

BT3040 – Bioinformatics

Practical 6

1

The given IDs in Set 1 were mapped using UniProt and the sequences were downloaded in FASTA format.

Retrieve/ID mapping | UniProt

https://www.uniprot.org/id-mapping

UniProt BLAST Align Peptide search ID mapping SPARQL UniProtKB Advanced | List Search Help

Retrieve/ID mapping

Enter one or more IDs (100,000 max). You may also load from a text file. Separate IDs by whitespace (space, tab, newline) or commas.

P69905 P01946 P01942 P01966 P01958 P01959 P01965 P06635 P60529 P80043 P01980

Your input contains 11 IDs

From database UniProtKB AC/ID To database UniProtKB

Name your ID Mapping job

P69905 +10 UniProtKB_AC-ID → UniProtKB

Reset Map 11 IDs

Retrieve/ID mapping results | UniProt

https://www.uniprot.org/id-mapping/uniprotkb/0e5cd162dc4a13d76244e11da9c723984a0904c1/overview

UniProt BLAST Align Peptide search ID mapping SPARQL Tool results Advanced | List Search Help

ID mapping 11 results found for UniProtKB_AC-ID → UniProtKB

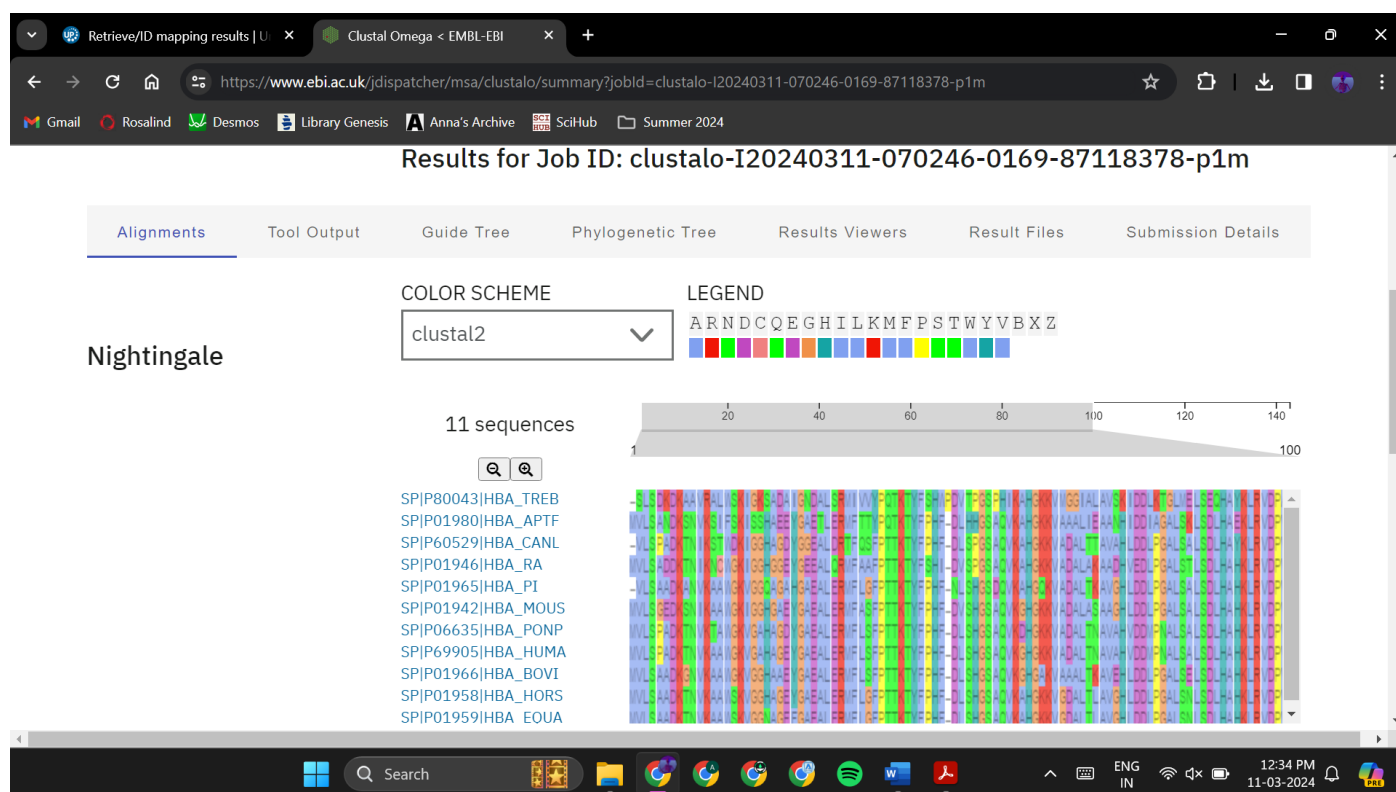
Overview Input Parameters API Request

BLAST Align Map IDs Download Add View: Cards Table Customize columns Resubmit Share

11 IDs were mapped to 11 results

From	Entry	Entry Name	Protein Names	Gene Names	Organism	Length
<input type="checkbox"/> P69905	P69905	HBA_HUMAN	Hemoglobin subunit alpha[...]	HBA1, HBA2	Homo sapiens (Human)	142 AA
<input type="checkbox"/> P01946	P01946	HBA_RAT	Hemoglobin subunit alpha-1/2[...]	Hba1, Hba-a1	Rattus norvegicus (Rat)	142 AA
<input type="checkbox"/> P01942	P01942	HBA_MOUSE	Hemoglobin subunit alpha[...]	Hba, Hba-a1	Mus musculus (Mouse)	142 AA
<input type="checkbox"/> P01966	P01966	HBA_BOVIN	Hemoglobin subunit	HBA	Bos taurus (Bovine)	142 AA

The FASTA file was fed into Clustal Omega to obtain the MSA. The result was downloaded in CLUSTAL format.



The file in CLUSTAL format was used as input for the AL2CO server along with the necessary scoring parameters.

Or upload a file: Choose File clustalo-I20...ln-clustal.txt

DATA SUBMIT

Enter email to receive the result (optional):

Enter a job name (optional): Submit Reset

PARAMETERS

- sequence weighting scheme: ☐ henikoff-henikoff ☐ independent count ☒ unweighted
- conservation calculation method: ☒ entropy ☐ variance ☐ sum-of-pairs
- For sum-of-pairs method only:
- scoring matrix: ☒ BLOSUM62 matrix ☐ identity matrix
- scoring matrix transformation: ☒ no transformation ☐ normalization ☐ adjustment
- normalize conservation values: ☐ True ☒ False
- window size used for averaging conservation (for smoothing purpose): 1
- gap fraction above which conservation calculation is not performed: 0.5
- exclude the first sequence from calculation: ☐ True ☒ False
- output alignment block size: 70
- pdb file for which b-factor field is replaced with conservation (optional): Choose File No file chosen

The results are shown below:

