



wwPDB EM Validation Summary Report ⓘ

May 19, 2025 – 06:48 PM EDT

PDB ID : 9BUT / pdb_00009but
EMDB ID : EMD-44919
Title : Single particle CryoEM structure of the Pf80S ribosome in the rotated-2 PRE state (rt state with P and E-site tRNA)
Authors : Anton, L.; Haile, M.; Ho, C.M.
Deposited on : 2024-05-17
Resolution : 2.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

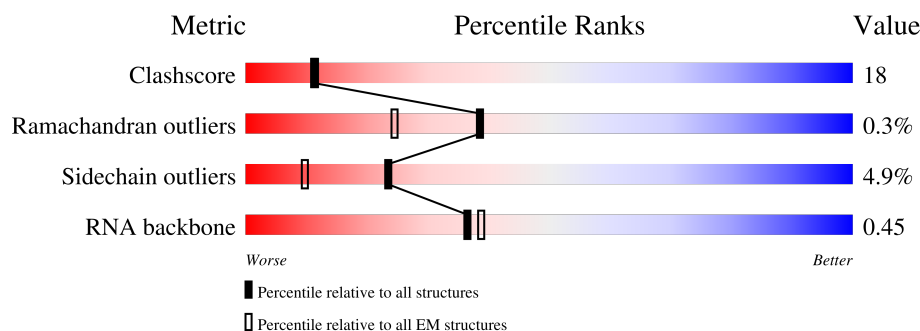
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.









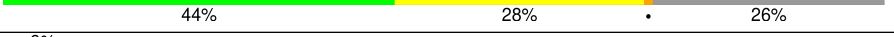
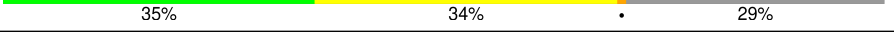
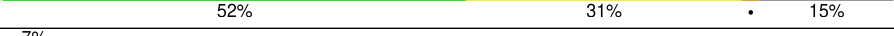

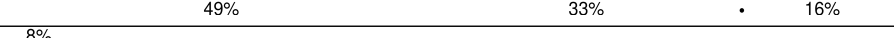
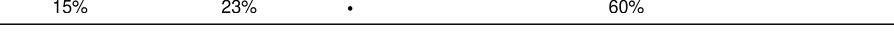

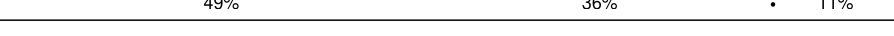


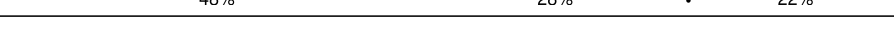

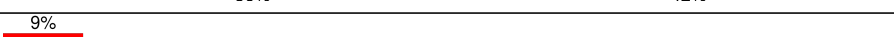






Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	S7	76	<div> <div>29%</div> <div>54%</div> <div>17%</div> </div>
1	S9	76	<div> <div>9%</div> <div>41%</div> <div>45%</div> <div>14%</div> </div>
2	AA	3788	<div> <div>32%</div> <div>41%</div> <div>11%</div> <div>16%</div> </div>
3	AC	159	<div> <div>36%</div> <div>47%</div> <div>13%</div> <div>5%</div> </div>
4	AB	119	<div> <div>29%</div> <div>48%</div> <div>22%</div> </div>
5	AL	215	<div> <div>62%</div> <div>36%</div> </div>
6	A1	146	<div> <div>16%</div> <div>51%</div> <div>44%</div> </div>









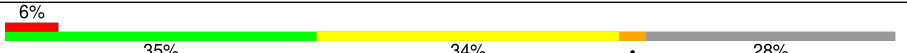
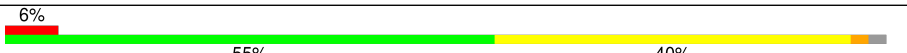
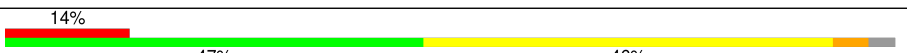
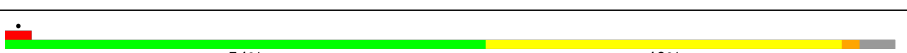
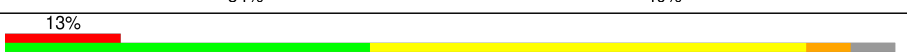
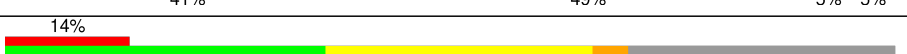
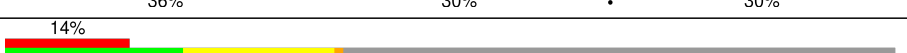


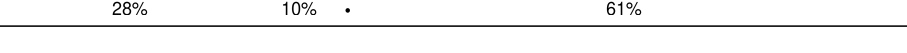







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Mol	Chain	Length	Quality of chain
7	A2	127	
8	A4	67	
9	A6	108	
10	A7	120	
11	AN	165	
12	A8	131	
13	A9	140	
14	Aa	150	
15	Ab	112	
16	Ad	87	
17	Ae	51	
18	Af	128	
19	AP	205	
20	Ah	96	
21	Ai	104	
22	AI	221	
23	AJ	283	
24	Ac	92	
25	AK	202	
26	AM	139	
27	AS	187	
28	AO	148	
29	AQ	219	
30	AR	294	
31	AW	173	


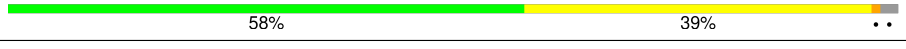
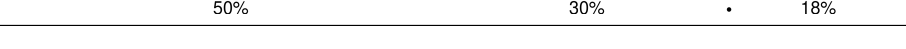




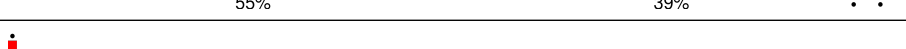
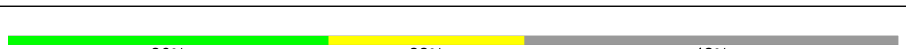


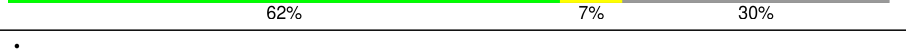
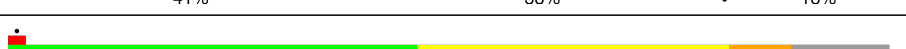
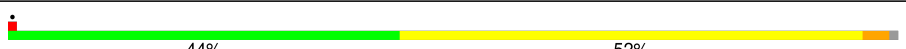

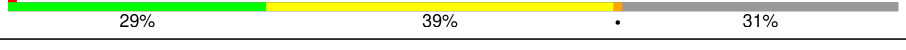
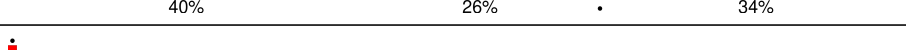






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Mol	Chain	Length	Quality of chain
32	AY	190	
33	AT	182	
34	AZ	126	
35	A3	124	
36	A5	257	
37	AD	260	
38	AE	386	
39	AF	411	
40	AG	173	
41	AU	184	
42	AH	190	
43	AV	161	
44	Ag	39	
45	AX	139	
46	A0	162	
47	S1	133	
48	S2	105	
49	S3	107	
50	S4	82	
51	S5	67	
52	S6	58	
53	SA	2092	
54	SB	262	
55	SC	263	
56	SD	221	

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Mol	Chain	Length	Quality of chain
57	SE	189	
58	SF	261	
59	SG	272	
60	SH	306	
61	SI	195	
62	SJ	194	
63	SK	130	
64	SL	218	
65	SM	144	
66	SN	118	
67	SO	137	
68	SP	151	
69	SQ	145	
70	SR	141	
71	SS	156	
72	ST	54	
73	SU	151	
74	SV	161	
75	SW	137	
76	SX	145	
77	SY	170	
78	SZ	82	
79	mR	9	

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 194842 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	S7	76	Total	C	N	O	P	0	0
			1620	723	295	527	75		
1	S9	76	Total	C	N	O	P	0	0
			1620	723	295	527	75		

- Molecule 2 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AA	3193	Total	C	N	O	P	0	0
			67884	30446	12053	22224	3161		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	151	Total	C	N	O	P	0	0
			3215	1444	589	1034	148		

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AB	118	Total	C	N	O	P	0	0
			2517	1126	457	817	117		

- Molecule 5 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AL	211	Total	C	N	O	S	0	0
			1761	1119	349	290	3		

- Molecule 6 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 7 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A2	105	Total	C	N	O	S	0	0
			837	534	152	148	3		

- Molecule 8 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 9 is a protein called 60S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A6	98	Total	C	N	O	S	0	0
			740	462	132	139	7		

- Molecule 10 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A7	96	Total	C	N	O	S	0	0
			793	508	151	129	5		

- Molecule 11 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AN	147	Total	C	N	O	S	0	0
			1210	787	212	205	6		

- Molecule 12 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A8	125	Total	C	N	O	S	0	0
			1036	660	206	163	7		

- Molecule 13 is a protein called 60S ribosomal protein L35ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A9	103	Total	C	N	O	S	0	0
			844	543	163	135	3		

- Molecule 14 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Aa	106	Total	C	N	O	S	0	0
			858	530	184	138	6		

- Molecule 15 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Ab	95	Total	C	N	O	S	0	0
			756	477	150	129			

- Molecule 16 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Ad	72	Total	C	N	O	S	0	0
			603	395	107	99	2		

- Molecule 17 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Ae	43	Total	C	N	O	S	0	0
			388	243	92	52	1		

- Molecule 18 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Af	51	Total	C	N	O	S	0	0
			413	255	87	66	5		

- Molecule 19 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AP	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 20 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Ah	85	Total	C	N	O	S	0	0
			658	417	127	107	7		

- Molecule 21 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Ai	95	Total	C	N	O	S	0	0
			778	490	152	127	9		

- Molecule 22 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AI	207	Total	C	N	O	S	0	0
			1685	1096	298	286	5		

- Molecule 23 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AJ	222	Total	C	N	O	S	0	0
			1813	1174	323	309	7		

- Molecule 24 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ac	89	Total	C	N	O	S	0	0
			709	441	150	113	5		

- Molecule 25 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AK	201	Total	C	N	O	S	0	0
			1659	1064	311	276	8		

- Molecule 26 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AM	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 27 is a protein called 60S ribosomal protein L18-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AS	186	Total	C	N	O	S	0	0
			1503	958	299	241	5		

- Molecule 28 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AO	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 29 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AQ	189	Total	C	N	O	S	0	0
			1544	984	291	261	8		

- Molecule 30 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AR	252	Total	C	N	O	S	0	0
			2049	1301	385	357	6		

- Molecule 31 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AW	170	Total	C	N	O	S	0	0
			1319	824	266	222	7		

- Molecule 32 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AY	101	Total	C	N	O	S	0	0
			796	502	144	144	6		

- Molecule 33 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AT	181	Total	C	N	O	S	0	0
			1509	952	309	244	4		

- Molecule 34 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AZ	121	Total	C	N	O	S	0	0
			1000	626	206	165	3		

- Molecule 35 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	A3	119	Total	C	N	O	S	0	0
			994	635	194	163	2		

- Molecule 36 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	A5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 37 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AD	247	Total	C	N	O	S	0	0
			1866	1166	374	317	9		

- Molecule 38 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AE	380	Total	C	N	O	S	0	0
			3061	1948	575	521	17		

- Molecule 39 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AF	390	Total	C	N	O	S	0	0
			3094	1962	594	527	11		

- Molecule 40 is a protein called 60S ribosomal protein L11a.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AG	124	Total	C	N	O	S	0	0
			1010	636	197	171	6		

- Molecule 41 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AU	180	Total	C	N	O	S	0	0
			1497	946	289	255	7		

- Molecule 42 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AH	185	Total	C	N	O	S	0	0
			1475	950	264	255	6		

- Molecule 43 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AV	155	Total	C	N	O	S	0	0
			1275	814	241	214	6		

- Molecule 44 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ag	37	Total	C	N	O	S	0	0
			343	210	86	45	2		

- Molecule 45 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AX	97	Total	C	N	O	S	0	0
			824	548	135	139	2		

- Molecule 46 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	A0	62	Total	C	N	O	S	0	0
			521	336	97	87	1		

- Molecule 47 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S1	120	Total	C	N	O	S	0	0
			985	632	189	162	2		

- Molecule 48 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	S2	41	Total	C	N	O	0	0
			320	208	56	56		

- Molecule 49 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S3	95	Total	C	N	O	S	0	0
			781	478	169	128	6		

- Molecule 50 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S4	76	Total	C	N	O	S	0	0
			586	368	102	107	9		

- Molecule 51 is a protein called 40S ribosomal protein S28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S5	59	Total	C	N	O	S	0	0
			465	290	94	80	1		

- Molecule 52 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	S6	43	Total	C	N	O	0	0
			345	213	75	57		

- Molecule 53 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SA	1608	Total	C	N	O	P	0	0
			34208	15346	6106	11170	1586		

- Molecule 54 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SB	210	Total	C	N	O	S	0	0
			1713	1097	301	303	12		

- Molecule 55 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SC	195	Total	C	N	O	S	0	0
			1538	990	266	273	9		

- Molecule 56 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SD	157	Total	C	N	O	S	0	0
			1228	782	225	214	7		

- Molecule 57 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SE	185	Total	C	N	O	S	0	0
			1514	962	290	260	2		

- Molecule 58 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SF	257	Total	C	N	O	S	0	0
			2061	1320	377	356	8		

- Molecule 59 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SG	224	Total	C	N	O	S	0	0
			1757	1132	307	309	9		

- Molecule 60 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SH	204	Total	C	N	O	S	0	0
			1651	1046	316	283	6		

- Molecule 61 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SI	180	Total	C	N	O	S	0	0
			1424	893	263	258	10		

- Molecule 62 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SJ	188	Total	C	N	O	S	0	0
			1528	982	264	278	4		

- Molecule 63 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SK	129	Total	C	N	O	S	0	0
			1037	665	189	178	5		

- Molecule 64 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SL	171	Total	C	N	O	S	0	0
			1383	872	264	243	4		

- Molecule 65 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SM	138	Total	C	N	O	S	0	0
			1098	704	200	193	1		

- Molecule 66 is a protein called 40S ribosomal protein S20e.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SN	98	Total	C	N	O	S	0	0
			772	484	135	148	5		

- Molecule 67 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SO	79	Total	C	N	O	S	0	0
			686	450	116	118	2		

- Molecule 68 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SP	127	Total	C	N	O	S	0	0
			954	591	184	176	3		

- Molecule 69 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SQ	144	Total	C	N	O	S	0	0
			1129	712	222	193	2		

- Molecule 70 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SR	98	Total	C	N	O	S	0	0
			746	474	123	145	4		

- Molecule 71 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SS	128	Total	C	N	O	S	0	0
			1046	657	205	180	4		

- Molecule 72 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	ST	48	Total	C	N	O	S	0	0
			405	252	85	64	4		

- Molecule 73 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SU	149	Total	C	N	O	S	0	0
			1202	769	220	210	3		

- Molecule 74 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SV	146	Total	C	N	O	S	0	0
			1206	772	227	200	7		

- Molecule 75 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SW	95	Total	C	N	O	S	0	0
			785	498	149	135	3		

- Molecule 76 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SX	96	Total	C	N	O	S	0	0
			776	497	137	138	4		

- Molecule 77 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SY	154	Total	C	N	O	S	0	0
			1266	811	239	214	2		

- Molecule 78 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SZ	72	Total	C	N	O	S	0	0
			557	346	102	105	4		

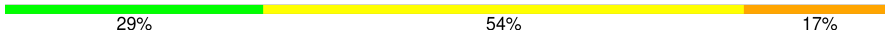
- Molecule 79 is a RNA chain called mRNA.

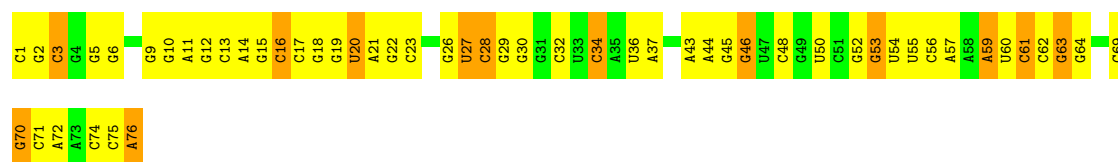
Mol	Chain	Residues	Atoms					AltConf	Trace
79	mR	9	Total	C	N	O	P	0	0
			180	81	18	72	9		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

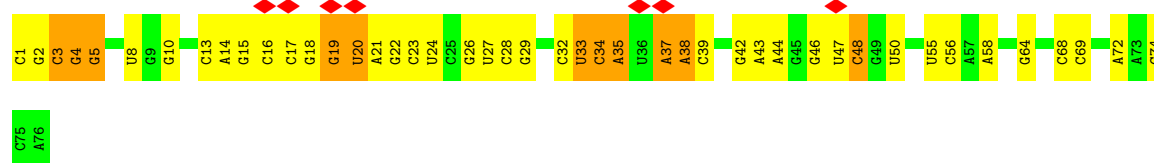
• Molecule 1: tRNA

Chain S7: 



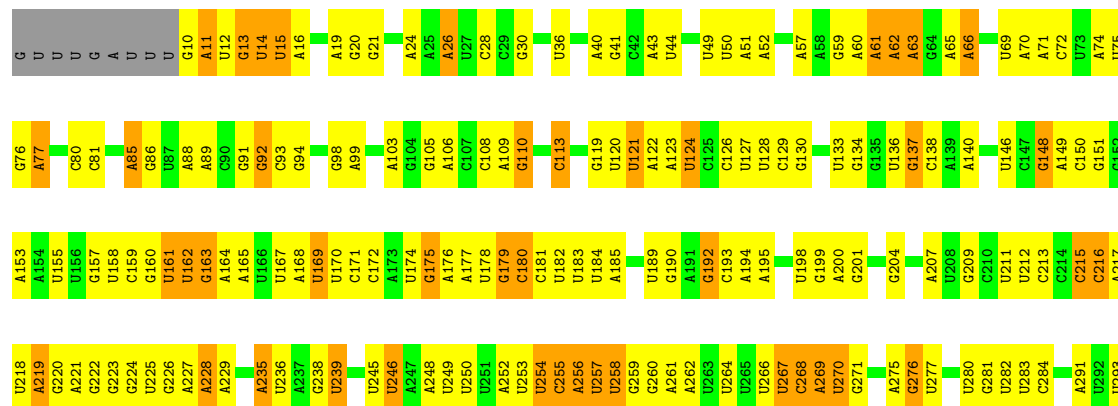
• Molecule 1: tRNA

Chain S9: 



