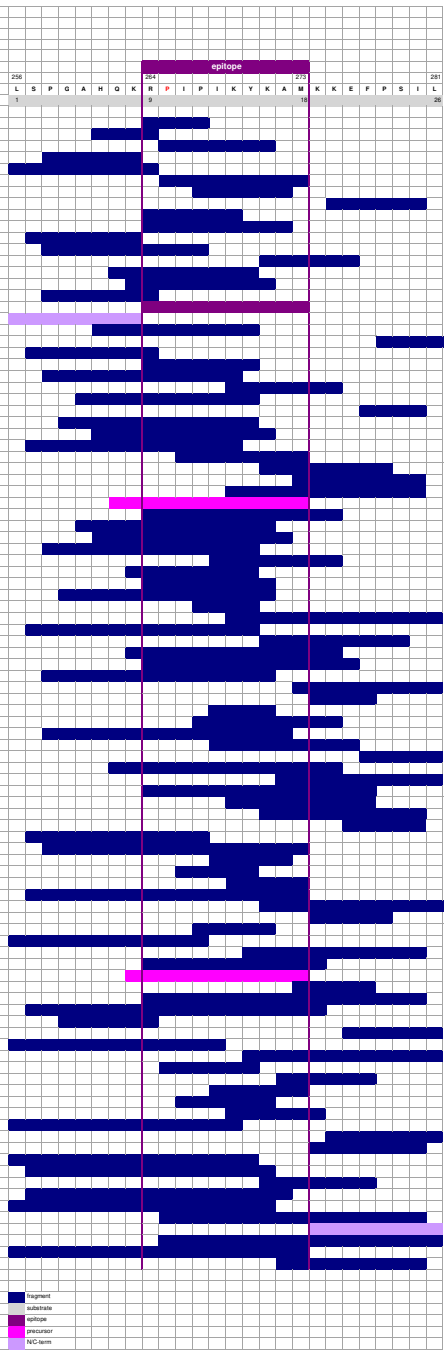
Supplementary Table 4: Summary of the peptides generated by the proteasome from the polypeptide substrate MyD88-L265P[256-281] in an in vitro digest.

RT alignment:		1. 180502_Cha45_Lcl_24h
identification:		2. 180502_Cha45_Ery_24h
		3. 180502_Cha45_Lcl_8h
		4. 180502_Cha45_Ery_8h

Cha-45 (MyD88$_{256-281}$ mut L265P)

LSPGAHQKRPIPIKYKAMKKEFPSIL

	m/z monoiso. Da			charge	sequence	RT	MW monoiso. Da			MS/MS
	detected	calculated	Δ	z		(min)	detected	calculated	Δ	Raw File
1	241.6578	241.6543	0.0036	2	R[9-12]P	20.3	481.3156	481.3085	0.0071	1
2	284.6687	284.6657	0.0030	2	H[6-9]R	12.6	567.3374	567.3314	0.0060	1
3	286.8528	286.8483	0.0045	3	P[10-16]K	27.2	857.5584	857.5448	0.0136	3,4
4	319.1746	319.1708	0.0038	2	P[3-8]K	18.3	636.3492	636.3416	0.0076	2,4
5	331.8578	331.8529	0.0049	3	L[1-9]R	24.1	992.5734	992.5588	0.0146	1,3,4
6	354.2118	354.2075	0.0043	3	P[10-18]M	35.0	1059.6354	1059.6224	0.0130	3,4
7	360.2266	360.2225	0.0041	2	P[12-17]A	24.2	718.4532	718.4450	0.0082	2,4
8	360.7004	360.6964	0.0041	2	K[20-25]I	39.6	719.4008	719.3927	0.0081	1-4
9	362.2473	362.2438	0.0035	2	R[9-14]K	20.6	722.4946	722.4876	0.0070	2,4
10	362.5664	362.5610	0.0054	3	R[9-17]A	24.1	1084.6992	1084.6830	0.0162	1-4
11	362.6903	362.6869	0.0034	2	S[2-8]K	19.0	723.3806	723.3737	0.0069	2,4
12	367.5489	367.5441	0.0048	3	P[3-12]P	21.8	1099.6467	1099.6322	0.0145	1,2,3
13	367.7151	367.7115	0.0036	2	K[16-21]E	14.8	733.4302	733.4229	0.0073	1-4
14	381.5725	381.5681	0.0044	3	Q[7-15]Y	26.3	1141.7175	1141.7044	0.0131	4
15	381.5854	381.5803	0.0051	3	K[8-16]K	19.2	1141.7562	1141.7408	0.0154	2-4
16	397.2250	397.2214	0.0036	2	P[3-9]R	12.3	792.4500	792.4428	0.0072	1-4
17	406.2462	406.2412	0.0050	3	R[9-18]M	25.4	1215.7386	1215.7235	0.0151	1-4
18	419.2325	419.2289	0.0036	2	L[1-8]K	20.4	836.4650	836.4577	0.0073	4
19	427.2589	427.2545	0.0044	3	H[6-15]Y	24.8	1278.7767	1278.7634	0.0133	1-4
20	429.2702	429.2708	-0.0006	1	P[23-26]L	51.4	428.2702	428.2708	-0.0006	1-4
