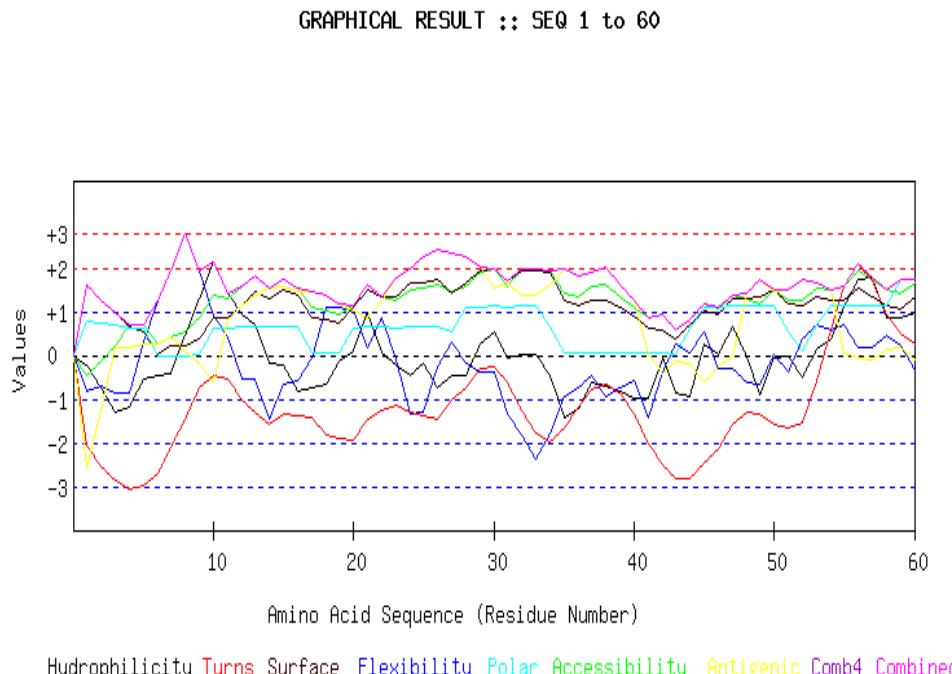


The server displays 1.[GRAPHICAL RESULT](#) 2.[TABULAR RESULT](#) 3.[Overlap Display](#)

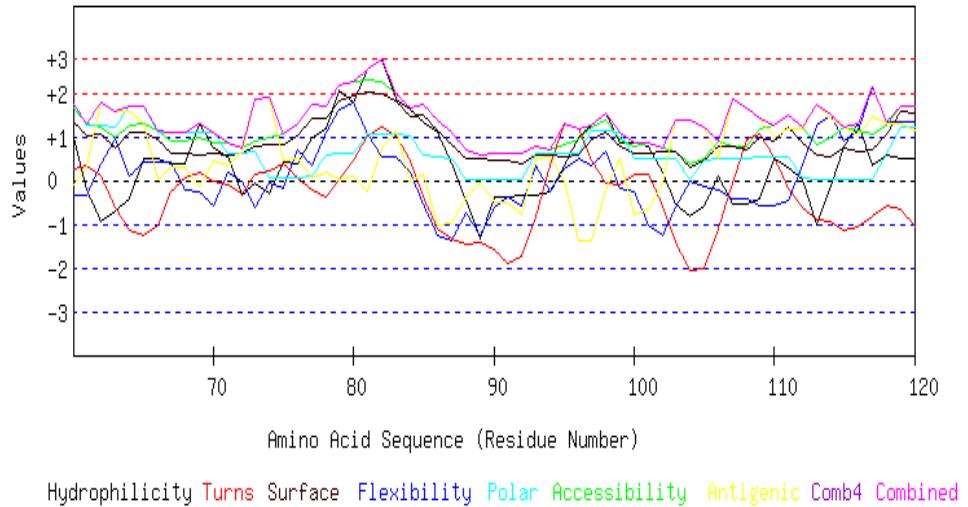
seqname=
Seq=MRGIILAGGSGTRLYPITMGISKQLPVYDKPMIYYPLTLMAGIRDIQLITTPHDAPG
FHRLLGDAHLGVNISYATQDQPDGLAQAFVIGANHIGADSVALVLGDNIFYGPGLGTSLKRFQ
SISGGAIFAYWVANPSAYGVVEFGAEGMALSLEEKPVTPKSNYAVPGLYFYDNDVIEIARGLKK
SARGEYEITEVNQVYLNQGRLLAVEVLARGTAWLDGTDFDSLLDAADFVRTLERRQGLKVSIE
EVAWRMGWIDDEQLVQRARALVKSGYGNYLLELLERN

