

Spot Number	Treatment	Raw file / Mascot DAT File Names	Protein name	Protein accession numbers	Protein molecular weight (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage	Peptide sequence	Previous amino acid	Next amino acid	Best Peptide Identification probability	Best Mascot Ion score	Best Mascot Identity score	Best Mascot Tandem (logE)	Number of identified +1H	Number of identified +2H spectra	Number of identified +3H spectra	Number of identified +4H spectra	Number of enzymatic termini	Calculated Peptide Mass (AMU)	Peptide Index	Peptide stop index
1	TI	PN_Gase_S_1,RAW (F02471)	Catalase, hydroperoxidase HPI(1) precur	O6682_YERP	81350.9	98.70%	1	1	1	0.03%	1.09%	TDSEFLPK	K	S	95.00%	0	0	3.5	0	0	0	0	2	970.49	29	36
1	TI	PN_Gase_S_1,RAW (F02471)	Envelope glycoprotein (Fragment)	ORFLFM9_GHIV	97730.8	98.40%	1	1	1	0.03%	1.74%	LISGNTSTLTOACP	K	A	95.00%	43.9	50.6	3.8	0	1	0	0	2	1693.83	105	209
2	TI	PN_Gase_S_2,RAW (F02482)	Envelope glycoprotein (Fragment)	O11506_GHIV1	43969.8	99.60%	2	2	2	0.07%	3.79%	VVTFIEPLGVPATK	K	A	95.00%	44.2	47.2	4.54	0	1	0	0	2	1323.79	361	373
2	TI	PN_Gase_S_2,RAW (F02482)	Envelope glycoprotein (Fragment)	O11506_GHIV1	43969.8	98.70%	2	2	2	0.07%	3.79%	VVTFIEPLGVPATK	K	A	95.00%	44.2	50.1	5	0	1	0	0	2	1323.79	361	373
2	TI	PN_Gase_S_2,RAW (F02482)	Envelope glycoprotein (Fragment)	O11506_GHIV1	43969.8	99.60%	2	2	2	0.07%	3.79%	VVTFIEPLGVPATK	K	A	95.00%	34.3	44.4	4.26	0	1	0	0	2	1614.95	359	373
2	TI	PN_Gase_S_2,RAW (F02482)	Envelope glycoprotein (Fragment)	O11506_GHIV1	43969.8	98.70%	2	2	2	0.07%	3.79%	VVTFIEPLGVPATK	K	A	95.00%	34.3	50.3	3.96	0	1	0	0	2	1614.95	359	373
2	TI	PN_Gase_S_2,RAW (F02482)	Polymerase	OR8344_9PAR	252728.1	99.50%	2	3	3	0.10%	1.07%	LGTLWLR	R	G	95.00%	18.1	45.3	3.1	0	2	0	0	2	842.49	1318	1324
2	TI	PN_Gase_S_2,RAW (F02482)	Q77981_9HIV1	Q77981_9HIV1	60168.8	97.30%	1	1	1	0.03%	2.79%	LISGNTSTLTOACP	R	V	95.00%	89.4	47.2	9.14	0	1	0	0	2	1692.83	218	232
3	TI	PN_Gase_S_3,RAW (F02495)	Alkaline nucleosidase	Q817C3_9GAM	55998.9	99.40%	1	1	1	0.03%	2.27%	DVGSVLLK	R	V	93.80%	48.5	47.8	-0.301	0	1	0	0	2	1146.67	134	144
3	TI	PN_Gase_S_3,RAW (F02495)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	8	9	0.29%	9.52%	AMYPAPIEGIR	K	C	95.00%	77	50.5	7.42	0	1	0	0	2	1361.69	433	444
3	TI	PN_Gase_S_3,RAW (F02495)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	8	9	0.29%	9.52%	LISGNTSTLTOACP	R	I	95.00%	113	50.6	6.88	0	1	0	0	2	1691.85	198	212
3	TI	PN_Gase_S_3,RAW (F02495)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	8	9	0.29%	9.52%	VVTFIEPLGVPATK	K	A	95.00%	35.4	48.3	5.17	0	1	0	0	2	1323.79	490	502
3	TI	PN_Gase_S_3,RAW (F02495)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	8	9	0.29%	9.52%	VVTFIEPLGVPATK	K	A	95.00%	37	50.1	2.41	0	2	0	0	2	1614.95	498	502
4	TI	PN_Gase_S_4,RAW (F02501)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	11	11	0.33%	9.99%	AMYPAPIEGIR	K	C	95.00%	65.5	50.5	4.29	0	1	0	0	2	1345.69	433	444
4	TI	PN_Gase_S_4,RAW (F02501)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	11	11	0.33%	9.99%	VVTFIEPLGVPATK	K	A	95.00%	84.1	51.3	6.77	0	1	0	0	2	1676.84	122	135
4	TI	PN_Gase_S_4,RAW (F02501)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	11	11	0.33%	9.99%	VVTFIEPLGVPATK	K	A	95.00%	0	0	5.96	0	1	0	0	2	2235.26	490	499
4	TI	PN_Gase_S_4,RAW (F02501)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	11	11	0.33%	9.99%	VVTFIEPLGVPATK	K	A	95.00%	0	0	5.96	0	1	0	0	2	2235.26	483	502
4	TI	PN_Gase_S_4,RAW (F02501)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	11	11	0.33%	9.99%	VVTFIEPLGVPATK	K	A	95.00%	71.5	50.1	1.33	0	1	1	0	2	1323.79	487	499
4	TI	PN_Gase_S_4,RAW (F02501)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	11	11	0.33%	9.99%	VVTFIEPLGVPATK	K	A	95.00%	71.5	50.1	1.33	0	1	1	0	2	1323.79	490	502
4	TI	PN_Gase_S_4,RAW (F02501)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	11	11	0.33%	9.99%	VVTFIEPLGVPATK	K	A	95.00%	0	0	3.11	0	2	0	0	2	1614.95	495	499
4	TI	PN_Gase_S_4,RAW (F02501)	Envelope glycoprotein	O90295_9HIV1	97601.4	100.00%	7	11	11	0.33%	9.99%	VVTFIEPLGVPATK	K	A	95.00%	0	0	3.11	0	2	0	0	2	1614.95	488	502
5	TI	PN_Gase_S_5,RAW (F02505)	Catalase, hydroperoxidase HPI(1) precur	O6682_YERP	81350.9	97.00%	1	1	1	0.03%	1.90%	YDGGRGADGGQOR	R	F	92.00%	0	0	2.6	0	1	0	0	2	1449.68	110	123
5	TI	PN_Gase_S_5,RAW (F02505)	Envelope glycoprotein (Fragment)	O41567_9HIV1	97453.3	98.30%	2	2	2	0.07%	3.14%	AMYPAPIEGIR	R	C	95.00%	48	50.5	1.96	0	1	0	0	2	1361.69	434	445
5	TI	PN_Gase_S_5,RAW (F02505)	Envelope glycoprotein (Fragment)	O90296_9HIV1	97048.4	99.60%	2	4	4	0.13%	5.02%	DGGEDTDTNTEIFRRGGGGR	K	V	92.00%	72	51.5	0.268	0	1	0	0	2	2193.03	75	82
5	TI	PN_Gase_S_5,RAW (F02505)	Envelope glycoprotein (Fragment)	O90296_9HIV1	97453.3	98.90%	2	2	2	0.07%	3.14%	LISGNTSTLTOACP	R	V	80.60%	0	0	1.92	0	1	0	0	2	1693.83	199	213
5	TI	PN_Gase_S_5,RAW (F02505)	Envelope glycoprotein (Fragment)	O90296_9HIV1	97048.4	100.00%	3	4	4	0.13%	5.02%	QINMWWK	K	V	95.00%	39.6	48.7	2.54	0	1	0	0	2	1076.56	422	429
5	TI	PN_Gase_S_5,RAW (F02505)	Envelope glycoprotein (Fragment)	O90296_9HIV1	97048.4	100.00%	3	4	4	0.13%	5.02%	VVTFIEPLGVPATK	K	V	95.00%	73.7	50	7.26	0	1	1	0	2	1323.79	490	502
10	TI	PN_Gase_S_10,RAW (F06223)	Envelope glycoprotein	O90296_9HIV1	97856.6	98.10%	2	2	2	0.04%	98.9%	FFVALISGK	R	A	90.80%	37	49.2	0.208	0	1	0	0	2	1508.26	192	202
10	TI	PN_Gase_S_10,RAW (F06223)	Envelope glycoprotein	O90296_9HIV1	97856.6	98.10%	2	2	2	0.04%	98.9%	VVTFIEPLGVPATK	R	V	95.00%	89.2	51	10.4	0	1	0	0	2	1692.83	218	232
10	TI	PN_Gase_S_10,RAW (F06223)	Envelope glycoprotein (Fragment)	Q71247_9HIV1	25578.2	96.00%	1	1	1	0.02%	2.79%	PVNLQGLQGMVHOAISPR	R	V	92.80%	46.1	51	-0.255	0	1	0	0	2	2032.08	1	18
10	TI	PN_Gase_S_10,RAW (F06223)	Hsp70 protein (Fragment)	Q6G211_9GAM	63826.5	99.30%	2	3	3	0.05%	12.8%	YKQKLVK	K	I	95.00%	58.1	48	0	0	1	0	0	2	744.45	450	455
10	TI	PN_Gase_S_10,RAW (F06223)	Pol polyprotein (Fragment)	Q36977_9RET	138983.1	98.70%	1	1	1	0.02%	0.80%	AVSQRGVLR	K	E	95.00%	38.9	49.1	4.13	0	1	0	0	2	1088.6	770	779
10	TI	PN_Gase_S_10,RAW (F06223)	Protein	Q68515_BVDV	446070.5	98.80%	1	2	3	0.06%	0.40%	TITLEVPSDITNVK	R	A	95.00%	55.3	51.9	1.96	0	1	0	0	2	1787.93	1602	1617
11	TI	PN_Gase_S_11,RAW (F06269)	Actin (Fragment)	Q6S5L7_9MOL	22796.9	99.50%	2	3	3	0.27%	10.10%	ELTALAPSTMK	K	I	95.00%	0	0	4.16	0	1	0	0	2	1177.61	192	202
11	TI	PN_Gase_S_11,RAW (F06269)	Actin (Fragment)	Q6S5L7_9MOL	22796.9	99.50%	2	3	3	0.27%	10.10%	ELTALAPSTMK	K	I	95.00%	0	0	4.16	0	1	0	0	2	1177.61	192	202
11	TI	PN_Gase_S_11,RAW (F06269)	Gag protein	OS2528_9HIV1	55642.5	98.40%	1	3	3	0.27%	2.20%	MYPSPSSIDIR	R	Q	95.00%	38.9	50.5	1.59	0	3	0	0	2	1281.65	276	286
12	TI	PN_Gase_S_12,RAW (F06209)	Envelope glycoprotein	O90296_9HIV1	97048.4	98.30%	2	2	3	0.11%	5.02%	LISGNTSTLTOACP	R	V	95.00%	96.7	51	6.5	0	2	0	0	2	1692.83	218	232
13	TI	PN_Gase_S_13,RAW (F02599)	Gag polyprotein (Fragment)	Q5W3W5_9HIV	24868.3	97.20%	1	1	1	0.02%	8.07%	LHMLKQDITNEEAAEWRD	K	T	83.20%	63	51.3	0.553	0	1	0	0	2	2193.03	60	77
13	TI	PN_Gase_S_13,RAW (F02599)	Gag polyprotein (Fragment)	Q92084_9HIV1	181758.7	99.00%	1	4	4	0.04%	16.70%	LHPVHAGPAPGQMR	K	E	95.00%	30.8	50.1	4.29	0	1	0	0	2	1507.96	215	229
13	TI	PN_Gase_S_13,RAW (F02599)	Gp160 protein	QB8L60_9HIV1	97007.2	98.90%	1	1	1	0.02%	1.75%	GDPRPEWEEGEGGR	R	D	86.40%	40.5	50	2.75	0	1	0	0	2	1626.74	725	739
13	TI	PN_Gase_S_13,RAW (F02599)	Protein	Q5EG67_9POT	347514.5	98.50%	2	2	2	0.04%	0.82%	LYKGLSGLWNSLK	R	A	82.20%	0	0	2.01	0	1	0	0	2	1535.86	2434	2447
14	TI	PN_Gase_S_14,RAW (F02600)	Gag-polyprotein (Fragment)	Q90292_9HIV1	270933.7	99.00%	1	1	1	0.02%	8.67%	LHPVHAGPAPGQMR	R	V	95.00%	69.7	49.8	3.96	0	1	0	0	2	1508.26	192	202
14	TI	PN_Gase_S_14,RAW (F02600)	Polymerase	OR8344_9PAR	252728.1	100.00%	2	3	4	0.08%	0.85%	LGTLWLR	R	G	82.50%	0	0	1.96	1	1	0	0	2	842.49	1318	1324
