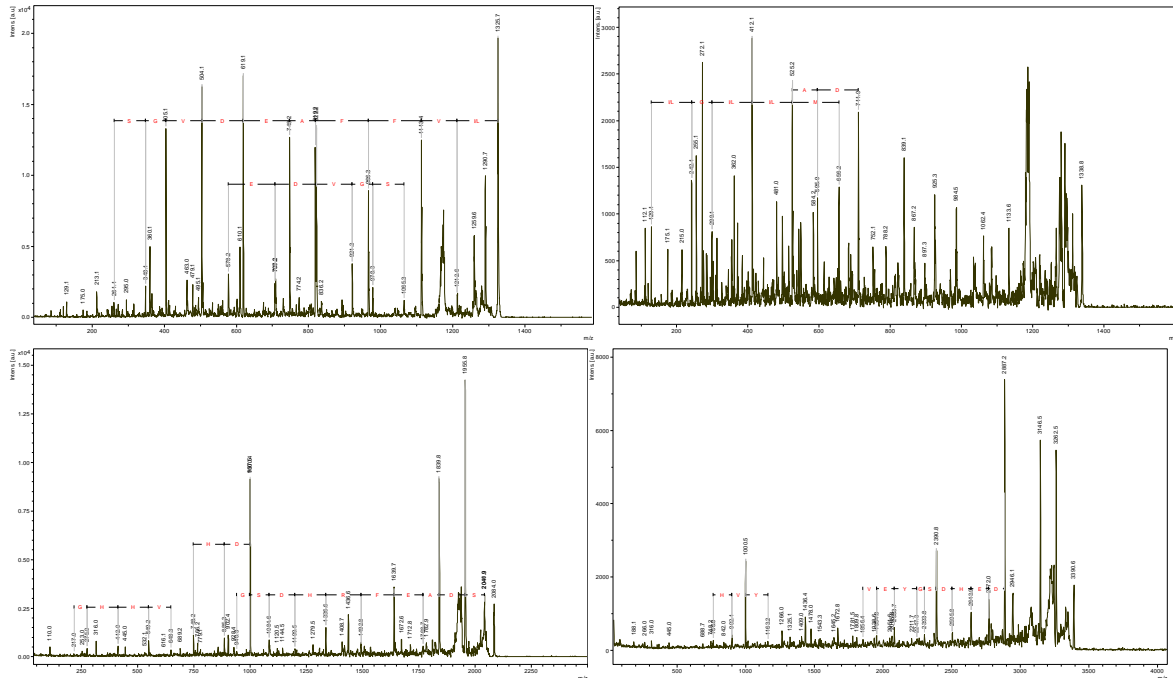


Table S2. Identification data of the proteins listed in Table 2.

A β -GFP

Mass-spectrum (MS/MS):



Identification:

[gi|253723204](#) **Mass:** 2176 **Score:** 137 **Matches:** 1 (1) **Sequences:** 1 (1)
Chain A, Zinc-Binding Domain Of Alzheimer's Disease Amyloid Beta- Peptide In Water Solution At Ph 6.5

