Thursday, January 21, 2010
2:34 PM

BcePred Prediction Server

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

seqname=RV1980C
Seq=   VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYY
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     GLDPVNYQNFAVTNDGVIFFFNPGELLPEAAGPTQVLVPRSAIDSMLA

Length=228

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

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

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
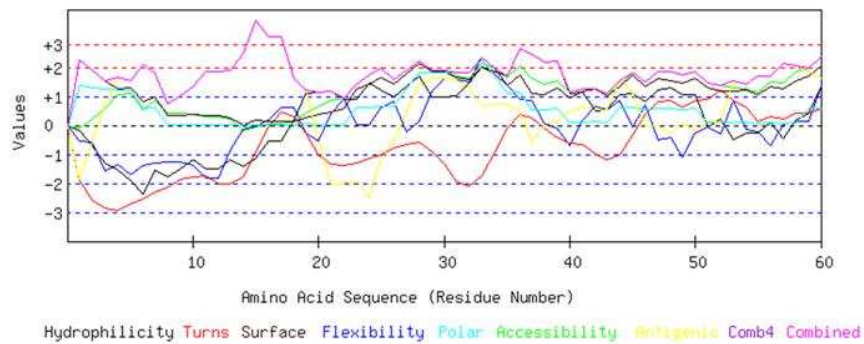
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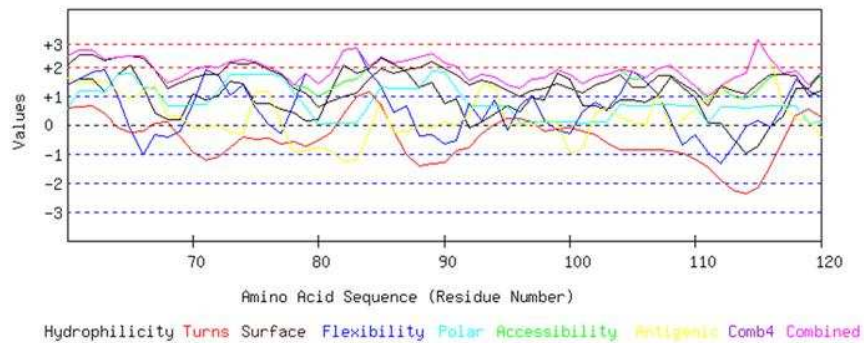
Length=228

A.A. ppppppppppppppppppppppppppppppp Parameter ppppppppppppppppppppppppppppppppppppppp Combined

