

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

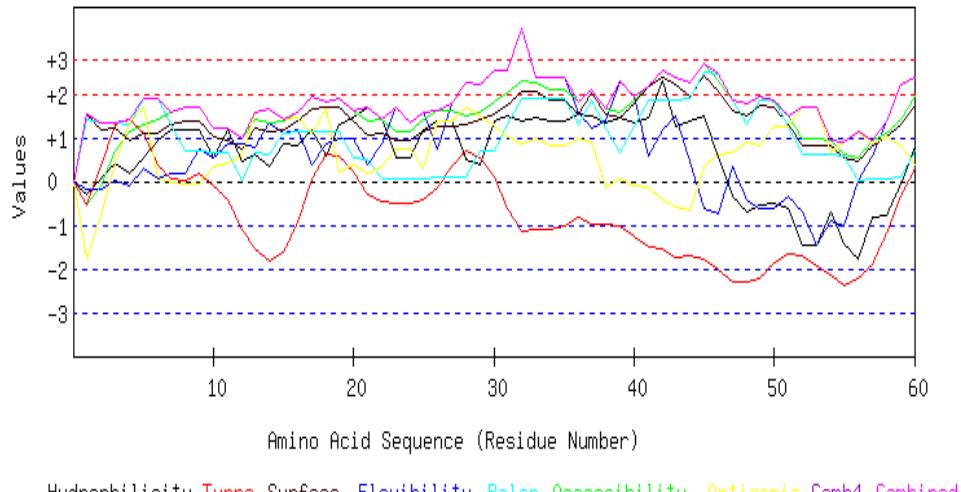
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GSDGINIRLILGNADVLQHLIAPDSLCGVRVFFPDPWPKARHKKRLLQPATMALIADRLVPS
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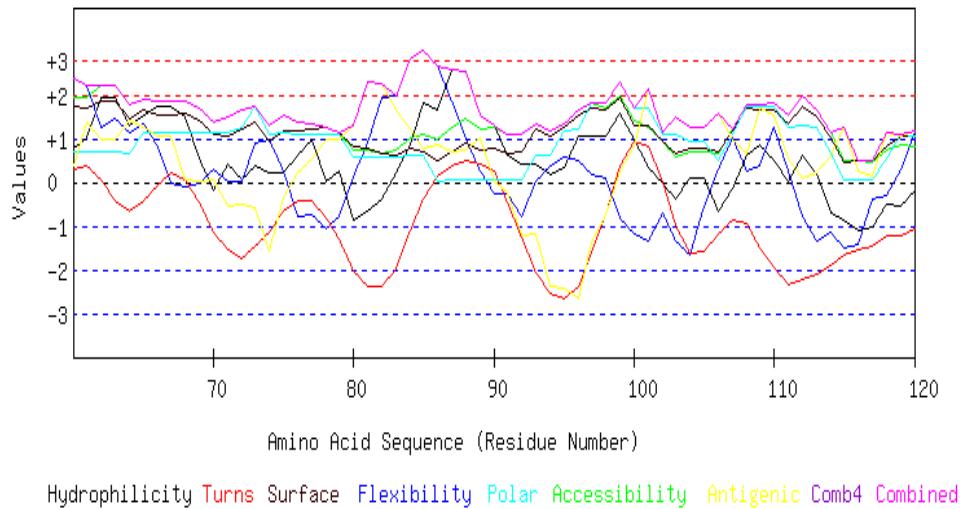
Length=263

