

Table S4. Peptides Derived from Protein Internal Cleavages Identified by N-CLAP Approach in Jurkat T-Cells

#	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	4 AAs Before Cleavage	Cleavage Site	Sample	Refs. Reported	Site Report (Y/N)
1	2	13.07	8.82	62.9	HSCH ₂ CH ₂ CO-	8	(R)K F L P L FD R(V)	K:PITC	629.8192	1258.611	0.02	15.9	10931.7	P61604	10 kDa heat shock protein, mitochondrial	GQAF	6	treated	1, 2	N
2	2	13.46	4.59	76.8	HSCH ₂ CH ₂ CO-	127	(C)N G Y L QSR(Y)		463.2093	925.42	-0.0083	-9	29458.7	P18405	3-oxo-5-alpha-steroid 4-dehydrogenase 1	MFCT	125	both	N	N
3	2	19.22	19.22	91.1	HSCH ₂ CH ₂ CO-	42	(L)Q G V D L L A D A V A V T M G PK G R(T)	K:PITC	1061.0093	2121.029	-0.0176	-8.3	61055	P10809	60 kDa heat shock protein, mitochondrial precursor	RALM	40	both	1	N
4	2	11.21	11.21	75.6	HSCH ₂ CH ₂ CO-	146	(K)L A T Q L T G PVM PVR(N)		735.8974	1470.781	0.0068	4.6	24261.6	P26373	60S ribosomal protein L13	AEEL	144	vehicle	N	N
5	2	19.22	7.34	82.9	HSCH ₂ CH ₂ CO-	167	(R)I A L T D N A L I A R(S)		629.8475	1258.682	0.0053	4.2	29225.9	P18124	60S ribosomal protein L7	INKK	165	treated	N	N
6	2	18.31	9.65	86.1	HSCH ₂ CH ₂ CO-	168	(I)A L T D N A L I A R(S)		573.2995	1145.598	-0.0066	-5.8	29225.9	P18124	60S ribosomal protein L7	NKKR	166	treated	N	N
7	3	10.27	10.27	60.2	HSCH ₂ CH ₂ CO-	206	(T)Q V N S E D K G A L L V E A I R(T)	K:PITC	767.0396	2299.103	0.0011	0.5	29995.8	P62424	60S ribosomal protein L7a	TVAF	204	treated	N	N
8	2	12.57	12.57	78.8	HSCH ₂ CH ₂ CO-	300	(N)V L S G G T T M Y P G I A R(M)		813.401	1625.766	0.0285	17.6	42009.2	P62736	Actin, aortic smooth muscle	LYAN	298	vehicle	1	N
9	3	10.63	10.63	67.5	HSCH ₂ CH ₂ CO-	161	(T)H T V P I Y E G Y A L P H A I R(L)		680.0301	2038.058	0.0179	8.8	41737	P60709	Actin, cytoplasmic 1	G D G V	159	vehicle	1, 2, 3	N
10	2	14.68	11.5	79.9	HSCH ₂ CH ₂ CO-	295	(Y)A N T V L S G G T T M Y P G I A R(M)		956.4683	1911.894	0.0354	18.5	41737	P60709	Actin, cytoplasmic 1	R K D L	293	vehicle	1, 2, 3	N
11	4	19.29	10.35	78.6	HSCH ₂ CH ₂ CO-	102	(R)Y S P H L L A N S K V E P I P W N Q A E G D L T P D E V V A L V G Q G L Q E G E R(D)	K:PITC	1170.5741	4679.255	0.0201	4.3	40764.7	P00813	Adenosine deaminase	Y V E V	100	vehicle	1, 2	N
12	2	15.15	15.15	69.5	HSCH ₂ CH ₂ CO-	5	(S)V P A A E P E Y P K G I R(A)	K:PITC	825.3979	1649.781	0.0071	4.3	26477.9	P54819	Adenylate kinase isoenzyme 2, mitochondrial	(-)M A P	3	treated	1	Y
13	2	17.10	6.88	84.8	HSCH ₂ CH ₂ CO-	366	(W)G V M V S H R(S)		437.2086	873.407	0.003	3.4	47169.2	P06733	Alpha-enolase	Q A N G	364	treated	1, 2	N
14	2	13.74	5.38	78.8	HSCH ₂ CH ₂ CO-	729	(R)A V F P S I V G R(P)		517.2773	1033.55	-0.0026	-2.5	121364.2	Q6S8J3	ANKRD26-like family C member 1A	D D A P	727	both	1	N
15	3	10.06	10.06	52.8	HSCH ₂ CH ₂ CO-	787	(W)H H T F Y N E L R(V)		435.5338	1304.584	0.0028	2.1	121364.2	Q6S8J3	ANKRD26-like family C member 1A	M E K I	785	treated	1	N
16	2	19.49	13.86	91.9	HSCH ₂ CH ₂ CO-	940	(S)Y E L P D G Q V I T I G N E R(F)		896.4328	1791.858	0.0001	0.1	121364.2	Q6S8J3	ANKRD26-like family C member 1A	S L E K	938	treated	1	N
17	4	11.76	11.76	65.9	HSCH ₂ CH ₂ CO-	500	(R)I L S L A T G H R E E G G E N L D Q A R(E)		592.5515	2367.172	0.012	5.1	75873.7	P08133	Annexin A6	G H F R	498	vehicle	N	N
