RI NSF/EPSCoR Proteomics Facility
Mass Spectrometry Report
Protein Groups and Peptide-Spectrum Matches (PSMs)

Sample:	Ctr
Researcher:	Djuro Josic
Data collected:	24 Aug 2011
Results filtering:	Unique PSMs; MOWSE Score > 20.6

MS data file:	Ctr_082511_224859.raw
Instrument type:	ESI-FTICR
Search engine:	Mascot
Parameter file:	N/D
Search database:	N/D (269577 entries)
Enzyme specificity:	Trypsin (2 missed cleavages allowed)
MS mass tolerance:	20 ppm; MS/MS tolerance 0.5 Da
Fixed modifications:	Carbamidomethyl (C)
Var. modifications:	[1] Oxidation (M)
Number of spectra:	3176
Input PSMs:	124 'Target'; 3 'Decoy'; 2.4% FDR
Output PSMs:	124

UniProt Human Protein IDs

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*

1	Q53H26	Transferrin variant (Fragment) OS=Homo sapiens PE=2 SV=1	2321.40	50	4 5 6 12 13 17 20 21 24 26 27 31 33 36 37 38 41 44 46 48 49 53 55 56 57 58 60 62 64 69 72 73 75 79 80 81 84 86 87 91 92 96 98 103 104 111 114 118 122 123		*56.6*
2	P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	293.28	6	8 10 23 39 45 109		*13.4*
	H0YA55	Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=4 SV=1	293.28	6	8 10 23 39 45 109		*13.4*
	F6KPG5	Albumin (Fragment) OS=Homo sapiens PE=2 SV=1	293.28	6	8 10 23 39 45 109		*13.4*
	B4DPR2	cDNA FLJ50830, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1	293.28	6	8 10 23 39 45 109		*13.4*
	B4DPP6	cDNA FLJ54371, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1	293.28	6	8 10 23 39 45 109		*13.4*
	B2RBS8	cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA OS=Homo sapiens PE=2 SV=1	293.28	6	8 10 23 39 45 109		*13.4*
	A8K9P0	cDNA FLJ78413, highly similar to Homo sapiens albumin, mRNA OS=Homo sapiens PE=2 SV=1	293.28	6	8 10 23 39 45 109		*13.4*
3	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1	267.11	5	1 28 61 102 119		*15.7*
	P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	267.11	5	1 28 61 102 119		*15.7*
	B7Z6P1	cDNA FLJ53662, highly similar to Actin, alpha skeletal muscle OS=Homo sapiens PE=2 SV=1	267.11	5	1 28 61 102 119		*15.7*
	A8K3K1	cDNA FLJ78096, highly similar to Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA OS=Homo sapiens PE=2 SV=1	267.11	5	1 28 61 102 119		*15.7*
4	Q8TCG3	TPMsk3 (Fragment) OS=Homo sapiens GN=TPM3 PE=2 SV=1	224.73	4	16 51 65 110		*27.4*
	Q5VU72	Tropomyosin 3, isoform CRA_a OS=Homo sapiens GN=TPM3 PE=3 SV=1	224.73	4	16 51 65 110		*27.4*
	Q5VU66	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=4 SV=1	224.73	4	16 51 65 110		*27.4*
	Q5VU59	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=3 SV=1	224.73	4	16 51 65 110		*27.4*
	Q5VU58	Tropomyosin 3, isoform CRA_b OS=Homo sapiens GN=TPM3 PE=3 SV=1	224.73	4	16 51 65 110		*27.4*
	Q5HYB6	Putative uncharacterized protein DKFZp686J1372 OS=Homo sapiens GN=DKFZp686J1372 PE=2 SV=1	224.73	4	16 51 65 110		*27.4*
	B2RDE1	cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1	224.73	4	16 51 65 110		*27.4*
5	Q6ZN40	Tropomyosin 1 (Alpha), isoform CRA_f OS=Homo sapiens GN=TPM1 PE=2 SV=1	202.67	7	19 42 54 63 99 105 120		*32.2*