15	TI	PN_Gase_S_15,RAW (F02602)	Gag polyprotein (Fragment)	Q5W3W5_9HIV	24868.3	99.50%	1	1	1	0.02%	11.70%	LHMLKQDITNEEAAEWRD	K	T	95.00%	54.1	51.7	0.824	0	2	0	0	2	2193.03	60	77
15	TI	PN_Gase_S_15,RAW (F02602)	Gag protein (Fragment)	Q673V1_9HIV1	56774.8	97.60%	1	2	2	0.04%	6.25%	ALGPAPALEEMTACGGVVK	K	A	95.00%	71.2	50.6	1.64	0	2	0	0	2	2413.13	341	364
15	TI	PN_Gase_S_15,RAW (F02602)	Gag protein (Fragment)	Q699A6_9HIV1	15732.3	99.00%																				

23	H9 PNase S_23_RAW (F029511)	Envelope glycoprotein (Fragment).	O11586_SHIV1	44992.5	99.30%	2	2	2	0.04%	6.20% CSSDTGLLTR	R	D	95.00%	52.5	50	4.92	0	1	0	0	2	1335.69	326	337
23	H9 PNase S_23_RAW (F029511)	Envelope glycoprotein (Fragment).	O90296_SHIV1	97048.4	100.00%	3	4	4	0.08%	6.07% DGGEDTDNDTEIFRRGGGCR	R	D	95.00%	69.9	51.5	3.19	0	1	0	0	2	2370.98	457	478
23	H9 PNase S_23_RAW (F029511)	Hydrophobic protein.	O81915_3CAU	29448.8	91.00%	1	1	1	0.00%	3.16% LKDAHLAK	L	D	95.00%	31.8	48.1	3.57	0	0	0	0	1	870.33	115	122
23	H9 PNase S_23_RAW (F029511)	Large T antigen.	O8JUDO_POJV	79254.1	98.00%	1	1	1	0.02%	1.31% CIVNLNPKL	K	R	95.00%	0	0	6.96	0	1	0	0	2	1084.66	412	420
23	H9 PNase S_23_RAW (F029511)	ORF1.	O6XZL4_RUBV	230674.8	97.00%	1	1	1	0.02%	0.61% DPPPLPPSPAPP	R	R	86.80%	0	0	2.06	0	1	0	0	2	1337.72	753	765
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein (Fragment).	O67002_SHIV1	95578.9	98.00%	1	1	1	0.02%	3.33% EATTLFCASDAK	K	S	95.00%	88.4	50.5	4.96	0	1	0	0	2	1414.65	54	66
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein (Fragment).	O77981_SHIV1	60168.8	97.70%	1	2	2	0.04%	5.21% EATTLFCASDAK	K	A	95.00%	88.4	50.5	4.96	0	1	0	0	2	1414.65	54	66
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein (Fragment).	O77981_SHIV1	60168.8	97.70%	1	2	2	0.04%	5.21% LISCDSVTIQAQCPK	R	V	95.00%	96.1	50.6	7.11	0	1	1	0	2	1692.83	218	232
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein (Fragment).	O97002_SHIV1	95578.9	98.90%	1	1	1	0.02%	3.32% YKVEIEERLGVAPTK	K	A	95.00%	46.6	50.1	2.96	0	1	0	0	2	1642.94	474	488
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein (Fragment).	O90296_SHIV1	97048.4	100.00%	4	5	5	0.09%	5.81% DGGEDTDNDTEIFRRGGGCR	R	D	95.00%	61.3	52.1	3.13	0	1	0	0	2	2258.03	457	478
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein.	O90295_SHIV1	97601.4	100.00%	4	5	5	0.09%	5.81% EATTLFCASDAK	K	A	95.00%	88.4	50.5	4.96	0	1	0	0	2	1414.65	46	58
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein.	O56567_SHIV1	96742.4	97.60%	1	1	1	0.02%	3.87% EATTLFCASDAK	K	A	95.00%	88.4	50.5	4.96	0	1	0	0	2	1414.65	46	58
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein.	O90295_SHIV1	97601.4	100.00%	4	5	5	0.09%	5.81% VVTIEPLGVAPTK	K	A	95.00%	17.6	50.1	3.57	0	1	0	0	2	1323.79	490	502
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein.	O90295_SHIV1	97601.4	100.00%	4	5	5	0.09%	5.81% YKVEIEERLGVAPTK	K	A	95.00%	46.6	50.1	3.43	0	1	0	0	2	1614.95	498	502
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein.	O90295_SHIV1	97601.4	100.00%	4	5	5	0.09%	5.81% EATTLFCASDAK	K	A	95.00%	88.4	50.5	4.96	0	1	0	0	2	1414.65	46	58
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein.	O90295_SHIV1	97601.4	100.00%	4	5	5	0.09%	5.81% LTPGLVLDCTDLR	K	N	95.00%	55.2	51.3	4.96	0	1	0	0	2	1676.84	121	134
24	H9 PNase S_24_RAW (F029514)	Envelope glycoprotein.	O90295_SHIV1	97601.4	100.00%	2	2	2	0.06%	8.77% VAEPSPPR	R	D	95.00%	0	0	2.52	0	1	0	0	2	842.44	117	124
25	H9 PNase S_25_RAW (F029515)	Envelope glycoprotein (Fragment).	O90296_SHIV1	97048.4	100.00%	5	6	7	0.13%	6.42% DGGEDTDNDTEIFRRGGGCR	R	D	95.00%	67.2	51.4	5.21	0	1	0	0	2	2370.98	457	478
25	H9 PNase S_25_RAW (F029515)	Envelope glycoprotein (Fragment).	O90296_SHIV1	97048.4	100.00%	5	6	7	0.13%	6.42% EATTLFCASDAK	K	A	95.00%	0	0	3.44	0	1	0	0	2	1414.65	46	58
25	H9 PNase S_25_RAW (F029515)	Envelope glycoprotein (Fragment).	O90296_SHIV1	97048.4	100.00%	5	6	7	0.13%	6.42% SELKYKVVITIEPLGVAPTK	R	A	86.80%	0	0	2.07	0	1	0	0	2	2235.26	483	502
25	H9 PNase S_25_RAW (F029515)	Envelope glycoprotein (Fragment).	O41627_SHIV1	46172.1	97.60%	1	1	1	0.02%	1.70% TIVMLK	K	E	94.00%	36.2	46.8	1.92	0	1	0	0	2	823.54	174	160
25	H9 PNase S_25_RAW (F029515)	Envelope glycoprotein (Fragment).	O90296_SHIV1	97048.4	100.00%	5	6	7	0.13%	6.42% VVTIEPLGVAPTK	K	A	95.00%	63.2	50.1	6.62	0	1	0	0	2	1323.79	490	502
25	H9 PNase S_25_RAW (F029515)	Envelope glycoprotein (Fragment).	O90296_SHIV1	97048.4	100.00%	5	6	7	0.13%	6.42% YKVVITIEPLGVAPTK	K	A	95.00%	42.7	50.3	4.01	0	2	0	0	2	1614.95	488	502
25	H9 PNase S_25_RAW (F029515)	Envelope glycoprotein.	O9W016_SHIV	37544.5	99.30%	2	2	2	0.04%	7.38% LISCDSVTIQAQCPK	R	V	95.00%	65.6	50.6	2.28	0	1	0	0	2	1692.83	65	79
25	H9 PNase S_25_RAW (F029515)	Envelope glycoprotein.	O9W016_SHIV	37544.5	99.30%	2	2	2	0.04%	7.38% NQTEVFRLLGK	R	-	86.80%	0	0	2.07	0	1	0	0	2	1040.54	330	339
25	H9 PNase S_25_RAW (F029515)	Gag protein (Fragment).	O699A6_SHIV1	15732.3	97.70%	1	1	1	0.02%	7.97% MYSPTSLDR	R	Q	95.00%	64.6	49.4	5	0	1	0	0	2	1297.65	7	17
25	H9 PNase S_25_RAW (F029515)	Hypothetical protein OSJNBa0090O10.	O8GXZ7_ORY2	20446.7	96.70%	1	1	1	0.02%	4.04% DAGSGVTR	A	R	90.20%	0	0	2.29	0	1	0	0	1	718.35	49	56
26	H9 PNase S_26_RAW (F029446)	Envelope glycoprotein.	O9W016_SHIV	37544.5	98.10%	1	1	1	0.02%	4.43% LISCDSVTIQAQCPK	R	V	95.00%	40.4	50.2	3.8	0	1	0	0	2	1692.83	65	79
26	H9 PNase S_26_RAW (F029446)	Envelope glycoprotein.	O6TAP1_SHIV1	97201.9	100.00%	3	3	3	0.06%	3.16% VFRFGGDMR	K	R	82.80%	0	0	1.92	0	1	0	0	2	1323.79	487	499
26	H9 PNase S_26_RAW (F029446)	Envelope glycoprotein.	O6TAP1_SHIV1	97201.9	100.00%	3	3	3	0.06%	3.16% YKVVITIEPLGVAPTK	K	A	95.00%	60.5	50.1	5	0	1	0	0	2	1323.79	487	499
26	H9 PNase S_26_RAW (F029446)	Envelope glycoprotein.	O6TAP1_SHIV1	97201.9	100.00%	3	3	3	0.06%	3.16% YKVVITIEPLGVAPTK	K	A	95.00%	46.9	50.1	2.88	0	1	0	0	2	1614.95	485	499
26	H9 PNase S_26_RAW (F029446)	Polyprotein (Fragment).	O98534_SPAK	257278.1	98.00%	1	1	1	0.02%	5.14% LKDAHLAK	L	D	95.00%	25	48	2.5	0	1	0	0	2	842.44	117	124
26	H9 PNase S_26_RAW (F029446)	Envelope glycoprotein (Fragment).	O6Y1M5_SHIV	89592.2	97.30%	1	1	1	0.02%	1.38% CSSDTGLLTR	R	D	93.00%	70.8	45.7	2.89	0	1	0	0	2	1335.69	363	474
26	H9 PNase S_26_RAW (F029446)	Putative tape-measure protein.	O9T1AT_BP411	186244.7	95.70%	1	1	1	0.02%	0.84% SGAKTAGGVISALK	K	G	81.80%	0	0	2.13	0	1	0	0	2	1387.79	285	299
29	H9 PNase S_29_RAW (F024697)	Hypothetical protein OSJNBa0090O10.	O8GXZ7_ORY2	20446.7	98.50%	1	1	1	0.02%	8.08% SCATGSRASASGTRRR	R	R	84.50%	0	0	2.3	0	1	0	0	2	1623.81	99	114
31	H9 PNase S_31_RAW (F024700)	Adp (Fragment).	O98534_SPAK	22796.9	98.00%	2	2	2	0.06%	1.89% GYSFTTAEK	R	E	95.00%	35.4	50.6	5.98	0	1	0	0	2	1153.23	263	268
32	H9 PNase S_32_RAW (F024700)	Gag protein (Fragment).	O9I0T5_SHIV1	25520.3	99.10%	1	1	1	0.02%	10.40% ALGPAATLEEMTACGGVIGK	A	A	95.00%	42.9	43	1.04	0	1	0	0	2	2429.13	204	227
32	H9 PNase S_32_RAW (F024700)	Gag-pol fusion polyprotein.	O92894_SHIV1	161758.7	97.90%	1	1	1	0.02%	1.67% ALGPAATLEEMTACGGVIGK	A	A	95.00%	54.3	43.7	1.92	0	1	0	0	2	2415.11	336	359
32	H9 PNase S_32_RAW (F024700)	Pestivirus type 1 cytopathic genomic RO11993_BVDV	O58885.1	98.50%	1	1	1	0.02%	0.18% ESTLHLVLR	K	L	87.70%	35.6	44.9	1.35	0	1	0	0	2	1067.62	2662	2670	
32	H9 PNase S_32_RAW (F024700)	Pestivirus type 1 cytopathic genomic RO11993_BVDV	O58885.1	98.50%	1	1	1	0.02%	0.18% TSLSDYNIKSTLHLVLR	R	L	95.00%	33.7	45.4	3.29	0	1	0	0	2	1076.59	119	127	
33	H9 PNase S_33_RAW (F006215)	Gene 12 protein.	O718G3_BPSF	46497.6	98.10%	1	1	1	0.02%	2.55% NSIGTLAAGAR	R	L	95.00%	0	0	2.29	0	1	0	0	2	1030.57	119	129
33	H9 PNase S_33_RAW (F006215)	Helicase.	O8S9NS_3CAU	14282.2	98.80%	1	1	1	0.02%	10.40% IDMLIVSLTKK	K	N	94.60%	41.1	50.3	1.2	0	1	0	0	2	1472.91	21	33