18	2	21.31	11.11	96.7	HSCH ₂ CH ₂ CO-	164	(I)V P I Y E G Y A L P H A I R(L)		900.4855	1799.951	0.0124	6.9	42003.4	Q562R1	Beta-actin-like protein 2	G V T H	162	both	N	N
19	3	10.27	3.92	61.7	HSCH ₂ CH ₂ CO-	169	(R)D V F H T T V N F I N Q N L R(T)		635.9855	1905.928	0.0144	7.5	21994.8	P55957	BH3-interacting domain death agonist	P S L L	167	vehicle	N	N
20	3	15.21	15.21	78.5	HSCH ₂ CH ₂ CO-	62	(I)L G G V I S A I S E A A A Q Y N P E P P P R(T)		808.0752	2422.207	0.0039	1.6	28315.9	P04632	Calpain small subunit 1	T A M R	60	both	N	N
21	2	18.11	5.18	89.8	HSCH ₂ CH ₂ CO-	112	(L)L V G T Q I D L R(D)		551.7977	1102.593	-0.0044	-4	21310.7	P60953	Cell division control protein 42 homolog precursor	K T P F	110	treated	N	N
22	3	10.37	10.37	55.4	HSCH ₂ CH ₂ CO-	22	(K)V E E A E P E F V E K V L D R R(V)	K:PITC	799.3807	2396.126	0.0015	0.6	20811.5	Q13185	Chromobox protein homolog 3	G K S K	20	treated	1, 4	Y

23	3	19.80	7.87	95.8	HSCH ₂ CH ₂ CO-	156	(S)V A E E A AD RH PE R(R)			489.8939	1467.665	0.0026	1.8	25835.4	Q96CT7	Coiled-coil domain-containing protein 124	IAVL	154	both	1	Y
24	3	14.86	5	76.4	HSCH ₂ CH ₂ CO-	157	(V)A E E A AD RH PE R(R)			456.8726	1368.596	0.0072	5.2	25835.4	Q96CT7	Coiled-coil domain-containing protein 124	AVLS	155	treated	1	N
25	3	15.17	15.17	75.2	HSCH ₂ CH ₂ CO-	89	(S)H TD IK V P D F SE Y R(R)	K:PITC		610.6085	1829.799	0.0124	6.8	30815.5	P0C7P4	Cytochrome b-c1 complex subunit Rieske-like protein 1	SVCY	87	both	1	N
26	3	12.02	3.32	56.8	HSCH ₂ CH ₂ CO-	28	(S)QGWVLPFGKIVPNTV F V G GIDA R(M)	K:PITC		892.4586	2675.347	0.014	5.2	82764.9	Q9NQZ3	Deleted in azoospermia protein 1	SAAA	26	vehicle	N	N
27	2	13.31	6.7	82.4	HSCH ₂ CH ₂ CO-	45	(S)NI P F ITV PLSR(T)			672.8709	1344.734	0.0001	0.1	87302.8	P54886	Delta-1-pyrroline-5-carboxylate synthetase	VRSW	43	both	1	Y
28	3	15.17	7.17	78.6	HSCH ₂ CH ₂ CO-	533	(R)NLHQSGF S LS GA Q ID D NI PR(R)			753.0311	2257.067	0.0121	5.4	62294	Q16555	Dihydropyrimidinase-related protein 2	APPV	531	both	1	N
29	3	15.80	15.8	65.1	HSCH ₂ CH ₂ CO-	230	(R)ETS S D V A L A SH I LTAL R(E)			624.6575	1871.953	0.0048	2.6	36522.1	Q00273	DNA fragmentation factor subunit alpha	TGIS	228	vehicle	N	N
30	3	13.01	2.51	50.7	HSCH ₂ CH ₂ CO-	264	(R)IAQPGDHVSV T GI F L PIL R(T)			707.7188	2121.153	-0.0107	-5	81308.4	P33993	DNA replication licensing factor MCM7	GENT	262	vehicle	N	N
31	2	23.33	13.03	91.8	HSCH ₂ CH ₂ CO-	269	(K)D G V PE GA QL Q G PV H R(N)			824.4014	1647.791	0.0048	2.9	40090.1	P16989	DNA-binding protein A	IGEM	267	vehicle	1, 3	N
32	2	13.78	13.78	72.1	HSCH ₂ CH ₂ CO-	92	(K)ED Y Y Q I L G V P R(N)			720.8533	1440.683	0.0165	11.5	52538.1	Q96EY1	DnaJ homolog subfamily A member 3, mitochondrial precursor	APLA	90	both	N	N
33	4	11.29	11.29	70.5	HSCH ₂ CH ₂ CO-	88	(R)IGPEPTTDSFIAVMHGPTEG V V PGNA L VVD P R(R)			840.919	3360.66	-0.0061	-1.8	60627.2	Q9H4M9	EH domain-containing protein 1	FPGM	86	vehicle	N	N
34	2	11.70	11.7	68.7	HSCH ₂ CH ₂ CO-	412	(C)VES F S D Y PPL GR(F)			727.8384	1454.662	0.0075	5.1	50141.1	P68104	Elongation factor 1-alpha 1	GKPM	410	vehicle	1, 2	N
