1020.5604
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2      : Deamidated (NQ)
Ions Score: 45   Expect: 0.0015
Matches : 17/84 fragment ions using 33 most intense peaks  (help)

```

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							9
2	217.0819	109.0446	200.0553	100.5313	199.0713	100.0393	N	920.5200	460.7636	903.4934	452.2504	902.5094	451.7584	8
3	330.1660	165.5866	313.1394	157.0733	312.1554	156.5813	L	805.4930	403.2502	788.4665	394.7369	787.4825	394.2449	7
4	417.1980	209.1026	400.1714	200.5894	399.1874	200.0974	S	692.4090	346.7081	675.3824	338.1949	674.3984	337.7028	6
5	488.2351	244.6212	471.2086	236.1079	470.2245	235.6159	A	605.3770	303.1921	588.3504	294.6788			5
6	587.3035	294.1554	570.2770	285.6421	569.2930	285.1501	V	534.3398	267.6736	517.3133	259.1603			4
7	700.3876	350.6974	683.3610	342.1842	682.3770	341.6921	L	435.2714	218.1394	418.2449	209.6261			3
8	847.4560	424.2316	830.4294	415.7184	829.4454	415.2264	F	322.1874	161.5973	305.1608	153.0840			2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of [TNLSAVLER](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.3	1020.5604	-0.0025	TNLSAVLER
14.0	1019.5611	0.9968	SQLSSTLKR
11.0	1020.5563	0.0016	SQLSSRKSK
10.0	1020.5604	-0.0024	SAYIQIAVR
8.2	1020.5604	-0.0024	KSIEFLER
8.2	1020.5604	-0.0024	KSLFEIQR
5.8	1018.5481	2.0098	TILEKMQR
4.8	1020.5538	0.0041	IANCKLFR
4.1	1018.5481	2.0098	KLLVDQMR
3.3	1019.5499	1.0081	NLTTNLKSK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGWNLSAVK**
Found in **F1RN76** in **uni_pig**, tr[F1RN76]F1RN76_PIG Uncharacterized protein OS=Sus scrofa GN=CD5L PE=4 SV=2

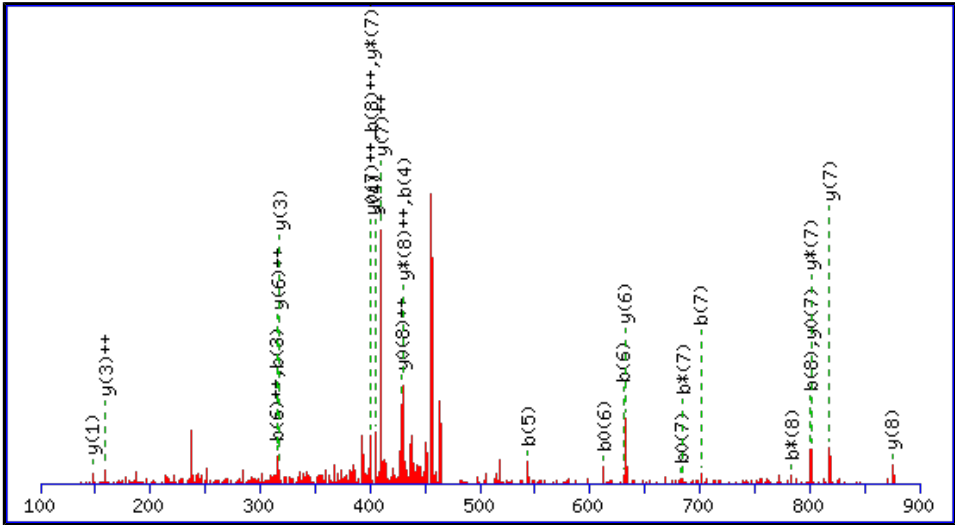
Match to Query 306: 945.490808 from(473.752680,2+) intensity(2916.8540) rtinseconds(1867) scans(3320) index(2812)
Title: 120325_Sunil_PigSerum_Glyco_P_06Spectrum2424_scans__3320
Data file
W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

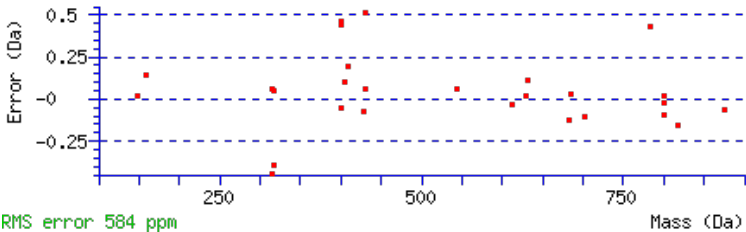
☐ Label all possible matches ☐ Label matches used for scoring

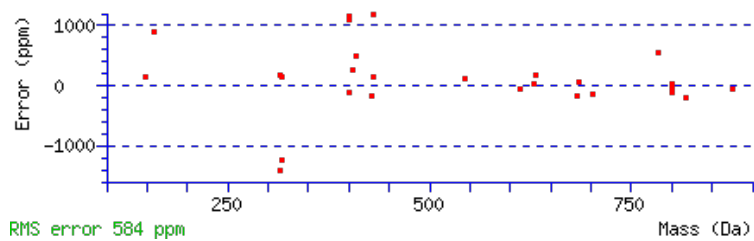
☐ Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 945.4920
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 46 Expect: 0.0017
Matches : 27/74 fragment ions using 40 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{++*}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{++*}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							9
2	129.0659	65.0366					G	875.4621	438.2347	858.4356	429.7214	857.4516	429.2294	8
3	315.1452	158.0762					W	818.4407	409.7240	801.4141	401.2107	800.4301	400.7187	7
4	430.1721	215.5897	413.1456	207.0764			N	632.3614	316.6843	615.3348	308.1710	614.3508	307.6790	6
5	543.2562	272.1317	526.2296	263.6185			L	517.3344	259.1709	500.3079	250.6576	499.3239	250.1656	5
6	630.2882	315.6477	613.2617	307.1345	612.2776	306.6425	S	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	4
7	701.3253	351.1663	684.2988	342.6530	683.3148	342.1610	A	317.2183	159.1128	300.1918	150.5995			3
8	800.3937	400.7005	783.3672	392.1872	782.3832	391.6952	V	246.1812	123.5942	229.1547	115.0810			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of [AGWNLSAVK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.9	945.4920	-0.0012	AGWNLSAVK
12.1	945.4992	-0.0084	KRSGGGGEAK
11.5	945.4992	-0.0084	EGSRDRVK
8.0	943.4916	1.9992	GAWSIPWK
7.3	945.4953	-0.0045	KGQQMPLK
7.0	945.4953	-0.0045	ATMAAAPAVK
6.9	945.4992	-0.0084	ASDRVDRK
6.8	945.4879	0.0029	EKGKENNK
6.8	944.4927	0.9981	EKGDLINR
6.2	944.4927	0.9981	NAKVEDLR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **VASVININPNTTNATGNCHSK**
Found in **F1RUC0** in **uni_pig**, tr[F1RUC0]F1RUC0_PIG Uncharacterized protein OS=Sus scrofa GN=LAMP2 PE=4 SV=2

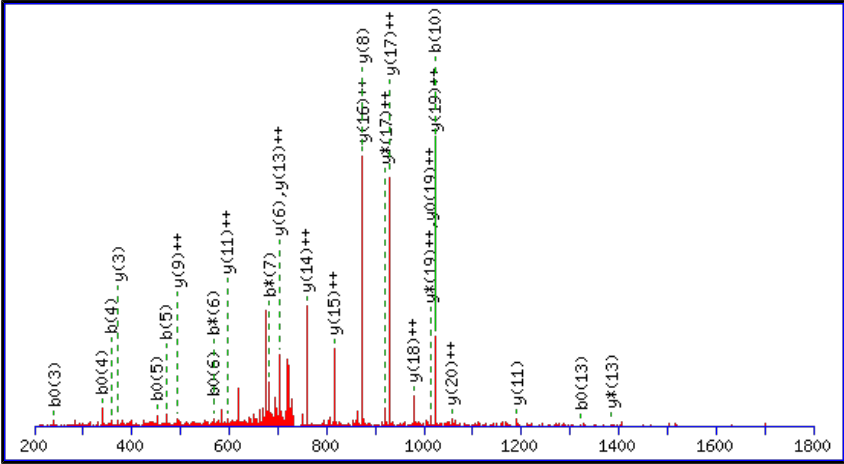
Match to Query 12455: 2213.041782 from(738.687870,3+) intensity(0.0000) rtinseconds(1519) scans(3160) index(8631)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_15Spectrum2582_scans__3160
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

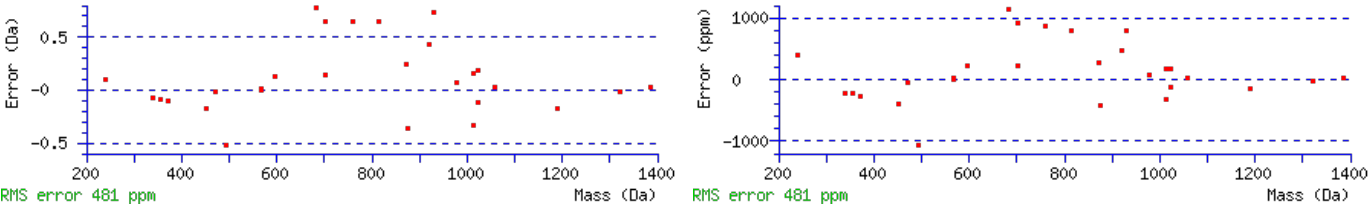
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2213.0382
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
N13 : Deamidated (NQ)
Ions Score: 46 Expect: 0.0018
Matches : 28/224 fragment ions using 55 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							21
2	171.1128	86.0600					A	2114.9771	1057.9922	2097.9506	1049.4789	2096.9666	1048.9869	20
3	258.1448	129.5761			240.1343	120.5708	S	2043.9400	1022.4736	2026.9135	1013.9604	2025.9294	1013.4684	19
4	357.2132	179.1103			339.2027	170.1050	V	1956.9080	978.9576	1939.8814	970.4444	1938.8974	969.9523	18
5	470.2973	235.6523			452.2867	226.6470	I	1857.8396	929.4234	1840.8130	920.9101	1839.8290	920.4181	17
6	585.3243	293.1658	568.2977	284.6525	567.3137	284.1605	N	1744.7555	872.8814	1727.7290	864.3681	1726.7449	863.8761	16
7	698.4083	349.7078	681.3818	341.1945	680.3978	340.7025	I	1629.7286	815.3679	1612.7020	806.8546	1611.7180	806.3626	15
8	812.4512	406.7293	795.4247	398.2160	794.4407	397.7240	N	1516.6445	758.8259	1499.6179	750.3126	1498.6339	749.8206	14
9	909.5040	455.2556	892.4775	446.7424	891.4934	446.2504	P	1402.6016	701.8044	1385.5750	693.2911	1384.5910	692.7991	13
10	1023.5469	512.2771	1006.5204	503.7638	1005.5364	503.2718	N	1305.5488	653.2780	1288.5223	644.7648	1287.5382	644.2728	12
11	1124.5946	562.8009	1107.5681	554.2877	1106.5840	553.7957	T	1191.5059	596.2566	1174.4793	587.7433	1173.4953	587.2513	11
12	1225.6423	613.3248	1208.6157	604.8115	1207.6317	604.3195	T	1090.4582	545.7327	1073.4317	537.2195	1072.4476	536.7275	10
13	1340.6692	670.8383	1323.6427	662.3250	1322.6587	661.8330	N	989.4105	495.2089	972.3840	486.6956	971.4000	486.2036	9
14	1411.7064	706.3568	1394.6798	697.8435	1393.6958	697.3515	A	874.3836	437.6954	857.3570	429.1822	856.3730	428.6901	8
15	1512.7540	756.8807	1495.7275	748.3674	1494.7435	747.8754	T	803.3465	402.1769	786.3199	393.6636	785.3359	393.1716	7
16	1569.7755	785.3914	1552.7489	776.8781	1551.7649	776.3861	G	702.2988	351.6530	685.2722	343.1398	684.2882	342.6477	6
17	1683.8184	842.4128	1666.7919	833.8996	1665.8079	833.4076	N	645.2773	323.1423	628.2508	314.6290	627.2668	314.1370	5
18	1843.8491	922.4282	1826.8225	913.9149	1825.8385	913.4229	C	531.2344	266.1208	514.2078	257.6076	513.2238	257.1156	4
19	1980.9080	990.9576	1963.8814	982.4444	1962.8974	981.9523	H	371.2037	186.1055	354.1772	177.5922	353.1932	177.1002	3
20	2067.9400	1034.4736	2050.9135	1025.9604	2049.9294	1025.4684	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
21							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VASVININPNTTNATGNCHSK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.7	2213.0382	0.0035	VASVININPNTTNATGNCHSK	Deamidated N6, N13 19.17%
45.6	2213.0382	0.0035	VASVININPNTTNATGNCHSK	Deamidated N10, N13 18.69%
45.6	2213.0382	0.0035	VASVININPNTTNATGNCHSK	Deamidated N8, N13 18.69%
44.1	2213.0382	0.0035	VASVININPNTTNATGNCHSK	Deamidated N10, N17 13.33%
44.1	2213.0382	0.0035	VASVININPNTTNATGNCHSK	Deamidated N8, N17 13.33%
42.9	2213.0382	0.0035	VASVININPNTTNATGNCHSK	Deamidated N8, N10 10.16%
39.6	2212.0542	0.9876	VASVININPNTTNATGNCHSK	
39.5	2212.0542	0.9876	VASVININPNTTNATGNCHSK	
37.9	2213.0382	0.0035	VASVININPNTTNATGNCHSK	Deamidated N6, N17 3.20%
34.1	2213.0382	0.0035	VASVININPNTTNATGNCHSK	Deamidated N13, N17 1.32%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAVQCPDAESQCHNNSTCCK**
Found in **F1RQZ0** in **uni_pig**, tr|F1RQZ0|F1RQZ0_PIG Uncharacterized protein OS=Sus scrofa GN=GRN PE=4 SV=1

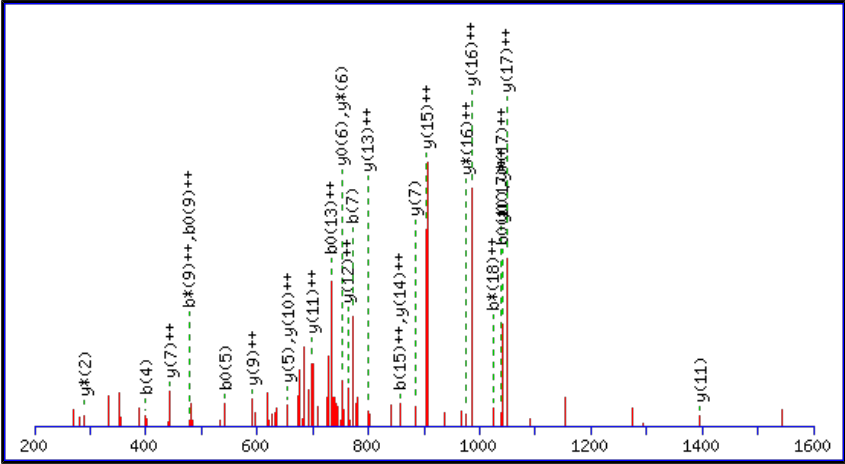
Match to Query 12820: 2366.895702 from(789.972510,3+) intensity(1149.9254) rtinseconds(863) scans(800) index(9820)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_09Spectrum256_scans_800
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

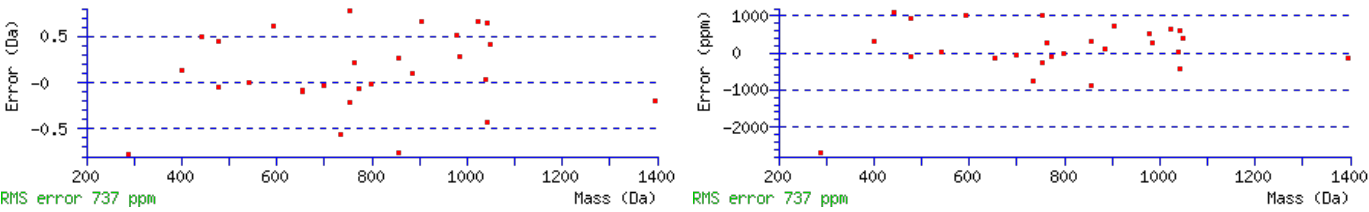
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2366.8984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N15 : Deamidated (NQ)
Ions Score: 29 Expect: 0.0019
Matches : 28/216 fragment ions using 63 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							20
2	173.0921	87.0497			155.0815	78.0444	A	2266.8580	1133.9326	2249.8315	1125.4194	2248.8474	1124.9274	19
3	272.1605	136.5839			254.1499	127.5786	V	2195.8209	1098.4141	2178.7944	1089.9008	2177.8103	1089.4088	18
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	Q	2096.7525	1048.8799	2079.7259	1040.3666	2078.7419	1039.8746	17
5	560.2497	280.6285	543.2232	272.1152	542.2391	271.6232	C	1968.6939	984.8506	1951.6674	976.3373	1950.6833	975.8453	16
6	657.3025	329.1549	640.2759	320.6416	639.2919	320.1496	P	1808.6633	904.8353	1791.6367	896.3220	1790.6527	895.8300	15
7	772.3294	386.6683	755.3029	378.1551	754.3189	377.6631	D	1711.6105	856.3089	1694.5839	847.7956	1693.5999	847.3036	14
8	843.3665	422.1869	826.3400	413.6736	825.3560	413.1816	A	1596.5836	798.7954	1579.5570	790.2821	1578.5730	789.7901	13
9	972.4091	486.7082	955.3826	478.1949	954.3986	477.7029	E	1525.5464	763.2769	1508.5199	754.7636	1507.5359	754.2716	12
10	1059.4412	530.2242	1042.4146	521.7109	1041.4306	521.2189	S	1396.5038	698.7556	1379.4773	690.2423	1378.4933	689.7503	11
11	1187.4997	594.2535	1170.4732	585.7402	1169.4892	585.2482	Q	1309.4718	655.2395	1292.4453	646.7263	1291.4613	646.2343	10
12	1347.5304	674.2688	1330.5038	665.7556	1329.5198	665.2635	C	1181.4132	591.2103	1164.3867	582.6970	1163.4027	582.2050	9
13	1484.5893	742.7983	1467.5627	734.2850	1466.5787	733.7930	H	1021.3826	511.1949	1004.3560	502.6817	1003.3720	502.1897	8
14	1598.6322	799.8197	1581.6057	791.3065	1580.6217	790.8145	N	884.3237	442.6655	867.2971	434.1522	866.3131	433.6602	7
15	1713.6592	857.3332	1696.6326	848.8199	1695.6486	848.3279	N	770.2808	385.6440	753.2542	377.1307	752.2702	376.6387	6
16	1800.6912	900.8492	1783.6646	892.3360	1782.6806	891.8440	S	655.2538	328.1305	638.2273	319.6173	637.2432	319.1253	5
17	1901.7389	951.3731	1884.7123	942.8598	1883.7283	942.3678	T	568.2218	284.6145	551.1952	276.1013	550.2112	275.6092	4
18	2061.7695	1031.3884	2044.7430	1022.8751	2043.7590	1022.3831	C	467.1741	234.0907	450.1476	225.5774			3
19	2221.8002	1111.4037	2204.7736	1102.8904	2203.7896	1102.3984	C	307.1435	154.0754	290.1169	145.5621			2
20							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [TAVQCPDAESQCHNNSTCCK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
28.8	2366.8984	-0.0027	TAVQCPDAESQCHNNSTCCK	Deamidated N15 48.26%
28.8	2366.8984	-0.0027	TAVQCPDAESQCHNNSTCCK	Deamidated N14 48.26%
15.4	2366.8984	-0.0027	TAVQCPDAESQCHNNSTCCK	Deamidated Q11 2.22%
12.9	2366.8984	-0.0027	TAVQCPDAESQCHNNSTCCK	Deamidated Q4 1.25%
4.1	2365.9144	0.9813	TAVQCPDAESQCHNNSTCCK	
2.9	2366.9123	-0.0166	QGENGQMMSCTCLGNGKGEFK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

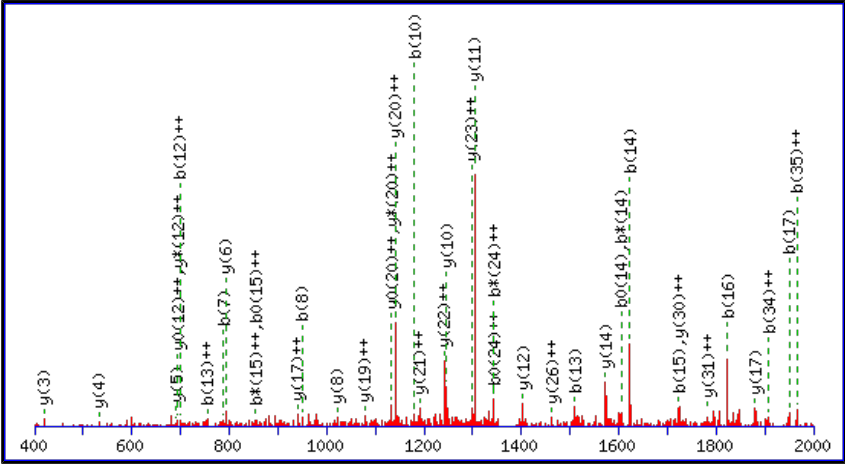
Peptide View

MS/MS Fragmentation of **LSVDQDKYTESEIITVQCDSGYGLVGPNITCIEDR**
Found in **F1S0J2** in **uni_pig**, tr[F1S0J2|F1S0J2_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPA PE=4 SV=2

Match to Query 13762: 4104.922272 from(1369.314700,3+) intensity(0.0000) rtinseconds(2850) scans(6781) index(3721)
Title: 120325_Sunil_PigSerum_Glyco_P_13Spectrum5803_scans__6781
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

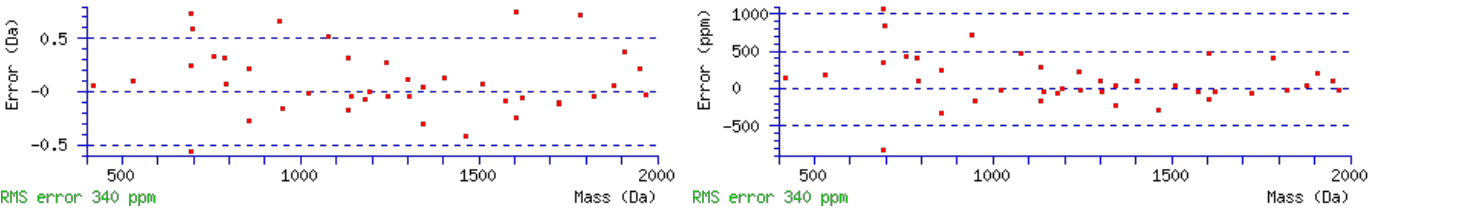
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 4103.8827
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Deamidated (NQ)
N29 : Deamidated (NQ)
Ions Score: 45 Expect: 0.0021
Matches : 41/408 fragment ions using 80 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							36
2	201.1234	101.0653			183.1128	92.0600	S	3991.8060	1996.4066	3974.7794	1987.8933	3973.7954	1987.4013	35
3	300.1918	150.5995			282.1812	141.5942	V	3904.7739	1952.8906	3887.7474	1944.3773	3886.7634	1943.8853	34
4	415.2187	208.1130			397.2082	199.1077	D	3805.7055	1903.3564	3788.6790	1894.8431	3787.6949	1894.3511	33
5	544.2613	272.6343	527.2348	264.1210	526.2508	263.6290	Q	3690.6786	1845.8429	3673.6520	1837.3296	3672.6680	1836.8376	32
6	659.2883	330.1478	642.2617	321.6345	641.2777	321.1425	D	3561.6360	1781.3216	3544.6094	1772.8084	3543.6254	1772.3163	31
7	787.3832	394.1953	770.3567	385.6820	769.3727	385.1900	K	3446.6090	1723.8082	3429.5825	1715.2949	3428.5985	1714.8029	30
8	950.4466	475.7269	933.4200	467.2136	932.4360	466.7216	Y	3318.5141	1659.7607	3301.4875	1651.2474	3300.5035	1650.7554	29
9	1051.4942	526.2508	1034.4677	517.7375	1033.4837	517.2455	T	3155.4507	1578.2290	3138.4242	1569.7157	3137.4402	1569.2237	28
10	1180.5368	590.7721	1163.5103	582.2588	1162.5263	581.7668	E	3054.4031	1527.7052	3037.3765	1519.1919	3036.3925	1518.6999	27
11	1267.5689	634.2881	1250.5423	625.7748	1249.5583	625.2828	S	2925.3605	1463.1839	2908.3339	1454.6706	2907.3499	1454.1786	26
12	1396.6114	698.8094	1379.5849	690.2961	1378.6009	689.8041	E	2838.3284	1419.6679	2821.3019	1411.1546	2820.3179	1410.6626	25
13	1509.6955	755.3514	1492.6690	746.8381	1491.6849	746.3461	I	2709.2858	1355.1466	2692.2593	1346.6333	2691.2753	1346.1413	24
14	1622.7796	811.8934	1605.7530	803.3802	1604.7690	802.8881	I	2596.2018	1298.6045	2579.1752	1290.0913	2578.1912	1289.5992	23
15	1723.8273	862.4173	1706.8007	853.9040	1705.8167	853.4120	T	2483.1177	1242.0625	2466.0912	1233.5492	2465.1072	1233.0572	22
16	1822.8957	911.9515	1805.8691	903.4382	1804.8851	902.9462	V	2382.0700	1191.5387	2365.0435	1183.0254	2364.0595	1182.5334	21
17	1950.9542	975.9808	1933.9277	967.4675	1932.9437	966.9755	Q	2283.0016	1142.0045	2265.9751	1133.4912	2264.9911	1132.9992	20
18	2110.9849	1055.9961	2093.9583	1047.4828	2092.9743	1046.9908	C	2154.9430	1077.9752	2137.9165	1069.4619	2136.9325	1068.9699	19
19	2226.0118	1113.5096	2208.9853	1104.9963	2208.0013	1104.5043	D	1994.9124	997.9598	1977.8858	989.4466	1976.9018	988.9546	18
20	2313.0439	1157.0256	2296.0173	1148.5123	2295.0333	1148.0203	S	1879.8855	940.4464	1862.8589	931.9331	1861.8749	931.4411	17
21	2370.0653	1185.5363	2353.0388	1177.0230	2352.0548	1176.5310	G	1792.8534	896.9304	1775.8269	888.4171	1774.8429	887.9251	16
22	2533.1287	1267.0680	2516.1021	1258.5547	2515.1181	1258.0627	Y	1735.8320	868.4196	1718.8054	859.9063	1717.8214	859.4143	15
23	2590.1501	1295.5787	2573.1236	1287.0654	2572.1396	1286.5734	G	1572.7686	786.8880	1555.7421	778.3747	1554.7581	777.8827	14

24	2703.2342	1352.1207	2686.2076	1343.6075	2685.2236	1343.1154	L	1515.7472	758.3772	1498.7206	749.8639	1497.7366	749.3719	13
25	2802.3026	1401.6549	2785.2761	1393.1417	2784.2920	1392.6497	V	1402.6631	701.8352	1385.6366	693.3219	1384.6525	692.8299	12
26	2859.3241	1430.1657	2842.2975	1421.6524	2841.3135	1421.1604	G	1303.5947	652.3010	1286.5681	643.7877	1285.5841	643.2957	11
27	2956.3768	1478.6921	2939.3503	1470.1788	2938.3663	1469.6868	P	1246.5732	623.7903	1229.5467	615.2770	1228.5627	614.7850	10
28	3084.4354	1542.7213	3067.4089	1534.2081	3066.4248	1533.7161	Q	1149.5205	575.2639	1132.4939	566.7506	1131.5099	566.2586	9
29	3199.4623	1600.2348	3182.4358	1591.7215	3181.4518	1591.2295	N	1021.4619	511.2346	1004.4353	502.7213	1003.4513	502.2293	8
30	3312.5464	1656.7768	3295.5199	1648.2636	3294.5358	1647.7716	I	906.4349	453.7211	889.4084	445.2078	888.4244	444.7158	7
31	3413.5941	1707.3007	3396.5675	1698.7874	3395.5835	1698.2954	T	793.3509	397.1791	776.3243	388.6658	775.3403	388.1738	6
32	3573.6247	1787.3160	3556.5982	1778.8027	3555.6142	1778.3107	C	692.3032	346.6552	675.2767	338.1420	674.2926	337.6500	5
33	3686.7088	1843.8580	3669.6823	1835.3448	3668.6982	1834.8528	I	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
34	3815.7514	1908.3793	3798.7248	1899.8661	3797.7408	1899.3741	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
35	3930.7783	1965.8928	3913.7518	1957.3795	3912.7678	1956.8875	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
36							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.0	4103.8827	1.0395	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, N29 47.77%
42.9	4103.8827	1.0395	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q28, N29 29.25%
39.3	4103.8827	1.0395	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q28 12.65%
38.8	4102.8987	2.0235	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
37.2	4103.8827	1.0395	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q17, N29 7.78%
33.4	4102.8987	2.0235	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	
31.9	4103.8827	1.0395	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q17, Q28 2.32%
21.7	4103.8827	1.0395	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q17 0.22%
15.7	4103.9447	0.9776	ILAPGEEENLEIEDDEDEGGAGAGAPDSFPARVPGTLLPR	
11.1	4102.8987	2.0235	LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

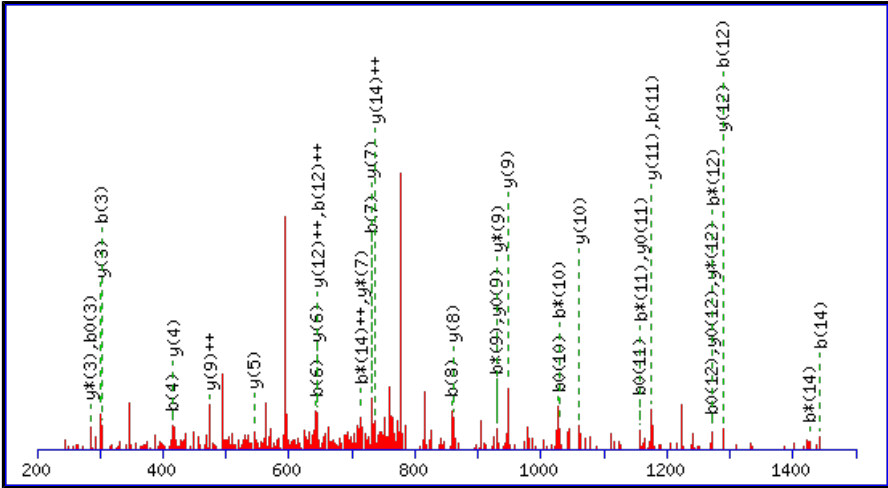
Peptide View

MS/MS Fragmentation of **DSVINLSESVEDGPK**
Found in **F1RM55** in **uni_pig**, tr|F1RM55|F1RM55_PIG Alpha-mannosidase OS=Sus scrofa GN=MAN2A1 PE=3 SV=1

Match to Query 5072: 1588.748348 from(795.381450,2+) intensity(1625.2358) rtinseconds(1986) scans(3634) index(9145)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_17Spectrum2605_scans__3634
