Table S6. Human ion-trap, V8, SM

Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\2008/043008HCGSLoMWCOV8
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 77 **Hits:** 87
beginning to assemble proteins .... proteins assembled 0.00512 sec
proteins filtered by unique peptides 0.007613 sec
proteins filtered by score
calculated protein coverage maps 0.040138 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.005337 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptide 12 Proteins listed

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
1	36	31	476.16	20	2.23e+009	4502807	chromogranin B precursor
2	5	5	88.47	12	1.38e+009	4502805	chromogranin A precursor
3	4	3	49.51	40	1.43e+009	4505449	neuropeptide Y
4	3	3	40.98	5	8.41e+008	68160947	secretogranin II precursor
5	2	2	28.11	6	8.15e+008	5453876	proenkephalin
6	2	2	26.25	7	2.40e+008	7019519	proprotein convertase subtilisin/kexin type 1 inhibitor precursor
7	2	2	24.99	7	6.09e+008	4506917	secretory granule, neuroendocrine protein 1 (7B2 protein)
8	1	1	16.17	1	1.35e+008	113418115	PREDICTED: similar to eyes shut CG33955-PB
8	1	1	16.17	3	1.35e+008	113417557	PREDICTED: similar to eyes shut CG33955-PB
9	1	1	14.83	2	2.12e+008	4507817	UDP glucuronosyltransferase 2 family, polypeptide B10
10	1	1	14.18	2	2.49e+009	21389569	tektin 5
11	2	1	13.72	1	3.77e+010	156151430	armadillo repeat containing 9
12	1	1	13.33	3	3.44e+007	156602655	septin 3 isoform A
12	1	1	13.33	3	3.44e+007	156602653	septin 3 isoform B
Totals:	62	55					

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
1	36	31	476.16	20	2.23e+009	4502807	chromogranin B precursor