35	2	14.89	3.15	82.2	HSCH ₂ CH ₂ CO-	417	(S)D Y P P L G R(F)			453.2153	905.419	0.0048	5.3	50141.1	P68104	Elongation factor 1-alpha 1	VESF	415	vehicle	1, 2	N
36	3	14.81	6.4	75.6	HSCH ₂ CH ₂ CO-	39	(F)EAVSS P P PADL CHAL R(W)			584.2809	1750.825	0.003	1.7	24763.9	P24534	Elongation factor 1-beta	DVAV	37	treated	1, 2	N
37	4	14.58	14.58	69.1	HSCH ₂ CH ₂ CO-	31	(R)VLSA P P HF H F GQTN R(T)			449.7252	1795.87	0.0093	5.2	50119.1	P26641	Elongation factor 1-gamma	GAQV	29	both	3	N
38	4	11.42	7.89	73.0	HSCH ₂ CH ₂ CO-	803	(S)NTG GQ A F PQC VFDHWQIL PGD PFD NSSRPSQVVAETR(K)			1048.0028	4188.929	0.0603	14.4	95338.7	P13639	Elongation factor 2	ADLR	801	treated	1, 5	N
39	4	14.25	14.25	77.9	HSCH ₂ CH ₂ CO-	512	(R)FQSSHPTD I T S L D Q Y V E R(M)			587.7738	2348.061	0.0122	5.2	92469.3	P14625	Endoplasmic precursor	AKLL	510	both	1, 4	N
40	3	13.48	13.48	75.6	HSCH ₂ CH ₂ CO-	15	(A)DA S K G D D L L PAGTEDYI HIR(I)	K:PITC		803.7035	2409.085	0.011	4.6	12732.6	P41567	Eukaryotic translation initiation factor 1	FDPF	13	treated	N	N
41	3	19.65	10.18	92.3	HSCH ₂ CH ₂ CO-	803	(R)LHLSGIDAN PN A L F P PVE F PAP R(G)			854.1137	2560.302	0.0249	9.7	273401	P49327	Fatty acid synthase	AGIG	801	vehicle	N	N
42	4	12.71	12.71	69.0	HSCH ₂ CH ₂ CO-	2052	(R)VSGQGLHEGHTFE PAE F I D T R(D)			632.8132	2528.187	0.0435	17.2	280740.4	P21333	Filamin-A	ASRV	2050	both	1	N
43	2	11.23	2.05	75.0	HSCH ₂ CH ₂ CO-	1708	(T)A P E PGKYVIT I R(F)	K:PITC		783.8786	1566.781	-0.0308	-19.7	290960.7	Q14315	Filamin-C	DIYY	1706	treated	N	N
44	3	11.64	11.64	62.2	HSCH ₂ CH ₂ CO-	363	(L)FS LSAAGVT QELA ISRRQ R(R)			726.7262	2178.145	0.0193	8.8	50708.7	Q14764	Gamma-aminobutyric acid receptor subunit delta precursor	NAIV	361	vehicle	N	N
45	2	14.49	2.33	79.3	HSCH ₂ CH ₂ CO-	321	(L)L A L LEAA L R(S)			529.3089	1057.607	0.0031	2.9	50509.7	Q6P531	Gamma-glutamyltransferase 6 precursor	AGPE	319	treated	N	N
46	2	19.71	19.71	91.5	HSCH ₂ CH ₂ CO-	257	(L)L SGDT Q T D A T S F YD R(V)			882.8773	1764.738	0.0092	5.2	59425.8	P14314	Glucosidase 2 subunit beta precursor	EAQA	255	both	N	N

47	2	10.66	10.66	68.3	HSCH ₂ CH ₂ CO-	171	(C)LDA\AF\PL/L\SAYVGR(L)			755.3916	1509.777	-0.0011	-0.7	23356	P09211	Glutathione S-transferase P	LAPG	169	vehicle	2	N
48	3	11.45	11.45	73.4	HSCH ₂ CH ₂ CO-	235	(R)VPTAN\VS\I/V/D/L/TC/R(L)			521.2676	1561.771	0.017	10.9	36053.4	P04406	Glyceraldehyde-3-phosphate dehydrogenase	GMAF	233	vehicle	4	N
49	2	10.41	10.41	55.9	HSCH ₂ CH ₂ CO-	299	(G)K\LT/G/M/A/F/R(V)	K:PITC		573.7689	1146.526	0.0048	4.2	44501.4	Q14556	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific	PELK	297	treated	2	N
50	2	10.33	2.98	59.0	HSCH ₂ CH ₂ CO-	318	(E)P\VE\K/A/L/R(D)	K:PITC		518.261	1035.511	0.0033	3.2	70375.4	P34931	Heat shock 70 kDa protein 1L	RGTL	316	treated	N	N
51	2	13.06	13.06	62.2	HSCH ₂ CH ₂ CO-	156	(S)VM\DA/T/Q/I/A/G/L/N/CL/R(L)			796.8985	1592.759	0.0304	19.1	94300.5	P34932	Heat shock 70 kDa protein 4	AERR	154	treated	1	N
52	3	16.44	16.44	79.7	HSCH ₂ CH ₂ CO-	457	(R)YHTSQSGD\E\M\T\S/L/S/E/Y/V/SR(M)			755.657	2264.943	0.013	5.7	83264.6	P08238	Heat shock protein HSP 90-beta	SELL	455	both	1, 3, 4	N
53	3	19.49	10.99	90.2	HSCH ₂ CH ₂ CO-	625	(K)H\LE\I\N/PD/H\PI/VETLR(Q)			624.3207	1870.948	-0.0004	-0.2	83264.6	P08238	Heat shock protein HSP 90-beta	MMAK	623	treated	1, 3, 4	N
