BcePred Prediction Server

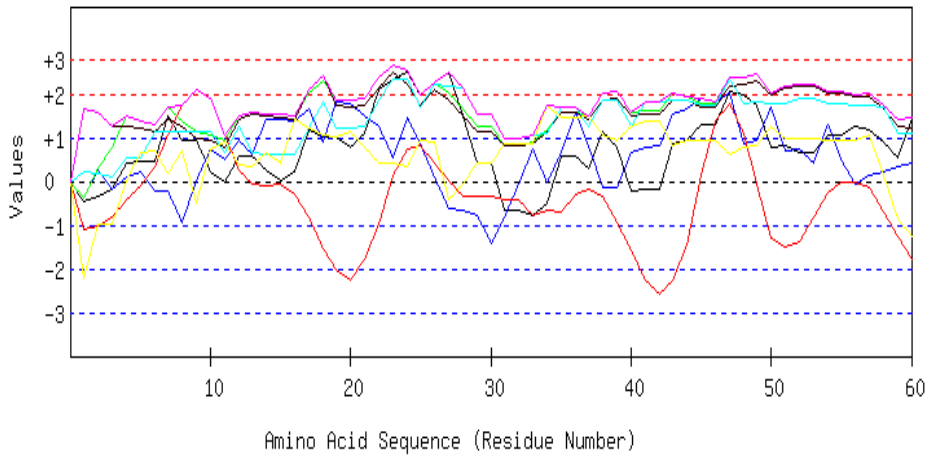The server displays 1.GRAPHICAL RESULT 2.TABULAR RESULT   3.Overlap Display

seqname=
Seq=MPLTPADVHNVAFSKPPIGKRGYNEDEVDAFLDLVENELTRLIEENSDLRQRINELDQELAAGGGAGVTPQA
TQAIPAYEPEPGKPAPAAVSAGMNEEQALKAARVLSLAQDTADRLTNTAKAESDKMLADARANAEQILGEARHTA
DATVAEARQRADAMLADAQSRSEAQLRQAQEKADALQADAERKHSEIMGTINQQRAVLEGRLEQLRTFEREYRT
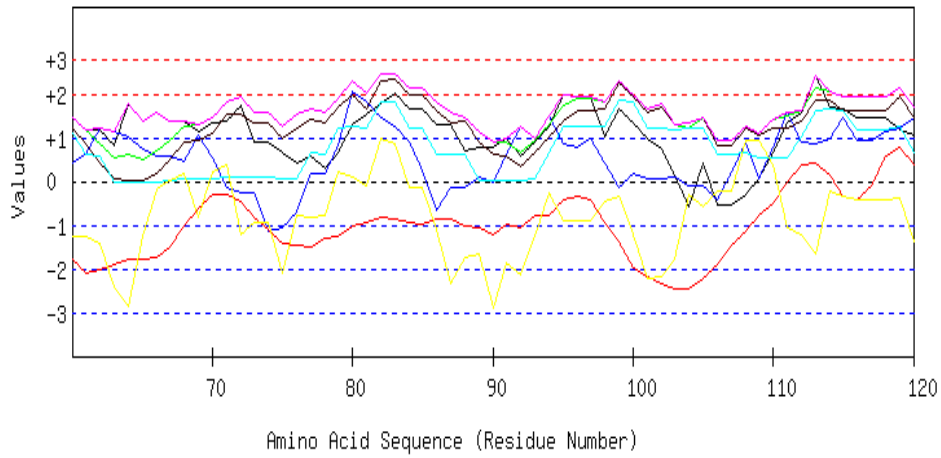RLKTYLESQLEELGQRGSAAPVDSNADAGGFDQFNRGKN

Length=260
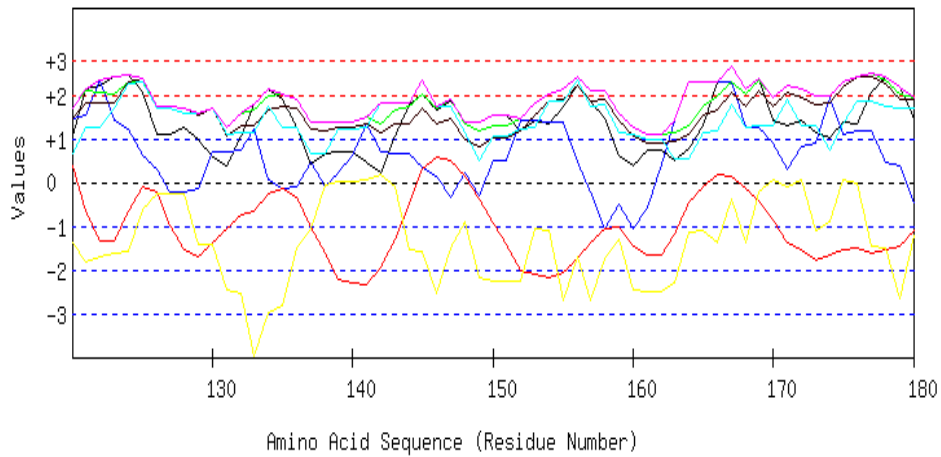
GRAPHICAL RESULT

GRAPHICAL RESULT :: SEQ 1 to 60

Amino Acid Sequence (Residue Number)

Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

GRAPHICAL RESULT :: SEQ 61 to 120

Values

+3
+2
+1
0
-1
-2
-3

70   80   90   100   110   120

Amino Acid Sequence (Residue Number)

Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

GRAPHICAL RESULT :: SEQ 121 to 180

Values

+3
+2
+1
0
-1
-2
-3

130   140   150   160   170   180

Amino Acid Sequence (Residue Number)

Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

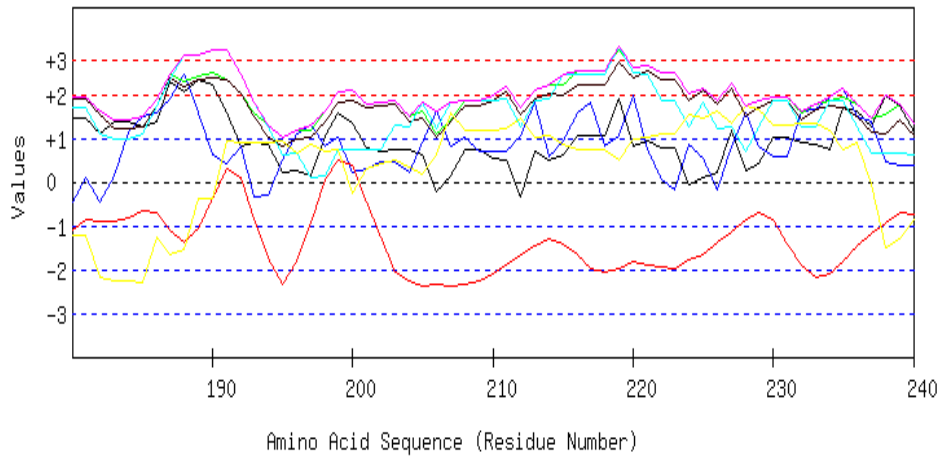# GRAPHICAL RESULT :: SEQ 181 to 240

Amino Acid Sequence (Residue Number)

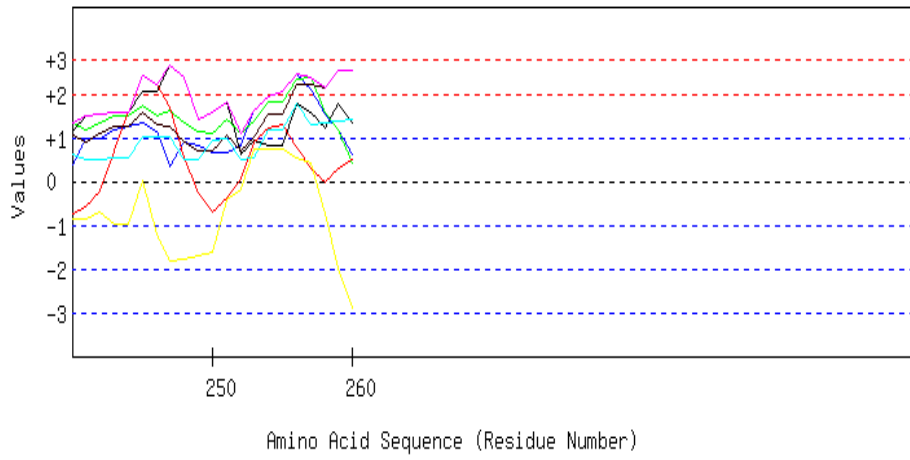Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

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

MPLTPADVHNVAFSKPPIGKRGYNEDEVDAFLDLVENELTRLIEENSDLRQRINELDQEL
AAGGGAGVTPQATQAIPAYEPEPGKPAPAAVSAGMNEEQALKAARVLSLAQDTADRLTNT
AKAESDKMLADARANAEQILGEARHTADATVAEARQRADAMLADAQSRSEAQLRQAQEKA
DALQADAERKHSEIMGTINQQRAVLEGRLEQLRTFEREYRTRLKTYLESQLEELGQRGSA
APVDSNADAGGFDQFNRGKN