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

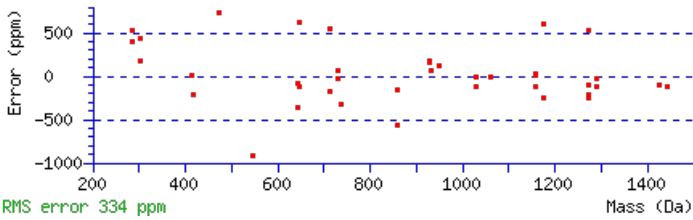
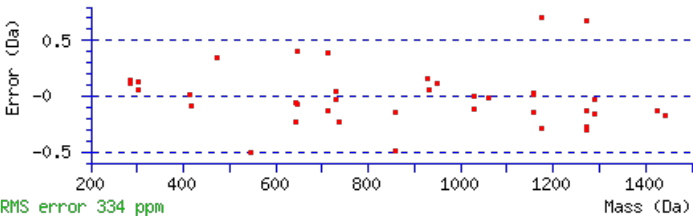
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1588.7468
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 44 Expect: 0.0022
Matches : 39/154 fragment ions using 72 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							15
2	203.0662	102.0368			185.0557	93.0315	S	1474.7271	737.8672	1457.7006	729.3539	1456.7166	728.8619	14
3	302.1347	151.5710			284.1241	142.5657	V	1387.6951	694.3512	1370.6686	685.8379	1369.6846	685.3459	13
4	415.2187	208.1130			397.2082	199.1077	I	1288.6267	644.8170	1271.6002	636.3037	1270.6161	635.8117	12
5	530.2457	265.6265	513.2191	257.1132	512.2351	256.6212	N	1175.5426	588.2750	1158.5161	579.7617	1157.5321	579.2697	11
6	643.3297	322.1685	626.3032	313.6552	625.3192	313.1632	L	1060.5157	530.7615	1043.4891	522.2482	1042.5051	521.7562	10
7	730.3618	365.6845	713.3352	357.1712	712.3512	356.6792	S	947.4316	474.2195	930.4051	465.7062	929.4211	465.2142	9
8	859.4044	430.2058	842.3778	421.6925	841.3938	421.2005	E	860.3996	430.7034	843.3731	422.1902	842.3890	421.6982	8
9	946.4364	473.7218	929.4098	465.2086	928.4258	464.7165	S	731.3570	366.1821	714.3305	357.6689	713.3464	357.1769	7
10	1045.5048	523.2560	1028.4782	514.7428	1027.4942	514.2508	V	644.3250	322.6661	627.2984	314.1529	626.3144	313.6608	6
11	1174.5474	587.7773	1157.5208	579.2641	1156.5368	578.7720	E	545.2566	273.1319	528.2300	264.6186	527.2460	264.1266	5
12	1289.5743	645.2908	1272.5478	636.7775	1271.5638	636.2855	D	416.2140	208.6106	399.1874	200.0974	398.2034	199.6053	4
13	1346.5958	673.8015	1329.5692	665.2883	1328.5852	664.7963	G	301.1870	151.0972	284.1605	142.5839			3
14	1443.6486	722.3279	1426.6220	713.8146	1425.6380	713.3226	P	244.1656	122.5864	227.1390	114.0731			2
15							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [DSVINLSESVEDGPK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.8	1588.7468	0.0016	DSVINLSESVEDGPK
8.8	1588.7482	0.0002	YHGGGGGDLKTTNPSK
5.0	1587.7376	1.0107	TAKAEVQQAPDGSQR
2.8	1588.7627	-0.0144	EGSCEEAPLSARRK
2.4	1587.7376	1.0108	QPSASQEEKELGER
2.4	1587.7376	1.0108	QPSASQEEKELGER
2.1	1586.7320	2.0163	ATEVMMQYVENLK
0.3	1586.7399	2.0085	NAQTFGENLSSLCK
0.3	1586.7399	2.0085	NAQTFGENLSSLCK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

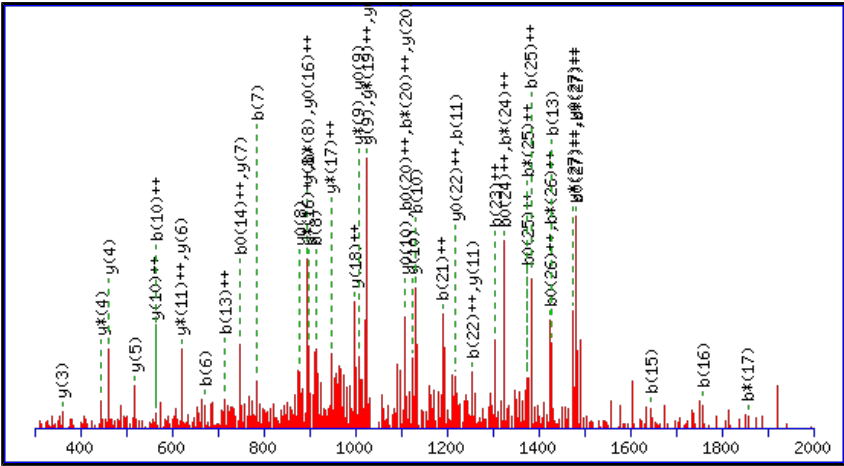
Peptide View

MS/MS Fragmentation of **CGPPPYLQFASPISELNETEFETGTTLK**
Found in **F1S0J2** in **uni_pig**, tr[F1S0J2|F1S0J2_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPA PE=4 SV=2

Match to Query 13373: 3127.447092 from(1043.489640,3+) intensity(11373.6504) rtinseconds(3318) scans(7936) index(3742)
Title: 120325_Sunil_PigSerum_Glyco_P_13Spectrum6798_scans__7936
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

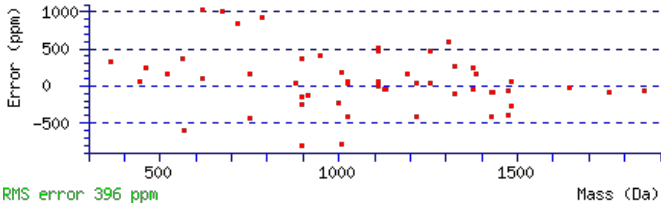
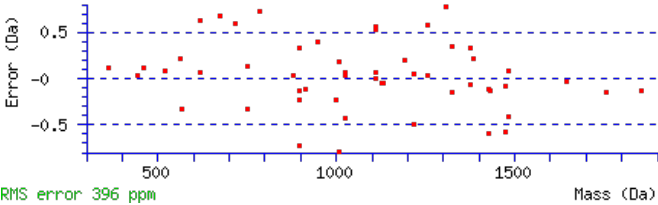
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 3127.4583
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Deamidated (NQ)
N17 : Deamidated (NQ)
Ions Score: 44 Expect: 0.0026
Matches : 53/286 fragment ions using 84 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	161.0379	81.0226					C							28
2	218.0594	109.5333					G	2968.4350	1484.7211	2951.4084	1476.2079	2950.4244	1475.7159	27
3	315.1122	158.0597					P	2911.4135	1456.2104	2894.3870	1447.6971	2893.4030	1447.2051	26
4	412.1649	206.5861					P	2814.3608	1407.6840	2797.3342	1399.1707	2796.3502	1398.6787	25
5	509.2177	255.1125					P	2717.3080	1359.1576	2700.2815	1350.6444	2699.2974	1350.1524	24
6	672.2810	336.6441					Y	2620.2552	1310.6313	2603.2287	1302.1180	2602.2447	1301.6260	23
7	785.3651	393.1862					L	2457.1919	1229.0996	2440.1654	1220.5863	2439.1813	1220.0943	22
8	914.4077	457.7075	897.3811	449.1942			Q	2344.1078	1172.5576	2327.0813	1164.0443	2326.0973	1163.5523	21
9	1061.4761	531.2417	1044.4495	522.7284			F	2215.0653	1108.0363	2198.0387	1099.5230	2197.0547	1099.0310	20
10	1132.5132	566.7602	1115.4866	558.2470			A	2067.9968	1034.5021	2050.9703	1025.9888	2049.9863	1025.4968	19
11	1219.5452	610.2763	1202.5187	601.7630	1201.5347	601.2710	S	1996.9597	998.9835	1979.9332	990.4702	1978.9492	989.9782	18
12	1316.5980	658.8026	1299.5714	650.2894	1298.5874	649.7973	P	1909.9277	955.4675	1892.9011	946.9542	1891.9171	946.4622	17
13	1429.6821	715.3447	1412.6555	706.8314	1411.6715	706.3394	I	1812.8749	906.9411	1795.8484	898.4278	1794.8644	897.9358	16
14	1516.7141	758.8607	1499.6875	750.3474	1498.7035	749.8554	S	1699.7909	850.3991	1682.7643	841.8858	1681.7803	841.3938	15
15	1645.7567	823.3820	1628.7301	814.8687	1627.7461	814.3767	E	1612.7588	806.8831	1595.7323	798.3698	1594.7483	797.8778	14
16	1758.8407	879.9240	1741.8142	871.4107	1740.8302	870.9187	L	1483.7162	742.3618	1466.6897	733.8485	1465.7057	733.3565	13
17	1873.8677	937.4375	1856.8411	928.9242	1855.8571	928.4322	N	1370.6322	685.8197	1353.6056	677.3065	1352.6216	676.8144	12
18	2002.9103	1001.9588	1985.8837	993.4455	1984.8997	992.9535	E	1255.6052	628.3063	1238.5787	619.7930	1237.5947	619.3010	11
19	2103.9580	1052.4826	2086.9314	1043.9693	2085.9474	1043.4773	T	1126.5626	563.7850	1109.5361	555.2717	1108.5521	554.7797	10
20	2233.0005	1117.0039	2215.9740	1108.4906	2214.9900	1107.9986	E	1025.5150	513.2611	1008.4884	504.7478	1007.5044	504.2558	9
21	2380.0690	1190.5381	2363.0424	1182.0248	2362.0584	1181.5328	F	896.4724	448.7398	879.4458	440.2266	878.4618	439.7345	8
22	2509.1116	1255.0594	2492.0850	1246.5461	2491.1010	1246.0541	E	749.4040	375.2056	732.3774	366.6923	731.3934	366.2003	7
23	2610.1592	1305.5833	2593.1327	1297.0700	2592.1487	1296.5780	T	620.3614	310.6843	603.3348	302.1710	602.3508	301.6790	6

24	2667.1807	1334.0940	2650.1541	1325.5807	2649.1701	1325.0887	G	519.3137	260.1605	502.2871	251.6472	501.3031	251.1552	5
25	2768.2284	1384.6178	2751.2018	1376.1046	2750.2178	1375.6125	T	462.2922	231.6498	445.2657	223.1365	444.2817	222.6445	4
26	2869.2761	1435.1417	2852.2495	1426.6284	2851.2655	1426.1364	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
27	2982.3601	1491.6837	2965.3336	1483.1704	2964.3496	1482.6784	L	260.1969	130.6021	243.1703	122.0888			2
28							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [CGPPPYLQFASPISELNETEFETGTTLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.9	3127.4583	-0.0113	CGPPPYLQFASPISELNETEFETGTTLK
41.5	3126.4743	0.9728	CGPPPYLQFASPISELNETEFETGTTLK
24.4	3126.4743	0.9728	CGPPPYLQFASPISELNETEFETGTTLK
6.8	3125.4532	1.9939	ANGNTASNKNSAAMDAELVLRPLMDFLDK
3.0	3127.4590	-0.0120	SLAVHTADTEGSSCTSLEYQMLYSAWR
2.4	3126.4128	1.0343	FEQLISIGSSYNYGNEDQAEFLCVVSR
2.4	3126.4128	1.0343	FEQLISIGSSYNYGNEDQAEFLCVVSR
1.4	3125.4607	1.9864	DNACNDMGKMLQFVLPVATQIQQEVIK
1.4	3125.4607	1.9864	DNACNDMGKMLQFVLPVATQIQQEVIK
1.1	3125.4607	1.9864	DNACNDMGKMLQFVLPVATQIQQEVIK

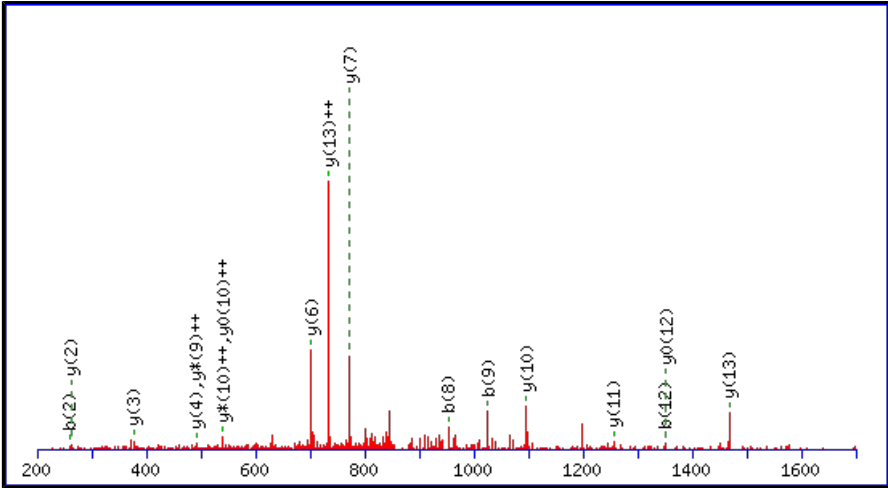
Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1SFI7** in **uni_pig**, tr|F1SFI7|F1SFI7_PIG Alpha-2-HS-glycoprotein (Fragment) OS=Sus scrofa GN=AHSG PE=4 SV=2

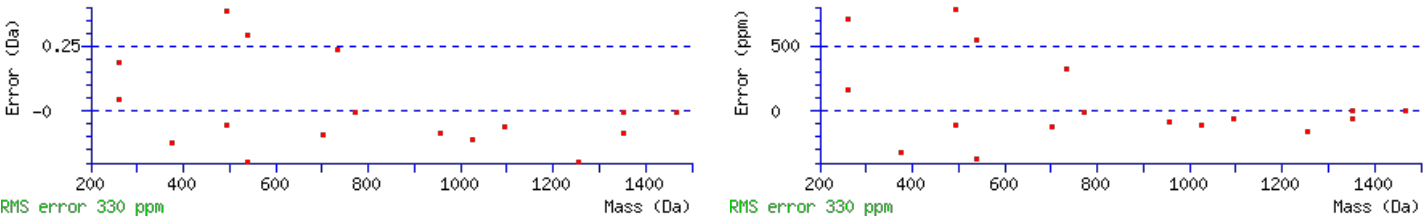
Match to Query 5737: 1725.816388 from(863.915470,2+) intensity(7536.2368) rtinseconds(2394) scans(5129) index(1869)
Title: 120325_Sunil_PigSerum_Glyco_D_15Spectrum4251_scans_5129
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1725.8178
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
 N12 : Deamidated (NQ)
Ions Score: 44 **Expect:** 0.0026
Matches : 17/136 fragment ions using 30 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							15
2	260.1063	130.5568					C	1627.7567	814.3820	1610.7301	805.8687	1609.7461	805.3767	14
3	357.1591	179.0832					P	1467.7260	734.3667	1450.6995	725.8534	1449.7155	725.3614	13
4	471.2020	236.1047	454.1755	227.5914			N	1370.6733	685.8403	1353.6467	677.3270	1352.6627	676.8350	12
5	631.2327	316.1200	614.2061	307.6067			C	1256.6303	628.8188	1239.6038	620.3055	1238.6198	619.8135	11
6	728.2854	364.6464	711.2589	356.1331			P	1096.5997	548.8035	1079.5732	540.2902	1078.5891	539.7982	10
7	841.3695	421.1884	824.3430	412.6751			L	999.5469	500.2771	982.5204	491.7638	981.5364	491.2718	9
8	954.4536	477.7304	937.4270	469.2171			L	886.4629	443.7351	869.4363	435.2218	868.4523	434.7298	8
9	1025.4907	513.2490	1008.4641	504.7357			A	773.3788	387.1930	756.3523	378.6798	755.3682	378.1878	7
10	1122.5434	561.7754	1105.5169	553.2621			P	702.3417	351.6745	685.3151	343.1612	684.3311	342.6692	6
11	1235.6275	618.3174	1218.6010	609.8041			L	605.2889	303.1481	588.2624	294.6348	587.2784	294.1428	5
12	1350.6545	675.8309	1333.6279	667.3176			N	492.2049	246.6061	475.1783	238.0928	474.1943	237.6008	4
13	1465.6814	733.3443	1448.6549	724.8311	1447.6708	724.3391	D	377.1779	189.0926	360.1514	180.5793	359.1674	180.0873	3
14	1552.7134	776.8604	1535.6869	768.3471	1534.7029	767.8551	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
15							R	175.1190	88.0631	158.0924	79.5498			1



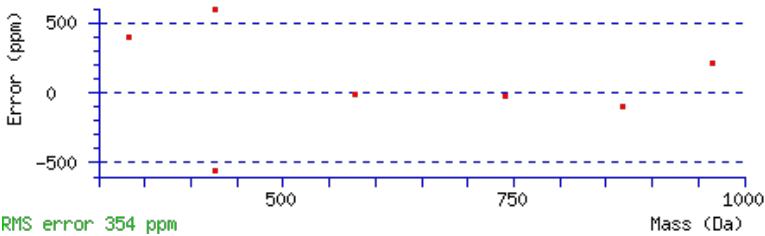
NCBI **BLAST** search of [VCPNCPLLAPLNSDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
43.9	1725.8178	-0.0014	VCPNCPLLAPLNSDR	Deamidated N12 99.91%
13.5	1725.8178	-0.0014	VCPNCPLLAPLNSDR	Deamidated N4 0.09%
3.5	1724.8138	1.0026	KEVAEKSQTSMDNK	
2.4	1725.8097	0.0067	FDYVAQQEQELDIK	
2.4	1725.8097	0.0067	FDYVAQQEQELDIK	
1.4	1723.8172	1.9992	NAAGTGRMSAPRNYSR	
1.4	1724.8012	1.0152	NAAGTGRMSAPRNYSR	
1.4	1725.8066	0.0098	CGDVKNVFMGLDNIK	
0.3	1723.8087	2.0077	EEQEKLGDICFSLR	
0.1	1724.8291	0.9873	NLFVMTLNGGGKENTK	

Mascot: <http://www.matrixscience.com/>

http:// MascotXP.student.main.ntu.edu.sg/Mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=726 [22/Apr/15 06:10:05 PM]



NCBI **BLAST** search of [NPQYNESAR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
38.1	1078.4679	-0.0032	NPQYNESAR	Deamidated N5 99.74%
12.0	1078.4679	-0.0032	NPQYNESAR	Deamidated Q3 0.24%
7.5	1078.4601	0.0047	LQEMDTQGR	
2.6	1077.4648	1.0000	LEQMDAENK	
1.3	1077.4648	0.9999	NDSMEAPLGK	
0.9	1078.4601	0.0047	DLSQAQCQK	
0.8	1078.4679	-0.0032	DGGNAGGIENR	
0.6	1078.4601	0.0047	DLSQAQCQK	
0.5	1078.4713	-0.0066	NLSDGQKCR	
0.2	1078.4601	0.0047	DLSQAQCQK	

Mascot: <http://www.matrixscience.com/>

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.8	1273.5509	-0.0012	RPGNYSCTYR
2.4	1271.5526	1.9971	DVDVCMGTFTK
1.9	1271.5373	2.0124	SLCSLNMNSTK
0.6	1272.5453	1.0044	YHIFQMMMR
0.6	1272.5453	1.0044	YHIFQMMMR
0.5	1273.5574	-0.0077	LESNNYNTYR
0.5	1273.5574	-0.0077	LESNNYNTYR
0.3	1272.5339	1.0158	SRNKCQYCR
0.1	1273.5476	0.0022	ENDNAWHDVR
0.1	1273.5476	0.0022	ENDNAWHDVR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

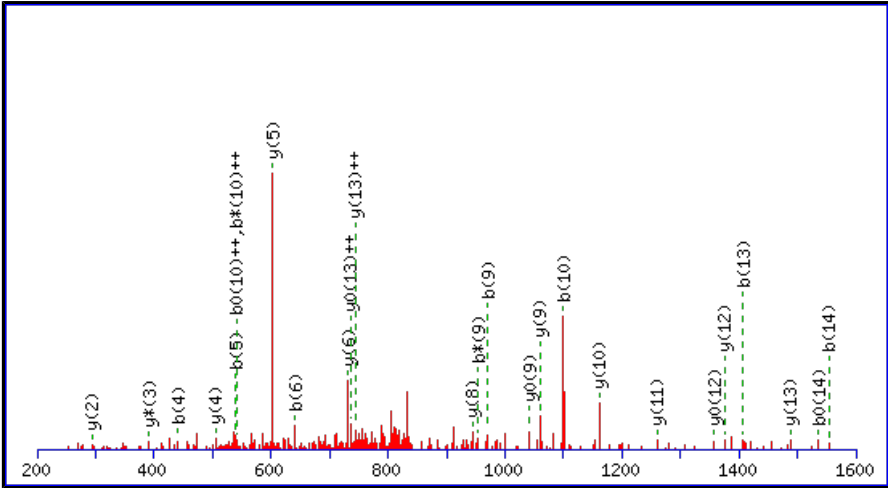
Peptide View

MS/MS Fragmentation of **VIINVTDVDEPPNFK**
Found in **O02840** in **uni_pig**, sp|O02840|CADH5_PIG Cadherin-5 OS=Sus scrofa GN=CDH5 PE=2 SV=1

Match to Query 5528: 1699.861548 from(850.938050,2+) intensity(3490.6619) rtinseconds(2177) scans(3961) index(8281)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_13Spectrum2784_scans__3961
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

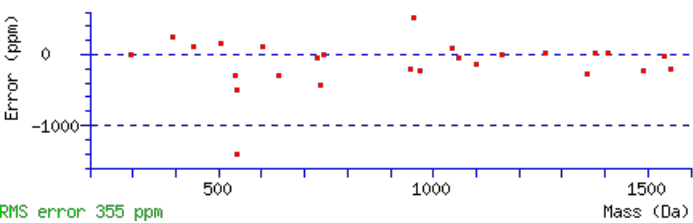
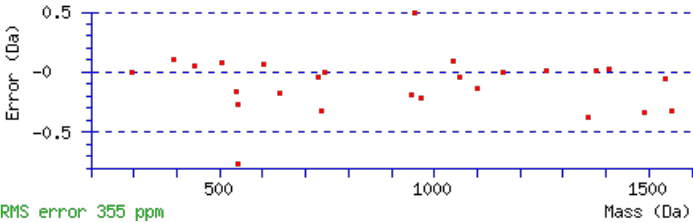
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1699.8669
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 44 Expect: 0.0027
Matches : 26/142 fragment ions using 66 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							15
2	213.1598	107.0835					I	1601.8057	801.4065	1584.7792	792.8932	1583.7952	792.4012	14
3	326.2438	163.6255					I	1488.7217	744.8645	1471.6951	736.3512	1470.7111	735.8592	13
4	441.2708	221.1390	424.2442	212.6257			N	1375.6376	688.3224	1358.6111	679.8092	1357.6270	679.3172	12
5	540.3392	270.6732	523.3126	262.1600			V	1260.6107	630.8090	1243.5841	622.2957	1242.6001	621.8037	11
6	641.3869	321.1971	624.3603	312.6838	623.3763	312.1918	T	1161.5422	581.2748	1144.5157	572.7615	1143.5317	572.2695	10
7	756.4138	378.7105	739.3872	370.1973	738.4032	369.7053	D	1060.4946	530.7509	1043.4680	522.2376	1042.4840	521.7456	9
8	855.4822	428.2447	838.4557	419.7315	837.4716	419.2395	V	945.4676	473.2374	928.4411	464.7242	927.4571	464.2322	8
9	970.5092	485.7582	953.4826	477.2449	952.4986	476.7529	D	846.3992	423.7032	829.3727	415.1900	828.3886	414.6980	7
10	1099.5517	550.2795	1082.5252	541.7662	1081.5412	541.2742	E	731.3723	366.1898	714.3457	357.6765	713.3617	357.1845	6
11	1196.6045	598.8059	1179.5780	590.2926	1178.5939	589.8006	P	602.3297	301.6685	585.3031	293.1552			5
12	1293.6573	647.3323	1276.6307	638.8190	1275.6467	638.3270	P	505.2769	253.1421	488.2504	244.6288			4
13	1407.7002	704.3537	1390.6737	695.8405	1389.6896	695.3485	N	408.2241	204.6157	391.1976	196.1024			3
14	1554.7686	777.8879	1537.7421	769.3747	1536.7581	768.8827	F	294.1812	147.5942	277.1547	139.0810			2
15							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [VIINVTDVDEPPNEFK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
44.1	1699.8669	-0.0053	VIINVTDVDEPPNEFK	Deamidated N4 99.26%
22.9	1699.8669	-0.0053	VIINVTDVDEPPNEFK	Deamidated N13 0.74%
9.6	1698.8498	1.0117	NVMTAQLHEGLVLQK	
4.8	1699.8740	-0.0125	NAKEEIDGLQGRLEK	
4.4	1699.8464	0.0152	MANLREYYERALR	
4.4	1699.8740	-0.0125	NAKEEIDGLQGRLEK	
3.1	1698.8433	1.0183	MHIKAMPEDAKGQVK	
2.8	1699.8740	-0.0125	ASQEADNVLILQDRK	
2.7	1699.8740	-0.0125	LQSNNNSAGIPRSVLK	
2.7	1699.8740	-0.0125	LQSNNNSAGIPRSVLK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

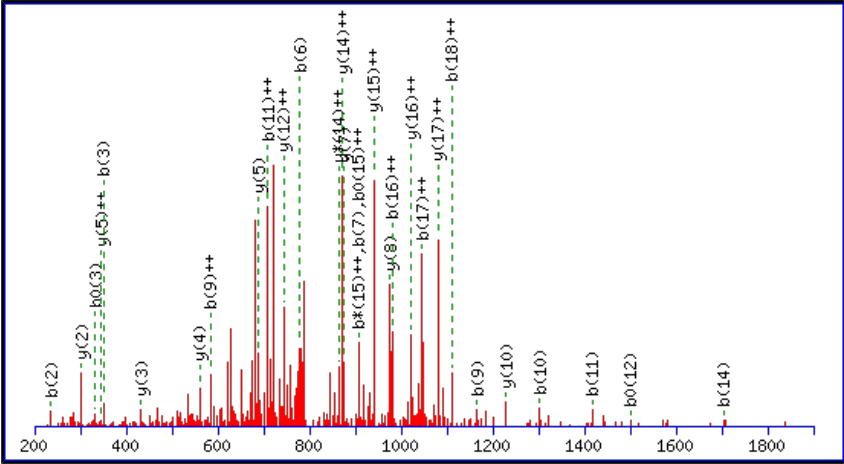
Peptide View

MS/MS Fragmentation of **AYDYHEETRHNTSVQEEQR**
Found in **I3L998** in **uni_pig**, tr|I3L998|I3L998_PIG Vitronectin OS=Sus scrofa GN=VTN PE=4 SV=1

Match to Query 12838: 2392.023162 from(798.348330,3+) intensity(4114.6250) rtinseconds(1083) scans(1675) index(1700)
Title: 120325_Sunil_PigSerum_Glyco_D_15Spectrum1182_scans__1675
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

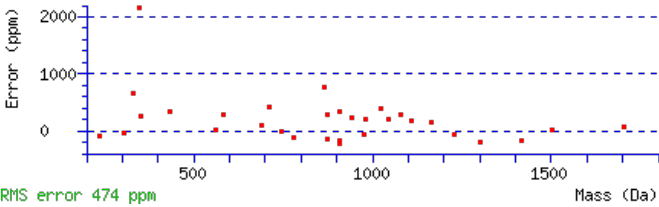
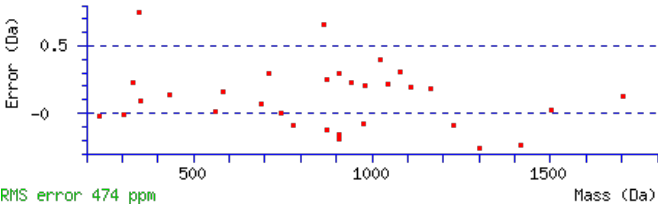
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2392.0316
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Ions Score: 38 Expect: 0.0028
Matches : 31/192 fragment ions using 60 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							19
2	235.1077	118.0575					Y	2322.0018	1161.5045	2304.9752	1152.9912	2303.9912	1152.4992	18
3	350.1347	175.5710			332.1241	166.5657	D	2158.9384	1079.9729	2141.9119	1071.4596	2140.9279	1070.9676	17
4	513.1980	257.1026			495.1874	248.0974	Y	2043.9115	1022.4594	2026.8849	1013.9461	2025.9009	1013.4541	16
5	650.2569	325.6321			632.2463	316.6268	H	1880.8482	940.9277	1863.8216	932.4144	1862.8376	931.9224	15
6	779.2995	390.1534			761.2889	381.1481	E	1743.7892	872.3983	1726.7627	863.8850	1725.7787	863.3930	14
7	908.3421	454.6747			890.3315	445.6694	E	1614.7467	807.8770	1597.7201	799.3637	1596.7361	798.8717	13
8	1009.3898	505.1985			991.3792	496.1932	T	1485.7041	743.3557	1468.6775	734.8424	1467.6935	734.3504	12
9	1165.4909	583.2491	1148.4643	574.7358	1147.4803	574.2438	R	1384.6564	692.8318	1367.6298	684.3186	1366.6458	683.8265	11
10	1302.5498	651.7785	1285.5232	643.2653	1284.5392	642.7733	H	1228.5553	614.7813	1211.5287	606.2680	1210.5447	605.7760	10
11	1417.5767	709.2920	1400.5502	700.7787	1399.5662	700.2867	N	1091.4964	546.2518	1074.4698	537.7385	1073.4858	537.2465	9
12	1518.6244	759.8158	1501.5979	751.3026	1500.6138	750.8106	T	976.4694	488.7383	959.4429	480.2251	958.4589	479.7331	8
13	1605.6564	803.3319	1588.6299	794.8186	1587.6459	794.3266	S	875.4217	438.2145	858.3952	429.7012	857.4112	429.2092	7
14	1704.7249	852.8661	1687.6983	844.3528	1686.7143	843.8608	V	788.3897	394.6985	771.3632	386.1852	770.3791	385.6932	6
15	1832.7834	916.8954	1815.7569	908.3821	1814.7729	907.8901	Q	689.3213	345.1643	672.2947	336.6510	671.3107	336.1590	5
16	1961.8260	981.4167	1944.7995	972.9034	1943.8155	972.4114	E	561.2627	281.1350	544.2362	272.6217	543.2522	272.1297	4
17	2090.8686	1045.9379	2073.8421	1037.4247	2072.8581	1036.9327	E	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
18	2218.9272	1109.9672	2201.9006	1101.4540	2200.9166	1100.9620	Q	303.1775	152.0924	286.1510	143.5791			2
19							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [AYDYHEETRHNTSVQEEQR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
38.1	2392.0316	-0.0084	AYDYHEETRHNTSVQEEQR	Deamidated N11 86.55%
27.8	2392.0316	-0.0084	AYDYHEETRHNTSVQEEQR	Deamidated Q15 7.95%
26.2	2392.0316	-0.0084	AYDYHEETRHNTSVQEEQR	Deamidated Q18 5.50%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLTQLPDGIPDAAR**

Found in **Q1KS52** in **uni_pig**, tr|Q1KS52|Q1KS52_PIG Acid-labile subunit OS=Sus scrofa GN=ALS PE=2 SV=1

Match to Query 4387: 1481.752488 from(741.883520,2+) intensity(2834.9927) rtinseconds(2118) scans(4215) index(13844)

Title: 120326_Sunil_PigSerum_Glyco_SsetB_18Spectrum2968_scans_4215

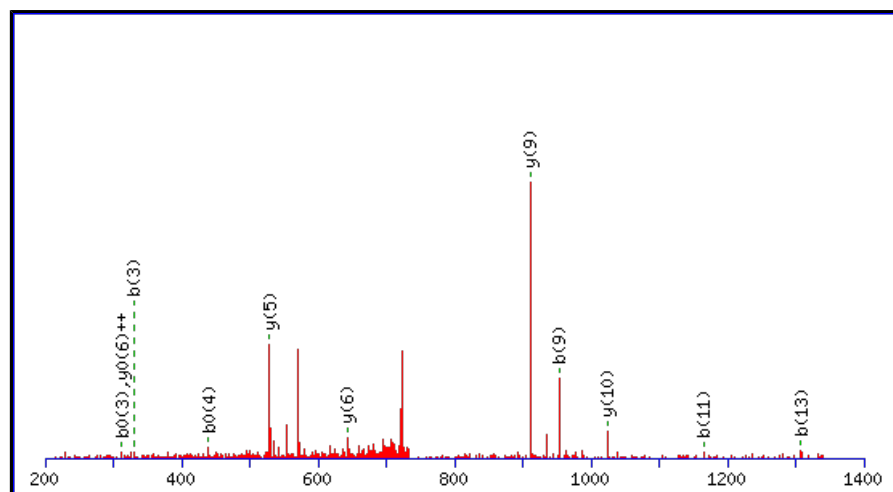
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1480.7522

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

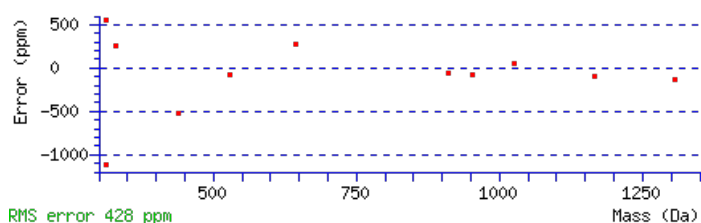
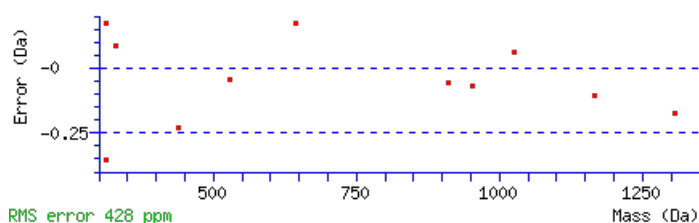
Variable modifications:

N1 : Deamidated (NQ)

