

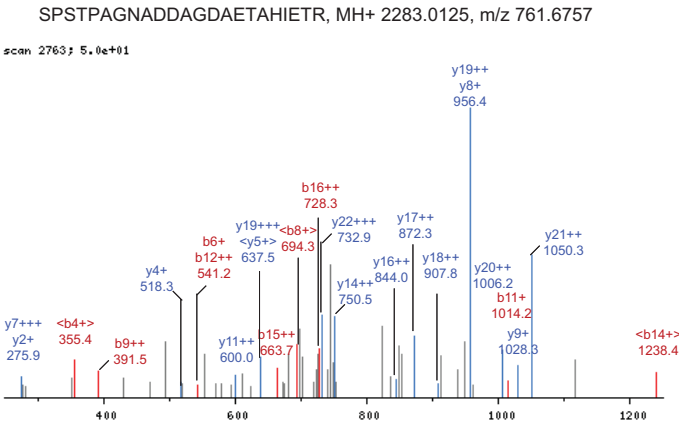
1. GvpH2 (GV fraction; delta mass = 0.0232 Da)

A

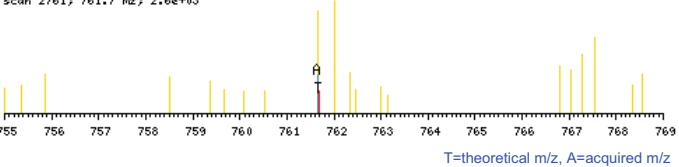
MPDDPSDRP SGLLDQLSRL IETLAELDDD NGEQHGHSIT DRGRTRIDYD YAVSIGLGSD
ARSPSTPAGN ADDAGDAETA HIETRASDDS DDLVVVADLP GVTDETAVDA AVEDTGALTI
SVGDDVVERL TLDDPGMTIT SLTVTNQILE LRVTPSEPSA TDT

Protein sequence coverage: 14.1%, MONO MW: 17096, pl: 3.84

B



D



C

b ⁺	b ²⁺	#	AA	#	y ⁺	y ²⁺	y ³⁺
88.0399	44.5238	1	S	23			
185.0926	93.0502	2	P	22	2195.9805	1098.4942	732.6654
272.1246	136.5662	3	S	21	2098.9277	1049.9678	700.3145
373.1723	187.0901	4	T	20	2011.8957	1006.4518	671.3038
470.2251	235.6165	5	P	19	1910.8480	955.9279	637.6212
541.2622	271.1350	6	A	18	1813.7953	907.4015	605.2703
598.2837	299.6457	7	G	17	1742.7582	871.8830	581.5913
712.3266	356.6672	8	N	16	1685.7367	843.3723	562.5841
783.3637	392.1858	9	A	15	1571.6938	786.3508	524.5698
898.3906	449.6992	10	D	14	1500.6567	750.8322	500.8908
1013.4176	507.2127	11	D	13	1385.6297	693.3188	462.5485
1084.4547	542.7313	12	A	12	1270.6028	635.8053	424.2061
1141.4762	571.2420	13	G	11	1199.5657	600.2867	400.5271
1256.5031	628.7555	14	D	10	1142.5442	571.7760	381.5199
1327.5402	664.2740	15	A	9	1027.5172	514.2625	343.1776
1456.5828	728.7953	16	E	8	956.4801	478.7440	319.4986
1557.6305	779.3192	17	T	7	827.4375	414.2227	276.4844
1628.6676	814.8377	18	A	6	726.3899	363.6988	242.8018
1765.7265	883.3672	19	H	5	655.3527	328.1803	219.1228
1878.8106	939.9092	20	I	4	518.2938	259.6508	173.4365
2007.8532	1004.4305	21	E	3	405.2098	203.1088	135.7418
2108.9009	1054.9543	22	T	2	276.1672	138.5875	92.7276
		23	R	1	175.1195	88.0637	59.0451