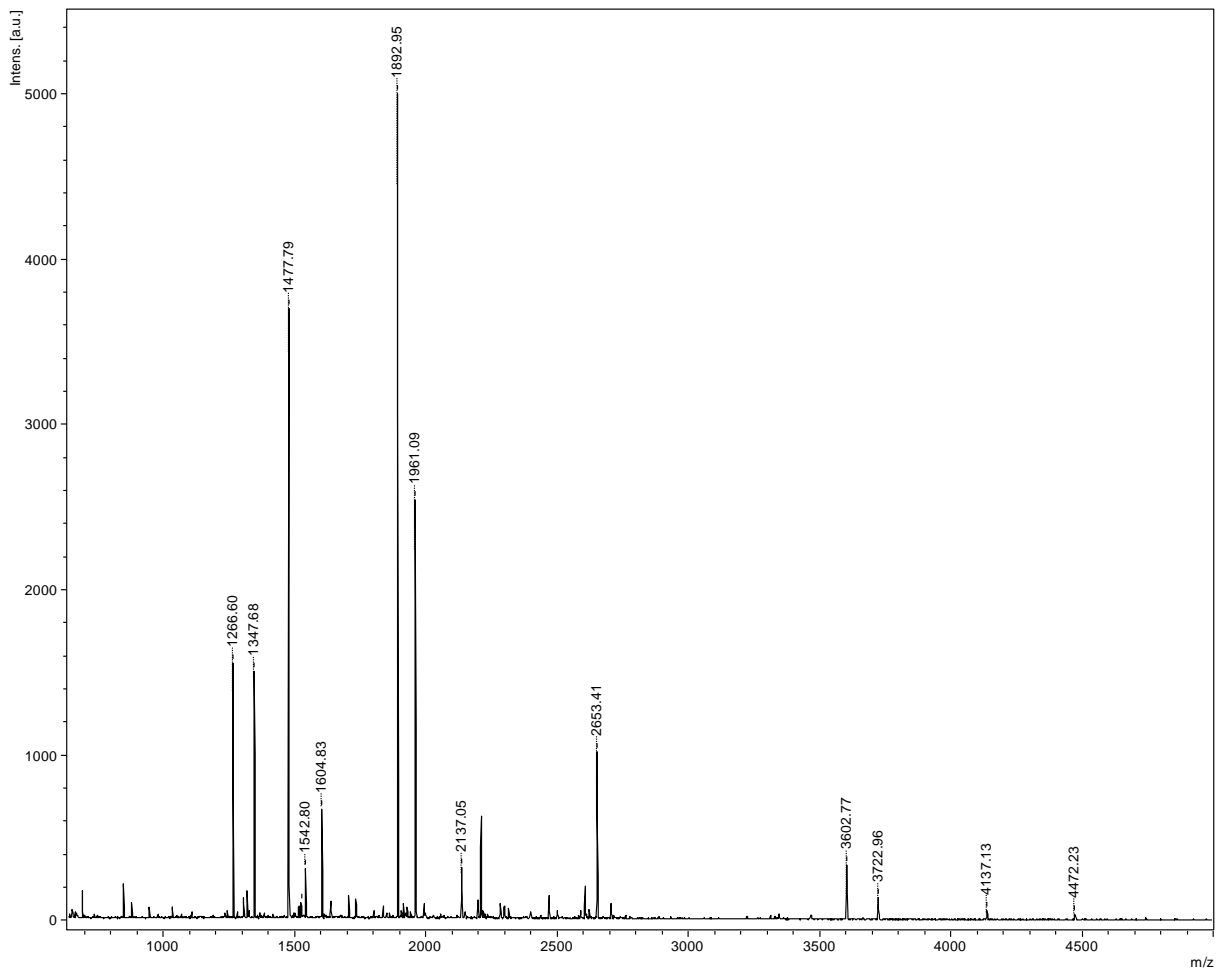
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
19	2083.9300	2082.9227	2082.9144	3.99	1	143	9e-11	1	U	-_SDAEFRHDSGYEVHHQK.X + Acetyl (Protein N-term)

[gi|177958](#) **Mass:** 3429 **Score:** 98 **Matches:** 1 (1) **Sequences:** 1 (1)
amyloid beta protein, partial [Homo sapiens]

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
8	1325.6741	1324.6668	1324.6663	0.39	0	98	5.5e-06	1	U	K.LVFFAEDVGSNK.G

PrP-GFP

Mass-spectrum:



Identification:

[gi|240104235](https://pubmed.ncbi.nlm.nih.gov/240104235/)