Set 1						
Position	Alignment	Score 1	Score 2	Score 3	Score 4	Score 5
1	:	0.000	1.021	5.000	1.019	0.943
2	S	-0.305	0.865	3.008	0.729	0.253
3	L	0.000	0.909	4.000	0.916	0.943
4	S	0.000	0.953	4.000	0.951	0.943
5	D	-1.121	0.527	1.149	0.492	-1.597
6	K	-1.160	0.561	1.157	0.439	-1.685
7	D	0.000	0.973	6.000	0.972	0.943
8	K	0.000	0.956	5.000	0.950	0.943
9	A	-1.169	0.541	1.868	0.465	-1.705
10	A	-0.305	0.917	4.661	0.770	0.253
11	V	-0.586	0.744	3.603	0.763	-0.385
12	R	-0.305	0.871	4.504	0.744	0.253
13	A	-1.034	0.567	1.909	0.566	-1.399
14	L	-1.160	0.559	1.521	0.415	-1.685
15	W	-0.305	0.943	9.306	0.888	0.253
16	S	-0.916	0.612	2.264	0.604	-1.134
17	K	0.000	0.956	5.000	0.950	0.943
18	I	-0.689	0.691	3.504	0.719	-0.618
19	G	-0.305	0.886	4.992	0.831	0.253
20	K	-1.034	0.613	2.405	0.502	-1.399
21	S	-0.886	0.713	4.372	0.627	-1.064
22	A	-0.474	0.740	2.876	0.767	-0.131
23	D	-1.034	0.624	2.240	0.517	-1.399
24	A	-0.908	0.665	2.455	0.593	-1.114
25	I	-0.886	0.757	4.314	0.679	-1.064
26	G	0.000	0.977	6.000	0.977	0.943
27	N	-0.886	0.650	1.826	0.561	-1.064
28	D	-0.305	0.922	4.512	0.784	0.253
29	A	-0.305	0.817	3.347	0.768	0.253
30	L	0.000	0.909	4.000	0.916	0.943
31	S	-0.886	0.749	3.298	0.628	-1.064
32	R	0.000	1.015	5.000	1.011	0.943
33	M	-0.305	0.933	4.008	0.944	0.253
34	I	-0.305	0.904	4.992	0.780	0.253
35	V	-1.295	0.470	0.959	0.373	-1.991
36	V	-1.367	0.472	1.132	0.386	-2.154
37	Y	-0.474	0.830	5.140	0.718	-0.131

38	P	0.000	0.993	7.000	0.993	0.943
39	Q	-0.474	0.821	3.215	0.715	-0.131
40	T	0.000	0.977	5.000	0.979	0.943
41	K	0.000	0.956	5.000	0.950	0.943
42	T	0.000	0.977	5.000	0.979	0.943
43	Y	0.000	1.016	7.000	1.012	0.943
44	F	0.000	0.988	6.000	0.989	0.943
45	S	-0.474	0.822	4.521	0.712	-0.131
46	H	0.000	0.969	8.000	0.972	0.943
47	W	-0.600	0.823	4.240	0.711	-0.417
48	P	-0.857	0.657	2.295	0.582	-1
49	D	-0.305	0.888	5.174	0.901	0.253
50	V	-0.586	0.674	2.810	0.621	-0.385
51	T	-0.600	0.776	2.752	0.605	-0.417
52	P	-0.586	0.745	3.959	0.689	-0.385
53	G	0.000	0.977	6.000	0.977	0.943
54	S	0.000	0.953	4.000	0.951	0.943
55	P	-0.600	0.730	2.322	0.628	-0.417
56	H	-0.305	0.936	4.198	0.800	0.253
57	I	-0.305	0.872	3.835	0.748	0.253
58	K	0.000	0.956	5.000	0.950	0.943
59	A	-0.860	0.596	1.835	0.687	-1.006
60	H	0.000	0.969	8.000	0.972	0.943
61	G	0.000	0.977	6.000	0.977	0.943
62	K	-0.600	0.777	3.405	0.812	-0.417
63	K	0.000	0.956	5.000	0.950	0.943
64	V	0.000	0.956	4.000	0.956	0.943
65	M	-0.760	0.660	2.124	0.612	-0.778
66	G	-0.760	0.704	2.694	0.561	-0.778
67	G	-0.305	0.817	3.355	0.692	0.253
68	I	-0.305	0.825	3.669	0.710	0.253
69	A	-0.860	0.643	2.190	0.545	-1.006
70	L	-1.673	0.360	0.124	0.382	-2.848
71	A	0.000	0.906	4.000	0.909	0.943
72	V	-0.586	0.701	2.413	0.682	-0.385
73	S	-1.594	0.406	0.934	0.359	-2.670
74	K	-0.305	0.879	6.488	0.745	0.253
75	I	-0.995	0.543	2.612	0.534	-1.312
76	D	-0.305	0.888	5.331	0.888	0.253

77	D	0.000	0.973	6.000	0.972	0.943
78	L	-0.760	0.675	3.140	0.683	-0.778
79	K	-0.600	0.807	4.446	0.618	-0.417
80	T	-0.760	0.733	3.149	0.664	-0.778
81	G	-0.305	0.817	3.355	0.692	0.253
82	L	0.000	0.909	4.000	0.916	0.943
83	M	-0.305	0.869	3.182	0.749	0.253
84	E	-1.414	0.451	0.678	0.428	-2.262
85	L	0.000	0.909	4.000	0.916	0.943
86	S	0.000	0.953	4.000	0.951	0.943
87	E	-0.305	0.888	5.331	0.763	0.253
88	Q	-0.305	0.826	3.017	0.715	0.253
89	H	0.000	0.969	8.000	0.972	0.943
90	A	0.000	0.906	4.000	0.909	0.943
91	Y	-0.760	0.731	4.967	0.618	-0.778
92	K	0.000	0.956	5.000	0.950	0.943
93	L	0.000	0.909	4.000	0.916	0.943
94	R	0.000	1.015	5.000	1.011	0.943
95	V	0.000	0.956	4.000	0.956	0.943
96	D	0.000	0.973	6.000	0.972	0.943
97	P	0.000	0.993	7.000	0.993	0.943
98	A	-0.305	0.860	3.339	0.715	0.253
99	N	0.000	1.012	6.000	1.011	0.943
100	F	0.000	0.988	6.000	0.989	0.943
101	K	0.000	0.956	5.000	0.950	0.943
102	I	-0.600	0.739	3.058	0.632	-0.417
103	L	0.000	0.909	4.000	0.916	0.943
104	N	-0.600	0.781	2.926	0.619	-0.417
105	H	-0.305	0.886	6.653	0.839	0.253
106	C	-0.305	0.937	7.306	0.962	0.253
107	I	-0.600	0.739	3.058	0.588	-0.417
108	L	-0.305	0.825	3.678	0.783	0.253
109	V	-0.474	0.784	2.215	0.844	-0.131
110	V	-0.474	0.806	3.479	0.677	-0.131
111	I	-0.600	0.735	3.240	0.580	-0.417
112	S	-0.305	0.814	3.504	0.683	0.253
113	T	-1.720	0.345	0.702	0.355	-2.955
114	M	-0.305	0.885	6.322	0.769	0.253
115	F	-0.935	0.559	1.207	0.529	-1.175

116	P	0.000	0.993	7.000	0.993	0.943
117	K	-1.846	0.302	0.562	0.299	-3.241
118	E	-0.916	0.633	3.008	0.584	-1.134
119	F	-0.305	0.893	4.992	0.837	0.253
120	T	-0.305	0.891	4.182	0.907	0.253
121	P	0.000	0.993	7.000	0.993	0.943
122	E	-0.760	0.660	2.182	0.589	-0.778
123	A	-0.886	0.695	2.736	0.519	-1.064
124	H	0.000	0.969	8.000	0.972	0.943
125	V	-0.305	0.814	3.339	0.685	0.253
126	S	0.000	0.953	4.000	0.951	0.943
127	L	0.000	0.909	4.000	0.916	0.943
128	D	0.000	0.973	6.000	0.972	0.943
129	K	0.000	0.956	5.000	0.950	0.943
130	F	0.000	0.988	6.000	0.989	0.943
131	L	-0.305	0.822	3.355	0.839	0.253
132	S	-0.860	0.595	2.289	0.528	-1.006
133	G	-1.414	0.459	1.496	0.400	-2.262
134	V	0.000	0.956	4.000	0.956	0.943
135	A	-0.600	0.769	2.909	0.577	-0.417
136	L	-0.600	0.796	3.231	0.615	-0.417
137	A	-0.305	0.860	3.339	0.715	0.253
138	L	0.000	0.909	4.000	0.916	0.943
139	A	-0.305	0.881	4.165	0.738	0.253
140	E	-0.305	0.868	3.347	0.743	0.253
141	R	-0.305	0.871	4.504	0.744	0.253
142	Y	0.000	1.016	7.000	1.012	0.943
143	R	0.000	1.015	5.000	1.011	0.943