E

#	Rank/Sp	(M+H) ⁺	deltCn	XCorr	Expect	Ions	Reference	Peptide
1.	1 / 1	2283.0120	0.0000	1.7669	0.6612	26/88	GVPH2_HALSA	R. SPSTPAGNADDAGDAETAHIETR .A
2.	2 / 7	2284.2547	0.1254	1.5454	2.5724	22/84	DECOY_2417	S. LAPLKNANILEAITQVFGDISG .D
3.	3 / 4	2283.1364	0.2263	1.3671	7.6800	22/88	DECOY_2331	D. AREALAGLVSNGYETLGHAPGEA .T
4.	4 / 57	2281.1419	0.2284	1.3634	7.8553	20/84	DECOY_1665	Q. ESLVPDRGTGSSLRTAGNSAVY .A
5.	5 /201	2285.0057	0.2301	1.3604	8.0014	18/88	DECOY_679	A. EVGPM*SAAAGAARDSTM*MGADTR .I
6.	6 /201	2285.0057	0.2441	1.3356	9.3153	18/88	DECOY_679	A. EVGPM*SAAAGAARDSTM*MGADTR .I
7.	7 /320	2284.1779	0.2524	1.3210	10.1882	19/88	Q9HHY8_HALSA	S. LAAKLNNESSTGISVPHTGLSTS .K
8.	8 / 63	2284.0601	0.2888	1.2566	15.1173	18/72	Q9HRD1_HALSA	Y. EQPRQLFEENGAM*TYNVLE .R
9.	9 /110	2282.2040	0.2891	1.2561	15.1688	19/84	Q9HNK7_HALSA	R. GVAPRRSFAAAGFDVTLVPVDH .P
10.	10 /157	2283.9757	0.3105	1.2182	19.1386	18/80	DECOY_1899	T. SDAAFSQAGDNPHMDTRMGly .S

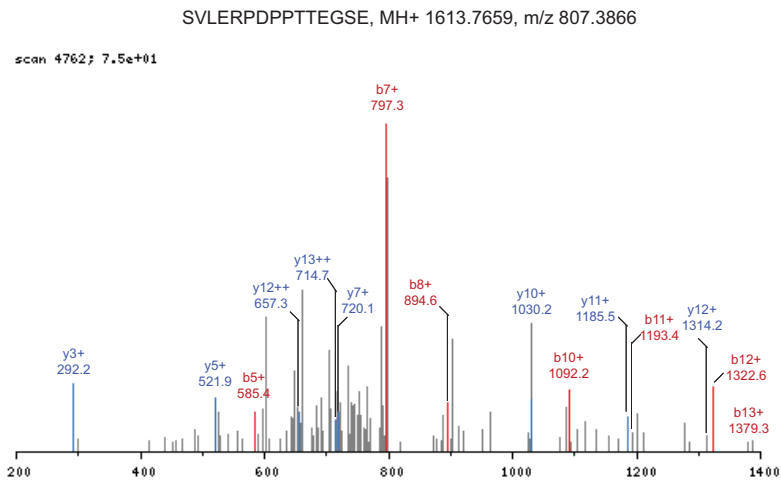
2. GvpJ2 (GV fraction; delta mass = 0.0157 Da)

A

MSDKPKPTRSQ GDLAETLELL LDKGVVNAD IAVSVGDEL LGVELRAAIA SFETAAEYGL
DFPTGTDMER VTAAAGVDAD DSKSVLERPD PPTTEGSE

Protein sequence coverage: 28.6%, MONO MW: 10202, pl: 4.00

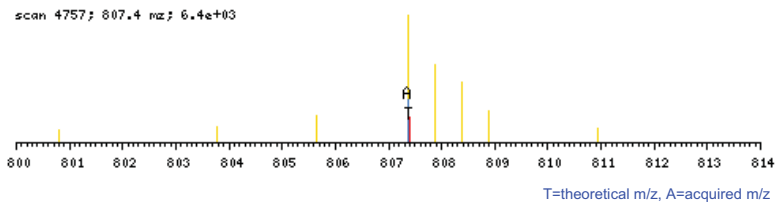
B



C

b ⁺	#	AA	#	y ⁺	y ²⁺
88.0399	1	S	15		
187.1083	2	V	14	1526.7338	763.8708
300.1923	3	L	13	1427.6654	714.3366
429.2349	4	E	12	1314.5814	657.7946
585.3360	5	R	11	1185.5388	593.2733
682.3888	6	P	10	1029.4377	515.2227
797.4157	7	D	9	932.3849	466.6964
894.4685	8	P	8	817.3580	409.1829
991.5213	9	P	7	720.3052	360.6565
1092.5689	10	T	6	623.2524	312.1301
1193.6166	11	T	5	522.2047	261.6063
1322.6592	12	E	4	421.1571	211.0824
1379.6807	13	G	3	292.1145	146.5611
1466.7127	14	S	2	235.0930	118.0504
	15	E	1	148.0610	74.5344