Length=260

A.A.					Parameter					Combined	
	Hydro	Flexi	Access	Turns	Surface	Polar	AntiPro	MAX	MIN	AVG
1 M	-0.465	-0.384	-0.382	-1.102	1.640	0.212	-2.208	1.640	-2.208	-0.384
2 P	-0.332	0.269	0.318	-1.025	1.595	0.170	-0.978	1.595	-1.025	0.003
3 L	-0.199	-0.186	0.776	-0.805	1.276	0.110	-0.978	1.276	-0.978	-0.001
4 T	0.433	0.109	1.505	-0.404	1.276	0.539	0.023	1.505	-0.404	0.497
5 P	0.465	0.227	1.393	-0.103	1.221	0.524	0.667	1.393	-0.103	0.628
6 A	0.465	-0.228	1.309	0.328	1.121	1.125	0.714	1.309	-0.228	0.691
7 D	1.489	-0.228	1.692	1.057	1.422	1.160	0.166	1.692	-0.228	0.965
8 V	0.926	-0.941	1.375	1.754	1.257	1.141	0.714	1.754	-0.941	0.890
9 H	0.926	0.011	1.132	2.091	0.984	1.122	-0.516	2.091	-0.516	0.821
10 N	0.212	0.752	1.066	1.880	0.938	1.127	0.746	1.880	0.212	0.960
11 V	-0.009	0.501	0.945	1.041	0.774	0.658	0.914	1.041	-0.009	0.689
12 A	0.585	0.956	1.515	0.273	1.422	1.251	0.391	1.515	0.273	0.913
13 F	0.585	0.632	1.599	-0.066	1.522	0.650	0.343	1.599	-0.066	0.752
14 S	0.275	1.433	1.543	-0.105	1.485	0.628	0.676	1.543	-0.105	0.848
15 K	0.003	1.409	1.524	-0.065	1.476	0.629	0.409	1.524	-0.065	0.769
16 P	0.231	1.391	1.515	-0.300	1.431	0.629	1.420	1.515	-0.300	0.902
17 P	1.173	1.660	2.029	-0.829	2.114	1.219	1.234	2.114	-0.829	1.228
18 I	1.028	0.894	2.309	-1.535	2.433	1.824	1.073	2.433	-1.535	1.146
19 G	1.028	1.828	1.851	-2.003	1.750	1.229	1.008	1.851	-2.003	0.956
20 K	0.775	1.776	1.860	-2.258	1.713	1.229	1.120	1.860	-2.258	0.888
21 R	1.084	1.483	1.917	-1.787	1.750	1.251	0.787	1.917	-1.787	0.926
22 G	2.083	1.245	2.384	-0.986	2.132	1.849	0.439	2.384	-0.986	1.307
23 Y	2.355	0.521	2.664	0.151	2.497	2.338	0.430	2.664	0.151	1.565
24 N	2.488	1.467	2.543	0.756	2.224	2.343	0.339	2.543	0.339	1.737
25 E	1.989	0.858	1.991	0.834	1.741	1.719	0.928	1.991	0.834	1.437
26 D	2.260	0.109	2.272	0.440	2.105	2.208	0.919	2.272	0.109	1.473
27 E	2.513	-0.635	2.019	0.002	1.868	2.189	-0.423	2.513	-0.635	1.076
28 V	1.489	-0.671	1.655	-0.323	1.513	2.153	-0.059	2.153	-0.671	0.822
29 D	0.414	-0.779	1.244	-0.344	1.157	1.558	0.402	1.558	-0.779	0.522
30 A	0.414	-1.414	1.244	-0.340	1.157	1.558	0.402	1.558	-1.414	0.432
31 F	-0.661	-0.839	0.832	-0.437	0.802	0.964	0.864	0.964	-0.839	0.218
32 L	-0.661	-0.056	0.832	-0.435	0.802	0.964	0.864	0.964	-0.661	0.330
33 D	-0.800	0.724	0.889	-0.796	0.847	1.075	0.846	1.075	-0.800	0.398
34 L	-0.490	-0.019	1.188	-0.651	1.157	1.116	1.743	1.743	-0.651	0.578
35 V	0.585	0.676	1.580	-0.687	1.567	1.711	1.466	1.711	-0.687	0.985
36 E	0.585	1.585	1.580	-0.281	1.567	1.711	1.466	1.711	-0.281	1.173
37 N	0.281	0.806	1.505	-0.178	1.403	1.242	1.516	1.516	-0.178	0.939
38 E	1.129	-0.128	2.019	-0.341	1.868	1.861	1.080	2.019	-0.341	1.070
39 L	0.781	-0.128	2.057	-0.946	1.886	1.865	0.926	2.057	-0.946	0.920