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH^+ Matched (Da)	MH^+ Mass Shift (Da)	MH^+ Error (ppm)
1	HCGSV8_043008_1.3475.3505.3	3	20.13	94.3	2.03e+009	423	(R)GGEPRAYFMSDTREE(K)	582.52	1744.760	0.7843	449.5
2	HCGSV8_043008_1.5596.5711.0	3	19.07	89.1	1.59e+010	521	(E)LFNPYYDPLQWKSSH(F)	632.56	1894.913	0.7515	396.6
3	HCGSV8_043008_1.2880.2880.0	3	18.77	82.2	3.82e+008	478	(E)GAPGKWQQQGDLQDTKE(N)	629.58	1885.904	0.8199	434.8
4	HCGSV8_043008_1.6224.6237.2	2	18.38	87.6	5.57e+008	521	(E)LFNPYYDPLQWKS(S)	836.11	1670.822	0.3903	233.6
5	HCGSV8_043008_1.4936.4936.2	2	18.14	85.2	1.34e+008	617	(K)SAEFPDFYDSEEPVSTHQE(A)	1107.89	2213.915	0.8571	387.1
6	HCGSV8_043008_1.7173.7188.3	3	18.05	87.2	1.35e+008	518	(R)LGELFNPYYDPLQWK(S)	628.75	1882.938	1.2964	688.5
7	HCGSV8_043008_1.5769.5769.2	2	17.31	75.0	3.38e+009	522	(L)FNPYYDPLQWKSSHFE(R)	1030.21	2057.940	1.4724	715.5
8	HCGSV8_043008_1.4705.4705.0	3	17.09	90.7	1.03e+008	602	(Y)DRVAQLDQLLH(Y)	436.97	1307.707	1.1872	907.8
9	HCGSV8_043008_1.6460.6467.0	3	16.97	86.8	7.09e+008	520	(G)ELFNPYYDPLQWKSSHFE(R)	767.97	2300.066	1.8279	794.7
10	HCGSV8_043008_1.5209.5275.0	3	16.96	85.1	6.14e+008	524	(N)PYYDPLQWKSSHFE(R)	599.90	1796.828	0.8559	476.3
11	HCGSV8_043008_1.5406.5406.2	2	16.94	85.8	5.12e+008	602	(Y)DRVAQLDQLL(H)	586.08	1170.648	0.5039	430.4
12	HCGSV8_043008_1.6333.6333.2	2	16.88	89.9	1.37e+009	521	(E)LFNPYYDPLQWK(S)	792.62	1583.790	0.4423	279.3
13	HCGSV8_043008_1.5575.5578.2	2	16.65	78.5	1.61e+009	522	(L)FNPYYDPLQWKSS(H)	823.22	1644.770	0.6623	402.7
14	HCGSV8_043008_1.2854.2854.2	2	16.45	84.7	1.82e+008	478	(E)GAPGKWQQQGDLQDTKE(N)	944.14	1885.904	1.3677	725.2
15	HCGSV8_043008_1.5548.5548.0	3	16.19	90.8	1.33e+008	602	(Y)DRVAQLDQLLHY(R)	491.05	1470.771	0.3638	247.4
16	HCGSV8_043008_1.3580.3580.2	2	16.04	90.3	2.37e+010	467	(E)LDRNYLNYGEE(G)	693.58	1385.634	0.5184	374.1
17	HCGSV8_043008_1.6200.6243.2	2	15.85	75.3	3.34e+009	521	(E)LFNPYYDPLQWKSSHFE(R)	1086.43	2171.024	0.8284	381.6
18	HCGSV8_043008_1.4942.4942.0	2	15.81	78.6	3.12e+007	619	(A)EFPDFYDSEEPVSTHQE(A)	1028.78	2055.846	0.7062	343.5
19	HCGSV8_043008_1.3844.3844.0	2	15.52	85.9	1.31e+008	602	(Y)DRVAQLDQL(L)	529.41	1057.564	0.2480	234.5
20	HCGSV8_043008_1.3805.3821.0	2	15.17	85.1	3.13e+008	466	(K)ELDRNYLNYGEE(G)	758.09	1514.676	0.4958	327.3
21	HCGSV8_043008_1.3457.3471.0	2	15.15	80.2	4.98e+008	467	(E)LDRNYLNYGE(E)	628.92	1256.591	0.2410	191.8
22	HCGSV8_043008_1.4994.4994.2	2	14.32	82.6	3.69e+007	617	(K)SAEFPDFYDSEEPVSTH(Q)	978.97	1956.814	0.1182	60.4
23	HCGSV8_043008_1.5789.5803.2	2	13.68	78.7	8.52e+008	522	(L)FNPYYDPLQWK(S)	736.07	1470.706	0.4264	289.9
24	HCGSV8_043008_1.5995.6111.2	2	13.30	72.6	1.97e+010	521	(E)LFNPYYDPLQWKSSHFE(R)	1086.60	2171.024	1.1684	538.2

25	HCGSV8_043008_1.5310.5310.2	2	13.01	80.3	3.27e+008	602	(Y)DRVAQLDQLL(H)	586.10	1170.648	0.5439	464.6
26	HCGSV8_043008_1.4157.4171.0	2	12.93	92.4	1.81e+008	40	(E)VLSNALSKSSAPPITPE(C)	856.22	1710.928	0.5044	294.8
27	HCGSV8_043008_1.5157.5157.1	1	12.31	80.2	9.49e+007	603	(D)RVAQLDQLL(H)	1055.81	1055.621	0.1887	178.8
28	HCGSV8_043008_1.4226.4226.2	2	12.30	78.3	7.24e+007	601	(Q)YDRVAQLDQL(L)	610.84	1220.628	0.0446	36.5
29	HCGSV8_043008_1.4934.4962.2	2	12.07	82.1	5.29e+007	525	(P)YYDPLQWKS(S)	600.37	1199.574	0.1585	132.1
30	HCGSV8_043008_1.7171.7220.0	2	12.04	77.3	3.01e+008	518	(R)LGELFNPYYDPLQWK(S)	942.36	1882.938	0.7742	411.2
31	HCGSV8_043008_1.3995.4028.0	2	11.99	86.4	3.27e+008	540	(R)DNMNDNFLE(G)	556.30	1111.437	0.1556	140.0
32	HCGSV8_043008_1.3688.3694.2	2	11.80	82.2	8.23e+008	467	(E)LDRNYLNYGEE(G)	693.41	1385.634	0.1784	128.7
33	HCGSV8_043008_1.4385.4385.2	2	11.46	79.0	2.77e+008	525	(P)YYDPLQWKSSH(F)	712.95	1423.665	1.2275	862.2
34	HCGSV8_043008_1.4973.4973.0	2	11.39	73.3	1.29e+008	588	(R)NLARVPKLDL(K)	570.16	1138.695	0.6174	542.2
35	HCGSV8_043008_1.4245.4245.2	2	11.38	95.0	2.32e+008	658	(E)NLAAMDLE(L)	438.76	876.414	0.0985	112.4
36	HCGSV8_043008_1.3368.3368.0	2	11.26	75.9	1.23e+009	588	(R)NLARVPKLD(L)	513.45	1025.611	0.2814	274.4