	Hydro	Flexi	Access	Turns	Surface	Polar	AntiPro	MAX	MIN	AVG

5	I	-1.893	-1.697	1.085	-2.693	1.285	1.220	1.520	1.520	-2.693	-0.168
6	F	-2.393	-1.372	0.533	-2.532	0.802	0.596	2.110	2.110	-2.532	-0.322
7	M	-1.558	-1.294	0.870	-2.295	0.975	0.615	1.829	1.829	-2.295	-0.123
8	L	-1.786	-1.276	0.421	-2.160	0.337	0.020	0.754	0.754	-2.160	-0.527
9	V	-1.514	-1.276	0.440	-1.858	0.346	0.020	1.021	1.021	-1.858	-0.403
10	T	-1.166	-1.384	0.384	-1.763	0.382	0.017	1.358	1.358	-1.763	-0.310
11	A	-1.482	-1.839	0.309	-1.758	0.346	0.005	1.849	1.849	-1.839	-0.367
12	V	-1.482	-1.803	0.309	-2.005	0.346	0.005	1.849	1.849	-2.005	-0.397
13	V	-1.160	-0.851	0.216	-2.031	0.264	0.022	1.882	1.882	-2.031	-0.237
14	L	-1.400	-0.128	-0.196	-1.769	0.018	0.019	2.464	2.464	-1.769	-0.142
15	L	-1.122	-0.019	-0.046	-0.927	0.173	0.039	3.634	3.634	-1.122	0.247
16	C	-0.528	0.185	0.066	-0.067	0.136	0.038	3.045	3.045	-0.528	0.411
17	C	-0.528	0.640	0.066	0.468	0.136	0.038	3.045	3.045	-0.528	0.552
18	S	0.187	0.604	0.150	0.285	0.127	0.032	1.600	1.600	0.032	0.426
19	G	1.097	-0.252	0.431	-0.269	0.273	0.047	1.206	1.206	-0.269	0.362
20	V	1.141	-0.520	0.646	-1.000	0.364	0.029	-0.427	1.141	-1.000	0.033
21	A	1.186	0.407	0.860	-1.356	0.455	0.011	-2.059	1.186	-2.059	-0.071
22	T	0.907	0.898	0.954	-1.394	0.574	0.010	-1.999	0.954	-1.999	-0.007
23	A	0.907	0.001	1.412	-1.318	1.257	0.605	-1.934	1.412	-1.934	0.133
24	A	1.470	0.037	1.730	-1.147	1.422	0.623	-2.482	1.730	-2.482	0.236
25	P	1.217	0.612	1.982	-1.028	1.658	0.643	-1.140	1.982	-1.140	0.563
26	K	0.977	0.828	1.571	-0.797	1.412	0.641	-0.558	1.571	-0.797	0.582
27	T	1.337	-0.208	1.898	-0.655	1.777	1.240	0.425	1.898	-0.655	0.831
28	Y	1.698	0.133	2.225	-0.569	2.142	1.840	1.409	2.225	-0.569	1.268
29	C	0.983	1.167	1.898	-0.905	1.877	1.826	1.624	1.898	-0.905	1.210
30	E	0.983	1.621	1.898	-1.351	1.877	1.826	1.624	1.898	-1.351	1.211
31	E	1.015	1.585	1.692	-1.932	1.677	1.806	1.584	1.806	-1.932	1.061
32	L	1.464	1.501	1.636	-2.103	1.595	1.807	1.293	1.807	-2.103	1.027
33	K	2.008	2.333	2.122	-1.754	2.005	2.278	0.661	2.333	-1.754	1.379
34	G	1.843	1.992	1.991	-0.932	1.795	1.698	0.728	1.992	-0.932	1.302
35	T	1.710	1.365	1.655	-0.097	1.385	1.099	0.755	1.710	-0.097	1.125
36	D	2.671	0.910	2.066	0.383	1.750	1.136	0.483	2.671	0.383	1.343
37	T	2.444	0.862	1.617	0.248	1.112	0.541	-0.592	2.444	-0.592	0.890
38	G	2.172	0.047	1.412	-0.107	1.066	0.559	0.030	2.172	-0.107	0.740
39	Q	2.222	-0.090	1.543	-0.412	1.285	0.581	0.153	2.222	-0.412	0.755
40	A	1.084	-0.695	1.132	-0.624	0.948	0.094	0.483	1.132	-0.695	0.346
41	C	1.135	0.161	1.262	-0.668	1.166	0.117	0.606	1.262	-0.668	0.540
42	Q	0.509	0.664	1.262	-0.982	1.257	0.134	0.550	1.262	-0.982	0.485
43	I	0.541	0.532	1.085	-1.196	1.039	0.111	0.547	1.085	-1.196	0.380
44	Q	1.040	0.856	1.356	-1.009	1.358	0.600	1.548	1.548	-1.009	0.821
45	M	1.084	-0.042	1.814	-0.353	1.722	0.602	1.146	1.814	-0.353	0.853
46	S	0.838	0.682	1.487	0.373	1.349	0.559	-0.028	1.487	-0.028	0.751
47	D	1.224	-0.498	1.879	0.835	1.604	0.577	-0.017	1.879	-0.498	0.800
48	P	1.287	-0.428	1.851	0.871	1.540	0.575	-0.294	1.851	-0.428	0.772
49	A	1.046	-1.111	1.720	0.620	1.476	0.560	0.083	1.720	-1.111	0.628
50	Y	1.078	-0.256	1.870	0.858	1.631	0.580	-0.190	1.870	-0.256	0.796
51	N	-0.060	-0.054	1.459	0.915	1.294	0.093	0.141	1.459	-0.060	0.541
52	I	0.218	-0.304	1.365	1.209	1.175	0.094	0.081	1.365	-0.304	0.548
53	N	-0.496	0.876	1.281	0.864	1.185	0.099	1.526	1.526	-0.496	0.762
54	I	-0.243	-0.140	1.272	0.615	1.221	0.099	1.414	1.414	-0.243	0.605
55	S	-0.275	-0.222	1.122	0.150	1.066	0.079	1.687	1.687	-0.275	0.515
56	L	0.111	-0.719	1.515	0.312	1.321	0.096	1.697	1.697	-0.719	0.619
57	P	-0.452	0.025	1.468	0.212	1.248	0.075	2.142	2.142	-0.452	0.674
58	S	0.187	0.157	1.851	0.433	1.540	0.092	2.040	2.040	0.092	0.900
59	Y	0.408	0.133	1.973	0.411	1.704	0.561	1.872	1.973	0.133	1.009
60	Y	1.369	1.395	2.384	0.561	2.069	0.598	1.600	2.384	0.561	1.425
61	P	1.597	1.597	2.589	0.622	2.433	1.174	1.445	2.589	0.622	1.637
62	D	1.597	1.814	2.589	0.662	2.433	1.174	1.445	2.589	0.662	1.673
63	Q	1.135	1.884	2.253	0.363	2.205	1.160	1.548	2.253	0.363	1.507
64	K	1.748	0.986	2.328	-0.109	2.333	1.740	1.190	2.333	-0.109	1.459
65	S	2.058	-0.170	2.384	-0.243	2.369	1.761	0.857	2.384	-0.243	1.288
66	L	1.306	-1.025	2.365	-0.200	2.287	1.292	1.198	2.365	-1.025	1.032
67	E	0.421	-0.330	1.898	0.047	1.895	1.251	1.356	1.898	-0.330	0.934
68	N	0.193	-0.414	1.449	0.087	1.257	0.657	0.281	1.449	-0.414	0.501
69	Y	0.161	-0.210	1.627	-0.400	1.476	0.679	0.284	1.627	-0.400	0.517
70	I	1.072	0.736	1.907	-0.935	1.622	0.694	-0.110	1.907	-0.935	0.712
71	A	0.844	1.892	2.010	-1.236	1.731	0.719	-0.084	2.010	-1.236	0.839
72	Q	1.034	1.718	1.982	-1.106	1.741	1.167	0.020	1.982	-1.106	0.936
73	T	1.514	1.022	2.178	-0.786	2.142	1.742	-0.247	2.178	-0.786	1.081
74	R	1.438	1.387	2.253	-0.413	2.114	1.745	-0.318	2.253	-0.413	1.172
75	D	0.724	0.574	2.169	-0.484	2.123	1.750	1.127	2.169	-0.484	1.140
76	K	0.756	0.035	1.991	-0.460	1.905	1.728	1.124	1.991	-0.460	1.011
77	F	0.560	-0.306	1.795	-0.657	1.750	1.708	0.073	1.795	-0.657	0.703
78	L	0.427	0.724	1.365	-0.591	1.276	1.083	-0.936	1.365	-0.936	0.478
79	S	0.123	1.784	1.290	-0.743	1.112	0.614	-0.887	1.784	-0.887	0.471
80	A	0.174	1.419	0.991	-0.549	0.629	0.040	-0.792	1.419	-0.792	0.273
81	A	1.167	1.778	1.206	-0.268	0.829	0.055	-0.883	1.778	-0.883	0.555
82	T	2.077	2.591	1.487	0.395	0.975	0.070	-1.277	2.591	-1.277	0.902
83	S	1.799	2.675	1.580	0.971	1.093	0.069	-1.217	2.675	-1.217	0.996
84	S	1.932	1.820	2.010	1.142	1.567	0.694	-0.208	2.010	-0.208	1.280
85	T	2.292	1.323	2.337	0.698	1.932	1.293	0.776	2.337	0.698	1.521
86	P	2.096	0.425	2.141	-0.238	1.777	1.273	-0.275	2.141	-0.275	1.028
87	R	1.818	0.642	2.234	-1.013	1.895	1.272	-0.215	2.234	-1.013	0.948
88	E	1.287	-0.376	2.337	-1.428	1.977	1.271	-0.043	2.337	-1.428	0.718
89	A	1.451	-0.342	2.468	-1.350	2.187	1.851	-0.110	2.468	-1.350	0.879
90	P	0.737	-0.667	2.141	-1.288	1.923	1.837	0.105	2.141	-1.288	0.684
91	Y	0.914	-0.534	2.010	-0.880	1.759	1.253	-0.007	2.010	-0.880	0.645
92	E	-0.085	0.728	1.543	-0.764	1.376	0.656	0.341	1.543	-0.764	0.542
93	L	0.111	0.153	1.739	-0.309	1.531	0.675	1.392	1.739	-0.309	0.756
94	N	0.389	0.848	1.646	0.039	1.412	0.677	1.332	1.646	0.039	0.906
95	I	0.642	-0.168	1.393	0.229	1.175	0.657	-0.010	1.393	-0.168	0.560
96	T	0.477	0.648	1.262	0.212	0.966	0.078	0.057	1.262	0.057	0.529
97	S	0.939	1.012	1.599	0.120	1.194	0.092	-0.046	1.599	-0.046	0.701
98	A	0.876	0.157	1.627	-0.213	1.257	0.093	0.230	1.627	-0.213	0.575
99	T	1.793	-0.168	1.917	-0.125	1.431	0.112	0.068	1.917	-0.168	0.718
100	Y	1.597	-0.300	1.720	-0.119	1.276	0.092	-0.983	1.720	-0.983	0.469
101	Q	0.680	0.465	1.431	-0.233	1.103	0.073	-0.821	1.431	-0.821	0.385
102	S	0.680	0.788	1.674	-0.332	1.376	0.092	0.409	1.674	-0.332	0.670
103	A	0.484	0.560	1.720	-0.632	1.494	0.091	0.588	1.720	-0.632	0.615
104	I	0.869	1.050	1.898	-0.853	1.731	0.697	0.256	1.898	-0.853	0.807