Mass: 13201

Score: 310

Expect: 2.7e-24

Matches: 4

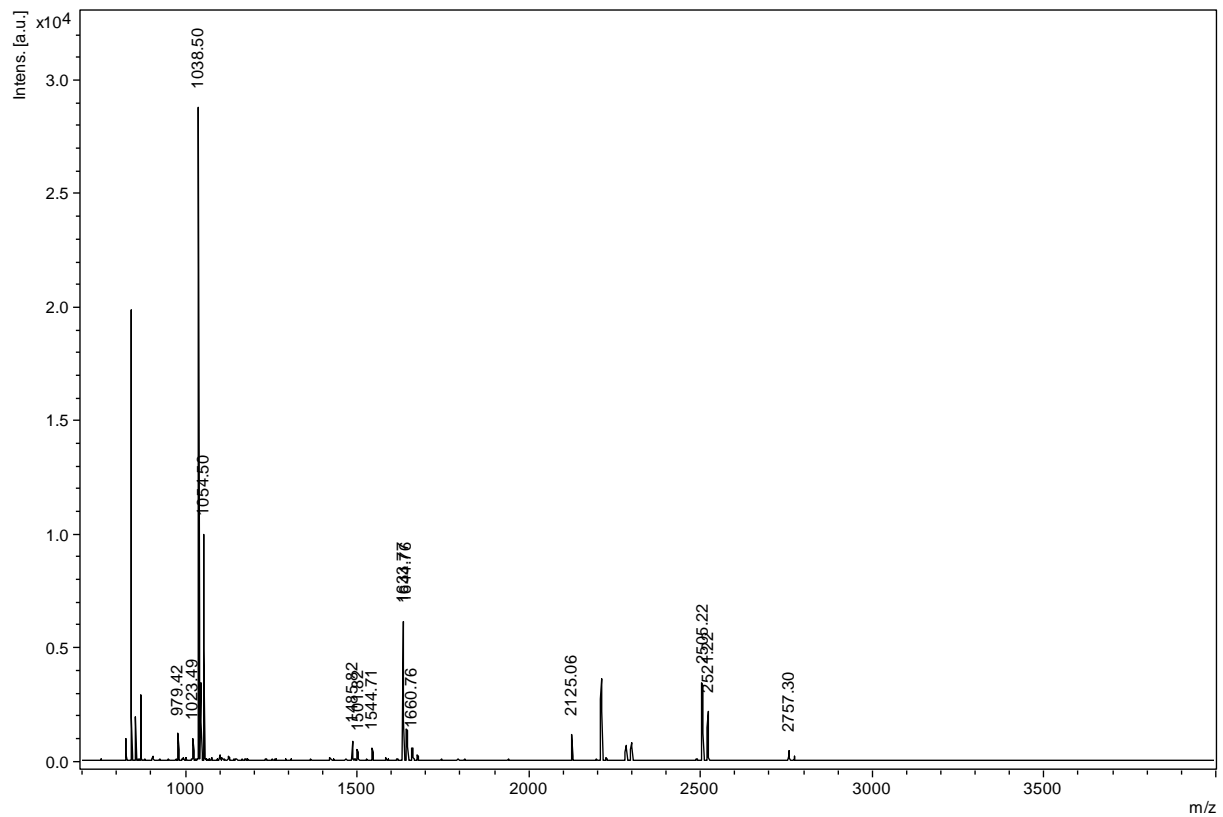
Chain A, Mouse Prion Protein (121-231) With Mutations Y225a And Y226a

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1526.7422	1525.7350	1525.7269	5.30	91	102	0	82	R.VVEQMCVTQYQK.E + Propionamide (C)
1542.7988	1541.7915	1541.7218	45.2	91	102	0	---	R.VVEQMCVTQYQK.E + Oxidation (M); Propionamide (C)
2137.0502	2136.0430	2136.0335	4.42	68	86	1	141	K.QHIVTTTIKGENFTETDVK.M
3602.7692	3601.7619	3601.7048	15.8	39	67	0	45	R.YPNQVYYRPVDQYSNQNNFVHDCVNITIK.Q + Propionamide (C)

No match to: 1266.5968, 1347.6805, 1477.7942, 1604.8267, 1892.9471, 1961.0884, 2653.4058, 3722.9558, 4137.1268, 4472.2296

Rnq1

Mass-spectrum:



Identification:

[gi|408368764](https://www.ncbi.nlm.nih.gov/nuclot/408368764)

Mass: 18836

Score: 94

Expect: 0.0091

Matches: 10

truncated Rnq1p [*Saccharomyces cerevisiae*]

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
979.4196	978.4123	978.4003	12.3	58	67	0	R.SGGSDASQDR.A
1038.5017	1037.4944	1037.4964	-1.90	49	57	0	K.IAGYVMDNR.S
1054.5032	1053.4959	1053.4913	4.39	49	57	0	K.IAGYVMDNR.S + Oxidation (M)
1485.8229	1484.8156	1484.8021	9.11	94	107	0	K.LALLATVMTHSSNK.G
1501.8173	1500.8100	1500.7970	8.67	94	107	0	K.LALLATVMTHSSNK.G + Oxidation (M)
1644.7597	1643.7525	1643.7283	14.7	68	84	0	R.AAGGGSSFMNLMADSK.G
1660.7558	1659.7485	1659.7233	15.2	68	84	0	R.AAGGGSSFMNLMADSK.G + Oxidation (M)
2125.0618	2124.0546	2124.0236	14.6	6	25	0	K.LISEAESHFSQGNHAEVAK.L
2505.2183	2504.2110	2504.2064	1.85	26	48	0	K.LTSAAQSNPNDEQMSTIESLIQK.I
2521.2183	2520.2111	2520.2013	3.86	26	48	0	K.LTSAAQSNPNDEQMSTIESLIQK.I + Oxidation (M)

No match to: 1023.4878, 1544.7086, 1633.7660, 2757.2960