Figure 1

Position in 1AO6	Position in Mature HSA	Position with Leader Sequence	Amino Acid	% SASA	B-Factor	SS	Align 1 (Mamm. W)	Adj. 100%'s (Align 1)	Align 2 (Var. Sps. V)	Polymorph.	Phenotype Change	Conserved Mutation *vs.* Cysteine
n/a	1	25	D	n/a	n/a	0	40	0	40	D25V	0	3
n/a	2	26	A	n/a	n/a	0	40	0	20			1
n/a	3	27	H	n/a	n/a	0	80	0	60	H27Q, H27Y	0	5
n/a	4	28	K	n/a	n/a	0	80	1	40			4
1	5	29	S	57.8	30.65	0	100	1	60			1
2	6	30	E	41.0	30.41	1	100	1	40			4
3	7	31	V	0.0	27.81	1	60	2	40			3
4	8	32	A	0.0	28.93	1	100	1	40			1
5	9	33	H	57.7	29.05	1	100	2	40			5
6	10	34	R	13.3	28.32	1	100	1	40			5
7	11	35	F	17.1	28.41	1	80	1	40			4
8	12	36	K	72.4	32.91	1	40	1	20			4
9	13	37	D	115.9	29.96	1	100	0	60			3
10	14	38	L	33.0	24.52	1	80	2	60			4
11	15	39	G	62.0	24.74	1	100	1	60			2
12	16	40	E	49.4	27.83	1	100	1	60			4
14	18	42	N	58.8	24.75	1	60	2	20			2
15	19	43	F	0.0	22.59	1	100	0	20			4
16	20	44	K	31.0	19.84	1	60	1	60			4
17	21	45	A	29.0	17.31	1	80	1	40			1
18	22	46	L	1.0	15.93	1	100	1	40			4
19	23	47	V	0.0	17.25	1	100	2	60			3
20	24	48	L	6.2	18.56	1	100	1	40			4

21	25	49	I	0.0	18.85	1	40	1	60			4
22	26	50	A	11.3	18.7	1	80	0	20			1
23	27	51	F	0.8	16.67	1	80	0	40			4
24	28	52	A	0.0	16.49	1	80	1	40			1
25	29	53	Q	3.1	18.47	1	100	0	40			3
26	30	54	Y	10.6	21.52	1	80	2	60			3
27	31	55	L	3.1	22.77	0	100	1	40			4
28	32	56	Q	8.7	19.2	0	100	1	60			3
29	33	57	Q	63.8	23.45	0	60	1	20			3
30	34	58	C	1.1	31.66	0	80	0	20			0
31	35	59	P	76.1	30.42	0	80	0	60			3
32	36	60	F	8.9	29.13	1	60	0	40			4
33	37	61	E	78.8	34.65	1	60	0	20			4
34	38	62	D	87.0	34.73	1	60	1	40			3
35	39	63	H	0.0	31.2	1	100	0	40			5
36	40	64	V	35.8	30.38	1	80	1	40			3
60	40	64	E	101.3	31.14	1	40	1	40			4
37	41	65	K	51.1	31.26	1	100	1	60			4
38	42	66	L	1.0	26.45	1	100	1	60			4
39	43	67	V	7.4	26.21	1	80	1	40			3
40	44	68	N	88.2	29.63	1	40	1	40			2
41	45	69	E	41.0	29.37	1	100	0	60			4
42	46	70	V	7.4	28.93	1	80	2	40			3
43	47	71	T	5.0	28.95	1	100	0	40			1
44	48	72	E	91.0	31.25	1	60	1	40			4
45	49	73	F	39.8	23.4	1	80	1	40	F73Y	0	4
46	50	74	A	0.0	23.04	1	100	0	60			1
47	51	75	K	53.4	28.74	1	80	1	60			4
48	52	76	T	86.3	35.9	1	40	1	20			1

49	53	77	C	0.0	36.73	1	100	0	60			0
50	54	78	V	60.5	39.55	1	60	1	40			3
51	55	79	A	148.4	43.59	1	80	0	40			1
52	56	80	D	117.4	45.92	0	80	0	40			3
53	57	81	E	54.5	48.38	0	80	0	40			4
54	58	82	S	164.1	53.12	0	80	0	40			1
55	59	83	A	54.8	52.13	0	60	0	40			1
56	60	84	E	110.3	53.87	0	40	0	20	E84K	0	4
57	61	85	N	54.1	43.73	0	80	1	40			2
58	62	86	C	1.1	36.08	0	100	0	80			0
59	63	87	D	189.9	35.65	0	80	2	40	D87N	1	3
60	64	88	K	32.2	32.63	0	100	0	60			4
61	65	89	S	93.8	26.67	0	80	1	60			1
62	66	90	L	9.3	23.68	1	80	0	40	L90P	1	4
63	67	91	H	20.0	20.17	1	80	0	40			5
64	68	92	T	45.0	22.6	1	80	0	40			1
65	69	93	L	22.7	18.5	1	80	0	60			4
66	70	94	F	13.0	19.27	1	80	1	60			4
67	71	95	G	4.0	23.14	1	100	1	40			2
68	72	96	D	113.0	24.53	1	100	1	60			3
69	73	97	K	32.2	22.59	1	80	1	40			4
70	74	98	L	1.0	19.05	1	80	1	40			4
71	75	99	C	20.7	24.72	1	100	0	80			0
72	76	100	T	105.0	32.05	1	40	1	20			1
73	77	101	V	27.2	42.97	1	60	0	20			3
74	78	102	A	0.0	53.66	1	60	0	20			1
75	79	103	T	103.8	67.13	0	40	0	20			1
76	80	104	L	106.2	79.71	0	80	0	40			4
77	81	105	R	87.2	90.39	1	80	0	40			5

78	82	106	E	130.1	96.77	1	60	0	40	E106K	0	4
79	83	107	T	113.8	98.21	1	60	1	20			1
80	84	108	Y	20.2	95.72	1	100	0	60			3
81	85	109	G	74.0	93.64	0	80	1	40			2
82	86	110	E	99.4	88.78	0	60	0	20			4
83	87	111	M	28.2	77.89	0	40	1	20			3
84	88	112	A	22.6	66.98	0	100	1	40			1
85	89	113	D	166.7	54.86	0	100	2	40			3
86	90	114	C	0.0	37.61	0	100	2	60			0
87	91	115	C	32.6	33.58	0	100	1	60			0
88	92	116	A	135.5	38.25	0	40	2	20			1
89	93	117	K	52.3	39.06	0	100	0	60			4
90	94	118	Q	121.3	41.84	0	60	1	40			3
91	95	119	E	28.2	35.82	0	80	1	40			4
92	96	120	P	125.4	32.16	0	100	0	60			3
93	97	121	E	63.5	28.49	1	80	2	60	E121G	0	4
94	98	122	R	7.6	26.53	1	100	0	60			5
95	99	123	N	1.2	30.02	1	80	2	40			2
96	100	124	E	71.8	31.84	1	100	1	60			4
97	101	125	C	2.2	28.44	1	100	2	80			0
98	102	126	F	3.3	22.56	1	100	2	60			4
99	103	127	L	22.7	26.39	1	100	1	60			4
100	104	128	Q	111.0	32.1	1	40	2	20			3
101	105	129	H	33.8	31.12	0	100	1	60			5
102	106	130	K	10.9	30.28	0	100	1	60			4
103	107	131	D	60.9	30.16	0	80	2	40			3
104	108	132	D	58.0	32.21	0	100	0	40			3
105	109	133	N	80.0	36.44	0	60	2	20			2
106	110	134	P	28.4	37.95	0	100	0	60			3

107	111	135	N	143.5	49.66	0	40	1	20			2
108	112	136	L	30.9	49.38	0	80	0	40			4
109	113	137	P	141.8	51.5	0	80	0	40			3
110	114	138	R	88.6	56.24	0	40	0	20	R138G	1	5
111	115	139	L	100.0	54.21	0	60	0	20			4
112	116	140	V	139.5	51.82	0	40	0	0			3
113	117	141	R	46.4	49.48	0	40	0	20			5
114	118	142	P	98.5	47.97	0	80	0	60			3
115	119	143	E	88.5	46.63	0	80	0	40	E143K	0	4
116	120	144	V	22.2	40.28	1	40	0	20			3
117	121	145	D	130.4	46.02	1	60	0	40			3
118	122	146	V	87.7	43.96	1	40	0	20	V146E	0	3
119	123	147	M	26.2	39.04	1	40	1	20			3
120	124	148	C	3.3	34.94	1	100	0	60			0
121	125	149	T	115.0	35.32	1	40	1	20			1
122	126	150	A	74.2	33.29	1	60	1	20			1
123	127	151	F	0.0	33.85	1	100	0	60			4
124	128	152	H	75.4	39.69	1	20	1	20	H152R	0	5
125	129	153	D	211.6	43.69	1	40	0	20			3
126	130	154	N	87.1	42.63	0	40	0	20			2
127	131	155	E	42.3	43.42	1	60	0	20			4
128	132	156	E	70.5	43.81	1	20	0	20			4
129	133	157	T	76.3	36.77	1	20	1	20			1
130	134	158	F	23.6	29.94	1	100	0	60			4
131	135	159	L	24.7	27.81	1	40	1	40			4
132	136	160	K	29.9	26.12	1	60	0	40			4
133	137	161	K	52.9	24.22	1	60	1	20			4
134	138	162	Y	26.0	20.68	1	100	1	60			3
135	139	163	L	13.4	19.07	1	100	1	60			4

136	140	164	Y	6.7	21.43	1	80	2	40	Y164C	0	3
137	141	165	E	17.9	22.66	1	100	0	60			4
138	142	166	I	50.0	19.7	1	60	1	40			4
139	143	167	A	0.0	16.68	1	80	1	60			1
140	144	168	R	11.4	16.35	1	100	1	60			5
141	145	169	R	22.7	20.06	1	100	2	60			5
142	146	170	H	37.7	23	0	100	2	60			5
143	147	171	P	3.0	22.35	0	100	2	60			3
144	148	172	Y	24.0	22.81	0	100	2	60			3
145	149	173	F	2.4	22.42	0	100	2	40			4
146	150	174	Y	16.3	20	0	100	1	60			3
147	151	175	A	0.0	22.17	1	80	2	40			1
148	152	176	P	9.0	23.4	1	100	1	60			3
149	153	177	E	4.5	23.39	1	100	2	40			4
150	154	178	L	1.0	20.61	1	100	2	40			4
151	155	179	L	14.4	22.22	1	100	1	60			4
152	156	180	F	12.2	22.38	1	60	1	40			4
153	157	181	F	1.6	24.28	1	40	1	20			4
154	158	182	A	21.0	24.88	1	100	0	60			1
155	159	183	K	45.4	27.29	1	20	1	20			4
156	160	184	R	33.2	25.89	1	40	1	20			5
157	161	185	Y	25.0	25.3	1	100	0	60			3
158	162	186	K	45.4	21.31	1	60	1	20			4
159	163	187	A	87.1	21.49	1	40	0	20			1
160	164	188	A	4.8	22.78	1	40	0	20			1
161	165	189	F	0.0	23.92	1	60	0	20			4
162	166	190	T	77.5	30.55	1	40	0	40			1
163	167	191	E	75.0	33.84	1	80	1	40			4
164	168	192	C	0.0	31.68	1	100	1	60			0

165	169	193	C	14.1	32.95	0	100	1	60			0
166	170	194	Q	124.4	34.61	0	40	1	20			3
167	171	195	A	58.1	31.57	0	80	0	40			1
168	172	196	A	183.9	30.74	0	40	1	40			1
169	173	197	D	155.1	29.21	0	100	1	60			3
170	174	198	K	32.2	30.28	1	100	1	60			4
171	175	199	A	74.2	27.97	1	40	1	40			1
172	176	200	A	93.5	29.27	1	80	1	40			1
173	177	201	C	30.4	28.29	1	100	1	80	C201F	2	0
174	178	202	L	0.0	28.43	1	100	1	40			4
175	179	203	L	70.1	27.06	1	40	2	20			4
176	180	204	P	111.9	28.36	1	100	1	40			3
177	181	205	K	33.3	27.16	1	100	1	60			4
178	182	206	L	10.3	24.64	1	60	1	20			4
179	183	207	D	52.2	26.6	1	60	0	40			3
180	184	208	E	80.8	28.49	1	40	0	20			4
181	185	209	L	8.2	26.58	1	60	0	40			4
182	186	210	R	59.2	29.18	1	40	0	20			5
183	187	211	D	118.8	28.69	1	60	0	40			3
184	188	212	E	35.9	27.68	1	60	0	40			4
185	189	213	G	20.0	22.68	1	20	0	20			2
186	190	214	K	37.9	23.57	1	60	0	40			4
187	191	215	A	58.1	22.4	1	40	0	20	A215V	0	1
188	192	216	S	32.8	23.5	1	80	0	40			1
189	193	217	S	21.9	21.41	1	60		40			1
190	194	218	A	45.2	21.45	1	80	0	40			1
191	195	219	K	55.2	24.21	1	40	0	20			4
192	196	220	Q	6.3	20.68	1	60	1	40	Q220L	0	3
193	197	221	R	9.0	16.53	1	100	0	40			5

194	198	222	L	27.8	18.26	1	80	1	40			4
195	199	223	K	20.1	19.76	1	60	1	40			4
196	200	224	C	2.2	20.47	1	100	0	80			0
197	201	225	A	4.8	21.9	1	60	2	20			1
198	202	226	S	17.2	25.36	1	100	0	40			1
199	203	227	L	19.6	28.06	1	40	1	40			4
200	204	228	Q	66.1	33.17	1	80	0	40			3
201	205	229	K	75.3	34.01	1	80	1	40			4
202	206	230	F	52.8	28.46	1	100	1	60			4
203	207	231	G	50.0	28.59	0	100	1	60			2
204	208	232	E	67.9	29.55	1	60	2	40			4
205	209	233	R	56.4	29.9	1	100	1	60			5
206	210	234	A	48.4	25.17	1	100	1	40			1
207	211	235	F	1.6	24.26	1	60	2	40			4
208	212	236	K	42.5	31.21	1	100	1	60			4
209	213	237	A	54.8	26.47	1	100	2	60			1
210	214	238	W	49.2	23.68	1	100	1	40			3
211	215	239	A	0.0	20.76	1	40	1	20			1
212	216	240	V	17.3	23.85	1	80	0	40			3
213	217	241	A	0.0	26.06	1	80	1	40			1
214	218	242	R	18.0	29.91	1	100	0	40	R242H, R242P	1	5
215	219	243	L	14.4	23.26	1	80	2	40			4
216	220	244	S	0.0	23.79	1	100	1	60			1
217	221	245	Q	2.4	24.52	1	100	1	60			3
218	222	246	R	19.0	24.02	1	40	2	40			5
219	223	247	F	2.4	26.59	0	100	1	60			4
220	224	248	P	4.5	29.7	0	100	1	60			3
221	225	249	K	54.6	37.85	0	80	2	60	K249Q	0	4

222	226	250	A	1.6	35.15	0	100	0	60			1
223	227	251	E	89.7	38.91	0	40	2	20			4
224	228	252	F	30.9	37.46	1	100	0	60			4
225	229	253	A	109.7	36.47	1	60	1	40			1
226	230	254	E	17.3	32.11	1	80	0	40			4
227	231	255	V	0.0	29.49	1	40	0	20			3
228	232	256	S	54.7	29.63	1	60	0	20			1
229	233	257	K	43.7	28.65	1	80	0	60			4
230	234	258	L	3.1	32.28	1	40	0	20			4
231	235	259	V	6.2	29.28	1	80	1	40			3
232	236	260	T	92.5	29.1	1	100	0	40			1
233	237	261	D	62.3	28.36	1	80	1	40			3
234	238	262	L	30.9	23.28	1	80	0	40			4
235	239	263	T	6.3	24.55	1	80	1	40			1
236	240	264	K	63.8	24.54	1	100	0	40	K264E	0	4
237	241	265	V	1.2	23.3	1	80	1	40			3
238	242	266	H	3.1	20.96	1	60	0	40			5
239	243	267	T	66.3	21.82	1	60	1	40			1
240	244	268	E	17.9	24.56	1	100	1	60			4
241	245	269	C	10.9	22.73	1	100	2	60			0
242	246	270	C	3.3	20.77	1	100	2	80			0
243	247	271	H	53.8	25.67	0	100	2	40			5
244	248	272	G	16.0	19.18	0	100	2	80			2
245	249	273	D	37.7	18.57	0	100	2	60			3
246	250	274	L	5.2	18.31	1	100	2	40			4
247	251	275	L	3.1	16.12	1	100	2	40			4
248	252	276	E	17.3	19.95	1	100	2	60			4
249	253	277	C	0.0	19.89	1	100	2	60			0
250	254	278	A	21.0	20.33	1	100	2	40			1

251	255	279	D	10.1	21.47	1	100	2	40			3
252	256	280	D	47.8	23.25	1	100	2	60			3
253	257	281	R	9.0	26.57	1	100	1	60			5
254	258	282	A	38.7	25.99	1	80	1	40			1
255	259	283	D	123.2	23.81	1	60	1	20			3
256	260	284	L	17.5	21.77	1	100	0	60			4
257	261	285	A	8.1	27.58	1	80	2	40			1
258	262	286	K	64.4	31.33	1	100	1	40			4
259	263	287	Y	51.0	30.7	1	100	1	60			3
260	264	288	I	14.3	32.27	1	40	2	20			4
261	265	289	C	18.5	38.84	1	100	0	80			0
262	266	290	E	83.3	41.21	1	80	1	40			4
263	267	291	N	54.1	36.4	0	60	1	20			2
264	268	292	Q	32.3	37.75	1	100	0	60	Q292R	0	3
265	269	293	D	229.0	45.46	1	60	1	60	D293G	1	3
266	270	294	S	114.1	43.53	1	40	0	20			1
267	271	295	I	2.4	35.55	1	80	1	40			4
268	272	296	S	7.8	36.26	0	100	0	60			1
269	273	297	S	112.5	40.24	0	60	1	40			1
270	274	298	K	23.6	38.39	0	80	1	60			4
271	275	299	L	0.0	37.35	0	100	0	80			4
272	276	300	K	64.9	45.27	0	80	1	40	K300N	1	4
273	277	301	E	79.5	46.31	0	60	1	20			4
274	278	302	C	1.1	40.66	0	100	1	80			0
275	279	303	C	20.7	40.94	0	100	1	80			0
276	280	304	E	99.4	44.93	0	60	2	40			4
277	281	305	K	59.2	41.28	0	100	0	60			4
278	282	306	P	116.4	40.02	0	80	1	60			3
279	283	307	L	87.6	36.51	1	40	1	20			4

280	284	308	L	22.7	33.27	1	100	0	60			4
281	285	309	E	32.7	32.98	1	60	2	40			4
282	286	310	K	26.4	30.79	1	100	0	40			4
283	287	311	S	12.5	31.54	1	80	1	40			1
284	288	312	H	27.7	33.63	1	80	1	40			5
285	289	313	C	22.8	34.65	1	100	0	80			0
286	290	314	I	14.3	34.3	1	60	1	40			4
287	291	315	A	53.2	35.49	1	60	0	40			1
288	292	316	E	58.3	40.82	0	80	0	40			4
289	293	317	V	32.1	40.52	0	60	0	40			3
290	294	318	E	89.1	40.97	0	40	0	40			4
291	295	319	N	65.9	40.65	0	20	1	20			2
292	296	320	D	15.9	44.56	0	100	0	60			3
293	297	321	E	80.8	49.85	0	40	1	20			4
294	298	322	M	84.5	53.49	0	20	1	20			3
295	299	323	P	44.8	59.14	0	100	0	60			3
296	300	324	A	180.6	63.75	0	40	1	40			1
297	301	325	D	218.8	64.56	0	60	1	40			3
298	302	326	L	44.3	61.34	0	100	0	60			4
299	303	327	P	119.4	59.59	0	80	1	60			3
300	304	328	S	134.4	57.01	0	20	0	20			1
301	305	329	L	13.4	53.51	0	80	0	40			4
302	306	330	A	33.9	49.21	1	60	0	20			1
303	307	331	A	67.7	48.5	1	60	0	40			1
304	308	332	D	131.9	47.92	1	80	0	40			3
305	309	333	F	10.6	43.2	1	80	0	40			4
306	310	334	V	25.9	50.47	0	60	1	40			3
307	311	335	E	92.9	55.73	0	100	0	60			4
308	312	336	S	75.0	57.48	0	60	1	40			1

309	313	337	K	92.0	64.18	0	80	0	40	K337N	1	4
310	314	338	D	131.9	65.86	0	40	0	40	D338G, D338V	1	3
311	315	339	V	2.5	62.66	1	80	1	60			3
312	316	340	C	23.9	62.19	1	100	1	80			0
313	317	341	K	79.3	62.49	1	100	1	60			4
314	318	342	N	107.1	59.91	1	80	1	40	N342K	0	2
315	319	343	Y	13.5	58.72	1	80	0	60			3
316	320	344	A	119.4	64	1	40	0	20	A344T	1	1
317	321	345	E	88.5	67.18	1	80	1	40	E345K	0	4
318	322	346	A	75.8	66.17	0	100	1	40			1
319	323	347	K	52.9	62.98	1	100	1	60			4
320	324	348	D	120.3	58.69	1	80	1	60			3
321	325	349	V	100.0	50.37	1	80	1	40			3
322	326	350	F	8.1	44.71	1	100	1	60			4
323	327	351	L	18.6	42.37	1	100	2	60			4
324	328	352	G	30.0	38.93	1	100	1	60			2
325	329	353	M	65.0	37.18	1	40	2	20			3
326	330	354	F	0.8	29.72	1	100	1	60			4
327	331	355	L	8.2	29.23	1	100	2	60			4
328	332	356	Y	13.5	30.36	1	100	2	60			3
329	333	357	E	23.7	29.68	1	100	2	60	E357K	0	4
330	334	358	Y	14.4	32.04	1	100	1	60			3
331	335	359	A	0.0	31.27	1	60	2	60			1
332	336	360	R	8.5	31.88	1	100	1	60			5
333	337	361	R	16.6	33.45	0	100	2	60			5
334	338	362	H	33.1	32.11	0	100	2	60			5
335	339	363	P	62.7	28.98	0	100	1	60			3
336	340	364	D	84.1	24.21	0	40	2	40			3

337	341	365	Y	24.0	20.57	0	100	0	40			3
338	342	366	S	0.0	20.06	0	80	1	60			1
339	343	367	V	2.5	23.25	1	80	0	40			3
340	344	368	V	14.8	24.72	1	60	0	20			3
341	345	369	L	0.0	25.04	1	60	1	40			4
342	346	370	L	0.0	25.17	1	100	1	60			4
343	347	371	L	16.5	25.68	1	100	2	60			4
344	348	372	R	3.3	24.63	1	100	1	60			5
345	349	373	L	0.0	26.75	1	60	1	40			4
346	350	374	A	27.4	27.71	1	80	1	60			1
347	351	375	K	60.3	33.28	1	100	0	60			4
348	352	376	T	33.8	31.6	1	20	2	20			1
349	353	377	Y	0.0	34.39	1	100	1	60			3
350	354	378	E	13.5	35.62	1	100	1	60	E378K	0	4
351	355	379	T	86.3	40.3	1	80	1	40			1
352	356	380	T	15.0	45.68	1	80	1	40			1
353	357	381	L	0.0	49.17	1	100	0	80			4
354	358	382	E	66.0	53.47	1	80	1	60	E382K	0	4
355	359	383	K	91.4	55.14	1	60	1	40	K383N	2	4
356	360	384	C	2.2	60.95	1	100	1	80			0
357	361	385	C	42.4	66.33	0	100	2	80			0
358	362	386	A	140.3	72.72	0	100	1	60			1
359	363	387	A	75.8	76.03	0	20	1	20			1
360	364	388	A	164.5	80.24	0	40	0	20			1
361	365	389	D	168.1	84.23	0	80	1	40	D389H, D389V	1	3
362	366	390	P	35.8	82.14	1	100	0	60			3
363	367	391	H	65.4	80.75	1	40	1	20			5
364	368	392	E	109.6	77.34	1	60	1	20			4

365	369	393	C	48.9	69.93	1	100	1	80			0
366	370	394	Y	1.9	65.2	0	100	1	60			3
367	371	395	A	100.0	63.92	0	60	1	40			1
368	372	396	K	73.0	64	0	40	1	20	K396E	0	4
369	373	397	V	0.0	58.46	1	100	0	40			3
370	374	398	F	51.2	53.71	1	60	1	40			4
371	375	399	D	152.2	50.78	1	80	0	40	D399N, D399H	0	3
372	376	400	E	66.0	44.4	1	60	0	20	E400K, E400Q	0	4
373	377	401	F	2.4	39.67	0	60	0	40			4
374	378	402	K	72.4	36.35	1	40	0	20			4
375	379	403	P	119.4	32.33	1	80	1	40			3
376	380	404	L	50.5	32.53	1	100	0	40			4
377	381	405	V	17.3	36.18	1	80	1	40			3
378	382	406	E	61.5	39.76	1	40	1	20	E406K	0	4
379	383	407	E	49.4	39.21	1	100	1	60			4
380	384	408	P	0.0	36.35	1	100	1	40			3
381	385	409	Q	68.5	41.13	1	40	1	20			3
382	386	410	N	94.1	42.58	1	80	1	40			2
383	387	411	L	21.6	44.35	1	100	0	60			4
384	388	412	I	11.9	45.79	1	60	1	40			4
385	389	413	K	69.5	50.24	1	80	0	60			4
386	390	414	Q	96.9	52.9	1	40	1	20			3
387	391	415	N	22.4	52.97	1	100	1	60			2
388	392	416	C	3.3	52.58	1	100	1	80			0
389	393	417	E	71.2	57.82	1	60	1	40			4
390	394	418	L	52.6	55.99	1	80	0	40			4
391	395	419	F	30.1	58.68	1	60	0	40			4

392	396	420	E	85.9	62.51	1	80	0	40	E420K	0	4
393	397	421	Q	101.6	58.94	1	40	0	20			3
394	398	422	L	21.6	53.27	1	60	1	40			4
395	399	423	G	62.0	50.77	0	100	0	60			2
396	400	424	E	51.9	50.07	1	80	2	40			4
397	401	425	Y	53.8	50.48	1	100	0	60			3
398	402	426	K	66.7	46.35	1	40	2	20			4
399	403	427	F	0.8	40.68	1	100	1	60			4
400	404	428	Q	0.8	37.32	1	100	2	40			3
401	405	429	N	21.2	34.37	1	100	2	60			2
402	406	430	A	54.8	29.99	1	100	1	40			1
403	407	431	L	8.2	28.56	1	80	1	60			4
404	408	432	L	0.0	32.59	1	40	1	40			4
405	409	433	V	34.6	36.52	1	100	1	60			3
406	410	434	R	31.8	38.85	1	100	2	60	R434C	1	5
407	411	435	Y	15.4	32.48	1	100	2	80			3
408	412	436	T	0.0	29.54	1	100	1	60			1
409	413	437	K	27.6	33.11	1	60	1	40			4
410	414	438	K	6.3	32.07	1	100	0	60			4
411	415	439	V	0.0	28.94	0	40	2	20			3
412	416	440	P	7.5	31.07	0	100	1	80			3
413	417	441	Q	45.7	31.05	0	100	2	60			3
414	418	442	V	3.7	28.94	0	100	2	60			3
415	419	443	S	98.4	27.89	0	100	2	60			1
416	420	444	T	13.8	27.97	1	100	2	40			1
417	421	445	P	132.8	24.74	1	100	2	40			3
418	422	446	T	18.8	25.07	1	100	2	60			1
419	423	447	L	3.1	24.57	1	100	2	60			4
420	424	448	V	6.2	25.83	1	100	2	60			3

421	425	449	E	48.1	30.55	1	100	1	60			4
422	426	450	V	3.7	28	1	40	1	20			3
423	427	451	S	1.6	31.38	1	40	1	20			1
424	428	452	R	18.0	30.58	1	100	0	40			5
425	429	453	N	22.4	29.18	1	20	2	20			2
426	430	454	L	7.2	31.68	1	100	1	40			4
427	431	455	G	0.0	35.59	1	100	1	40			2
428	432	456	K	27.6	36.58	0	60	2	40			4
429	433	457	V	17.3	37.59	0	100	1	60			3
430	434	458	G	4.0	40.74	1	100	1	60			2
431	435	459	S	73.4	41.51	1	40	1	20			1
432	436	460	K	58.0	40.92	1	60	1	40			4
433	437	461	C	2.2	41.74	1	100	1	80			0
434	438	462	C	13.0	46.67	0	100	1	80			0
435	439	463	K	106.3	52.99	0	40	1	20			4
436	440	464	H	44.6	54.37	0	40	1	20			5
437	441	465	P	119.4	55.7	0	100	1	60			3
438	442	466	E	112.8	57.25	0	100	1	60			4
439	443	467	A	93.5	55.15	0	40	1	20			1
440	444	468	K	63.8	50.64	0	40	1	20			4
441	445	469	R	24.2	42.52	1	100	0	60			5
442	446	470	M	8.7	35.96	1	40	1	20			3
443	447	471	P	35.8	36.33	1	60	1	40			3
444	448	472	C	43.5	35.54	1	100	0	80			0
445	449	473	A	3.2	33.69	1	40	2	20			1
446	450	474	E	0.0	29.58	1	100	0	60			4
447	451	475	D	42.0	25.46	1	80	1	40			3
448	452	476	Y	34.6	20.82	1	80	1	40			3
449	453	477	L	20.6	21.5	1	100	0	60			4

450	454	478	S	23.4	20.37	1	80	1	40			1
451	455	479	V	23.5	16.54	1	40	0	20			3
452	456	480	V	3.7	20.05	1	40	1	20			3
453	457	481	L	3.1	17.71	1	100	1	60			4
454	458	482	N	3.5	19.76	1	100	1	40			2
455	459	483	Q	25.2	25.52	1	80	1	40			3
456	460	484	L	2.1	26.58	1	80	1	40			4
457	461	485	C	7.6	27.06	1	100	0	80			0
458	462	486	V	12.3	25.4	1	80	2	40			3
459	463	487	L	17.5	29.09	1	100	1	40			4
460	464	488	H	6.9	35.51	1	100	2	40			5
461	465	489	E	60.3	42.01	1	100	2	60			4
462	466	490	K	54.0	45.63	1	100	2	60	K490E	0	4
463	467	491	T	111.3	47.62	0	100	2	60			1
464	468	492	P	128.4	44.24	0	100	2	40			3
465	469	493	V	97.5	41.69	0	100	2	40			3
466	470	494	S	4.7	43.02	0	100	1	40			1
467	471	495	D	205.8	45.67	1	80	1	40			3
468	472	496	R	25.6	43.1	1	40	0	20			5
469	473	497	V	0.0	35.26	1	80	1	60			3
470	474	498	T	66.3	36.92	1	100	1	40			1
471	475	499	K	63.2	36.72	1	100	2	40			4
472	476	500	C	2.2	29.85	1	100	2	80			0
473	477	501	C	9.8	29.96	1	100	1	80			0
474	478	502	T	125.0	35	1	60	1	40			1
475	479	503	E	94.2	40.83	1	60	1	20	E503K	0	4
476	480	504	S	62.5	40.31	0	100	1	60			1
477	481	505	L	34.0	34.26	0	100	1	40			4
478	482	506	V	32.1	32.41	0	80	1	40			3