Length=288

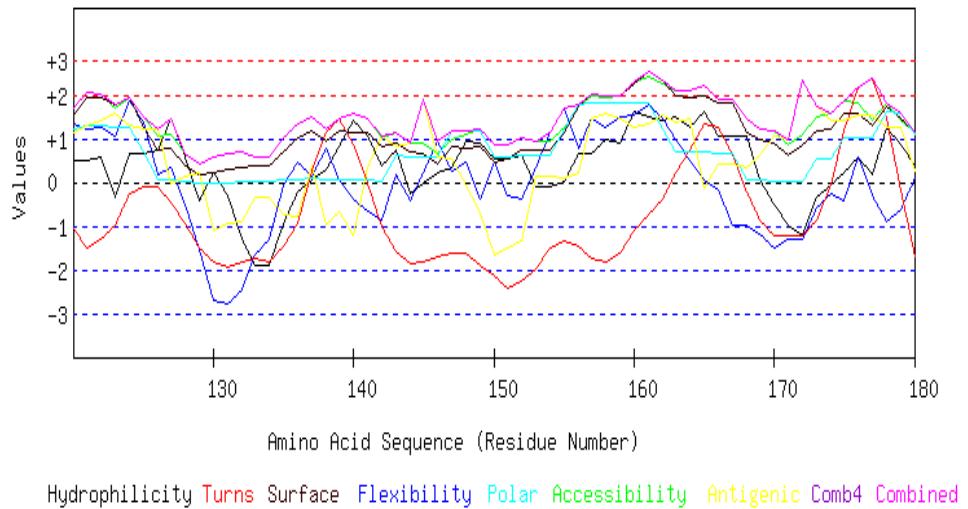
GRAPHICAL RESULT



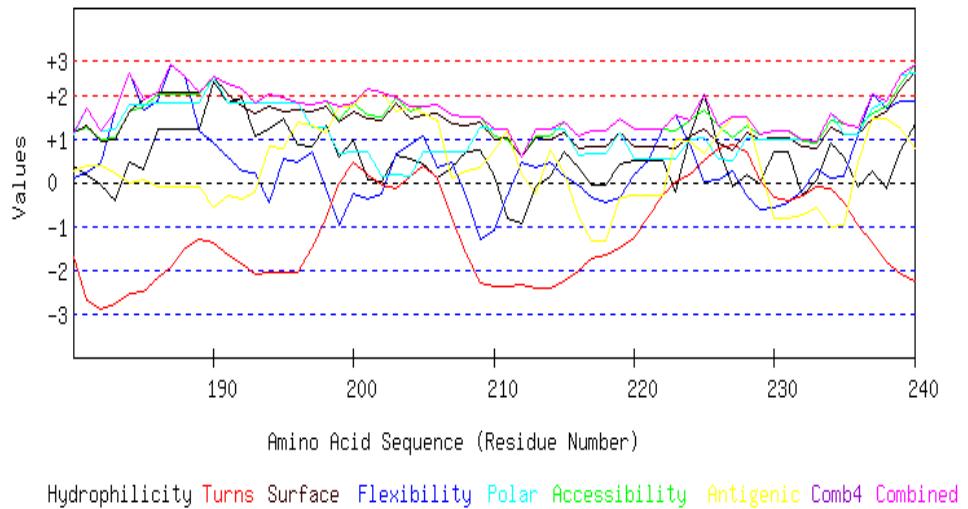
GRAPHICAL RESULT :: SEQ 61 to 120



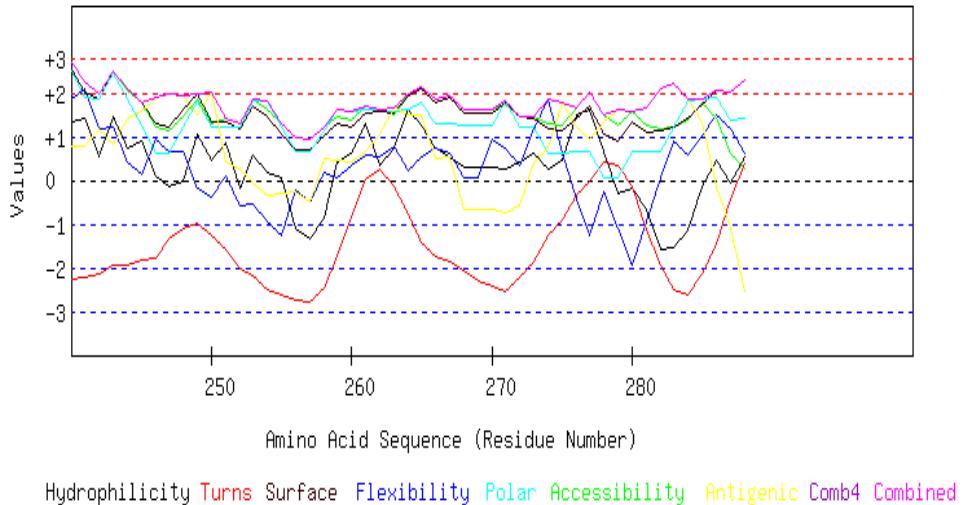
GRAPHICAL RESULT :: SEQ 121 to 180



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

MRGIIILAGGS GTRLYPITMGISKQLLPVYDKPMIYYPLTTLMMAGIRDIQ LITT PHDAPG
FHRLLG DGAHLGVNIS YATQD QPDGLA QAFVIGANHIGAD SV ALVLGD NIFYGP GLGTSL
KRFQSISGGAI FAYW VANPSA YGVVEFGAEGM ALSLEEKPVTPKS NYAVPG LYFYDNDVI
EIARGLKKSARGEYEITEVNQVYLNQGR LAVEV LARGTA WLD TGT FDSLLDAADF VRTLE
RRQGLKVSIP EEEVAWR MGWIDDEQLVQRARALVKSGYGN YLLELLERN

Length=288

A.A.

Parameter
Combined

Hydro	Flexi	Access	Turns	Surface	Polar	AntiPro	MAX
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29 Y	0.244	-0.390	1.898	-0.286	1.941	1.118	2.034	2.034
-0.390	0.937							
30 D	0.560	-0.390	1.973	-0.246	1.977	1.129	1.543	1.977
-0.390	0.935							
31 K	-0.079	-1.336	1.589	-0.629	1.686	1.112	1.645	1.686
-1.336	0.570							
32 P	0.035	-1.809	1.963	-1.241	1.932	1.130	1.388	1.963
-1.809	0.486							
33 M	0.035	-2.372	1.963	-1.781	1.932	1.130	1.388	1.963
-2.372	0.328							
34 I	-0.465	-1.767	1.935	-1.980	1.886	0.660	1.617	1.935
-1.980	0.270							
35 Y	-1.407	-0.951	1.403	-1.645	1.257	0.071	1.987	1.987
-1.645	0.102							
36 Y	-1.211	-0.749	1.356	-1.190	1.139	0.072	1.808	1.808
-1.211	0.175							
37 P	-0.616	-0.456	1.561	-0.779	1.248	0.075	1.904	1.904
-0.779	0.420							
38 L	-0.692	-0.929	1.617	-0.643	1.276	0.078	2.017	2.017
-0.929	0.389							