33	H9 PNase S_33_RAW (F006215)	RNA polymerase.	O33334_3CAU	217255.7	97.00%	1	1	1	0.02%	4.48% LKDAHLAK	L	N	95.00%	34.1	50	1.28	0	1	0	0	2	1029.55	302	318
33	H9 PNase S_33_RAW (F006215)	Pestivirus type 1 cytopathic genomic RO11993_BVDV	O58885.1	100.00%	2	4	5	0.11%	1.20% AKIQDKGIPPPDOOR	K	L	83.80%	0	0	1.77	0	1	0	0	2	1722.91	2622	2636	
33	H9 PNase S_33_RAW (F006215)	Pestivirus type 1 cytopathic genomic RO11993_BVDV	O58885.1	100.00%	2	4	5	0.11%	1.20% ESTLHLVLR	K	L	95.00%	67.4	48.9	-2.63	0	6	0	0	2	1067.62	2662	2670	
33	H9 PNase S_33_RAW (F006215)	Pestivirus type 1 cytopathic genomic RO11993_BVDV	O58885.1	100.00%	2	4	5	0.11%	1.20% IQDKEGIPPPDOOR	K	L	95.00%	49	51.1	1.48	0	8	7	0	2	1523.78	2624	2636	
33	H9 PNase S_33_RAW (F006215)	Pestivirus type 1 cytopathic genomic RO11993_BVDV	O58885.1	100.00%	2	4	5	0.11%	1.20% TSLSDYNIKSTLHLVLR	R	L	95.00%	45.1	48.5	0	0	4	0	0	2	1081.55	356	323	
33	H9 PNase S_33_RAW (F006215)	Pestivirus type 1 cytopathic genomic RO11993_BVDV	O58885.1	100.00%	2	4	5	0.11%	1.20% TSLSDYNIKSTLHLVLR	R	L	95.00%	0	0	3.52	0	1	0	0	2	2130.16	2653	2670	
33	H9 PNase S_33_RAW (F006215)	Polyprotein (Fragment).	O91N44_BVDV	62402.2	97.70%	1	2	4	0.09%	12.80% AKIQDKGIPPPDOOR	K	L	83.80%	0	0	1.77	0	1	0	0	2	1722.9		

Spot Number	Treatment	Raw file / Mascot DAT File Names	Protein name	Protein accession numbers	Protein molecular weight (Da)	Protein identification probability	Number of unique peptides	Number of spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage	Peptide sequence	Previous amino acid	Next amino acid	Best Peptide identification probability	Best Mascot Ion score	Best Mascot Ion score	Best X! Tandem log(e)	Number of identified +H1	Number of identified +H2	Number of identified +H3	Number of identified +H4	Number of enzymatic tryptic	Calculate Peptide Mass	Peptide start index	Peptide stop index
1	T1 PNGase	S_1.RAW (F025142)	beta actin	gi 30355057	41986.2	99.90%	3	4	4	0.13%	13.60% LDLAGRLDLYTLK	R	I	95.00%	41.9	41.4	2.24	0	0	0	0	0	2	1630.84	179	192
1	T1 PNGase	S_1.RAW (F025142)	beta actin	gi 30355057	41986.2	99.90%	3	4	4	0.13%	13.60% VAPEHDPILLTEAPLNK	R	I	88.50%	0	0	2.1	0	0	0	0	0	2	1954.07	97	114
1	T1 PNGase	S_1.RAW (F025142)	chaperonin containing TCP1, subunit 8 (theta)	gi 1136741.gi 31418053.gi	59633.1	99.90%	2	2	2	0.07%	3.83% EDGASITVLR	K	G	90.20%	35.2	42.1	1.28	0	1	0	0	0	2	1173.65	368	378
1	T1 PNGase	S_1.RAW (F025142)	chaperonin containing TCP1, subunit 8 (theta)	gi 1136741.gi 31418053.gi	59633.1	99.90%	2	2	2	0.07%	3.83% FAEAFEAAPR	K	A	95.00%	30.3	40.5	5.02	0	1	0	0	0	2	1150.59	441	450
1	T1 PNGase	S_1.RAW (F025142)	stimulator of TAR RNA binding	gi 1200184.gi 7682790	57908	99.90%	2	2	2	0.07%	4.27% IGLSVSEVIEGEGR	R	C	95.00%	40.0	0	2.82	0	0	1	0	0	2	1960.55	9	21
1	T1 PNGase	S_1.RAW (F025142)	stimulator of TAR RNA binding	gi 1200184.gi 7682790	57908	99.90%	2	2	2	0.07%	4.27% SHIDALCYR	R	C	95.00%	37.5	42.1	2.85	0	1	0	0	0	2	1183.63	404	413
2	T1 PNGase	S_2.RAW (F025143)	chaperonin containing TCP1, subunit 8 (theta)	gi 1136741.gi 31418053.gi	58485	100.00%	3	3	3	0.10%	6.68% AIADTGANVVTGGK	R	V	95.00%	10.7	42	7.6	0	1	0	0	0	2	1372.74	282	296
2	T1 PNGase	S_2.RAW (F025143)	chaperonin containing TCP1, subunit 8 (theta)	gi 1136741.gi 31418053.gi	58485	100.00%	3	3	3	0.10%	6.68% DIDEVSSLLR	R	T	95.00%	50.6	42.4	4	0	1	0	0	0	2	1146.6	156	165
2	T1 PNGase	S_2.RAW (F025143)	chaperonin containing TCP1, subunit 8 (theta)	gi 1136741.gi 31418053.gi	58485	100.00%	3	3	3	0.10%	6.68% DIDEVSSLLR	R	T	95.00%	66	41.8	2.02	0	1	0	0	0	2	1173.65	368	378
3	T1 PNGase	S_3.RAW (F025145)	chaperonin containing TCP1, subunit 5 (epsilon)	gi 12804225.gi 24307939.gi	59654.3	100.00%	5	5	5	0.15%	12.60% AVTIFR	R	G	95.00%	40.7	43.1	9	0	1	0	0	0	2	819.51	382	388
3	T1 PNGase	S_3.RAW (F025145)	chaperonin containing TCP1, subunit 5 (epsilon)	gi 12804225.gi 24307939.gi	59654.3	100.00%	5	5	5	0.15%	12.60% ENMFLGIDGLHK	R	G	89.20%	40.3	41.4	-0.672	0	1	0	0	0	2	1513.71	484	496
3	T1 PNGase	S_3.RAW (F025145)	chaperonin containing TCP1, subunit 5 (epsilon)	gi 12804225.gi 24307939.gi	59654.3	100.00%	5	5	5	0.15%	12.60% ISDVLVQDKDTPLQTK	K	T	95.00%	54.9	39.4	3.26	0	1	0	0	0	2	2185.2	151	170
3	T1 PNGase	S_3.RAW (F025145)	chaperonin containing TCP1, subunit 5 (epsilon)	gi 12804225.gi 24307939.gi	59654.3	100.00%	5	5	5	0.15%	12.60% LDVTSVDYD	K	A	95.00%	55	41.7	2.09	0	1	0	0	0	2	1168.57	286	275
3	T1 PNGase	S_3.RAW (F025145)	chaperonin containing TCP1, subunit 5 (epsilon)	gi 12804225.gi 24307939.gi	59654.3	100.00%	5	5	5	0.15%	12.60% QMAEIAVAVLTVADMER	R	R	95.00%	74	39	3.8	0	1	0	0	0	2	1992.97	184	201
3	T1 PNGase	S_3.RAW (F025145)	chaperonin containing TCP1, subunit 8 (theta)	gi 1136741.gi 40789055	58485	100.00%	4	4	4	0.12%	9.28% APFGAQMLK	K	E	95.00%	43.9	42.8	2.38	0	1	0	0	0	2	978.51	8	16
3	T1 PNGase	S_3.RAW (F025145)	chaperonin containing TCP1, subunit 8 (theta)	gi 1136741.gi 40789055	58485	100.00%	4	4	4	0.12%	9.28% IGLSVSEVIEGEGYIACR	R	K	95.00%	65	40.8	4.52	0	1	0	0	0	2	1894.96	121	137
3	T1 PNGase	S_3.RAW (F025145)	copine I	gi 23397704.gi 48145697.gi	59088.6	99.50%	2	2	2	0.06%	5.03% GTTIVSAQELK	R	D	95.00%	67.1	42.4	4.2	0	1	0	0	0	2	1146.64	125	135
3	T1 PNGase	S_3.RAW (F025145)	copine I	gi 23397704.gi 48145697.gi	59088.6	99.50%	2	2	2	0.06%	5.03% LYGFNFAPINHVAR	R	F	95.00%	42.3	40.2	1.6	0	1	0	0	0	2	1782.97	385	400
3	T1 PNGase	S_3.RAW (F025145)	dihydropyrimidinase-like 2 variant	gi 45501286	62276	100.00%	3	3	3	0.09%	6.29% GLVDYGPVCEVYTFK	R	T	95.00%	53.1	41.5	6.32	0	1	0	0	0	2	1620.8	497	511
3	T1 PNGase	S_3.RAW (F025145)	dihydropyrimidinase-like 2 variant	gi 45501286	62276	100.00%	3	3	3	0.09%	6.29% ILEVDGTHVTEGSSGR	K	Y	95.00%	33.3	41.2	2.96	0	1	0	0	0	2	1682.87	452	467
3	T1 PNGase	S_3.RAW (F025145)	ER-60 protease (Protein disulfide isomerase family A)	gi 1208427.gi 21361657.gi	56767.6	99.50%	2	2	2	0.06%	4.75% LAPEVEAATR	R	V	95.00%	86	42.7	2.64	0	1	0	0	0	2	1191.6	63	73
3	T1 PNGase	S_3.RAW (F025145)	ER-60 protease (Protein disulfide isomerase family A)	gi 1208427.gi 21361657.gi	56767.6	99.50%	2	2	2	0.06%	4.75% SEPFSNDQVPK	K	V	95.00%	50.5	42.3	3.25	0	1	0	0	0	2	1368.17	367	379
3	T1 PNGase	S_3.RAW (F025145)	Heterogeneous nuclear ribonucleoprotein K, isoform 1	gi 15292044.gi 460789.gi	50960.5	98.70%	2	2	2	0.06%	3.89% ILLDLSGAPQMLK	K	G	95.00%	65	40.8	4.52	0	1	0	0	0	2	1340.8	106	117
3	T1 PNGase	S_3.RAW (F025145)	Heterogeneous nuclear ribonucleoprotein K, isoform 2	gi 15292044.gi 460789.gi	50960.5	98.70%	2	2	2	0.06%	3.89% VYKEDKLLDSESPK	K	G	86.60%	38.6	40.7	-0.644	0	1	0	0	0	2	2012.17	207	219
4	T1 PNGase	S_4.RAW (F025146)	chaperonin containing TCP1, subunit 5 (epsilon)	gi 12804225.gi 24307939.gi	60918.7	100.00%	3	3	3	0.09%	9.04% ISDVLVQDKDTPLQTK	K	T	95.00%	49.1	38.9	4.92	0	1	0	0	0	2	2186.2	163	182
4	T1 PNGase	S_4.RAW (F025146)	chaperonin containing TCP1, subunit 5 (epsilon)	gi 12804225.gi 24307939.gi	60918.7	100.00%	3	3	3	0.09%	9.04% VYGGGAEISALASVDEAKR	K	N	95.00%	38.7	40.5	3.54	0	1	0	0	0	2	2195.07	430	451
4	T1 PNGase	S_4.RAW (F025146)	chaperonin containing TCP1, subunit 8 (theta)	gi 1136741.gi 31418053.gi	58485	100.00%	6	6	6	0.18%	17.40% AIADTGANVVTGGK	R	V	95.00%	110	41.5	6.08	0	1	0	0	0	2	1372.74	282	296
4	T1 PNGase	S_4.RAW (F025146)	chaperonin containing TCP1, subunit 8 (theta)	gi 1136741.gi 31418053.gi	58485	100.00%	6	6	6	0.18%	17.40% IGLSVSEVIEGEGYIACR	R	K	95.00%	37.9	40.1	3.77	0	1	0	0	0	2	1894.96	121	137
4	T1 PNGase	S_4.RAW (F025146)	copine I	gi 23397704.gi 48145697.gi	58485	100.00%	4	4	4	0.12%	8.82% DTVQFVYR	R	R	81.90%	74.6	39	1.27	0	1	0	0	0	2	1933.23	182	203
4	T1 PNGase	S_4.RAW (F025146)	copine I	gi 23397704.gi 48145697.gi	58485	100.00%	4	4	4	0.12%	8.82% DTVQFVYR	R	R	81.90%	62.5	40.7	1.07	0	1	0	0	0	2	1136.61	478	486
4	T1 PNGase	S_4.RAW (F025146)	copine I	gi 23397704.gi 48145697.gi	58485	100.00%	4	4	4	0.12%	8.82% GYDVIDMK	R	T	95.00%	35.5	41.5	2.62	0	1	0	0	0	2	1084.53	76	84
