

Supplementary material for:

The 1.7 Å Resolution Crystal Structure of AT2G44920, a Pentapeptide Repeat Protein in the Thylakoid Lumen of *Arabidopsis thaliana*

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Figure S1: Sequence analysis of AT2G44920 showing PRP motifs and secondary structure elements.

Figure S2: Electrostatic surface potential rendering of AT2G44920.

Figure S3: Multiple sequence alignment used for Consurf analysis.

Figure S4: Size exclusion chromatography analysis of AT2G44920.

Table S1: Consurf analysis results.

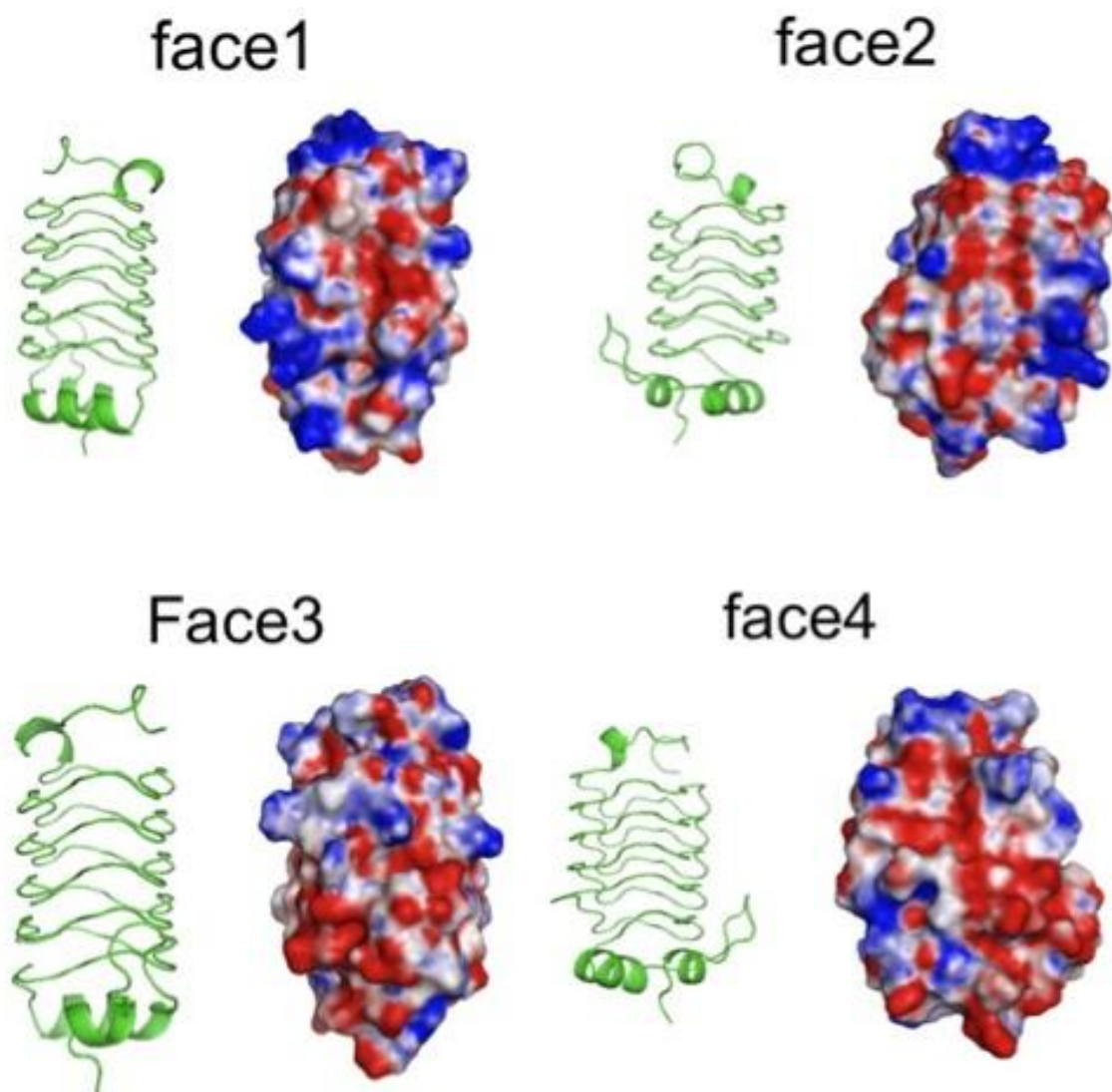


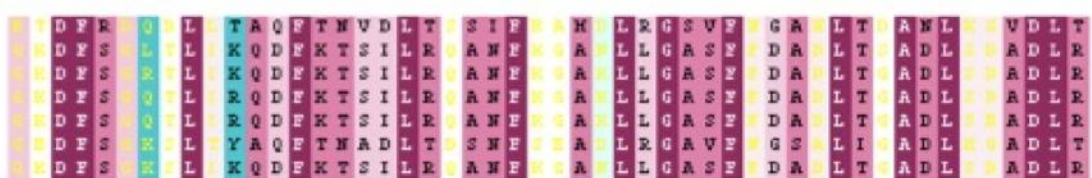
Figure S2. Electrostatic surface plots of four faces of AT2G44920. Plots were generated using the APBS (Baker et al., 2001) plug-in in Pymol (The PyMOL Molecular Graphics System, Version 1.3, Schrödinger, LLC.).

Baker NA, Sept D, Joseph S, Holst MJ, McCammon JA. Electrostatics of nanosystems: application to microtubules and the ribosome. *Proc. Natl. Acad. Sci. USA* 98, 10037-10041 2001.

