

**Table S1. Peptides Derived from Protein N-terminus Identified by N-CLAP Approach**

#	z	Score	Fwd-Rev Score	SPI %	N-terminal Modification	Start AA Position	Sequence Map	Modification	m/z Measured (Da)	MH <sup>+</sup> Matched (Da)	MH <sup>+</sup> Mass Shift (Da)	MH <sup>+</sup> Error (ppm)	Protein MW (Da)	Accession #	Protein Name	Sample*
1	2	19.49	19.49	90.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)Q A W Y M D D/A PGD PR(Q)		805.3312	1609.641	0.0141	8.8	21498.5	Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	both
2	2	16.13	16.13	81.8	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)LEN L E E E G L P K N PD L R(I)	K:PITC	1044.994	2088.973	0.0078	3.8	45531.6	Q15008	26S proteasome non-ATPase regulatory subunit 6	both
3	3	12.29	12.29	71.4	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)GV TVKDV N Q Q E F V R(A)	K:PITC	614.6296	1841.867	0.0069	3.8	16060.6	P39019	40S ribosomal protein S19	treated
4	3	15.2	15.2	76.8	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(G)H QQL Y W S H P R(K)		480.5624	1439.664	0.0089	6.2	6676.8	P62273	40S ribosomal protein S29	vehicle
5	2	16.83	2.59	93.8	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)V H G S LA R(A)		414.2123	827.419	-0.0019	-2.3	6647.9	P62861	40S ribosomal protein S30	both
6	2	13.50	13.50	65.1	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)K F N P F V T SDR(S)	K:PITC	717.323	1433.634	0.0047	3.3	17256.3	Q9UNX3	60S ribosomal protein L26-like 1	both
7	2	21.39	4.29	98.1	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)I L L E V N N R(I)		529.7906	1058.566	0.0076	7.2	34333.2	O15144	Actin-related protein 2/3 complex subunit 2	both
8	3	15.11	15.11	71.4	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)AYHSSLM D PDT K L I GNM A L L PI R(S)	K:PITC	927.1183	2779.344	-0.0035	-1.3	20546.8	O15145	Actin-related protein 2/3 complex subunit 3	both
9	3	10.18	10.18	64.1	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)AHL LQDD IS SSYTTT TTL T/A PPS R(V)		888.7698	2664.282	0.0127	4.8	41522.9	O00767	Acyl-CoA desaturase	vehicle
10	2	15.80	5.40	86.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)T V E E L Y R(N)		499.2368	997.466	0.0004	0.4	57561.4	Q9BZZ5	Apoptosis inhibitor 5	both
11	2	17.35	10.02	89.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)L A E L Y V S D R(E)		577.2843	1153.556	0.0055	4.8	62943.3	O43776	Asparaginyl-tRNA synthetase, cytoplasmic	both
12	2	12.42	12.42	82.9	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)P P V Q V S PLIKL GR(Y)	K:PITC	813.947	1626.886	0.0009	0.5	7933.2	P56385	ATP synthase subunit e, mitochondrial	treated
13	2	12.81	12.81	64.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)E L S A E Y L R(E)		534.7564	1068.503	0.0025	2.3	10116.6	Q9H3K6	BolA-like protein 2	vehicle
14	2	23.72	23.72	100.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)VGG E A A A A V E E L V S GV R(Q)		851.4279	1701.848	0.0009	0.5	13196	Q96HQ2	CDKN2AIP N-terminal-like protein	both
15	2	22.45	22.45	97.8	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)GGEA A A A V E E L V S GV R(Q)		801.8925	1602.779	-0.0015	-0.9	13196	Q96HQ2	CDKN2AIP N-terminal-like protein	both
16	2	10.23	10.23	58.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(A)L S A E TE S HI Y R(A)		697.3228	1393.642	-0.0033	-2.4	23973.8	O14569	Cytochrome b561 domain-containing protein 2	both
17	2	10.33	4.21	69.3	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)A PE V L PK PR(M)	K:PITC	615.3123	1229.617	0.0004	0.3	8781.5	P09669	Cytochrome c oxidase polypeptide VIc precursor	both