4	T1 PNGase	S_4.RAW (F025146)	copine I	gi 23397704.gi 48145697.gi	58485	100.00%	4	4	4	0.12%	8.82% LYGFNFAPINHVAR	R	F	95.00%	49.7	41.1	1.92	0	1	0	0	0	2	1782.97	385	400
4	T1 PNGase	S_4.RAW (F025146)	ER-60 protease (Protein disulfide isomerase family A)	gi 1208427.gi 21361657.gi	56767.6	100.00%	4	4	4	0.15%	10.50% LQYEFYFETVYK	R	A	83.90%	38	41.3	0	0	1	0	0	0	2	1654.88	81	93
4	T1 PNGase	S_4.RAW (F025146)	ER-60 protease (Protein disulfide isomerase family A)	gi 1208427.gi 21361657.gi	56767.6	100.00%	4	4	4	0.15%	10.50% FLDQYFDQNLK	R	Y	95.00%	45.3	41.6	0	0	1	0	0	0	2	1515.76	352	363
4	T1 PNGase	S_4.RAW (F025146)	ER-60 protease (Protein disulfide isomerase family A)	gi 1208427.gi 21361657.gi	56767.6	100.00%	4	4	4	0.15%	10.50% IFRDGEEAGVYDPR	K	T	95.00%	51.5	41.6	3.6	0	1	0	0	0	2	1652.77	105	119
4	T1 PNGase	S_4.RAW (F025146)	ER-60 protease (Protein disulfide isomerase family A)	gi 1208427.gi 21361657.gi	56767.6	100.00%	4	4	4	0.15%	10.50% LQYEFYFETVYK	K	A	95.00%	64.5	41.1	3.37	0	1	0	0	0	2	1937.72	461	476
4	T1 PNGase	S_4.RAW (F025146)	ER-60 protease (Protein disulfide isomerase family A)	gi 1208427.gi 21361657.gi	56767.6	100.00%	4	4	4	0.15%	10.50% MDATANDVPSPPYR	K	G	95.00%	0	0	8.64	0	2	0	0	0	2	1664.76	434	448
4	T1 PNGase	S_4.RAW (F025146)	T complex protein 1	gi 36796.gi 5786325.gi 57	4389	100.00%	3	3	3	0.09%	10.50% ICDDLELLK	R	N	95.00%	59	42.3	1.7	0	1	0	0	0	2	1233.66	201	210
4	T1 PNGase	S_4.RAW (F025146)	T complex protein 1	gi 36796.gi 5786325.gi 57	4389	100.00%	3	3	3	0.09%	10.50% ILATGANVLTGGIDMCLK	K	Y	95.00%	44.7	40.7	3.48	0	1	0	0	0	2	2192.13	123	143
4	T1 PNGase	S_4.RAW (F025146)	T complex protein 1	gi 36796.gi 5786325.gi 57	4389	100.00%	3	3	3	0.09%	10.50% ILATGANVLTGGIDMCLK	K	Y	95.00%	61.7	40.3	5.29	0	1	0	0	0	2	1231.65	106	156
5	T1 PNGase	S_5.RAW (F025147)	beta actin	gi 14250401	40987.9	99.90%	3	3	3	0.10%	10.90% LVDNDSGMCK	-	A	86.20%	0	0	1.89	0	0	1	0	0	2	1195.55	1	11
5	T1 PNGase	S_5.RAW (F025147)	beta actin	gi 14250401	40987.9	99.90%	3	3	3	0.10%	10.90% QEYDESGPSIVHR	K	K	95.00%	45.8	41.9	0.886	0	1	0	0	0	2	1516.7	353	365
5	T1 PNGase	S_5.RAW (F025147)	beta actin	gi 14250401	40987.9	99.90%	3	3	3	0.10%	10.90% SYELPQDQVITGNER	K	F	90.70%	22.5	41.2	2.66	0	1							

18	T1	PN	Gase	S.18.RAW (F025164)	Vmenin	gi 16552261.gi 21043084.g	53562.6	100.00%	3	3	3	0.06%	8.58%	FADLSEANRRNDLALR	K	Q	87.30%	0	0	1.92	0	0	1	0	0	2	1776.86	295	310	
19	T1	PN	Gase	S.19.RAW (F025165)	actin prepeptide	gi 178027.gi 178067.gi 383	41908.2	100.00%	4	4	5	0.10%	14.40%	AVFVPSIVGR	R	P	92.40%	41	0	2	0	2	0	0	0	0	2	945.55	30	38
19	T1	PN	Gase	S.19.RAW (F025165)	actin prepeptide	gi 178027.gi 178067.gi 383	41908.2	100.00%	4	4	5	0.10%	14.40%	ETALAPSTMK	K	I	95.00%	41	42	0.444	0	0	1	0	0	2	1171.61	96	113	
19	T1	PN	Gase	S.19.RAW (F025165)	actin prepeptide	gi 178027.gi 178067.gi 383	41908.2	100.00%	4	4	5	0.10%	14.40%	VAPEHFLLTLEAPLNK	R	A	95.00%	43.8	40.6	0.7	0	0	1	0	0	2	1956.05	97	114	
19	T1	PN	Gase	S.19.RAW (F025165)	Calpain, small subunit 1	gi 40674605	28212.6	100.00%	10	12	13	0.25%	18.70%	GGGGGGGGGGGGGGGGGGGTTG	I	I	87.30%	0	0	1.1	0	0	1	0	0	1	1771.85	38	60	
19	T1	PN	Gase	S.19.RAW (F025165)	Calpain, small subunit 1	gi 40674605	28212.6	100.00%	10	12	13	0.25%	18.70%	GGGGGGGGGGGGGGGGGGGTTG	I	I	92.70%	0	0	1.4	0	0	1	0	0	2	1742.26	39	60	
19	T1	PN	Gase	S.19.RAW (F025165)	Calpain, small subunit 1	gi 40674605	28212.6	100.00%	10	12	13	0.25%	18.70%	GGGGGGGGGGGGGGGGGGTAMG	I	I	85.00%	0	0	2.08	0	0	1	0	0	1	1657.81	40	60	
19	T1	PN	Gase	S.19.RAW (F025165)	Calpain, small subunit 1	gi 40674605	28212.6	100.00%	10	12	13	0.25%	18.70%	GGGGGGGGGGGGGGGGGGTAMR	I	I	86.50%	0	0	1.07	0	0	1	0	0	1	1470.56	41	60	
19	T1	PN	Gase	S.19.RAW (F025165)	Calpain, small subunit 1	gi 40674605	28212.6	100.00%	10	12	13	0.25%	18.70%	GGGGGGGGGGGGGGGGGGTAMR	G	I	95.00%	0	0	2.09	0	0	2	0	0	1	1333.57	42	60	
19	T1	PN	Gase	S.19.RAW (F025165)	Calpain, small subunit 1	gi 40674605	28212.6	100.00%	10	12	13	0.25%	18.70%	GGGGGGGGGGGGGGGGGGTAMR	G	I	89.70%	0	0	1.11	0	0	1	0	0	1	1276.55	43	60	
19	T1	PN	Gase	S.19.RAW (F025165)	Calpain, small subunit 1	gi 40674605	28212.6	100.00%	10	12	13	0.25%	18.70%	GGGGGGGGGGGGGGGGGGTAMR	G	I	95.00%	0	0	1.98	0	0	1	0	0	1	1162.5	45	60	
19	T1	PN	Gase	S.19.RAW (F025165)	Calpain, small subunit 1	gi 40674605	28212.6	100.00%	10	12	13	0.25%	18.70%	GGGGGGGGGGGGGGGGGGTAMR	G	I	87.20%	0	0	1.09	0	0	1	0	0	1	1596.81	10	32	
19	T1	PN	Gase	S.19.RAW (F025165)	Calpain, small subunit 1	gi 40674605	28212.6	100.00%	10	12	13	0.25%	18.70%	GGGGGGGGGGGGGGGGGGTAMR	G	I	90.40%	0	0	1.24	0	0	1	0	0	1	1064.45	47	60	
19	T1	PN	Gase	S.19.RAW (F025165)	c-Myc-responsive protein Rcl	gi 40354201.gi 5454002	16169.4	99.50%	2	2	2	0.04%	21.60%	TEHVAALGKLR	R	G	95.00%	77	39	6	3.26	0	0	1	0	0	2	1741.92	49	85
19	T1	PN	Gase	S.19.RAW (F025165)	c-Myc-responsive protein Rcl	gi 40354201.gi 5454002	16169.4	99.50%	2	2	2	0.04%	21.60%	GEPRPALVFCOSR	R	G	89.80%	32.5	39.9	0.824	0	0	1	0	0	1	2	1679.83	16	30
19	T1	PN	Gase	S.19.RAW (F025165)	eukaryotic initiation factor 5A	gi 89031353	25721.4	100.00%	4	4	4	0.08%	21.40%	KYEDPCPTHMMDVSNIK	K	R	95.00%	75.4	40.7	3.92	0	0	1	0	0	2	2177	152	169	
19	T1	PN	Gase	S.19.RAW (F025165)	eukaryotic initiation factor 5A	gi 89031353	25721.4	100.00%	4	4	4	0.08%	21.40%	LVKQIDFTTK	K	K	95.00%	40.6	41.9	3.11	0	0	0	0	0	2	1298.75	140	151	
19	T1	PN	Gase	S.19.RAW (F025165)	Plasminogen [Homo sapiens]	gi 38051823	90565.4	99.70%	2	2	2	0.04%	2.59%	LESPADITDK	K	V	95.00%	39.8	42.7	0.959	0	0	1	0	0	0	2	1046.54	671	680
19	T1	PN	Gase	S.19.RAW (F025165)	Titin	gi 17066105.gi 50659088	3815862.5	100.00%	4	4	4	0.08%	0.17%	GDQAQVTCYASNIAGK	K	D	80.10%	0	0	0.886	0	0	1	0	0	0	2	1618.72	8204	8219
19	T1	PN	Gase	S.19.RAW (F025165)	Titin	gi 17066105.gi 50659088	3815862.5	100.00%	4	4	4	0.08%	0.17%	VGLEATSVPGTKVPEDK	K	L	92.00%	0	0	1.35	0	0	1	0	0	1	2	1783.94	24268	24945
20	T1	PN	Gase	S.20.RAW (F025166)	polyubiquitin C	gi 13569612	16157.7	100.00%	3	4	4	0.08%	33.30%	IQZKGGGGPPDQR	K	L	95.00%	62.9	41.6	3.02	0	0	1	0	0	2	1523.76	43	55	
20	T1	PN	Gase	S.20.RAW (F025166)	polyubiquitin C	gi 13569612	16157.7	100.00%	3	4	4	0.08%	33.30%	TITLEVPSDITNKK	K	A	95.00%	69.4	41.6	6.72	0	0	1	0	0	0	2	1787.93	25	40
20	T1	PN	Gase	S.20.RAW (F025166)	polyubiquitin C	gi 13569612	16157.7	100.00%	3	4	4	0.08%	33.30%	TLSDYNIKKESTLHLVLR	R	L	95.00%	61.1	40.6	2.6	0	0	1	0	0	0	2	2130.16	68	85
20	T1	PN	Gase	S.20.RAW (F025166)	serum albumin	gi 28590	69277.9	99.50%	2	2	2	0.04%	3.61%	KVPEVSTPLTVEVSR	K	N	95.00%	0	0	4.64	0	0	1	0	0	0	2	1640.92	438	452
20	T1	PN	Gase	S.20.RAW (F025166)	serum albumin	gi 28590	69277.9	99.50%	2	2	2	0.04%	3.61%	YLYEAKR	K	R	92.30%	40.4	41.9	0.796	0	0	1	0	0	0	2	927.49	162	168
21	H9	PN	Gase	S.21.RAW (F025168)	beta actin	gi 14250401.gi 15277503.g	41719.8	99.70%	2	3	3	0.06%	14.70%	MKEITALAPSTMK	K	I	95.00%	33.4	40.8	1.96	0	0	1	0	0	0	2	1580.8	313	326
21	H9	PN	Gase	S.21.RAW (F025168)	beta actin	gi 14250401.gi 15277503.g	41719.8	99.70%	2	3	3	0.06%	14.70%	RIGLTK	K	Y	95.00%	38	42.7	1.72	0	0	1	0	0	0	2	800.54	62	68
21	H9	PN	Gase	S.21.RAW (F025168)	beta actin	gi 14250401.gi 15277503.g	41719.8	99.70%	2	3	3	0.06%	14.70%	SVELPDQVITGNER	K	F	95.00%	32.7	41.2	1.96	0	0	1	0	0	0	2	1790.89	239	254
21	H9	PN	Gase	S.21.RAW (F025168)	beta actin	gi 14250401.gi 15277503.g	41719.8	99.70%	2	3	3	0.06%	14.70%	VAPEHFLLTLEAPLNK	R	A	95.00%	40.6	40.8	0.67	0	0	1	0	0	0	2	1984.07	40	46
21	H9	PN	Gase	S.21.RAW (F025168)	chaperonin (HSP60)	gi 306890	61007.7	100.00%	7	8	8	0.16%	16.60%	AAVEGHLGGGALLLR	R	C	95.00%	52.4	41.1	2.96	0	0	0	0	0	0	2	1684.91	300	346
21	H9	PN	Gase	S.21.RAW (F025168)	chaperonin (HSP60)	gi 306890	61007.7	100.00%	7	8	8	0.16%	16.60%	CFEQDAVLLSEKK	R	I	94.90%	39.7	41.4	1.06	0	0	1	0	0	0	2	1729.85	237	250