The same steps were repeated for Set 2. The results are shown below:

Set 2						
Position	Alignment	Score 1	Score 2	Score 3	Score 4	Score 5
1	M	-1.216	0.529	1.306	0.494	-1
2	A	-1.216	0.529	1.306	0.494	-1
3	S	-0.974	0.648	1.328	0.666	-0.56
4	K	-1.494	0.426	1.109	0.365	-1.507

5	P	-0.377	0.882	3.5	0.827	0.529
6	Q	-0.736	0.726	2.938	0.641	-0.125
7	P	-0.377	0.884	3.828	0.83	0.529
8	I	-0.736	0.769	3.172	0.713	-0.125
9	A	-0.377	0.801	3.125	0.739	0.529
10	A	-0.377	0.812	4.656	0.754	0.529
11	A	-0.377	0.812	4.656	0.754	0.529
12	N	0	0.995	6	0.994	1.215
13	W	-0.349	0.909	8.963	0.876	0.58
14	K	0	0.962	5	0.966	1.215
15	C	-0.937	0.679	2.395	0.639	-0.492
16	N	0	0.995	6	0.994	1.215
17	G	-0.349	0.835	4	0.81	0.58
18	S	-1.311	0.51	0.79	0.53	-1.173
19	E	-1.303	0.553	1.568	0.515	-1.159
20	S	-1.523	0.401	0.901	0.372	-1.56
21	L	-1.581	0.481	0.519	0.482	-1.666
22	L	-1.061	0.526	2.667	0.514	-0.718
23	V	-1.677	0.317	0.198	0.27	-1.841
24	P	-1.003	0.64	2.025	0.597	-0.612
25	L	-0.687	0.664	3.012	0.656	-0.036
26	I	-0.965	0.55	2.716	0.557	-0.543
27	E	-1.735	0.362	0.136	0.393	-1.946
28	T	-1.003	0.663	1.815	0.595	-0.612
29	L	-0.349	0.859	3.235	0.826	0.58
30	N	-0.349	0.888	4.988	0.885	0.58
31	A	-1.003	0.591	1.951	0.549	-0.612
32	A	-0.684	0.691	2.716	0.676	-0.031
33	T	-1.889	0.305	0.383	0.302	-2.227
34	F	-1.581	0.426	0.457	0.364	-1.666
35	D	-1.149	0.604	1.543	0.553	-0.879
36	H	-1.677	0.372	0.383	0.348	-1.841
37	D	-1.523	0.429	1.259	0.421	-1.56
38	:	-1.216	0.529	1.306	0.494	-1
39	:	-1.216	0.529	1.306	0.494	-1
40	V	-0.687	0.645	2.222	0.684	-0.036
41	Q	-0.849	0.671	3.432	0.623	-0.331
42	C	-0.349	0.829	3.074	0.795	0.58
43	V	0	0.93	4	0.93	1.215

44	V	-1.061	0.545	2.136	0.563	-0.718
45	A	-1.003	0.594	2.062	0.557	-0.612
46	P	-0.349	0.893	5.049	0.894	0.58
47	T	-0.349	0.889	5.395	0.855	0.58
48	F	-1.215	0.498	0.889	0.51	-0.998
49	L	-1.677	0.321	0.593	0.294	-1.841
50	H	-0.684	0.808	5.247	0.771	-0.031
51	I	-0.687	0.664	3.012	0.686	-0.036
52	P	-1.149	0.595	1.272	0.564	-0.879
53	M	-1.465	0.504	1.704	0.492	-1.454
54	T	-1.149	0.509	1.704	0.45	-0.879
55	K	-0.937	0.625	2.37	0.582	-0.492
56	A	-1.215	0.541	1.556	0.505	-0.998
57	R	-1.427	0.462	0.889	0.399	-1.385
58	L	-0.349	0.85	3.407	0.809	0.58
59	T	-1.216	0.529	1.306	0.494	-1
60	N	-1.523	0.455	0.877	0.44	-1.56
61	P	-1.149	0.584	1.667	0.551	-0.879
62	K	-1.427	0.467	1.469	0.421	-1.385
63	F	-1.311	0.477	1.852	0.497	-1.173
64	Q	-1.831	0.321	-0.222	0.292	-2.121
65	I	-1.003	0.611	2.531	0.549	-0.612
66	A	-0.684	0.691	2.716	0.623	-0.031
67	A	-0.349	0.798	3.235	0.793	0.58
68	Q	0	0.994	5	0.993	1.215
69	N	0	0.995	6	0.994	1.215
70	A	-0.687	0.669	3.568	0.649	-0.036
71	I	-0.849	0.723	4	0.666	-0.331
72	:	-1.074	0.596	1.234	0.506	-0.741
73	T	-1.149	0.532	0.827	0.465	-0.879
74	R	-1.523	0.408	0.654	0.38	-1.56
75	S	-1.369	0.453	1.358	0.446	-1.279
76	G	0	0.944	6	0.951	1.215
77	A	0	0.909	4	0.905	1.215
78	F	0	1.001	6	1.006	1.215
79	T	0	0.983	5	0.984	1.215
80	G	0	0.944	6	0.951	1.215
81	E	0	0.962	5	0.96	1.215
82	V	-1.149	0.559	2	0.478	-0.879

83	S	-0.349	0.873	3.235	0.84	0.58
84	L	-1.149	0.562	1.568	0.469	-0.879
85	Q	-1.465	0.391	0.741	0.375	-1.454
86	I	-0.684	0.811	3.235	0.744	-0.031
87	L	-0.937	0.601	2.914	0.557	-0.492
88	K	-0.349	0.849	3.605	0.848	0.58
89	D	-0.349	0.883	5.012	0.878	0.58
90	Y	-1.523	0.43	1.123	0.415	-1.56
91	G	0	0.944	6	0.951	1.215
92	I	-1.003	0.58	1.778	0.529	-0.612
93	S	-1.677	0.406	0.778	0.368	-1.841
94	W	0	1.013	11	1.013	1.215
95	V	0	0.93	4	0.93	1.215
96	V	-0.687	0.644	3.506	0.676	-0.036
97	L	0	0.963	4	0.959	1.215
98	G	0	0.944	6	0.951	1.215
99	H	0	1.017	8	1.017	1.215
100	S	0	0.979	4	0.977	1.215
101	E	0	0.962	5	0.96	1.215
102	R	0	0.999	5	1	1.215
103	R	0	0.999	5	1	1.215
104	L	-1.149	0.592	1.728	0.522	-0.879
105	Y	-1.273	0.484	1.827	0.463	-1.104
106	:	-1.216	0.529	1.306	0.494	-1
107	:	-1.216	0.529	1.306	0.494	-1
108	Y	-0.849	0.703	3.346	0.65	-0.331
109	G	-0.684	0.735	3.074	0.682	-0.031
110	E	0	0.962	5	0.96	1.215
111	T	-0.684	0.768	2.704	0.7	-0.031
112	N	-0.53	0.796	4.272	0.765	0.25
113	E	-1.149	0.546	1.605	0.484	-0.879
114	I	-1.149	0.577	1.642	0.508	-0.879
115	V	-0.53	0.762	3.654	0.726	0.25
116	A	-0.687	0.601	2.42	0.643	-0.036
117	E	-1.311	0.505	1.914	0.499	-1.173
118	K	0	0.962	5	0.966	1.215
119	V	-0.995	0.535	1.679	0.492	-0.598
120	A	-1.303	0.475	1.21	0.465	-1.159
121	Q	-1.149	0.638	3.346	0.569	-0.879

