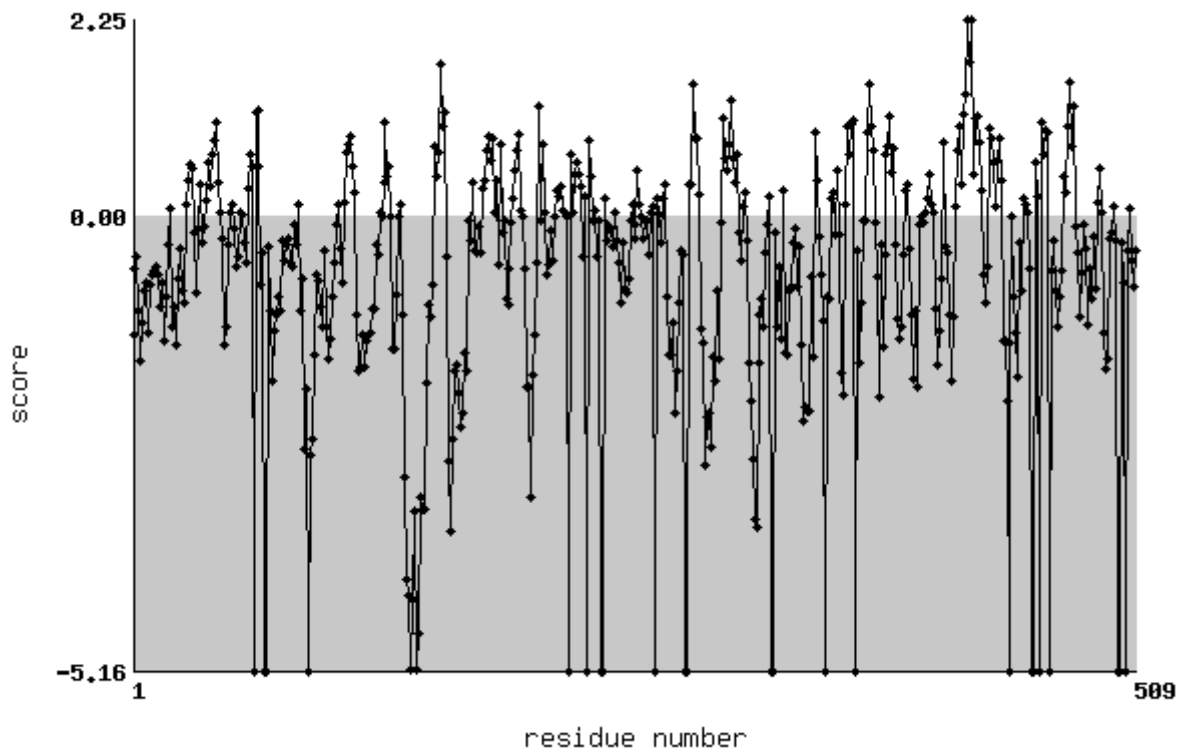


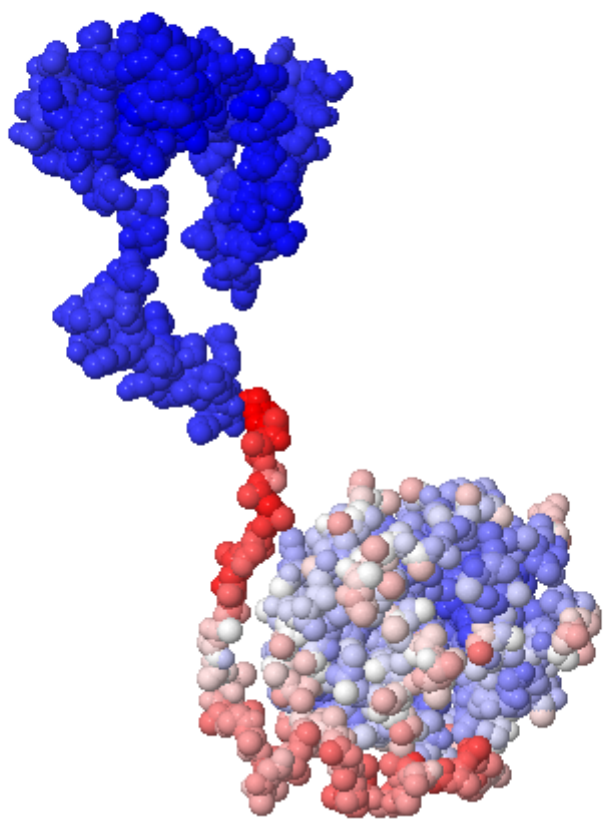
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# RNA Interface Residue Prediction



**RNA interface prediction by averaged ((averaged singlet) + doublet) [ $A^2SD$ ]**  
The higher the propensity is, the more likely it is to be an interface.

