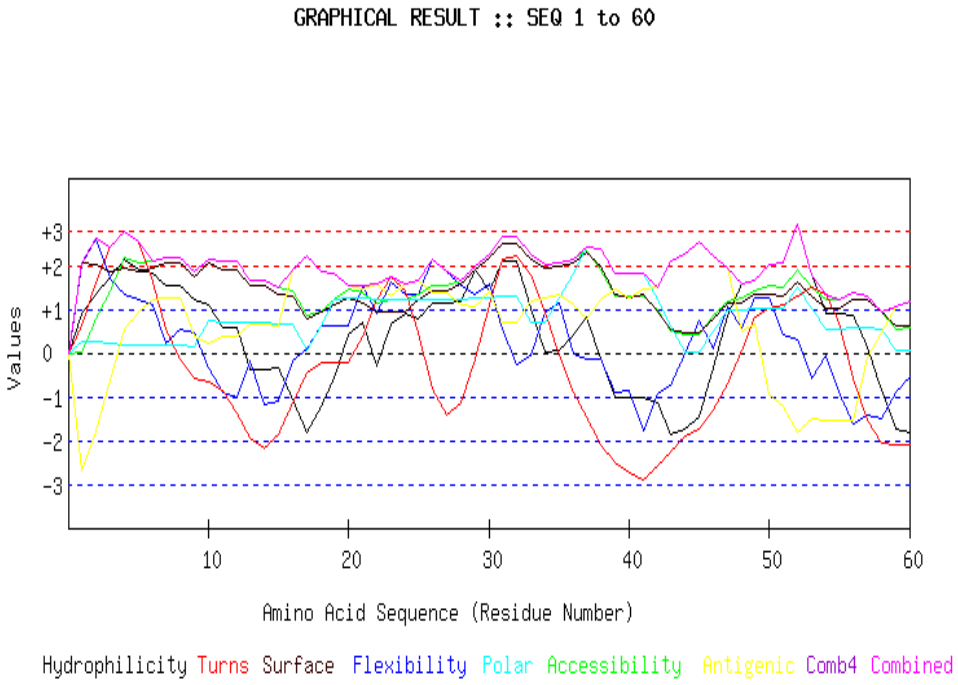
BcePred Prediction Server

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

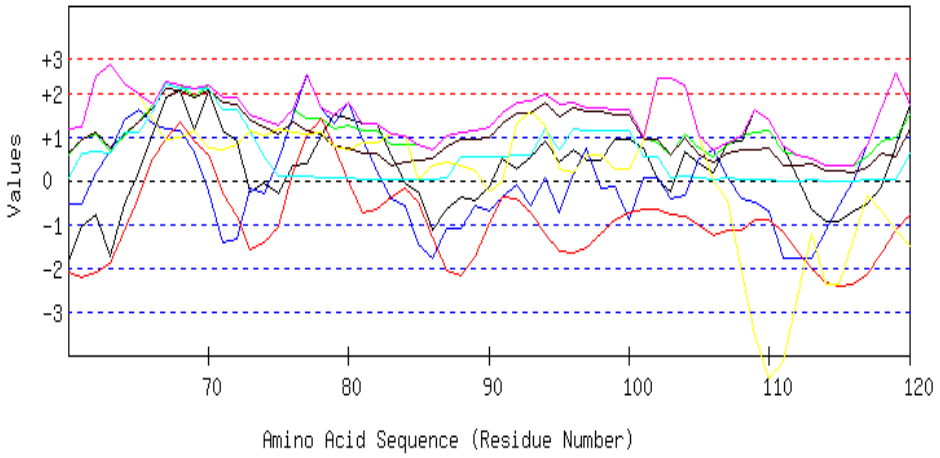
seqname=
Seq=MNSQNSQIQPQARYILPSFIEHSSFGVKESNPYNKLFEERIIFLGVQVDDASANDIMAQLLVLESLDPDRDIT
MYINSPGGGFTSLMAIYDTMQYVRADIQTVCLGQAASAAAVLLAAGTPGKRMALPNARVLIHQPSLSGVIQGQFS
DLEIQAAEIERMRTLMETTLARHTGKDAGVIRKDTDRDKILTAEEAKDYGIIDTVLEYRKLSAQTA