Ions Score: 44 Expect: 0.0028

Matches : 11/146 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							14
2	229.1183	115.0628	212.0917	106.5495			L	1366.7325	683.8699	1349.7060	675.3566	1348.7219	674.8646	13
3	330.1660	165.5866	313.1394	157.0733	312.1554	156.5813	T	1253.6484	627.3279	1236.6219	618.8146	1235.6379	618.3226	12
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	Q	1152.6008	576.8040	1135.5742	568.2907	1134.5902	567.7987	11
5	571.3086	286.1579	554.2821	277.6447	553.2980	277.1527	L	1024.5422	512.7747	1007.5156	504.2615	1006.5316	503.7694	10
6	668.3614	334.6843	651.3348	326.1710	650.3508	325.6790	P	911.4581	456.2327	894.4316	447.7194	893.4476	447.2274	9
7	783.3883	392.1978	766.3618	383.6845	765.3777	383.1925	D	814.4054	407.7063	797.3788	399.1930	796.3948	398.7010	8
8	840.4098	420.7085	823.3832	412.1953	822.3992	411.7032	G	699.3784	350.1928	682.3519	341.6796	681.3678	341.1876	7
9	953.4938	477.2506	936.4673	468.7373	935.4833	468.2453	I	642.3570	321.6821	625.3304	313.1688	624.3464	312.6768	6
10	1050.5466	525.7769	1033.5201	517.2637	1032.5360	516.7717	P	529.2729	265.1401	512.2463	256.6268	511.2623	256.1348	5
11	1165.5735	583.2904	1148.5470	574.7771	1147.5630	574.2851	D	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	4
12	1236.6107	618.8090	1219.5841	610.2957	1218.6001	609.8037	A	317.1932	159.1002	300.1666	150.5870			3
13	1307.6478	654.3275	1290.6212	645.8143	1289.6372	645.3222	A	246.1561	123.5817	229.1295	115.0684			2
14							R	175.1190	88.0631	158.0924	79.5498			1

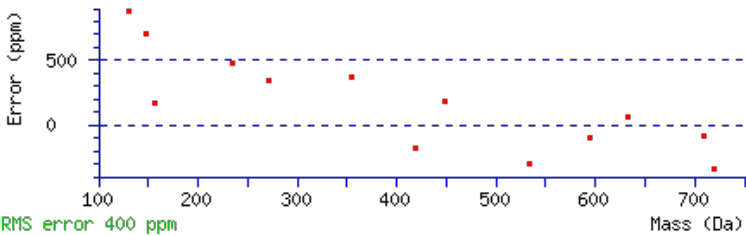


NCBI **BLAST** search of [NLTQLPDGIPDAAR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
43.8	1480.7522	1.0003	NLTQLPDGIPDAAR	Deamidated N1 93.23%
32.4	1480.7522	1.0003	NLTQLPDGIPDAAR	Deamidated Q4 6.77%
12.6	1480.7634	0.9891	TNQIPRQIPEQR	
12.6	1480.7634	0.9891	TNQIPRQIPEQR	
12.3	1480.7634	0.9891	LAASNLPISSSQHR	
7.0	1480.7521	1.0004	QTEVLLQPNPNAR	
6.7	1479.7317	2.0208	NILDVARQLNDAH	
6.1	1479.7317	2.0208	NILDVARQLNDAH	
6.1	1480.7521	1.0004	QTEVLLQPNPNAR	
5.4	1481.7474	0.0051	VNYDTTESKLRR	

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [GVNENVSK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.9	864.4341	1.0026	GVNENVSK	Deamidated N5 99.39%
28.4	864.4310	1.0058	RMMNVSK	
19.8	864.4341	1.0026	GVNENVSK	Deamidated N3 0.61%
15.6	864.4341	1.0026	AQAFVNSK	
9.7	863.4348	2.0019	QSSSGALSK	
8.4	864.4341	1.0026	FQEQVSK	
7.6	863.4357	2.0011	RMMNAIK	
7.3	865.4406	-0.0039	ETHQVPR	
7.2	863.4236	2.0131	EVSSLNSK	
6.3	864.4375	0.9993	KINEMSK	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1RPW2** in **uni_pig**, tr|F1RPW2|F1RPW2_PIG Coagulation factor V OS=Sus scrofa GN=F5 PE=4 SV=2

Title: 120325_Sunil_PigSerum_Glyco_S_14Spectrum1363_scans__1724

Data file

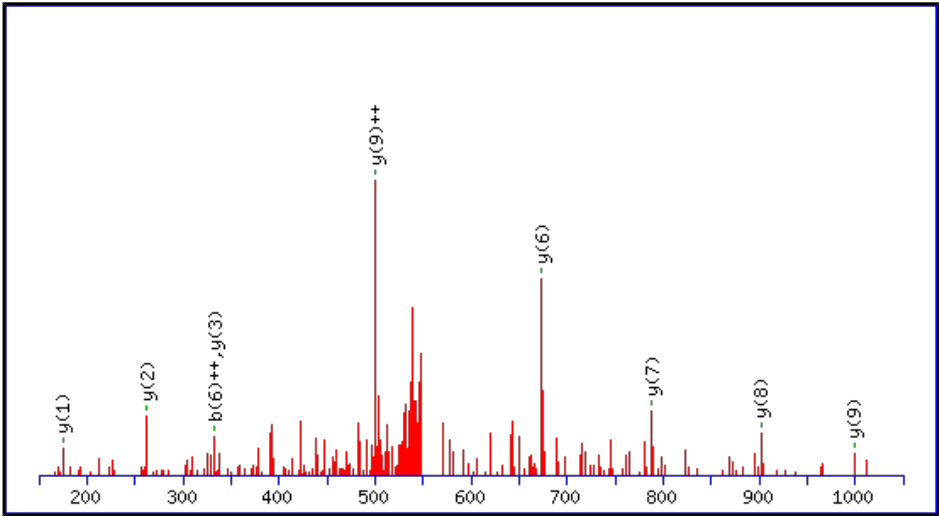
W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1111.5258

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

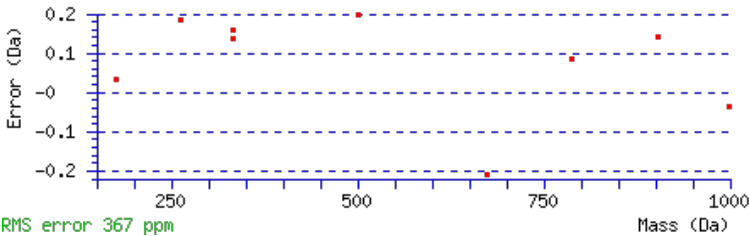
Q6 : Deamidated (NQ)

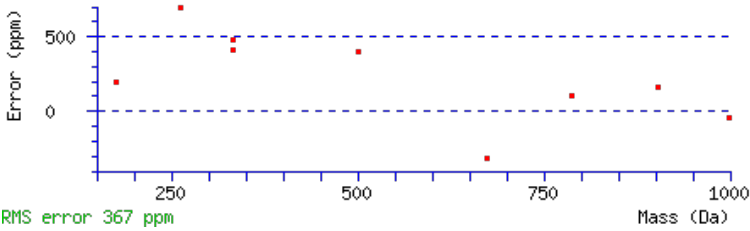
N7 : Deamidated (NQ)

Ions Score: 40 Expect: 0.0031
Matches: 2/26 fragment ions: 1

Matches : 9/86 fragment ions using 18 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							10
2	211.1441	106.0757					P	999.4490	500.2281	982.4225	491.7149	981.4384	491.2229	9
3	325.1870	163.0972	308.1605	154.5839			N	902.3962	451.7018	885.3697	443.1885	884.3857	442.6965	8
4	439.2300	220.1186	422.2034	211.6053			N	788.3533	394.6803	771.3268	386.1670	770.3428	385.6750	7
5	536.2827	268.6450	519.2562	260.1317			P	674.3104	337.6588	657.2838	329.1456	656.2998	328.6536	6
6	665.3253	333.1663	648.2988	324.6530			Q	577.2576	289.1325	560.2311	280.6192	559.2471	280.1272	5
7	780.3523	390.6798	763.3257	382.1665			N	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4
8	851.3894	426.1983	834.3628	417.6850			A	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
9	938.4214	469.7143	921.3949	461.2011	920.4108	460.7091	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of [LPNNPQNASR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
39.9	1111.5258	-0.0040	LPNNPQNASR	Deamidated Q6, N7 39.62%
37.0	1111.5258	-0.0040	LPNNPQNASR	Deamidated N3, N7 20.14%
36.6	1111.5258	-0.0040	LPNNPQNASR	Deamidated N4, N7 18.58%
36.6	1111.5258	-0.0040	LPNNPQNASR	Deamidated N4, Q6 18.58%
28.5	1111.5258	-0.0040	LPNNPQNASR	Deamidated N3, Q6 2.86%
17.5	1111.5258	-0.0040	LPNNPQNASR	Deamidated N3, N4 0.23%
5.9	1111.5220	-0.0002	LFSQDVMEK	
5.3	1110.5267	0.9951	LESEMDFLK	
3.6	1111.5258	-0.0040	TEAHQDVVGR	
0.7	1110.5080	1.0137	SENIQLDYK	

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGHFYYNISEVK**

Found in **F1SC57** in **uni_pig**, tr|F1SC57|F1SC57_PIG Uncharacterized protein OS=Sus scrofa GN=PLTP PE=4 SV=1

Match to Query 4446: 1485.670068 from(743.842310,2+) intensity(2711.3606) rtinseconds(1868) scans(4048) index(12930)

Title: 120326_Sunil_PigSerum_Glyco_SsetB_13Spectrum3288_scans_4048

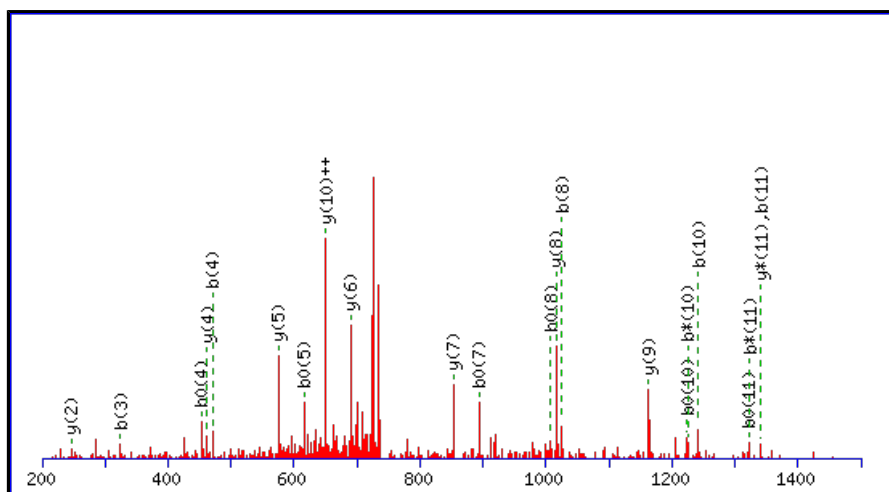
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1485.6776

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

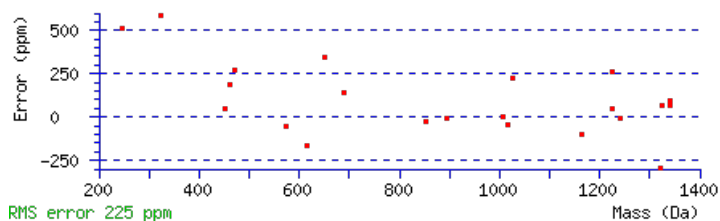
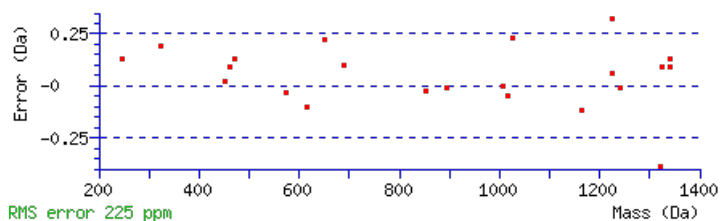
Variable modifications:

N7 : Deamidated (NQ)

Ions Score: 40 Expect: 0.0031

Matches : 22/116 fragment ions using 38 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							12
2	187.0713	94.0393			169.0608	85.0340	G	1357.6423	679.3248	1340.6157	670.8115	1339.6317	670.3195	11
3	324.1302	162.5688			306.1197	153.5635	H	1300.6208	650.8141	1283.5943	642.3008	1282.6103	641.8088	10
4	471.1987	236.1030			453.1881	227.0977	F	1163.5619	582.2846	1146.5354	573.7713	1145.5514	573.2793	9
5	634.2620	317.6346			616.2514	308.6293	Y	1016.4935	508.7504	999.4670	500.2371	998.4829	499.7451	8
6	797.3253	399.1663			779.3148	390.1610	Y	853.4302	427.2187	836.4036	418.7055	835.4196	418.2134	7
7	912.3523	456.6798	895.3257	448.1665	894.3417	447.6745	N	690.3668	345.6871	673.3403	337.1738	672.3563	336.6818	6
8	1025.4363	513.2218	1008.4098	504.7085	1007.4258	504.2165	I	575.3399	288.1736	558.3134	279.6603	557.3293	279.1683	5
9	1112.4684	556.7378	1095.4418	548.2245	1094.4578	547.7325	S	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
10	1241.5109	621.2591	1224.4844	612.7458	1223.5004	612.2538	E	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
11	1340.5794	670.7933	1323.5528	662.2800	1322.5688	661.7880	V	246.1812	123.5942	229.1547	115.0810			2
12							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of EGHFYYNISEVK

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.3	1485.6776	-0.0075	EGHFYYNISEVK
3.7	1485.6657	0.0043	DSNFDSSVQIMVK
2.6	1483.6765	1.9936	SYWEMRGNALEK

Mascot: <http://www.matrixscience.com/>

http:// MascotXP.student.main.ntu.edu.sg/mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=3152 [22/Apr/15 06:10:32 PM]

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.0	1354.7456	1.0032	LNITINDLPGKR
20.1	1355.7409	0.0079	LDNLTTSFILNR
18.4	1355.7408	0.0079	DLISKNIAEPTR
12.2	1353.7326	2.0162	QICAVILESPPK
9.7	1354.7391	1.0097	KTNLNRLHIVM
9.0	1354.7456	1.0032	INLLQQQIQVR
9.0	1354.7456	1.0032	INLLQQQIQVR
9.0	1354.7456	1.0032	INLLQQQIQVR
7.6	1354.7357	1.0131	LVETPGRELWR
6.5	1353.7292	2.0196	NNILFGKKYEK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLNTSSLLK**
Found in **F1RJS2** in **uni_pig**, tr|F1RJS2|F1RJS2_PIG Clusterin OS=Sus scrofa GN=CLU PE=3 SV=2

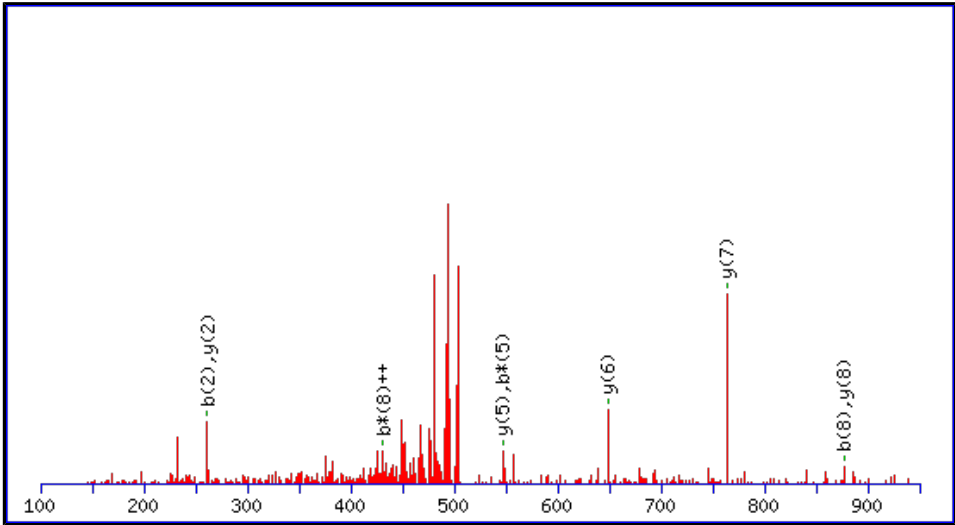
Match to Query 559: 1022.530308 from(512.272430,2+) intensity(7587.6728) rtinseconds(1688) scans(3951) index(1508)
Title: 120325_Sunil_PigSerum_Glyco_D_14Spectrum3348_scans__3951
Data file
W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

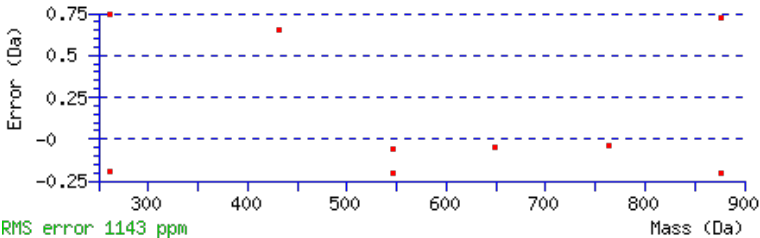
☐ Label all possible matches ☐ Label matches used for scoring

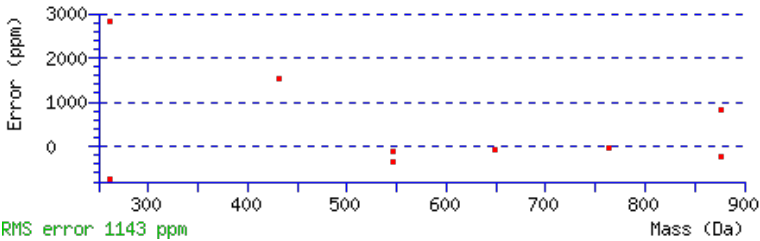
☐ Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1022.5318
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N3 : Deamidated (NQ)
Ions Score: 42 Expect: 0.0034
Matches : 9/118 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0427	74.5250					M							9
2	261.1267	131.0670					L	876.5037	438.7555	859.4771	430.2422	858.4931	429.7502	8
3	376.1537	188.5805	359.1271	180.0672			N	763.4196	382.2134	746.3931	373.7002	745.4090	373.2082	7
4	477.2014	239.1043	460.1748	230.5910	459.1908	230.0990	T	648.3927	324.7000	631.3661	316.1867	630.3821	315.6947	6
5	564.2334	282.6203	547.2068	274.1071	546.2228	273.6151	S	547.3450	274.1761	530.3184	265.6629	529.3344	265.1708	5
6	651.2654	326.1363	634.2389	317.6231	633.2549	317.1311	S	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
7	764.3495	382.6784	747.3229	374.1651	746.3389	373.6731	L	373.2809	187.1441	356.2544	178.6308			3
8	877.4335	439.2204	860.4070	430.7071	859.4230	430.2151	L	260.1969	130.6021	243.1703	122.0888			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of [MLNTSSLLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.1	1022.5318	-0.0015	MLNTSSLLK
17.3	1022.5253	0.0051	KMDKMOVQK
14.6	1022.5396	-0.0093	FLLSNVSSR
14.3	1022.5397	-0.0094	TATTQNFLK
14.0	1022.5253	0.0051	MLSNMVGKK
12.1	1022.5396	-0.0093	SYRLENLK
11.7	1022.5284	0.0019	LFTDQISAK
11.6	1022.5371	-0.0068	FGWIKMNK
10.8	1022.5284	0.0019	EQVATDTLK
10.6	1021.5300	1.0003	LMNEMKIK

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1SQX9** in **uni_pig**, tr|F1SQX9|F1SQX9_PIG Uncharacterized protein OS=Sus scrofa GN=APOD PE=4 SV=3

Title: 120325_Sunil_PigSerum_Glyco_P_07Spectrum1324_scans__2140

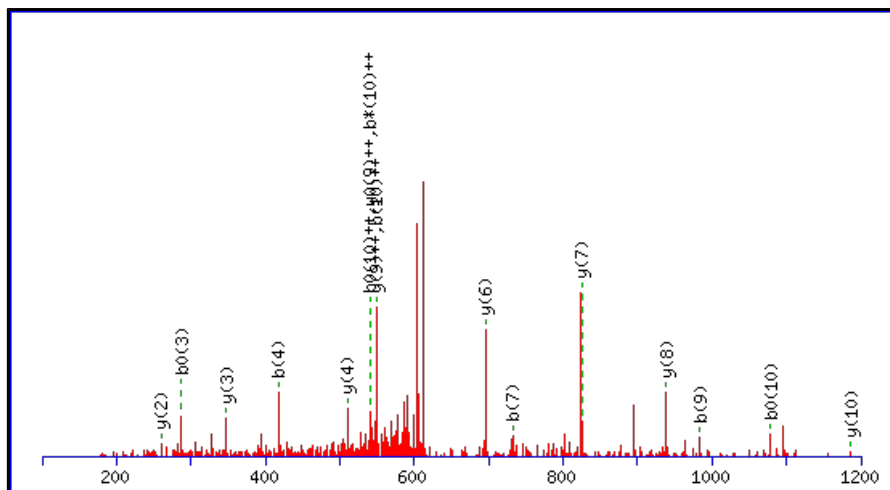
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

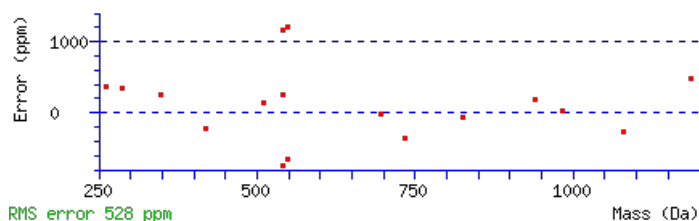
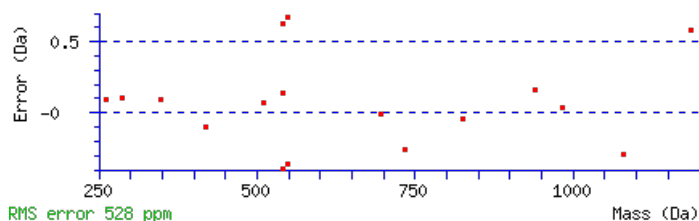
Q5 : Deamidated (NQ)

N7 : Deamidated (NQ)

Ions Score: 39 Expect: 0.0038

Matches : 17/106 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							11
2	145.0608	73.0340			127.0502	64.0287	S	1185.5456	593.2764	1168.5191	584.7632	1167.5351	584.2712	10
3	305.0914	153.0493			287.0809	144.0441	C	1098.5136	549.7604	1081.4870	541.2472	1080.5030	540.7552	9
4	418.1755	209.5914			400.1649	200.5861	I	938.4829	469.7451	921.4564	461.2318	920.4724	460.7398	8
5	547.2181	274.1127	530.1915	265.5994	529.2075	265.1074	Q	825.3989	413.2031	808.3723	404.6898	807.3883	404.1978	7
6	618.2552	309.6312	601.2286	301.1180	600.2446	300.6260	A	696.3563	348.6818	679.3297	340.1685	678.3457	339.6765	6
7	733.2821	367.1447	716.2556	358.6314	715.2716	358.1394	N	625.3192	313.1632	608.2926	304.6499	607.3086	304.1579	5
8	896.3455	448.6764	879.3189	440.1631	878.3349	439.6711	Y	510.2922	255.6498	493.2657	247.1365	492.2817	246.6445	4
9	983.3775	492.1924	966.3509	483.6791	965.3669	483.1871	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
10	1096.4616	548.7344	1079.4350	540.2211	1078.4510	539.7291	L	260.1969	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1



(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

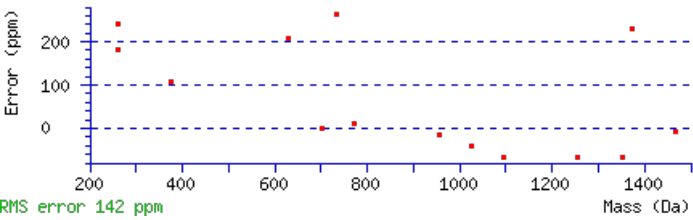
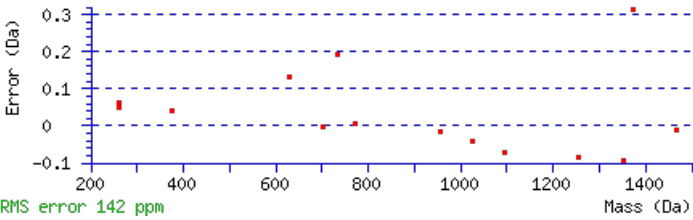
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.7	1241.5598	0.0020	GSCIQANYSLK
16.9	1240.5679	0.9938	EMTEMTGVSLK
13.3	1240.5679	0.9938	EMTEMTGVSLK
8.9	1240.5468	1.0150	QNFMEQMALK
7.1	1241.5679	-0.0061	MTGRSPRMMK
6.0	1241.5598	0.0020	IPPPNNNSQMK
6.0	1241.5598	0.0020	IPPPNNNSQMK
6.0	1241.5598	0.0020	IPPPNNNSQMK
5.7	1240.5468	1.0150	QNFMEQMALK
5.3	1240.5646	0.9972	FTVQASPTMDK

Mascot: <http://www.matrixscience.com/>

http://masscop.student.main.ntu.edu.sg/mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=5797 [22/Apr/15 06:10:40 PM]



NCBI **BLAST** search of [VCPNCPLLAPLNDSR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.2	1726.8018	-0.0060	VCPNCPLLAPLNDSR
1.7	1726.7906	0.0052	LPNMPLSGMYNKSGGK
1.5	1724.8012	1.9946	NAAGTGRMSAPRNYSR
1.1	1726.7971	-0.0013	MDVENLEYSEEILK
0.6	1726.8130	-0.0172	LAQLFMMSQQQGRR
0.6	1726.8130	-0.0172	LAQLFMMSQQQGRR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

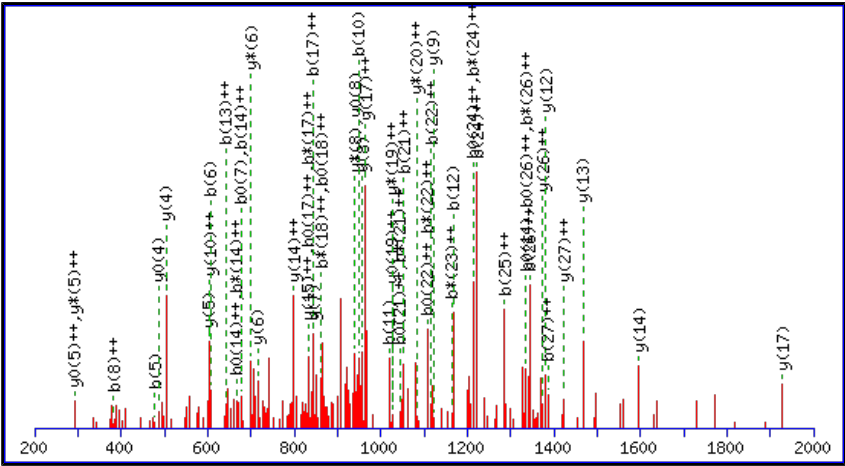
Peptide View

MS/MS Fragmentation of **VVHAAESALAAFNAQSNQSYLQLVEISR**
Found in **F1SFI7** in **uni_pig**, tr[F1SFI7|F1SFI7_PIG Alpha-2-HS-glycoprotein (Fragment) OS=Sus scrofa GN=AHSG PE=4 SV=2

Match to Query 13331: 2947.500882 from(983.507570,3+) intensity(0.0000) rtinseconds(2925) scans(6163) index(6071)
Title: 120325_Sunil_PigSerum_Glyco_S_12Spectrum4716_scans_6163
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

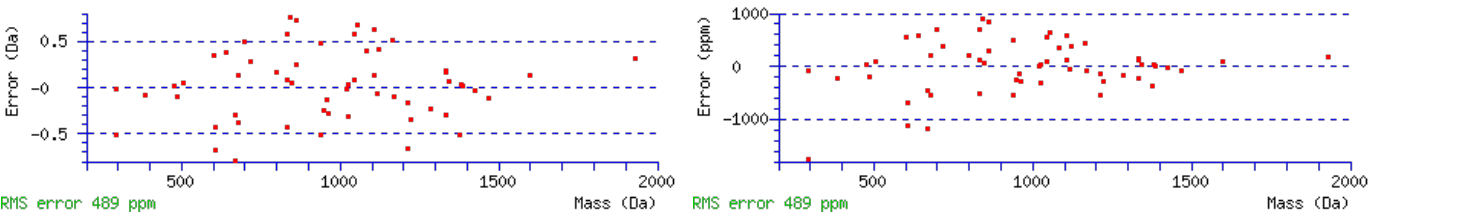
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2946.4723
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N17 : Deamidated (NQ)
Q22 : Deamidated (NQ)
Ions Score: 43 Expect: 0.0041
Matches : 57/288 fragment ions using 122 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							28
2	199.1441	100.0757					V	2848.4112	1424.7092	2831.3846	1416.1960	2830.4006	1415.7039	27
3	336.2030	168.6051					H	2749.3428	1375.1750	2732.3162	1366.6617	2731.3322	1366.1697	26
4	407.2401	204.1237					A	2612.2839	1306.6456	2595.2573	1298.1323	2594.2733	1297.6403	25
5	478.2772	239.6423					A	2541.2467	1271.1270	2524.2202	1262.6137	2523.2362	1262.1217	24
6	607.3198	304.1636			589.3093	295.1583	E	2470.2096	1235.6085	2453.1831	1227.0952	2452.1991	1226.6032	23
7	694.3519	347.6796			676.3413	338.6743	S	2341.1670	1171.0872	2324.1405	1162.5739	2323.1565	1162.0819	22
8	765.3890	383.1981			747.3784	374.1928	A	2254.1350	1127.5711	2237.1085	1119.0579	2236.1244	1118.5659	21
9	878.4730	439.7402			860.4625	430.7349	L	2183.0979	1092.0526	2166.0713	1083.5393	2165.0873	1083.0473	20
10	949.5102	475.2587			931.4996	466.2534	A	2070.0138	1035.5106	2052.9873	1026.9973	2052.0033	1026.5053	19
11	1020.5473	510.7773			1002.5367	501.7720	A	1998.9767	999.9920	1981.9502	991.4787	1980.9661	990.9867	18
12	1167.6157	584.3115			1149.6051	575.3062	F	1927.9396	964.4734	1910.9130	955.9602	1909.9290	955.4682	17
13	1281.6586	641.3329	1264.6321	632.8197	1263.6480	632.3277	N	1780.8712	890.9392	1763.8446	882.4260	1762.8606	881.9339	16
14	1352.6957	676.8515	1335.6692	668.3382	1334.6852	667.8462	A	1666.8283	833.9178	1649.8017	825.4045	1648.8177	824.9125	15
15	1480.7543	740.8808	1463.7278	732.3675	1462.7437	731.8755	Q	1595.7911	798.3992	1578.7646	789.8859	1577.7806	789.3939	14
16	1567.7863	784.3968	1550.7598	775.8835	1549.7758	775.3915	S	1467.7326	734.3699	1450.7060	725.8566	1449.7220	725.3646	13
17	1682.8133	841.9103	1665.7867	833.3970	1664.8027	832.9050	N	1380.7005	690.8539	1363.6740	682.3406	1362.6900	681.8486	12
18	1739.8347	870.4210	1722.8082	861.9077	1721.8242	861.4157	G	1265.6736	633.3404	1248.6470	624.8272	1247.6630	624.3352	11
19	1826.8668	913.9370	1809.8402	905.4237	1808.8562	904.9317	S	1208.6521	604.8297	1191.6256	596.3164	1190.6416	595.8244	10
20	1989.9301	995.4687	1972.9035	986.9554	1971.9195	986.4634	Y	1121.6201	561.3137	1104.5936	552.8004	1103.6095	552.3084	9
21	2103.0142	1052.0107	2085.9876	1043.4974	2085.0036	1043.0054	L	958.5568	479.7820	941.5302	471.2688	940.5462	470.7767	8
22	2232.0568	1116.5320	2215.0302	1108.0187	2214.0462	1107.5267	Q	845.4727	423.2400	828.4462	414.7267	827.4621	414.2347	7
23	2345.1408	1173.0740	2328.1143	1164.5608	2327.1303	1164.0688	L	716.4301	358.7187	699.4036	350.2054	698.4196	349.7134	6

24	2444.2092	1222.6083	2427.1827	1214.0950	2426.1987	1213.6030	V	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
25	2573.2518	1287.1296	2556.2253	1278.6163	2555.2413	1278.1243	E	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
26	2686.3359	1343.6716	2669.3093	1335.1583	2668.3253	1334.6663	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
27	2773.3679	1387.1876	2756.3414	1378.6743	2755.3574	1378.1823	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
28							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [VVHAAESALAAFNAQSNGSYLQLVEISR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
43.0	2946.4723	1.0286	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated N17, Q22 37.97%
42.5	2946.4723	1.0286	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated Q15, Q22 34.00%
38.9	2946.4723	1.0286	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated Q15, N17 14.84%
36.1	2946.4723	1.0286	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated N13, Q22 7.77%
32.5	2946.4723	1.0286	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated N13, N17 3.42%
30.2	2946.4723	1.0286	VVHAAESALAAFNAQSNGSYLQLVEISR	Deamidated N13, Q15 2.01%
27.0	2945.4883	2.0126	VVHAAESALAAFNAQSNGSYLQLVEISR	
25.2	2945.4883	2.0126	VVHAAESALAAFNAQSNGSYLQLVEISR	
23.0	2945.4883	2.0126	VVHAAESALAAFNAQSNGSYLQLVEISR	
18.2	2945.4883	2.0126	VVHAAESALAAFNAQSNGSYLQLVEISR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **YPHKPEVNSTMYPGADLR**

Found in **F1SIB1** in **uni_pig**, tr|F1SIB1|F1SIB1_PIG Prothrombin OS=Sus scrofa GN=F2 PE=3 SV=2

Match to Query 11911: 2074.970592 from(692.664140,3+) intensity(3511.0659) rtinseconds(1516) scans(2216) index(7305)

Title: 120326 Sunil PigSerum Glyco DsetB 03Spectrum1319 scans 2216

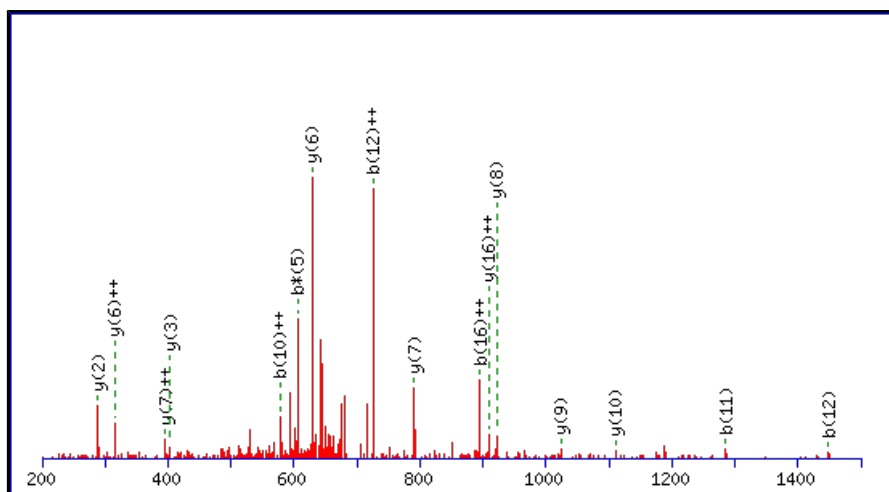
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point.