GRAPHICAL RESULT

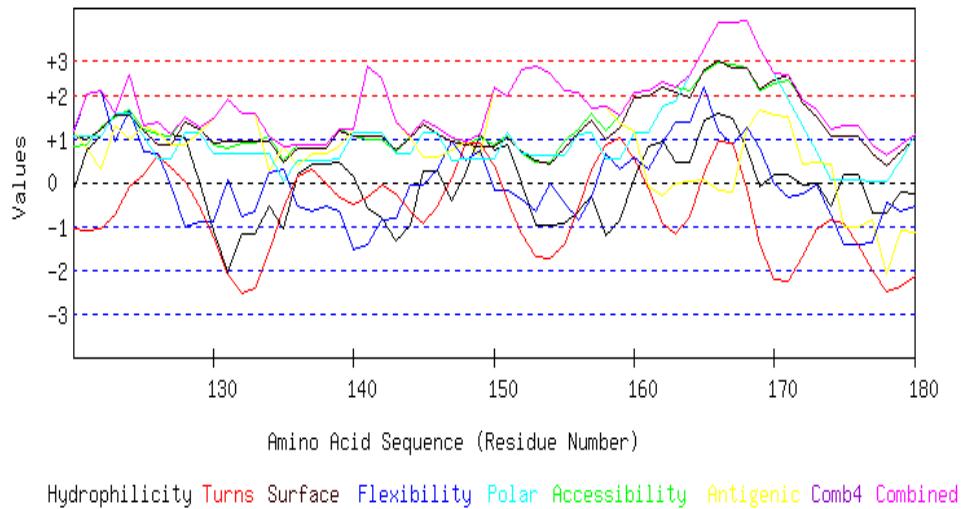
GRAPHICAL RESULT :: SEQ 1 to 60



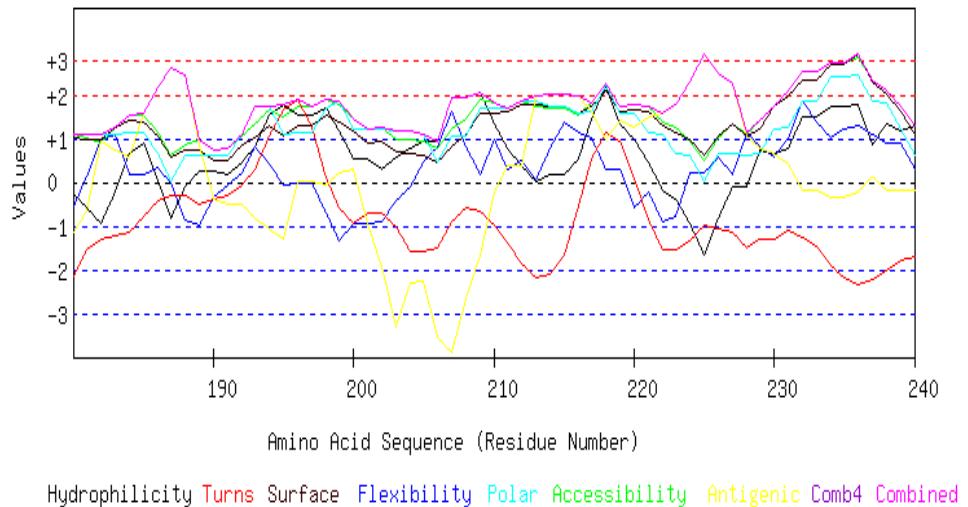
GRAPHICAL RESULT :: SEQ 61 to 120



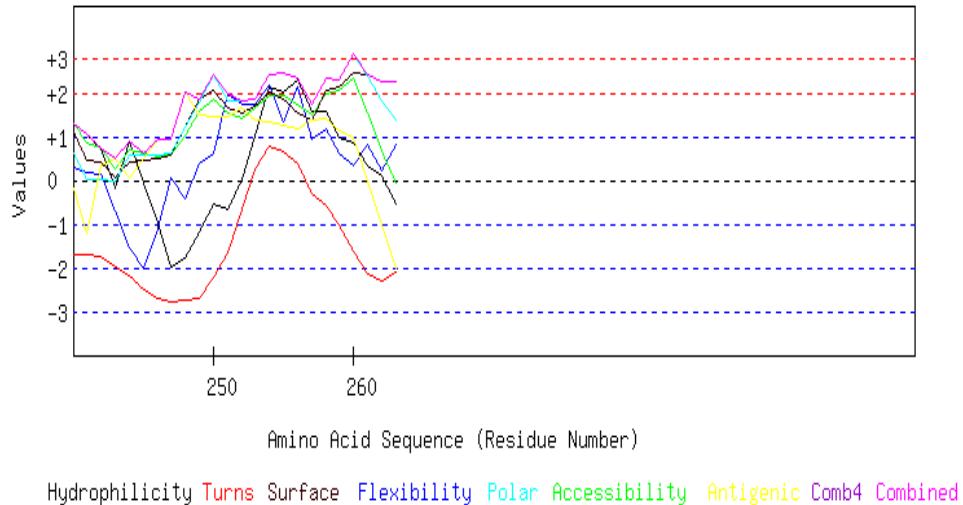
GRAPHICAL RESULT :: SEQ 121 to 180



GRAPHICAL RESULT :: SEQ 181 to 240



GRAPHICAL RESULT :: SEQ 241 to 300



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

MVHHGQMHAQPGVGLRPDTPVASGQLPSTSIRSRRSGISKAQRETWERLWPELGLLALPQ
SPRGTPVDTRAWFGRDAPPVLEIGSGSGTSTLAMAKAEPHVDVIAVDVYRRGLAQQLLCI
DKVGSDGINIRLILGNAVDVLQHLIAPDSLCGVRVFFPDWPWPKARHKRRLLQPATMALI
ADRLVPSGVLAATDHPGYAEHIAAGDAEPRIVRVDPDTELLPISVVRPATKYERKAQL
GGGAVIELLWKKHGCSERDLKIR

Length=263

A.A.

Parameter
Combined

Hydro	Flexi	Access	Turns	Surface	Polar	AntiPro	MAX
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29 T	0.383	0.383	2.231	1.589	0.546	1.403	0.681	1.518	2.231		
30 S	0.081	1.193	1.375	2.553	1.823	0.081	1.549	0.695	1.243	2.553	
31 I	-0.637	1.331	1.508	2.553	2.010	-0.637	1.750	1.301	1.022	2.553	
32 R	-1.128	1.358	1.363	3.505	2.290	-1.128	2.069	1.906	0.861	3.505	
33 S	-1.106	1.415	1.445	2.367	2.244	-1.106	2.069	1.906	0.980	2.367	
34 R	-1.098	1.415	1.394	2.367	2.085	-1.098	1.868	1.886	0.821	2.367	
35 R	-1.009	1.332	1.394	2.385	2.085	-1.009	1.868	1.886	0.821	2.385	
36 S	-0.823	1.347	1.540	1.571	1.804	-0.823	1.549	1.281	0.982	1.804	
37 G	-0.966	1.129	1.489	1.207	2.103	-0.966	2.032	1.856	0.887	2.103	