110Q	0.920	-0.348	1.346	-1.166	1.139	0.660	0.553	1.346	-1.166	0.443
111A	0.073	-0.935	0.832	-1.476	0.674	0.041	0.988	0.988	-1.476	0.028
112V	0.073	-1.342	1.290	-1.919	1.358	0.635	1.053	1.358	-1.919	0.164
113V	-0.490	-0.755	0.973	-2.271	1.194	0.617	1.601	1.601	-2.271	0.124
114L	-0.989	-0.050	0.898	-2.384	1.057	0.594	1.770	1.770	-2.384	0.128
115K	-0.743	0.155	1.225	-2.194	1.431	0.636	2.943	2.943	-2.194	0.493
116V	-0.066	-0.050	1.646	-1.420	1.750	0.675	2.242	2.242	-1.420	0.682
117Y	0.300	0.674	1.767	-0.547	1.759	0.674	0.643	1.767	-0.547	0.753
118Q	1.242	1.571	1.842	0.339	1.704	0.668	0.208	1.842	0.208	1.082
119N	1.242	1.171	1.384	0.558	1.020	0.074	0.143	1.384	0.074	0.799
120A	1.805	0.920	1.702	0.242	1.185	0.092	-0.405	1.805	-0.405	0.792
121G	2.058	1.411	1.608	-0.067	1.121	0.693	-0.469	2.058	-0.469	0.908
122G	1.812	1.275	1.524	0.146	1.020	0.669	-0.413	1.812	-0.413	0.862
123T	1.698	1.139	1.421	0.699	0.866	0.649	-0.259	1.698	-0.259	0.887
124H	1.894	0.241	1.617	1.361	1.020	0.669	0.792	1.894	0.241	1.085
125P	1.862	0.982	1.823	1.441	1.221	0.688	0.832	1.862	0.688	1.264
126T	1.382	0.624	2.085	0.992	1.504	0.708	1.164	2.085	0.624	1.208
127T	1.413	-0.042	2.337	0.329	1.987	1.282	1.188	2.337	-0.042	1.214
128T	1.413	0.007	2.178	-0.451	1.813	0.663	-0.089	2.178	-0.451	0.791
129Y	0.699	-0.987	1.870	-0.973	1.494	0.648	-0.058	1.870	-0.987	0.385
130K	1.002	-0.042	1.945	-1.085	1.658	1.117	-0.107	1.945	-1.085	0.641
131A	0.041	-0.382	1.767	-0.921	1.522	1.122	-0.126	1.767	-0.921	0.432
132F	0.345	-0.382	1.842	-0.240	1.686	1.591	-0.176	1.842	-0.382	0.666
133D	0.844	-0.615	1.917	0.288	1.823	1.614	-0.344	1.917	-0.615	0.790
134W	0.617	-0.340	1.468	0.553	1.185	1.020	-1.420	1.468	-1.420	0.440
135D	0.364	0.994	1.720	0.359	1.422	1.039	-0.077	1.720	-0.077	0.832
136Q	1.211	0.814	2.216	-0.175	1.941	1.659	-0.329	2.216	-0.329	1.048
137A	0.939	-0.001	2.393	-0.991	2.260	1.765	-0.255	2.393	-0.991	0.873
138Y	1.704	0.489	2.617	-1.406	2.515	1.759	-0.058	2.617	-1.406	1.089
139R	0.566	0.489	2.206	-1.837	2.178	1.272	0.273	2.206	-1.837	0.735
140K	0.515	0.215	2.075	-1.735	1.959	1.249	0.150	2.075	-1.735	0.633
141P	0.263	-0.126	2.328	-1.537	2.196	1.269	1.493	2.328	-1.537	0.841
142I	1.015	-0.689	2.346	-1.066	2.278	1.738	1.151	2.346	-1.066	0.968
143T	1.078	-0.867	2.113	-0.538	1.959	1.133	1.193	2.113	-0.867	0.867
144Y	0.136	-0.867	1.580	0.003	1.330	0.544	1.563	1.580	-0.867	0.613
145D	-0.629	-0.460	1.356	0.025	1.075	0.550	1.365	1.365	-0.629	0.469
146T	0.256	-0.460	1.823	-0.202	1.467	0.591	1.207	1.823	-0.460	0.669
147L	0.060	-0.460	1.627	-0.890	1.312	0.571	0.156	1.627	-0.890	0.339
148W	0.813	0.283	1.646	-1.043	1.394	1.041	-0.185	1.646	-1.043	0.564
149Q	0.509	1.145	1.571	-0.887	1.230	0.572	-0.135	1.571	-0.887	0.572
150A	0.813	0.449	1.646	-0.073	1.394	1.041	-0.185	1.646	-0.185	0.726
151D	1.527	0.808	1.973	0.736	1.658	1.054	-0.400	1.973	-0.400	1.051
152T	1.578	0.173	1.870	1.193	1.649	1.034	0.013	1.870	0.013	1.073
153D	1.331	-0.414	1.786	1.130	1.549	1.011	0.069	1.786	-0.414	0.923
154P	0.964	-1.127	1.664	0.647	1.540	1.013	1.668	1.668	-1.127	0.910
155L	0.098	-1.127	1.272	-0.148	1.212	0.525	2.266	2.266	-1.127	0.585
156P	-0.812	-1.248	1.010	-0.697	1.011	0.509	2.476	2.476	-1.248	0.321
157V	-1.312	-1.703	0.982	-0.964	0.966	0.040	2.705	2.705	-1.703	0.102
158V	-1.950	-1.115	0.599	-1.079	0.674	0.022	2.807	2.807	-1.950	-0.006
159F	-1.603	-0.392	0.561	-1.013	0.656	0.019	2.961	2.961	-1.603	0.170
160P	-1.356	0.357	0.646	-1.183	0.756	0.042	2.904	2.904	-1.356	0.309
161I	-0.762	-0.206	0.758	-1.370	0.720	0.040	2.316	2.316	-1.370	0.214
162V	-0.035	0.974	1.206	-1.543	1.093	0.638	1.701	1.701	-1.543	0.576
163Q	-0.035	1.902	1.188	-1.659	1.148	0.640	1.884	1.902	-1.659	0.724
164G	0.244	1.902	1.094	-1.561	1.030	0.641	1.824	1.902	-1.561	0.739
165E	1.110	1.766	1.683	-1.430	1.686	1.233	1.568	1.766	-1.430	1.088
166L	1.723	1.818	2.132	-1.119	2.069	1.274	1.142	2.132	-1.119	1.291
167S	1.672	2.513	2.001	-0.854	1.850	1.252	1.020	2.513	-0.854	1.351
168K	1.672	2.148	2.001	-0.633	1.850	1.252	1.020	2.148	-0.633	1.330
169Q	1.559	1.221	2.001	-0.562	1.859	0.695	1.209	2.001	-0.562	1.140