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2074.9782

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

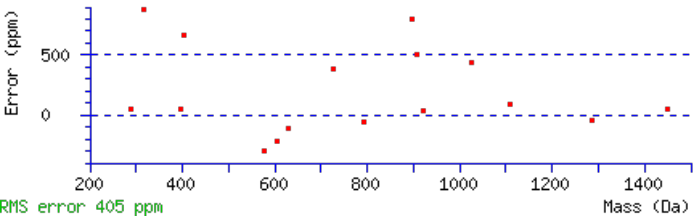
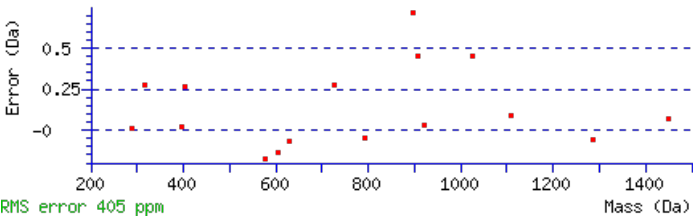
Variable modifications:

N8 : Deamidated (NQ)

Ions Score: 41 Expect: 0.0045

Matches : 16/184 fragment ions using 25 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							18
2	261.1234	131.0653					P	1912.9222	956.9647	1895.8956	948.4515	1894.9116	947.9594	17
3	398.1823	199.5948					H	1815.8694	908.4383	1798.8429	899.9251	1797.8588	899.4331	16
4	526.2772	263.6423	509.2507	255.1290			K	1678.8105	839.9089	1661.7840	831.3956	1660.7999	830.9036	15
5	623.3300	312.1686	606.3035	303.6554			P	1550.7155	775.8614	1533.6890	767.3481	1532.7050	766.8561	14
6	752.3726	376.6899	735.3461	368.1767	734.3620	367.6847	E	1453.6628	727.3350	1436.6362	718.8217	1435.6522	718.3297	13
7	851.4410	426.2241	834.4145	417.7109	833.4304	417.2189	V	1324.6202	662.8137	1307.5936	654.3005	1306.6096	653.8084	12
8	966.4680	483.7376	949.4414	475.2243	948.4574	474.7323	N	1225.5518	613.2795	1208.5252	604.7662	1207.5412	604.2742	11
9	1053.5000	527.2536	1036.4734	518.7404	1035.4894	518.2483	S	1110.5248	555.7660	1093.4983	547.2528	1092.5143	546.7608	10
10	1154.5477	577.7775	1137.5211	569.2642	1136.5371	568.7722	T	1023.4928	512.2500	1006.4662	503.7368	1005.4822	503.2448	9
11	1285.5882	643.2977	1268.5616	634.7844	1267.5776	634.2924	M	922.4451	461.7262	905.4186	453.2129	904.4345	452.7209	8
12	1448.6515	724.8294	1431.6249	716.3161	1430.6409	715.8241	Y	791.4046	396.2060	774.3781	387.6927	773.3941	387.2007	7
13	1545.7042	773.3558	1528.6777	764.8425	1527.6937	764.3505	P	628.3413	314.6743	611.3148	306.1610	610.3307	305.6690	6
14	1602.7257	801.8665	1585.6992	793.3532	1584.7151	792.8612	G	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	5
15	1673.7628	837.3850	1656.7363	828.8718	1655.7523	828.3798	A	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
16	1788.7898	894.8985	1771.7632	886.3852	1770.7792	885.8932	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
17	1901.8738	951.4406	1884.8473	942.9273	1883.8633	942.4353	L	288.2030	144.6051	271.1765	136.0919			2
18							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [YPHKPEVNSTMYPGADLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.2	2074.9782	-0.0076	YPHKPEVNSTMYPGADLR
9.6	2074.9816	-0.0110	WLTVEMMQDGHQVSLLR
4.6	2073.9790	0.9916	TFSCQSALVVHQSSHTGVK
3.2	2074.9737	-0.0031	VMMTYQVPSSRDMASVLK
3.2	2074.9737	-0.0031	VMMTYQVPSSRDMASVLK
0.3	2074.9816	-0.0110	KVLMDDALWETIMGHER
0.2	2074.9841	-0.0135	SIEQHKSDIETDKQMIR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of NESKPDVDTER

Found in **F1RMN7** in **uni_pig**, tr|F1RMN7|F1RMN7_PIG Hemopexin OS=Sus scrofa GN=HPX PE=4 SV=2

Match to Query 3313: 1386.624762 from(463.215530,3+) intensity(11408.0664) rtinseconds(635) scans(1177) index(6119)

Title: 120325_Sunil_PigSerum_Glyco_S_14Spectrum891_scans__1177

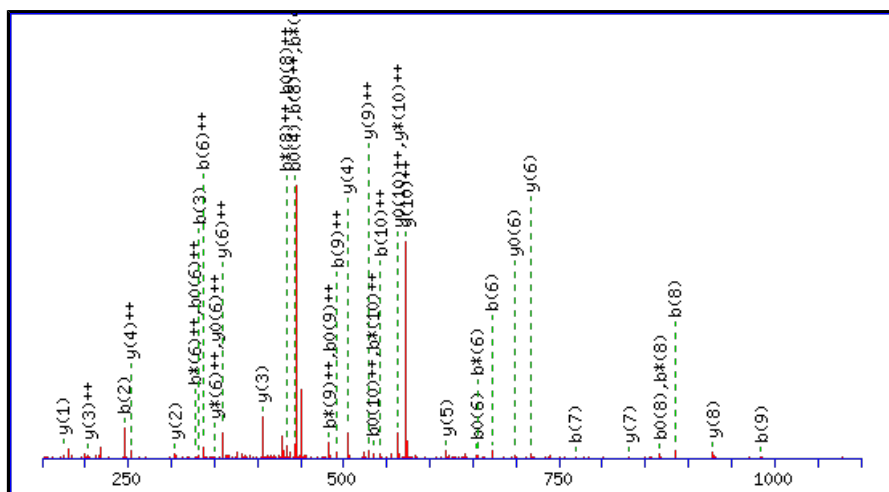
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1386.6263

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

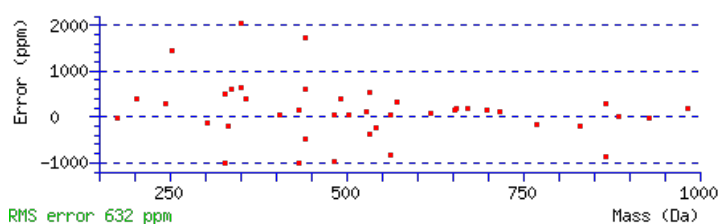
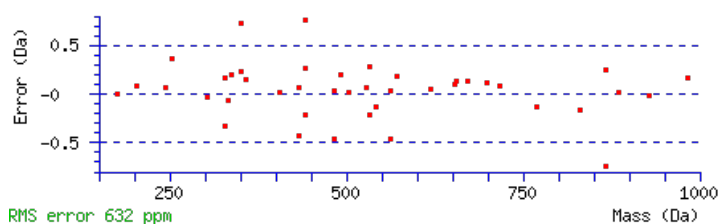
Variable modifications:

N1 : Deamidated (NQ)

Ions Score: 38 Expect: 0.0046

Matches : 42/128 fragment ions using 68 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							12
2	245.0768	123.0420	228.0503	114.5288	227.0662	114.0368	E	1272.6066	636.8070	1255.5801	628.2937	1254.5961	627.8017	11
3	332.1088	166.5581	315.0823	158.0448	314.0983	157.5528	S	1143.5640	572.2857	1126.5375	563.7724	1125.5535	563.2804	10
4	460.2038	230.6055	443.1773	222.0923	442.1932	221.6003	K	1056.5320	528.7696	1039.5055	520.2564	1038.5215	519.7644	9
5	557.2566	279.1319	540.2300	270.6186	539.2460	270.1266	P	928.4371	464.7222	911.4105	456.2089	910.4265	455.7169	8
6	672.2835	336.6454	655.2570	328.1321	654.2729	327.6401	D	831.3843	416.1958	814.3577	407.6825	813.3737	407.1905	7
7	769.3363	385.1718	752.3097	376.6585	751.3257	376.1665	P	716.3573	358.6823	699.3308	350.1690	698.3468	349.6770	6
8	884.3632	442.6852	867.3367	434.1720	866.3527	433.6800	D	619.3046	310.1559	602.2780	301.6427	601.2940	301.1506	5
9	983.4316	492.2195	966.4051	483.7062	965.4211	483.2142	V	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
10	1084.4793	542.7433	1067.4528	534.2300	1066.4687	533.7380	T	405.2092	203.1082	388.1827	194.5950	387.1987	194.1030	3
11	1213.5219	607.2646	1196.4954	598.7513	1195.5113	598.2593	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of NESKPDVTER

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.3	1386.6263	-0.0015	NESKPPDPDVTER
6.6	1386.6337	-0.0089	ENAEQPNLVPMK
4.2	1386.6337	-0.0089	ENAEQPNLVPMK
4.1	1386.6337	-0.0089	ENAEQPNLVPMK
2.7	1386.6263	-0.0015	NQAQDEGILPSGR
2.3	1386.6303	-0.0055	LQEEYYEEKR
1.6	1385.6284	0.9964	GAGGSRQGGQPGAQR
1.5	1384.6268	1.9980	CFHKMISYNGK
1.5	1386.6262	-0.0015	NNNEANQVVRPK
1.4	1384.6292	1.9955	YMGKQESLEER

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of GSEILYNETLR

Found in **F1RSK4** in **uni_pig**, tr|F1RSK4|F1RSK4_PIG Uncharacterized protein OS=Sus scrofa GN=ICAM2 PE=4 SV=2

Match to Query 2554: 1294.633788 from(648.324170,2+) intensity(4718.0127) rtinseconds(1781) scans(3854) index(8689)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_15Spectrum3205_scans__3854

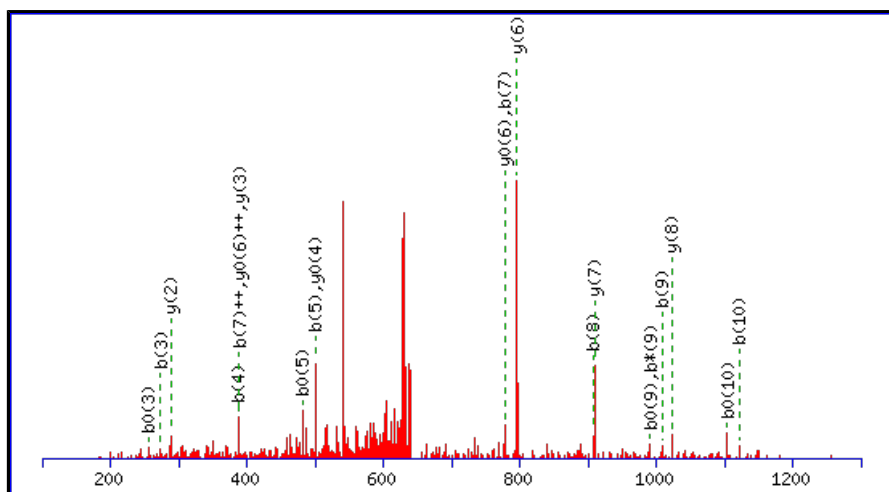
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1294.6405

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

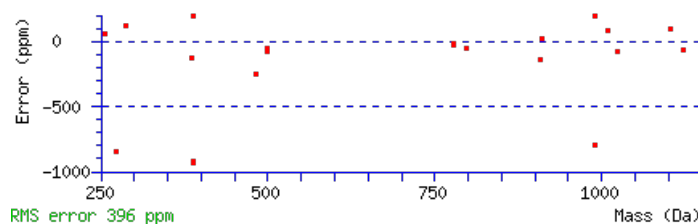
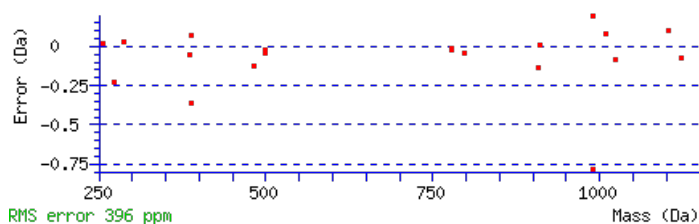
Variable modifications:

N7 : Deamidated (NQ)

Ions Score: 41 Expect: 0.0053

Matches : 21/102 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							11
2	145.0608	73.0340			127.0502	64.0287	S	1238.6263	619.8168	1221.5998	611.3035	1220.6157	610.8115	10
3	274.1034	137.5553			256.0928	128.5500	E	1151.5943	576.3008	1134.5677	567.7875	1133.5837	567.2955	9
4	387.1874	194.0974			369.1769	185.0921	I	1022.5517	511.7795	1005.5251	503.2662	1004.5411	502.7742	8
5	500.2715	250.6394			482.2609	241.6341	L	909.4676	455.2374	892.4411	446.7242	891.4571	446.2322	7
6	663.3348	332.1710			645.3243	323.1658	Y	796.3836	398.6954	779.3570	390.1821	778.3730	389.6901	6
7	778.3618	389.6845	761.3352	381.1712	760.3512	380.6792	N	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	5
8	907.4044	454.2058	890.3778	445.6925	889.3938	445.2005	E	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	4
9	1008.4520	504.7297	991.4255	496.2164	990.4415	495.7244	T	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
10	1121.5361	561.2717	1104.5095	552.7584	1103.5255	552.2664	L	288.2030	144.6051	271.1765	136.0919			2
11							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [GSEILYNETLR](#)

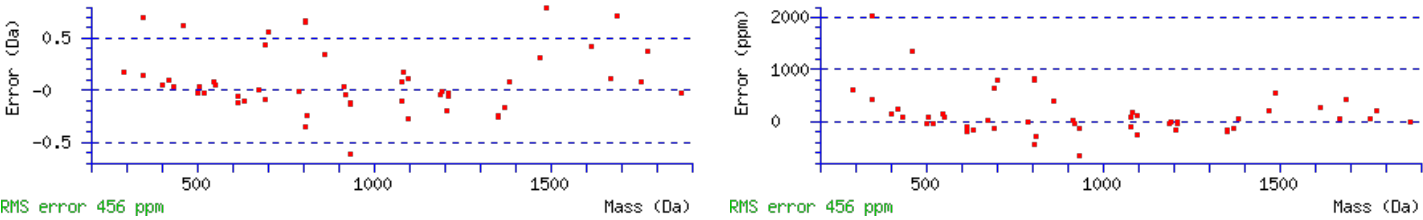
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.8	1294.6405	-0.0067	GSEILYNETLR
7.8	1294.6340	-0.0002	VKGTNEDMVFR
7.2	1294.6340	-0.0002	CLLFSENTGVR
6.5	1294.6306	0.0032	AEWLYSQGKGR
6.1	1294.6227	0.0111	LCDLTFEQIR
1.3	1294.6378	-0.0040	EPSGQEHKRAR
0.9	1294.6265	0.0073	SDANASYLRAAR
0.7	1294.6227	0.0110	NDTVFEMPSVLR
0.6	1294.6340	-0.0002	FGESTIVCNIR
0.6	1294.6340	-0.0002	FGESTIVCNLR

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [EYQTIGNQCIYNDSSLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
39.0	2032.9048	1.0222	EYQTIGNQCIYNDSSLK	Deamidated N7 71.32%
32.4	2032.9048	1.0222	EYQTIGNQCIYNDSSLK	Deamidated Q8 15.64%
31.2	2032.9048	1.0222	EYQTIGNQCIYNDSSLK	Deamidated N12 11.94%
20.9	2032.9048	1.0222	EYQTIGNQCIYNDSSLK	Deamidated Q3 1.10%
3.4	2031.9207	2.0062	EYQTIGNQCIYNDSSLK	

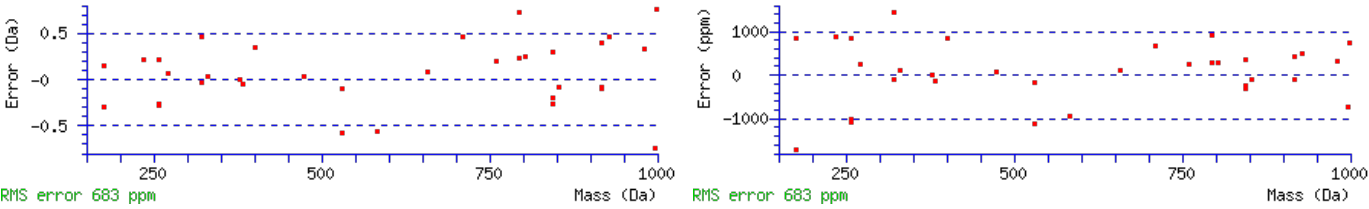
Mascot: <http://www.matrixscience.com/>

Peptide View

Match to Query 12818: 2361.021696 from(591.262700,4+) intensity(6131.1738) rtinseconds(949) scans(1251) index(6631)
Title: 120325_Sunil_PigSerum_Glyco_S_16Spectrum584_scans_1251
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Monoisotopic mass of neutral peptide Mr(calc): 2361.0257
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
 N11 : Deamidated (NQ)
Ions Score: 37 **Expect:** 0.0057
Matches : 34/192 fragment ions using 47 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							19
2	235.1077	118.0575					Y	2290.9959	1146.0016	2273.9694	1137.4883	2272.9854	1136.9963	18
3	350.1347	175.5710			332.1241	166.5657	D	2127.9326	1064.4699	2110.9061	1055.9567	2109.9221	1055.4647	17
4	513.1980	257.1026			495.1874	248.0974	Y	2012.9057	1006.9565	1995.8791	998.4432	1994.8951	997.9512	16
5	650.2569	325.6321			632.2463	316.6268	H	1849.8423	925.4248	1832.8158	916.9115	1831.8318	916.4195	15
6	779.2995	390.1534			761.2889	381.1481	E	1712.7834	856.8954	1695.7569	848.3821	1694.7729	847.8901	14
7	908.3421	454.6747			890.3315	445.6694	E	1583.7408	792.3741	1566.7143	783.8608	1565.7303	783.3688	13
8	1009.3898	505.1985			991.3792	496.1932	T	1454.6982	727.8528	1437.6717	719.3395	1436.6877	718.8475	12
9	1165.4909	583.2491	1148.4643	574.7358	1147.4803	574.2438	R	1353.6506	677.3289	1336.6240	668.8156	1335.6400	668.3236	11
10	1302.5498	651.7785	1285.5232	643.2653	1284.5392	642.7733	H	1197.5495	599.2784	1180.5229	590.7651	1179.5389	590.2731	10
11	1417.5767	709.2920	1400.5502	700.7787	1399.5662	700.2867	N	1060.4905	530.7489	1043.4640	522.2356	1042.4800	521.7436	9
12	1518.6244	759.8158	1501.5979	751.3026	1500.6138	750.8106	T	945.4636	473.2354	928.4371	464.7222	927.4530	464.2302	8
13	1605.6564	803.3319	1588.6299	794.8186	1587.6459	794.3266	S	844.4159	422.7116	827.3894	414.1983	826.4054	413.7063	7
14	1704.7249	852.8661	1687.6983	844.3528	1686.7143	843.8608	V	757.3839	379.1956	740.3573	370.6823	739.3733	370.1903	6
15	1832.7834	916.8954	1815.7569	908.3821	1814.7729	907.8901	Q	658.3155	329.6614	641.2889	321.1481	640.3049	320.6561	5
16	1961.8260	981.4167	1944.7995	972.9034	1943.8155	972.4114	E	530.2569	265.6321	513.2304	257.1188	512.2463	256.6268	4
17	2090.8686	1045.9379	2073.8421	1037.4247	2072.8581	1036.9327	E	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
18	2187.9214	1094.4643	2170.8948	1085.9511	2169.9108	1085.4590	P	272.1717	136.5895	255.1452	128.0762			2
19							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [AYDYHEETRHNTSVQEEPR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
36.9	2361.0257	-0.0040	AYDYHEETRHNTSVQEEPR	Deamidated N11 95.69%
23.4	2361.0257	-0.0040	AYDYHEETRHNTSVQEEPR	Deamidated Q15 4.31%
22.1	2360.0417	0.9800	AYDYHEETRHNTSVQEEPR	
17.3	2360.0314	0.9903	YDPHQNQWTVCRPMKEPR	
9.7	2361.0385	-0.0168	ELSMENQCSLDMKSKLNTSK	
9.2	2360.0187	1.0030	MAADSDDGAASAPAVSDGGVHQSTK	
9.2	2361.0027	0.0190	MAADSDDGAASAPAVSDGGVHQSTK	
6.9	2361.0267	-0.0050	DLPMHNKFSDWCGVQDGSPR	
5.6	2359.0274	1.9943	YIAETMKSDQESNNAAEWK	
4.4	2359.0249	1.9968	EFYMKDMYTFDSSPEAARR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **AYDYHEETRHNTSVQEEQR**
Found in **I3L998** in **uni_pig**, tr|I3L998|I3L998_PIG Vitronectin OS=Sus scrofa GN=VTN PE=4 SV=1

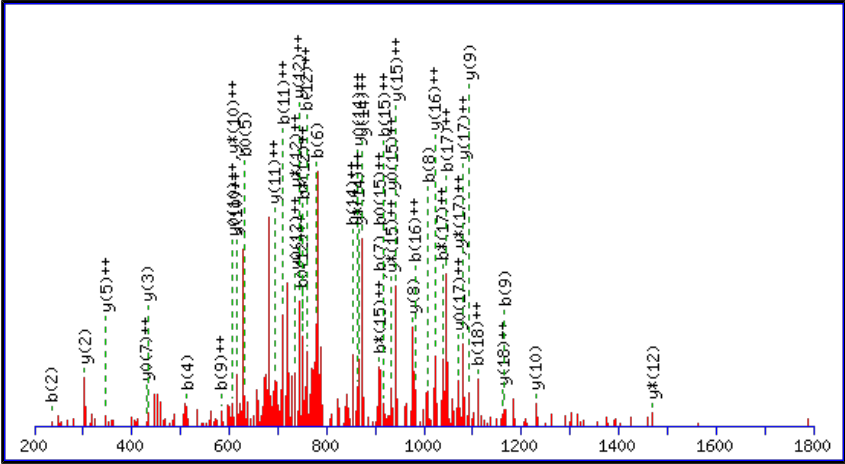
Match to Query 12858: 2394.010632 from(799.010820,3+) intensity(3758.2600) rtinseconds(915) scans(1391) index(13758)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_18Spectrum871_scans__1391
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

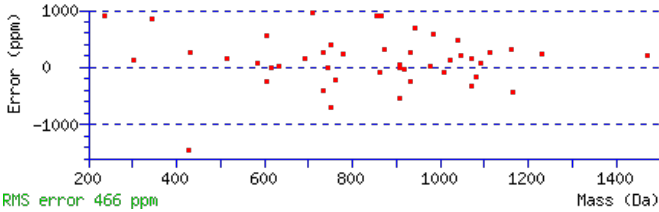
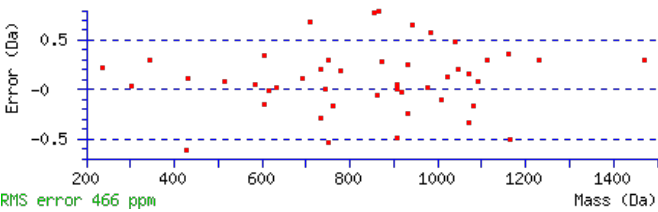
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2393.0156
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Q15 : Deamidated (NQ)
Ions Score: 35 Expect: 0.0058
Matches : 46/192 fragment ions using 122 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							19
2	235.1077	118.0575					Y	2322.9858	1161.9965	2305.9592	1153.4833	2304.9752	1152.9912	18
3	350.1347	175.5710			332.1241	166.5657	D	2159.9224	1080.4649	2142.8959	1071.9516	2141.9119	1071.4596	17
4	513.1980	257.1026			495.1874	248.0974	Y	2044.8955	1022.9514	2027.8690	1014.4381	2026.8849	1013.9461	16
5	650.2569	325.6321			632.2463	316.6268	H	1881.8322	941.4197	1864.8056	932.9065	1863.8216	932.4144	15
6	779.2995	390.1534			761.2889	381.1481	E	1744.7733	872.8903	1727.7467	864.3770	1726.7627	863.8850	14
7	908.3421	454.6747			890.3315	445.6694	E	1615.7307	808.3690	1598.7041	799.8557	1597.7201	799.3637	13
8	1009.3898	505.1985			991.3792	496.1932	T	1486.6881	743.8477	1469.6615	735.3344	1468.6775	734.8424	12
9	1165.4909	583.2491	1148.4643	574.7358	1147.4803	574.2438	R	1385.6404	693.3238	1368.6138	684.8106	1367.6298	684.3186	11
10	1302.5498	651.7785	1285.5232	643.2653	1284.5392	642.7733	H	1229.5393	615.2733	1212.5127	606.7600	1211.5287	606.2680	10
11	1417.5767	709.2920	1400.5502	700.7787	1399.5662	700.2867	N	1092.4804	546.7438	1075.4538	538.2306	1074.4698	537.7385	9
12	1518.6244	759.8158	1501.5979	751.3026	1500.6138	750.8106	T	977.4534	489.2304	960.4269	480.7171	959.4429	480.2251	8
13	1605.6564	803.3319	1588.6299	794.8186	1587.6459	794.3266	S	876.4058	438.7065	859.3792	430.1932	858.3952	429.7012	7
14	1704.7249	852.8661	1687.6983	844.3528	1686.7143	843.8608	V	789.3737	395.1905	772.3472	386.6772	771.3632	386.1852	6
15	1833.7674	917.3874	1816.7409	908.8741	1815.7569	908.3821	Q	690.3053	345.6563	673.2788	337.1430	672.2947	336.6510	5
16	1962.8100	981.9087	1945.7835	973.3954	1944.7995	972.9034	E	561.2627	281.1350	544.2362	272.6217	543.2522	272.1297	4
17	2091.8526	1046.4300	2074.8261	1037.9167	2073.8421	1037.4247	E	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
18	2219.9112	1110.4592	2202.8847	1101.9460	2201.9006	1101.4540	Q	303.1775	152.0924	286.1510	143.5791			2
19							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [AYDYHEETRHNTSVQEEQR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
34.7	2393.0156	0.9951	AYDYHEETRHNTSVQEEQR	Deamidated N11, Q15 63.23%
34.5	2393.9996	0.0111	AYDYHEETRHNTSVQEEQR	
30.1	2393.0156	0.9951	AYDYHEETRHNTSVQEEQR	Deamidated Q15, Q18 22.28%
28.3	2393.0156	0.9951	AYDYHEETRHNTSVQEEQR	Deamidated N11, Q18 14.49%

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **VASVININPNTTNATGNCHSK**
Found in **F1RUC0** in **uni_pig**, tr[F1RUC0]F1RUC0_PIG Uncharacterized protein OS=Sus scrofa GN=LAMP2 PE=4 SV=2

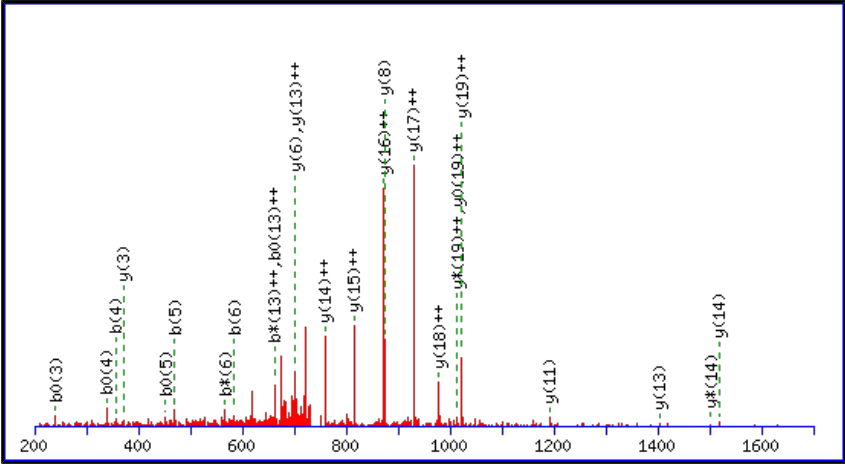
Match to Query 12457: 2214.037602 from(739.019810,3+) intensity(4777.8755) rtinseconds(1619) scans(3082) index(1745)
Title: 120325_Sunil_PigSerum_Glyco_D_15Spectrum2414_scans__3082
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

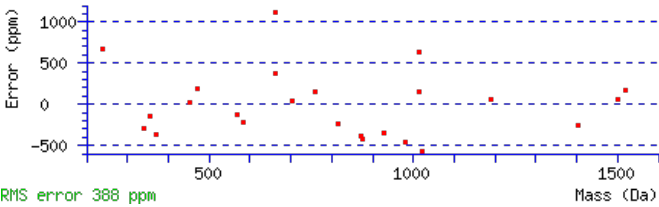
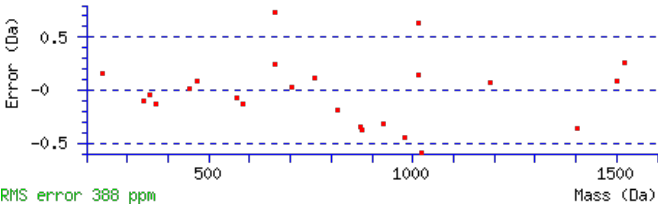
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2214.0222
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
N10 : Deamidated (NQ)
N13 : Deamidated (NQ)
Ions Score: 40 Expect: 0.0063
Matches : 25/224 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							21
2	171.1128	86.0600					A	2115.9611	1058.4842	2098.9346	1049.9709	2097.9506	1049.4789	20
3	258.1448	129.5761			240.1343	120.5708	S	2044.9240	1022.9657	2027.8975	1014.4524	2026.9135	1013.9604	19
4	357.2132	179.1103			339.2027	170.1050	V	1957.8920	979.4496	1940.8654	970.9364	1939.8814	970.4444	18
5	470.2973	235.6523			452.2867	226.6470	I	1858.8236	929.9154	1841.7970	921.4022	1840.8130	920.9101	17
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	N	1745.7395	873.3734	1728.7130	864.8601	1727.7290	864.3681	16
7	697.4243	349.2158	680.3978	340.7025	679.4137	340.2105	I	1631.6966	816.3519	1614.6700	807.8387	1613.6860	807.3467	15
8	812.4512	406.7293	795.4247	398.2160	794.4407	397.7240	N	1518.6125	759.8099	1501.5860	751.2966	1500.6020	750.8046	14
9	909.5040	455.2556	892.4775	446.7424	891.4934	446.2504	P	1403.5856	702.2964	1386.5590	693.7832	1385.5750	693.2911	13
10	1024.5310	512.7691	1007.5044	504.2558	1006.5204	503.7638	N	1306.5328	653.7700	1289.5063	645.2568	1288.5223	644.7648	12
11	1125.5786	563.2930	1108.5521	554.7797	1107.5681	554.2877	T	1191.5059	596.2566	1174.4793	587.7433	1173.4953	587.2513	11
12	1226.6263	613.8168	1209.5998	605.3035	1208.6157	604.8115	T	1090.4582	545.7327	1073.4317	537.2195	1072.4476	536.7275	10
13	1341.6533	671.3303	1324.6267	662.8170	1323.6427	662.3250	N	989.4105	495.2089	972.3840	486.6956	971.4000	486.2036	9
14	1412.6904	706.8488	1395.6638	698.3355	1394.6798	697.8435	A	874.3836	437.6954	857.3570	429.1822	856.3730	428.6901	8
15	1513.7380	757.3727	1496.7115	748.8594	1495.7275	748.3674	T	803.3465	402.1769	786.3199	393.6636	785.3359	393.1716	7
16	1570.7595	785.8834	1553.7330	777.3701	1552.7489	776.8781	G	702.2988	351.6530	685.2722	343.1398	684.2882	342.6477	6
17	1684.8024	842.9049	1667.7759	834.3916	1666.7919	833.8996	N	645.2773	323.1423	628.2508	314.6290	627.2668	314.1370	5
18	1844.8331	922.9202	1827.8065	914.4069	1826.8225	913.9149	C	531.2344	266.1208	514.2078	257.6076	513.2238	257.1156	4
19	1981.8920	991.4496	1964.8654	982.9364	1963.8814	982.4444	H	371.2037	186.1055	354.1772	177.5922	353.1932	177.1002	3
20	2068.9240	1034.9657	2051.8975	1026.4524	2050.9135	1025.9604	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
21							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [VASVININPNTTNATGNCHSK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

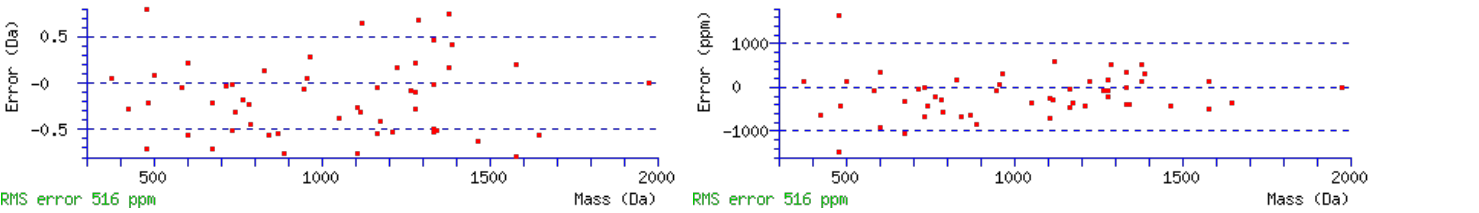
All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
40.2	2214.0222	0.0154	VASVININPNTTNATGNCHSK	Deamidated N8, N10, N13 53.07%
37.3	2213.0382	0.9994	VASVININPNTTNATGNCHSK	
37.3	2213.0382	0.9994	VASVININPNTTNATGNCHSK	
33.5	2214.0222	0.0154	VASVININPNTTNATGNCHSK	Deamidated N8, N10, N17 11.53%
31.2	2214.0222	0.0154	VASVININPNTTNATGNCHSK	Deamidated N8, N13, N17 6.71%
31.0	2213.0382	0.9994	VASVININPNTTNATGNCHSK	
30.8	2213.0382	0.9994	VASVININPNTTNATGNCHSK	
30.7	2214.0222	0.0154	VASVININPNTTNATGNCHSK	Deamidated N6, N10, N13 6.01%
30.7	2214.0222	0.0154	VASVININPNTTNATGNCHSK	Deamidated N6, N8, N13 6.01%
28.9	2214.0222	0.0154	VASVININPNTTNATGNCHSK	Deamidated N6, N13, N17 3.99%

Mascot: <http://www.matrixscience.com/>

http:// MascotXP.student.main.ntu.edu.sg/Mascot/cgi/peptide_view.pl?file=F:/data/20150422/F033714.dat&hit=1&px=1&query=13336[22/Apr/15 06:11:23 PM]

24	2445.1932	1223.1003	2428.1667	1214.5870	2427.1827	1214.0950	V	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
25	2574.2358	1287.6216	2557.2093	1279.1083	2556.2253	1278.6163	E	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
26	2687.3199	1344.1636	2670.2934	1335.6503	2669.3093	1335.1583	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
27	2774.3519	1387.6796	2757.3254	1379.1663	2756.3414	1378.6743	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
28							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [VVHAAESALAAFNAQSNQSYLQLVEISR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
40.7	2947.4563	1.0143	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated Q15, N17, Q22 89.67%
37.5	2946.4723	1.9983	VVHAAESALAAFNAQSNQSYLQLVEISR	
33.5	2946.4723	1.9983	VVHAAESALAAFNAQSNQSYLQLVEISR	
31.8	2946.4723	1.9983	VVHAAESALAAFNAQSNQSYLQLVEISR	
29.2	2947.4563	1.0143	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated N13, N17, Q22 6.39%
26.2	2947.4563	1.0143	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated N13, Q15, Q22 3.19%
22.1	2946.4723	1.9983	VVHAAESALAAFNAQSNQSYLQLVEISR	
22.0	2946.4723	1.9983	VVHAAESALAAFNAQSNQSYLQLVEISR	
19.9	2947.4563	1.0143	VVHAAESALAAFNAQSNQSYLQLVEISR	Deamidated N13, Q15, N17 0.74%
14.4	2946.4723	1.9983	VVHAAESALAAFNAQSNQSYLQLVEISR	

Mascot: <http://www.matrixscience.com/>

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Mascot Search Results

Peptide View

MS/MS Fragmentation of **GCLLLSHLNETVTVSASLESLENR**
Found in **F1SLX2** in **uni_pig**, tr[F1SLX2]F1SLX2_PIG Uncharacterized protein OS=Sus scrofa GN=A2M PE=4 SV=2

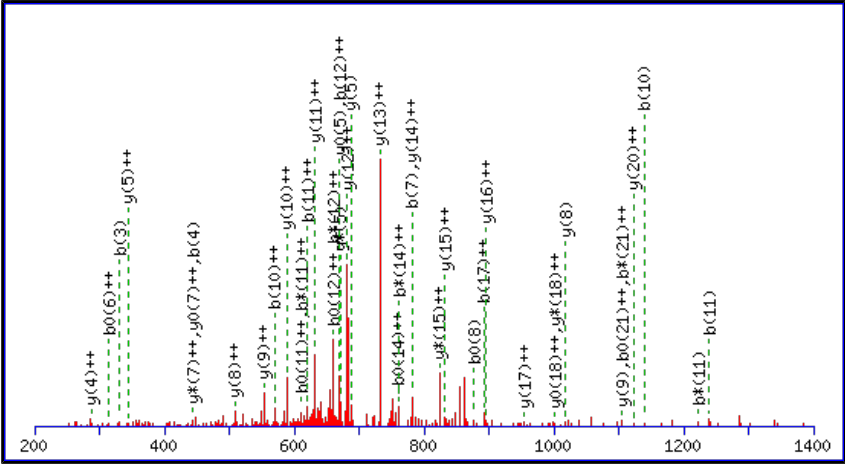
Match to Query 13225: 2800.404656 from(701.108440,4+) intensity(1816.7742) rtinseconds(2803) scans(5236) index(5683)
Title: 120325_Sunil_PigSerum_Glyco_S_10Spectrum3629_scans_5236
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

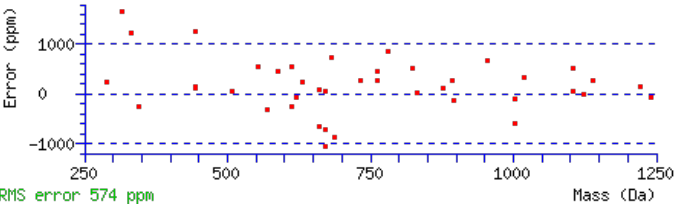
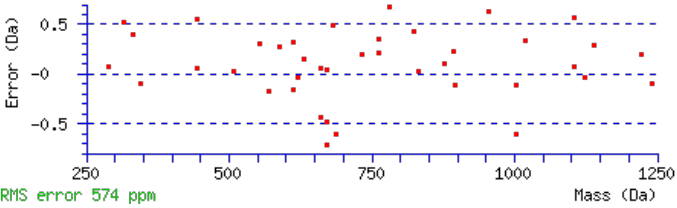
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2799.4072
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
N24 : Deamidated (NQ)
Ions Score: 39 Expect: 0.01
Matches : 43/258 fragment ions using 100 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							25
2	218.0594	109.5333					C	2743.3931	1372.2002	2726.3665	1363.6869	2725.3825	1363.1949	24
3	331.1435	166.0754					L	2583.3624	1292.1849	2566.3359	1283.6716	2565.3519	1283.1796	23
4	444.2275	222.6174					L	2470.2784	1235.6428	2453.2518	1227.1295	2452.2678	1226.6375	22
5	557.3116	279.1594					L	2357.1943	1179.1008	2340.1678	1170.5875	2339.1837	1170.0955	21