122	A	0	0.909	4	0.905	1.215
123	C	-0.349	0.861	3.074	0.824	0.58
124	A	-1.427	0.419	1.136	0.381	-1.385
125	:	-1.216	0.529	1.306	0.494	-1
126	A	-1.061	0.514	1.63	0.491	-0.718
127	G	-0.349	0.837	4.79	0.813	0.58
128	F	-1.003	0.642	2.444	0.566	-0.612
129	H	-0.937	0.592	1.444	0.573	-0.492
130	V	0	0.93	4	0.93	1.215
131	I	-0.349	0.858	3.802	0.849	0.58
132	V	-1.303	0.492	0.901	0.401	-1.159
133	C	0	1.017	9	1.018	1.215
134	V	-0.53	0.762	3.654	0.726	0.25
135	G	0	0.944	6	0.951	1.215
136	E	0	0.962	5	0.96	1.215
137	T	-0.965	0.592	1.333	0.598	-0.543
138	N	-0.349	0.859	2.642	0.819	0.58
139	E	-0.637	0.706	3.778	0.782	0.056
140	E	-0.349	0.857	4.407	0.85	0.58
141	R	-0.349	0.89	4.407	0.856	0.58
142	E	-0.349	0.853	4.21	0.816	0.58
143	A	-0.349	0.802	3.407	0.766	0.58
144	G	0	0.944	6	0.951	1.215
145	R	-1.677	0.414	-0.222	0.387	-1.841
146	T	0	0.983	5	0.984	1.215
147	A	-1.831	0.35	-0.062	0.283	-2.121
148	A	-1.311	0.452	0.988	0.454	-1.173
149	V	0	0.93	4	0.93	1.215
150	V	-0.684	0.726	1.84	0.692	-0.031
151	L	-1.273	0.497	0.395	0.44	-1.104
152	T	-1.215	0.533	1.309	0.562	-0.998
153	Q	0	0.994	5	0.993	1.215
154	L	-0.965	0.604	1.543	0.623	-0.543
155	A	-1.427	0.481	0.951	0.424	-1.385
156	A	-0.637	0.629	2.222	0.712	0.056
157	V	-1.149	0.562	2.407	0.491	-0.879
158	A	-1.003	0.581	1.852	0.507	-0.612
159	Q	-0.995	0.612	3.037	0.569	-0.598
160	K	-1.215	0.519	1.593	0.511	-0.998

161	L	-1.215	0.484	1.802	0.458	-0.998
162	S	-1.216	0.529	1.306	0.494	-1
163	K	-1.216	0.529	1.306	0.494	-1
164	E	-1.003	0.635	2.136	0.568	-0.612
165	A	-0.684	0.766	3.407	0.718	-0.031
166	W	0	1.013	11	1.013	1.215
167	S	-1.003	0.658	2.086	0.617	-0.612
168	R	-1.215	0.549	2	0.558	-0.998
169	V	-0.349	0.822	3.802	0.815	0.58
170	V	0	0.93	4	0.93	1.215
171	I	-1.099	0.495	2.667	0.518	-0.787
172	A	0	0.909	4	0.905	1.215
173	Y	0	1.013	7	1.011	1.215
174	E	0	0.962	5	0.96	1.215
175	P	0	0.995	7	0.997	1.215
176	V	0	0.93	4	0.93	1.215
177	W	0	1.013	11	1.013	1.215
178	A	0	0.909	4	0.905	1.215
179	I	0	0.971	4	0.97	1.215
180	G	0	0.944	6	0.951	1.215
181	T	0	0.983	5	0.984	1.215
182	G	0	0.944	6	0.951	1.215
183	K	-0.684	0.75	2.914	0.718	-0.031
184	V	-0.937	0.591	2.037	0.535	-0.492
185	A	0	0.909	4	0.905	1.215
186	T	-0.349	0.876	4.198	0.87	0.58
187	P	-0.349	0.884	5.21	0.88	0.58
188	Q	-1.215	0.53	2.185	0.514	-0.998
189	Q	-0.349	0.888	4.025	0.853	0.58
190	A	0	0.909	4	0.905	1.215
191	Q	-0.349	0.885	4.407	0.852	0.58
192	E	-0.684	0.753	3.852	0.689	-0.031
193	V	-0.349	0.822	3.802	0.788	0.58
194	H	0	1.017	8	1.017	1.215
195	E	-0.637	0.669	2.222	0.641	0.056
196	L	-1.677	0.389	-0.074	0.351	-1.841
197	L	-0.849	0.656	2.914	0.592	-0.331
198	R	0	0.999	5	1	1.215
199	R	-1.677	0.35	0.383	0.319	-1.841

200	W	-0.53	0.822	7.296	0.792	0.25
201	V	-0.349	0.85	3.407	0.808	0.58
202	R	-1.149	0.545	1.827	0.476	-0.879
203	S	-1.303	0.564	1.778	0.525	-1.159
204	K	-0.637	0.724	3.222	0.69	0.056
205	L	-1.149	0.516	2.173	0.471	-0.879
206	G	-0.849	0.673	2.296	0.656	-0.331
207	T	-1.215	0.555	1.42	0.532	-0.998
208	D	-1.677	0.333	0.543	0.319	-1.841
209	I	-0.684	0.707	3.012	0.633	-0.031
210	A	-0.349	0.802	3.407	0.796	0.58
211	A	-1.465	0.426	1.012	0.405	-1.454
212	Q	-1.003	0.651	2.099	0.575	-0.612
213	L	-0.637	0.713	2.222	0.68	0.056
214	R	0	0.999	5	1	1.215
215	I	0	0.971	4	0.97	1.215
216	L	-0.937	0.612	1.963	0.586	-0.492
217	Y	0	1.013	7	1.011	1.215
218	G	0	0.944	6	0.951	1.215
219	G	0	0.944	6	0.951	1.215
220	S	0	0.979	4	0.977	1.215
221	V	-0.349	0.815	3.21	0.776	0.58
222	T	-0.684	0.773	3.346	0.711	-0.031
223	A	-0.965	0.53	1.765	0.521	-0.543
224	K	-1.003	0.592	1.642	0.518	-0.612
225	N	-0.637	0.733	3.222	0.814	0.056
226	A	-0.687	0.669	3.568	0.65	-0.036
227	R	-1.303	0.523	1.593	0.429	-1.159
228	T	-0.849	0.666	2.272	0.596	-0.331
229	L	-0.349	0.859	3.235	0.823	0.58
230	Y	-1.003	0.59	1.383	0.52	-0.612
231	Q	-1.465	0.444	1.111	0.427	-1.454
232	M	-0.937	0.637	2.457	0.601	-0.492
233	R	-0.684	0.777	3.802	0.707	-0.031
234	D	-0.349	0.883	5.012	0.852	0.58
235	I	-0.687	0.637	3.506	0.638	-0.036
236	N	-0.349	0.883	5.012	0.847	0.58
237	G	0	0.944	6	0.951	1.215
238	F	0	1.001	6	1.006	1.215

