

BcePred Prediction Server

The server displays 1.[GRAPHICAL RESULT](#) 2.[TABULAR RESULT](#) 3.[Overlap Display](#)

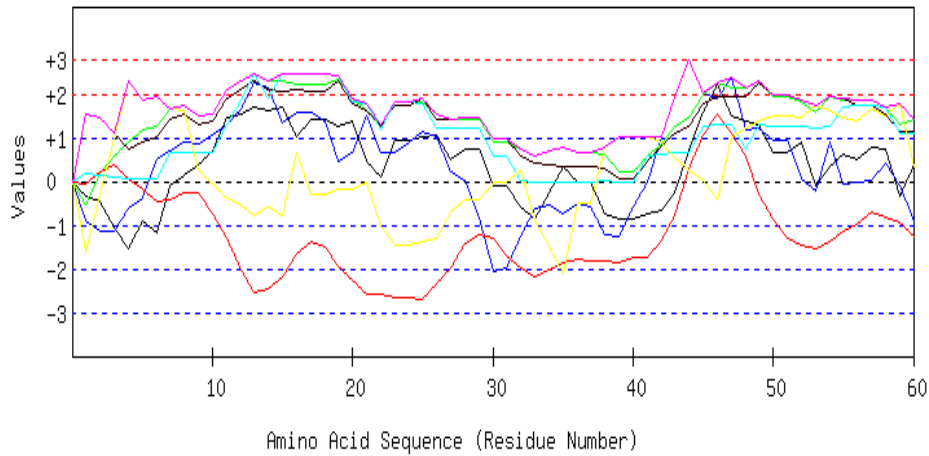
seqname=

Seq=VSFPYFISPEQAMRERSELARKGIARAKSVVALAYAGGVLFVAENPSRSLQKISELYDRVGFAAAGKFNEFD
NLRRGGIQFADTRGYAYDRRDVTGRQLANVYAQTLGTIFTEQAKPYEVELCVAEVAHYGETKRPELYRITYDGSIA
DEPHFVVMGGTTEPIANALKESYAENASLTDALRIAVAALRAGSADTSGGDQPTLGVASLEVAVLDANRPRRAFR
RITGSALQALLVDQESPQSDGESSG

Length=248

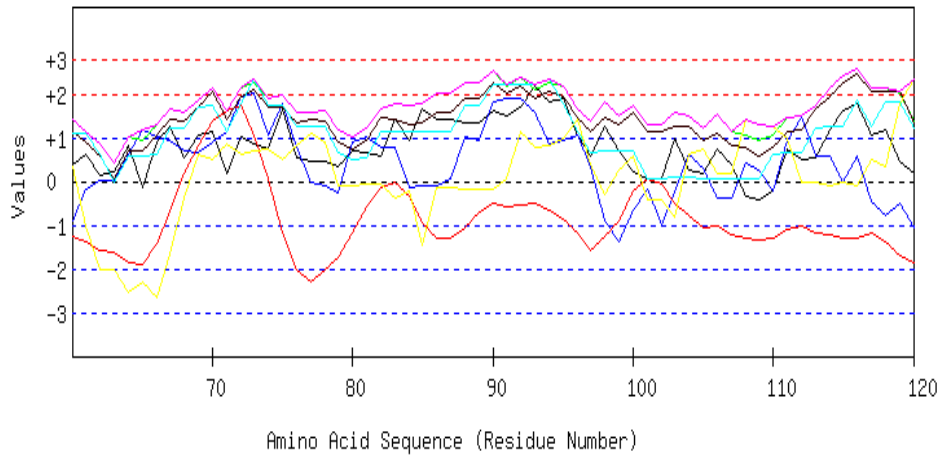
GRAPHICAL RESULT

GRAPHICAL RESULT :: SEQ 1 to 60



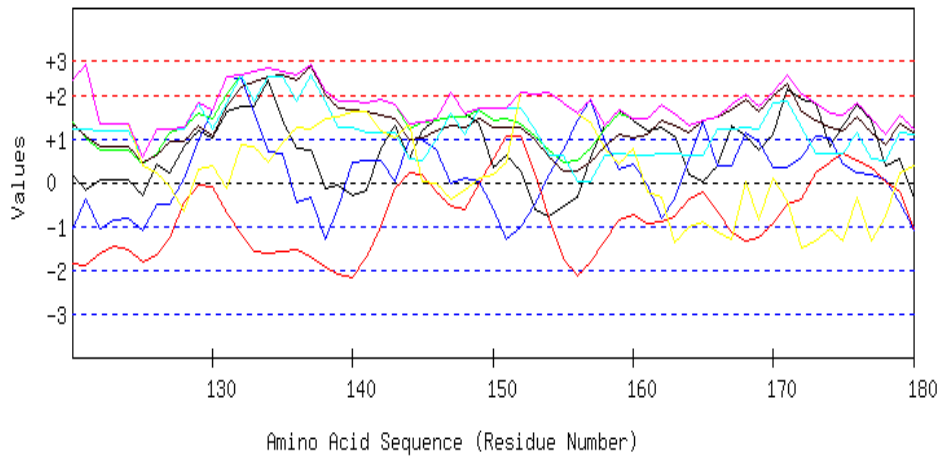
Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