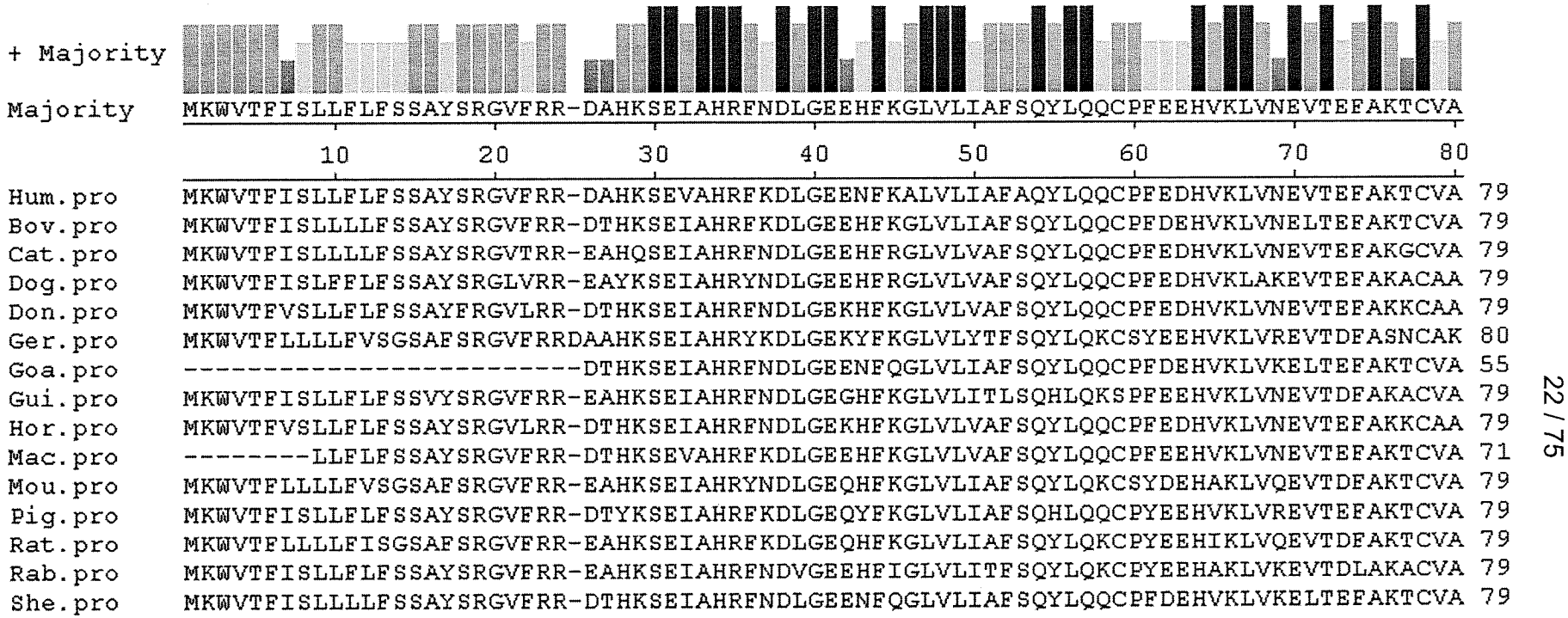
479	483	507	N	85.9	30.93	0	60	1	40			2
480	484	508	R	8.1	26.02	1	100	1	60			5
481	485	509	R	2.4	27.43	1	100	2	60			5
482	486	510	P	26.9	27.41	1	100	2	60			3
483	487	511	C	34.8	28.7	1	100	2	80			0
484	488	512	F	0.0	26.54	1	100	2	60			4
485	489	513	S	39.1	29.37	1	100	1	40			1
486	490	514	A	130.6	32.03	1	80	2	40			1
487	491	515	L	12.4	36.77	0	100	0	60			4
488	492	516	E	83.3	48.42	0	40	1	20			4
489	493	517	V	67.9	54.02	0	40	1	20			3
490	494	518	D	26.1	62.32	0	100	1	60	D518N	1	3
491	495	519	E	100.6	69.16	0	100	1	60			4
492	496	520	T	148.8	70.07	0	60	2	40			1
493	497	521	Y	46.2	69.63	0	100	0	60			3
494	498	522	V	149.4	74.11	0	80	2	60			3
495	499	523	P	89.6	78.71	0	100	1	80			3
496	500	524	K	86.8	87.39	0	100	1	40			4
497	501	525	E	99.4	95.25	0	60	2	40	E525K	0	4
498	502	526	F	48.8	97.09	0	100	0	60			4
499	503	527	N	81.2	99.86	0	40	1	20			2
500	504	528	A	108.1	98.55	0	60	0	40			1
501	505	529	E	105.8	93.84	0	60	0	40	E529K	0	4
502	506	530	T	92.5	88	0	60	1	40			1
503	507	531	F	3.3	82.27	0	100	1	60			4
504	508	532	T	100.0	80.18	0	100	2	40			1
505	509	533	F	13.8	78.2	0	100	2	60			4
506	510	534	H	88.5	76.46	0	100	1	60			5
507	511	535	A	48.4	69.68	0	80	1	40			1

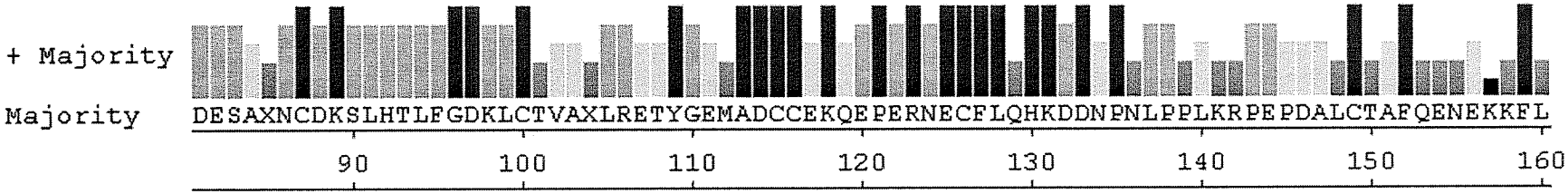
508	512	536	D	139.1	61.05	0	80	0	40			3
509	513	537	I	4.8	50.62	0	60	1	40			4
510	514	538	C	45.7	44.69	0	100	1	80			0
511	515	539	T	145.0	40.33	0	100	2	60			1
512	516	540	L	46.4	40.23	0	100	1	40			4
513	517	541	S	78.1	46.03	0	60	1	40			1
514	518	542	E	51.9	49.65	1	60	0	40			4
515	519	543	K	62.6	49.4	1	40	1	20			4
516	520	544	E	23.7	43.06	1	100	0	60			4
517	521	545	R	16.6	40.16	1	80	1	40			5
518	522	546	Q	37.0	39.72	1	80	0	60			3
519	523	547	I	71.4	36.13	1	60	0	40			4
520	524	548	K	60.3	34.29	1	80	1	60			4
521	525	549	K	6.9	35.18	1	100	1	60			4
522	526	550	Q	0.0	30.63	1	100	1	60			3
523	527	551	T	53.8	28.26	1	60	2	20			1
524	528	552	A	6.5	31.62	1	100	1	40			1
525	529	553	L	7.2	30.26	1	100	1	80			4
526	530	554	V	0.0	33.2	1	60	2	40			3
527	531	555	E	28.2	41.25	1	100	1	60			4
528	532	556	L	14.4	49.88	1	100	1	60			4
529	533	557	V	2.5	54.97	1	60	2	40	V557M	0	3
530	534	558	K	10.9	60.16	0	100	1	60			4
531	535	559	H	27.7	70.44	0	100	2	60			5
532	536	560	K	23.0	79.19	0	100	1	60	K560E	0	4
533	537	561	P	34.3	87.27	0	100	1	60			3
534	538	562	K	115.5	96.73	0	80	2	40			4
535	539	563	A	90.3	99.48	0	100	0	40			1
536	540	564	T	26.3	97.44	0	80	1	60			1

537	541	565	K	98.3	96.84	0	20	0	20	K565E	1	4
538	542	566	E	105.8	96.98	1	80	1	60			4
539	543	567	Q	53.5	92.83	1	100	0	60			3
540	544	568	L	6.2	91.34	1	80	1	60			4
541	545	569	K	63.8	92.51	1	80	0	60			4
542	546	570	A	80.6	91.51	1	60	1	40			1
543	547	571	V	27.2	88.34	1	100	0	60			3
544	548	572	M	8.7	86.47	1	60	1	40			3
545	549	573	D	146.4	84.68	1	40	0	20			3
546	550	574	D	94.2	80.18	1	40	1	20	D574G, D574A	0	3
547	551	575	F	0.8	74.2	1	100	0	80			4
548	552	576	A	38.7	71.8	1	40	1	20			1
549	553	577	A	69.4	71.17	1	60	0	40			1
550	554	578	F	0.8	71.18	1	80	0	40			4
551	555	579	V	1.2	73.7	1	60	0	60			3
552	556	580	E	60.9	77.5	1	40	0	20			4
553	557	581	K	71.8	77.55	1	80	1	60			4
554	558	582	C	1.1	76.28	1	100	1	80			0
555	559	583	C	40.2	71.47	0	100	1	80			0
556	560	584	K	92.5	81.9	0	40	1	20	K584E	0	4
557	561	585	A	77.4	89.44	0	80	0	60			1
558	562	586	D	217.4	95.72	0	40	0	40			3
559	563	587	D	63.8	98.46	0	80	0	60	D587N	1	3
560	564	588	K	97.1	100.08	0	80	0	40			4
561	565	589	E	87.8	98.18	0	80	0	40	E589K	0	4
562	566	590	T	86.3	94.83	1	40	1	40			1
563	567	591	C	25.0	92.56	1	100	1	80			0
564	568	592	F	1.6	95.34	1	100	1	60			4

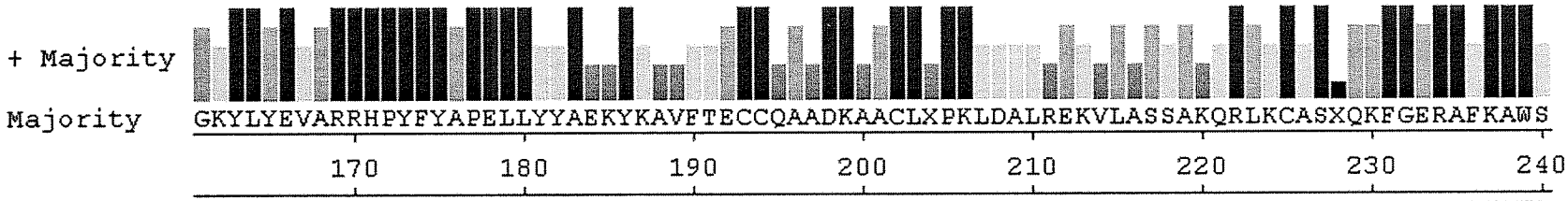
565	569	593	A	74.2	96.55	1	60	1	20			1
566	570	594	E	73.1	97.9	1	40	0	40	E594K	2	4
567	571	595	E	48.7	96.74	1	80	1	60			4
568	572	596	G	6.0	97.47	1	100	0	60			2
569	573	597	K	81.6	98.2	1	80	1	40	K597E	0	4
570	574	598	K	90.8	99.51	1	80	0	40	K598N	0	4
571	575	599	L	33.0	99.45	1	80	1	60			4
572	576	600	V	25.9	98.42	1	100	0	60			3
573	577	601	A	93.5	97.86	1	60	1	40			1
574	578	602	A	96.8	98.62	1	20	0	20			1
575	579	603	S	21.9	100.74	1	40	0	40			1
576	580	604	Q	86.6	101.91	1	60	0	40			3
577	581	605	A	133.9	103.91	1	40	0	40			1
578	582	606	A	88.7	106.05	0	80	1	40			1
n/a	583	607	L	n/a	n/a	0	100	0	60			4
n/a	584	608	G	n/a	n/a	0	60	1	40			2
n/a	585	609	L	n/a	n/a	0	0	0	0			4

Figure 2

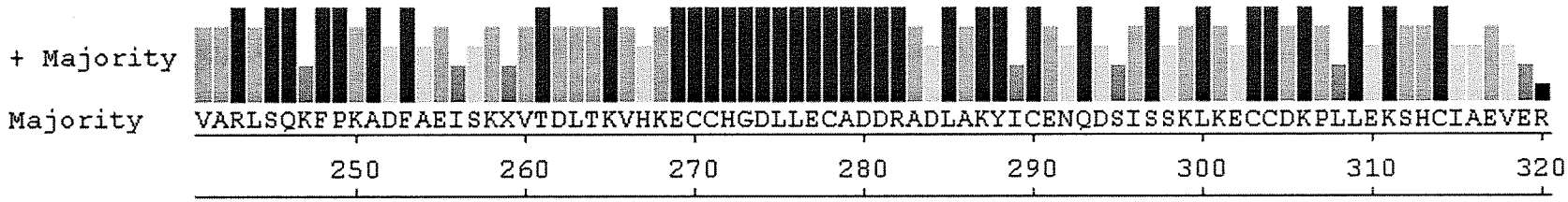

+ Majority
Majority MKWVTFISLLFLFSSAYSRGVFRR-DAHKSEIAHRFNDLGEEHFKGLVLIAFSQYLQQCPFEEHVKLVNEVTEFAKTCVA
10 20 30 40 50 60 70 80
Hum.pro MKWVTFISLLFLFSSAYSRGVFRR-DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVA 79
Bov.pro MKWVTFISLLLLFSSAYSRGVFRR-DTHKSEIAHRFKDLGEEHFKGLVLIAFSQYLQQCPFDEHVKLVNELTEFAKTCVA 79
Cat.pro MKWVTFISLLLLFSSAYSRGVTRR-EAHQSEIAHRFNDLGEEHFRGLVLVAFSQYLQQCPFEDHVKLVNEVTEFAKGCVA 79
Dog.pro MKWVTFISLFFLFSSAYSRGLVRR-EAYKSEIAHRYNDLGEEHFRGLVLVAFSQYLQQCPFEDHVKLAKEVTEFAKACAA 79
Don.pro MKWVTFVSLLFLFSSAYFRGVLRR-DTHKSEIAHRFNDLGEKHFKGLVLVAFSQYLQQCPFEDHVKLVNEVTEFAKKCAA 79
Ger.pro MKWVTFLLLLFVSGSAFSRGVFRRDAAHKSEIAHRYKDLGEKYFKGLVLYTFSQYLQKCSYEEHVKLVREVTDFASNCAK 80
Goa.pro ----------DTHKSEIAHRFNDLGEENFQGLVLIAFSQYLQQCPFDEHVKLVKELTEFAKTCVA 55
Gui.pro MKWVTFISLLFLFSSVYSRGVFRR-EAHKSEIAHRFNDLGEGHFKGLVLITLSQHLQKSPFEEHVKLVNEVTDFAKACVA 79
Hor.pro MKWVTFVSLLFLFSSAYSRGVLRR-DTHKSEIAHRFNDLGEKHFKGLVLVAFSQYLQQCPFEDHVKLVNEVTEFAKKCAA 79
Mac.pro --------LLFLFSSAYSRGVFRR-DTHKSEVAHRFKDLGEEHFKGLVLVAFSQYLQQCPFEEHVKLVNEVTEFAKTCVA 71
Mou.pro MKWVTFLLLLFVSGSAFSRGVFRR-EAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVA 79
Pig.pro MKWVTFISLLFLFSSAYSRGVFRR-DTYKSEIAHRFKDLGEQYFKGLVLIAFSQHLQQCPYEEHVKLVREVTEFAKTCVA 79
Rat.pro MKWVTFLLLLFISGSAFSRGVFRR-EAHKSEIAHRFKDLGEQHFKGLVLIAFSQYLQKCPYEEHIKLVQEVTDFAKTCVA 79
Rab.pro MKWVTFISLLFLFSSAYSRGVFRR-EAHKSEIAHRFNDVGEEHFIGLVLITFSQYLQKCPYEEHAKLVKEVTDLAKACVA 79
She.pro MKWVTFISLLLLFSSAYSRGVFRR-DTHKSEIAHRFNDLGEENFQGLVLIAFSQYLQQCPFDEHVKLVKELTEFAKTCVA 79



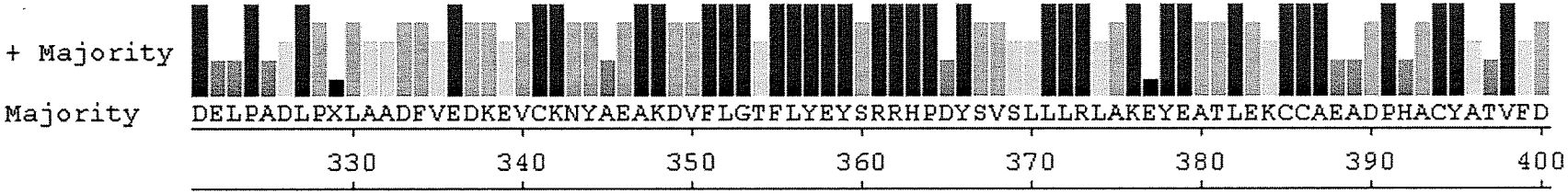

```
Hum.pro    DESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFL 159
Bov.pro    DESHAGCEKSLHTLFGDELCKVASLRETYGDMADCCEKQEPERNECFLSHKDDSPDLPKLK-PDPNTLCDEFKADEKKFW 158
Cat.pro    DQSAANCEKSLHELLGDKLCTVASLRDKYGEMADCCEKKEPERNECFLQHKDDNPGFGQLVTPEADAMCTAFHENEQRFL 159
Dog.pro    EESGANCDKSLHTLFGDKLCTVASLRDKYGDMADCCEKQEPDRNECFLAHKDDNPGFPPLVAPEPDALCAAFQDNEQLFL 159
Don.pro    DESAENCDKSLHTLFGDKLCTVATLRATYGELADCCEKQEPERNECFLTHKDDHPNLPKLK-PEPDAQCAAFQEDPDKFL 158
Ger.pro    DESAENCDKSLHTLFGDKLCSLPNFGEKYAEMADCCAKQEPERNECFLQHKDDNPQLPPFKRAEPDAMCTAFQENAEAFM 160
Goa.pro    DESHAGCDKSLHTLFGDELCKVATLRETYGDMADCCEKQEPERNECFLKHKDDSPDLPKLK-PEPDTLCAEFKADEKKFW 134
Gui.pro    DESAQNCGKAIATLFGDKVCAIPSLRETYGELADCCAKEDPDRVECFLQHKDDNPNLPPFERPEPEALCTAFKENNDRFI 159
Hor.pro    DESAENCDKSLHTLFGDKLCTVATLRATYGELADCCEKQEPERNECFLTHKDDHPNLPKLK-PEPDAQCAAFQEDPDKFL 158
Mac.pro    DESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPPLVRPEVDVMCTAFHDNEATFL 151
Mou.pro    DESAANCDKSLHTLFGDKLCAIPNLRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFM 159
Pig.pro    DESAENCDKSIHTLFGDKLCAIPSLREHYGDLADCCEKEEPERNECFLQHKNDNPDIPKLK-PDPVALCADFQEDEQKFW 158
Rat.pro    DENAENCDKSIHTLFGDKLCAIPKLRDNYGELADCCAKQEPERNECFLQHKDDNPNLPPFQRPEAEAMCTSFQENPTSFL 159
Rab.pro    DESAANCDKSLHDIFGDKICALPSLRDTYGDVADCCEKKEPERNECFLHHKDDKPDLPPFARPEADVLCKAFHDDEKAFF 159
She.pro    DESHAGCDKSLHTLFGDELCKVATLRETYGDMADCCEKQEPERNECFLNHKDDSPDLPKLK-PEPDTLCAEFKADEKKFW 158
```




```
Hum.pro    KKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWA 239
Bov.pro    GKYLYEIARRHPYFYAPELLYYANKYNGVFQECCQAEDKGACLLPKIETMREKVLASSARQRLRCASIQKFGERALKAWS 238
Cat.pro    GKYLYEIARRHPYFYAPELLYYAEEYKGVFTECCEAADKAACLTPKVDALREKVLASSAKERLKCASLQKFGERAFKAWS 239
Dog.pro    GKYLYEIARRHPYFYAPELLYYAQQYKGVFAECCQAADKAACLGPKIEALREKVLLSSAKERFKCASLQKFGDRAFKAWS 239
Don.pro    GKYLYEVARRHPYFYGPELLFHAEEYKADFTECCPADDKAGCLIPKLDALKERILLSSAKERLKCSSFQKFGERAFKAWS 238
Ger.pro    GHYLHEVARRHPYFYGPELLYLADKYTAVLTECCAADDKGACLTPKLDALKEKALVSAVRQRLKCSSMKKFGERAFKAWA 240
Goa.pro    GKYLYEVARRHPYFYAPELLYYANKYNGVFQECCQAEDKGACLLPKIETMREKVLASSARQRLRCASIQKFGERALKAWS 214
Gui.pro    GHYLYEVSRRHPYFYAPELLYYAEKYKNALTECCEAADKAACLTPKLDAIKEKALVSSAQQRLKCASLQKFGERAFKAWS 239
Hor.pro    GKYLYEVARRHPYFYGPELLFHAEEYKADFTECCPADDKLACLIPKLDALKERILLSSAKERLKCSSFQNFGERAVKAWS 238
Mac.pro    KKYLYEVARRHPYFYAPELLFFAARYKAAFAECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGDRAFKAWA 231
Mou.pro    GHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTPKLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWA 239
Pig.pro    GKYLYEIARRHPYFYAPELLYYAIIYKDVFSECCQAADKAACLLPKIEHLREKVLTSAAKQRLKCASIQKFGERAFKAWS 238
Rat.pro    GHYLHEVARRHPYFYAPELLYYAEKYNEVLTQCCTESDKAACLTPKLDAVKEKALVAAVRQRMKCSSMQRFGERAFKAWA 239
Rab.pro    GHYLYEVARRHPYFYAPELLYYAQKYKAILTECCEAADKGACLTPKLDALEGKSLISAAQERLRCASIQKFGDRAYKAWA 239
She.pro    GKYLYEVARRHPYFYAPELLYYANKYNGVFQECCQAEDKGACLLPKIDAMREKVLASSARQRLRCASIQKFGERALKAWS 238
```



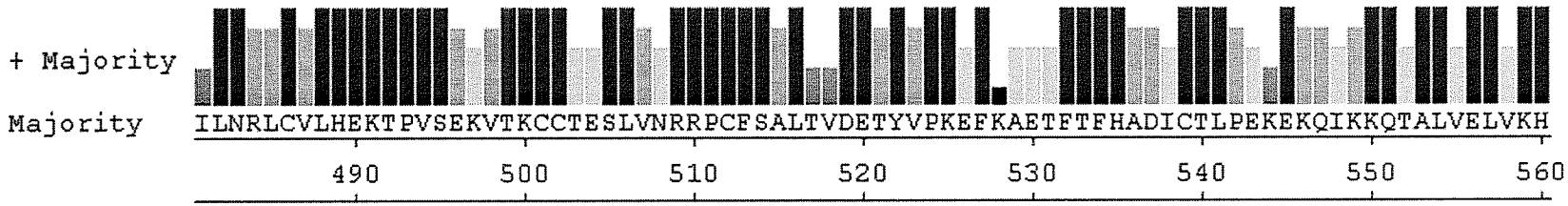

```
Hum.pro    VARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVEN 319
Bov.pro    VARLSQKFPKAEFVEVTKLVTDLTKVHKECCHGDLLECADDRADLAKYICDNQDTISSKLKECCDKPLLEKSHCIAEVEK 318
Cat.pro    VARLSQKFPKAEFAEISKLVTDLAKIHKECCHGDLLECADDRADLAKYICENQDSISTKLKECCGKPVLEKSHCISEVER 319
Dog.pro    VARLSQRFPKADFAEISKVVTDLTKVHKECCHGDLLECADDRADLAKYMCENQDSISTKLKECCDKPVLEKSQCLAEVER 319
Don.pro    VARLSQKFPKADFAEVSKIVTDLTKVHKECCHGDLLECADDRADLTKYICEHQDSISGKLKACCDKPLLQKSHCIAEVKE 318
Ger.pro    VARMSQTFPNADFAEITKLATDLTKVTQECCHGDLLECADDRAELAKYMCENQASISSKLQACCDKEMLQKSQCLAEVEH 320
Goa.pro    VARLSQKFPKADFTDVTKIVTDLTKVHKECCHGDLLECADDRADLAKYICDHQDTLSSKLKECCDKPVLEKSHCIAEIDK 294
Gui.pro    VARLSQKFPKAEFAEISTIVTSLTKVTKECCHGDLLECADDRQELAKYMCEHQDSISSKLKECCVKPTLQKAHCILEIQR 319
Hor.pro    VARLSQKFPKADFAEVSKIVTDLTKVHKECCHGDLLECADDRADLAKYICEHQDSISGKLKACCDKPLLQKSHCIAEVKE 318
Mac.pro    VARLSQKFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYMCENQDSISSKLKECCDKPLLEKSHCLAEVEN 311
Mou.pro    VARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDKPLLKKAHCLSEVEH 319
Pig.pro    LARLSQRFPKADFTEISKIVTDLAKVHKECCHGDLLECADDRADLAKYICENQDTISTKLKECCDKPLLEKSHCIAEAKR 318
Rat.pro    VARMSQRFPNAEFAEITKLATDVTKINKECCHGDLLECADDRAELAKYMCENQATISSKLQACCDKPVLQKSQCLAEIEH 319
Rab.pro    LVRLSQRFPKADFTDISKIVTDLTKVHKECCHGDLLECADDRADLAKYMCEHQETISSHLKECCDKPILEKAHCIYGLHN 319
She.pro    VARLSQKFPKADFTDVTKIVTDLTKVHKECCHGDLLECADDRADLAKYICDHQDALSSKLKECCDKPVLEKSHCIAEVDK 318
```



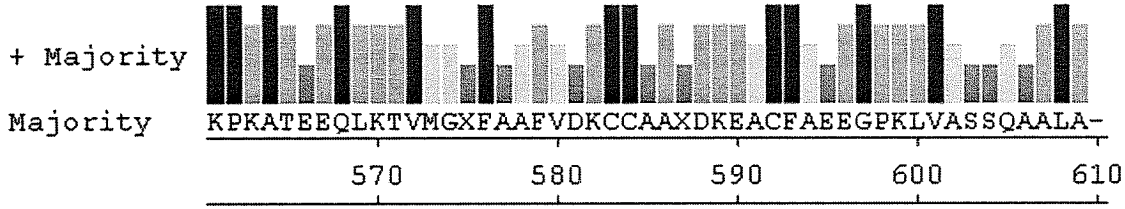

```
Majority  DELPADLPXLAADFVEDKEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKEYEATLEKCCAEADPHACYATVFD
                    330       340       350       360       370       380       390       400
Hum.pro   DEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFD 399
Bov.pro   DAIPENLPPLTADFAEDKDVCKNYQEAKDAFLGSFLYEYSRRHPEYAVSVLLRLAKEYEATLEECCAKDDPHACYSTVFD 398
Cat.pro   DELPADLPPLAVDFVEDKEVCKNYQEAKDVFLGTFLYEYSRRHPEYSVSLLLRLAKEYEATLEKCCATDDPPACYAHVFD 399
Dog.pro   DELPGDLPSLAADFVEDKEVCKNYQEAKDVFLGTFLYEYARRHPEYSVSLLLRLAKEYEATLEKCCATDDPPTCYAKVLD 399
Don.pro   DDLPSDLPALAADFAEDKEICKHYKDAKDVFLGTFLYEYSRRHPDYSVSLLLRIAKTYEATLEKCCAEADPPACYATVFD 398
Ger.pro   DDMPADLPALTADFVEDKDVCKNYAEAKDVFLGTFLYEYSRRHPEYSVSLLLRLAKKYEATLEKCCAEADPHACYGHVFD 400
Goa.pro   DAVPENLPPLTADFAEDKEVCKNYQEAKDVFLGSFLYEYSRRHPEYAVSVLLRLAKEYEATLEDCCAKEDPHACYATVFD 374
Gui.pro   DELPTELPDLAVDFVEDKEVCKNFAEAKDVFLGTFLYEYSRRHPEYSIGMLLRIAKGYEAKLEKCCAEADPHACYAKVFD 399
Hor.pro   DDLPSDLPALAADFAEDKEICKHYKDAKDVFLGTFLYEYSRRHPDYSVSLLLRIAKTYEATLEKCCAEADPPACYRTVFD 398
Mac.pro   DEMPADLPSLAADYVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVMLLLRLAKAYEATLEKCCAAADPHECYAKVFD 391
Mou.pro   DTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLA 399
Pig.pro   DELPADLNPLEHDFVEDKEVCKNYKEAKHVFLGTFLYEYSRRHPDYSVSLLLRIAKIYEATLEDCCAKEDPPACYATVFD 398
Rat.pro   DNIPADLPSIAADFVEDKEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEGDPPACYGTVLA 399
Rab.pro   DETPAGLPAVAEEFVEDKDVCKNYEEAKDLFLGKFLYEYSRRHPDYSVVLLLRLGKAYEATLKKCCATDDPHACYAKVLD 399
She.pro   DAVPENLPPLTADFAEDKEVCKNYQEAKDVFLGSFLYEYSRRHPEYAVSVLLRLAKEYEATLEDCCAKEDPHACYATVFD 398
```




```
Hum.pro    EFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSV 479
Bov.pro    KLKHLVDEPQNLIKQNCDQFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTRCCTKPESERMPCTEDYLSL 478
Cat.pro    EFKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSKCCTHPEAERLSCAEDYLSV 479
Dog.pro    EFKPLVDEPQNLVKTNCELFEKLGEYGFQNALLVRYTKKAPQVSTPTLVEVSRKLGKVGTKCCKKPESERMSCAEDFLSV 479
Don.pro    QFTPLVEEPKSLVKKNCDLFEEVGEYDFQNALIVRYTKKAPQVSTPTLVEIGRTLGKVGSRCCKLPESERLPCSENHLAL 478
Ger.pro    EFKPLVEEPQNLVKSNCELYEKLGEYGFQNAVLVRYTKKAPQVSTPTLVEAARSLGRVGTHCCALPEKKRLPCVEDYLSA 480
Goa.pro    KLKHLVDEPQNLIKKNCELFEKHGEYGFQNALIVRYTRKAPQVSTPTLVEISRSLGKVGTKCCAKPESERMPCTEDYLSL 454
Gui.pro    ELQPLIDEPKKLVQQNCELFDKLGEYGFQNALAVRYTQKAPQVSTPTLVEYARKLGSVGTKCCSLPETERLSCTENYLAL 479
Hor.pro    QFTPLVEEPKSLVKKNCDLFEEVGEYDFQNALIVRYTKKAPQVSTPTLVEIGRTLGKVGSRCCKLPESERLPCSENHLAL 478
Mac.pro    EFQPLVEEPQNLVKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGAKCCKLPEAKRMPCAEDYLSV 471
Mou.pro    EFQPLVEEPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSA 479
Pig.pro    KFQPLVDEPKNLIKQNCELFEKLGEYGFQNALIVRYTKKVPQVSTPTLVEVARKLGLVGSRCCKRPEEERLSCAEDYLSL 478
Rat.pro    EFQPLVEEPKNLVKTNCELYEKLGEYGFQNAVLVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEAQRLPCVEDYLSA 479
Rab.pro    EFQPLVDEPKNLVKQNCELYEQLGDYNFQNALLVRYTKKVPQVSTPTLVEISRSLGKVGSKCCKHPEAERLPCVEDYLSV 479
She.pro    KLKHLVDEPQNLIKKNCELFEKHGEYGFQNALIVRYTRKAPQVSTPTLVEISRSLGKVGTKCCAKPESERMPCTEDYLSL 478
```