21	440.7411	440.7374	0.0037	2	S[2-9]R	12.4	879.4822	879.4748	0.0074	2-4
22	443.7794	443.7755	0.0040	2	R[9-15]Y	30.4	885.5588	885.5509	0.0079	1-4
23	447.9404	447.9371	0.0033	3	P[3-14]K	22.1	1340.8212	1340.8114	0.0098	2-4
24	448.7730	448.7693	0.0037	2	K[14-20]K	10.9	895.5460	895.5386	0.0074	1-4
25	450.9387	450.9335	0.0052	3	A[5-15]Y	23.3	1349.8161	1349.8005	0.0156	1-4
26	463.2555	463.2551	0.0004	1	F[22-25]I	60.2	462.2555	462.2551	0.0004	1-4
27	469.9461	469.9406	0.0055	3	G[4-15]Y	27.3	1406.8383	1406.8219	0.0164	1-4
28	469.9586	469.9528	0.0058	3	H[6-16]K	20.0	1406.8758	1406.8583	0.0175	4
29	476.9536	476.9478	0.0058	3	S[2-14]K	22.7	1427.8608	1427.8434	0.0174	3,4
30	482.2897	482.2848	0.0049	2	E[1-18]M	35.2	962.5794	962.5696	0.0098	4
31	489.7760	489.7721	0.0040	2	K[16-23]P	18.9	977.5520	977.5441	0.0079	1-4
32	490.2676	490.2641	0.0036	2	M[18-25]I	33.5	978.5352	978.5281	0.0071	1-4
33	490.6119	490.6062	0.0057	3	K[14-25]I	30.4	1468.8357	1468.8185	0.0172	3,4
34	491.6313	491.6257	0.0056	3	Q[7-18]M	25.5	1471.8939	1471.8770	0.0169	4
35	491.6432	491.6378	0.0054	3	R[9-20]K	20.4	1471.9286	1471.9134	0.0162	1,2,4
36	493.6372	493.6318	0.0054	3	A[5-16]K	19.8	1477.9116	1477.8954	0.0162	4
37	493.6381	493.6318	0.0063	3	H[6-17]A	20.9	1477.9143	1477.8954	0.0189	4
38	502.2982	502.2916	0.0066	3	P[3-15]Y	27.4	1503.8946	1503.8747	0.0199	1-4
39	505.3194	505.3114	0.0080	2	I[13-20]K	14.9	1008.6388	1008.6228	0.0160	4
40	507.8265	507.8230	0.0036	2	K[8-15]Y	24.5	1013.6530	1013.6459	0.0071	1,2,4
41	507.8266	507.8230	0.0036	2	R[9-16]K	22.9	1013.6532	1013.6459	0.0073	1-4
42	512.6464	512.6390	0.0074	3	G[4-16]K	22.5	1534.9392	1534.9169	0.0223	3,4
43	520.3136	520.3130	0.0006	1	P[12-15]Y	34.4	519.3136	519.3130	0.0006	3,4
44	528.3059	528.3009	0.0050	3	K[14-26]L	34.6	1581.9177	1581.9026	0.0151	3,4
45	531.3074	531.3022	0.0052	3	S[2-15]Y	26.3	1590.9222	1590.9067	0.0155	1-4
46	533.2922	533.2881	0.0041	2	K[16-24]S	17.8	1064.5844	1064.5761	0.0083	1,3
47	534.3415	534.3361	0.0054	3	K[8-20]K	20.1	1600.0245	1600.0084	0.0161	4