21	H9	PN	Gase	S.21.RAW (F025168)	chaperonin (HSP60)	gi 306890	61007.7	100.00%	7	8	8	0.16%	16.60%	ISGQDQVPLAEVNAHR	R	A	95.00%	67.0	75	4.1	3.59	0	0	0	0	0	2	1916.07	257	260
21	H9	PN	Gase	S.21.RAW (F025168)	chaperonin (HSP60)	gi 306890	61007.7	100.00%	7	8	8	0.16%	16.60%	LKVGLOVAVK	K	A	84.50%	0	0	1.42	0	0	1	0	0	0	2	1153.77	291	301
21	H9	PN	Gase	S.21.RAW (F025168)	chaperonin (HSP60)	gi 306890	61007.7	100.00%	7	8	8	0.16%	16.60%	LSDGAVLK	K	V	87.80%	0	0	1.57	1	0	1	0	0	0	2	901.54	397	405
21	H9	PN	Gase	S.21.RAW (F025168)	chaperonin (HSP60)	gi 306890	61007.7	100.00%	7	8	8	0.16%	16.60%	TKLIPAMTIAR	R	N	86.00%	33.6	42.6	1.18	0	0	1	0	0	0	2	1186.72	471	481
21	H9	PN	Gase	S.21.RAW (F025168)	chaperonin (HSP60)	gi 306890	61007.7	100.00%	7	8	8	0.16%	16.60%	VGVEVTKDDMALLK	K	L	85.60%	43.6	40.7	5.22	0	0	0	0	0	0	2	1068.69	367	359
21	H9	PN	Gase	S.21.RAW (F025168)	serum albumin	gi 25058739	71866.9	100.00%	3	3	3	0.06%	5.90%	KVPOVSTPLTVEVSR	K	N	95.00%	60.7	40.1	0	0	0	1	0	0	0	2	1639.94	438	452
21	H9	PN	Gase	S.21.RAW (F025168)	serum albumin	gi 25058739	71866.9	100.00%	3	3	3	0.06%	5.90%	LVNVEVFAK	K	T	95.00%	67.3	42.2	4.42	0	0	1	0	0	0	2	1149.62	66	75
21	H9	PN	Gase	S.21.RAW (F025168)	serum albumin	gi 25058739	71866.9	100.00%	3	3	3	0.06%	5.90%	YKVDQDISISK	K	L	95.00%	67	41.8	5.39	0	0	1	0	0	0	2	1444.84	267	298
21	H9	PN	Gase	S.21.RAW (F025168)	similar to Prostate, ovary, testis expressed protein	gi 88953569.gi 88953569	107266.5	100.00%	2	2	2	0.04%	2.42%	SVELPDQVITGNER	K	F	95.00%	32.7	41.2	1.96	0	0	1	0	0	0	2	1793.89	816	817
22	H9	PN	Gase	S.22.RAW (F025169)	beta actin variant	gi 62897825	41747.9	100.00%	4	4	4	0.08%	11.50%	AVFVPSIVGR	R	P	91.60%	0	0	2.06	0	0	1	0	0	0	2	945.55	29	37
22	H9	PN	Gase	S.22.RAW (F025169)	beta actin variant	gi 62897825	41747.9	100.00%	4	4	4	0.08%	11.50%	ETALAPSTMK	K	I	95.00%	30.5	42.5	1.5	0	0	0	0	0	0	2	1171.61	96	113
22	H9	PN	Gase	S.22.RAW (F025169)	beta actin variant	gi 62897825	41747.9	100.00%	4	4	4	0.08%	11.50%	KOLYANTVLSGGTMYPIQADR	R	M	95.00%	53.5	40.1	1.18	0	0	0	0	0	0	2	2359.16	291	312
22	H9	PN	Gase	S.22.RAW (F025169)	beta actin variant	gi 62897825	41747.9	100.00%	4	4	4	0.08%	11.50%	KETALAPSTMK	R	I	83.50%	0	0	1.52	0	0	1	0	0	0	2	1305.71	313	326
22	H9	PN	Gase	S.22.RAW (F025169)	cytokeratin 2	gi 31074629.gi 7705545	65883.4	99.30%	2	2	2	0.04%	3.76%	FLEQGKIVLETK	R	W	95.00%	60.2	42	4.42	0	0	1	0	0	0	2	1476.81	203	214
22	H9	PN	Gase	S.22.RAW (F025169)	cytokeratin 2	gi 31074629.gi 7705545	65883.4	99.30%	2	2	2	0.04%	3.76%	GAAGAGVLETK	R	S	95.00%	60.2	42	4.42	0	0	1	0	0	0	2	1576.64	36	47
22	H9	PN	Gase	S.22.RAW (F025169)	glucose regulated protein 58kD (GRP58)	gi 27805905	56913.7	100.00%	4	4	4	0.08%	9.31%	DPNVIK	K	M	90.10%	43.1	41.7	-3.22	0	0	1	0	0	0	2	869.51	426	433
22	H9	PN	Gase	S.2																										

23	H9	PNGas5	S_23_RAW	(F025170)	serum albumin	gii11493459.gii178345.gi2	69207.8	100.00%	3	3	3	0.06%	5.58%	KVPOVSTPTLVEVSR	K	L	84.30%	32.8	39.8	1.15	0	0	1	0	0	2	1639.94	438	452
23	H9	PNGas5	S_23_RAW	(F025170)	serum albumin	gii11493459.gii178345.gi2	69207.8	100.00%	3	3	3	0.06%	5.58%	YICENQDSSISK	K	N	95.00%	42.3	41.8	5.68	0	1	0	0	0	2	1443.64	297	298
23	H9	PNGas5	S_23_RAW	(F025170)	serum albumin	gii11493459.gii178345.gi2	69207.8	100.00%	3	3	3	0.06%	5.58%	YICENQDSSISK	K	R	95.00%	48.4	41.9	1.6	0	1	0	0	0	2	1522.8	162	168
23	H9	PNGas5	S_23_RAW	(F025170)	vacuolar H-ATPase B2	gii13938355.gii19913428.g	55384.7	98.80%	2	2	2	0.04%	5.79%	AVVOVFQEGSDIADK	K	K	95.00%	77.3	40.8	9.07	0	1	0	0	0	2	1520.8	84	98
23	H9	PNGas5	S_23_RAW	(F025170)	vacuolar H-ATPase B2	gii13938355.gii19913428.g	55384.7	98.80%	2	2	2	0.04%	5.79%	Y9AEVHLPLDGTGK	R	R	91.80%	26.5	39.9	3.66	0	0	1	0	0	2	1556.83	58	71
24	H9	PNGas5	S_24_RAW	(F025171)	beta actin	gii63355057	41986.2	99.70%	2	2	2	0.04%	8.51%	VADEHPILLTEAPLNKR	R	I	95.00%	48.2	35.2	1.2	0	0	1	0	0	2	1954.07	179	114
24	H9	PNGas5	S_24_RAW	(F025171)	chaperonin containing TCP1, subunit 8 (beta)	gii1136741	58485	100.00%	3	3	3	0.06%	7.61%	AIDTGANVVTGGK	K	V	95.00%	116	40.6	1.34	0	0	1	0	0	2	1372.74	282	296
24	H9	PNGas5	S_24_RAW	(F025171)	chaperonin containing TCP1, subunit 8 (beta)	gii1136741	58485	100.00%	3	3	3	0.06%	7.61%	NIQAQKELATGR	R	T	95.00%	55.3	41	0.721	0	0	0	1	0	2	1532.79	32	44
24	H9	PNGas5	S_24_RAW	(F025171)	chaperonin containing TCP1, subunit 8 (beta)	gii1136741	58485	100.00%	3	3	3	0.06%	7.61%	NIQAQKELATGR	R	V	95.00%	35.6	41.1	7.02	0	0	0	1	0	2	1528.83	153	164
24	H9	PNGas5	S_24_RAW	(F025171)	copine 1	gii23397704.gii48145697	59088.6	99.90%	2	2	2	0.04%	5.59%	YGTIVYAEQDKDNR	R	V	95.00%	48	41.7	1.89	0	0	1	0	0	2	1531.81	125	138
24	H9	PNGas5	S_24_RAW	(F025171)	copine 1	gii23397704.gii48145697	59088.6	99.90%	2	2	2	0.04%	5.59%	LYGTNFAPIINHAVR	R	F	95.00%	55.3	41.8	1.96	0	0	0	1	0	2	1782.97	385	400
24	H9	PNGas5	S_24_RAW	(F025171)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	9	9	10	0.19%	21.60%	FEDKTVAYTEGK	K	M	95.00%	33.8	41.6	2.96	0	0	1	0	0	2	1458.71	215	226
24	H9	PNGas5	S_24_RAW	(F025171)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	9	9	10	0.19%	21.60%	LDAGHGLNFAVSR	K	K	95.00%	72.9	40.8	4.36	0	0	1	0	0	2	1645.89	290	304
24	H9	PNGas5	S_24_RAW	(F025171)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	9	9	10	0.19%	21.60%	FVMEEFPSR	K	D	95.00%	41	42.5	1.38	0	1	0	0	0	2	1188.54	336	344
24	H9	PNGas5	S_24_RAW	(F025171)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	9	9	10	0.19%	21.60%	IFRDGEEAGYDGGPR	K	T	94.20%	0	0	2.42	0	0	2	0	0	2	1652.77	105	119
24	H9	PNGas5	S_24_RAW	(F025171)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	9	9	10	0.19%	21.60%	LDAGHGLNFAVSR	K	V	95.00%	27.8	42.1	2.5	0	1	0	0	2	1308.64	74	82	
24	H9	PNGas5	S_24_RAW	(F025171)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	9	9	10	0.19%	21.60%	LSKDPNVIADK	K	M	92.50%	20.9	42.1	2.24	0	1	0	0	0	2	1197.72	423	433
24	H9	PNGas5	S_24_RAW	(F025171)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	9	9	10	0.19%	21.60%	QAQPASVPLRTEFFPKK	K	F	94.40%	0	0	2.44	0	0	1	0	0	2	1887	131	147
24	H9	PNGas5	S_24_RAW	(F025171)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	9	9	10	0.19%	21.60%	TADIVSHLKK	R	Q	93.50%	44.2	42.1	0.0809	0	0	0	1	0	2	1168.67	120	130
24	H9	PNGas5	S_24_RAW	(F025171)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	9	9	10	0.19%	21.60%	YGVSYGYPTLTK	K	I	95.00%	61.1	40.7	6	0	1	0	0	2	1084.57	95	104	
24	H9	PNGas5	S_24_RAW	(F025171)	integrin alpha-4 subunit	gii34190805.gii67191027	114883.8	99.70%	2	2	2	0.04%	3.68%	SQHTTEVGGAPQHQEIQK	R	A	95.00%	32.4	40.9	2.34	0	0	1	0	0	2	2003	262	280
24	H9	PNGas5	S_24_RAW	(F025171)	integrin alpha-4 subunit	gii34190805.gii67191027	114883.8	99.70%	2	2	2	0.04%	3.68%	TRPVVDASSLHSEPVNR	R	T	95.00%	57.1	40.7	6.82	0	0	1	0	0	2	2076.12	463	481
25	H9	PNGas5	S_25_RAW	(F025173)	cell division cycle 2-like 5 (cholesterase-relat)	gii1110387.gii14110390.gi	164910.6	99.50%	2	2	2	0.04%	1.26%	GQIKLADFLGAR	R	L	88.50%	29.3	40.6	1.59	0	0	1	0	0	2	1288.74	849	860
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	DPNVIADK	K	M	87.50%	40.1	41.7	0.102	1	0	0	0	0	2	869.51	426	433
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	ELSDSIFLOR	R	E	95.00%	0	0	3.25	0	1	0	0	0	2	1370.7	472	482
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	FLDAGHGLNFAVSR	K	K	95.00%	0	0	3.55	0	1	0	0	0	2	1645.88	290	304
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	FLDQVFDGKLR	K	R	95.00%	51.3	40.6	1	0	1	0	0	0	2	1515.76	352	363
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	FVMEEFPSR	K	D	95.00%	68.5	42.3	1.7	0	0	0	0	2	1172.54	161	174	
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	FVMEEFPSRDKG	K	A	95.00%	38.5	41.5	3.48	0	0	1	0	0	2	1488.68	336	347
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	IFRDGEEAGYDGGPR	K	T	95.00%	37	41.4	3.16	0	0	3	0	0	2	1652.77	105	119
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	IFRDGEEAGYDGGPR	K	V	95.00%	40.4	42.3	0.9	0	0	1	0	0	2	1123.66	153	164