39 T	-0.838	-0.725	1.356	-0.876	1.084	0.076	1.630	1.630
-0.876	0.244							
40 T	-0.983	-0.589	1.094	-1.339	0.893	0.074	1.243	1.243
-1.339	0.056							
41 L	-0.983	-1.404	0.851	-2.030	0.619	0.055	0.013	0.851
-2.030	-0.411							
42 M	-0.041	-0.386	0.926	-2.514	0.565	0.049	-0.422	0.926
-2.514	-0.260							
43 M	-0.876	0.267	0.589	-2.818	0.392	0.031	-0.141	0.589
-2.818	-0.365							
44 A	-0.939	0.057	0.823	-2.836	0.711	0.636	-0.183	0.823
-2.836	-0.247							
45 G	0.275	0.548	1.178	-2.449	1.020	1.120	-0.627	1.178
-2.449	0.152							
46 I	0.035	-0.284	1.047	-2.131	0.957	1.104	-0.250	1.104
-2.131	0.068							
47 R	0.680	-0.284	1.384	-1.578	1.285	1.129	-0.031	1.384
-1.578	0.369							
48 D	-0.035	-0.607	1.300	-1.298	1.294	1.135	1.414	1.414
-1.298	0.458							
49 I	-0.901	-0.655	1.169	-1.328	1.321	1.137	1.735	1.735
-1.328	0.354							
50 Q	-0.066	0.029	1.505	-1.567	1.494	1.155	1.454	1.505
-1.567	0.572							
51 L	-0.003	-0.372	1.272	-1.680	1.175	0.550	1.496	1.496
-1.680	0.348							
52 I	-0.503	0.371	1.244	-1.544	1.130	0.080	1.725	1.725
-1.544	0.358							
53 T	0.136	0.696	1.543	-0.570	1.321	0.698	1.671	1.671
-0.570	0.785							
54 T	0.389	0.564	1.487	0.583	1.267	1.145	1.498	1.498
0.389	0.990							
55 P	1.103	0.700	1.571	1.564	1.257	1.139	0.053	1.571
0.053	1.055							
56 H	1.742	0.167	1.954	2.090	1.549	1.156	-0.049	2.090
-0.049	1.230							
57 D	1.774	0.167	1.748	1.690	1.349	1.137	-0.089	1.774
-0.089	1.111							
58 A	0.863	0.441	1.487	0.939	1.148	1.121	0.121	1.487