18	2	12.15	5.27	78.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(A)P E V L PK PR(M)	K:PITC	579.7951	1158.58	0.0031	2.7	8781.5	P09669	Cytochrome c oxidase polypeptide VIc precursor	treated
19	2	23.47	18.17	100.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)F L E L D T N L P A N R(V)		745.8717	1490.731	0.0053	3.6	14195.4	A6NHG4	D-dopachrome decarboxylase-like protein	both
20	2	14.06	14.06	69.4	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)FV L V E M V D TV R(I)		698.3548	1395.701	0.0013	0.9	22918	Q9Y535	DNA-directed RNA polymerase III subunit RPC8	treated
21	2	12.04	12.04	57.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(G)K D Y YQ T L G L A R(G)	K:PITC	775.8754	1550.713	0.0305	19.7	38044.3	P25685	DnaJ homolog subfamily B member 1	both
22	2	11.26	11.26	61.9	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)DY Y E V LG V Q R(H)		665.3156	1329.614	0.0096	7.2	36087.2	O75190	DnaJ homolog subfamily B member 6	both
23	2	10.02	10.02	61.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)V N F T V D Q I R(A)		590.295	1179.583	0.0001	0	95338.7	P13639	Elongation factor 2	vehicle
24	2	16.18	3.06	84.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)N F T VD Q I R(A)		540.7636	1080.514	0.0057	5.2	95338.7	P13639	Elongation factor 2	both
25	2	14.94	5.26	68.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)K P L L Q GHE R(S)	K:PITC	707.3579	1413.713	-0.0044	-3.1	36502	Q13347	Eukaryotic translation initiation factor 3 subunit I	both
26	2	11.16	11.16	62.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)A I M T M L A D HAA R(Q)		694.8341	1388.648	0.0126	9.1	123386.6	O14980	Exportin-1	both
27	2	11.34	2.67	62.9	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)K P I NV R(V)	K:PITC	475.2422	949.475	0.0025	2.6	69413.2	P15311	Ezrin	treated
28	3	10.70	10.70	60.1	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(A)V GN I NE L PENILLELF TH V PAR(Q)		859.4567	2576.354	0.0014	0.6	29746.9	Q9H4M3	F-box only protein 44	both
29	2	19.64	19.64	98.4	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(G)V Q V E T I S PGD GR(T)		673.3286	1345.642	0.0083	6.2	11950.8	P62942	FK506-binding protein 1A	both
30	2	17.34	17.34	85.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	4	(V)Q V E T I S PGD G R(T)		623.7907	1246.573	0.0009	0.7	11950.8	P62942	FK506-binding protein 1A	both
31	2	15.54	11.28	79.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(G)I Q G L A K L I A D V A PSA R(E)	K:PITC	980.0361	1959.055	0.0095	4.8	42593.2	P39748	Flap endonuclease 1	vehicle
32	4	12.19	12.19	69.9	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)Y Q YPALTPEQKK E L SD I AHR(I)	K:PITC	687.075	2745.262	0.016	5.8	39420.2	P04075	Fructose-bisphosphate aldolase A	both
33	3	10.70	10.70	68.8	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)H S YPA L SAE Q KK E L S D I AL R(I)	K:PITC	872.0858	2614.225	0.0177	6.8	39456.1	P09972	Fructose-bisphosphate aldolase C	vehicle
34	2	19.14	19.14	81.3	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(C)G I F A Y L N Y H V P R(T)		769.3835	1537.762	-0.0023	-1.5	78806.9	Q06210	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	vehicle
35	2	11.84	11.84	59.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)P P Y T V V Y F PVR(G)		713.3692	1425.724	0.0076	5.3	23356	P09211	Glutathione S-transferase P	treated
36	2	17.45	17.45	95.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)P Y T V V Y F PV R(G)		664.841	1328.671	0.004	3	23356	P09211	Glutathione S-transferase P	both
37	2	20.94	20.94	96.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)P M F I V N T N V P R(A)		688.3584	1375.686	0.0234	17	12476.4	P14174	Macrophage migration inhibitory factor	both