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	LAPEYEAATR	R	L	91.60%	40.4	42.8	7.96	1	1	0	0	0	2	1119.61	63	73
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	LSKDPNVIADK	K	M	95.00%	49.1	42.1	2.47	0	0	1	0	0	2	1197.72	423	433
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	QAQPASVPLR	K	T	95.00%	84.3	42	2.22	0	1	0	0	0	2	995.56	131	140
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	YGVSYGYPTLTK	K	I	95.00%	61.1	40.7	6	0	1	0	0	2	1084.57	95	104	
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	VVAENFENNVNENK	K	D	94.30%	43.2	40.2	-0.0792	0	0	1	0	0	2	1832.9	380	395
25	H9	PNGas5	S_25_RAW	(F025173)	ER-60 protease (Protein disulfide isomerase fa)	gii1208427.gii21361657.gi	56780.5	100.00%	15	17	19	0.36%	29.70%	YGVSYGYPTLTK	K	I	95.00%	46.2	42.1	4.66	0	2	0	0	0	2	1084.57	95	104
25	H9	PNGas5	S_25_RAW	(F025173)	heat shock 70kDa protein B isoform 2 variant	gii62898815	53482.8	99.80%	2	2	2	0.04%	5.88%	STAGDTLGGDFDNRK	M	N	95.00%	32.5	38.7	1.85	0	0	1	0	0	2	1691.73	221	236
25	H9	PNGas5	S_25_RAW	(F025173)	heat shock 70kDa protein B isoform 2 variant	gii62898815	53482.8	99.80%	2	2	2	0.04%	5.88%	STAGDTLGGDFDNRK	R	N	95.00%	47.8	39.9	0.42	0	0	1	0	0	2	1407.67	201	210
25	H9	PNGas5	S_25_RAW	(F025173)	T complex protein 1	gii36796.gii57863257.gii57	43869	100.00%	3	3	3	0.06%	9.23%	LGQVIVITPEKDLDIR	K	Q	95.00%	61.6	39.6	5	0	0	1	0	0	2	1923.09	333	349
25	H9	PNGas5	S_25_RAW	(F025173)	T complex protein 1	gii36796.gii57863257.gii57	43869	100.00%	3	3	3	0.06%	9.23%	YGVSYGYPTLTK	K	I	95.00%	59.5	42.4	4.64	0	0	1	0	0	2	1465.05	25	35
26	H9	PNGas5	S_26_RAW	(F025174)	glucose regulated protein 58kD (GRP58)	gii27805905	56913.7	100.00%	3	4	5	0.10%	5.94%	FVMEEFPSR	K	L	95.00%	57.4	42.3	3.47	0	2	0	0	0	2	1172.54	336	344
26	H9	PNGas5	S_26_RAW	(F025174)	glucose regulated protein 58kD (GRP58)	gii27805905	56913.7	100.00%	3	4	5	0.10%	5.94%	LAPEYEAATR	K	L	95.00%	83.8	42.8	6.28	0	2	0	0	0	2	1191.63	63	73
26	H9	PNGas5	S_26_RAW	(F025174)	glucose regulated protein 58kD (GRP58)	gii27805905	56913.7	100.00%	3	4	5	0.10%	5.94%	YGVSYGYPTLTK	K	I	95.00%	22.3	41.3	2.24	0	1	0	0	0	2	1084.57	95	104
27	H9	PNGas5	S_27_RAW	(F025175)	beta actin	gii178045	25861.8	100.00%	4	4	4	0.08%	19.40%	YQSFYTTAER	R	E	95.00%	86.1	42.4	5.14	0	1	0	0	0	2	1132.53	54	63
27	H9	PNGas5	S_27_RAW	(F025175)	beta actin	gii178045	25861.8	100.00%	4	4	4	0.08%	19.40%	MOKKITALPSTMK	R	I	81.90%	20.4	41.6	1.57	0	0	1	0	0	2	1579		

32	H9	PNase	S_32 RAW (F025181)	pan-leukocyte antigen	g 180139.g 48146141.g 5	27665.4	100.00%	6	9	9	0.17%	24.70%	IKLQVLDVPPKVIK	K	I	82.30%	0	0	1.84	0	1	0	2	1687.09	123	137	
32	H9	PNase	S_32 RAW (F025181)	pan-leukocyte antigen	g 180139.g 48146141.g 5	27665.4	100.00%	6	9	9	0.17%	24.70%	LQVLDVPPKVIK	K	I	95.00%	68.1	40.8	3.96	0	1	1	0	2	1445.91	125	137
32	H9	PNase	S_32 RAW (F025181)	RAN protein 2	g 32425497.g 4902954.g 2	24437.9	99.40%	2	2	2	0.04%	10.30%	LVLDVPPKQEK	K	F	90.00%	69.2	41	0.77	0	0	1	0	2	1294.61	61	71
32	H9	PNase	S_32 RAW (F025181)	RAN protein	g 32425497.g 4902954.g 2	24437.9	99.40%	2	2	2	0.04%	10.20%	LVLDGDDGKTK	K	N	90.30%	31.3	40.9	1.75	0	1	0	0	2	1015.58	13	23
32	H9	PNase	S_32 RAW (F025181)	triosephosphate isomerase 1	g 17398915.g 4507645.g 1	26193.9	99.90%	2	2	2	0.04%	12.50%	IVYGSVITGATCK	R	E	95.00%	96.6	41.8	1.19	0	1	0	0	2	1326.67	206	218
32	H9	PNase	S_32 RAW (F025181)	triosephosphate isomerase 1	g 17398915.g 4507645.g 1	26193.9	99.90%	2	2	2	0.04%	12.50%	IVYGSVITGATCK	R	E	95.00%	96.6	41.8	1.19	0	1	0	0	2	1807.89	113	130
33	H9	PNase	S_33 RAW (F025182)	polyubiquitin C	g 1304129	68708.4	100.00%	8	9	11	0.22%	9.88%	LIFAGKQLEDRG	R	T	95.00%	29.7	40.7	4.38	0	1	0	0	2	1346.74	43	54
33	H9	PNase	S_33 RAW (F025182)	polyubiquitin C	g 1304128	68708.4	100.00%	8	9	11	0.22%	9.88%	TITLEVFPSTIEANVK	K	A	95.00%	66.9	41.6	7.22	0	1	0	0	2	1789.93	12	27
33	H9	PNase	S_33 RAW (F025182)	polyubiquitin C	g 1304128	68708.4	100.00%	8	9	11	0.22%	9.88%	TLSYDVIQIK	R	E	95.00%	68.9	42	-2.79	0	2	0	0	2	1081.55	55	63
34	T1	control	S_34 RAW (F025183)	Dystonin	g 34570747.g 34577049.g 0	587668.8	99.90%	2	2	2	0.04%	8.41%	SDLEAGVDELK	K	E	83.00%	75.5	42.2	5	0	1	0	0	2	1408.66	289	261
34	T1	control	S_34 RAW (F025183)	Dystonin	g 34577047.g 34577049.g 0	587668.8	99.90%	2	2	2	0.04%	0.41%	SPASKLQK	R	E	95.00%	32.4	41.9	21.3	0	1	0	0	2	845.47	5133	5104
34	T1	control	S_34 RAW (F025183)	fas-like protein	g 1040970	5359.1	99.90%	2	2	2	0.04%	5.11%	GGMGSDRRGGFNK	R	F	95.00%	31.9	42	2.05	0	1	0	0	2	1255.55	255	267
36	T1	control	S_36 RAW (F025185)	type I keratin	g 186685	50682.1	99.50%	2	2	2	0.04%	5.75%	ALEEANADLVYK	R	I	95.00%	86	40.3	4.46	0	1	0	0	2	1301.86	135	146
36	T1	control	S_36 RAW (F025185)	type I keratin	g 186685	50682.1	99.50%	2	2	2	0.04%	5.75%	YVGGGGGGSSSR	K	I	89.10%	0	0	2.86	0	0	1	0	2	1235.98	16	30
36	T1	control	S_36 RAW (F025185)	type I keratin	g 2950168	47213.6	99.30%	2	3	3	0.06%	8.41%	LNVEVDAPTVLNR	R	V	95.00%	62.8	41.6	7.5	0	1	0	0	2	1625.85	209	223
36	T1	control	S_36 RAW (F025185)	type I keratin	g 2950168	47213.6	99.30%	2	3	3	0.06%	8.41%	LVQVINDAK	R	L	85.00%	40.3	42.4	-0.94	1	1	0	0	2	999.58	127	135
36	T1	control	S_36 RAW (F025185)	type I keratin	g 2950168	47213.6	99.30%	2	3	3	0.06%	8.41%	SDLEAGVDELK	K	E	83.00%	75.5	42.2	5	0	1	0	0	2	1218.52	174	184
37	T1	control	S_37 RAW (F025186)	migration inhibitory factor-related protein 14	g 20150236.g 29126810.g 0	13077	99.90%	2	2	2	0.04%	20.40%	KOLNLFK	K	K	95.00%	53.3	42.7	1.02	0	1	0	0	2	1005.57	42	49
37	T1	control	S_37 RAW (F025186)	migration inhibitory factor-related protein 14	g 20150236.g 29126810.g 0	13077	99.90%	2	2	2	0.04%	20.40%	VEIHMDLDTNAIK	K	Q	95.00%	64.8	40.5	4.27	0	1	0	0	2	1758.82	57	71
37	T1	control	S_37 RAW (F025186)	psoriasis	g 12053626.g 29168101.g 0	10399.8	99.30%	2	2	2	0.04%	13.50%	GTVNLADVFEK	K	K	95.00%	41.1	42.1	5.08	0	1	0	0	2	1256.62	51	61
37	T1	control	S_37 RAW (F025186)	psoriasis	g 12053626.g 29168101.g 0	10399.8	99.30%	2	2	2	0.04%	13.50%	GTVNLADVFEK	K	D	86.30%	38.8	40.1	0.469	0	1	0	0	2	1384.71	51	62
38	T1	control	S_38 RAW (F025187)	annexin VIII isoform 1	g 4502111.g 4809279.g 5	52722.5	99.90%	2	2	2	0.05%	6.56%	FGTDEQAQVIVANR	K	S	95.00%	70.2	42.3	6.25	0	1	0	0	2	1690.84	200	215
38	T1	control	S_38 RAW (F025187)	annexin VIII isoform 1	g 4502111.g 4809279.g 5	52722.5	99.90%	2	2	2	0.05%	6.56%	TLGTMIADGTSQDYYR	K	L	95.00%	47.7	41.4	1.35	0	1	0	0	2	1729.82	465	480
38	T1	control	S_38 RAW (F025187)	RuvB-like 2	g 12653319	51140.1	99.80%	2	2	2	0.05%	4.75%	QVTVVDQDK	K	R	95.00%	64.6	42.4	3.54	0	1	0	0	2	1320.63	224	234
38	T1	control	S_38 RAW (F025187)	RuvB-like 2	g 12653319	51140.1	99.80%	2	2	2	0.05%	4.75%	QVTVVDQDK	K	R	95.00%	61.5	41	1.17	0	0	1	0	2	1259.66	418	428
38	T1	control	S_38 RAW (F025187)	serum albumin	g 11493459.g 178345.g 2	69376.1	99.80%	2	2	2	0.05%	3.61%	KVQVSTPTLVEYSR	K	N	95.00%	90.9	41.4	2.34	0	1	0	0	2	1639.94	438	452
38	T1	control	S_38 RAW (F025187)	serum albumin	g 11493459.g 178345.g 2	69376.1	99.80%	2	2	2	0.05%	3.61%	VPQVSTPTLVEYSR	K	N	95.00%	82.4	41.6	0	0	1	0	0	2	1511.84	439	452
38	T1	control	S_38 RAW (F025187)	serum albumin	g 11493459.g 178345.g 2	69376.1	99.80%	2	2	2	0.05%	3.61%	YLYEAYR	K	R	95.00%	46.3	41.9	1.13	0	1	0	0	2	1277.41	162	168
39	T1	control	S_39 RAW (F025188)	beta actin variant	g 62897625	41747.9	100.00%	4	4	4	0.10%	10.90%	LDLTKLTK	K	I	95.00%	41.7	41.5	2.82	0	1	0	0	2	1014.48	316	329
39	T1	control	S_39 RAW (F025188)	beta actin variant	g 62897625	41747.9	100.00%	4	4	4	0.10%	10.90%	EYLAARSTMK	K	I	95.00%	33.8	42.3	2.36	0	1	0	0	2	927.89	316	326
39	T1	control	S_39 RAW (F025188)	beta actin variant	g 62897625	41747.9	100.00%	4	4	4	0.10%	10.90%	LDLADGKLDLTKML	R	I	81.60%	28	41.3	1.51	0	0	1	0	2	1639.84	178	191
39	T1	control	S_39 RAW (F025188)	beta actin variant	g 62897625	41747.9	100.00%	4	4	4	0.10%	10.90%	SEFVPLDQVQNGER	K	R	95.00%	24.4	42.4	2.86	0	1	0	0	2	1760.89	259	290
