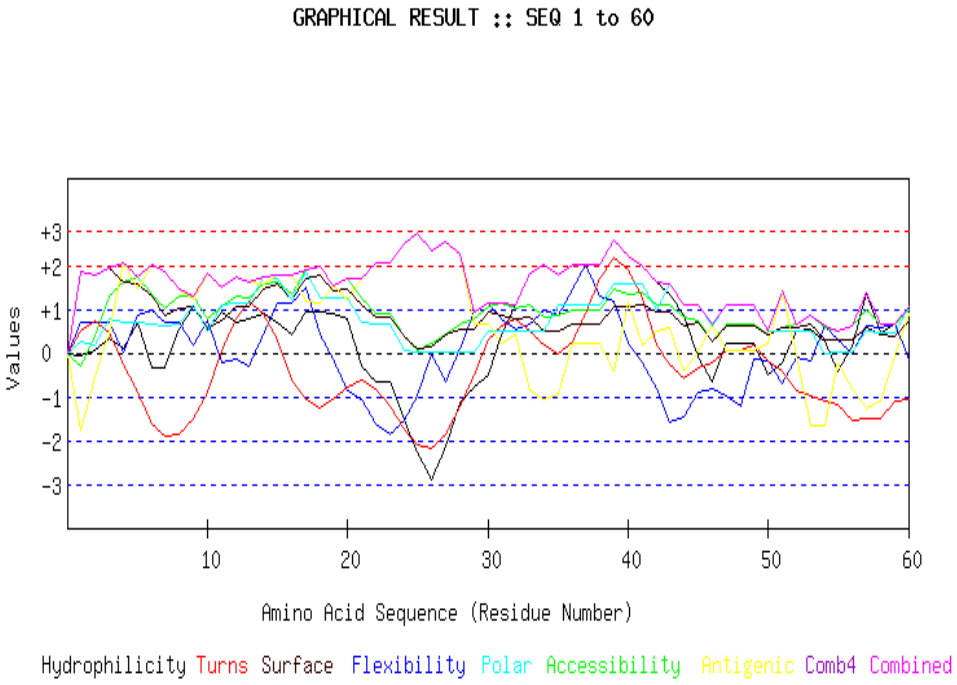
BcePred Prediction Server

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

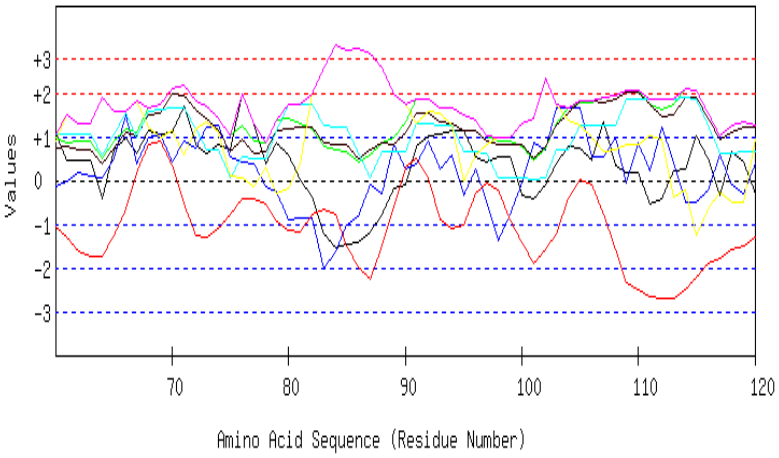
seqname=
Seq= VNQLPRVGLGTDVHPIEPGRPCWLVGLLFPSADGCAGHSDGDVAVHALCDAVLSAAGLGD
IGEVFGVDDPRWQGVSGADMLRHVVVLITQHGYRVGNAVVQVIGNRPKIGWRRLEAQAVL
SRLLNAPVSVSATTTDGLGLTGRGEGLAAIATALVVSLR