38	2	22.24	22.24	95.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)M/F I V N/T/N/V PR(A)		639.8228	1278.633	0.005	3.9	12476.4	P14174	Macrophage migration inhibitory factor	both
39	2	17.01	5.13	87.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	4	(M)F I V N/T/NV P/R(A)		574.3038	1147.593	0.0075	6.5	12476.4	P14174	Macrophage migration inhibitory factor	vehicle
40	2	13.72	3.99	83.6	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)V N L L Q I/V/R(D)		521.8081	1042.608	0.0012	1.1	6961.2	O75438	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1	vehicle
41	2	11.40	2.32	71.5	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)N L L Q I/V/R(D)		472.2796	943.539	0.0126	13.3	6961.2	O75438	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1	vehicle
42	2	24.15	24.15	98.9	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)V/N PT V F F D I A V D G/E/PL GR(V)		1017.5043	2034	0.0012	0.6	18012.6	P62937	Peptidyl-prolyl cis-trans isomerase A	both
43	2	23.89	23.89	98.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)N/PT V F F D I A V D G/E/PL GR(V)		967.9696	1934.932	0.0002	0.1	18012.6	P62937	Peptidyl-prolyl cis-trans isomerase A	both
44	2	22.41	22.41	99.3	HSCH <sub>2</sub> CH <sub>2</sub> CO-	4	(N)PT V F F D I A V D G/E/PL GR(V)		910.9378	1820.889	-0.0204	-11.2	18012.6	P62937	Peptidyl-prolyl cis-trans isomerase A	both
45	2	26.97	21.75	100.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)GGL L L G D V A PNF/E/A/N TT/V GR(I)		1045.0237	2089.038	0.0019	0.9	25035.1	P30041	Peroxiredoxin-6	both
46	2	15.71	11.03	72.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)G/H L Q E GF/GCV/V TN/R(F)		802.871	1604.731	0.0039	2.4	44965.6	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	both
47	2	10.33	3.62	75.6	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)L P/V/A LQTR(L)		493.2815	985.55	0.0058	5.9	30472.4	O60828	Polyglutamine-binding protein 1	both
48	2	13.39	8.50	82.1	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)G/P T P/S GTNV/G SSGR(S)		681.3101	1361.611	0.0015	1.1	9974.5	P60468	Protein transport protein Sec61 subunit beta	vehicle
49	2	14.47	14.47	71.5	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)M E K P/S PLL/V G/R(E)	K:PITC	725.3602	1449.705	0.008	5.5	52164.5	Q13283	Ras GTPase-activating protein-binding protein 1	both
50	3	21.08	11.82	91.9	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)N I V L F/S GSS/H QD/L SQ/R(V)		625.9763	1875.902	0.0126	6.7	34769.3	P11908	Ribose-phosphate pyrophosphokinase 2	both
51	2	12.25	8.73	66.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)K L F I/G NL P/R(E)	K:PITC	640.838	1280.664	0.0045	3.5	40149.8	Q9BQ04	RNA-binding protein 4B	both
52	2	15.32	15.32	80.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(A)P V E H V V A D AGAF L/R(H)		784.9009	1568.789	0.0055	3.5	46675.2	Q9ULX3	RNA-binding protein NOB1	vehicle
53	2	13.43	13.43	67.9	HSCH <sub>2</sub> CH <sub>2</sub> CO-	4	(P)V E H V V A D AGAF L/R(H)		736.3746	1471.736	0.0057	3.9	46675.2	Q9ULX3	RNA-binding protein NOB1	treated
54	2	16.44	2.53	94.9	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)L D L D L F/R(V)		490.2506	979.492	0.0022	2.2	58777.6	P49591	Seryl-tRNA synthetase, cytoplasmic	both
55	2	19.45	8.31	92.1	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)L S L D F L D D V/R(R)		640.8162	1280.619	0.006	4.7	20625.4	P67812	Signal peptidase complex catalytic subunit SEC11A	both