39	T1	control	S_39 RAW (F025188)	chaperonin containing TCP1, subunit 5 (epsilon)	g 14495685.g 0	43014.6	100.00%	2	2	2	0.05%	4.91%	MLVROCK	K	N	95.00%	32.4	42.4	2.24	0	1	0	0	2	1020.52	217	224
39	T1	control	S_39 RAW (F025188)	chaperonin containing TCP1, subunit 5 (epsilon)	g 14495685.g 0	43014.6	100.00%	2	2	2	0.05%	4.91%	QQISLATQMYR	K	V	95.00%	49.6	40.7	1.03	0	1	0	0	2	1290.68	361	371
39	T1	control	S_39 RAW (F025188)	chaperonin containing TCP1, subunit 8 (theta)	g 1136741.g 31418053.g 0	58485	99.80%	2	2	2	0.05%	4.82%	AIADTGANVITGGK	K	M	95.00%	134	41.1	2.89	0	1	0	0	2	1372.74	282	296
39	T1	control	S_39 RAW (F025188)	chaperonin containing TCP1, subunit 8 (theta)	g 1136741.g 31418053.g 0	58485	99.80%	2	2	2	0.05%	4.82%	IFNMGVTLVLR	R	I	95.00%	32.5	42	3.11	0	1	0	0	2	1282.67	505	519
39	T1	control	S_39 RAW (F025188)	dihydropyrimidinase-like 2 variant	g 45501286.g 62898846	62276	99.90%	2	2	2	0.05%	6.47%	DIGAAPVHAENDIGAEQQOR	R	I	95.00%	53.1	40.1	3.15	0	1	0	0	2	2377.18	190	211
39	T1	control	S_39 RAW (F025188)	dihydropyrimidinase-like 2 variant	g 45501286.g 62898846	62276	99.90%	2	2	2	0.05%	6.47%	GLDYGQVCEVSTPK	R	I	95.00%	76	41.5	4.8	0	1	0	0	2	1620.8	497	511
39	T1	control	S_39 RAW (F025188)	protein disulfide isomerase family A, member	g 1208427.g 21361657.g 0	56663.5	100.00%	6	9	9	0.22%	13.70%	FLDAGHKLNFVAYSR	K	K	95.00%	47.9	41.5	0.638	0	2	0	0	2	1645.88	290	304
39	T1	control	S_39 RAW (F025188)	protein disulfide isomerase family A, member	g 1208427.g 21361657.g 0	56663.5	100.00%	6	9	9	0.22%	13.70%	FLDAGHKLNFVAYSR	K	R	95.00%	47.9	41.5	0.638	0	2	0	0	2	1645.88	290	304
39	T1	control	S_39 RAW (F025188)	protein disulfide isomerase family A, member	g 1208427.g 21361657.g 0	56663.5	100.00%	6	9	9	0.22%	13.70%	IFRDDEEAGAYDQPR	K	T	95.00%	36	41.7	1.92	0	1	0	0	2	1652.77	105	119
39	T1	control	S_39 RAW (F025188)	protein disulfide isomerase family A, member	g 1208427.g 21361657.g 0	56663.5	100.00%	6	9	9	0.22%	13.70%	LSKDPNVIK	K	M	95.00%	76.5	41.2	4.02	0	1	1	0	2	1197.72	423	433
39	T1	control	S_39 RAW (F025188)	protein disulfide isomerase family A, member	g 1208427.g 21361657.g 0	56663.5	100.00%	6	9	9	0.22%	13.70%	SEFVPLDQVQNGER	K	R	95.00%	24.4	42.4	2.86	0	1	0	0	2	1368.57	367	379
39	T1	control	S_39 RAW (F025188)	protein disulfide isomerase family A, member	g 1208427.g 21361657.g 0	56663.5	100.00%	6	9	9	0.22%	13.70%	YLYKSEIPESNDQPK	K	V	95.00%	41.2	39.6	1.7	0	1	0	0	2	1177.91	364	379
39	T1	control	S_39 RAW (F025188)	serum albumin	g 28590	69277.9	99.50%	2	3	3	0.07%	3.61%	KVPEVSTPTLVEYSR	K	N	90.40%	0	0	2.14	0	1	0	0	2	1640.92	438	452
39	T1	control	S_39 RAW (F025188)	serum albumin	g 28590	69277.9	99.50%	2	3	3	0.07%	3.61%	YLYEAYR	K	R	95.00%	44.1	41.9	0.678	0	2	0	0	2	927.49	162	168
40	H9	control	S_40 RAW (F025189)	ER-60 protease (Protein disulfide isomerase family A, member)	g 1208427.g 21361657.g 0	56780.5	100.00%	8	10	11	0.26%	22.80%	FLDAGHKLNFVAYSR	K	R	95.00%	47.9	41.5	0.638	0	2	0	0	2	1645.88	290	304
40	H9	control	S_40 RAW (F025189)	ER-60 protease (Protein disulfide isomerase family A, member)	g 1208427.g 21361657.g 0	56780.5	100.00%	8	10	11	0.26%	22.80%	FLODYGDKLNR	K	Y	95.00%	46.9	40	-0.255	0	1	0	0	2	1515.76	352	363
40	H9	control	S_40 RAW (F025189)	ER-60 protease (Protein disulfide isomerase family A, member)	g 1208427.g 21361657.g 0	56780.5	100.00%	8	10	11	0.26%	22.80%	FVMEFSESR	K	D	95.00%	61.9	42.3	3.1	0	2	0	0	2	1172.54	336	344
40	H9	control	S_40 RAW (F025189)	ER-60 protease (Protein disulfide isomerase family A, member)	g 1208427.g 21361657.g 0																						

Supplemental Table 3: gp120 Quantitation data (Raw data from progenesis)

Ref. Spot	hiv h9 pngase (762 matches)	hiv h9 wt (810 matches)	hiv t1 png (936 matches)	hiv t1 wt (1433 matches)	siv 239 png (602 matches)	siv 239 wt (892 matches)	siv mne png (843 matches)	siv mne wt (823 matches)
1790	0.05	0.941	0.046	0.15	0.028	0.835	0.055	4.119
1802	0.87	0.064	0.892	0.345	1.09	0.85	0.548	0.507
1806	0.13	0.196	0.027	0.019	0.02	0.041	1.207	0.006

PRESENTED IN PAPER

PRESENTED IN PAPER		RATIOS (GRAPHS)				COMPARISONS (RATIOS)
REGION	SPOT	DEGLYCOSYLATED hiv h9 pngase (762 matches)	GLYCOSYLATED hiv h9 wt (810 matches)	DEGLYCOSYLATED hiv h9 pngase (762 matches)	GLYCOSYLATED hiv h9 wt (810 matches)	COMPARISONS (RATIOS)
REGION A	SPOT	1790	0.05	0.941	5.045408678	SIV MNE TO HIV H9 (GLYCOSYLATED) 4.377258236
		1790	0.055	4.119	1.317680882	98.68231912
REGION B	SPOT	1802	0.87	0.064	93.14775161	SIV MNE TO HIV H9 (DEGLYCOSYLATED) 1.387356322
		1802	0.548	0.507	51.94312796	48.05687204
REGION C	SPOT	1806	0.13	0.196	39.87730061	HIV H9 TO HIV T1 (GLYCOSYLATED) 6.273333333
		1806	1.207	0.006	99.50535862	0.494641385

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REGION A	SPOT	1790	0.046	0.15	23.46938776	HIV T1 TO SIV 239 (GLYCOSYLATED) 5.566666667
		1790	0.028	0.835	3.244495944	96.75550406
						SIV MNE TO SIV 239 (GLYCOSYLATED) 4.932934132
REGION B	SPOT	1802	0.892	0.345	72.10994341	SIV MNE TO SIV 239 (DEGLYCOSYLATED) NO MATCHING SPOTS
		1802	1.09	0.85	56.18556701	43.81443299
REGION C	SPOT	1806	0.027	0.019	58.69565217	
		1806	0.02	0.041	32.78688525	67.21311475

SUPPLEMENTAL TABLE 4: Viral Peptides - Orbirap

M/SMS sample	Protein name	Protein accession	Protein molecular weight (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage	Assigned	Spectrum name	Peptide sequence	Previous amino acid	Next amino acid	Peptide identification probability	Variable modifications identified by spectrum	Observed m/z	Actual peptide mass	Calculated Peptide Mass	Spectrum charge	Actual minus calculated	Actual minus calculated	Peptide start index	Peptide stop index
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q2_SHV1	24781.5	76.30%	1	1	1	0.02%	3.15%	TRUE	pppHH9H_0163.0163.2.0a	DKHSSTK	A		95.00% Q1: Deamidation (+0.98), T6: Phospho (+79.97)	422.7687	843.2578	843.2578	2	-0.1543	-0.1543	130	136	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q3_SHV1	22759.3	76.30%	1	1	1	0.02%	4.21%	TRUE	pppHH9H_0234.0234.3.0a	LRKQFGFK	T		95.00% Q4: Deamidation (+0.98), N8: Deamidation (+0.98)	383.88	1146.617	1146.6018	3	-0.0226	19.64	86	86	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q4_SHV1	98209.5	76.30%	1	1	1	0.02%	1.05%	TRUE	pppHH9H_0286.0286.3.0a	TLVEQAR	T		95.00% Q5: Deamidation (+0.98), N8: Deamidation (+0.98)	383.1892	1146.544	1147.5749	3	-0.023055	-20.11	335	343	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q5_SHV1	22292.4	76.30%	1	2	6	0.10%	5.42%	TRUE	pppHH9H_0562.0562.3.0a	QVTKLRACK	N		95.00% Q1: Deamidation (+0.98)	444.8997	1331.676	1332.8004	3	-0.1169	-87.75	81	91	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q6_SHV1	22292.4	76.30%	1	2	6	0.10%	5.42%	TRUE	pppHH9H_0573.0573.2.0a	QVTKLRACK	N		95.00% Q1: Deamidation (+0.98)	666.8477	1331.676	1332.8004	3	-0.1129	-84.73	81	91	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q7_SHV1	22292.4	76.30%	1	2	6	0.10%	5.42%	TRUE	pppHH9H_0576.0576.2.0a	QVTKLRACK	N		95.00% Q9: Deamidation (+0.98)	666.8484	1331.677	1332.8004	3	-0.1154	-86.56	81	91	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q8_SHV1	22292.4	76.30%	1	2	6	0.10%	5.42%	TRUE	pppHH9H_0638.0638.3.0a	QVTKLRACK	N		95.00% Q1: Deamidation (+0.98)	444.8997	1331.676	1332.8004	3	-0.1169	-87.75	81	91	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q9_SHV1	22292.4	76.30%	1	2	6	0.10%	5.42%	TRUE	pppHH9H_0656.0656.2.0a	QVTKLRACK	N		95.00% Q9: Deamidation (+0.98)	666.8467	1331.676	1332.8004	3	-0.1149	-85.18	81	91	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q0_SHV1	22292.4	76.30%	1	2	6	0.10%	5.42%	TRUE	pppHH9H_0660.0660.2.0a	QVTKLRACK	N		95.00% Q9: Deamidation (+0.98)	666.8476	1331.676	1332.8004	3	-0.113	-84.82	81	91	
