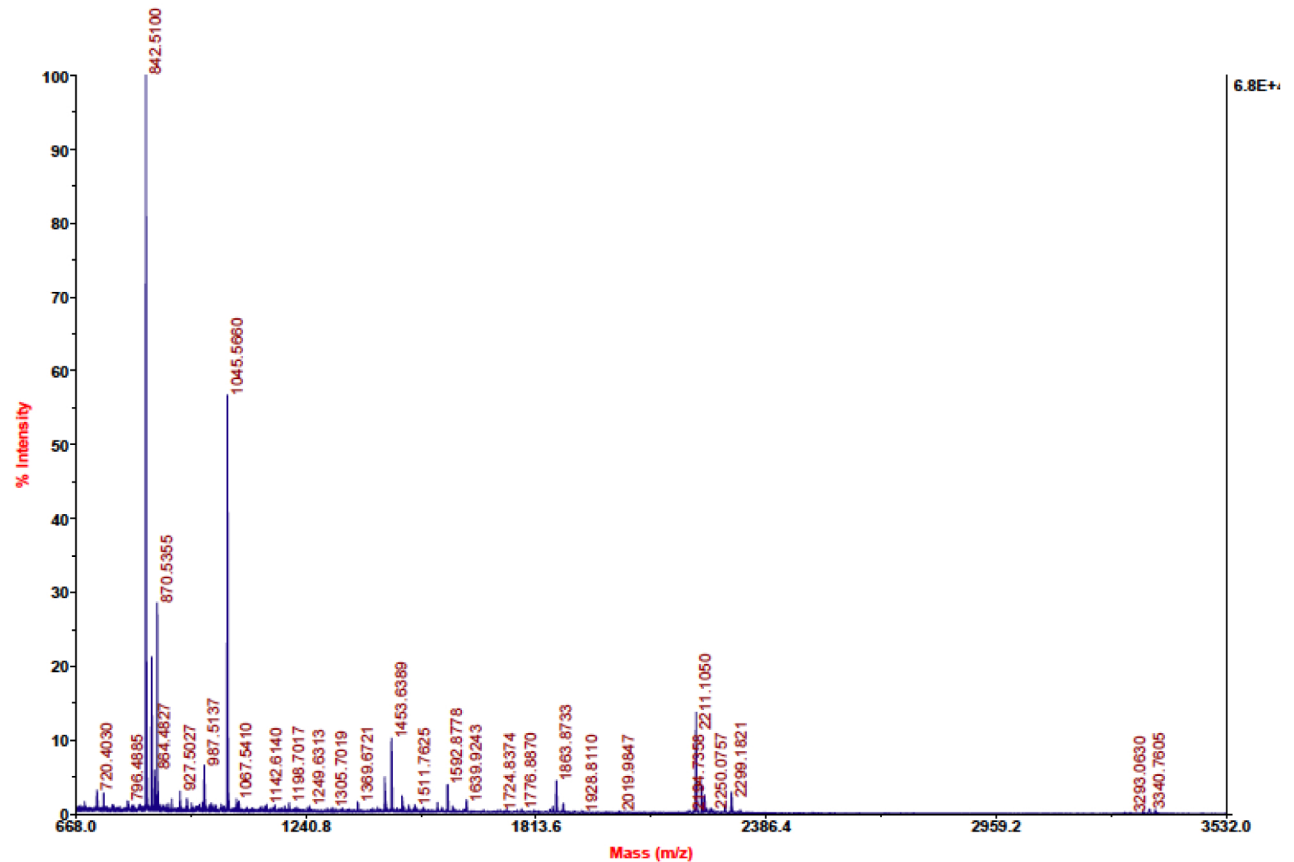
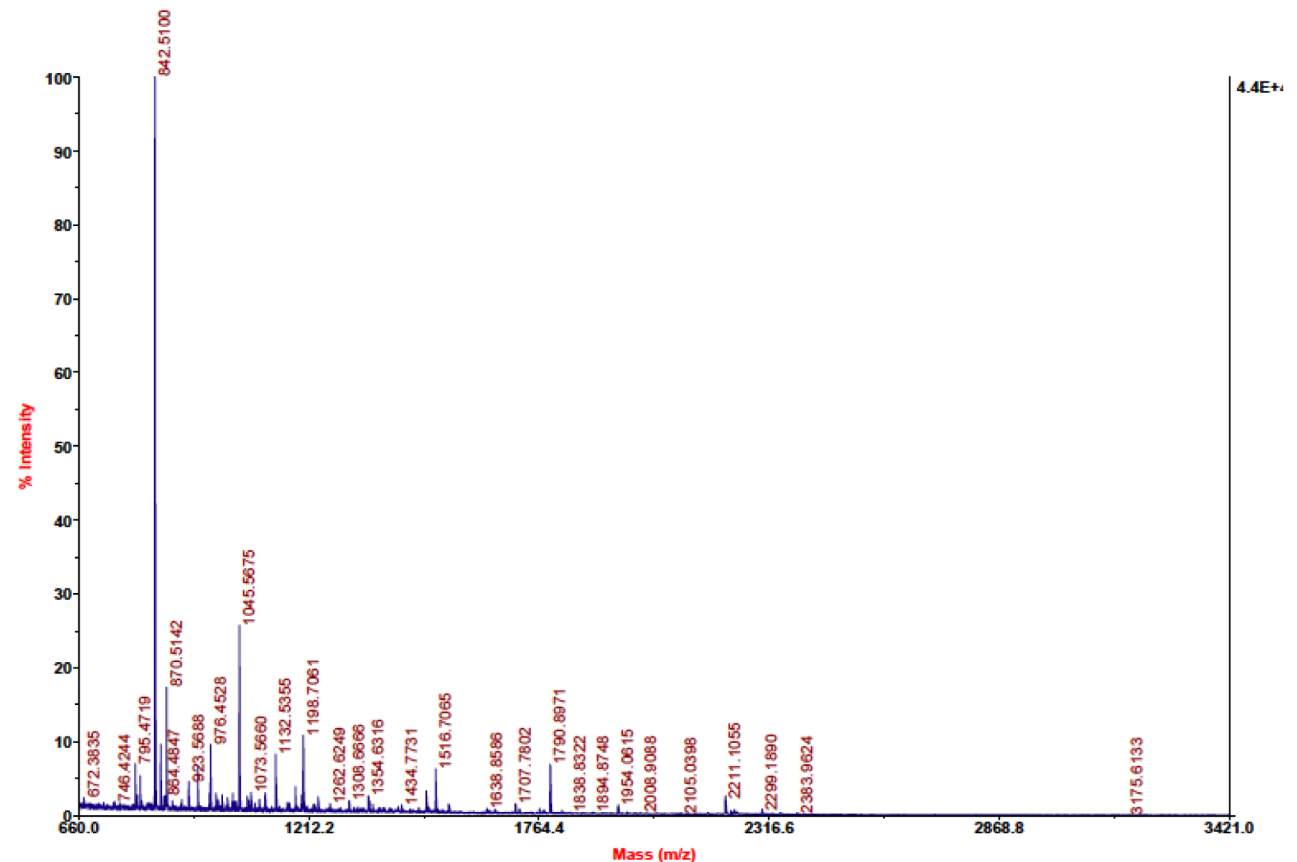


Match to: **gi|17549909** Score: **263** Expect: **4e-020**
ASpartyl Protease family member (asp-4) [Caenorhabditis elegans]



Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss Sequence
228 - 239	1479.7979	1478.7906	1478.7670	16	0 K.VPSNLFSEFWLNR.N
228 - 239	1479.7979	1478.7906	1478.7670	16	0 K.VPSNLFSEFWLNR.N
240 - 257	1863.8732	1862.8659	1862.8646	1	0 R.NPDSEIGGEITFGGIDSR.R (Ions score 94)
240 - 257	1863.8732	1862.8659	1862.8646	1	0 R.NPDSEIGGEITFGGIDSR.R
258 - 270	1592.8778	1591.8705	1591.8722	-1	1 R.RYVEPITYVPVTR.K (Ions score 21)
258 - 270	1592.8778	1591.8705	1591.8722	-1	1 R.RYVEPITYVPVTR.K
259 - 270	1436.7776	1435.7703	1435.7711	-1	0 R.YVEPITYVPVTR.K (Ions score 31)
259 - 270	1436.7776	1435.7703	1435.7711	-1	0 R.YVEPITYVPVTR.K
272 - 280	1218.5554	1217.5481	1217.5539	-5	1 K.GYWQFKMDK.V Oxidation (M)