170T	2.520	1.585	2.412	-0.493	2.224	0.732	0.938	2.520	-0.493	1.417
171G	1.875	0.770	2.141	-0.649	2.060	0.713	1.366	2.141	-0.649	1.182
172Q	1.925	0.143	1.842	-0.474	1.576	0.139	1.461	1.925	-0.474	0.945
173Q	1.040	0.011	1.375	-0.574	1.185	0.098	1.620	1.620	-0.574	0.679
174V	0.844	0.129	1.178	-0.678	1.030	0.078	0.569	1.178	-0.678	0.450
175S	0.617	0.225	1.431	-0.830	1.349	0.097	0.788	1.431	-0.830	0.525
176I	0.680	-0.003	1.403	-0.601	1.285	0.095	0.512	1.403	-0.601	0.482
177A	0.433	0.117	1.075	-0.228	0.911	0.053	-0.661	1.075	-0.661	0.243
178P	1.028	0.656	1.188	0.494	0.875	0.051	-1.250	1.188	-1.250	0.434
179N	0.035	0.656	0.954	0.524	0.729	0.037	-0.975	0.954	-0.975	0.280
180A	1.173	-0.050	1.365	0.369	1.066	0.524	-1.305	1.365	-1.305	0.449
181G	1.173	0.560	1.608	-0.080	1.339	0.543	-0.075	1.608	-0.080	0.724
182L	0.806	-0.474	1.244	-0.161	1.057	0.525	0.294	1.244	-0.474	0.470
183D	0.806	0.221	1.244	0.268	1.057	0.525	0.294	1.244	0.221	0.631
184P	0.553	0.291	1.496	0.820	1.294	0.545	1.636	1.636	0.291	0.948
185V	0.572	-0.242	1.832	1.168	1.713	0.587	1.799	1.832	-0.242	1.061
186N	1.597	-0.146	2.216	1.536	2.014	0.622	1.251	2.216	-0.146	1.299
187Y	0.383	-0.851	1.879	1.647	1.649	0.138	1.511	1.879	-0.851	0.908
188Q	0.383	0.047	1.636	1.649	1.376	0.119	0.281	1.649	0.047	0.784
189N	0.383	0.165	1.636	1.391	1.376	0.119	0.281	1.636	0.119	0.764
190F	0.269	0.095	1.533	0.582	1.221	0.098	0.435	1.533	0.095	0.605
191A	0.832	0.896	1.580	0.181	1.294	0.119	-0.010	1.580	-0.010	0.699
192V	1.084	0.800	1.524	0.388	1.239	0.566	-0.183	1.524	-0.183	0.774
193T	1.002	0.572	1.216	1.002	0.884	0.525	-0.069	1.216	-0.069	0.733
194N	1.350	-0.094	1.160	1.609	0.920	0.522	0.268	1.609	-0.094	0.819
195D	0.711	-0.877	1.019	1.255	0.902	0.524	1.600	1.600	-0.877	0.734
196G	0.364	-1.590	1.075	0.189	0.866	0.527	1.262	1.262	-1.590	0.385
197V	-0.547	-1.608	0.814	-0.893	0.665	0.511	1.473	1.473	-1.608	0.059
198I	-1.571	-1.154	0.449	-1.369	0.310	0.475	1.837	1.837	-1.571	-0.146
199F	-1.761	-0.202	0.477	-0.765	0.300	0.026	1.733	1.733	-1.761	-0.027
200F	-1.988	0.548	0.730	0.291	0.619	0.045	1.953	1.953	-1.988	0.314
201F	-1.394	0.517	0.842	1.209	0.583	0.044	1.364	1.364	-1.394	0.452
202N	-0.395	0.487	1.309	1.477	0.966	0.642	1.016	1.477	-0.395	0.786
203P	-0.395	0.237	1.290	0.845	1.020	0.643	1.200	1.290	-0.395	0.692
204G	-0.395	0.453	1.272	-0.346	1.075	0.644	1.384	1.384	-0.395	0.584
205E	0.319	-0.174	1.580	-1.241	1.394	0.659	1.353	1.580	-1.241	0.556
206L	0.370	-0.749	1.608	-1.825	1.449	1.218	1.439	1.608	-1.825	0.501
207L	0.370	0.083	1.365	-1.749	1.175	1.199	0.209	1.365	-1.749	0.379
208P	0.142	0.646	1.375	-1.621	1.221	1.199	-0.801	1.375	-1.621	0.309
209E	0.010	0.778	1.038	-1.619	0.811	0.599	-0.775	1.038	-1.619	0.120

```
215Q        0.073   -0.007    1.075   -0.830    0.948    0.060    2.219    2.219   -0.830    0.505
216V       -0.155    0.357    1.328   -1.225    1.267    0.079    2.438    2.438   -1.225    0.584
217L       -0.022    0.453    1.515   -1.592    1.467    0.684    2.217    2.217   -1.592    0.675
218V        0.060    0.333    1.468   -1.342    1.467    0.684    2.336    2.336   -1.342    0.715
219P       -0.186    0.968    1.141   -1.050    1.093    0.642    1.163    1.163   -1.050    0.539
220R       -0.458    1.465    1.122   -0.808    1.084    0.642    0.896    1.465   -0.808    0.563
221S        0.756    0.538    1.477   -0.683    1.394    1.126    0.452    1.477   -0.683    0.723
222A        1.401   -0.522    1.748   -0.498    1.558    1.144    0.023    1.748   -0.522    0.693
223I        1.002   -0.522    1.496   -0.383    1.330    1.143   -0.252    1.496   -0.522    0.545
224D        0.155    0.057    0.982   -0.124    0.866    0.523    0.184    0.982   -0.124    0.377
225S       -0.123   -0.228    0.832   -0.434    0.711    0.503   -0.986    0.832   -0.986    0.039
226M       -0.256   -0.829    0.375   -0.964    1.030    0.563   -0.986    1.030   -0.986   -0.152
227L        0.250   -0.460    0.057   -1.409    1.367    0.622   -2.318    1.367   -2.318   -0.270
228A       -0.382   -0.001   -0.672   -1.504    1.367    0.193   -3.319    1.367   -3.319   -0.617
```

