

BcePred Prediction Server

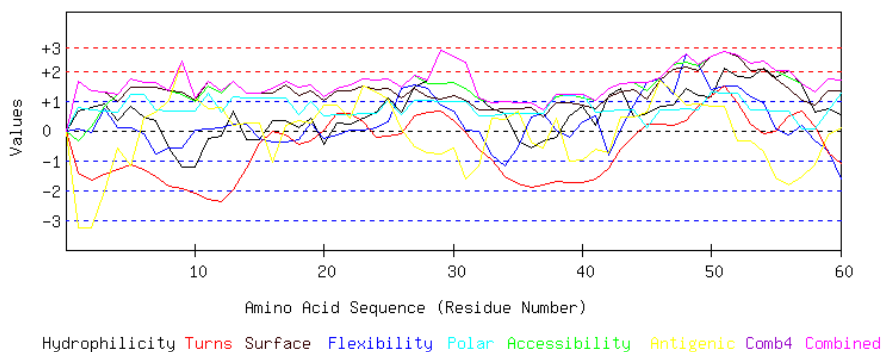
The server displays 1. [GRAPHICAL RESULT](#) 2. [TABULAR RESULT](#) 3. [Overlap Display](#)

seqname=
Seq= VAETAPLRVQLIAKTDFLAPPDVPWTTDADGGPALVEFAGRACYQSWKPNPKTATNAGY
LRHIIDVGHFVLEHASVSFYITGISRSCTHELIRHRHFSYSQLSQRYVPEKDSRVVVP
GMEDDADLRHILTEAADAARATYSELLAKLEAKFADQPNAILRRKQARQAARAVLPNATE
TRIVVTGNYRAWRHFIAMRASEHADVEIRRLAIECLRQLAAVAPAVFADFEVTTLDGTE
VATSPLATEA

