Table S2. Peptides Derived from Proteins with Removed Signal or Transit Peptides

#	z	Score	Fwd-Rev Score	SPI %	N-terminal Modification	Start AA Position	Sequence Map	Modification	m/z Measured (Da)	MH^+ Matched (Da)	MH^+ Mass Shift (Da)	MH^+ Error (ppm)	Protein MW (Da)	Accession #	Protein Name	Signal Peptide Annotated in Swiss-Prot**	4 AAs Before Cleavage	Cleavage Site	Sample***
1	2	11.64	11.64	56.3	$HSCH_2CH_2CO$-	28	(L)SG|A/PQ/A/SAADV/V/V/V/HGR(R)		854.923	1708.843	-0.0048	-2.8	44292.3	P09110	3-ketoacyl-CoA thiolase, peroxisomal precursor	1-26	AAPC	26	treated
2	2	22.60	14.72	96.2	$HSCH_2CH_2CO$-	70	(S)D/M|P|P\L|T|L/E/GI/QD/R(V)		786.8759	1572.74	0.0049	3.1	17417.4	O14561	Acyl carrier protein, mitochondrial precursor	1-68 (similarity)	CRQY	68	both
3	2	15.88	15.88	69.7	$HSCH_2CH_2CO$-	45	(Q)K|T/GT/A/E/M/S/SI/L/E/E/R(I)	K:PITC	887.8983	1774.781	0.0085	4.8	59750.9	P25705	ATP synthase subunit alpha, mitochondrial precursor	1-43 (similarity)	NTHL	43	both
4	2	11.69	2.88	70.7	$HSCH_2CH_2CO$-	44	(P)V/P|PL/PEYGGKV/R(Y)	K:PITC	767.8823	1534.755	0.0028	1.8	28908.8	P24539	ATP synthase subunit b, mitochondrial precursor	1-42	PHLV	42	both
5	2	14.69	8.01	75.2	$HSCH_2CH_2CO$-	48	(A)A\Q\T|S|PS/PK/A/GA/A/TGR(I)	K:PITC	811.8756	1622.741	0.0026	1.6	56560.2	P06576	ATP synthase subunit beta, mitochondrial precursor	1-47 (similarity)	VRDY	46	both
6	3	11.56	11.56	51.2	$HSCH_2CH_2CO$-	25	(F)AK/L/V/R/PPVQV/Y/GIE/G/R(Y)	K:PITC	669.0219	2005.051	0.0001	0.1	23277.4	P48047	ATP synthase subunit O, mitochondrial precursor	1-23	VVRP	23	treated
7	3	10.23	10.23	59.1	$HSCH_2CH_2CO$-	26	(F)GS|D/Q/SE/N/V/D/RGAGSIR(E)		579.2645	1735.766	0.0125	7.2	12248.9	Q9UII2	ATPase inhibitor, mitochondrial precursor	1-25 (similarity)	QARG	24	vehicle
8	3	16.73	16.73	75.7	$HSCH_2CH_2CO$-	27	(G)S/D/Q/S/E/N/V/D/RGA/GSI/R(E)		560.2573	1678.745	0.0124	7.4	12248.9	Q9UII2	ATPase inhibitor, mitochondrial precursor	1-25 (similarity)	ARGF	25	both
9	3	13.22	7.05	68.9	$HSCH_2CH_2CO$-	28	(S)D|Q/S/E/N/V/D/RGAGSIR(E)		531.2425	1591.713	0	0	12248.9	Q9UII2	ATPase inhibitor, mitochondrial precursor	1-25 (similarity)	RGFG	26	treated
10	3	20.04	20.04	94.1	$HSCH_2CH_2CO$-	36	(T)AT\F\A\QA\L\QF\V/PETQ/V/S/L/L/D/NGL/R(V)		869.4581	2606.328	0.0314	12.1	52646.1	P31930	Cytochrome b-c1 complex subunit 1, mitochondrial precursor	1-34	ALRS	34	both
11	2	23.94	23.94	98.4	$HSCH_2CH_2CO$-	15	(G)D/PEEE\E\E\E\E|E|E|L|V|D/PL/T/T/V/R(E)		1238.0355	2475.06	0.0034	1.4	10738.8	P07919	Cytochrome b-c1 complex subunit 6, mitochondrial precursor	1-13	LTES	13	both
12	3	18.24	14.34	87.6	$HSCH_2CH_2CO$-	24	(A)H\E\S\V\V\KSED/F/S/L/P/A/YMD/R(R)	K:PITC	778.3432	2333.003	0.0115	4.9	19576.8	P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor	1-22	VCVR	22	both
13	2	15.29	15.29	77.9	$HSCH_2CH_2CO$-	43	(S)H|G|SQ|E|T/D|E/E/FD|AR(W)		804.8168	1608.623	0.0032	2	16774.3	P20674	Cytochrome c oxidase subunit 5A, mitochondrial precursor	1-41	VRCY	41	both