ID_H9	Envelope glycoprotein (Fragment)	Q10701_SHV1	12921.9	76.30%	1	1	2	0.03%	7.83%	TRUE	pppHH9H_0681.0681.2.0a	KVQQQLR	K		95.00% Q4: Deamidation (+0.98), T8: Phospho (+79.97)	590.8142	1179.613	1180.6456	2	-0.0205	-21.2	68	76	
ID_H9	Envelope glycoprotein (Fragment)	Q10701_SHV1	12921.9	76.30%	1	1	2	0.03%	7.83%	TRUE	pppHH9H_0688.0688.2.0a	KVQQQLR	K		95.00% Q4: Deamidation (+0.98), T8: Phospho (+79.97)	590.8144	1179.613	1180.6456	2	-0.0205	-21.2	68	76	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q2_SHV1	11638.2	76.30%	1	1	2	0.03%	12.10%	TRUE	pppHH9H_0719.0719.3.0a	TLLQVEAHR	F		94.00% T1: Phospho (+79.97), N11: Deamidation (+0.98)	497.2613	1488.76	1489.7417	3	-0.02847	-17.78	72	83	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q2_SHV1	11638.2	76.30%	1	1	2	0.03%	12.10%	TRUE	pppHH9H_0725.0725.3.0a	TLLQVEAHR	F		95.00% T1: Phospho (+79.97), N11: Deamidation (+0.98)	497.2618	1488.762	1489.7417	3	-0.02906	-18.85	72	83	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9Q3_SHV1	13852.4	76.30%	1	1	1	0.02%	6.03%	TRUE	pppHH9H_0746.0746.2.0a	ESHSVKK	T		95.00% N5: Deamidation (+0.98)	414.2086	826.4016	827.8263	2	-0.016949	-20.43	1	7	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9C1_SHV1	98354.6	76.30%	1	1	1	0.02%	1.98%	TRUE	pppHH9H_0772.0772.2.0a	AEGNSITLK	K		95.00% N4: Deamidation (+0.98)	616.8036	1231.592	1232.5947	2	0.006348	3.763	417	428	
ID_H9	Envelope glycoprotein (Fragment)	Q7SSY1_SHV1	52567.3	76.30%	1	1	1	0.02%	1.82%	TRUE	pppHH9H_1156.1156.2.0a	QVTKLKR	F		95.00% Q1: Deamidation (+0.98)	564.5402	1127.065	1127.7154	2	0.3572	316.6	311	319	
ID_H9	Envelope glycoprotein (Fragment)	Q8J8RS_SHV1	17801.9	67.00%	1	1	1	0.02%	4.40%	TRUE	pppHH9H_1272.1272.2.0a	IRGLVK	P		92.30% Q4: Deamidation (+0.98)	414.3403	826.6649	827.5007	2	0.112	135.3	1	7	
ID_H9	Envelope glycoprotein (Fragment)	Q8ZHF5_SHV1	7530.9	76.30%	1	1	1	0.02%	6.86%	TRUE	pppHH9H_1277.1277.2.0a	LEEQYMK	K		95.00% Q4: Deamidation (+0.98), N7: Deamidation (+0.98)	527.3062	1052.705	1053.5106	2	0.202	191.7	101	108	
ID_H9	Envelope glycoprotein (Fragment)	Q8ZL09_SHV1	97281.5	99.10%	1	1	2	0.03%	0.82%	TRUE	pppHH9H_1306.1306.2.0a	AHWVPR	R		95.00% N4: Deamidation (+0.98)	404.2023	806.389	807.4477	2	-0.05068	-63.05	842	848	
ID_H9	Envelope glycoprotein (Fragment)	Q8ZL09_SHV1	97281.5	99.10%	1	1	2	0.03%	0.82%	TRUE	pppHH9H_1312.1312.2.0a	AHWVPR	R		95.00% N4: Deamidation (+0.98)	404.2025	806.391	807.4477	2	-0.04855	-60.1	842	848	
ID_H9	Envelope glycoprotein (Env protein)	Q8Q7G2_SHV1	100595.4	76.30%	1	1	2	0.03%	0.79%	TRUE	pppHH9H_1430.1430.2.0a	GWNVPR	R		95.00% N4: Deamidation (+0.98)	421.7588	841.502	842.4524	2	0.05737	66.1	873	879	
ID_H9	Envelope glycoprotein (Env protein)	Q8Q7G2_SHV1	100595.4	76.30%	1	1	2	0.03%	0.79%	TRUE	pppHH9H_1436.1436.2.0a	GWNVPR	R		95.00% N4: Deamidation (+0.98)	421.7587	841.5017	842.4524	2	0.057055	67.74	873	879	
ID_H9	Envelope protein (Fragment)	Q77028_SHV1	10476.4	74.30%	1	1	1	0.02%	14.70%	TRUE	pppHH9H_1551.1551.3.0a	IVRSNLT	T		94.50% N7: Deamidation (+0.98)	499.2756	1494.803	1495.8232	3	-0.012067	-8.079	1	13	
ID_H9	Envelope protein (v1 region) (Fragment)	Q77443_SHV1	1744.6	76.30%	1	1	1	0.02%	7.62%	TRUE	pppHH9H_1765.1765.2.0a	QVDSLR	K		95.00% Q1: Deamidation (+0.98), S3: Phospho (+79.97), Q5: Deamidation (+0.98)	501.748	1013.474	1014.4396	2	-0.02116	-81.7	80	87	
ID_H9	Envelope glycoprotein (Fragment)	Q8P031_SHV1	22638.8	76.30%	1	1	1	0.02%	4.46%	TRUE	pppHH9H_1864.1864.2.0a	LGQGFQMK	K		95.00% Q4: Deamidation (+0.98), M7: Oxidation (+16.00), N8: Deamidation (+0.98)	485.2556	988.4957	989.4353	2	0.068156	70.32	82	90	
ID_H9	Envelope glycoprotein (Fragment)	Q8J5U7_SHV1	15081.3	76.30%	1	1	1	0.02%	14.00%	TRUE	pppHH9H_1915.1915.2.0a	STNTDNTK	E		95.00% N2: Deamidation (+0.98), N6: Deamidation (+0.98), S16: Phospho (+79.97)	1041.5092	2081.003	2081.8154	2	0.1951	93.69	25	43	
ID_H9	Envelope glycoprotein (Fragment)	Q8P084_SHV1	16340.8	76.30%	1	1	1	0.02%	8.22%	TRUE	pppHH9H_1974.1974.2.0a	KLSTFHTK	F		95.00% T3: Phospho (+79.97), N6: Deamidation (+0.98)	778.9079	1951.8	1952.8143	2	-0.006959	-4.481	59	70	
ID_H9	Envelope glycoprotein (Fragment)	Q81290_SHV1	8669.4	76.30%	1	1	1	0.02%	22.20%	TRUE	pppHH9H_2558.2558.3.0a	LNSVIVRK	I		95.00% N2: Deamidation (+0.98), N3: Deamidation (+0.98), T10: Phospho (+79.97)	694.6727	2080.995	2081.9802	3	0.02225	10.67	22	39	
ID_H9	Envelope glycoprotein (Fragment)	Q8J8A8_SHV1	98561.6	76.30%	1	1	1	0.02%	1.61%	TRUE	pppHH9H_2841.2841.3.0a	WSDTNTK	S		95.00% Q1: Deamidation (+0.98), N11: Deamidation (+0.98), S13: Phospho (+79.97)	503.3473	1508.899	1507.559	3	0.3474	230.4	413	426	
ID_H9	Envelope glycoprotein (Fragment)	Q8L0T7_SHV1	16540.5	76.30%	1	1	1	0.02%	11.80%	TRUE	pppHH9H_3638.3638.3.0a	QAHVQGR	Y		95.00% Q1: Deamidation (+0.98), N12: Deamidation (+0.98)	620.4375	1658.298	1658.9122	3	0.3946	208.9	49	65	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9D13_SHV1	21535.9	76.30%	1	1	1	0.02%	14.00%	TRUE	pppHH9H_3651.3651.3.0a	VQGMVPR	D		95.00% Q11: Deamidation (+0.98), M15: Oxidation (+16.00)	978.523	2932.546	2933.5413	3	0.012249	4.161	154	180	
ID_H9	Envelope glycoprotein (Fragment)	Q8Q9N8_SHV1	22607	76.30%	1	1	1	0.02%	5.45%	TRUE	pppHH9H_4496.4496.3.0a	KLGEQGR	I		95.00% Q5: Deamidation (+0.98), N9: Deamidation (+0.98)	437.3271	1308.958	1309.6577	3	0.3081	235.2	81	91	
ID_H9	Envelope glycoprotein (Fragment)	Q72618_SHV1	12471.3	76.30%	1	1	1	0.02%	9.17%	TRUE	pppHH9H_4738.4738.3.0a	LLNLSLAE	I		95.00% N4: Deamidation (+0.98), S8: Phospho (+79.97)	423.3355	926.974	927.8169	3	0.3826	286.2	1	11	
ID_H9	Envelope glycoprotein (Fragment)	Q8L184_SHV1	43100	76.30%	1	1	1	0.02%	3.87%	TRUE	pppHH9H_5092.5092.2.0a	LDVPIGNSR	Y		95.00% Q4: Deamidation (+0.98), S10: Phospho (+79.97)	522.5549	1564.041	1564.7628	3	0.2864	183	63	77	
ID_H9	Envelope glycoprotein (Fragment)	Q81023_SHV1	23953.1	61.40%	1	1	1	0.02%	3.65%	TRUE	pppHH9H_5378.5378.2.0a	DDDSNTRK	S		90.40% S4: Phospho (+79.97), N5: Deamidation (+16.00), N8: Deamidation (+0.98)	496.6944	989.1932	990.2941	2	-0.099152	-84.96	15	22	
ID_MNE	Envelope glycoprotein (Fragment)	Q8D923_SHV1	9745.2	70.10%	1	1	1	0.02%	11.40%	TRUE	pppMNEH_046.046.3.0a	LDDSPK	K		93.30% Q2: Deamidation (+0.98)	378.1614	1125.661	1126.5383	3	-0.0697	-81.89	79	88	
ID_MNE	Env glycoprotein (Fragment)	Q8H1T4_SHV1	18333.2	76.30%	1	1	1	0.02%	5.88%	TRUE	pppMNEH_0492.0492.3.0a	LAQVMRR	R		95.00% Q4: Deamidation (+0.98), M6: Oxidation (+16.00), S9: Phospho (+79.97)	424.5749	1270.701	1271.6071	3	0.102	80.25	3	12	
ID_MNE	Envelope glycoprotein (Fragment)	Q8D973_SHV1	11205.9	76.30%	1	1	1	0.02%	10.90%	TRUE	pppMNEH_0709.0709.3.0a	WNETLQHK	L		95.00% T4: Phospho (+79.97), Q6: Deamidation (+0.98)	492.2446	1383.71	1384.6515	3	0.06677	48.22	66	76	
ID_MNE	Envelope glycoprotein (Env protein)	Q8Q7G2_SHV1	100595.4	76.30%	1	3	3	0.06%	0.79%	TRUE	pppMNEH_1022.1022.2.0a	GWNVPR	R		95.00% N4: Deamidation (+0.98)	421.7591	841.5026	842.4524	2	0.05765	68.75	873	879	
ID_MNE	Envelope glycoprotein (Env protein)	Q8Q7G2_SHV1	100595.4	76.30%	1	3	3	0.06%	0.79%	TRUE	pppMNEH_1057.1057.2.0a	GWNVPR	R		95.00% N4: Deamidation (+0.98)	421.7591	841.5025	842.4524	2	0.057854	68.68	873	879	
ID_MNE	Envelope glycoprotein (Env protein)	Q8Q7G2_SHV1	100595.4	76.30%	1	3	3	0.06%	0.79%	TRUE	pppMNEH_1058.1058.2.0a	GWNVPR	R		95.00% N4: Deamidation (+0.98)	421.7591	841.5025	842.4524	2	0.057854	68.68	873	879	
ID_MNE	Envelope glycoprotein (Fragment)	Q8H8C1_SHV1	24554.8	76.30%	1	1	1	0.02%	5.46%	TRUE	pppMNEH_1080.1080.2.0a	ALCEVQK	F		95.00% Q3: Deamidation (+0.98), S6: Phospho (+79.97), Q8: Deamidation (+0.98)	681.5288	1380.642	1381.673	2	-0.02319	-16.79	69	80	
ID_MNE	Envelope glycoprotein (Fragment)	Q8H8C1_SHV1	24554.8	76.30%	1	1	1	0.02%	6.52%	TRUE	pppMNEH_1102.1102.3.0a</													