239	L	0	0.963	4	0.959	1.215
240	V	0	0.93	4	0.93	1.215
241	G	0	0.944	6	0.951	1.215
242	G	0	0.944	6	0.951	1.215
243	A	0	0.909	4	0.905	1.215
244	S	0	0.979	4	0.977	1.215
245	L	-0.349	0.862	3.617	0.829	0.58
246	K	0	0.962	5	0.966	1.215
247	P	0	0.995	7	0.997	1.215
248	E	-0.684	0.752	3.309	0.713	-0.031
249	F	0	1.001	6	1.006	1.215
250	V	-0.684	0.715	3.259	0.678	-0.031
251	E	-0.849	0.682	3.469	0.628	-0.331
252	I	0	0.971	4	0.97	1.215
253	I	-0.349	0.858	3.802	0.824	0.58
254	E	-0.684	0.782	3.988	0.714	-0.031
255	A	-0.53	0.714	2.963	0.663	0.25
256	T	-1.465	0.462	1.062	0.457	-1.454
257	K	-1.427	0.502	1.519	0.451	-1.385
258	:	-1.216	0.529	1.306	0.494	-1
259	:	-1.216	0.529	1.306	0.494	-1
260	:	-1.216	0.529	1.306	0.494	-1
261	:	-1.216	0.529	1.306	0.494	-1
262	:	-1.216	0.529	1.306	0.494	-1
263	:	-1.216	0.529	1.306	0.494	-1
264	:	-1.216	0.529	1.306	0.494	-1

2

The top 10 residues with the highest scores in Set 1 and Set 2 obtained by unweighted frequency and entropy-based measure are:

Set 1			Set 2		
1	:	0.00	12	N	0.00
3	L	0.00	14	K	0.00
4	S	0.00	16	N	0.00
7	D	0.00	43	V	0.00

8	K	0.00	68	Q	0.00
17	K	0.00	69	N	0.00
26	G	0.00	76	G	0.00
30	L	0.00	77	A	0.00
32	R	0.00	78	F	0.00
38	P	0.00	79	T	0.00

The top 10 residues with the lowest scores in Set 1 and Set 2 obtained by unweighted frequency and entropy-based measure are:

Set 1			Set 2		
117	K	-1.85	33	T	-1.889
113	T	-1.72	64	Q	-1.831
70	L	-1.67	147	A	-1.831
73	S	-1.59	27	E	-1.735
84	E	-1.41	23	V	-1.677
133	G	-1.41	36	H	-1.677
36	V	-1.37	49	L	-1.677
35	V	-1.30	93	S	-1.677
9	A	-1.17	145	R	-1.677
6	K	-1.16	196	L	-1.677

3

The Python code to compute the conservation score from MSA using unweighted frequency, and entropy, variance and sum of pairs-based measures is given below:

```
import numpy as np
import pandas as pd

blosum62 = {
    ('W', 'F'): 1, ('L', 'R'): -2, ('S', 'P'): -1, ('V', 'T'): 0,
    ('Q', 'Q'): 5, ('N', 'A'): -2, ('Z', 'Y'): -2, ('W', 'R'): -3,
    ('Q', 'A'): -1, ('S', 'D'): 0, ('H', 'H'): 8, ('S', 'H'): -1,
    ('H', 'D'): -1, ('L', 'N'): -3, ('W', 'A'): -3, ('Y', 'M'): -1,
    ('G', 'R'): -2, ('Y', 'I'): -1, ('Y', 'E'): -2, ('B', 'Y'): -3,
    ('Y', 'A'): -2, ('V', 'D'): -3, ('B', 'S'): 0, ('Y', 'Y'): 7,
    ('G', 'N'): 0, ('E', 'C'): -4, ('Y', 'Q'): -1, ('Z', 'Z'): 4,
    ('V', 'A'): 0, ('C', 'C'): 9, ('M', 'R'): -1, ('V', 'E'): -2,
    ('T', 'N'): 0, ('P', 'P'): 7, ('V', 'I'): 3, ('V', 'S'): -2,
    ('Z', 'P'): -1, ('V', 'M'): 1, ('T', 'F'): -2, ('V', 'Q'): -2,
    ('K', 'K'): 5, ('P', 'D'): -1, ('I', 'H'): -3, ('I', 'D'): -3,
    ('T', 'R'): -1, ('P', 'L'): -3, ('K', 'G'): -2, ('M', 'N'): -2,
    ('P', 'H'): -2, ('F', 'Q'): -3, ('Z', 'G'): -2, ('X', 'L'): -1,
```

```

('T', 'M'): -1, ('Z', 'C'): -3, ('X', 'H'): -1, ('D', 'R'): -2,
('B', 'W'): -4, ('X', 'D'): -1, ('Z', 'K'): 1, ('F', 'A'): -2,
('Z', 'W'): -3, ('F', 'E'): -3, ('D', 'N'): 1, ('B', 'K'): 0,
('X', 'X'): -1, ('F', 'I'): 0, ('B', 'G'): -1, ('X', 'T'): 0,
('F', 'M'): 0, ('B', 'C'): -3, ('Z', 'I'): -3, ('Z', 'V'): -2,
('S', 'S'): 4, ('L', 'Q'): -2, ('W', 'E'): -3, ('Q', 'R'): 1,
('N', 'N'): 6, ('W', 'M'): -1, ('Q', 'C'): -3, ('W', 'I'): -3,
('S', 'C'): -1, ('L', 'A'): -1, ('S', 'G'): 0, ('L', 'E'): -3,
('W', 'Q'): -2, ('H', 'G'): -2, ('S', 'K'): 0, ('Q', 'N'): 0,
('N', 'R'): 0, ('H', 'C'): -3, ('Y', 'N'): -2, ('G', 'Q'): -2,
('Y', 'F'): 3, ('C', 'A'): 0, ('V', 'L'): 1, ('G', 'E'): -2,
('G', 'A'): 0, ('K', 'R'): 2, ('E', 'D'): 2, ('Y', 'R'): -2,
('M', 'Q'): 0, ('T', 'I'): -1, ('C', 'D'): -3, ('V', 'F'): -1,
('T', 'A'): 0, ('T', 'P'): -1, ('B', 'P'): -2, ('T', 'E'): -1,
('V', 'N'): -3, ('P', 'G'): -2, ('M', 'A'): -1, ('K', 'H'): -1,
('V', 'R'): -3, ('P', 'C'): -3, ('M', 'E'): -2, ('K', 'L'): -2,
('V', 'V'): 4, ('M', 'I'): 1, ('T', 'Q'): -1, ('I', 'G'): -4,
('P', 'K'): -1, ('M', 'M'): 5, ('K', 'D'): -1, ('I', 'C'): -1,
('Z', 'D'): 1, ('F', 'R'): -3, ('X', 'K'): -1, ('Q', 'D'): 0,
('X', 'G'): -1, ('Z', 'L'): -3, ('X', 'C'): -2, ('Z', 'H'): 0,
('B', 'L'): -4, ('B', 'H'): 0, ('F', 'F'): 6, ('X', 'W'): -2,
('B', 'D'): 4, ('D', 'A'): -2, ('S', 'L'): -2, ('X', 'S'): 0,
('F', 'N'): -3, ('S', 'R'): -1, ('W', 'D'): -4, ('V', 'Y'): -1,
('W', 'L'): -2, ('H', 'R'): 0, ('W', 'H'): -2, ('H', 'N'): 1,
('W', 'T'): -2, ('T', 'T'): 5, ('S', 'F'): -2, ('W', 'P'): -4,
('L', 'D'): -4, ('B', 'I'): -3, ('L', 'H'): -3, ('S', 'N'): 1,
('B', 'T'): -1, ('L', 'L'): 4, ('Y', 'K'): -2, ('E', 'Q'): 2,
('Y', 'G'): -3, ('Z', 'S'): 0, ('Y', 'C'): -2, ('G', 'D'): -1,
('B', 'V'): -3, ('E', 'A'): -1, ('Y', 'W'): 2, ('E', 'E'): 5,
('Y', 'S'): -2, ('C', 'N'): -3, ('V', 'C'): -1, ('T', 'H'): -2,
('P', 'R'): -2, ('V', 'G'): -3, ('T', 'L'): -1, ('V', 'K'): -2,
('K', 'Q'): 1, ('R', 'A'): -1, ('I', 'R'): -3, ('T', 'D'): -1,
('P', 'F'): -4, ('I', 'N'): -3, ('K', 'I'): -3, ('M', 'D'): -3,
('V', 'W'): -3, ('W', 'W'): 11, ('M', 'H'): -2, ('P', 'N'): -2,
('K', 'A'): -1, ('M', 'L'): 2, ('K', 'E'): 1, ('Z', 'E'): 4,
('X', 'N'): -1, ('Z', 'A'): -1, ('Z', 'M'): -1, ('X', 'F'): -1,
('K', 'C'): -3, ('B', 'Q'): 0, ('X', 'B'): -1, ('B', 'M'): -3,
('F', 'C'): -2, ('Z', 'Q'): 3, ('X', 'Z'): -1, ('F', 'G'): -3,
('B', 'E'): 1, ('X', 'V'): -1, ('F', 'K'): -3, ('B', 'A'): -2,
('X', 'R'): -1, ('D', 'D'): 6, ('W', 'G'): -2, ('Z', 'F'): -3,
('S', 'Q'): 0, ('W', 'C'): -2, ('W', 'K'): -3, ('H', 'Q'): 0,
('L', 'C'): -1, ('W', 'N'): -4, ('S', 'A'): 1, ('L', 'G'): -4,
('W', 'S'): -3, ('S', 'E'): 0, ('H', 'E'): 0, ('S', 'I'): -2,
('H', 'A'): -2, ('S', 'M'): -1, ('Y', 'L'): -1, ('Y', 'H'): 2,
('Y', 'D'): -3, ('E', 'R'): 0, ('X', 'P'): -2, ('G', 'G'): 6,
('G', 'C'): -3, ('E', 'N'): 0, ('Y', 'T'): -2, ('Y', 'P'): -3,
('T', 'K'): -1, ('A', 'A'): 4, ('P', 'Q'): -1, ('T', 'C'): -1,
('V', 'H'): -3, ('T', 'G'): -2, ('I', 'Q'): -3, ('Z', 'T'): -1,
('C', 'R'): -3, ('V', 'P'): -2, ('P', 'E'): -1, ('M', 'C'): -1,
('K', 'N'): 0, ('I', 'I'): 4, ('P', 'A'): -1, ('M', 'G'): -3,
('T', 'S'): 1, ('I', 'E'): -3, ('P', 'M'): -2, ('M', 'K'): -1,
('I', 'A'): -1, ('P', 'I'): -3, ('R', 'R'): 5, ('X', 'M'): -1,
('L', 'I'): 2, ('X', 'I'): -1, ('Z', 'B'): 1, ('X', 'E'): -1,
('Z', 'N'): 0, ('X', 'A'): 0, ('B', 'R'): -1, ('B', 'N'): 3,
('F', 'D'): -3, ('X', 'Y'): -1, ('Z', 'R'): 0, ('F', 'H'): -1,
('B', 'F'): -3, ('F', 'L'): 0, ('X', 'Q'): -1, ('B', 'B'): 4
}

def compute_conservation_scores(msa):
    n = len(msa)
    residues = ["-", "A", "R", "N", "D", "C", "Q", "E", "G", "H", "I", "L", "K", "M",
"F", "P", "S", "T", "W", "Y", "V"]

    overall_freq = {residue: 0 for residue in residues}

    for i in range(n):