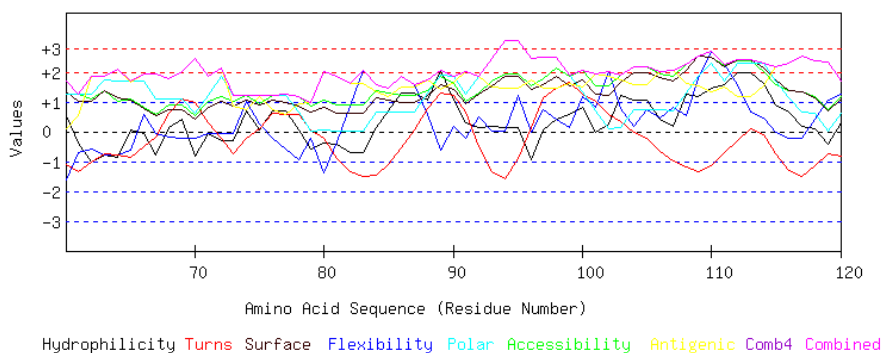
Length=250

GRAPHICAL RESULT

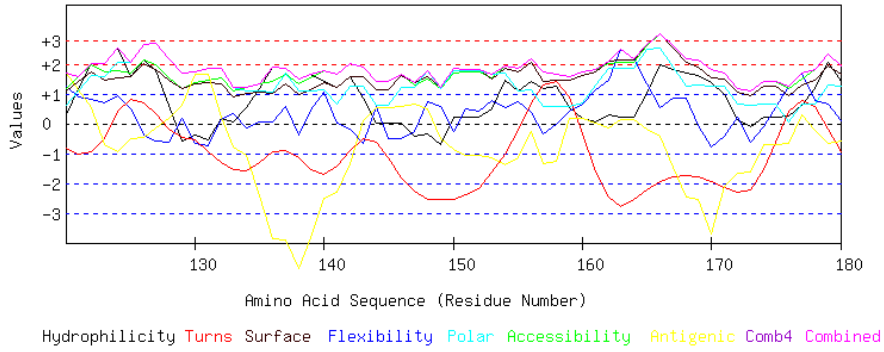
GRAPHICAL RESULT :: SEQ 1 to 60



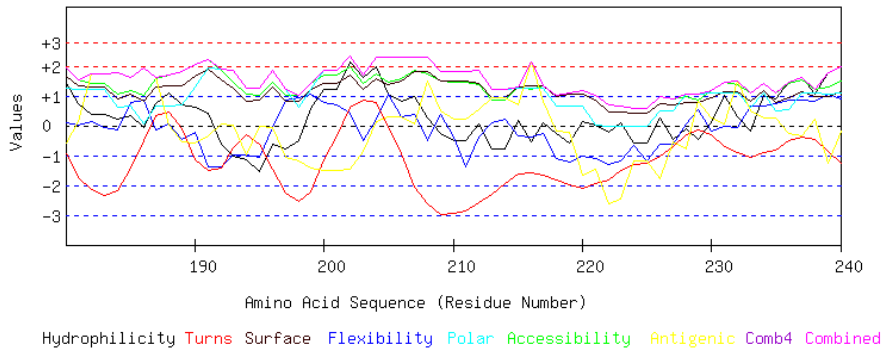
GRAPHICAL RESULT :: SEQ 61 to 120



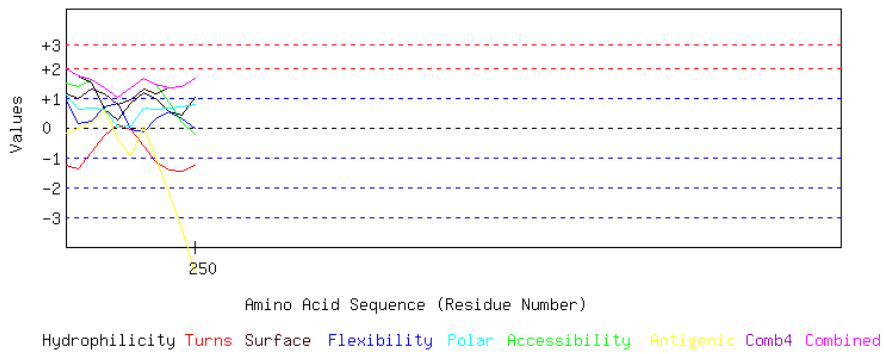
GRAPHICAL RESULT :: SEQ 121 to 180



GRAPHICAL RESULT :: SEQ 181 to 240



GRAPHICAL RESULT :: SEQ 241 to 300



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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

VAETAPLRVQLIAKTDFLAPPDVPFWTTDADGGPALVEFAGRACYQSWSKPNPKTATNAGY
LRHIIDVGHFVLEHASVSFYITGISRSCTHELIRRRHFSYSQLSQRYVPEKDSRVVFP
GMEDDADLRHILTEAADAARATYSSELLAKLEAKFADQPNAILRRKQARQAARAVLPNATE
TRIVVTGNYRAWRHFIAMRASEHADVEIRRLATECLRLQAAVAVPAVFADFVETTLADGTE
VATSPLATEA

Length=250

A.A. ppp Combined

Table with 11 columns: Hydro, Flexi, Access, Turns, Surface, Polar, AntiPro, MAX, MIN, AVG. Rows 1-87 represent various amino acid positions and their values across the different parameters.