D



E

#	Rank/Sp	(M+H) ⁺	deltCn	XCorr	Expect	Ions	Reference	Peptide
1.	1 / 1	1613.7653	0.0000	2.1497	0.0299	13/28	GVPJ2_HALSA	K. SVLERPDPPTTEGSE .-
2.	2 / 25	1614.8311	0.1673	1.7900	0.3085	11/28	DECOY_134	D. RTRAVHMAVATKCGC .T
3.	3 / 11	1615.8075	0.3037	1.4969	2.0688	12/28	DECOY_1471	Y. ERGDAFLKIGNDSPP .N
4.	4 / 137	1615.7751	0.3273	1.4461	2.8785	8/26	DECOY_483	S. PSDAPIESPHYQFK .N
5.	5 / 13	1615.8398	0.3308	1.4386	3.0221	11/30	DECOY_138	V. VDAADLRGRADALTTA .E
6.	6 / 288	1614.8823	0.3541	1.3885	4.1833	9/28	DECOY_416	D. AHLVTPGVRVRHDSA .D
7.	7 / 21	1612.7489	0.3687	1.3572	5.1271	12/30	DECOY_463	L. GVAALYDAFGDLQTGD .P
8.	8 / 38	1614.7857	0.3836	1.3251	6.3130	11/30	Q9HQP5_HALSA	G. EATLAVPDTDDNVVGV .G
9.	9 / 41	1615.8424	0.3849	1.3224	6.4273	13/30	DECOY_1241	P. GPM*RARGVAFAAPGEI .V
10.	10 / 60	1612.8177	0.3888	1.3140	6.7858	11/30	DECOY_2109	S. EPALSVLPTGARESDA .V

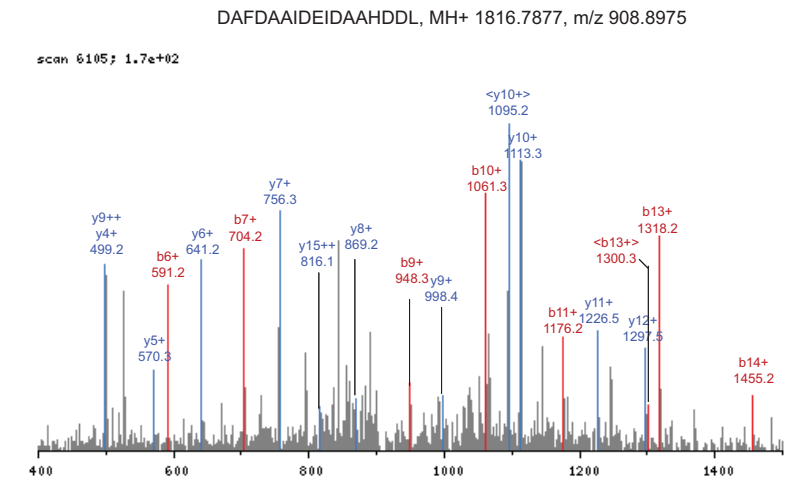
3. GvpF2 (GVD fraction; delta mass = -1.0055 Da)

A

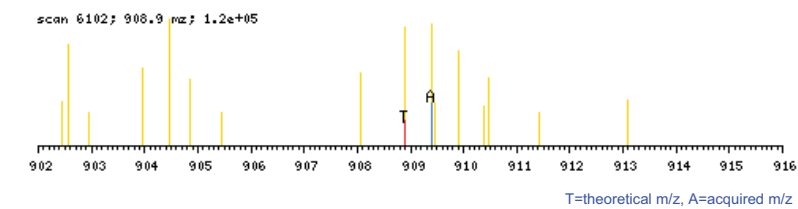
MSESHLYTYG IIDDNESLAL NVDGVAGATR AYTVSYSRLS AVVSDIETTD PERTDAAVEA HNTVLQAVLE
HDATRAVVP SFGMAFKNAR TLKGVLRGAR RALRSTLTEI AGTVELGVKV LAPGDDTAVD TAAVRSDVTA
RLSALSVGET ENDCFTDRLI INKSYLVEHD TRDAFDAAID EIDAAHDDL T VRYTGPWPPY NFVDIHIGAE
QAQQGGR