54	2	13.96	8.33	69.1	HSCH ₂ CH ₂ CO-	626	(H)L\E\I\N/PD/H\PIVETLR(Q)			867.4439	1733.889	-0.0086	-4.9	83264.6	P08238	Heat shock protein HSP 90-beta	MAKK	624	treated	1, 3, 4	N
55	3	10.66	10.66	56.1	HSCH ₂ CH ₂ CO-	215	(T)I\EDG\I\F\VK/S/T/A/GDTHLGGEDFDNR(M)	K:PITC		982.4357	2945.272	0.0209	7.1	70021.3	P54652	Heat shock-related 70 kDa protein 2	VSIL	213	treated	4	N
56	3	16.18	16.18	79.7	HSCH ₂ CH ₂ CO-	19	(V)GAHAG\E\Y\G\A/E/A/L/E/R(M)			506.8991	1518.664	0.0186	12.2	15257.6	P69905	Hemoglobin subunit alpha	AWGK	17	treated	N	N
57	2	12.04	12.04	70.0	HSCH ₂ CH ₂ CO-	185	(I)FV\G\G\L\I\S\PD\T/PEEKIR(E)	K:PITC		934.4395	1867.872	0	0	38434.4	Q14103	Heterogeneous nuclear ribonucleoprotein D0	PVKK	183	treated	1, 2	N
58	3	12.55	12.55	64.2	HSCH ₂ CH ₂ CO-	415	(R)HESGA\SI\KI\I\D/E\I\G\SED/R(I)	K:PITC		764.6828	2291.991	0.0431	18.8	50976.5	P61978	Heterogeneous nuclear ribonucleoprotein K	IKQI	413	vehicle	1, 5, 6, 7	N
59	5	13.12	13.12	63.7	HSCH ₂ CH ₂ CO-	96	(R)M\VV\NEGSDGGQSV\Y/HV/HL/H/V/LGGR(Q)			527.8602	2635.25	0.0215	8.2	13802	P49773	Histidine triad nucleotide-binding protein 1	NKGY	94	vehicle	1	N
60	3	12.08	12.08	65.4	HSCH ₂ CH ₂ CO-	32	(A)AGV\T\DGNEVAKAQA\T\PGGA/A\PI\FSR(I)	K:PITC		946.4547	2837.334	0.015	5.3	17161.8	Q9BX68	Histidine triad nucleotide-binding protein 2	QVRG	30	treated	1	Y
61	2	11.85	3.34	71.1	HSCH ₂ CH ₂ CO-	22	(R)A\G\L\Q\F\PV\G/R(I)			516.7703	1032.53	0.0038	3.7	14233.6	Q96QV6	Histone H2A type 1-A	SRSS	20	vehicle	1	N
62	2	13.64	13.64	78.1	HSCH ₂ CH ₂ CO-	57	(L)EY\L\T\AE\I\I\I\I\A/G/NAAR(D)			911.4504	1821.905	-0.0116	-6.4	14135.6	P04908	Histone H2A type 1-B	LAAY	55	treated	1	N
63	2	16.54	16.54	83.5	HSCH ₂ CH ₂ CO-	59	(Y)LT\A\E\I\I\I\I\A/G/NAAR(D)			765.3982	1529.799	-0.0101	-6.6	14135.6	P04908	Histone H2A type 1-B	AVLE	57	treated	1	N
64	2	14.60	10.58	85.3	HSCH ₂ CH ₂ CO-	61	(T)AE\I\I\I\I\A/G/NAAR(D)			658.3392	1315.668	0.0037	2.8	14135.6	P04908	Histone H2A type 1-B	LEYL	59	both	1	N
65	2	15.59	15.59	79.3	HSCH ₂ CH ₂ CO-	62	(G)I\M\N\I\F/V\NDI\FE/R(I)			786.8751	1572.718	0.0244	15.5	13950.3	P33778	Histone H2B type 1-B	SKAM	60	treated	1, 3	N
66	2	15.04	8.83	84.1	HSCH ₂ CH ₂ CO-	63	(I)M\N\I\F/V\NDI\FE/R(I)			730.3321	1459.634	0.0225	15.4	13950.3	P33778	Histone H2B type 1-B	KAMG	61	vehicle	1, 3	N
67	2	17.92	7.59	88.8	HSCH ₂ CH ₂ CO-	66	(S)F\I\N\DI\FE/R(I)			564.2667	1127.519	0.0071	6.3	13950.3	P33778	Histone H2B type 1-B	GIMN	64	treated	1, 3	N
68	2	14.67	14.67	83.0	HSCH ₂ CH ₂ CO-	25	(R)D\N\I\Q\G\I\T\K\PAI/R(R)	K:PITC		774.8876	1548.766	0.0018	1.2	11367.4	P62805	Histone H4	RKVL	23	both	3	N
69	2	10.88	4.1	79.0	HSCH ₂ CH ₂ CO-	47	(R)I\I\G\L\I\Y/E/ETR(G)			634.8136	1268.619	0.0008	0.6	11367.4	P62805	Histone H4	GGVK	45	treated	3	N
70	2	16.85	4.81	89.8	HSCH ₂ CH ₂ CO-	50	(G)L\I\Y/E/T/R(R)			506.2452	1011.482	0.0016	1.5	11009.2	Q99525	Histone H4-like protein type G	KRIL	48	treated	N	N
71	3	10.70	5.23	66.5	HSCH ₂ CH ₂ CO-	45	(R)LAVHPSG\I\A\I\Q/D/R(V)			484.2563	1450.747	0.0072	5	17887.6	P05161	Interferon-induced 17 kDa protein precursor	AFQQ	43	vehicle	N	N