Length=159

GRAPHICAL RESULT

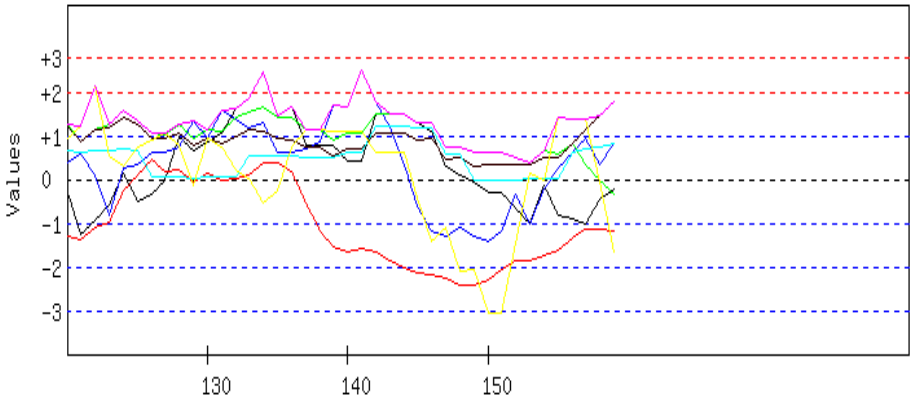


GRAPHICAL RESULT :: SEQ 61 to 120



Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

GRAPHICAL RESULT :: SEQ 121 to 180



Hydrophilicity Turns Surface Flexibility Polar Accessibility Antigenic Comb4 Combined

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

VNQLPRVGLGTDVHPIEPGRPCWLVGLLFPSADGCAGHSDGDVAVHALCDAVLSAAGLGD
IGEVFGVDDPRWQGVSGADMLRHVVVLITQHGYRVGNAVVQVIGNRPKIGWRRLEAQAVL
SRLLNAPVSVSATTTDGLGLTGRGEGLAAIATALVVSLR

Length=159

A.A.		Parameter						Combined		
		Hydro	Flexi	Access	Turns	Surface	Polar	AntiPro	MAX	MIN	AVG
1	V	-0.073	0.698	-0.308	0.512	1.841	0.240	-1.775	1.841	-1.775	0.162
2	N	0.060	0.698	0.393	0.747	1.795	0.199	-0.544	1.795	-0.544	0.478
3	Q	0.326	0.716	1.281	0.449	1.950	0.764	0.465	1.950	0.326	0.850
4	L	0.092	0.021	1.617	-0.253	1.622	0.705	2.064	2.064	-0.253	0.838
5	P	0.686	0.852	1.730	-0.915	1.586	0.703	1.475	1.730	-0.915	0.874
6	R	-0.338	0.984	1.346	-1.608	1.285	0.668	2.023	2.023	-1.608	0.623
7	V	-0.357	0.710	1.010	-1.902	0.866	0.626	1.860	1.860	-1.902	0.402
8	G	0.553	0.710	1.290	-1.872	1.011	0.640	1.466	1.466	-1.872	0.543
9	L	1.053	0.173	1.318	-1.514	1.057	1.110	1.237	1.318	-1.514	0.633
10	G	0.553	0.736	0.767	-0.909	0.574	0.487	1.827	1.827	-0.909	0.576
11	T	0.920	-0.216	1.047	0.059	0.756	1.106	1.505	1.505	-0.216	0.740
12	D	0.692	-0.132	1.300	0.785	1.075	1.125	1.725	1.725	-0.132	0.939
13	V	0.768	-0.312	1.244	1.167	1.048	1.121	1.612	1.612	-0.312	0.950
14	H	0.901	0.411	1.580	0.905	1.458	1.720	1.585	1.720	0.411	1.223
15	P	0.705	1.135	1.627	0.287	1.576	1.720	1.764	1.764	0.287	1.259