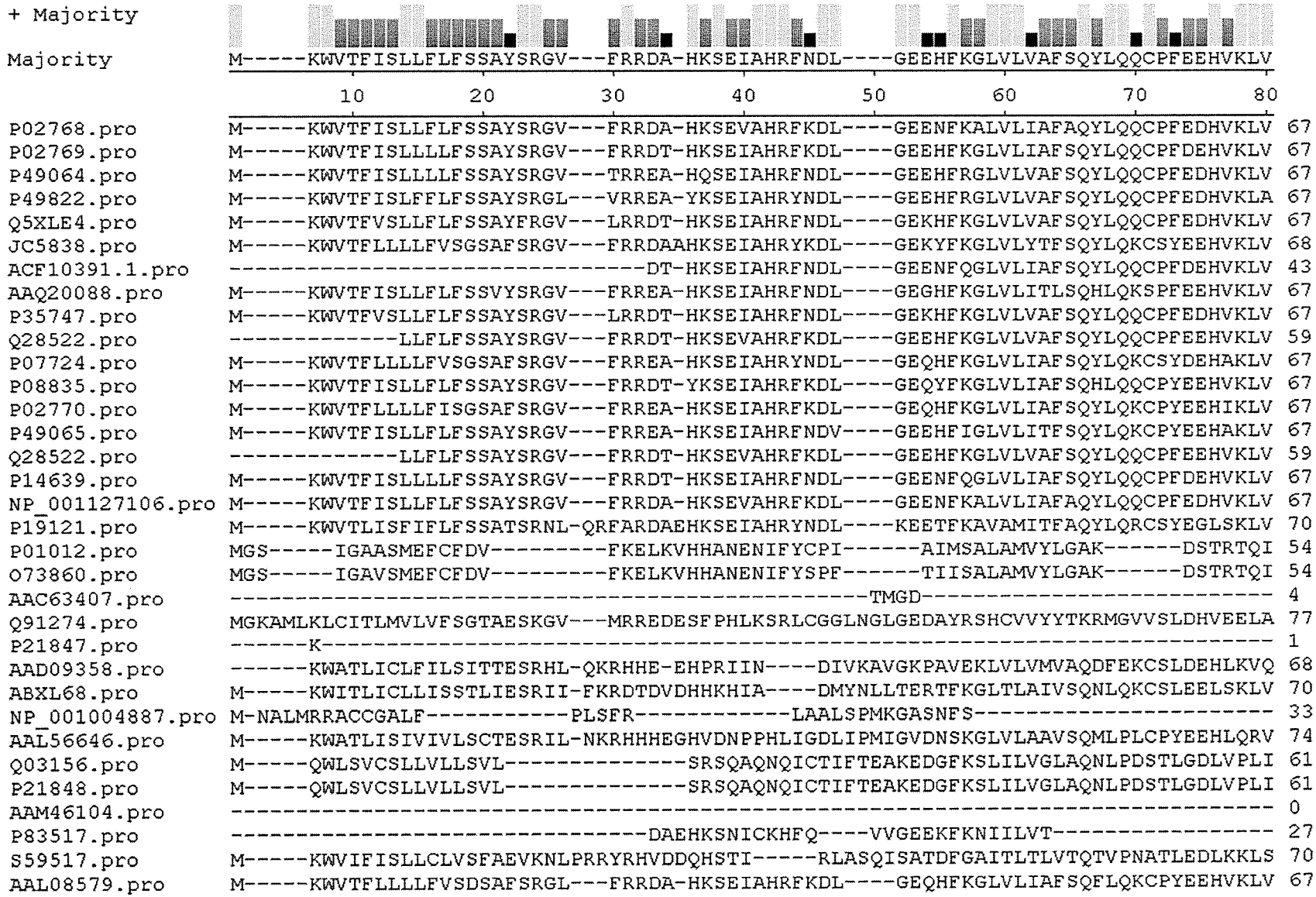


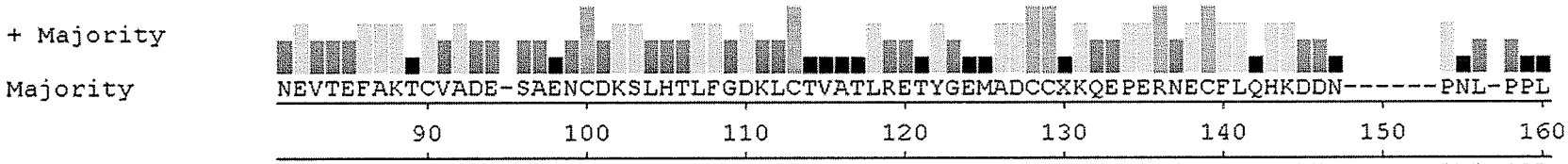

```
Hum.pro    VLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKH 559
Bov.pro    ILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDETYVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKH 558
Cat.pro    VLNRLCVLHEKTPVSERVTKCCTESLVNRRPCFSALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKH 559
Dog.pro    VLNRLCVLHEKTPVSERVTKCCSESLVNRRPCFSGLEVDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQTALVELLKH 559
Don.pro    ALNRLCVLHEKTPVSEKITKCCTDSLAERRPCFSALELDEGYIPKEFKAETFTFHADICTLPEDEKQIKKQSALAELVKH 558
Ger.pro    ILNRVCLLHEKTPVSEQVTKCCSGSLVERRPCFSALPVDETYVPKEFKAETFTFHANICTLPEKEKQMEKQTALAELVKH 560
Goa.pro    ILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSDLTLDETYVPKPFDGESFTFHADICTLPDTEKQIKKQTALVELLKH 534
Gui.pro    ILNRLCILHEKTPVSERVTKCCTESLVNRRPCFSALHVDETYVPKPFHADSFTFHADICTLPEKEKQVKKQMALVELVKH 559
Hor.pro    ALNRLCVLHEKTPVSEKITKCCTDSLAERRPCFSALELDEGYVPKEFKAETFTFHADICTLPEDEKQIKKQSALAELVKH 558
Mac.pro    VLNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALELDEAYVPKAFNAETFTFHADMCTLSEKEKQVKKQTALVELVKH 551
Mou.pro    ILNRVCLLHEKTPVSEHVTKCCSGSLVERRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKH 559
Pig.pro    VLNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDETYKPKEFVEGTFTFHADLCTLPEDEKQIKKQTALVELLKH 558
Rat.pro    ILNRLCVLHEKTPVSEKVTKCCSGSLVERRPCFSALTVDETYVPKEFKAETFTFHSDICTLPDKEKQIKKQTALAELVKH 559
Rab.pro    VLNRLCVLHEKTPVSEKVTKCCSESLVDRRPCFSALGPDETYVPKEFNAETFTFHADICTLPETERKIKKQTALVELVKH 559
She.pro    ILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSDLTLDETYVPKPFDEKFFTFHADICTLPDTEKQIKKQTALVELLKH 558
```



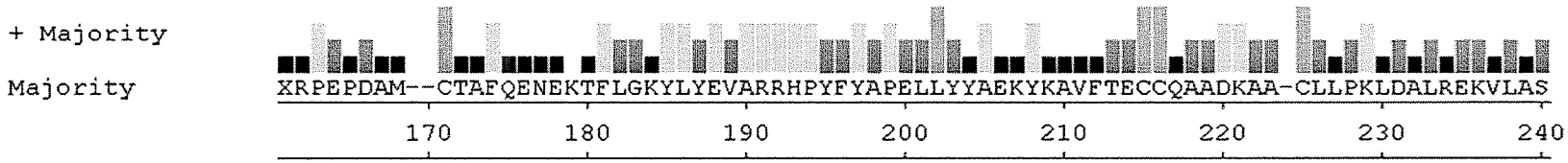
Hum.pro	KPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL	609
Bov.pro	KPKATEEQLKTVMENFVAFVDKCCAADDKEACFAVEGPKLVVSTQTALA	607
Cat.pro	KPKATEEQLKTVMGDFGSFVDKCCAAEDKEACFAEEGPKLVAAAQAALA	608
Dog.pro	KPKATDEQLKTVMGDFGAFVEKCCAAENKEGCFSEEGPKLVAAAQAALV	608
Don.pro	KPKATKEQLKTVLGNFSAFVAKCCGAEDKEACFAEEGPKLVASSQLALA	607
Ger.pro	KPQATEEQLKKVMGDFAEFLEKCCKQEDKEACFSTEGPKLVAESQKALA	609
Goa.pro	KPKATDEQLKTVMENFVAFVDKCCAADDKEGCFLLEGPKLVASTQAALA	583
Gui.pro	KPKASEEQMKTVMGDFAAFLKKCCDADNKEACFTEDGPKLVAKCQATLA	608
Hor.pro	KPKATKEQLKTVLGNFSAFVAKCCGREDKEACFAEEGPKLVASSQLALA	607
Mac.pro	KPKATKEQLKGVMDNFAAFVEKCCKADDKEACFAEEGPKFVAASQAALA	600
Mou.pro	KPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA	608
Pig.pro	KPHATEEQLRTVLGNFAAFVQKCCAAPDHEACFAVEGPKFVIEIRGILA	607
Rat.pro	KPKATEDQLKTVMGDFAQFVDKCCKAADKDNCFATEGPNLVARSKEALA	608
Rab.pro	KPHATNDQLKTVVGEFTALLDKCCSAEDKEACFAVEGPKLVESSKATLG	608
She.pro	KPKATDEQLKTVMENFVAFVDKCCAADDKEGCFVLEGPKLVASTQAALA	607

Figure 3

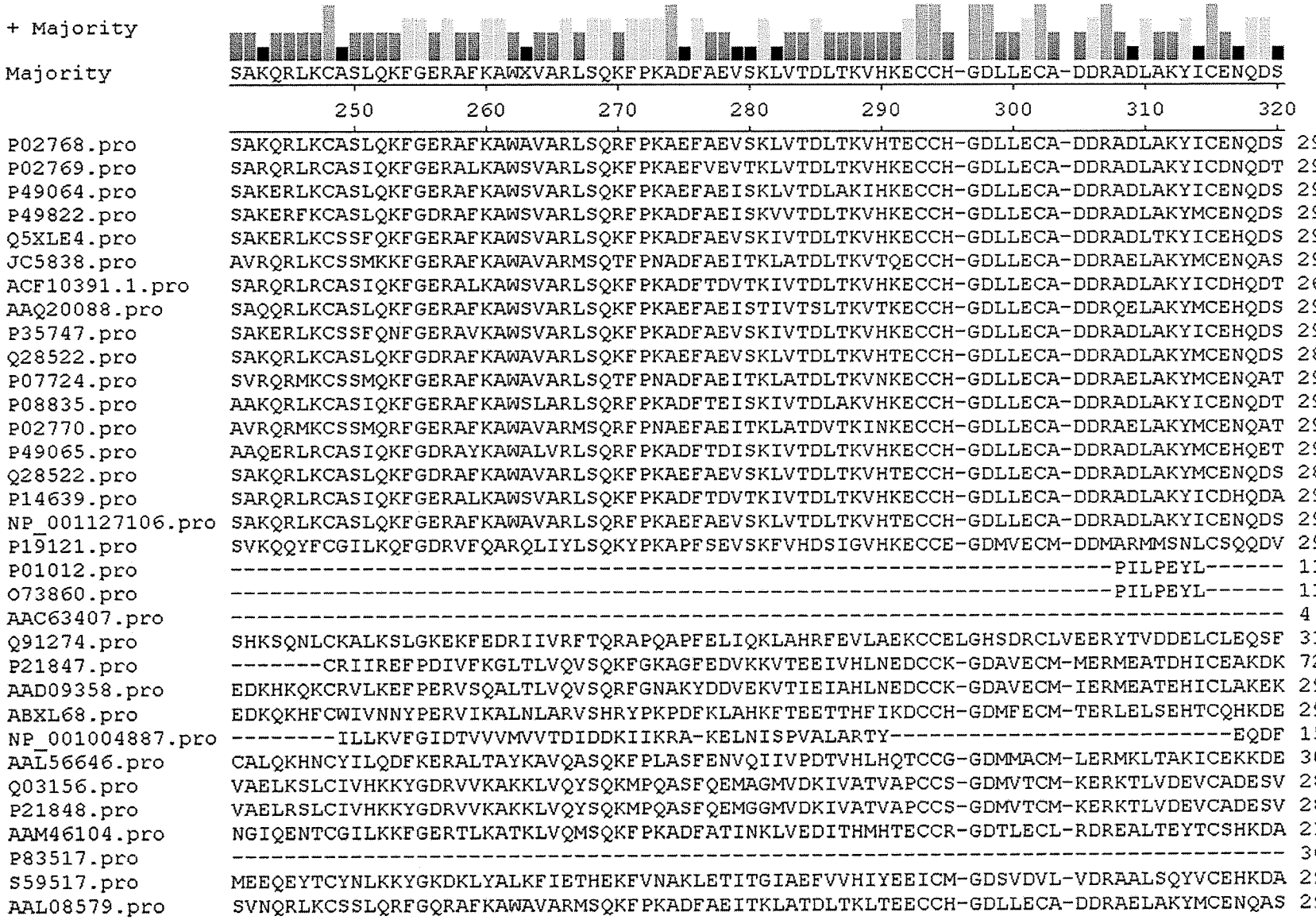

+ Majority
Majority
M-----KWVTFISLLFLFSSAYSRGV---FRRDA-HKSEIAHRFNDL----GEEHFKGLVLVAFSQYLQQCPFEEHVKLV
10
20
30
40
50
60
70
80
P02768.pro M-----KWVTFISLLFLFSSAYSRGV---FRRDA-HKSEVAHRFKDL----GEENFKALVLIAFAQYLQQCPFEDHVKLV 67
P02769.pro M-----KWVTFISLLLLFSSAYSRGV---FRRDT-HKSEIAHRFKDL----GEEHFKGLVLIAFSQYLQQCPFDEHVKLV 67
P49064.pro M-----KWVTFISLLLLFSSAYSRGV---TRREA-HQSEIAHRFNDL----GEEHFRGLVLVAFSQYLQQCPFEDHVKLV 67
P49822.pro M-----KWVTFISLFFLFSSAYSRGL---VRREA-YKSEIAHRYNDL----GEEHFRGLVLVAFSQYLQQCPFEDHVKLA 67
Q5XLE4.pro M-----KWVTFVSLLFLFSSAYFRGV---LRRDT-HKSEIAHRFNDL----GEKHFKGLVLVAFSQYLQQCPFEDHVKLV 67
JC5838.pro M-----KWVTFLLLLFVSGSAFSRGV---FRRDAAHKSEIAHRYKDL----GEKYFKGLVLYTFSQYLQKCSYEEHVKLV 68
ACF10391.1.pro ------------------------------DT-HKSEIAHRFNDL----GEENFQGLVLIAFSQYLQQCPFDEHVKLV 43
AAQ20088.pro M-----KWVTFISLLFLFSSVYSRGV---FRREA-HKSEIAHRFNDL----GEGHFKGLVLITLSQHLQKSPFEEHVKLV 67
P35747.pro M-----KWVTFVSLLFLFSSAYSRGV---LRRDT-HKSEIAHRFNDL----GEKHFKGLVLVAFSQYLQQCPFEDHVKLV 67
Q28522.pro -------------LLFLFSSAYSRGV---FRRDT-HKSEVAHRFKDL----GEEHFKGLVLVAFSQYLQQCPFEEHVKLV 59
P07724.pro M-----KWVTFLLLLFVSGSAFSRGV---FRREA-HKSEIAHRYNDL----GEQHFKGLVLIAFSQYLQKCSYDEHAKLV 67
P08835.pro M-----KWVTFISLLFLFSSAYSRGV---FRRDT-YKSEIAHRFKDL----GEQYFKGLVLIAFSQHLQQCPYEEHVKLV 67
P02770.pro M-----KWVTFLLLLFISGSAFSRGV---FRREA-HKSEIAHRFKDL----GEQHFKGLVLIAFSQYLQKCPYEEHIKLV 67
P49065.pro M-----KWVTFISLLFLFSSAYSRGV---FRREA-HKSEIAHRFNDV----GEEHFIGLVLITFSQYLQKCPYEEHAKLV 67
Q28522.pro -------------LLFLFSSAYSRGV---FRRDT-HKSEVAHRFKDL----GEEHFKGLVLVAFSQYLQQCPFEEHVKLV 59
P14639.pro M-----KWVTFISLLLLFSSAYSRGV---FRRDT-HKSEIAHRFNDL----GEENFQGLVLIAFSQYLQQCPFDEHVKLV 67
NP_001127106.pro M-----KWVTFISLLFLFSSAYSRGV---FRRDA-HKSEVAHRFKDL----GEENFKALVLIAFAQYLQQCPFEDHVKLV 67
P19121.pro M-----KWVTLISFIFLFSSATSRNL-QRFARDAEHKSEIAHRYNDL----KEETFKAVAMITFAQYLQRCSYEGLSKLV 70
P01012.pro MGS-----IGAASMEFCFDV---------FKELKVHHANENIFYCPI------AIMSALAMVYLGAK------DSTRTQI 54
O73860.pro MGS-----IGAVSMEFCFDV---------FKELKVHHANENIFYSPF------TIISALAMVYLGAK------DSTRTQI 54
AAC63407.pro --TMGD---------- 4
Q91274.pro MGKAMLKLCITLMVLVFSGTAESKGV---MRREDESFPHLKSRLCGGLNGLGEDAYRSHCVVYYTKRMGVVSLDHVEELA 77
P21847.pro ------K---------- 1
AAD09358.pro ------KWATLICLFILSITTESRHL-QKRHHE-EHPRIIN----DIVKAVGKPAVEKLVLVMVAQDFEKCSLDEHLKVQ 68
ABXL68.pro M-----KWITLICLLISSTLIESRII-FKRDTDVDHHKHIA----DMYNLLTERTFKGLTLAIVSQNLQKCSLEELSKLV 70
NP_001004887.pro M-NALMRRACCGALF-----------PLSFR------------LAALSPMKGASNFS---------- 33
AAL56646.pro M-----KWATLISIVIVLSCTESRIL-NKRHHHEGHVDNPPHLIGDLIPMIGVDNSKGLVLAAVSQMLPLCPYEEHLQRV 74
Q03156.pro M-----QWLSVCSLLVLLSVL--------------SRSQAQNQICTIFTEAKEDGFKSLILVGLAQNLPDSTLGDLVPLI 61
P21848.pro M-----QWLSVCSLLVLLSVL--------------SRSQAQNQICTIFTEAKEDGFKSLILVGLAQNLPDSTLGDLVPLI 61
AAM46104.pro ---------- 0
P83517.pro ------------------------------DAEHKSNICKHFQ----VVGEEKFKNIILVT---------- 27
S59517.pro M-----KWVIFISLLCLVSFAEVKNLPRRYRHVDDQHSTI-----RLASQISATDFGAITLTLVTQTVPNATLEDLKKLS 70
AAL08579.pro M-----KWVTFLLLLFVSDSAFSRGL---FRRDA-HKSEIAHRFKDL----GEQHFKGLVLIAFSQFLQKCPYEEHVKLV 67

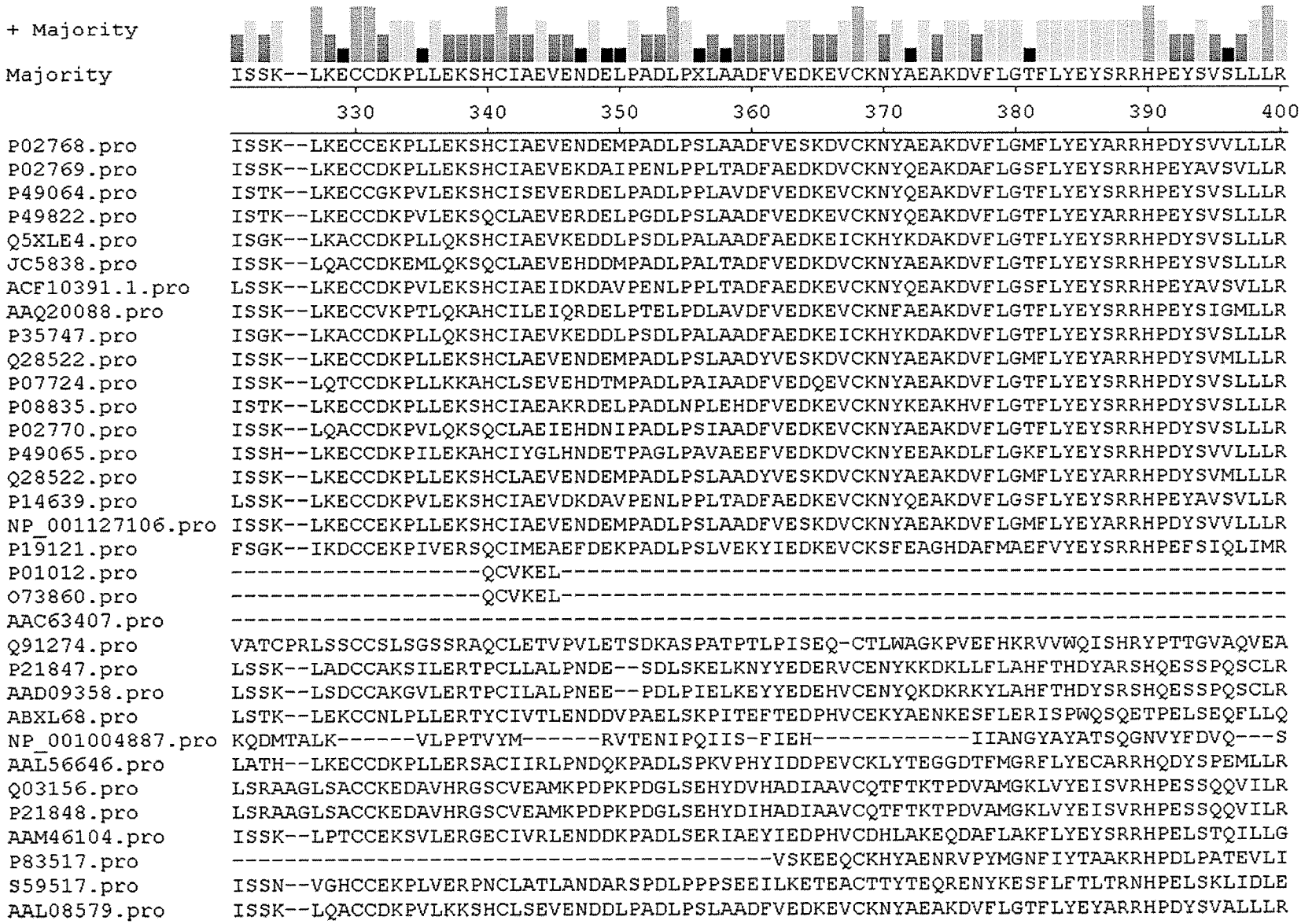


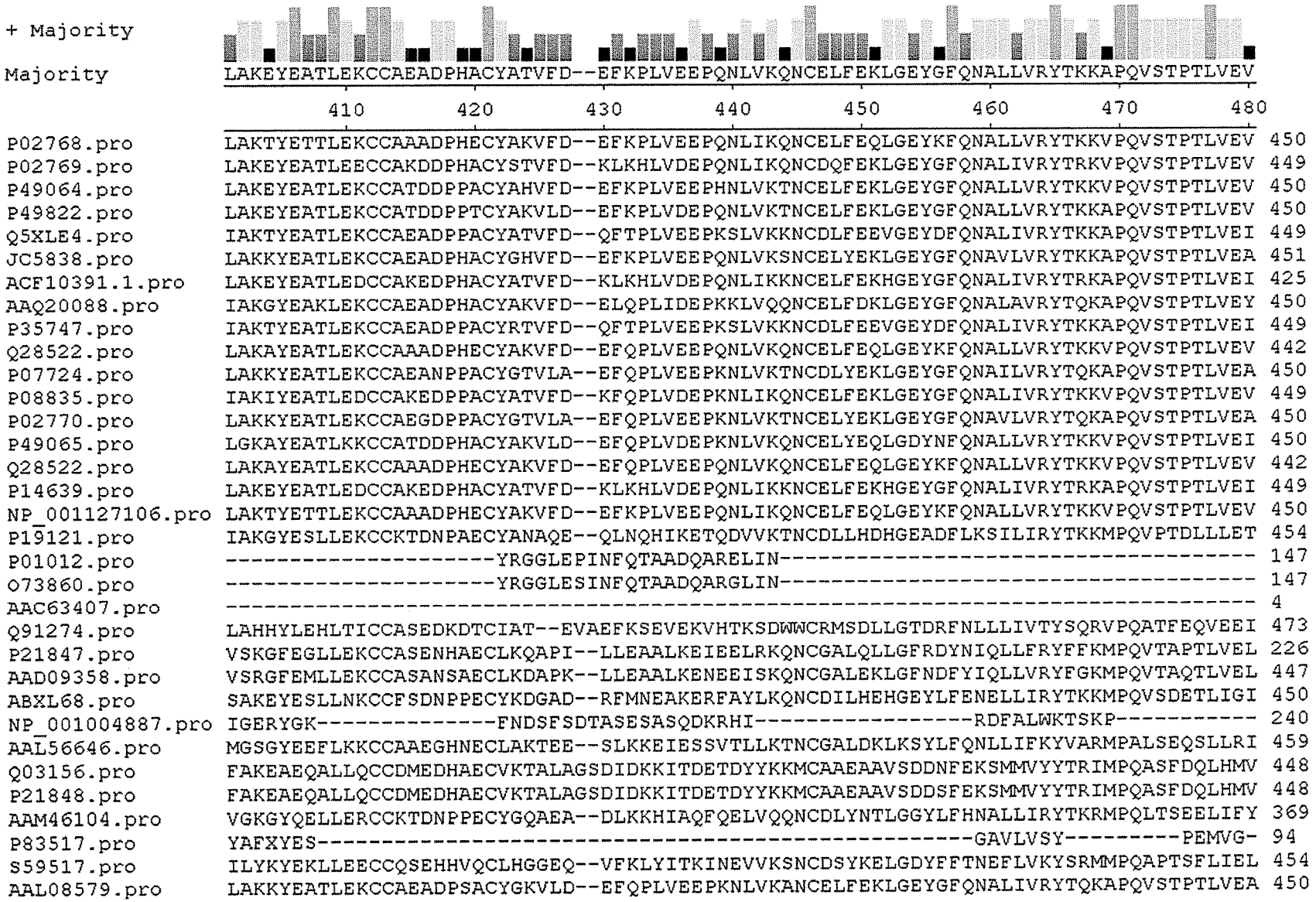

```
P02768.pro          NEVTEFAKTCVADE-SAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN------PNL-PRL 139
P02769.pro          NELTEFAKTCVADE-SHAGCEKSLHTLFGDELCKVASLRETYGDMADCCEKQEPERNECFLSHKDDS------PDL-PKL 139
P49064.pro          NEVTEFAKGCVADQ-SAANCEKSLHELLGDKLCTVASLRDKYGEMADCCEKKEPERNECFLQHKDDN------PGF-GQL 139
P49822.pro          KEVTEFAKACAAEE-SGANCDKSLHTLFGDKLCTVASLRDKYGDMADCCEKQEPDRNECFLAHKDDN------PGF-PPL 139
Q5XLE4.pro          NEVTEFAKKCAADE-SAENCDKSLHTLFGDKLCTVATLRATYGELADCCEKQEPERNECFLTHKDDH------PNL-PKL 139
JC5838.pro          REVTDFASNCAKDE-SAENCDKSLHTLFGDKLCSLPNFGEKYAEMADCCAKQEPERNECFLQHKDDN------PQL-PPF 140
ACF10391.1.pro      KELTEFAKTCVADE-SHAGCDKSLHTLFGDELCKVATLRETYGDMADCCEKQEPERNECFLKHKDDS------PDL-PKL 115
AAQ20088.pro        NEVTDFAKACVADE-SAQNCGKAIATLFGDKVCAIPSLRETYGELADCCAKEDPDRVECFLQHKDDN------PNL-PPF 139
P35747.pro          NEVTEFAKKCAADE-SAENCDKSLHTLFGDKLCTVATLRATYGELADCCEKQEPERNECFLTHKDDH------PNL-PKL 139
Q28522.pro          NEVTEFAKTCVADE-SAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN------PNL-PPL 131
P07724.pro          QEVTDFAKTCVADE-SAANCDKSLHTLFGDKLCAIPNLRENYGELADCCTKQEPERNECFLQHKDDN------PSL-PPF 139
P08835.pro          REVTEFAKTCVADE-SAENCDKSIHTLFGDKLCAIPSLREHYGDLADCCEKEEPERNECFLQHKNDN------PDI-PKL 139
P02770.pro          QEVTDFAKTCVADE-NAENCDKSIHTLFGDKLCAIPKLRDNYGELADCCAKQEPERNECFLQHKDDN------PNL-PPF 139
P49065.pro          KEVTDLAKACVADE-SAANCDKSLHDIFGDKICALPSLRDTYGDVADCCEKKEPERNECFLHHKDDK------PDL-PPF 139
Q28522.pro          NEVTEFAKTCVADE-SAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN------PNL-PPL 131
P14639.pro          KELTEFAKTCVADE-SHAGCDKSLHTLFGDELCKVATLRETYGDMADCCEKQEPERNECFLNHKDDS------PDL-PKL 139
NP_001127106.pro    NEVTEFAKTCVADE-SAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN------PNL-PRL 139
P19121.pro          KDVVDLAQKCVANE-DAPECSKPLPSIILDEICQVEKLRDSYGAMADCCSKADPERNECFLSFKVSQ------PDFVQPY 143
P01012.pro          NKVVRFDKLPGFGDSIEAQCGTSVNV----------------------------------------------HSSLRDILNQI 91
O73860.pro          NKVVRFDKLPGFGDSVEAQCGTSVNV----------------------------------------------HSSLRDILNQI 91
AAC63407.pro        ------------------------------------------------------------------------------- 4
Q91274.pro          NHCLRIVKQCCAEG-AADDCLQTELAAVQEQVCTRMSEAKDVPLVGRCCALAGSERHDCFHHAGGVAEGEGAWPHALPVT 156
P21847.pro          ------------------------------------------------------------------------------- 1
AAD09358.pro        AKIIEAVDNCEKHP-EEAECKKPAIELYHDIVCKEEDIDQLYPWTTECCGKAEAERTKCFYEHREVR------VE---EY 138
ABXL68.pro          NEINDFAKSCTGND-KTPECEKPIGTLFYDKLCADPKVGVNYEWSKECCSKQDPERAQCFRAHRVFE------HN---PV 140
NP_001004887.pro    --------------------CGN---------VCASP--------------------AGCWAPPSGHDTGIKVYNSLTRRK 65
AAL56646.pro        EDVMQIADLCAKGA-RHANCAKSPMTIILDELCKKPENAEKYPFHQECCKKEDPERHKCFVEHKMAN------HEELTKY 147
Q03156.pro          AEALAMGVKCCSDT-PPEDCERDVADLFQSAVCSSETLVEK-NDLKMCCEKTAAERTHCFVDHKAKI------PRDLSLK 133
P21848.pro          AEALAMGVKCCSDT-PPEDCERDVADLFQSAVCSSETLVEK-NDLKMCCEKTAAERTHCFVDHKAKI------PRDLSLK 133
AAM46104.pro        ---------------EDPTCLKSLDTIFLDEICHEEGFAAKY-DLAACCAKAEVERKECLLAHKNAT------PGFIPAF 58
P83517.pro          ------------------------------------------------------------------------------- 27
S59517.pro          AEIIELHKKCVASEFSDPPCTKPLGIVFLDVLCHNEEFSNKYG-INDCCAKADPDRNECVLSHKTSS------TGTISPF 143
AAL08579.pro        NEVTDFAKTCVADE-SAENCDKSLHTLFGDKLCAIPTLRDSYGELADCCAKKEPERNECFLKHKDDH------PNL-PPF 139
```