72	3	16.47	8.16	74.3	HSCH ₂ CH ₂ CO-	298	(R)VTGNFKHASPILPI/T/E/F/SDI/P/R(R)	K:PITC	888.1116	2662.316	0.0046	1.7	50670.5	P42167	Lamina-associated polypeptide 2, isoforms beta/gamma	LVVN	296	both	1, 5	N
73	2	23.38	15.58	98.1	HSCH ₂ CH ₂ CO-	305	(H)A/S/P/I/L/P/I/TE/FSD/I/P/R(R)		872.4476	1743.899	-0.0107	-6.1	50670.5	P42167	Lamina-associated polypeptide 2, isoforms beta/gamma	GNFK	303	treated	1, 5	N
74	4	10.05	2.06	57.7	HSCH ₂ CH ₂ CO-	513	(A)HPFRDLPLGREQHCKL/P/GVADI/R(A)	K:PITC	748.3802	2990.506	-0.0073	-2.4	71190.5	Q8NA19	Lethal(3)malignant brain tumor-like 4 protein	STVS	511	vehicle	N	N
75	3	10.07	2.89	72.0	HSCH ₂ CH ₂ CO-	311	(R)VLHVSENPV/PL/TV/R(V)		549.9685	1647.889	0.0023	1.4	63473.3	Q8N1G4	Leucine-rich repeat-containing protein 47	RLLL	309	both	1	N
76	2	21.38	14.39	95.1	HSCH ₂ CH ₂ CO-	603	(S)P\A L T E N E H I/R(A)		690.8507	1380.694	0.0001	0.1	113744.7	O00754	Lysosomal alpha-mannosidase precursor	RRSW	601	treated	N	N
77	2	12.98	12.98	83.3	HSCH ₂ CH ₂ CO-	203	(E)IV\ A D V L DN DSWR(L)		802.3897	1603.778	-0.0063	-4	47079.5	P22234	Multifunctional protein ADE2	VTTK	201	treated	N	N
78	2	15.08	15.08	85.7	HSCH ₂ CH ₂ CO-	678	(A)V\S L L E E V I T/P/R(K)		672.3633	1343.724	-0.0046	-3.4	115704.5	Q9H0A0	N-acetyltransferase 10	VSSE	676	treated	N	N
79	3	12.63	12.63	63.5	HSCH ₂ CH ₂ CO-	94	(R)DPAETLHLSEP\LGGK/L/L/E/E/Y/T/Q/L/A/R(E)	K:PITC	1001.8295	3003.459	0.0149	5	35896.7	Q86X76	Nitrilase homolog 1	DFIA	92	vehicle	N	N
80	3	12.45	12.45	67.5	HSCH ₂ CH ₂ CO-	220	(E)GA D N Q G A GEQGRPV/R(Q)		533.9176	1599.729	0.009	5.6	35924.3	P67809	Nuclease-sensitive element-binding protein 1	GEVM	218	treated	1	N
81	2	12.02	6.71	84.2	HSCH ₂ CH ₂ CO-	9	(F)DI A V D G E PLGR(V)		615.2949	1229.583	-0.0005	-0.4	18012.6	P62937	Peptidyl-prolyl cis-trans isomerase A	PTVF	7	treated	1, 2	N
82	2	11.24	3.12	70.9	HSCH ₂ CH ₂ CO-	98	(K)RTVPTGDL/A/L/R(P)		643.8433	1286.689	-0.0092	-7.2	155004.6	Q9BXM0	Periaxin	SFCL	96	treated	N	N
83	4	17.36	9.8	93.3	HSCH ₂ CH ₂ CO-	272	(R)DQHDTFFLRDPA E A L Q L P M/D/YVQ/R(V)		749.1136	2993.392	0.0405	13.5	57563.9	Q9Y285	Phenylalanyl-tRNA synthetase alpha chain	QHPA	270	both	N	N
84	2	20.30	20.3	97.7	HSCH ₂ CH ₂ CO-	109	(C)AN P A A G S V I L E N L R(F)		813.4362	1625.868	-0.0028	-1.7	44615	P00558	Phosphoglycerate kinase 1	VEKA	107	vehicle	2	N
85	2	13.23	2.17	77.9	HSCH ₂ CH ₂ CO-	116	(S)V I L L E N L R(F)		529.3077	1057.607	0.0007	0.7	44615	P00558	Phosphoglycerate kinase 1	PAAG	114	vehicle	2	N
86	3	11.73	11.73	67.5	HSCH ₂ CH ₂ CO-	11	(R)HGESA W N L E N R(F)		467.5428	1400.601	0.0127	9	28804.1	P18669	Phosphoglycerate mutase 1	LVLI	9	treated	1, 2	N
87	4	11.02	11.02	56.4	HSCH ₂ CH ₂ CO-	127	(R)LSFAHPPSAEVE A A L A T L HD R(M)		609.0639	2433.223	0.0107	4.4	144665	Q15067	Phosphoribosylformylglyc inamidase synthase	TRRY	125	vehicle	N	N
88	2	17.37	9.88	86.1	HSCH ₂ CH ₂ CO-	518	(N)DD I I V N W V N E TL R(E)		837.9106	1674.816	-0.0017	-1	70289.7	P13796	Plastin-2	GQKV	516	treated	N	N
89	2	16.46	16.46	58.0	HSCH ₂ CH ₂ CO-	230	(T)I/S PLD L A K L N Q V A R(Q)	K:PITC	880.95	1760.919	-0.0259	-14.7	37498	Q15365	Poly(rC)-binding protein 1	QGQH	228	vehicle	1	N