Length=214

GRAPHICAL RESULT

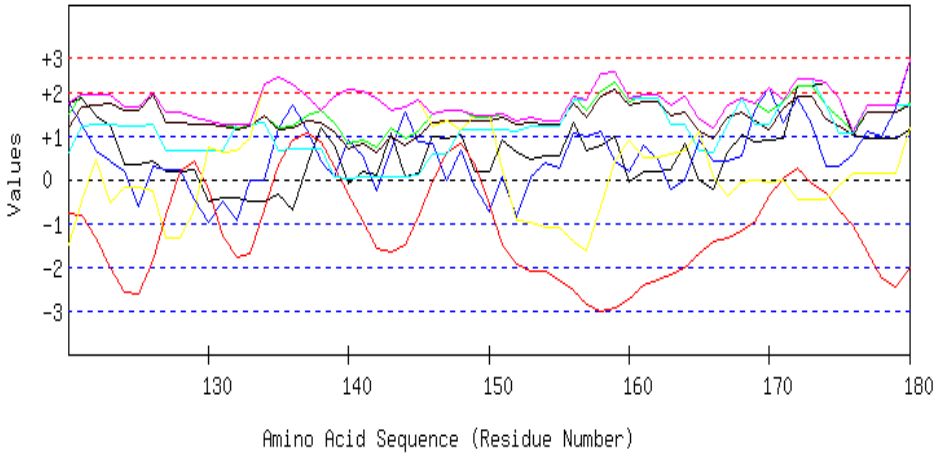


GRAPHICAL RESULT :: SEQ 61 to 120



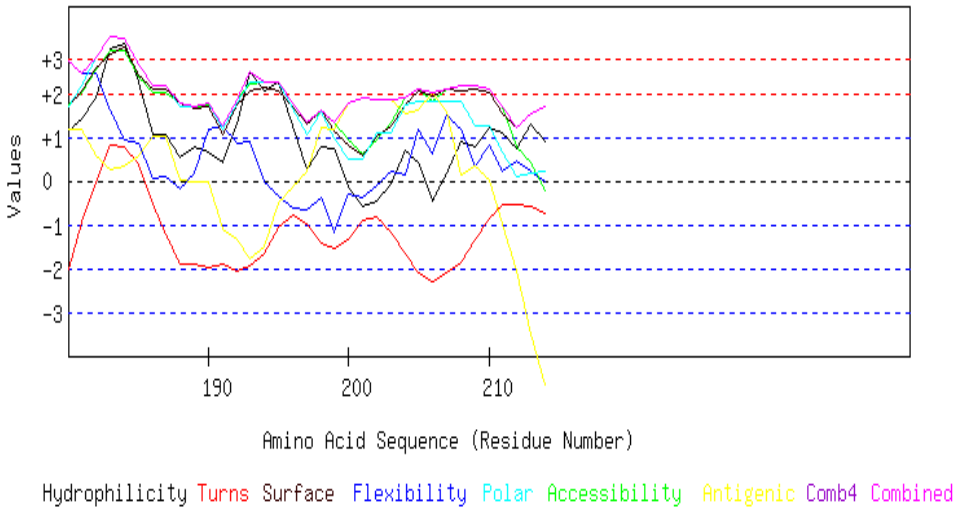
Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

GRAPHICAL RESULT :: SEQ 121 to 180



Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

GRAPHICAL RESULT :: SEQ 181 to 240



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

**MNSQNSQIQPQARYILPSFIEHSSFGVKESNPYNKLFEERIIFLGVQVDDASANDIMAQL
LVLESLDPDRDITMYINSPGGGFTSLMAIYDTMQYVRADIQTVCLGQAASAAAVLLAAGT
PGKRMALPNARVLIHQPSLSGVIQGQFSDLEIQAAEIERMRTLMETTLARHTGKDAGVIR
KDTDRDKILTAEEAKDYGIIDTVLEYRKLSAQTA**