• Molecule 2: 28S ribosomal RNA

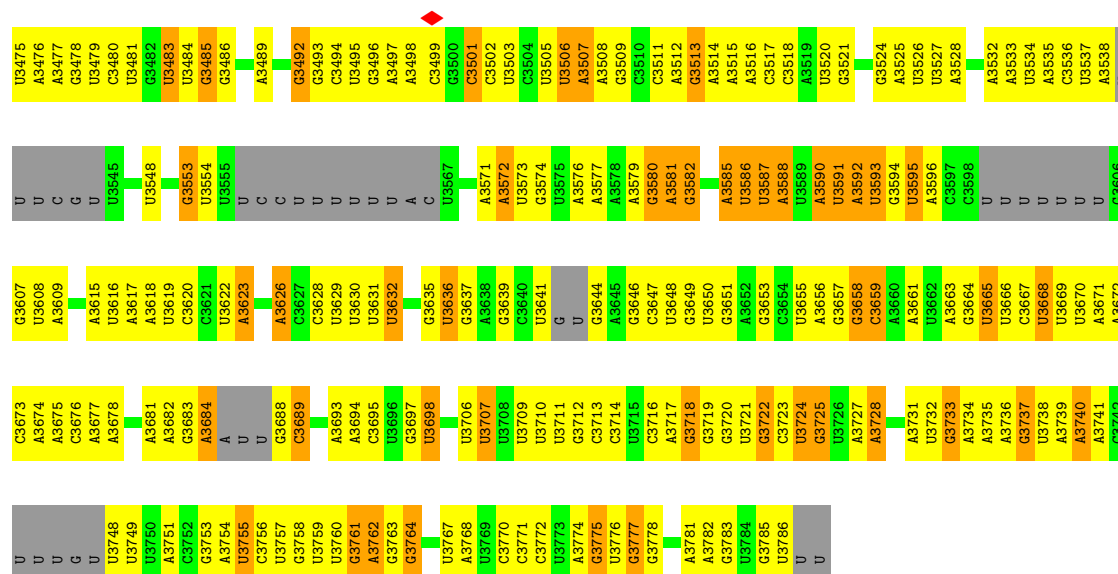
Chain AA: 





C	A1458	U1527	A1594	C1681	G1757	U1819	A1888	U	C2015	U2083	A2151	A	G
G	U1459	G1528	A1595	U1682	C1758	U1820	A1889	U	U2016	U2084	A2152	A	A
A	C1461	G1529	A1596	G1685	A1759	A1821	G1890	U	U2017	A2085	A2153	A	A
A	U1597	G1530	U1597	G1685	G1762	A1822	A1891	U	G2018	A2086	A2154	U	U
U	C1462	G1531	A1601	G1691	U1763	C1825	G1892	A	A2019	U2087	A2155	G	A
U	A1463	U1532	A1602	C1692	U1764	U1826	U1893	U	A2020	A2088	A2156	C	A
C	A1464	U1533	A1603	G1693	U1765	C1827	G1894	U	A2021	G2089	G2157	C	A
C	A1465	U1534	C1603	G1694	U1766	G1828	U1895	U	A2022	U2090	G2157	U	U
G	C1466	G1535	U1604	A1695	U1767	G1829	C1896	U1956		U2091	G2160	U	U
U	U1467	U1536	G1603	G1695	U1768	G1830	A1897	U1961	G2026	G2092	G2161	G	G
U	A1468	U1537	U1604	A1605	U1769	G1831	U1898	U1962	A2027	U2093	U2162	A	U
A	U1469	U1538	U1611	G1699	U1770	G1835	U1899	U1963	G2028	A2094	A2163	A	A
A	U1470	U1539	U1612	U1700	U1771	U1836	G1900	G1964	G2029	U2095	A2164	U	U
G	A1471	G1540	G1613	U1703	A1772	U1837	A1901	A1965	A2030	G2096	A2167	C	A
G	A1472	A1542	G1619	U1704	U1773	U1838	A1902	A1966	A2031	A2097	G2167	C	A
A	A1473	A1542	U1620	U1705	U1773	U1839	A1903	A1967	A2032	G2100	G2174	C	A
G	A1474	A1542	U1621	A1706	U1774	C1840	U1904	G1967	C2033	U2101	C2175	G	A
U	G1475	A1546	G1622	A1707	U	U1841	C1905	C1968	G2034	A2102	A2176	U	U
U	A1476	A1547	U1622	A	C	U1842	U1906	A1969	G2035	G2103	A2177	U	U
G	U1477	A1548	U1622	G	U	U1843	U1907	A1970	C2036	C2104	A2178	G	A
G	C	A1549	U1622	G	U	U1844	U1908	A1971	U2037	A2105	U2179	U	U
U	U1478	U1550	U1622	G	U	U1844	U1909	A1972	U2038	C2106	U2180	U	U
A	A1481	G1551	U1622	G	U	U1844	C1910	U1973	U2041	C2107	A2181	C	A
A	A1482	C1552	U1622	G	U	U1844	A1911	U1974	A	A2108	G2182	U	U
A	A1483	U1553	U1622	G	U	U1844	A1912	A1975	A	A2109	A2183	A	A
A	A1484	U1554	U1622	G	U	U1844	A1913	A1976	A	C2110	U2184	U	U
A	A1485	A1555	U1622	G	U	U1844	A1914	A1977	C	C2111	C2185	U	U
U	U1486	G1556	U1622	G	U	U1844	A1915	U1978	U	G2112	C2186	C	A
C	U1487	U1556	U1622	G	U	U1844	A	C1979	U	C2113	U2188	U	U
C	U1493	U1557	U1622	G	U	U1844	U	G1980	G	A2117	A2189	A	A
C	U1498	A1558	U1622	G	U	U1844	U	U1981	U	G2118	A2190	A	A
G	U1499	A1559	U1622	G	U	U1844	U	U1982	U	U2119	U	C	A
A	U1500	U1560	U1622	G	U	U1844	U	U1983	U	U2120	U	U	U
U1416	A1501	U1561	U1622	G	U	U1844	U	U1984	U	C2121	U	U	U
C1420	G1502	U1562	U1622	G	U	U1844	U	U1985	U	U2122	U	C	A
G1423	A1503	G1563	U1622	G	U	U1844	U	U1986	U	G2123	U	C	A
U1433	A1504	C1574	U1622	G	U	U1844	U	U1987	U	C2124	U	C	A
G1434	U1505	U1575	U1622	G	U	U1844	U	U1988	U	A2125	U	C	A
A1436	U1506	A1577	U1622	G	U	U1844	U	U1989	U	A2126	U	C	A
U1437	U1510	U1577	U1622	G	U	U1844	U	U1990	U	G2127	U	U	U
G1441	U1511	G1580	U1622	G	U	U1844	U	U1991	U	U2128	U	U	U
A1444	A1512	U1581	U1622	G	U	U1844	U	U1992	U	U2129	U	U	U
A1445	A1520	A1582	U1622	G	U	U1844	U	U1993	U	U2130	U	C	A
A1521	A1522	U1583	U1622	G	U	U1844	U	U1994	U	A2131	U	C	A
A1522	U1588	G1584	U1622	G	U	U1844	U	U1995	U	A2132	U	C	A
C1525	G1592	U1585	U1622	G	U	U1844	U	U1996	U	G2133	U	C	A
G1526	G1593	U1586	U1622	G	U	U1844	U	U1997	U	U2134	U	C	A
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		U1594	U1622	G	U	U1844	U	U2005	U	A2145	U	C	A
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		U1596	U1622	G	U	U1844	U	U2007	U	A2147	U	C	A
		U1597	U1622	G	U	U1844	U	U2008	U				
		U1598	U1622	G	U	U1844	U	U2009	U				
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		U1612	U1622	G	U	U1844	U	U2023	U				
		U1613	U1622	G	U	U1844	U	U2024	U				
		U1614	U1622	G	U	U1844	U	U2025	U				
		U1615	U1622	G	U	U1844	U	U2026	U				
		U1616	U1622	G	U	U1844	U	U2027	U				
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		U1618	U1622	G	U	U1844	U	U2029	U				
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		U1627	U1622	G	U	U1844	U	U2038	U				
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		U1630	U1622	G	U	U1844	U	U2041	U				
		U1631	U1622	G	U	U1844	U	U2042	U				
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		U1635	U1622	G	U	U1844	U	U2046	U				
		U1636	U1622	G	U	U1844	U	U2047	U				
		U1637	U1622	G	U	U1844	U	U2048	U				
		U1638	U1622	G	U	U1844	U	U2049	U				
		U1639	U1622	G	U	U1844	U	U2050	U				
		U1640	U1622	G	U	U1844	U	U2051	U				
		U1641	U1622	G	U	U1844	U	U2052	U				
		U1642	U1622	G	U	U1844	U	U2053	U				
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		U1656	U1622	G	U	U1844	U	U2067	U				
		U1657	U1622	G	U	U1844	U	U2068	U				
		U1658	U1622	G	U	U1844	U	U2069	U				
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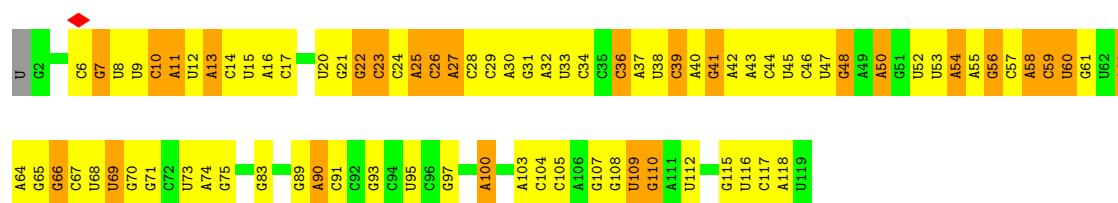
• Molecule 3: 5.8S ribosomal RNA

Chain AC: 36% 47% 13% 5%



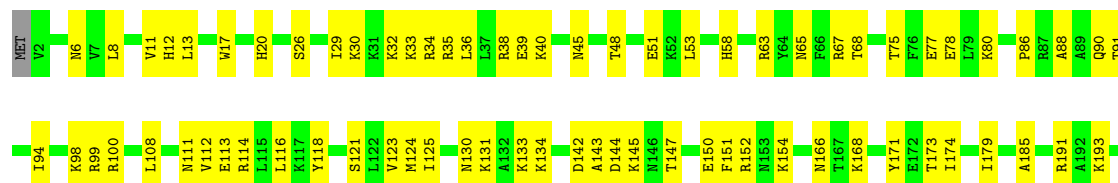
• Molecule 4: 5S ribosomal RNA

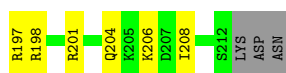
Chain AB: 29% 48% 22%



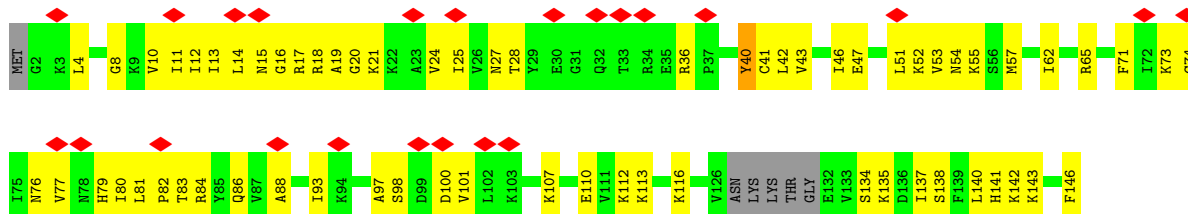
• Molecule 5: 60S ribosomal protein L13

Chain AL: 62% 36%

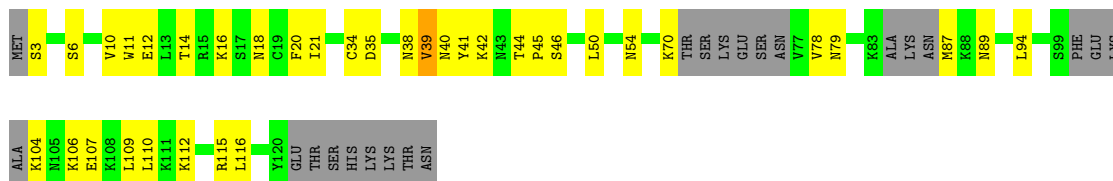




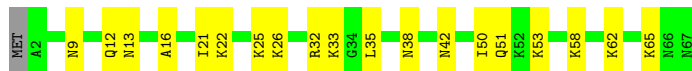
- Molecule 6: 60S ribosomal protein L27



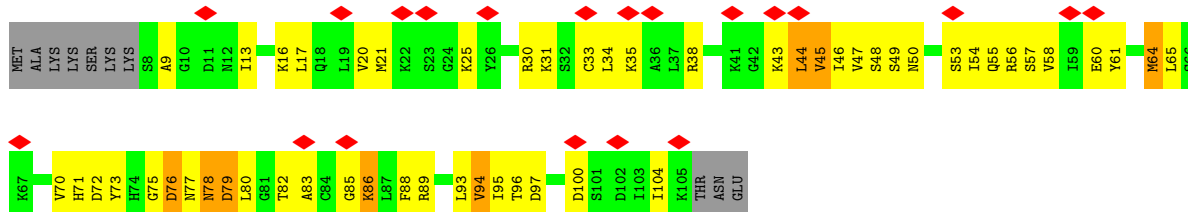
- Molecule 7: 60S ribosomal protein L28



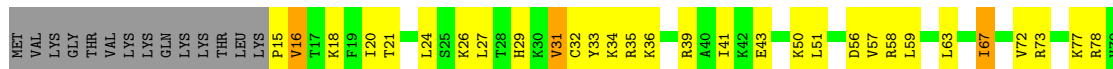
- Molecule 8: 60S ribosomal protein L29



- Molecule 9: 60S ribosomal protein L30e

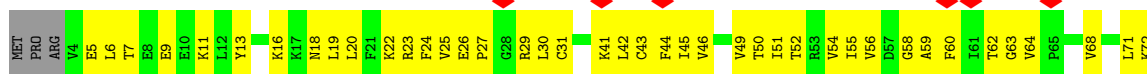


- Molecule 10: 60S ribosomal protein L31

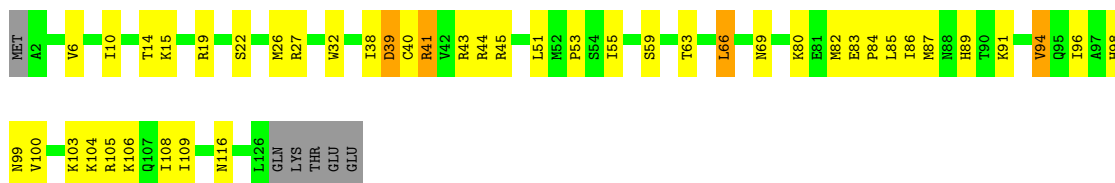




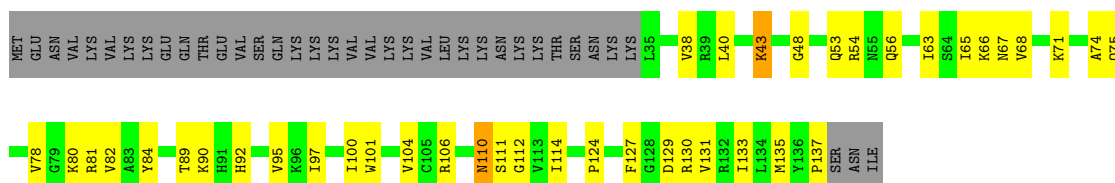
- Molecule 11: 60S ribosomal protein L14



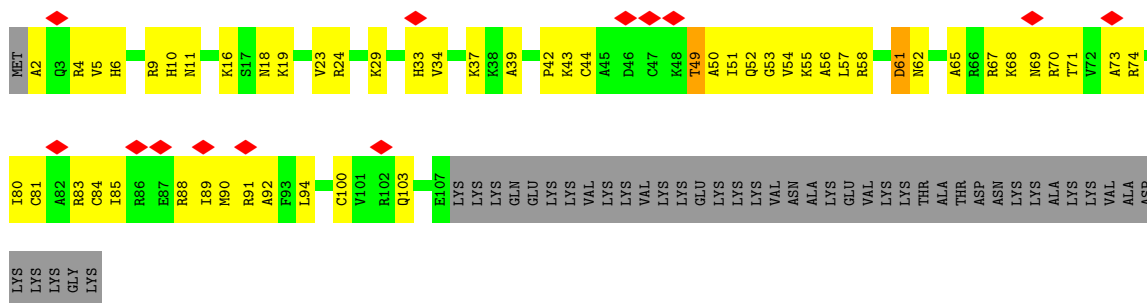
- Molecule 12: 60S ribosomal protein L32



- Molecule 13: 60S ribosomal protein L35ae

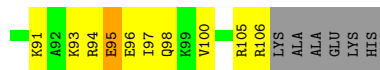


- Molecule 14: 60S ribosomal protein L34



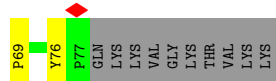
- Molecule 15: 60S ribosomal protein L36

Response	Percentage
Yes	52%
No	31%
Don't know	1%
No answer	15%



- Molecule 16: 60S ribosomal protein L38

Frequency	Percentage
Very often	7%
Often	38%
Sometimes	41%
Never	17%



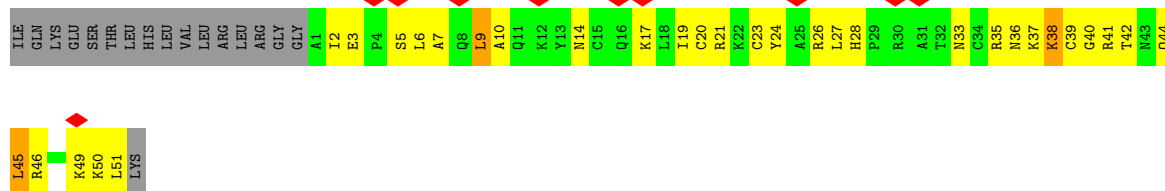
- Molecule 17: 60S ribosomal protein L39