90	4	10.23	4.59	68.3	HSCH ₂ CH ₂ CO-	16	(P)GDAPRAEL VAL TAVQSEQGEAGGG GS P/R(R)		692.8437	2768.327	0.0262	9.5	77092.2	P56696	Potassium voltage-gated channel subfamily KQT member 4	LGPP	14	vehicle	N	N
91	2	23.56	23.56	97.8	HSCH ₂ CH ₂ CO-	196	(G)DV\C QD C I Q M V T D I Q T A V R(T)		1063.4758	2125.939	0.0058	2.7	58113.1	P07602	Proactivator polypeptide precursor	PKDN	194	both	1	N
92	2	14.82	8.69	84.5	HSCH ₂ CH ₂ CO-	81	(R)ELS E L V Y T DV L DR(S)		820.3973	1639.788	-0.001	-0.6	20694.6	Q8WU39	Proapoptotic caspase adapter protein precursor	SGGR	79	treated	N	N
93	2	14.83	14.83	63.8	HSCH ₂ CH ₂ CO-	43	(N)I T PAE V G V L V GKDR(S)	K:PITC	838.9307	1676.85	0.0043	2.5	15054.3	P07737	Profilin-1	KTFV	41	treated	N	N
94	2	17.13	17.13	86.4	HSCH ₂ CH ₂ CO-	147	(H)E E A T M T I E E L L T R(Y)		812.3834	1623.76	-0.0009	-0.6	59271.9	Q15355	Protein phosphatase 1G	AALL	145	vehicle	1	N
95	4	15.15	11.04	84.5	HSCH ₂ CH ₂ CO-	100	(F)VNHPQVSA L L G E E DEE ALH YLTR(V)		677.8332	2708.298	0.0125	4.6	33489	Q01105	Protein SET	WVTT	98	treated	3, 8	N

96	2	13.44	3.96	86.0	HSCH ₂ CH ₂ CO-	180	(E)E\L I PE\YLN\I/R(G)			747.892	1494.766	0.0106	7.1	47712.1	Q58FG1	Putative heat shock protein HSP 90-alpha A4	MDNC	178	vehicle	N	N
97	3	18.08	8.46	90.5	HSCH ₂ CH ₂ CO-	66	(A)AP\V\PTAPAAGA\PLMDF\GND\FV\PPA\PR(G)			888.7714	2664.295	0.0048	1.8	129932	Q9NQC3	Reticulon-4	AGLS	64	treated	1	Y
98	2	19.13	10.86	94.2	HSCH ₂ CH ₂ CO-	93	(G)P\L P A A P PV\APER(Q)			651.8457	1302.688	-0.0033	-2.6	129932	Q9NQC3	Reticulon-4	PAPR	91	treated	1	N
99	2	23.51	23.51	96.6	HSCH ₂ CH ₂ CO-	289	(L)A\M P L PE PE PL PL PLEVV\R(G)			1043.0656	2085.112	0.0116	5.6	50414.3	Q9BTD8	RNA-binding protein 42	LPLA	287	both	N	N
100	3	13.53	7.25	54.3	HSCH ₂ CH ₂ CO-	127	(M)ALAFS\EQEE\HE\L PV\LS\R(Q)			681.6784	2042.985	0.0355	17.4	41595.7	Q75995	SAM and SH3 domain-containing protein 3	GPEK	125	vehicle	N	N
101	2	10.35	2.22	65.9	HSCH ₂ CH ₂ CO-	290	(M)YT I MNPIQGAG\R(A)			733.3459	1465.693	-0.0081	-5.5	39388.6	Q9BWG4	Single-stranded DNA-binding protein 4	SSEN	288	vehicle	N	N
102	2	10.21	2.21	60.6	HSCH ₂ CH ₂ CO-	289	(I)EIFLVY I V P R(A)			668.8712	1336.733	0.0018	1.3	127617.7	Q9UHW9	Solute carrier family 12 member 6	ILGA	287	both	N	N
103	3	12.58	5.57	69.3	HSCH ₂ CH ₂ CO-	249	(R)IVNHPTM\L Q D PD V R(E)			574.9495	1722.83	0.0038	2.2	59069.8	Q13596	Sorting nexin-1	RYLQ	247	both	N	N
104	4	10.47	10.47	68.0	HSCH ₂ CH ₂ CO-	1845	(R)MHTTFEHD I Q A\L GT QV R(Q)			518.751	2071.969	0.0134	6.5	274610.6	Q01082	Spectrin beta chain, brain 1	ETLQ	1843	treated	N	N
105	2	12.10	12.1	63.6	HSCH ₂ CH ₂ CO-	15	(R)AS\G Q A\F E\L I SP R(S)			738.8804	1476.752	0.002	1.4	17302.6	P16949	Stathmin	ELEK	13	vehicle	1, 2	N
106	2	15.60	2.16	84.7	HSCH ₂ CH ₂ CO-	21	(F)E\L I L S P R(S)			458.26	915.497	0.0159	17.4	17302.6	P16949	Stathmin	SGQA	19	treated	1, 2	N
107	3	13.06	13.06	57.3	HSCH ₂ CH ₂ CO-	89	(N)IVAYHDSI M N PD Y N V E FFR(Q)			806.7029	2418.089	0.0048	2	71224	Q9UBT2	SUMO-activating enzyme subunit 2	YPKA	87	treated	N	N
108	2	10.01	3.32	67.2	HSCH ₂ CH ₂ CO-	32	(E)DIVFETDH I L ESLYRD I R(D)			1161.5724	2322.144	-0.0059	-2.6	33196	Q75558	Syntaxin-11	DSPH	30	treated	N	N
109	3	12.71	7.11	64.9	HSCH ₂ CH ₂ CO-	439	(R)VGKVEHGSV A L P A IM R(S)	K:PITC		629.6569	1886.944	0.0124	6.6	269768.5	Q9Y490	Talin-1	QQYN	437	vehicle	1	N