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	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Hydrophilicity	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Flexibility	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Accessibility	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Turns	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Exposed Surface	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Polarity	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Antigenic Propensity	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT

TOP

Home

BcePred Prediction Server

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

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Seq=   VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYY
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    GLDPVNYQNFAVTNDGVIFFFNPGELLPEAAGPTQVLVPRSAIDSMLA

Length=228

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

TOP

TABULAR RESULT

Selected Programs: hydro flexi access turns surface polar antipro
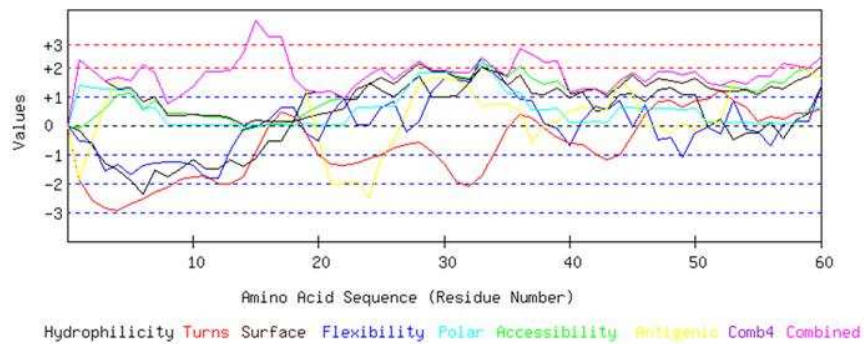
Respective Threshold: 1.9 2 1.9 2.4 2.3 1.8 1.9

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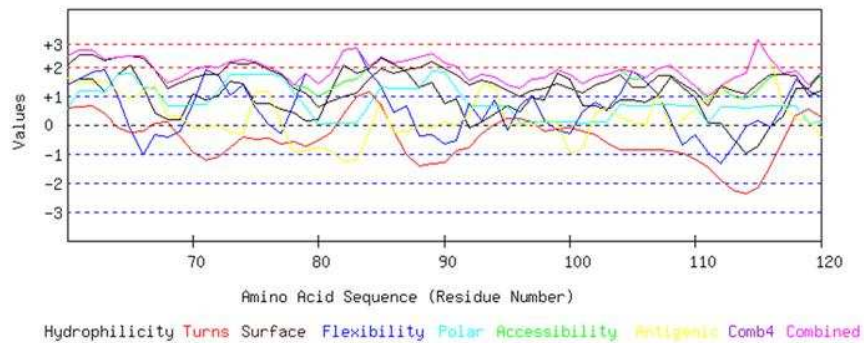
Length=228

A.A. ppppppppppppppppppppppppppppppp Parameter ppppppppppppppppppppppppppppppppppppppp Combined

