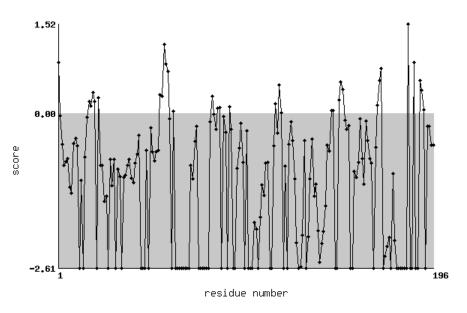
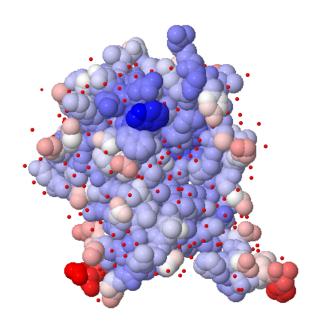
RNA Interface Residue Prediction



RNA interface prediction by averaged ((averaged singlet) + doublet) [A^2SD] 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	DITE	0.55
11	-	-0.55
12	-	-2.61
13	-	-1.13
14		-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	-	-1.22
30	LEU	-0.77
31	SER	-2.61
32		-0.94
33	1	-1.06
34	 	-2.61
35		-1.08
36		-1.04
37		-0.87
H=	SER	
38		-0.77
39	_	-1.09
40	-	-1.17
41	+	-0.84
42	-	-0.68
43	-	-0.37
44		-2.61
45	-	-2.61
46		-2.61
47	-	-0.62
48		-2.61
49		-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		-2.61
64		-2.61
65	-	-2.61
66		-2.61
67	LEU	-2.61
68		-2.61
		01
11		