16 I	0.433	1.135	1.346	-0.619	1.212	1.231	1.773	1.773	-0.619	0.930
17 E	0.933	1.495	1.898	-1.076	1.695	1.854	1.184	1.898	-1.076	1.140
18 P	0.933	0.417	1.982	-1.270	1.795	1.253	1.136	1.982	-1.270	0.892
19 G	0.888	-0.146	1.524	-1.058	1.431	1.252	1.539	1.539	-1.058	0.776
20 R	0.762	-0.869	1.683	-0.772	1.467	1.275	1.239	1.683	-0.869	0.684
21 P	-0.313	-1.055	1.272	-0.616	1.112	0.681	1.701	1.701	-1.055	0.397
22 C	-0.680	-1.618	0.907	-0.817	0.829	0.663	2.069	2.069	-1.618	0.193
23 W	-0.680	-1.859	0.907	-1.231	0.829	0.663	2.069	2.069	-1.859	0.100
24 L	-1.527	-1.530	0.393	-1.723	0.364	0.044	2.505	2.505	-1.723	-0.210
25 V	-2.241	-0.967	0.066	-2.105	0.100	0.031	2.720	2.720	-2.241	-0.342
26 G	-2.911	-0.015	0.216	-2.170	0.146	0.017	2.349	2.349	-2.911	-0.339
27 L	-2.146	-0.643	0.440	-1.864	0.401	0.011	2.547	2.547	-2.146	-0.179
28 L	-1.154	0.101	0.674	-1.208	0.547	0.025	2.272	2.272	-1.208	0.179
29 F	-0.787	0.932	0.795	-0.508	0.556	0.024	0.673	0.932	-0.787	0.241
30 P	-0.515	1.143	1.075	0.297	0.920	0.513	0.664	1.143	-0.515	0.585
31 S	0.427	0.784	1.150	0.608	0.866	0.507	0.229	1.150	0.229	0.653
32 A	1.097	0.556	1.019	0.768	0.765	0.520	0.416	1.097	0.416	0.735
33 D	1.812	0.646	1.085	0.482	0.811	0.516	-0.845	1.812	-0.845	0.644
34 G	2.039	0.962	0.832	0.176	0.492	0.497	-1.065	2.039	-1.065	0.562
35 C	1.761	0.874	0.842	-0.019	0.510	1.096	-0.957	1.761	-0.957	0.587
36 A	2.039	1.465	0.991	0.261	0.665	1.116	0.213	2.039	0.213	0.964
37 G	2.039	2.004	0.991	0.904	0.665	1.116	0.213	2.039	0.213	1.133
38 H	2.039	1.281	0.991	1.682	0.665	1.116	0.213	2.039	0.213	1.141
39 S	2.583	1.191	1.477	2.166	1.075	1.588	-0.418	2.583	-0.418	1.380
40 D	2.216	0.239	1.356	1.896	1.066	1.589	1.180	2.216	0.239	1.363
41 G	1.989	-0.210	1.365	1.258	1.112	1.589	0.170	1.989	-0.210	1.039
42 D	1.622	-0.837	1.085	0.191	0.929	0.971	0.491	1.622	-0.837	0.636
43 V	1.344	-1.580	1.094	-0.261	0.948	1.571	0.599	1.571	-1.580	0.531
44 A	0.844	-1.448	0.823	-0.592	0.629	1.082	-0.402	1.082	-1.448	0.134
45 V	-0.098	-0.909	0.748	-0.343	0.683	1.087	0.032	1.087	-0.909	