```

```

        for residue in residues:
            overall_freq[residue] += msa[i].count(residue)
        gap_count = overall_freq["-"]
        overall_freq = {residue: overall_freq[residue] / (n * len(msa[0]) - gap_count) for
residue in residues}

    entropy_scores = []
    variance_scores = []
    sum_of_pairs_scores = []

    for i in range(len(msa[0])):
        freq = {residue: 0 for residue in residues}
        count = 0
        for j in range(n):
            if msa[j][i] != "-":
                freq[msa[j][i]] += 1
                count += 1
        freq = {residue: freq[residue] / count for residue in residues}

        entropy_score = 0
        variance_score = 0
        sum_of_pairs_score = 0

        for residue in residues:
            if freq[residue] != 0:
                entropy_score += freq[residue] * np.log(freq[residue])
                variance_score += (freq[residue] - overall_freq[residue]) ** 2

        variance_score = np.sqrt(variance_score)

        for residue1 in residues:
            for residue2 in residues:
                if (residue1, residue2) in blosum62:
                    sum_of_pairs_score += freq[residue1] * freq[residue2] *
blosum62[(residue1, residue2)]
                elif (residue2, residue1) in blosum62:
                    sum_of_pairs_score += freq[residue1] * freq[residue2] *
blosum62[(residue2, residue1)]

        entropy_scores.append(round(entropy_score, 3))
        variance_scores.append(round(variance_score, 3))
        sum_of_pairs_scores.append(round(sum_of_pairs_score, 3))

    df = pd.DataFrame(
        data=([residue for residue in msa[0]], entropy_scores, variance_scores,
sum_of_pairs_scores)).transpose()
    df.columns = ["Residue", "Entropy", "Variance", "Sum of Pairs"]

    return df

msa = [
    "_",
    "SLSDKDKAAVRALWSKIGKSADAIGNDALSRMIVVYPQTKTYFSHWPDVTPGSPHIKAHGKKVMGGIALAVSKIDDLKTGLMELSEQ",
    "HAYKLRVDPANFKILNHCILVVISTMFPKEFTPEAHVSLDKFLSGVALALAERYR",
    "MVLSANDKSNVKSIFSKISSHAEYYGAETLERMFTTYPQTKTYFPHF-",
    "DLHHGSAQVKAHGKKVAAALIEAANHIDDIAGALSKLSDLHA EKLRVDPVNFKLLGQCFMVVVAIHHPSALTPEIHASLDKFLCAVG",
    "NVLTSKYR",
    "-VLSPADKTNIKSTWDKIGGHAGDYGGEALDRTFQSFPPTTKTYFPHF-",
    "DLSPGSAQVKAHGKKVADALTAVAHLDLPGALSALSDLHAYKLRVDPVNFKLLSHCLLVTLACHHPTEFTP AVHASLDKFFAAVS",
    "TVLTSKYR",
    "MVLSADDKTNIKNCWGKIGGHGGEYGEEALQRMFAAFPTTKTYFSHI-",
    "DVSPGSAQVKAHGKKVADALAKAADHVEDLPGALSTLSDLHAHKL RVDPVNFKFLSHCLLVTLACHHPGDFTPAMHASLDKFLASVS",
    "TVLTSKYR",
    "-VLSAADKANVKA AWGKVGGQAGAHGA EALERMFLGFPTTKTYFPHF-",
    "NLSHGSDQVKAHGQKVADALTKAVGHLDDLPGALSALSDLHAHKL RVDPVNFKLLSHCLLVTLAAHHPDDFNPSVHASLDKFLANVS",
    "TVLTSKYR",

```



```

"MVLSGEDKSNIAAWGKIGGHGAHEYGAELERMFLSFPTTKTYFPHF-
DVSHGSAQVKGHGKKVADALASAAGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLASHHPADFTP AVHASL DKFLASVS
TVLTSKYR",
"MVLSPADKTNVKTAWGKVGAGHAGDYGAELERMFLSFPTTKTYFPHF-
DLSHGSAQVKDHGKKVADALTNVAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLP AEFTP AVHASL DKFLASVS
TVLTSKYR",
"MVLSPADKTNVKAAWGKVGAGHAGEYGAELERMFLSFPTTKTYFPHF-
DLSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLP AEFTP AVHASL DKFLASVS
TVLTSKYR",
"MVLSAADKGNVKAAWGKVGGHAAHEYGAELERMFLSFPTTKTYFPHF-
DLSHGSAQVKGHGAKVAAALTKAVEHLDDLPGALSELSDLHAHKLRVDPVNFKLLSHSLVTLASHLP SDFTP AVHASL DKFLANVS
TVLTSKYR",
"MVLSAADKTNVKAAWSKVGGHAGEYGAELERMFLGFPTTKTYFPHF-
DLSHGSAQVKAHGKKVGDALTLAVGHLDDLPGALSNLSDLHAHKLRVDPVNFKLLSHCLLVTLAVHLP NDFTP AVHASL DKFLSSVS
TVLTSKYR",
"MVLSAADKTNVKAAWSKVGGNAGEFGAEALERMFLGFPTTKTYFPHF-
DLSHGSAQVKAHGKKVGDALTLAVGHLDDLPGALSNLSDLHAHKLRVDPVNFKLLSHCLLVTLAVHLP NDFTP AVHASL DKFLSTVS
TVLTSKYR"]

result = compute_conservation_scores(msa)
print(result)

