Supplementary Table III: List of identified peptides and corresponding proteins during the LC-MS/MS analysis of the proteasome assembly complexes.

1. Mass spectrometry results[a] of the proteasome assembly intermedate 15S*.

a: Mass spectrometry was done in A. Emili's lab.
b: the statistical confidence percentage that this protein was correctly identified
c: the percentage of residues in protein sequence that are represented by at least one peptide passing the criteria.
d: the number of peptides in the protein that were found.

IDS	sequence	[b]statistical confidence	[c]percentage of residues	[d]the numbers of peptides
β4/Pre1		99.6	21.2	14
	EDYELSPQAVSSFV			
	EDYELSPQAVSSFV			
	EDYELSPQAVSSFV			
	RPYQVNVLIGGYD			
	RPYQVNVLIGGYDK			
	RPYQVNVLIGGYDK			
	KNKPELYQIDYLGT			
	NKPELYQIDYLGT			
	NKPELYQIDYLGT			
	NKPELYQIDYLGT			
β3/Pup3		99.6	16.1	9
	AIEPETFTQLVSSSLYE			
	AIEPETFTQLVSSSLYE			
	RFGPYFVGPVVAGINS			
	RFGPYFVGPVVAGINS			
	FGPYFVGPVVAGINS			
	FGPYFVGPVVAGINS			
	FGPYFVGPVVAGINS			
	FGPYFVGPVVAGINS			
α1/Scl1		99.6	20.6	23
	HITIFSPEG			
	HITIFSPEG			
	HITIFSPEG			
	LYQVEYAF			
	LYQVEYAF			
	LYQVEYAF			
	TIGMVVNGPIPDA			
	TIGMVVNGPIPDA			
	MANLSQIYTQ			
	MANLSQIYTQ			
	MANLSQIYTQ			
	MANLSQIYTQ			
	MANLSQIYTQ			
	QQEITTNLENHF			
	QQEITTNLENHF			

Supplementary Table III: List of identified peptides and corresponding proteins during the LC-MS/MS analysis of the proteasome assembly complexes.

α3/Pre9		99.6	14.7	8
	TYNEDIPVEILV			
	TYNEDIPVEILV			
	YGYQLYTSNPSGNYTGW			
	VDDAIELAL			
	VDDAIELAL			
α5/Doa5		69.5	8.5	4
	LFQVEYSLEAIKLGSTAIGIAT			
Pba1		99.6	12.7	9
	NLLQLTSIGEI			
	NLLQLTSIGEI			
	HSWNYDENFPNEVDPDQ			
	HSWNYDENFPNEVDPDQ			
α2/Pre8		99.6	22	15
	YSFSLTTFSPSG			
	YSFSLTTFSPSG			
	LGQIDYALTAV			
	LGQIDYALTAV			
	KSSSPLAMSETLS			
	KSSSPLAMSETLS			
	SSSPLAMSETLS			
	SSSPLAMSETLS			
	VSLLTPDIGAVYSGMGPDY			
	VSLLTPDIGAVYSGMGPDY			
α6/Pre5		99.6	35	17
	LFQVEYALEAI			
	LFQVEYALEAI			
	SNTHAVLVAL			
	SNTHAVLVAL			
	SNTHAVLVALK			
	NTQSYGGRPYGVGLLIIGYD			
	NTQSYGGRPYGVGLLIIGYD			
	SGAHLLEFQPSGNVTELYG			
	SGAHLLEFQPSGNVTELYG			
	SGAHLLEFQPSGNVTELYGTAIGA			
	SGAHLLEFQPSGNVTELYGTAIGA			
	TLDTFIKIDGNPDELI			
	TLDTFIKIDGNPDELI			
	TLDTFIKIDGNPDELI			
	TLDTFIKIDGNPDELI			
α4/Pre6		99.6	22.8	15
	IDSHVVLSFSGLNADS			
	IDSHVVLSFSGLNADS			

Supplementary Table III: List of identified peptides and corresponding proteins during the LC-MS/MS analysis of the proteasome assembly complexes.

	IDSHVVLSFSGLNADS			
	IDSHVVLSFSGLNADS			
	TLEDPVTVEYLT			
	LYQTEPSGIYSSWSAQTIG			
	LYQTEPSGIYSSWSAQTIG			
	SLLEVVQTGA			
	SLLEVVQTGA			
	SLLEVVQTGA			
α7/Pre10		99.6	9	6
	TPIPIPAFAD			
	TPIPIPAFAD			
	AELEKLVDHHPEGLSA			
	AELEKLVDHHPEGLSA			

2. Mass spectrometry results for the proteasome assembly intermediate 15S .

a: Protein name identified by searching the database
b: This column contains the sequences of the peptides that were matched to the MS/MS spectra with high enough scores.
c: Molecular weight of the peptide
d: Peptide charge. Possible values: +1, +2 or +3
e: Xcorr score shows how good the match is between the observed peptide fragment mass spectrum and the one theoretically predicted based on this sequence.
We want to see XC higher than 1.5-1.7 for peptides charged +1, higher than 2.0-2.5 for peptides charged +2 and higher that 2.5-3.5 for peptides charged +3.
f: This score shows the change in XC between the best match and the next possible peptide match. We want this score to be higher than 0.08.
g: Displays the percent of peptide fragment ions in an MS/MS spectrum that match with the experimental data; Sp is a preliminary score to shortlist the data for the final correlation analysis.
h: Accession number in the protein lane is the protein database gi number. Rsp value in peptide lane displays the ranking of the particular match during the preliminary scoring (Sp).
i: Ions lane shows how many of the experimental fragment ions matched with the theoretical ions: 21/28 means that 21 fragments (out of 28 that should be\ theoretically produced by given peptide) were actually observed in the experiment.
j: Displays number of duplicate entries found for each DTA file.

