



wwPDB EM Validation Summary Report ⓘ

Nov 21, 2023 – 01:18 PM JST

PDB ID : 8HL4
EMDB ID : EMD-34869
Title : Cryo-EM Structures and Translocation Mechanism of Crenarchaeota Ribosome
Authors : Wang, Y.H.; Zhou, J.
Deposited on : 2022-11-28
Resolution : 4.62 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.dev70
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

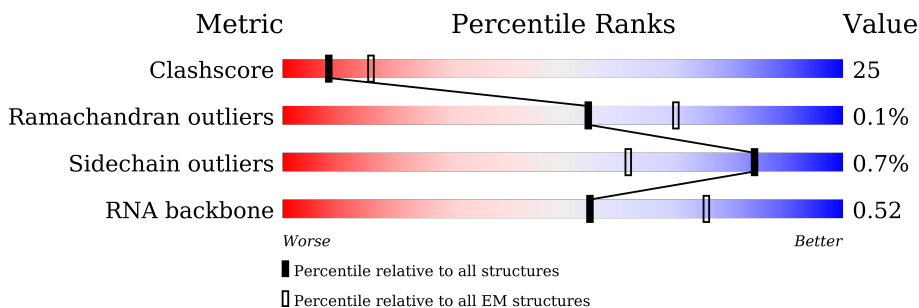
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.62 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	A23S	3022	 75% 23% ..
2	A16S	1503	 66% 29% ..
3	A5S	122	 45% 45% 10%
4	AL2P	234	 9% 100%
5	AL3P	339	 13% 100%
6	AL4P	251	 8% 100%
7	AL5P	168	 12% 98% .

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Mol	Chain	Length	Quality of chain
8	AL6P	181	17% 99%
9	ALX0	76	17% 97%
10	L10E	164	11% 99%
11	L13P	140	16% 99%
12	L141	86	16% 100%
12	L142	86	21% 100%
13	L14P	134	18% 100%
14	L15E	169	7% 100%
15	L18E	112	6% 99%
16	L18P	193	6% 99%
17	L19E	144	. 100%
18	L22P	150	7% 99%
19	L23P	81	11% 100%
20	L24E	54	6% 98%
21	L24P	122	7% 100%
22	L29P	63	14% 100%
23	L30E	94	6% 100%
24	L30P	155	15% 100%
25	L31E	75	7% 100%
26	L32E	123	20% 98%
27	L34E	77	38% 96%
28	L37A	65	. 100%
29	L37E	54	11% 98%
30	L39E	49	20% 100%
31	L40E	55	47% 98%

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Mol	Chain	Length	Quality of chain
32	L44E	92	5% 99%
33	L7A1	123	12% 100%
33	L7A2	123	22% 99%
33	SL7A	123	75% 100%
34	L15P	144	5% 65% 35%
35	L21E	97	7% 100%
36	L45A	101	8% 96%
37	L46A	70	34% 100%
38	L47A	80	92% 99%
39	AL1P	216	90% 100%
40	AS2P	196	34% 100%
41	AS4E	240	11% 98%
42	AS4P	166	11% 98%
43	AS5P	204	6% 100%
44	AS6E	105	28% 100%
45	AS8E	126	18% 99%
46	AS8P	130	• 100%
47	S11P	128	15% 99%
48	S12P	143	14% 100%
49	S15P	149	7% 98%
50	S17P	111	15% 97%
51	S24E	96	• 97%
52	S27E	59	14% 100%
53	S3AE	189	13% 98%
54	AS3P	201	16% 100%

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Mol	Chain	Length	Quality of chain
55	AS7P	193	46% 99%
56	S10P	100	29% 100%
57	S13P	147	31% 99%
58	S14P	52	8% 100%
59	S17E	62	50% 100%
60	S19P	115	19% 99%
61	AS9P	136	34% 99%
62	S28E	63	51% 100%
63	S27A	54	33% 93% 7%
64	AMRN	9	89% 11%
65	APTN	76	72% 22% 5%
66	APTP	6	100% 100%
67	S19E	150	31% 100%
68	AEFG	729	45% 98%