Length=214

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

1	M	0.888	2.032	0.038	0.631	2.041	0.270	-2.694	2.041	-2.694	0.458
2	N	1.331	2.637	0.795	1.619	2.032	0.251	-1.797	2.637	-1.797	0.981
3	S	1.742	1.704	1.403	2.424	1.868	0.211	-0.627	2.424	-0.627	1.246
4	Q	2.121	1.339	2.188	2.765	1.923	0.193	0.547	2.765	0.193	1.582
5	N	1.881	1.207	2.057	2.544	1.859	0.178	0.924	2.544	0.178	1.521
6	S	1.818	1.089	2.085	1.635	1.923	0.180	1.200	2.085	0.180	1.418
7	Q	1.540	0.233	2.178	0.558	2.041	0.179	1.260	2.178	0.179	1.141
8	I	1.540	0.556	2.178	-0.159	2.041	0.179	1.260	2.178	-0.159	1.085
9	Q	1.230	0.473	1.879	-0.586	1.731	0.138	0.363	1.879	-0.586	0.747
10	P	1.084	-0.342	2.160	-0.666	2.050	0.743	0.202	2.160	-0.666	0.747
11	Q	0.585	-0.905	2.085	-0.879	1.914	0.719	0.371	2.085	-0.905	0.556
12	A	0.585	-1.037	2.085	-1.361	1.914	0.719	0.371	2.085	-1.361	0.468
13	R	-0.376	-0.182	1.674	-1.928	1.549	0.682	0.643	1.674	-1.928	0.295
14	Y	-0.376	-1.170	1.674	-2.176	1.549	0.682	0.643	1.674	-2.176	0.118
15	I	-0.344	-1.087	1.496	-1.874	1.330	0.660	0.639	1.496	-1.874	0.117
16	L	-1.059	-0.188	1.431	-1.158	1.285	0.664	1.901	1.901	-1.158	0.411
17	P	-1.830	0.107	0.860	-0.443	0.793	0.041	2.223	2.223	-1.830	0.250
18	S	-1.217	0.604	0.935	-0.233	0.920	0.622	1.865	1.865	-1.217	0.499
19	F	-0.578	0.604	1.234	-0.229	1.112	1.240	1.810	1.810	-0.578	0.742
20	I	0.414	0.604	1.468	-0.228	1.257	1.254	1.535	1.535	-0.228	0.901
21	E	0.692	1.555	1.375	0.376	1.139	1.255	1.475	1.555	0.376	1.124
22	H	-0.300	0.884	1.160	1.234	0.938	1.240	1.566	1.566	-0.300	0.960
23	S	0.642	1.625	1.216	1.755	0.938	1.235	1.316	1.755	0.642	1.247
24	S	0.914	1.345	1.234	1.425	0.948	1.235	1.583	1.583	0.914	1.240
25	F	0.781	1.345	1.356	0.442	1.221	1.230	1.674	1.674	0.442	1.150
26	G	1.141	2.128	1.524	-0.832	1.412	1.210	1.380	2.128	-0.832	1.138
27	V	1.141	1.860	1.524	-1.435	1.412	1.210	1.380	1.860	-1.435	1.013
28	K	1.173	1.549	1.674	-1.147	1.567	1.230	1.108	1.674	-1.147	1.022
29	E	1.887	1.327	1.982	-0.121	1.886	1.245	1.076	1.982	-0.121	1.326