	60	****	0.04
ļ	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
Ī	76	LEU	-2.61
ĺ	77	PHE	-2.61
أ	78	HIS	-2.61
İ	79	VAL	-2.61
ľ	80	SER	-0.14
ľ	81	SER	0.30
ľ	82	MET	-0.01
ŀ	83	SER	-0.26
ŀ	84	VAL	0.09
ŀ	=	PHE	
	85	PRO	0.10
	86	_	-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
Ī	99	LYS	-0.29
Ī	100	LYS	-2.61
	101	ALA	-2.61
Ī	102	GLY	-2.61
Ī	103	VAL	-1.84
İ	104	GLY	-1.96
ľ	105	ILE	-2.61
ľ	106	GLU	-1.75
ľ	107	GLY	-1.20
ľ	108	ASP	-1.39
ŀ	109	GLN	-0.84
	110	TRP	-0.83
	111	LYS	-2.61
	111	LEU	-2.61
			-0.55
	113		
	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
-		0.64
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	
1 40		-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
155	ш	-0.50
1 F.C	TXC	1 00
156	LYS	-1.08
156 157	LYS ASP	-1.08 -0.83
-		
157	ASP	-0.83
157 158 159	ASP LYS SER	-0.83 -0.09 -0.76
157 158 159 160	ASP LYS SER ILE	-0.83 -0.09 -0.76 -1.19
157 158 159 160 161	ASP LYS SER ILE ARG	-0.83 -0.09 -0.76 -1.19 -0.13
157 158 159 160	ASP LYS SER ILE	-0.83 -0.09 -0.76 -1.19
157 158 159 160 161	ASP LYS SER ILE ARG	-0.83 -0.09 -0.76 -1.19 -0.13
157 158 159 160 161	ASP LYS SER ILE ARG CYS	-0.83 -0.09 -0.76 -1.19 -0.13 -0.45
157 158 159 160 161 162 163	ASP LYS SER ILE ARG CYS SER	-0.83 -0.09 -0.76 -1.19 -0.13 -0.45 -0.76 -0.84
157 158 159 160 161 162 163 164 165	ASP LYS SER ILE ARG CYS SER ASN TRP	-0.83 -0.09 -0.76 -1.19 -0.13 -0.45 -0.76 -0.84 -2.61
157 158 159 160 161 162 163 164 165	ASP LYS SER ILE ARG CYS SER ASN TRP	-0.83 -0.09 -0.76 -1.19 -0.13 -0.45 -0.76 -0.84 -2.61 -0.57
157 158 159 160 161 162 163 164 165 166	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14
157 158 159 160 161 162 163 164 165 166 167	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14 0.56
157 158 159 160 161 162 163 164 165 166	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14
157 158 159 160 161 162 163 164 165 166 167	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14 0.56
157 158 159 160 161 162 163 164 165 166 167	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14 0.56 0.77
157 158 159 160 161 162 163 164 165 166 167 168 169	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR	-0.83 -0.09 -0.76 -1.19 -0.45 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.41
157 158 159 160 161 162 163 164 165 166 167 168 169 170 171	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.41 -2.25
157 158 159 160 161 162 163 164 165 166 167 168 170 171 172 173	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU ASP	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.25 -2.29
157 158 159 160 161 162 163 164 165 166 167 168 170 171 172 173	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.41 -2.25
157 158 159 160 161 162 163 164 165 166 167 168 170 171 172 173	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU ASP	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.25 -2.29
157 158 159 160 161 162 163 164 165 166 167 168 170 171 172 173	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU ASP	-0.83 -0.09 -0.76 -1.19 -0.45 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.25 -2.09 -2.61
157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU ASP GLN LYS	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.41 -2.25 -2.09 -2.61
157 158 159 160 161 162 163 164 165 166 167 170 171 172 173 174 175 176	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU ASP GLN LYS LEU TYR	-0.83 -0.09 -0.76 -1.19 -0.45 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.25 -2.09 -2.61 -1.01 -2.15
157 158 159 160 161 162 163 164 165 166 167 170 171 172 173 174 175 176 177	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU ASP GLN LYS LYS LYS	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.41 -2.25 -2.09 -2.61 -1.01 -2.15 -2.61
157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU ASP GLN LYS LYS LYS ALA ALA	-0.83 -0.09 -0.76 -1.19 -0.45 -0.45 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.25 -2.25 -2.09 -2.61 -1.01 -2.15 -2.61 -2.61 -2.61
157 158 159 160 161 162 163 164 165 166 167 168 170 171 172 173 174 175 176 177 178	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU ASP GLN LYS LYS LYS	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.41 -2.25 -2.09 -2.61 -1.01 -2.15 -2.61
157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU ASP GLN LYS LYS LYS ALA ALA	-0.83 -0.09 -0.76 -1.19 -0.45 -0.45 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.25 -2.25 -2.09 -2.61 -1.01 -2.15 -2.61 -2.61 -2.61
157 158 159 160 161 162 163 164 165 166 167 168 170 171 172 173 174 175 176 177 178	ASP LYS SER ILE ARG CYS SER ASN TRP SER PHE PRO LEU THR GLU ASP GLN LYS LYS LYS LYS TYR ALA ALA THR	-0.83 -0.09 -0.76 -1.19 -0.45 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.25 -2.09 -2.61 -1.01 -2.15 -2.61 -2.61 -2.61 -2.61
157 158 159 160 161 162 163 164 165 166 167 170 171 172 173 174 175 176 177 178 179 180 181	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU ASP GLN LYS LEU TYR ALA ALA THR ASP	-0.83 -0.09 -0.76 -1.19 -0.45 -0.84 -2.61 -0.57 0.14 0.56 0.77 -2.61 -2.25 -2.09 -2.61 -1.01 -2.15 -2.61 -2.61 -2.61 -2.61
157 158 159 160 161 162 163 164 165 166 167 170 171 172 173 174 175 176 177 178 179 180 181	ASP LYS SER ILE ARG CYS SER ASN TRP SER LYS PHE PRO LEU THR GLU ASP GLN LYS LYS LYS ALA ALA THR ASP	-0.83 -0.09 -0.76 -1.19 -0.45 -0.76 -0.84 -2.61 -0.57 -2.61 -2.25 -2.09 -2.61 -1.01 -2.15 -2.61 -2.61 -2.61 -2.61 -2.61 -2.61 -2.61 -2.61

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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
105		
195	LEU	-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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