14	2	22.04	15.26	96.2	$HSCH_2CH_2CO$-	33	(A)SGG\G\V|P/TD/E/E/Q/A/T/GL/E/R(E)		895.8989	1790.786	0.0044	2.5	13695.8	P10606	Cytochrome c oxidase subunit 5B, mitochondrial precursor	1-31	MRSM	31	both
15	3	15.38	15.38	73.9	$HSCH_2CH_2CO$-	86	(S)DL\ELH|PPS\Y/P/W/SH/R(G)		607.9597	1821.838	0.0268	14.7	35390.1	P08574	Cytochrome c1, heme protein, mitochondrial precursor	1-84	AVSA	84	vehicle
16	2	14.85	6.35	80.0	$HSCH_2CH_2CO$-	69	(D)DL\V|T\V|K|T|PAF/A/ESV/TE/GDVR(W)	K:PITC	1179.0588	2357.115	-0.0049	-2.1	48640.5	P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor	1-67 (similarity)	AVCK	67	treated
17	2	14.41	14.41	78.3	$HSCH_2CH_2CO$-	23	(D)D\E\V\D\V|DGT|V/E/E/DL/GK/S/R(E)	K:PITC	1043.4306	2085.874	-0.02	-9.6	92469.3	P14625	Endoplasmin precursor	1-21	SVRA	21	treated
18	2	22.62	9.95	96.7	$HSCH_2CH_2CO$-	25	(E)E|Q|P/P/E/T/A/A/Q/R(C)		607.7791	1214.547	0.0039	3.2	54393	Q96HE7	ERO1-like protein alpha precursor	1-23	SGHG	23	both
19	2	12.34	2.33	83.4	$HSCH_2CH_2CO$-	29	(R)E\V\L|V|PE/GPLY/R(V)		680.3482	1359.698	-0.0086	-6.3	65034.6	Q969P0	Immunoglobulin superfamily member 8 precursor	1-27 (potential)	GCWA	27	both

20	2	19.64	4.58	95.8	HSCH$_2$CH$_2$CO-	26	(K)V|F|E|V/H/V/R(P)		487.2515	973.492	0.0033	3.4	30654.5	P13598	Intercellular adhesion molecule 2 precursor	1-24 (predicted)*	GSDE	24	both
21	2	18.86	18.86	90.9	HSCH$_2$CH$_2$CO-	45	(S)TQA\A|T|Q/V|V|L/N/V|PE/T/R(V)		857.9441	1714.879	0.0017	1	54366.5	O75439	Mitochondrial-processing peptidase subunit beta, mitochondrial precursor	1-45 (potential)	NRLR	43	vehicle
22	2	12.57	12.57	74.3	HSCH$_2$CH$_2$CO-	35	(A)G\GG\V/H/I/E/P/R(Y)		505.2492	1009.488	0.0027	2.7	12058.5	O95178	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial precursor	1-33 (similarity)	GVRH	33	vehicle
23	2	23.92	14.32	100.0	HSCH$_2$CH$_2$CO-	34	(G)A|G|G|A|L|F/V/H/R(D)		508.2618	1015.514	0.0021	2.1	27391.7	P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial precursor	1-32	VMQN	32	both
24	3	9.43****	9.43	62.4	HSCH$_2$CH$_2$CO-	38	(E)S/A/G|AD/TRPTVRPR(N)		491.2547	1471.743	0.0061	4.2	30241.7	O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor	1-36 (similarity)	PVRR	36	treated
25	2	13.19	6	77.5	HSCH$_2$CH$_2$CO-	39	(W)E|T/E/E/R/P/R(T)		502.7278	1004.447	0.0018	1.7	30540.1	Q13162	Peroxiredoxin-4	1-37 (predicted)*	AVQG	37	treated
26	3	12.03	12.03	71.3	HSCH$_2$CH$_2$CO-	23	(L)R\PGDCE\V/C|I/S/YL/G/R(F)		552.5879	1655.734	0.0153	9.2	20256.7	P55145	Protein ARMET precursor	1-21	GSRA	21	vehicle
27	2	23.72	20.54	100.0	HSCH$_2$CH$_2$CO-	26	(S)DV|L|E|L|T|D/D/N/F/E/S/R(I)		820.8607	1640.711	0.0033	2	56782.7	P30101	Protein disulfide-isomerase A3 precursor	1-24	LAAA	24	both
28	2	18.02	18.02	94.8	HSCH$_2$CH$_2$CO-	21	(L)YSSSDD\V|I|E|L|T|P/SNFN/R(E)		1016.4674	2031.896	0.0311	15.3	48121.6	Q15084	Protein disulfide-isomerase A6 precursor	1-19 (potential)	AVNG	19	both
29	2	26.66	16.1	98.1	HSCH$_2$CH$_2$CO-	19	(D)A/P/E/E/E/D/H|V|L/V|L/R(K)		747.8721	1494.726	0.0112	7.5	57116.6	P07237	Protein disulfide-isomerase precursor	1-17	LVRA	17	both