309 - 325	1855.0264	1854.0191	1854.0251	-3	0 K.AQIEAIQNFIGAEPLIK.G
396 - 406	1453.6389	1452.6316	1452.6310	0	0 R.YYSVFDFDQNR.V (Ions score 71)
396 - 406	1453.6389	1452.6316	1452.6310	0	0 R.YYSVFDFDQNR.V
407 - 413	720.4031	719.3959	719.3966	-1	0 R.VGFAQAK.T (Ions score 18)
407 - 413	720.4031	719.3959	719.3966	-1	0 R.VGFAQAK.T

Match to: **gi|71994099** Score: **295** Expect: **8.7e-026**
ACTin family member (act-4) [Caenorhabditis elegans]



Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence
6 - 15	976.4528	975.4455	975.4410	5	0	R.AGFAGDDAPR.A (Ions score 34)
6 - 15	976.4528	975.4455	975.4410	5	0	R.AGFAGDDAPR.A
16 - 26	1198.7059	1197.6986	1197.6982	0	0	R.AVFPSIVGRPR.H (Ions score 23)
16 - 26	1198.7059	1197.6986	1197.6982	0	0	R.AVFPSIVGRPR.H
38 - 49	1354.6316	1353.6243	1353.6161	6	1	K.DSYVGDEAQSKR.G (Ions score 31)