2 Entry composition i

There are 70 unique types of molecules in this entry. The entry contains 171780 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 23s rRNA (3000-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A23S	2995	64339	28665	11911	20768	2995	0	0

- Molecule 2 is a RNA chain called 16s rRNA (1493-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A16S	1492	32040	14269	5925	10354	1492	0	0

- Molecule 3 is a RNA chain called 5s rRNA (122-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	A5S	122	2609	1163	476	849	121	0	0

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AL2P	234	1754	1101	344	307	2	0	0

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AL3P	339	2695	1730	484	477	4	0	0

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AL4P	251	1926	1223	356	345	2	0	0

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	AL5P	168	1343	854	253	232	4	0	0

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	AL6P	181	1431	920	246	264	1	0	0

- Molecule 9 is a protein called 50S ribosomal protein L18Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	ALX0	76	629	403	110	115	1	0	0

- Molecule 10 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	L10E	164	1310	837	239	227	7	0	0

- Molecule 11 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L13P	140	1109	707	208	190	4	0	0

- Molecule 12 is a protein called 50S ribosomal protein L14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L141	86	669	417	123	127	2	0	0
12	L142	86	669	417	123	127	2	0	0

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L14P	134	1034	655	194	181	4	0	0

- Molecule 14 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	L15E	169	1423	899	283	236	5	0	0

- Molecule 15 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	L18E	112	895	576	163	153	3	0	0

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	L18P	193	1539	990	274	274	1	0	0

- Molecule 17 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	L19E	144	1206	753	247	206	0	0

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	L22P	150	1223	782	225	213	3	0	0

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	L23P	81	650	419	109	121	1	0	0

- Molecule 20 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	L24E	54	441	282	80	73	6	0	0

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L24P	122	Total	C	N	O	S	0	0
			989	620	189	176	4		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L29P	63	Total	C	N	O	S	0	0
			513	319	95	96	3		

- Molecule 23 is a protein called 50S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L30E	94	Total	C	N	O	S	0	0
			729	474	116	136	3		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L30P	155	Total	C	N	O	S	0	0
			1254	804	222	223	5		

- Molecule 25 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	L31E	75	Total	C	N	O	S	0	0
			625	398	126	97	4		

- Molecule 26 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	L32E	123	Total	C	N	O	S	0	0
			1010	650	193	166	1		

- Molecule 27 is a protein called 50S ribosomal protein L34e.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L34E	77	Total	C	N	O	S	0	0
			629	395	119	110	5		

- Molecule 28 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	L37A	65	527	335	99	87	6	0	0

- Molecule 29 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	L37E	54	436	267	94	69	6	0	0

- Molecule 30 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	L39E	49	414	265	88	61	0	0

- Molecule 31 is a protein called 50S ribosomal protein L40E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	L40E	55	439	273	89	72	5	0	0

- Molecule 32 is a protein called 50S ribosomal protein L44e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	L44E	92	753	474	144	129	6	0	0

- Molecule 33 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	L7A1	123	935	593	155	184	3	0	0
33	L7A2	123	935	593	155	184	3	0	0
33	SL7A	123	935	593	155	184	3	0	0

- Molecule 34 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	L15P	94	752	487	131	133	1	0	0

- Molecule 35 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	L21E	97	785	502	152	129	2	0	0

- Molecule 36 is a protein called DUF2280 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	L45A	101	816	515	141	156	4	0	0

- Molecule 37 is a protein called Conserved protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	L46A	70	586	382	101	102	1	0	0

- Molecule 38 is a protein called 50S ribosomal protein L47A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	L47A	80	648	405	113	128	2	0	0

- Molecule 39 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	AL1P	216	1715	1096	303	312	4	0	0

- Molecule 40 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	AS2P	196	1587	1022	277	286	2	0	0

- Molecule 41 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	AS4E	240	1925	1238	335	348	4	0	0

- Molecule 42 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AS4P	166	Total	C	N	O	S	0	0
			1370	874	252	241	3		

- Molecule 43 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AS5P	204	Total	C	N	O	S	0	0
			1600	1028	277	287	8		

- Molecule 44 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AS6E	105	Total	C	N	O	S	0	0
			805	506	149	147	3		