GRAPHICAL RESULT :: SEQ 61 to 120



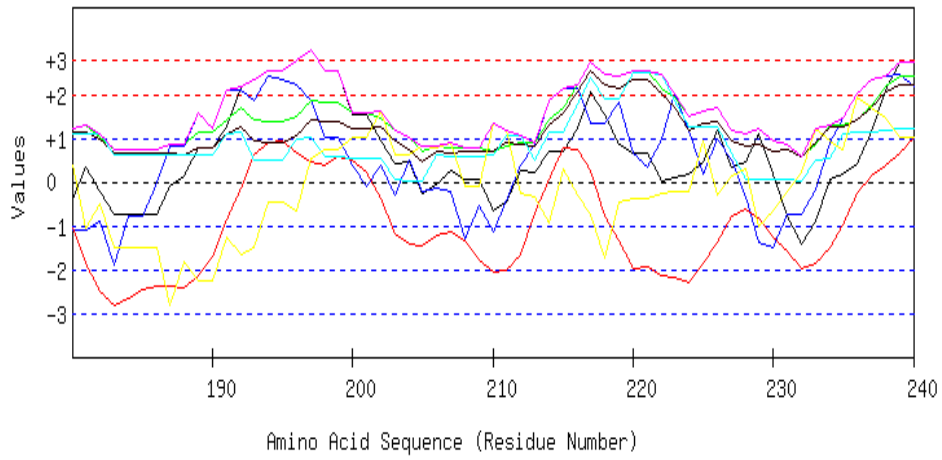
Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

GRAPHICAL RESULT :: SEQ 121 to 180



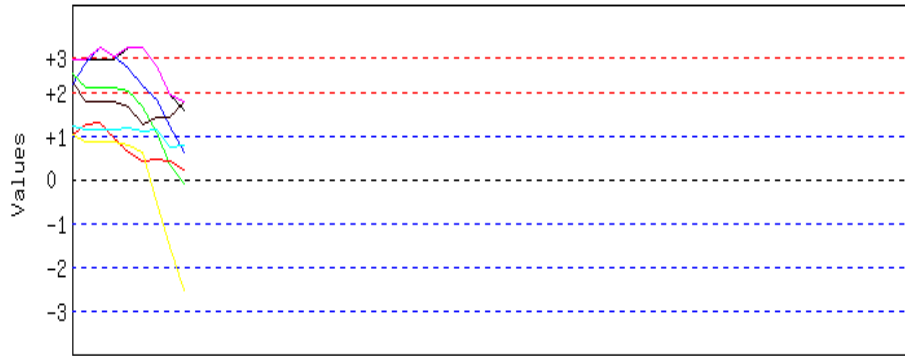
Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

GRAPHICAL RESULT :: SEQ 181 to 240



Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

GRAPHICAL RESULT :: SEQ 241 to 300



Amino Acid Sequence (Residue Number)

Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

[TOP](#)

TABULAR RESULT

Selected Programs: hydro flexi access turns surface polar antipro

Respective Threshold: 1.9 2 1.9 2.4 2.3 1.8 1.9

**VSPYFISPEQAMRERSELARKGIARAKSVVALAYAGGVLFVAENPSRSLQKISELYDRV
 GFAAAGKFNFDNLRRGGIQFADTRGYAYDRRDVTGRQLANVYAQTLGTIFTEQAKPYEV
 ELCVAEVAHYGETKRPELYRITYDGSIADEPHFVVMGGTTEPIANALKESYAENASLTDA
 LRIAVAALRAGSADTSGGDQPTLGVASLEVAVLDANRPRRAFRRITGSALQALLVDQESP
 QSDGESSG**

Length=248

A.A.	Parameter							Combined		
	Hydro	Flexi	Access	Turns	Surface	Polar	AntiPro	MAX	MIN	AVG