88 Q	-0.471	-0.751	0.692	-1.446	0.483	0.023	-0.400	0.692
-1.446	-0.267							
89 A	-1.337	-1.242	0.561	-1.414	0.510	0.025	-0.079	0.561
-1.414	-0.425							
90 F	-0.395	-0.633	0.636	-1.579	0.455	0.020	-0.513	0.636
-1.579	-0.287							
91 V	-0.395	-0.368	0.636	-1.897	0.455	0.020	-0.513	0.636
-1.897	-0.295							
92 I	-0.332	-0.597	0.608	-1.736	0.392	0.018	-0.790	0.608
-1.736	-0.348							
93 G	-0.332	0.355	0.767	-0.820	0.565	0.638	0.488	0.767
-0.820	0.237							
94 A	-0.256	-0.272	0.692	0.352	0.592	0.635	0.558	0.692
-0.272	0.329							
95 N	0.338	0.267	0.804	1.287	0.556	0.634	-0.030	1.287
-0.030	0.551							
96 H	0.977	0.513	0.945	1.200	0.574	0.632	-1.362	1.200
-1.362	0.497							
97 I	1.249	0.327	1.225	0.464	0.938	1.121	-1.371	1.249
-1.371	0.565							
98 G	1.527	0.652	1.375	-0.065	1.093	1.141	-0.201	1.527
-0.201	0.789							
99 A	0.850	-0.180	0.954	-0.109	0.774	1.102	0.501	1.102
-0.180	0.556							
100D	0.850	-0.276	0.795	0.135	0.601	0.482	-0.777	0.850
-0.777	0.259							
101S	0.775	-1.019	0.851	0.134	0.629	0.486	-0.664	0.851
-1.019	0.170							
102V	0.180	-1.248	0.739	-0.580	0.665	0.487	-0.075	0.739
-1.248	0.024							
103A	-0.534	-0.613	0.655	-1.439	0.674	0.493	1.370	1.370
-1.439	0.087							
104L	-0.806	-0.003	0.375	-2.077	0.310	0.004	1.379	1.379
-2.077	-0.117							
105V	-0.585	-0.124	0.496	-2.025	0.474	0.473	1.210	1.210
-2.025	-0.012							
106L	0.092	-0.202	0.917	-1.108	0.793	0.512	0.509	0.917
-1.108	0.216							
107G	-0.547	-0.404	0.776	-0.075	0.774	0.514	1.840	1.840
-0.547	0.411							
108D	-0.547	-0.404	0.795	0.927	0.720	0.512	1.657	1.657
-0.547	0.523							
109N	-0.433	-0.585	1.169	1.077	0.966	0.530	1.400	1.400
-0.585	0.589							
110I	0.509	-0.566	1.244	0.544	0.911	0.525	0.965	1.244
-0.566	0.590							
111F	0.281	-0.446	1.496	-0.161	1.230	0.544	1.185	1.496
-0.446	0.590							
112Y	0.010	0.355	1.216	-0.626	0.866	0.055	1.194	1.216
-0.626	0.438							
113G	-1.015	1.253	0.832	-0.905	0.565	0.020	1.742	1.742
-1.015	0.356							
114P	-0.148	1.481	0.963	-0.924	0.537	0.018	1.421	1.481
-0.924	0.478							
115G	0.762	0.918	1.225	-1.131	0.738	0.034	1.210	1.225
-1.131	0.537							
116L	1.293	1.123	1.122	-1.077	0.656	0.034	1.038	1.293
-1.077	0.598							
117G	0.351	2.140	1.047	-0.833	0.711	0.040	1.473	2.140