48	534.6572	534.6520	0.0052	3	R[9-21]E	21.6	1600.9716	1600.9560	0.0156	2-4
49	544.9952	544.9899	0.0053	3	P[3-16]K	23.3	1631.9856	1631.9697	0.0159	2-4
50	546.8099	546.8061	0.0038	2	M[18-26]L	44.6	1091.6198	1091.6122	0.0076	1-4
51	551.3195	551.3188	0.0007	1	K[19-22]F	14.8	550.3195	550.3188	0.0007	1-4
52	551.3557	551.3552	0.0005	1	I[13-16]K	18.7	550.3557	550.3552	0.0005	1,3,4
53	553.8427	553.8378	0.0050	2	P[12-20]K	21.5	1105.6854	1105.6755	0.0099	4
54	568.6744	568.6689	0.0055	3	P[3-17]A	24.2	1703.0252	1703.0068	0.0164	2,4
55	569.8362	569.8327	0.0036	2	I[13-21]E	15.5	1137.6724	1137.6653	0.0071	3,4
56	576.3395	576.3392	0.0003	1	F[22-26]L	64.9	575.3395	575.3392	0.0003	1-4
57	577.0275	577.0223	0.0052	3	Q[7-20]K	20.2	1728.0825	1728.0669	0.0156	4
58	582.3397	582.3347	0.0041	2	A[17-26]L	47.8	1162.6574	1162.6493	0.0081	1-4
59	583.6798	583.6748	0.0050	3	R[9-22]F	30.0	1748.0394	1748.0244	0.0150	4
60	586.8276	586.8248	0.0028	2	K[14-22]F	17.9	1171.6552	1171.6496	0.0056	1-4
61	589.8353	589.8301	0.0052	2	K[16-25]I	26.1	1177.6706	1177.6602	0.0104	1-4
62	592.2981	592.2977	0.0004	1	E[21-25]I	65.8	591.2981	591.2977	0.0004	1,2
63	594.3356	594.3322	0.0034	2	S[2-12]P	21.6	1186.6712	1186.6644	0.0068	1
64	612.3531	612.3491	0.0040	3	P[3-18]M	29.7	1834.0593	1834.0473	0.0120	4
65	622.3926	622.3923	0.0003	1	I[13-17]A	15.8	621.3926	621.3923	0.0003	2-4
66	633.3966	633.3970	-0.0004	1	I[11-15]Y	39.3	632.3966	632.3970	-0.0004	1-4
67	640.3483	640.3487	-0.0004	1	K[14-18]M	14.9	639.3483	639.3487	-0.0004	3,4
68	641.3646	641.3598	0.0048	3	S[2-18]M	24.6	1921.0938	1921.0793	0.0145	4
69	646.3749	646.3722	0.0027	2	K[16-26]L	52.6	1290.7498	1290.7443	0.0055	1,3,4
70	648.3718	648.3715	0.0003	1	K[19-23]P	18.0	647.3718	647.3715	0.0003	2
71	648.4076	648.4079	-0.0003	1	P[12-16]K	18.6	647.4076	647.4079	-0.0003	1-4
72	650.8774	650.8742	0.0032	2	L[1-12]P	21.4	1299.7548	1299.7484	0.0064	1-4
73	671.3655	671.3618	0.0037	2	Y[15-25]I	33.6	1340.7310	1340.7235	0.0075	4