38 I	-0.982	1.230	1.356	1.393	1.674	-0.982	1.558	1.231	-0.123	1.674	
39 S	-1.032	0.873	1.470	2.293	1.571	-1.032	1.458	0.649	0.042	2.293	
40 K	-1.276	0.921	1.325	1.928	1.851	-1.276	1.777	1.253	-0.119	1.928	
41 A	-1.490	0.963	1.457	0.594	2.188	-1.490	2.187	1.853	-0.146	2.188	
42 Q	-1.553	0.949	2.292	1.169	2.524	-1.553	2.360	1.871	-0.427	2.524	
43 R	-1.760	1.177	1.249	1.491	2.393	-1.760	2.224	1.876	-0.564	2.393	
44 E	-1.719	0.987	1.382	0.473	2.272	-1.719	1.950	1.881	-0.655	2.272	
45 T	-1.791	0.798	1.514	-0.605	2.702	-1.791	2.424	2.506	0.354	2.702	
46 W	-2.022	1.015	0.553	-0.737	2.290	-2.022	2.060	2.469	0.625	2.469	
47 E	-2.291	0.748	-0.344	0.341	1.879	-2.291	1.604	1.869	0.649	1.879	
48 R	-2.307	0.529	-0.705	-0.438	1.795	-2.307	1.513	1.289	0.895	1.795	
49 L	-2.215	0.292	-0.540	-0.625	1.926	-2.215	1.722	1.868	0.828	1.926	
50 W	-1.862	0.423	-0.490	-0.625	1.823	-1.862	1.713	1.849	1.240	1.849	
51 P	-1.657	0.521	-0.623	-0.326	1.487	-1.657	1.303	1.249	1.267	1.487	
52 E	-1.944	0.386	-1.470	-0.685	0.973	-1.696	0.838	0.630	1.703	1.703	
53 L	-1.944	-0.105	-1.470	-1.464	0.973	-1.944	0.838	0.630	1.703	1.703	
54 G	-2.152	0.042	-1.470	-0.705	-0.901	0.954	-2.152	0.820	0.605	0.671	0.954
55 L	-2.373	-0.101	-1.419	-1.037	0.627	-2.373	0.556	0.591	0.886	0.886	
56 L	-2.230	-0.310	-1.780	0.023	0.543	-2.230	0.465	0.010	1.132	1.132	
57 A	-1.898	-0.262	-0.819	0.586	0.954	-1.898	0.829	0.047	0.860	0.954	
58 L	0.080	-0.768	0.399	1.113	-1.185	1.030	0.068	1.020	1.399		

