

Figure 2 - Source Data 1

Top ten non-redundant proteins identified in the three samples by MS analysis

	Name	Length (aa)	MolWt (Da)	Sequence Count	Spectrum Count	Functional Annotation	Sequence Coverage
65kDa – WT <sub>v</sub> /PNGaseF (-) sample	GENSCAN_GS00000231568	209	22371	4	13	ref[NP_002761.1] trypsin-2 preproprotein [Homo sapiens]	14.80%
	comp5_c0_seq1 GENSCAN_predicted_peptide_1 608_aa	608	68682	3	11	ref[NP_000468.1] 609 serum albumin preproprotein [Homo sapiens]	4.30%
	ENSTBEP0000000142	128	14403	2	13	ref[NP_003372.1] VIP peptides isoform 1 preproprotein [Homo sapiens]	9.40%
	comp7554_c0_seq2 GENSCAN_predicted_peptide_1 379_aa	379	41483	2	8	ref[NP_003040.1] 349 sodium/bile acid cotransporter [Homo sapiens]	6.60%
	GENSCAN_GS00000235950	102	10754	1	1	ref[NP_004474.2] glycine cleavage system H protein, mitochondrial precursor [Homo sapiens]	21.80%
	comp376_c0_seq1 GENSCAN_predicted_peptide_1 733_aa	733	84789	1	1	ref[NP_005339.3] 732 heat shock protein HSP 90-alpha isoform 2 [Homo sapiens]	2.50%
	comp59_c0_seq2 GENSCAN_predicted_peptide_1 330_aa	330	37147	1	2	ref[NP_995584.1] 265 UDP-glucuronosyltransferase 1-6 isoform 2 [Homo sapiens]	2.40%
	GENSCAN_GS00000261263	802	84357	1	4	ref[NP_006112.3] keratin, type II cytoskeletal 1 [Homo sapiens]	1.50%
	GENSCAN_GS00000252787	713	73842	1	2	ref[NP_000412.3] keratin, type I cytoskeletal 10 [Homo sapiens]	1.30%
	comp218_c0_seq1 GENSCAN_predicted_peptide_1 1178_aa	1178	129710	1	4	ref[NP_071504.2] 1178 pyruvate carboxylase, mitochondrial precursor [Homo sapiens]	1.20%
43 kDa – WT <sub>v</sub> /PNGaseF (+) sample	GENSCAN_GS00000231568	209	22371	5	25	ref[NP_002761.1] trypsin-2 preproprotein [Homo sapiens]	12.90%
	comp7554_c0_seq2 GENSCAN_predicted_peptide_1 379_aa	379	41483	3	6	ref[NP_003040.1] 349 sodium/bile acid cotransporter [Homo sapiens]	6.60%
	comp5_c0_seq1 GENSCAN_predicted_peptide_1 608_aa	608	68682	8	32	ref[NP_000468.1] 609 serum albumin preproprotein [Homo sapiens]	6.20%
	comp218_c0_seq1 GENSCAN_predicted_peptide_1 1178_aa	1178	129710	2	5	ref[NP_071504.2] 1178 pyruvate carboxylase, mitochondrial precursor [Homo sapiens]	2.00%
	ENSTBEP0000000142	128	14403	1	4	ref[NP_003372.1] VIP peptides isoform 1 preproprotein [Homo sapiens]	9.40%
	GENSCAN_GS00000279109	265	28676	1	2	~ref[NP_037362.1] signal transducer CD24 precursor [Homo sapiens]	7.90%
	ENSTBEP00000001232	676	75890	1	1	ref[NP_659001.2] sciellin isoform 1 [Homo sapiens]	6.70%
	GENSCAN_GS00000184315	322	34272	1	1	ref[NP_001989.2] fibulin-2 isoform b precursor [Homo sapiens]	5.30%
	GENSCAN_GS00000184883	238	25776	1	1	Uncharacterized protein	2.90%
	comp5222_c0_seq1 GENSCAN_predicted_peptide_1 1285_aa	1285	148568	1	1	ref[NP_004990.3] 1285 myosin-VI [Homo sapiens]	1.50%
43 kDa – N9K <sub>v</sub> /PNGaseF (+) sample	GENSCAN_GS00000203437	578	61569	14	45	ref[NP_005546.2] keratin, type II cytoskeletal 6B [Homo sapiens]	15.80%
	GENSCAN_GS00000261263	802	84357	10	46	ref[NP_006112.3] keratin, type II cytoskeletal 1 [Homo sapiens]	6.50%
	GENSCAN_GS00000261502	378	40781	8	24	ref[NP_000517.2] keratin, type I cytoskeletal 14 [Homo sapiens]	20.10%
	GENSCAN_GS00000252787	713	73842	8	24	ref[NP_000412.3] keratin, type I cytoskeletal 10 [Homo sapiens]	7.90%
	ENSTBEP00000007380	537	59027	6	28	ref[NP_000414.2] keratin, type II cytoskeletal 2 epidermal [Homo sapiens]	7.10%
	comp5_c0_seq1 GENSCAN_predicted_peptide_1 608_aa	608	68682	6	24	ref[NP_000468.1] 609 serum albumin preproprotein [Homo sapiens]	3.90%
	GENSCAN_GS00000214315	505	55293	5	13	ref[NP_005548.2] keratin, type I cytoskeletal 16 [Homo sapiens]	9.10%
	GENSCAN_GS00000261260	1169	125254	4	16	ref[NP_778253.2] keratin, type II cytoskeletal 1b [Homo sapiens]	3.20%
	GENSCAN_GS00000211249	815	90386	4	13	ref[NP_002266.2] keratin, type I cytoskeletal 15 [Homo sapiens]	3.70%
	GENSCAN_GS00000223539	804	89223	4	7	ref[NP_000415.2] keratin, type II cytoskeletal 5 [Homo sapiens]	4.60%
<p><b>Name:</b> target protein name in the database. <b>Length:</b> number of amino acids. <b>MolWt:</b> calculated molecular weight (Dalton). <b>Sequence Count:</b> distinct peptides identified in a protein. <b>Spectrum Count:</b> number of spectrum identified in MS/MS. <b>Functional Annotation:</b> annotation of the protein according to their homolog in human. <b>Sequence Coverage:</b> percentage of the protein sequences that covered by identified peptides.</p>							