1 V	-0.351	-0.911	-0.523	-0.047	1.531	0.195	-1.629	1.531	-1.629	-0.248
2 S	-0.471	-1.140	0.188	0.210	1.449	0.154	-0.287	1.449	-1.140	0.015
3 F	-1.053	-1.140	0.580	0.394	1.084	0.098	0.975	1.084	-1.140	0.134
4 P	-1.558	-0.607	0.898	0.065	0.747	0.040	2.306	2.306	-1.558	0.270
5 Y	-0.913	-0.390	1.169	-0.162	0.911	0.059	1.877	1.877	-0.913	0.364
6 F	-1.192	0.507	1.262	-0.472	1.030	0.057	1.938	1.938	-1.192	0.447
7 I	-0.117	0.682	1.655	-0.412	1.440	0.653	1.660	1.660	-0.412	0.794
8 S	0.130	0.892	1.739	-0.266	1.540	0.676	1.603	1.739	-0.266	0.902
9 P	0.383	0.850	1.487	-0.271	1.303	0.657	0.261	1.487	-0.271	0.667
10 E	0.699	1.066	1.543	-0.729	1.394	0.670	-0.045	1.543	-0.729	0.657
11 Q	1.470	1.305	2.113	-1.310	1.886	1.293	-0.368	2.113	-1.310	0.913
12 A	1.552	1.670	2.290	-2.036	2.096	1.872	-0.554	2.290	-2.036	0.984
13 M	1.685	2.245	2.477	-2.558	2.296	2.478	-0.775	2.478	-2.558	1.121
14 R	1.603	2.154	2.300	-2.465	2.087	1.898	-0.588	2.300	-2.465	0.998
15 E	1.717	1.341	2.300	-2.191	2.078	2.456	-0.778	2.456	-2.191	0.989
16 R	1.002	1.579	2.216	-1.657	2.087	2.461	0.667	2.461	-1.657	1.194
17 S	1.401	1.597	2.225	-1.367	2.041	2.444	-0.288	2.444	-1.367	1.150
18 E	1.401	1.369	2.225	-1.489	2.041	2.444	-0.288	2.444	-1.489	1.100
19 L	1.268	0.469	2.346	-1.938	2.315	2.439	-0.197	2.439	-1.938	0.958
20 A	1.363	0.674	1.907	-2.251	1.795	1.814	-0.195	1.907	-2.251	0.730
21 R	0.446	1.487	1.617	-2.587	1.622	1.796	-0.034	1.796	-2.587	0.621
22 K	0.085	0.674	1.290	-2.594	1.257	1.196	-1.017	1.290	-2.594	0.127
23 G	0.933	0.674	1.804	-2.649	1.722	1.816	-1.453	1.816	-2.649	0.407
24 I	0.933	0.902	1.804	-2.670	1.722	1.816	-1.453	1.816	-2.670	0.436
25 A	1.028	1.131	1.823	-2.685	1.886	1.786	-1.387	1.886	-2.685	0.512
26 R	1.078	1.034	1.524	-2.344	1.403	1.211	-1.292	1.524	-2.344	0.373
27 A	0.484	0.221	1.412	-1.977	1.440	1.213	-0.704	1.440	-1.977	0.298
28 K	0.756	0.017	1.431	-1.420	1.449	1.212	-0.437	1.449	-1.420	0.430
29 S	0.756	-0.815	1.431	-1.200	1.449	1.212	-0.437	1.449	-1.200	0.342
30 V	-0.092	-2.077	0.917	-1.298	0.984	0.593	-0.001	0.984	-2.077	-0.139
31 V	-0.092	-1.981	0.917	-1.716	0.984	0.593	-0.001	0.984	-1.981	-0.185
32 A	-0.572	-1.258	0.720	-1.972	0.583	0.018	0.266	0.720	-1.972	-0.316
33 L	-0.850	-0.631	0.571	-2.167	0.428	-0.002	-0.904	0.571	-2.167	-0.508
34 A	-0.256	-0.522	0.683	-2.011	0.392	-0.004	-1.492	0.683	-2.011	-0.459
35 Y	0.338	-0.727	0.795	-1.859	0.355	-0.005	-2.081	0.795	-2.081	-0.455
36 A	-0.028	-0.494	0.674	-1.783	0.346	-0.004	-0.482	0.674	-1.783	-0.253
37 G	-0.028	-0.591	0.674	-1.820	0.346	-0.004	-0.482	0.674	-1.820	-0.272
38 G	-0.743	-1.218	0.608	-1.812	0.300	0.000	0.779	0.779	-1.812	-0.298
39 V	-0.857	-1.270	0.234	-1.845	0.054	-0.017	1.036	1.036	-1.845	-0.381
40 L	-0.857	-0.564	0.234	-1.755	0.054	-0.017	1.036	1.036	-1.755	-0.267
41 F	-0.724	-0.001	0.571	-1.750	0.465	0.582	1.009	1.009	-1.750	0.022
42 V	-0.642	1.028	0.879	-1.357	0.820	0.623	0.896	1.028	-1.357	0.321
43 A	-0.275	1.938	1.244	-0.794	1.103	0.640	0.527	1.938	-0.794	0.626
44 E	0.718	2.794	1.477	0.317	1.248	0.655	0.252	2.794	0.252	1.066
45 N	1.565	2.014	1.973	1.053	1.768	1.275	0.000	2.014	0.000	1.378
46 P	2.210	1.896	2.244	1.543	1.932	1.294	-0.429	2.244	-0.429	1.527
47 S	1.495	2.369	2.160	1.082	1.941	1.299	1.016	2.369	1.016	1.623
48 R	1.382	1.189	2.160	0.566	1.950	0.742	1.206	2.160	0.566	1.313
49 S	1.299	1.231	2.309	-0.297	2.278	1.296	1.384	2.309	-0.297	1.357
50 L	0.661	0.950	1.926	-0.848	1.987	1.279	1.486	1.987	-0.848	1.063
51 Q	0.661	0.950	1.926	-1.298	1.987	1.279	1.486	1.987	-1.298	0.999
52 K	0.888	0.053	1.823	-1.459	1.877	1.254	1.460	1.877	-1.459	0.842
53 I	-0.104	-0.240	1.589	-1.528	1.731	1.239	1.735	1.735	-1.528	0.632
54 S	0.357	0.898	1.926	-1.364	1.959	1.253	1.632	1.959	-1.364	0.952
55 E	0.610	-0.054	1.870	-1.124	1.905	1.700	1.460	1.905	-1.124	0.910
56 L	0.515	-0.001	1.851	-0.992	1.741	1.730	1.394	1.851	-0.992	0.891
57 Y	0.787	0.029	1.870	-0.712	1.750	1.729	1.661	1.870	-0.712	1.016
58 D	0.737	0.435	1.711	-0.817	1.549	1.709	1.502	1.711	-0.817	0.975
59 R	-0.338	-0.104	1.318	-0.927	1.139	1.114	1.779	1.779	-0.927	0.569