88 G	2.532	0.986	1.468	0.520	0.884	0.070	0.743	2.532
0.070	1.029							
89 T	1.540	0.245	1.234	0.411	0.738	0.055	1.019	1.540
0.055	0.749							
90 S	1.312	-0.246	1.244	0.273	0.784	0.055	0.008	1.312
-0.246	0.490							
91 T	0.636	-0.270	1.085	-0.448	0.674	0.052	-0.207	1.085
-0.448	0.217							
92 L	0.408	-0.761	1.094	-1.259	0.720	0.052	-1.217	1.094
-1.259	-0.138							
93 A	0.440	0.019	1.346	-2.074	1.203	0.627	-1.193	1.346
-2.074	0.053							
94 M	0.161	0.377	1.197	-2.546	1.048	0.607	-2.363	1.197
-2.546	-0.217							
95 A	0.326	0.582	1.328	-2.663	1.257	1.187	-2.430	1.328
-2.663	-0.059							
96 K	1.040	0.485	1.655	-2.361	1.522	1.200	-2.645	1.655
-2.645	0.128							
97 A	1.040	0.193	1.814	-1.633	1.695	1.820	-1.368	1.820
-1.633	0.509							
98 E	1.072	0.097	1.702	-0.724	1.640	1.804	-0.724	1.804
-0.724	0.695							
99 P	1.571	-0.803	1.973	0.397	1.959	2.293	0.277	2.293
-0.803	1.095							
100H	0.977	-1.162	1.403	0.950	1.312	1.700	0.801	1.700
-1.162	0.855							
101V	0.338	-1.348	1.262	0.821	1.294	1.702	2.133	2.133
-1.348	0.886							
102D	-0.022	-0.713	0.935	0.025	0.929	1.103	1.149	1.149
-0.713	0.487							
103V	-0.389	-1.348	0.571	-0.981	0.647	1.085	1.518	1.518
-1.348	0.158							
104I	0.111	-1.658	0.683	-1.632	0.793	0.954	1.242	1.242
-1.658	0.070							
105A	0.111	-0.520	0.683	-1.577	0.793	0.954	1.242	1.242
-1.577	0.241							
106V	-0.642	0.293	0.664	-1.189	0.711	0.485	1.583	1.583
-1.189	0.272							
107D	-0.142	1.016	1.216	-0.866	1.194	1.108	0.993	1.216
-0.866	0.646							
108V	0.629	0.273	1.786	-0.948	1.686	1.731	0.671	1.786
-0.948	0.832							
109Y	0.857	0.369	1.776	-1.480	1.640	1.731	1.681	1.776
-1.480	0.939							
110R	0.509	1.267	1.814	-1.957	1.658	1.734	1.527	1.814
-1.957	0.936							
111R	0.010	0.249	1.543	-2.339	1.339	1.245	0.526	1.543
-2.339	0.368							
112G	0.623	-0.769	1.991	-2.226	1.722	1.286	0.101	1.991
-2.226	0.390							
113L	0.161	-1.360	1.655	-2.093	1.494	1.272	0.203	1.655
-2.093	0.191							
114A	-0.686	-1.156	1.141	-1.908	1.030	0.653	0.639	1.141
-1.908	-0.041							
115Q	-0.863	-1.480	0.496	-1.663	0.465	0.046	1.262	1.262
-1.663	-0.248							
116L	-1.090	-1.432	0.505	-1.546	0.510	0.046	0.252	0.510
-1.546	-0.393							
117L	-1.015	-0.396	0.449	-1.467	0.483	0.043	0.139	0.483