30	S	1.407	1.583	2.244	1.104	2.169	1.265	1.408	2.244	1.104	1.597
31	N	2.083	0.523	2.664	2.127	2.488	1.304	0.706	2.664	0.523	1.699
32	P	2.083	-0.260	2.664	2.211	2.488	1.304	0.706	2.664	-0.260	1.599
33	Y	1.009	-0.044	2.253	1.773	2.132	0.709	1.168	2.253	-0.044	1.286
34	N	0.016	0.938	2.038	0.940	1.932	0.694	1.259	2.038	0.016	1.117
35	K	0.067	1.143	2.066	-0.059	1.987	1.253	1.346	2.066	-0.059	1.114
36	L	0.427	-0.013	2.150	-0.902	2.078	1.833	1.099	2.150	-0.902	0.953
37	F	0.813	-0.134	2.328	-1.476	2.315	2.438	0.766	2.438	-1.476	1.007
38	E	-0.136	-0.134	1.889	-2.115	1.987	2.400	1.201	2.400	-2.115	0.727
39	E	-1.002	-0.913	1.300	-2.515	1.330	1.807	1.458	1.807	-2.515	0.209
40	R	-1.002	-0.861	1.318	-2.760	1.276	1.806	1.274	1.806	-2.760	0.150
41	I	-1.002	-1.771	1.300	-2.893	1.330	1.807	1.458	1.807	-2.893	0.033
42	I	-1.135	-0.955	0.963	-2.597	0.920	1.207	1.484	1.484	-2.597	-0.016
43	F	-1.862	-0.727	0.515	-2.266	0.547	0.609	2.099	2.099	-2.266	-0.155
44	L	-1.748	-0.013	0.412	-1.899	0.446	0.027	2.264	2.264	-1.899	-0.073
45	G	-1.476	0.730	0.431	-1.735	0.455	0.027	2.531	2.531	-1.735	0.137
46	V	-0.338	0.103	0.842	-1.289	0.793	0.514	2.200	2.200	-1.289	0.403
47	Q	0.876	1.054	1.178	-0.697	1.157	0.999	1.940	1.940	-0.697	0.930
48	V	1.590	0.564	1.262	0.079	1.148	0.993	0.495	1.590	0.079	0.876
49	D	1.641	1.269	1.421	0.808	1.349	1.013	0.654	1.641	0.654	1.165
50	D	2.008	1.269	1.543	1.000	1.358	1.012	-0.944	2.008	-0.944	1.035
51	A	2.071	0.405	1.515	1.120	1.294	1.010	-1.221	2.071	-1.221	0.885
52	S	2.937	0.291	1.907	1.301	1.622	1.497	-1.818	2.937	-1.818	1.105
53	A	1.799	-0.564	1.496	1.502	1.285	1.010	-1.488	1.799	-1.488	0.720
54	N	0.901	-0.074	1.216	1.349	1.011	0.538	-1.534	1.349	-1.534	0.487
55	D	0.901	-0.887	1.216	0.684	1.011	0.538	-1.534	1.216	-1.534	0.276
56	I	0.869	-1.630	1.393	-0.594	1.230	0.561	-1.531	1.393	-1.630	0.043
57	M	0.155	-1.402	1.309	-1.533	1.239	0.566	-0.086	1.309	-1.533	0.036
58	A	-0.869	-1.492	0.926	-2.050	0.938	0.531	0.462	0.938	-2.050	-0.222