[a]Scan	[b]Sequence	[c]MH+	[d]Charge	[e]XC
α1/Scl1				
862 - 867	-.SKIDHINEESWEK.-	1614.78	3	3.65
863	-.SKIDHINEESWEK.-	1614.78	2	4.21
879	-.IDHINEESWEK.-	1399.65	2	2.92
903 - 910	-.TDPAGYYVGYK.-	1233.58	2	3.04
931 - 938	-.M*ANLSQIYTQR.-	1340.67	2	4.85
956 - 963	-.HITIFSPEGR.-	1156.61	2	3.27
974 - 982	-.TIGM*VVNGPIPDAR.-	1455.77	2	3.56
984 - 990	-.QQEITTNLENHFK.-	1601.79	2	3.20
1006 - 1015	-.MANLSQIYTQR.-	1324.67	2	4.67
1063 - 1070	-.LYQVEYAFK.-	1160.60	2	3.41
1067 - 1076	-.TIGMVVNGPIPDAR.-	1439.77	2	4.13
1072	-.LYQVEYAFK.-	1160.60	1	2.06
1344 - 1348	-.VVEFAITHM*IDALGTEFSK.-	2124.07	2	3.74
1395 - 1407	-.VVEFAITHM*IDALGTEFSKNDLEVGVATK.-	3150.61	3	4.08
1570 - 1578	-.AYM*RPLGVILTFVSVDEELGPSIYK.-	2813.48	3	3.73
1572 - 1575	-.VVEFAITHMIDALGTEFSK.-	2108.07	2	4.61
1583 - 1592	-.VVEFAITHMIDALGTEFSKNDLEVGVATK.-	3134.61	3	6.50
1662 - 1671	-.AYMRPLGVILTFVSVDEELGPSIYK.-	2797.49	3	3.11
α2/Pre8				
871 - 875	-.SSSPLAM*SETLSK.-	1353.66	2	2.51
998 - 1007	-.SSSPLAMSETLSK.-	1337.66	2	2.99
1074	-.KLTSQEINDRLEAL.-	1629.88	2	3.06
1207 - 1214	-.YSFSLTTFSPSGK.-	1421.69	2	3.75
1332	-.VSLLTPDIGAVYSGMGPDYR.-	2111.05	2	3.59
1602 - 1607	-.RWNDELELEDAIHIALLTLK.-	2392.29	3	5.61
1651 - 1658	-.WNDELELEDAIHIALLTLK.-	2236.19	3	3.97
α3/Pre9				
870	-.KVTSTLLEQDTSTEK.-	1679.87	3	4.04
1116 - 1120	-.YGYQLYTSNPSGNYTGWK.-	2098.95	2	3.59
1135	-.YGYQLYTSNPSGNYTGWK.-	2098.95	2	3.20
1170 - 1178	-.TTDSSALTYDRLEFATIR.-	2060.03	2	3.12
1263 - 1270	-.TYNEDIPVEILVR.-	1560.83	2	3.97
1519 - 1527	-.IAVAVAGLTADAEILINTAR.-	1982.13	2	4.81
Pba1				
1036 - 1047	-.IM*NPLFPK.-	975.54	2	2.57
1294 - 1302	-.NLLQLTSIGEIK.-	1328.78	2	4.70
1299	-.NLLQLTSIGEIK.-	1328.78	1	1.85
1444	-.NDTADETVYGFSFPIYSFGK.-	2258.03	2	3.81
1642 - 1646	-.TLLFSMEENFISISPIFGNM*ISR.-	2662.33	2	3.43
1643	-.TLLFSMEENFISISPIFGNM*ISR.-	2662.33	2	3.05
α4/Pre6				
1056 - 1060	-.SLLEVVQTGAK.-	1144.66	1	2.78
1172 - 1179	-.LYQTEPSGIYSSWSAQTIGR.-	2244.09	2	4.75
1258 - 1267	-.LTLEDPVTVEYLTR.-	1648.88	2	4.01
1370 - 1378	-.YTQSGGVRPFGVSTLIAGFDPR.-	2325.20	3	3.12
1482 - 1486	-.ALSIFSPDGHIFQVEYALEAVK.-	2434.27	3	3.39
Pba2				
1038 - 1048	-.ISVDQPIFK.-	1046.59	2	2.85
1144	-.YSSALEVFYNK.-	1320.65	2	3.23
1227 - 1236	-.YLVEFVGPLDRPEDGSDSLYKDADM*K.-	2975.40	3	4.09
1279 - 1284	-.YLVEFVGPLDRPEDGSDSLYK.-	2399.18	2	3.68
Ump1				
970 - 979	-.TDFNPLSTNGSIHR.-	1558.76	2	3.08
972 - 980	-.TDFNPLSTNGSIHR.-	1558.76	3	3.09
1196	-.SQVSTDQDKSVLSSAVPSLPDTLR.-	2530.30	2	3.49
1218 - 1224	-.SVLSSAVPSLPDTLR.-	1541.85	2	2.59
α5/Doa5				
960 - 966	-.ATSPLLESDSIEK.-	1389.71	2	3.34
1268 - 1276	-.LFQVEYSLEAIK.-	1439.78	2	4.69
1311	-.AIGSGSEGAQAELLNEWHSSLTLK.-	2498.25	2	3.52
α6/Pre5				
923 - 930	-.NNYDGDTVTFSPTGR.-	1643.73	2	4.68
1303	-.NTQSYGGRPYGVGLLIIGYDK.-	2271.18	3	3.71
1454 - 1462	-.AGVEAISQSLRDESLTVDNLSIAIVGK.-	2785.50	3	4.22
α7/Pre10				
1359 - 1366	-.GDLLQEAIDFAQK.-	1447.74	2	4.15
β3/Pup3				
1307	-.FGPYFVGPVVAGINSK.-	1651.89	2	3.62
1452	-.DALSGWGAVVYIIK.-	1491.82	2	3.89
1492	-.IFHYGHVFLGITGLATDVTTLNEM*FR.-	2968.51	3	3.88
β4/Pre1				
1068	-.RPYQVNVLIGGYDK.-	1621.87	3	3.16
β2/Pup1				
911 - 918	-.FNNGVVIAADTR.-	1276.67	2	4.54

	F	G	H	I	J
1					
2					
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6					
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11					
12					
13					
14					
15					
16					
17					
18					
19	[f]Delta Cn	[g]Sp	[h]RSp	[i]Ions	[j]Count
20					
21	180.33	11513433.0		18 (18 0 0 0 0)	
22	0.19	1258.0	4	0.541666667	2
23	0.39	1286.9	1	0.708333333	2
24	0.18	828.2	1	0.8	2
25	0.37	379.5	2	0.8	2
26	0.31	1780.2	1	0.85	5
27	0.23	485.5	1	0.722222222	40
28	0.32	893.0	1	0.653846154	2
29	0.36	303.7	1	0.583333333	2
30	0.00	1393.2	1	0.85	5
31	0.23	997.2	1	0.875	37
32	0.39	1194.5	1	0.653846154	2
33	0.11	502.2	16	0.625	37
34	0.42	916.8	1	0.555555556	2
35	0.26	857.6	1	0.276785714	2
36	0.41	932.1	1	0.302083333	2
37	0.49	1148.0	1	0.555555556	2
38	0.54	1696.4	1	0.330357143	2
39	0.37	919.7	1	0.28125	2
40					
41	70.28	575711.0		7 (7 0 0 0 0)	
42	0.05	491.9	2	0.625	
43	0.26	715.3	1	0.625	
44	0.26	1802.9	1	0.692307692	
45	0.42	1143.6	1	0.708333333	14
46	0.33	764.0	1	0.552631579	
47	0.30	2313.7	1	0.434210526	1
48	0.12	1068.9	1	0.361111111	1
49					
50	60.24	1323225.0		6 (6 0 0 0 0)	
51	0.16	1401.0	1	0.482142857	3
52	0.42	1089.0	1	0.617647059	3
53	0.44	541.3	1	0.470588235	3
54	0.18	204.9	9	0.382352941	2
55	0.35	900.8	1	0.833333333	2
56	0.51	2006.1	1	0.684210526	2
57					
58	60.23	37362679.0		6 (6 0 0 0 0)	
59	0.09	663.5	166	0.857142857	
60	0.25	1783.7	1	0.863636364	1
61	0.14	297.1	67	0.5	1
62	0.46	892.9	1	0.447368421	1
63	0.30	471.1	1	0.409090909	1
64	0.28	562.7	1	0.431818182	1
65					
66	50.24	11514008.0		5 (5 0 0 0 0)	
67	0.15	477.5	11	0.6	11
68	0.42	1136.8	1	0.657894737	2
69	0.00	1231.2	1	0.769230769	3
70	0.24	1043.9	1	0.357142857	3
71	0.02	1587.3	1	0.392857143	4
72					
73	40.20	486367.0		4 (4 0 0 0 0)	
74	0.14	892.1	2	0.875	
75	0.41	1253.8	1	0.8	
76	0.27	807.7	1	0.27	
77	0.39	455.4	2	0.375	
78					
79	40.17	2911543.0		4 (4 0 0 0 0)	
80	0.20	1204.5	1	0.730769231	
81	0.22	676.7	1	0.480769231	
82	0.31	401.3	1	0.369565217	
83	0.30	364.7	6	0.535714286	
84					
85	30.23	11513430.0		3 (3 0 0 0 0)	
86	0.21	1009.6	1	0.666666667	5
87	0.24	2414.7	2	0.909090909	14
88	0.19	1097.7	1	0.456521739	2
89					
90	30.23	11513431.0		3 (3 0 0 0 0)	
91	0.50	2562.7	1	0.857142857	6
92	0.37	1635.5	1	0.4	1
93	0.31	971.4	1	0.307692308	2
94					
95	30.23	11513431.0		3 (3 0 0 0 0)	
96	0.36	1742.4	1	0.75	3
97					
98	30.19	11514014.0		3 (3 0 0 0 0)	
99	0.36	1030.3	1	0.6	3
100	0.40	1811.6	1	0.730769231	3
101	0.38	1255.1	1	0.33	1
102					
103	10.24	311329.0		1 (1 0 0 0 0)	
104	0.22	1021.4	5	0.461538462	
105					
106	10.23	1420391.0		1 (1 0 0 0 0)	
107	0.35	1358.7	1	0.818181818	2