Response	Percentage
Yes	49%
No	33%
Don't know	1%
No answer	16%



- Molecule 18: Ubiquitin-60S ribosomal protein L40

Response	Percentage
Very bad	8%
Bad	15%
Okay	23%
Good	60%



- Molecule 19: Ribosomal protein L15

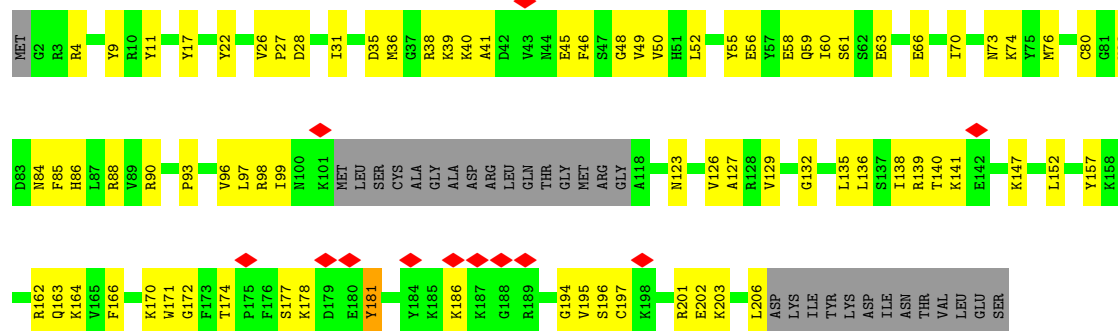
Response	Percentage
Yes, the U.S. is a threat to my country	58%
No, the U.S. is not a threat to my country	39%



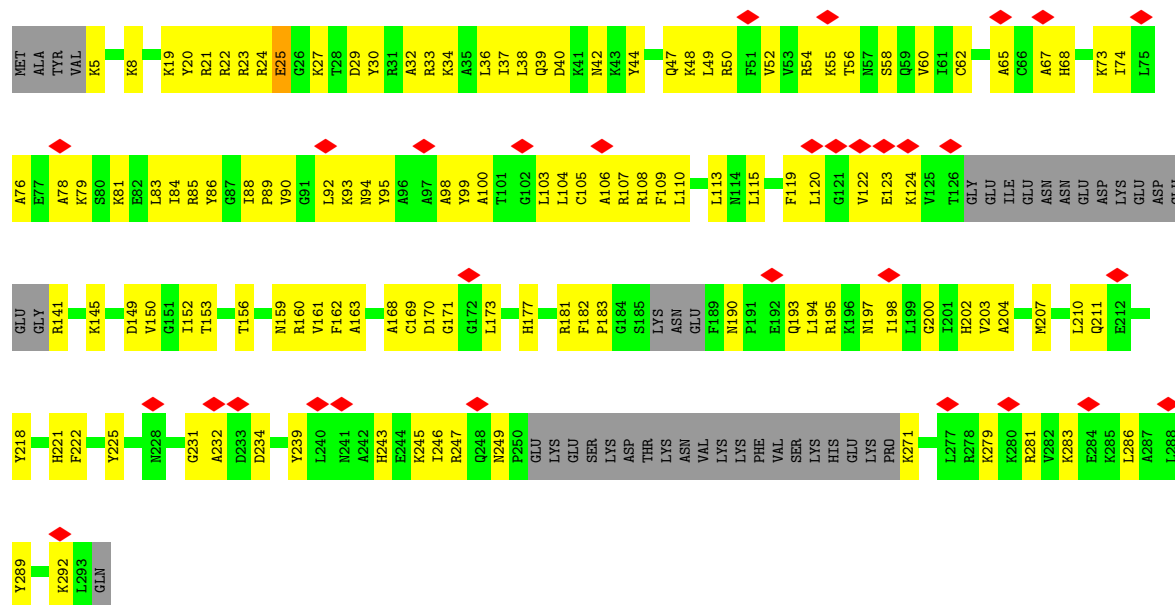
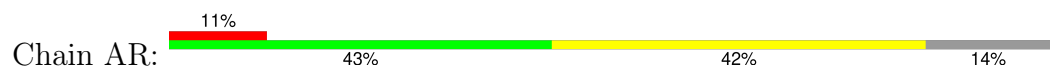




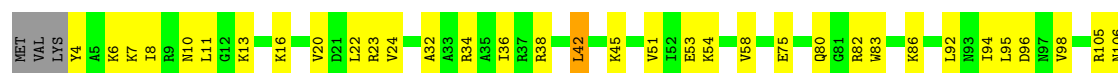
- Molecule 29: 60S ribosomal protein L10



- Molecule 30: 60S ribosomal protein L5

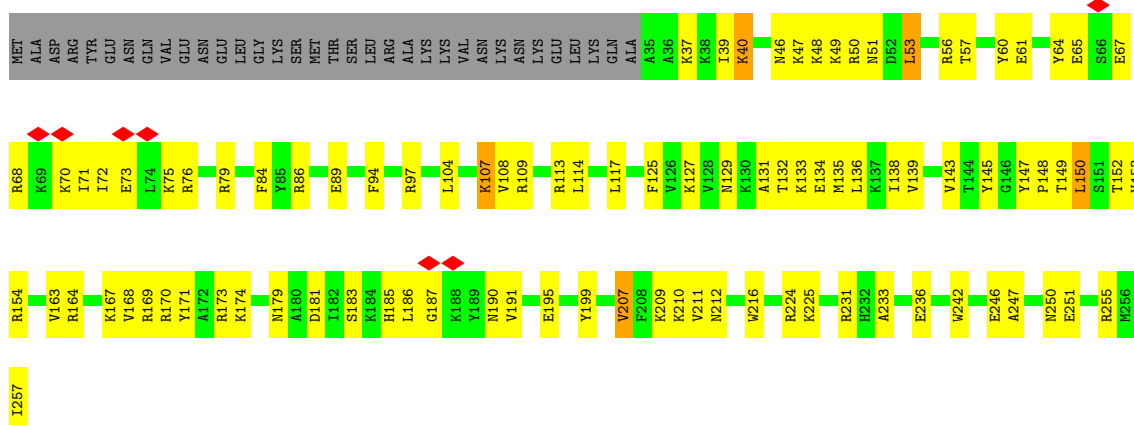


- Molecule 31: 60S ribosomal protein L17

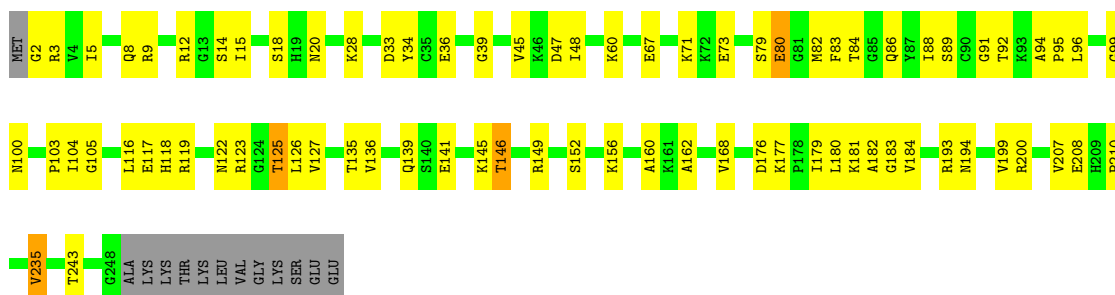




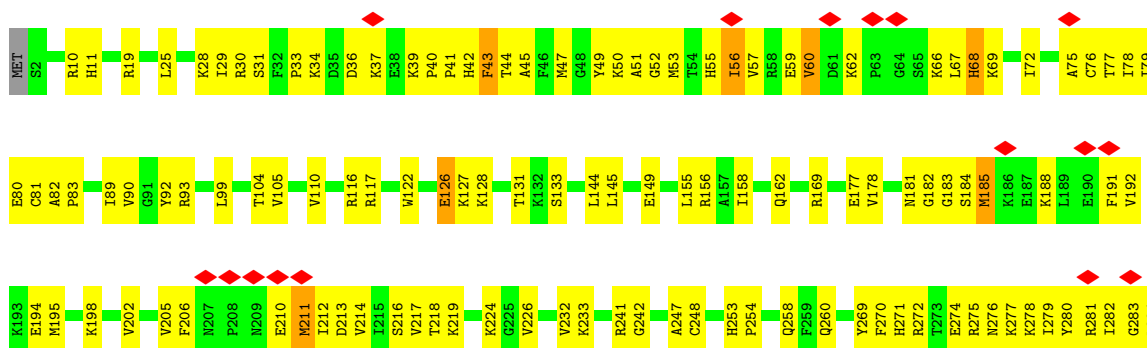
• Molecule 36: 60S ribosomal protein L7

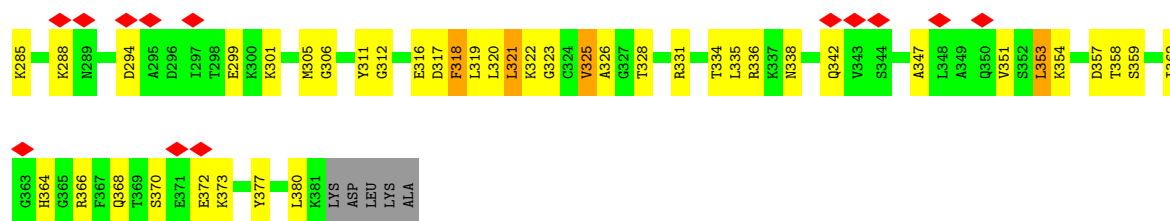


• Molecule 37: 60S ribosomal protein L2



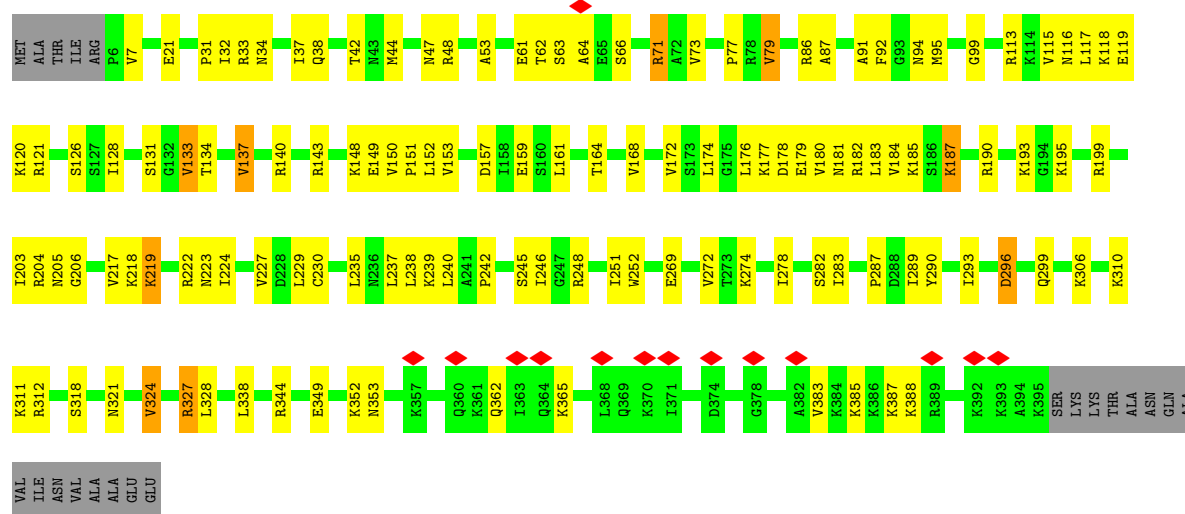
• Molecule 38: 60S ribosomal protein L3





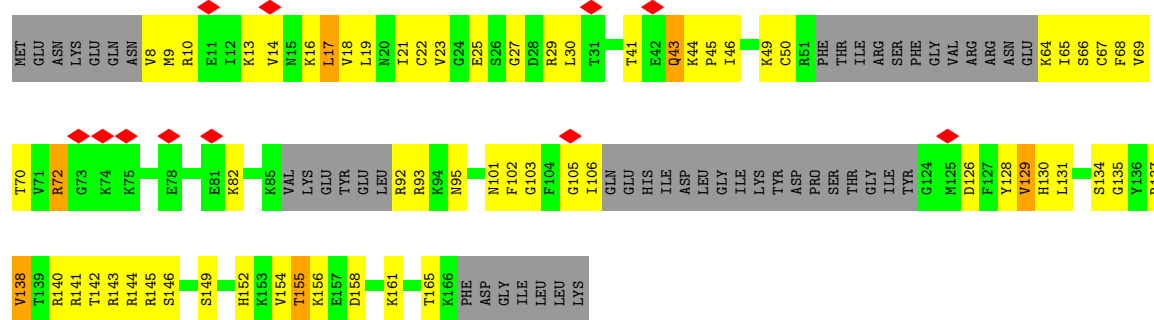
• Molecule 39: 60S ribosomal protein L4

Chain AF: 64% 29% • 5%



• Molecule 40: 60S ribosomal protein L11a

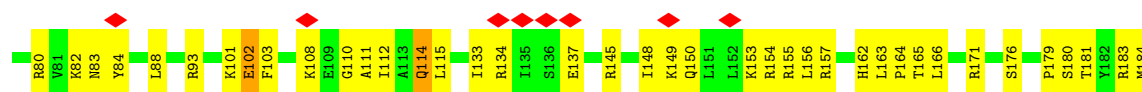
Chain AG: 6% 35% 34% • 28%



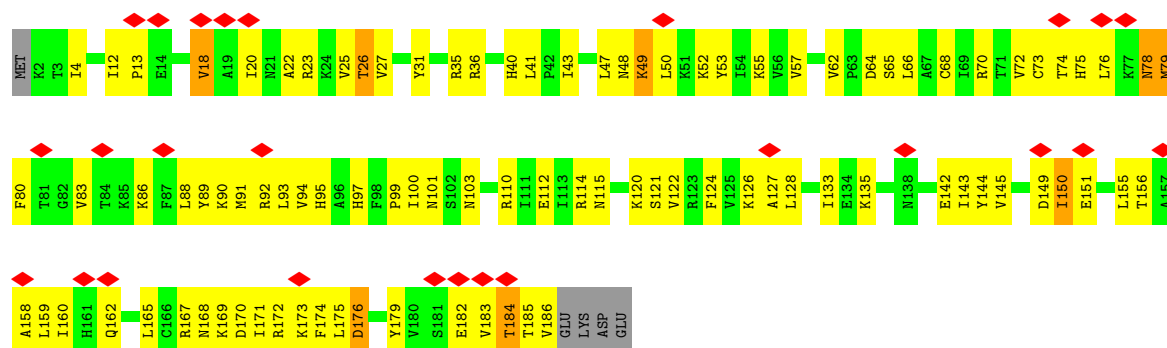
• Molecule 41: 60S ribosomal protein L18a

Chain AU: 6% 55% 40% • •





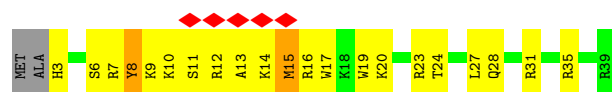
• Molecule 42: 60S ribosomal protein L6



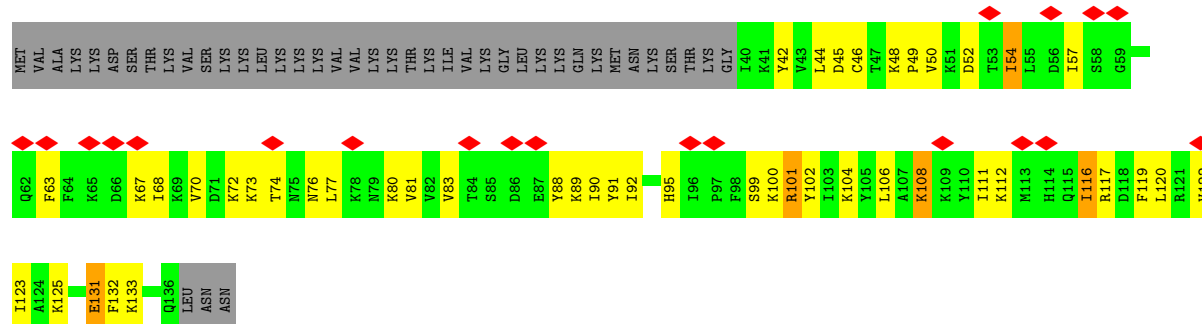
• Molecule 43: 60S ribosomal protein L21



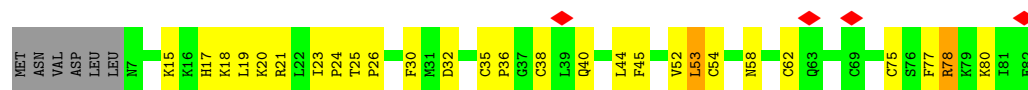
• Molecule 44: 60S ribosomal protein L41



• Molecule 45: 60S ribosomal protein L22



- Chain S4: 



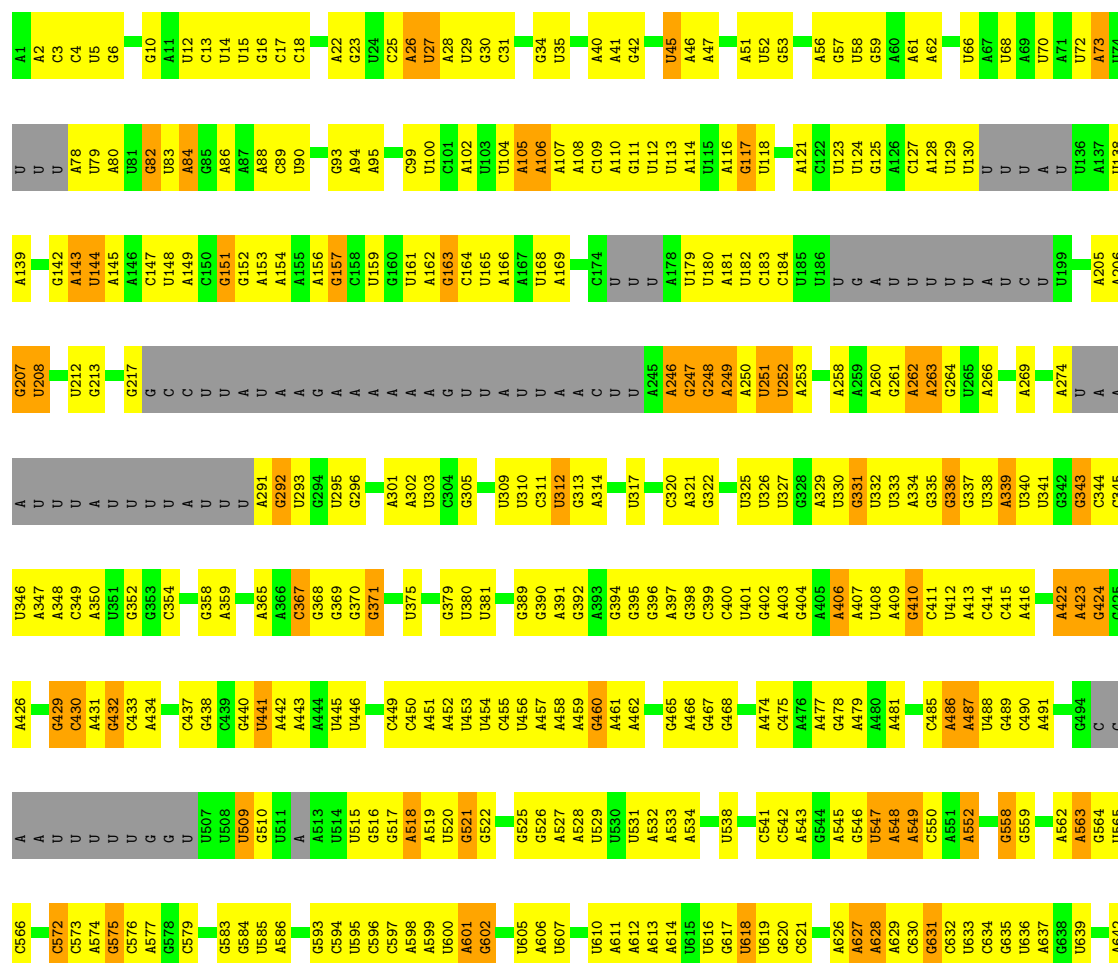
- Molecule 51: 40S ribosomal protein S28e



