

Table S3. Peptides Derived from Caspase Cleavage Sites Identified by N-CLAP Approach after Drug Treatment of 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 Sites	Cleavage Site	Sample	Refs. Reported	Site Report (Y/N)
1	3	15.47	15.47	64.8	HSCH ₂ CH ₂ CO-	159	(G)VTHTV PI YEG Y/A/L/P/HAIL/R(L)		746.7372	2238.174	0.0231	10.3	41737	P60709	Actin, cytoplasmic 1	DSGD	157	treated	1	N
2	2	9.89	5.6	66.6	HSCH ₂ CH ₂ CO-	266	(M)SK/P/DL/T/A/ALR(D)	K:PITC	647.818	1294.628	0.0005	0.4	53536	P17661	Desmin *	VEMD	264	treated	2	Y
3	2	13.96	13.96	78.9	HSCH ₂ CH ₂ CO-	8	(F)L/GQSDSGG S EE V V L/T/PAE/L/IE/R(L)		1201.5707	2402.139	-0.005	-2.1	26047	Q9BRT9	DNA replication complex GINS protein SLD5	EEVD	6	treated	N/A	N
4	2	12.69	12.69	61.2	HSCH ₂ CH ₂ CO-	95	(S)LKE A L T Y D G AL/L/GDR(S)	K:PITC	929.4416	1857.887	-0.0114	-6.2	27385.2	Q15056	Eukaryotic translation initiation factor 4H	DEVD	93	treated	3	Y
5	2	12.78	-0.16	71.1	HSCH ₂ CH ₂ CO-	137	(L)S/P/P/PQ/AA/R(R)		456.2223	911.44	-0.003	-3.3	23410.1	P63118	HERV-H_3q26 provirus ancestral Gag polyprotein **	DPSD	135	treated	N/A	N
6	3	18.72	18.72	65.7	HSCH ₂ CH ₂ CO-	1003	(G)ASA E T E PWA A A V PPEWV PII QQDIQ/SQR(K)		1069.1866	3205.562	-0.017	-5.3	119409.3	P46379	Large proline-rich protein BAT3	DEQD	1001	treated	4	Y
7	2	14.28	6.81	79.4	HSCH ₂ CH ₂ CO-	1162	(T)T/A A/Q/Q/E/L/R(T)		502.7451	1004.483	0	0	228940.2	P35580	Myosin-10 ***	DTLD	1160	treated	N/A	N
8	2	23.97	14.28	94.8	HSCH ₂ CH ₂ CO-	59	(G)LV E T P T G/Y I/E/S/L/PR(V)		831.9247	1662.841	0.0014	0.8	45374.4	P55209	Nucleosome assembly protein 1-like 1	ERLD	57	treated	3, 5	Y
9	2	19.34	10.84	89.1	HSCH ₂ CH ₂ CO-	520	(D)II V N W V N/E/T/L/R(E)		722.8809	1444.762	-0.0072	-5	70289.7	P13796	Plastin-2	KVND	518	treated	N/A	N
10	2	15.01	7.43	81.5	HSCH ₂ CH ₂ CO-	16	(A)L P Y F D QGY E/A PGVR(E)		850.3974	1699.778	0.0091	5.3	26131.6	O75934	Pre-mRNA-splicing factor SPF27	VVVD	14	treated	N/A	N
11	3	17.41	17.41	78.9	HSCH ₂ CH ₂ CO-	195	(N)GDV C QDC I Q M V T D I Q T/A VR(T)		728.3306	2182.96	0.0173	7.9	58113.1	P07602	Proactivator polypeptide precursor	QPKD	193	both	N/A	N
12	3	15.19	15.19	79.1	HSCH ₂ CH ₂ CO-	140	(N)EE A A LLHEEAT M T I E E/L/L/T/R(Y)		796.3898	2387.147	0.008	3.3	59271.9	O15355	Protein phosphatase 1G	DEDD	138	treated	N/A	N
13	2	20.63	20.63	98.8	HSCH ₂ CH ₂ CO-	586	(A)A E L V E T I A/A/T/A/R(E)		666.8489	1332.683	0.0077	5.8	86707.4	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	DNVD	584	treated	N/A	N
14	2	19.13	19.13	91.2	HSCH ₂ CH ₂ CO-	7	(G)DD S L Y PI A VL I D E LR(N)		910.4593	1819.915	-0.0033	-1.8	65309	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	AAAD	5	treated	6	N
15	3	20.87	20.87	94.7	HSCH ₂ CH ₂ CO-	130	(G)L A V T PT PV P V V GSQMT/R(Q)		614.3298	1840.966	0.0089	4.8	53501.3	P26368	Splicing factor U2AF 65 kDa subunit	MTPD	128	treated	3	Y
16	2	19.26	10.08	81.0	HSCH ₂ CH ₂ CO-	219	(S)I E A N V E S SEV HV E/R(A)		843.393	1685.78	-0.0012	-0.7	31642.1	Q86Y82	Syntaxin-12	DLID	217	treated	3	Y
17	3	23.97	13.63	100.0	HSCH ₂ CH ₂ CO-	206	(S)I E A N V E N/A/E/V HVQQANQQLSR(A)		822.4052	2465.184	0.0173	7	29815.7	O15400	Syntaxin-7	DVID	204	treated	7	Y
18	2	15.32	6.81	85.6	HSCH ₂ CH ₂ CO-	154	(A)GL D A L S S I S/R(Q)		610.3203	1219.635	-0.0018	-1.5	26906.8	Q9UNK0	Syntaxin-8	QEQD	152	treated	8	N
19	2	19.45	19.45	90.6	HSCH ₂ CH ₂ CO-	8	(Q)Q Q T T N T V E E PL D LI/R(L)		922.9606	1844.906	0.0081	4.4	11845.5	P62310	U6 snRNA-associated Sm-like protein LSm3	DDVD	6	treated	3	Y
20	2	10.63	5.2	71.5	HSCH ₂ CH ₂ CO-	54	(A)SS T VP SLCTEAR(A)		669.8173	1338.603	0.0245	18.3	14269.2	Q96NJ1	Uncharacterized protein FLJ30774	GFPD	52	treated	N/A	N
21	2	18.70	18.7	93.1	HSCH ₂ CH ₂ CO-	159	(Q)IG SE I I E E L G/E Q/R(D)		780.8819	1560.757	-0.0009	-0.6	26688.6	Q9UEU0	Vesicle transport	TETD	157	treated	N/A	N