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200A	1.224	0.786	1.702	-1.138	1.412	<u>1.851</u>	-1.494	1.851	-1.494	0.621
201S	1.224	0.690	1.702	-0.331	1.412	<u>1.851</u>	-1.494	1.851	-1.494	0.722
202E	<u>2.121</u>	0.409	<u>1.982</u>	0.607	1.686	<u>2.323</u>	-1.447	2.323	-1.447	1.097
203H	1.622	-0.490	1.431	0.846	1.203	1.700	-0.858	1.700	-0.858	0.779
204A	<u>1.982</u>	0.233	1.758	0.768	1.567	<u>2.299</u>	0.126	2.299	0.126	1.248
205D	1.065	1.046	1.468	-0.078	1.394	<u>2.281</u>	0.288	2.281	-0.078	1.066
206V	0.838	0.303	1.571	-0.924	1.504	<u>2.306</u>	0.313	2.306	-0.924	0.844
207E	0.971	0.399	1.842	-2.074	1.804	<u>2.311</u>	0.045	2.311	-2.074	0.757
208I	0.256	-0.500	1.758	-2.625	1.813	<u>2.316</u>	1.490	2.316	-2.625	0.644
209R	-0.243	0.399	1.487	-2.973	1.494	<u>1.828</u>	0.489	1.828	-2.973	0.354
210R	-0.515	-0.378	1.468	-2.939	1.485	<u>1.828</u>	0.222	1.828	-2.939	0.167
211L	-0.515	-1.396	1.468	-2.859	1.485	<u>1.828</u>	0.222	1.828	-2.859	0.033
212A	0.079	-0.378	1.393	-2.592	1.412	<u>1.844</u>	0.523	1.844	-2.592	0.326
213I	-0.768	0.113	0.879	-2.316	0.948	1.224	0.958	1.224	-2.316	0.148
214E	-0.768	0.233	0.879	-1.948	0.948	1.224	0.958	1.224	-1.948	0.218
215C	0.193	-0.342	1.290	-1.627	1.312	1.261	0.687	1.312	-1.627	0.396
216L	-0.521	-0.378	1.206	-1.592	1.321	1.267	<u>2.132</u>	2.132	-1.592	0.491
217R	0.117	-0.270	1.346	-1.668	1.339	1.265	0.800	1.346	-1.668	0.419
218Q	-0.243	-1.083	1.019	-1.802	0.975	0.666	-0.184	1.019	-1.802	-0.093
219L	-0.566	-1.216	1.113	-1.990	1.057	0.649	-0.217	1.113	-1.990	-0.167
220A	0.149	-1.011	1.197	-2.082	1.048	0.644	-1.662	1.197	-2.082	-0.245
221A	0.016	-1.107	1.010	-1.959	0.847	0.038	-1.442	1.010	-1.959	-0.371
222V	-0.231	-1.282	0.683	-1.829	0.474	-0.004	-2.615	0.683	-2.615	-0.686
223A	0.117	-1.186	0.646	-1.519	0.455	-0.008	-2.461	0.646	-2.461	-0.565
224P	-0.597	-0.647	0.580	-1.289	0.410	-0.004	-1.200	0.580	-1.289	-0.392
225A	-0.597	-1.180	0.580	-1.251	0.410	-0.004	-1.200	0.580	-1.251	-0.463
226V	0.269	-0.605	0.973	-1.037	0.738	0.484	-1.798	0.973	-1.798	-0.140
227F	-0.446	-0.605	0.907	-0.690	0.692	0.488	-0.536	0.907	-0.690	-0.027
228A	-0.085	0.061	0.991	-0.319	0.784	1.068	-0.783	1.068	-0.783	0.245
229D	-0.452	0.552	0.870	-0.154	0.774	1.070	0.816	1.070	-0.452	0.497
230F	0.111	-0.192	1.188	-0.301	0.938	1.088	0.268	1.188	-0.301	0.443
231E	1.021	-0.017	1.449	-0.704	1.139	1.104	0.058	1.449	-0.704	0.579
232V	0.307	-0.054	1.365	-0.911	1.148	1.109	1.503	1.503	-0.911	0.638
233T	-0.193	0.670	1.094	-1.074	0.829	0.620	0.502	1.094	-1.074	0.350
234T	1.021	0.670	1.431	-0.910	1.194	1.105	0.242	1.431	-0.910	0.679
235L	0.888	0.754	1.094	-0.802	0.784	0.506	0.268	1.094	-0.802	0.499
236A	1.451	0.862	1.412	-0.498	0.948	0.524	-0.280	1.451	-0.498	0.631
237D	1.616	0.862	1.543	-0.372	1.157	1.104	-0.347	1.616	-0.372	0.795
238G	1.053	0.814	1.225	-0.447	0.993	1.085	0.201	1.225	-0.447	0.704
239T	1.767	1.042	1.309	-0.874	0.984	1.080	-1.244	1.767	-1.244	0.581
240E	<u>1.963</u>	0.910	1.505	-1.250	1.139	1.100	-0.193	1.963	-1.250	0.739
241V	1.742	0.131	1.384	-1.372	0.975	0.631	-0.024	1.742	-1.372	0.495
242A	1.514	0.227	1.636	-0.827	1.294	0.650	0.195	1.636	-0.827	0.670
243T	0.604	0.718	1.356	-0.243	1.148	0.635	0.590	1.356	-0.243	0.687
244S	0.244	0.802	1.029	0.110	0.784	0.036	-0.394	1.029	-0.394	0.373
245P	0.806	-0.054	1.346	-0.060	0.948	0.054	-0.942	1.346	-0.942	0.300
246L	1.167	-0.158	1.674	-0.622	1.312	0.654	0.042	1.674	-0.622	0.581
247A	0.971	0.301	1.477	-1.149	1.157	0.634	-1.009	1.477	-1.149	0.340
248T	0.560	0.556	0.870	-1.432	1.321	0.674	-2.179	1.321	-2.179	0.053
249E	0.427	0.319	0.169	-1.449	1.367	0.715	-3.409	1.367	-3.409	-0.266
250A	1.009	-0.001	-0.205	-1.250	1.677	0.770	-4.854	1.677	-4.854	-0.408