6	P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	141.29	4	30 85 100 108		*36.6*
	I1VZV6	Hemoglobin alpha 1 OS=Homo sapiens GN=HBA1 PE=3 SV=1	141.29	4	30 85 100 108		*36.6*
	E9M4D4	Hemoglobin alpha-1 globin chain (Fragment) OS=Homo sapiens GN=HBA1 PE=3 SV=1	141.29	4	30 85 100 108		*36.6*
	D1MGQ2	Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=2 SV=1	141.29	4	30 85 100 108		*36.6*
7	P13533	Myosin-6 OS=Homo sapiens GN=MYH6 PE=1 SV=5	118.42	3	34 89 115		*4.8*
	P12883	Myosin-7 OS=Homo sapiens GN=MYH7 PE=1 SV=5	118.42	3	34 89 115		*4.8*
	D9YZU2	Myosin, heavy chain 6, cardiac muscle, alpha OS=Homo sapiens GN=MYH6 PE=2 SV=1	118.42	3	34 89 115		*4.8*
	A5YM51	MYH7 protein (Fragment) OS=Homo sapiens GN=MYH7 PE=2 SV=1	118.42	3	34 89 115		*4.8*
8	P01185	Vasopressin-neurophysin 2-copeptin OS=Homo sapiens GN=AVP PE=1 SV=2	111.88	4	3 74 88 106		*12.2*
9	P01308	Insulin OS=Homo sapiens GN=INS PE=1 SV=1	100.84	2	35 70		*25.5*
	I3WAC9	Preproinsulin OS=Homo sapiens GN=INS PE=3 SV=1	100.84	2	35 70		*25.5*
	F6MZK5	Insulin (Precursor) OS=Homo sapiens GN=INS PE=2 SV=1	100.84	2	35 70		*25.5*
	A6XGL2	Insulin OS=Homo sapiens GN=INS PE=3 SV=1	100.84	2	35 70		*25.5*
10	P30049	ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2	97.02	2	47 50		*7.1*
11	G3V1N2	HCG1745306, isoform CRA_a OS=Homo sapiens GN=HBA2 PE=3 SV=1	75.60	3	43 107 113		*29.1*
12	H7BZJ3	Thioredoxin (Fragment) OS=Homo sapiens GN=PDIA3 PE=2 SV=1	73.00	1	52		*11.4*
13	A7XZE4	Beta tropomyosin isoform OS=Homo sapiens GN=TPM2b PE=2 SV=1	72.44	3	25 32 117		*28.9*
14	Q59FG9	Chondroitin sulfate proteoglycan 2 (Versican) variant (Fragment) OS=Homo sapiens PE=2 SV=1	64.82	1	101		*36.6*
	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3	64.82	1	101		*36.6*
15	Q6LAM1	Heavy chain of factor I (Fragment) OS=Homo sapiens PE=2 SV=1	60.03	1	121		*7.2*
16	P17540	Creatine kinase S-type, mitochondrial OS=Homo sapiens GN=CKMT2 PE=1 SV=2	59.29	1	40		*5.7*
	D6RHV3	Creatine kinase S-type, mitochondrial (Fragment) OS=Homo sapiens GN=CKMT2 PE=2 SV=1	59.29	1	40		*5.7*
	D6R998	Creatine kinase S-type, mitochondrial (Fragment) OS=Homo sapiens GN=CKMT2 PE=2 SV=1	59.29	1	40		*5.7*

	B3KVA7	cDNA FLJ16309 fis, clone SKMUS2007816, highly similar to Creatine kinase, sarcomeric mitochondrial (EC 2.7.3.2) OS=Homo sapiens PE=2 SV=1	59.29	1	40		*5.7*
	B2R8A3	cDNA, FLJ93805, highly similar to Homo sapiens creatine kinase, mitochondrial 2 (sarcomeric) (CKMT2), nuclear gene encoding mitochondrial protein, mRNA OS=Homo sapiens PE=2 SV=1	59.29	1	40		*5.7*
17	B4E1B2	cDNA FLJ53691, highly similar to Serotransferrin OS=Homo sapiens PE=2 SV=1	56.27	1	18		*54.7*
18	Q6FHV6	ENO2 protein OS=Homo sapiens GN=ENO2 PE=2 SV=1	53.23	1	77		*3.2*
	P09104	Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3	53.23	1	77		*3.2*
	F5H0C8	Enolase OS=Homo sapiens GN=ENO2 PE=2 SV=1	53.23	1	77		*3.2*
	B7Z2X9	Enolase OS=Homo sapiens GN=ENO2 PE=2 SV=1	53.23	1	77		*3.2*
	A8K3B0	cDNA FLJ77877, highly similar to Human ENO2 neuron specific (gamma) enolase OS=Homo sapiens PE=2 SV=1	53.23	1	77		*3.2*
19	Q08043	Alpha-actinin-3 OS=Homo sapiens GN=ACTN3 PE=1 SV=2	51.37	1	82		*2.8*
	P35609	Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1	51.37	1	82		*2.8*
	B7Z4V1	cDNA FLJ55401, highly similar to Alpha-actinin-2 OS=Homo sapiens PE=2 SV=1	51.37	1	82		*2.8*
	B4DZQ2	cDNA FLJ58651, highly similar to Alpha-actinin-3 OS=Homo sapiens PE=2 SV=1	51.37	1	82		*2.8*
	B2R8Y4	cDNA, FLJ94117, highly similar to Homo sapiens actinin, alpha 3 (ACTN3), mRNA OS=Homo sapiens PE=2 SV=1	51.37	1	82		*2.8*
20	Q0QEN7	ATP synthase subunit beta (Fragment) OS=Homo sapiens GN=ATP5B PE=2 SV=1	49.48	1	94		*5.4*
	P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	49.48	1	94		*5.4*
	F8W079	ATP synthase subunit beta, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5B PE=2 SV=1	49.48	1	94		*5.4*
	F8VQY0	ATP synthase subunit beta, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5B PE=2 SV=1	49.48	1	94		*5.4*
	F8VPV9	ATP synthase subunit beta OS=Homo sapiens GN=ATP5B PE=2 SV=1	49.48	1	94		*5.4*
21	P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	46.17	1	11		*4.0*
	H7C5W9	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (Fragment) OS=Homo sapiens GN=ATP2A2 PE=3 SV=1	46.17	1	11		*4.0*
22	Q53HG2	NADH dehydrogenase (Ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase) variant (Fragment) OS=Homo sapiens PE=2 SV=1	43.40	1	124		*5.0*
	O75306	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens GN=NDUFS2 PE=1 SV=2	43.40	1	124		*5.0*
23	Q6FI52	TAGLN protein OS=Homo sapiens GN=TAGLN PE=2 SV=1	41.32	1	112		*6.0*
	Q5U0D2	Putative uncharacterized protein DKFZp686P11128 OS=Homo sapiens GN=TAGLN PE=2 SV=1	41.32	1	112		*6.0*
	Q53GC9	Transgelin variant (Fragment) OS=Homo sapiens PE=2 SV=1	41.32	1	112		*6.0*