147P	-0.439	0.938	1.001	0.093	0.948	0.510	0.734	1.001
-0.439	0.541							
148D	0.231	0.483	0.870	0.899	0.847	0.523	0.921	0.921
0.231	0.682							
149S	1.097	0.758	1.001	0.912	0.820	0.521	0.600	1.097
0.521	0.816							
150L	0.730	-0.194	0.879	0.394	0.811	0.523	2.199	2.199
-0.194	0.763							
151C	0.863	-0.164	1.066	-0.435	1.011	1.128	1.978	1.978
-0.435	0.778							
152G	-0.003	-0.374	0.674	-1.180	0.683	0.641	2.576	2.576
-1.180	0.431							
153V	-0.996	-0.643	0.459	-1.711	0.483	0.625	2.667	2.667
-1.711	0.126							
154R	-0.996	-0.007	0.477	-1.739	0.428	0.624	2.483	2.483
-1.739	0.181							
155V	-0.951	-0.462	0.935	-1.430	0.793	0.625	2.081	2.081
-1.430	0.227							
156F	-0.680	-0.869	1.216	-0.600	1.157	1.114	2.072	2.072
-0.869	0.487							
157F	-0.313	-0.336	1.580	0.291	1.440	1.131	1.703	1.703
-0.336	0.785							
158P	-1.211	0.670	1.169	0.858	0.984	0.532	1.726	1.726
-1.211	0.675							
159D	-0.844	0.311	1.533	1.036	1.267	0.549	1.357	1.533
-0.844	0.744							
160P	0.098	0.586	2.047	0.556	1.950	1.140	1.171	2.047
0.098	1.078							
161W	0.813	0.317	2.113	-0.139	1.996	1.136	-0.090	2.113
-0.139	0.878							
162P	0.945	0.910	2.300	-0.943	2.196	1.741	-0.311	2.300
-0.943	0.977							
163K	0.446	1.383	2.188	-1.189	2.050	1.872	-0.035	2.188
-1.189	0.959							
164A	0.446	1.365	2.103	-0.762	1.950	2.473	0.013	2.473
-0.762	1.084							
165R	1.438	2.178	2.533	0.205	2.570	3.042	0.056	3.042
0.056	1.718							
166H	1.571	1.161	2.720	0.926	2.770	3.648	-0.165	3.648
-0.165	1.804							
167H	1.476	0.866	2.702	0.880	2.606	3.678	-0.231	3.678
-0.231	1.711							
168K	0.762	1.267	2.617	-0.151	2.615	3.684	1.214	3.684
-0.151	1.715							
169R	-0.085	0.794	2.103	-1.408	2.151	3.064	1.650	3.064
-1.408	1.181							
170R	0.161	-0.019	2.272	-2.233	2.351	2.487	1.546	2.487
-2.233	0.938							
171L	0.161	-0.342	2.356	-2.259	2.451	1.886	1.498	2.451
-2.259	0.822							
172L	-0.066	-0.252	1.907	-1.710	1.813	1.291	0.423	1.907
-1.710	0.487							
173Q	-0.003	-0.048	1.674	-1.071	1.494	0.687	0.465	1.674
-1.071	0.457							
174P	-0.534	-0.743	1.234	-0.841	1.066	0.079	0.410	1.234
-0.841	0.096							
175A	0.180	-1.426	1.318	-0.960	1.057	0.074	-1.035	1.318
-1.426	-0.113							
176T	0.180	-1.426	1.318	-1.436	1.057	0.074	-1.035	1.318