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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	<u>¹VAETAPLRVQLIAKTDFLAPPDVPWTTDADGGPALVEFAGRACYQSWSKPNPKTATNAGYLRHII</u> DVGHFSVLEHASVSFYITGISRSCTHELIRHRHFSYQLSQRYVPEKDSRVVPPGMEDDADLF
Hydrophilicity	<u>¹VAETAPLRVQLIAKTDFLAPPDVPWTTDADGGPALVEFAGRACYQSWSKPNPKTATNAGYLRHII</u> DVGHFSVLEHASVSFYITGISRSCTHELIRHRHFSYQLSQRYVPEKDSRVVPPGMEDDADLF
Flexibility	<u>¹VAETAPLRVQLIAKTDFLAPPDVPWTTDADGGPALVEFAGRACYQSWSKPNPKTATNAGYLRHII</u> DVGHFSVLEHASVSFYITGISRSCTHELIRHRHFSYQLSQRYVPEKDSRVVPPGMEDDADLF
Accessibility	<u>¹VAETAPLRVQLIAKTDFLAPPDVPWTTDADGGPALVEFAGRACYQSWSKPNPKTATNAGYLRHII</u> DVGHFSVLEHASVSFYITGISRSCTHELIRHRHFSYQLSQRYVPEKDSRVVPPGMEDDADLF
Turns	<u>¹VAETAPLRVQLIAKTDFLAPPDVPWTTDADGGPALVEFAGRACYQSWSKPNPKTATNAGYLRHII</u> DVGHFSVLEHASVSFYITGISRSCTHELIRHRHFSYQLSQRYVPEKDSRVVPPGMEDDADLF
Exposed Surface	<u>¹VAETAPLRVQLIAKTDFLAPPDVPWTTDADGGPALVEFAGRACYQSWSKPNPKTATNAGYLRHII</u> DVGHFSVLEHASVSFYITGISRSCTHELIRHRHFSYQLSQRYVPEKDSRVVPPGMEDDADLF
Polarity	<u>¹VAETAPLRVQLIAKTDFLAPPDVPWTTDADGGPALVEFAGRACYQSWSKPNPKTATNAGYLRHII</u> DVGHFSVLEHASVSFYITGISRSCTHELIRHRHFSYQLSQRYVPEKDSRVVPPGMEDDADLF
Antigenic Propensity	<u>¹VAETAPLRVQLIAKTDFLAPPDVPWTTDADGGPALVEFAGRACYQSWSKPNPKTATNAGYLRHII</u> DVGHFSVLEHASVSFYITGISRSCTHELIRHRHFSYQLSQRYVPEKDSRVVPPGMEDDADLF

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