147F	0.351	0.267	0.982	-1.610	0.820	1.176	0.548	1.176
-1.610	0.362							
148G	0.945	0.441	1.094	-1.619	0.784	1.175	-0.040	1.175
-1.619	0.397							
149A	0.914	-0.390	1.206	-1.882	0.838	1.190	-0.684	1.206
-1.882	0.170							
150E	0.553	0.465	0.879	-2.123	0.474	0.591	-1.668	0.879
-2.123	-0.118							
151G	0.553	-0.314	0.860	-2.415	0.528	0.592	-1.484	0.860
-2.415	-0.240							
152M	0.604	-0.366	1.019	-2.257	0.729	0.612	-1.325	1.019
-2.257	-0.141							
153A	-0.111	0.323	0.935	-1.988	0.738	0.617	0.120	0.935
-1.988	0.091							
154L	-0.111	1.155	0.935	-1.512	0.738	0.617	0.120	1.155
-1.512	0.278							
155S	0.022	1.718	1.272	-1.342	1.148	1.217	0.094	1.718
-1.342	0.590							
156L	0.648	0.766	1.730	-1.464	1.741	1.794	0.214	1.794
-1.464	0.775							
157E	0.648	1.461	1.973	-1.735	2.014	1.813	1.444	2.014
-1.735	1.088							
158E	0.996	1.245	1.935	-1.827	1.996	1.810	1.598	1.996
-1.827	1.107							
159K	0.914	1.501	1.982	-1.634	1.996	1.809	1.479	1.996
-1.634	1.150							
160P	1.628	1.525	2.309	-1.108	2.260	1.823	1.264	2.309
-1.108	1.386							
161V	1.495	1.776	2.431	-0.738	2.533	1.818	1.355	2.533
-0.738	1.524							
162T	1.413	1.465	2.253	-0.376	2.324	1.239	1.541	2.324
-0.376	1.408							
163P	1.495	0.974	2.103	0.213	1.996	0.685	1.363	2.103
0.213	1.261							
164K	1.242	0.519	2.113	0.754	1.959	0.685	1.475	2.113
0.519	1.250							
165S	1.609	0.047	2.234	1.321	1.968	0.683	-0.124	2.234
-0.124	1.106							
166N	1.046	-0.182	1.917	1.247	1.804	0.665	0.424	1.917
-0.182	0.989							
167Y	1.046	-0.995	1.917	0.612	1.804	0.665	0.424	1.917
-0.995	0.782							
168A	1.046	-0.995	1.459	-0.227	1.121	0.070	0.360	1.459
-0.995	0.405							
169V	0.054	-1.170	1.225	-0.865	0.975	0.056	0.635	1.225
-1.170	0.130							
170P	-0.509	-1.480	1.178	-1.221	0.902	0.034	1.080	1.178
-1.480	-0.002							
171G	-0.970	-1.300	0.860	-1.211	0.619	0.019	0.999	0.999
-1.300	-0.140							
172L	-1.223	-1.318	1.113	-1.216	0.856	0.039	2.341	2.341
-1.318	0.085							
173Y	-0.357	-0.574	1.505	-0.849	1.185	0.526	1.743	1.743
-0.849	0.454							
174F	-0.047	-0.264	1.561	-0.051	1.221	0.548	1.410	1.561
-0.264	0.626							
175Y	0.225	-0.414	1.842	1.169	1.586	1.037	1.401	1.842
-0.414	0.978							
176D	0.572	0.568	1.804	2.184	1.567	1.033	1.555	2.184