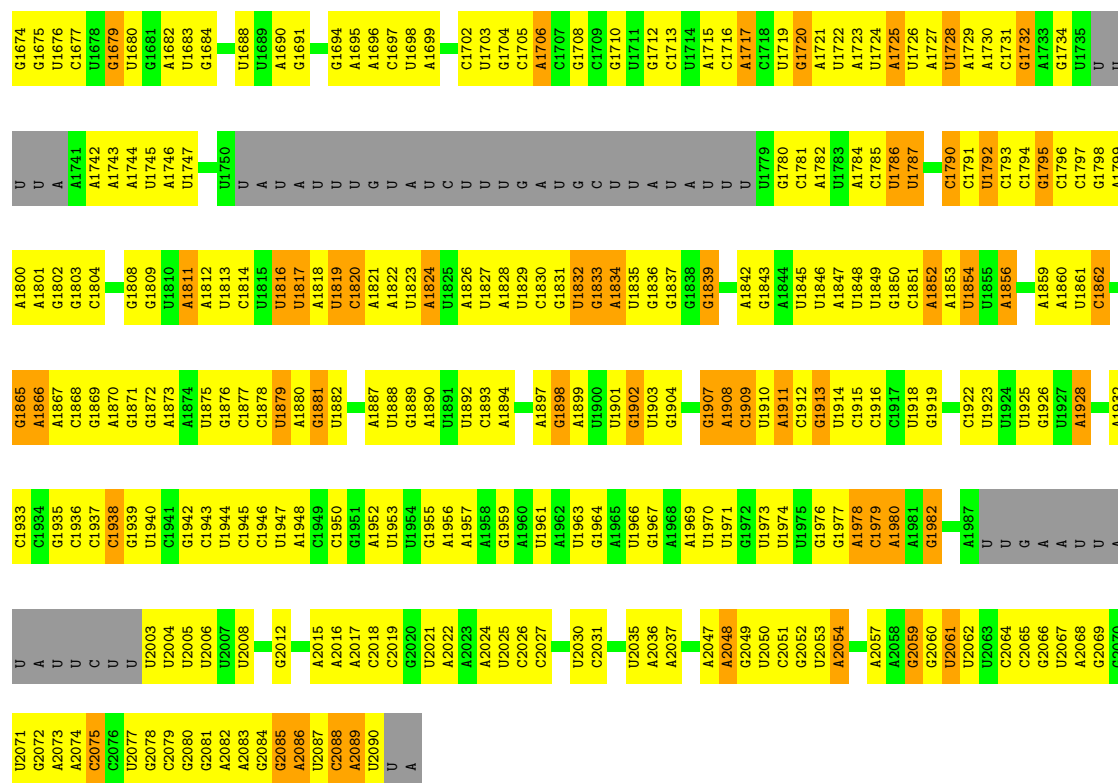
- Molecule 52: 40S ribosomal protein S30



- Molecule 53: 18S ribosomal RNA

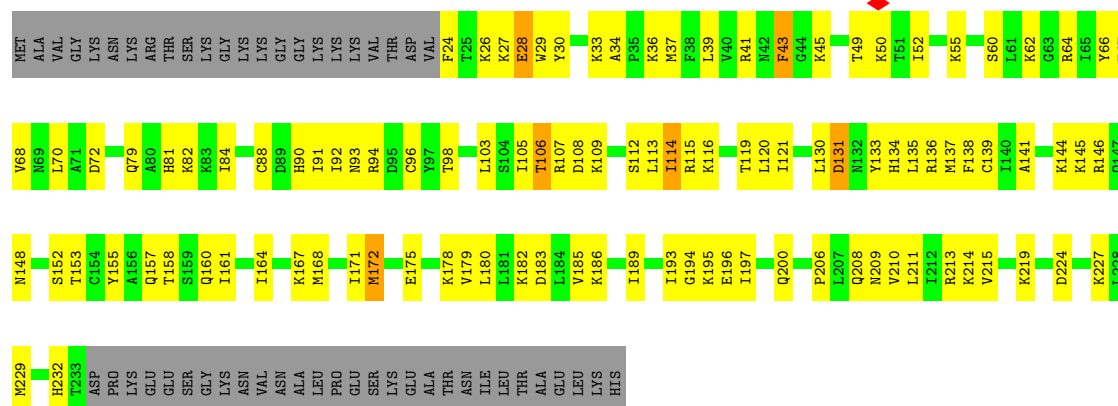


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U1608	C1609	U1610	U	C	A	A1428	A	A1295	A1225	C	U1093	C959	U894	G829	U	U	U	U644
U1609	U1610	U	C	C	U	C1429	U	A1296	A1226	U	A1094	A960	U895	U850	U	A	A	U645
U	G	C	U	U	U	C1430	U	A1297	A1227	U	A1095	U1025	U896	U831	U	A	U	U646
U	G	C	U	C	U	C1431	C	C1298	C1228	U	A1096	A962	U897	A832	G	A	U	U647
A	U	U	G	G	U	A1432	U1362	G1300	A1233	A	C1097	U963	U897	A833	C	C	C	U648
U	U	U	U	U	U	A1433	U1363	G1301	A1234	G	C1098	G964	U	A834	U	U	U	U649
U	U	U	U	U	U	A1434	U1364	G1302	U1237	A	C1099	U965	U	G835	C	G	U	U650
G	U	C	C	C	U	C1435	G1365	A1303	A1238	G	U1100	U966	C	G836	U	C	C	U651
A	U	U	U	U	U	A1436	A1366	A1304	U1239	U	C1101	A967	U	A837	U	U	U	U652
A	U	U	U	U	U	U1437	U1367	A1305	A1238	G1165	C1102	G968	U	U838	G	C	C	U653
A	U	U	U	U	U	A1438	G1368	C1306	A1239	U	C1103	A969	U	U	U	U	U	U654
A	U	U	U	U	U	A1439	G1369	U1307	A1240	U1168	G1104	G970	U	U	C	C	C	C855
U	U	U	U	U	U	A1440	U1370	C1308	A1241	C1169	A1105	G971	U905	A	U	U	U	G
U	U	U	U	U	U	C1441	U1371	A1309	G1242	C1170	C1106	U972	U906	C	U	U	U	A
U	U	U	U	U	U	U1442	U	A1310	A1243	C1171	U1107	U973	U907	U843	U	U	U	U
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U	U	U	U	U	U	A1462	U1396	U	A1266	U1194	A	A1002	A932	U863	A	A	A	U
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U	U	U	U	U	U	A	A	G	U1269	U1199	A	A999	U936	A866	A	A	A	G
U	U	U	U	U	U	U	U	C	G1270	U1200	U	C1000	U937	A867	A	A	A	G
U	U	U	U	U	U	U	U	C	A1271	G1203	A	A1001	U938	U868	A	A	A	U
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U	U	U	U	U	U	U	U	C	U1277	C1206	A	U1004	C941	A871	U745	U	U	U
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U	U	U	U	U	U	U	U	C	G1279	G1208	U	C1006	U943	A873	U747	U	U	A
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U	U	U	U	U	U	U	U	C	A1284	G1213	U	U1011	A948	A878	U752	U	U	A
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U	U	U	U	U	U	U	U	C	U1301	G1231	U	U1025	U964	A895	U	U	U	U
U	U	U	U	U	U	U	U	C	U1302	G1232	U	U1026	U965	A896	U	U	U	U
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U	U	U	U	U	U	U	U	C	U1304	G1234	U	U1028	U967	A898	U	U	U	U
U	U	U	U	U	U	U	U	C	U1305	G1235	U	U1029	U968	A899	U	U	U	U
U	U	U	U	U	U	U	U	C	U1306	G1236	U	U1030	U969	A900	U	U	U	U
U	U	U	U	U	U	U	U	C	U1307	G1237	U	U1031	U970	A901	U	U	U	U
U	U	U	U	U	U	U	U	C	U1308	G1238	U	U1032	U971	A902	U	U	U	U
U	U	U	U	U	U	U	U	C	U1309	G1239	U	U1033	U972	A903	U	U	U	U
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U	U	U	U	U	U	U	U	C	U1317	G1247	U	U1041	U980	A911	U	U	U	U
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U																		



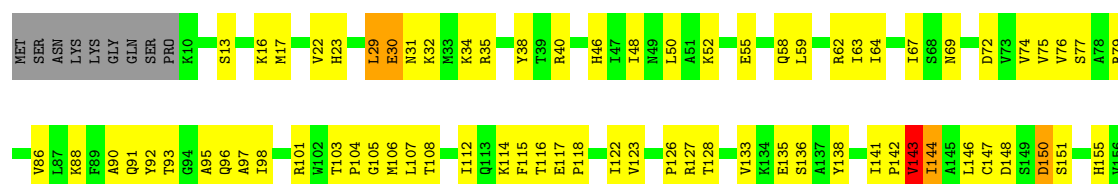
• Molecule 54: 40S ribosomal protein S3a

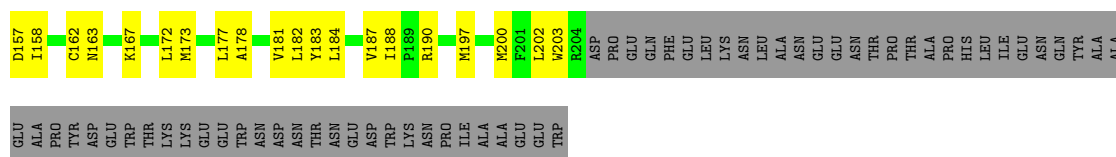
Chain SB:



• Molecule 55: 40S ribosomal protein SA

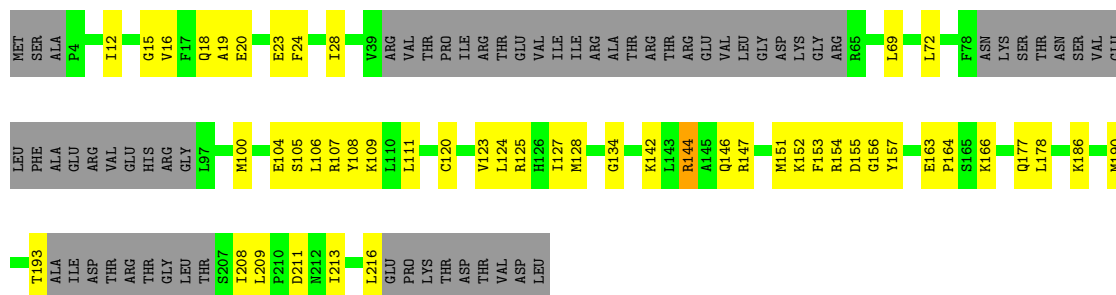
Chain SC:





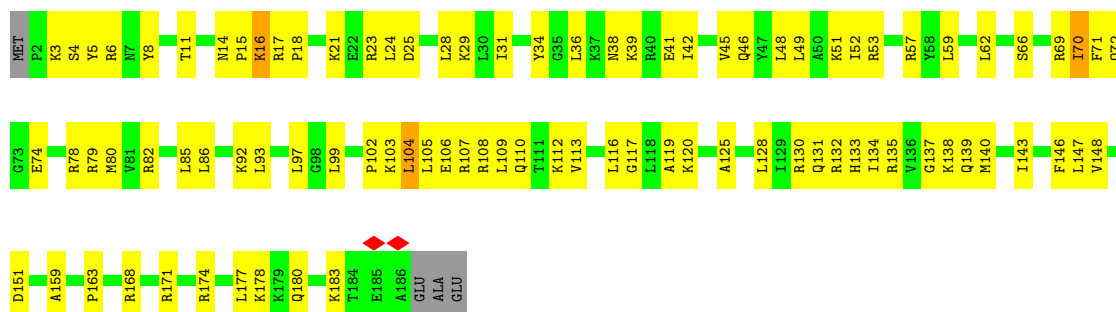
• Molecule 56: 40S ribosomal protein S3

Chain SD: 48% 22% 29%



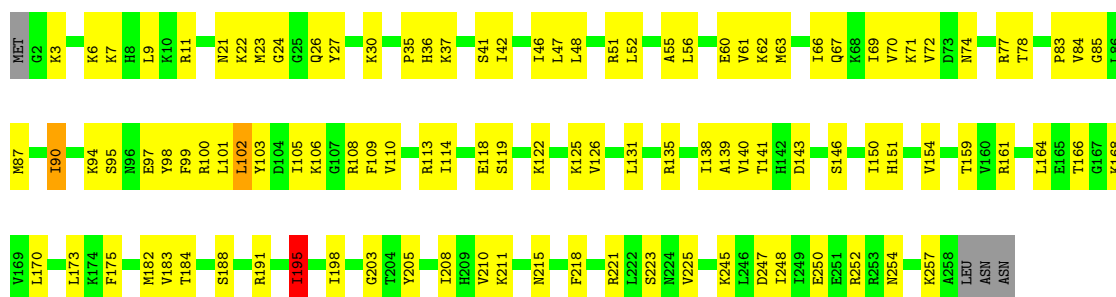
• Molecule 57: 40S ribosomal protein S9

Chain SE: 50% 47% ..



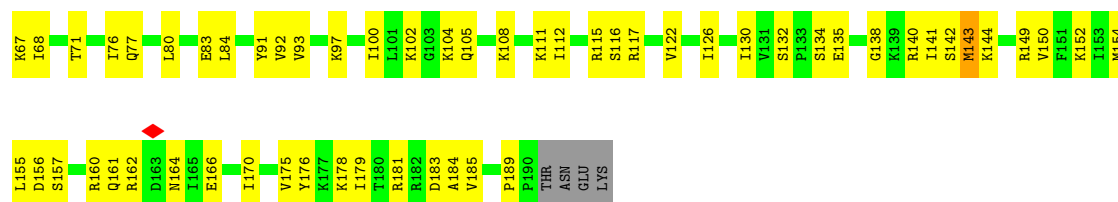
• Molecule 58: 40S ribosomal protein S4

Chain SF: 58% 39% ..



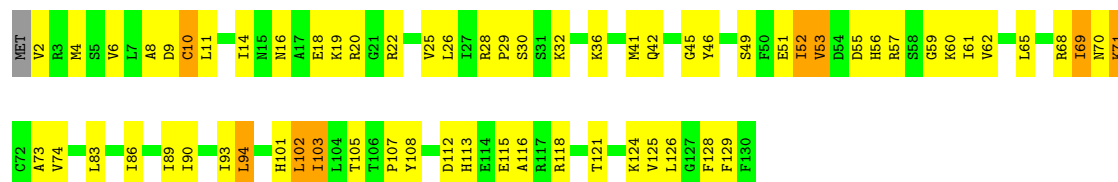
• Molecule 59: 40S ribosomal protein S5

Chain SG: 50% 30% 18%



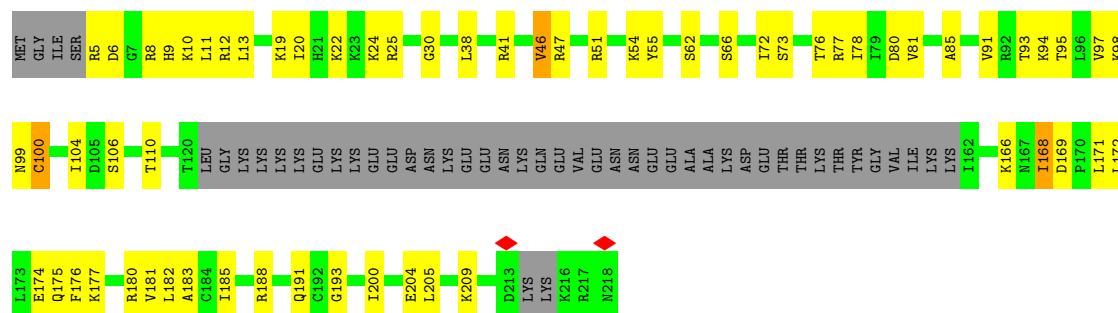
• Molecule 63: 40S ribosomal protein S15A

Chain SK: 49% 44% 6%



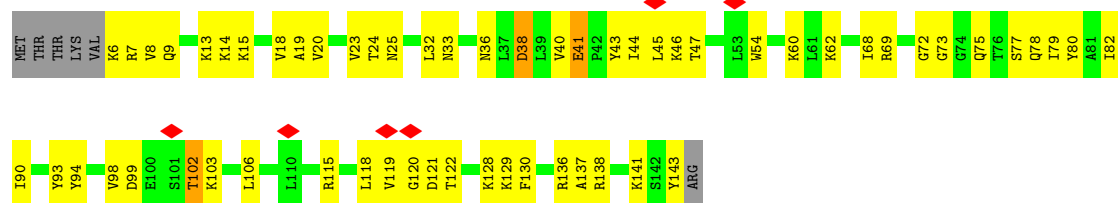
• Molecule 64: 40S ribosomal protein S8

Chain SL: 50% 28% 22%



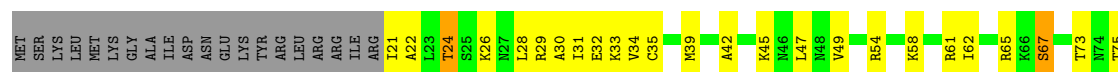
• Molecule 65: 40S ribosomal protein S16

Chain SM: 55% 39%



• Molecule 66: 40S ribosomal protein S20e

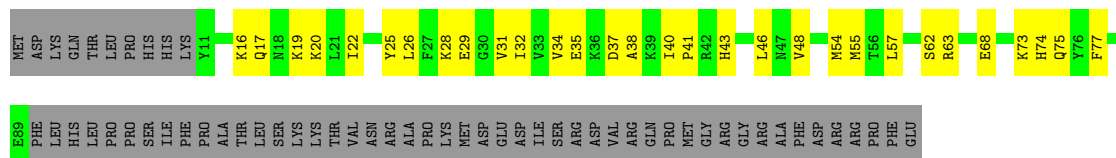
Chain SN: 49% 32% 17%





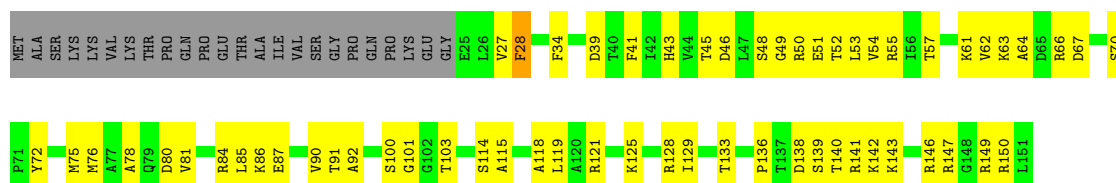
- Molecule 67: 40S ribosomal protein S10