6	644.3436	322.6754			626.3330	313.6702	S	2244.1102	1122.5588	2227.0837	1114.0455	2226.0997	1113.5535	20
7	781.4025	391.2049			763.3920	382.1996	H	2157.0782	1079.0427	2140.0517	1070.5295	2139.0677	1070.0375	19
8	894.4866	447.7469			876.4760	438.7416	L	2020.0193	1010.5133	2002.9928	1002.0000	2002.0087	1001.5080	18
9	1009.5135	505.2604	992.4870	496.7471	991.5030	496.2551	N	1906.9352	953.9713	1889.9087	945.4580	1888.9247	944.9660	17
10	1138.5561	569.7817	1121.5296	561.2684	1120.5456	560.7764	E	1791.9083	896.4578	1774.8817	887.9445	1773.8977	887.4525	16
11	1239.6038	620.3055	1222.5773	611.7923	1221.5932	611.3003	T	1662.8657	831.9365	1645.8392	823.4232	1644.8551	822.9312	15
12	1338.6722	669.8397	1321.6457	661.3265	1320.6616	660.8345	V	1561.8180	781.4127	1544.7915	772.8994	1543.8075	772.4074	14
13	1439.7199	720.3636	1422.6933	711.8503	1421.7093	711.3583	T	1462.7496	731.8784	1445.7231	723.3652	1444.7390	722.8732	13
14	1538.7883	769.8978	1521.7618	761.3845	1520.7777	760.8925	V	1361.7019	681.3546	1344.6754	672.8413	1343.6914	672.3493	12
15	1625.8203	813.4138	1608.7938	804.9005	1607.8098	804.4085	S	1262.6335	631.8204	1245.6070	623.3071	1244.6230	622.8151	11
16	1696.8574	848.9324	1679.8309	840.4191	1678.8469	839.9271	A	1175.6015	588.3044	1158.5749	579.7911	1157.5909	579.2991	10
17	1783.8895	892.4484	1766.8629	883.9351	1765.8789	883.4431	S	1104.5644	552.7858	1087.5378	544.2726	1086.5538	543.7805	9
18	1896.9735	948.9904	1879.9470	940.4771	1878.9630	939.9851	L	1017.5323	509.2698	1000.5058	500.7565	999.5218	500.2645	8
19	2026.0161	1013.5117	2008.9896	1004.9984	2008.0056	1004.5064	E	904.4483	452.7278	887.4217	444.2145	886.4377	443.7225	7
20	2113.0482	1057.0277	2096.0216	1048.5144	2095.0376	1048.0224	S	775.4057	388.2065	758.3791	379.6932	757.3951	379.2012	6
21	2226.1322	1113.5698	2209.1057	1105.0565	2208.1217	1104.5645	L	688.3737	344.6905	671.3471	336.1772	670.3631	335.6852	5
22	2382.2333	1191.6203	2365.2068	1183.1070	2364.2228	1182.6150	R	575.2896	288.1484	558.2630	279.6352	557.2790	279.1432	4
23	2511.2759	1256.1416	2494.2494	1247.6283	2493.2654	1247.1363	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3

24	2626.3029	1313.6551	2609.2763	1305.1418	2608.2923	1304.6498	N	290.1459	145.5766	273.1193	137.0633			2
25							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [GCLLLSHLNETVTVSASLESLREN](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.2	2799.4072	0.9974	GCLLLSHLNETVTVSASLESLREN
25.3	2798.4232	1.9814	GCLLLSHLNETVTVSASLESLREN
19.2	2798.4232	1.9814	GCLLLSHLNETVTVSASLESLREN
9.9	2800.4065	-0.0019	DGGELPDPDRMVVSGRELNILELNK
8.4	2799.3836	1.0210	LGQAGFMQRQFGAMLQPGVNKFSLR
6.6	2799.3836	1.0210	LGQAGFMQRQFGAMLQPGVNKFSLR
5.8	2799.4225	0.9822	NSGKTPHLLMLLPSYGLESQQSNR
3.8	2799.4151	0.9895	WRSLGSLSQGSTNATVLDVAQTGGHKK
3.6	2799.4113	0.9934	VTEQEVEAVGKMLVDPGQPLQARFR
3.5	2800.3967	0.0080	GPLGKPGLPGMPGADGPPGHPGKEGPPGEK

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLTNGSTTPGDAGR**

Found in **I3LM17** in **uni_pig**, tr|I3LM17|I3LM17_PIG Uncharacterized protein OS=Sus scrofa GN=HEG1 PE=4 SV=1

Match to Query 3049: 1333.609588 from(667.812070,2+) intensity(1770.3756) rtinseconds(915) scans(1165) index(6629)

Title: 120325_Sunil_PigSerum_Glyco_S_16Spectrum528_scans__1165

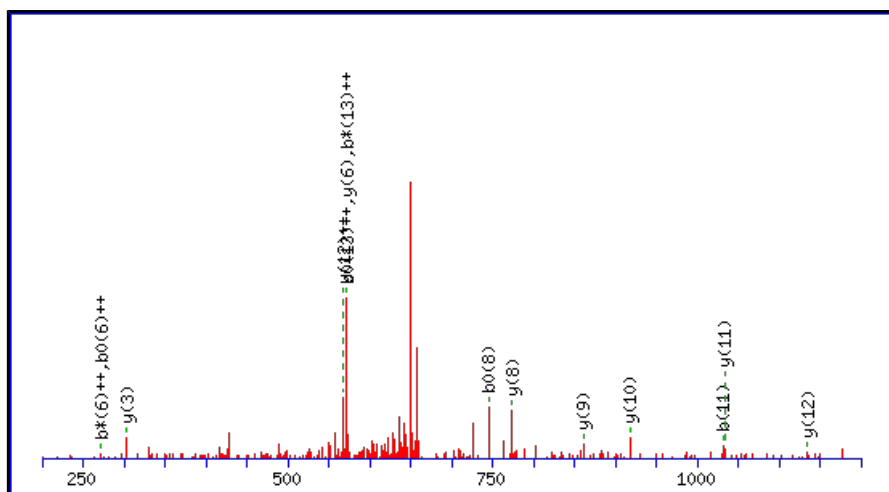
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1333.6110

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

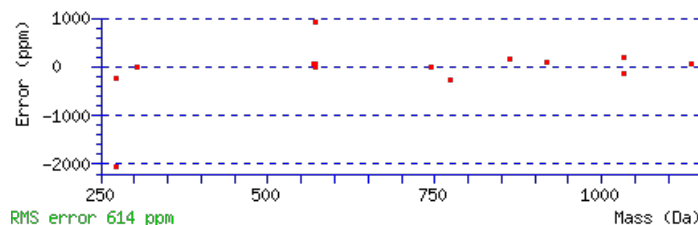
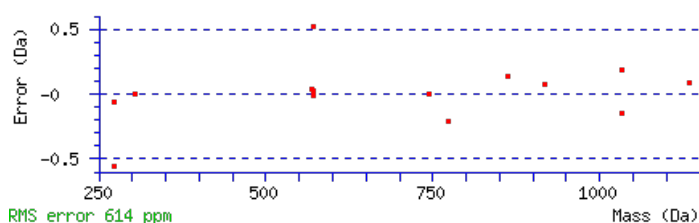
Variable modifications:

N4 : Deamidated (NQ)

Ions Score: 35 Expect: 0.012

Matches : 14/144 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	201.1234	101.0653			183.1128	92.0600	L	1247.5862	624.2968	1230.5597	615.7835	1229.5757	615.2915	13
3	302.1710	151.5892			284.1605	142.5839	T	1134.5022	567.7547	1117.4756	559.2415	1116.4916	558.7494	12
4	417.1980	209.1026	400.1714	200.5894	399.1874	200.0974	N	1033.4545	517.2309	1016.4279	508.7176	1015.4439	508.2256	11
5	474.2195	237.6134	457.1929	229.1001	456.2089	228.6081	G	918.4276	459.7174	901.4010	451.2041	900.4170	450.7121	10
6	561.2515	281.1294	544.2249	272.6161	543.2409	272.1241	S	861.4061	431.2067	844.3795	422.6934	843.3955	422.2014	9
7	662.2992	331.6532	645.2726	323.1399	644.2886	322.6479	T	774.3741	387.6907	757.3475	379.1774	756.3635	378.6854	8
8	763.3468	382.1771	746.3203	373.6638	745.3363	373.1718	T	673.3264	337.1668	656.2998	328.6536	655.3158	328.1615	7
9	860.3996	430.7034	843.3731	422.1902	842.3890	421.6982	P	572.2787	286.6430	555.2522	278.1297	554.2681	277.6377	6
10	917.4211	459.2142	900.3945	450.7009	899.4105	450.2089	G	475.2259	238.1166	458.1994	229.6033	457.2154	229.1113	5
11	1032.4480	516.7276	1015.4215	508.2144	1014.4374	507.7224	D	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	4
12	1103.4851	552.2462	1086.4586	543.7329	1085.4746	543.2409	A	303.1775	152.0924	286.1510	143.5791			3
13	1160.5066	580.7569	1143.4800	572.2437	1142.4960	571.7517	G	232.1404	116.5738	215.1139	108.0606			2
14							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [SLTNGSTTPGDAGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.2	1333.6110	-0.0014	SLTNGSTTPGDAGR
7.1	1333.6110	-0.0014	AEKSGDASDLQGR
5.9	1333.6183	-0.0088	ADQIETQQLMR
4.5	1331.5953	2.0143	SQEAQDLQQQR
4.2	1331.5953	2.0143	SQEAQDLQQQR
2.1	1331.5928	2.0168	TQRYFMEANR
2.1	1333.6183	-0.0088	ADQIETQQLMR
2.0	1333.6110	-0.0014	NPSSTLGSKNGDR
1.6	1333.6157	-0.0061	AENGRQSRVCR
1.0	1333.6044	0.0052	IREMEGEGQNR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

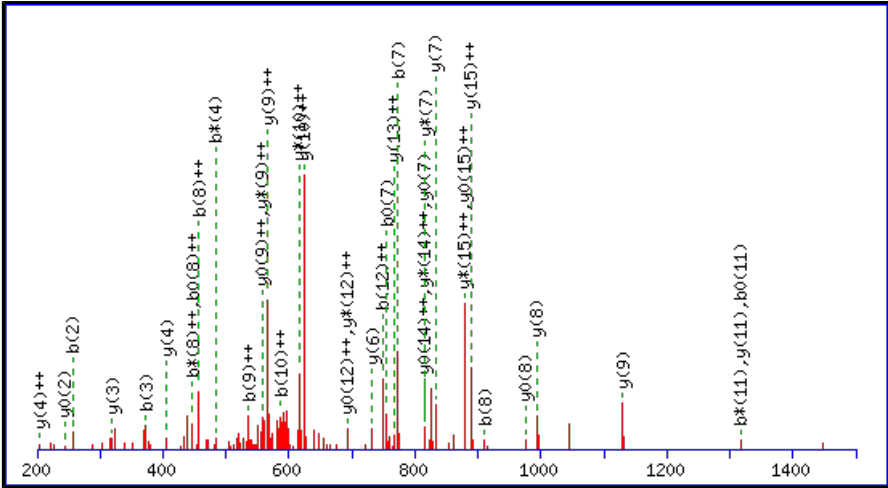
Peptide View

MS/MS Fragmentation of **KKNQSANHCTYYSGDK**
Found in **F1S0J2** in **uni_pig**, tr[F1S0J2]F1S0J2_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPA PE=4 SV=2

Match to Query 7844: 1901.818392 from(634.946740,3+) intensity(1239.5211) rtinseconds(265) scans(311) index(10163)
Title: 120326_Sunil_PigSerum_Glyco_PsetB_12Spectrum166_scans__311
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

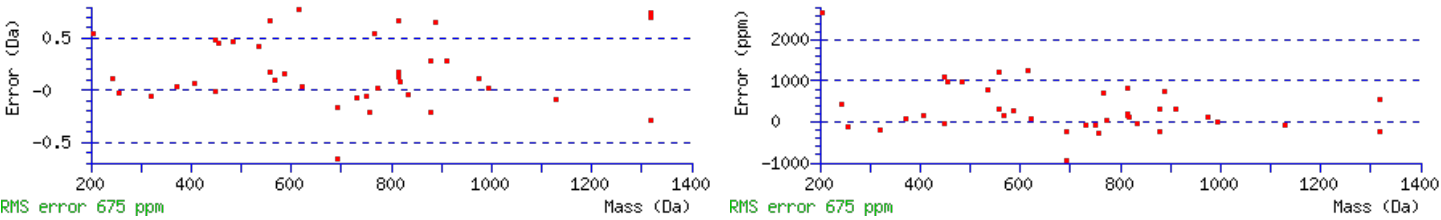
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1901.8213
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
N7 : Deamidated (NQ)
Ions Score: 32 Expect: 0.014
Matches : 40/170 fragment ions using 60 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							16
2	257.1972	129.1022	240.1707	120.5890			K	1774.7337	887.8705	1757.7072	879.3572	1756.7231	878.8652	15
3	372.2241	186.6157	355.1976	178.1024			N	1646.6387	823.8230	1629.6122	815.3097	1628.6282	814.8177	14
4	500.2827	250.6450	483.2562	242.1317			Q	1531.6118	766.3095	1514.5853	757.7963	1513.6012	757.3043	13
5	587.3148	294.1610	570.2882	285.6477	569.3042	285.1557	S	1403.5532	702.2802	1386.5267	693.7670	1385.5427	693.2750	12
6	658.3519	329.6796	641.3253	321.1663	640.3413	320.6743	A	1316.5212	658.7642	1299.4946	650.2510	1298.5106	649.7590	11
7	773.3788	387.1930	756.3523	378.6798	755.3682	378.1878	N	1245.4841	623.2457	1228.4575	614.7324	1227.4735	614.2404	10
8	910.4377	455.7225	893.4112	447.2092	892.4272	446.7172	H	1130.4571	565.7322	1113.4306	557.2189	1112.4466	556.7269	9
9	1070.4684	535.7378	1053.4418	527.2245	1052.4578	526.7325	C	993.3982	497.2028	976.3717	488.6895	975.3877	488.1975	8
10	1171.5160	586.2617	1154.4895	577.7484	1153.5055	577.2564	T	833.3676	417.1874	816.3410	408.6742	815.3570	408.1821	7
11	1334.5794	667.7933	1317.5528	659.2801	1316.5688	658.7880	Y	732.3199	366.6636	715.2933	358.1503	714.3093	357.6583	6
12	1497.6427	749.3250	1480.6162	740.8117	1479.6321	740.3197	Y	569.2566	285.1319	552.2300	276.6186	551.2460	276.1266	5
13	1584.6747	792.8410	1567.6482	784.3277	1566.6642	783.8357	S	406.1932	203.6003	389.1667	195.0870	388.1827	194.5950	4
14	1641.6962	821.3517	1624.6696	812.8385	1623.6856	812.3465	G	319.1612	160.0842	302.1347	151.5710	301.1506	151.0790	3
15	1756.7231	878.8652	1739.6966	870.3519	1738.7126	869.8599	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [KKNQSANHCTYYSGDK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
32.3	1901.8213	-0.0030	KKNQSANHCTYYSGDK	Deamidated N3, N7 49.81%
31.4	1901.8213	-0.0030	KKNQSANHCTYYSGDK	Deamidated Q4, N7 40.68%
25.1	1901.8213	-0.0030	KKNQSANHCTYYSGDK	Deamidated N3, Q4 9.51%
12.2	1900.8075	1.0109	ENGSKSPAHSYSSYDSGK	
10.9	1901.8023	0.0161	MQEVVANLQYDDGSGMK	
4.5	1899.8235	1.9949	ENGSKSPAHSYSSYDSGK	
4.2	1899.8230	1.9954	DQEMVPQPPNPESGMK	
2.7	1901.8023	0.0161	MQEVVANLQYDDGSGMK	
2.2	1900.8183	1.0001	MQEVVANLQYDDGSGMK	
2.0	1901.8335	-0.0151	CMPQGDWSPAAPRCAAK	

Mascot: <http://www.matrixscience.com/>

Peptide View

MS/MS Fragmentation of **YKVDYESQSTDTQNFSSSKR**

Match to Query 13007: 2500.107096 from(626.034050,4+) intensity(3487.8245) rtinseconds(1280) scans(2891) index(1463)

Title: 120325 Sunil PigSerum Glyco D 14Spectrum2422 scans 2891

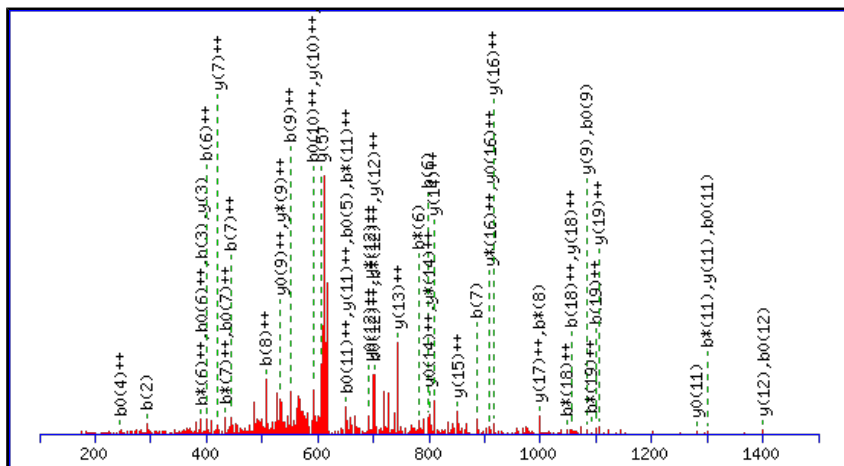
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2500.0877

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

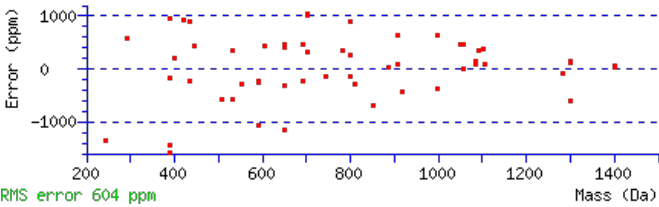
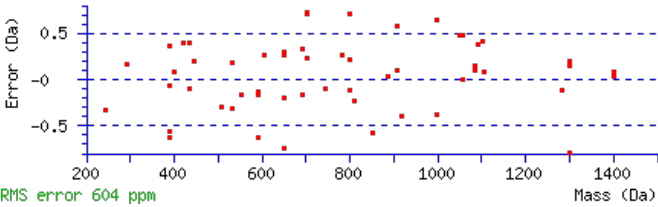
Q8 : Deamidated (NQ)

N14 : Deamidated (NQ)

Ions Score: 34 Expect: 0.014

Matches : 55/228 fragment ions using 97 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							21
2	292.1656	146.5864	275.1390	138.0731			K	2338.0317	1169.5195	2321.0052	1161.0062	2320.0212	1160.5142	20
3	391.2340	196.1206	374.2074	187.6074			V	2209.9368	1105.4720	2192.9102	1096.9587	2191.9262	1096.4667	19
4	506.2609	253.6341	489.2344	245.1208	488.2504	244.6288	D	2110.8683	1055.9378	2093.8418	1047.4245	2092.8578	1046.9325	18
5	669.3243	335.1658	652.2977	326.6525	651.3137	326.1605	Y	1995.8414	998.4243	1978.8149	989.9111	1977.8308	989.4191	17
6	798.3668	399.6871	781.3403	391.1738	780.3563	390.6818	E	1832.7781	916.8927	1815.7515	908.3794	1814.7675	907.8874	16
7	885.3989	443.2031	868.3723	434.6898	867.3883	434.1978	S	1703.7355	852.3714	1686.7089	843.8581	1685.7249	843.3661	15
8	1014.4415	507.7244	997.4149	499.2111	996.4309	498.7191	Q	1616.7035	808.8554	1599.6769	800.3421	1598.6929	799.8501	14
9	1101.4735	551.2404	1084.4469	542.7271	1083.4629	542.2351	S	1487.6609	744.3341	1470.6343	735.8208	1469.6503	735.3288	13
10	1202.5212	601.7642	1185.4946	593.2510	1184.5106	592.7589	T	1400.6288	700.8181	1383.6023	692.3048	1382.6183	691.8128	12
11	1317.5481	659.2777	1300.5216	650.7644	1299.5376	650.2724	D	1299.5811	650.2942	1282.5546	641.7809	1281.5706	641.2889	11
12	1418.5958	709.8015	1401.5692	701.2883	1400.5852	700.7963	T	1184.5542	592.7807	1167.5277	584.2675	1166.5436	583.7755	10
13	1546.6544	773.8308	1529.6278	765.3176	1528.6438	764.8255	Q	1083.5065	542.2569	1066.4800	533.7436	1065.4960	533.2516	9
14	1661.6813	831.3443	1644.6548	822.8310	1643.6708	822.3390	N	955.4479	478.2276	938.4214	469.7143	937.4374	469.2223	8
15	1808.7497	904.8785	1791.7232	896.3652	1790.7392	895.8732	F	840.4210	420.7141	823.3945	412.2009	822.4104	411.7089	7
16	1895.7818	948.3945	1878.7552	939.8812	1877.7712	939.3892	S	693.3526	347.1799	676.3260	338.6667	675.3420	338.1747	6
17	1982.8138	991.9105	1965.7872	983.3973	1964.8032	982.9053	S	606.3206	303.6639	589.2940	295.1506	588.3100	294.6586	5
18	2111.8564	1056.4318	2094.8298	1047.9186	2093.8458	1047.4265	E	519.2885	260.1479	502.2620	251.6346	501.2780	251.1426	4
19	2198.8884	1099.9478	2181.8619	1091.4346	2180.8778	1090.9426	S	390.2459	195.6266	373.2194	187.1133	372.2354	186.6213	3
20	2326.9834	1163.9953	2309.9568	1155.4821	2308.9728	1154.9900	K	303.2139	152.1106	286.1874	143.5973			2
21							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [YKVDYESQSTDTQNFSESSESKR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
34.4	2500.0877	0.0194	YKVDYESQSTDTQNFSESSESKR	Deamidated Q8, N14 41.34%
34.4	2500.0877	0.0194	YKVDYESQSTDTQNFSESSESKR	Deamidated Q8, Q13 41.34%
30.7	2499.1037	1.0034	YKVDYESQSTDTQNFSESSESKR	
30.7	2499.1037	1.0034	YKVDYESQSTDTQNFSESSESKR	
30.7	2500.0877	0.0194	YKVDYESQSTDTQNFSESSESKR	Deamidated Q13, N14 17.31%
21.7	2498.1197	1.9874	YKVDYESQSTDTQNFSESSESKR	
20.8	2499.1037	1.0034	YKVDYESQSTDTQNFSESSESKR	
6.8	2498.1199	1.9872	SNSTSSMSSGLPEQDRMAMTLPR	
4.5	2499.1039	1.0032	SNSTSSMSSGLPEQDRMAMTLPR	
4.0	2499.1039	1.0032	SNSTSSMSSGLPEQDRMAMTLPR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFLVHPNYTR**

Found in **I3LRJ4** in **uni_pig**, tr|I3LRJ4|I3LRJ4_PIG Vitamin K-dependent protein C OS=Sus scrofa GN=PROC PE=3 SV=1

Match to Query 2366: 1275.622568 from(638.818560,2+) intensity(8615.8906) rtinseconds(1605) scans(3367) index(12872)

Title: 120326_Sunil_PigSerum_Glyco_SsetB_13Spectrum2689_scans__3367

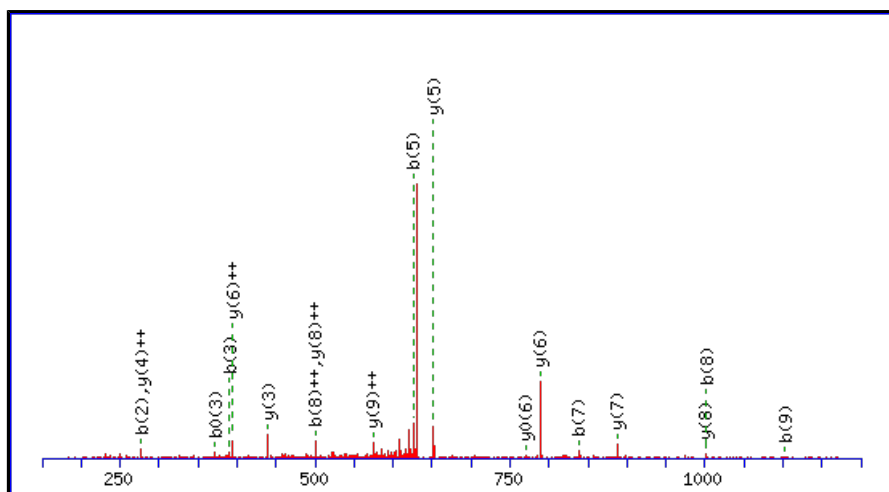
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1275.6248

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

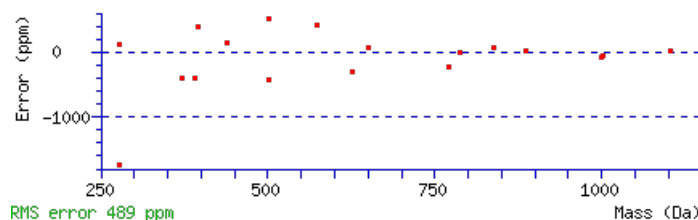
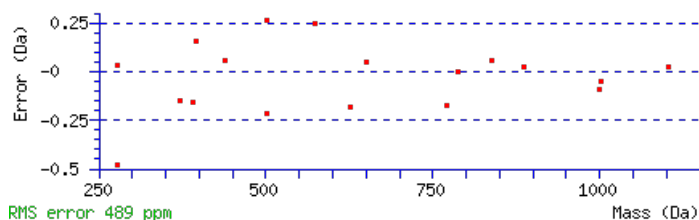
Variable modifications:

N7 : Deamidated (NQ)

Ions Score: 36 Expect: 0.016

Matches : 18/94 fragment ions using 30 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							10
2	277.1183	139.0628			259.1077	130.0575	F	1147.5895	574.2984	1130.5629	565.7851	1129.5789	565.2931	9
3	390.2023	195.6048			372.1918	186.5995	L	1000.5211	500.7642	983.4945	492.2509	982.5105	491.7589	8
4	489.2708	245.1390			471.2602	236.1337	V	887.4370	444.2221	870.4104	435.7089	869.4264	435.2169	7
5	626.3297	313.6685			608.3191	304.6632	H	788.3686	394.6879	771.3420	386.1747	770.3580	385.6826	6
6	723.3824	362.1949			705.3719	353.1896	P	651.3097	326.1585	634.2831	317.6452	633.2991	317.1532	5
7	838.4094	419.7083	821.3828	411.1951	820.3988	410.7030	N	554.2569	277.6321	537.2304	269.1188	536.2463	268.6268	4
8	1001.4727	501.2400	984.4462	492.7267	983.4621	492.2347	Y	439.2300	220.1186	422.2034	211.6053	421.2194	211.1133	3
9	1102.5204	551.7638	1085.4938	543.2506	1084.5098	542.7585	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
10							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [EFLVHPNYTR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.2	1275.6248	-0.0022	EFLVHPNYTR
28.3	1274.6142	1.0083	GDAKQQAWLQK
11.4	1274.6078	1.0148	DCLVGLWEAGR
11.4	1274.6176	1.0049	NCLVGENQVIK
11.4	1274.6176	1.0049	NCLVGENQVIK
11.2	1273.6262	1.9964	RINDENQKQK
11.2	1274.6102	1.0124	RINDENQKQK
11.2	1273.6262	1.9964	RINDENQKQK
11.2	1274.6102	1.0124	RINDENQKQK
10.5	1274.6223	1.0002	KNCPACRLQK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **VMVDLCNSTR**

Found in **F1RYN3** in **uni_pig**, tr|F1RYN3|F1RYN3_PIG Uncharacterized protein OS=Sus scrofa GN=GLDN PE=4 SV=1

Match to Query 1472: 1194.531988 from(598.273270,2+) intensity(8484.1875) rtinseconds(1781) scans(3206) index(8100)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_12Spectrum2218_scans_3206

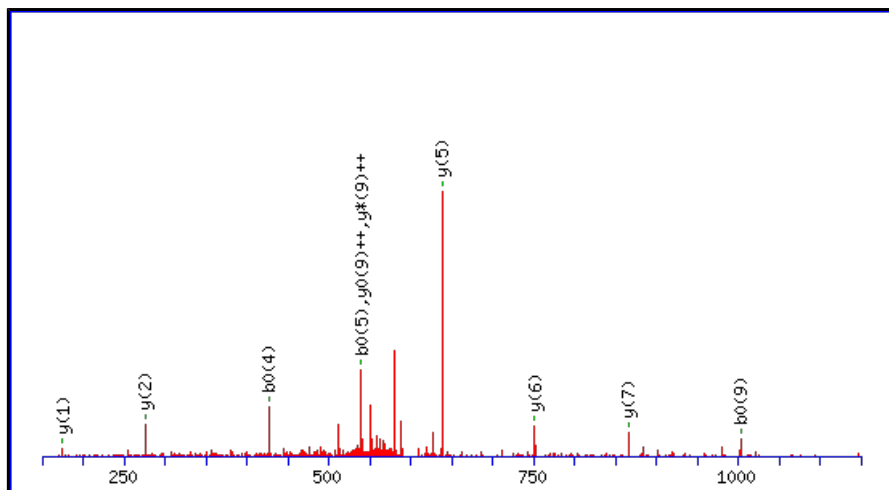
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1194.5373

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

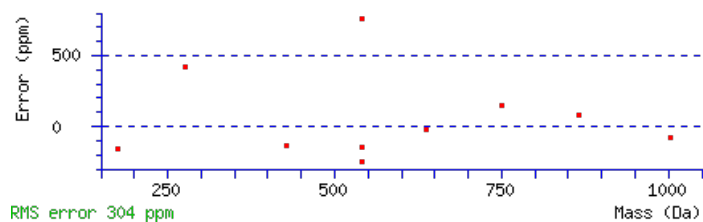
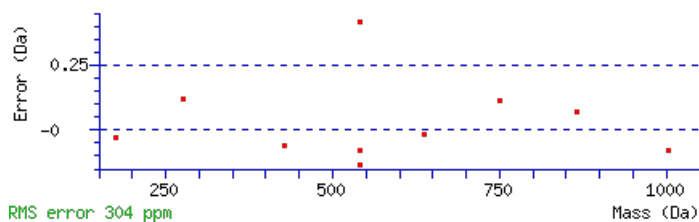
Variable modifications:

N7 : Deamidated (NQ)

Ions Score: 32 Expect: 0.017

Matches : 10/88 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							10
2	231.1162	116.0617					M	1096.4762	548.7417	1079.4496	540.2284	1078.4656	539.7364	9
3	330.1846	165.5959					V	965.4357	483.2215	948.4091	474.7082	947.4251	474.2162	8
4	445.2115	223.1094			427.2010	214.1041	D	866.3673	433.6873	849.3407	425.1740	848.3567	424.6820	7
5	558.2956	279.6514			540.2850	270.6462	L	751.3403	376.1738	734.3138	367.6605	733.3298	367.1685	6
6	718.3262	359.6668				700.3157	C	638.2563	319.6318	621.2297	311.1185	620.2457	310.6265	5
7	833.3532	417.1802	816.3266	408.6670	815.3426	408.1749	N	478.2256	239.6164	461.1991	231.1032	460.2150	230.6112	4
8	920.3852	460.6962	903.3587	452.1830	902.3747	451.6910	S	363.1987	182.1030	346.1721	173.5897	345.1881	173.0977	3
9	1021.4329	511.2201	1004.4063	502.7068	1003.4223	502.2148	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
10							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [VMVDLCNSTR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.4	1194.5373	-0.0053	VMVDLCNSTR
10.8	1193.5175	1.0144	FYVQGYCTR
4.5	1192.5248	2.0072	NPDNKEFAEK
4.4	1194.5373	-0.0053	DEVTMKEMGR
2.1	1194.5352	-0.0033	QEWNFCRR
2.1	1194.5339	-0.0019	NTVQDPAYMR
1.6	1193.5313	1.0007	ADGPFRDSDSK
0.3	1192.5360	1.9960	HANSVDTSESK
0.3	1192.5335	1.9984	FYVQGYCTR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

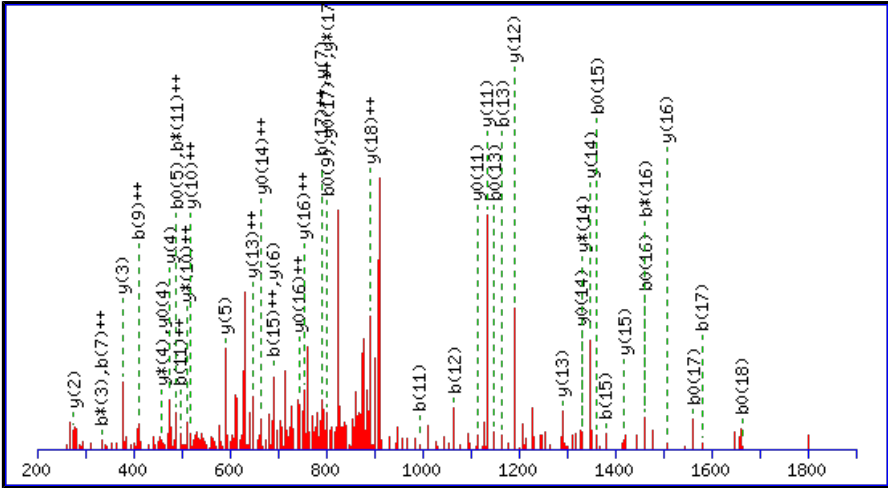
Peptide View

MS/MS Fragmentation of **AYNSAGTGPSSATVNVTTTR**
Found in **F1SFM0** in **uni_pig**, tr|F1SFM0|F1SFM0_PIG Uncharacterized protein (Fragment) OS=Sus scrofa GN=CNTN4 PE=4 SV=2

Match to Query 6942: 1854.852488 from(928.433520,2+) intensity(2677.9006) rtinseconds(1263) scans(2797) index(13159)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_14Spectrum2270_scans_2797
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

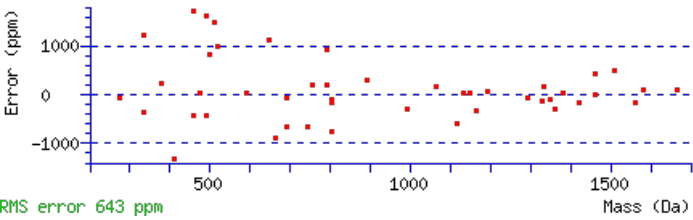
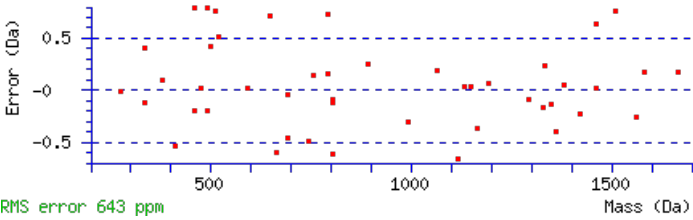
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1854.8595
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
N15 : Deamidated (NQ)
Ions Score: 35 Expect: 0.018
Matches : 46/204 fragment ions using 121 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							19
2	235.1077	118.0575					Y	1784.8297	892.9185	1767.8032	884.4052	1766.8192	883.9132	18
3	350.1347	175.5710	333.1081	167.0577			N	1621.7664	811.3868	1604.7398	802.8736	1603.7558	802.3815	17
4	437.1667	219.0870	420.1401	210.5737	419.1561	210.0817	S	1506.7394	753.8734	1489.7129	745.3601	1488.7289	744.8681	16
5	508.2038	254.6055	491.1773	246.0923	490.1932	245.6003	A	1419.7074	710.3573	1402.6809	701.8441	1401.6969	701.3521	15
6	565.2253	283.1163	548.1987	274.6030	547.2147	274.1110	G	1348.6703	674.8388	1331.6438	666.3255	1330.6597	665.8335	14
7	666.2729	333.6401	649.2464	325.1268	648.2624	324.6348	T	1291.6488	646.3281	1274.6223	637.8148	1273.6383	637.3228	13
8	723.2944	362.1508	706.2679	353.6376	705.2838	353.1456	G	1190.6012	595.8042	1173.5746	587.2909	1172.5906	586.7989	12
9	820.3472	410.6772	803.3206	402.1640	802.3366	401.6719	P	1133.5797	567.2935	1116.5531	558.7802	1115.5691	558.2882	11
10	907.3792	454.1932	890.3527	445.6800	889.3686	445.1880	S	1036.5269	518.7671	1019.5004	510.2538	1018.5164	509.7618	10
11	994.4112	497.7093	977.3847	489.1960	976.4007	488.7040	S	949.4949	475.2511	932.4684	466.7378	931.4843	466.2458	9
12	1065.4483	533.2278	1048.4218	524.7145	1047.4378	524.2225	A	862.4629	431.7351	845.4363	423.2218	844.4523	422.7298	8
13	1166.4960	583.7517	1149.4695	575.2384	1148.4855	574.7464	T	791.4258	396.2165	774.3992	387.7032	773.4152	387.2112	7
14	1265.5644	633.2859	1248.5379	624.7726	1247.5539	624.2806	V	690.3781	345.6927	673.3515	337.1794	672.3675	336.6874	6
15	1380.5914	690.7993	1363.5648	682.2861	1362.5808	681.7940	N	591.3097	296.1585	574.2831	287.6452	573.2991	287.1532	5
16	1479.6598	740.3335	1462.6332	731.8203	1461.6492	731.3283	V	476.2827	238.6450	459.2562	230.1317	458.2722	229.6397	4
17	1580.7075	790.8574	1563.6809	782.3441	1562.6969	781.8521	T	377.2143	189.1108	360.1878	180.5975	359.2037	180.1055	3
18	1681.7552	841.3812	1664.7286	832.8679	1663.7446	832.3759	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
19							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [AYNSAGTGPSSATVNVTTTR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

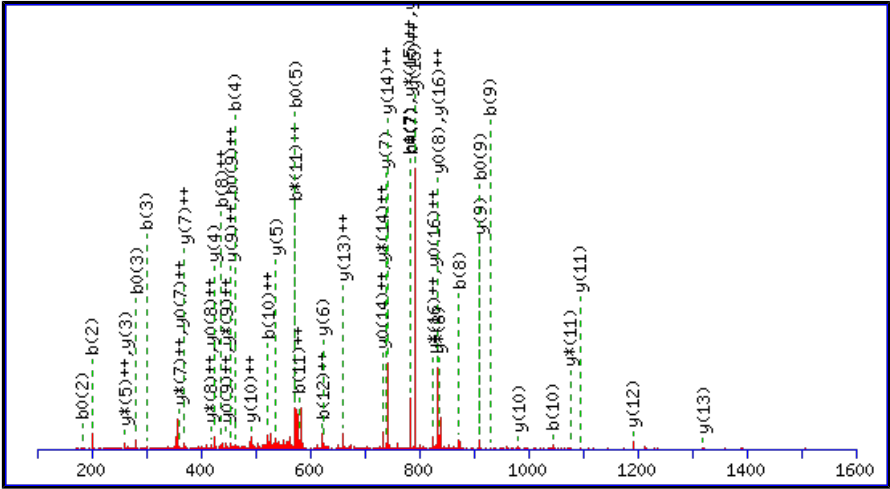
Score	Mr(calc)	Delta	Sequence
34.8	1854.8595	-0.0071	AYNSAGTGPSSATVNVTTTR

Mascot: <http://www.matrixscience.com/>

Peptide View

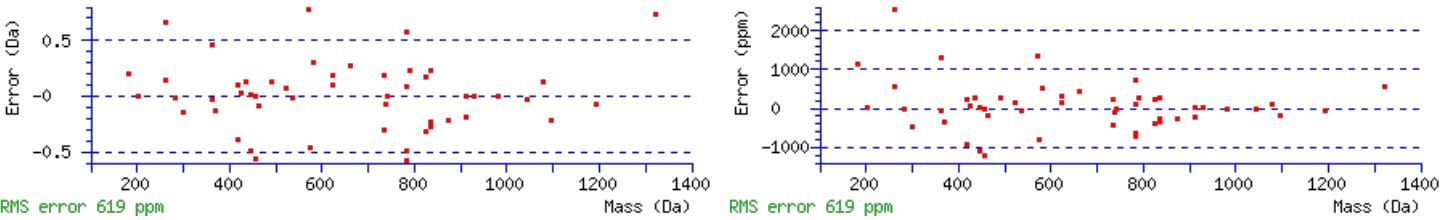
Match to Query 6567: 1780.932702 from(594.651510,3+) intensity(16616.0918) rtinseconds(1866) scans(4086) index(6001)
Title: 120325_Sunil_PigSerum_Glyco_S_12Spectrum3272_scans_4086
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, to Da
 Label all possible matches Label matches used for scoring
 Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1780.9359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
 N10 : Deamidated (NQ)
Ions Score: 35 **Expect:** 0.018
Matches : 51/172 fragment ions using 112 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							17
2	201.1234	101.0653			183.1128	92.0600	S	1668.8592	834.9332	1651.8326	826.4199	1650.8486	825.9279	16
3	300.1918	150.5995			282.1812	141.5942	V	1581.8271	791.4172	1564.8006	782.9039	1563.8166	782.4119	15
4	463.2551	232.1312			445.2445	223.1259	Y	1482.7587	741.8830	1465.7322	733.3697	1464.7482	732.8777	14
5	591.3501	296.1787	574.3235	287.6654	573.3395	287.1734	K	1319.6954	660.3513	1302.6688	651.8381	1301.6848	651.3461	13
6	688.4028	344.7051	671.3763	336.1918	670.3923	335.6998	P	1191.6004	596.3039	1174.5739	587.7906	1173.5899	587.2986	12