```

The output is shown below:

Residue	Entropy	Variance	Sum of Pairs
0	-	0.0	1.021
1	S	-0.305	0.865
2	L	0.0	0.909
3	S	0.0	0.953
4	D	-1.121	0.527
...
138	A	-0.305	0.881
139	E	-0.305	0.868
140	R	-0.305	0.871
141	Y	0.0	1.016
142	R	0.0	1.015

[143 rows x 4 columns]

Process finished with exit code 0

This matches the results obtained in Question 1 using AL2CO.

4

Multiple sequence alignments for Set 1 from Question 1 were obtained using Clustal Omega, MAFFT, and MUSCLE. These were used as input to the previous program to obtain the conservation score at each residue for each of these alignments.

The Python code used for this is shown below:

```

clustal = [
    "_
SLSDKDKAAVRALWSKIGKSADAIGNDALSRMIVVYPQTKTYFSHWPDVTPGSPHIKAHGKKVMGGIALAVSKIDDLKTGLMELSEQ
HAYKLRVDPANFKILNHCILVVISTMFPKEFTPEAHVSLDKFLSGVALALAERYR",
    "MVLSANDKSNVKSIFSKISSHAEEYGAETLERMFTTYPQTKTYFPHF-
DLHHGSAQVKAHGKKVAAALIEAANHIDDIAGALSKLSDLHAEKLRVDPVNFKLLGQCFMVVVAIHHP SALTPEIHASL DKFLCAVG
NVLTSKYR",

```

```
"-VLSPADKTNIKSTWDKIGGHAGDYGGEALDRTFQSFPPTTKTYFPHF-
DLSPGSAQVKAHGKKVADALTTAVAHLLDLPGALSALSDLHAYKLRVDPVNFKLLSHCLLVTLACHHPTEFTPAVHASLKDFFAAVS
TVLTSKYR",
"MVLSADDKTNIKNCWKGKIGGHGGEYGEEALQRMFAAFPTTKTYFSHI-
DVSPGSAQVKAHGKKVADALAKAADHVEDLPGALSTLSDLHAHKLRVDPVNFKFLSHCLLVTLACHHPGDFTPAMHASLKDFLASVS
TVLTSKYR",
"-VLSAADKANVKAAWGKVGQGAGAHGAEALERMFLGFPTTKTYFPHF-
NLSHGSDQVKAHGQKVADALTKAVGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHHPDDFNPSVHASLKDFLANVS
TVLTSKYR",
"MVLSGEDKSNIAAWGKIGGHGAEYGAELERMFLSFPTTKTYFPHF-
DVSHGSAQVKGHGKKVADALASAAGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLASHHPADFTPAVHASLKDFLASVS
TVLTSKYR",
"MVLSPADKTNVKTAWGKVGGAHAGDYGAEALERMFLSFPTTKTYFPHF-
DLSHGSAQVKDHGKKVADALTNAAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLKDFLASVS
TVLTSKYR",
"MVLSPADKTNVKAAWGKVGGAHAGEYGAELERMFLSFPTTKTYFPHF-
DLSHGSAQVKGHGKKVADALTNAAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLKDFLASVS
TVLTSKYR",
"MVLSAADKGNVKAAWGKVGGHAAEYGAELERMFLSFPTTKTYFPHF-
DLSHGSAQVKGHGAKVAAALTKAVEHLDDLPGALSELSDLHAHKLRVDPVNFKLLSHSLLVTLASHLPSDFTPAVHASLKDFLANVS
TVLTSKYR",
"MVLSAADKTNVKAAWSKVGGHAGEYGAELERMFLGFPTTKTYFPHF-
DLSHGSAQVKAHGKKVGDALTLAVGHLDDLPGALSNLSDLHAHKLRVDPVNFKLLSHCLLSTLAVHLPNDFTPAVHASLDKFLSSVS
TVLTSKYR",
"MVLSAADKTNVKAAWSKVGGNAGEFGAEALERMFLGFPTTKTYFPHF-
DLSHGSAQVKAHGKKVGDALTLAVGHLDDLPGALSNLSDLHAHKLRVDPVNFKLLSHCLLSTLAVHLPNDFTPAVHASLDKFLSTVS
TVLTSKYR"]
```

```
mafft = [
    "MVLSGEDKSNIAAWGKIGGHGAEYGAELERMFLSFPTTKTYFPHF-
DVSHGSAQVKGHGKKVADALASAAGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLASHHPADFTPAVHASLKDFLASVS
TVLTSKYR",
    "MVLSAADKTNVKAAWSKVGGHAGEYGAELERMFLGFPTTKTYFPHF-
DLSHGSAQVKAHGKKVGDALTLAVGHLDDLPGALSNLSDLHAHKLRVDPVNFKLLSHCLLSTLAVHLPNDFTPAVHASLDKFLSSVS
TVLTSKYR",
    "MVLSAADKTNVKAAWSKVGGNAGEFGAEALERMFLGFPTTKTYFPHF-
DLSHGSAQVKAHGKKVGDALTLAVGHLDDLPGALSNLSDLHAHKLRVDPVNFKLLSHCLLSTLAVHLPNDFTPAVHASLDKFLSTVS
TVLTSKYR",
    "MVLSAADKGNVKAAWGKVGGHAAEYGAELERMFLSFPTTKTYFPHF-
DLSHGSAQVKGHGAKVAAALTKAVEHLDDLPGALSELSDLHAHKLRVDPVNFKLLSHSLLVTLASHLPSDFTPAVHASLKDFLANVS
TVLTSKYR",
    "MVLSPADKTNVKTAWGKVGGAHAGDYGAEALERMFLSFPTTKTYFPHF-
DLSHGSAQVKDHGKKVADALTNAAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLKDFLASVS
TVLTSKYR",
    "MVLSPADKTNVKAAWGKVGGAHAGEYGAELERMFLSFPTTKTYFPHF-
DLSHGSAQVKGHGKKVADALTNAAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLKDFLASVS
TVLTSKYR",
    "-VLSAADKANVKAAWGKVGQGAGAHGAEALERMFLGFPTTKTYFPHF-
NLSHGSDQVKAHGQKVADALTKAVGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHHPDDFNPSVHASLKDFLANVS
TVLTSKYR",
    "MVLSADDKTNIKNCWKGKIGGHGGEYGEEALQRMFAAFPTTKTYFSHI-
DVSPGSAQVKAHGKKVADALAKAADHVEDLPGALSTLSDLHAHKLRVDPVNFKFLSHCLLVTLACHHPGDFTPAMHASLKDFLASVS
TVLTSKYR",
    "-VLSPADKTNIKSTWDKIGGHAGDYGGEALDRTFQSFPPTTKTYFPHF-
DLSPGSAQVKAHGKKVADALTTAVAHLLDLPGALSALSDLHAYKLRVDPVNFKLLSHCLLVTLACHHPTEFTPAVHASLKDFFAAVS
TVLTSKYR",
    "MVLSANDKSNVKSIFSISKISSHAEYGAETLERMFTTYPQTKTYFPHF-
DLHHGSAQVKAHGKKVAAALIEAANHIDDIAGALSKLSDLHAEKLRVDPVNFKLLGQCFMVVVAIHHPALTPEIHASLDKFLCAVG
NVLTSKYR",
    "_"
]

SLSDKDKAAVRALWSKIGKSADAIGNDALSRMIVVYPQTKTYFSHWPDVTPGSPHIKAHGKKVMGGIALAVSKIDDLKTGLMELSEQ
HAYKLRVDPANFKILNHCILVVISTMFPKEFTPEAHVSLDKFLSGVALALAEERYR"]
```

```
muscle = [
    "_"
]

SLSDKDKAAVRALWSKIGKSADAIGNDALSRMIVVYPQTKTYFSHWPDVTPGSPHIKAHGKKVMGGIALAVSKIDDLKTGLMELSEQ
HAYKLRVDPANFKILNHCILVVISTMFPKEFTPEAHVSLDKFLSGVALALAEERYR",
```

```

"MVLSANDKSNVKSIFSKISSHAEYGAETLERMFTTYPQTKTYFPHF-
DLHHGSAQVKAHGKKVAAALIEAANHIDDIAGALSKLSDLHAEKLRVDPVNFKLLGQCQFMVVVAIHHPALTPEIHASLDKFLCAVG
NVLTISKYR",
"-VLSPADKTNIKSTWDKIGGHAGDYGGEEALDRFTQSFPTTKTYFPHF-
DLSPGSAQVKAHGKKVADALTTAVAHLDLPGALSALSDLHAYKLRVDPVNFKLLSHCLLVTLACHHPTEFTPAVHASLDKFFAAVS
TVLTISKYR",
"MVLSADDKTNIKNCWGKIGGHGGEYGEELQRMFAAFPTTKTYFSHI-
DVSPGSAQVKAHGKKVADALAKAADHVEDLPGALSTLSDLHAHKLRVDPVNFKFLSHCLLVTLACHHPGDFTPAMHASLDKFLASVS
TVLTISKYR",
"-VLSAADKANVKAAGWKVGGQAGAHGAEALERMFLGFPTTKTYFPHF-
NLSHGSDQVKAHGQKVADALTKAVGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHHPDDFNPSVHASLDKFLANVS
TVLTISKYR",
"MVLSGEDKSNIAAWGKIGGHGAEYGAELERMFAFPTTKTYFPHF-
DVSHGSAQVKGHGKKVADALASAAGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLASHHPADFTPAVHASLDKFLASVS
TVLTISKYR",
"MVLSPADKTNVKTAWGKVGAGAHAGDYGAELERMFLSFPTTKTYFPHF-
DLSHGSAQVKDHGKKVADALTNAAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS
TVLTISKYR",
"MVLSPADKTNVKAAGWKVGAHAGEYGAELERMFLSFPTTKTYFPHF-
DLSHGSAQVKGHGKKVADALTNAAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVS
TVLTISKYR",
"MVLSAADKGNVKAAGWKVGGHAAEYGAELERMFLSFPTTKTYFPHF-
DLSHGSAQVKGHGKAVAAALTKAVEHLDDLPGALSELSDLHAHKLRVDPVNFKLLSHSLLVTLASHLPSTFTPAVHASLDKFLANVS
TVLTISKYR",
"MVLSAADKTNVKAAWSKVGGHAGEYGAELERMFLGFPTTKTYFPHF-
DLSHGSAQVKAHGKKVGDALTLAVGHLDDLPGALSNLSDLHAHKLRVDPVNFKLLSHCLLSTLAVHLPNDFTPAVHASLDKFLSSVS
TVLTISKYR",
"MVLSAADKTNVKAAWSKVGGNAGEFGAEALERMFLGFPTTKTYFPHF-
DLSHGSAQVKAHGKKVGDALTLAVGHLDDLPGALSNLSDLHAHKLRVDPVNFKLLSHCLLSTLAVHLPNDFTPAVHASLDKFLSTVS
TVLTISKYR"]

df =
pd.DataFrame([compute_conservation_scores(clustal)["Entropy"],compute_conservation_scor
es(mafft)["Entropy"],compute_conservation_scores(muscle)["Entropy"]]).transpose()
df.columns = ["Clustal Omega","MAFFT","MUSCLE"]
print(df)

print("\nThe correlation between the conservation scores of the different alignments
are:\n")
print(df.corr())