	Q01995	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4	41.32	1	112		*6.0*
	E9PJ32	Transgelin (Fragment) OS=Homo sapiens GN=TAGLN PE=2 SV=1	41.32	1	112		*6.0*
24	Q5JQ13	Vinculin (Fragment) OS=Homo sapiens GN=VCL PE=2 SV=1	41.25	1	22		*1.1*
	P18206	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	41.25	1	22		*1.1*
	B4E3Q9	cDNA FLJ59659, highly similar to Vinculin OS=Homo sapiens PE=2 SV=1	41.25	1	22		*1.1*
	B3KXA2	cDNA FLJ45031 fis, clone BRAWH3018548, highly similar to Vinculin OS=Homo sapiens PE=2 SV=1	41.25	1	22		*1.1*
25	P06753	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1	40.15	1	93		*19.3*
	J3KN67	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=3 SV=1	40.15	1	93		*19.3*
26	A1A5C4	RRBP1 protein OS=Homo sapiens GN=RRBP1 PE=2 SV=1	38.79	1	59		*1.1*
27	A0N4V7	HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1	34.78	1	95		*38.1*
28	Q96BA4	NUCB1 protein OS=Homo sapiens PE=2 SV=1	34.55	1	2		*6.5*
	Q53GX6	Nucleobindin 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	34.55	1	2		*6.5*
	Q02818	Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4	34.55	1	2		*6.5*
	B4DZX0	cDNA FLJ52898, highly similar to Nucleobindin-1 OS=Homo sapiens PE=2 SV=1	34.55	1	2		*6.5*
	B3KUR6	cDNA FLJ40471 fis, clone TESTI2042508, highly similar to Nucleobindin-1 OS=Homo sapiens PE=2 SV=1	34.55	1	2		*6.5*
	A8K7Q1	cDNA FLJ77770, highly similar to Homo sapiens nucleobindin 1 (NUCB1), mRNA OS=Homo sapiens PE=2 SV=1	34.55	1	2		*6.5*

UniProt Human Protein IDs, *cont.*

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*
29	Q9Y2G9	Protein strawberry notch homolog 2 OS=Homo sapiens GN=SBNO2 PE=2 SV=3	34.02	1	29		*1.2*
	K7ES28	Protein strawberry notch homolog 2 OS=Homo sapiens GN=SBNO2 PE=4 SV=1	34.02	1	29		*1.2*
30	B4DUA3	cDNA FLJ50067, weakly similar to Dynamin-binding protein OS=Homo sapiens PE=2 SV=1	33.75	1	66		*27.4*