- Molecule 45 is a protein called 30S ribosomal protein S8e.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	AS8E	126	Total	C	N	O	0	0
			993	619	187	187		

- Molecule 46 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AS8P	130	Total	C	N	O	S	0	0
			1028	661	181	182	4		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S11P	128	Total	C	N	O	S	0	0
			960	595	190	173	2		

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S12P	143	Total	C	N	O	S	0	0
			1103	701	209	189	4		

- Molecule 49 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S15P	149	Total	C	N	O	S	0	0
			1225	778	228	214	5		

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S17P	111	Total	C	N	O	S	0	0
			885	557	165	160	3		

- Molecule 51 is a protein called 30S ribosomal protein S24e.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	S24E	96	Total	C	N	O	0	0
			759	479	133	147		

- Molecule 52 is a protein called 30S ribosomal protein S27e.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S27E	59	Total	C	N	O	S	0	0
			458	294	83	76	5		

- Molecule 53 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S3AE	189	Total	C	N	O	S	0	0
			1545	1004	264	276	1		

- Molecule 54 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AS3P	201	Total	C	N	O	S	0	0
			1576	1020	274	278	4		

- Molecule 55 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AS7P	193	Total	C	N	O	S	0	0
			1537	969	285	279	4		

- Molecule 56 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S10P	100	Total	C	N	O	S	0	0
			824	522	154	142	6		

- Molecule 57 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S13P	147	Total	C	N	O	S	0	0
			1204	753	230	217	4		

- Molecule 58 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	S14P	52	Total	C	N	O	S	0	0
			432	273	85	69	5		

- Molecule 59 is a protein called 30S ribosomal protein S17e.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	S17E	62	Total	C	N	O	0	0
			517	326	92	99		

- Molecule 60 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	S19P	115	Total	C	N	O	S	0	0
			968	620	181	162	5		

- Molecule 61 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AS9P	136	Total	C	N	O	S	0	0
			1096	692	200	197	7		

- Molecule 62 is a protein called 30S ribosomal protein S28e.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	S28E	63	Total	C	N	O	0	0
			498	308	99	91		

- Molecule 63 is a protein called 30S ribosomal protein S27ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	S27A	54	Total	C	N	O	S	0	0
			435	274	79	76	6		

- Molecule 64 is a RNA chain called mRNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*U)-3').

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

- Molecule 65 is a RNA chain called tRNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
65	APTN	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 66 is a protein called PHE-PHE-PHE-PHE-PHE-PHE.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	APTP	6	Total	C	N	O	0	0
			67	54	6	7		

- Molecule 67 is a protein called 30S ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	S19E	150	Total	C	N	O	S	0	0
			1239	801	223	213	2		

- Molecule 68 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AEFG	724	Total	C	N	O	S	0	0
			5668	3604	983	1064	17		

- Molecule 69 is UNKNOWN (three-letter code: UNK) (formula: C₄H₉NO₂) (labeled as "Ligand of Interest" by depositor).

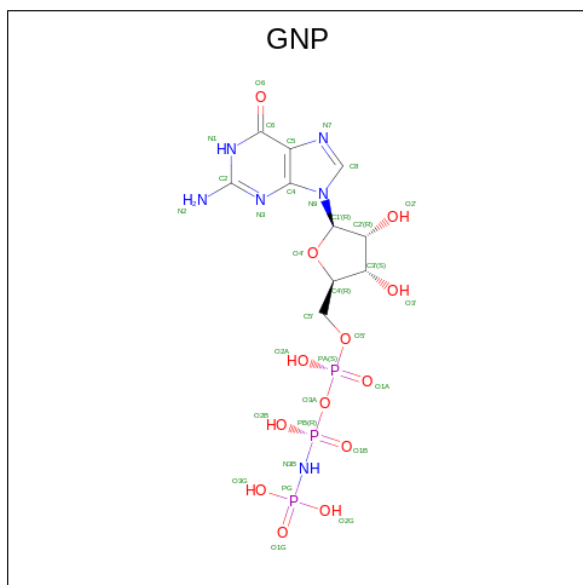
Mol	Chain	Residues	Atoms				AltConf
69	AS2P	37	Total	C	N	O	0
			186	111	37	38	
69	AS5P	13	Total	C	N	O	0
			65	39	13	13	