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JSmol

15	THR	-1.03
16	TYR	-0.74
17	GLU	-1.41
18	THR	-0.90
19	MET	-0.31
20	PHE	0.09
21	ALA	-1.25
22	PRO	-1.03
23	GLU	-1.45
24	PHE	-0.70
25	GLY	-0.35
26	PRO	-0.85
27	GLU	-0.97
28	ASN	0.13
29	PRO	0.41
30	PHE	0.60
31	ARG	0.56
32	THR	-0.17
33	GLN	-0.86

34	GLN	-0.13
35	MET	0.36
36	ALA	-0.30
37	ALA	-0.11
38	PRO	0.19
39	ARG	0.62
40	ASN	0.34
41	MET	0.70
42	LEU	0.87
43	SER	1.07
44	GLY	0.40
45	TYR	0.05
46	ALA	-0.25
47	GLU	-1.45
48	PRO	-1.26
49	ALA	-0.31
50	HIS	0.06
51	ILE	0.14
52	ASN	-0.13
53	ASP	-0.56
54	PHE	-0.46
55	MET	0.04
56	PHE	0.03
57	GLU	-0.30
58	GLN	-0.53
59	GLN	0.33
60	ARG	0.70
61	ARG	0.57
62	THR	-5.16
63	PHE	1.19
64	ALA	1.22
65	THR	0.57
66	TYR	-0.76
67	GLY	-0.41
68	TYR	-5.16
69	ALA	-5.16
70	LEU	-0.33
71	ASP	-1.07
72	PRO	-1.87
73	SER	-1.30
74	LEU	-1.11

75	ASP	-0.91
76	ASN	-1.06
77	HIS	-0.28
78	GLN	-0.49
79	VAL	-0.32
80	SER	-0.24
81	ALA	-0.51
82	LYS	-0.56
83	TYR	-0.09
84	ILE	-0.32
85	GLY	0.14
86	SER	-1.07
87	VAL	-0.71
88	GLU	-2.63
89	GLU	-1.96
90	ALA	-5.16
91	GLU	-2.72
92	LYS	-2.53
93	ASN	-1.57
94	GLN	-0.65
95	GLY	-0.73
96	LEU	-1.03
97	THR	-1.26
98	VAL	-0.39
99	PHE	-1.24
100	GLU	-1.61
101	THR	-1.38
102	GLY	-0.91
103	GLN	-0.53
104	LYS	-0.09
105	LYS	0.15
106	THR	-0.36
107	GLU	-0.75
108	LYS	0.17
109	ARG	0.73
110	LYS	0.82
111	LYS	0.92
112	PHE	0.58
113	LYS	0.27
114	GLU	-1.11
115	ASN	-1.75

116	ASP	-1.71
117	ALA	-1.35
118	SER	-1.70
119	ASN	-1.42
120	ILE	-1.35
121	ASP	-1.31
122	GLY	-1.05
123	PHE	-1.04
124	LEU	-0.31
125	GLY	-0.43
126	PRO	0.04
127	TRP	0.01
128	ALA	0.39
129	LYS	1.08
130	TYR	0.46
131	VAL	0.58
132	ASP	-0.00
133	GLU	-1.50
134	LYS	-1.51
135	ASP	-0.88
136	VAL	0.00
137	ALA	0.15
138	LYS	-1.11
139	PRO	-2.96
140	SER	-4.13
141	GLU	-4.31
142	GLU	-5.14
143	GLU	-4.35
144	GLN	-3.34
145	LYS	-5.14
146	GLU	-4.74
147	LEU	-3.18
148	ASP	-3.33
149	GLU	-3.32
150	ILE	-1.89
151	THR	-0.99
152	ALA	-1.13
153	LYS	-0.77
154	ARG	0.80
155	GLN	0.46

