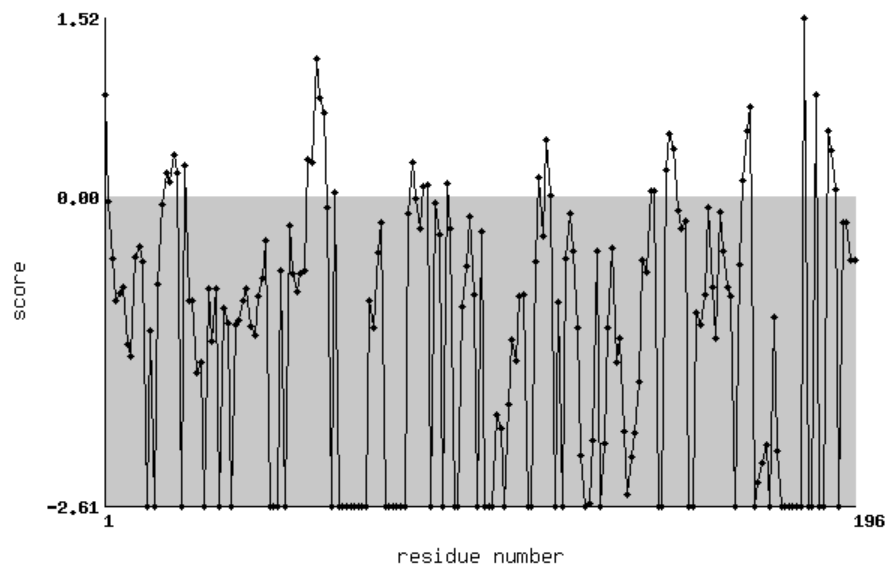
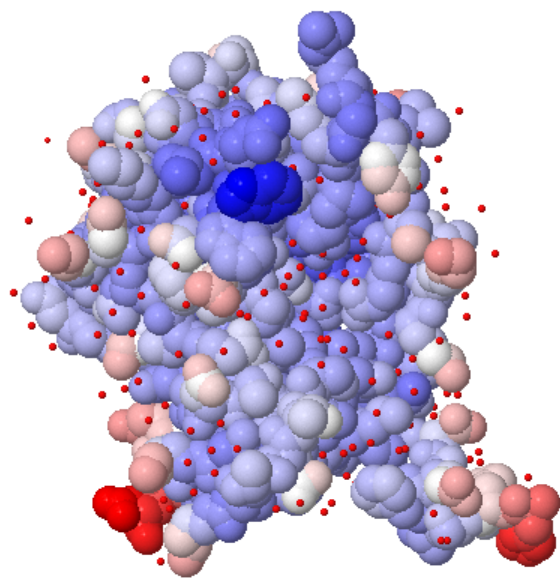


RNA Interface Residue Prediction



RNA interface prediction by averaged ((averaged singlet) + doublet) [A²SD]
The higher the propensity is, the more likely it is to be an interface.



JSmol



Raw Prediction Value

No.	aa	score
1	HIS	0.86
2	HIS	-0.04
3	SER	-0.52
4	VAL	-0.88
5	PHE	-0.81
6	GLU	-0.76
7	ASP	-1.25
8	ASP	-1.35
9	LEU	-0.51
10	PRO	-0.42

11	PHE	-0.55
12	LEU	-2.61
13	GLU	-1.13
14	PHE	-2.61
15	THR	-0.74
16	GLY	-0.06
17	SER	0.21
18	ILE	0.13
19	VAL	0.36
20	TYR	0.20
21	SER	-2.61
22	TYR	0.27
23	ASP	-0.88
24	ALA	-0.88
25	SER	-1.49
26	ASP	-1.40
27	CYS	-2.61
28	SER	-0.77
29	PHE	-1.22
30	LEU	-0.77
31	SER	-2.61
32	GLU	-0.94
33	ASP	-1.06
34	ILE	-2.61
35	SER	-1.08
36	MET	-1.04
37	SER	-0.87
38	LEU	-0.77
39	SER	-1.09
40	ASP	-1.17
41	GLY	-0.84
42	ASP	-0.68
43	VAL	-0.37
44	VAL	-2.61
45	GLY	-2.61
46	PHE	-2.61
47	ASP	-0.62
48	MET	-2.61
49	GLU	-0.24
50	TRP	-0.65
51	PRO	-0.80
52	PRO	-0.65
53	LEU	-0.62
54	TYR	0.32
55	ASN	0.29
56	ARG	1.17
57	GLY	0.84
58	LYS	0.71
59	LEU	-0.09
60	GLY	-2.61
61	LYS	0.04
62	VAL	-2.61
63	ALA	-2.61
64	LEU	-2.61
65	ILE	-2.61
66	GLN	-2.61
67	LEU	-2.61
68	CYS	-2.61