56	2	24.47	14.48	100.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)V/L/L/E/S/E/Q/F/L/T/E/L/T/R(L)		883.4541	1765.904	-0.0031	-1.8	14570	P37108	Signal recognition particle 14 kDa protein	treated
57	2	24.22	24.22	100.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)L/L/E/S/E/Q/F/L/T/E/L/T/R(L)		833.9189	1666.836	-0.0051	-3.1	14570	P37108	Signal recognition particle 14 kDa protein	both
58	2	19.72	11.04	89.4	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)Q Y Q T W E E F SR(A)		731.3139	1461.61	0.0102	7	10111.8	P49458	Signal recognition particle 9 kDa protein	both
59	4	16.43	10.92	87.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)AGPV Q A V PPPPV PTEPKQPTTEEEASSK EDSA/P/SK/PVV/GI/I/Y/PPPEVR(N)	K:PITC	1372.9214	5488.64	0.0237	4.3	88886.6	Q15459	Splicing factor 3 subunit 1	vehicle
60	2	15.62	5.12	81.9	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)F/L Y NL/T/L/Q/R(A)		628.3305	1255.65	0.0034	2.7	135578.1	Q15393	Splicing factor 3B subunit 3	both
61	2	25.22	25.22	100.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(G)Q ND L M G T A E D F A D Q F L R(V)		1029.9505	2058.89	0.0042	2	30394.2	O15260	Surfeit locus protein 4	both
62	2	13.04	3.92	79.5	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)E N V A P R(S)		387.1853	773.361	0.0023	2.9	57924.6	P50991	T-complex protein 1 subunit delta	treated
63	2	20.17	20.17	86.9	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(A)V L A P L T A I V Y S V PR(L)		799.9727	1598.934	0.0043	2.7	34037.8	Q9Y320	Thioredoxin domain-containing protein 14 precursor	vehicle
64	2	15.26	5.36	75.3	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(S)PT P PL F S L PE A R(T)		706.8635	1412.724	-0.0045	-3.2	75666.7	Q96FV9	THO complex subunit 1	vehicle
65	2	19.43	6.42	95.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)V A G S E L P R(R)		458.7322	916.456	0.0014	1.6	35716.2	P04818	Thymidylate synthase	both
66	2	19.71	11.31	84.6	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)Q L T H Q L D L F PE C R(V)		844.405	1687.793	0.0097	5.7	19661	Q9Y3C4	TP53RK-binding protein	vehicle
67	2	12.12	6.79	71.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(T)V H N L Y LFD R(N)		632.8132	1264.614	0.0048	3.8	16831.7	Q9Y5R8	Trafficking protein particle complex subunit 1	both
68	3	16.30	16.30	51.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)K L LT H N L L S SHV R(G)	K:PITC	580.9749	1740.904	0.0065	3.7	14199.5	Q9UI30	TRM112-like protein	vehicle
69	2	24.39	24.39	94.8	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)NSEPASL L E L F N S A T Q GE L V R(S)		1238.628	2476.239	0.0099	4	53165.7	P23381	Tryptophanyl-tRNA synthetase, cytoplasmic	both
70	2	14.02	6.73	83.1	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)D P A A H L PFFYGSIS R(A)		883.425	1765.837	0.0061	3.4	69872.7	P43403	Tyrosine-protein kinase ZAP-70	both
71	2	20.03	20.03	92.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)KLTAEL L I EQ A Q Y T N A V R(D)	K:PITC	1121.5485	2242.099	-0.0098	-4.4	28415.7	P09661	U2 small nuclear ribonucleoprotein A'	both
72	2	11.81	5.40	78.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)I E V V C ND R(L)		518.239	1035.46	0.0109	10.6	8547	Q9BZL1	Ubiquitin-like protein 5	vehicle
73	3	23.98	14.79	98.7	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)N V DHEVN L L V E E I H R(L)		635.3199	1903.933	0.0121	6.3	9056.5	Q9P1F3	Uncharacterized protein C6orf115	both
74	3	11.28	11.28	59.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(N)VDHE V NL L V E E I H R(L)		597.3037	1789.89	0.0064	3.6	9056.5	Q9P1F3	Uncharacterized protein C6orf115	vehicle
75	2	14.98	14.98	77.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)FV E L NN L L NT T PD R(A)		867.428	1733.853	-0.004	-2.3	29793.5	Q0PNE2	UPF0405 protein TMEM103	vehicle
76	2	19.42	12.82	91.1	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)F E S V V V D V L N R(F)		682.8467	1364.688	-0.0017	-1.3	360278	Q96RL7	Vacuolar protein sorting-associated protein 13A	vehicle
77	2	18.46	11.19	95.0	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)L E S V V A D LL N R(F)		658.8478	1316.688	0.0005	0.3	422392.3	Q709C8	Vacuolar protein sorting-associated protein 13C	both

78	3	12.52	12.52	68.2	HSCH <sub>2</sub> CH <sub>2</sub> CO-	2	(-)LVILV/L/GDL/HL/PH/R(C)		523.9766	1569.893	0.0219	13.9	20505.8	Q9UBQ0	Vacuolar protein sorting-associated protein 29	treated	
79	2	15.64	2.50	89.8	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(V)L[L]T[M]I/A/R(V)		453.2532	905.495	0.0044	4.9	24740.7	O75396	Vesicle-trafficcking protein SEC22b	both	
80	2	10.94	10.94	56.6	HSCH <sub>2</sub> CH <sub>2</sub> CO-	3	(P)P[K]V/T/S/E/L/L/R(Q)	K:PITC	633.3253	1265.638	0.0052	4.1	69918.2	Q9NQW7	Xaa-Pro aminopeptidase 1	treated	

\* The N-CLAP peptides are either detected in vehicle, cisplatin treated or both samples.