0.172									
46 H	-0.642	-0.813	0.262	-0.219	0.273	0.616	0.664	0.664	-0.813
0.020									
47 A	0.225	-0.999	0.655	0.045	0.601	1.103	0.066	1.103	-0.999
0.242									
48 L	0.225	-1.204	0.655	0.055	0.601	1.103	0.066	1.103	-1.204
0.215									
49 C	0.225	-0.144	0.655	0.179	0.601	1.103	0.066	1.103	-0.144
0.384									
50 D	-0.490	-0.180	0.412	-0.166	0.437	0.489	0.234	0.489	-0.490
0.105									
51 A	-0.212	-0.719	0.561	-0.412	0.592	0.509	1.403	1.403	-0.719
0.246									
52 V	0.503	-0.092	0.646	-0.840	0.583	0.504	-0.042	0.646	-0.840
0.180									
53 L	0.547	-0.200	0.860	-0.996	0.674	0.486	-1.674	0.860	-1.674
-0.043									
54 S	0.275	0.632	0.580	-1.088	0.310	-0.003	-1.665	0.632	-1.665
-0.137									
55 A	-0.439	0.315	0.496	-1.190	0.319	0.002	-0.220	0.496	-1.190
-0.102									
56 A	0.155	-0.009	0.608	-1.530	0.282	0.001	-0.808	0.608	-1.530
-0.186									
57 G	1.369	0.618	0.963	-1.505	0.592	0.484	-1.252	1.369	-1.505
0.181									
58 L	0.452	0.566	0.674	-1.481	0.419	0.466	-1.090	0.674	-1.481
0.001									
59 G	0.680	0.674	0.664	-1.087	0.373	0.466	-0.080	0.680	-1.087
0.241									
60 D	1.040	-0.128	0.991	-1.042	0.738	1.066	0.904	1.066	-1.042
0.510									
61 I	0.446	-0.040	0.879	-1.300	0.774	1.067	1.493	1.493	-1.300
0.474									
62 G	0.446	0.189	0.898	-1.631	0.720	1.066	1.309	1.309	-1.631
0.428									
63 E	0.446	0.101	0.898	-1.738	0.720	1.066	1.309	1.309	-1.738
0.400									
64 V	-0.420	0.065	0.505	-1.748	0.392	0.579	1.906	1.906	-1.748
0.183									
65 F	0.718	0.519	0.917	-1.247	0.729	1.066	1.576	1.576	-1.247
0.611									
66 G	0.990	1.507	1.197	-0.646	1.093	1.555	1.566	1.566	-0.646
1.037									
67 V	0.629	0.377	1.113	0.187	1.002	0.974	1.813	1.813	0.187
0.871									
68 D	1.129	0.964	1.664	0.837	1.485	1.597	1.223	1.664	0.837
1.271									
69 D	1.078	1.052	1.748	0.897	1.549	1.618	0.994	1.748	0.897
1.277									
70 P	1.097	0.417	2.085	0.327	1.968	1.661	1.157	2.085	0.327
1.245									
71 R	1.691	0.914	2.197	-0.520	1.932	1.659	0.569	2.197	-0.520
1.206									
72 W	0.825	0.728	1.804	-1.247	1.604	1.172	1.166	1.804	-1.247
0.865									
73 Q	0.604	1.231	1.683	-1.305	1.440	0.703	1.335	1.683	-1.305
0.813									
74 G	0.832	1.279	1.431	-1.103	1.121	0.684	1.116	1.431	-1.103
0.765									