110	4	15.63	15.63	54.1	HSCH ₂ CH ₂ CO-	1691	(R)EGIS\QEALHTQML T A VQ\EISHL E PL ANAAR(A)			865.4453	3458.741	0.0187	5.4	269768.5	Q9Y490	Talin-1	QLAP	1689	vehicle	1	N
111	2	20.75	20.75	91.8	HSCH ₂ CH ₂ CO-	2495	(M)VGG I A Q I I A Q E E M L R(K)			893.9595	1786.919	-0.0073	-4.1	269768.5	Q9Y490	Talin-1	VKEK	2493	both	1	N
112	2	23.54	23.54	93.8	HSCH ₂ CH ₂ CO-	342	(E)AA M L G Q A E E V V Q E R(I)			809.881	1618.756	-0.0016	-1	60343.9	P17987	T-complex protein 1 subunit alpha	EETF	340	treated	3, 4	N
113	2	18.50	10.35	83.3	HSCH ₂ CH ₂ CO-	345	(M)L G Q A E E V V Q E R(I)			673.3245	1345.642	0.0001	0.1	60343.9	P17987	T-complex protein 1 subunit alpha	FEAA	343	treated	3, 4	N
114	3	19.89	15.48	91.5	HSCH ₂ CH ₂ CO-	456	(A)DA M E V I PSTLAENA GL N PIST V TE L R(N)			943.807	2829.401	0.0056	2	57924.6	P50991	T-complex protein 1 subunit delta	VRAF	454	treated	1, 3, 4	N
115	2	13.40	7.81	74.8	HSCH ₂ CH ₂ CO-	114	(A)GAL L E E AE Q L L DR(G)			772.8848	1544.763	-0.0002	-0.1	59671.4	P48643	T-complex protein 1 subunit epsilon	VVVL	112	treated	1, 2, 3	N
116	4	15.11	15.11	65.6	HSCH ₂ CH ₂ CO-	40	(R)GLDPSLSPPLNLPQPGALPTEQENILHTTQDCYNNL AA CL L Q M E PV N YE R(V)			1465.9624	5860.797	0.0312	5.3	20012.7	Q8N5M4	Tetratricopeptide repeat protein 9C	LLQL	38	vehicle	5	N
117	2	12.50	3.04	73.4	HSCH ₂ CH ₂ CO-	731	(S)L\D Q P GGT LDLT L I R(A)			800.4191	1599.841	-0.0101	-6.3	88550.2	Q13263	Transcription intermediary factor 1-beta	DSTF	729	treated	3	N
118	2	13.57	2.87	76.7	HSCH ₂ CH ₂ CO-	553	(F)G E S E A N V R(E)			475.2093	949.404	0.007	7.3	89322.3	P55072	Transitional endoplasmic reticulum ATPase	LTMW	551	vehicle	N	N
119	3	11.62	11.62	70.9	HSCH ₂ CH ₂ CO-	568	(G)IG E A V SSA V V GE PGITVTHL AVNR(V)			822.1044	2464.286	0.0122	5	67878	P29401	Transketolase	YYEG	566	vehicle	N	N
120	3	16.51	7.67	85.6	HSCH ₂ CH ₂ CO-	167	(R)PLHIST F I N E L D S GF R(L)			645.3258	1933.948	0.0152	7.9	26183.1	Q15631	Translin	GDYS	165	both	N	N

121	2	21.74	12.09	95.6	HSCH ₂ CH ₂ CO-	48	(R)E A P V D V L T Q I GR(S)		693.3574	1385.709	-0.0018	-1.3	26210.1	Q9BVC6	Transmembrane protein 109 precursor	GQQK	46	both	N	N
122	2	12.55	4.62	80.2	HSCH ₂ CH ₂ CO-	197	(L)H L G V T PSVI(R(K)		583.8193	1166.635	-0.0037	-3.2	61248.2	Q14773	Tripeptidyl-peptidase 1 precursor	GTVG	195	both	1	Y
123	3	13.96	3.61	63.7	HSCH ₂ CH ₂ CO-	65	(R)AVFVDLEPT V I D E V R(T)		597.3097	1789.904	0.0105	5.9	50135.9	Q71U36	Tubulin alpha-1A chain	KHVP	63	vehicle	1, 9	N
124	2	17.87	9.5	92.2	HSCH ₂ CH ₂ CO-	66	(A)VFV D L E PTV IDE V R(T)		859.9339	1718.867	-0.0064	-3.7	50135.9	Q71U36	Tubulin alpha-1A chain	HVPR	64	treated	1, 9	N
125	2	11.23	11.23	68.6	HSCH ₂ CH ₂ CO-	67	(V)FV D L E PTVIDE V R(T)		810.4092	1619.799	0.0126	7.8	50135.9	Q71U36	Tubulin alpha-1A chain	VPRA	65	vehicle	1, 9	N
126	2	10.78	7.18	78.4	HSCH ₂ CH ₂ CO-	250	(N)VDL T E F Q TNL V PY PR(I)		940.4655	1879.926	-0.0021	-1.1	50135.9	Q71U36	Tubulin alpha-1A chain	DGAL	248	treated	1, 9	N
127	2	10.90	5.6	71.2	HSCH ₂ CH ₂ CO-	63	(R)A L V D L E PGTMD SV R(S)		852.4119	1703.834	-0.0177	-10.4	49907.3	Q13885	Tubulin beta-2A chain	KYVP	61	vehicle	1, 5	N