40 T	-0.218	0.652	1.589	-1.569	1.504	1.267	1.274	1.589	-1.569	0.643
41 R	-0.167	0.770	1.617	-2.251	1.558	1.826	1.361	1.826	-2.251	0.673
42 L	-0.167	0.812	1.617	-2.585	1.558	1.826	1.361	1.826	-2.585	0.632
43 I	0.857	1.555	2.001	-2.258	1.859	1.861	0.813	2.001	-2.258	0.955
44 E	0.939	1.676	1.954	-1.444	1.859	1.862	0.932	1.954	-1.444	1.111
45 E	1.306	1.914	1.795	0.152	1.704	1.726	0.924	1.914	0.152	1.360
46 N	1.306	1.830	1.795	1.365	1.704	1.726	0.924	1.830	0.924	1.521
47 S	2.077	2.034	2.365	1.785	2.196	2.349	0.601	2.365	0.601	1.915
48 D	1.963	0.854	2.365	1.106	2.205	1.791	0.791	2.365	0.791	1.582
49 L	1.736	0.924	2.468	-0.044	2.315	1.817	0.816	2.468	-0.044	1.433
50 R	0.787	1.704	2.029	-1.293	1.987	1.778	1.251	2.029	-1.293	1.177
51 Q	0.819	0.686	2.178	-1.494	2.142	1.798	0.978	2.178	-1.494	1.015
52 R	0.680	0.734	2.234	-1.385	2.187	1.909	0.961	2.234	-1.385	1.046
53 I	0.680	0.411	2.234	-0.806	2.187	1.909	0.961	2.234	-0.806	1.082
54 N	1.046	1.311	2.075	-0.243	2.032	1.773	0.953	2.075	-0.243	1.278
55 E	1.046	0.497	2.075	-0.014	2.032	1.773	0.953	2.075	-0.014	1.195
56 L	1.274	-0.078	1.973	-0.016	1.923	1.748	0.927	1.973	-0.078	1.107
57 D	1.198	0.127	2.029	-0.133	1.950	1.752	1.040	2.029	-0.133	1.138
58 Q	0.888	0.215	1.730	-0.714	1.640	1.711	0.143	1.730	-0.714	0.802
59 E	0.528	0.351	1.403	-1.273	1.276	1.112	-0.840	1.403	-1.273	0.365
60 L	1.470	0.403	1.477	-1.768	1.221	1.106	-1.275	1.477	-1.768	0.376
61 A	1.198	0.608	1.197	-2.099	0.856	0.617	-1.266	1.198	-2.099	0.159
62 A	1.179	1.235	0.860	-2.035	0.437	0.575	-1.429	1.235	-2.035	0.118
63 G	0.819	1.139	0.533	-1.883	0.073	-0.025	-2.413	1.139	-2.413	-0.251
64 G	1.761	1.002	0.608	-1.776	0.018	-0.030	-2.847	1.761	-2.847	-0.181
65 G	1.394	0.734	0.487	-1.793	0.009	-0.029	-1.249	1.394	-1.793	-0.064
66 A	1.590	0.598	0.683	-1.720	0.164	-0.009	-0.198	1.590	-1.720	0.158
67 G	1.363	0.598	0.935	-1.487	0.483	0.010	0.022	1.363	-1.487	0.275
68 V	1.382	0.461	1.272	-1.037	0.902	0.053	0.185	1.382	-1.037	0.460
69 T	1.154	1.048	1.281	-0.615	0.948	0.053	-0.825	1.281	-0.825	0.435
70 P	1.350	0.558	1.477	-0.305	1.103	0.073	0.225	1.477	-0.305	0.640
71 Q	1.369	-0.126	1.814	-0.311	1.522	0.115	0.388	1.814	-0.311	0.682
72 A	1.736	-0.258	1.935	-0.473	1.531	0.114	-1.210	1.935	-1.210	0.482
73 T	0.901	-0.258	1.599	-0.830	1.358	0.095	-0.929	1.599	-0.929	0.276
74 Q	0.901	-1.156	1.599	-1.086	1.358	0.095	-0.929	1.599	-1.156	0.112
75 A	0.655	-1.071	1.272	-1.410	0.984	0.053	-2.103	1.272	-2.103	-0.232
76 I	0.402	-0.713	1.524	-1.455	1.221	0.072	-0.761	1.524	-1.455	0.042
77 P	0.566	0.187	1.655	-1.501	1.431	0.652	-0.828	1.655	-1.501	0.309
78 A	0.319	0.187	1.571	-1.314	1.330	0.629	-0.771	1.571	-1.314	0.279
79 Y	0.680	0.814	1.898	-1.277	1.695	1.228	0.213	1.898	-1.277	0.750
80 E	1.318	2.052	2.281	-1.002	1.987	1.245	0.111	2.281	-1.002	1.142
81 P	1.546	1.836	2.029	-0.944	1.668	1.226	-0.109	2.029	-0.944	1.036
82 E	1.774	1.477	2.477	-0.821	2.306	1.821	0.966	2.477	-0.821	1.429
83 P	2.026	1.261	2.468	-0.847	2.342	1.821	0.854	2.468	-0.847	1.418
84 G	1.666	0.902	2.141	-0.948	1.977	1.221	-0.129	2.141	-0.948	0.976
85 K	1.666	0.275	2.141	-0.968	1.977	1.221	-0.129	2.141	-0.968	0.883
86 P	1.306	-0.653	1.814	-0.877	1.613	0.621	-1.113	1.814	-1.113	0.387
87 A	1.306	-0.156	1.571	-0.862	1.339	0.602	-2.343	1.571	-2.343	0.208
88 P	0.711	-0.156	1.459	-1.037	1.376	0.604	-1.755	1.459	-1.755	0.172
89 A	0.762	0.113	1.160	-1.065	0.893	0.029	-1.660	1.160	-1.660	0.033
90 A	0.762	-0.001	0.917	-1.217	0.619	0.010	-2.890	0.917	-2.890	-0.257
91 V	0.990	0.608	0.907	-0.978	0.574	0.010	-1.880	0.990	-1.880	0.033
92 S	0.591	1.279	0.655	-1.042	0.346	0.009	-2.155	1.279	-2.155	-0.045
93 A	0.901	0.998	0.954	-0.776	0.656	0.049	-1.258	0.998	-1.258	0.218
94 G	1.261	1.489	1.281	-0.762	1.020	0.649	-0.274	1.489	-0.762	0.667
95 M	1.989	0.862	1.730	-0.424	1.394	1.247	-0.889	1.989	-0.889	0.844
96 N	1.957	0.772	1.907	-0.335	1.613	1.269	-0.886	1.957	-0.886	0.900
97 E	1.957	0.994	1.907	-0.417	1.613	1.269	-0.886	1.957	-0.886	0.920
98 E	1.015	0.419	1.832	-0.946	1.668	1.275	-0.451	1.832	-0.946	0.687