75 V	0.699	0.538	1.001	-0.774	0.647	0.059	0.106	1.001	-0.774
0.325									
76 S	1.963	0.429	1.253	-0.423	0.948	0.523	0.075	1.963	-0.423
0.681									
77 G	1.318	0.387	0.917	-0.428	0.619	0.498	-0.143	1.318	-0.428
0.453									
78 A	0.376	-0.150	0.842	-0.539	0.674	0.503	0.291	0.842	-0.539
0.285									
79 D	0.876	-0.246	1.393	-0.930	1.157	1.126	-0.298	1.393	-0.930
0.440									
80 M	0.598	-0.881	1.403	-1.143	1.175	1.726	-0.191	1.726	-1.143
0.384									
81 L	0.003	-0.863	1.290	-1.198	1.212	1.727	0.398	1.727	-1.198
0.367									
82 R	-0.363	-0.863	1.169	-0.780	1.203	1.729	1.997	1.997	-0.863
0.584									
83 H	-1.230	-2.001	0.776	-0.679	0.875	1.242	2.594	2.594	-2.001
0.225									
84 V	-1.546	-1.600	0.702	-0.782	0.838	1.230	3.084	3.084	-1.600
0.275									
85 V	-1.470	-1.013	0.646	-1.499	0.811	1.226	2.971	2.971	-1.499
0.239									
86 V	-1.407	-0.827	0.412	-1.967	0.492	0.622	3.013	3.013	-1.967
0.048									
87 L	-1.160	-0.104	0.580	-2.259	0.692	0.044	2.909	2.909	-2.259
0.100									
88 I	-0.793	-0.306	0.860	-1.519	0.875	0.662	2.587	2.587	-1.519
0.338									
89 T	-0.199	0.832	0.973	-0.624	0.838	0.661	1.999	1.999	-0.624
0.640									
90 Q	-0.085	0.245	1.346	0.311	1.084	0.679	1.742	1.742	-0.085
0.760									
91 H	0.762	0.381	1.860	0.498	1.549	1.298	1.306	1.860	0.381
1.094									
92 G	1.034	0.900	1.879	0.062	1.558	1.298	1.573	1.879	0.062
1.186									
93 Y	1.065	0.273	1.674	-0.896	1.358	1.278	1.533	1.674	-0.896
0.898									
94 R	1.129	0.584	1.646	-1.120	1.294	1.276	1.257	1.646	-1.120
0.866									
95 V	1.129	-0.326	1.487	-1.036	1.121	0.656	-0.021	1.487	-1.036
0.430									
96 G	0.534	0.261	1.375	-0.302	1.157	0.658	0.568	1.375	-0.302
0.607									
97 N	0.421	-0.462	1.001	-0.052	0.911	0.640	0.824	1.001	-0.462
0.469									
98 A	0.534	-1.396	0.898	-0.234	0.811	0.058	0.988	0.988	-1.396
0.237									
99 V	0.534	-0.769	0.898	-0.898	0.811	0.058	0.988	0.988	-0.898
0.232									
100V	-0.332	-0.064	0.767	-1.409	0.838	0.059	1.310	1.310	-1.409
0.167									
101Q	-0.414	0.846	0.459	-1.888	0.483	0.019	1.423	1.423	-1.888
0.133									
102V	-0.104	0.714	0.758	-1.583	0.793	0.059	2.320	2.320	-1.583
0.422									
103I	0.395	1.641	1.309	-1.236	1.276	0.682	1.731	1.731	-1.236
0.828									
104G	0.762	1.641	1.674	-0.409	1.558	0.700	1.362	1.674	-0.409

1.041									
105N	0.743	1.641	1.795	0.005	1.823	1.252	1.264	1.823	0.005
1.217									
106R	0.471	0.529	1.776	-0.085	1.813	1.252	0.997	1.813	-0.085
0.965									
107P	1.337	0.529	1.907	-0.782	1.786	1.251	0.675	1.907	-0.782
0.958									
108K	0.345	0.984	1.935	-1.564	1.850	1.276	0.697	1.935	-1.564
0.789									
109I	0.168	-0.052	2.066	-2.323	2.014	1.860	0.809	2.066	-2.323
0.649									
110G	0.168	0.848	2.066	-2.498	2.014	1.860	0.809	2.066	-2.498
0.752									
111W	-0.547	0.221	1.739	-2.672	1.750	1.846	1.024	1.846	-2.672
0.480									
112R	-0.414	1.215	1.617	-2.710	1.476	1.851	0.933	1.851	-2.710
0.567									
113R	0.225	0.401	1.758	-2.682	1.494	1.849	-0.399	1.849	-2.682
0.378									
114L	0.244	-0.508	2.094	-2.519	1.914	1.892	-0.236	2.094	-2.519
0.411									
115E	1.009	-0.508	2.075	-2.235	1.895	1.867	-1.268	2.075	-2.235
0.405									
116A	0.509	-0.228	1.524	-1.912	1.412	1.243	-0.679	1.524	-1.912
0.267									
117Q	-0.338	0.586	1.010	-1.776	0.948	0.624	-0.243	1.010	-1.776
0.116									
118A	0.655	-0.110	1.244	-1.572	1.093	0.639	-0.518	1.244	-1.572
0.204									
119V	0.427	-0.314	1.346	-1.506	1.203	0.664	-0.492	1.346	-1.506
0.190									
120L	-0.288	0.391	1.262	-1.308	1.212	0.669	0.953	1.262	-1.308
0.413									
121S	-1.249	0.596	0.851	-1.367	0.847	0.632	1.224	1.224	-1.367
0.219									
122R	-0.939	0.099	1.150	-1.108	1.157	0.673	2.121	2.121	-1.108
0.451									
123L	-0.572	-0.811	1.272	-0.963	1.166	0.671	0.523	1.272	-0.963
0.184									
124L	0.142	0.249	1.599	-0.254	1.431	0.685	0.308	1.599	-0.254
0.594									
125N	-0.503	0.357	1.328	0.084	1.267	0.666	0.736	1.328	-0.503
0.562									
126A	-0.357	0.604	1.047	0.464	0.948	0.062	0.897	1.047	-0.357
0.523									
127P	-0.009	0.604	1.010	0.183	0.929	0.058	1.051	1.051	-0.009
0.547									
128V	0.983	0.736	1.244	0.220	1.075	0.073	0.776	1.244	0.073
0.729									
129S	0.673	1.323	0.945	-0.063	0.765	0.032	-0.121	1.323	-0.121
0.508									
130V	0.869	0.958	1.141	0.124	0.920	0.052	0.930	1.141	0.052
0.714									
131S	1.065	1.593	1.094	-0.021	0.802	0.053	0.750	1.593	-0.021
0.762									
132A	1.628	1.365	1.412	0.015	0.966	0.071	0.202	1.628	0.015
0.809									
133T	1.849	1.161	1.533	0.085	1.130	0.540	0.034	1.849	0.034
0.905									