	B4DTT4	cDNA FLJ54440, weakly similar to Dynamin-binding protein OS=Homo sapiens PE=2 SV=1	33.75	1	66		*27.4*
	A1IGU5	Rho guanine nucleotide exchange factor 37 OS=Homo sapiens GN=ARHGEF37 PE=2 SV=2	33.75	1	66		*27.4*
31	P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	33.35	1	97		*5.4*
	B7Z5E7	cDNA FLJ51046, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1	33.35	1	97		*5.4*
	B7Z597	cDNA FLJ54373, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1	33.35	1	97		*5.4*
	B7Z532	cDNA FLJ51028, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1	33.35	1	97		*5.4*
	B3GQS7	Mitochondrial heat shock 60kD protein 1 variant 1 OS=Homo sapiens GN=HSPD1 PE=2 SV=1	33.35	1	97		*5.4*
32	Q567R0	UQCRH protein OS=Homo sapiens GN=UQCRH PE=2 SV=1	31.31	1	78		*8.2*
	P07919	Cytochrome b-c1 complex subunit 6, mitochondrial OS=Homo sapiens GN=UQCRH PE=1 SV=2	31.31	1	78		*8.2*
33	B8ZZ54	10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=3 SV=1	30.40	1	90		*53.2*
34	F4MHR1	Ubiquitously transcribed tetratricopeptide repeat protein Y-linked transcript variant 83 OS=Homo sapiens GN=UTY PE=2 SV=1	30.01	1	67		*27.4*
35	Q99798	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2	27.89	1	116		*3.0*
	Q71UF1	Aconitase OS=Homo sapiens GN=ACO2 PE=2 SV=1	27.89	1	116		*3.0*
	O75944	Aconitase (Fragment) OS=Homo sapiens GN=ACON PE=2 SV=1	27.89	1	116		*3.0*
	B4DZ08	cDNA FLJ51705, highly similar to Aconitate hydratase, mitochondrial (EC 4.2.1.3) OS=Homo sapiens PE=2 SV=1	27.89	1	116		*3.0*
	B4DW08	cDNA FLJ50886, highly similar to Aconitate hydratase, mitochondrial(EC 4.2.1.3) OS=Homo sapiens PE=2 SV=1	27.89	1	116		*3.0*
	B4DLY4	cDNA FLJ52327, highly similar to Aconitate hydratase, mitochondrial (EC 4.2.1.3) OS=Homo sapiens PE=2 SV=1	27.89	1	116		*3.0*
	B4DJW1	cDNA FLJ54329, highly similar to Aconitate hydratase, mitochondrial(EC 4.2.1.3) OS=Homo sapiens PE=2 SV=1	27.89	1	116		*3.0*
	B4DEC3	cDNA FLJ60429, highly similar to Aconitate hydratase, mitochondrial (EC 4.2.1.3) OS=Homo sapiens PE=2 SV=1	27.89	1	116		*3.0*
	B2RBW5	cDNA, FLJ95737, highly similar to Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear geneencoding mitochondrial protein, mRNA OS=Homo sapiens PE=2 SV=1	27.89	1	116		*3.0*
	A2A274	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=4 SV=1	27.89	1	116		*3.0*
36	D9YZV8	Tropomyosin 1 (Alpha) isoform 7 OS=Homo sapiens GN=TPM1 PE=3 SV=1	27.22	1	76		*35.6*
37	Q5CZ94	Putative uncharacterized protein DKFZp781M0386 OS=Homo sapiens GN=DKFZp781M0386 PE=2 SV=1	26.67	1	9		*13.4*

38	Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	25.18	1	83		*2.6*
39	H0Y450	Probable arginine--tRNA ligase, mitochondrial (Fragment) OS=Homo sapiens GN=RARS2 PE=3 SV=1	24.66	1	71		*25.5*
40	Q05CG0	ARID4A protein (Fragment) OS=Homo sapiens GN=ARID4A PE=2 SV=1	24.65	1	7		*56.6*
	P29374	AT-rich interactive domain-containing protein 4A OS=Homo sapiens GN=ARID4A PE=1 SV=3	24.65	1	7		*6.5*
	C9J1W3	AT-rich interactive domain-containing protein 4A (Fragment) OS=Homo sapiens GN=ARID4A PE=2 SV=1	24.65	1	7		*6.5*
41	Q02045	Myosin light chain 5 OS=Homo sapiens GN=MYL5 PE=2 SV=1	23.73	1	68		*9.5*
	D6RJ91	Myosin light chain 5 (Fragment) OS=Homo sapiens GN=MYL5 PE=2 SV=1	23.73	1	68		*9.5*
	D6RA88	Myosin light chain 5 OS=Homo sapiens GN=MYL5 PE=2 SV=1	23.73	1	68		*9.5*
42	Q7Z3Z1	Myosin light chain 2 OS=Homo sapiens PE=2 SV=1	23.73	1	14		*6.0*
	Q6IB42	MYL2 protein OS=Homo sapiens GN=MYL2 PE=2 SV=1	23.73	1	14		*6.0*
	Q14908	Cardiac ventricular myosin light chain-2 OS=Homo sapiens PE=2 SV=1	23.73	1	14		*6.0*
	P10916	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform OS=Homo sapiens GN=MYL2 PE=1 SV=3	23.73	1	14		*6.0*
	F8VWQ7	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform (Fragment) OS=Homo sapiens GN=MYL2 PE=2 SV=1	23.73	1	14		*6.0*
43	Q6MZX0	Putative uncharacterized protein DKFZp686B12213 (Fragment) OS=Homo sapiens GN=DKFZp686B12213 PE=2 SV=1	20.72	1	15		*6.0*
	Q13099	Intraflagellar transport protein 88 homolog OS=Homo sapiens GN=IFT88 PE=2 SV=2	20.72	1	15		*6.0*
	F5H6C2	Intraflagellar transport protein 88 homolog OS=Homo sapiens GN=IFT88 PE=2 SV=1	20.72	1	15		*6.0*
	E7EW86	Intraflagellar transport protein 88 homolog OS=Homo sapiens GN=IFT88 PE=2 SV=1	20.72	1	15		*6.0*
	B3KX42	cDNA FLJ44712 fis, clone BRACE3019941, highly similar to Intraflagellar transport 88 homolog OS=Homo sapiens PE=2 SV=1	20.72	1	15		*6.0*