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
69	AS8P	7	35	21	7	7	0

- Molecule 70 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

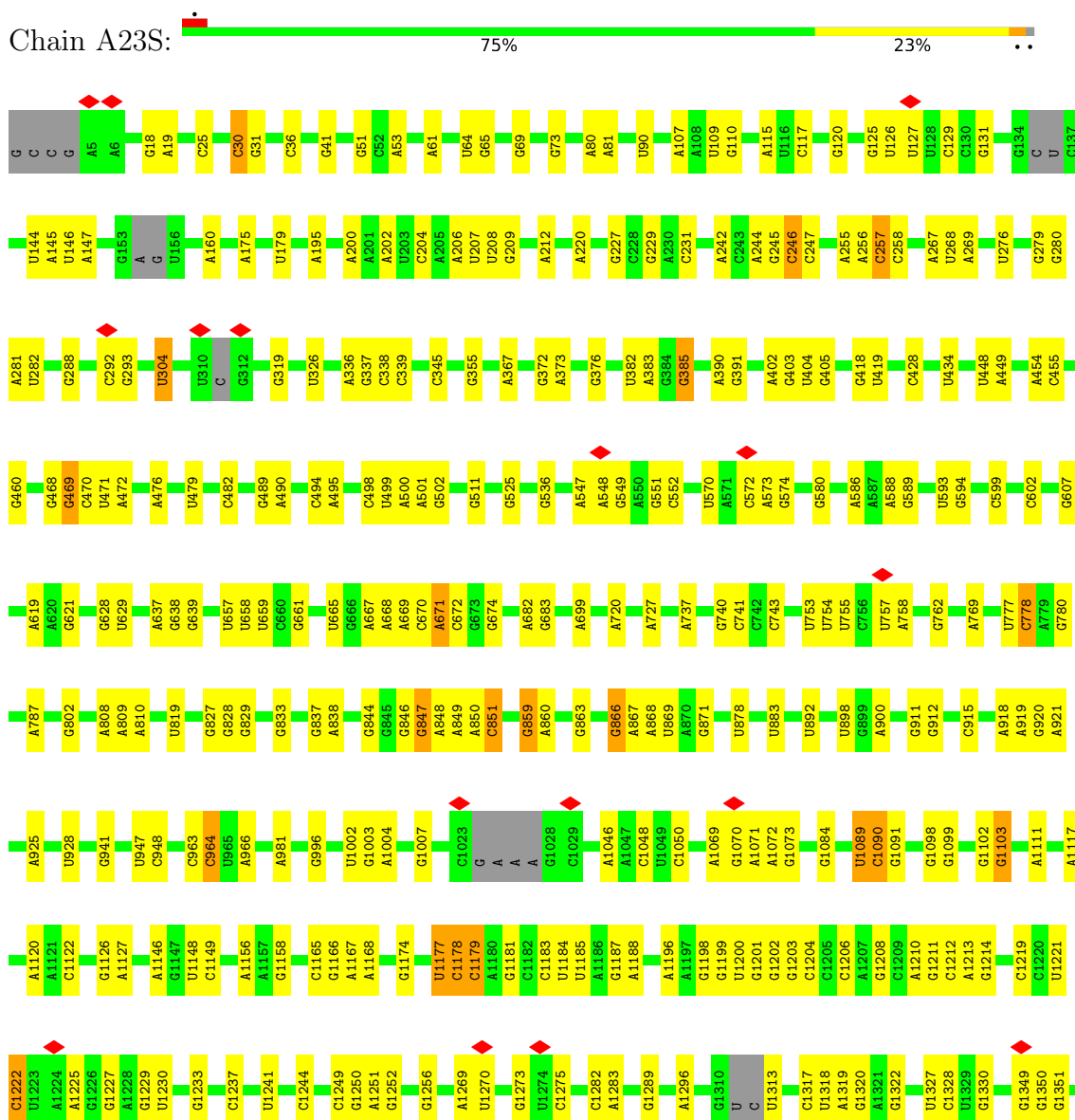