60 V	0.376	-0.917	1.403	-1.244	1.130	1.109	0.334	1.403	-1.244	0.313
61 G	0.629	-0.194	1.150	-1.387	0.893	1.089	-1.008	1.150	-1.387	0.168
62 F	0.130	0.011	0.879	-1.579	0.574	0.600	-2.009	0.879	-2.009	-0.199
63 A	0.225	0.011	0.440	-1.622	0.054	-0.024	-2.008	0.440	-2.008	-0.418
64 A	0.819	0.620	1.010	-1.845	0.701	0.569	-2.532	1.010	-2.532	-0.094
65 A	-0.123	1.195	0.954	-1.890	0.701	0.573	-2.281	1.195	-2.281	-0.124
66 G	0.901	1.020	1.318	-1.427	1.057	0.609	-2.645	1.318	-2.645	0.119
67 K	1.261	0.932	1.646	-0.720	1.422	1.209	-1.661	1.646	-1.661	0.584
68 F	0.547	0.710	1.580	0.181	1.376	1.213	-0.400	1.580	-0.400	0.744
69 N	1.046	0.680	1.851	0.831	1.695	1.702	0.601	1.851	0.601	1.201
70 E	1.129	0.884	2.160	1.382	2.050	1.743	0.488	2.160	0.488	1.405
71 F	0.187	1.123	1.627	1.622	1.422	1.153	0.858	1.627	0.187	1.142
72 D	1.034	1.924	2.122	1.748	1.941	1.774	0.606	2.122	0.606	1.593
73 N	0.857	2.012	2.253	1.063	2.105	2.358	0.718	2.358	0.718	1.624
74 L	0.724	1.078	1.917	0.057	1.695	1.758	0.745	1.917	0.057	1.139
75 R	1.666	1.774	1.973	-1.195	1.695	1.754	0.494	1.973	-1.195	1.166
76 R	0.528	0.786	1.561	-2.026	1.358	1.267	0.824	1.561	-2.026	0.614
77 G	0.465	-0.028	1.589	-2.298	1.422	1.269	1.101	1.589	-2.298	0.503
78 G	0.465	-0.116	1.608	-2.038	1.367	1.268	0.917	1.608	-2.038	0.496
79 I	0.332	-0.252	1.178	-1.739	0.893	0.643	-0.092	1.178	-1.739	0.138
80 Q	0.699	0.886	1.019	-1.162	0.738	0.507	-0.101	1.019	-1.162	0.370
81 F	0.667	1.022	1.225	-0.583	0.938	0.527	-0.060	1.225	-0.583	0.534
82 A	0.572	0.790	1.664	-0.157	1.458	1.152	-0.061	1.664	-0.157	0.774
83 D	1.438	0.790	1.795	-0.023	1.431	1.150	-0.383	1.795	-0.383	0.886
84 T	0.939	-0.156	1.720	-0.353	1.294	1.127	-0.214	1.720	-0.353	0.623
85 R	1.653	-0.108	1.786	-0.941	1.339	1.123	-1.475	1.786	-1.475	0.483
86 G	1.401	-0.108	2.038	-1.309	1.576	1.142	-0.133	2.038	-1.309	0.658
87 Y	1.401	0.079	2.038	-1.303	1.576	1.142	-0.133	2.038	-1.303	0.686
88 A	1.337	1.024	2.272	-1.049	1.895	1.747	-0.175	2.272	-1.049	1.007
89 Y	1.337	0.928	2.272	-0.715	1.895	1.747	-0.175	2.272	-0.715	1.041
90 D	1.609	1.826	2.552	-0.496	2.260	2.236	-0.184	2.552	-0.496	1.400
91 R	1.495	1.914	2.178	-0.577	2.014	2.218	0.073	2.218	-0.577	1.331
92 R	1.691	1.914	2.374	-0.525	2.169	2.238	1.124	2.374	-0.525	1.569
93 D	2.172	1.591	2.113	-0.490	1.886	2.219	0.792	2.219	-0.490	1.469
94 V	1.805	0.848	2.272	-0.651	2.041	2.354	0.800	2.354	-0.651	1.353
95 T	1.919	0.944	2.169	-0.850	1.941	1.772	0.964	2.169	-0.850	1.266
96 G	1.072	1.062	1.655	-1.186	1.476	1.153	1.400	1.655	-1.186	0.947
97 R	0.572	0.339	1.384	-1.593	1.157	0.664	0.399	1.384	-1.593	0.417
98 Q	1.249	-0.881	1.804	-1.275	1.476	0.703	-0.303	1.804	-1.275	0.396
99 L	0.686	-1.372	1.487	-0.897	1.312	0.684	0.245	1.487	-1.372	0.307
100A	0.206	-0.677	1.748	-0.228	1.595	0.704	0.577	1.748	-0.677	0.561
101N	0.073	-0.186	1.318	0.075	1.121	0.079	-0.432	1.318	-0.432	0.293
102V	0.073	-0.999	1.318	-0.078	1.121	0.079	-0.432	1.318	-0.999	0.155
103Y	0.983	-0.276	1.599	-0.498	1.267	0.094	-0.827	1.599	-0.827	0.335
104A	0.269	0.622	1.515	-0.781	1.276	0.099	0.619	1.515	-0.781	0.517
105Q	0.187	0.297	1.206	-1.070	0.920	0.059	0.732	1.206	-1.070	0.333
106T	0.749	-0.368	1.524	-1.002	1.084	0.077	0.184	1.524	-1.002	0.321
107L	0.364	-0.368	1.132	-1.222	0.829	0.059	0.173	1.132	-1.222	0.138
108G	-0.351	0.411	1.066	-1.311	0.784	0.064	1.435	1.435	-1.311	0.300
109T	-0.401	0.275	0.935	-1.346	0.565	0.041	1.312	1.312	-1.346	0.197
110I	-0.237	-0.216	1.066	-1.293	0.774	0.621	1.245	1.245	-1.293	0.280
111F	0.724	0.940	1.477	-1.081	1.139	0.658	0.973	1.477	-1.081	0.690
112T	0.496	1.473	1.487	-1.009	1.185	0.658	-0.037	1.487	-1.009	0.608
113E	0.528	0.576	1.739	-1.167	1.668	1.232	-0.013	1.739	-1.167	0.652
114Q	1.167	0.576	2.122	-1.218	1.959	1.250	-0.114	2.122	-1.218	0.820
115A	1.628	-0.011	2.440	-1.317	2.242	1.265	-0.034	2.440	-1.317	0.888
116K	1.793	0.564	2.571	-1.285	2.451	1.844	-0.101	2.571	-1.285	1.120
117P	1.065	-0.472	2.122	-1.200	2.078	1.246	0.514	2.122	-1.200	0.765
118Y	1.179	-0.795	2.122	-1.373	2.069	1.803	0.325	2.122	-1.373	0.761