59 Q	-1.735	-0.917	0.533	-2.119	0.610	0.044	1.060	1.060	-2.119	-0.361
60 L	-1.811	-0.552	0.589	-2.083	0.638	0.047	1.173	1.173	-2.083	-0.286
61 L	-1.053	-0.552	0.926	-2.231	0.957	0.630	1.202	1.202	-2.231	-0.017
62 V	-0.774	0.191	1.075	-2.106	1.112	0.650	2.372	2.372	-2.106	0.360
63 L	-1.735	0.646	0.664	-1.890	0.747	0.613	2.644	2.644	-1.890	0.241
64 E	-0.521	1.389	1.019	-1.123	1.057	1.096	2.200	2.200	-1.123	0.731
65 S	0.193	1.627	1.346	-0.381	1.321	1.110	1.985	1.985	-0.381	1.029
66 L	1.059	1.311	1.739	0.507	1.649	1.597	1.387	1.739	0.507	1.321
67 D	1.906	1.191	2.253	0.931	2.114	2.216	0.951	2.253	0.931	1.652
68 P	2.045	1.143	2.197	1.332	2.069	2.106	0.969	2.197	0.969	1.694
69 D	1.129	0.670	1.907	0.891	1.895	2.087	1.131	2.087	0.670	1.387
70 R	2.039	-0.276	2.188	0.569	2.041	2.102	0.736	2.188	-0.276	1.343
71 D	1.141	-1.414	1.907	-0.297	1.768	1.630	0.690	1.907	-1.414	0.775
72 I	0.888	-1.344	1.917	-0.833	1.731	1.631	0.802	1.917	-1.344	0.685
73 T	-0.250	-0.164	1.505	-1.586	1.394	1.144	1.133	1.505	-1.586	0.454
74 M	-0.073	-0.296	1.375	-1.429	1.230	0.559	1.021	1.375	-1.429	0.341
75 Y	-0.294	0.445	1.253	-1.062	1.066	0.091	1.190	1.253	-1.062	0.384
76 I	0.345	1.479	1.636	0.163	1.358	0.108	1.088	1.636	0.108	0.882
77 N	0.376	2.431	1.431	1.037	1.157	0.088	1.047	2.431	0.088	1.081
78 S	1.002	1.648	1.431	1.421	1.066	0.071	1.103	1.648	0.071	1.106
79 P	1.483	1.283	1.169	0.778	0.784	0.051	0.771	1.483	0.051	0.903
80 G	1.407	1.780	1.244	-0.002	0.756	0.054	0.701	1.780	-0.002	0.848
81 G	1.293	0.948	1.141	-0.749	0.601	0.033	0.854	1.293	-0.749	0.589
82 G	1.293	0.207	1.141	-0.659	0.601	0.033	0.854	1.293	-0.659	0.496
83 F	0.579	-0.420	0.814	-0.366	0.337	0.019	1.069	1.069	-0.420	0.290
84 T	-0.047	-0.570	0.814	-0.168	0.428	0.037	1.014	1.014	-0.570	0.215
85 S	-0.275	-1.468	0.823	-0.494	0.474	0.037	0.003	0.823	-1.468	-0.129
86 L	-1.141	-1.785	0.692	-1.283	0.501	0.038	0.325	0.692	-1.785	-0.379
87 M	-0.680	-1.089	1.010	-2.069	0.784	0.054	0.406	1.010	-2.069	-0.226
88 A	-0.376	-1.089	1.085	-2.193	0.948	0.523	0.356	1.085	-2.193	-0.107