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
2	5	5	88.47	12	1.38e+009	4502805	chromogranin A precursor

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH^+ Matched (Da)	MH^+ Mass Shift (Da)	MH^+ Error (ppm)
1	HCGSV8_043008_1.3480.3484.0	3	18.51	87.1	5.21e+008	139	(E)AEKSGEATDGARPQALPEPMQE(S)	771.70	2312.083	1.0015	433.2
2	HCGSV8_043008_1.3607.3714.2	2	18.31	91.7	2.91e+009	145	(E)ATDGARPQALPEPMQE(S)	856.03	1710.812	0.2401	140.3
3	HCGSV8_043008_1.3255.3268.0	3	18.29	82.8	3.10e+009	180	(E)ATNTHPPASLPSQKYPGPQAE(G)	731.29	2191.078	0.7760	354.2
4	HCGSV8_043008_1.3249.3249.0	3	16.74	79.2	1.66e+008	183	(N)THPPASLPSQKYPGPQAE(G)	636.07	1904.951	1.2437	652.9
5	HCGSV8_043008_1.4713.4713.0	2	16.62	87.2	2.24e+008	405	(E)AGLPLQVRGYPE(E)	650.72	1299.706	0.7261	558.7

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
3	4	3	49.51	40	1.43e+009	4505449	neuropeptide Y

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH^+ Matched (Da)	MH^+ Mass Shift (Da)	MH^+ Error (ppm)
1	HCGSV8_043008_1.5338.5338.0	2	19.06	73.2	1.09e+008	72	(E)TLISDLLMRE(S)	595.17	1190.646	-1.3133	-1103.0
2	HCGSV8_043008_1.2449.2449.2	2	15.65	82.5	1.14e+009	29	(A)YPSKPDNPGEDAPAED(M)	851.87	1701.724	1.0078	592.2
3	HCGSV8_043008_1.4690.4690.2	2	14.80	77.1	4.27e+009	85	(E)NVPRTRLEDPAMW(-)	793.43	1584.796	1.0565	666.6
4	HCGSV8_043008_1.6498.6498.0	2	12.29	81.4	1.82e+008	72	(E)TLISDLLMRE(S)	596.35	1190.646	1.0467	879.1

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
4	3	3	40.98	5	8.41e+008	68160947	secretogranin II precursor

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH^+ Matched (Da)	MH^+ Mass Shift (Da)	MH^+ Error (ppm)
1	HCGSV8_043008_1.3375.3375.0	2	17.12	88.8	3.77e+008	232	(D)DIYKANNIAYE(D)	657.52	1313.638	0.3944	300.2
2	HCGSV8_043008_1.4491.4491.2	2	12.75	85.7	1.10e+009	243	(E)DVVGGEDWNPVEE(K)	722.93	1444.623	0.2289	158.4
3	HCGSV8_043008_1.5638.5638.2	2	11.11	98.4	1.05e+009	588	(E)DLLMKVLE(Y)	480.85	960.544	0.1482	154.3

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
5	2	2	28.11	6	8.15e+008	5453876	proenkephalin