3. Mass spectrometry results for the proteasome assembly intermediate 15S-Blm10 (I-2).

Scan(s)	Sequence	MH+	Charge	XC
α1/Scl1				
887 - 894	-.TDPAGYYVGYK.-	1233.58	2	3.50
914	-.M*ANLSQIYTQR.-	1340.67	2	3.98
942 - 947	-.HITIFSPEGR.-	1156.61	2	2.69
956 - 962	-.TIGM*VVNGPIPDAR.-	1455.77	2	3.86
1042 - 1047	-.LYQVEYAFK.-	1160.60	2	3.61
1091 - 1096	-.DKFFTLSAENIEER.-	1698.83	3	4.63
1092 - 1098	-.DKFFTLSAENIEER.-	1698.83	2	4.62
1356	-.VVEFAITHM*IDALGTEFSKNDLEVGVATK.-	3150.61	3	4.71
1530 - 1535	-.AYM*RPLGVILTFVSVDEELGPSIYK.-	2813.48	3	3.84
1615	-.AYMRPLGVILTFVSVDEELGPSIYK.-	2797.49	3	3.03
α4/Pre6				
1030 - 1034	-.SLLEVVQTGAK.-	1144.66	2	4.01
1135	-.IDSHVVLSFSGLNADSR.-	1816.92	2	3.23
1151	-.LYQTEPSGIYSSWSAQTIGR.-	2244.09	2	2.52
1226 - 1230	-.LTLEDPVTVEYLTR.-	1648.88	2	4.19
α2/Pre8				
1100 - 1108	-.LTSQEINDRLEAL.-	1501.79	2	3.12
1180	-.YSFSLTTFSPSGK.-	1421.69	2	3.25
1219 - 1223	-.VSLLTPDIGAVYSGM*GPDYR.-	2127.05	2	4.07
1603 - 1608	-.WNDELELEDAIHIALLTLK.-	2236.19	3	4.08
β4/Pre1				
1038	-.RPYQVNVLIGGYDK.-	1621.87	2	4.63
1054 - 1058	-.NKPELYQIDYLGTK.-	1681.88	3	4.21
1171 - 1178	-.EDYELSPQAVSSFVR.-	1726.83	2	4.05
Blm10				
1183	-.IISLSDYEYDITR.-	1587.79	2	3.54
1264 - 1271	-.NLEDSVVGLNPQQFIK.-	1800.95	2	3.88
1438	-.ASFNTEELEDLEGVLWR.-	2007.97	2	4.41
β3/Pup3				
1263	-.FGPYFVGPVVAGINSK.-	1651.89	2	3.48
1375 - 1382	-.AIEPETFTQLVSSSLYER.-	2070.04	2	4.74
α6/Pre5				
911 - 924	-.NNYDGDTVTFSPTGR.-	1643.73	2	4.16
1251 - 1256	-.DESLTVDNLSIAIVGK.-	1673.90	2	3.45
Cdc48				
1504	-.AAAPTVVFLDELDSIAK.-	1759.95	2	4.08
1523	-.NAPAIIFIDEIDSIAPK.-	1826.99	2	3.50
Pba1				
1215	-.VEFPQDLDVPQYSTAVITTK.-	2251.15	2	3.26
1515	-.SIISQLAQFSPDIIVIGTSDK.-	2232.21	2	3.95
α5/Doa5				
944 - 950	-.ATSPLLESDSIEK.-	1389.71	2	3.12
1236	-.LFQVEYSLEAIK.-	1439.78	2	3.62
α3/Pre9				
1139 - 1143	-.TTDSSALTYDRLEFATIR.-	2060.03	3	3.29
1234 - 1242	-.TYNEDIPVEILVR.-	1560.83	2	3.21
α7/Pre10				
1359 - 1366	-.GDLLQEAIDFAQK.-	1447.74	2	4.15
β2/Pup1				
895 - 899	-.FNNGVVIAADTR.-	1276.67	2	3.53

	F	G	H	I	J
1					
2	Score	Accession		Peptides (Hits)	
3					
4	Delta Cn	Sp	RSp	Ions	Count
5					
6	100.24	11513433.0		10 (10 0 0 0 0)	
7	0.39	547.5	1	0.8	2
8	0.00	2084.8	1	0.9	5
9	0.21	712.3	1	0.833333333	40
10	0.27	1137.6	1	0.692307692	2
11	0.24	1119.0	1	0.875	37
12	0.19	1441.6	1	0.480769231	2
13	0.45	1789.1	1	0.807692308	2
14	0.50	603.5	1	0.267857143	2
15	0.37	763.6	1	0.3125	2
16	0.36	610.7	3	0.260416667	2
17					
18	40.23	11514008.0		4 (4 0 0 0 0)	
19	0.23	1304.0	1	0.85	11
20	0.42	1306.1	1	0.65625	2
21	0.17	434.5	1	0.447368421	2
22	0.44	1017.1	1	0.692307692	3
23					
24	40.20	575711.0		4 (4 0 0 0 0)	
25	0.19	735.5	1	0.583333333	
26	0.46	833.5	1	0.625	14
27	0.45	715.5	1	0.526315789	
28	0.07	1383.4	1	0.402777778	1
29					
30	30.23	311329.0		3 (3 0 0 0 0)	
31	0.44	1349.0	1	0.807692308	
32	0.18	1839.3	1	0.538461538	
33	0.40	1095.3	1	0.714285714	
34					
35	30.22	37362646.0		3 (3 0 0 0 0)	
36	0.32	891.9	1	0.708333333	1
37	0.37	1400.3	1	0.7	
38	0.39	1527.3	1	0.625	1
39					
40	20.24	11513435.0		2 (2 0 0 0 0)	
41	0.37	785.5	1	0.6	3
42	0.47	1219.6	1	0.647058824	1
43					
44	20.21	984687.0		2 (2 0 0 0 0)	
45	0.51	1059.5	1	0.678571429	6
46	0.43	673.6	1	0.566666667	2
47					
48					
49	0.44	1172.0	1	0.65625	5
50	0.00	1159.9	1	0.59375	5
51					
52	20.20	37362679.0		2 (2 0 0 0 0)	
53	0.38	415.4	1	0.447368421	
54	0.37	600.8	1	0.425	1
55					
56	20.18	1323460.0		2 (2 0 0 0 0)	
57	0.22	580.5	1	0.583333333	5
58	0.27	1517.4	2	0.818181818	14
59					
60					
61	0.34	754.8	1	0.411764706	2
62	0.36	483.3	1	0.666666667	2
63					
64					
65	0.36	1742.4	1	0.75	3
66	10.21	14488825.0		1 (1 0 0 0 0)	
67	10.19	14488827.0		1 (1 0 0 0 0)	
68	0.28	1376.6	1	0.818181818	2
69					
70					
71					
72					