Chain SO:



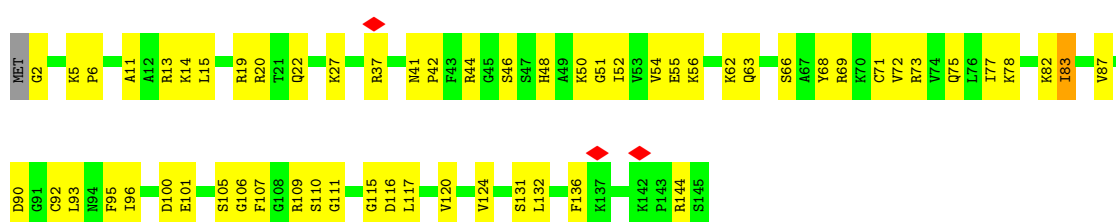
- Molecule 68: 40S ribosomal protein S11

Chain SP:



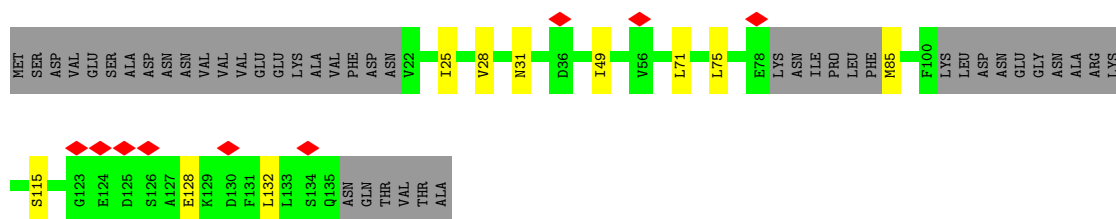
- Molecule 69: 40S ribosomal protein S23

Chain SQ:



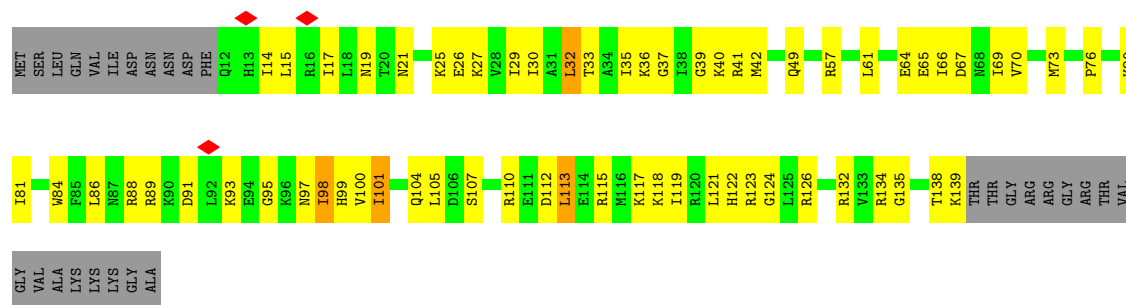
- Molecule 70: 40S ribosomal protein S12

Chain SR:



- Molecule 71: 40S ribosomal protein S18

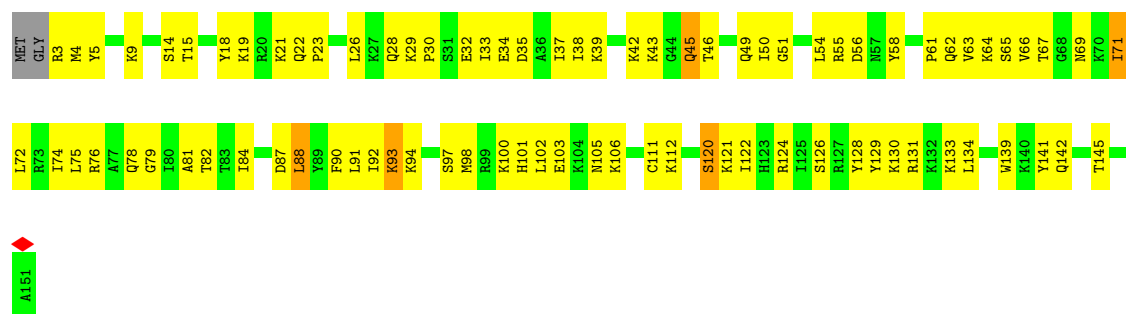
Chain SS:



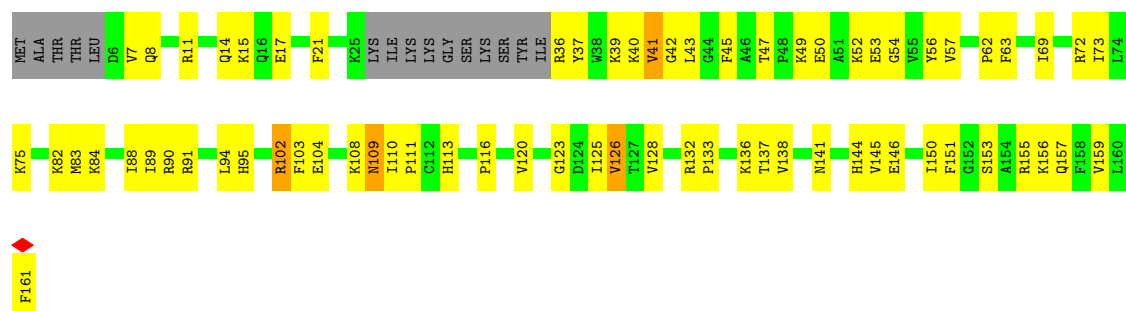
• Molecule 72: 40S ribosomal protein S29



• Molecule 73: 40S ribosomal protein S15

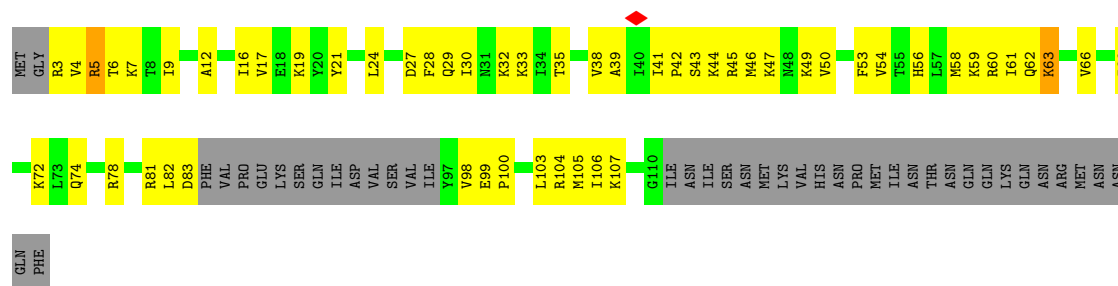


• Molecule 74: 40S ribosomal protein S11



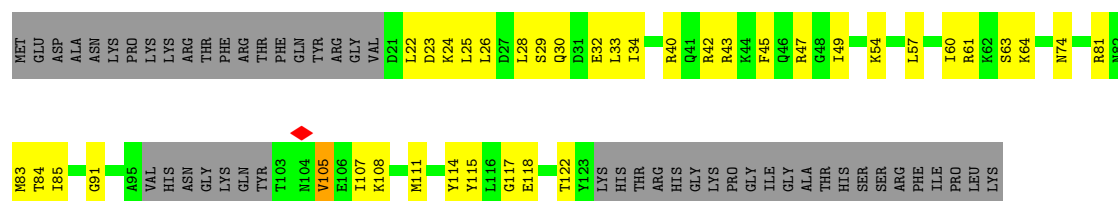
• Molecule 75: 40S ribosomal protein S17





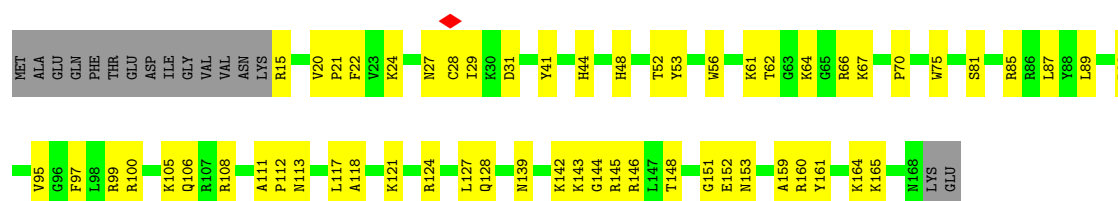
- Molecule 76: 40S ribosomal protein S19

Chain SX: 40% 26% 34%



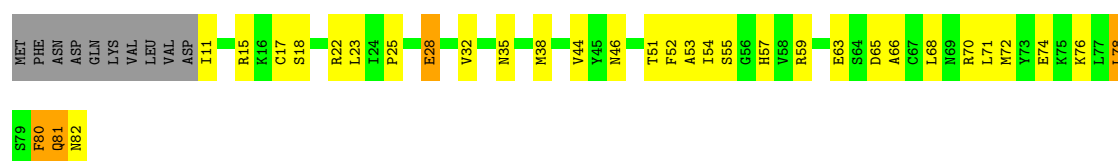
- Molecule 77: 40S ribosomal protein S19

Chain SY: 56% 34% 9%



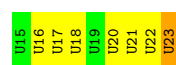
- Molecule 78: 40S ribosomal protein S21

Chain SZ: 48% 35% 5% 12%



- Molecule 79: mRNA

Chain mR: 22% 67% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	69147	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.068	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00277	Depositor
Map size (Å)	415.0, 415.0, 415.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	S7	0.11	0/1810	0.28	0/2821
1	S9	0.09	0/1810	0.25	0/2821
2	AA	0.13	0/75947	0.30	0/118255
3	AC	0.12	0/3599	0.27	0/5603
4	AB	0.15	0/2816	0.34	0/4388
5	AL	0.14	0/1793	0.40	0/2387
6	A1	0.15	0/1151	0.44	0/1531
7	A2	0.14	0/846	0.39	0/1124
8	A4	0.16	0/564	0.38	0/737
9	A6	0.18	0/748	0.48	0/1001
10	A7	0.16	0/805	0.40	0/1073
11	AN	0.13	0/1226	0.38	0/1632
12	A8	0.16	0/1053	0.47	0/1399
13	A9	0.16	0/864	0.44	0/1160
14	Aa	0.18	0/871	0.52	0/1161
15	Ab	0.16	0/762	0.43	0/1008
16	Ad	0.15	0/611	0.45	0/812
17	Ae	0.12	0/396	0.30	0/521
18	Af	0.16	0/418	0.48	0/556
19	AP	0.14	0/1735	0.40	1/2320 (0.0%)
20	Ah	0.16	0/667	0.43	0/887
21	Ai	0.12	0/788	0.36	0/1032
22	AI	0.14	0/1708	0.37	0/2274
23	AJ	0.14	0/1840	0.37	0/2456
24	Ac	0.13	0/722	0.37	0/951
25	AK	0.14	0/1689	0.35	0/2260
26	AM	0.15	0/1012	0.43	0/1363
27	AS	0.13	0/1531	0.36	0/2040
28	AO	0.15	0/1199	0.38	0/1597
29	AQ	0.14	0/1579	0.41	0/2113
30	AR	0.18	0/2078	0.45	1/2776 (0.0%)
31	AW	0.14	0/1244	0.37	0/1663
32	AY	0.16	0/805	0.40	0/1074
33	AT	0.15	0/1525	0.42	0/2016

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	AZ	0.14	0/1012	0.41	0/1339
35	A3	0.21	0/1004	0.48	0/1329
36	A5	0.16	0/1917	0.45	0/2562
37	AD	0.14	0/1901	0.35	0/2544
38	AE	0.14	0/3129	0.38	0/4195
39	AF	0.14	0/3144	0.36	0/4205
40	AG	0.16	0/1020	0.45	1/1349 (0.1%)
41	AU	0.16	0/1527	0.41	0/2043
42	AH	0.18	0/1500	0.51	0/2025
43	AV	0.18	0/1300	0.44	0/1732
44	Ag	0.18	0/348	0.45	0/448
45	AX	0.12	0/841	0.38	0/1125
46	A0	0.13	0/533	0.36	0/711
47	S1	0.10	0/998	0.31	0/1321
48	S2	0.09	0/323	0.26	0/435
49	S3	0.16	0/793	0.45	0/1055
50	S4	0.24	0/597	0.50	0/801
51	S5	0.11	0/466	0.35	0/616
52	S6	0.16	0/348	0.54	0/458
53	SA	0.10	0/38276	0.25	0/59598
54	SB	0.15	0/1737	0.42	0/2321
55	SC	0.15	0/1569	0.41	0/2129
56	SD	0.15	0/1240	0.44	0/1652
57	SE	0.13	0/1538	0.38	0/2055
58	SF	0.12	0/2097	0.35	0/2819
59	SG	0.16	0/1799	0.40	0/2429
60	SH	0.12	0/1668	0.35	0/2214
61	SI	0.14	0/1443	0.42	0/1936
62	SJ	0.20	0/1544	0.46	1/2064 (0.0%)
63	SK	0.16	0/1054	0.43	0/1411
64	SL	0.12	0/1407	0.35	0/1879
65	SM	0.12	0/1113	0.36	0/1487
66	SN	0.15	0/780	0.38	0/1053
67	SO	0.14	0/705	0.39	0/950
68	SP	0.15	0/966	0.44	0/1295
69	SQ	0.14	0/1149	0.37	0/1532
70	SR	0.09	0/754	0.28	0/1013
71	SS	0.15	0/1062	0.46	0/1425
72	ST	0.16	0/412	0.42	0/544
73	SU	0.15	0/1223	0.43	0/1634
74	SV	0.17	0/1233	0.47	0/1645
75	SW	0.16	0/792	0.47	0/1053
76	SX	0.12	0/787	0.44	0/1050

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	SY	0.11	0/1294	0.32	0/1742
78	SZ	0.14	0/565	0.46	0/758
79	mR	0.10	0/197	0.29	0/302
All	All	0.13	0/209317	0.33	4/307095 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
9	A6	0	1
50	S4	0	1
62	SJ	0	2
All	All	0	4

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	SJ	51	GLU	CA-CB-CG	7.04	128.17	114.10
19	AP	156	VAL	N-CA-C	-6.40	107.25	113.53
30	AR	48	LYS	CB-CA-C	-5.11	104.64	111.89
40	AG	155	THR	CB-CA-C	-5.08	109.75	115.79

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	A6	64	MET	Peptide
50	S4	78	ARG	Sidechain
62	SJ	50	ILE	Peptide
62	SJ	51	GLU	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S7	1620	0	827	29	0
1	S9	1620	0	827	38	0
2	AA	67884	0	34243	1768	0
3	AC	3215	0	1633	86	0
4	AB	2517	0	1275	108	0
5	AL	1761	0	1896	77	0
6	A1	1134	0	1245	58	0
7	A2	837	0	896	21	0
8	A4	555	0	599	20	0
9	A6	740	0	763	49	0
10	A7	793	0	869	51	0
11	AN	1210	0	1329	58	0
12	A8	1036	0	1139	36	0
13	A9	844	0	886	32	0
14	Aa	858	0	912	54	0
15	Ab	756	0	842	32	0
16	Ad	603	0	686	40	0
17	Ae	388	0	421	18	0
18	Af	413	0	452	35	0
19	AP	1697	0	1802	74	0
20	Ah	658	0	727	37	0
21	Ai	778	0	859	29	0
22	AI	1685	0	1849	70	0
23	AJ	1813	0	1985	73	0
24	Ac	709	0	761	30	0
25	AK	1659	0	1782	63	0
26	AM	996	0	1044	57	0
27	AS	1503	0	1636	40	0
28	AO	1172	0	1230	43	0
29	AQ	1544	0	1582	71	0
30	AR	2049	0	2145	119	0
31	AW	1319	0	1303	42	0
32	AY	796	0	850	36	0
33	AT	1509	0	1682	75	0
34	AZ	1000	0	1099	52	0
35	A3	994	0	1121	59	0
36	A5	1879	0	2005	91	0
37	AD	1866	0	1964	56	0
38	AE	3061	0	3205	135	0
39	AF	3094	0	3333	102	0
40	AG	1010	0	1073	66	0
41	AU	1497	0	1556	67	0
42	AH	1475	0	1574	94	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	AV	1275	0	1355	60	0
44	Ag	343	0	388	23	0
45	AX	824	0	882	34	0
46	A0	521	0	539	33	0
47	S1	985	0	1076	54	0
48	S2	320	0	338	10	0
49	S3	781	0	820	45	0
50	S4	586	0	604	18	0
51	S5	465	0	505	19	0
52	S6	345	0	381	21	0
53	SA	34208	0	17266	1074	0
54	SB	1713	0	1838	91	0
55	SC	1538	0	1600	66	0
56	SD	1228	0	1311	46	0
57	SE	1514	0	1605	89	0
58	SF	2061	0	2200	93	0
59	SG	1757	0	1811	76	0
60	SH	1651	0	1807	72	0
61	SI	1424	0	1471	80	0
62	SJ	1528	0	1680	70	0
63	SK	1037	0	1099	67	0
64	SL	1383	0	1434	57	0
65	SM	1098	0	1183	53	0
66	SN	772	0	813	37	0
67	SO	686	0	695	19	0
68	SP	954	0	997	52	0
69	SQ	1129	0	1196	52	0
70	SR	746	0	754	7	0
71	SS	1046	0	1101	54	0
72	ST	405	0	419	27	0
73	SU	1202	0	1299	77	0
74	SV	1206	0	1239	62	0
75	SW	785	0	858	50	0
76	SX	776	0	832	33	0
77	SY	1266	0	1316	55	0
78	SZ	557	0	558	29	0
79	mR	180	0	91	3	0
All	All	194842	0	145268	5896	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

The worst 5 of 5896 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AA:1132:G:H1	2:AA:1163:A:N6	1.42	1.17
2:AA:3410:A:H62	2:AA:3417:G:N2	1.48	1.09
2:AA:3410:A:N6	2:AA:3417:G:H21	1.50	1.08
2:AA:541:A:C2	2:AA:611:G:N1	2.24	1.05
53:SA:956:A:N6	53:SA:994:G:H1	1.54	1.04