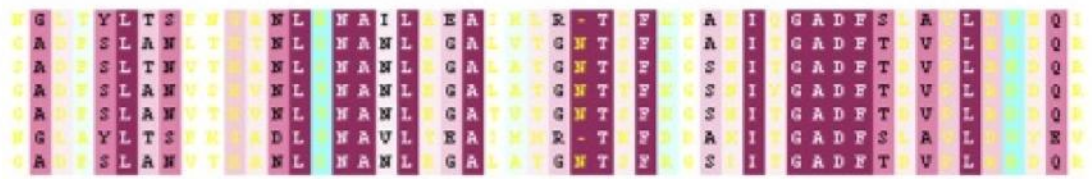
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Populus
Oryza
Arabidopsis
Cyanothece
Vitis



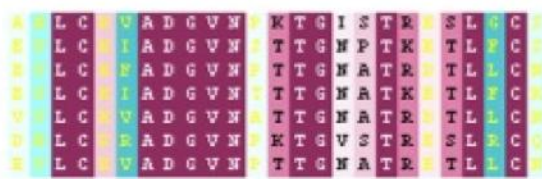
Synechocystis
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Cyanothece
Vitis



Synechocystis
Sorghum
Populus
Oryza
Arabidopsis
Cyanothece
Vitis



Synechocystis
Sorghum
Populus
Oryza
Arabidopsis
Cyanothece
Vitis



1 2 3 4 5 6 7 8 9
Variable Average Conserved

⊠ - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.

Figure S3. Multiple sequence alignment used for Consurf analysis. The genes and plant species included in the alignment are as follows: *Synechocystis* sp. PCC6803 (sll0577); *Sorghum bicolor* (sorghum) (SORBI 03g006310); *Populus trichocarpa* (black cottonwood) (POPTR 563930); *Oryza sativa japonica* (Japanese rice) (Os01g0144100); *Arabidopsis thaliana* (mouseear cress) (AT2G44920); *Cyanothece* 51142 (RFR32); *Vitis vinifera* (wine grape) (Vvi 100244370).