134T	2.444	1.297	1.646	0.378	1.093	0.539	-0.555	2.444	-0.555
0.977									
135T	1.451	0.602	1.412	0.397	0.948	0.524	-0.280	1.451	-0.280
0.722									
136D	1.679	0.602	1.403	0.178	0.902	0.524	0.731	1.679	0.178
0.860									
137G	0.768	0.690	1.122	-0.521	0.756	0.509	1.125	1.125	-0.521
0.636									
138L	0.768	0.876	1.122	-1.182	0.756	0.509	1.125	1.125	-1.182
0.568									
139G	0.800	1.708	0.917	-1.546	0.556	0.490	1.084	1.708	-1.546
0.573									
140L	0.433	1.656	1.075	-1.674	0.711	0.625	1.093	1.656	-1.674
0.560									
141T	0.433	2.487	1.075	-1.599	0.711	0.625	1.093	2.487	-1.599
0.689									
142G	1.508	1.792	1.487	-1.677	1.066	1.219	0.631	1.792	-1.677
0.861									
143R	1.508	1.165	1.487	-1.871	1.066	1.219	0.631	1.508	-1.871
0.744									
144G	1.508	0.351	1.487	-2.021	1.066	1.219	0.631	1.508	-2.021
0.606									
145E	1.312	-0.601	1.290	-2.131	0.911	1.199	-0.420	1.312	-2.131
0.223									
146G	1.084	-1.176	1.300	-2.174	0.957	1.199	-1.430	1.300	-2.174
-0.034									
147L	0.313	-1.312	0.730	-2.269	0.465	0.577	-1.107	0.730	-2.269
-0.372									
148A	0.085	-1.107	0.739	-2.424	0.510	0.577	-2.118	0.739	-2.424
-0.534									
149A	-0.079	-1.312	0.608	-2.417	0.300	-0.003	-2.051	0.608	-2.417
-0.708									
150I	-0.307	-1.408	0.618	-2.312	0.346	-0.003	-3.061	0.618	-3.061
-0.875									
151A	-0.307	-1.180	0.618	-2.045	0.346	-0.003	-3.061	0.618	-3.061
-0.805									
152T	-0.673	-0.324	0.496	-1.856	0.337	-0.001	-1.462	0.496	-1.856
-0.498									
153A	-1.040	-1.019	0.375	-1.877	0.328	0.000	0.136	0.375	-1.877
-0.442									
154L	-0.123	-0.206	0.664	-1.759	0.501	0.018	-0.025	0.664	-1.759
-0.133									
155V	-0.838	0.253	0.580	-1.618	0.510	0.024	1.420	1.420	-1.618
0.047									
156V	-0.901	0.604	0.814	-1.360	0.829	0.629	1.378	1.378	-1.360
0.285									
157S	-1.034	0.954	0.356	-1.155	1.148	0.689	1.378	1.378	-1.155
0.334									
158L	-0.452	0.353	-0.018	-1.145	1.458	0.743	-0.067	1.458	-1.145
0.125									
159R	-0.218	0.812	-0.354	-1.195	1.786	0.802	-1.666	1.786	-1.666
-0.005									