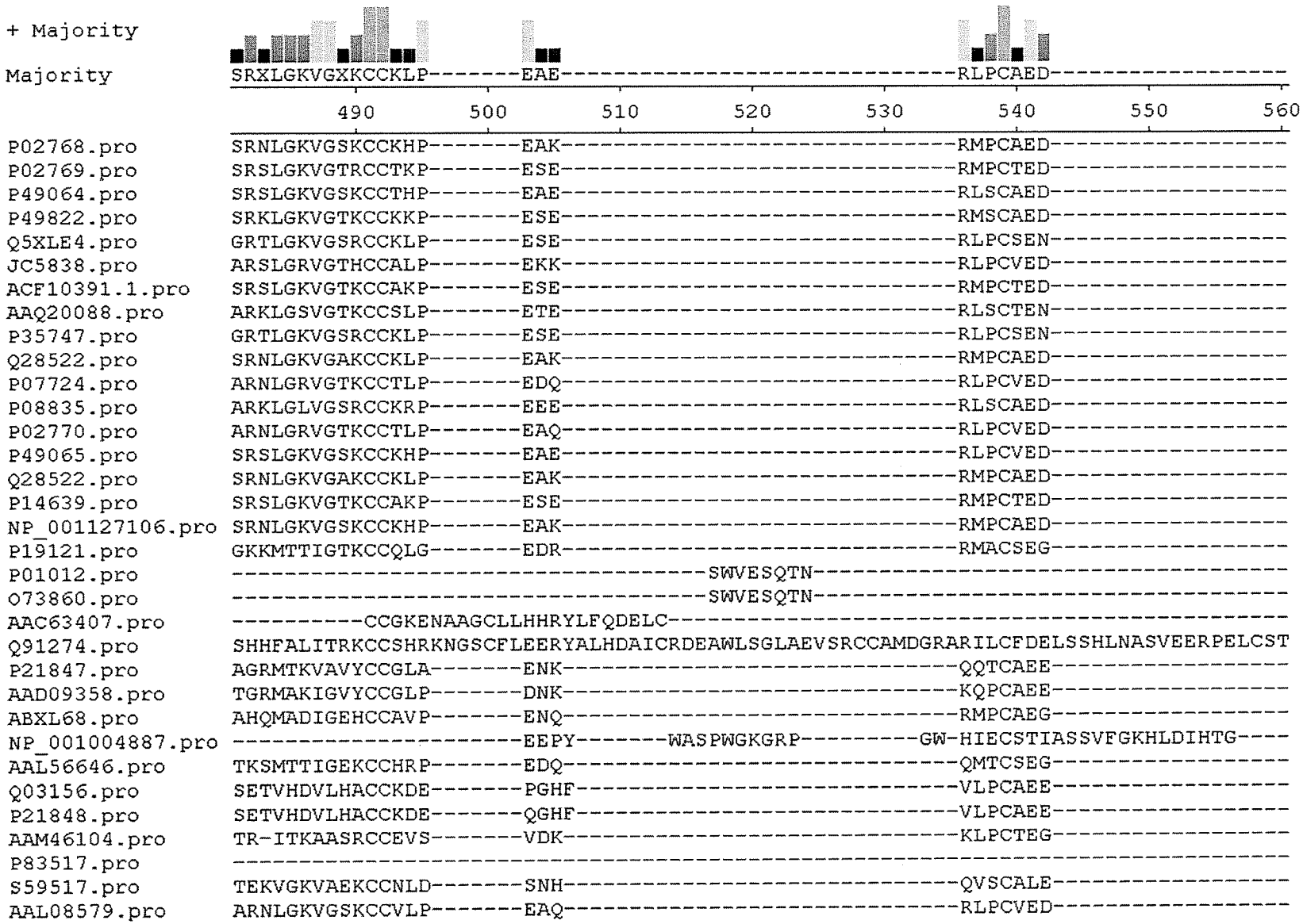


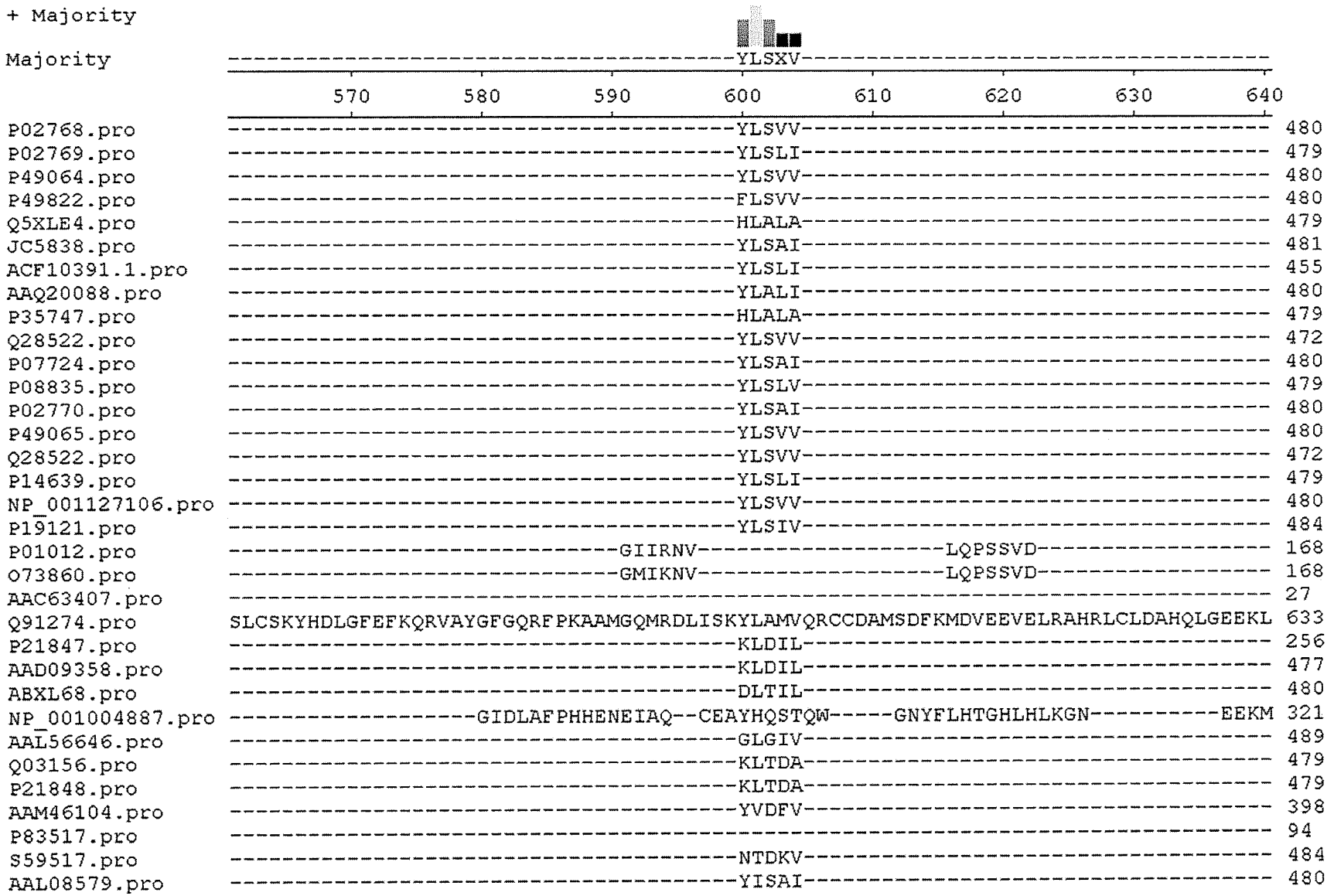

```
P02768.pro          VRPEVDVM--CTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAA-CLLPKLDELRDEGKAS 216
P02769.pro          -KPDPNTL--CDEFKADEKKFWGKYLYEIARRHPYFYAPELLYYANKYNGVFQECCQAEDKGA-CLLPKIETMREKVLAS 215
P49064.pro          VTPEADAM--CTAFHENEQRFLGKYLYEIARRHPYFYAPELLYYAEEYKGVFTECCEAADKAA-CLTPKVDALREKVLAS 216
P49822.pro          VAPEPDAL--CAAFQDNEQLFLGKYLYEIARRHPYFYAPELLYYAQQYKGVFAECCQAADKAA-CLGPKIEALREKVLLS 216
Q5XLE4.pro          -KPEPDAQ--CAAFQEDPDKFLGKYLYEVARRHPYFYGPELLFHAEEYKADFTECCPADDKAG-CLIPKLDALKERILLS 215
JC5838.pro          KRAEPDAM--CTAFQENAEAFMGHYLHEVARRHPYFYGPELLYLADKYTAVLTECCAADDKGA-CLTPKLDALKEKALVS 217
ACF10391.1.pro      -KPEPDTL--CAEFKADEKKFWGKYLYEVARRHPYFYAPELLYYANKYNGVFQECCQAEDKGA-CLLPKIETMREKVLAS 191
AAQ20088.pro        ERPEPEAL--CTAFKENNDRFIGHYLYEVSRRHPYFYAPELLYYAEKYKNALTECCEAADKAA-CLTPKLDAIKEKALVS 216
P35747.pro          -KPEPDAQ--CAAFQEDPDKFLGKYLYEVARRHPYFYGPELLFHAEEYKADFTECCPADDKLA-CLIPKLDALKERILLS 215
Q28522.pro          VRPEVDVM--CTAFHDNEATFLKKYLYEVARRHPYFYAPELLFFAARYKAAFAECCQAADKAA-CLLPKLDELRDEGKAS 208
P07724.pro          ERPEAEAM--CTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKES-CLTPKLDGVKEKALVS 216
P08835.pro          -KPDPVAL--CADFQEDEQKFWGKYLYEIARRHPYFYAPELLYYAIIYKDVFSECCQAADKAA-CLLPKIEHLREKVLTS 215
P02770.pro          QRPEAEAM--CTSFQENPTSFLGHYLHEVARRHPYFYAPELLYYAEKYNEVLTQCCTESDKAA-CLTPKLDAVKEKALVA 216
P49065.pro          ARPEADVL--CKAFHDDEKAFFGHYLYEVARRHPYFYAPELLYYAQKYKAILTECCEAADKGA-CLTPKLDALEGKSLIS 216
Q28522.pro          VRPEVDVM--CTAFHDNEATFLKKYLYEVARRHPYFYAPELLFFAARYKAAFAECCQAADKAA-CLLPKLDELRDEGKAS 208
P14639.pro          -KPEPDTL--CAEFKADEKKFWGKYLYEVARRHPYFYAPELLYYANKYNGVFQECCQAEDKGA-CLLPKIDAMREKVLAS 215
NP_001127106.pro    VRPEVDVM--CTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAA-CLLPKLDELRDEGKAS 216
P19121.pro          QRPASDVI--CQEYQDNRVSFLGHFIYSVARRHPFLYAPAILSFAVDFEHALQSCCKESDVGA-CLDTKEIVMREKAKGV 220
P01012.pro          TKPN------------------DVYSFSLASR---------LYAEERY------------------------------ 112
O73860.pro          TKPN------------------DVYSFSLASR---------LYAEETY------------------------------ 112
AAC63407.pro        ------------------------------------------------------------------------------- 4
Q91274.pro          SPPEYDSVTVCALHATANARLYDTLLWEFSRRYPSASDSHLIALANEFITGLTTCCLVEEEHGACLATLREDFKHKLTEA 236
P21847.pro          ------------------------------------------------------------------------------- 1
AAD09358.pro        KIPNIEES--CKEHKEHPQRAFSYYLSNIAKRHSKLYPPAVLGFAIQYNEITTECCAAEDKA-KCFGERMPQVKKLTNYL 215
ABXL68.pro          R-PKPEET--CALFKEHPDDLLSAFIHEEARNHPDLYPPAVLLLTQQYGKLVEHCCEEEDKD-KCFAEKMKELMKHSHSI 216
NP_001004887.pro    DPLILADPTVATWYSCGPTVY-----------------------------------DHAHLGHACSYVRFDIIRR----- 105
AAL56646.pro        VRPAPEQI--CKDHAENRGPLLARYIFMLAIGHPHMYIPAILGFAQRFDGIVSHCCKDVETAGQCFNDKMPEHKQEVEYV 225
Q03156.pro          AELPAADQ--CEDFKKDHKAFVGRFIFKFSKSNPMLPPHVVLAIAKGYGEVLTTCCGEAE-AQTCFDTKKATFQHAIAKR 210
P21848.pro          AELPAADQ--CEDFKKDHKAFVGRFIFKFSKSNPMLPPHVVLAIAKGYGEVLTTCCGEAE-AQTCFDTKKATFQHAVMKR 210
AAM46104.pro        QRPGIEVS--CKLYQDDRLTLLGNYIYEVARRHPYLQVPPVFATASLYDEALKTCCQTADKAT-CFHPRIPPLIEYLKMS 135
P83517.pro          -------------QDGHGPFIQ------------------------------------------------------- 36
S59517.pro          VHPNAEEA--CQAFQNDRDSVLAQYIFELSRRYPTALSVVILESTKTYKKILETCCAEADKDA-CIHEKATEAKKKFREI 220
AAL08579.pro        VRPDAEAM--CTSFQENAVTFMGHYLHEVARRHPYFYAPELLYYAEKYSAIMTECCGEADKAA-CITPKLDALKEKALAS 216
```

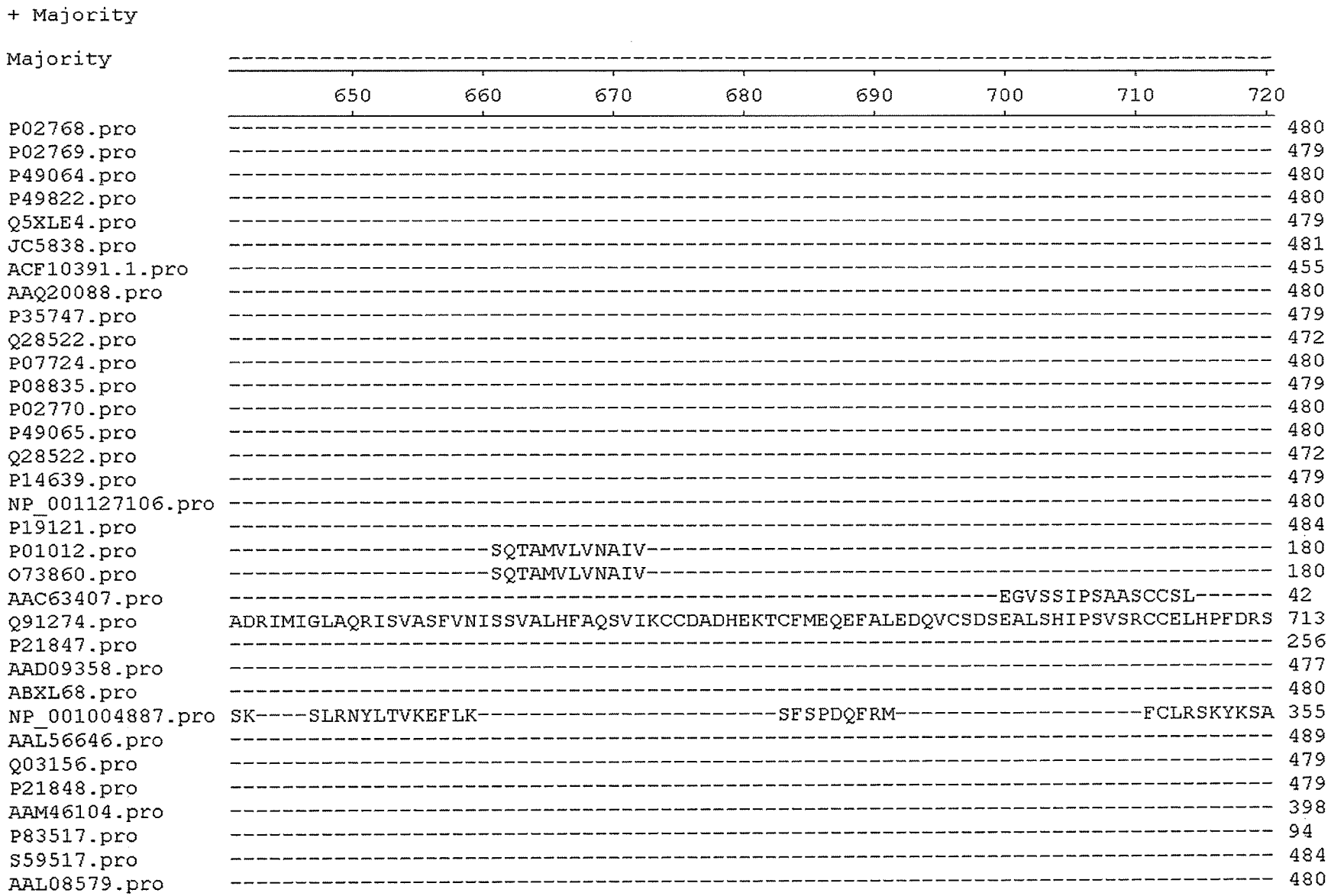

+ Majority
Majority
SAKQRLKCASLQKFGERAFKAWXVARLSQKFPKADFAEVSKLVTDLTKVHKECCH-GDLLECA-DDRADLAKYICENQDS
250
260
270
280
290
300
310
320
P02768.pro SAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCH-GDLLECA-DDRADLAKYICENQDS 294
P02769.pro SARQRLRCASIQKFGERALKAWSVARLSQKFPKAEFVEVTKLVTDLTKVHKECCH-GDLLECA-DDRADLAKYICDNQDT 293
P49064.pro SAKERLKCASLQKFGERAFKAWSVARLSQKFPKAEFAEISKLVTDLAKIHKECCH-GDLLECA-DDRADLAKYICENQDS 294
P49822.pro SAKERFKCASLQKFGDRAFKAWSVARLSQRFPKADFAEISKVVTDLTKVHKECCH-GDLLECA-DDRADLAKYMCENQDS 294
Q5XLE4.pro SAKERLKCSSFQKFGERAFKAWSVARLSQKFPKADFAEVSKIVTDLTKVHKECCH-GDLLECA-DDRADLTKYICEHQDS 293
JC5838.pro AVRQRLKCSSMKKFGERAFKAWAVARMSQTFPNADFAEITKLATDLTKVTQECCH-GDLLECA-DDRAELAKYMCENQAS 295
ACF10391.1.pro SARQRLRCASIQKFGERALKAWSVARLSQKFPKADFTDVTKIVTDLTKVHKECCH-GDLLECA-DDRADLAKYICDHQDT 269
AAQ20088.pro SAQQRLKCASLQKFGERAFKAWSVARLSQKFPKAEFAEISTIVTSLTKVTKECCH-GDLLECA-DDRQELAKYMCEHQDS 294
P35747.pro SAKERLKCSSFQNFGERAVKAWSVARLSQKFPKADFAEVSKIVTDLTKVHKECCH-GDLLECA-DDRADLAKYICEHQDS 293
Q28522.pro SAKQRLKCASLQKFGDRAFKAWAVARLSQKFPKAEFAEVSKLVTDLTKVHTECCH-GDLLECA-DDRADLAKYMCENQDS 286
P07724.pro SVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCH-GDLLECA-DDRAELAKYMCENQAT 294
P08835.pro AAKQRLKCASIQKFGERAFKAWSLARLSQRFPKADFTEISKIVTDLAKVHKECCH-GDLLECA-DDRADLAKYICENQDT 293
P02770.pro AVRQRMKCSSMQRFGERAFKAWAVARMSQRFPNAEFAEITKLATDVTKINKECCH-GDLLECA-DDRAELAKYMCENQAT 294
P49065.pro AAQERLRCASIQKFGDRAYKAWALVRLSQRFPKADFTDISKIVTDLTKVHKECCH-GDLLECA-DDRADLAKYMCEHQET 294
Q28522.pro SAKQRLKCASLQKFGDRAFKAWAVARLSQKFPKAEFAEVSKLVTDLTKVHTECCH-GDLLECA-DDRADLAKYMCENQDS 286
P14639.pro SARQRLRCASIQKFGERALKAWSVARLSQKFPKADFTDVTKIVTDLTKVHKECCH-GDLLECA-DDRADLAKYICDHQDA 293
NP_001127106.pro SAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCH-GDLLECA-DDRADLAKYICENQDS 294
P19121.pro SVKQQYFCGILKQFGDRVFQARQLIYLSQKYPKAPFSEVSKFVHDSIGVHKECCE-GDMVECM-DDMARMMSNLCSQQDV 298
P01012.pro ----------PILPEYL------ 119
O73860.pro ----------PILPEYL------ 119
AAC63407.pro ---------- 4
Q91274.pro SHKSQNLCKALKSLGKEKFEDRIIVRFTQRAPQAPFELIQKLAHRFEVLAEKCCELGHSDRCLVEERYTVDDELCLEQSF 316
P21847.pro -------CRIIREFPDIVFKGLTLVQVSQKFGKAGFEDVKKVTEEIVHLNEDCCK-GDAVECM-MERMEATDHICEAKDK 72
AAD09358.pro EDKHKQKCRVLKEFPERVSQALTLVQVSQRFGNAKYDDVEKVTIEIAHLNEDCCK-GDAVECM-IERMEATEHICLAKEK 293
ABXL68.pro EDKQKHFCWIVNNYPERVIKALNLARVSHRYPKPDFKLAHKFTEETTHFIKDCCH-GDMFECM-TERLELSEHTCQHKDE 294
NP_001004887.pro --------ILLKVFGIDTVVVMVVTDIDDKIIKRA-KELNISPVALARTY----------EQDF 150
AAL56646.pro CALQKHNCYILQDFKERALTAYKAVQASQKFPLASFENVQIIVPDTVHLHQTCCG-GDMMACM-LERMKLTAKICEKKDE 303
Q03156.pro VAELKSLCIVHKKYGDRVVKAKKLVQYSQKMPQASFQEMAGMVDKIVATVAPCCS-GDMVTCM-KERKTLVDEVCADESV 288
P21848.pro VAELRSLCIVHKKYGDRVVKAKKLVQYSQKMPQASFQEMGGMVDKIVATVAPCCS-GDMVTCM-KERKTLVDEVCADESV 288
AAM46104.pro NGIQENTCGILKKFGERTLKATKLVQMSQKFPKADFATINKLVEDITHMHTECCR-GDTLECL-RDREALTEYTCSHKDA 213
P83517.pro ---------- 36
S59517.pro MEEQEYTCYNLKKYGKDKLYALKFIETHEKFVNAKLETITGIAEFVVHIYEEICM-GDSVDVL-VDRAALSQYVCEHKDA 298
AAL08579.pro SVNQRLKCSSLQRFGQRAFKAWAVARMSQKFPKADFAEITKLATDLTKLTEECCH-GDLLECA-DDRAELAKYMCENQAS 294

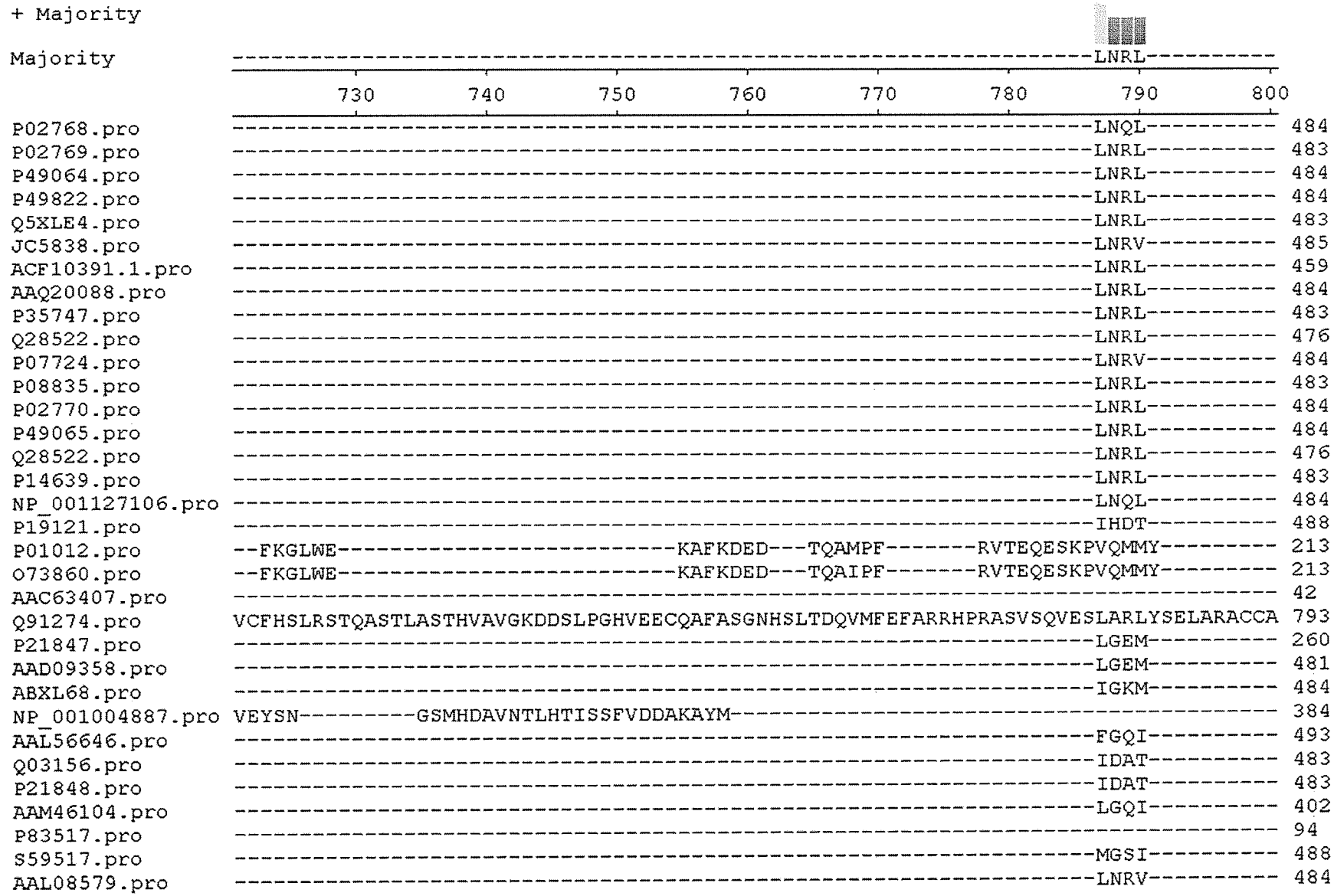

+ Majority
Majority
ISSK--LKECCDKPLLEKSHCIAEVENDELPADLPXLAADFVEDKEVCKNYAEAKDVFLGTFLYEYSRRHPEYSVSLLLR
330
340
350
360
370
380
390
400
P02768.pro ISSK--LKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLR 372
P02769.pro ISSK--LKECCDKPLLEKSHCIAEVEKDAIPENLPPLTADFAEDKDVCKNYQEAKDAFLGSFLYEYSRRHPEYAVSVLLR 371
P49064.pro ISTK--LKECCGKPVLEKSHCISEVERDELPADLPPLAVDFVEDKEVCKNYQEAKDVFLGTFLYEYSRRHPEYSVSLLLR 372
P49822.pro ISTK--LKECCDKPVLEKSQCLAEVERDELPGDLPSLAADFVEDKEVCKNYQEAKDVFLGTFLYEYARRHPEYSVSLLLR 372
Q5XLE4.pro ISGK--LKACCDKPLLQKSHCIAEVKEDDLPSDLPALAADFAEDKEICKHYKDAKDVFLGTFLYEYSRRHPDYSVSLLLR 371
JC5838.pro ISSK--LQACCDKEMLQKSQCLAEVEHDDMPADLPALTADFVEDKDVCKNYAEAKDVFLGTFLYEYSRRHPEYSVSLLLR 373
ACF10391.1.pro LSSK--LKECCDKPVLEKSHCIAEIDKDAVPENLPPLTADFAEDKEVCKNYQEAKDVFLGSFLYEYSRRHPEYAVSVLLR 347
AAQ20088.pro ISSK--LKECCVKPTLQKAHCILEIQRDELPTELPDLAVDFVEDKEVCKNFAEAKDVFLGTFLYEYSRRHPEYSIGMLLR 372
P35747.pro ISGK--LKACCDKPLLQKSHCIAEVKEDDLPSDLPALAADFAEDKEICKHYKDAKDVFLGTFLYEYSRRHPDYSVSLLLR 371
Q28522.pro ISSK--LKECCDKPLLEKSHCLAEVENDEMPADLPSLAADYVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVMLLLR 364
P07724.pro ISSK--LQTCCDKPLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLR 372
P08835.pro ISTK--LKECCDKPLLEKSHCIAEAKRDELPADLNPLEHDFVEDKEVCKNYKEAKHVFLGTFLYEYSRRHPDYSVSLLLR 371
P02770.pro ISSK--LQACCDKPVLQKSQCLAEIEHDNIPADLPSIAADFVEDKEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLR 372
P49065.pro ISSH--LKECCDKPILEKAHCIYGLHNDETPAGLPAVAEEFVEDKDVCKNYEEAKDLFLGKFLYEYSRRHPDYSVVLLLR 372
Q28522.pro ISSK--LKECCDKPLLEKSHCLAEVENDEMPADLPSLAADYVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVMLLLR 364
P14639.pro LSSK--LKECCDKPVLEKSHCIAEVDKDAVPENLPPLTADFAEDKEVCKNYQEAKDVFLGSFLYEYSRRHPEYAVSVLLR 371
NP_001127106.pro ISSK--LKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLR 372
P19121.pro FSGK--IKDCCEKPIVERSQCIMEAEFDEKPADLPSLVEKYIEDKEVCKSFEAGHDAFMAEFVYEYSRRHPEFSIQLIMR 376
P01012.pro ----------QCVKEL---------- 125
O73860.pro ----------QCVKEL---------- 125
AAC63407.pro ---------- 4
Q91274.pro VATCPRLSSCCSLSGSSRAQCLETVPVLETSDKASPATPTLPISEQ-CTLWAGKPVEFHKRVVWQISHRYPTTGVAQVEA 395
P21847.pro LSSK--LADCCAKSILERTPCLLALPNDE--SDLSKELKNYYEDERVCENYKKDKLLFLAHFTHDYARSHQESSPQSCLR 148
AAD09358.pro LSSK--LSDCCAKGVLERTPCILALPNEE--PDLPIELKEYYEDEHVCENYQKDKRKYLAHFTHDYSRSHQESSPQSCLR 369
ABXL68.pro LSTK--LEKCCNLPLLERTYCIVTLENDDVPAELSKPITEFTEDPHVCEKYAENKESFLERISPWQSQETPELSEQFLLQ 372
NP_001004887.pro KQDMTALK------VLPPTVYM------RVTENIPQIIS-FIEH----------IIANGYAYATSQGNVYFDVQ---S 202
AAL56646.pro LATH--LKECCDKPLLERSACIIRLPNDQKPADLSPKVPHYIDDPEVCKLYTEGGDTFMGRFLYECARRHQDYSPEMLLR 381
Q03156.pro LSRAAGLSACCKEDAVHRGSCVEAMKPDPKPDGLSEHYDVHADIAAVCQTFTKTPDVAMGKLVYEISVRHPESSQQVILR 368
P21848.pro LSRAAGLSACCKEDAVHRGSCVEAMKPDPKPDGLSEHYDIHADIAAVCQTFTKTPDVAMGKLVYEISVRHPESSQQVILR 368
AAM46104.pro ISSK--LPTCCEKSVLERGECIVRLENDDKPADLSERIAEYIEDPHVCDHLAKEQDAFLAKFLYEYSRRHPELSTQILLG 291
P83517.pro ----------VSKEEQCKHYAENRVPYMGNFIYTAAKRHPDLPATEVLI 75
S59517.pro ISSN--VGHCCEKPLVERPNCLATLANDARSPDLPPPSEEILKETEACTTYTEQRENYKESFLFTLTRNHPELSKLIDLE 376
AAL08579.pro ISSK--LQACCDKPVLKKSHCLSEVENDDLPADLPSLAADFVEDKEVCKNYAEAKDVFLGTFLYEYARRHPDYSVALLLR 372