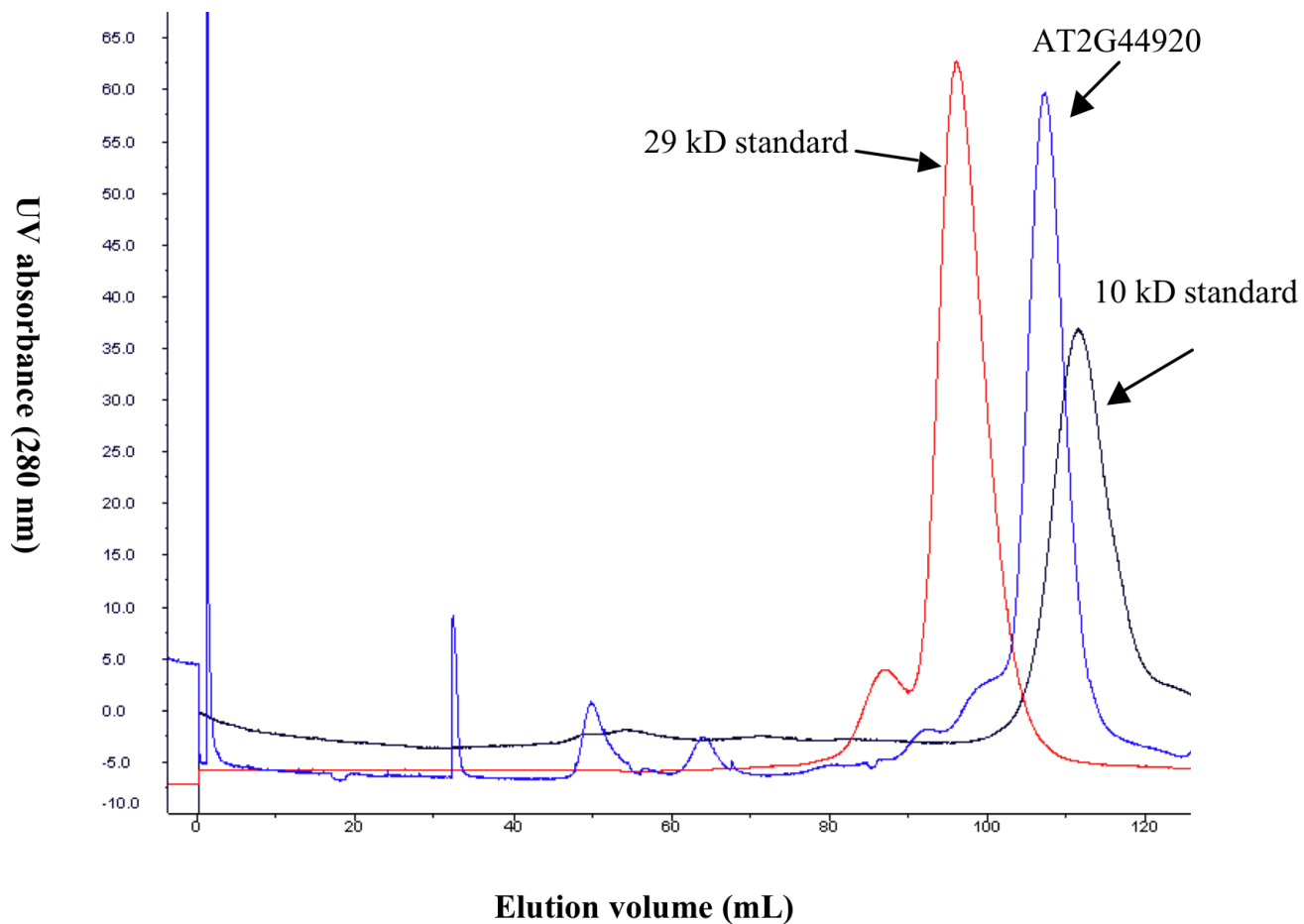


Figure S4. Overlay of SEC chromatogram of AT2G44920 with two protein standards (29 kD carbonic anhydrase and 10 kD 6XHis-tagged ubiquitin run with a flow rate of 1 ml/min on a preparative Superdex 200 column attached to AKTA (GE life science).

Table S1. Consurf analysis for multiple sequence alignment depicted in Figure S3.

Amino Acid Conservation Scores

- POS: The position of the AA in the SEQRES derived sequence.
- SEQ: The SEQRES derived sequence in one letter code.
- 3LATOM: The ATOM derived sequence in three letter code, including the AA's positions as they appear in the PDB file and the chain identifier.
- SCORE: The normalized conservation scores.
- COLOR: The color scale representing the conservation scores (9 - conserved, 1 - variable).
- CONFIDENCE INTERVAL: When using the bayesian method for calculating rates, a confidence interval is assigned to each of the inferred evolutionary conservation scores.
- CONFIDENCE INTERVAL COLORS: When using the bayesian method for calculating rates. The color scale representing the lower and upper bounds of the confidence interval.
- MSA DATA: The number of aligned sequences having an amino acid (non-gapped) from the overall number of sequences at each position.
- RESIDUE VARIETY: The residues variety at each position of the multiple sequence alignment.

