Table S.1. Mass spectrometry data for 0305ϕ8-36 proteins detected by HPLC-ESI-MS/MS.

Protein identifier (gp)	Protein molecular weight (kDa)	Protein identification probability (%)[1]	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage sequence coverage (%)
113	20.4	100	11	26	64	66
114	26.4	100	4	5	8	24
116	20.2	98	1	1	3	8
118	49.1	100	1	1	1	3
119	43.2	100	23	68	223	66
122	72.8	100	13	28	50	25
124	40.1	100	20	47	128	72
125	44.4	100	14	71	190	45
127	37.0	100	5	8	13	16
128	16.5	99	1	2	4	8
129	110.8	100	42	118	307	54
130	123.3	100	3	3	3	4
131	13.2	100	4	13	34	46
132	41.6	100	5	9	12	18
133	100.4	100	15	28	43	22
134	14.0	100	2	6	9	25
135	32.6	100	4	6	7	14
136	20.7	100	3	3	5	16
137	60.4	100	3	3	3	9

Protein identifier (gp)	Protein molecular weight (kDa)	Protein identification probability (%)[1]	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage sequence coverage (%)
138	26.4	100	6	13	21	26
139	78.2	100	45	148	373	69
140	27.9	100	14	62	188	65
141	54.8	100	4	6	10	8
142	63.2	100	16	27	43	35
145	220.4	100	5	6	6	3
146	287.6	100	69	100	144	31
151	30.3	100	9	19	34	37
152	29.9	100	11	22	42	45
153	43.5	100	7	8	12	26
154	136.6	100	34	58	98	32
155	106.8	100	23	37	59	33
156	22.6	100	3	6	9	24
157	14.7	98	1	2	3	7
158	32.8	100	8	21	36	31
159	30.5	100	8	12	21	28
160	29.3	100	6	10	22	33
161	12.8	100	6	13	28	69
162	44.1	81	1	1	1	2
163	243.7	100	68	121	206	35
164	122.2	100	17	33	49	20
165	48.5	100	6	8	12	18
166	46.1	100	6	9	14	19

Protein identifier (gp)	Protein molecular weight (kDa)	Protein identification probability (%)[1]	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage sequence coverage (%)
167	65.9	100	13	26	49	32
168	77.3	100	23	65	141	41
171	88.5	100	18	27	41	22
172	68.5	100	1	2	3	2
173	79.9	99	1	1	1	2
174	9.5	100	2	3	5	26
175	46.2	100	6	9	13	23
197	9.0	88	1	1	3	14
198	15.4	100	2	3	3	16
199	54.4	100	10	21	39	25
205	18.8	100	2	2	2	14
209	66.0	100	2	2	4	3
81	9.3	100	3	5	23	69

[1] The protein identity probability was determined by Scaffold (Proteome Software).