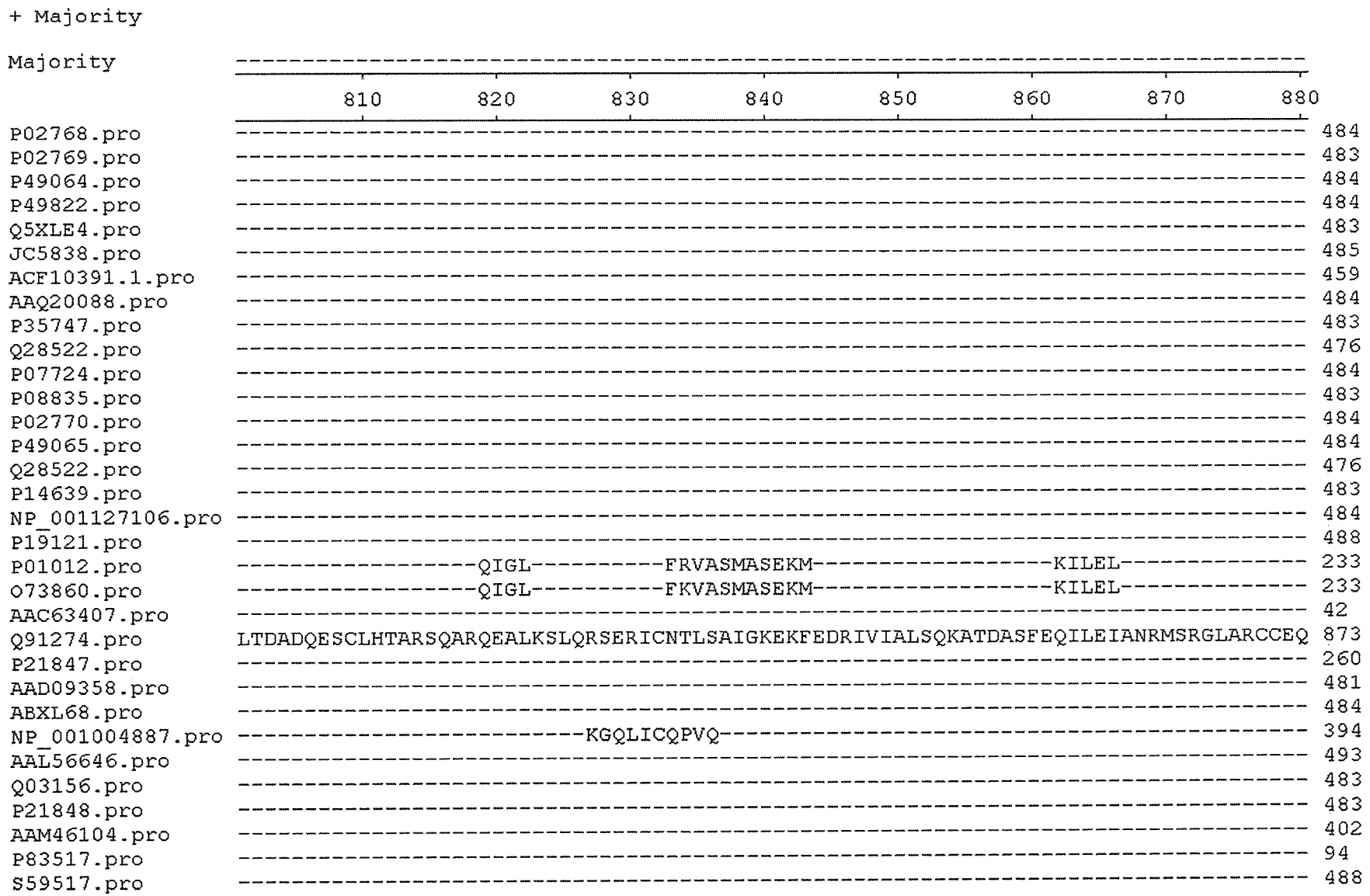

+ Majority
Majority
LAKEYEATLEKCCAEADPHACYATVFD--EFKPLVEEPQNLVKQNCELFEKLGEYGFQNALLVRYTKKAPQVSTPTLVEV
410
420
430
440
450
460
470
480
P02768.pro LAKTYETTLEKCCAAADPHECYAKVFD--EFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEV 450
P02769.pro LAKEYEATLEECCAKDDPHACYSTVFD--KLKHLVDEPQNLIKQNCDQFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEV 449
P49064.pro LAKEYEATLEKCCATDDPPACYAHVFD--EFKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEV 450
P49822.pro LAKEYEATLEKCCATDDPPTCYAKVLD--EFKPLVDEPQNLVKTNCELFEKLGEYGFQNALLVRYTKKAPQVSTPTLVEV 450
Q5XLE4.pro IAKTYEATLEKCCAEADPPACYATVFD--QFTPLVEEPKSLVKKNCDLFEEVGEYDFQNALIVRYTKKAPQVSTPTLVEI 449
JC5838.pro LAKKYEATLEKCCAEADPHACYGHVFD--EFKPLVEEPQNLVKSNCELYEKLGEYGFQNAVLVRYTKKAPQVSTPTLVEA 451
ACF10391.1.pro LAKEYEATLEDCCAKEDPHACYATVFD--KLKHLVDEPQNLIKKNCELFEKHGEYGFQNALIVRYTRKAPQVSTPTLVEI 425
AAQ20088.pro IAKGYEAKLEKCCAEADPHACYAKVFD--ELQPLIDEPKKLVQQNCELFDKLGEYGFQNALAVRYTQKAPQVSTPTLVEY 450
P35747.pro IAKTYEATLEKCCAEADPPACYRTVFD--QFTPLVEEPKSLVKKNCDLFEEVGEYDFQNALIVRYTKKAPQVSTPTLVEI 449
Q28522.pro LAKAYEATLEKCCAAADPHECYAKVFD--EFQPLVEEPQNLVKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEV 442
P07724.pro LAKKYEATLEKCCAEANPPACYGTVLA--EFQPLVEEPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEA 450
P08835.pro IAKIYEATLEDCCAKEDPPACYATVFD--KFQPLVDEPKNLIKQNCELFEKLGEYGFQNALIVRYTKKVPQVSTPTLVEV 449
P02770.pro LAKKYEATLEKCCAEGDPPACYGTVLA--EFQPLVEEPKNLVKTNCELYEKLGEYGFQNAVLVRYTQKAPQVSTPTLVEA 450
P49065.pro LGKAYEATLKKCCATDDPHACYAKVLD--EFQPLVDEPKNLVKQNCELYEQLGDYNFQNALLVRYTKKVPQVSTPTLVEI 450
Q28522.pro LAKAYEATLEKCCAAADPHECYAKVFD--EFQPLVEEPQNLVKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEV 442
P14639.pro LAKEYEATLEDCCAKEDPHACYATVFD--KLKHLVDEPQNLIKKNCELFEKHGEYGFQNALIVRYTRKAPQVSTPTLVEI 449
NP_001127106.pro LAKTYETTLEKCCAAADPHECYAKVFD--EFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEV 450
P19121.pro IAKGYESLLEKCCKTDNPAECYANAQE--QLNQHIKETQDVVKTNCDLLHDHGEADFLKSILIRYTKKMPQVPTDLLLET 454
P01012.pro ----------YRGGLEPINFQTAADQARELIN---------- 147
O73860.pro ----------YRGGLESINFQTAADQARGLIN---------- 147
AAC63407.pro ---------- 4
Q91274.pro LAHHYLEHLTICCASEDKDTCIAT--EVAEFKSEVEKVHTKSDWWCRMSDLLGTDRFNLLLIVTYSQRVPQATFEQVEEI 473
P21847.pro VSKGFEGLLEKCCASENHAECLKQAPI--LLEAALKEIEELRKQNCGALQLLGFRDYNIQLLFRYFFKMPQVTAPTLVEL 226
AAD09358.pro VSRGFEMLLEKCCASANSAECLKDAPK--LLEAALKENEEISKQNCGALEKLGFNDFYIQLLVRYFGKMPQVTAQTLVEL 447
ABXL68.pro SAKEYESLLNKCCFSDNPPECYKDGAD--RFMNEAKERFAYLKQNCDILHEHGEYLFENELLIRYTKKMPQVSDETLIGI 450
NP_001004887.pro IGERYGK----------FNDSFSDTASESASQDKRHI----------RDFALWKTSKP---------- 240
AAL56646.pro MGSGYEEFLKKCCAAEGHNECLAKTEE--SLKKEIESSVTLLKTNCGALDKLKSYLFQNLLIFKYVARMPALSEQSLLRI 459
Q03156.pro FAKEAEQALLQCCDMEDHAECVKTALAGSDIDKKITDETDYYKKMCAAEAAVSDDNFEKSMMVYYTRIMPQASFDQLHMV 448
P21848.pro FAKEAEQALLQCCDMEDHAECVKTALAGSDIDKKITDETDYYKKMCAAEAAVSDDSFEKSMMVYYTRIMPQASFDQLHMV 448
AAM46104.pro VGKGYQELLERCCKTDNPPECYGQAEA--DLKKHIAQFQELVQQNCDLYNTLGGYLFHNALLIRYTKRMPQLTSEELIFY 369
P83517.pro YAFXYES----------GAVLVSY---------PEMVG- 94
S59517.pro ILYKYEKLLEECCQSEHHVQCLHGGEQ--VFKLYITKINEVVKSNCDSYKELGDYFFTNEFLVKYSRMMPQAPTSFLIEL 454
AAL08579.pro LAKKYEATLEKCCAEADPSACYGKVLD--EFQPLVEEPKNLVKANCELFEKLGEYGFQNALIVRYTQKAPQVSTPTLVEA 450

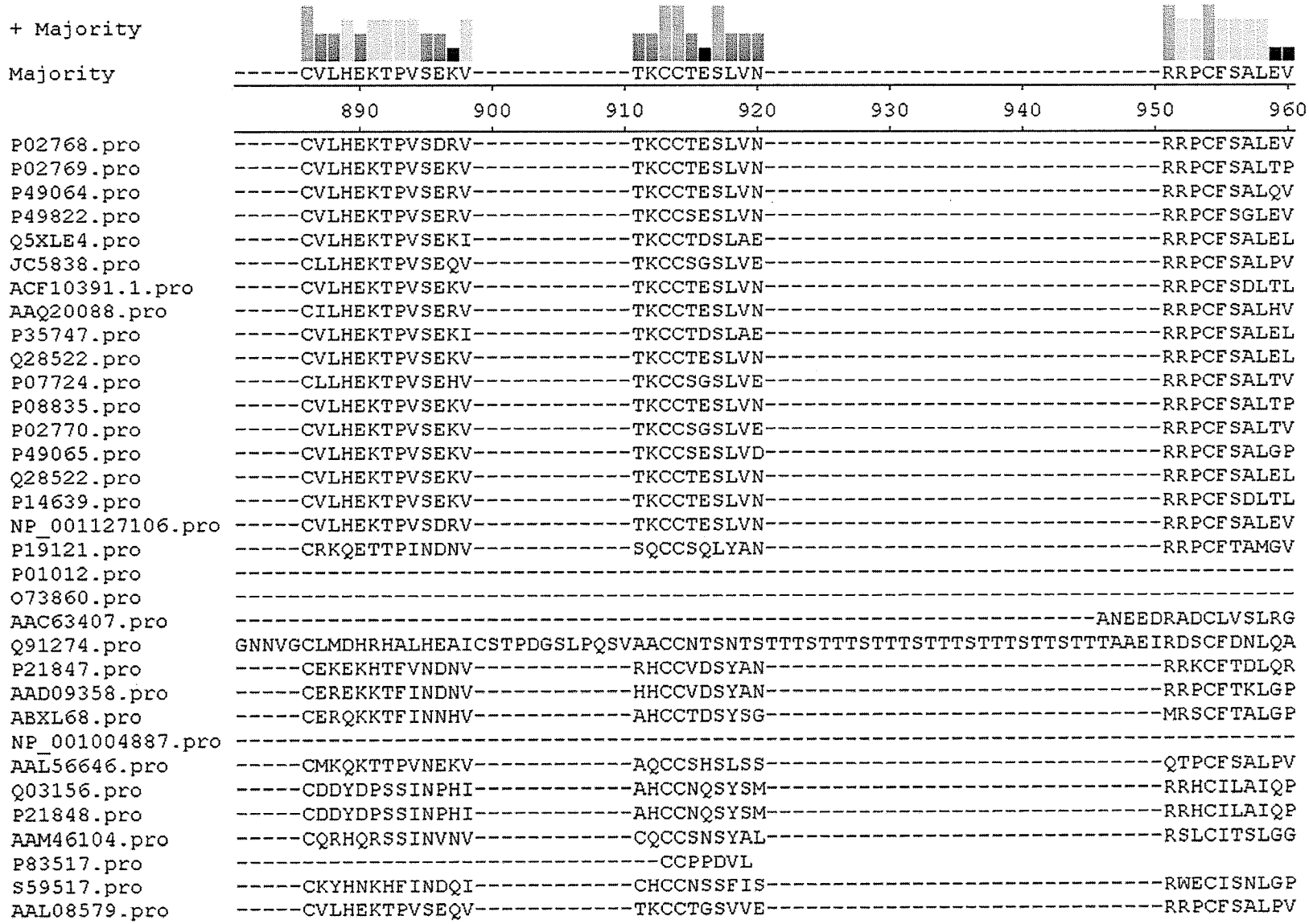

+ Majority
Majority
SRXLGKVGXKCCKLP-------EAE--------------------------------RLPCAED----------
490
500
510
520
530
540
550
560
P02768.pro SRNLGKVGSKCCKHP-------EAK--------------------------------RMPCAED---------- 475
P02769.pro SRSLGKVGTRCCTKP-------ESE--------------------------------RMPCTED---------- 474
P49064.pro SRSLGKVGSKCCTHP-------EAE--------------------------------RLSCAED---------- 475
P49822.pro SRKLGKVGTKCCKKP-------ESE--------------------------------RMSCAED---------- 475
Q5XLE4.pro GRTLGKVGSRCCKLP-------ESE--------------------------------RLPCSEN---------- 474
JC5838.pro ARSLGRVGTHCCALP-------EKK--------------------------------RLPCVED---------- 476
ACF10391.1.pro SRSLGKVGTKCCAKP-------ESE--------------------------------RMPCTED---------- 450
AAQ20088.pro ARKLGSVGTKCCSLP-------ETE--------------------------------RLSCTEN---------- 475
P35747.pro GRTLGKVGSRCCKLP-------ESE--------------------------------RLPCSEN---------- 474
Q28522.pro SRNLGKVGAKCCKLP-------EAK--------------------------------RMPCAED---------- 467
P07724.pro ARNLGRVGTKCCTLP-------EDQ--------------------------------RLPCVED---------- 475
P08835.pro ARKLGLVGSRCCKRP-------EEE--------------------------------RLSCAED---------- 474
P02770.pro ARNLGRVGTKCCTLP-------EAQ--------------------------------RLPCVED---------- 475
P49065.pro SRSLGKVGSKCCKHP-------EAE--------------------------------RLPCVED---------- 475
Q28522.pro SRNLGKVGAKCCKLP-------EAK--------------------------------RMPCAED---------- 467
P14639.pro SRSLGKVGTKCCAKP-------ESE--------------------------------RMPCTED---------- 474
NP_001127106.pro SRNLGKVGSKCCKHP-------EAK--------------------------------RMPCAED---------- 475
P19121.pro GKKMTTIGTKCCQLG-------EDR--------------------------------RMACSEG---------- 479
P01012.pro ----------SWVESQTN---------- 155
O73860.pro ----------SWVESQTN---------- 155
AAC63407.pro ----------CCGKENAAGCLLHHRYLFQDELC---------- 27
Q91274.pro SHHFALITRKCCSHRKNGSCFLEERYALHDAICRDEAWLSGLAEVSRCCAMDGRARILCFDELSSHLNASVEERPELCST 553
P21847.pro AGRMTKVAVYCCGLA-------ENK--------------------------------QQTCAEE---------- 251
AAD09358.pro TGRMAKIGVYCCGLP-------DNK--------------------------------KQPCAEE---------- 472
ABXL68.pro AHQMADIGEHCCAVP-------ENQ--------------------------------RMPCAEG---------- 475
NP_001004887.pro ----------EEPY-------WASPWGKGRP---------GW-HIECSTIASSVFGKHLDIHTG---- 277
AAL56646.pro TKSMTTIGEKCCHRP-------EDQ--------------------------------QMTCSEG---------- 484
Q03156.pro SETVHDVLHACCKDE-------PGHF--------------------------------VLPCAEE---------- 474
P21848.pro SETVHDVLHACCKDE-------QGHF--------------------------------VLPCAEE---------- 474
AAM46104.pro TR-ITKAASRCCEVS-------VDK--------------------------------KLPCTEG---------- 393
P83517.pro ---------- 94
S59517.pro TEKVGKVAEKCCNLD-------SNH--------------------------------QVSCALE---------- 479
AAL08579.pro ARNLGKVGSKCCVLP-------EAQ--------------------------------RLPCVED---------- 475

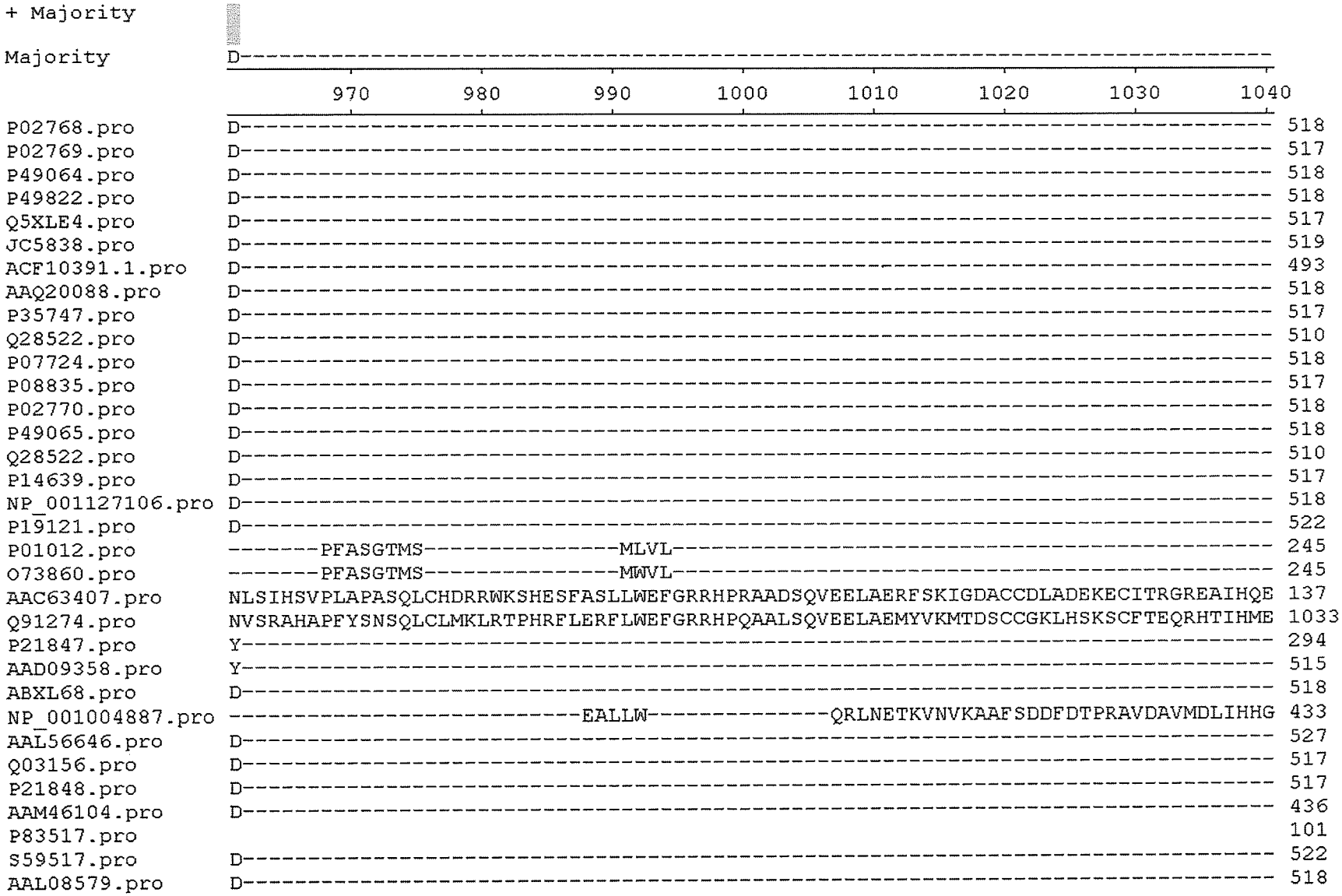

+ Majority
Majority
570
580
590
600
610
620
630
640
P02768.pro
P02769.pro
P49064.pro
P49822.pro
Q5XLE4.pro
JC5838.pro
ACF10391.1.pro
AAQ20088.pro
P35747.pro
Q28522.pro
P07724.pro
P08835.pro
P02770.pro
P49065.pro
Q28522.pro
P14639.pro
NP_001127106.pro
P19121.pro
P01012.pro
O73860.pro
AAC63407.pro
Q91274.pro
P21847.pro
AAD09358.pro
ABXL68.pro
NP_001004887.pro
AAL56646.pro
Q03156.pro
P21848.pro
AAM46104.pro
P83517.pro
S59517.pro
AAL08579.pro

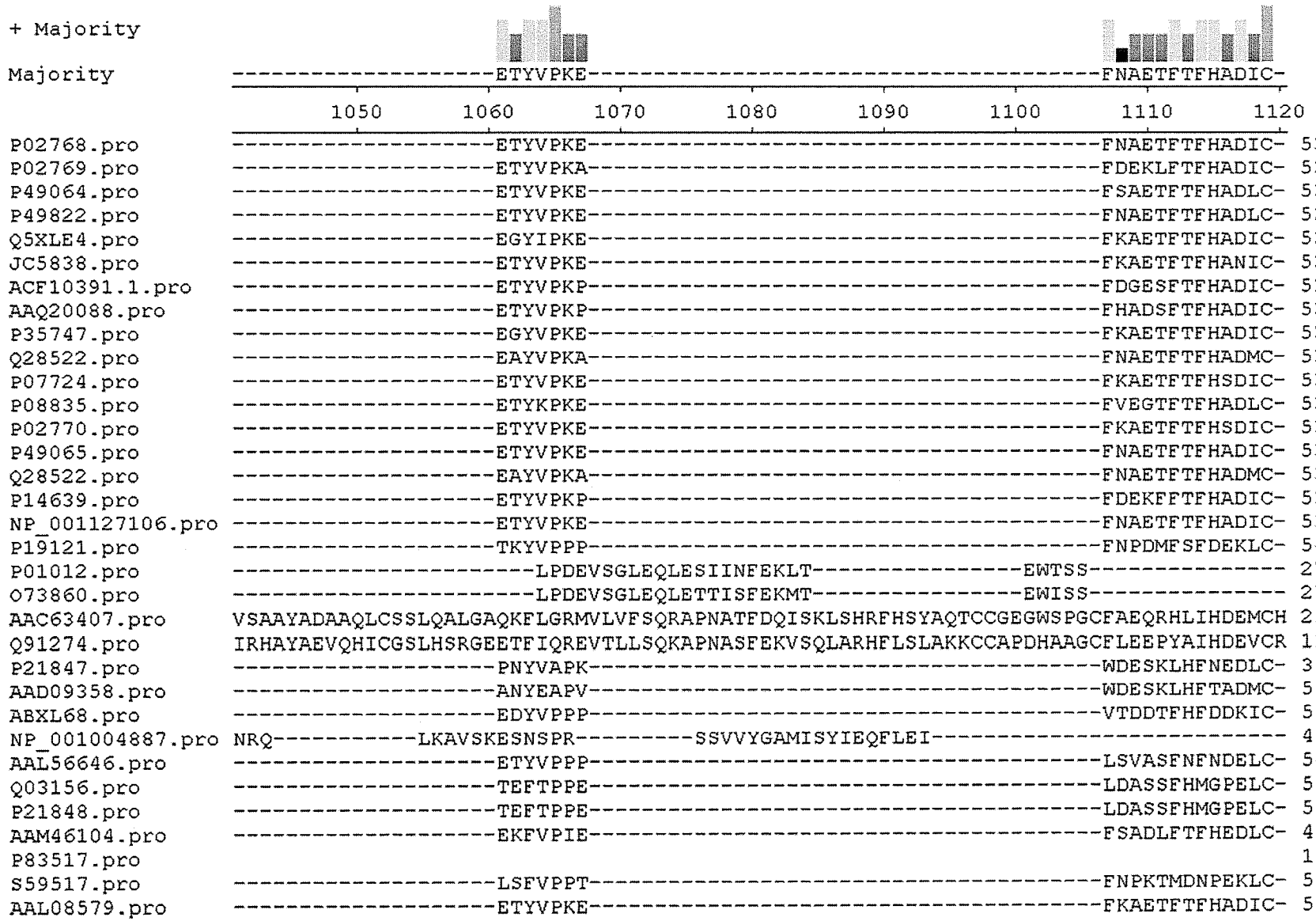

+ Majority
Majority
650
660
670
680
690
700
710
720
P02768.pro 480
P02769.pro 479
P49064.pro 480
P49822.pro 480
Q5XLE4.pro 479
JC5838.pro 481
ACF10391.1.pro 455
AAQ20088.pro 480
P35747.pro 479
Q28522.pro 472
P07724.pro 480
P08835.pro 479
P02770.pro 480
P49065.pro 480
Q28522.pro 472
P14639.pro 479
NP_001127106.pro 480
P19121.pro 484
P01012.pro SQTAMVLVNAIV 180
O73860.pro SQTAMVLVNAIV 180
AAC63407.pro EGVSSIPSAASCCSL 42
Q91274.pro ADRIMIGLAQRISVASFVNISSVALHFAQSVIKCCDADHEKTCFMEQEFALEDQVCSDSEALSHIPSVSRCCELHPFDRS 713
P21847.pro 256
AAD09358.pro 477
ABXL68.pro 480
NP_001004887.pro SK----SLRNYLTVKEFLK----------SFSPDQFRM----------FCLRSKYKSA 355
AAL56646.pro 489
Q03156.pro 479
P21848.pro 479
AAM46104.pro 398
P83517.pro 94
S59517.pro 484
AAL08579.pro 480

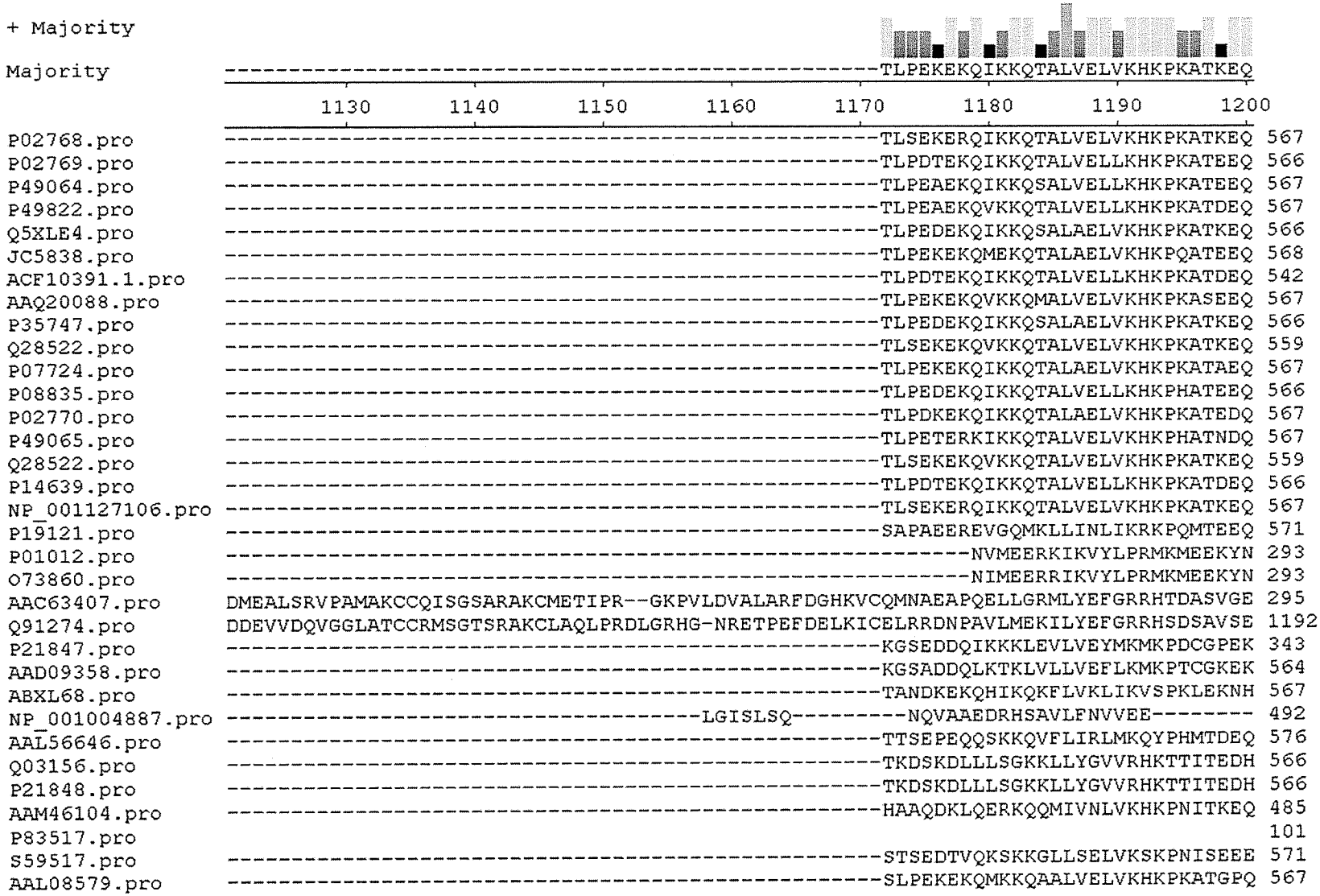

+ Majority
Majority
730
740
750
760
770
780
790
800
P02768.pro
P02769.pro
P49064.pro
P49822.pro
Q5XLE4.pro
JC5838.pro
ACF10391.1.pro
AAQ20088.pro
P35747.pro
Q28522.pro
P07724.pro
P08835.pro
P02770.pro
P49065.pro
Q28522.pro
P14639.pro
NP_001127106.pro
P19121.pro
P01012.pro
O73860.pro
AAC63407.pro
Q91274.pro
P21847.pro
AAD09358.pro
ABXL68.pro
NP_001004887.pro
AAL56646.pro
Q03156.pro
P21848.pro
AAM46104.pro
P83517.pro
S59517.pro
AAL08579.pro

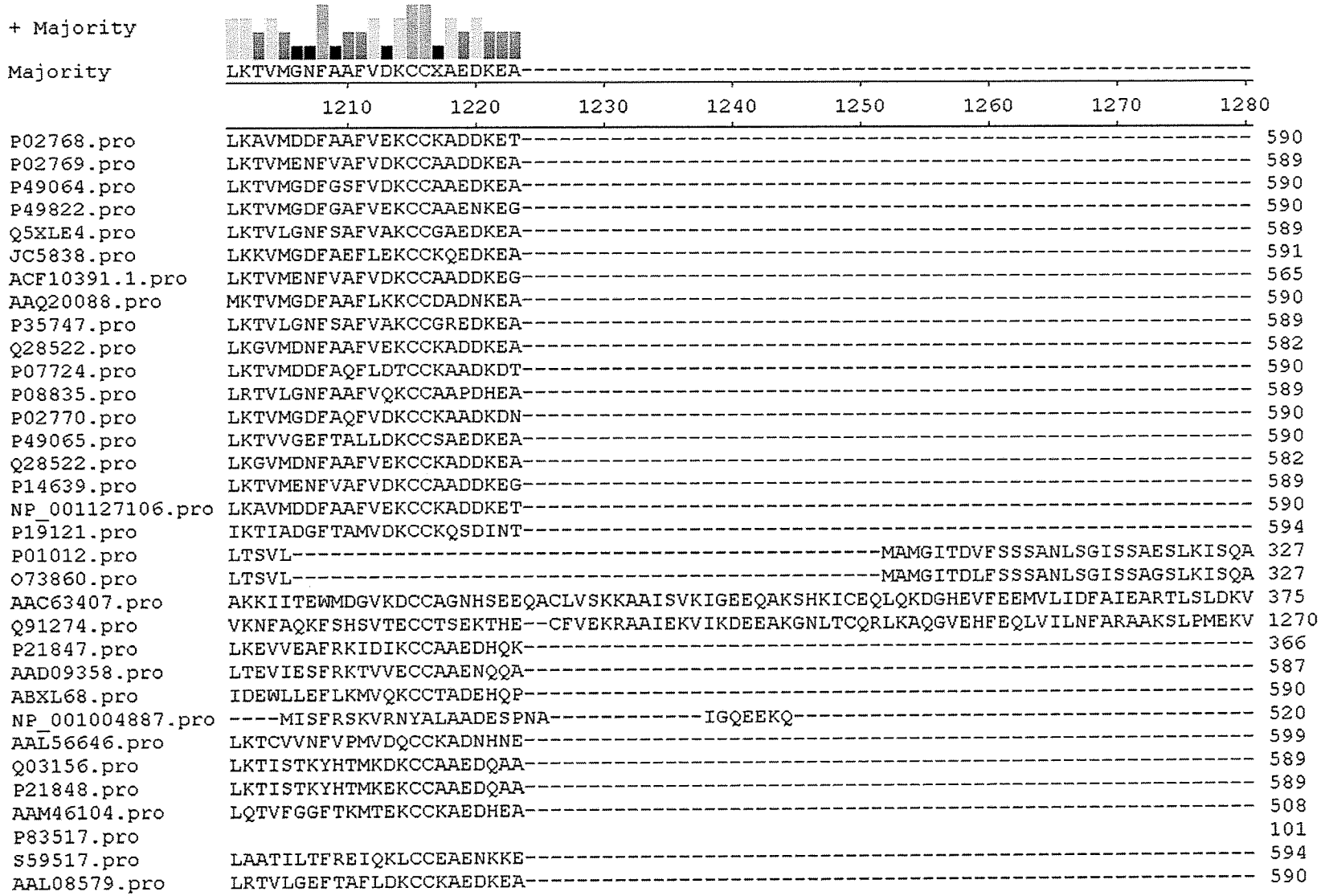

+ Majority
Majority
810
820
830
840
850
860
870
880
P02768.pro 484
P02769.pro 483
P49064.pro 484
P49822.pro 484
Q5XLE4.pro 483
JC5838.pro 485
ACF10391.1.pro 459
AAQ20088.pro 484
P35747.pro 483
Q28522.pro 476
P07724.pro 484
P08835.pro 483
P02770.pro 484
P49065.pro 484
Q28522.pro 476
P14639.pro 483
NP_001127106.pro 484
P19121.pro 488
P01012.pro QIGL FRVASMASEKM KILEL 233
O73860.pro QIGL FKVASMASEKM KILEL 233
AAC63407.pro 42
Q91274.pro LTDADQESCLHTARSQARQEALKSLQRSERICNTLSAIGKEKFEDRIVIALSQKATDASFEQILEIANRMSRGLARCCEQ 873
P21847.pro 260
AAD09358.pro 481
ABXL68.pro 484
NP_001004887.pro KGQLICQPVQ 394
AAL56646.pro 493
Q03156.pro 483
P21848.pro 483
AAM46104.pro 402
P83517.pro 94
S59517.pro 488