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	AL	209/215 (97%)	197 (94%)	12 (6%)	0	100	100
6	A1	136/146 (93%)	122 (90%)	14 (10%)	0	100	100
7	A2	97/127 (76%)	93 (96%)	4 (4%)	0	100	100
8	A4	64/67 (96%)	60 (94%)	4 (6%)	0	100	100
9	A6	96/108 (89%)	88 (92%)	7 (7%)	1 (1%)	13	39
10	A7	92/120 (77%)	91 (99%)	1 (1%)	0	100	100
11	AN	145/165 (88%)	132 (91%)	13 (9%)	0	100	100
12	A8	123/131 (94%)	109 (89%)	14 (11%)	0	100	100
13	A9	101/140 (72%)	95 (94%)	6 (6%)	0	100	100
14	Aa	104/150 (69%)	94 (90%)	10 (10%)	0	100	100
15	Ab	91/112 (81%)	85 (93%)	6 (7%)	0	100	100
16	Ad	68/87 (78%)	61 (90%)	7 (10%)	0	100	100
17	Ae	39/51 (76%)	38 (97%)	1 (3%)	0	100	100
18	Af	49/128 (38%)	42 (86%)	7 (14%)	0	100	100
19	AP	202/205 (98%)	185 (92%)	16 (8%)	1 (0%)	25	56
20	Ah	83/96 (86%)	77 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	Ai	93/104 (89%)	85 (91%)	8 (9%)	0	100	100
22	AI	203/221 (92%)	190 (94%)	11 (5%)	2 (1%)	13	39
23	AJ	216/283 (76%)	204 (94%)	11 (5%)	1 (0%)	25	56
24	Ac	87/92 (95%)	76 (87%)	11 (13%)	0	100	100
25	AK	199/202 (98%)	191 (96%)	7 (4%)	1 (0%)	25	56
26	AM	130/139 (94%)	124 (95%)	6 (5%)	0	100	100
27	AS	184/187 (98%)	173 (94%)	11 (6%)	0	100	100
28	AO	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
29	AQ	185/219 (84%)	163 (88%)	21 (11%)	1 (0%)	25	56
30	AR	244/294 (83%)	227 (93%)	17 (7%)	0	100	100
31	AW	149/173 (86%)	143 (96%)	6 (4%)	0	100	100
32	AY	99/190 (52%)	95 (96%)	4 (4%)	0	100	100
33	AT	179/182 (98%)	170 (95%)	9 (5%)	0	100	100
34	AZ	119/126 (94%)	112 (94%)	7 (6%)	0	100	100
35	A3	117/124 (94%)	110 (94%)	7 (6%)	0	100	100
36	A5	221/257 (86%)	203 (92%)	18 (8%)	0	100	100
37	AD	245/260 (94%)	229 (94%)	14 (6%)	2 (1%)	16	44
38	AE	378/386 (98%)	356 (94%)	22 (6%)	0	100	100
39	AF	388/411 (94%)	369 (95%)	19 (5%)	0	100	100
40	AG	116/173 (67%)	97 (84%)	19 (16%)	0	100	100
41	AU	178/184 (97%)	169 (95%)	9 (5%)	0	100	100
42	AH	183/190 (96%)	168 (92%)	14 (8%)	1 (0%)	25	56
43	AV	153/161 (95%)	147 (96%)	6 (4%)	0	100	100
44	Ag	35/39 (90%)	27 (77%)	8 (23%)	0	100	100
45	AX	95/139 (68%)	92 (97%)	3 (3%)	0	100	100
46	A0	60/162 (37%)	54 (90%)	6 (10%)	0	100	100
47	S1	118/133 (89%)	116 (98%)	2 (2%)	0	100	100
48	S2	35/105 (33%)	35 (100%)	0	0	100	100
49	S3	93/107 (87%)	84 (90%)	9 (10%)	0	100	100
50	S4	74/82 (90%)	61 (82%)	13 (18%)	0	100	100
51	S5	55/67 (82%)	53 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	S6	41/58 (71%)	35 (85%)	5 (12%)	1 (2%)	5	18
54	SB	208/262 (79%)	191 (92%)	17 (8%)	0	100	100
55	SC	193/263 (73%)	176 (91%)	15 (8%)	2 (1%)	13	39
56	SD	149/221 (67%)	144 (97%)	5 (3%)	0	100	100
57	SE	183/189 (97%)	170 (93%)	13 (7%)	0	100	100
58	SF	255/261 (98%)	244 (96%)	10 (4%)	1 (0%)	30	61
59	SG	222/272 (82%)	208 (94%)	14 (6%)	0	100	100
60	SH	200/306 (65%)	192 (96%)	7 (4%)	1 (0%)	25	56
61	SI	176/195 (90%)	160 (91%)	16 (9%)	0	100	100
62	SJ	186/194 (96%)	170 (91%)	15 (8%)	1 (0%)	25	56
63	SK	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
64	SL	165/218 (76%)	151 (92%)	13 (8%)	1 (1%)	22	51
65	SM	136/144 (94%)	128 (94%)	7 (5%)	1 (1%)	19	48
66	SN	96/118 (81%)	90 (94%)	6 (6%)	0	100	100
67	SO	77/137 (56%)	72 (94%)	4 (5%)	1 (1%)	10	32
68	SP	125/151 (83%)	115 (92%)	10 (8%)	0	100	100
69	SQ	142/145 (98%)	132 (93%)	9 (6%)	1 (1%)	19	48
70	SR	92/141 (65%)	86 (94%)	6 (6%)	0	100	100
71	SS	126/156 (81%)	111 (88%)	13 (10%)	2 (2%)	8	27
72	ST	46/54 (85%)	46 (100%)	0	0	100	100
73	SU	147/151 (97%)	136 (92%)	11 (8%)	0	100	100
74	SV	142/161 (88%)	133 (94%)	8 (6%)	1 (1%)	19	48
75	SW	91/137 (66%)	86 (94%)	3 (3%)	2 (2%)	5	20
76	SX	92/145 (63%)	81 (88%)	11 (12%)	0	100	100
77	SY	152/170 (89%)	147 (97%)	5 (3%)	0	100	100
78	SZ	70/82 (85%)	65 (93%)	4 (6%)	1 (1%)	9	30
All	All	10114/12049 (84%)	9412 (93%)	676 (7%)	26 (0%)	38	67

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	AJ	75	ILE
42	AH	53	TYR

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Mol	Chain	Res	Type
62	SJ	112	ILE
65	SM	41	GLU
71	SS	101	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	AL	190/194 (98%)	187 (98%)	3 (2%)	58	85
6	A1	127/132 (96%)	122 (96%)	5 (4%)	27	61
7	A2	98/118 (83%)	94 (96%)	4 (4%)	26	59
8	A4	60/61 (98%)	58 (97%)	2 (3%)	33	67
9	A6	83/92 (90%)	74 (89%)	9 (11%)	5	17
10	A7	90/112 (80%)	81 (90%)	9 (10%)	6	20
11	AN	136/152 (90%)	130 (96%)	6 (4%)	24	56
12	A8	114/120 (95%)	106 (93%)	8 (7%)	12	36
13	A9	90/127 (71%)	85 (94%)	5 (6%)	17	47
14	Aa	89/128 (70%)	86 (97%)	3 (3%)	32	66
15	Ab	82/97 (84%)	76 (93%)	6 (7%)	11	34
16	Ad	69/83 (83%)	64 (93%)	5 (7%)	12	34
17	Ae	40/48 (83%)	38 (95%)	2 (5%)	20	51
18	Af	45/114 (40%)	42 (93%)	3 (7%)	13	38
19	AP	179/180 (99%)	168 (94%)	11 (6%)	15	43
20	Ah	70/80 (88%)	65 (93%)	5 (7%)	12	35
21	Ai	87/93 (94%)	85 (98%)	2 (2%)	45	78
22	AI	189/203 (93%)	175 (93%)	14 (7%)	11	33
23	AJ	204/260 (78%)	198 (97%)	6 (3%)	37	71
24	Ac	74/77 (96%)	73 (99%)	1 (1%)	62	87
25	AK	181/182 (100%)	173 (96%)	8 (4%)	24	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	AM	106/110 (96%)	98 (92%)	8 (8%)	11	33
27	AS	158/159 (99%)	152 (96%)	6 (4%)	28	62
28	AO	121/122 (99%)	116 (96%)	5 (4%)	26	59
29	AQ	165/190 (87%)	159 (96%)	6 (4%)	30	64
30	AR	215/254 (85%)	207 (96%)	8 (4%)	29	63
31	AW	128/131 (98%)	121 (94%)	7 (6%)	18	47
32	AY	90/177 (51%)	86 (96%)	4 (4%)	24	56
33	AT	162/163 (99%)	157 (97%)	5 (3%)	35	69
34	AZ	111/115 (96%)	101 (91%)	10 (9%)	8	25
35	A3	110/115 (96%)	101 (92%)	9 (8%)	9	29
36	A5	201/231 (87%)	191 (95%)	10 (5%)	20	51
37	AD	191/202 (95%)	182 (95%)	9 (5%)	22	54
38	AE	335/340 (98%)	311 (93%)	24 (7%)	12	34
39	AF	336/352 (96%)	322 (96%)	14 (4%)	25	58
40	AG	110/155 (71%)	100 (91%)	10 (9%)	7	24
41	AU	162/166 (98%)	153 (94%)	9 (6%)	17	47
42	AH	168/173 (97%)	158 (94%)	10 (6%)	16	44
43	AV	140/144 (97%)	134 (96%)	6 (4%)	25	57
44	Ag	34/35 (97%)	31 (91%)	3 (9%)	8	26
45	AX	92/131 (70%)	84 (91%)	8 (9%)	8	26
46	A0	53/146 (36%)	50 (94%)	3 (6%)	17	46
47	S1	104/115 (90%)	103 (99%)	1 (1%)	73	91
48	S2	35/88 (40%)	33 (94%)	2 (6%)	17	46
49	S3	87/98 (89%)	79 (91%)	8 (9%)	7	24
50	S4	70/76 (92%)	68 (97%)	2 (3%)	37	71
51	S5	48/54 (89%)	47 (98%)	1 (2%)	48	80
52	S6	36/47 (77%)	34 (94%)	2 (6%)	17	47
54	SB	195/238 (82%)	182 (93%)	13 (7%)	13	38
55	SC	167/227 (74%)	157 (94%)	10 (6%)	16	44
56	SD	132/188 (70%)	129 (98%)	3 (2%)	45	78
57	SE	161/167 (96%)	156 (97%)	5 (3%)	35	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	SF	233/237 (98%)	223 (96%)	10 (4%)	25	57
59	SG	191/222 (86%)	179 (94%)	12 (6%)	15	42
60	SH	182/279 (65%)	177 (97%)	5 (3%)	40	74
61	SI	154/165 (93%)	148 (96%)	6 (4%)	27	61
62	SJ	177/183 (97%)	171 (97%)	6 (3%)	32	66
63	SK	115/116 (99%)	106 (92%)	9 (8%)	10	31
64	SL	151/193 (78%)	147 (97%)	4 (3%)	41	75
65	SM	116/122 (95%)	113 (97%)	3 (3%)	41	75
66	SN	91/109 (84%)	88 (97%)	3 (3%)	33	67
67	SO	76/129 (59%)	75 (99%)	1 (1%)	65	88
68	SP	99/119 (83%)	94 (95%)	5 (5%)	20	51
69	SQ	120/121 (99%)	114 (95%)	6 (5%)	20	51
70	SR	83/121 (69%)	82 (99%)	1 (1%)	67	89
71	SS	114/136 (84%)	109 (96%)	5 (4%)	24	56
72	ST	43/48 (90%)	38 (88%)	5 (12%)	4	15
73	SU	132/133 (99%)	125 (95%)	7 (5%)	19	49
74	SV	131/144 (91%)	126 (96%)	5 (4%)	28	62
75	SW	86/127 (68%)	83 (96%)	3 (4%)	31	65
76	SX	88/130 (68%)	85 (97%)	3 (3%)	32	66
77	SY	137/151 (91%)	136 (99%)	1 (1%)	81	94
78	SZ	60/70 (86%)	52 (87%)	8 (13%)	3	10
All	All	9099/10617 (86%)	8653 (95%)	446 (5%)	23	52

5 of 446 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	AF	133	VAL
78	SZ	63	GLU
45	AX	123	ILE
78	SZ	11	ILE
68	SP	85	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
40	AG	20	ASN
58	SF	176	GLN
42	AH	168	ASN
52	S6	38	GLN
60	SH	59	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S7	75/76 (98%)	30 (40%)	2 (2%)
1	S9	75/76 (98%)	15 (20%)	1 (1%)
2	AA	3162/3788 (83%)	768 (24%)	57 (1%)
3	AC	148/159 (93%)	34 (22%)	4 (2%)
4	AB	117/119 (98%)	41 (35%)	1 (0%)
53	SA	1587/2092 (75%)	360 (22%)	24 (1%)
79	mR	8/9 (88%)	6 (75%)	0
All	All	5172/6319 (81%)	1254 (24%)	89 (1%)

5 of 1254 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	S7	3	C
1	S7	6	G
1	S7	9	G
1	S7	10	G
1	S7	11	A

5 of 89 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	AA	3658	G
53	SA	844	G
3	AC	35	A
53	SA	246	A
53	SA	1182	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
31	AW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	154:ASN	C	197:UNK	N	32.90

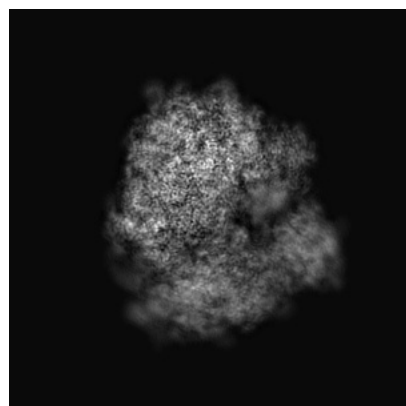
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44919. These allow visual inspection of the internal detail of the map and identification of artifacts.

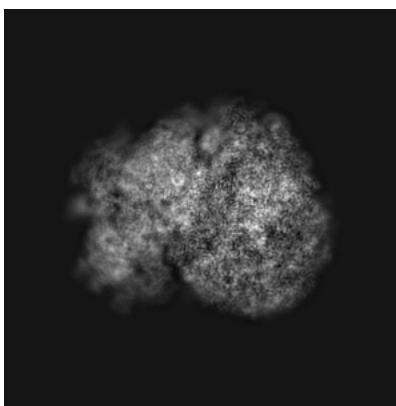
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

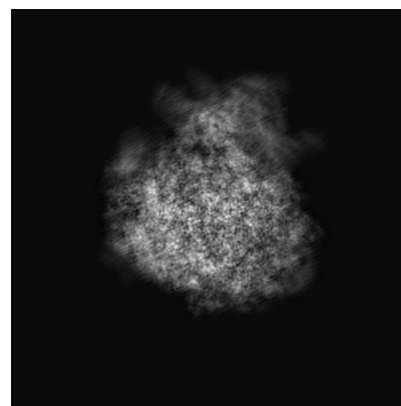
6.1.1 Primary map



X

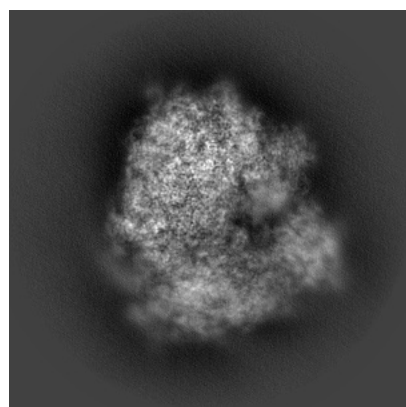


Y

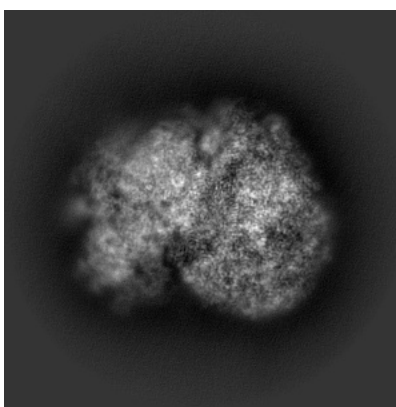


Z

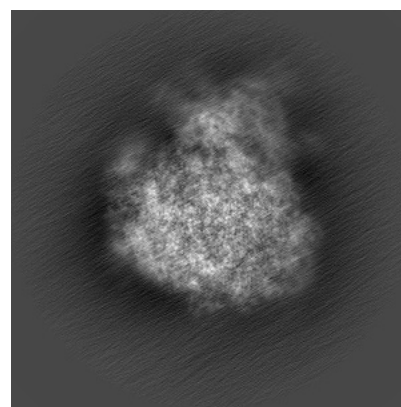
6.1.2 Raw map



X



Y

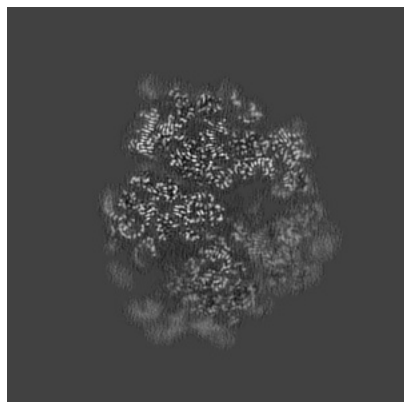


Z

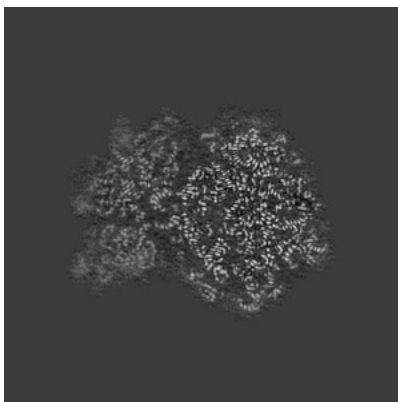
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