128	2	22.94	13.17	99.1	HSCH ₂ CH ₂ CO-	64	(A)IL V D L E P GT MD SV R(S)		816.9012	1632.797	-0.002	-1.2	49907.3	Q13885	Tubulin beta-2A chain	YVPR	62	treated	1, 5	N
129	3	17.00	17	84.6	HSCH ₂ CH ₂ CO-	102	(W)AKGHYTEGA E L V D S V L DV V R(K)	K:PITC	794.3895	2381.126	0.0275	11.6	49907.3	Q13885	Tubulin beta-2A chain	AGNN	100	treated	1, 5	N
130	3	14.31	14.31	69.9	HSCH ₂ CH ₂ CO-	104	(K)GHYTEGA E L V D S V L D VV R(K)		682.9989	2046.98	0.0021	1	49907.3	Q13885	Tubulin beta-2A chain	NNWA	102	both	1, 5	N
131	3	17.36	17.36	90.8	HSCH ₂ CH ₂ CO-	105	(G)H Y TEG A E L V D SV L D VV R(K)		663.995	1989.959	0.0118	5.9	49907.3	Q13885	Tubulin beta-2A chain	NWAK	103	vehicle	1, 5	N
132	3	12.86	12.86	69.9	HSCH ₂ CH ₂ CO-	106	(H)YTEGAE L V D S V L D VV R(K)		618.3078	1852.9	0.0091	4.9	49907.3	Q13885	Tubulin beta-2A chain	WAKG	104	treated	1, 5	N
133	2	20.08	20.08	95.9	HSCH ₂ CH ₂ CO-	108	(T)E G A E L V DSV L D V V R(K)		794.8973	1588.789	-0.0014	-0.9	49907.3	Q13885	Tubulin beta-2A chain	KGHY	106	both	1, 5	N
134	3	13.50	13.5	77.3	HSCH ₂ CH ₂ CO-	800	(R)AVTHTS PED V SF A E S R(R)		607.6113	1820.812	0.0074	4.1	132528.6	Q9BTW9	Tubulin-specific chaperone D	LTGL	798	vehicle	N	N
135	3	10.65	10.65	66.8	HSCH ₂ CH ₂ CO-	64	(K)ESTL H LV L R(L)		385.8804	1155.619	0.0076	6.6	8564.9	P62988	Ubiquitin	YNIQ	62	vehicle	N	N
136	2	12.36	2.64	67.0	HSCH ₂ CH ₂ CO-	90	(A)AS P L PEEPPV P R(P)		688.8522	1376.688	0.0093	6.7	35187.1	A8MZF0	Uncharacterized protein LOC728008	TTVQ	88	both	N	N
137	2	11.29	5.66	65.2	HSCH ₂ CH ₂ CO-	88	(S)L A D A I N T E FK NT R(T)	K:PITC	858.4	1715.788	0.0047	2.8	53651.9	P08670	Vimentin	SVDF	86	treated	1, 3	Y

- Mahrus S, *et al.* (2008) Global sequencing of proteolytic cleavage sites in apoptosis by specific labeling of protein N termini. *Cell* 134:866-876.
- Thiede B, Siejak F, Dimmler C, Jungblut PR, & Rudel T (2000) A two dimensional electrophoresis database of a human Jurkat T-cell line. *Electrophoresis* 21:2713-2720.
- Van Damme P, *et al.* (2005) Caspase-specific and nonspecific *in vivo* protein processing during Fas-induced apoptosis. *Nat Methods* 2:771-777.
- Thiede B & Rudel T (2004) Proteome analysis of apoptotic cells. *Mass Spectrom Rev* 23:333-349.
- Schmidt F, *et al.* (2007) Quantitative proteome analysis of cisplatin-induced apoptotic Jurkat T cells by stable isotope labeling with amino acids in cell culture, SDS-PAGE, and LC-MALDI-TOF/TOF MS. *Electrophoresis* 28:4359-4368.
- Thiede B, Treumann A, Kretschmer A, Sohlke J, & Rudel T (2005) Shotgun proteome analysis of protein cleavage in apoptotic cells. *Proteomics* 5:2123-2130.
- Thiede B, Kretschmer A, & Rudel T (2006) Quantitative proteome analysis of CD95 (Fas/Apo-1)-induced apoptosis by stable isotope labeling with amino acids in cell culture, 2-DE and MALDI-MS. *Proteomics* 6:614-622.
- Yuan X, *et al.* (2007) Nuclear protein profiling of Jurkat cells during heat stress-induced apoptosis by 2-DE and MS/MS. *Electrophoresis* 28:2018-2026.
- Short DM, *et al.* (2007) Apoptosis induced by staurosporine alters chaperone and endoplasmic reticulum proteins: Identification by quantitative proteomics. *Proteomics* 7:3085-3096.