Group Nr.

By the rule of parsimony, we have gathered all proteins sharing the same identified peptides into a single group.
Accession Nr.

The accession number from the searched database (DB).
Protein Name

The protein name in the DB.
Protein Score

Sum of the contributing peptide scores.

NOTE: This score can only be used to support the identification of **one** protein per group.
Unique PSMs.

The number of unique peptide-spectrum matches that contribute to the protein assignment.
PSM Serial Nrs.

Sequential number of assigned peptide (in the following table.)
Other Grp.

If the protein is assigned to another group, that (those) group number(s).
% Seq. Cover.

Percent sequence coverage of this protein.

Assigned Peptides

#	Sequence	PTM Site	Nr. Scans	Mascot Score	Expectation	Isolated Mass	Delta Mass	Charge State	Matched Ions	Scan Nr.
1	R.GYSFVTTAER.E		1	39.900	0.012	565.78	0.1	2	'7/18	2270
2	R.FEEELAAR.E		1	34.550	0.047	482.74	1.7	2	'7/14	1776
3	R.QCLPCGPGGKGR.C		2	31.680	0.081	429.54	-0.1	3	'7/22	1939
4	K.CSTSSLLEACTFR.R		4	99.580	5.9e-009	766.35	-1.5	2	'10/24	3100
5	K.YLGEEYVK.A		2	31.820	0.061	500.75	0.7	2	'11/14	2464
6	K.YLGEEYVKAVGNLRK.C		4	25.160	0.34	435.49	-0.1	4	'10/28	4035
7	K.FYSIAR.K		3	24.650	0.24	378.70	-15.0	2	'4/10	3010
8	K.LVTDLTK.V		11	44.370	0.0043	395.24	-0.6	2	'6/12	1539
9	R.TLIYDTSAK.H		1	26.670	0.21	506.28	11.0	2	'4/16	1985
10	R.YLYEIAR.R		5	31.910	0.075	464.25	0.0	2	'6/12	2602
11	K.TASEMVLADDNFSTIVAAVEEGR.A	0.00001000000000000000000.0	2	46.170	0.0027	814.39	-1.4	3	'22/44	4852
12	K.EGYYGYTGAFR.C		2	56.700	0.0001	642.29	-0.2	2	'8/20	2969
13	K.SVIPSDGPSVACVK.K		6	74.760	3.9e-006	708.36	0.4	2	'8/26	2338
14	K.EAFTIMDQNR.D	0.0000010000.0	1	23.730	0.25	620.78	-1.8	2	'5/18	1869