206Q	0.085	0.085	0.357	1.776	0.110	1.567	0.708	1.434	1.776
0.085	0.863	0.863	0.338	0.441	1.524	-0.826	1.330	0.688	0.091
207G	-0.826	0.513	0.686	-0.282	1.487	-1.636	1.312	0.684	0.245
-1.636	0.357	0.357	0.737	-1.300	1.515	-2.301	1.367	1.243	1.487
209L	-2.301	0.228	0.123	-1.095	1.066	-2.394	0.984	1.203	0.757
-2.394	0.092	0.092	-0.819	-0.282	0.991	-2.387	1.039	1.208	1.208
211V	-2.387	0.135	-0.951	0.441	0.561	-2.357	0.565	0.583	0.183
-2.357	-0.139	-0.139	-0.104	0.357	1.075	-2.403	1.030	1.203	0.583
213V	-2.403	0.129	0.123	0.453	1.066	-2.409	0.984	1.203	1.203
-2.409	0.311	0.311	0.686	0.155	1.384	-2.266	1.148	1.221	0.209
215A	-2.266	0.363	0.326	-0.050	1.057	-2.022	0.784	0.621	0.057
-2.022	-0.008	-0.008	-0.073	-0.324	1.197	-1.751	0.811	0.645	-1.341
217G	-1.751	-0.119	-0.073	-0.460	1.197	-1.646	0.811	0.645	-1.197
-1.646	-0.124	-0.124	0.427	-0.324	1.468	-1.484	1.130	1.134	-0.340
219A	-1.484	0.287	0.490	0.167	1.234	-1.247	0.811	0.529	-0.298
220W	-1.247	0.241	0.490	0.495	1.234	-0.764	0.811	0.529	-0.298
221L	-0.764	0.357	0.490	1.239	1.234	-0.283	0.811	0.529	-0.298
222D	-0.298	0.532	-0.224	1.555	1.169	0.012	0.765	0.533	1.239
223T	-0.224	0.682	1.040	0.860	1.421	0.179	1.066	0.997	0.963
224G	0.179	0.928	2.033	0.029	1.655	0.514	1.212	1.012	0.435
225T	0.029	1.016	0.819	0.077	1.300	0.773	0.902	0.528	2.033
226F	0.077	0.786	-0.092	0.251	1.019	0.867	0.756	0.514	1.300
227D	-0.092	0.687	0.180	-0.288	1.300	0.690	1.121	1.495	1.495
-0.288	0.785	-0.016	-0.605	1.103	0.074	0.966	0.983	1.486	1.103
229L	-0.605	0.420	-0.294	-0.654	1.169	-0.351	1.011	0.979	1.169
-0.827	0.301	0.305	0.170	-0.192	0.954	-0.318	0.811	0.963	-0.827
231D	-0.827	0.305	0.054	0.299	0.917	-0.119	0.793	0.959	-0.735
-0.735	0.332	0.332	0.901	0.095	1.431	-0.129	1.257	0.581	0.959
233A	-0.581	0.588	0.598	0.131	1.356	-0.467	1.093	1.109	1.578
-1.017	0.598	0.598	0.598	0.131	1.356	-0.467	1.093	-0.968	1.356