119E	0.465	-0.484	2.038	-1.717	2.078	1.809	1.770	2.078	-1.717	0.851
120V	0.193	-1.059	1.375	-1.846	1.349	1.232	2.327	2.327	-1.846	0.510
121E	-0.174	-0.388	1.010	-1.887	1.066	1.215	2.696	2.696	-1.887	0.505
122L	0.079	-1.059	0.758	-1.614	0.829	1.195	1.354	1.354	-1.614	0.220
123C	0.079	-0.855	0.758	-1.455	0.829	1.195	1.354	1.354	-1.455	0.272
124V	0.079	-0.801	0.758	-1.536	0.829	1.195	1.354	1.354	-1.536	0.268
125A	-0.281	-1.111	0.431	-1.840	0.465	0.596	0.370	0.596	-1.840	-0.196
126E	0.433	-0.484	0.674	-1.648	0.629	1.210	0.202	1.210	-1.648	0.145
127V	0.225	-0.484	1.141	-1.276	0.957	1.212	-0.088	1.212	-1.276	0.241
128A	0.819	0.103	1.253	-0.473	0.920	1.210	-0.676	1.253	-0.676	0.451
129H	1.179	0.934	1.580	-0.075	1.285	1.810	0.308	1.810	-0.075	1.003
130Y	1.015	1.658	1.449	-0.104	1.075	1.230	0.375	1.658	-0.104	0.957
131G	1.609	2.423	2.019	-0.683	1.722	1.823	-0.149	2.423	-0.683	1.252
132E	1.742	2.371	2.449	-1.181	2.196	2.448	0.860	2.449	-1.181	1.555
133T	1.742	1.591	2.533	-1.560	2.296	1.847	0.813	2.533	-1.560	1.323
134K	2.355	0.694	2.608	-1.606	2.424	2.427	0.454	2.608	-1.606	1.337
135R	1.413	0.676	2.533	-1.596	2.479	2.433	0.889	2.533	-1.596	1.261
136P	0.800	-0.462	2.459	-1.548	2.351	1.852	1.247	2.459	-1.548	0.957
137E	0.737	-0.330	2.692	-1.697	2.670	2.457	1.206	2.692	-1.697	1.105
138L	-0.129	-1.312	2.103	-1.947	2.014	1.864	1.462	2.103	-1.947	0.579
139Y	-0.066	-0.568	1.870	-2.086	1.695	1.260	1.504	1.870	-2.086	0.515
140R	-0.319	0.465	1.879	-2.191	1.658	1.260	1.616	1.879	-2.191	0.624
141I	-0.180	0.507	1.823	-1.682	1.613	1.149	1.634	1.823	-1.682	0.695
142T	0.762	0.507	1.898	-1.032	1.558	1.144	1.199	1.898	-1.032	0.862
143Y	1.293	0.017	1.795	-0.151	1.476	1.145	1.027	1.795	-0.151	0.943
144D	0.522	0.962	1.225	0.210	0.984	0.522	1.349	1.349	0.210	0.825
145G	1.160	0.998	1.365	0.193	1.002	0.520	0.017	1.365	0.017	0.751
146S	1.464	0.730	1.440	-0.202	1.166	0.989	-0.032	1.464	-0.202	0.793
147I	2.077	-0.036	1.515	-0.544	1.294	1.569	-0.391	2.077	-0.544	0.784
148A	1.578	0.115	1.487	-0.608	1.248	1.099	-0.162	1.578	-0.608	0.679
149D	1.350	0.019	1.655	-0.023	1.467	1.719	0.105	1.719	-0.023	0.899
150E	0.357	-0.617	1.440	0.536	1.267	1.703	0.197	1.703	-0.617	0.698
151P	0.629	-1.306	1.459	1.065	1.276	1.703	0.464	1.703	-1.306	0.756
152H	0.263	-1.037	1.337	1.054	1.267	1.705	2.062	2.062	-1.037	0.950
153F	-0.635	-0.500	1.057	0.210	0.993	1.233	2.016	2.016	-0.635	0.625
154V	-0.768	0.165	0.720	-0.807	0.583	0.633	2.043	2.043	-0.807	0.367
155V	-0.540	0.752	0.468	-1.747	0.264	0.614	1.823	1.823	-1.747	0.233
156M	-0.344	1.423	0.505	-2.133	0.246	0.014	1.597	1.597	-2.133	0.187
157G	0.566	1.896	0.767	-1.833	0.446	0.030	1.386	1.896	-1.833	0.465
158G	1.293	0.944	1.216	-1.333	0.820	0.628	0.771	1.293	-1.333	0.620
159T	1.660	0.317	1.580	-0.844	1.103	0.645	0.402	1.660	-0.844	0.695
160T	1.420	0.435	1.449	-0.746	1.039	0.630	0.779	1.449	-0.746	0.715
161E	1.192	-0.056	1.459	-0.938	1.084	0.630	-0.231	1.459	-0.938	0.449
162P	1.274	-0.835	1.767	-0.898	1.440	0.671	-0.344	1.767	-0.898	0.439
163I	1.078	-0.362	1.571	-0.763	1.285	0.651	-1.395	1.571	-1.395	0.295
164A	0.168	0.538	1.290	-0.381	1.139	0.636	-1.001	1.290	-1.001	0.341
165N	0.035	1.393	1.412	-0.216	1.412	0.631	-0.910	1.412	-0.910	0.537
166A	0.395	0.377	1.496	-0.664	1.504	1.212	-1.156	1.504	-1.156	0.452
167L	1.312	0.377	1.786	-1.147	1.677	1.230	-1.318	1.786	-1.318	0.560
168K	1.059	1.157	2.038	-1.359	1.914	1.249	0.024	2.038	-1.359	0.869
169E	0.749	0.934	1.739	-1.277	1.604	1.209	-0.873	1.739	-1.277	0.584
170S	1.110	0.359	2.066	-0.940	1.968	1.808	0.111	2.066	-0.940	0.926
171Y	2.134	0.359	2.449	-0.519	2.269	1.844	-0.437	2.449	-0.519	1.157
172A	1.906	0.562	2.001	-0.390	1.631	1.249	-1.512	2.001	-1.512	0.778
173E	1.824	1.052	1.823	0.216	1.422	0.669	-1.326	1.824	-1.326	0.811
174N	0.832	1.016	1.589	0.459	1.276	0.655	-1.051	1.589	-1.051	0.682
175A	1.280	0.407	1.533	0.662	1.194	0.655	-1.342	1.533	-1.342	0.627
176S	1.780	0.203	1.804	0.507	1.513	1.144	-0.341	1.804	-0.341	0.944
177L	1.420	0.161	1.477	0.358	1.148	0.545	-1.325	1.477	-1.325	0.541