15	K.EALRNDSSCTEALYNIGLTYEKLNR.L		1	20.720	1.2	489.25	9.0	6	'7/48	4532
16	K.IQVLQQQADDAEER.A		1	87.950	2.3e-007	821.91	0.4	2	'9/26	2070
17	K.DCHLAQVPSHTVVAR.S		8	54.680	0.00051	563.95	-0.4	3	'11/28	2376
18	K.SVEEYANCHLAR.A		2	56.270	0.00074	724.83	-0.3	2	'9/22	2182
19	R.SKQLEEDIAAKEK.L		2	21.490	1.2	496.94	2.1	3	'12/24	2132
20	K.ASYLDCIR.A		4	48.130	0.0015	499.24	2.8	2	'12/14	2527
21	K.IECVSAETTEDCIAK.I		4	77.330	9.2e-007	863.39	-0.7	2	'9/28	2018
22	R.ELTPQVVSAAR.I		1	41.250	0.017	585.83	1.1	2	'7/20	2101
23	K.VPQVSTPTLVEVSR.N		1	52.860	0.00049	756.43	0.2	2	'9/26	2906
24	R.DDTVCLAK.L		2	35.020	0.039	461.22	0.4	2	'7/14	1385
25	R.ARQLEEELR.T		1	20.950	2.2	381.88	-0.3	3	'7/16	2242
26	R.SAGWNIPIGLLYCDLPEPRKPLEK.A		1	55.210	0.00024	692.37	4.0	4	'14/46	4991
27	K.DSGFQMNQLRGK.K		2	28.200	0.21	460.90	1.4	3	'8/22	2453
28	K.IWHHTFYNELR.V		4	24.350	0.48	505.92	-2.4	3	'8/20	4315
29	K.AVLDLQNK.L		2	34.020	0.06	450.76	-0.3	2	'5/14	2680
30	K.VGAHAGEYGAEALER.M		2	57.510	0.00018	510.58	-0.1	3	'7/28	2950
31	R.KCSTSSLLEACTFRRP.-		6	37.390	0.026	638.32	0.1	3	'7/30	3333
32	R.QLEEELR.T		1	24.190	0.6	458.74	-1.0	2	'4/12	1670
33	K.CDEWSVNSVGK.I		2	65.220	1.1e-005	640.78	0.0	2	'8/20	2217
34	R.ELEEISERLEEAGGATSVQIEMNK.K	0.000000000000000000000100.0	5	67.440	1.9e-005	893.43	0.5	3	'17/46	3840
35	R.GFFYTPK.T		1	28.340	0.15	430.22	-0.5	2	'5/12	3008
36	K.KSASDLTWDNLK.G		2	26.550	0.37	459.91	-0.1	3	'12/22	2794
37	K.SASDLTWDNLK.G		2	65.950	3.8e-005	625.31	1.2	2	'8/20	3041
38	R.LKCDEWSVNSVGK.I		4	74.770	5e-006	761.37	1.2	2	'19/24	2566
39	K.CCTESLVNR.R		1	46.630	0.00083	569.75	-1.2	2	'7/16	1482
40	K.TVGMVAGDEESYEVFADLFDPVIK.L	0.00010000000000000000000.0	1	59.290	0.00013	883.09	-0.2	3	'23/46	5334
41	K.HSTIFENLANK.A		4	68.970	2.4e-005	637.33	0.0	2	'9/20	3402
42	R.KLVIIESDLER.A		4	34.360	0.038	657.89	3.7	2	'6/20	3485
43	-.MFLSFPTTK.T		1	23.880	0.48	536.28	-0.7	2	'7/16	3786
44	K.SVIPSDGPSVACVKK.A		6	43.190	0.0079	772.41	0.0	2	'7/28	2261
45	K.CASLQKFGER.A		2	49.980	0.0013	598.30	-0.4	2	'7/18	2062
46	K.SASDLTWDNLKGK.K		4	83.010	8e-007	717.86	-0.8	2	'10/24	2647
47	R.IEANEALVKALE.-		1	57.940	0.00031	650.36	2.9	2	'18/22	3636
48	K.SDNCEDTPEAGYFAVAVVKK.S		2	62.150	5.3e-005	734.01	-1.1	3	'19/38	3272
49	R.WCAVSEHEATK.C		10	57.410	0.0001	659.30	2.6	2	'9/20	1756
50	R.IEANEALVK.A		1	39.080	0.02	493.78	0.0	2	'8/16	1701