POS	SEQ	3LATOM	SCORE (normalized)	COLOR	CONFIDENCE INTERVAL	CONFIDENCE INTERVAL COLORS	MSA DATA	RESIDUE VARIETY
1	M	-	-0.344	6*	-1.258,-0.016	9,5	1/7	M
2	V	-	-0.344	6*	-1.258, 0.292	9,4	1/7	V
3	I	-	-0.344	6*	-1.258, 0.292	9,4	1/7	I
4	L	-	0.308	4*	-0.790, 0.704	8,2	2/7	ML
5	S	-	1.176	1*	-0.260, 3.024	6,1	3/7	A,S,M
6	N	-	1.614	1*	0.292, 3.024	4,1	3/7	A,N,L
7	V	-	0.285	4*	-0.790, 0.704	8,2	3/7	L,V
8	S	-	0.313	4*	-0.790, 0.704	8,2	3/7	S,L
9	L	-	0.360	4*	-0.790, 1.339	8,1	3/7	N,L
10	F	-	0.234	4*	-0.925, 0.704	8,2	3/7	F,V
11	S	-	0.019	5*	-0.925, 0.704	8,2	3/7	S,Y
12	C	-	0.500	3*	-0.790, 1.339	8,1	3/7	C,L
13	C	-	0.206	4*	-0.925, 0.704	8,2	3/7	S,C
14	N	-	0.676	3*	-0.463, 1.339	7,1	3/7	S,T,N
15	I	-	0.377	4*	-0.790, 1.339	8,1	3/7	I,K
16	S	-	1.295	1*	-0.016, 3.024	5,1	3/7	S,L,L
17	Q	-	0.176	4*	-0.925, 0.704	8,2	3/7	Q,P
18	K	-	0.542	3*	-0.637, 1.339	7,1	3/7	K,P
19	P	-	1.881	1*	0.292, 3.024	4,1	3/7	F,P,K
20	S	-	0.122	5*	-0.925, 0.704	8,2	3/7	S,P
21	L	-	1.296	1*	-0.016, 3.024	5,1	3/7	H,I,L
22	F	-	0.945	2*	-0.260, 1.339	6,1	4/7	F,M,L
23	S	-	0.812	2*	-0.463, 1.339	7,1	4/7	A,S,K
24	P	-	0.644	3*	-0.637, 1.339	7,1	3/7	P,I
25	S	-	1.933	1*	0.292, 3.024	4,1	4/7	H,S,M,P
26	S	-	1.980	1*	0.292, 3.024	4,1	5/7	S,A,T,L,L
27	R	-	1.326	1*	-0.016, 3.024	5,1	5/7	S,T,R,I
28	S	-	1.867	1*	0.292, 3.024	4,1	5/7	F,S,K,L
29	S	-	0.794	2*	-0.463, 1.339	7,1	5/7	S,P,G
30	H	-	1.665	1*	0.292, 3.024	4,1	5/7	H,S,A,K
31	C	-	1.100	1*	-0.260, 3.024	6,1	5/7	C,P,L
32	P	-	1.819	1*	0.292, 3.024	4,1	5/7	H,S,P,K
33	I	-	0.786	2*	-0.463, 1.339	7,1	5/7	I,L
34	R	-	2.212	1*	0.704, 3.024	2,1	5/7	A,T,N,R,P
35	C	-	1.599	1*	0.292, 3.024	4,1	5/7	S,H,C,P
36	S	-	0.347	4*	-0.637, 0.704	7,2	5/7	S,C,L
37	Q	-	0.786	2*	-0.463, 1.339	7,1	5/7	Q,P,L