206A	0.939	0.826	0.767	-1.484	0.455	0.461	-3.546	0.939
-3.546	-0.226							
207G	1.938	1.639	1.234	-0.903	0.838	1.058	-3.894	1.938
-3.894	0.273							
208D	1.938	0.808	1.477	-0.579	1.112	1.077	-2.664	1.938
-2.664	0.453							
209A	2.071	0.173	1.907	-0.664	1.586	1.702	-1.654	2.071
-1.654	0.731							
210E	1.356	0.986	1.823	-0.988	1.595	1.707	-0.209	1.823
-0.988	0.896							
211P	0.762	0.315	1.711	-1.372	1.631	1.709	0.379	1.711
-1.372	0.734							
212R	0.395	0.495	1.870	-1.875	1.786	1.845	0.387	1.870
-1.875	0.700							
213L	0.029	0.041	1.748	-2.194	1.777	1.846	1.986	1.986
-2.194	0.748							
214V	0.168	0.784	1.692	-2.081	1.731	1.736	2.003	2.003
-2.081	0.862							
215R	0.168	1.371	1.692	-1.652	1.731	1.736	2.003	2.003
-1.652	1.007							
216V	0.534	1.133	1.533	-0.544	1.576	1.600	1.995	1.995
-0.544	1.118							
217D	1.445	1.024	1.814	0.524	1.722	1.614	1.601	1.814
0.524	1.392							
218P	2.172	0.281	2.262	1.141	2.096	2.212	0.986	2.262
0.281	1.593							
219D	1.325	0.281	1.748	0.946	1.631	1.593	1.422	1.748
0.281	1.278							
220T	0.977	-0.583	1.786	0.116	1.649	1.597	1.268	1.786
-0.583	0.973							
221E	0.477	-0.218	1.758	-0.871	1.604	1.127	1.497	1.758
-0.871	0.768							
222L	-0.161	-0.889	1.375	-1.551	1.312	1.110	1.599	1.599
-1.551	0.399							
223L	-0.382	-0.781	1.253	-1.548	1.148	0.641	1.768	1.768
-1.548	0.300							
224P	-0.945	0.237	0.935	-1.329	0.984	0.623	2.316	2.316
-1.329	0.403							
225I	-1.672	0.237	0.487	-0.986	0.610	0.025	2.931	2.931
-1.672	0.233							
226S	-0.825	0.562	1.001	-1.055	1.075	0.644	2.495	2.495
-1.055	0.557							
227V	-0.111	0.197	1.328	-1.139	1.339	0.657	2.280	2.280
-1.139	0.650							
228V	-0.111	1.125	1.085	-1.489	1.066	0.638	1.050	1.125
-1.489	0.481							
229R	0.724	0.814	1.421	-1.316	1.239	0.657	0.769	1.421
-1.316	0.615							
230P	0.673	0.576	1.720	-1.311	1.722	1.231	0.674	1.722
-1.311	0.755							
231A	0.787	1.030	2.094	-1.104	1.968	1.249	0.417	2.094
-1.104	0.920							
232T	1.514	1.862	2.543	-1.244	2.342	1.847	-0.198	2.543
-1.244	1.238							
233K	1.514	1.371	2.543	-1.474	2.342	1.847	-0.198	2.543
-1.474	1.135							
234Y	1.742	1.030	2.748	-1.916	2.707	2.423	-0.353	2.748
-1.916	1.197							
235E	1.742	1.233	2.748	-2.179	2.707	2.423	-0.353	2.748