89 I	-0.458	-0.599	1.132	-1.748	0.948	0.522	0.237	1.132	-1.748	0.005
90 Y	-0.142	-0.681	1.206	-0.967	0.984	0.534	-0.253	1.206	-0.967	0.097
91 D	0.503	-0.370	1.543	-0.370	1.312	0.559	-0.035	1.543	-0.370	0.449
92 T	0.250	-0.096	1.795	-0.401	1.549	0.579	1.308	1.795	-0.401	0.712
93 M	0.522	-0.587	1.814	-0.750	1.558	0.579	1.575	1.814	-0.750	0.673
94 Q	0.907	0.067	1.991	-1.219	1.795	1.184	1.242	1.991	-1.219	0.852
95 Y	0.408	-0.749	1.720	-1.635	1.476	0.695	0.240	1.720	-1.635	0.308
96 V	0.711	0.149	1.795	-1.653	1.640	1.164	0.191	1.795	-1.653	0.571
97 R	0.471	0.736	1.664	-1.555	1.576	1.149	0.568	1.664	-1.555	0.658
98 A	0.471	-0.174	1.664	-1.221	1.576	1.149	0.568	1.664	-1.221	0.576
99 D	0.920	-0.138	1.608	-0.905	1.494	1.149	0.276	1.608	-0.905	0.629
100I	0.920	-0.881	1.608	-0.750	1.494	1.149	0.276	1.608	-0.881	0.545
101Q	0.743	0.071	0.963	-0.660	0.929	0.542	0.899	0.963	-0.660	0.498
102T	0.029	0.071	0.879	-0.658	0.938	0.548	2.345	2.345	-0.658	0.593
103V	-0.243	-0.420	0.599	-0.792	0.574	0.059	2.354	2.354	-0.792	0.304
104C	0.642	-0.324	1.066	-0.817	0.966	0.099	2.195	2.195	-0.817	0.547
105L	0.395	0.495	0.739	-1.035	0.592	0.057	1.022	1.022	-1.035	0.324
106G	0.199	0.700	0.543	-1.272	0.437	0.037	-0.029	0.700	-1.272	0.088
107Q	0.844	0.073	0.814	-1.155	0.601	0.056	-0.458	0.844	-1.155	0.111
108A	0.888	-0.418	1.029	-1.125	0.692	0.038	-2.090	1.029	-2.090	-0.141
109A	1.603	-0.514	1.113	-0.892	0.683	0.032	-3.535	1.603	-3.535	-0.216
110S	1.375	-0.719	1.122	-0.899	0.729	0.032	-4.546	1.375	-4.546	-0.415
111A	0.762	-1.779	0.674	-1.175	0.346	-0.009	-4.120	0.762	-4.120	-0.757
112A	0.048	-1.779	0.589	-1.630	0.355	-0.003	-2.675	0.589	-2.675	-0.728
113A	-0.667	-1.779	0.505	-2.012	0.364	0.002	-1.230	0.505	-2.012	-0.688
114V	-0.945	-1.152	0.356	-2.352	0.209	-0.018	-2.400	0.356	-2.400	-0.900
115L	-0.945	-0.564	0.356	-2.407	0.209	-0.018	-2.400	0.356	-2.407	-0.824
116L	-0.717	-0.001	0.346	-2.370	0.164	-0.018	-1.390	0.346	-2.370	-0.569
117A	-0.521	0.830	0.543	-2.139	0.319	0.002	-0.339	0.830	-2.139	-0.186