38	S	-	0.537	3*	-0.637, 1.339	7,1	5/7	F,S,P
39	Q	-	2.050	1*	0.704, 3.024	2,1	5/7	H,S,A,Q,L
40	E	-	2.151	1*	0.704, 3.024	2,1	5/7	A,S,N,E,L
41	G	-	1.938	1*	0.292, 3.024	4,1	5/7	F,A,T,G
42	K	-	1.514	1*	-0.016, 3.024	5,1	4/7	S,N,K,G
43	E	-	1.824	1*	0.292, 3.024	4,1	4/7	S,H,A,E
44	V	-	0.728	2*	-0.463, 1.339	7,1	4/7	A,C,V
45	V	-	2.003	1*	0.704, 3.024	2,1	4/7	T,D,P,V
46	T	-	1.268	1*	-0.016, 3.024	5,1	4/7	T,K,P
47	S	-	1.465	1*	-0.016, 3.024	5,1	5/7	S,A,Q,P
48	P	-	2.425	1*	0.704, 3.024	2,1	5/7	Q,T,P,G,V
49	L	-	2.055	1*	0.704, 3.024	2,1	5/7	A,S,N,R,L
50	R	-	1.457	1*	-0.016, 3.024	5,1	5/7	S,R,G,L
51	S	-	0.672	3*	-0.463, 1.339	7,1	5/7	S,I,P
52	V	-	1.561	1*	0.292, 3.024	4,1	5/7	A,N,P,V
53	V	-	2.198	1*	0.704, 3.024	2,1	5/7	F,S,N,R,V
54	W	-	1.893	1*	0.292, 3.024	4,1	5/7	S,W,D,K
55	S	-	0.442	3*	-0.637, 1.339	7,1	5/7	H,S,Q
56	L	-	0.106	5*	-0.790, 0.704	8,2	6/7	M,L,V
57	G	-	1.460	1*	-0.016, 3.024	5,1	6/7	H,G,L,V
58	E	-	2.089	1	0.704, 3.024	2,1	7/7	F,M,K,L,E
59	E	-	2.281	1	0.704, 3.024	2,1	7/7	S,H,D,K,E,V
60	V	-	1.594	1	0.292, 3.024	4,1	7/7	F,Y,L,V
61	S	-	1.240	1*	-0.016, 3.024	5,1	7/7	S,A,T,R,L
62	K	-	1.020	1*	-0.260, 1.339	6,1	7/7	Q,N,R,K,L
63	R	-	1.685	1	0.292, 3.024	4,1	7/7	A,S,T,R,G
64	S	-	1.492	1*	-0.016, 3.024	5,1	7/7	S,F,G,L
65	L	-	1.677	1	0.292, 3.024	4,1	7/7	F,A,T,L
66	F	-	1.052	1*	-0.260, 1.339	6,1	7/7	F,A,I,L,V
67	A	-	-0.881	8	-1.352,-0.637	9,7	7/7	A,V
68	L	-	0.119	5*	-0.790, 0.704	8,2	7/7	I,L,V
69	V	-	0.985	1*	-0.260, 1.339	6,1	7/7	F,T,L,V
70	S	-	-0.138	5*	-0.925, 0.292	8,4	7/7	S,A,V
71	A	-	-0.140	5*	-0.925, 0.292	8,4	7/7	A,L,V
72	S	-	-0.297	6*	-1.046,-0.016	9,5	7/7	S,C,L
73	L	-	-0.470	7*	-1.157,-0.016	9,5	7/7	W,L
74	F	-	0.663	3*	-0.463, 1.339	7,1	7/7	F,I,L