265L	1.255	0.544	2.122	-1.403	2.105	1.775	1.496	2.122
-1.403	1.128							
266V	0.756	0.748	1.851	-1.728	1.786	1.286	0.495	1.851
-1.728	0.742							
267Q	0.528	0.640	1.954	-1.850	1.895	1.311	0.520	1.954
-1.850	0.714							
268R	0.281	0.053	1.627	-2.071	1.522	1.269	-0.653	1.627
-2.071	0.290							
269A	0.281	0.071	1.627	-2.291	1.522	1.269	-0.653	1.627
-2.291	0.261							
270R	0.281	0.926	1.627	-2.414	1.522	1.269	-0.653	1.627
-2.414	0.365							
271A	0.263	0.740	1.748	-2.527	1.786	1.821	-0.751	1.821
-2.527	0.440							
272L	0.408	0.333	1.468	-2.209	1.467	1.216	-0.591	1.468
-2.209	0.299							
273V	0.636	1.165	1.459	-1.846	1.422	1.216	0.420	1.459
-1.846	0.639							
274K	0.250	1.870	1.281	-1.253	1.185	0.611	0.753	1.870
-1.253	0.671							
275S	0.477	0.632	1.272	-0.881	1.139	0.611	1.763	1.763
-0.881	0.716							
276G	1.502	-0.428	1.655	-0.329	1.440	0.646	1.215	1.655
-0.428	0.814							
277Y	1.616	-1.260	2.029	-0.014	1.686	0.664	0.958	2.029
-1.260	0.811							
278G	0.673	-0.278	1.496	0.435	1.057	0.075	1.328	1.496
-0.278	0.684							
279N	-0.319	-1.109	1.262	0.339	0.911	0.060	1.603	1.603
-1.109	0.392							
280Y	-0.186	-1.923	1.599	-0.150	1.321	0.660	1.577	1.599
-1.923	0.414							
281L	-0.648	-0.941	1.262	-1.144	1.093	0.646	1.680	1.680
-1.144	0.278							
282L	-1.590	0.077	1.188	-1.923	1.148	0.651	2.114	2.114
-1.923	0.238							
283E	-1.539	0.890	1.216	-2.509	1.203	1.210	2.201	2.201
-2.509	0.382							
284L	-1.154	0.570	1.393	-2.609	1.440	1.815	1.868	1.868
-2.609	0.475							
285L	-0.129	1.028	1.776	-2.133	1.741	1.850	1.320	1.850
-2.133	0.779							
286E	0.452	1.487	1.403	-1.445	2.050	1.905	-0.125	2.050
-1.445	0.818							
287R	-0.041	1.167	0.618	-0.402	2.005	1.366	-1.109	2.005
-1.109	0.515							
288N	0.541	0.608	0.244	0.365	2.315	1.420	-2.554	2.315
-2.554	0.420							