118A	-0.155	1.662	0.907	-1.675	0.601	0.020	-0.707	1.662	-1.675	0.093
119G	0.787	2.475	0.982	-1.141	0.547	0.014	-1.142	2.475	-1.142	0.360
120T	1.729	1.734	1.515	-0.763	1.175	0.603	-1.512	1.734	-1.512	0.640
121P	1.862	1.243	1.945	-0.818	1.649	1.228	-0.503	1.945	-0.818	0.944
122G	1.464	0.680	1.935	-1.344	1.695	1.245	0.452	1.935	-1.344	0.875
123K	1.236	0.411	1.945	-2.028	1.741	1.245	-0.558	1.945	-2.028	0.570
124R	0.326	0.189	1.664	-2.593	1.595	1.231	-0.164	1.664	-2.593	0.321
125M	0.326	-0.625	1.664	-2.634	1.595	1.231	-0.164	1.664	-2.634	0.199
126A	0.408	0.303	1.973	-1.863	1.950	1.271	-0.277	1.973	-1.863	0.538
127L	0.180	0.207	1.524	-0.808	1.312	0.677	-1.353	1.524	-1.353	0.249
128P	0.180	0.207	1.524	0.170	1.312	0.677	-1.353	1.524	-1.353	0.388
129N	0.212	-0.476	1.412	0.416	1.257	0.661	-0.709	1.412	-0.709	0.396
130A	-0.503	-0.995	1.328	-0.221	1.267	0.666	0.736	1.328	-0.995	0.325
131R	-0.427	-0.504	1.272	-1.317	1.239	0.663	0.623	1.272	-1.317	0.221
132V	-0.427	-0.959	1.188	-1.771	1.139	1.264	0.671	1.264	-1.771	0.158
133L	-0.490	-0.007	1.216	-1.718	1.203	1.266	0.947	1.266	-1.718	0.345
134I	-0.490	-0.007	1.459	-0.718	1.476	1.285	2.177	2.177	-0.718	0.740
135H	-0.344	1.173	1.178	0.336	1.157	0.680	2.338	2.338	-0.344	0.931
136Q	-0.692	1.710	1.216	0.912	1.175	0.684	2.184	2.184	-0.692	1.027
137P	0.300	1.123	1.449	1.078	1.321	0.698	1.909	1.909	0.300	1.126
138S	1.167	0.439	1.580	0.848	1.294	0.697	1.587	1.587	0.439	1.087
139L	0.800	0.075	1.300	0.293	1.112	0.078	1.909	1.909	0.075	0.795
140S	-0.085	0.906	0.832	-0.329	0.720	0.038	2.067	2.067	-0.329	0.593
141G	0.161	0.542	0.917	-0.927	0.820	0.061	2.010	2.010	-0.927	0.512
142V	0.111	-0.260	0.758	-1.585	0.619	0.041	1.851	1.851	-1.585	0.219
143I	1.072	0.692	1.169	-1.648	0.984	0.078	1.579	1.579	-1.648	0.561
144Q	0.079	1.555	0.954	-1.517	0.784	0.062	1.671	1.671	-1.517	0.513
145G	0.130	0.860	1.113	-0.856	0.984	0.082	1.830	1.830	-0.856	0.592
146Q	0.996	0.808	1.505	-0.058	1.312	0.570	1.232	1.505	-0.058	0.909
147F	0.920	-0.007	1.561	0.616	1.339	0.573	1.346	1.561	-0.007	0.907
148S	1.034	0.658	1.561	0.812	1.330	1.130	1.156	1.561	0.658	1.097
149D	0.168	-0.198	1.431	0.324	1.358	1.132	1.477	1.477	-0.198	0.813
150L	0.168	-0.737	1.431	-0.577	1.358	1.132	1.477	1.477	-0.737	0.607
151E	0.882	0.043	1.496	-1.506	1.403	1.128	0.216	1.496	-1.506	0.523
152I	0.604	-0.857	1.346	-1.959	1.248	1.108	-0.954	1.346	-1.959	0.077
153Q	0.465	0.043	1.403	-2.101	1.294	1.219	-0.971	1.403	-2.101	0.193
154A	0.541	0.365	1.346	-2.088	1.267	1.215	-1.084	1.346	-2.088	0.223
155A	0.541	0.251	1.346	-2.292	1.267	1.215	-1.084	1.346	-2.292	0.178
156E	1.312	1.064	1.917	-2.552	1.759	1.838	-1.407	1.917	-2.552	0.561
157I	0.667	0.980	1.580	-2.871	1.431	1.813	-1.625	1.813	-2.871	0.282
158E	0.800	1.101	2.010	-3.016	1.905	2.437	-0.616	2.437	-3.016	0.660
159R	0.996	0.411	2.206	-2.924	2.060	2.457	0.435	2.457	-2.924	0.806
160M	-0.079	0.173	1.795	-2.738	1.704	1.863	0.896	1.863	-2.738	0.516
161R	0.161	0.778	1.926	-2.439	1.768	1.878	0.519	1.926	-2.439	0.656
162T	0.161	0.455	1.926	-2.289	1.768	1.878	0.519	1.926	-2.289	0.631
163L	0.225	-0.240	1.692	-2.190	1.449	1.274	0.561	1.692	-2.190	0.396
164M	0.819	-0.036	1.898	-2.033	1.558	1.276	0.657	1.898	-2.033	0.591
165E	-0.028	0.892	1.384	-1.720	1.093	0.657	1.093	1.384	-1.720	0.482
166T	-0.224	0.407	1.188	-1.417	0.938	0.637	0.042	1.188	-1.417	0.224
167T	0.623	0.407	1.702	-1.351	1.403	1.257	-0.394	1.702	-1.351	0.521
168L	1.021	0.544	1.870	-1.192	1.531	1.859	-0.072	1.870	-1.192	0.794
169A	0.857	1.579	1.739	-0.969	1.321	1.280	-0.005	1.739	-0.969	0.829
170R	0.888	2.118	1.533	-0.389	1.121	1.260	-0.045	2.118	-0.389	0.927
171H	0.920	1.305	1.786	0.003	1.604	1.834	-0.021	1.834	-0.021	1.062
172T	2.134	1.842	2.141	0.243	1.914	2.318	-0.465	2.318	-0.465	1.447
173G	2.134	1.255	2.141	-0.120	1.914	2.318	-0.465	2.318	-0.465	1.311
174K	2.229	0.303	1.702	-0.309	1.394	1.693	-0.464	2.229	-0.464	0.935
175D	1.862	0.285	1.421	-0.700	1.212	1.075	-0.142	1.862	-0.700	0.716
176A	1.028	0.578	1.085	-1.046	1.039	1.057	0.139	1.085	-1.046	0.554