75	F	-	1.117	1*	-0.260, 3.024	6,1	7/7	F,W,I,V
76	V	-	0.822	2*	-0.260, 1.339	6,1	7/7	A,S,T,V
77	D	-	-0.068	5*	-0.925, 0.292	8,4	7/7	A,D,P
78	P	-	-0.583	7	-1.157,-0.260	9,6	7/7	T,P
79	A	-	-1.247	9	-1.520,-1.157	9,9	7/7	A
80	L	-	0.950	2*	-0.260, 1.339	6,1	7/7	I,Y,L,V
81	A	ALA81:A	-1.247	9	-1.520,-1.157	9,9	7/7	A
82	F	PHE82:A	-0.390	6*	-1.157,-0.016	9,5	7/7	F,A
83	K	LYS83:A	-0.080	5*	-0.925, 0.292	8,4	7/7	S,K,I
84	G	GLY84:A	-0.730	8	-1.258,-0.463	9,7	7/7	S,G
85	G	GLY85:A	-0.730	8	-1.258,-0.463	9,7	7/7	S,G
86	G	GLY86:A	-0.187	6*	-0.925, 0.292	8,4	7/7	A,S,G
87	P	PRO87:A	-0.440	7*	-1.157,-0.016	9,5	7/7	P,V
88	Y	TYR88:A	-0.467	7*	-1.157,-0.016	9,5	7/7	T,Y
89	G	GLY89:A	-1.083	9	-1.520,-0.925	9,8	7/7	G
90	Q	GLN90:A	1.077	1*	-0.260, 3.024	6,1	7/7	S,A,Q,K
91	G	GLY91:A	1.142	1*	-0.016, 3.024	5,1	7/7	A,S,Q,G,E
92	V	VAL92:A	-0.425	7*	-1.046,-0.016	9,5	7/7	S,A,V
93	T	THR93:A	-0.099	5*	-0.790, 0.292	8,4	7/7	F,T,Y
94	R	ARG94:A	-0.525	7	-1.157,-0.260	9,6	7/7	R,E
95	G	GLY95:A	-0.082	5*	-0.925, 0.292	8,4	7/7	D,N,G
96	Q	GLN96:A	-0.082	5*	-0.925, 0.292	8,4	7/7	Q,M,V
97	D	ASP97:A	0.265	4*	-0.637, 0.704	7,2	7/7	D,K,V
98	L	LEU98:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
99	S	SER99:A	0.061	5*	-0.790, 0.704	8,2	7/7	S,A,T,I
100	G	GLY100:A	-0.492	7*	-1.157,-0.016	9,5	7/7	G,E
101	K	LYS101:A	0.011	5*	-0.790, 0.292	8,4	7/7	T,K,E
102	D	ASP102:A	-1.201	9	-1.520,-1.046	9,9	7/7	D
103	F	PHE103:A	-1.077	9	-1.520,-0.925	9,8	7/7	F
104	S	SER104:A	-0.875	8	-1.352,-0.637	9,7	7/7	S,R
105	G	GLY105:A	-0.495	7*	-1.157,-0.016	9,5	7/7	D,G
106	Q	GLN106:A	0.984	1*	-0.260, 1.339	6,1	7/7	Q,K,R,L
107	T	THR107:A	0.129	5*	-0.637, 0.704	7,2	7/7	S,T,D
108	L	LEU108:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
109	I	ILE109:A	-0.255	6*	-0.925, 0.292	8,4	7/7	T,I,L
110	R	ARG110:A	1.593	1	0.292, 3.024	4,1	7/7	T,R,K,Y
111	Q	GLN111:A	-0.707	8	-1.258,-0.463	9,7	7/7	A,Q
112	D	ASP112:A	-0.616	7	-1.157,-0.260	9,6	7/7	Q,D
113	F	PHE113:A	-1.077	9	-1.520,-0.925	9,8	7/7	F
114	K	LYS114:A	-0.748	8	-1.258,-0.463	9,7	7/7	T,K
115	T	THR115:A	-0.891	8	-1.352,-0.637	9,7	7/7	T,N
116	S	SER116:A	-0.500	7	-1.046,-0.260	9,6	7/7	A,S,V
117	I	ILE117:A	-0.569	7	-1.157,-0.260	9,6	7/7	D,I
118	L	LEU118:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
119	R	ARG119:A	-0.725	8	-1.258,-0.463	9,7	7/7	T,R
120	Q	GLN120:A	0.032	5*	-0.790, 0.704	8,2	7/7	S,Q,D
121	A	ALA121:A	-0.912	8	-1.352,-0.637	9,7	7/7	A,S
122	N	ASN122:A	-0.853	8	-1.352,-0.637	9,7	7/7	N,I