Protein sequence coverage: 7.8%, MONO MW: 23384, pl: 4.65

B



D



C

b ⁺	#	AA	#	y ⁺	y ²⁺
116.0348	1	D	17		
187.0719	2	A	16	1701.7608	851.3843
334.1403	3	F	15	1630.7237	815.8657
449.1672	4	D	14	1483.6553	742.3315
520.2044	5	A	13	1368.6283	684.8181
591.2415	6	A	12	1297.5912	649.2995
704.3255	7	I	11	1226.5541	613.7810
819.3525	8	D	10	1113.4700	557.2389
948.3951	9	E	9	998.4431	499.7255
1061.4791	10	I	8	869.4005	435.2042
1176.5061	11	D	7	756.3164	378.6621
1247.5432	12	A	6	641.2895	321.1487
1318.5803	13	A	5	570.2524	285.6301
1455.6392	14	H	4	499.2153	250.1115
1570.6662	15	D	3	362.1563	181.5821
1685.6931	16	D	2	247.1294	124.0686
	17	L	1	132.1025	66.5551

E

#	Rank/Sp	(M+H) ⁺	deltCn	XCorr	Expect	Ions	Reference	Peptide
1.	1 / 1	1816.7872	0.0000	4.7798	0.0001	23/32	GVPF2_HALSA	R. DAFDAAIDEIDAAHDDL .T
2.	2 /111	1817.7977	0.4686	2.5401	0.8148	12/32	O54605_HALSA	A. FEGDHAVVEEGFEANP .R
3.	3 / 34	1816.8712	0.4902	2.4367	1.2471	11/28	DECOY_457	E. SVFEEESLRQHVDE .R
4.	4 / 20	1817.9392	0.5333	2.2308	2.9102	13/32	DECOY_2137	H. FVSGEANPEVQSISRNV .W
5.	5 /244	1817.8148	0.5641	2.0837	5.3332	12/34	Q9HR29_HALSA	G. DEVAGVSVRAADQADGEE .-
6.	6 /124	1816.8684	0.5653	2.0777	5.4660	10/30	DECOY_433	H. LNADIDNM*LPIVNEET .D
7.	7 /104	1816.8937	0.5706	2.0522	6.0710	11/32	DECOY_429	E. EALRVAHGLNAADHEDV .G
8.	8 / 4	1817.8157	0.5811	2.0022	7.4600	15/30	DECOY_383	L. MTHEAREKEDALMEGA .L
9.	9 /250	1816.7229	0.5895	1.9623	8.7902	10/32	AROE_HALSA	G. M*DDPDTSPVSADALHDD .L
10.	10 /421	1815.9521	0.5915	1.9527	9.1435	9/30	DECOY_563	F. EIIDGIDSMREQLALI .Q

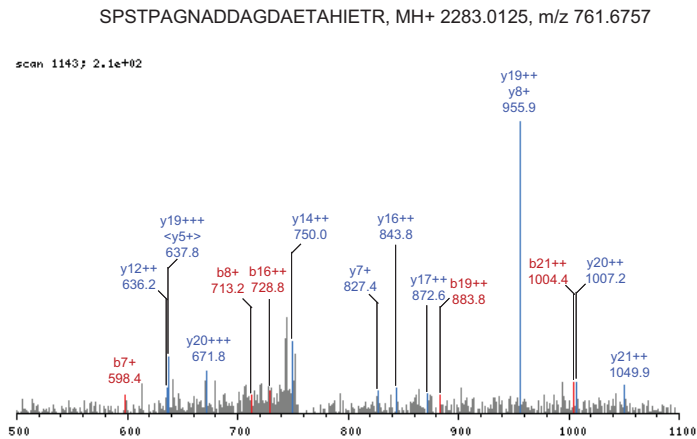
4. GvpH2 (GVD fraction; delta mass = -0.005 Da)