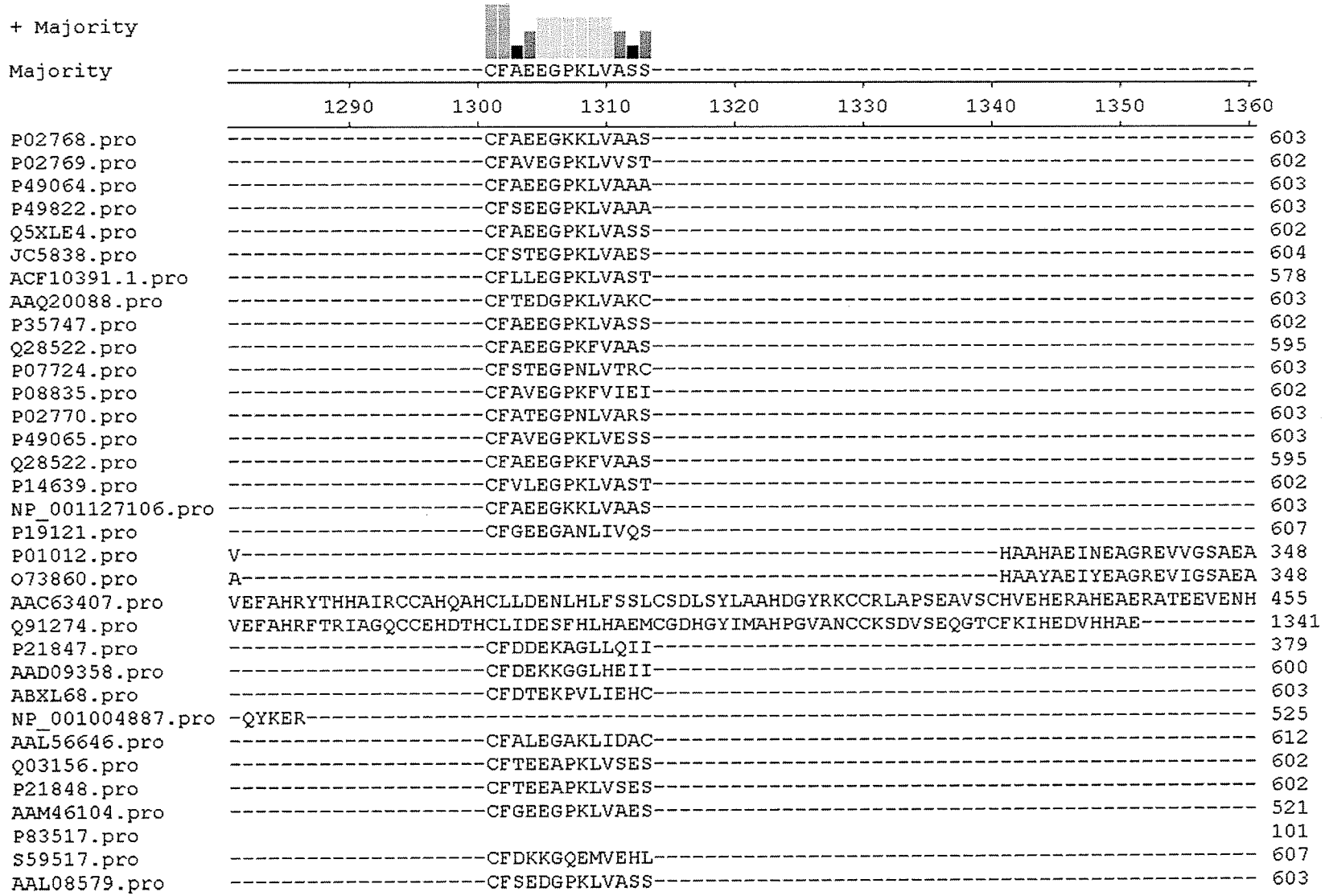

+ Majority
Majority
-----CVLHEKTPVSEKV----------TKCCTESLVN----------RRPCFSALEV
890 900 910 920 930 940 950 960
P02768.pro -----CVLHEKTPVSDRV----------TKCCTESLVN----------RRPCFSALEV 517
P02769.pro -----CVLHEKTPVSEKV----------TKCCTESLVN----------RRPCFSALTP 516
P49064.pro -----CVLHEKTPVSERV----------TKCCTESLVN----------RRPCFSALQV 517
P49822.pro -----CVLHEKTPVSERV----------TKCCSESLVN----------RRPCFSGLEV 517
Q5XLE4.pro -----CVLHEKTPVSEKI----------TKCCTDSLAE----------RRPCFSALEL 516
JC5838.pro -----CLLHEKTPVSEQV----------TKCCSGSLVE----------RRPCFSALPV 518
ACF10391.1.pro -----CVLHEKTPVSEKV----------TKCCTESLVN----------RRPCFSDLTL 492
AAQ20088.pro -----CILHEKTPVSERV----------TKCCTESLVN----------RRPCFSALHV 517
P35747.pro -----CVLHEKTPVSEKI----------TKCCTDSLAE----------RRPCFSALEL 516
Q28522.pro -----CVLHEKTPVSEKV----------TKCCTESLVN----------RRPCFSALEL 509
P07724.pro -----CLLHEKTPVSEHV----------TKCCSGSLVE----------RRPCFSALTV 517
P08835.pro -----CVLHEKTPVSEKV----------TKCCTESLVN----------RRPCFSALTP 516
P02770.pro -----CVLHEKTPVSEKV----------TKCCSGSLVE----------RRPCFSALTV 517
P49065.pro -----CVLHEKTPVSEKV----------TKCCSESLVD----------RRPCFSALGP 517
Q28522.pro -----CVLHEKTPVSEKV----------TKCCTESLVN----------RRPCFSALEL 509
P14639.pro -----CVLHEKTPVSEKV----------TKCCTESLVN----------RRPCFSDLTL 516
NP_001127106.pro -----CVLHEKTPVSDRV----------TKCCTESLVN----------RRPCFSALEV 517
P19121.pro -----CRKQETTPINDNV----------SQCCSQLYAN----------RRPCFTAMGV 521
P01012.pro ---------- 233
O73860.pro ---------- 233
AAC63407.pro ----------ANEEDRADCLVSLRG 57
Q91274.pro GNNVGCLMDHRHALHEAICSTPDGSLPQSVAACCNTSNTSTTTSTTTSTTTSTTTSTTTSTTTSTTTAAEIRDSCFDNLQA 953
P21847.pro -----CEKEKHTFVNDNV----------RHCCVDSYAN----------RRKCFTDLQR 293
AAD09358.pro -----CEREKKTFINDNV----------HHCCVDSYAN----------RRPCFTKLGP 514
ABXL68.pro -----CERQKKTFINNHV----------AHCCTDSYSG----------MRSCFTALGP 517
NP_001004887.pro ---------- 394
AAL56646.pro -----CMKQKTTPVNEKV----------AQCCSHSLSS----------QTPCFSALPV 526
Q03156.pro -----CDDYDPSSINPHI----------AHCCNQSYSM----------RRHCILAIQP 516
P21848.pro -----CDDYDPSSINPHI----------AHCCNQSYSM----------RRHCILAIQP 516
AAM46104.pro -----CQRHQRSSINVNV----------CQCCSNSYAL----------RSLCITSLGG 435
P83517.pro ----------CCPPDVL 101
S59517.pro -----CKYHNKHFINDQI----------CHCCNSSFIS----------RWECISNLGP 521
AAL08579.pro -----CVLHEKTPVSEQV----------TKCCTGSVVE----------RRPCFSALPV 517

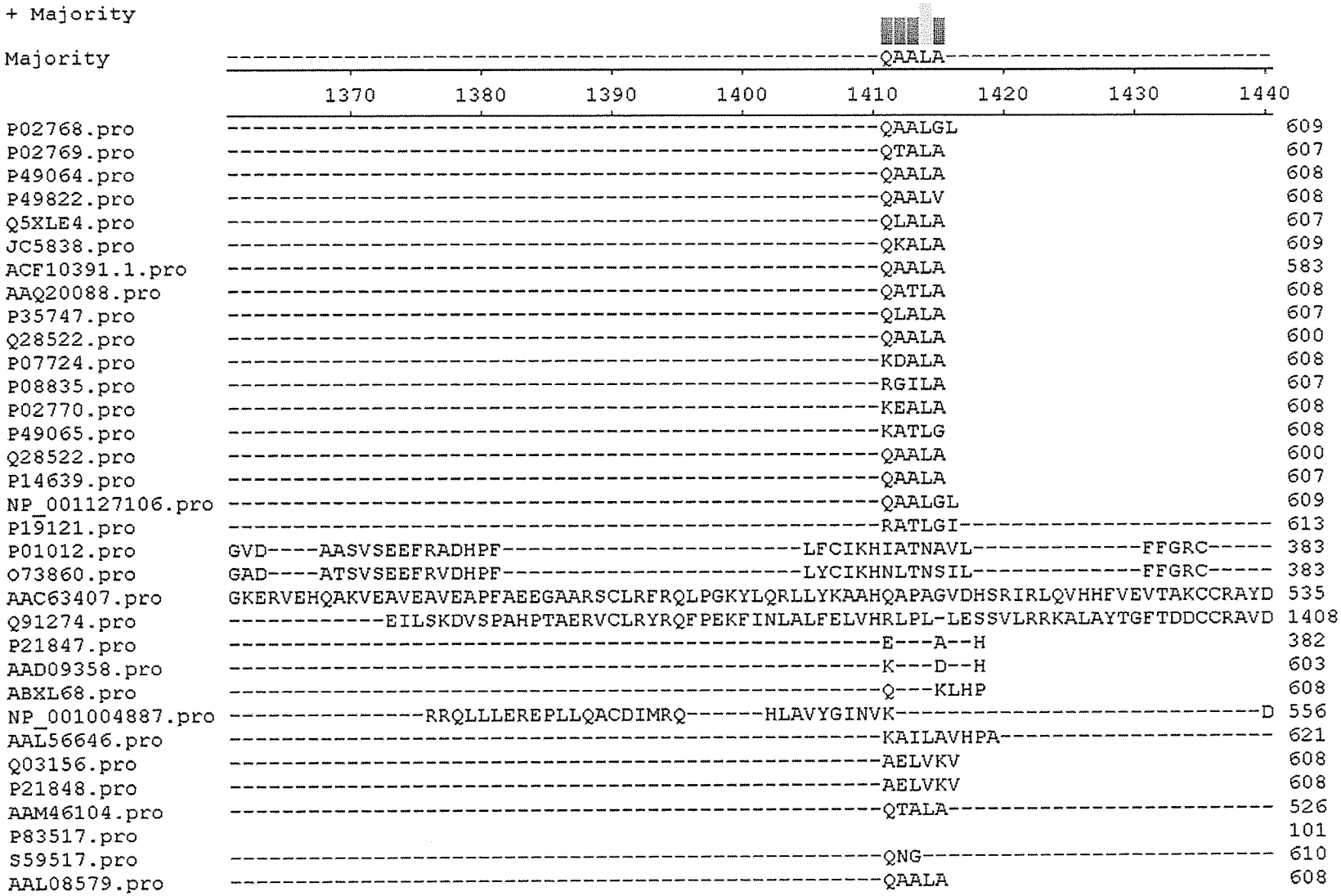

+ Majority
Majority
970
980
990
1000
1010
1020
1030
1040
P02768.pro 518
P02769.pro 517
P49064.pro 518
P49822.pro 518
Q5XLE4.pro 517
JC5838.pro 519
ACF10391.1.pro 493
AAQ20088.pro 518
P35747.pro 517
Q28522.pro 510
P07724.pro 518
P08835.pro 517
P02770.pro 518
P49065.pro 518
Q28522.pro 510
P14639.pro 517
NP_001127106.pro 518
P19121.pro 522
P01012.pro 245
O73860.pro 245
AAC63407.pro 137
Q91274.pro 1033
P21847.pro 294
AAD09358.pro 515
ABXL68.pro 518
NP_001004887.pro 433
AAL56646.pro 527
Q03156.pro 517
P21848.pro 517
AAM46104.pro 436
P83517.pro 101
S59517.pro 522
AAL08579.pro 518

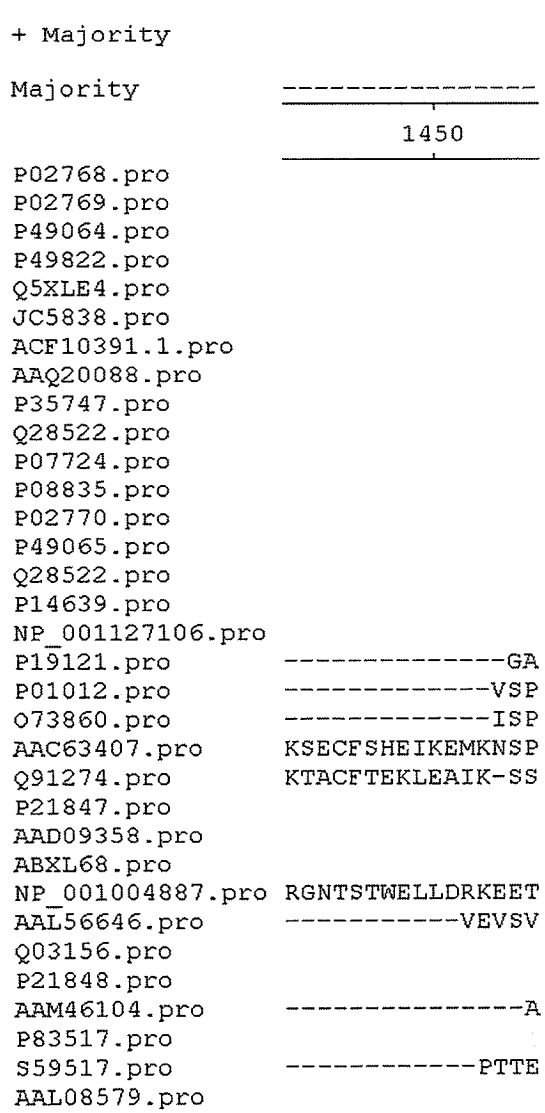

+ Majority
Majority
1050
1060
1070
1080
1090
1100
1110
1120
P02768.pro
P02769.pro
P49064.pro
P49822.pro
Q5XLE4.pro
JC5838.pro
ACF10391.1.pro
AAQ20088.pro
P35747.pro
Q28522.pro
P07724.pro
P08835.pro
P02770.pro
P49065.pro
Q28522.pro
P14639.pro
NP_001127106.pro
P19121.pro
P01012.pro
O73860.pro
AAC63407.pro
Q91274.pro
P21847.pro
AAD09358.pro
ABXL68.pro
NP_001004887.pro
AAL56646.pro
Q03156.pro
P21848.pro
AAM46104.pro
P83517.pro
S59517.pro
AAL08579.pro


+ Majority
Majority
1130
1140
1150
1160
1170
1180
1190
1200
P02768.pro
P02769.pro
P49064.pro
P49822.pro
Q5XLE4.pro
JC5838.pro
ACF10391.1.pro
AAQ20088.pro
P35747.pro
Q28522.pro
P07724.pro
P08835.pro
P02770.pro
P49065.pro
Q28522.pro
P14639.pro
NP_001127106.pro
P19121.pro
P01012.pro
O73860.pro
AAC63407.pro
Q91274.pro
P21847.pro
AAD09358.pro
ABXL68.pro
NP_001004887.pro
AAL56646.pro
Q03156.pro
P21848.pro
AAM46104.pro
P83517.pro
S59517.pro
AAL08579.pro


+ Majority
Majority LKTVMGNFAAFVDKCCXAEDKEA----------
1210 1220 1230 1240 1250 1260 1270 1280
P02768.pro LKAVMDDFAAFVEKCCKADDKET---------- 590
P02769.pro LKTVMENFVAFVDKCCAADDKEA---------- 589
P49064.pro LKTVMGDFGSFVDKCCAAEDKEA---------- 590
P49822.pro LKTVMGDFGAFVEKCCAAENKEG---------- 590
Q5XLE4.pro LKTVLGNFSAFVAKCCGAEDKEA---------- 589
JC5838.pro LKKVMGDFAEFLEKCCKQEDKEA---------- 591
ACF10391.1.pro LKTVMENFVAFVDKCCAADDKEG---------- 565
AAQ20088.pro MKTVMGDFAAFLKKCCDADNKEA---------- 590
P35747.pro LKTVLGNFSAFVAKCCGREDKEA---------- 589
Q28522.pro LKGVMDNFAAFVEKCCKADDKEA---------- 582
P07724.pro LKTVMDDFAQFLDTCCKAADKDT---------- 590
P08835.pro LRTVLGNFAAFVQKCCAAPDHEA---------- 589
P02770.pro LKTVMGDFAQFVDKCCKAADKDN---------- 590
P49065.pro LKTVVGEFTALLDKCCSAEDKEA---------- 590
Q28522.pro LKGVMDNFAAFVEKCCKADDKEA---------- 582
P14639.pro LKTVMENFVAFVDKCCAADDKEG---------- 589
NP_001127106.pro LKAVMDDFAAFVEKCCKADDKET---------- 590
P19121.pro IKTIADGFTAMVDKCCKQSDINT---------- 594
P01012.pro LTSVL----------MAMGITDVFSSSANLSGISSAESLKISQA 327
O73860.pro LTSVL----------MAMGITDLFSSSANLSGISSAGSLKISQA 327
AAC63407.pro AKKIITEWMDGVKDCCAGNHSEEQACLVSKKAAISVKIGEEQAKSHKICEQLQKDGHEVFEEMVLIDFAIEARTLSLDKV 375
Q91274.pro VKNFAQKFSHSVTECCTSEKTHE--CFVEKRAAIEKVIKDEEAKGNLTCQRLKAQGVEHFEQLVILNFARAAKSLPMEKV 1270
P21847.pro LKEVVEAFRKIDIKCCAAEDHQK---------- 366
AAD09358.pro LTEVIESFRKTVVECCAAENQQA---------- 587
ABXL68.pro IDEWLLEFLKMVQKCCTADEHQP---------- 590
NP_001004887.pro ----MISFRSKVRNYALAADESPNA----------IGQEEKQ---------- 520
AAL56646.pro LKTCVVNFVPMVDQCCKADNHNE---------- 599
Q03156.pro LKTISTKYHTMKDKCCAAEDQAA---------- 589
P21848.pro LKTISTKYHTMKEKCCAAEDQAA---------- 589
AAM46104.pro LQTVFGGFTKMTEKCCKAEDHEA---------- 508
P83517.pro 101
S59517.pro LAATILTFREIQKLCCEAENKKE---------- 594
AAL08579.pro LRTVLGEFTAFLDKCCKAEDKEA---------- 590


+ Majority
Majority
1290
1300
1310
1320
1330
1340
1350
1360
P02768.pro
P02769.pro
P49064.pro
P49822.pro
Q5XLE4.pro
JC5838.pro
ACF10391.1.pro
AAQ20088.pro
P35747.pro
Q28522.pro
P07724.pro
P08835.pro
P02770.pro
P49065.pro
Q28522.pro
P14639.pro
NP_001127106.pro
P19121.pro
P01012.pro
O73860.pro
AAC63407.pro
Q91274.pro
P21847.pro
AAD09358.pro
ABXL68.pro
NP_001004887.pro
AAL56646.pro
Q03156.pro
P21848.pro
AAM46104.pro
P83517.pro
S59517.pro
AAL08579.pro


+ Majority
Majority
1370
1380
1390
1400
1410
1420
1430
1440
P02768.pro
P02769.pro
P49064.pro
P49822.pro
Q5XLE4.pro
JC5838.pro
ACF10391.1.pro
AAQ20088.pro
P35747.pro
Q28522.pro
P07724.pro
P08835.pro
P02770.pro
P49065.pro
Q28522.pro
P14639.pro
NP_001127106.pro
P19121.pro
P01012.pro
O73860.pro
AAC63407.pro
Q91274.pro
P21847.pro
AAD09358.pro
ABXL68.pro
NP_001004887.pro
AAL56646.pro
Q03156.pro
P21848.pro
AAM46104.pro
P83517.pro
S59517.pro
AAL08579.pro



609
607
608
608
607
609
583
608
607
600
608
607
608
608
600
607
609
615
386
386
551
1423
382
603
608
572
626
608
608
527
101
614
608

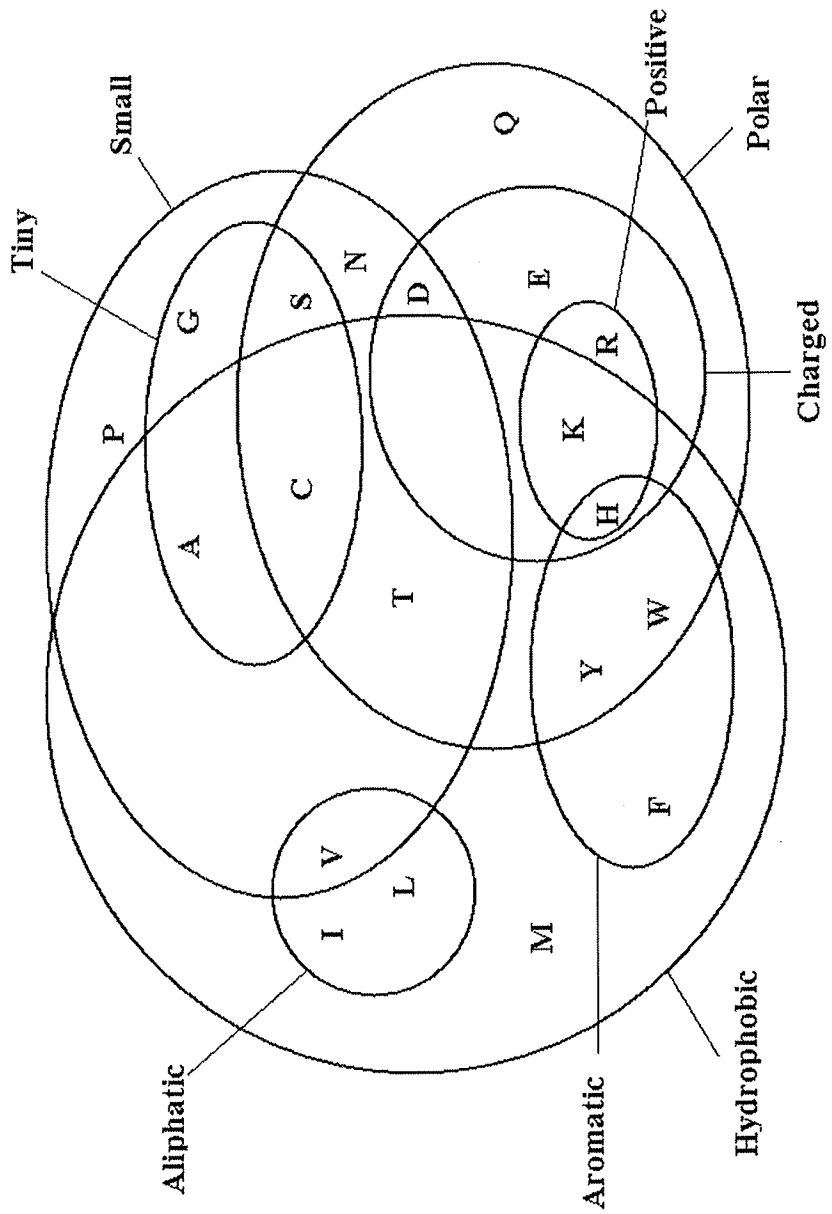

Tiny
Small
Polar
Positive
Charged
Aliphatic
Aromatic
Hydrophobic
A
G
P
C
S
N
T
D
Q
E
R
K
H
I
V
L
M
Y
W
F

Figure 4

Figure 5A

Position in 1AO6	Position in Mature HSA	Position with Leader Sequence	Amino Acid	% SASA	B-Factor	SS	Align 1 (Mamm. W)	Adj. 100%'s (Align 1)	Align 2 (Var. Sps. V)	Polymorph.	Phenotype Change	Conserved Mutation *vs.* Cysteine
n/a	1	25	D	n/a	n/a	0	40	0	40	D25V	0	3
n/a	585	609	L	n/a	n/a	0	0	0	0			4
n/a	2	26	A	n/a	n/a	0	40	0	20			1
558	562	586	D	217.4	95.72	0	40	0	40			3
360	364	388	A	164.5	80.24	0	40	0	20			1
500	504	528	A	108.1	98.55	0	60	0	40			1
501	505	529	E	105.8	93.84	0	60	0	40	E529K	0	4
75	79	103	T	103.8	67.13	0	40	0	20			1
82	86	110	E	99.4	88.78	0	60	0	20			4

Figure 5B

Position in 1AO6	Position in Mature HSA	Position with Leader Sequence	Amino Acid	% SASA	B-Factor	SS	Align 1 (Mamm. W)	Adj. 100%'s (Align 1)	Align 2 (Var. Sps. V)	Polymorph.	Phenotype Change	Conserved Mutation *vs.* Cysteine
125	129	153	D	211.6	43.69	1	40	0	20			3
545	549	573	D	146.4	84.68	1	40	0	20			3
577	581	605	A	133.9	103.91	1	40	0	40			1
117	121	145	D	130.4	46.02	1	60	0	40			3
78	82	106	E	130.1	96.77	1	60	0	40	E106K	0	4
266	270	294	S	114.1	43.53	1	40	0	20			1
393	397	421	Q	101.6	58.94	1	40	0	20			3
574	578	602	A	96.8	98.62	1	20	0	20			1

Figure 5C

Position in 1AO6	Position in Mature HSA	Position with Leader Sequence	Amino Acid	% SASA	B-Factor	SS	Align 1 (Mamm. W)	Adj. 100%'s (Align 1)	Align 2 (Var. Sps. V)	Polymorph.	Phenotype Change	Conserved Mutation *vs.* Cysteine
n/a	585	609	L	n/a	n/a	0	0	0	0			4
n/a	2	26	A	n/a	n/a	0	40	0	20			1
n/a	1	25	D	n/a	n/a	0	40	0	40	D25V	0	3
n/a	584	608	G	n/a	n/a	0	60	1	40			2
n/a	4	28	K	n/a	n/a	0	80	1	40			4
297	301	325	D	218.8	64.56	0	60	1	40			3
558	562	586	D	217.4	95.72	0	40	0	40			3
296	300	324	A	180.6	63.75	0	40	1	40			1
361	365	389	D	168.1	84.23	0	80	1	40	D389H, D389V	1	3
360	364	388	A	164.5	80.24	0	40	0	20			1
54	58	82	S	164.1	53.12	0	80	0	40			1
494	498	522	V	149.4	74.11	0	80	2	60			3
492	496	520	T	148.8	70.07	0	60	2	40			1
109	113	137	P	141.8	51.5	0	80	0	40			3
112	116	140	V	139.5	51.82	0	40	0	0			3
508	512	536	D	139.1	61.05	0	80	0	40			3
300	304	328	S	134.4	57.01	0	20	0	20			1
310	314	338	D	131.9	65.86	0	40	0	40	D338G, D338V	1	3
299	303	327	P	119.4	59.59	0	80	1	60			3
534	538	562	K	115.5	96.73	0	80	2	40			4
56	60	84	E	110.3	53.87	0	40	0	20	E84K	0	4

Position in 1AO6	Position in Mature HSA	Position with Leader Sequence	Amino Acid	% SASA	B-Factor	SS	Align 1 (Mamm. W)	Adj. 100%'s (Align 1)	Align 2 (Var. Sps. V)	Polymorph.	Phenotype Change	Conserved Mutation *vs.* Cysteine
500	504	528	A	108.1	98.55	0	60	0	40			1
435	439	463	K	106.3	52.99	0	40	1	20			4
76	80	104	L	106.2	79.71	0	80	0	40			4
501	505	529	E	105.8	93.84	0	60	0	40	E529K	0	4
75	79	103	T	103.8	67.13	0	40	0	20			1
111	115	139	L	100.0	54.21	0	60	0	20			4
367	371	395	A	100.0	63.92	0	60	1	40			1
82	86	110	E	99.4	88.78	0	60	0	20			4
497	501	525	E	99.4	95.25	0	60	2	40	E525K	0	4
537	541	565	K	98.3	96.84	0	20	0	20	K565E	1	4
560	564	588	K	97.1	100.08	0	80	0	40			4
439	443	467	A	93.5	55.15	0	40	1	20			1
556	560	584	K	92.5	81.9	0	40	1	20	K584E	0	4
502	506	530	T	92.5	88	0	60	1	40			1
309	313	337	K	92.0	64.18	0	80	0	40	K337N	1	4
578	582	606	A	88.7	106.05	0	80	1	40			1
561	565	589	E	87.8	98.18	0	80	0	40	E589K	0	4
294	298	322	M	84.5	53.49	0	20	1	20			3
499	503	527	N	81.2	99.86	0	40	1	20			2

Figure 5D

Position in 1AO6	Position in Mature HSA	Position with Leader Sequence	Amino Acid	% SASA	B-Factor	SS	Align 1 (Mamm. W)	Adj. 100%'s (Align 1)	Align 2 (Var. Sps. V)	Polymorph.	Phenotype Change	Conserved Mutation *vs.* Cysteine
265	269	293	D	229.0	45.46	1	60	1	60	D293G	1	3
125	129	153	D	211.6	43.69	1	40	0	20			3
467	471	495	D	205.8	45.67	1	80	1	40			3
371	375	399	D	152.2	50.78	1	80	0	40	D399N, D399H	0	3
51	55	79	A	148.4	43.59	1	80	0	40			1
545	549	573	D	146.4	84.68	1	40	0	20			3
577	581	605	A	133.9	103.91	1	40	0	40			1
304	308	332	D	131.9	47.92	1	80	0	40			3
486	490	514	A	130.6	32.03	1	80	2	40			1
117	121	145	D	130.4	46.02	1	60	0	40			3
78	82	106	E	130.1	96.77	1	60	0	40	E106K	0	4
474	478	502	T	125.0	35	1	60	1	40			1
320	324	348	D	120.3	58.69	1	80	1	60			3
375	379	403	P	119.4	32.33	1	80	1	40			3
316	320	344	A	119.4	64	1	40	0	20	A344T	1	1
121	125	149	T	115.0	35.32	1	40	1	20			1
266	270	294	S	114.1	43.53	1	40	0	20			1
79	83	107	T	113.8	98.21	1	60	1	20			1
100	104	128	Q	111.0	32.1	1	40	2	20			3
225	229	253	A	109.7	36.47	1	60	1	40			1
364	368	392	E	109.6	77.34	1	60	1	20			4
314	318	342	N	107.1	59.91	1	80	1	40	N342K	0	2
538	542	566	E	105.8	96.98	1	80	1	60			4

Position in 1AO6	Position in Mature HSA	Position with Leader Sequence	Amino Acid	% SASA	B-Factor	SS	Align 1 (Mamm. W)	Adj. 100%'s (Align 1)	Align 2 (Var. Sps. V)	Polymorph.	Phenotype Change	Conserved Mutation *vs.* Cysteine
72	76	100	T	105.0	32.05	1	40	1	20			1
393	397	421	Q	101.6	58.94	1	40	0	20			3
60	40	64	E	101.3	31.14	1	40	1	40			4
321	325	349	V	100.0	50.37	1	80	1	40			3
386	390	414	Q	96.9	52.9	1	40	1	20			3
574	578	602	A	96.8	98.62	1	20	0	20			1
475	479	503	E	94.2	40.83	1	60	1	20	E503K	0	4
546	550	574	D	94.2	80.18	1	40	1	20	D574G, D574A	0	3
382	386	410	N	94.1	42.58	1	80	1	40			2
573	577	601	A	93.5	97.86	1	60	1	40			1
44	48	72	E	91.0	31.25	1	60	1	40			4
570	574	598	K	90.8	99.51	1	80	0	40	K598N	0	4
317	321	345	E	88.5	67.18	1	80	1	40	E345K	0	4
118	122	146	V	87.7	43.96	1	40	0	20	V146E	0	3
279	283	307	L	87.6	36.51	1	40	1	20			4
34	38	62	D	87.0	34.73	1	60	1	40			3
576	580	604	Q	86.6	101.91	1	60	0	40			3
562	566	590	T	86.3	94.83	1	40	1	40			1
48	52	76	T	86.3	35.9	1	40	1	20			1
351	355	379	T	86.3	40.3	1	80	1	40			1
392	396	420	E	85.9	62.51	1	80	0	40	E420K	0	4
262	266	290	E	83.3	41.21	1	80	1	40			4
569	573	597	K	81.6	98.2	1	80	1	40	K597E	0	4
542	546	570	A	80.6	91.51	1	60	1	40			1