99 Q	1.641	-0.156	2.290	-1.391	2.260	1.852	-0.331	2.290	-1.391	0.881
100A	1.331	0.167	1.991	-1.968	1.950	1.811	-1.228	1.991	-1.968	0.579
101L	0.971	0.071	1.664	-2.183	1.586	1.212	-2.212	1.664	-2.212	0.158
102K	0.743	0.071	1.767	-2.351	1.695	1.237	-2.186	1.767	-2.351	0.139
103A	0.130	0.095	1.318	-2.459	1.312	1.196	-1.761	1.318	-2.459	-0.024
104A	-0.585	-0.110	1.234	-2.476	1.321	1.202	-0.316	1.321	-2.476	0.039
105R	0.408	-0.110	1.468	-2.209	1.467	1.216	-0.591	1.468	-2.209	0.236
106V	-0.534	-0.432	0.935	-1.902	0.838	0.627	-0.221	0.935	-1.902	-0.098
107L	-0.534	0.203	0.935	-1.453	0.838	0.627	-0.221	0.935	-1.453	0.057
108S	-0.288	0.898	1.262	-1.148	1.212	0.669	0.953	1.262	-1.148	0.508
109L	0.079	0.043	1.103	-0.794	1.057	0.534	0.945	1.103	-0.794	0.424
110A	0.642	0.786	1.421	-0.491	1.221	0.552	0.397	1.421	-0.491	0.647
111Q	1.356	1.599	1.505	-0.028	1.212	0.547	-1.049	1.599	-1.049	0.735
112D	1.578	0.904	1.627	0.368	1.376	1.015	-1.217	1.627	-1.217	0.807
113T	2.425	0.856	2.141	0.432	1.841	1.635	-1.653	2.425	-1.653	1.097
114A	1.710	0.974	2.057	0.139	1.850	1.640	-0.208	2.057	-0.208	1.166
115D	1.660	1.465	1.926	-0.336	1.631	1.618	-0.331	1.926	-0.336	1.090
116R	1.470	0.926	1.954	-0.419	1.622	1.169	-0.435	1.954	-0.435	0.898
117L	1.470	0.944	1.954	-0.117	1.622	1.169	-0.435	1.954	-0.435	0.944
118T	1.470	1.149	1.954	0.596	1.622	1.169	-0.435	1.954	-0.435	1.075
119N	1.198	1.233	2.132	0.770	1.941	1.275	-0.361	2.132	-0.361	1.170
120T	1.065	1.479	1.702	0.390	1.467	0.650	-1.370	1.702	-1.370	0.769
121A	2.140	1.527	2.113	-0.643	1.823	1.245	-1.831	2.140	-1.831	0.910
122K	2.222	2.359	2.066	-1.326	1.823	1.245	-1.712	2.359	-1.712	0.954
123A	2.412	1.413	2.038	-1.338	1.832	1.693	-1.608	2.412	-1.608	0.920
124E	2.444	1.209	2.290	-0.671	2.315	2.268	-1.584	2.444	-1.584	1.181
125S	2.045	0.634	2.281	-0.101	2.360	2.285	-0.629	2.360	-0.629	1.268
126D	1.103	0.317	1.748	-0.201	1.731	1.696	-0.259	1.748	-0.259	0.877
127K	1.103	-0.222	1.748	-0.976	1.731	1.696	-0.259	1.748	-0.976	0.689
128M	1.242	-0.240	1.692	-1.534	1.686	1.585	-0.242	1.692	-1.534	0.599
129L	0.964	-0.126	1.543	-1.713	1.531	1.565	-1.412	1.565	-1.713	0.336
130A	0.598	0.688	1.702	-1.385	1.686	1.701	-1.403	1.702	-1.403	0.512
131D	0.370	0.688	1.253	-1.080	1.048	1.106	-2.479	1.253	-2.479	0.129
132A	1.078	0.724	1.561	-0.745	1.312	1.129	-2.536	1.561	-2.536	0.361
133R	1.793	1.215	1.646	-0.665	1.303	1.124	-3.981	1.793	-3.981	0.348
134A	2.153	0.077	1.973	-0.265	1.668	1.724	-2.998	2.153	-2.998	0.619
135N	1.900	-0.128	2.029	-0.121	1.722	1.277	-2.825	2.029	-2.825	0.551
136A	1.261	-0.110	1.889	-0.331	1.704	1.279	-1.494	1.889	-1.494	0.600
137E	0.414	0.465	1.375	-1.005	1.239	0.660	-1.058	1.375	-1.058	0.299
138Q	0.642	-0.110	1.365	-1.639	1.194	0.660	-0.047	1.365	-1.639	0.295
139I	0.692	0.213	1.393	-2.227	1.248	1.219	0.039	1.393	-2.227	0.368
140L	0.692	0.628	1.393	-2.320	1.248	1.219	0.039	1.393	-2.320	0.414
141G	0.465	1.323	1.496	-2.328	1.358	1.244	0.065	1.496	-2.328	0.517
142E	0.218	0.696	1.328	-1.954	1.157	1.821	0.169	1.821	-1.954	0.491
143A	1.053	0.660	1.664	-1.309	1.330	1.839	-0.112	1.839	-1.309	0.732
144R	1.767	0.660	1.748	-0.497	1.321	1.834	-1.557	1.834	-1.557	0.754
145H	2.039	0.337	2.029	0.282	1.686	2.323	-1.566	2.323	-1.566	1.018
146T	1.679	0.151	1.702	0.561	1.321	1.723	-2.550	1.723	-2.550	0.655
147A	1.875	-0.340	1.898	0.485	1.476	1.743	-1.499	1.898	-1.499	0.805
148D	1.375	0.235	1.346	0.154	0.993	1.120	-0.910	1.375	-0.910	0.616
149A	1.375	-0.304	1.188	-0.396	0.820	0.500	-2.187	1.375	-2.187	0.142
150T	1.540	0.509	1.318	-0.956	1.030	1.080	-2.254	1.540	-2.254	0.324
151V	1.540	0.509	1.318	-1.421	1.030	1.080	-2.254	1.540	-2.254	0.257
152A	1.173	1.419	1.477	-2.002	1.185	1.216	-2.246	1.477	-2.246	0.317
153E	1.420	1.419	1.804	-2.103	1.558	1.258	-1.073	1.804	-2.103	0.612
154A	1.356	1.383	2.038	-2.200	1.877	1.863	-1.114	2.038	-2.200	0.743
155R	1.723	1.383	2.160	-2.070	1.886	1.861	-2.713	2.160	-2.713	0.604
156Q	2.222	0.455	2.431	-1.724	2.205	2.350	-1.712	2.431	-1.724	0.890
157R	1.862	-0.240	2.103	-1.369	1.841	1.751	-2.696	2.103	-2.696	0.465