177G	0.933	1.117	1.524	-1.664	1.558	1.681	0.138	1.681	-1.664	0.755
178V	0.933	0.980	1.524	-2.246	1.558	1.681	0.138	1.681	-2.246	0.653
179I	0.933	1.615	1.524	-2.456	1.558	1.681	0.138	1.681	-2.456	0.713
180R	1.129	2.754	1.720	-2.013	1.713	1.701	1.188	2.754	-2.013	1.170
181K	1.401	2.479	2.001	-0.939	2.078	2.190	1.179	2.479	-0.939	1.484
182D	1.900	2.479	2.552	-0.022	2.561	2.813	0.590	2.813	-0.022	1.839
183T	3.038	1.615	2.963	0.808	2.898	3.301	0.259	3.301	0.259	2.126
184D	3.133	0.920	2.982	0.769	3.062	3.271	0.325	3.271	0.325	2.066
185R	2.267	0.872	2.393	0.373	2.406	2.678	0.582	2.678	0.373	1.653
186D	1.053	0.059	2.038	-0.554	2.096	2.194	1.025	2.194	-0.554	1.130
187K	1.053	0.095	2.038	-1.227	2.096	2.194	1.025	2.194	-1.227	1.039
188I	0.553	-0.162	1.767	-1.882	1.777	1.705	0.024	1.777	-1.882	0.540
189L	0.781	0.163	1.664	-1.916	1.668	1.680	-0.001	1.680	-1.916	0.577
190T	0.642	1.199	1.720	-1.974	1.713	1.791	-0.018	1.791	-1.974	0.725
191A	0.414	1.247	1.272	-1.912	1.075	1.196	-1.094	1.272	-1.912	0.314
192E	1.280	0.840	1.860	-2.068	1.731	1.789	-1.350	1.860	-2.068	0.583
193E	2.494	0.892	2.216	-1.936	2.041	2.272	-1.794	2.494	-1.936	0.884
194A	2.045	-0.007	2.272	-1.660	2.123	2.272	-1.503	2.272	-1.660	0.792
195K	2.273	-0.332	2.262	-1.044	2.078	2.272	-0.492	2.273	-1.044	1.002
196D	1.274	-0.625	1.795	-0.762	1.695	1.674	-0.144	1.795	-0.762	0.701
197Y	0.275	-0.673	1.328	-0.989	1.312	1.076	0.203	1.328	-0.989	0.362
198G	0.775	-0.362	1.599	-1.406	1.631	1.565	1.205	1.631	-1.406	0.715
199I	0.743	-1.194	1.346	-1.560	1.148	0.991	1.180	1.346	-1.560	0.379
200I	-0.123	-0.294	0.954	-1.348	0.820	0.503	1.778	1.778	-1.348	0.327
201D	-0.585	-0.376	0.618	-0.885	0.592	0.489	1.881	1.881	-0.885	0.248
202T	-0.452	-0.102	0.954	-0.817	1.002	1.089	1.854	1.854	-0.817	0.504
203V	-0.066	0.239	1.346	-1.182	1.257	1.106	1.865	1.865	-1.182	0.652
204L	0.705	0.131	1.917	-1.673	1.750	1.729	1.542	1.917	-1.673	0.871
205E	0.433	1.191	2.094	-2.107	2.069	1.835	1.616	2.094	-2.107	1.019
206Y	-0.477	0.616	1.814	-2.281	1.923	1.820	2.010	2.010	-2.281	0.775
207R	0.168	1.513	2.085	-2.103	2.087	1.839	1.582	2.087	-2.103	1.024
208K	0.882	1.191	2.169	-1.877	2.078	1.834	0.136	2.169	-1.877	0.916
209L	0.768	0.359	2.169	-1.328	2.087	1.276	0.326	2.169	-1.328	0.808
210S	1.217	0.818	2.113	-0.844	2.005	1.277	0.035	2.113	-0.844	0.946
211A	1.084	0.217	1.683	-0.540	1.531	0.652	-0.975	1.683	-0.975	0.522
212Q	0.724	0.471	0.776	-0.522	1.212	0.118	-2.050	1.212	-2.050	0.104
213T	1.306	0.235	0.403	-0.584	1.522	0.172	-3.495	1.522	-3.495	-0.063
214A	0.895	-0.001	-0.205	-0.732	1.686	0.212	-4.665	1.686	-4.665	-0.402

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	[1]MNSQNSQIQPQARYILPSFIEHSSFGVKESNPYNKLFEERIIFLGVQVDDASANDIMAQLLVLESLDP DRDITMYINSPGGGFTSLMAIYDTMQYVRADIQTVCLGQAASAAAVLLAAGTPGKRMALPNARVLIHQ PSLSGVIQGQFSDLEIQAAEIERMRTLMETTLARHTGKDAGVIRKDTDRDKILTAEEAKDYGIIDTVLEY RKLSAQTA[214]
Hydrophilicity	[1]MNSQNSQIQPQARYILPSFIEHSSFGVKESNPYNKLFEERIIFLGVQVDDASANDIMAQLLVLESLDP DRDITMYINSPGGGFTSLMAIYDTMQYVRADIQTVCLGQAASAAAVLLAAGTPGKRMALPNARVLIHQ PSLSGVIQGQFSDLEIQAAEIERMRTLMETTLARHTGKDAGVIRKDTDRDKILTAEEAKDYGIIDTVLEY RKLSAQTA[214]
Flexibility	[1]