	A	B	C	D	E
1					
2	4. Mass spectrometry results for the proteasome assembly intermediate half-mer (-β7).				
3					
4	Scan(s)	Sequence	MH+	Charge	XC
5					
6	α1/Scl1				
7	886	-.SKIDHINEESWEK.-	1614.78	3	2.69
8	926 - 934	-.TDPAGYYVGYK.-	1233.58	2	3.56
9	951 - 959	-.M*ANLSQIYTQR.-	1340.67	2	4.41
10	984 - 991	-.HITIFSPEGR.-	1156.61	2	3.30
11	998 - 1006	-.TIGM*VVNGPIPDAR.-	1455.77	2	3.10
12	1004	-.QQEITTNLENHFK.-	1601.79	2	2.20
13	1016 - 1030	-.MANLSQIYTQR.-	1324.67	2	3.75
14	1034 - 1038	-.MANLSQIYTQR.-	1324.67	2	3.93
15	1082 - 1091	-.LYQVEYAFK.-	1160.60	2	3.57
16	1092	-.TIGMVVNGPIPDAR.-	1439.77	2	3.07
17	1142 - 1152	-.DKFFTLSAENIEER.-	1698.83	2	4.53
18	1147	-.DKFFTLSAENIEER.-	1698.83	3	3.68
19	1186	-.FFTLSAENIEER.-	1455.71	2	2.54
20	1551 - 1558	-.AYM*RPLGVILTFVSVDEELGPSIYK.-	2813.48	3	2.78
21					
22	β5/Doa3				
23	922 - 932	-.ATAGNWVASQTVK.-	1332.69	2	3.90
24	928 - 939	-.KEGPTIYYVDSDGTR.-	1700.81	3	3.35
25	931 - 936	-.KEGPTIYYVDSDGTR.-	1700.81	2	4.59
26	978 - 987	-.EGPTIYYVDSDGTR.-	1572.72	2	2.68
27	1090 - 1100	-.ILSNLVYQYK.-	1240.69	2	3.54
28	1376	-.LAPSLTVPPIASPQQFLR.-	1935.11	2	2.94
29					
30	Pba1				
31	967 - 974	-.QWNDLPEPK.-	1126.55	2	2.07
32	1055 - 1063	-.IM*NPLFPK.-	975.54	2	2.74
33	1134 - 1143	-.HLLDLPEISK.-	1164.66	2	3.75
34	1266 - 1275	-.VEFPQDLDVPQYSTAVITTK.-	2251.15	2	4.04
35	1311 - 1314	-.NLLQLTSIGEIK.-	1328.78	2	4.53
36	1538 - 1542	-.SIISQLAQFSPDIIVIGTSDK.-	2232.21	2	4.40
37					
38	α2/Pre8				
39	1019 - 1027	-.SSSPLAMSETLSK.-	1337.66	2	2.95
40	1123 - 1131	-.LGQIDYALTAVK.-	1291.73	2	4.11
41	1150 - 1154	-.LTSQEINDRLEAL.-	1501.79	2	3.19
42	1223 - 1232	-.YSFSLTTFSPSGK.-	1421.69	2	3.94
43	1272 - 1278	-.VSLLTPDIGAVYSGM*GPDYR.-	2127.05	2	4.53
44	1340	-.VSLLTPDIGAVYSGMGPDYR.-	2111.05	2	3.47
45					
46	α6/Pre5				
47	947 - 955	-.NNYDGDTVTFSPTGR.-	1643.73	2	4.52
48	960 - 966	-.IDGNPDELIK.-	1113.58	2	3.27
49	964	-.IDGNPDELIK.-	1113.58	1	1.66
50	1114 - 1122	-.DTPFTIYDGEAVAK.-	1526.74	2	2.97
51	1298 - 1303	-.SGAHLLEFQPSGNVTELYGTAIGAR.-	2588.31	3	4.02
52	1447	-.AGVEAISQSLRDESLTVDNLSIAIVGK.-	2785.50	2	2.09
53					
54	α5/Doa5				
55	943 - 952	-.RATSPLLESDSIEK.-	1545.81	2	4.43
56	948	-.RATSPLLESDSIEK.-	1545.81	3	2.77
57	983 - 990	-.ATSPLLESDSIEK.-	1389.71	2	3.54
58	1102 - 1112	-.EAELLVLK.-	914.56	1	1.86
59	1299	-.LFQVEYSLEAIK.-	1439.78	2	2.44
60					
61	α4/Pre6				
62	1078 - 1083	-.SLLEVVQTGAK.-	1144.66	1	2.43
63	1187	-.IDSHVVLSFSGLNADSR.-	1816.92	2	3.82
64	1190 - 1199	-.LYQTEPSGIYSSWSAQTIGR.-	2244.09	2	4.52
65	1280 - 1287	-.LTLEDPVTVEYLTR.-	1648.88	2	4.72
66					
67	Pba2				
68	1035	-.GLFAIQQR.-	932.53	2	3.26
69	1059 - 1066	-.ISVDQPIFK.-	1046.59	2	2.79
70	1071	-.FVRPISWQGAYGM*ADAR.-	1940.95	3	4.77
71	1158 - 1168	-.YSSALEVFYNK.-	1320.65	2	3.76
72					
73	β6/Pre7				
74	1115 - 1124	-.GAVYSFDPVGSYER.-	1546.72	2	3.69
75	1116 - 1130	-.YLSVEEVIK.-	1079.60	2	2.29
76	1132 - 1136	-.YLSVEEVIK.-	1079.60	1	1.79
77	1135 - 1138	-.YLSVEEVIK.-	1079.60	2	2.56
78					
79	Ump1				
80	956 - 963	-.QQEGGAVPLSTQLNDR.-	1712.86	2	3.18
81	992 - 1000	-.QIFGIAEPM*KR.-	1305.70	2	2.25
82	995 - 1003	-.TDFNPLSTNGSIHR.-	1558.76	2	2.68
83	1007 - 1014	-.TDFNPLSTNGSIHR.-	1558.76	3	2.56
84					
85	α3/Pre9				
86	914	-.VTSTLLEQDTSTEK.-	1551.78	2	3.17
87	1159	-.YGYQLYTSNPSGNYTGWK.-	2098.95	2	2.95
88	1159	-.AISVGANTSAAQTLLQM*DYK.-	2098.05	2	2.99
89	1279 - 1286	-.TYNEDIPVEILVR.-	1560.83	2	3.88
90					
91	β3/Pup3				
92	918 - 923	-.LGSQSLGVSNKFEK.-	1493.80	2	2.99
93	1310 - 1320	-.FGPYFVGPVVAGINSK.-	1651.89	2	3.80
94	1406 - 1410	-.AIEPETFTQLVSSSLYER.-	2070.04	2	4.52
95					
96	α7/Pre10				
97	1203 - 1210	-.TPIPIPAFADR.-	1197.66	2	2.51
98	1395 - 1398	-.GDLLQEAIDFAQK.-	1447.74	2	4.68
99					
100	β4/Pre1				
101	1108 - 1120	-.NKPELYQIDYLGTK.-	1681.88	2	4.30
102	1230 - 1236	-.EDYELSPQAVSSFVR.-	1726.83	2	3.76
103					
104	β1/Pre3				
105	976 - 979	-.NKGEVYTIPLGGSVHK.-	1698.92	3	3.01
106	1024 - 1031	-.MVVLTAAGVER.-	1145.64	2	4.05
107					
108	β2/Pup1				
109	935 - 942	-.FNNGVVIAADTR.-	1276.67	2	4.07