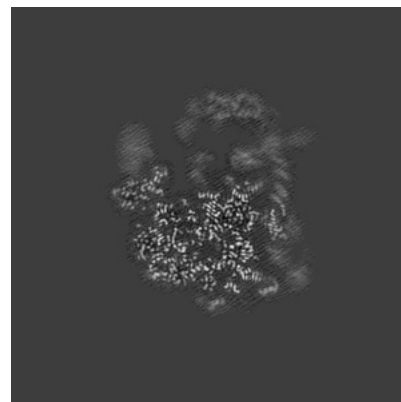
6.2.1 Primary map



X Index: 250

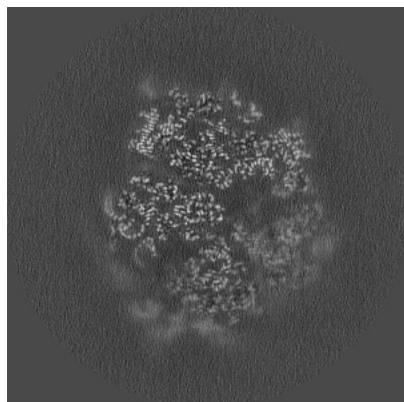


Y Index: 250

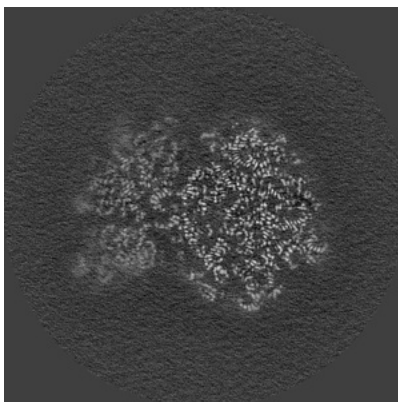


Z Index: 250

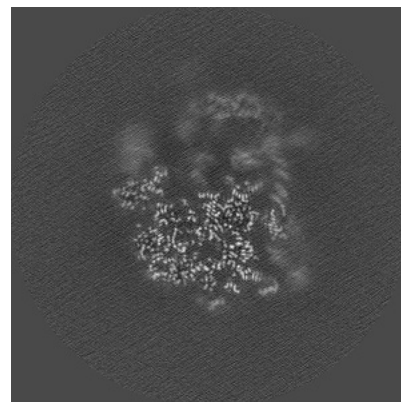
6.2.2 Raw map



X Index: 250



Y Index: 250

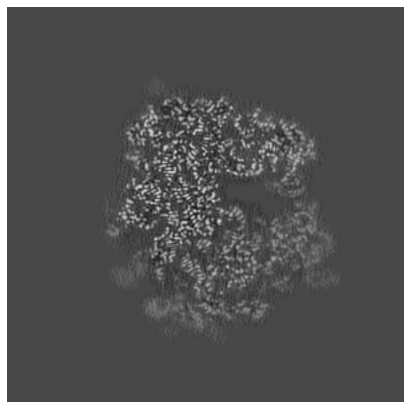


Z Index: 250

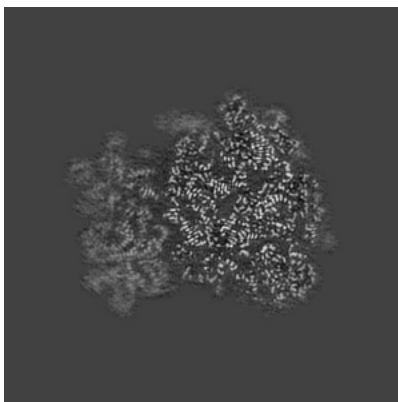
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

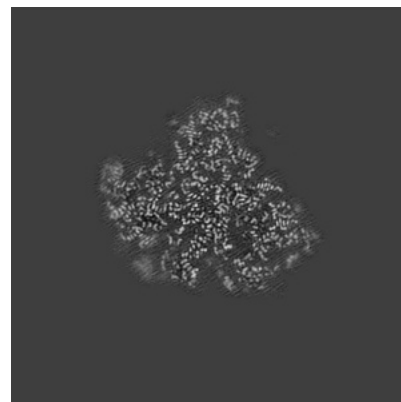
6.3.1 Primary map



X Index: 269

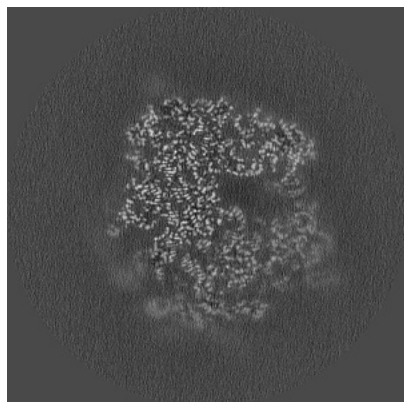


Y Index: 222

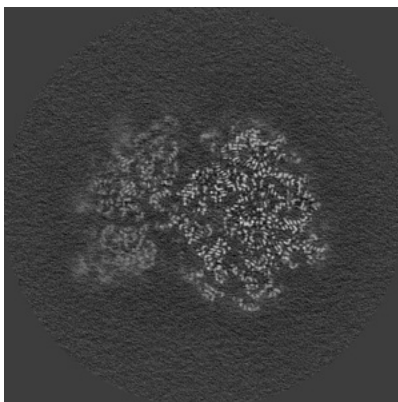


Z Index: 310

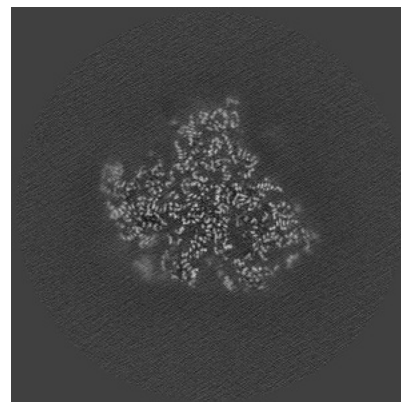
6.3.2 Raw map



X Index: 269



Y Index: 251

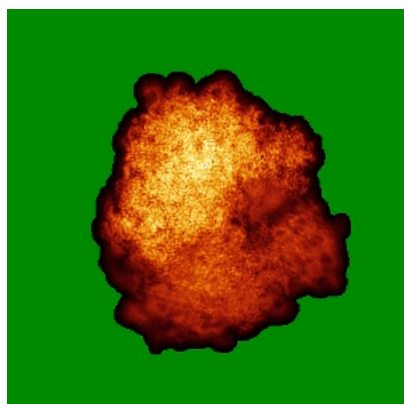


Z Index: 310

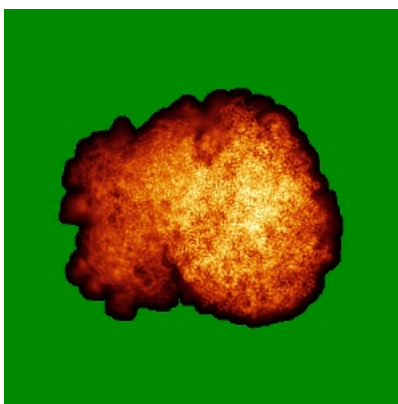
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

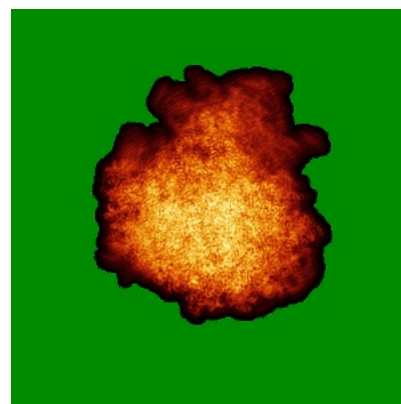
6.4.1 Primary map



X

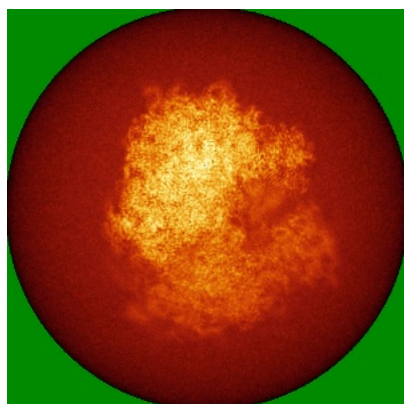


Y

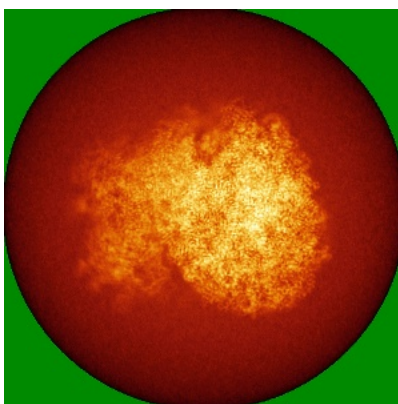


Z

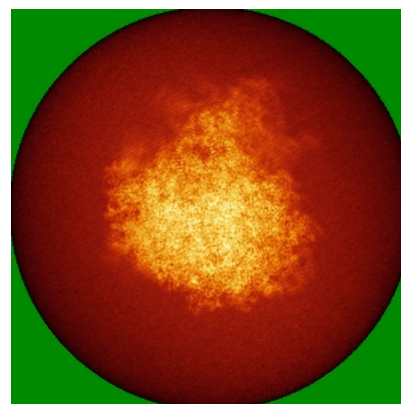
6.4.2 Raw map



X



Y



Z

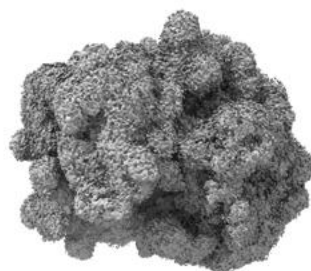
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

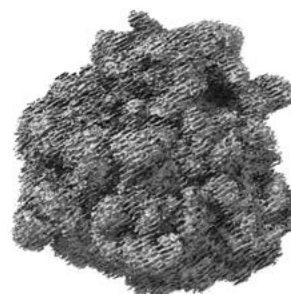
6.5.1 Primary map



X



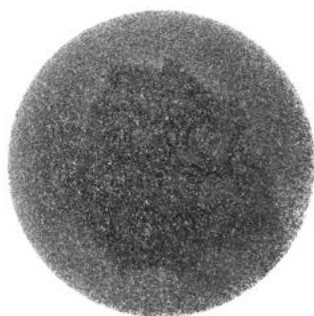
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00277. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

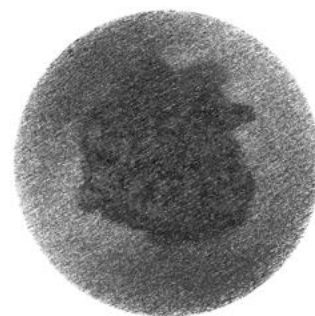
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

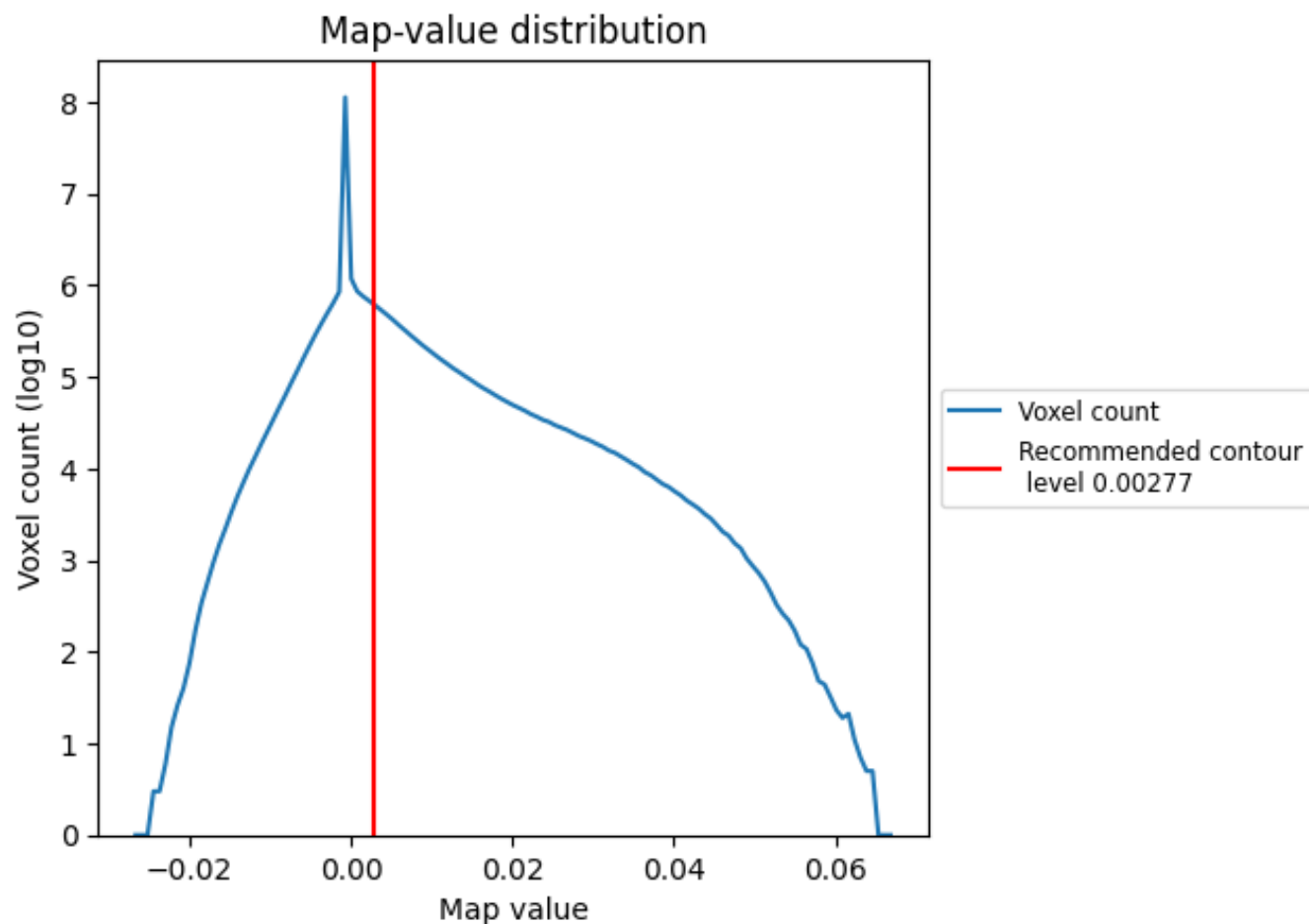
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

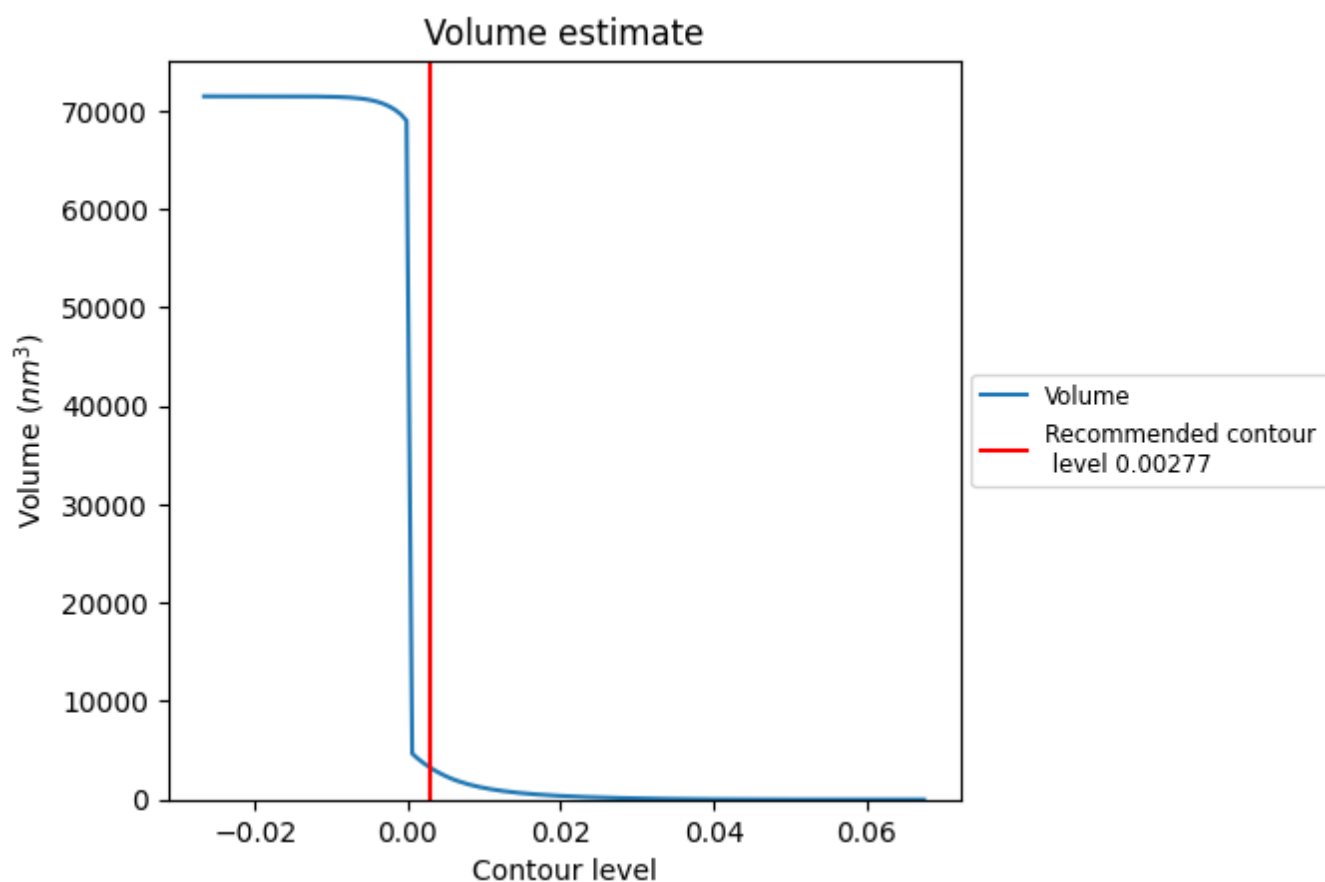
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