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 MVHHGQMHAQPGVGLRPDTPVASGQLPSTSIRSRRSGISKA <u>QRETWERLWPELGLLALPQS</u> PRGTPVDTRAFFGRDAPVVLEIGSGSGTSTLAMAKAEPHVDVIAVDVYRRGLAQLLCIADK VGSDGINIRLILGNAVDVLQHLIAPDSL CGVRVFFPDPWP KARHHKRRLLQPATMALIADRL VPSGV L HAA <u>TDHPGYAEHIAAAGDAEPR</u> L V RVDPDTELLPISVVRPATKYERKAQLGGGAVI ELLWKKHGCSERDLKIR ²⁶³
Hydrophobicity	¹ MVHHGQMHAQPGVGLRPDTPVASGQLPSTSIRSRRSGIS <u>SKAQRETWERLWPELGLLALPQS</u> <u>PRGTP</u> VDTRAFFGRDAPVVLE <u>IGSGSGT</u> STLAMAKAEPHVDVIAVDVYRRGLAQLLCIADK VGSDGINIRLILGNAVDVLQHLIAPDSL CGVRVFFPDPWP <u>PKARHHK</u> RRLQPATMALIADRL VPSGV L HAA <u>TDHPGYAEHI</u> <u>AAAGDAEPR</u> L <u>V</u> RVDPDTELLPISVVRPATKYERKAQLGGGAVI ELLW <u>KKHGCSERD</u> LKIR ²⁶³
Flexibility	¹ MVHHGQMHAQPGVGLRPDTPVASG <u>QLPSTSIRSRRSGISKAQ</u> RETWERLWPELGLLALPQS PRGTPVDTRAFFGRDAPVV <u>LEIGSGSGT</u> STLAMAKAEPHVDVIAVDVYRRGLAQLLCIADK VGSDGINIRLILGNAVDVLQHLIAPDSL CGVRVFFPDPWP <u>PKARHHK</u> RRLQPATMALIADRL VPSGV L HAA <u>TDHPGYAEHIAAAGDAEPR</u> L V RVDPDTELLPISVVRPATKYERKAQLGGGAVI ELLW <u>KKHGCSERD</u> LKIR ²⁶³
Accessibility	¹ MVHHGQMHAQPGV <u>GLRPDTPVA</u> SGQLPSTSIRSRRSGISKA <u>QRETWERLWPELGLLALPQS</u> PRGTPVDTRAFFGRDAPVVLEIGSGSGTSTLAMAKAEPHVDVIAVDVY <u>RRGLAQL</u> LLCAIDK VGSDGINIRLILGNAVDVLQHLIAPDSL CGVRVFFPDPWP <u>KARHHKRRLLQPA</u> TMALIADRL VPSGV L HAA <u>TDHPGYAEHIAAAGDAEPR</u> L <u>V</u> RVDPDTELLPISV <u>VRPATKYERKAQLG</u> GGAVI ELLW <u>KKHGCSERD</u> LKIR ²⁶³
Turns	¹ MVHHGQMHAQPGVGLRPDTPVASGQLPSTSIRSRRSGISKA <u>QRETWERLWPELGLLALPQS</u> PRGTPVDTRAFFGRDAPVVLEIGSGSGTSTLAMAKAEPHVDVIAVDVYRRGLAQLLCIADK VGSDGINIRLILGNAVDVLQHLIAPDSL CGVRVFFPDPWP KARHHKRRLLQPATMALIADRL VPSGV L HAA <u>TDHPGYAEHIAAAGDAEPR</u> L V RVDPDTELLPISVVRPATKYERKAQLGGGAVI ELLWKKHGCSERDLKIR ²⁶³
Exposed Surface	¹ MVHHGQMHAQPGVGLRPDTPVASGQLPSTSIRSRRSGIS <u>SKAQRETWERLWPELGLLALPQS</u> PRGTPVDTRAFFGRDAPVVLEIGSGSGTSTLAMAKAEPHVDVIAVDVYRRGLAQLLCIADK

	VGSDGINIRLILGNAVDVLQHLIAPDSLCGVRVFFPDPW <u>PKARHHKRRLLQP</u> ATMALIADRL VPSGVLAATDHPGYAEHIAAAGDAEPRLVRVDPDTTELLPISVV <u>RPATKYERKAQ</u> LGGA ELLWKKHGCS <u>ERDLKIR</u> ²⁶³
Polarity	¹ <u>MVHHGQMHAQPGVGLRPDTPVASQLPSTSIRSRRSGISKAQRETWERLWPEL</u> GLLALPQS PRGTPVDTRAFFGRDAPVVLEIGSGSGTSTLA <u>MAKAEPHV</u> DVIAVDVYRRGLAQLLCAIDK VGSDGINIRLILGNAVDVLQHLIAPDSLCGVRVFFPD <u>PWPKARHHKRRLLQP</u> ATMALIADRL VPSGVLAATD <u>HPGYAEHIAAAGD</u> AEPRLVRVDPDTTELLPISVV <u>RPATKYERKAQ</u> LG ELLWKKHGCS <u>ERDLKIR</u> ²⁶³
Antigenic Propensity	¹ <u>MVHHGQMHAQPGVGLRPDTPVASQLPSTSIRSRRSGISKAQRETWERLWPEL</u> GLLALPQS PRGTPVDTRAFFGRDAP <u>PVVLEIGS</u> GSGTSTLA <u>MAKAEPHV</u> DVIAVDVYRRGLAQLLCAIDK VGSDG <u>INIRLIL</u> GNA <u>VDVLQHLIAPDSLCGVRVFFPD</u> PWPKARHHKRRLLQPATMALIAD <u>RL</u> <u>VPSGVLAATDHPGYAEHIAAAGDA</u> EPRLVRVDPDTTELLPISVV <u>RPATKYERKAQ</u> LG <u>ELLWK</u> HGCS <u>ERDLKIR</u> ²⁶³

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