178T	0.395	0.041	1.094	0.018	0.847	0.510	-0.777	1.094	-0.777	0.304
179D	0.528	-0.450	1.524	-0.231	1.321	1.134	0.232	1.524	-0.450	0.580
180A	-0.389	-1.085	1.234	-1.044	1.148	1.116	0.394	1.234	-1.085	0.196
181L	0.326	-1.085	1.318	-1.857	1.139	1.111	-1.051	1.318	-1.857	-0.014
182R	-0.237	-0.881	1.001	-2.513	0.975	1.092	-0.503	1.092	-2.513	-0.152
183I	-0.736	-1.899	0.730	-2.808	0.656	0.603	-1.504	0.730	-2.808	-0.708
184A	-0.736	-0.761	0.730	-2.659	0.656	0.603	-1.504	0.730	-2.659	-0.525
185V	-0.736	-0.761	0.730	-2.464	0.656	0.603	-1.504	0.730	-2.464	-0.497
186A	-0.736	-0.038	0.730	-2.385	0.656	0.603	-1.504	0.730	-2.385	-0.382
187A	-0.098	0.818	0.870	-2.382	0.674	0.601	-2.836	0.870	-2.836	-0.336
188L	0.130	0.818	0.860	-2.432	0.629	0.601	-1.825	0.860	-2.432	-0.174
189R	0.775	1.561	1.132	-2.136	0.793	0.620	-2.254	1.561	-2.254	0.070
190A	0.775	1.239	1.132	-1.700	0.793	0.620	-2.254	1.239	-2.254	0.086
191G	1.274	2.094	1.403	-0.852	1.112	1.109	-1.253	2.094	-1.253	0.698
192S	2.185	2.094	1.683	-0.136	1.257	1.123	-1.647	2.185	-1.647	0.937
193A	2.330	1.866	1.403	0.609	0.938	0.519	-1.487	2.330	-1.487	0.883
194D	2.558	2.405	1.393	0.891	0.893	0.519	-0.476	2.558	-0.476	1.169
195T	2.558	2.357	1.393	0.932	0.893	0.519	-0.476	2.558	-0.476	1.168
196S	2.779	2.225	1.515	0.651	1.057	0.988	-0.645	2.779	-0.645	1.224
197G	3.025	1.860	1.842	0.460	1.431	1.030	0.528	3.025	0.460	1.454
198G	2.526	1.028	1.814	0.373	1.385	0.560	0.757	2.526	0.373	1.206
199D	2.526	1.028	1.814	0.563	1.385	0.560	0.757	2.526	0.560	1.233
200Q	1.533	0.393	1.580	0.515	1.239	0.546	1.032	1.580	0.393	0.977
201P	1.533	-0.098	1.580	0.212	1.239	0.546	1.032	1.580	-0.098	0.864
202T	0.939	0.399	1.468	-0.399	1.276	0.547	1.621	1.621	-0.399	0.836
203L	0.440	-0.296	1.197	-1.174	0.957	0.058	0.620	1.197	-1.174	0.257
204G	0.471	0.483	1.019	-1.420	0.738	0.036	0.616	1.019	-1.420	0.278
205V	-0.243	-0.240	0.692	-1.445	0.474	0.022	0.831	0.831	-1.445	0.013
206A	-0.079	-0.144	0.823	-1.215	0.683	0.602	0.764	0.823	-1.215	0.205
207S	0.269	-0.240	0.786	-1.124	0.665	0.598	0.918	0.918	-1.124	0.267
208L	0.041	-1.300	0.795	-1.354	0.711	0.598	-0.092	0.795	-1.354	-0.086
209E	0.041	-0.556	0.795	-1.778	0.711	0.598	-0.092	0.795	-1.778	-0.040
210V	-0.673	-1.131	0.711	-2.079	0.720	0.603	1.353	1.353	-2.079	-0.071
211A	-0.452	-0.426	0.832	-2.020	0.884	1.072	1.184	1.184	-2.020	0.153
212V	0.263	0.387	0.917	-1.649	0.875	1.067	-0.261	1.067	-1.649	0.228
213L	0.212	0.842	0.889	-0.686	0.820	0.508	-0.348	0.889	-0.686	0.319
214D	0.711	1.860	1.440	0.044	1.303	1.131	-0.938	1.860	-0.938	0.793
215A	0.711	2.134	1.683	0.788	1.576	1.150	0.293	2.134	0.293	1.191
216N	1.211	2.134	2.234	0.721	2.060	1.773	-0.297	2.234	-0.297	1.405
217R	2.058	1.351	2.748	0.264	2.524	2.392	-0.733	2.748	-0.733	1.515
218P	1.559	1.351	2.477	-0.782	2.205	1.903	-1.734	2.477	-1.734	0.997
219R	0.844	1.806	2.412	-1.360	2.160	1.908	-0.473	2.412	-1.360	1.042
220R	0.667	0.668	2.543	-1.962	2.324	2.492	-0.361	2.543	-1.962	0.910
221A	0.667	0.345	2.543	-1.938	2.324	2.492	-0.361	2.543	-1.938	0.867
222F	0.029	0.972	2.160	-2.135	2.032	2.475	-0.259	2.475	-2.135	0.753
223R	0.092	2.002	1.926	-2.183	1.713	1.870	-0.217	2.002	-2.183	0.743
224R	0.187	1.189	1.487	-2.289	1.194	1.245	-0.216	1.487	-2.289	0.399
225I	0.465	0.171	1.636	-1.879	1.349	1.265	0.954	1.636	-1.879	0.566
226T	1.179	0.986	1.702	-1.377	1.394	1.261	-0.307	1.702	-1.377	0.691
227G	0.332	0.495	1.188	-0.799	0.929	0.642	0.128	1.188	-0.799	0.417
228S	0.446	-0.336	1.085	-0.637	0.829	0.059	0.293	1.085	-0.637	0.248
229A	1.084	-1.396	1.225	-0.821	0.847	0.058	-1.039	1.225	-1.396	-0.006
230L	0.174	-1.492	0.945	-1.276	0.701	0.043	-0.645	0.945	-1.492	-0.221
231Q	-0.768	-0.749	0.870	-1.600	0.756	0.049	-0.210	0.870	-1.600	-0.236
232A	-1.413	-0.749	0.599	-1.968	0.592	0.030	0.219	0.599	-1.968	-0.384
233L	-0.913	-0.174	0.870	-1.875	0.911	0.519	1.220	1.220	-1.875	0.080
234L	0.048	0.886	1.281	-1.513	1.276	0.556	0.948	1.281	-1.513	0.497
235V	0.161	1.449	1.281	-0.964	1.267	1.113	0.758	1.449	-0.964	0.724
236D	0.440	2.036	1.431	-0.279	1.422	1.133	1.928	2.036	-0.279	1.159