```

The results obtained from this is shown below:

```

Run - Anirudh-Python
workboard
C:\Users\anira\PycharmProjects\Anirudh-Python\venv\Scripts\python.exe C:/Users/anira/P
Clustal Omega  MAFFT  MUSCLE
0      0.000  0.000  0.000
1     -0.305 -0.305 -0.305
2      0.000  0.000  0.000
3      0.000  0.000  0.000
4     -1.121 -1.121 -1.121
..      ...   ...   ...
138    -0.305 -0.305 -0.305
139    -0.305 -0.305 -0.305
140    -0.305 -0.305 -0.305
141      0.000  0.000  0.000
142      0.000  0.000  0.000

[143 rows x 3 columns]

The correlation between the conservation scores of the different alignments are:

      Clustal Omega  MAFFT  MUSCLE
Clustal Omega      1.0    1.0    1.0
MAFFT              1.0    1.0    1.0
MUSCLE             1.0    1.0    1.0

Process finished with exit code 0

```

From this, we can say that the conservation scores obtained from the three alignment methods are identical.

The manual verification of the unweighted frequency entropy scores at the given positions is shown below:

Pos. 9 = A, S, T, T, A, S, T, T, G, T, T

$$f(A) = \frac{2}{11}, f(S) = \frac{2}{11}, f(T) = \frac{6}{11}, f(G) = \frac{1}{11}$$

$$= 0.182 \quad = 0.182 \quad = 0.545 \quad = 0.091$$

$$\text{Entropy score} = \sum f(i) \ln(f(i))$$

$$= 0.182(-1.704) + 0.182(-1.704) + 0.545(-0.607) + 0.091(-2.397)$$

$$= -1.169 \Rightarrow \text{verified}$$

Pos. 11 = V, V, I, I, V, I, V, V, V, V, V

$$f(V) = \frac{8}{11}, f(I) = \frac{3}{11}$$

$$= 0.727 \quad = 0.273$$

$$\text{Entropy score} = 0.727(-0.319) + 0.273(-1.293)$$

$$= -0.586 \Rightarrow \text{verified}$$

Pos. 20 = K, S, G, G, G, G, A, A, G, G, G

$$f(K) = \frac{1}{11}, f(S) = \frac{1}{11}, f(G) = \frac{7}{11}, f(A) = \frac{2}{11}$$

$$= 0.091 \quad = 0.091 \quad = 0.636 \quad = 0.182$$

$$\text{Entropy score} = 0.091(-2.397) + 0.091(-2.397) + 0.636(-0.453) + 0.182(-1.704)$$

$$= -1.034 \Rightarrow \text{verified}$$

Pos. 22 = A, A, A, G, A, G, A, A, A, A, A

$$f(A) = \frac{9}{11}, f(G) = \frac{2}{11}$$

$$= 0.818 \quad = 0.182$$

$$\text{Entropy score} = 0.818(-0.201) + 0.182(-1.704)$$

$$= -0.474 \Rightarrow \text{verified}$$

Pos. 30 = L, L, L, L, L, L, L, L, L, L, L

$$f(L) = \frac{11}{11} = 1$$

$$\text{Entropy score} = 1(0)$$

$$= 0 \Rightarrow \text{verified}$$

The conservation scores for 1BTM Chain A were obtained used ConSurf. The results are shown below:

[illegible]