7	801.4869	401.2471	784.4604	392.7338	783.4763	392.2418	L	1094.5477	547.7775	1077.5211	539.2642	1076.5371	538.7722	11
8	872.5240	436.7656	855.4975	428.2524	854.5135	427.7604	A	981.4636	491.2354	964.4371	482.7222	963.4530	482.2302	10
9	929.5455	465.2764	912.5189	456.7631	911.5349	456.2711	G	910.4265	455.7169	893.3999	447.2036	892.4159	446.7116	9
10	1044.5724	522.7898	1027.5459	514.2766	1026.5619	513.7846	N	853.4050	427.2061	836.3785	418.6929	835.3945	418.2009	8
11	1158.6154	579.8113	1141.5888	571.2980	1140.6048	570.8060	N	738.3781	369.6927	721.3515	361.1794	720.3675	360.6874	7
12	1245.6474	623.3273	1228.6208	614.8141	1227.6368	614.3220	S	624.3352	312.6712	607.3086	304.1579	606.3246	303.6659	6
13	1358.7314	679.8694	1341.7049	671.3561	1340.7209	670.8641	L	537.3031	269.1552	520.2766	260.6419			5
14	1521.7948	761.4010	1504.7682	752.8877	1503.7842	752.3957	Y	424.2191	212.6132	407.1925	204.0999			4
15	1578.8162	789.9118	1561.7897	781.3985	1560.8057	780.9065	G	261.1557	131.0815	244.1292	122.5682			3
16	1635.8377	818.4225	1618.8112	809.9092	1617.8271	809.4172	G	204.1343	102.5708	187.1077	94.0575			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [LSVYKPLAGNNSLYGGK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
35.5	1780.9359	-0.0032	LSVYKPLAGNNSLYGGK	Deamidated N10 53.68%
34.8	1780.9359	-0.0032	LSVYKPLAGNNSLYGGK	Deamidated N11 46.32%
7.1	1780.9406	-0.0079	SLVRNPHLCCLGPYVR	
1.9	1779.9189	1.0138	SLVANLAAANCYKKEK	
1.7	1778.9414	1.9913	TPQPLNQSDSPIVLLR	
1.5	1778.9414	1.9913	TPQPLNQSDSPIVLLR	
1.5	1778.9414	1.9913	TPQPLNQSDSPIVLLR	
1.5	1779.9254	1.0073	TPQPLNQSDSPIVLLR	
0.7	1778.9097	2.0230	MVAPPAEPARQQPSKR	
0.7	1778.9097	2.0230	MVAPPAEPARQQPSKR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSNLTGISDQR**

Found in **F1RKY2** in **uni_pig**, tr|F1RKY2|F1RKY2_PIG Uncharacterized protein OS=Sus scrofa GN=SERPIND1 PE=3 SV=1

Match to Query 1653: 1206.530788 from(604.272670,2+) intensity(2897.9646) rtinseconds(1314) scans(2332) index(13529)

Title: 120326_Sunil_PigSerum_Glyco_SsetB_16Spectrum1474_scans_2332

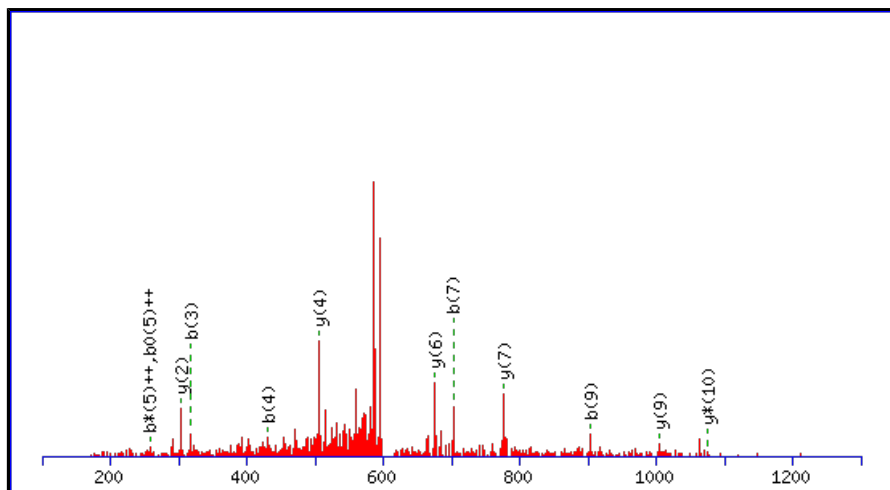
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1206.5364

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

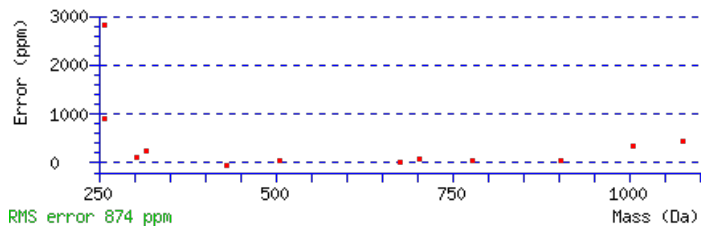
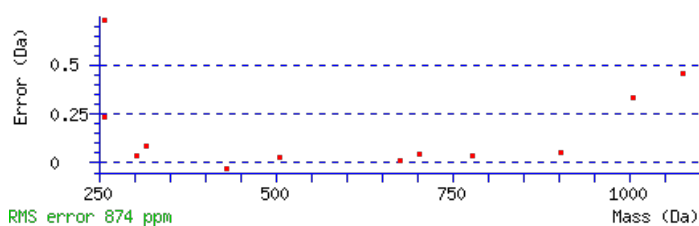
N1 : Deamidated (NQ)

N3 : Deamidated (NQ)

Q10 : Deamidated (NQ)

Ions Score: 31 **Expect:** 0.019
Matches : 12/114 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							11
2	203.0662	102.0368	186.0397	93.5235	185.0557	93.0315	S	1092.5168	546.7620	1075.4902	538.2487	1074.5062	537.7567	10
3	318.0932	159.5502	301.0666	151.0370	300.0826	150.5450	N	1005.4847	503.2460	988.4582	494.7327	987.4742	494.2407	9
4	431.1773	216.0923	414.1507	207.5790	413.1667	207.0870	L	890.4578	445.7325	873.4312	437.2193	872.4472	436.7272	8
5	532.2249	266.6161	515.1984	258.1028	514.2144	257.6108	T	777.3737	389.1905	760.3472	380.6772	759.3632	380.1852	7
6	589.2464	295.1268	572.2198	286.6136	571.2358	286.1216	G	676.3260	338.6667	659.2995	330.1534	658.3155	329.6614	6
7	702.3305	351.6689	685.3039	343.1556	684.3199	342.6636	I	619.3046	310.1559	602.2780	301.6427	601.2940	301.1506	5
8	789.3625	395.1849	772.3359	386.6716	771.3519	386.1796	S	506.2205	253.6139	489.1940	245.1006	488.2100	244.6086	4
9	904.3894	452.6984	887.3629	444.1851	886.3789	443.6931	D	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
10	1033.4320	517.2197	1016.4055	508.7064	1015.4215	508.2144	Q	304.1615	152.5844	287.1350	144.0711			2
11							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [NSNLTGISDOR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.8	1206.5364	-0.0056	NSNLTGISDQR
8.0	1206.5364	-0.0056	SNNITDSLNR
6.6	1206.5377	-0.0069	NTRGSWSNER
6.3	1206.5299	0.0009	MGDGVQQTSER
2.3	1206.5411	-0.0103	NSQCSRGLER
1.9	1205.5346	0.9962	EKSPMESQDR
0.7	1205.5346	0.9962	LSLNEEGQCR
0.2	1206.5339	-0.0031	ADMPAAPSQR
0.1	1206.5265	0.0043	TWRQQDSER

Mascot: <http://www.matrixscience.com/>

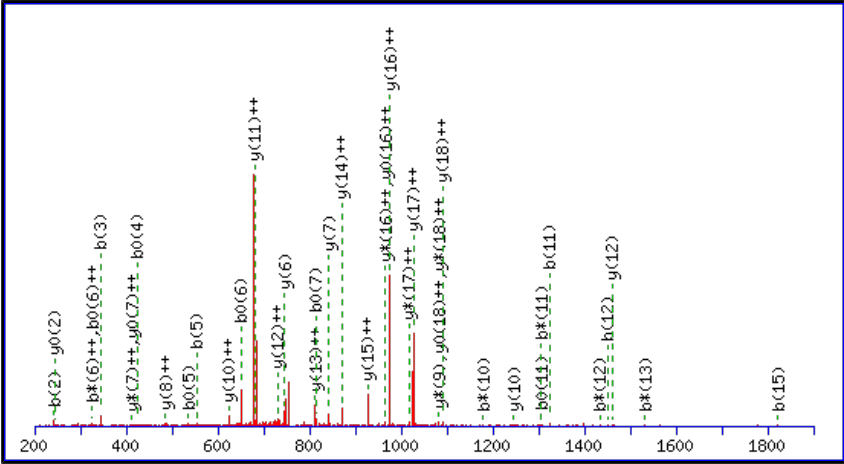
Peptide View

MS/MS Fragmentation of **LETPLNYTDFQKPICLPSR**
Found in **F1RZN7** in **uni_pig**, tr|F1RZN7|F1RZN7_PIG Uncharacterized protein OS=Sus scrofa GN=KLKB1 PE=3 SV=2

Match to Query 12681: 2292.145422 from(765.055750,3+) intensity(6553.1309) rtinseconds(2589) scans(5513) index(11462)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_01Spectrum4466_scans_5513
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

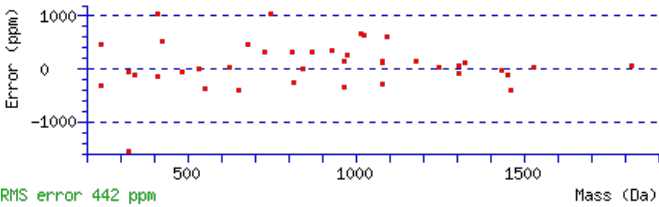
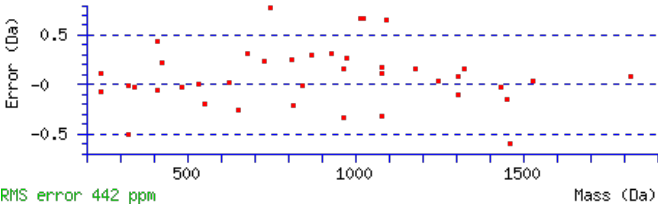
Click mouse within plot area to zoom in by factor of two about that point

Or,	to	Da
Label all possible matches		Label matches used for scoring
Show Y-axis		



Monoisotopic mass of neutral peptide Mr(calc): 2292.1460
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 N6 : Deamidated (NQ)
 Ions Score: 36 Expect: 0.02
 Matches : 41/202 fragment ions using 81 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							19
2	243.1339	122.0706			225.1234	113.0653	E	2180.0692	1090.5383	2163.0427	1082.0250	2162.0587	1081.5330	18
3	344.1816	172.5944			326.1710	163.5892	T	2051.0266	1026.0170	2034.0001	1017.5037	2033.0161	1017.0117	17
4	441.2344	221.1208			423.2238	212.1155	P	1949.9790	975.4931	1932.9524	966.9798	1931.9684	966.4878	16
5	554.3184	277.6629			536.3079	268.6576	L	1852.9262	926.9667	1835.8996	918.4535	1834.9156	917.9615	15
6	669.3454	335.1763	652.3188	326.6631	651.3348	326.1710	N	1739.8421	870.4247	1722.8156	861.9114	1721.8316	861.4194	14
7	832.4087	416.7080	815.3822	408.1947	814.3981	407.7027	Y	1624.8152	812.9112	1607.7886	804.3980	1606.8046	803.9060	13
8	933.4564	467.2318	916.4298	458.7186	915.4458	458.2266	T	1461.7519	731.3796	1444.7253	722.8663	1443.7413	722.3743	12
9	1048.4833	524.7453	1031.4568	516.2320	1030.4728	515.7400	D	1360.7042	680.8557	1343.6776	672.3425	1342.6936	671.8504	11
10	1195.5517	598.2795	1178.5252	589.7662	1177.5412	589.2742	F	1245.6772	623.3423	1228.6507	614.8290	1227.6667	614.3370	10
11	1323.6103	662.3088	1306.5838	653.7955	1305.5998	653.3035	Q	1098.6088	549.8081	1081.5823	541.2948	1080.5983	540.8028	9
12	1451.7053	726.3563	1434.6787	717.8430	1433.6947	717.3510	K	970.5502	485.7788	953.5237	477.2655	952.5397	476.7735	8
13	1548.7581	774.8827	1531.7315	766.3694	1530.7475	765.8774	P	842.4553	421.7313	825.4287	413.2180	824.4447	412.7260	7
14	1661.8421	831.4247	1644.8156	822.9114	1643.8316	822.4194	I	745.4025	373.2049	728.3760	364.6916	727.3920	364.1996	6
15	1821.8728	911.4400	1804.8462	902.9267	1803.8622	902.4347	C	632.3185	316.6629	615.2919	308.1496	614.3079	307.6576	5
16	1934.9568	967.9821	1917.9303	959.4688	1916.9463	958.9768	L	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
17	2032.0096	1016.5084	2014.9830	1007.9952	2013.9990	1007.5032	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
18	2119.0416	1060.0244	2102.0151	1051.5112	2101.0311	1051.0192	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
19							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LETPLNYTDFQKPICLPSR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
36.5	2292.1460	-0.0006	LETPLNYTDFQKPICLPSR	Deamidated N6 87.99%
27.8	2292.1460	-0.0006	LETPLNYTDFQKPICLPSR	Deamidated Q11 12.01%
12.8	2291.1620	0.9834	LETPLNYTDFQKPICLPSR	
8.0	2291.1315	1.0140	LEPQTVEERSSVTMAVELTR	
7.8	2290.1475	1.9980	LEPQTVEERSSVTMAVELTR	
6.7	2290.1337	2.0117	SLFGEIGHTIMNLLVDLMNR	
4.3	2290.1191	2.0264	IYNKCYLDINALQELYQK	
4.3	2290.1191	2.0264	IYNKCYLDINALQELYQK	
3.6	2291.1613	0.9841	LEVNERILNSCTDLMKAIR	
3.3	2292.1274	0.0181	LNGLEDSPVKEYQQNIDSPK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

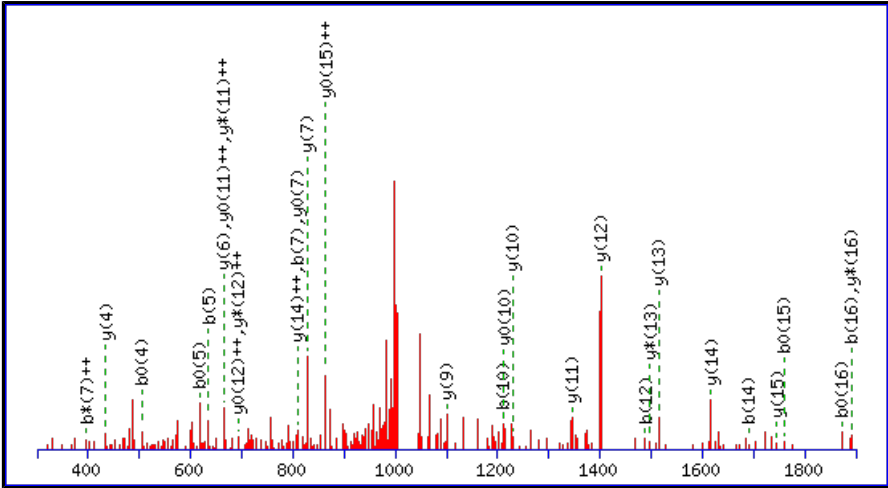
Peptide View

MS/MS Fragmentation of **EYQTIGNQCIYNDSSLK**
Found in **F1SN68** in **uni_pig**, tr|F1SN68|F1SN68_PIG Alpha-1-acid glycoprotein OS=Sus scrofa GN=ORM1 PE=3 SV=1

Match to Query 11801: 2035.852508 from(1018.933530,2+) intensity(979.4328) rtinseconds(2077) scans(3663) index(2272)
Title: 120325_Sunil_PigSerum_Glyco_D_17Spectrum2555_scans__3663
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

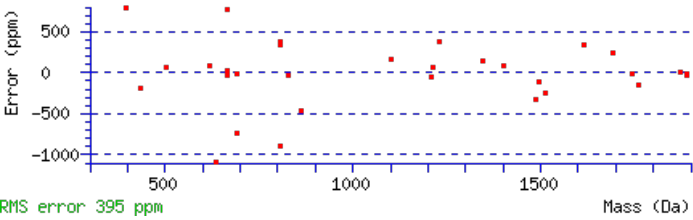
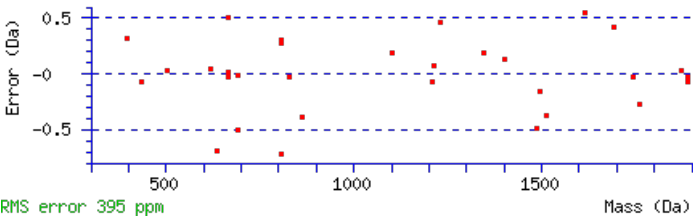
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2035.8568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N7 : Deamidated (NQ)
Q8 : Deamidated (NQ)
N12 : Deamidated (NQ)
Ions Score: 28 Expect: 0.021
Matches : 31/184 fragment ions using 92 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	293.1132	147.0602			275.1026	138.0550	Y	1907.8215	954.4144	1890.7950	945.9011	1889.8110	945.4091	16
3	422.1558	211.5815	405.1292	203.0683	404.1452	202.5763	Q	1744.7582	872.8827	1727.7316	864.3695	1726.7476	863.8775	15
4	523.2035	262.1054	506.1769	253.5921	505.1929	253.1001	T	1615.7156	808.3614	1598.6890	799.8482	1597.7050	799.3562	14
5	636.2875	318.6474	619.2610	310.1341	618.2770	309.6421	I	1514.6679	757.8376	1497.6414	749.3243	1496.6574	748.8323	13
6	693.3090	347.1581	676.2825	338.6449	675.2984	338.1529	G	1401.5839	701.2956	1384.5573	692.7823	1383.5733	692.2903	12
7	808.3359	404.6716	791.3094	396.1583	790.3254	395.6663	N	1344.5624	672.7848	1327.5358	664.2716	1326.5518	663.7796	11
8	937.3785	469.1929	920.3520	460.6796	919.3680	460.1876	Q	1229.5354	615.2714	1212.5089	606.7581	1211.5249	606.2661	10
9	1097.4092	549.2082	1080.3826	540.6950	1079.3986	540.2029	C	1100.4929	550.7501	1083.4663	542.2368	1082.4823	541.7448	9
10	1210.4932	605.7503	1193.4667	597.2370	1192.4827	596.7450	I	940.4622	470.7347	923.4357	462.2215	922.4516	461.7295	8
11	1373.5566	687.2819	1356.5300	678.7687	1355.5460	678.2766	Y	827.3781	414.1927	810.3516	405.6794	809.3676	405.1874	7
12	1488.5835	744.7954	1471.5570	736.2821	1470.5730	735.7901	N	664.3148	332.6610	647.2883	324.1478	646.3042	323.6558	6
13	1603.6105	802.3089	1586.5839	793.7956	1585.5999	793.3036	D	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
14	1690.6425	845.8249	1673.6159	837.3116	1672.6319	836.8196	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
15	1777.6745	889.3409	1760.6480	880.8276	1759.6640	880.3356	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
16	1890.7586	945.8829	1873.7320	937.3697	1872.7480	936.8776	L	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1

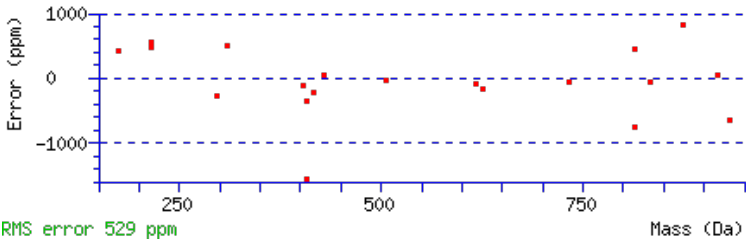


NCBI **BLAST** search of [EYQTIGNQCIYNDSSLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.2	2035.8568	-0.0043	EYQTIGNQCIYNDSSLK

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [LTVNLTNDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
35.1	1045.5404	-0.0021	LTVNLTNDR	Deamidated N4 97.02%
20.0	1045.5404	-0.0021	LTVNLTNDR	Deamidated N7 2.98%
11.7	1045.5339	0.0044	LECGGKGLGR	
10.1	1045.5404	-0.0021	LLIQGDSSGR	
8.8	1045.5404	-0.0021	ESLVAVESGR	
8.3	1045.5404	-0.0021	IQALDTGTAR	
7.1	1045.5451	-0.0068	IRMDSRPR	
7.1	1045.5451	-0.0068	LRMDSRPR	
6.8	1045.5451	-0.0068	VSARGACLGR	
6.6	1045.5404	-0.0021	LGELQTTAGR	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQCIVDDITYNVNDTFHK**
Found in **F1SS24** in **uni_pig**, tr|F1SS24|F1SS24_PIG Uncharacterized protein OS=Sus scrofa GN=FN1 PE=4 SV=1

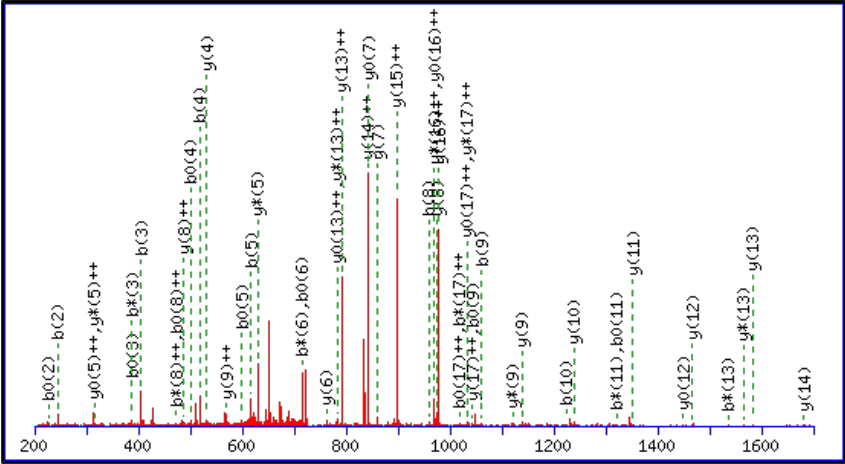
Match to Query 12346: 2197.941282 from(733.654370,3+) intensity(15515.0322) rtinseconds(2640) scans(6531) index(3935)
Title: 120325_Sunil_PigSerum_Glyco_P_14Spectrum5539_scans__6531
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

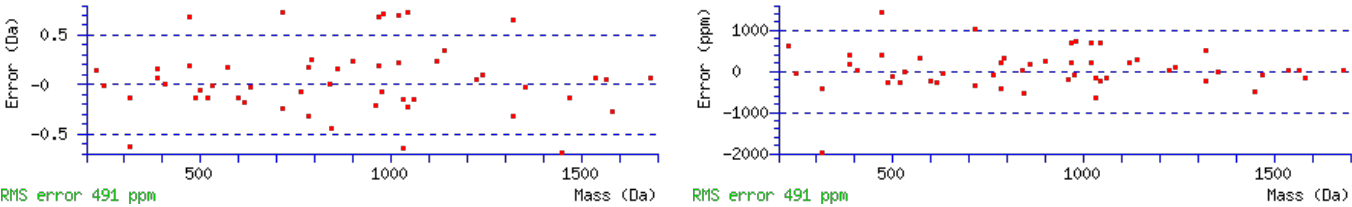
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2197.9474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Deamidated (NQ)
N13 : Deamidated (NQ)
Ions Score: 30 Expect: 0.023
Matches : 52/196 fragment ions using 128 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							18
2	245.0768	123.0420	228.0503	114.5288	227.0662	114.0368	Q	2083.9277	1042.4675	2066.9012	1033.9542	2065.9171	1033.4622	17
3	405.1075	203.0574	388.0809	194.5441	387.0969	194.0521	C	1954.8851	977.9462	1937.8586	969.4329	1936.8746	968.9409	16
4	518.1915	259.5994	501.1650	251.0861	500.1810	250.5941	I	1794.8545	897.9309	1777.8279	889.4176	1776.8439	888.9256	15
5	617.2599	309.1336	600.2334	300.6203	599.2494	300.1283	V	1681.7704	841.3888	1664.7439	832.8756	1663.7598	832.3836	14
6	732.2869	366.6471	715.2603	358.1338	714.2763	357.6418	D	1582.7020	791.8546	1565.6754	783.3414	1564.6914	782.8494	13
7	847.3138	424.1606	830.2873	415.6473	829.3033	415.1553	D	1467.6751	734.3412	1450.6485	725.8279	1449.6645	725.3359	12
8	960.3979	480.7026	943.3713	472.1893	942.3873	471.6973	I	1352.6481	676.8277	1335.6216	668.3144	1334.6375	667.8224	11
9	1061.4456	531.2264	1044.4190	522.7131	1043.4350	522.2211	T	1239.5640	620.2857	1222.5375	611.7724	1221.5535	611.2804	10
10	1224.5089	612.7581	1207.4823	604.2448	1206.4983	603.7528	Y	1138.5164	569.7618	1121.4898	561.2485	1120.5058	560.7565	9
11	1338.5518	669.7796	1321.5253	661.2663	1320.5413	660.7743	N	975.4530	488.2302	958.4265	479.7169	957.4425	479.2249	8
12	1437.6202	719.3138	1420.5937	710.8005	1419.6097	710.3085	V	861.4101	431.2087	844.3836	422.6954	843.3995	422.2034	7
13	1552.6472	776.8272	1535.6206	768.3140	1534.6366	767.8219	N	762.3417	381.6745	745.3151	373.1612	744.3311	372.6692	6
14	1667.6741	834.3407	1650.6476	825.8274	1649.6636	825.3354	D	647.3148	324.1610	630.2882	315.6477	629.3042	315.1557	5
15	1768.7218	884.8645	1751.6953	876.3513	1750.7112	875.8593	T	532.2878	266.6475	515.2613	258.1343	514.2772	257.6423	4
16	1915.7902	958.3987	1898.7637	949.8855	1897.7797	949.3935	F	431.2401	216.1237	414.2136	207.6104			3
17	2052.8491	1026.9282	2035.8226	1018.4149	2034.8386	1017.9229	H	284.1717	142.5895	267.1452	134.0762			2
18							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [DQCIVDDITYNVNDTFHK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
29.7	2197.9474	-0.0061	DQCIVDDITYNVNDTFHK	Deamidated Q2, N13 72.14%
23.4	2197.9474	-0.0061	DQCIVDDITYNVNDTFHK	Deamidated Q2, N11 16.91%
21.5	2197.9474	-0.0061	DQCIVDDITYNVNDTFHK	Deamidated N11, N13 10.94%
1.6	2197.9394	0.0018	ELQENQDEIENMMNAIFK	
1.6	2197.9394	0.0018	ELQENQDEIENMMNAIFK	
1.6	2197.9394	0.0018	ELQENQDEIENMMNAIFK	
1.6	2196.9554	0.9859	ELQENQDEIENMMNAIFK	
1.6	2196.9554	0.9859	ELQENQDEIENMMNAIFK	
1.6	2196.9554	0.9859	ELQENQDEIENMMNAIFK	
1.5	2197.9554	-0.0142	AGEFLDMKDQSCKPCAAGR	

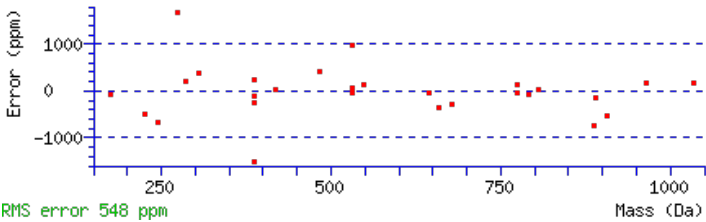
Mascot: <http://www.matrixscience.com/>

NCBI **BLAST** search of [EMQNLSQHGSIQR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.1	1529.6780	-0.0131	EMQNLSQHGSIQR
17.1	1529.6780	-0.0131	CDTNEVDIPPNTR
6.3	1529.6733	-0.0084	YDTTDTTNNIKDK
0.2	1527.6525	2.0125	QPHHYSEQMSQR
0.2	1529.6676	-0.0027	MASVNMDPALMER

Mascot: <http://www.matrixscience.com/>



NCBI **BLAST** search of [ENCCILDER](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.1	1208.4801	-0.0032	ENCCILDER
1.1	1208.4847	-0.0077	ANDHGYDNER
0.7	1207.4840	0.9929	NESAEASENQK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **KKNQSANHCTYYSGDK**
Found in **F1S0J2** in **uni_pig**, tr[F1S0J2]F1S0J2_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPA PE=4 SV=2

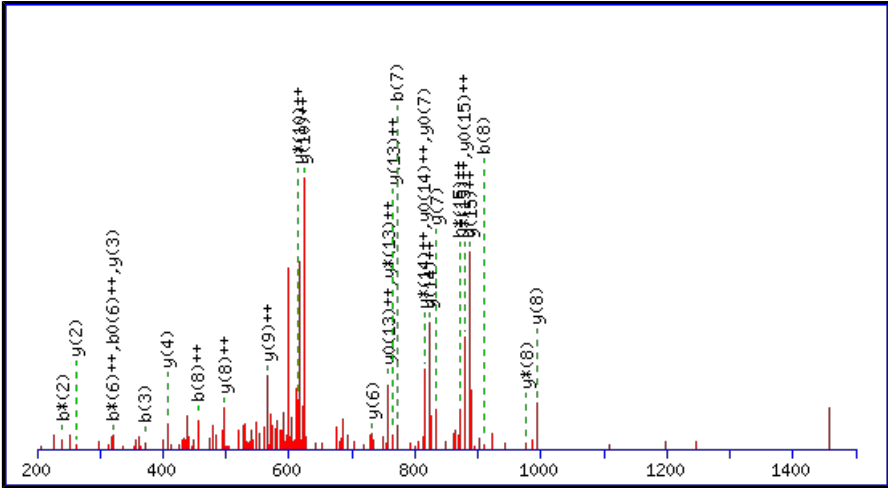
Match to Query 7835: 1900.832022 from(634.617950,3+) intensity(1934.5333) rtinseconds(140) scans(129) index(2922)
Title: 120325_Sunil_PigSerum_Glyco_P_08Spectrum48_scans__129
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

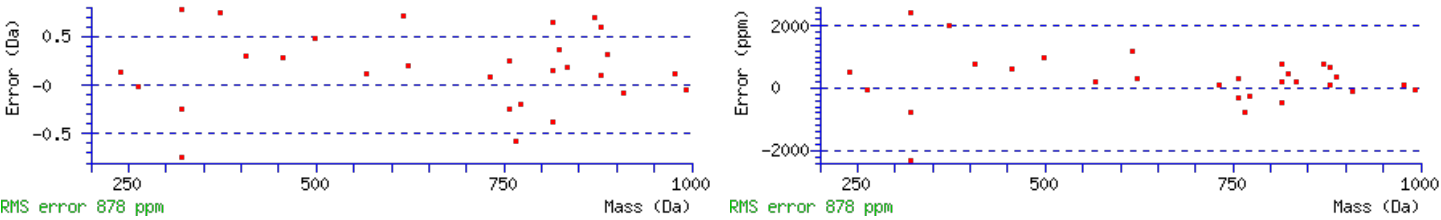
☐ Label all possible matches ☐ Label matches used for scoring

☐ Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1900.8373
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 31 Expect: 0.023
Matches : 30/170 fragment ions using 59 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							16
2	257.1972	129.1022	240.1707	120.5890			K	1773.7497	887.3785	1756.7231	878.8652	1755.7391	878.3732	15
3	371.2401	186.1237	354.2136	177.6104			N	1645.6547	823.3310	1628.6282	814.8177	1627.6442	814.3257	14
4	499.2987	250.1530	482.2722	241.6397			Q	1531.6118	766.3095	1514.5853	757.7963	1513.6012	757.3043	13
5	586.3307	293.6690	569.3042	285.1557	568.3202	284.6637	S	1403.5532	702.2802	1386.5267	693.7670	1385.5427	693.2750	12
6	657.3678	329.1876	640.3413	320.6743	639.3573	320.1823	A	1316.5212	658.7642	1299.4946	650.2510	1298.5106	649.7590	11
7	772.3948	386.7010	755.3682	378.1878	754.3842	377.6958	N	1245.4841	623.2457	1228.4575	614.7324	1227.4735	614.2404	10
8	909.4537	455.2305	892.4272	446.7172	891.4431	446.2252	H	1130.4571	565.7322	1113.4306	557.2189	1112.4466	556.7269	9
9	1069.4844	535.2458	1052.4578	526.7325	1051.4738	526.2405	C	993.3982	497.2028	976.3717	488.6895	975.3877	488.1975	8
10	1170.5320	585.7697	1153.5055	577.2564	1152.5215	576.7644	T	833.3676	417.1874	816.3410	408.6742	815.3570	408.1821	7
11	1333.5954	667.3013	1316.5688	658.7880	1315.5848	658.2960	Y	732.3199	366.6636	715.2933	358.1503	714.3093	357.6583	6
12	1496.6587	748.8330	1479.6321	740.3197	1478.6481	739.8277	Y	569.2566	285.1319	552.2300	276.6186	551.2460	276.1266	5
13	1583.6907	792.3490	1566.6642	783.8357	1565.6802	783.3437	S	406.1932	203.6003	389.1667	195.0870	388.1827	194.5950	4
14	1640.7122	820.8597	1623.6856	812.3465	1622.7016	811.8544	G	319.1612	160.0842	302.1347	151.5710	301.1506	151.0790	3
15	1755.7391	878.3732	1738.7126	869.8599	1737.7286	869.3679	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [KKNQSANHCTYYSGDK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
31.0	1900.8373	-0.0053	KKNQSANHCTYYSGDK	Deamidated N7 35.76%
31.0	1900.8373	-0.0053	KKNQSANHCTYYSGDK	Deamidated Q4 35.43%
30.1	1900.8373	-0.0053	KKNQSANHCTYYSGDK	Deamidated N3 28.80%
9.3	1900.8183	0.0138	MQEVVANLQYDDGSGMK	
9.2	1900.8183	0.0138	MQEVVANLQYDDGSGMK	
3.0	1900.8183	0.0138	MQEVVANLQYDDGSGMK	
2.9	1899.8343	0.9978	MQEVVANLQYDDGSGMK	
2.2	1900.8304	0.0016	FTCACPDGMLLAKDMR	
0.5	1899.8428	0.9892	MDRAVPDTRHDQCQR	
0.5	1900.8268	0.0052	MDRAVPDTRHDQCQR	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1RPW2** in **uni_pig**, tr|F1RPW2|F1RPW2_PIG Coagulation factor V OS=Sus scrofa GN=F5 PE=4 SV=2

Title: 120325_Sunil_PigSerum_Glyco_D_15Spectrum735_scans__1146

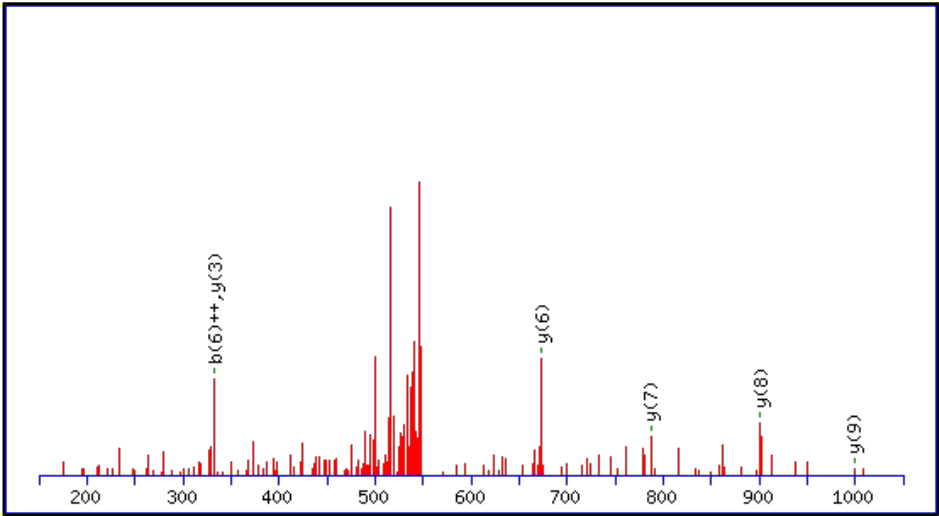
W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

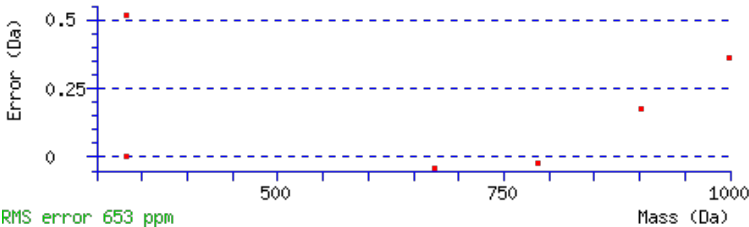
Label all possible matches Label matches used for scoring

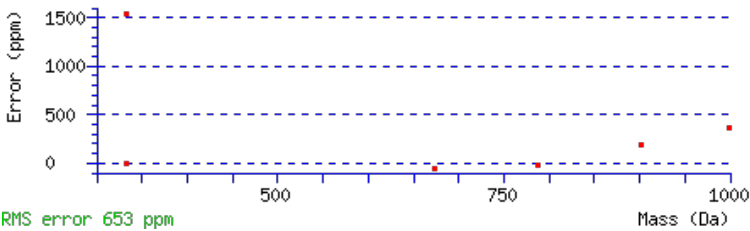
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1110.5417
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 N7 : Deamidated (NQ)
 Ions Score: 33 Expect: 0.025
 Matches : 6/86 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							10
2	211.1441	106.0757					P	998.4650	499.7361	981.4384	491.2229	980.4544	490.7309	9
3	325.1870	163.0972	308.1605	154.5839			N	901.4122	451.2098	884.3857	442.6965	883.4017	442.2045	8
4	439.2300	220.1186	422.2034	211.6053			N	787.3693	394.1883	770.3428	385.6750	769.3587	385.1830	7
5	536.2827	268.6450	519.2562	260.1317			P	673.3264	337.1668	656.2998	328.6536	655.3158	328.1615	6
6	664.3413	332.6743	647.3148	324.1610			Q	576.2736	288.6404	559.2471	280.1272	558.2630	279.6352	5
7	779.3682	390.1878	762.3417	381.6745			N	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4
8	850.4054	425.7063	833.3788	417.1930			A	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
9	937.4374	469.2223	920.4108	460.7091	919.4268	460.2170	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of [LPNNPQNASR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
32.6	1110.5417	-0.0012	LPNNPQNASR	Deamidated N7 47.51%
32.6	1110.5417	-0.0012	LPNNPQNASR	Deamidated Q6 47.51%
20.3	1110.5417	-0.0012	LPNNPQNASR	Deamidated N4 2.75%
19.4	1110.5417	-0.0012	LPNNPQNASR	Deamidated N3 2.24%
7.2	1110.5417	-0.0012	SQRYKDASR	
4.6	1108.5434	1.9971	DTKTTVDAMK	
4.5	1110.5458	-0.0052	YDYERLPR	
4.0	1110.5458	-0.0052	QAEVAAYFGR	
3.9	1110.5305	0.0100	SAGGYQTITGR	
2.6	1110.5418	-0.0012	AQPAESPGAQR	

Mascot: <http://www.matrixscience.com/>

MS/MS Fragmentation of **IIVPLNNRENISDPTSPLR**

Title: 120325 Sunil PigSerum Glyco P 13Spectrum4201 scans 4989

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

The plot displays the 14th order Legendre polynomial, $P_{14}(x)$, with its roots and extrema. The x-axis ranges from 200 to 1600. The roots are marked by red vertical lines, and the extrema are marked by green dashed vertical lines. The labels for the roots and extrema are as follows:

- Roots (red lines): $-b(2)$, $y0(4)$, $-y(5)$, $-b(6)$, $y0(6)$, $-y(6)$, $y(7)$, $y0(4)$, $-y(4)$, $-b0(10)$, $y(5)$, $-b(10)$, $y(6)$, $-b(13)$, $y0(13)$, $-y(13)$, $y(15)$, $-y(8)$, $-b0(16)$, $y(16)$, $-y0(17)$, $y(17)$, $-y(14)$, $y(18)$, $-y(10)$, $-b(10)$, $-b(11)$, $-b(12)$, $-y0(12)$, $y(12)$, $-b(13)$, $-y(13)$.