Figure 6A

Position in 1AO6	Position in Mature HSA	Position with Leader Sequence	Amino Acid	% SASA	B-Factor	SS	Align 1 (Mamm. W)	Adj. 100%'s (Align 1)	Align 2 (All Sps. V)	Disulphide Information	(Polymorp.) Phenotype Change	Modification Score
71	75	99	C	20.7	24.72	1	100	0	80	pairs with C91		high
87	91	115	C	32.6	33.58	0	100	1	60	pairs with C75		high
120	124	148	C	3.3	34.94	1	100	0	60	pairs with C169		high
164	168	192	C	0.0	31.68	1	100	1	60	pairs with C177		high
165	169	193	C	14.1	32.95	0	100	1	60	pairs with C124		high
312	316	340	C	23.9	62.19	1	100	1	80	pairs with C361		high
356	360	384	C	2.2	60.95	1	100	1	80	pairs with C369		high
357	361	385	C	42.4	66.33	0	100	2	80	pairs with C316		high
554	558	582	C	1.1	76.28	1	100	1	80	pairs with C567		high
563	567	591	C	25.0	92.56	1	100	1	80	pairs with C558		high

Figure 6B

Position in 1AO6	Position in Mature HSA	Position with Leader Sequence	Amino Acid	% SASA	B-Factor	SS	Align 1 (Mamm. W)	Adj. 100%'s (Align 1)	Align 2 (All Sps. V)	Disulphide Information	(Polymorp.) Phenotype Change	Modification Score
71	75	99	C	20.7	24.72	1	100	0	80	pairs with C91		high
87	91	115	C	32.6	33.58	0	100	1	60	pairs with C75		high
120	124	148	C	3.3	34.94	1	100	0	60	pairs with C169		high
165	169	193	C	14.1	32.95	0	100	1	60	pairs with C124		high
173	177	201	C	30.4	28.29	1	100	1	80	pairs with C168	(C201F) 2	medium
312	316	340	C	23.9	62.19	1	100	1	80	pairs with C361		high
357	361	385	C	42.4	66.33	0	100	2	80	pairs with C316		high
365	369	393	C	48.9	69.93	1	100	1	80	pairs with C360		medium
554	558	582	C	1.1	76.28	1	100	1	80	pairs with C567		high
563	567	591	C	25.0	92.56	1	100	1	80	pairs with C558		high

Figure 7

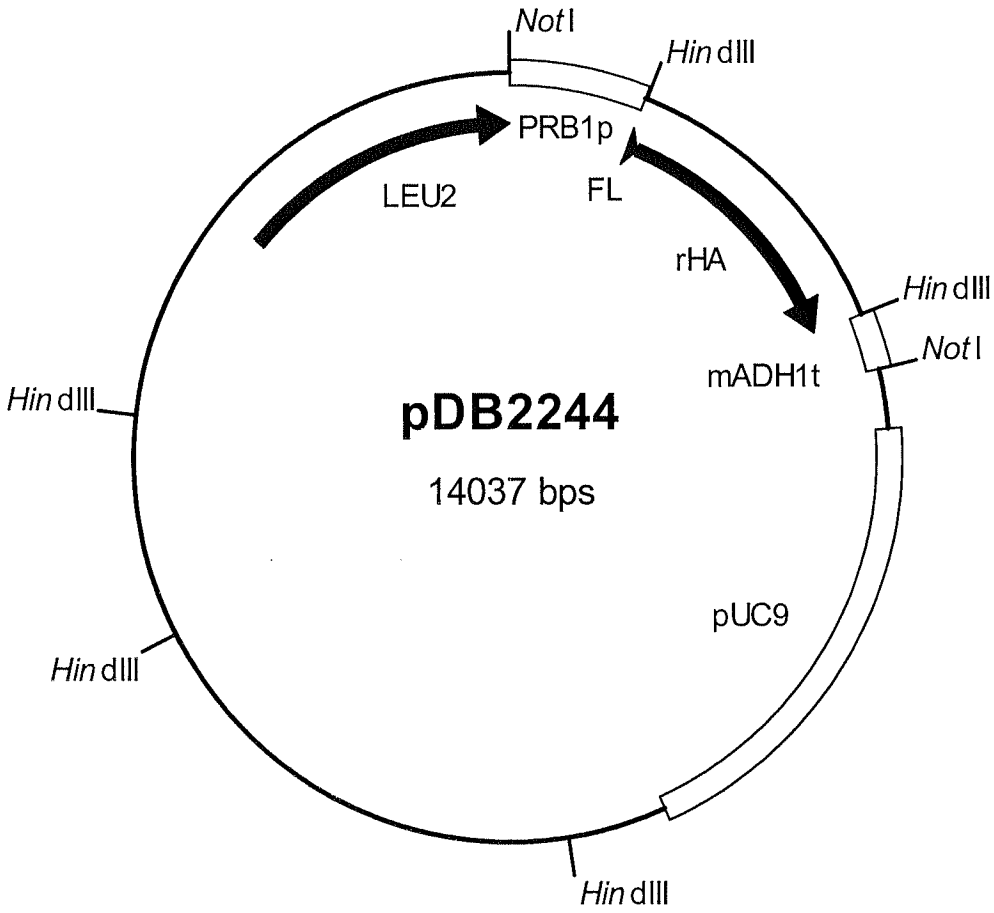

NotI
HindIII
PRB1p
LEU2
FL
rHA
HindIII
NotI
mADH1t
HindIII
pDB2244
14037 bps
pUC9
HindIII
HindIII

Figure 8

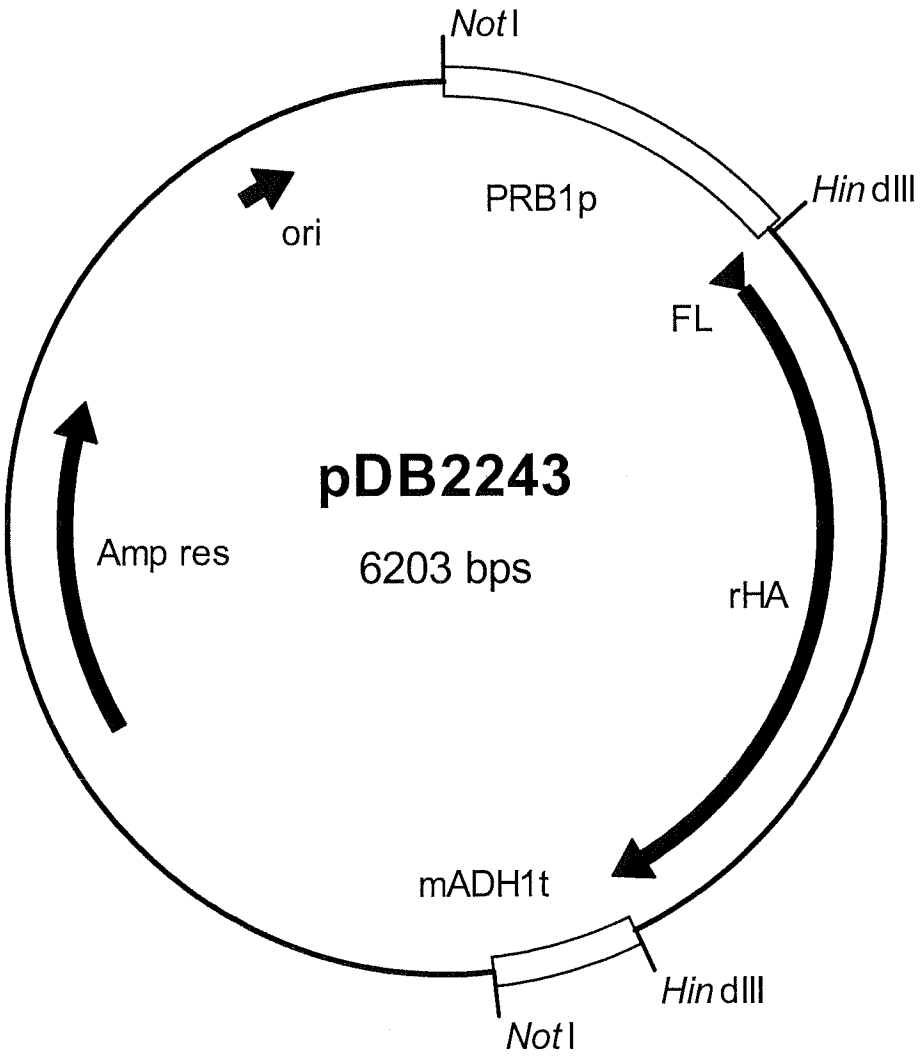

NotI
PRB1p
HindIII
ori
FL
pDB2243
6203 bps
Amp res
rHA
mADH1t
HindIII
NotI

Figure 9

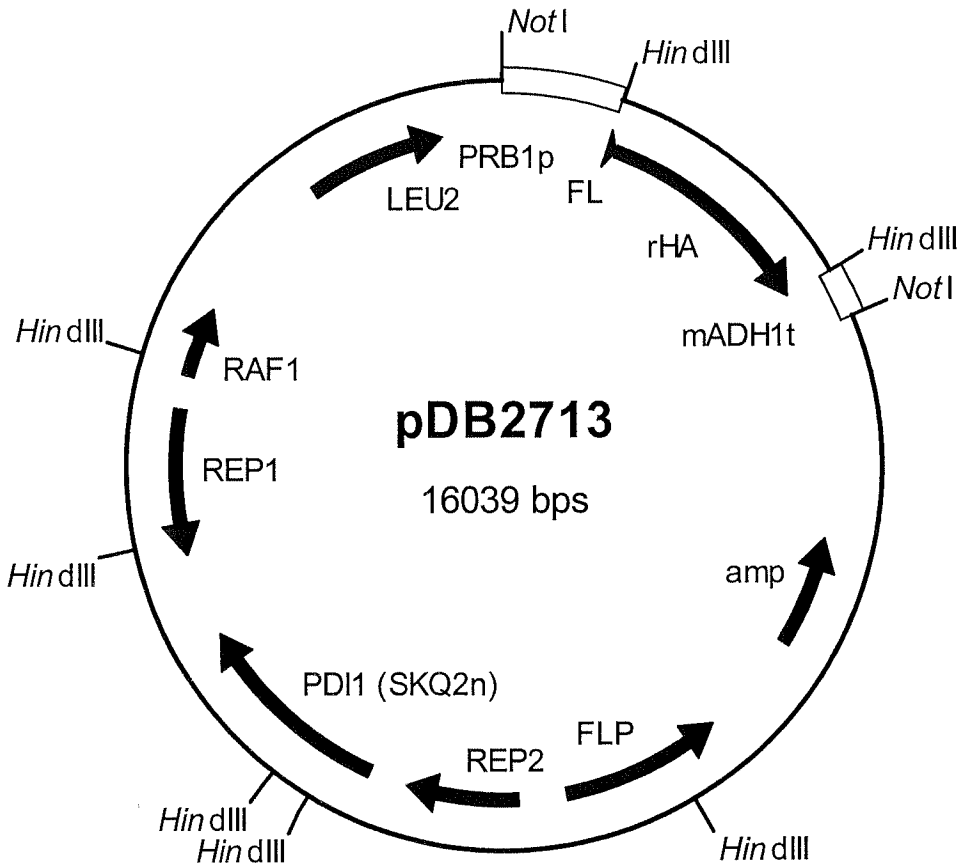

Not I
Hin dIII
PRB1p
LEU2
FL
rHA
Hin dIII
Not I
mADH1t
Hin dIII
RAF1
pDB2713
16039 bps
REP1
Hin dIII
amp
PDI1 (SKQ2n)
FLP
REP2
Hin dIII
Hin dIII
Hin dIII

Figure 10

Position in 1AO6	Position in Mature HSA	Position with Leader Sequence	Amino Acid	% SASA	B-Factor	SS	Align 1 (Mamm. W)	Adj. 100%'s (Align 1)	Align 2 (Var. Sps. V)	(Polymorp.) Phenotype Change	Selection Group	Proximity Group
n/a	1	25	D	n/a	n/a	0	40	0	40	(D25V) 0	1	E
n/a	2	26	A	n/a	n/a	0	40	0	20		1	E
71	75	99	C	20.7	24.72	1	100	0	80		3	K
75	79	103	T	103.8	67.13	0	40	0	20		1	A
78	82	106	E	130.1	96.77	1	60	0	40	(E106K) 0	2	F
82	86	110	E	99.4	88.78	0	60	0	20		1	A
87	91	115	C	32.6	33.58	0	100	1	60		3	K
117	121	145	D	130.4	46.02	1	60	0	40		2	H
120	124	148	C	3.3	34.94	1	100	0	60		3	L
125	129	153	D	211.6	43.69	1	40	0	20		2	H
165	169	193	C	14.1	32.95	0	100	1	60		3	L
173	177	201	C	30.4	28.29	1	100	1	80	(C201F) 2	3	L
266	270	294	S	114.1	43.53	1	40	0	20		2	G
312	316	340	C	23.9	62.19	1	100	1	80		3	M
357	361	385	C	42.4	66.33	0	100	2	80		3	M
360	364	388	A	164.5	80.24	0	40	0	20		1	C
365	369	393	C	48.9	69.93	1	100	1	80		3	M
393	397	421	Q	101.6	58.94	1	40	0	20		2	J
500	504	528	A	108.1	98.55	0	60	0	40		1	D
501	505	529	E	105.8	93.84	0	60	0	40	(E529K) 0	1	D
545	549	573	D	146.4	84.68	1	40	0	20		2	J

Position in 1AO6	Position in Mature HSA	Position with Leader Sequence	Amino Acid	% SASA	B-Factor	SS	Align 1 (Mamm. W)	Adj. 100%'s (Align 1)	Align 2 (Var. Sps. V)	(Polymorp.) Phenotype Change	Selection Group	Proximity Group
554	558	582	C	1.1	76.28	1	100	1	80		3	N
558	562	586	D	217.4	95.72	0	40	0	40		1	B
563	567	591	C	25	92.56	1	100	1	80		3	N
574	578	602	A	96.8	98.62	1	20	0	20		2	I
577	581	605	A	133.9	103.91	1	40	0	40		2	I
n/a	585	609	L	n/a	n/a	0	0	0	0		1	D

Figure 11

Construct Reference	Mutation	Plasmid Name	Transformant	Yeast Stock Number	Positions Modified in SEQ ID N0.2	Original Codon	Original Residue	Mutant Codon	Mutant Residue	DNA SEQ ID No.	Protein SEQ ID No.
TA1	A2C	pDB4029	B	9012	4-6	GCA	A	TGT	C	5	50
TA2	D1C	pDB4030	B	9013	1-3	GAT	D	TGT	C	6	51
TA3	C75S	pDB4031	A	9014	223-225	TGC	C	TCT	S	7	52
TA4	T79C	pDB4032	D	9015	235-237	ACT	T	TGT	C	8	53
TA5	E82C	pDB4033	D	9016	244-246	GAA	E	TGT	C	9	54
TA6	E86C	pDB4034	A	9017	256-258	GAA	E	TGT	C	10	55
TA7	C124S	pDB4035	D	9018	370-372	TGC	C	TCT	S	11	56
TA8	C168S	pDB4036	B	9019	502-504	TGT	C	TCT	S	12	57
TA9	C169S	pDB4037	B	9020	505-507	TGC	C	TCT	S	13	58
TA10	C91S	pDB4038	B	9021	271-273	TGT	C	TCT	S	14	59
TA11	D121C	pDB4039	B	9022	361-363	GAT	D	TGT	C	15	60

Construct Reference	Mutation	Plasmid Name	Transformant	Yeast Stock Number	Positions Modified in SEQ ID N0.2	Original Codon	Original Residue	Mutant Codon	Mutant Residue	DNA SEQ ID No.	Protein SEQ ID No.
TA12	D129C	pDB4040	C	9023	385-387	GAC	D	TGT	C	16	61
TA13	S270C	pDB4041	D	9024	808-810	TCG	S	TGT	C	17	62
TA14	C316A	pDB4042	B	9025	946-948	TGC	C	GCT	A	18	63
TA16	C360S	pDB4044	B	9026	1078-1080	TGC	C	TCT	S	19	64
TA17	C361A	pDB4045	A	9027	1081-1083	TGT	C	GCT	A	20	65
TA18	C361S	pDB4046	C	9028	1081-1083	TGT	C	TCT	S	21	66
TA19	A364C	pDB4047	D	9029	1090-1092	GCT	A	TGT	C	22	67
TA20	Q397C	pDB4048	A	9030	1189-1191	CAG	Q	TGT	C	23	68
TA21	A504C	pDB4049	A	9031	1510-1512	GCT	A	TGT	C	24	69
TA22	A578C	pDB4050	D	9032	1732-1734	GCA	A	TGT	C	25	70
TA23	A581C	pDB4051	C	9033	1741-1743	GCT	A	TGT	C	26	71
TA24	C558S	pDB4052	D	9034	1672-1674	TGC	C	TCT	S	27	72
TA25	C567S	pDB4053	B	9035	1699-1701	TGC	C	TCT	S	28	73
TA26	D549C	pDB4054	B	9036	1645-1647	GAT	D	TGT	C	29	74
TA27	D562C	pDB4055	B	9037	1684-1686	GAC	D	TGT	C	30	75
TA28	E505C	pDB4056	D	9038	1513-1515	GAA	E	TGT	C	31	76
TA29	L585C	pDB4057	B	9039	1753-1755	TTA	L	TGT	C	32	77
TA30	N/A	pDB3927	A	9040	N/A	N/A	N/A	N/A	N/A	2	1
TA31	N/A	pDB3964	D	9041	N/A	N/A	N/A	N/A	N/A	4	1
TA32	N/A	pDB2244	B	9042	N/A	N/A	N/A	N/A	N/A	2	1

Figure 12

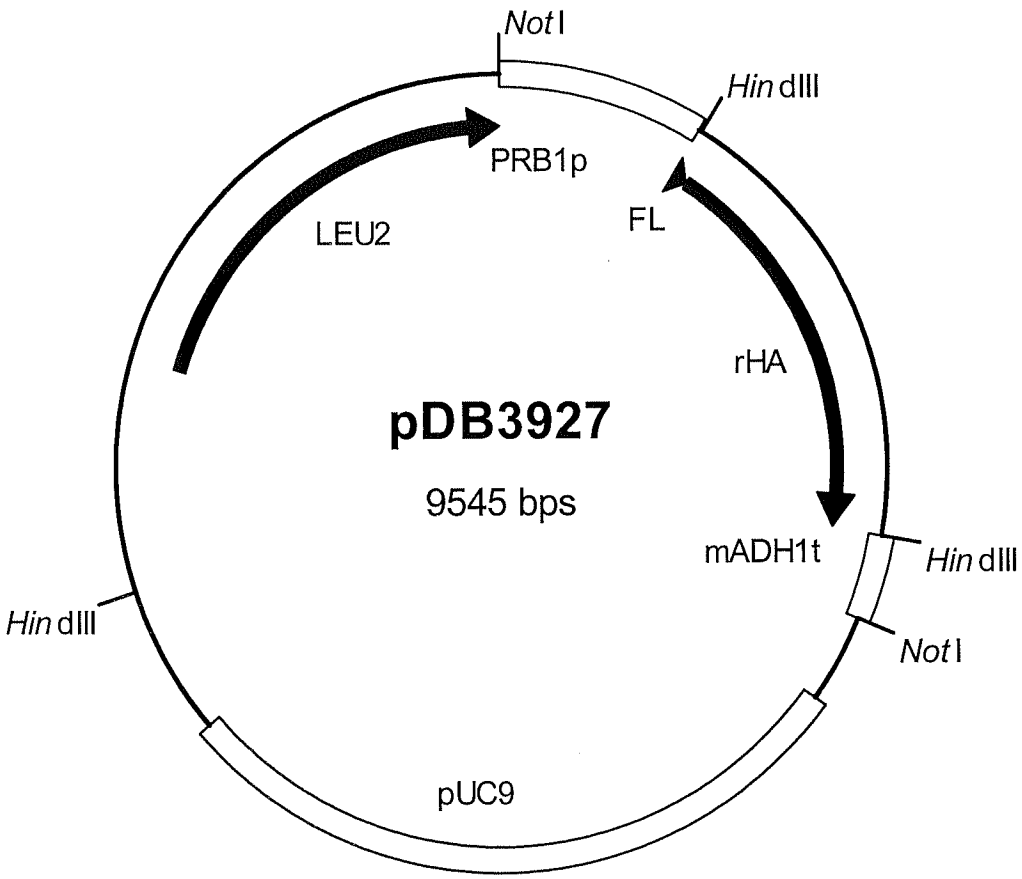

NotI
HindIII
PRB1p
LEU2
FL
rHA
pDB3927
9545 bps
mADH1t
HindIII
NotI
HindIII
pUC9

Figure 13

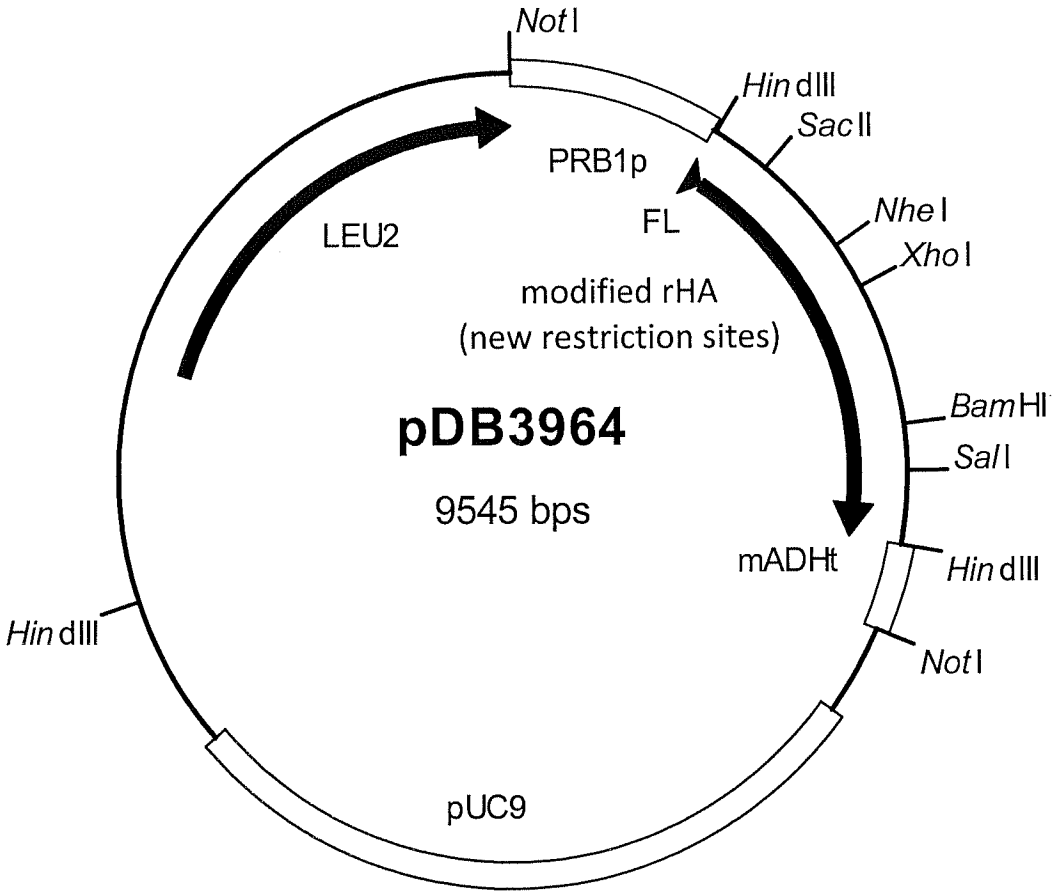

NotI
HindIII
SacII
PRB1p
NheI
FL
XhoI
LEU2
modified rHA
(new restriction sites)
pDB3964
9545 bps
BamHI
SalI
mADHt
HindIII
NotI
HindIII
pUC9

Figure 14

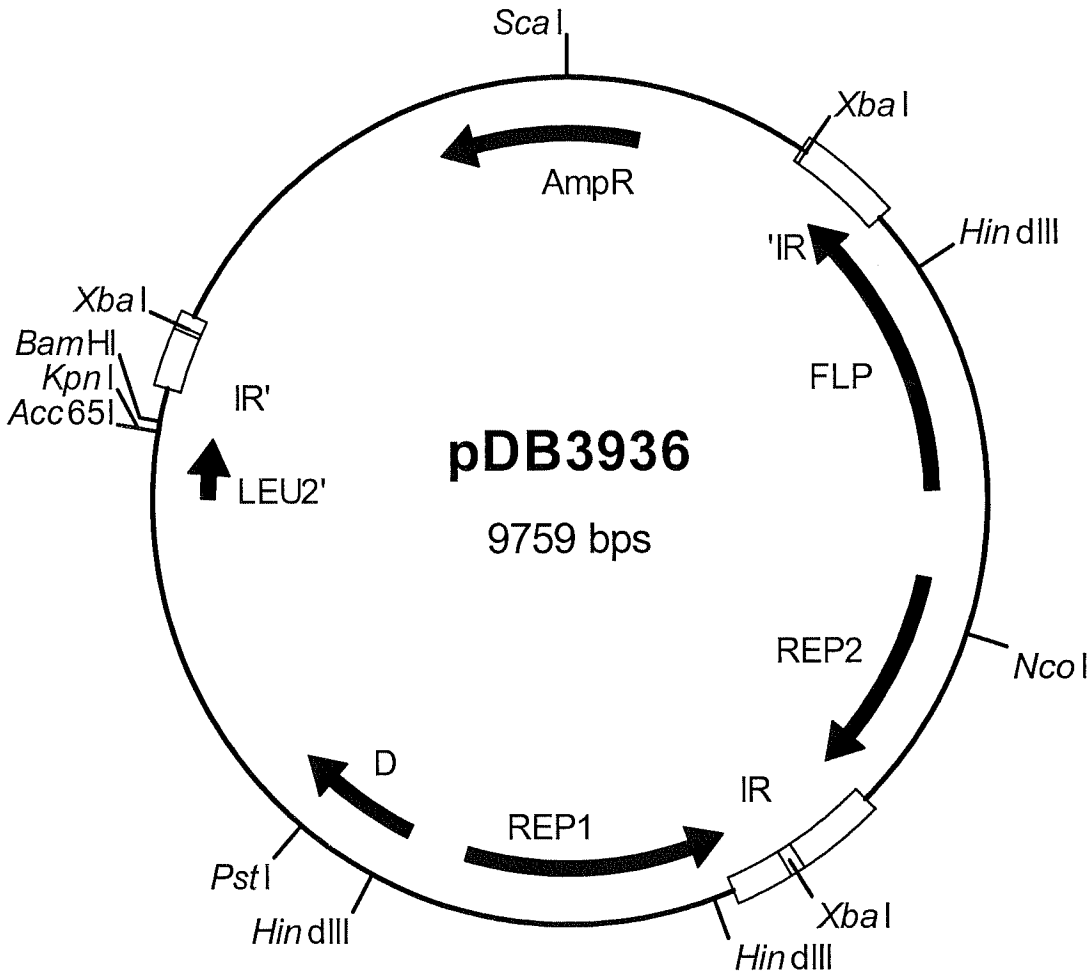

ScaI
XbaI
AmpR
HindIII
'IR
XbaI
BamHI
KpnI
Acc65I
IR'
FLP
pDB3936
9759 bps
LEU2'
REP2
NcoI
D
IR
REP1
PstI
HindIII
XbaI
HindIII

Figure 15

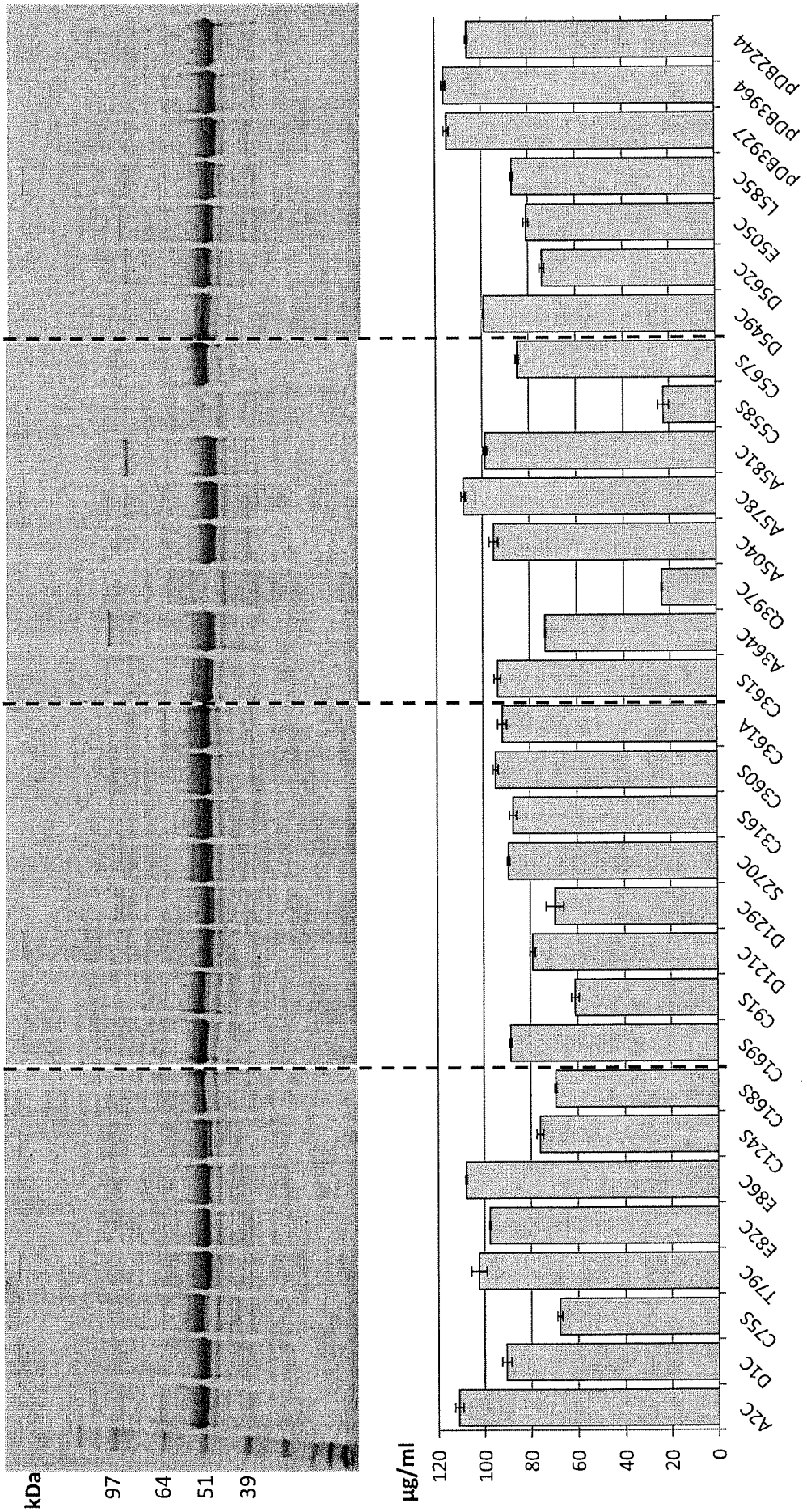

kDa
97
64
51
39
µg/ml
120
100
80
60
40
20
0
A2C
D1C
C75S
T79C
E82C
E86C
C124S
C168S
C169S
C9S
D12AC
D129C
S270C
C316S
C360S
C361A
C361S
A364C
Q397C
A504C
A578C
A581C
C558S
C567S
D549C
D562C
E505C
L585C
PDB3927
PDB3964
PDB2244

Figure 16

Construct Reference	Mutation(s)	Plasmid Number	Transformant	Yeast Stock Number	Combination of Single Mutants	Additional Mutation(s)				DNA SEQ ID No.	Protein SEQ ID No.
						Additional Mutations	Positions Modified in SEQ ID N0. 2	Original Codon	Mutant Codon(s)		
TA33	**A2C, L585C**	**pDB4058**	**C**	**9116**	**SEQ ID 5 SEQ ID 33**	**N/A**	**N/A**	**N/A**	**N/A**	**33**	**78**
TA34	A2C, A504C	pDB4059	B	9117	SEQ ID 5 SEQ ID 25	N/A	N/A	N/A	N/A	34	79
TA35	**A2C, A364C, D562C**	**pDB4060**	**B**	**9118**	**SEQ ID 5 SEQ ID 23 SEQ ID 31**	**N/A**	**N/A**	**N/A**	**N/A**	**35**	**80**
TA36	A2C, C34A, A364C, D562C	pDB4061	A	9119	SEQ ID 5 SEQ ID 23 SEQ ID 31	C34A	100-102	TGT	GCT	36	81
TA38	**A2C, A364C, D562C, L585C**	**pDB4062**	**C**	**9130**	**SEQ ID 5 SEQ ID 23 SEQ ID 31 SEQ ID 33**	**N/A**	**N/A**	**N/A**	**N/A**	**37**	**82**
TA39	C34A, A504C, E505C	pDB4063	C	9120	SEQ ID 25 SEQ ID 32	C34A	100-102	TGT	GCT	38	83
TA41	S270C, A581C	pDB4064	A	9121	SEQ ID 17 SEQ ID 27	N/A	N/A	N/A	N/A	39	84
TA43	D129C, S270C, A581C	pDB4065	A	9122	SEQ ID 16 SEQ ID 17 SEQ ID 27	N/A	N/A	N/A	N/A	40	85
TA46	C169S, C316A	pDB4066	A	9123	SEQ ID 13 SEQ ID 18	N/A	N/A	N/A	N/A	41	86
TA47	**D129C, C360S, L585C**	**pDB4067**	**B**	**9124**	**SEQ ID 16 SEQ ID 20**	**N/A**	**N/A**	**N/A**	**N/A**	**42**	**87**