	Hydro	Flexi	Access	Turns	Surface	Polar	AntiPro	MAX	MIN	AVG

5	I	-1.893	-1.697	1.085	-2.693	1.285	1.220	1.520	1.520	-2.693	-0.168
6	F	-2.393	-1.372	0.533	-2.532	0.802	0.596	2.110	2.110	-2.532	-0.322
7	M	-1.558	-1.294	0.870	-2.295	0.975	0.615	1.829	1.829	-2.295	-0.123
8	L	-1.786	-1.276	0.421	-2.160	0.337	0.020	0.754	0.754	-2.160	-0.527
9	V	-1.514	-1.276	0.440	-1.858	0.346	0.020	1.021	1.021	-1.858	-0.403
10	T	-1.166	-1.384	0.384	-1.763	0.382	0.017	1.358	1.358	-1.763	-0.310
11	A	-1.482	-1.839	0.309	-1.758	0.346	0.005	1.849	1.849	-1.839	-0.367
12	V	-1.482	-1.803	0.309	-2.005	0.346	0.005	1.849	1.849	-2.005	-0.397
13	V	-1.160	-0.851	0.216	-2.031	0.264	0.022	1.882	1.882	-2.031	-0.237
14	L	-1.400	-0.128	-0.196	-1.769	0.018	0.019	2.464	2.464	-1.769	-0.142
15	L	-1.122	-0.019	-0.046	-0.927	0.173	0.039	3.634	3.634	-1.122	0.247
16	C	-0.528	0.185	0.066	-0.067	0.136	0.038	3.045	3.045	-0.528	0.411
17	C	-0.528	0.640	0.066	0.468	0.136	0.038	3.045	3.045	-0.528	0.552
18	S	0.187	0.604	0.150	0.285	0.127	0.032	1.600	1.600	0.032	0.426
19	G	1.097	-0.252	0.431	-0.269	0.273	0.047	1.206	1.206	-0.269	0.362
20	V	1.141	-0.520	0.646	-1.000	0.364	0.029	-0.427	1.141	-1.000	0.033
21	A	1.186	0.407	0.860	-1.356	0.455	0.011	-2.059	1.186	-2.059	-0.071
22	T	0.907	0.898	0.954	-1.394	0.574	0.010	-1.999	0.954	-1.999	-0.007
23	A	0.907	0.001	1.412	-1.318	1.257	0.605	-1.934	1.412	-1.934	0.133
24	A	1.470	0.037	1.730	-1.147	1.422	0.623	-2.482	1.730	-2.482	0.236
25	P	1.217	0.612	1.982	-1.028	1.658	0.643	-1.140	1.982	-1.140	0.563
26	K	0.977	0.828	1.571	-0.797	1.412	0.641	-0.558	1.571	-0.797	0.582
27	T	1.337	-0.208	1.898	-0.655	1.777	1.240	0.425	1.898	-0.655	0.831
28	Y	1.698	0.133	2.225	-0.569	2.142	1.840	1.409	2.225	-0.569	1.268
29	C	0.983	1.167	1.898	-0.905	1.877	1.826	1.624	1.898	-0.905	1.210
30	E	0.983	1.621	1.898	-1.351	1.877	1.826	1.624	1.898	-1.351	1.211
31	E	1.015	1.585	1.692	-1.932	1.677	1.806	1.584	1.806	-1.932	1.061
32	L	1.464	1.501	1.636	-2.103	1.595	1.807	1.293	1.807	-2.103	1.027
33	K	2.008	2.333	2.122	-1.754	2.005	2.278	0.661	2.333	-1.754	1.379
34	G	1.843	1.992	1.991	-0.932	1.795	1.698	0.728	1.992	-0.932	1.302
35	T	1.710	1.365	1.655	-0.097	1.385	1.099	0.755	1.710	-0.097	1.125
36	D	2.671	0.910	2.066	0.383	1.750	1.136	0.483	2.671	0.383	1.343
37	T	2.444	0.862	1.617	0.248	1.112	0.541	-0.592	2.444	-0.592	0.890
38	G	2.172	0.047	1.412	-0.107	1.066	0.559	0.030	2.172	-0.107	0.740
39	Q	2.222	-0.090	1.543	-0.412	1.285	0.581	0.153	2.222	-0.412	0.755
40	A	1.084	-0.695	1.132	-0.624	0.948	0.094	0.483	1.132	-0.695	0.346
41	C	1.135	0.161	1.262	-0.668	1.166	0.117	0.606	1.262	-0.668	0.540
42	Q	0.509	0.664	1.262	-0.982	1.257	0.134	0.550	1.262	-0.982	0.485
43	I	0.541	0.532	1.085	-1.196	1.039	0.111	0.547	1.085	-1.196	0.380
44	Q	1.040	0.856	1.356	-1.009	1.358	0.600	1.548	1.548	-1.009	0.821
45	M	1.084	-0.042	1.814	-0.353	1.722	0.602	1.146	1.814	-0.353	0.853
46	S	0.838	0.682	1.487	0.373	1.349	0.559	-0.028	1.487	-0.028	0.751
47	D	1.224	-0.498	1.879	0.835	1.604	0.577	-0.017	1.879	-0.498	0.800
48	P	1.287	-0.428	1.851	0.871	1.540	0.575	-0.294	1.851	-0.428	0.772
49	A	1.046	-1.111	1.720	0.620	1.476	0.560	0.083	1.720	-1.111	0.628
50	Y	1.078	-0.256	1.870	0.858	1.631	0.580	-0.190	1.870	-0.256	0.796
51	N	-0.060	-0.054	1.459	0.915	1.294	0.093	0.141	1.459	-0.060	0.541
52	I	0.218	-0.304	1.365	1.209	1.175	0.094	0.081	1.365	-0.304	0.548
53	N	-0.496	0.876	1.281	0.864	1.185	0.099	1.526	1.526	-0.496	0.762
54	I	-0.243	-0.140	1.272	0.615	1.221	0.099	1.414	1.414	-0.243	0.605
55	S	-0.275	-0.222	1.122	0.150	1.066	0.079	1.687	1.687	-0.275	0.515
56	L	0.111	-0.719	1.515	0.312	1.321	0.096	1.697	1.697	-0.719	0.619
57	P	-0.452	0.025	1.468	0.212	1.248	0.075	2.142	2.142	-0.452	0.674
58	S	0.187	0.157	1.851	0.433	1.540	0.092	2.040	2.040	0.092	0.900
59	Y	0.408	0.133	1.973	0.411	1.704	0.561	1.872	1.973	0.133	1.009
60	Y	1.369	1.395	2.384	0.561	2.069	0.598	1.600	2.384	0.561	1.425
61	P	1.597	1.597	2.589	0.622	2.433	1.174	1.445	2.589	0.622	1.637
62	D	1.597	1.814	2.589	0.662	2.433	1.174	1.445	2.589	0.662	1.673
63	Q	1.135	1.884	2.253	0.363	2.205	1.160	1.548	2.253	0.363	1.507
64	K	1.748	0.986	2.328	-0.109	2.333	1.740	1.190	2.333	-0.109	1.459
65	S	2.058	-0.170	2.384	-0.243	2.369	1.761	0.857	2.384	-0.243	1.288
66	L	1.306	-1.025	2.365	-0.200	2.287	1.292	1.198	2.365	-1.025	1.032
67	E	0.421	-0.330	1.898	0.047	1.895	1.251	1.356	1.898	-0.330	0.934
68	N	0.193	-0.414	1.449	0.087	1.257	0.657	0.281	1.449	-0.414	0.501
69	Y	0.161	-0.210	1.627	-0.400	1.476	0.679	0.284	1.627	-0.400	0.517
70	I	1.072	0.736	1.907	-0.935	1.622	0.694	-0.110	1.907	-0.935	0.712
71	A	0.844	1.892	2.010	-1.236	1.731	0.719	-0.084	2.010	-1.236	0.839
72	Q	1.034	1.718	1.982	-1.106	1.741	1.167	0.020	1.982	-1.106	0.936
73	T	1.514	1.022	2.178	-0.786	2.142	1.742	-0.247	2.178	-0.786	1.081
74	R	1.438	1.387	2.253	-0.413	2.114	1.745	-0.318	2.253	-0.413	1.172
75	D	0.724	0.574	2.169	-0.484	2.123	1.750	1.127	2.169	-0.484	1.140
76	K	0.756	0.035	1.991	-0.460	1.905	1.728	1.124	1.991	-0.460	1.011
77	F	0.560	-0.306	1.795	-0.657	1.750	1.708	0.073	1.795	-0.657	0.703
78	L	0.427	0.724	1.365	-0.591	1.276	1.083	-0.936	1.365	-0.936	0.478
79	S	0.123	1.784	1.290	-0.743	1.112	0.614	-0.887	1.784	-0.887	0.471
80	A	0.174	1.419	0.991	-0.549	0.629	0.040	-0.792	1.419	-0.792	0.273
81	A	1.167	1.778	1.206	-0.268	0.829	0.055	-0.883	1.778	-0.883	0.555
82	T	2.077	2.591	1.487	0.395	0.975	0.070	-1.277	2.591	-1.277	0.902
83	S	1.799	2.675	1.580	0.971	1.093	0.069	-1.217	2.675	-1.217	0.996
84	S	1.932	1.820	2.010	1.142	1.567	0.694	-0.208	2.010	-0.208	1.280
85	T	2.292	1.323	2.337	0.698	1.932	1.293	0.776	2.337	0.698	1.521
86	P	2.096	0.425	2.141	-0.238	1.777	1.273	-0.275	2.141	-0.275	1.028
87	R	1.818	0.642	2.234	-1.013	1.895	1.272	-0.215	2.234	-1.013	0.948
88	E	1.287	-0.376	2.337	-1.428	1.977	1.271	-0.043	2.337	-1.428	0.718
89	A	1.451	-0.342	2.468	-1.350	2.187	1.851	-0.110	2.468	-1.350	0.879
90	P	0.737	-0.667	2.141	-1.288	1.923	1.837	0.105	2.141	-1.288	0.684
91	Y	0.914	-0.534	2.010	-0.880	1.759	1.253	-0.007	2.010	-0.880	0.645
92	E	-0.085	0.728	1.543	-0.764	1.376	0.656	0.341	1.543	-0.764	0.542
93	L	0.111	0.153	1.739	-0.309	1.531	0.675	1.392	1.739	-0.309	0.756
94	N	0.389	0.848	1.646	0.039	1.412	0.677	1.332	1.646	0.039	0.906
95	I	0.642	-0.168	1.393	0.229	1.175	0.657	-0.010	1.393	-0.168	0.560
96	T	0.477	0.648	1.262	0.212	0.966	0.078	0.057	1.262	0.057	0.529
97	S	0.939	1.012	1.599	0.120	1.194	0.092	-0.046	1.599	-0.046	0.701
98	A	0.876	0.157	1.627	-0.213	1.257	0.093	0.230	1.627	-0.213	0.575
99	T	1.793	-0.168	1.917	-0.125	1.431	0.112	0.068	1.917	-0.168	0.718
100	Y	1.597	-0.300	1.720	-0.119	1.276	0.092	-0.983	1.720	-0.983	0.469
101	Q	0.680	0.465	1.431	-0.233	1.103	0.073	-0.821	1.431	-0.821	0.385
102	S	0.680	0.788	1.674	-0.332	1.376	0.092	0.409	1.674	-0.332	0.670
103	A	0.484	0.560	1.720	-0.632	1.494	0.091	0.588	1.720	-0.632	0.615
104	I	0.869	1.050	1.898	-0.853	1.731	0.697	0.256	1.898	-0.853	0.807