A

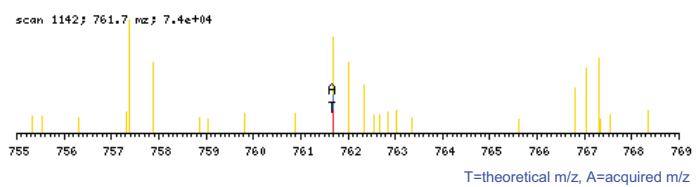
MPTDDPSDRP SGLLDQLSRL IETLAELDDD NGEQHGHSIT DRGRTRIDYD YAVSIGLGSD
ARSPSTPAGN ADDAGDAETA HIETRASDDS DDLVVADLP GVTDETAVDA AVEDTGALTI
SVGDDVVERL TLDDPGMTIT SLVTINQILE LRVTPSEPSA TDT

Protein sequence coverage: 14.1%, MONO MW: 17096, pl: 3.84

B



D



C

b ⁺	b ²⁺	#	AA	#	y ⁺	y ²⁺	y ³⁺
88.0399	44.5238	1	S	23			
185.0926	93.0502	2	P	22	2195.9805	1098.4942	732.6654
272.1246	136.5662	3	S	21	2098.9277	1049.9678	700.3145
373.1723	187.0901	4	T	20	2011.8957	1006.4518	671.3038
470.2251	235.6165	5	P	19	1910.8480	955.9279	637.6212
541.2622	271.1350	6	A	18	1813.7953	907.4015	605.2703
598.2837	299.6457	7	G	17	1742.7582	871.8830	581.5913
712.3266	356.6672	8	N	16	1685.7367	843.3723	562.5841
783.3637	392.1858	9	A	15	1571.6938	786.3508	524.5698
898.3906	449.6992	10	D	14	1500.6567	750.8322	500.8908
1013.4176	507.2127	11	D	13	1385.6297	693.3188	462.5485
1084.4547	542.7313	12	A	12	1270.6028	635.8053	424.2061
1141.4762	571.2420	13	G	11	1199.5657	600.2867	400.5271
1256.5031	628.7555	14	D	10	1142.5442	571.7760	381.5199
1327.5402	664.2740	15	A	9	1027.5172	514.2625	343.1776
1456.5828	728.7953	16	E	8	956.4801	478.7440	319.4986
1557.6305	779.3192	17	T	7	827.4375	414.2227	276.4844
1628.6676	814.8377	18	A	6	726.3899	363.6988	242.8018
1765.7265	883.3672	19	H	5	655.3527	328.1803	219.1228
1878.8106	939.9092	20	I	4	518.2938	259.6508	173.4365
2007.8532	1004.4305	21	E	3	405.2098	203.1088	135.7418
2108.9009	1054.9543	22	T	2	276.1672	138.5875	92.7276
		23	R	1	175.1195	88.0637	59.0451

E

#	Rank/Sp	(M+H) ⁺	deltCn	XCorr	Expect	Ions	Reference	Peptide
1.	1 / 1	2283.0120	0.0000	4.0211	0.0280	25/88	GVPH2_HALSA	R. SPSTPAGNADDAGDAETAHIETR .A
2.	2 / 7	2283.8122	0.3116	2.7682	1.9425	25/100	DNAK_HALSA	G. AGGMGGMGGM*ADGPGGAADADGDDEE .Y
3.	3 / 205	2283.0962	0.3344	2.6764	2.6499	18/80	DECOY_2015	D. ALTAMFDDYQDGLERLLGTP .T
4.	4 / 364	2283.1013	0.3575	2.5837	3.6272	17/76	RL5_HALSA	Q. EYDPNIGIYGM*DVTVNLTRP .G
5.	5 / 11	2283.8122	0.3599	2.5738	3.7502	24/100	DNAK_HALSA	G. AGGMGGM*GGMADGPGGAADADGDDEE .Y
6.	6 / 253	2284.1034	0.3711	2.5291	4.3633	18/84	DECOY_1251	I. LCM*PVGIGPTTNAGTFYLGDLA .T
7.	7 / 4	2284.1027	0.3859	2.4695	5.3374	21/76	DECOY_2004	L. DTRAMGNLFHKITSITDSNY .F
8.	8 / 53	2283.2832	0.4185	2.3383	8.3209	19/84	DECOY_1223	P. LAASQAPYVLQNALALLPM*VAL .V
9.	9 / 256	2282.3568	0.4496	2.2131	12.7085	17/80	Q9HRJO_HALSA	L. LRTPVVGTAVFNALVSRRLR .C
10.	10 / 489	2284.1264	0.4512	2.2068	12.9845	18/84	DECOY_1945	P. AASALRN*AHMTPAPELPAVGY .A