	F	G	H	I	J
1					
2					
3					
4	Delta Cn	Sp	RSp	Ions	Count
5					
6	140.23	11513433.0		14 (14 0 0 0 0)	
7	0.12	344.7	227	0.395833333	2
8	0.40	343.9	1	0.75	2
9	0.00	1788.8	1	0.85	5
10	0.33	654.9	1	0.833333333	40
11	0.28	872.7	1	0.615384615	2
12	0.32	280.0	1	0.5	2
13	0.25	1289.9	1	0.8	5
14	0.00	1703.0	1	0.8	5
15	0.21	1020.6	1	0.875	37
16	0.20	636.3	8	0.538461538	2
17	0.44	2039.9	1	0.846153846	2
18	0.21	778.0	9	0.423076923	2
19	0.41	858.6	1	0.636363636	2
20	0.10	536.0	9	0.239583333	2
21					
22	60.23	914974.0		6 (6 0 0 0 0)	
23	0.44	1183.4	1	0.791666667	4
24	0.19	794.9	3	0.375	8
25	0.45	1486.0	1	0.75	8
26	0.26	322.2	3	0.5	10
27	0.04	986.3	1	0.888888889	5
28	0.36	357.2	1	0.5	1
29					
30	60.23	37362679.0		6 (6 0 0 0 0)	
31	0.13	197.2	73	0.5625	
32	0.07	601.2	162	0.857142857	
33	0.12	1342.3	1	0.888888889	
34	0.37	450.8	1	0.473684211	
35	0.26	1787.4	1	0.818181818	1
36	0.49	827.6	1	0.45	1
37					
38	60.23	575711.0		6 (6 0 0 0 0)	
39	0.40	1133.4	1	0.708333333	
40	0.25	1456.2	1	0.863636364	1
41	0.28	682.4	7	0.583333333	
42	0.44	966.6	1	0.666666667	14
43	0.50	879.1	1	0.605263158	
44	0.21	946.1	1	0.552631579	
45					
46	60.23	984687.0		6 (6 0 0 0 0)	
47	0.51	1427.7	1	0.714285714	6
48	0.11	656.8	3	0.833333333	2
49	0.04	230.0	257	0.5	2
50	0.11	715.5	1	0.653846154	2
51	0.18	886.2	1	0.302083333	2
52	0.17	489.0	1	0.346153846	2
53					
54	50.22	1041976.0		5 (5 0 0 0 0)	
55	0.34	1440.9	1	0.730769231	5
56	0.03	844.4	20	0.442307692	5
57	0.27	903.4	1	0.708333333	5
58	0.06	225.6	159	0.642857143	5
59	0.14	934.5	1	0.727272727	14
60					
61	40.35	11514008.0		4 (4 0 0 0 0)	
62	0.30	600.0	1	0.6	11
63	0.42	1325.6	1	0.59375	2
64	0.42	813.8	1	0.605263158	2
65	0.00	1344.9	1	0.846153846	3
66					
67	40.24	486367.0		4 (4 0 0 0 0)	
68	0.16	1095.4	4	0.857142857	
69	0.15	689.7	6	0.8125	
70	0.44	2435.0	1	0.546875	
71	0.33	1692.1	1	0.85	
72					
73	40.18	11513438.0		4 (4 0 0 0 0)	
74	0.39	1052.4	1	0.615384615	4
75	0.12	322.3	221	0.6875	1
76	0.08	479.4	5	0.6875	1
77	0.09	472.5	26	0.8125	1
78					
79	40.16	2911543.0		4 (4 0 0 0 0)	
80	0.40	365.0	1	0.566666667	
81	0.10	339.6	22	0.55	
82	0.23	910.5	1	0.692307692	
83	0.10	457.3	6	0.423076923	
84					
85	38.19	1323225.0		4 (3 1 0 0 0)	
86	0.31	785.9	1	0.615384615	3
87	0.40	574.5	1	0.441176471	3
88	0.02	371.9	2	0.368421053	3
89	0.33	569.5	1	0.708333333	2
90					
91	30.23	11514014.0		3 (3 0 0 0 0)	
92	0.28	525.0	1	0.538461538	1
93	0.35	891.1	1	0.666666667	3
94	0.46	1157.9	1	0.617647059	1
95					
96	20.23	1420786.0		2 (2 0 0 0 0)	
97	0.14	347.7	9	0.6	3
98	0.39	1497.8	1	0.75	3
99					
100	20.21	311329.0		2 (2 0 0 0 0)	
101	0.22	881.5	1	0.730769231	
102	0.40	1377.0	1	0.785714286	
103					
104	20.20	2131077.0		2 (2 0 0 0 0)	
105	0.07	803.0	5	0.383333333	3
106	0.32	2217.0	1	0.95	3
107					
108	10.20	1420391.0		1 (1 0 0 0 0)	
109	0.29	1744.9	1	0.863636364	2