[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 MRIIILAGGSCTRYPITMGISKQLLPVYDKPMIYYPLTTLMMAGIRDIQLITTPHD APGFHRLLDGAHLGVNISYATQDQPDGLAQAFVIGANHIGADSVALVLGDNIFYG PGLGTSKRFQSISGGAIWVANPSAYGVVEFGAEGMALSLEEKPVTPKSNYAV PGLYFYDNDVIEIARGLKKSARGEYEITEVNQVYLNQGRLAVEVLARGTAWLDTG TFDSLLDAADFVRTLERRQGLKVSIPPEVAWRMGWIDDEQLVQRARALVKSGYGN YLLELLERN ²⁸⁸
Hydrophobicity	¹ MRIIIL <u>AGGSCTR</u> YPITMGISKQLLPVYDKPMIYYPLTTLMMAGIRDIQLITTPHD APGFHRLLDGAHLGVNISYAT <u>QDQPDGL</u> AQAFVIGANHIGADSVALVLGDNIFYG PGLGTSKRFQSISGGAIWVANPSAYGVVEFGAEGMALSLEEKPVTPKSNYAV PGLYFYDNDVIEIARGL <u>KKSARGEYE</u> ITEVNQVYLNQGRLAVEVLARGTAWL <u>DTG</u> <u>TFDS</u> LLDAADFVRTLERRQGLKVSIPPEVAWRMGWIDDEQLVQRARALVKSGYGN YLLELLERN ²⁸⁸
Flexibility	¹ MRII <u>LAGGSCTR</u> YPITMGISKQLLPVYDKPMIYYPLTTLMMAGIRDIQLITTPHD APGFHRLLDGAHLGVNISYATQDQPDGLAQAFVIGANHIGADSVALVLGDNIFYG <u>PGLGTSK</u> RKFQSISGGAIWVANPSAYGVVEFGAEGMALSLEEKPVTPKSNYAV PGLYFYDNDVIEI <u>ARGLKKSAR</u> GEYEITEVNQVYLNQGRLAVEVLARGTAWLDTG TFDSLLDAAD <u>DFVRTLERRQGLK</u> VSIPEEVAWRMGWIDDEQLVQRARALVKSGYGN YLLELLERN ²⁸⁸
Accessibility	¹ MRIIILAGGSCTRYPITMGISKQLLPVY <u>DKPMIYYPLTTLMMAGIRDIQLITTPHD</u> APGFHRLLDGAHLGVNISYAT <u>QDQPDGL</u> AQAFVIGANHIGADSVALVLGDNIFYG PGLG <u>TSLKRFQSISGGAIWVANPSAYGVVEFGAEGMALSLEEKPVTPKSNYAV</u> PGLYFYDNDVIEI <u>ARGLKKSARGEYEITEVNQVYLNQ</u> GRLAVEVLARGTAWLDTG TFDSLLDAADF <u>VRTLERRQGLK</u> VSIPEEVAWRMGWIDDEQLVQRARALVKSGYGN YLLELLERN ²⁸⁸
Turns	¹ MRIIILAGGSCTRYPITMGISKQLLPVYDKPMIYYPLTTLMMAGIRDIQLITTPHD APGFHRLLDGAHLGVNISYATQDQPDGLAQAFVIGANHIGADSVALVLGDNIFYG PGLGTSKRFQSISGGAIWVANPSAYGVVEFGAEGMALSLEEKPVTPKSNYAV PGLYFYDNDVIEIARGLKKSARGEYEITEVNQVYLNQGRLAVEVLARGTAWLDTG TFDSLLDAADFVRTLERRQGLKVSIPPEVAWRMGWIDDEQLVQRARALVKSGYGN YLLELLERN ²⁸⁸
Exposed Surface	¹ MRIIILAGGSCTRYPITMGISKQLLPVYDKPMIYYPLTTLMMAGIRDIQLITTPHD APGFHRLLDGAHLGVNISYATQDQPDGLAQAFVIGANHIGADSVALVLGDNIFYG PGLGTSKRFQSISGGAIWVANPSAYGVVEFGAEGMALS <u>EKPVTPKS</u> NYAV PGLYFYDNDVIEIARGL <u>KKSARGEYEITEVNQVYLNQ</u> GRLAVEVLARGTAWLDTG

	TFDSLDAADFVRTLERRQGLKVSIEEVAWRMGWIDDEQLVQRARALVKSGYGN YLLELLERN ²⁸⁸
Polarity	¹ MRGIILAGGSGTRLYPITMGISKQLLPVYDKPMIYYPLTLMAGIRDIQLITTPHD APGFHRLLDGAHLGVNISYATQDQPDGLAQAFVIGANHIGADSVALVLGDNIFYG PGLGTSLKRFQSISGGAIFAYWVANPSAYGVVEFGAEGMALSLEEKPVTPKSNYAV PGLYFYDNDVIEI <u>ARGLKK</u> SARGEYEITEV <u>NQVYLN</u> QGRALAVEVLARGTAWLDTG TFDSLDAAD <u>FVRTLERRQGLK</u> VSIPEEVAWRMGWIDDEQLVQRARALVKSGYGN YLLELLERN ²⁸⁸
Antigenic Propensity	¹ MRGIILAGGSGTRLYPITMG <u>ISKQLLPVYDKPMIYYPLTL</u> MMAGIRDIQLITTPHD APGFHRLLDGAH <u>LGVNISY</u> ATQDQPDGLAQAFVIGANHIGADSVALVLGDNIFYG PGLGTSLKRFQSISGGAIFAYWVANPSA <u>YGVVEFGAEGMALSLEEKPVTPKSNYAV</u> <u>PGLYFY</u> DNDVIEIARGLKK <u>SARGEYEIT</u> <u>EVNQVYLN</u> QGRALAVEVLARGTAWLDTG TFDSLDAADFVRTLERR <u>QGLKVSIEEV</u> AWRMGWIDDEQLVQRARALVKSGYGN YLLELLERN ²⁸⁸

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