51	R.EQAEAEVASLNR.R		1	39.670	0.013	658.83	2.2	2	'8/22	1844
52	-.SDVLELTDDNFESR.I		1	73.000	3.5e-006	820.38	1.6	2	'9/26	3507
53	K.KSASDLTWDNLKGK.K		2	73.960	8.2e-006	521.61	0.3	3	'10/26	2697
54	K.KATDAEADVASLNRR.I		2	24.120	0.62	539.62	-0.7	3	'8/28	2116
55	R.CLVEKGDVAFVK.H		2	63.220	0.00011	455.58	-0.1	3	'11/22	2973
56	R.KCSTSSLLEACTFR.R		2	35.640	0.027	553.93	2.1	3	'7/26	3051
57	K.SKEFQLFSSPHGK.D		4	43.840	0.0088	497.92	-1.3	3	'6/24	3482
58	K.LHDRNTYEKYLGEEYVK.A		2	22.680	0.75	540.02	-0.3	4	'9/32	3810
59	R.EQEITAVQAR.M		1	38.790	0.021	572.80	3.8	2	'7/18	1452
60	R.EGTCPEAPTDECKPVKWCALSHHER.L		6	25.370	0.22	749.34	1.3	4	'18/48	3596
61	K.LCYVALDFENEMATAASSSSLEK.S		3	78.030	1.1e-006	846.06	-0.4	3	'22/44	4704
62	K.YLGEEYVKAVGNLR.K		2	21.260	1	537.62	0.5	3	'12/26	4192
63	K.HIAEDADRKYEEVAR.K		2	27.720	0.2	451.22	-4.0	4	'12/28	2533
64	R.FDEFFSEGCAPGSKK.D		2	22.750	0.35	569.26	0.8	3	'11/28	3330
65	R.IQLVEEELDR.A		6	62.070	8.9e-005	622.33	0.2	2	'8/18	3000
66	R.QAGLNKDPR.C		1	33.750	0.045	499.77	-9.3	2	'6/16	1794
67	K.KMMEGK.A	0.011000.0	1	30.010	0.048	378.18	13.1	2	'5/10	2377
68	K.EAFTLMDQNR.D	0.0000010000.0	1	23.730	0.25	620.78	-1.8	2	'5/18	1869
69	K.CLKDGAGDVAFVK.H		2	54.850	0.00065	460.57	-1.1	3	'19/24	2890
70	R.GIVEQCCTSICSLYQLENYCN.-		3	72.500	9.9e-007	871.04	-0.2	3	'18/40	4389
71	-.TFQSVESSTR.K		1	24.660	0.43	381.19	15.7	3	'4/18	2488
72	K.DKEACVHKILR.Q		4	32.260	0.069	456.92	0.4	3	'11/20	2830
73	R.EGTCPEAPTDECKPVK.W		4	54.160	0.00018	909.41	-0.4	2	'8/30	1455
74	R.AMSDLELR.Q	0.01000000.0	1	25.740	0.41	475.74	7.1	2	'6/14	1685
75	R.DDTVCLAKLHDR.N		2	38.660	0.016	481.57	0.3	3	'13/22	2428
76	K.AEADVASLNRR.I		1	27.220	0.27	401.21	-0.1	3	'5/20	1574
77	R.IEEELGDEAR.F		1	53.230	0.00032	580.78	0.0	2	'16/18	1570
78	R.LELCDER.V		1	31.310	0.069	467.72	3.0	2	'6/12	1625
79	K.HSTIFENLANKADR.D		2	42.490	0.0092	539.28	1.4	3	'14/26	3751
80	R.SETKDLLFRDDTVCLAK.L		4	31.370	0.1	671.01	-0.3	3	'10/32	3553
81	R.SETKDLLFR.D		4	37.330	0.025	554.80	0.2	2	'12/16	2821
82	K.AIMTYVSCFYHAFAGAEQAETAANR.I	0.0010000000000000000000000.0	1	51.370	0.00053	932.43	4.1	3	'12/48	4840
83	R.IGCIITAR.K		1	25.180	0.54	452.26	2.5	2	'6/14	2206
84	K.MYLGYEYVTAIR.N	0.100000000000.0	4	70.690	1.2e-005	747.87	3.0	2	'8/22	3885