5. Mass spectrometry results of the proteasome assembly intermediate: precursor dimer.

Scan(s)	Sequence	MH+	Charge	XC
α1/Scl1				
366 - 374	-.LVAIAEQD.-	858.46	1	1.87
402 - 416	-.ATNQTNINSLAVR.-	1401.75	2	4.07
414 - 420	-.TDPAGYYVGYK.-	1233.58	2	2.89
456	-.QQEITTNLENHFK.-	1601.79	2	2.61
460 - 466	-.TIGM*VVNGPIPDAR.-	1455.77	2	2.67
492 - 494	-.LYQVEYAFK.-	1160.60	1	2.27
518 - 526	-.DKFFTLSAENIEER.-	1698.83	2	4.78
α5/Doa5				
332	-.EKEAAESPEEADVEM*S.-	1766.73	2	3.88
352 - 358	-.GVSTFSPEGR.-	1036.51	2	3.02
403 - 412	-.LGSTAIGIATK.-	1031.61	2	3.76
438 - 448	-.ATSPLLESDSIEK.-	1389.71	2	3.23
479 - 487	-.EAELLVLK.-	914.56	2	2.09
480 - 495	-.EAELLVLK.-	914.56	1	2.24
β1/Pre3				
299 - 306	-.TTTGAYIANR.-	1067.55	2	2.92
367 - 376	-.DGVILGADSR.-	1002.52	2	3.16
435	-.EETVDFIK.-	980.49	1	1.60
590 - 598	-.LIFYPDEYEQL.-	1429.69	1	2.03
596 - 608	-.LIFYPDEYEQL.-	1429.69	1	2.09
602 - 616	-.LIFYPDEYEQL.-	1429.69	2	4.40
β6/Pre7				
288	-.DSFTSATER.-	1013.45	2	2.41
396	-.NITDYSINSR.-	1182.58	2	3.57
410 - 418	-.EFYELK.-	828.41	1	1.92
503 - 511	-.YLSVEEVIK.-	1079.60	1	1.55
504 - 508	-.YLSVEEVIK.-	1079.60	2	2.49
512	-.GAVYSFDPVGSYER.-	1546.72	2	3.62
α3/Pre9				
323 - 336	-.TTDSSALTYDR.-	1229.56	2	3.70
355 - 360	-.TTDSSALTYDR.-	1229.56	2	2.36
384 - 392	-.KVTSTLLEQDTSTEK.-	1679.87	2	5.25
411	-.TTIFSPEGR.-	1007.52	2	2.49
571 - 579	-.TYNEDIPVEILVR.-	1560.83	2	4.84
α6/Pre5				
316 - 320	-.NADELSSYQK.-	1154.53	2	3.22
419 - 428	-.IDGNPDELIK.-	1113.58	1	1.95
426 - 439	-.NNYDGDTVTFSPTGR.-	1643.73	2	4.51
442 - 451	-.TLDTFIK.-	837.47	1	1.69
499 - 506	-.DTPFTIYDGEAVAK.-	1526.74	2	4.52
β7/Pre4				
356	-.NTGLTFK.-	780.43	1	1.85
510	-.TTVQVAEEAIVNAM*R.-	1647.84	2	3.95
531 - 539	-.NFSLAIIDK.-	1020.57	1	2.22
611	-.TTVQVAEEAIVNAMR.-	1631.84	2	4.21
β2/Pup1				
326	-.QDLTKEEAIK.-	1174.63	2	2.67
359	-.NNFLAENSHTQPK.-	1499.72	2	3.73
363	-.ATSTGTTIVGVK.-	1134.64	2	3.34
432	-.FNNGVVIAADTR.-	1276.67	2	2.77
α2/Pre8				
339 - 348	-.ATNGVVIATEK.-	1102.61	2	2.54
368	-.KSSSPLAM*SETLSK.-	1481.76	2	3.38
387 - 391	-.SSSPLAM*SETLSK.-	1353.66	2	2.71
516 - 520	-.LTSQEINDRLEAL.-	1501.79	2	2.97
β5/Doa3				
436	-.VKEEEGSFNNVIG.-	1421.69	2	2.50
444	-.EGPTIYYVDSDGTR.-	1572.72	2	2.34
572 - 578	-.ELQYDNEQNLESDFVTGASQFQR.-	2718.23	2	4.18
β4/Pre1				
382 - 388	-.VQDSVILASSK.-	1146.64	2	3.91
383	-.VQDSVILASSK.-	1146.64	1	1.77
559	-.EDYELSPQAVSSFVR.-	1726.83	2	2.57
β3/Pup3				
334	-.LGSQSLGVSNK.-	1089.59	2	2.77
415	-.LGSQSLGVSNKFEK.-	1493.80	2	3.25
656	-.AIEPETFTQLVSSSLYER.-	2070.04	2	3.50
α7/Pre10				
311 - 319	-.LVDHHPEGLSAR.-	1330.69	2	2.70
375 - 378	-.AVENGTTSIGIK.-	1189.64	2	2.87
634	-.GDLLQEAIDFAQK.-	1447.74	2	3.49
α4/Pre6				
476 - 483	-.SLLEVVQTGAK.-	1144.66	2	4.00
576 - 580	-.LTLEDPVTVEYLTR.-	1648.88	2	3.58
Ump1				
286 - 296	-.TM*EM*EIVNR.-	1154.53	2	2.34
[a]Pba2				
484	-.GLFAIQQR.-	932.53	2	2.95
[a]Pba1				
666	K.VEFPQDLDVPQYSTAVITTK.I	2251.15000	2	2.89
670	K.VEFPQDLDVPQYSTAVITTK.I	2251.15000	2	3.16
676	K.VEFPQDLDVPQYSTAVITTK.I	2251.15000	2	2.89
927	R.SIISQLAQFSPDIIVIGTSDK.I	2232.21000	2	3.19

	A	B	C	D	E
106	931	R.SIISQLAQFSPDIIVIGTSDK.I	2232.21219	2	2.59
107	935	R.SIISQLAQFSPDIIVIGTSDK.I	2232.21219	2	4.18
108					
109					
110	a: identified from a separate scan for the precursordimer particle.				