237Q	1.154	<u>2.353</u>	1.758	0.143	1.686	1.147	1.713	2.353	0.143	1.422
238E	<u>2.115</u>	<u>2.401</u>	<u>2.169</u>	0.363	2.050	1.184	1.442	2.401	0.363	1.675
239S	<u>2.760</u>	<u>2.453</u>	<u>2.440</u>	0.676	2.214	1.202	1.013	2.760	0.676	1.823
240P	<u>2.760</u>	<u>2.172</u>	<u>2.440</u>	1.011	2.214	1.202	1.013	2.760	1.011	1.830
241Q	<u>2.741</u>	<u>2.669</u>	<u>2.103</u>	1.273	1.795	1.160	0.850	2.741	0.850	1.799
242S	<u>2.741</u>	<u>3.034</u>	<u>2.103</u>	1.283	1.795	1.160	0.850	3.034	0.850	1.852
243D	<u>2.741</u>	<u>2.806</u>	<u>2.103</u>	0.943	1.795	1.160	0.850	2.806	0.850	1.771
244G	<u>3.019</u>	<u>2.521</u>	<u>2.010</u>	0.601	1.677	1.161	0.790	3.019	0.601	1.683
245E	<u>3.000</u>	<u>2.148</u>	1.674	0.430	1.257	1.119	0.627	3.000	0.430	1.465
246S	<u>2.589</u>	1.828	1.066	0.480	1.422	1.159	-0.543	2.589	-0.543	1.143
247S	<u>1.957</u>	1.227	0.337	0.430	1.422	0.730	-1.544	1.957	-1.544	0.651
248G	1.597	0.626	-0.111	0.229	1.786	0.790	-2.555	1.786	-2.555	0.337

[TOP](#)

Overlap Display

Selected Programs: hydro flexi access turns surface polar antipro

Respective Threshold: 1.9 2 1.9 2.4 2.3 1.8 1.9

The predicted B-cell epitopes are shown in blue colour and underlined.