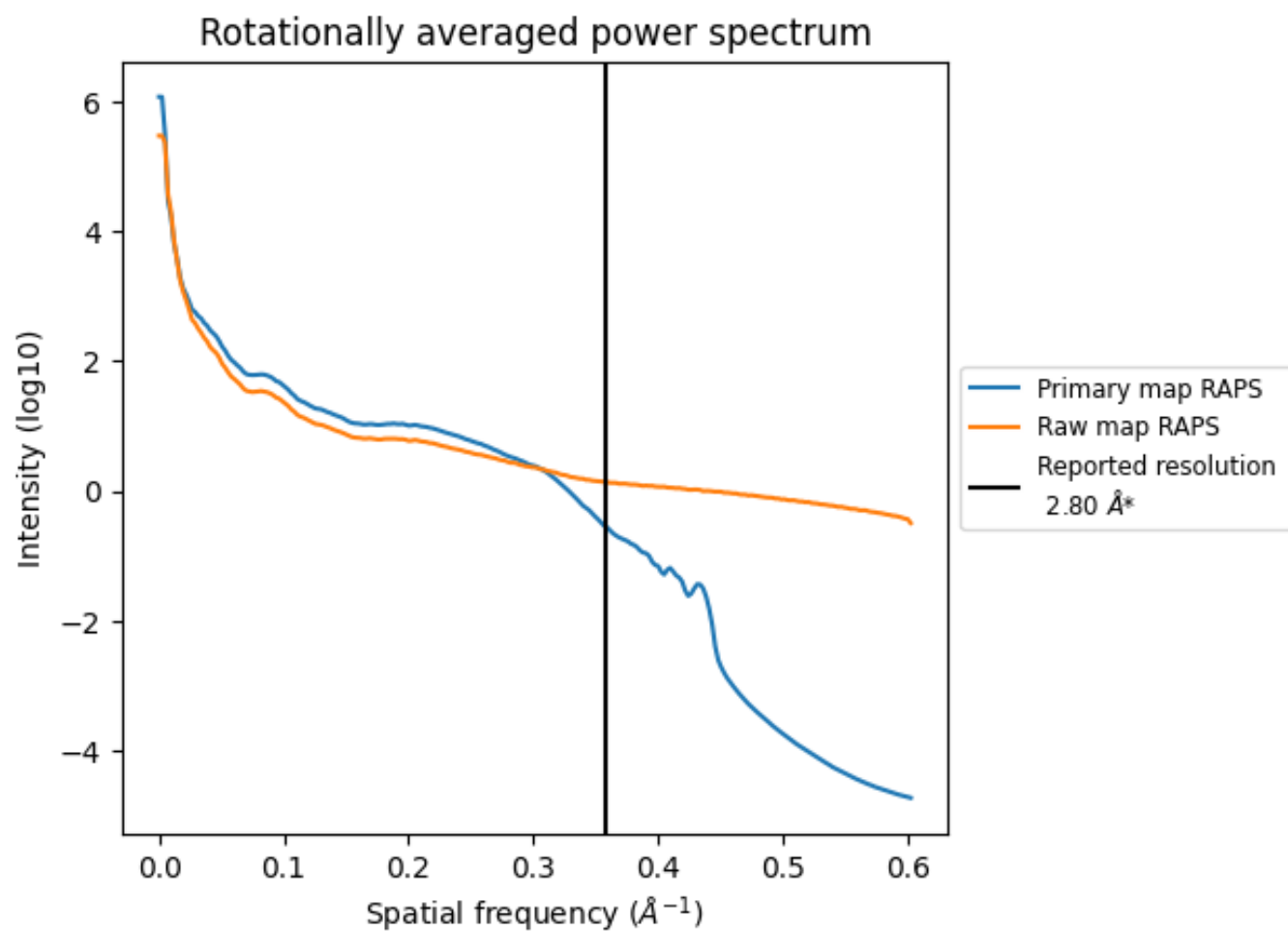
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3322 nm³; this corresponds to an approximate mass of 3000 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

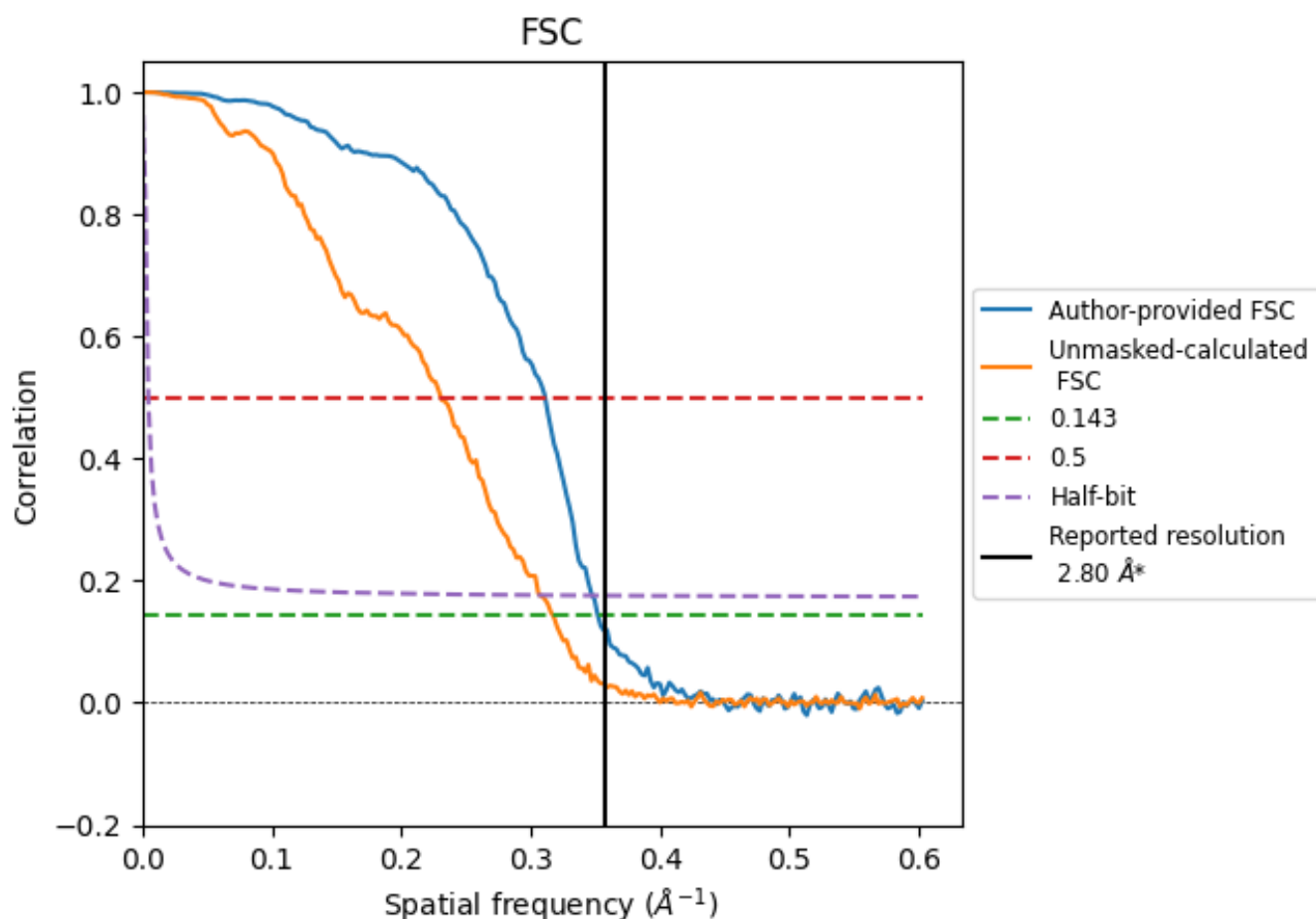


*Reported resolution corresponds to spatial frequency of 0.357 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.357 \AA^{-1}

8.2 Resolution estimates [i](#)

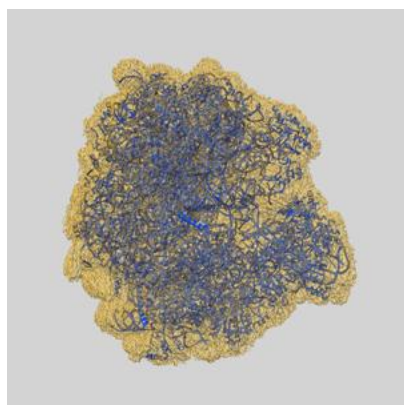
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.84	3.21	2.88
Unmasked-calculated*	3.15	4.33	3.25

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.15 differs from the reported value 2.8 by more than 10 %

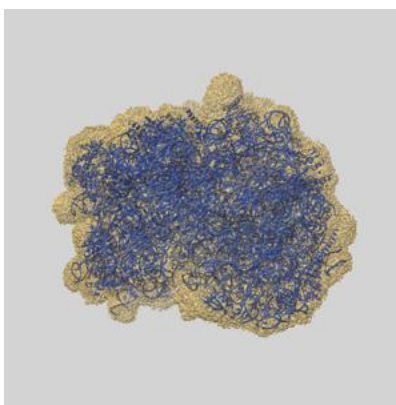
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-44919 and PDB model 9BUT. Per-residue inclusion information can be found in section 3 on page 18.

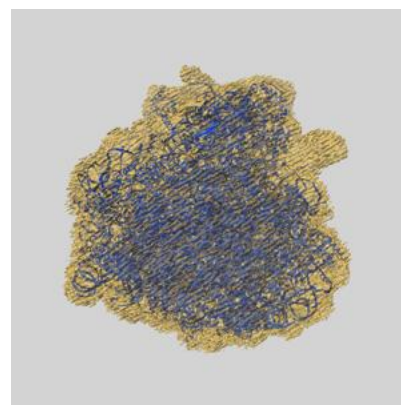
9.1 Map-model overlay [i](#)



X



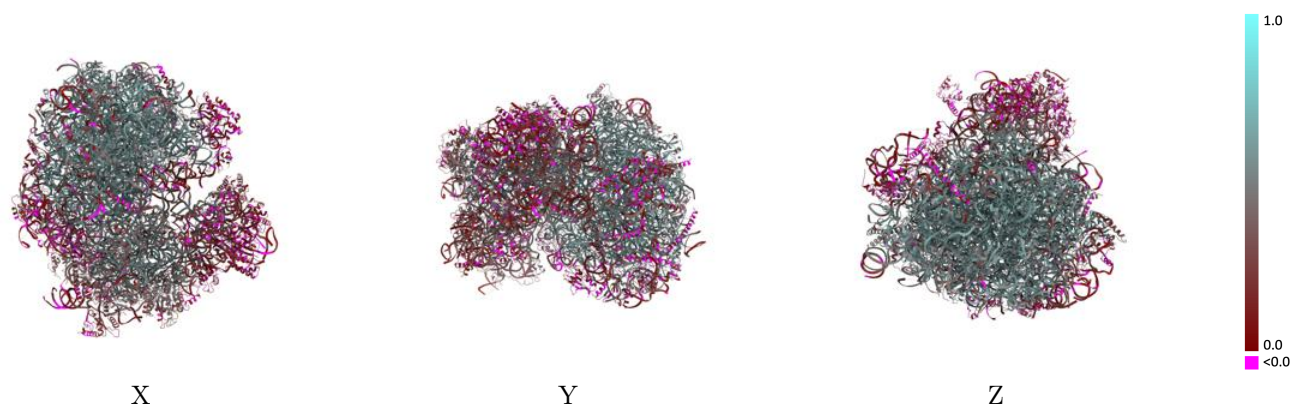
Y



Z

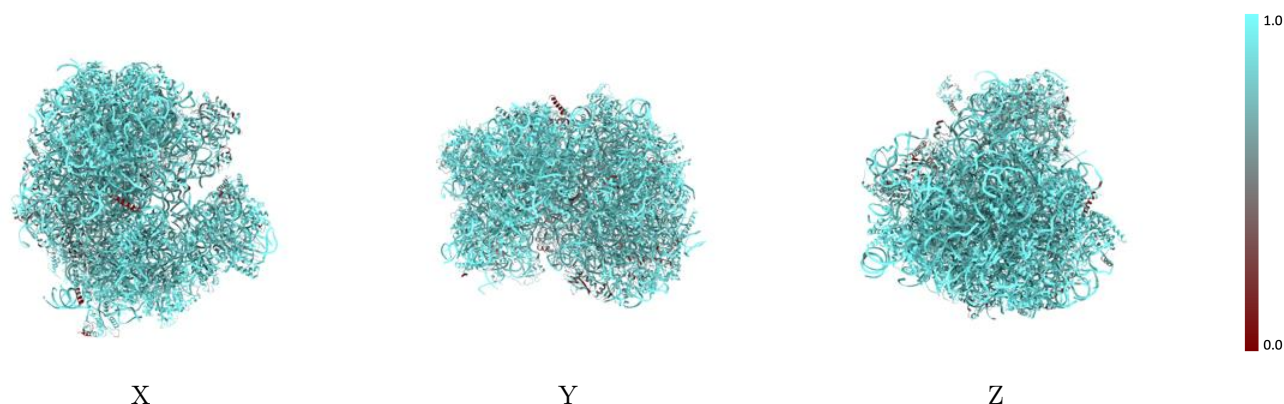
The images above show the 3D surface view of the map at the recommended contour level 0.00277 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



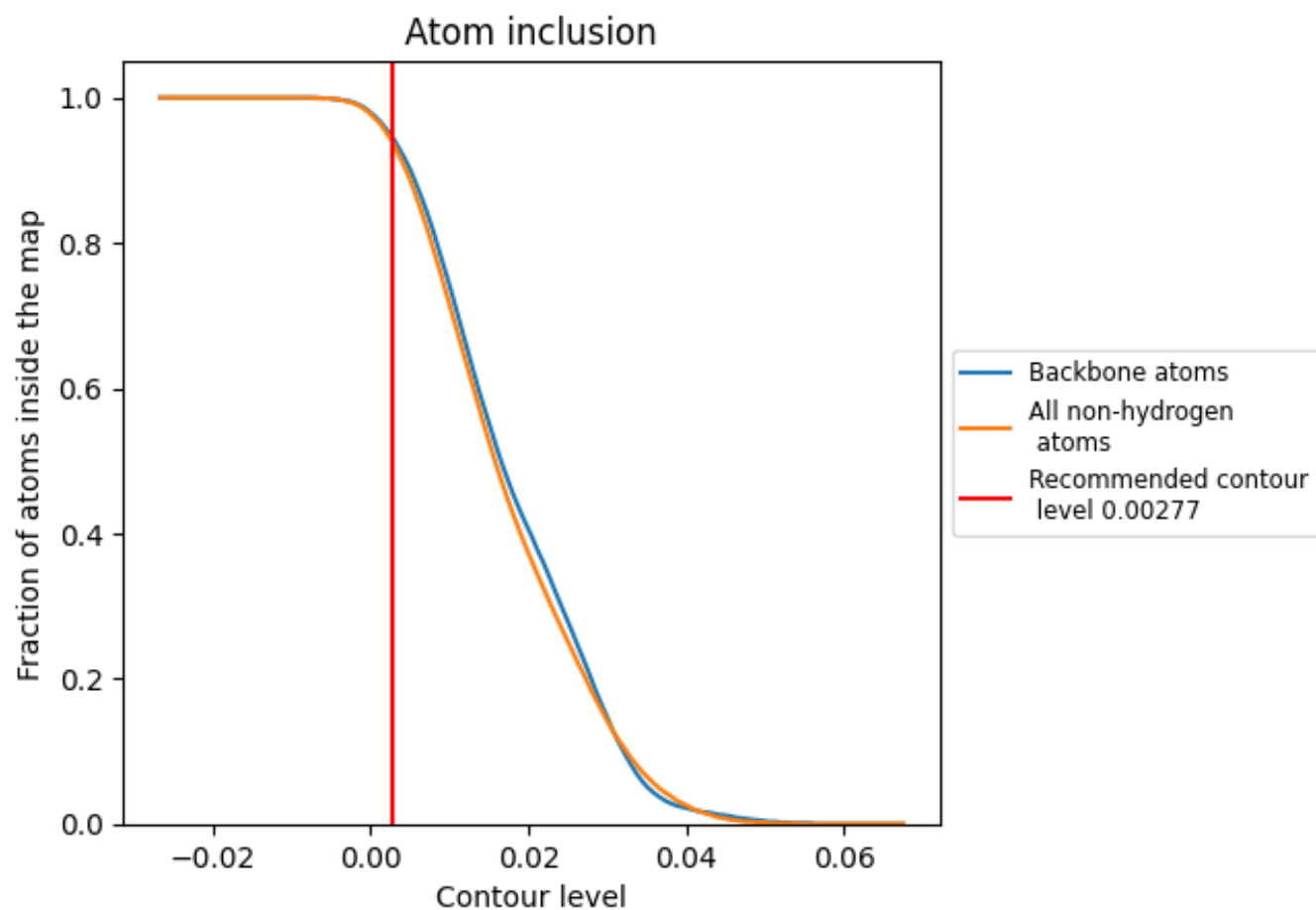
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00277).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.00277) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9390	 0.4120
A0	 0.5860	 0.1210
A1	 0.7370	 0.1510
A2	 0.9630	 0.5330
A3	 0.8730	 0.3190
A4	 0.9490	 0.4440
A5	 0.9170	 0.4390
A6	 0.6920	 0.1620
A7	 0.9210	 0.4350
A8	 0.9670	 0.5730
A9	 0.9850	 0.5930
AA	 0.9690	 0.4960
AB	 0.9030	 0.2660
AC	 0.9890	 0.5240
AD	 0.9760	 0.5890
AE	 0.8760	 0.4080
AF	 0.9260	 0.4930
AG	 0.8190	 0.2030
AH	 0.7310	 0.1770
AI	 0.9840	 0.5250
AJ	 0.8350	 0.3580
AK	 0.9800	 0.5670
AL	 0.9640	 0.5070
AM	 0.8280	 0.3920
AN	 0.8690	 0.3210
AO	 0.9890	 0.5910
AP	 0.9870	 0.5980
AQ	 0.8400	 0.3320
AR	 0.7850	 0.1750
AS	 0.9840	 0.5930
AT	 0.6760	 0.2100
AU	 0.8350	 0.3430
AV	 0.9250	 0.4680
AW	 0.9870	 0.5770
AX	 0.6750	 0.1580










Continued on next page...

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Chain	Atom inclusion	Q-score
AY	 0.8690	 0.3510
AZ	 0.9670	 0.4850
Aa	 0.7860	 0.3000
Ab	 0.9780	 0.5220
Ac	 0.9800	 0.5790
Ad	 0.7960	 0.1890
Ae	 0.9810	 0.5660
Af	 0.7520	 0.1890
Ag	 0.7640	 0.3090
Ah	 0.8780	 0.4310
Ai	 0.9710	 0.5700
S1	 0.9320	 0.1980
S2	 0.5570	 0.0970
S3	 0.9670	 0.4470
S4	 0.8430	 0.2350
S5	 0.8100	 0.1290
S6	 0.8890	 0.2070
S7	 0.9650	 0.3200
S9	 0.7470	 0.1840
SA	 0.9860	 0.3800
SB	 0.9290	 0.3840
SC	 0.9610	 0.3740
SD	 0.9070	 0.1930
SE	 0.9190	 0.2830
SF	 0.9520	 0.3210
SG	 0.9430	 0.3990
SH	 0.9440	 0.2720
SI	 0.8600	 0.1400
SJ	 0.8520	 0.2520
SK	 0.9630	 0.4680
SL	 0.9370	 0.3440
SM	 0.8740	 0.1120
SN	 0.8970	 0.1580
SO	 0.9330	 0.1380
SP	 0.9600	 0.4100
SQ	 0.8870	 0.4070
SR	 0.8170	 0.0640
SS	 0.8890	 0.2190
ST	 0.8920	 0.2030
SU	 0.9260	 0.4010
SV	 0.9290	 0.4170
SW	 0.9010	 0.1400

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Chain	Atom inclusion	Q-score
SX	 0.9370	 0.2260
SY	 0.9230	 0.1670
SZ	 0.9630	 0.3980
mR	 0.9560	 0.3810