69	VAL	-2.61
70	SER	-0.88
71	GLU	-1.10
72	SER	-0.47
73	LYS	-0.22
74	CYS	-2.61
75	TYR	-2.61
76	LEU	-2.61
77	PHE	-2.61
78	HIS	-2.61
79	VAL	-2.61
80	SER	-0.14
81	SER	0.30
82	MET	-0.01
83	SER	-0.26
84	VAL	0.09
85	PHE	0.10
86	PRO	-2.61
87	GLN	-0.05
88	GLY	-0.31
89	LEU	-2.61
90	LYS	0.11
91	MET	-0.26
92	LEU	-2.61
93	LEU	-2.61
94	GLU	-0.93
95	ASN	-0.58
96	LYS	-0.16
97	ALA	-0.83
98	VAL	-2.61
99	LYS	-0.29
100	LYS	-2.61
101	ALA	-2.61
102	GLY	-2.61
103	VAL	-1.84
104	GLY	-1.96
105	ILE	-2.61
106	GLU	-1.75
107	GLY	-1.20
108	ASP	-1.39
109	GLN	-0.84
110	TRP	-0.83
111	LYS	-2.61
112	LEU	-2.61
113	LEU	-0.55
114	ARG	0.17
115	ASP	-0.33
116	PHE	0.49
117	ASP	0.02
118	ILE	-2.61
119	LYS	-0.89
120	LEU	-2.61
121	LYS	-0.52
122	ASN	-0.14
123	PHE	-0.45
124	VAL	-1.11
125	GLU	-2.19
126	LEU	-2.61

127	THR	-2.59
128	ASP	-2.06
129	VAL	-0.46
130	ALA	-2.61
131	ASN	-2.08
132	LYS	-1.10
133	LYS	-0.43
134	LEU	-1.40
135	LYS	-1.19
136	CYS	-1.98
137	THR	-2.52
138	GLU	-2.20
139	THR	-2.00
140	TRP	-1.56
141	SER	-0.53
142	LEU	-0.63
143	ASN	0.05
144	SER	0.05
145	LEU	-2.61
146	VAL	-2.61
147	LYS	0.23
148	HIS	0.54
149	LEU	0.41
150	LEU	-0.11
151	GLY	-0.26
152	LYS	-0.20
153	GLN	-2.61
154	LEU	-2.61
155	LEU	-0.98
156	LYS	-1.08
157	ASP	-0.83
158	LYS	-0.09
159	SER	-0.76
160	ILE	-1.19
161	ARG	-0.13
162	CYS	-0.45
163	SER	-0.76
164	ASN	-0.84
165	TRP	-2.61
166	SER	-0.57
167	LYS	0.14
168	PHE	0.56
169	PRO	0.77
170	LEU	-2.61
171	THR	-2.41
172	GLU	-2.25
173	ASP	-2.09
174	GLN	-2.61
175	LYS	-1.01
176	LEU	-2.15
177	TYR	-2.61
178	ALA	-2.61
179	ALA	-2.61
180	THR	-2.61
181	ASP	-2.61
182	ALA	-2.61
183	TYR	1.52
184	ALA	-2.61

185	GLY	-2.61
186	PHE	0.86
187	ILE	-2.61
188	ILE	-2.61
189	TYR	0.56
190	ARG	0.40
191	ASN	0.06
192	LEU	-2.61
193	GLU	-0.22
194	ILE	-0.22
195	LEU	-0.53
196	ASP	-0.53

How to visualize the prediction result at hand

1. Download the prediction result file (PDB format) from the following link; [Prediction Result](#)
 2. Launch Rasmol by the following way;
 - % rasmol -script (downloaded file)
 3. The protein is colour coded residue-wise as shown bellow;

 - **red**: highly likely to be an interface
 - **light blue**: unlikely to be an interface
 - **deep blue**: buried residue (not considered as an interface residue)
 4. The scores of the prediction are the numbers between columns 61 and 66 (temperature factor column) of ATOM rows in the file.
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