85	R.MFLSFPTTK.T	0.100000000.0	2	28.670	0.17	544.28	-3.1	2	'5/16	3579
86	K.DGAGDVAFVK.H		2	67.570	2.7e-005	489.75	0.0	2	'9/18	2147
87	K.MYLGYEYVTAIRNLR.E	0.100000000000000.0	10	22.980	0.75	626.66	-0.1	3	'8/28	4586
88	R.AMSDLELRQCLPCGPGGKGR.C	0.01000000000000000000.0	1	27.530	0.18	555.27	-0.9	4	'20/38	3201
89	K.EKSEFKLELDDVTSNMEQIIK.A	0.000000000000000100000.0	1	23.600	0.5	628.82	2.0	4	'7/40	4180
90	R.DGDILGKYVD.-		1	30.400	0.12	547.77	1.6	2	'6/18	3219
91	R.LKCDEWSVNSVGKIECVSAETTEDCIAK.I		2	27.880	0.13	807.88	0.0	4	'19/54	4057
92	K.HQTVPQNTGGKNPDPWAK.N		4	36.330	0.036	659.00	0.6	3	'16/34	2457
93	K.AADAEAEVASLNR.R		1	40.150	0.012	658.83	2.2	2	'8/24	1844
94	K.SLQDIIAILGMDELSEEDKLTVSR.A	0.000000000010000000000000.0	1	49.480	0.0015	897.80	-1.5	3	'11/46	5351
95	K.GITLSVRP.-		1	34.780	0.029	421.76	0.6	2	'4/14	1888
96	K.KASYLDCIR.A		4	44.520	0.0042	563.29	-2.0	2	'6/16	2579
97	R.KPLVIIAEDVDGEALSTLVLNR.L		1	33.350	0.018	789.12	-1.4	3	'17/42	5386
98	K.DLLFRDDTVCLAK.L		4	54.180	0.0015	783.40	1.3	2	'7/24	3752
99	K.ATDAEADVASLNRR.I		2	26.140	0.35	496.92	-1.0	3	'7/26	1866
100	K.AAWGKVGAHAGEYGAEALER.M		1	31.230	0.11	511.51	-1.1	4	'7/38	3996
101	R.AQCGGGLLGVR.T		1	64.820	5.5e-005	544.29	-0.5	2	'9/20	2492
102	K.AGFAGDDAPR.A		2	46.260	0.0015	488.73	0.9	2	'8/18	1460
103	K.EACVHKILR.Q		2	27.940	0.19	375.88	-0.9	3	'8/16	2662
104	K.MYLGYEYVTAIRNLR.E		2	23.450	0.67	621.33	-0.5	3	'7/28	4687
105	R.KLVIIESDLERAEER.A		2	27.580	0.2	600.67	0.7	3	'7/28	3939
106	R.QCLPCGPGGK.G		1	26.930	0.097	537.25	0.7	2	'7/18	1511
107	M.FLSFPTTK.T		1	23.050	0.41	470.76	1.2	2	'4/14	3119
108	R.MFLSFPTTK.T		1	23.880	0.48	536.28	-0.7	2	'7/16	3786
109	K.KVPQVSTPTLVEVSR.N		19	67.530	1.1e-005	820.47	-0.5	2	'12/28	2929
110	R.IQLVEEELDRAQER.L		6	35.040	0.048	576.64	0.9	3	'7/26	3190
111	R.NLREGTCPEAPTDECKPVK.W		2	22.220	1.7	551.01	0.8	4	'13/36	2314
112	K.YDEELEER.L		1	41.320	0.0028	541.74	0.1	2	'6/14	1457
113	-.MFLSFPTTK.T	0.100000000.0	2	28.670	0.17	544.28	-3.1	2	'5/16	3579
114	K.EFQLFSSPHGK.D		2	33.860	0.064	426.22	0.2	3	'6/20	3327
115	R.SEAPPHIFSISDNAYQYMLTDRENQSILITGESGAGK.T	0.0000000000000000010000000000000000000.0	1	27.380	0.13	1014.74	6.0	4	'6/72	4312

116	K.HPNGTQETILLNHTFNETQIEWFR.A		1	27.890	0.19	732.11	1.9	4	'25/46	4829
117	K.HIAEDSDRKYEEVAR.K		1	27.300	0.27	455.23	4.7	4	'14/28	2315
118	K.CSTSSLLEACTFRRP.-		10	36.680	0.024	595.62	-1.5	3	'8/28	3341
119	K.LCYVALDFENEMATAASSSSLEK.S	0.00000000000100000000000.0	7	78.570	8.3e-007	851.39	-2.1	3	'22/44	4247
120	K.SIDDLEEK.V		2	41.260	0.014	474.73	0.4	2	'11/14	1591
121	-.KVTYTSQEDLVEKK.C		1	60.030	0.00013	556.63	-1.3	3	'10/26	1984
122	K.DSGFQMNQLR.G		2	55.380	0.0003	598.28	4.3	2	'9/18	2581
123	K.SVIPSDGPSVACVKKASYLDCIR.A		4	26.680	0.3	631.32	-0.6	4	'17/44	3827
124	K.GHMLADVVAIIGTQDIVFGEVDR.-	0.00100000000000000000000.0	1	43.400	0.0068	824.42	-3.2	3	'17/44	5288

#

Serial (sequential) number for peptide.
Sequence

Assigned peptide sequence. Periods (".") delimit the sequence for internal peptides.
PTM Site

Location of the post-translational modification (PTM) in the peptide.

Modification codes: [1] Oxidation (M)
Nr. Scans

The number of MS/MS scans that were matched to this peptide.
Mascot Score

Score given to this peptide/spectrum match by Mascot.
Expectation

The number of matches with equal or better scores that are expected to occur by chance alone.
Isolated Mass

"Mass" in the Orbitrap analyzer.
Delta Mass

Difference between the observed and theoretical masses, in ppm.
Charge State

Inferred ionic state of the peptide.
Matched Ions

Number of matched MS/MS ions, as reported by Mascot.
Scan Nr.

MS/MS scan number in the original Xcalibur RAW file.