Sequence	<u>1VSFPYFISPEQAMRERSELARKGIARAKSVVALAYAGGVLVFAENPSRSLQKISELYDRVGFAAAG</u> KFNEFDNLRRGGIQFADTRGYAYDRRDVTGRQLANVYAQTLGTIFTEQAKPYEVELCVAEVAHYGE TKRPELYRITYDGSIADEPHFVVMGGTTEPIANALKESYAENASLTDALRIAVAALRAGSADTSSGD QPTLGVASLEVAVL <u>DANRPRRAFRRITGSALQALLVDQESPQSDGESSG</u> ²⁴⁸
Hydrophilicity	<u>1VSFPYFISPEQAMRERSELARKGIARAKSVVALAYAGGVLVFAENPSRSLQKISELYDRVGFAAAG</u> KFNEFDNLRRGGIQFADTRGYAY <u>DRRDVTGRQLANVYAQTLGTIFTEQAKPYEVELCVAEVAHYGE</u> <u>TKRPELYRITYDGSIADEPHFVVMGGTTEPIANALKESYAENASLTDALRIAVAALRAGSADTSSGD</u> <u>QPTLGVASLEVAVL</u> <u>DANRPRRAFRRITGSALQALLVDQESPQSDGESSG</u> ²⁴⁸
Flexibility	<u>1VSFPYFISP</u> <u>EQAMRERS</u> ELARKGIARAKSVVALAYAGGVL <u>VFAENPSRSL</u> QKISELYDRVGFAAAG KFNE <u>FDNLRR</u> GGIQFADTRGYAYDRRDVTGRQLANVYAQTLGTIFTEQAKPYEVELCVAEVA <u>HYGE</u> <u>TKRPELYRITYDGSIADEPHFVVMGGTTEPIANALKESYAENASLTDALRIAVAALRAGSADTSSGD</u> QPTLGVASLEVA <u>VL</u> <u>DANRPRRAFRRITGSALQALLVDQESPQSDGESSG</u> ²⁴⁸
Accessibility	<u>1VSFPYFISPEQAMRERSELARKGIARAKSVVALAYAGGVLVFAENPSRSLQKISELYDRVGFAAAG</u> <u>KFNEFDNLRRGGIQFADTRGYAYDRRDVTGRQLANVYAQTLGTIFTEQAKPYEVELCVAEVAHYGE</u> <u>TKRPELYRITYDGSIADEPHFVVMGGTTEPIANALKESYAENASLTDALRIAVAALRAGSADTSSGD</u> QPTLGVASLEVAVL <u>DANRPRRAFRRITGSALQALLVDQESPQSDGESSG</u> ²⁴⁸
Turns	<u>1VSFPYFISPEQAMRERSELARKGIARAKSVVALAYAGGVLVFAENPSRSLQKISELYDRVGFAAAG</u> KFNEFDNLRRGGIQFADTRGYAYDRRDVTGRQLANVYAQTLGTIFTEQAKPYEVELCVAEVAHYGE TKRPELYRITYDGSIADEPHFVVMGGTTEPIANALKESYAENASLTDALRIAVAALRAGSADTSSGD QPTLGVASLEVAVL <u>DANRPRRAFRRITGSALQALLVDQESPQSDGESSG</u> ²⁴⁸

Exposed Surface	¹ VSFPYFISPEQAMRE <u>RSELARK</u> GIARAKSVVALAYAGGVLFVAENPSRSLQKISELYDRVGF ²⁴⁸ AAAG KFNEFDNLRRGGIQFADTRGYAYDRRDVTGRQLANVYAQTLGTIFT <u>EQAKPYE</u> VELCVAEVAHY <u>GE</u> <u>TKRPELYR</u> ITYDGSIADEPHFVVMGGTTEPIANALKESYAENASLTDALRIAVAALRAGSADTSGGD QPTLGVASLEVAVL <u>DANRPRRAFRR</u> ITGSALQALLVDQESPQSDGESSG ²⁴⁸
Polarity	¹ VSFPYFIS <u>PEQAMRERSELARK</u> GIARAKSVVALAYAGGVLFVAENPSRSLQKISELYDRVGF ²⁴⁸ AAAG KFNE <u>FDNLRR</u> GGIQFADTRG <u>YAYDRRDVTGR</u> QLANVYAQTLGTIFT <u>EQAKPYE</u> VELCVAEVAHY <u>GE</u> <u>TKRPELYR</u> ITYDGSIADEPHFVVMGGTTEPIANA <u>LKESYAEN</u> ASLTDALRIAVAALRAGSADTSGGD QPTLGVASLEVAVL <u>DANRPRRAFRR</u> ITGSALQALLVDQESPQSDGESSG ²⁴⁸
Antigenic Propensity	¹ <u>VSFPYFIS</u> PEQAMRERSELARKGIARAKSVVALAYAGGVLFVAENPSRSLQKISELYDRVGF ²⁴⁸ AAAG KFNEFDNLRRGGIQFADTRGYAYDRRDVTGRQLANVYAQTLGTIFTEQAK <u>PYEVELC</u> VAEVAHYGE TKRPELYRITYDGSIA <u>DEPHFVVM</u> GGTTEPIANALKESYAENASLTDALRIAVAALRAGSADTSGGD QPTLGVASLEVAVLDANRPRRAFRRITGSALQA <u>LLVDQES</u> PQSDGESSG ²⁴⁸

[TOP](#)

[Home](#)