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH^+ Matched (Da)	MH^+ Mass Shift (Da)	MH^+ Error (ppm)
1	HCGSV8_043008_1.4347.4347.2	2	15.98	95.6	5.76e+008	143	(K)DAEEDDSLANSSDLLKE(L)	926.69	1850.814	1.5578	841.7
2	HCGSV8_043008_1.4076.4169.0	2	12.13	84.2	1.05e+009	146	(E)EDDSLANSSDLLKE(L)	768.53	1535.708	0.3445	224.3

Distinct Mean

Group (#)	Spectra (#)	Distinct Peptides (#)	Summed MS/MS Search Score	% AA Coverage	Peptide Spectral Intensity	Database Accession #	Protein Name
6	2	2	26.25	7	2.40e+008	7019519	proprotein convertase subtilisin/kexin type 1 inhibitor precursor

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH+ Matched (Da)	MH+ Mass Shift (Da)	MH+ Error (ppm)
1	HCGSV8_043008_1.6245.6245.2	2	14.39	86.7	3.71e+008	221	(R)AADHDVGSELPPEGVLGAL(L)	924.15	1846.919	0.3735	202.2
2	HCGSV8_043008_1.4748.4752.0	2	11.86	71.3	1.09e+008	221	(R)AADHDVGSELPPEGVLGA(L)	867.71	1733.835	0.5776	333.1

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
7	2	2	24.99	7	6.09e+008	4506917	secretory granule, neuroendocrine protein 1 (7B2 protein)

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH+ Matched (Da)	MH+ Mass Shift (Da)	MH+ Error (ppm)
1	HCGSV8_043008_1.4812.4812.0	2	12.89	74.1	8.11e+008	181	(R)SVNPYLQGQRLDNVV(A)	851.99	1701.892	1.0798	634.5
2	HCGSV8_043008_1.3458.3467.0	2	12.10	80.8	4.08e+008	181	(R)SVNPYLQGQRLDN(V)	752.55	1503.756	0.3366	223.8

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
8	1	1	16.17	1	1.35e+008	113418115	PREDICTED: similar to eyes shut CG33955-PB

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH+ Matched (Da)	MH+ Mass Shift (Da)	MH+ Error (ppm)
1	HCGSV8_043008_1.5533.5539.3	3	16.17	81.1	1.35e+008	512	(G)STWHIIKAGRVGAEG(Y)	528.50	1581.850	1.6342	1033.1

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
9	1	1	14.83	2	2.12e+008	4507817	UDP glucuronosyltransferase 2 family, polypeptide B10

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH+ Matched (Da)	MH+ Mass Shift (Da)	MH+ Error (ppm)
1	HCGSV8_043008_1.4129.4129.2	2	14.83	87.0	2.12e+008	34	(S)LWMNMKTILKE(L)	704.04	1406.754	0.3182	226.2

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
10	1	1	14.18	2	2.49e+009	21389569	tektin 5

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH+ Matched (Da)	MH+ Mass Shift (Da)	MH+ Error (ppm)
1	HCGSV8_043008_1.5148.5148.2	2	14.18	79.5	2.49e+009	403	(P)NMELCRDIPQL(K)	666.59	1331.645	0.5270	395.8

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
11	2	1	13.72	1	3.77e+010	156151430	armadillo repeat containing 9

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH+ Matched (Da)	MH+ Mass Shift (Da)	MH+ Error (ppm)
1	HCGSV8_043008_1.6465.6465.2	2	13.72	93.8	2.90e+010	425	(E)EDKDIITRENVL(G)	723.15	1444.765	0.5274	365.0
2	HCGSV8_043008_1.6332.6351.2	2	11.92	89.4	4.64e+010	425	(E)EDKDIITRENVL(G)	723.13	1444.765	0.4874	337.4

Group (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Mean Peptide Spectral Intensity	Database Accession #	Protein Name
12	1	1	13.33	3	3.44e+007	156602655	septin 3 isoform A

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Start AA Position	Sequence	m/z Measured (Da)	MH^+ Matched (Da)	MH^+ Mass Shift (Da)	MH^+ Error (ppm)
1	HCGSV8_043008_1.2589.2595.2	2	13.33	85.7	3.44e+007	146	(Y)INEQYEKFLKEE(V)	785.32	1569.780	-0.1479	-94.2