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]VNQLPRVGLGTDVHPIEPGRPCWLVGLLFPSADGCAGHSDGDVAVHALCDAVLSAAGLGDIGEVFGVDDPRWQGV SGADMLRHVVVLITQHGYRVGNAVVQVIGNRPKIGWRRLEAQAVLSRLLNAPVSVSATTTDGLGLTGRGEGLAAIAT ALVVSLR[159]
Hydrophilicity	[1]VNQLPRVGLGTDVHPIEPGRPCWLVGLLFPSADGCAGHSDGDVAVHALCDAVLSAAGLGDIGEVFGVDDPRWQGV SGADMLRHVVVLITQHGYRVGNAVVQVIGNRPKIGWRRLEAQAVLSRLLNAPVSVSATTTDGLGLTGRGEGLAAIAT ALVVSLR[159]
Flexibility	[1]VNQLPRVGLGTDVHPIEPGRPCWLVGLLFPSADGCAGHSDGDVAVHALCDAVLSAAGLGDIGEVFGVDDPRWQGV SGADMLRHVVVLITQHGYRVGNAVVQVIGNRPKIGWRRLEAQAVLSRLLNAPVSVSATTTDGLGLTGRGEGLAAIAT ALVVSLR[159]
Accessibility	[1]VNQLPRVGLGTDVHPIEPGRPCWLVGLLFPSADGCAGHSDGDVAVHALCDAVLSAAGLGDIGEVFGVDDPRWQGV SGADMLRHVVVLITQHGYRVGNAVVQVIGNRPKIGWRRLEAQAVLSRLLNAPVSVSATTTDGLGLTGRGEGLAAIAT ALVVSLR[159]
Turns	[1]VNQLPRVGLGTDVHPIEPGRPCWLVGLLFPSADGCAGHSDGDVAVHALCDAVLSAAGLGDIGEVFGVDDPRWQGV SGADMLRHVVVLITQHGYRVGNAVVQVIGNRPKIGWRRLEAQAVLSRLLNAPVSVSATTTDGLGLTGRGEGLAAIAT ALVVSLR[159]
Exposed Surface	[1]VNQLPRVGLGTDVHPIEPGRPCWLVGLLFPSADGCAGHSDGDVAVHALCDAVLSAAGLGDIGEVFGVDDPRWQGV SGADMLRHVVVLITQHGYRVGNAVVQVIGNRPKIGWRRLEAQAVLSRLLNAPVSVSATTTDGLGLTGRGEGLAAIAT ALVVSLR[159]
Polarity	[1]VNQLPRVGLGTDVHPIEPGRPCWLVGLLFPSADGCAGHSDGDVAVHALCDAVLSAAGLGDIGEVFGVDDPRWQGV SGADMLRHVVVLITQHGYRVGNAVVQVIGNRPKIGWRRLEAQAVLSRLLNAPVSVSATTTDGLGLTGRGEGLAAIAT ALVVSLR[159]
Antigenic Propensity	[1]VNQLPRVGLGTDVHPIEPGRPCWLVGLLFPSADGCAGHSDGDVAVHALCDAVLSAAGLGDIGEVFGVDDPRWQGV SGADMLRHVVVLITQHGYRVGNAVVQVIGNRPKIGWRRLEAQAVLSRLLNAPVSVSATTTDGLGLTGRGEGLAAIAT ALVVSLR[159]

TOP

Home