74	672.9124	672.9092	0.0032	2	R[9-19]K	23.7	1343.8248	1343.8184	0.0064	2,4
75	672.9127	672.9092	0.0035	2	K[8-18]M	25.3	1343.8254	1343.8184	0.0070	4
76	682.3593	682.3593	0.0000	1	M[18-22]F	18.1	681.3593	681.3593	0.0000	1-4
77	682.7376	682.7311	0.0065	3	R[9-25]I	39.0	2045.2128	2045.1933	0.0195	4
78	684.0626	684.0581	0.0045	3	S[2-19]K	22.0	2049.1878	2049.1743	0.0135	4
79	696.3897	696.3300	0.0597	1	Q[4-9]R	12.6	695.3897	695.3300	0.0597	1-4
80	705.3822	705.3818	0.0004	1	E[21-26]L	68.7	704.3822	704.3818	0.0004	1-4
81	707.4193	707.4163	0.0032	2	L[1-13]I	30.0	1412.8392	1412.8329	0.0065	4
82	727.9081	727.9038	0.0043	2	Y[15-26]L	42.6	1453.8162	1453.8076	0.0086	3,4
83	730.4495	730.4498	-0.0003	1	P[10-15]Y	39.5	729.4495	729.4498	-0.0003	1-4
84	753.3965	753.3964	0.0001	1	A[17-22]F	18.1	752.3965	752.3964	0.0001	1-4
85	753.4333	753.4328	0.0005	1	I[13-18]M	21.5	752.4333	752.4328	0.0005	2-4
86	761.4927	761.4920	0.0007	1	I[11-16]K	23.9	760.4927	760.4920	0.0007	1,3
87	768.4433	768.4437	-0.0004	1	K[14-19]K	12.8	767.4433	767.4437	-0.0004	4
88	771.4677	771.4638	0.0040	2	L[1-14]K	21.7	1540.9354	1540.9275	0.0079	1,3,4
89	833.4762	833.4767	-0.0005	1	K[20-26]L	60.2	832.4762	832.4767	-0.0005	1-4
90	848.4894	848.4876	0.0018	1	K[19-25]I	30.1	847.4894	847.4876	0.0018	1-4
91	852.9981	852.9954	0.0027	2	L[1-15]Y	26.1	1703.9962	1703.9908	0.0054	2-4
92	860.5056	860.5009	0.0047	2	S[2-16]K	20.9	1719.0112	1719.0017	0.0095	2-4
93	881.4908	881.4913	-0.0005	1	K[16-22]F	19.6	880.4908	880.4913	-0.0005	1-4
94	896.0245	896.0194	0.0051	2	S[2-17]A	21.6	1790.0490	1790.0388	0.0102	2,4
95	917.0485	917.0429	0.0056	2	L[1-16]K	24.0	1832.0970	1832.0858	0.0112	4
96	945.5517	945.5461	0.0056	2	P[10-25]I	45.1	1889.1034	1889.0921	0.0113	4
97	961.5740	961.5717	0.0023	1	K[19-26]L	43.1	960.5740	960.5717	0.0023	1-4
98	1002.0928	1002.0881	0.0047	2	P[10-26]L	51.7	2002.1856	2002.1762	0.0094	4
99	1018.0857	1018.0817	0.0040	2	L[1-18]M	29.4	2034.1714	2034.1634	0.0080	4
100	1050.5660	1050.5652	0.0008	1	A[17-25]I	34.4	1049.5660	1049.5652	0.0008	1-4