	F	G	H	I	J	K
1						
2	Score	Accession		Peptides (Hits)		
3						
4	Delta Cn	Sp	RSp	Ions	Count	
5						
6	70.24	11513433.0		7 (7 0 0 0 0)		
7	0.18	513.5	1	0.714285714	5	
8	0.00	1206.8	1	0.708333333	2	
9	0.35	463.7	2	0.8	2	
10	0.16	184.3	83	0.416666667	2	
11	0.08	651.5	3	0.615384615	2	
12	0.22	775.9	1	0.75	37	
13	0.40	1416.0	1	0.807692308	2	
14						
15	60.19	312258.0		6 (6 0 0 0 0)		
16	0.45	856.4	1	0.6	1	
17	0.08	816.9	1	0.833333333	10	
18	0.28	1233.8	1	0.85	4	
19	0.31	926.2	1	0.708333333	5	
20	0.02	390.5	101	0.714285714	5	
21	0.00	256.5	32	0.785714286	5	
22						
23	58.22	476044.0		6 (5 1 0 0 0)		
24	0.29	903.9	1	0.833333333	17	
25	0.16	1614.6	1	0.944444444	14	
26	0.05	251.0	2	0.714285714	3	
27	0.04	523.6	17	0.55	3	
28	0.03	487.3	63	0.5	3	
29	0.29	1368.3	1	0.85	3	
30						
31	54.18	463267.0		6 (5 0 0 1 0)		
32	0.15	749.6	2	0.75	1	
33	0.31	602.6	1	0.777777778	1	
34	0.02	247.9	35	0.8	2	
35	0.03	292.9	226	0.5625	1	
36	0.02	515.3	11	0.875	1	
37	0.34	795.8	1	0.615384615	4	
38						
39	50.26	11514007.0		5 (5 0 0 0 0)		
40	0.42	1819.0	1	0.9	2	
41	0.14	361.7	42	0.6	2	
42	0.38	2056.8	1	0.75	3	
43	0.05	528.4	9	0.6875	46	
44	0.42	782.5	1	0.791666667	2	
45						
46	44.23	11513431.0		5 (3 1 1 0 0)		
47	0.30	1078.2	1	0.833333333	5	
48	0.03	295.8	12	0.555555556	2	
49	0.49	1326.8	1	0.714285714	6	
50	0.01	367.6	119	0.666666667	2	
51	0.31	1668.6	1	0.884615385	2	
52						
53	40.21	4223.0		4 (4 0 0 0 0)		
54	0.08	156.2	17	0.666666667	2	
55	0.41	1666.9	1	0.714285714	2	
56	0.01	454.6	15	0.75	2	
57	0.36	1493.9	1	0.714285714	2	
58						
59	40.19	1420391.0		4 (4 0 0 0 0)		
60	0.11	326.5	4	0.777777778	2	
61	0.35	1042.0	1	0.666666667		
62	0.18	840.9	5	0.727272727	2	
63	0.10	1074.3	1	0.727272727	2	
64						
65	38.17	575711.0		4 (3 1 0 0 0)		
66	0.22	970.0	4	0.75	3	
67	0.37	595.5	1	0.692307692		
68	0.13	555.2	1	0.666666667		
69	0.09	477.3	60	0.5		
70						
71	30.21	914974.0		3 (3 0 0 0 0)		
72	0.15	593.8	1	0.541666667	4	
73	0.28	394.8	1	0.576923077	10	
74	0.48	1027.8	1	0.477272727	1	
75						
76	30.20	311329.0		3 (3 0 0 0 0)		
77	0.41	886.0	1	0.85		
78	0.27	234.8	40	0.45		
79	0.39	654.3	1	0.607142857		
80						
81	30.17	11514014.0		3 (3 0 0 0 0)		
82	0.34	1069.2	1	0.75	1	
83	0.34	514.7	2	0.5	1	
84	0.41	1044.5	1	0.558823529	1	
85						
86	30.17	1420786.0		3 (3 0 0 0 0)		
87	0.30	487.5	4	0.681818182	3	
88	0.26	622.1	3	0.636363636	3	
89	0.39	1235.5	1	0.708333333	3	
90						
91	20.20	11514008.0		2 (2 0 0 0 0)		
92	0.19	1644.5	1	0.85	11	
93	0.00	1000.1	1	0.692307692	3	
94						
95	10.12	2911543.0		1 (1 0 0 0 0)		
96	0.13	660.3	33	0.6875		
97						
98	10.15	486367.0		1 (1 0 0 0 0)		
99	0.11	1071.3	7	0.857142857		
100						
101		30675.4	37362679	6 (6 0 0 0 0)		
102	0.55	447.3	1	18/38	1	
103	0.49	357.6	1	18/38	1	
104	0.42	434.8	1	18/38	1	
105	0.60	590.4	1	17/40	1	

	F	G	H	I	J	K
106	0.40	241.7	1	12/40	1	
107	0.65	907.4	1	20/40	1	
108						
109						
110						

	A	B	C	D	E
1					
2	6. Mass spectrometry results of mature 20S proteasome.				
3					
4	Scan(s)	Sequence	MH+	Charge	XC
5					
6	α1/Scl1				
7	404 - 411	-.NDLEVGVATK.-	1045.55	1	2.51
8	406 - 414	-.LVAIAEQD.-	858.46	1	1.96
9	442	-.ATNQTNINSLAVR.-	1401.75	2	3.15
10	456 - 464	-.TDPAGYYVGYK.-	1233.58	2	3.34
11	496 - 500	-.QQEITTNLENHFK.-	1601.79	2	2.53
12	498 - 507	-.TIGM*VVNGPIPDAR.-	1455.77	2	3.54
13	539	-.LYQVEYAFK.-	1160.60	1	1.82
14	547	-.TIGMVVNGPIPDAR.-	1439.77	2	2.97
15	566 - 574	-.DKFFTLSAENIEER.-	1698.83	2	4.57
16					
17	β1/Pre3				
18	298 - 310	-.TTTGAYIANR.-	1067.55	2	2.84
19	316	-.TTTGAYIANR.-	1067.55	2	2.35
20	420	-.WDGSSGGVIR.-	1033.51	2	2.87
21	476 - 479	-.EETVDFIK.-	980.49	1	2.04
22	560	-.DNLTAGIIVAGYDDK.-	1564.79	2	4.33
23	654 - 662	-.LIFYPDEYEQL.-	1429.69	1	2.20
24	659 - 666	-.LIFYPDEYEQL.-	1429.69	1	3.16
25	664 - 671	-.LIFYPDEYEQL.-	1429.69	2	3.61
26					
27	α6/Pre5				
28	327	-.NADELSSYQK.-	1154.53	2	3.21
29	390 - 399	-.QGSVTVGLR.-	916.52	2	2.39
30	466 - 470	-.IDGNPDELIK.-	1113.58	1	2.15
31	468	-.IDGNPDELIK.-	1113.58	2	2.18
32	474	-.NNYDGDTVTFSPTGR.-	1643.73	2	3.37
33	546 - 554	-.DTPFTIYDGEAVAK.-	1526.74	2	3.55
34	556	-.DTPFTIYDGEAVAK.-	1526.74	1	2.72
35	686	-.LFQVEYALEAIK.-	1423.78	2	4.26
36					
37	β7/Pre4				
38	388 - 403	-.NTGLTFK.-	780.43	1	2.00
39	536	-.TQQPIVTGTSVISMK.-	1589.86	2	3.83
40	582 - 590	-.NFSLAIIDK.-	1020.57	1	2.26
41	588 - 599	-.NFSLAIIDK.-	1020.57	2	2.57
42	670 - 678	-.TTVQVAEEAIVNAMR.-	1631.84	2	4.62
43	695	-.YDNGVIIAADNLGSYGSLLR.-	2111.08	2	2.81
44					
45	α7/Pre10				
46	331 - 339	-.LVDHHPEGLSAR.-	1330.69	2	2.71
47	415 - 422	-.AVENGTTSIGIK.-	1189.64	2	2.99
48	478 - 492	-.NFQVEYAVK.-	1097.56	1	2.74
49	596 - 604	-.TPIPIPAFADR.-	1197.66	2	2.32
50	694 - 702	-.GDLLQEAIDFAQK.-	1447.74	2	4.27
51					
52	α5/Doa5				
53	359 - 371	-.EKEAAESPEEADVEM*S.-	1766.73	2	4.13
54	394 - 402	-.GVSTFSPEGR.-	1036.51	2	2.61
55	434 - 444	-.EGVVLGVEK.-	929.53	1	2.70
56	483 - 488	-.ATSPLLESDSIEK.-	1389.71	2	2.97
57	528 - 534	-.EAELLVLK.-	914.56	1	1.96
58					
59	α3/Pre9				
60	344 - 350	-.TTDSSALTYDR.-	1229.56	2	3.44
61	436	-.VTSTLLEQDTSTEK.-	1551.78	2	3.48
62	443 - 447	-.TTIFSPEGR.-	1007.52	2	2.15
63	594	-.TTDSSALTYDRLEFATIR.-	2060.03	2	2.76
64	627 - 634	-.TYNEDIPVEILVR.-	1560.83	2	3.95
65					
66	α2/Pre8				
67	370 - 378	-.ATNGVVIATEK.-	1102.61	2	2.73
68	375	-.ATNGVVIATEK.-	1102.61	1	1.98
69	543	-.KLTSQEINDRLEAL.-	1629.88	2	3.19
70	562 - 567	-.LTSQEINDRLEAL.-	1501.79	2	3.04
71	640	-.VSLLTPDIGAVYSGM*GPDYR.-	2127.05	2	2.85
72					
73	α4/Pre6				
74	511 - 527	-.SLLEVVQTGAK.-	1144.66	2	3.62
75	523 - 531	-.SLLEVVQTGAK.-	1144.66	1	2.93
76	532	-.SLLEVVQTGAK.-	1144.66	2	3.92
77	631 - 642	-.LTLEDPVTVEYLTR.-	1648.88	2	4.30
78					
79	β5/Doa3				
80	452	-.ATAGNWVASQTVK.-	1332.69	2	2.79
81	460 - 462	-.KEGPTIYYVDSDGTR.-	1700.81	2	4.72
82	490 - 503	-.EGPTIYYVDSDGTR.-	1572.72	2	3.16
83					
84	β6/Pre7				
85	550 - 558	-.YLSVEEVIK.-	1079.60	1	1.92
86	552	-.YLSVEEVIK.-	1079.60	2	2.74
87	559	-.GAVYSFDPVGSYER.-	1546.72	2	3.40
88					
89	β3/Pup3				
90	364 - 367	-.LGSQSLGVSNK.-	1089.59	2	3.23
91	710 - 718	-.AIEPETFTQLVSSSLYER.-	2070.04	2	5.75
92					
93	β4/Pre1				
94	423 - 431	-.VQDSVILASSK.-	1146.64	1	2.53
95	607 - 615	-.EDYELSPQAVSSFVR.-	1726.83	2	4.20
96	423 - 431	-.VKDSVILASSK.-	1146.67	1	2.53
97					
98	Sem1				
99	584 - 587	-.LGEHNIDVLEGNEQFINAAK.-	2211.11	2	5.47
100					
101	β2/Pup1				
102	363	-.QDLTKEEAIK.-	1174.63	2	2.80
103					
104	Non-identified peptides				
105	588 - 599	-.FSDIAILSR.-	1021.57	2	2.59
106	576	-.NGQM*NLDLR.-	1076.52	2	2.52
107	386 - 400	-.PAGAGRAASKAPR.-	1209.68	2	2.32
108	416	-.DRLLDEDK.-	1003.51	2	2.31
109	535 - 538	-.EALENVIK.-	915.52	1	1.88