38 - 49	1354.6316	1353.6243	1353.6161	6	1	K.DSYVGDEAQSKR.G
49 - 55	800.5206	799.5134	799.5280	-18	1	K.RGILTILK.Y
83 - 100	1954.0614	1953.0541	1953.0571	-2	0	R.VAPEEHPVLLTEAPLNPK.A
184 - 193	1132.5358	1131.5285	1131.5197	8	0	R.GYSFTTTAER.E (Ions score 41)
184 - 193	1132.5358	1131.5285	1131.5197	8	0	R.GYSFTTTAER.E
226 - 241	1776.8818	1775.8745	1775.8690	3	0	K.SYELPDGQVITVGNER.F
279 - 299	2231.0725	2230.0652	2230.0576	3	0	K.DLIYANTVLSGGTTMYPGIADR.M Oxidation (M)
316 - 322	795.4719	794.4646	794.4650	-0	0	K.IIAPPER.K (Ions score 18)
316 - 322	795.4719	794.4646	794.4650	-0	0	K.IIAPPER.K
316 - 323	923.5689	922.5616	922.5600	2	1	K.IIAPPERK.Y (Ions score 2)
316 - 323	923.5689	922.5616	922.5600	2	1	K.IIAPPERK.Y
347 - 359	1516.7065	1515.6992	1515.6954	3	0	K.QEYDESGPSIVHR.K (Ions score 85)
347 - 359	1516.7065	1515.6992	1515.6954	3	0	K.QEYDESGPSIVHR.K
347 - 360	1644.8157	1643.8084	1643.7903	11	1	K.QEYDESGPSIVHRK.C