156	LYS	0.74
157	LYS	1.74
158	GLY	1.02
159	LYS	1.20
160	GLN	-0.46
161	GLU	-2.77
162	GLU	-3.58
163	GLU	-2.52
164	LYS	-1.76
165	PRO	-1.68
166	GLY	-2.01
167	GLU	-2.39
168	GLU	-2.23
169	LYS	-1.54
170	THR	-1.74
171	ILE	-0.04
172	LEU	-0.28
173	HIS	0.39
174	VAL	-0.39
175	LYS	-0.40
176	GLU	-0.10
177	MET	-0.40
178	TYR	0.32
179	ASP	0.42
180	TYR	0.76
181	GLN	0.92
182	GLY	0.64
183	ARG	0.90
184	SER	0.06
185	TYR	0.42
186	LEU	-0.54
187	HIS	0.82
188	ILE	-0.18
189	PRO	-0.04
190	GLN	-0.92
191	ASP	-0.99
192	VAL	-0.59
193	GLY	-0.06
194	VAL	0.20
195	ASN	0.52
196	LEU	0.76

197	ARG	0.95
198	SER	0.07
199	THR	0.01
200	MET	-0.58
201	PRO	-1.93
202	PRO	-1.94
203	GLU	-3.18
204	LYS	-1.79
205	CYS	-1.34
206	TYR	-0.52
207	LEU	1.26
208	PRO	-0.04
209	LYS	0.83
210	LYS	0.04
211	GLN	-0.66
212	ILE	-0.55
213	HIS	-0.15
214	VAL	-0.49
215	TRP	-0.00
216	SER	0.31
217	GLY	0.23
218	HIS	0.34
219	THR	0.07
220	LYS	0.06
221	GLY	0.01
222	VAL	-5.16
223	SER	0.70
224	ALA	0.04
225	VAL	0.48
226	ARG	0.62
227	LEU	0.49
228	PHE	0.35
229	PRO	-0.45
230	LEU	0.24
231	SER	-5.16
232	GLY	0.86
233	HIS	0.46
234	LEU	-0.03
235	LEU	0.08
236	LEU	-0.46
237	SER	-0.04

238	CYS	-5.16
239	SER	-5.16
240	MET	0.22
241	ASP	-0.27
242	CYS	-0.12
243	LYS	-0.13
244	ILE	-0.34
245	LYS	0.06
246	LEU	-0.28
247	TRP	-0.51
248	GLU	-0.98
249	VAL	-0.29
250	TYR	-0.81
251	GLY	-0.86
252	GLU	-0.71
253	ARG	-0.03
254	ARG	0.13
255	CYS	-0.24
256	LEU	-0.09
257	ARG	0.54
258	THR	0.15
259	PHE	0.01
260	ILE	-0.25
261	GLY	-0.03
262	HIS	-0.04
263	SER	-0.42
264	LYS	0.05
265	ALA	0.11
266	VAL	-5.16
267	ARG	0.20
268	ASP	0.02
269	ILE	-0.30
270	CYS	0.20
271	PHE	0.37
272	ASN	-0.91
273	THR	-1.58
274	ALA	-1.56
275	GLY	-1.20
276	THR	-2.22
277	GLN	-1.74



278	PHE	-0.97
279	LEU	-0.38
280	SER	-0.44
281	ALA	-5.16
282	ALA	-5.16
283	TYR	0.36
284	ASP	0.37
285	ARG	1.50
286	TYR	0.90
287	LEU	0.90
288	LYS	0.25
289	LEU	-1.28
290	TRP	-1.44
291	ASP	-2.83
292	THR	-2.27
293	GLU	-2.23
294	THR	-2.61
295	GLY	-1.60
296	GLN	-1.87
297	CYS	-0.85
298	ILE	-1.62
299	SER	-0.06
300	ARG	1.13
301	PHE	0.67
302	THR	0.54
303	ASN	0.83
304	ARG	1.32
305	LYS	0.67
306	VAL	0.39
307	PRO	0.70
308	TYR	-0.17
309	CYS	-0.50
310	VAL	0.12
311	LYS	0.28
312	PHE	-0.27
313	ASN	-1.67
314	PRO	-2.10
315	ASP	-2.75
316	GLU	-3.43
317	ASP	-3.53
318	LYS	-1.66

319	GLN	-1.12
320	ASN	-0.92
321	LEU	-1.26
322	PHE	-0.41
323	VAL	-0.08
324	ALA	0.23
325	GLY	-5.16
326	MET	-5.16
327	SER	-0.18
328	ASP	-1.26
329	LYS	-0.57
330	LYS	-1.39
331	ILE	0.29
332	VAL	-1.55
333	GLN	-1.56
334	TRP	-0.85
335	ASP	-0.80
336	ILE	-0.29
337	ARG	-0.13
338	SER	-0.79
339	GLY	-0.34
340	GLU	-1.45
341	ILE	-2.31
342	VAL	-2.16
343	GLN	-2.20
344	GLU	-2.21
345	TYR	-0.68
346	ASP	-1.59
347	ARG	0.97
348	HIS	0.42
349	LEU	-0.23
350	GLY	-0.65
351	ALA	-1.19
352	VAL	-5.16
353	ASN	-0.91
354	THR	-0.92
355	ILE	0.20
356	VAL	0.28
357	PHE	-0.21
358	VAL	0.54
359	ASP	-0.19