- Extrema (green dashed lines): $-b(5)$, $y(6)$, $-y(7)$, $y(4)$, $-b(10)$, $y(5)$, $-b(10)$, $y(6)$, $-b(13)$, $y0(13)$, $-y(13)$, $y(15)$, $-y(8)$, $-b0(16)$, $y(16)$, $-y0(17)$, $y(17)$, $-y(14)$, $y(18)$, $-y(10)$, $-b(10)$, $-b(11)$, $-b(12)$, $-y0(12)$, $y(12)$, $-b(13)$, $-y(13)$.

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

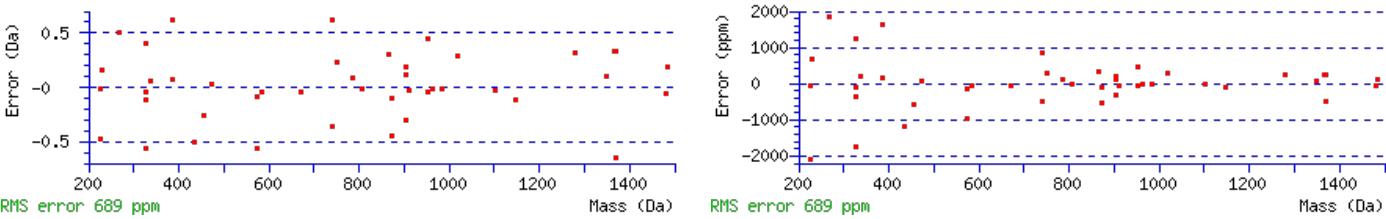
Variable modifications:

N10 : Deamidated (NQ)

Ions Score: 33 Expect: 0.025

Matches : 44/184 fragment ions using 107 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							19
2	227.1754	114.0913					I	2036.0771	1018.5422	2019.0505	1010.0289	2018.0665	1009.5369	18
3	326.2438	163.6255					V	1922.9930	962.0002	1905.9665	953.4869	1904.9825	952.9949	17
4	423.2966	212.1519					P	1823.9246	912.4659	1806.8981	903.9527	1805.9141	903.4607	16
5	536.3806	268.6940					L	1726.8719	863.9396	1709.8453	855.4263	1708.8613	854.9343	15
6	650.4236	325.7154	633.3970	317.2022			N	1613.7878	807.3975	1596.7612	798.8843	1595.7772	798.3922	14
7	764.4665	382.7369	747.4400	374.2236			N	1499.7449	750.3761	1482.7183	741.8628	1481.7343	741.3708	13
8	920.5676	460.7874	903.5411	452.2742			R	1385.7019	693.3546	1368.6754	684.8413	1367.6914	684.3493	12
9	1049.6102	525.3087	1032.5837	516.7955	1031.5996	516.3035	E	1229.6008	615.3040	1212.5743	606.7908	1211.5903	606.2988	11
10	1164.6371	582.8222	1147.6106	574.3089	1146.6266	573.8169	N	1100.5582	550.7828	1083.5317	542.2695	1082.5477	541.7775	10
11	1277.7212	639.3642	1260.6947	630.8510	1259.7106	630.3590	I	985.5313	493.2693	968.5047	484.7560	967.5207	484.2640	9
12	1364.7532	682.8803	1347.7267	674.3670	1346.7427	673.8750	S	872.4472	436.7272	855.4207	428.2140	854.4367	427.7220	8
13	1479.7802	740.3937	1462.7536	731.8805	1461.7696	731.3884	D	785.4152	393.2112	768.3886	384.6980	767.4046	384.2060	7
14	1576.8329	788.9201	1559.8064	780.4068	1558.8224	779.9148	P	670.3883	335.6978	653.3617	327.1845	652.3777	326.6925	6
15	1677.8806	839.4440	1660.8541	830.9307	1659.8701	830.4387	T	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
16	1764.9127	882.9600	1747.8861	874.4467	1746.9021	873.9547	S	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
17	1861.9654	931.4863	1844.9389	922.9731	1843.9549	922.4811	P	385.2558	193.1315	368.2292	184.6183			3
18	1975.0495	988.0284	1958.0229	979.5151	1957.0389	979.0231	L	288.2030	144.6051	271.1765	136.0919			2
19							R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [IIVPLNNRENISDPTSPLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
33.4	2148.1538	-0.0072	IIVPLNNRENISDPTSPLR	Deamidated N10 57.74%
29.0	2148.1538	-0.0072	IIVPLNNRENISDPTSPLR	Deamidated N6 21.16%
29.0	2148.1538	-0.0072	IIVPLNNRENISDPTSPLR	Deamidated N7 21.11%
3.3	2148.1547	-0.0081	MEVNPPKQEHLALVKMR	
1.5	2147.1521	0.9946	MHTAVKLNEVIVNKSHEAK	
1.3	2148.1341	0.0126	AAWLAKVGHPRALNTWDR	
1.1	2146.1238	2.0228	EIRNAVEMMIARLDTQLK	
1.0	2147.1474	0.9993	SIPFKPIQTTIAETRTEK	
0.8	2148.1651	-0.0185	LQEQVGQLVPQGRVAELQR	
0.5	2146.1238	2.0228	EIRNAVEMMIARLDTQLK	

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

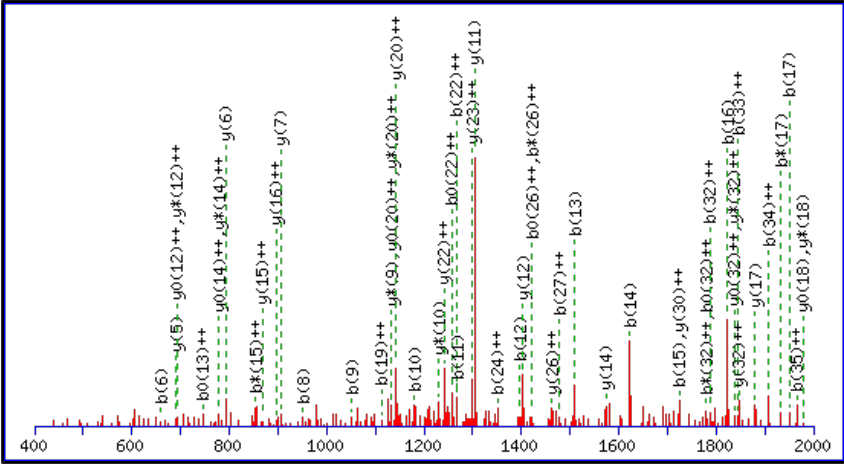
Peptide View

MS/MS Fragmentation of **LSVDQDKYTESEIITVQCDSGYGLVGPQNITCIEDR**
Found in **F1S0J2** in **uni_pig**, tr[F1S0J2|F1S0J2_PIG Uncharacterized protein OS=Sus scrofa GN=C4BPA PE=4 SV=2

Match to Query 13764: 4105.877892 from(1369.633240,3+) intensity(2625.4981) rtinseconds(2761) scans(5710) index(3512)
Title: 120325_Sunil_PigSerum_Glyco_P_12Spectrum4334_scans__5710
Data file W:\Documents\NewmanPaper\Sunil\PigPlasmaGlyco\mgf\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

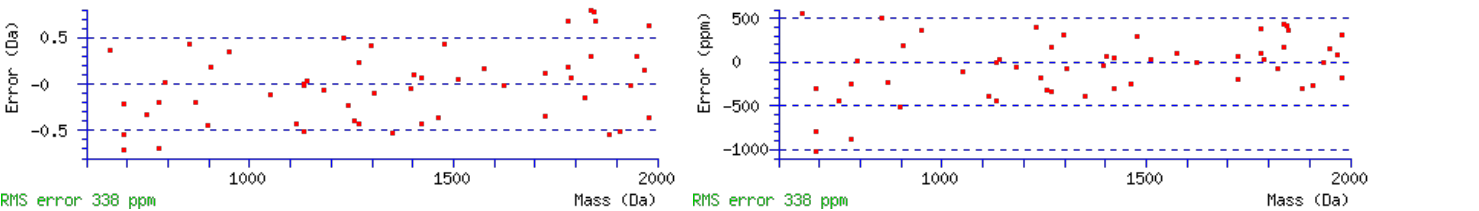
Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 4104.8667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Deamidated (NQ)
Q28 : Deamidated (NQ)
N29 : Deamidated (NQ)
Ions Score: 33 Expect: 0.026
Matches : 54/408 fragment ions using 140 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							36
2	201.1234	101.0653			183.1128	92.0600	S	3992.7900	1996.8986	3975.7634	1988.3853	3974.7794	1987.8933	35
3	300.1918	150.5995			282.1812	141.5942	V	3905.7579	1953.3826	3888.7314	1944.8693	3887.7474	1944.3773	34
4	415.2187	208.1130			397.2082	199.1077	D	3806.6895	1903.8484	3789.6630	1895.3351	3788.6790	1894.8431	33
5	544.2613	272.6343	527.2348	264.1210	526.2508	263.6290	Q	3691.6626	1846.3349	3674.6360	1837.8217	3673.6520	1837.3296	32
6	659.2883	330.1478	642.2617	321.6345	641.2777	321.1425	D	3562.6200	1781.8136	3545.5934	1773.3004	3544.6094	1772.8084	31
7	787.3832	394.1953	770.3567	385.6820	769.3727	385.1900	K	3447.5930	1724.3002	3430.5665	1715.7869	3429.5825	1715.2949	30
8	950.4466	475.7269	933.4200	467.2136	932.4360	466.7216	Y	3319.4981	1660.2527	3302.4715	1651.7394	3301.4875	1651.2474	29
9	1051.4942	526.2508	1034.4677	517.7375	1033.4837	517.2455	T	3156.4348	1578.7210	3139.4082	1570.2077	3138.4242	1569.7157	28
10	1180.5368	590.7721	1163.5103	582.2588	1162.5263	581.7668	E	3055.3871	1528.1972	3038.3605	1519.6839	3037.3765	1519.1919	27
11	1267.5689	634.2881	1250.5423	625.7748	1249.5583	625.2828	S	2926.3445	1463.6759	2909.3179	1455.1626	2908.3339	1454.6706	26
12	1396.6114	698.8094	1379.5849	690.2961	1378.6009	689.8041	E	2839.3125	1420.1599	2822.2859	1411.6466	2821.3019	1411.1546	25
13	1509.6955	755.3514	1492.6690	746.8381	1491.6849	746.3461	I	2710.2699	1355.6386	2693.2433	1347.1253	2692.2593	1346.6333	24
14	1622.7796	811.8934	1605.7530	803.3802	1604.7690	802.8881	I	2597.1858	1299.0965	2580.1592	1290.5833	2579.1752	1290.0913	23
15	1723.8273	862.4173	1706.8007	853.9040	1705.8167	853.4120	T	2484.1017	1242.5545	2467.0752	1234.0412	2466.0912	1233.5492	22
16	1822.8957	911.9515	1805.8691	903.4382	1804.8851	902.9462	V	2383.0541	1192.0307	2366.0275	1183.5174	2365.0435	1183.0254	21
17	1950.9542	975.9808	1933.9277	967.4675	1932.9437	966.9755	Q	2283.9856	1142.4965	2266.9591	1133.9832	2265.9751	1133.4912	20
18	2110.9849	1055.9961	2093.9583	1047.4828	2092.9743	1046.9908	C	2155.9271	1078.4672	2138.9005	1069.9539	2137.9165	1069.4619	19
19	2226.0118	1113.5096	2208.9853	1104.9963	2208.0013	1104.5043	D	1995.8964	998.4518	1978.8699	989.9386	1977.8858	989.4466	18
20	2313.0439	1157.0256	2296.0173	1148.5123	2295.0333	1148.0203	S	1880.8695	940.9384	1863.8429	932.4251	1862.8589	931.9331	17
21	2370.0653	1185.5363	2353.0388	1177.0230	2352.0548	1176.5310	G	1793.8374	897.4224	1776.8109	888.9091	1775.8269	888.4171	16
22	2533.1287	1267.0680	2516.1021	1258.5547	2515.1181	1258.0627	Y	1736.8160	868.9116	1719.7894	860.3984	1718.8054	859.9063	15
23	2590.1501	1295.5787	2573.1236	1287.0654	2572.1396	1286.5734	G	1573.7527	787.3800	1556.7261	778.8667	1555.7421	778.3747	14

24	2703.2342	1352.1207	2686.2076	1343.6075	2685.2236	1343.1154	L	1516.7312	758.8692	1499.7046	750.3560	1498.7206	749.8639	13
25	2802.3026	1401.6549	2785.2761	1393.1417	2784.2920	1392.6497	V	1403.6471	702.3272	1386.6206	693.8139	1385.6366	693.3219	12
26	2859.3241	1430.1657	2842.2975	1421.6524	2841.3135	1421.1604	G	1304.5787	652.7930	1287.5522	644.2797	1286.5681	643.7877	11
27	2956.3768	1478.6921	2939.3503	1470.1788	2938.3663	1469.6868	P	1247.5572	624.2823	1230.5307	615.7690	1229.5467	615.2770	10
28	3085.4194	1543.2133	3068.3929	1534.7001	3067.4089	1534.2081	Q	1150.5045	575.7559	1133.4779	567.2426	1132.4939	566.7506	9
29	3200.4464	1600.7268	3183.4198	1592.2135	3182.4358	1591.7215	N	1021.4619	511.2346	1004.4353	502.7213	1003.4513	502.2293	8
30	3313.5304	1657.2689	3296.5039	1648.7556	3295.5199	1648.2636	I	906.4349	453.7211	889.4084	445.2078	888.4244	444.7158	7
31	3414.5781	1707.7927	3397.5516	1699.2794	3396.5675	1698.7874	T	793.3509	397.1791	776.3243	388.6658	775.3403	388.1738	6
32	3574.6088	1787.8080	3557.5822	1779.2947	3556.5982	1778.8027	C	692.3032	346.6552	675.2767	338.1420	674.2926	337.6500	5
33	3687.6928	1844.3500	3670.6663	1835.8368	3669.6823	1835.3448	I	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
34	3816.7354	1908.8713	3799.7089	1900.3581	3798.7248	1899.8661	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
35	3931.7624	1966.3848	3914.7358	1957.8715	3913.7518	1957.3795	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
36							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
33.0	4104.8667	1.0111	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q28, N29 52.77%
28.6	4104.8667	1.0111	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q17, Q28, N29 19.03%
27.3	4103.8827	1.9952	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
27.3	4103.8827	1.9952	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
27.3	4104.8667	1.0111	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q17, N29 14.10%
27.3	4104.8667	1.0111	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	Deamidated Q5, Q17, Q28 14.10%
26.7	4103.8827	1.9952	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
26.7	4103.8827	1.9952	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
26.4	4105.8508	0.0271	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	
22.2	4103.8827	1.9952	LSVDQDKYTESEITVQCDSGYGLVGPQNITCIEDR	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1SLX2** in **uni_pig**, tr|F1SLX2|F1SLX2_PIG Uncharacterized protein OS=Sus scrofa GN=A2M PE=4 SV=2

Title: 120325_Sunil_PigSerum_Glyco_S_10Spectrum3761_scans__5469

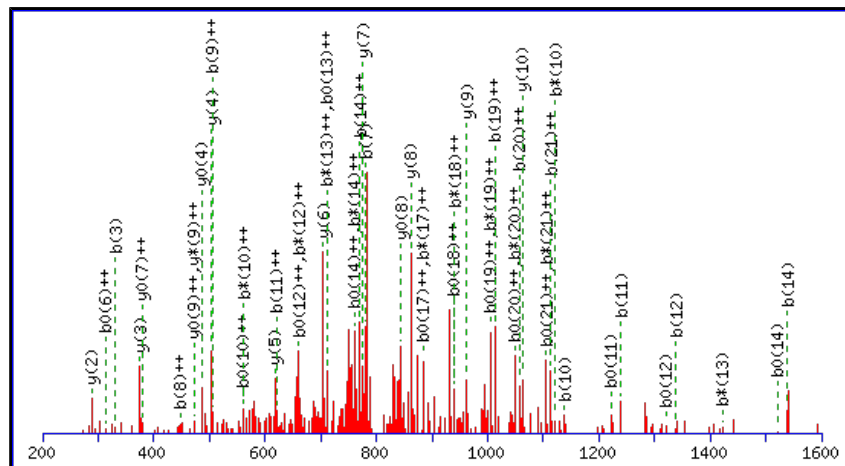
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

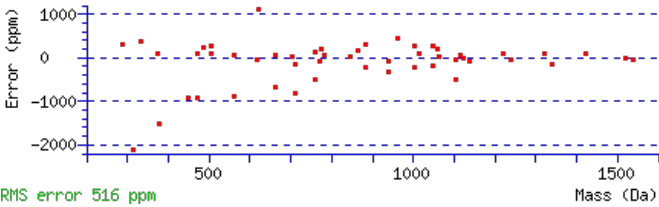
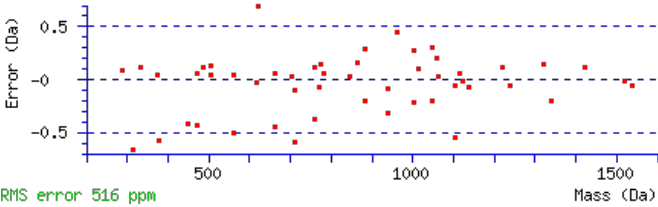
Variable modifications:

N9 : Deamidated (N0)

Ions Score: 35 Expect: 0.028

Matches : 51/222 fragment ions using 107 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							22
2	218.0594	109.5333					C	2343.2224	1172.1149	2326.1959	1163.6016	2325.2119	1163.1096	21
3	331.1435	166.0754					L	2183.1918	1092.0995	2166.1652	1083.5863	2165.1812	1083.0942	20
4	444.2275	222.6174					L	2070.1077	1035.5575	2053.0812	1027.0442	2052.0972	1026.5522	19
5	557.3116	279.1594					L	1957.0237	979.0155	1939.9971	970.5022	1939.0131	970.0102	18
6	644.3436	322.6754			626.3330	313.6702	S	1843.9396	922.4734	1826.9130	913.9602	1825.9290	913.4682	17
7	781.4025	391.2049			763.3920	382.1996	H	1756.9076	878.9574	1739.8810	870.4441	1738.8970	869.9521	16
8	894.4866	447.7469			876.4760	438.7416	L	1619.8487	810.4280	1602.8221	801.9147	1601.8381	801.4227	15
9	1009.5135	505.2604	992.4870	496.7471	991.5030	496.2551	N	1506.7646	753.8859	1489.7380	745.3727	1488.7540	744.8807	14
10	1138.5561	569.7817	1121.5296	561.2684	1120.5456	560.7764	E	1391.7377	696.3725	1374.7111	687.8592	1373.7271	687.3672	13
11	1239.6038	620.3055	1222.5773	611.7923	1221.5932	611.3003	T	1262.6951	631.8512	1245.6685	623.3379	1244.6845	622.8459	12
12	1338.6722	669.8397	1321.6457	661.3265	1320.6616	660.8345	V	1161.6474	581.3273	1144.6208	572.8141	1143.6368	572.3220	11
13	1439.7199	720.3636	1422.6933	711.8503	1421.7093	711.3583	T	1062.5790	531.7931	1045.5524	523.2798	1044.5684	522.7878	10
14	1538.7883	769.8978	1521.7618	761.3845	1520.7777	760.8925	V	961.5313	481.2693	944.5047	472.7560	943.5207	472.2640	9
15	1625.8203	813.4138	1608.7938	804.9005	1607.8098	804.4085	S	862.4629	431.7351	845.4363	423.2218	844.4523	422.7298	8
16	1696.8574	848.9324	1679.8309	840.4191	1678.8469	839.9271	A	775.4308	388.2191	758.4043	379.7058	757.4203	379.2138	7
17	1783.8895	892.4484	1766.8629	883.9351	1765.8789	883.4431	S	704.3937	352.7005	687.3672	344.1872	686.3832	343.6952	6
18	1896.9735	948.9904	1879.9470	940.4771	1878.9630	939.9851	L	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
19	2026.0161	1013.5117	2008.9896	1004.9984	2008.0056	1004.5064	E	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
20	2113.0482	1057.0277	2096.0216	1048.5144	2095.0376	1048.0224	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
21	2226.1322	1113.5698	2209.1057	1105.0565	2208.1217	1104.5645	L	288.2030	144.6051	271.1765	136.0919			2
22							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [GCLLLSHLNETVTVSASLESLR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.8	2399.2366	-0.0119	GCLLLSHLNETVTVSASLESLR
9.7	2399.2168	0.0079	FMPPDDPLGRRGPTLNNELSR
7.2	2397.2176	2.0071	DHHQIQQTSEYLQLSITKVK
7.2	2397.2176	2.0071	DHHQIQQTSEYLQLSITKVK
7.2	2397.2176	2.0071	DHHQIQQTSEYLQLSITKVK
5.1	2397.2176	2.0071	DHHQIQQTSEYLQLSITKVK
5.1	2397.2176	2.0071	DHHQIQQTSEYLQLSITKVK
3.9	2397.2032	2.0214	TSLQPMVSALNISVGGTGMFTVR
2.9	2397.2288	1.9959	NTRIKDTSQNFQVSLNVLR
2.9	2398.2128	1.0119	NTRIKDTSQNFQVSLNVLR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIPVNSPELEEPLNHSIAK**

Found in **F1SFI4** in **uni_pig**, tr|F1SFI4|F1SFI4_PIG Uncharacterized protein OS=Sus scrofa GN=KNG1 PE=4 SV=2

Match to Query 11958: 2103.045788 from(1052.530170,2+) intensity(4283.4956) rtinseconds(2090) scans(3985) index(11950)

Title: 120326_Sunil_PigSerum_Glyco_SsetB_06Spectrum2842_scans__3985

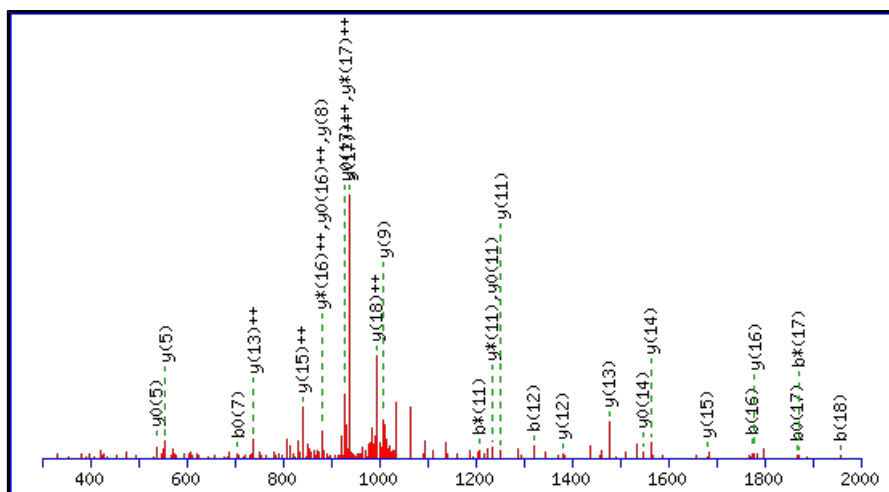
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2103.0371

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

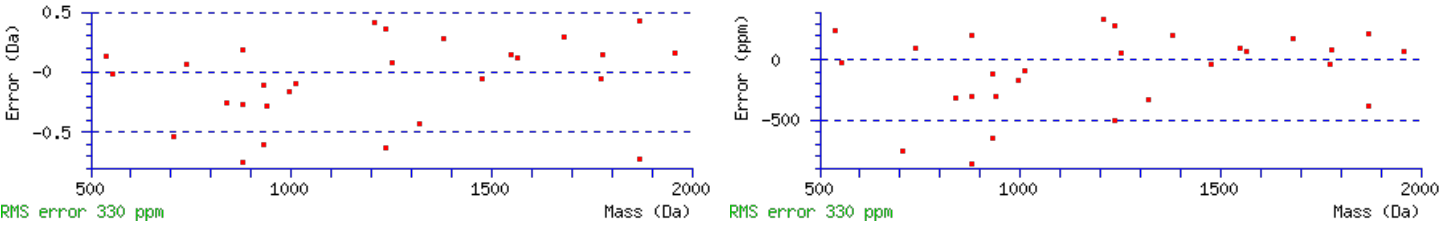
N5 : Deamidated (NQ)

N14 : Deamidated (NQ)

Ions Score: 35 Expect: 0.029

Matches : 28/202 fragment ions using 63 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							19
2	229.1183	115.0628			211.1077	106.0575	I	1989.0175	995.0124	1971.9910	986.4991	1971.0069	986.0071	18
3	326.1710	163.5892			308.1605	154.5839	P	1875.9334	938.4704	1858.9069	929.9571	1857.9229	929.4651	17
4	425.2395	213.1234			407.2289	204.1181	V	1778.8807	889.9440	1761.8541	881.4307	1760.8701	880.9387	16
5	540.2664	270.6368	523.2399	262.1236	522.2558	261.6316	N	1679.8123	840.4098	1662.7857	831.8965	1661.8017	831.4045	15
6	627.2984	314.1529	610.2719	305.6396	609.2879	305.1476	S	1564.7853	782.8963	1547.7588	774.3830	1546.7748	773.8910	14
7	724.3512	362.6792	707.3246	354.1660	706.3406	353.6740	P	1477.7533	739.3803	1460.7268	730.8670	1459.7427	730.3750	13
8	853.3938	427.2005	836.3672	418.6873	835.3832	418.1953	E	1380.7005	690.8539	1363.6740	682.3406	1362.6900	681.8486	12
9	966.4779	483.7426	949.4513	475.2293	948.4673	474.7373	L	1251.6579	626.3326	1234.6314	617.8193	1233.6474	617.3273	11
10	1095.5204	548.2639	1078.4939	539.7506	1077.5099	539.2586	E	1138.5739	569.7906	1121.5473	561.2773	1120.5633	560.7853	10
11	1224.5630	612.7852	1207.5365	604.2719	1206.5525	603.7799	E	1009.5313	505.2693	992.5047	496.7560	991.5207	496.2640	9
12	1321.6158	661.3115	1304.5893	652.7983	1303.6052	652.3063	P	880.4887	440.7480	863.4621	432.2347	862.4781	431.7427	8
13	1434.6999	717.8536	1417.6733	709.3403	1416.6893	708.8483	L	783.4359	392.2216	766.4094	383.7083	765.4254	383.2163	7
14	1549.7268	775.3670	1532.7003	766.8538	1531.7162	766.3618	N	670.3519	335.6796	653.3253	327.1663	652.3413	326.6743	6
15	1686.7857	843.8965	1669.7592	835.3832	1668.7752	834.8912	H	555.3249	278.1661	538.2984	269.6528	537.3144	269.1608	5
16	1773.8178	887.4125	1756.7912	878.8992	1755.8072	878.4072	S	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
17	1886.9018	943.9545	1869.8753	935.4413	1868.8912	934.9493	I	331.2340	166.1206	314.2074	157.6074			3
18	1957.9389	979.4731	1940.9124	970.9598	1939.9284	970.4678	A	218.1499	109.5786	201.1234	101.0653			2
19							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [DIPVNSPELEEPLNHSLAK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.8	2103.0371	0.0087	DIPVNSPELEEPLNHSLAK
23.6	2102.0531	0.9927	DIPVNSPELEEPLNHSLAK
14.5	2103.0524	-0.0066	DLYQLNPNAEWVSKPS
14.5	2103.0524	-0.0066	DLYQLNPNAEWVSKPS
12.9	2103.0457	0.0001	DPRQQNTPQAANSPPNLGAK
10.3	2103.0524	-0.0066	DLYQLNPNAEWVSKPS
7.5	2102.0579	0.9879	GATTNICYNVLDRIVHEK
7.1	2103.0419	0.0039	GATTNICYNVLDRIVHEK
6.3	2103.0582	-0.0125	SGLSQKEEEDAIVIEKQLK
2.8	2103.0596	-0.0138	LDEEEHKNLKLQHVVDK

Mascot: <http://www.matrixscience.com/>

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SCIENCE

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENESSSLIK**
Found in **I3LBJ0** in **uni_pig**, tr|I3LBJ0|I3LBJ0_PIG Uncharacterized protein OS=Sus scrofa GN=LRRCC1 PE=4 SV=1

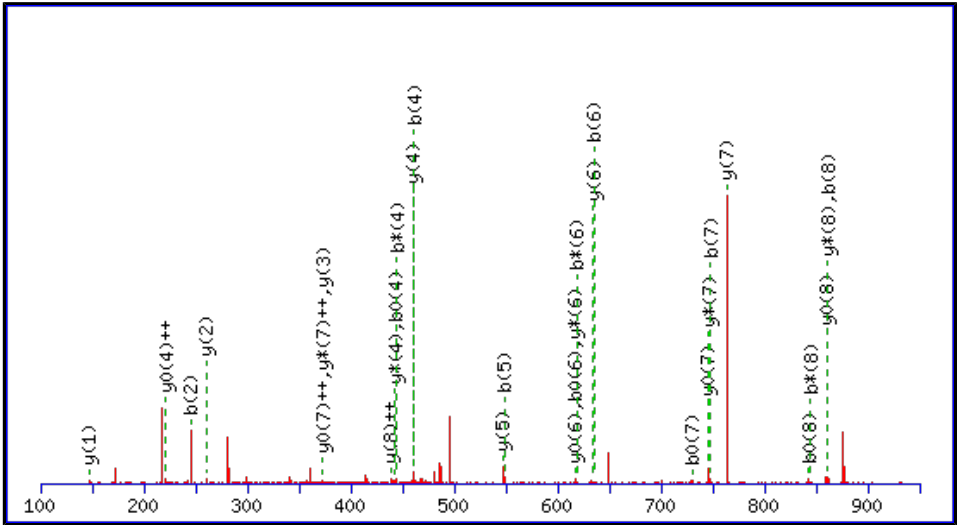
Match to Query 434: 1006.487948 from(504.251250,2+) intensity(0.0000) rtinseconds(1948) scans(4573) index(6322)
Title: 120325_Sunil_PigSerum_Glyco_S_14Spectrum3825_scans__4573
Data file
W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

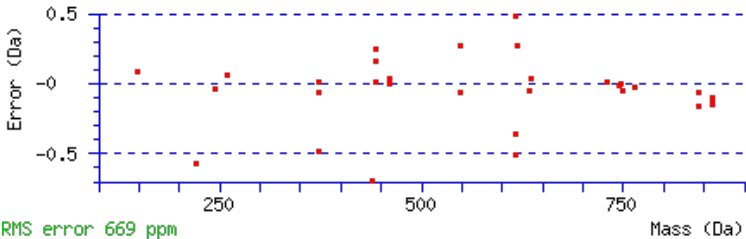
Label all possible matches Label matches used for scoring

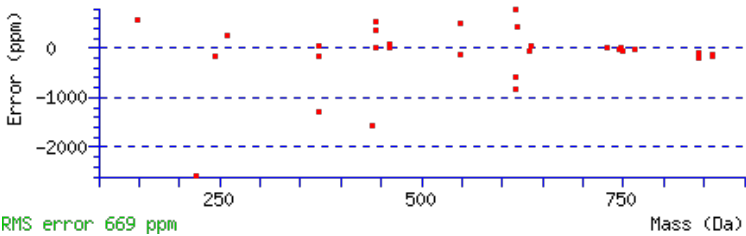
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1006.4818
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Ions Score: 32 Expect: 0.032
Matches : 31/88 fragment ions using 64 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							9
2	245.0768	123.0420	228.0503	114.5288	227.0662	114.0368	N	878.4466	439.7269	861.4200	431.2136	860.4360	430.7216	8
3	374.1194	187.5633	357.0929	179.0501	356.1088	178.5581	E	763.4196	382.2134	746.3931	373.7002	745.4090	373.2082	7
4	461.1514	231.0794	444.1249	222.5661	443.1409	222.0741	S	634.3770	317.6921	617.3505	309.1789	616.3665	308.6869	6
5	548.1835	274.5954	531.1569	266.0821	530.1729	265.5901	S	547.3450	274.1761	530.3184	265.6629	529.3344	265.1708	5
6	635.2155	318.1114	618.1889	309.5981	617.2049	309.1061	S	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
7	748.2996	374.6534	731.2730	366.1401	730.2890	365.6481	L	373.2809	187.1441	356.2544	178.6308			3
8	861.3836	431.1954	844.3571	422.6822	843.3731	422.1902	I	260.1969	130.6021	243.1703	122.0888			2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of [ENESSSLIK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.7	1006.4818	0.0061	ENESSSLIK
15.3	1006.4793	0.0086	MPFNKEPK
14.1	1004.4774	2.0105	EINQTRDK
9.6	1005.4767	1.0112	EIEFQPSR
9.4	1005.4767	1.0113	ENFPKENK
8.3	1006.4939	-0.0060	MLPKTMNR
8.3	1004.4848	2.0031	QQLNEMLK
8.0	1004.4774	2.0105	QIENASQSK
7.8	1006.4939	-0.0060	MLSPMREK
7.8	1006.4971	-0.0091	ENIQLENK

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **K7GKE7** in **uni_pig**, tr|K7GKE7|K7GKE7_PIG Haptoglobin OS=Sus scrofa GN=HP PE=3 SV=1

Title: 120325 Sunil PigSerum Glyco S 14Spectrum3755 scans 4495

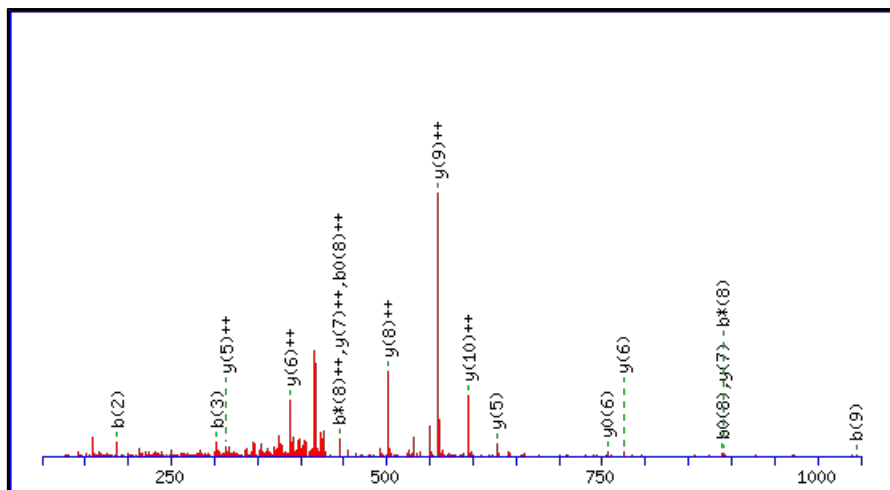
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325 Sunil PigSerum Glyco DSP uni pigPTM 2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

N1 : Deamidated (NQ)

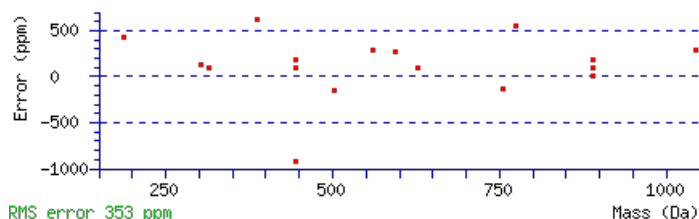
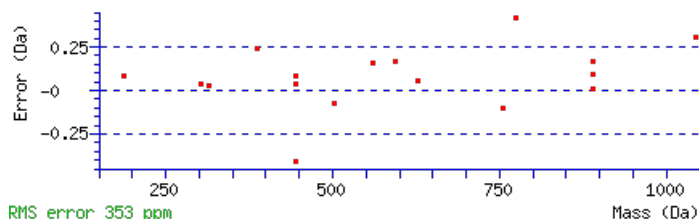
N3 : Deamidated (NQ)

N5 : Deamidated (NQ)

Ions Score: 30 Expect: 0.033