158A	1.464	-1.053	2.094	-1.069	1.886	1.768	-1.741	2.094	-1.741	0.478
159D	0.617	-0.514	1.580	-1.037	1.422	1.148	-1.305	1.580	-1.305	0.273
160A	0.370	-1.053	1.253	-1.446	1.048	1.106	-2.479	1.253	-2.479	-0.172
161M	0.737	-0.562	1.094	-1.677	0.893	0.970	-2.487	1.094	-2.487	-0.147
162L	0.737	0.407	1.094	-1.642	0.893	0.970	-2.487	1.094	-2.487	-0.004
163A	0.484	1.425	1.150	-1.197	0.948	0.524	-2.314	1.425	-2.314	0.146
164D	0.762	2.281	1.300	-0.471	1.103	0.544	-1.144	2.281	-1.144	0.625
165A	1.293	2.317	1.739	-0.082	1.531	1.151	-1.090	2.317	-1.090	0.980
166Q	2.286	2.317	1.973	0.164	1.677	1.166	-1.365	2.317	-1.365	1.174
167S	2.646	2.317	2.300	0.125	2.041	1.766	-0.381	2.646	-0.381	1.545
168R	2.147	1.257	2.029	-0.138	1.722	1.277	-1.383	2.147	-1.383	0.987
169S	2.393	1.257	2.356	-0.424	2.096	1.319	-0.209	2.393	-0.424	1.255
170E	1.432	0.892	1.945	-0.844	1.731	1.282	0.062	1.945	-0.844	0.929
171A	1.287	0.317	2.225	-1.367	2.050	1.887	-0.098	2.225	-1.367	0.900
172Q	1.401	0.808	2.122	-1.532	1.950	1.304	0.066	2.122	-1.532	0.874
173L	1.122	0.892	1.973	-1.797	1.795	1.284	-1.104	1.973	-1.797	0.595
174R	1.009	1.928	1.973	-1.679	1.804	0.727	-0.914	1.973	-1.679	0.692
175Q	1.369	1.115	2.300	-1.559	2.169	1.327	0.069	2.300	-1.559	0.970
176A	1.350	1.163	2.421	-1.508	2.433	1.879	-0.029	2.433	-1.508	1.101
177Q	2.064	1.163	2.505	-1.606	2.424	1.874	-1.474	2.505	-1.606	0.993
178E	2.431	0.467	2.346	-1.522	2.269	1.738	-1.482	2.431	-1.522	0.893
179K	2.185	0.383	2.019	-1.461	1.895	1.695	-2.655	2.185	-2.655	0.580
180A	1.470	-0.448	1.935	-1.093	1.905	1.701	-1.210	1.935	-1.210	0.608
181D	1.470	0.091	1.935	-0.873	1.905	1.701	-1.210	1.935	-1.210	0.717
182A	1.110	-0.448	1.608	-0.908	1.540	1.101	-2.194	1.608	-2.194	0.258
183L	1.382	0.127	1.431	-0.893	1.221	0.996	-2.268	1.431	-2.268	0.285
184Q	1.382	1.145	1.431	-0.810	1.221	0.996	-2.268	1.431	-2.268	0.442
185A	1.242	1.485	1.487	-0.668	1.267	1.106	-2.286	1.487	-2.286	0.519
186D	1.375	1.575	1.917	-0.697	1.741	1.731	-1.276	1.917	-1.276	0.909
187A	2.317	1.892	2.449	-1.096	2.369	2.320	-1.646	2.449	-1.646	1.229
188E	2.071	2.467	2.281	-1.396	2.169	2.898	-1.542	2.898	-1.542	1.278
189R	2.349	1.567	2.431	-1.064	2.324	2.918	-0.372	2.918	-1.064	1.450
190K	2.210	0.640	2.487	-0.367	2.369	3.028	-0.390	3.028	-0.390	1.425
191H	1.571	0.435	2.346	0.306	2.351	3.030	0.942	3.030	0.306	1.569
192S	0.813	0.836	2.010	0.117	2.032	2.448	0.913	2.448	0.117	1.310
193E	0.907	-0.344	1.571	-0.851	1.513	1.823	0.914	1.823	-0.851	0.791
194I	0.876	-0.310	1.318	-1.753	1.030	1.248	0.890	1.318	-1.753	0.471
195M	0.237	0.505	1.019	-2.343	0.838	0.630	0.945	1.019	-2.343	0.262
196G	0.269	1.111	1.169	-1.801	0.993	0.651	0.672	1.169	-1.801	0.438
197T	0.155	1.297	1.169	-0.948	1.002	0.094	0.861	1.297	-0.948	0.519
198I	1.040	0.806	1.636	0.062	1.394	0.134	0.703	1.636	0.062	0.825
199N	1.571	1.034	2.075	0.507	1.823	0.742	0.757	2.075	0.507	1.216
200Q	1.344	0.221	2.085	0.375	1.868	0.742	-0.253	2.085	-0.253	0.912
201Q	0.781	0.305	1.767	-0.477	1.704	0.723	0.295	1.767	-0.477	0.728
202R	0.705	0.441	1.823	-1.256	1.731	0.727	0.408	1.823	-1.256	0.654
203A	0.756	0.441	1.851	-2.070	1.786	1.286	0.495	1.851	-2.070	0.649
204V	0.737	0.237	1.515	-2.279	1.367	1.243	0.332	1.515	-2.279	0.450
205L	0.623	0.908	1.617	-2.383	1.467	1.826	0.168	1.826	-2.383	0.604
206E	-0.224	1.603	1.103	-2.356	1.002	1.206	0.603	1.603	-2.356	0.420
207G	0.136	0.824	1.431	-2.398	1.367	1.806	1.587	1.806	-2.398	0.679
208R	0.749	1.010	1.879	-2.330	1.750	1.847	1.162	1.879	-2.330	0.867
209L	0.749	0.688	1.879	-2.240	1.750	1.847	1.162	1.879	-2.240	0.834
210E	0.522	0.718	1.982	-2.080	1.859	1.872	1.187	1.982	-2.080	0.866
211Q	0.490	0.718	2.188	-1.902	2.060	1.892	1.228	2.188	-1.902	0.953
212L	-0.357	1.040	1.692	-1.675	1.540	1.271	1.480	1.692	-1.675	0.713
213R	0.718	1.820	2.103	-1.479	1.895	1.866	1.019	2.103	-1.479	1.134
214T	0.490	0.600	2.206	-1.319	2.005	1.891	1.044	2.206	-1.319	0.988
215F	0.604	0.922	2.206	-1.429	1.996	2.448	0.854	2.448	-1.429	1.086
216E	1.065	1.587	2.543	-1.669	2.224	2.462	0.751	2.543	-1.669	1.280