123	F	PHE123:A	-1.077	9	-1.520,-0.925	9,8	7/7	F
124	K	LYS124:A	0.102	5*	-0.790, 0.704	8,2	7/7	S,K,E
125	G	GLY125:A	0.010	5*	-0.790, 0.292	8,4	7/7	A,G,E
126	A	ALA126:A	-0.709	8	-1.258,-0.463	9,7	7/7	A,M
127	K	LYS127:A	0.506	3*	-0.463, 1.339	7,1	7/7	N,D,K
128	L	LEU128:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
129	L	LEU129:A	-0.532	7	-1.157,-0.260	9,6	7/7	R,L
130	G	GLY130:A	-1.083	9	-1.520,-0.925	9,8	7/7	G
131	A	ALA131:A	-0.837	8	-1.352,-0.637	9,7	7/7	A,S
132	S	SER132:A	-0.732	8	-1.258,-0.463	9,7	7/7	S,V
133	F	PHE133:A	-1.077	9	-1.520,-0.925	9,8	7/7	F
134	F	PHE134:A	-0.404	6*	-1.046,-0.016	9,5	7/7	F,N
135	D	ASP135:A	-0.658	7	-1.258,-0.260	9,6	7/7	D,G
136	A	ALA136:A	-0.861	8	-1.352,-0.637	9,7	7/7	S,A
137	D	ASP137:A	-0.227	6*	-0.925, 0.292	8,4	7/7	A,D,N
138	L	LEU138:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
139	T	THR139:A	-0.902	8	-1.352,-0.637	9,7	7/7	T,I
140	G	GLY140:A	0.093	5*	-0.790, 0.704	8,2	7/7	S,D,G
141	A	ALA141:A	-1.247	9	-1.520,-1.157	9,9	7/7	A
142	D	ASP142:A	-0.778	8	-1.258,-0.463	9,7	7/7	D,N
143	L	LEU143:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
144	S	SER144:A	-0.149	6*	-0.925, 0.292	8,4	7/7	H,S,K
145	E	GLU145:A	-0.165	6*	-0.925, 0.292	8,4	7/7	D,G,E
146	A	ALA146:A	-0.847	8	-1.352,-0.637	9,7	7/7	A,V
147	D	ASP147:A	-1.201	9	-1.520,-1.046	9,9	7/7	D
148	L	LEU148:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
149	R	ARG149:A	-0.725	8	-1.258,-0.463	9,7	7/7	T,R
150	G	GLY150:A	-0.114	5*	-0.925, 0.292	8,4	7/7	S,N,G
151	A	ALA151:A	-0.759	8	-1.258,-0.463	9,7	7/7	A,G
152	D	ASP152:A	-0.354	6*	-1.046,-0.016	9,5	7/7	D,L
153	F	PHE153:A	0.198	4*	-0.637, 0.704	7,2	7/7	A,F,T
154	S	SER154:A	-0.743	8	-1.258,-0.463	9,7	7/7	S,Y
155	L	LEU155:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
156	A	ALA156:A	-0.554	7	-1.157,-0.260	9,6	7/7	A,T
157	N	ASN157:A	-0.945	8	-1.352,-0.790	9,8	7/7	S,N
158	V	VAL158:A	-0.099	5*	-0.925, 0.292	8,4	7/7	F,L,V
159	T	THR159:A	0.022	5*	-0.790, 0.292	8,4	7/7	S,T,N,K
160	K	LYS160:A	-0.427	7*	-1.157,-0.016	9,5	7/7	K,G
161	V	VAL161:A	-0.350	6*	-1.046,-0.016	9,5	7/7	A,T,V
162	N	ASN162:A	-0.903	8	-1.352,-0.637	9,7	7/7	D,N
163	L	LEU163:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
164	T	THR164:A	0.861	2*	-0.260, 1.339	6,1	7/7	S,T,E
165	N	ASN165:A	-1.258	9	-1.520,-1.157	9,9	7/7	N
166	A	ALA166:A	-1.247	9	-1.520,-1.157	9,9	7/7	A
167	N	ASN167:A	-0.313	6	-0.925,-0.016	8,5	7/7	N,I,V