Matches : 17/102 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	99.0077	50.0075			N							11
2	187.0713	94.0393	170.0448	85.5260			A	1188.5895	594.7984	1171.5630	586.2851	1170.5790	585.7931	10
3	302.0983	151.5528	285.0717	143.0395			N	1117.5524	559.2798	1100.5259	550.7666	1099.5419	550.2746	9
4	415.1823	208.0948	398.1558	199.5815			L	1002.5255	501.7664	985.4989	493.2531	984.5149	492.7611	8
5	530.2093	265.6083	513.1827	257.0950			N	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	7
6	677.2777	339.1425	660.2511	330.6292			F	774.4145	387.7109	757.3879	379.1976	756.4039	378.7056	6
7	778.3254	389.6663	761.2988	381.1531	760.3148	380.6610	T	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	5
8	907.3680	454.1876	890.3414	445.6743	889.3574	445.1823	E	526.2984	263.6528	509.2718	255.1396	508.2878	254.6475	4
9	1044.4269	522.7171	1027.4003	514.2038	1026.4163	513.7118	H	397.2558	199.1315	380.2292	190.6183			3
10	1157.5109	579.2591	1140.4844	570.7458	1139.5004	570.2538	L	260.1969	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [NANLNFTEHLK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.4	1302.6091	-0.0016	NANLNFTEHLK
11.4	1301.6099	0.9976	VSNGISEDQGPAK
10.2	1301.6099	0.9976	VSNGISEDQGPAK
8.7	1302.5952	0.0123	WAREEEEEAQR
6.5	1302.5979	0.0096	NAVESYTYNIK
5.5	1301.6139	0.9936	NAVESYTYNIK
4.4	1301.5960	1.0116	ANNSGEAGLQEGR
4.3	1302.6051	0.0024	AEARTSEGEKPK
2.0	1301.6098	0.9977	NNAQAEKNGKPK
2.0	1302.5986	0.0089	GTKENMHREGK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

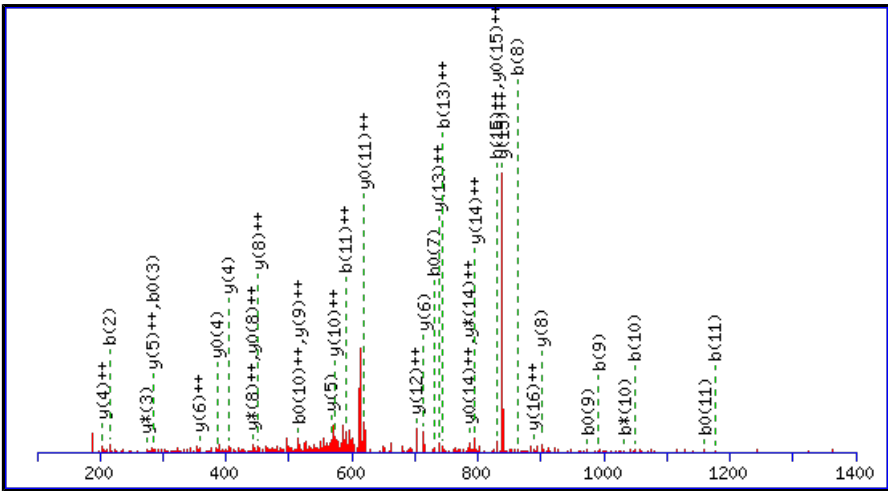
Peptide View

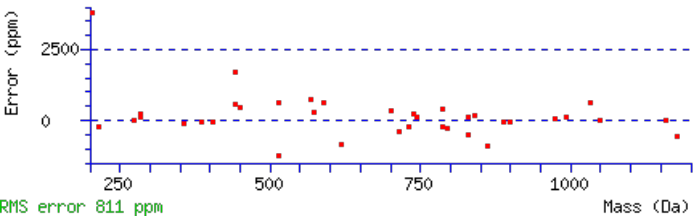
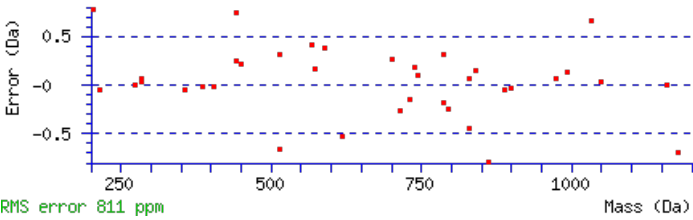
MS/MS Fragmentation of **NVSNAFLDKGEFYIGSK**
Found in **F1SKB1** in **uni_pig**, tr|F1SKB1|F1SKB1_PIG Uncharacterized protein OS=Sus scrofa GN=CP PE=4 SV=3

Match to Query 7676: 1889.919192 from(630.980340,3+) intensity(1002.4272) rtinseconds(2387) scans(4809) index(11583)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_02Spectrum3662_scans_4809
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis





NCBI **BLAST** search of [NVSNAFLDKGEFYIGSK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.0	1889.9047	0.0145	NVSNAFLDKGEFYIGSK
33.1	1888.9207	0.9985	NVSNAFLDKGEFYIGSK
25.3	1888.9207	0.9985	NVSNAFLDKGEFYIGSK
5.3	1887.9050	2.0142	CPWQEEAFIRRGPGK
4.7	1889.9014	0.0178	NVSNQEGSMDVVARTQR
2.8	1887.9070	2.0122	MKAVVHQTDNIMDQLK
2.1	1888.9200	0.9992	VLLDDDLSDIECAKR
1.8	1888.9312	0.9880	ERLEQDLQMQAKVR
1.8	1888.9312	0.9880	ERLEQDLQMQAKVR
1.8	1888.9312	0.9880	ERLEQDLQMQAKVR

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

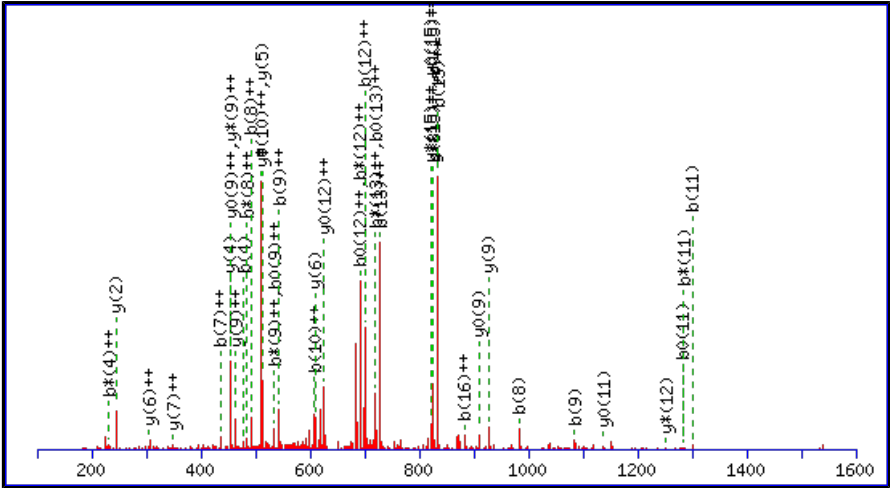
Peptide View

MS/MS Fragmentation of **LHINYNNLTESVGPLPK**
Found in **F1SQ09** in **uni_pig**, tr|F1SQ09|F1SQ09_PIG Uncharacterized protein OS=Sus scrofa GN=LUM PE=4 SV=1

Match to Query 7870: 1910.994732 from(638.005520,3+) intensity(2993.6592) rtinseconds(2082) scans(4903) index(8505)
Title: 120326_Sunil_PigSerum_Glyco_DsetB_14Spectrum4202_scans__4903
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

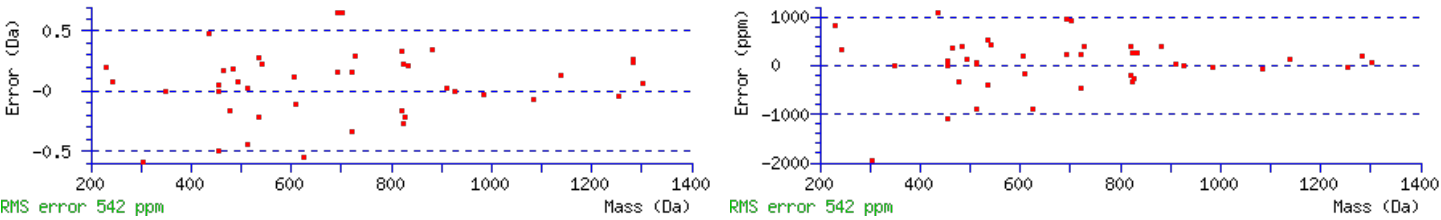
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches Label matches used for scoring
Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 1908.9945
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 33 Expect: 0.035
Matches : 43/158 fragment ions using 70 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							17
2	251.1503	126.0788					H	1796.9177	898.9625	1779.8912	890.4492	1778.9072	889.9572	16
3	364.2343	182.6208					I	1659.8588	830.4331	1642.8323	821.9198	1641.8483	821.4278	15
4	478.2772	239.6423	461.2507	231.1290			N	1546.7748	773.8910	1529.7482	765.3777	1528.7642	764.8857	14
5	641.3406	321.1739	624.3140	312.6606			Y	1432.7318	716.8696	1415.7053	708.3563	1414.7213	707.8643	13
6	755.3835	378.1954	738.3569	369.6821			N	1269.6685	635.3379	1252.6420	626.8246	1251.6579	626.3326	12
7	870.4104	435.7089	853.3839	427.1956			N	1155.6256	578.3164	1138.5990	569.8032	1137.6150	569.3111	11
8	983.4945	492.2509	966.4680	483.7376			L	1040.5986	520.8030	1023.5721	512.2897	1022.5881	511.7977	10
9	1084.5422	542.7747	1067.5156	534.2615	1066.5316	533.7694	T	927.5146	464.2609	910.4880	455.7477	909.5040	455.2556	9
10	1213.5848	607.2960	1196.5582	598.7828	1195.5742	598.2907	E	826.4669	413.7371	809.4403	405.2238	808.4563	404.7318	8
11	1300.6168	650.8120	1283.5903	642.2988	1282.6062	641.8068	S	697.4243	349.2158	680.3978	340.7025	679.4137	340.2105	7
12	1399.6852	700.3462	1382.6587	691.8330	1381.6747	691.3410	V	610.3923	305.6998	593.3657	297.1865			6
13	1456.7067	728.8570	1439.6801	720.3437	1438.6961	719.8517	G	511.3239	256.1656	494.2973	247.6523			5
14	1553.7594	777.3834	1536.7329	768.8701	1535.7489	768.3781	P	454.3024	227.6548	437.2758	219.1416			4
15	1666.8435	833.9254	1649.8170	825.4121	1648.8329	824.9201	L	357.2496	179.1285	340.2231	170.6152			3
16	1763.8963	882.4518	1746.8697	873.9385	1745.8857	873.4465	P	244.1656	122.5864	227.1390	114.0731			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [LHINYNNLTESVGPLPK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
32.6	1908.9945	2.0002	LHINYNNLTESVGPLPK	Deamidated N7 43.49%
32.6	1908.9945	2.0002	LHINYNNLTESVGPLPK	Deamidated N6 43.49%
31.9	1909.9785	1.0162	LHINYNNLTESVGPLPK	
27.3	1908.9945	2.0002	LHINYNNLTESVGPLPK	Deamidated N4 13.01%
22.7	1909.9785	1.0162	LHINYNNLTESVGPLPK	
22.7	1909.9785	1.0162	LHINYNNLTESVGPLPK	
5.4	1908.9908	2.0039	KMALNSLSMLKLMGPK	
4.4	1909.9785	1.0162	DLKPENLVDDDFHIK	
4.4	1910.0070	0.9877	IQDLLELTPVSICPSK	
2.8	1909.9753	1.0194	QMEKIQPALQEKHAMK	

Mascot: <http://www.matrixscience.com/>

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
58.9	1205.5524	-0.0030	NSNLTGISDQR	Deamidated N3, Q10 68.73%
55.5	1205.5524	-0.0030	NSNLTGISDQR	Deamidated N1, Q10 31.27%
29.6	1205.5524	-0.0029	SNNITDSLNR	
23.9	1205.5524	-0.0029	SNNITDSLNR	
14.2	1205.5459	0.0035	LSGGQSGGVCER	
9.0	1205.5459	0.0036	MRAEGDGGLER	
8.4	1205.5598	-0.0103	INELPSTMQR	
7.1	1205.5411	0.0083	LLTEDSENQR	
6.8	1205.5571	-0.0077	NSQCSRGLER	
6.6	1205.5524	-0.0029	SKQQLSDNQR	

Mascot: <http://www.matrixscience.com/>

Peptide View

Found in **F1S3J9** in **uni_pig**, tr|F1S3J9|F1S3J9_PIG Intercellular adhesion molecule 1 OS=Sus scrofa GN=ICAM-1 PE=2 SV=1

Title: 120326_Sunil_PigSerum_Glyco_SsetB_13Spectrum2462_scans__3115

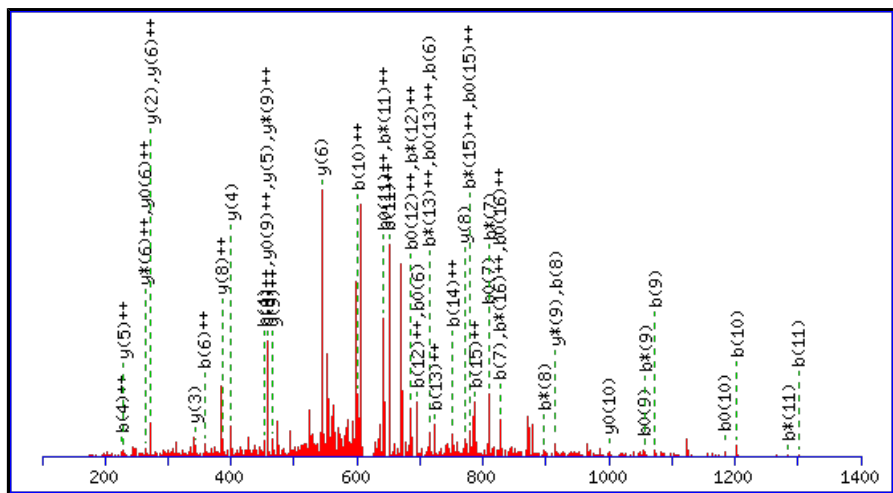
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring

Show Y-axis



Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

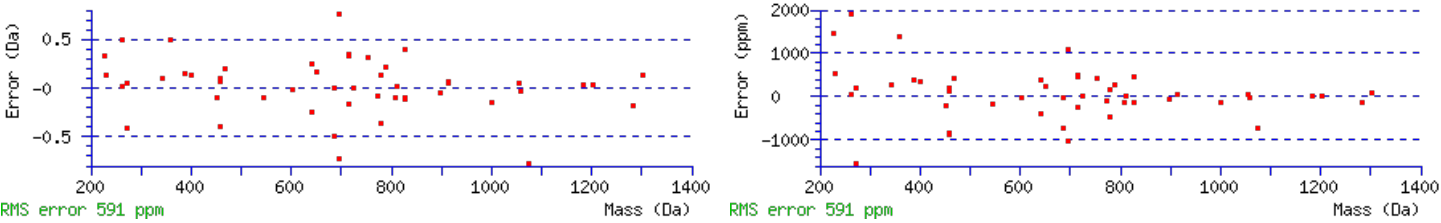
Variable modifications:

N6 : Deamidated (NQ)

Ions Score: 30 Expect: 0.04

Matches : 50/178 fragment ions using 97 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	187.0713	94.0393			169.0608	85.0340	G	1715.7918	858.3996	1698.7653	849.8863	1697.7813	849.3943	16
3	315.1299	158.0686	298.1034	149.5553	297.1193	149.0633	Q	1658.7704	829.8888	1641.7438	821.3755	1640.7598	820.8835	15
4	452.1888	226.5980	435.1623	218.0848	434.1783	217.5928	H	1530.7118	765.8595	1513.6852	757.3463	1512.7012	756.8542	14
5	599.2572	300.1323	582.2307	291.6190	581.2467	291.1270	F	1393.6529	697.3301	1376.6263	688.8168	1375.6423	688.3248	13
6	714.2842	357.6457	697.2576	349.1325	696.2736	348.6404	N	1246.5845	623.7959	1229.5579	615.2826	1228.5739	614.7906	12
7	827.3682	414.1878	810.3417	405.6745	809.3577	405.1825	L	1131.5575	566.2824	1114.5310	557.7691	1113.5470	557.2771	11
8	914.4003	457.7038	897.3737	449.1905	896.3897	448.6985	S	1018.4735	509.7404	1001.4469	501.2271	1000.4629	500.7351	10
9	1074.4309	537.7191	1057.4044	529.2058	1056.4204	528.7138	C	931.4414	466.2244	914.4149	457.7111	913.4309	457.2191	9
10	1202.4895	601.7484	1185.4630	593.2351	1184.4789	592.7431	Q	771.4108	386.2090	754.3842	377.6958	753.4002	377.2037	8
11	1301.5579	651.2826	1284.5314	642.7693	1283.5473	642.2773	V	643.3522	322.1797	626.3257	313.6665	625.3416	313.1745	7
12	1388.5899	694.7986	1371.5634	686.2853	1370.5794	685.7933	S	544.2838	272.6455	527.2572	264.1323	526.2732	263.6402	6
13	1445.6114	723.3093	1428.5849	714.7961	1427.6008	714.3041	G	457.2518	229.1295	440.2252	220.6162			5
14	1502.6329	751.8201	1485.6063	743.3068	1484.6223	742.8148	G	400.2303	200.6188	383.2037	192.1055			4
15	1573.6700	787.3386	1556.6434	778.8254	1555.6594	778.3333	A	343.2088	172.1081	326.1823	163.5948			3
16	1670.7227	835.8650	1653.6962	827.3517	1652.7122	826.8597	P	272.1717	136.5895	255.1452	128.0762			2
17							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [EGQHFNLSQVSGGAPR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
30.1	1843.8271	-0.0016	EGQHFNLSQVSGGAPR	Deamidated N6 46.37%
29.0	1843.8271	-0.0016	EGQHFNLSQVSGGAPR	Deamidated Q3 35.67%
26.0	1843.8271	-0.0016	EGQHFNLSQVSGGAPR	Deamidated Q10 17.96%
14.4	1843.8112	0.0144	NLIDEDGNNQWPEGLK	
14.4	1843.8112	0.0144	NLIDEDGNNQWPEGLK	
9.0	1843.8112	0.0144	NLIDEDGNNQWPEGLK	
8.0	1842.8271	0.9984	NLIDEDGNNQWPEGLK	
8.0	1842.8271	0.9984	NLIDEDGNNQWPEGLK	
8.0	1842.8271	0.9984	NLIDEDGNNQWPEGLK	
8.0	1843.8112	0.0144	NLIDEDGNNQWPEGLK	

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

MS/MS Fragmentation of **YKVDYESQSTDQNFSSESK**

Found in **F1ST75** in **uni_pig**, tr|F1ST75|F1ST75_PIG Insulin-like growth factor-binding protein 3 (Fragment) OS=Sus scrofa GN=IGFBP3 PE=4 SV=2

Match to Query 12756: 2344.000632 from(782.340820,3+) intensity(684.5981) rtinseconds(1321) scans(2144) index(8057)

Title: 120326_Sunil_PigSerum_Glyco_DsetB_12Spectrum1385_scans__2144

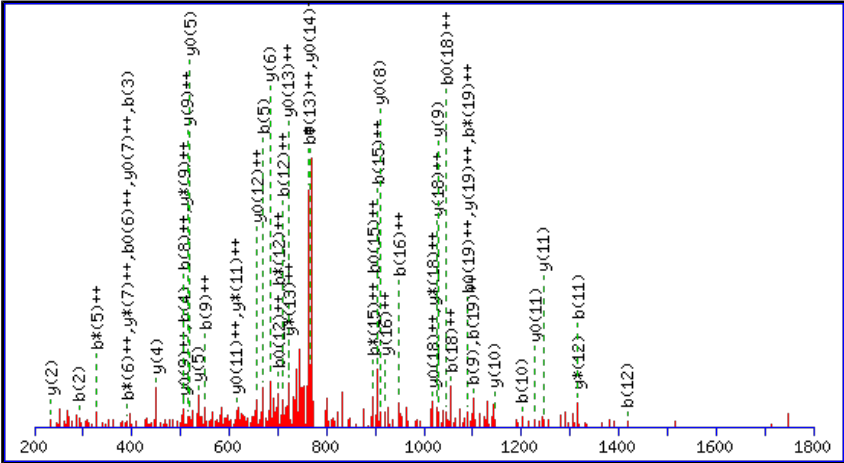
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, _____ to _____ Da _____

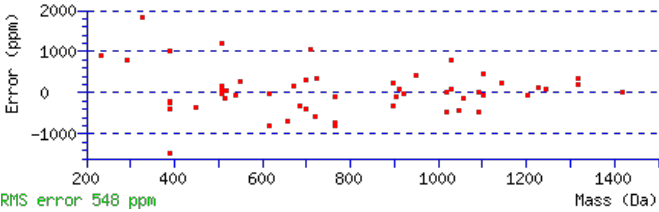
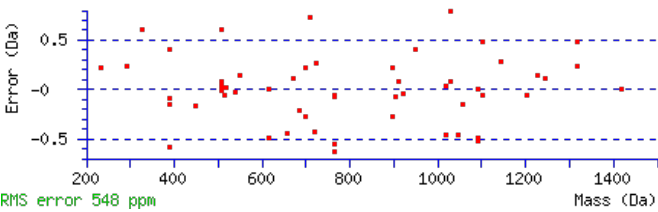
Label all possible matches Label matches used for scoring

Show Y-axis



Monoisotopic mass of neutral peptide Mr(calc): 2343.9866
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
 Q13 : Deamidated (NQ)
 N14 : Deamidated (NQ)
Ions Score: 27 **Expect:** 0.04
Matches : 55/218 fragment ions using 106 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							20
2	292.1656	146.5864	275.1390	138.0731			K	2181.9306	1091.4689	2164.9041	1082.9557	2163.9200	1082.4637	19
3	391.2340	196.1206	374.2074	187.6074			V	2053.8356	1027.4215	2036.8091	1018.9082	2035.8251	1018.4162	18
4	506.2609	253.6341	489.2344	245.1208	488.2504	244.6288	D	1954.7672	977.8873	1937.7407	969.3740	1936.7567	968.8820	17
5	669.3243	335.1658	652.2977	326.6525	651.3137	326.1605	Y	1839.7403	920.3738	1822.7137	911.8605	1821.7297	911.3685	16
6	798.3668	399.6871	781.3403	391.1738	780.3563	390.6818	E	1676.6770	838.8421	1659.6504	830.3288	1658.6664	829.8368	15
7	885.3989	443.2031	868.3723	434.6898	867.3883	434.1978	S	1547.6344	774.3208	1530.6078	765.8075	1529.6238	765.3155	14
8	1013.4575	507.2324	996.4309	498.7191	995.4469	498.2271	Q	1460.6023	730.8048	1443.5758	722.2915	1442.5918	721.7995	13
9	1100.4895	550.7484	1083.4629	542.2351	1082.4789	541.7431	S	1332.5438	666.7755	1315.5172	658.2622	1314.5332	657.7702	12
10	1201.5372	601.2722	1184.5106	592.7589	1183.5266	592.2669	T	1245.5117	623.2595	1228.4852	614.7462	1227.5012	614.2542	11
11	1316.5641	658.7857	1299.5376	650.2724	1298.5535	649.7804	D	1144.4641	572.7357	1127.4375	564.2224	1126.4535	563.7304	10
12	1417.6118	709.3095	1400.5852	700.7963	1399.6012	700.3042	T	1029.4371	515.2222	1012.4106	506.7089	1011.4265	506.2169	9
13	1546.6544	773.8308	1529.6278	765.3176	1528.6438	764.8255	Q	928.3894	464.6984	911.3629	456.1851	910.3789	455.6931	8
14	1661.6813	831.3443	1644.6548	822.8310	1643.6708	822.3390	N	799.3468	400.1771	782.3203	391.6638	781.3363	391.1718	7
15	1808.7497	904.8785	1791.7232	896.3652	1790.7392	895.8732	F	684.3199	342.6636	667.2933	334.1503	666.3093	333.6583	6
16	1895.7818	948.3945	1878.7552	939.8812	1877.7712	939.3892	S	537.2515	269.1294	520.2249	260.6161	519.2409	260.1241	5
17	1982.8138	991.9105	1965.7872	983.3973	1964.8032	982.9053	S	450.2195	225.6134	433.1929	217.1001	432.2089	216.6081	4
18	2111.8564	1056.4318	2094.8298	1047.9186	2093.8458	1047.4265	E	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
19	2198.8884	1099.9478	2181.8619	1091.4346	2180.8778	1090.9426	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
20							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [YKVDYESQSTDTQNFSESSESK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
27.5	2343.9866	0.0140	YKVDYESQSTDTQNFSESSESK	Deamidated Q13, N14 39.59%
27.0	2343.9866	0.0140	YKVDYESQSTDTQNFSESSESK	Deamidated Q8, N14 35.61%
26.6	2343.0026	0.9980	YKVDYESQSTDTQNFSESSESK	
26.6	2343.0026	0.9980	YKVDYESQSTDTQNFSESSESK	
25.5	2343.9866	0.0140	YKVDYESQSTDTQNFSESSESK	Deamidated Q8, Q13 24.81%
18.2	2343.0026	0.9980	YKVDYESQSTDTQNFSESSESK	

Mascot: <http://www.matrixscience.com/>

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
69.6	1205.5524	-0.0015	NSNLTGISDQR	Deamidated N1, N3 100.00%
29.2	1205.5524	-0.0015	SNNITDSLNR	
22.4	1205.5524	-0.0015	NSNLTGISDQR	Deamidated N1, Q10 0.00%
19.3	1205.5524	-0.0015	NSNLTGISDQR	Deamidated N3, Q10 0.00%
13.0	1205.5420	0.0089	MAPEVMEQVR	
10.2	1205.5524	-0.0015	QDVDTESQKR	
9.8	1205.5459	0.0050	MRAEGDGGLER	
9.2	1205.5537	-0.0028	NTRGSWSNER	
8.6	1204.5472	1.0036	RYPSDPAQDR	
8.0	1205.5499	0.0010	ADMPAAPSFQR	

Mascot: <http://www.matrixscience.com/>

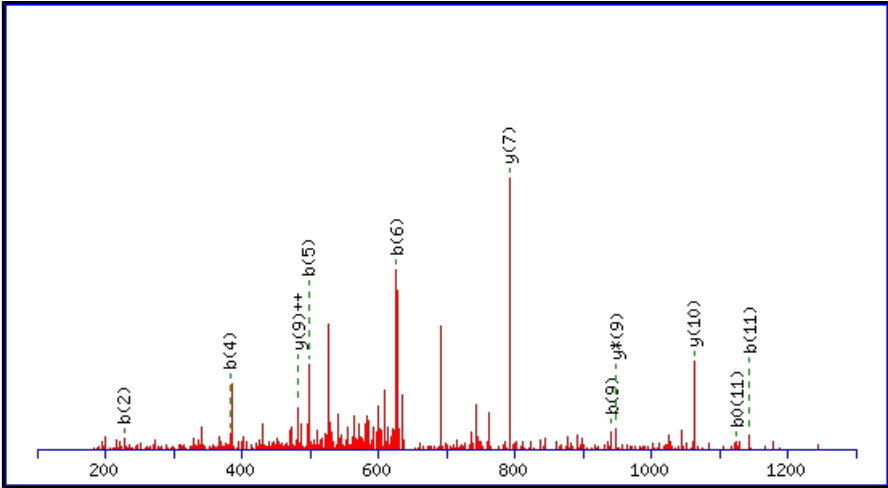
Peptide View

Found in **Q06AU7** in **uni_pig**, sp|Q06AU7|RAB1B_PIG Ras-related protein Rab-1B OS=Sus scrofa GN=RAB1B PE=2 SV=1

Match to Query 2442: 1288.717828 from(645.366190,2+) intensity(914.1672) rtinseconds(1768) scans(3358) index(12150)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_08Spectrum2425_scans__3358
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

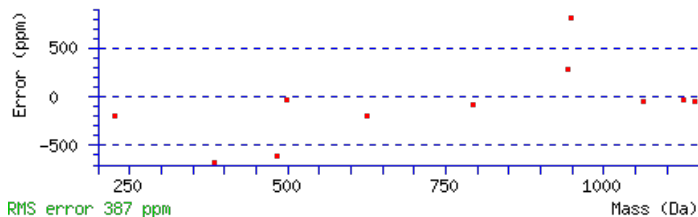
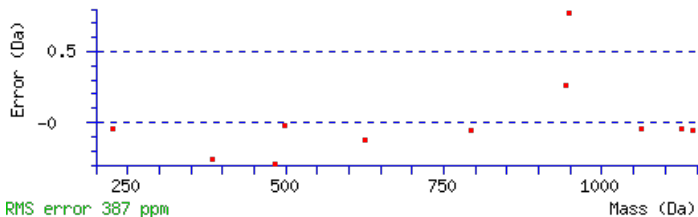
Click mouse within plot area to zoom in by factor of two about that point

Or,	to	Da
Label all possible matches		Label matches used for scoring
Show Y-axis		



Monoisotopic mass of neutral peptide Mr(calc): 1288.7238
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 N5 : Deamidated (NQ)
 Ions Score: 31 Expect: 0.044
 Matches : 11/110 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							12
2	227.1754	114.0913					L	1176.6470	588.8272	1159.6205	580.3139	1158.6365	579.8219	11
3	326.2438	163.6255					V	1063.5630	532.2851	1046.5364	523.7719	1045.5524	523.2798	10
4	383.2653	192.1363					G	964.4946	482.7509	947.4680	474.2376	946.4840	473.7456	9
5	498.2922	249.6498	481.2657	241.1365			N	907.4731	454.2402	890.4466	445.7269	889.4625	445.2349	8
6	626.3872	313.6972	609.3606	305.1840			K	792.4462	396.7267	775.4196	388.2134	774.4356	387.7214	7
7	713.4192	357.2132	696.3927	348.7000	695.4087	348.2080	S	664.3512	332.6792	647.3246	324.1660	646.3406	323.6740	6
8	828.4462	414.7267	811.4196	406.2134	810.4356	405.7214	D	577.3192	289.1632	560.2926	280.6499	559.3086	280.1579	5
9	941.5302	471.2687	924.5037	462.7555	923.5197	462.2635	L	462.2922	231.6498	445.2657	223.1365	444.2817	222.6445	4
10	1042.5779	521.7926	1025.5514	513.2793	1024.5673	512.7873	T	349.2082	175.1077	332.1816	166.5944	331.1976	166.1024	3
11	1143.6256	572.3164	1126.5990	563.8032	1125.6150	563.3111	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
12							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [LLVGNKSDLTTK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.8	1288.7238	-0.0060	LLVGNKSDLTTK
10.0	1288.7139	0.0039	AFSKSSALTCHK
6.0	1288.7139	0.0039	RLDIFAQNLAK
6.0	1288.7139	0.0039	RLDIFAQNLAK
4.5	1286.7082	2.0097	VVVGDASESALLK
3.7	1286.7082	2.0097	LDLQEQTLCHK
3.7	1288.7173	0.0006	ITGANAKKEMVK
0.2	1287.7121	1.0057	GLGNKMKFLHK

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

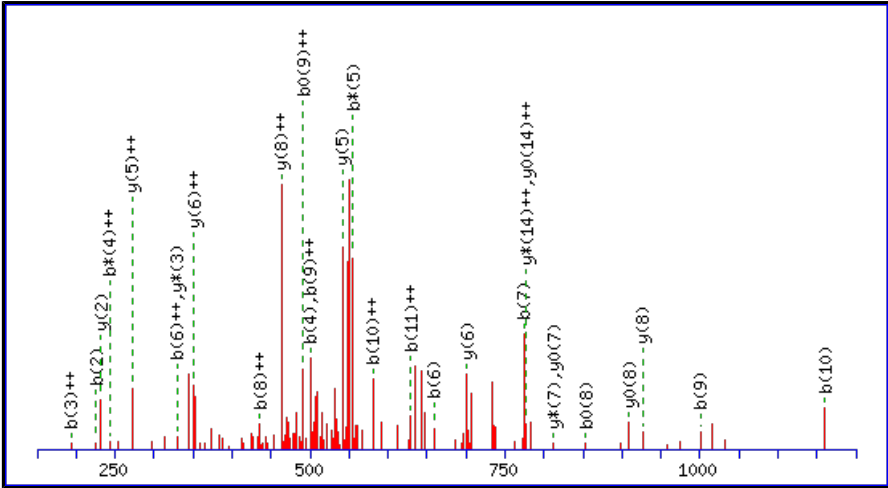
Peptide View

MS/MS Fragmentation of **KPCNASDPQCPPDGR**
Found in **F1S3Q8** in **uni_pig**, tr|F1S3Q8|F1S3Q8_PIG Uncharacterized protein OS=Sus scrofa GN=VNN3 PE=4 SV=2

Match to Query 5515: 1699.706862 from(567.576230,3+) intensity(468.0324) rtinseconds(654) scans(768) index(12354)
Title: 120326_Sunil_PigSerum_Glyco_SsetB_10Spectrum384_scans__768
Data file W:\\Documents\\NewmanPaper\\Sunil\\PigPlasmaGlyco\\mgf\\T120325_Sunil_PigSerum_Glyco_DSP_uni_pigPTM_2D.mgf

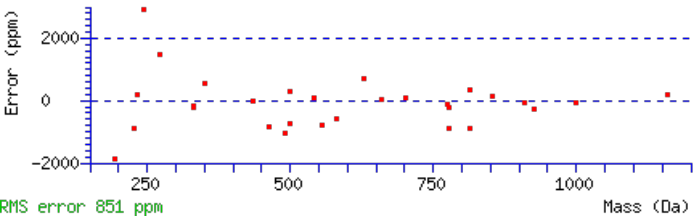
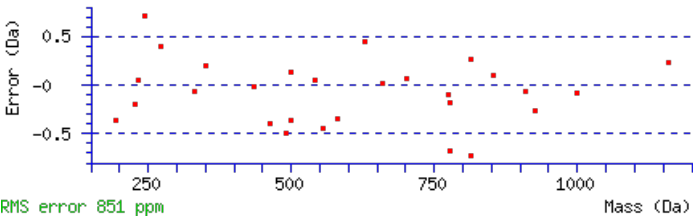
Click mouse within plot area to zoom in by factor of two about that point

Or, to Da
Label all possible matches ☐ Label matches used for scoring ☐
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1699.6930
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Q9 : Deamidated (NQ)
Ions Score: 24 Expect: 0.046
Matches : 29/154 fragment ions using 55 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							15
2	226.1550	113.5811	209.1285	105.0679			P	1572.6053	786.8063	1555.5788	778.2930	1554.5948	777.8010	14
3	386.1857	193.5965	369.1591	185.0832			C	1475.5526	738.2799	1458.5260	729.7666	1457.5420	729.2746	13
4	501.2126	251.1099	484.1860	242.5967			N	1315.5219	658.2646	1298.4954	649.7513	1297.5114	649.2593	12
5	572.2497	286.6285	555.2232	278.1152			A	1200.4950	600.7511	1183.4684	592.2379	1182.4844	591.7458	11
6	659.2817	330.1445	642.2552	321.6312	641.2712	321.1392	S	1129.4579	565.2326	1112.4313	556.7193	1111.4473	556.2273	10
7	774.3087	387.6580	757.2821	379.1447	756.2981	378.6527	D	1042.4258	521.7166	1025.3993	513.2033	1024.4153	512.7113	9
8	871.3614	436.1844	854.3349	427.6711	853.3509	427.1791	P	927.3989	464.2031	910.3723	455.6898	909.3883	455.1978	8
9	1000.4040	500.7057	983.3775	492.1924	982.3935	491.7004	Q	830.3461	415.6767	813.3196	407.1634	812.3356	406.6714	7
10	1160.4347	580.7210	1143.4081	572.2077	1142.4241	571.7157	C	701.3035	351.1554	684.2770	342.6421	683.2930	342.1501	6
11	1257.4875	629.2474	1240.4609	620.7341	1239.4769	620.2421	P	541.2729	271.1401	524.2463	262.6268	523.2623	262.1348	5
12	1354.5402	677.7737	1337.5137	669.2605	1336.5296	668.7685	P	444.2201	222.6137	427.1936	214.1004	426.2096	213.6084	4
13	1469.5672	735.2872	1452.5406	726.7739	1451.5566	726.2819	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
14	1526.5886	763.7979	1509.5621	755.2847	1508.5781	754.7927	G	232.1404	116.5738	215.1139	108.0606			2
15							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [KPCNASDPQCPPDGR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.4	1699.6930	0.0139	KPCNASDPQCPPDGR
22.5	1698.7090	0.9979	KPCNASDPQCPPDGR
21.5	1698.7090	0.9979	KPCNASDPQCPPDGR
2.0	1699.6970	0.0098	FLDYQMEHSNECK

Mascot: <http://www.matrixscience.com/>