217R	1.065	1.826	2.543	-1.988	2.224	2.462	0.751	2.543	-1.988	1.269
218E	1.065	0.808	2.543	-2.044	2.224	2.462	0.751	2.543	-2.044	1.116
219Y	1.913	1.064	3.038	-1.985	2.743	3.082	0.499	3.082	-1.985	1.479
220R	0.838	1.962	2.627	-1.824	2.388	2.488	0.961	2.627	-1.824	1.349
221T	0.933	0.742	2.646	-1.891	2.552	2.458	1.027	2.646	-1.891	1.209
222R	0.768	0.047	2.515	-1.936	2.342	1.878	1.094	2.515	-1.936	0.958
223L	0.768	-0.192	2.515	-1.978	2.342	1.878	1.094	2.515	-1.978	0.918
224K	-0.079	0.868	2.001	-1.766	1.877	1.259	1.530	2.001	-1.766	0.813
225T	0.085	0.527	2.132	-1.651	2.087	1.839	1.462	2.132	-1.651	0.926
226Y	0.231	-0.168	1.851	-1.360	1.768	1.234	1.623	1.851	-1.360	0.740
227L	1.192	0.814	2.262	-1.154	2.132	1.271	1.351	2.262	-1.154	1.124
228E	0.250	1.593	1.730	-0.841	1.504	0.682	1.721	1.730	-0.841	0.948
229S	0.414	0.814	1.860	-0.706	1.713	1.262	1.654	1.860	-0.706	1.002
230Q	1.028	0.586	1.935	-0.880	1.841	1.842	1.296	1.935	-0.880	1.092
231L	1.028	0.586	1.935	-1.412	1.841	1.842	1.296	1.935	-1.412	1.016
232E	0.895	1.603	1.599	-1.913	1.431	1.242	1.323	1.603	-1.913	0.883
233E	0.863	1.656	1.776	-2.164	1.649	1.265	1.326	1.776	-2.164	0.910
234L	0.749	1.936	1.879	-2.087	1.750	1.847	1.162	1.936	-2.087	1.034
235G	1.691	2.140	1.954	-1.825	1.695	1.841	0.727	2.140	-1.825	1.175
236Q	1.609	1.513	1.776	-1.469	1.485	1.262	0.913	1.776	-1.469	1.013
237R	1.249	1.381	1.449	-1.198	1.121	0.662	-0.070	1.449	-1.198	0.656
238G	1.963	0.471	1.533	-0.920	1.112	0.657	-1.516	1.963	-1.516	0.472
239S	1.736	0.383	1.786	-0.698	1.431	0.676	-1.296	1.786	-1.296	0.574
240A	1.122	0.383	1.337	-0.757	1.048	0.635	-0.870	1.337	-0.870	0.414
241A	1.489	0.992	1.178	-0.590	0.893	0.499	-0.879	1.489	-0.879	0.512
242P	1.540	0.992	1.337	-0.209	1.093	0.519	-0.719	1.540	-0.719	0.651
243V	1.571	1.173	1.487	0.692	1.248	0.540	-0.992	1.571	-0.992	0.817
244D	1.571	1.269	1.487	1.581	1.248	0.540	-0.992	1.581	-0.992	0.958
245S	2.071	1.357	1.758	2.408	1.567	1.029	0.009	2.408	0.009	1.457
246N	2.071	1.129	1.515	2.236	1.294	1.010	-1.221	2.236	-1.221	1.148
247A	2.665	0.345	1.627	1.685	1.257	1.008	-1.809	2.665	-1.809	0.968
248D	2.393	0.884	1.346	0.559	0.893	0.519	-1.800	2.393	-1.800	0.685
249A	1.401	0.836	1.132	-0.246	0.692	0.504	-1.709	1.401	-1.709	0.373
250G	1.590	0.662	1.103	-0.686	0.701	0.952	-1.605	1.590	-1.605	0.388
251G	1.837	0.644	1.431	-0.378	1.075	0.994	-0.431	1.837	-0.431	0.739
252F	0.623	0.830	1.094	0.066	0.711	0.510	-0.171	1.094	-0.171	0.523
253D	0.933	1.631	1.393	0.886	1.020	0.550	0.726	1.631	0.550	1.020
254Q	0.838	1.924	1.832	1.225	1.540	1.175	0.725	1.924	0.725	1.323
255F	0.838	2.042	1.832	1.300	1.540	1.175	0.725	2.042	0.725	1.350
256N	1.780	2.471	2.346	0.779	2.224	1.765	0.539	2.471	0.539	1.701
257R	1.590	2.116	2.374	0.319	2.214	1.317	0.435	2.374	0.319	1.481
258G	1.211	1.557	1.589	-0.036	2.160	1.335	-0.739	2.160	-0.739	1.011
259K	1.793	1.185	1.197	0.280	2.524	1.390	-2.000	2.524	-2.000	0.910
260N	1.350	0.608	0.440	0.491	2.533	1.410	-2.897	2.533	-2.897	0.562