360	GLU	-1.77
361	ASN	-2.02
362	ARG	0.15
363	ARG	1.04
364	PHE	0.71
365	VAL	1.05
366	SER	1.10
367	THR	-5.16
368	SER	-0.38
369	ASP	-1.67
370	ASP	-0.98
371	LYS	-0.03
372	SER	-0.03
373	LEU	0.97
374	ARG	1.52
375	VAL	1.04
376	TRP	0.76
377	GLU	-0.07
378	TRP	-0.68
379	ASP	-2.04
380	ILE	-0.31
381	PRO	-1.47
382	VAL	-0.44
383	ASP	0.70
384	PHE	0.81
385	LYS	1.15
386	TYR	0.51
387	ILE	0.78
388	ALA	-0.31
389	GLU	-1.15
390	PRO	-1.39
391	SER	-1.26
392	MET	-0.44
393	HIS	0.31
394	SER	0.37
395	MET	-0.36
396	PRO	-1.12
397	ALA	-1.85
398	VAL	-1.07
399	THR	-1.94

400	LEU	-0.08
401	SER	0.00
402	PRO	-0.06
403	ASN	0.04
404	GLY	0.20
405	LYS	0.49
406	TRP	0.15
407	LEU	0.06
408	ALA	-1.04
409	CYS	-1.69
410	GLN	-1.30
411	SER	-0.71
412	MET	0.84
413	ASP	-0.34
414	ASN	-0.40
415	GLN	-1.12
416	ILE	-1.86
417	LEU	-1.13
418	ILE	0.12
419	PHE	0.75
420	GLY	1.03
421	ALA	0.38
422	GLN	1.17
423	ASN	1.39
424	ARG	2.23
425	PHE	1.77
426	ARG	2.25
427	LEU	0.49
428	ASN	1.12
429	LYS	1.15
430	LYS	0.84
431	LYS	0.31
432	ILE	-0.65
433	PHE	-0.97
434	LYS	-0.57
435	GLY	1.00
436	HIS	0.90
437	MET	0.63
438	VAL	0.11
439	ALA	0.64
440	GLY	0.90

441	TYR	0.41
442	ALA	-1.40
443	CYS	-1.41
444	GLN	-2.09
445	VAL	-5.16
446	ASP	-1.43
447	PHE	0.00
448	SER	-0.90
449	PRO	-1.32
450	ASP	-1.81
451	MET	-0.29
452	SER	-0.84
453	TYR	0.21
454	VAL	0.15
455	ILE	0.06
456	SER	-0.58
457	GLY	-5.16
458	ASP	-5.16
459	GLY	0.63
460	ASN	0.24
461	GLY	-5.16
462	LYS	1.08
463	LEU	0.70
464	ASN	0.99
465	ILE	0.97
466	TRP	-5.16
467	ASP	-0.61
468	TRP	-0.27
469	LYS	-0.83
470	THR	-1.25
471	THR	-0.91
472	LYS	-0.61
473	LEU	0.45
474	TYR	0.27
475	SER	1.02
476	ARG	1.53
477	PHE	0.80
478	LYS	1.26
479	ALA	-0.10
480	HIS	-0.41
481	ASP	-1.13

482	LYS	-0.63
483	VAL	-0.09
484	CYS	-0.35
485	ILE	-1.23
486	GLY	-0.59
487	ALA	-0.92
488	VAL	-0.23
489	TRP	-0.82
490	HIS	0.16
491	PRO	0.55
492	HIS	0.04
493	GLU	-1.31
494	THR	-1.72
495	SER	-1.61
496	LYS	-0.25
497	VAL	-0.18
498	ILE	0.12
499	THR	-0.27
500	CYS	-5.16
501	GLY	-5.16
502	TRP	-0.29
503	ASP	-0.74
504	GLY	-5.16
505	LEU	-0.38
506	ILE	0.09
507	LYS	-0.50
508	LEU	-0.79
509	TRP	-0.39

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## 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.