Construct Reference	Mutation(s)	Plasmid Number	Transformant	Yeast Stock Number	Combination of Single Mutants	Additional Mutation(s)				DNA SEQ ID No.	Protein SEQ ID No.
						Additional Mutations	Positions Modified in SEQ ID N0. 2	Original Codon	Mutant Codon(s)		
					SEQ ID 33						
TA51	**A2C, rHA-Cys**	**pDB4068**	**A**	**9125**	**SEQ ID 5**	**-Cys**	**Addition before 1756**	**N/A**	**TGT**	**43**	**88**
TA57	A2C, G584_L585insC	pDB4069	C	9126	SEQ ID 5	G584_L585insC	Addition before 1753	N/A	TGT	44	89
TA60	A2C, C316del	pDB4070	A	9127	SEQ ID 5	C316del	946-948 (deletion)	TGC	N/A	45	90
TA63	H39C, C253P	pDB4071	A	9128	N/A	H39C, C253P	115-117, 757-759	CAT, TGT	TGT, CCA	46	91
TA64	C177F	pDB4072	C	9129	N/A	C177F	529-531	TGC	TTT	47	92
TA65	Cys-rHA-Ala-Cys	4073	D	9131	N/A	Cys-and -Ala-Cys	Additions before 1 and 1756	N/A	TGT, GCTTGT	48	93

Figure 17

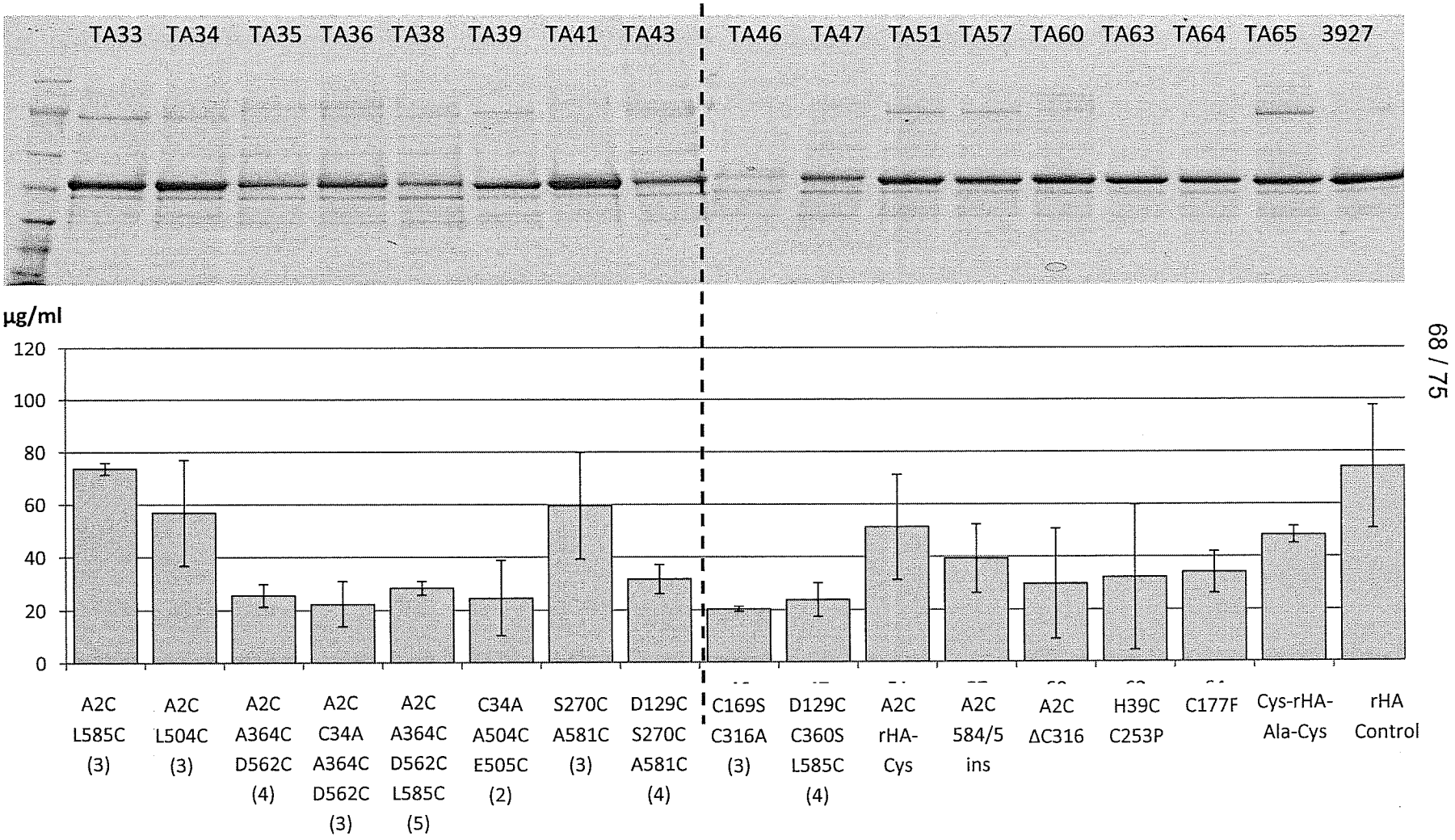

TA33
TA34
TA35
TA36
TA38
TA39
TA41
TA43
TA46
TA47
TA51
TA57
TA60
TA63
TA64
TA65
3927
µg/ml
120
100
80
60
40
20
0
A2C L585C (3)
A2C L504C (3)
A2C A364C D562C (4)
A2C C34A A364C D562C (3)
A2C A364C D562C L585C (5)
C34A A504C E505C (2)
S270C A581C (3)
D129C S270C A581C (4)
C169S C316A (3)
D129C C360S L585C (4)
A2C rHA-Cys
A2C 584/5 ins
A2C ΔC316
H39C C253P
C177F
Cys-rHA-Ala-Cys
rHA Control

Figure 18

Protein	Construct Reference	SEQ ID No.	Fermentation Yield (g/L supernatant)	Colour Intensity after DTNB Treatment
Negative Control (Transferrin)	N/A	N/A	N/A	-
Positive Control (rHA, Human Albumin, Recombumin®)	N/A	50	N/A	+
rHA (A2C, L585C)	TA33	80	2.8	++++
rHA (A2C, A364C, D562C)	TA35	82	1.1	++++
rHA (A2C, A364C, D562C, L585C)	TA38	84	1.3	++++
rHA (D129C, C360S, L585C)	TA47	89	1.6	++++
A2C, rHA-Cys	TA51	90	2.9	++++

Figure 19

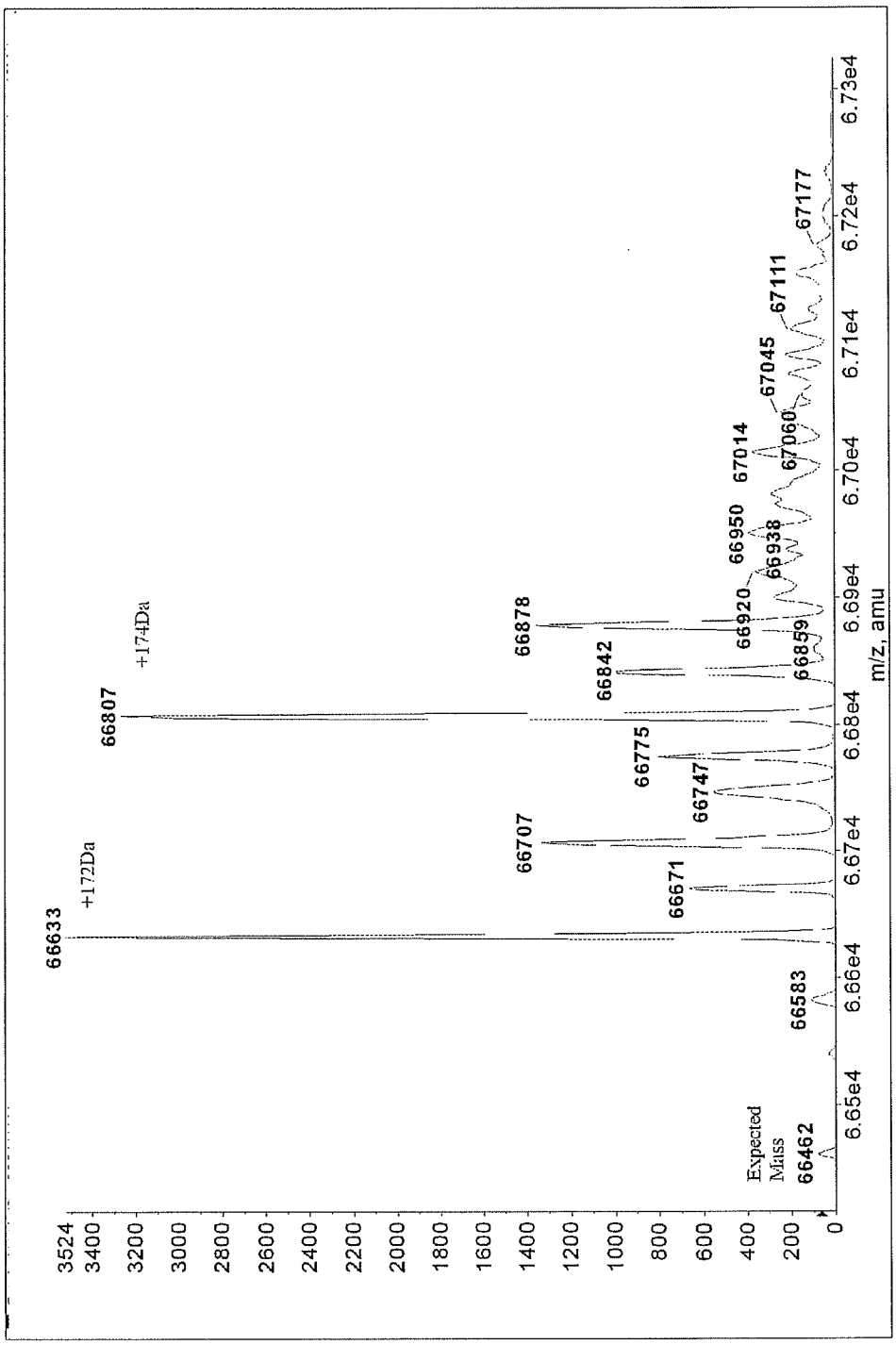

3524
3400
3200
3000
2800
2600
2400
2200
2000
1800
1600
1400
1200
1000
800
600
400
200
0
Expected Muss
66462
66583
66633
+172Da
66671
66707
66747
66775
66807
+174Da
66842
66878
66859
66920
66938
66950
67014
67060
67045
67111
67177
6.65e4
6.66e4
6.67e4
6.68e4
6.69e4
6.70e4
6.71e4
6.72e4
6.73e4
m/z, amu

Figure 20

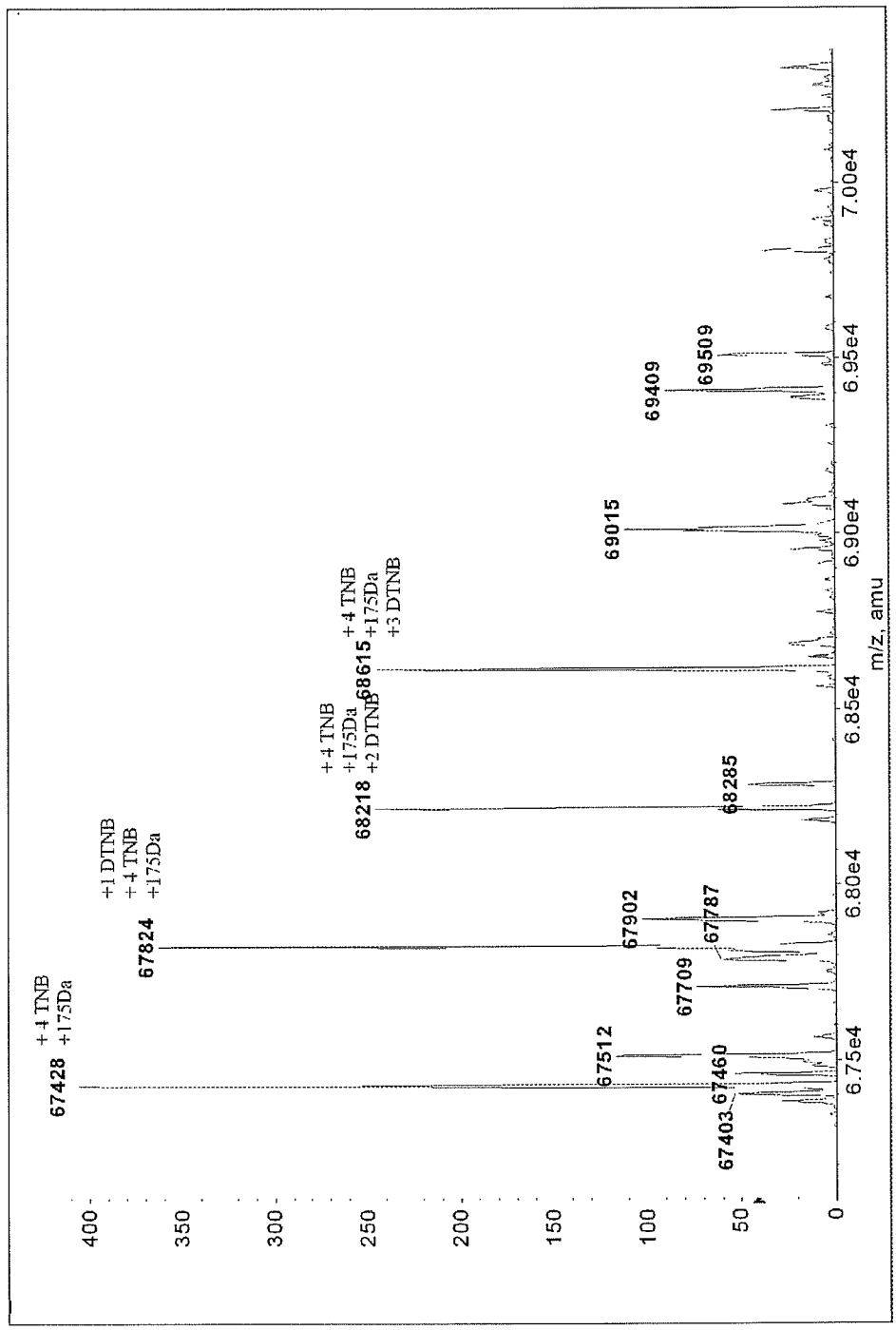

67428
+4 TNB
+175Da
67824
+1 DTNB
+4 TNB
+175Da
68218
+4 TNB
+175Da
+2 DTNB
68615
+4 TNB
+175Da
+3 DTNB
69015
69409
69509
67403
67460
67512
67709
67787
67902
68285
400
350
300
250
200
150
100
50
0
6.75e4
6.80e4
6.85e4
6.90e4
6.95e4
7.00e4
m/z, amu

Figure 21

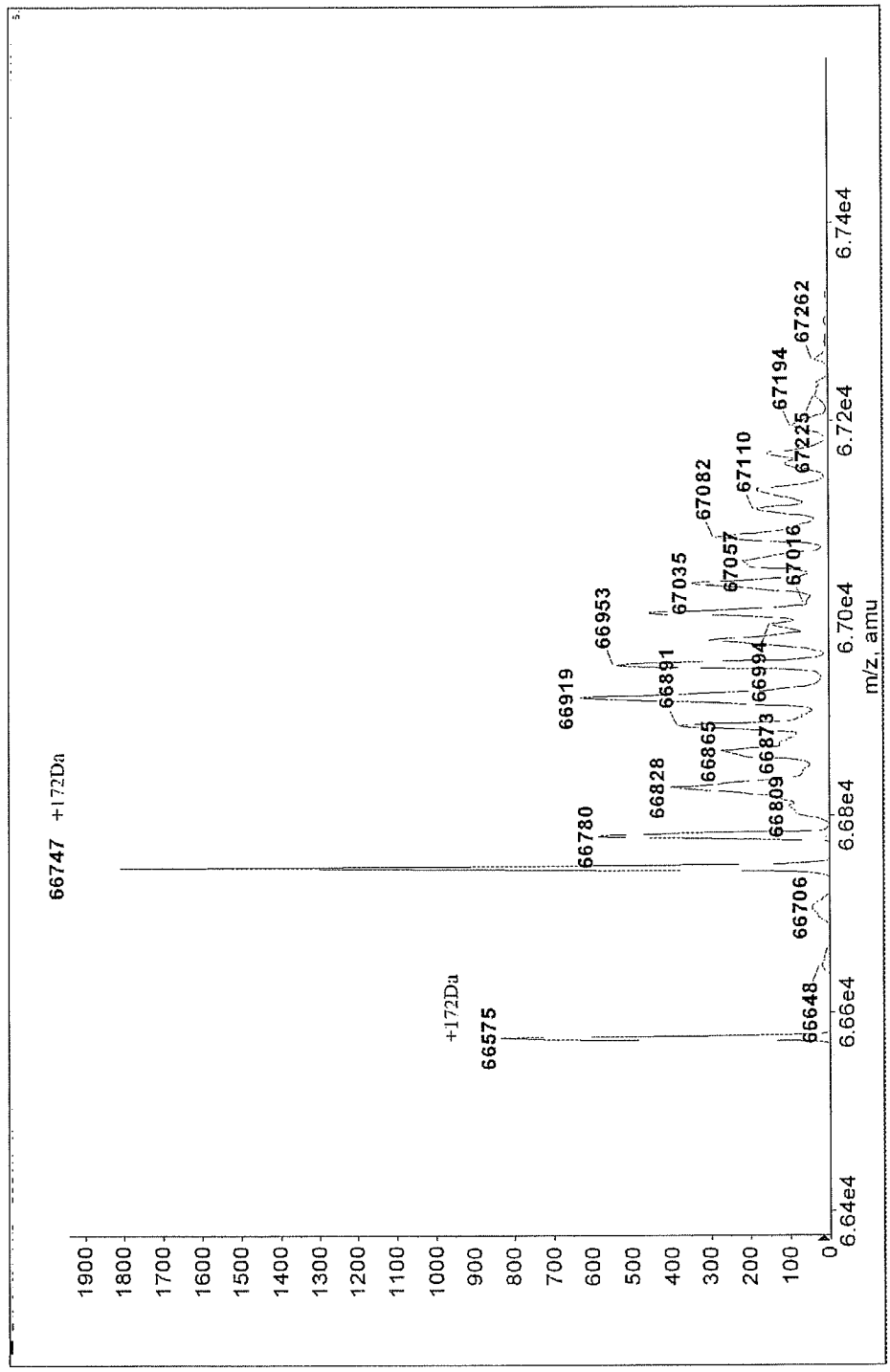

66747 +172Da
+172Da
66575
66648
66706
66780
66809
66828
66865
66873
66891
66919
66953
66994
67016
67035
67057
67082
67110
67225
67194
67262
1900
1800
1700
1600
1500
1400
1300
1200
1100
1000
900
800
700
600
500
400
300
200
100
0
6.64e4
6.66e4
6.68e4
6.70e4
6.72e4
6.74e4
m/z, amu

Figure 22

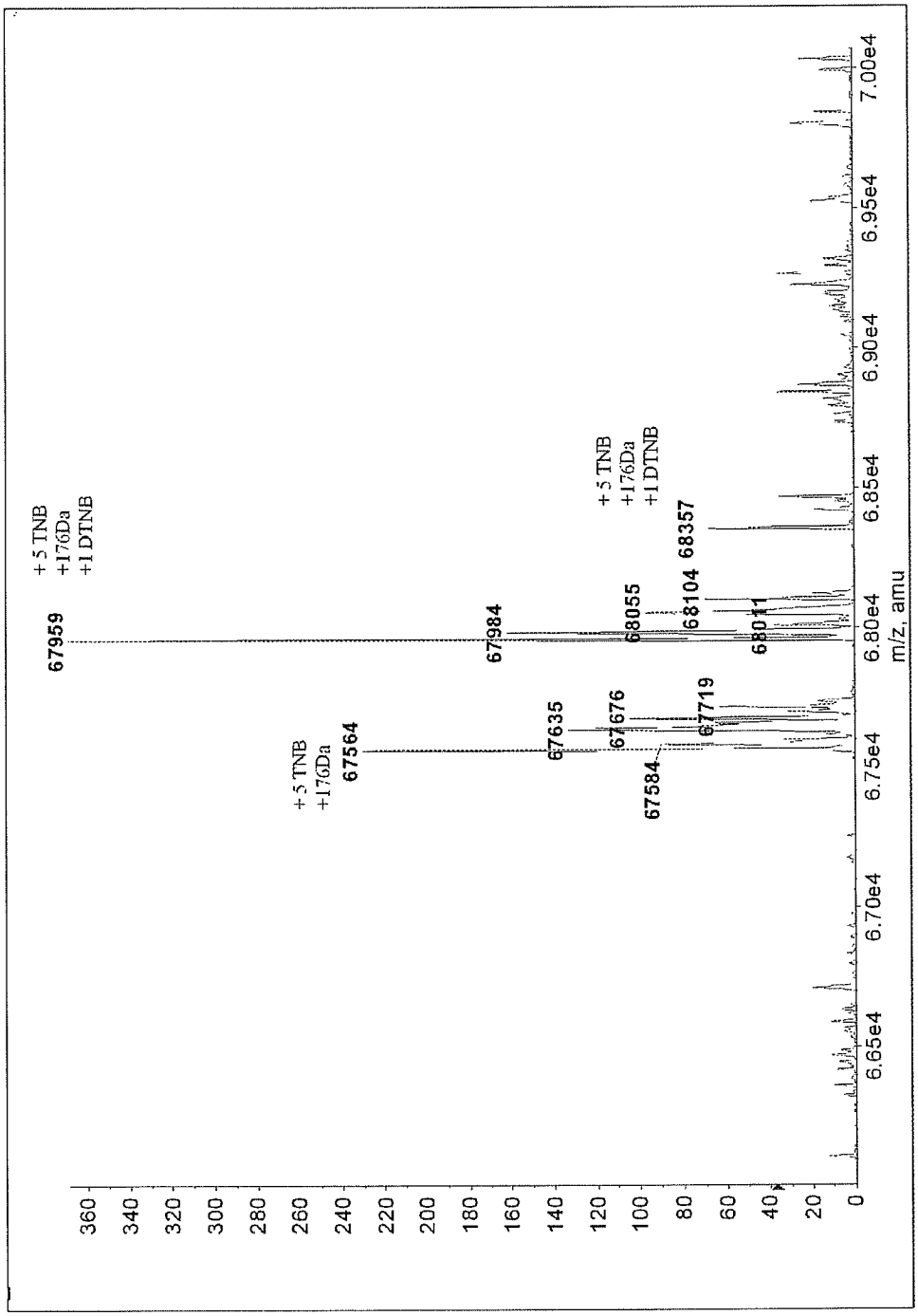

+5 TNB
+176Da
+1 DTNB
67959
+5 TNB
+176Da
67564
67984
67635
67676
67584
67719
+5 TNB
+176Da
+1 DTNB
68055
68104
68357
68011
360
340
320
300
280
260
240
220
200
180
160
140
120
100
80
60
40
20
0
6.65e4
6.70e4
6.75e4
6.80e4
6.85e4
6.90e4
6.95e4
7.00e4
m/z, amu

Figure 23

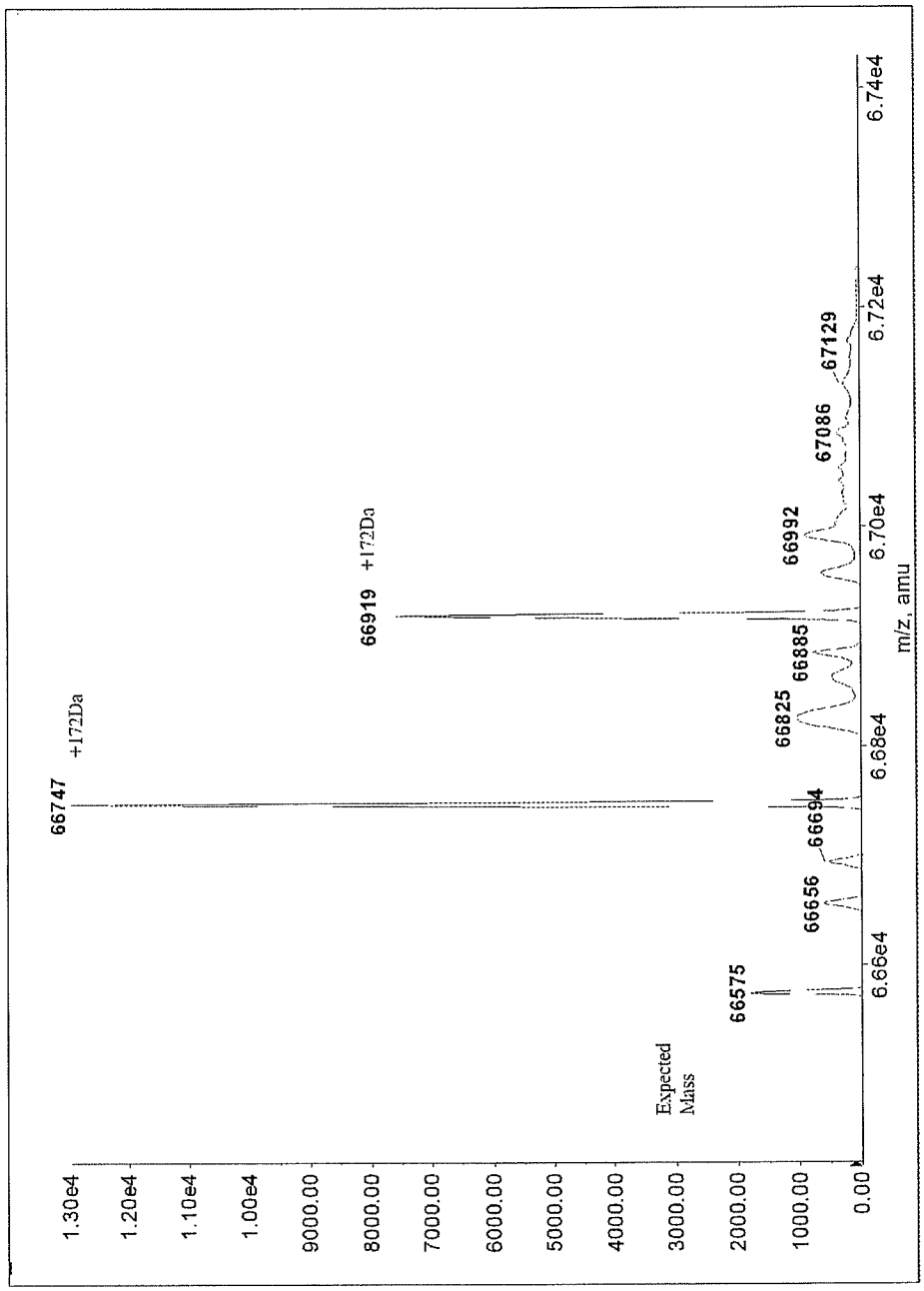
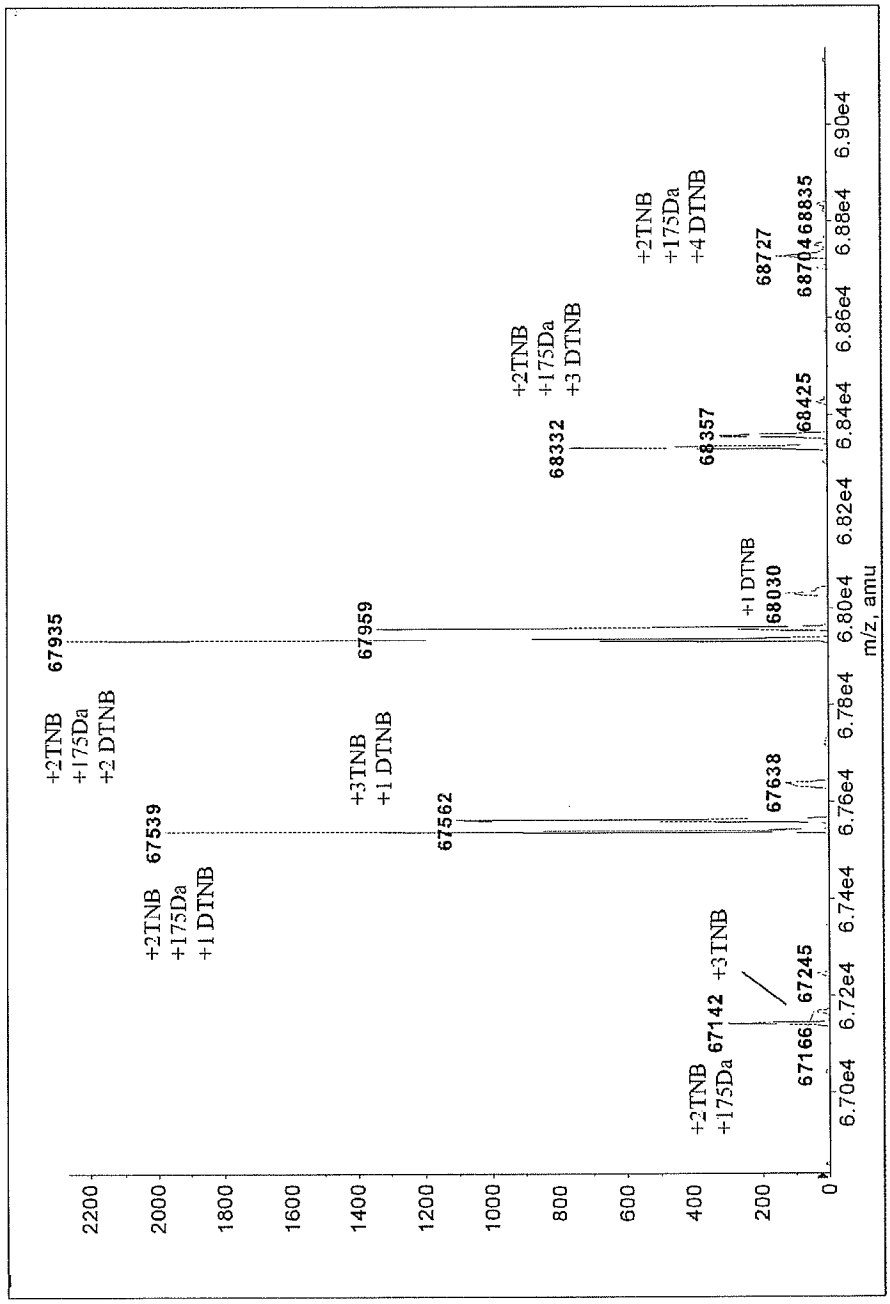

1.30e4
1.20e4
1.10e4
1.00e4
9000.00
8000.00
7000.00
6000.00
5000.00
4000.00
3000.00
2000.00
1000.00
0.00
Expected Mass
66575
66656
66694
66747
+172Da
66825
66885
66919
+172Da
66992
67086
67129
6.66e4
6.68e4
6.70e4
6.72e4
6.74e4
m/z, amu

Figure 24


+2TNB
+175Da
+2 DTNB
67935
+2TNB
+175Da
+1 DTNB
67539
+3TNB
+1 DTNB
67562
67959
+2TNB
+175Da
+3 DTNB
68332
+2TNB
+175Da
+4 DTNB
68357
68425
68727
68704
68835
+1 DTNB
68030
67638
+2TNB
+175Da
67166
67142
+3TNB
67245
2200
2000
1800
1600
1400
1200
1000
800
600
400
200
0
6.70e4
6.72e4
6.74e4
6.76e4
6.78e4
6.80e4
6.82e4
6.84e4
6.86e4
6.88e4
6.90e4
m/z, amu