30	2	22.30	14.24	98.3	HSCH$_2$CH$_2$CO-	32	(D)GV|G\GD|P|A|V|A/L/PH/R(R)		667.3379	1333.668	0.0004	0.3	57549.2	P49257	Protein ERGIC-53 precursor	1-30	FVRG	30	treated
31	2	22.36	10.74	97.6	HSCH$_2$CH$_2$CO-	58	(P)L/I|P|I/V/V/E/Q|T/G/R(G)		656.8659	1312.729	-0.0048	-3.7	30180.2	Q16740	Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial precursor	1-? (potential)	TRAL	56	both
32	2	17.12	17.12	91.4	HSCH$_2$CH$_2$CO-	18	(E)SE/T|T/T/S/L/V/L/E/R(S)		662.3325	1323.646	0.0117	8.8	17259.8	Q04837	Single-stranded DNA-binding protein, mitochondrial precursor	1-16 (similarity)	FVRH	16	both
33	2	13.11	13.11	69.8	HSCH$_2$CH$_2$CO-	30	(A)Q|T|A/A/A/T/A/P/R(I)		487.7408	974.472	0.0019	2	31629.9	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial precursor	1-28	ASRG	28	treated
34	2	15.11	4.06	79.0	HSCH$_2$CH$_2$CO-	23	(F)K|I|P/I/EE/LED/R(V)	K:PITC	732.8484	1464.686	0.0034	2.3	18929.7	P04234	T-cell surface glycoprotein CD3 delta chain precursor	1-21	QVSP	21	both
35	2	20.76	13.57	97.7	HSCH$_2$CH$_2$CO-	61	(T)TF\N|I|Q/D/G/PDF/Q/D/R(V)		820.8636	1640.701	0.019	11.6	18383.4	Q99757	Thioredoxin, mitochondrial precursor	1-59 (similarity)	RISL	59	both
36	2	14.67	9.57	78.7	HSCH$_2$CH$_2$CO-	25	(A)G/P|P/PI\Q|DGE/FTF/L/L/PAGR(K)		1000.5047	1999.995	0.0075	3.8	25205.9	Q13445	Transmembrane emp24 domain-containing protein 1 precursor	1-23 (potential)	EVGG	23	treated
37	2	11.84	6.21	74.6	HSCH$_2$CH$_2$CO-	33	(I)SF/H|L/PINS/R(K)		579.7898	1158.572	-0.0001	-0.1	24976.1	P49755	Transmembrane emp24 domain-containing protein 10 precursor	1-31 (potential)	LVLA	31	both
38	2	19.63	19.63	88.0	HSCH$_2$CH$_2$CO-	33	(V)SE/P/T/T/V/A/F/D/V/R(P)		655.3098	1309.609	0.003	2.3	18795.3	Q969H8	UPF0556 protein C19orf10 precursor	1-31 (potential)	PAEA	31	both

*The signal peptides are predicted by SignalP 3.0 (Emanuelsson O, Brunak S, von Heijne G, & Nielsen H (2007) Locating proteins in the cell using TargetP, SignalP and related tools. *Nat Protoc* 2:953-971.)

** The term ‘potential’ and 'similarity' are qulifiers used in the Swiss-Prot database for the annotatoin describing information that is not based on experimental findings.'Potential' indicates that there is some logical or conclusive evidence that the given annotation could apply. This non-experimental qualifier is often used to present results from protein sequence analysis software tools, which are only annotated if the result makes sense in the biological context of a given protein. When an biological information was experimentally obtained for a given protein (or part of it), it may be transferred to other protein family members within a certain taxonomic range, dependent on the biological event or characteristic. The propagated information is tagged with the term ‘similarity’.
*** The N-CLAP peptides are either detected in vehicle, cisplatin treated or both samples.
**** This N-CLAP peptide has a lower score, which is also included in the list because this peptide is derived from the removal of the transit peptide annotated in Swiss-Prot database.