110Q	0.920	-0.348	1.346	-1.166	1.139	0.660	0.553	1.346	-1.166	0.443
111A	0.073	-0.935	0.832	-1.476	0.674	0.041	0.988	0.988	-1.476	0.028
112V	0.073	-1.342	1.290	-1.919	1.358	0.635	1.053	1.358	-1.919	0.164
113V	-0.490	-0.755	0.973	-2.271	1.194	0.617	1.601	1.601	-2.271	0.124
114L	-0.989	-0.050	0.898	-2.384	1.057	0.594	1.770	1.770	-2.384	0.128
115K	-0.743	0.155	1.225	-2.194	1.431	0.636	2.943	2.943	-2.194	0.493
116V	-0.066	-0.050	1.646	-1.420	1.750	0.675	2.242	2.242	-1.420	0.682
117Y	0.300	0.674	1.767	-0.547	1.759	0.674	0.643	1.767	-0.547	0.753
118Q	1.242	1.571	1.842	0.339	1.704	0.668	0.208	1.842	0.208	1.082
119N	1.242	1.171	1.384	0.558	1.020	0.074	0.143	1.384	0.074	0.799
120A	1.805	0.920	1.702	0.242	1.185	0.092	-0.405	1.805	-0.405	0.792
121G	2.058	1.411	1.608	-0.067	1.121	0.693	-0.469	2.058	-0.469	0.908
122G	1.812	1.275	1.524	0.146	1.020	0.669	-0.413	1.812	-0.413	0.862
123T	1.698	1.139	1.421	0.699	0.866	0.649	-0.259	1.698	-0.259	0.887
124H	1.894	0.241	1.617	1.361	1.020	0.669	0.792	1.894	0.241	1.085
125P	1.862	0.982	1.823	1.441	1.221	0.688	0.832	1.862	0.688	1.264
126T	1.382	0.624	2.085	0.992	1.504	0.708	1.164	2.085	0.624	1.208
127T	1.413	-0.042	2.337	0.329	1.987	1.282	1.188	2.337	-0.042	1.214
128T	1.413	0.007	2.178	-0.451	1.813	0.663	-0.089	2.178	-0.451	0.791
129Y	0.699	-0.987	1.870	-0.973	1.494	0.648	-0.058	1.870	-0.987	0.385
130K	1.002	-0.042	1.945	-1.085	1.658	1.117	-0.107	1.945	-1.085	0.641
131A	0.041	-0.382	1.767	-0.921	1.522	1.122	-0.126	1.767	-0.921	0.432
132F	0.345	-0.382	1.842	-0.240	1.686	1.591	-0.176	1.842	-0.382	0.666
133D	0.844	-0.615	1.917	0.288	1.823	1.614	-0.344	1.917	-0.615	0.790
134W	0.617	-0.340	1.468	0.553	1.185	1.020	-1.420	1.468	-1.420	0.440
135D	0.364	0.994	1.720	0.359	1.422	1.039	-0.077	1.720	-0.077	0.832
136Q	1.211	0.814	2.216	-0.175	1.941	1.659	-0.329	2.216	-0.329	1.048
137A	0.939	-0.001	2.393	-0.991	2.260	1.765	-0.255	2.393	-0.991	0.873
138Y	1.704	0.489	2.617	-1.406	2.515	1.759	-0.058	2.617	-1.406	1.089
139R	0.566	0.489	2.206	-1.837	2.178	1.272	0.273	2.206	-1.837	0.735
140K	0.515	0.215	2.075	-1.735	1.959	1.249	0.150	2.075	-1.735	0.633
141P	0.263	-0.126	2.328	-1.537	2.196	1.269	1.493	2.328	-1.537	0.841
142I	1.015	-0.689	2.346	-1.066	2.278	1.738	1.151	2.346	-1.066	0.968
143T	1.078	-0.867	2.113	-0.538	1.959	1.133	1.193	2.113	-0.867	0.867
144Y	0.136	-0.867	1.580	0.003	1.330	0.544	1.563	1.580	-0.867	0.613
145D	-0.629	-0.460	1.356	0.025	1.075	0.550	1.365	1.365	-0.629	0.469
146T	0.256	-0.460	1.823	-0.202	1.467	0.591	1.207	1.823	-0.460	0.669
147L	0.060	-0.460	1.627	-0.890	1.312	0.571	0.156	1.627	-0.890	0.339
148W	0.813	0.283	1.646	-1.043	1.394	1.041	-0.185	1.646	-1.043	0.564
149Q	0.509	1.145	1.571	-0.887	1.230	0.572	-0.135	1.571	-0.887	0.572
150A	0.813	0.449	1.646	-0.073	1.394	1.041	-0.185	1.646	-0.185	0.726
151D	1.527	0.808	1.973	0.736	1.658	1.054	-0.400	1.973	-0.400	1.051
152T	1.578	0.173	1.870	1.193	1.649	1.034	0.013	1.870	0.013	1.073
153D	1.331	-0.414	1.786	1.130	1.549	1.011	0.069	1.786	-0.414	0.923
154P	0.964	-1.127	1.664	0.647	1.540	1.013	1.668	1.668	-1.127	0.910
155L	0.098	-1.127	1.272	-0.148	1.212	0.525	2.266	2.266	-1.127	0.585
156P	-0.812	-1.248	1.010	-0.697	1.011	0.509	2.476	2.476	-1.248	0.321
157V	-1.312	-1.703	0.982	-0.964	0.966	0.040	2.705	2.705	-1.703	0.102
158V	-1.950	-1.115	0.599	-1.079	0.674	0.022	2.807	2.807	-1.950	-0.006
159F	-1.603	-0.392	0.561	-1.013	0.656	0.019	2.961	2.961	-1.603	0.170
160P	-1.356	0.357	0.646	-1.183	0.756	0.042	2.904	2.904	-1.356	0.309
161I	-0.762	-0.206	0.758	-1.370	0.720	0.040	2.316	2.316	-1.370	0.214
162V	-0.035	0.974	1.206	-1.543	1.093	0.638	1.701	1.701	-1.543	0.576
163Q	-0.035	1.902	1.188	-1.659	1.148	0.640	1.884	1.902	-1.659	0.724
164G	0.244	1.902	1.094	-1.561	1.030	0.641	1.824	1.902	-1.561	0.739
165E	1.110	1.766	1.683	-1.430	1.686	1.233	1.568	1.766	-1.430	1.088
166L	1.723	1.818	2.132	-1.119	2.069	1.274	1.142	2.132	-1.119	1.291
167S	1.672	2.513	2.001	-0.854	1.850	1.252	1.020	2.513	-0.854	1.351
168K	1.672	2.148	2.001	-0.633	1.850	1.252	1.020	2.148	-0.633	1.330
169Q	1.559	1.221	2.001	-0.562	1.859	0.695	1.209	2.001	-0.562	1.140
170T	2.520	1.585	2.412	-0.493	2.224	0.732	0.938	2.520	-0.493	1.417
171G	1.875	0.770	2.141	-0.649	2.060	0.713	1.366	2.141	-0.649	1.182
172Q	1.925	0.143	1.842	-0.474	1.576	0.139	1.461	1.925	-0.474	0.945
173Q	1.040	0.011	1.375	-0.574	1.185	0.098	1.620	1.620	-0.574	0.679
174V	0.844	0.129	1.178	-0.678	1.030	0.078	0.569	1.178	-0.678	0.450
175S	0.617	0.225	1.431	-0.830	1.349	0.097	0.788	1.431	-0.830	0.525
176I	0.680	-0.003	1.403	-0.601	1.285	0.095	0.512	1.403	-0.601	0.482
177A	0.433	0.117	1.075	-0.228	0.911	0.053	-0.661	1.075	-0.661	0.243
178P	1.028	0.656	1.188	0.494	0.875	0.051	-1.250	1.188	-1.250	0.434
179N	0.035	0.656	0.954	0.524	0.729	0.037	-0.975	0.954	-0.975	0.280
180A	1.173	-0.050	1.365	0.369	1.066	0.524	-1.305	1.365	-1.305	0.449
181G	1.173	0.560	1.608	-0.080	1.339	0.543	-0.075	1.608	-0.080	0.724
182L	0.806	-0.474	1.244	-0.161	1.057	0.525	0.294	1.244	-0.474	0.470
183D	0.806	0.221	1.244	0.268	1.057	0.525	0.294	1.244	0.221	0.631
184P	0.553	0.291	1.496	0.820	1.294	0.545	1.636	1.636	0.291	0.948
185V	0.572	-0.242	1.832	1.168	1.713	0.587	1.799	1.832	-0.242	1.061
186N	1.597	-0.146	2.216	1.536	2.014	0.622	1.251	2.216	-0.146	1.299
187Y	0.383	-0.851	1.879	1.647	1.649	0.138	1.511	1.879	-0.851	0.908
188Q	0.383	0.047	1.636	1.649	1.376	0.119	0.281	1.649	0.047	0.784
189N	0.383	0.165	1.636	1.391	1.376	0.119	0.281	1.636	0.119	0.764
190F	0.269	0.095	1.533	0.582	1.221	0.098	0.435	1.533	0.095	0.605
191A	0.832	0.896	1.580	0.181	1.294	0.119	-0.010	1.580	-0.010	0.699
192V	1.084	0.800	1.524	0.388	1.239	0.566	-0.183	1.524	-0.183	0.774
193T	1.002	0.572	1.216	1.002	0.884	0.525	-0.069	1.216	-0.069	0.733
194N	1.350	-0.094	1.160	1.609	0.920	0.522	0.268	1.609	-0.094	0.819
195D	0.711	-0.877	1.019	1.255	0.902	0.524	1.600	1.600	-0.877	0.734
196G	0.364	-1.590	1.075	0.189	0.866	0.527	1.262	1.262	-1.590	0.385
197V	-0.547	-1.608	0.814	-0.893	0.665	0.511	1.473	1.473	-1.608	0.059
198I	-1.571	-1.154	0.449	-1.369	0.310	0.475	1.837	1.837	-1.571	-0.146
199F	-1.761	-0.202	0.477	-0.765	0.300	0.026	1.733	1.733	-1.761	-0.027
200F	-1.988	0.548	0.730	0.291	0.619	0.045	1.953	1.953	-1.988	0.314
201F	-1.394	0.517	0.842	1.209	0.583	0.044	1.364	1.364	-1.394	0.452
202N	-0.395	0.487	1.309	1.477	0.966	0.642	1.016	1.477	-0.395	0.786
203P	-0.395	0.237	1.290	0.845	1.020	0.643	1.200	1.290	-0.395	0.692
204G	-0.395	0.453	1.272	-0.346	1.075	0.644	1.384	1.384	-0.395	0.584
205E	0.319	-0.174	1.580	-1.241	1.394	0.659	1.353	1.580	-1.241	0.556
206L	0.370	-0.749	1.608	-1.825	1.449	1.218	1.439	1.608	-1.825	0.501
207L	0.370	0.083	1.365	-1.749	1.175	1.199	0.209	1.365	-1.749	0.379
208P	0.142	0.646	1.375	-1.621	1.221	1.199	-0.801	1.375	-1.621	0.309
209E	0.010	0.778	1.038	-1.619	0.811	0.599	-0.775	1.038	-1.619	0.120