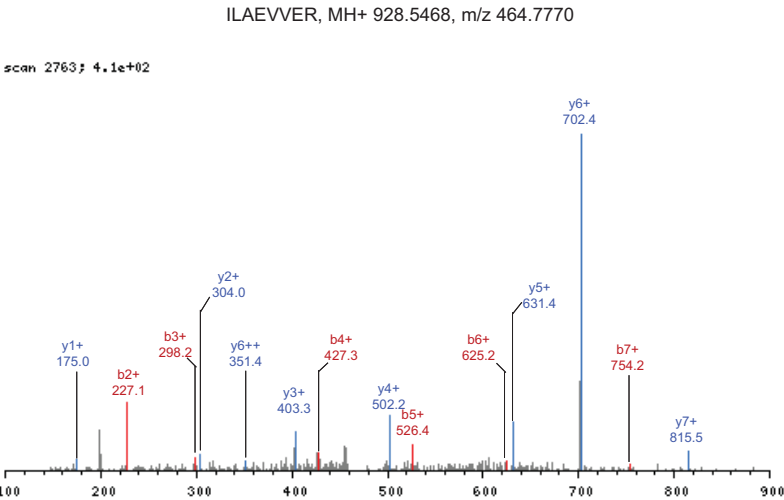
5. GvpO2 (GVD fraction; delta mass = 0.001 Da)

A

MDDPVADQPD GTDETPDGD T AGSSPIGLAD AQARAREAVA ELLEHPFDGI ITAESGADGG WR ILAEVVER
SAVPDTQDII GRYEITLDDG GRVTGYELRE RYRRGEMKEE L

Protein sequence coverage: 7.2%, MONO MW: 12010, pl: 4.15

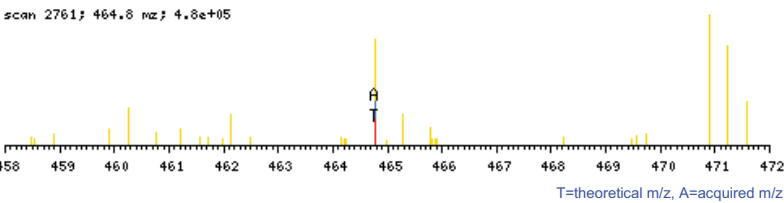
B



C

b ⁺	#	AA	#	y ⁺	y ²⁺
114.0919	1	I	8		
227.1760	2	L	7	815.4627	408.2353
298.2131	3	A	6	702.3786	351.6932
427.2557	4	E	5	631.3415	316.1747
526.3241	58	V	4	502.2989	251.6534
625.3925	6	V	3	403.2305	202.1192
754.4351	7	E	2	304.1621	152.5850
	8	R	1	175.1195	88.0637

D



E

#	Rank/Sp	(M+H) ⁺	deltCn	XCorr	Expect	Ions	Reference	Peptide
1.	1 / 1	928.5462	0.0000	2.7491	0.2081	13/14	GVPO2_HALSA	R. ILAEVVER .S
2.	2 /243	928.6077	0.2752	1.9924	5.3092	10/16	Q9HN44_HALSA	E. LLSVLVTAL .D
3.	3 /367	928.4734	0.3007	1.9225	7.1627	9/14	DECOY_393	V. EPIDLGER .L
4.	4 / 6	927.6237	0.3010	1.9217	7.1854	12/16	Q9HNS6_HALSA	M. LIKVVITAL .G
5.	5 /365	928.5826	0.3013	1.9208	7.2144	9/14	Q9HRZ5_HALSA	D. ILIALTER .T
6.	6 /234	928.5211	0.3117	1.8922	8.1531	11/18	DECOY_1580	L. LGGAVVAER .L
7.	7 /412	928.5687	0.3186	1.8732	8.8447	10/16	054596_HALSA	G. LGGSVLARR .G
8.	8 / 71	928.4986	0.3384	1.8189	11.1608	10/16	DECOY_2354	D. LLAETDVA .L
9.	9 /181	928.5574	0.3584	1.7637	14.1321	11/18	054662_HALSA	T. LLAGSALGAR .I
10.	10 /126	927.5370	0.3595	1.7607	14.3149	11/14	COFH_HALSA	A. IGRTPVER .S