168	L	LEU168:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
169	E	GLU169:A	-0.204	6*	-0.925, 0.292	8,4	7/7	A.T.E
170	G	GLY170:A	-0.564	7	-1.157,-0.260	9,6	7/7	G.E
171	A	ALA171:A	-1.247	9	-1.520,-1.157	9,9	7/7	A
172	T	THR172:A	0.025	5*	-0.790, 0.704	8,2	7/7	T.I.L
173	V	MET173:A	0.156	4*	-0.637, 0.704	7,2	7/7	A.M.V
174	T	MET174:A	-0.369	6*	-1.046,-0.016	9,5	7/7	M.T.L
175	G	GLY175:A	-0.640	7	-1.258,-0.260	9,6	7/7	R.G
176	N	ASN176:A	-0.994	9*	-1.520,-0.790	9,8	5/7	N
177	T	THR177:A	-1.265	9	-1.520,-1.157	9,9	7/7	T
178	S	SER178:A	-0.298	6*	-1.046,-0.016	9,5	7/7	S.T.K
179	F	PHE179:A	-1.077	9	-1.520,-0.925	9,8	7/7	F
180	K	LYS180:A	0.652	3*	-0.463, 1.339	7,1	7/7	D.R.K
181	G	GLY181:A	-0.082	5*	-0.925, 0.292	8,4	7/7	D.N.G
182	S	SER182:A	-0.560	7	-1.157,-0.260	9,6	7/7	S.A
183	N	ASN183:A	-0.382	6*	-1.046,-0.016	9,5	7/7	N.I.K
184	I	ILE184:A	-1.245	9	-1.520,-1.157	9,9	7/7	I
185	T	THR185:A	-0.248	6*	-1.046, 0.292	9,4	7/7	Q.T.Y
186	G	GLY186:A	-1.083	9	-1.520,-0.925	9,8	7/7	G
187	A	ALA187:A	-1.247	9	-1.520,-1.157	9,9	7/7	A
188	D	ASP188:A	-1.201	9	-1.520,-1.046	9,9	7/7	D
189	F	PHE189:A	-1.077	9	-1.520,-0.925	9,8	7/7	F
190	T	THR190:A	-0.942	8	-1.352,-0.790	9,8	7/7	S.T
191	D	ASP191:A	-0.354	6*	-1.046,-0.016	9,5	7/7	D.L
192	V	VAL192:A	-0.884	8	-1.352,-0.637	9,7	7/7	A.V
193	P	PRO193:A	-0.440	7*	-1.157,-0.016	9,5	7/7	P.V
194	L	LEU194:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
195	R	ARG195:A	-0.465	7*	-1.157,-0.016	9,5	7/7	D.R
196	D	ASP196:A	0.877	2*	-0.260, 1.339	6,1	7/7	T.D.E.V
197	D	ASP197:A	-0.181	6*	-0.925, 0.292	8,4	7/7	D.Y.E
198	Q	GLN198:A	-0.812	8	-1.352,-0.637	9,7	7/7	Q.E
199	R	ARG199:A	-0.132	5*	-0.925, 0.292	8,4	7/7	R.I.V
200	V	VAL200:A	0.341	4*	-0.637, 0.704	7,2	7/7	A.D.E.V
201	Y	TYR201:A	0.770	2*	-0.463, 1.339	7,1	7/7	A.K.Y
202	L	LEU202:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
203	C	CYS203:A	-1.052	9	-1.520,-0.790	9,8	7/7	C
204	K	LYS204:A	-0.462	7*	-1.157,-0.016	9,5	7/7	D.K
205	V	VAL205:A	1.090	1*	-0.260, 3.024	6,1	7/7	F.R.I.V
206	A	ALA206:A	-1.247	9	-1.520,-1.157	9,9	7/7	A
207	D	ASP207:A	-1.201	9	-1.520,-1.046	9,9	7/7	D
208	G	GLY208:A	-1.083	9	-1.520,-0.925	9,8	7/7	G
209	V	VAL209:A	-1.237	9	-1.520,-1.157	9,9	7/7	V
210	N	ASN210:A	-1.258	9	-1.520,-1.157	9,9	7/7	N
211	A	ALA211:A	0.213	4*	-0.637, 0.704	7,2	7/7	A.S.T.P
212	T	THR212:A	-0.792	8	-1.258,-0.463	9,7	7/7	T.K
213	T	THR213:A	-1.265	9	-1.520,-1.157	9,9	7/7	T
214	G	GLY214:A	-1.083	9	-1.520,-0.925	9,8	7/7	G
215	N	ASN215:A	-0.313	6	-0.925,-0.016	8,5	7/7	N.I.V
216	A	ALA216:A	-0.525	7	-1.157,-0.260	9,6	7/7	A.S.P
217	T	THR217:A	-1.265	9	-1.520,-1.157	9,9	7/7	T
218	R	ARG218:A	-0.801	8	-1.258,-0.463	9,7	7/7	K.R
219	D	ASP219:A	-0.250	6*	-0.925, 0.292	8,4	7/7	D.E
220	T	THR220:A	-0.942	8	-1.352,-0.790	9,8	7/7	S.T
221	L	LEU221:A	-1.082	9	-1.520,-0.925	9,8	7/7	L
222	L	LEU222:A	1.148	1*	-0.260, 3.024	6,1	7/7	F.R.G.L
223	C	CYS223:A	-1.052	9	-1.520,-0.790	9,8	7/7	C
224	N	ASN224:A	0.688	3*	-0.463, 1.339	7,1	7/7	S.Q.N.K

*Below the confidence cut-off - The calculations for this site were performed on less than 6 non-gapped homologue sequences, or the confidence interval for the estimated score is equal to- or larger than- 4 color grades.