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	[1]MPLTPADVHNVAFSKPPIGKRGYNEDEVDAFLDLVENELTRLIEENSDLRQRINELDQELAAGGGAGVTPQATQAIPAYEPEPGKPAPAAVSAGMNEEQALKAARVLSLAQDTADRLTNTAKAESDKMLADARANAEQILGEARHTADATVAEARQRADAMLADAQSRSEAQLRQAQEKADALQADAERKHSEIMGTINQQRAVLEGRLEQLRTFEREYRTRLKTYLESQLEELGQRGSAAPVDSNADAGGFDQFNRGKN[260]
Hydrophilicity	[1]MPLTPADVHNVAFSKPPI<u>GKRGYNEDEVDA</u>FLDLVENELTRLI<u>EENSDLRQ</u>RINELDQELAAGGGAGVTPQATQAIPAY<u>EPEPGKP</u>APAAVS<u>SAGMNEEQAL</u>KAARVLSL<u>AQDTADRL</u><u>TNTAKAESDKM</u>LA<u>DARA</u><u>NAEQ</u>ILG<u>EARHTAD</u>ATVA<u>EARQRAD</u>AML<u>ADAQSRSEAQL</u><u>RQAQEKADAL</u><u>QADAERKHSE</u>IMGTINQQRAVLEGRLEQLRTF<u>EREYRTR</u>LKTYLESQLEEL<u>GQRGSAAPVDSNADAGG</u>FDQFNRGKN[260]
Flexibility	[1]MPLTPADVHNVAFSKPPIGKRGYNEDEVDAFLDLVENELTRLI<u>EENSDLR</u>QRINELDQELAAGGGAGVTPQATQAI<u>PAYEPEP</u>GKPAPAAVSAGMNEEQALKAARVLSLAQDTADRLT<u>NTAKAES</u>DKMLADARANAEQILGEARHTADATVAEARQRADA<u>MLADAQSRSE</u>AQLRQAQEKADAL<u>QADAERKH</u>SEIMGTINQQRAVLEGRLEQLRTFEREYRTRLKTYLESQL<u>EELGQRG</u>SAAPVDSNADAGG<u>FDQFNRGKN</u>[260]
Accessibility	[1]MPLTPADVHNVAF<u>SKPPIGKRGYNEDEVDA</u>FLDL<u>VENELTRLIEENSDLRQRINELDQEL</u>AAGGGAGV<u>TPQATQAI</u><u>PAYEPEPGKPAP</u>AAVS<u>AGMNEEQALKA</u>ARVLSL<u>AQDTADRLTNTAKAESDKM</u>LA<u>DARA</u><u>NAEQ</u>ILG<u>EARHTAD</u>AT<u>VAEARQRADAM</u><u>LADAQSRSEAQLRQAQEKADALQADAERKHSEIMGTINQ</u><u>QRA</u>VLE<u>GRLEQLRTFEREYRTRLKTYLESQLEELGQRG</u>SAAPVDSNADAGGF<u>DQFNRGKN</u>[260]
Turns	[1]MPLTPADVHNVAFSKPPIGKRGYNEDEVDAFLDLVENELTRLIEENSDLRQRINELDQELAAGGGAGVTPQATQAIPAYEPEPGKPAPAAVSAGMNEEQALKAARVLSLAQDTADRLTNTAKAESDKMLADARANAEQILGEARHTADATVAEARQRADAMLADAQSRSEAQLRQAQEKADALQADAERKHSEIMGTINQQRAVLEGRLEQLRTFEREYRTRLKTYLESQLEELGQRGSAA<u>PVDSNAD</u>AGGFDQFNRGKN[260]
Exposed Surface	[1]MPLTPADVHNVAFS<u>KPPIGKRGYNED</u>EVDAFLDLVENELTRLIEE<u>NSDLRQR</u>INELDQELAAGGGAGVTPQATQAIPA<u>YEPEPGKP</u>APAAVSAGMNEEQALKAARVLSLAQDTADRLTNT<u>AKAESDKM</u>LADARANAEQILGEARHTADATVAEARQRADAMLADAQSRSEAQ<u>LRQAQEKA</u>DAL<u>QADAERKHSEI</u>MGTINQQRAVLEGRLEQLRTF<u>EREYRTRLKTY</u>LESQLEELGQRGSAAPVDSNADAGGFDQF<u>NRGKN</u>[260]
Polarity	[1]MPLTPADVHNVAFS<u>KPPIGKRGYNEDEVDAF</u>LDL<u>VENELTRLIEENSDLRQRINEL</u>DQELAAGGGAGVTPQATQAIPA<u>YEPEPGKP</u>APAAVSAGM<u>NEEQALKA</u>ARVLSLAQDTADRLTNT<u>AKAESDKM</u>LADARANAEQ<u>ILGEARHTAD</u>AT<u>VAEARQRAD</u>AMLADAQS<u>RSEAQLRQAQEKA</u>DAL<u>QADAERKHSEIMG</u>TINQQ<u>RAVLEGRLEQLRTFEREYRTRLKTYLESQLEELGQRG</u>SAAPVDSNADAGGFDQFNRGKN[260]
Antigenic Propensity	[1]MPLTPADVHNVAFSKPPIGKRGYNEDEVDAFLDLVENELTRLIEENSDLRQRINELDQELAAGGGAGVTPQATQAIPAYEPEPGKPAPAAVSAGMNEEQALKAARVLSLAQDTADRLTNTAKAESDKMLADARANAEQILGEARHTADATVAEARQRADAMLADAQSRSEAQLRQAQEKADALQADAERKHSEIMGTINQQRAVLEGRLEQLRTFEREYRTRLKTYLESQLEELGQRGSAAPVDSNADAGGFDQFNRGKN[260]