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215Q      0.073   -0.007    1.075   -0.830    0.948    0.060    2.219    2.219   -0.830    0.505
216V     -0.155    0.357    1.328   -1.225    1.267    0.079    2.438    2.438   -1.225    0.584
217L     -0.022    0.453    1.515   -1.592    1.467    0.684    2.217    2.217   -1.592    0.675
218V      0.060    0.333    1.468   -1.342    1.467    0.684    2.336    2.336   -1.342    0.715
219P     -0.186    0.968    1.141   -1.050    1.093    0.642    1.163    1.163   -1.050    0.539
220R     -0.458    1.465    1.122   -0.808    1.084    0.642    0.896    1.465   -0.808    0.563
221S      0.756    0.538    1.477   -0.683    1.394    1.126    0.452    1.477   -0.683    0.723
222A      1.401   -0.522    1.748   -0.498    1.558    1.144    0.023    1.748   -0.522    0.693
223I      1.002   -0.522    1.496   -0.383    1.330    1.143   -0.252    1.496   -0.522    0.545
224D      0.155    0.057    0.982   -0.124    0.866    0.523    0.184    0.982   -0.124    0.377
225S     -0.123   -0.228    0.832   -0.434    0.711    0.503   -0.986    0.832   -0.986    0.039
226M     -0.256   -0.829    0.375   -0.964    1.030    0.563   -0.986    1.030   -0.986   -0.152
227L      0.250   -0.460    0.057   -1.409    1.367    0.622   -2.318    1.367   -2.318   -0.270
228A     -0.382   -0.001   -0.672   -1.504    1.367    0.193   -3.319    1.367   -3.319   -0.617
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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	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Hydrophilicity	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Flexibility	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Accessibility	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Turns	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Exposed Surface	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Polarity	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT
Antigenic Propensity	¹VRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGTQAVVLKVYQNAGGT

TOP

Home