	F	G	H	I	J
1					
2					
3					
4	Delta Cn	Sp	RSp	Ions	Count
5					
6	90.23	11513433.0		9 (9 0 0 0 0)	
7	0.24	420.7	1	0.666666667	2
8	0.17	682.3	1	0.785714286	5
9	0.00	789.0	2	0.625	2
10	0.33	488.0	1	0.8	2
11	0.21	320.0	8	0.5	2
12	0.24	861.7	1	0.615384615	2
13	0.16	500.8	27	0.625	37
14	0.21	882.7	1	0.653846154	2
15	0.43	2053.2	1	0.769230769	2
16					
17	80.22	3114290.0		8 (8 0 0 0 0)	
18	0.31	1020.4	1	0.888888889	17
19	0.19	812.1	1	0.777777778	17
20	0.25	1192.7	1	0.833333333	12
21	0.00	262.6	293	0.642857143	3
22	0.50	1623.4	1	0.714285714	4
23	0.25	664.5	4	0.6	3
24	0.12	721.5	21	0.6	3
25	0.21	1050.0	1	0.85	3
26					
27	80.21	11513431.0		8 (8 0 0 0 0)	
28	0.26	1088.5	1	0.833333333	5
29	0.17	406.1	1	0.75	4
30	0.18	397.9	8	0.611111111	2
31	0.13	204.7	260	0.555555556	2
32	0.38	946.8	1	0.607142857	6
33	0.29	736.9	1	0.769230769	2
34	0.18	636.9	1	0.538461538	2
35	0.00	1910.9	1	0.863636364	10
36					
37	58.23	11513439.0		6 (5 1 0 0 0)	
38	0.03	169.3	36	0.666666667	2
39	0.40	1210.8	1	0.75	
40	0.03	430.5	83	0.625	2
41	0.03	688.6	3	0.8125	2
42	0.46	1855.4	1	0.714285714	2
43	0.21	951.9	1	0.473684211	2
44					
45	50.21	14488825.0		5 (5 0 0 0 0)	
46	0.33	395.0	10	0.636363636	3
47	0.29	1152.5	1	0.818181818	3
48	0.17	652.9	4	0.75	7
49	0.10	287.9	23	0.6	3
50	0.43	1438.6	1	0.75	3
51					
52	50.21	1323460.0		5 (5 0 0 0 0)	
53	0.50	1305.1	1	0.666666667	1
54	0.14	1031.4	1	0.888888889	10
55	0.11	465.7	1	0.8125	5
56	0.14	873.1	1	0.666666667	5
57	0.04	332.8	24	0.714285714	5
58					
59	50.20	11514007.0		5 (5 0 0 0 0)	
60	0.33	1290.7	1	0.8	2
61	0.30	804.6	1	0.615384615	3
62	0.06	684.1	2	0.75	46
63	0.15	195.2	42	0.323529412	2
64	0.43	899.1	1	0.833333333	2
65					
66	46.16	575711.0		5 (3 2 0 0 0)	
67	0.24	1067.6	2	0.75	3
68	0.33	461.9	2	0.6	3
69	0.17	975.1	2	0.538461538	
70	0.24	725.8	5	0.583333333	
71	0.38	462.2	1	0.473684211	
72					
73	40.21	11514008.0		4 (4 0 0 0 0)	
74	0.11	1150.5	2	0.8	11
75	0.26	678.6	1	0.65	11
76	0.16	1527.5	1	0.85	11
77	0.41	1034.3	1	0.769230769	3
78					
79	30.26	14488830.0		3 (3 0 0 0 0)	
80	0.25	852.3	1	0.666666667	4
81	0.49	1267.9	1	0.714285714	8
82	0.39	622.7	1	0.653846154	10
83					
84	30.17	11513438.0		3 (3 0 0 0 0)	
85	0.05	603.3	61	0.6875	1
86	0.16	462.6	7	0.8125	1
87	0.35	1046.3	1	0.653846154	4
88					
89	20.29	11514014.0		2 (2 0 0 0 0)	
90	0.34	1107.5	1	0.8	1
91	0.51	1554.4	1	0.676470588	1
92					
93	20.21	311329.0		2 (2 0 0 0 0)	
94	0.00	747.1	2	0.7	
95	0.45	1160.3	1	0.714285714	
96	0.29	747.1	2	0.7	
97					
98	10.27	3318722.0		1 (1 0 0 0 0)	
99	0.13	2869.8	1	0.684210526	5
100					
101	10.14	1420391.0		1 (1 0 0 0 0)	
102	0.21	282.9	27	0.722222222	2
103					
104	10.13	663258.0		1 (1 0 0 0 0)	
105	0.01	460.2	46	0.75	1
106	0.00	950.3	51	0.8125	
107	0.03	386.4	72	0.5	
108	0.03	761.4	1	0.785714286	
109	0.13	209.6	242	0.642857143	2