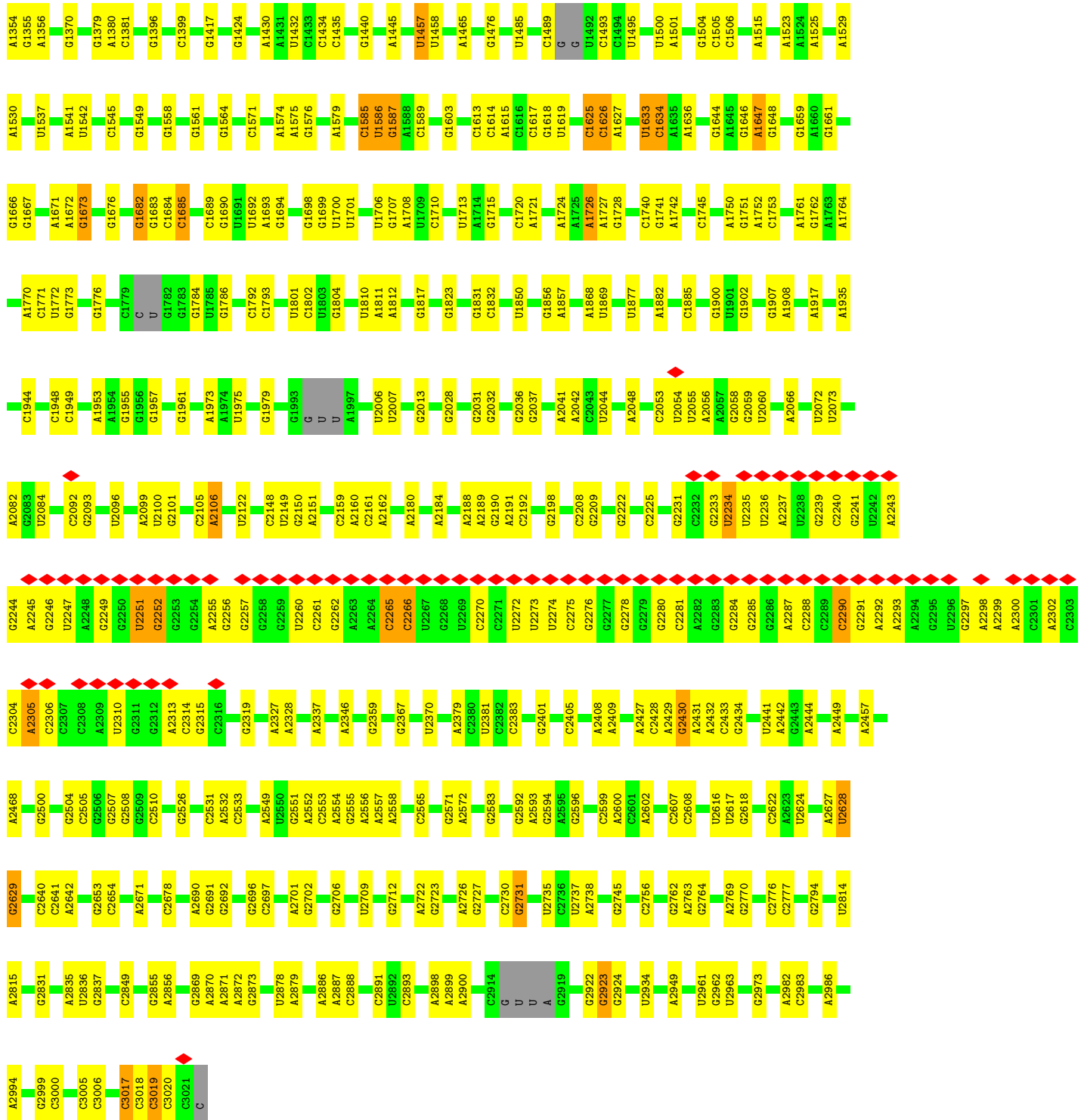
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
70	AEFG	1	32	10	6	13	3	0

3 Residue-property plots [i](#)

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.

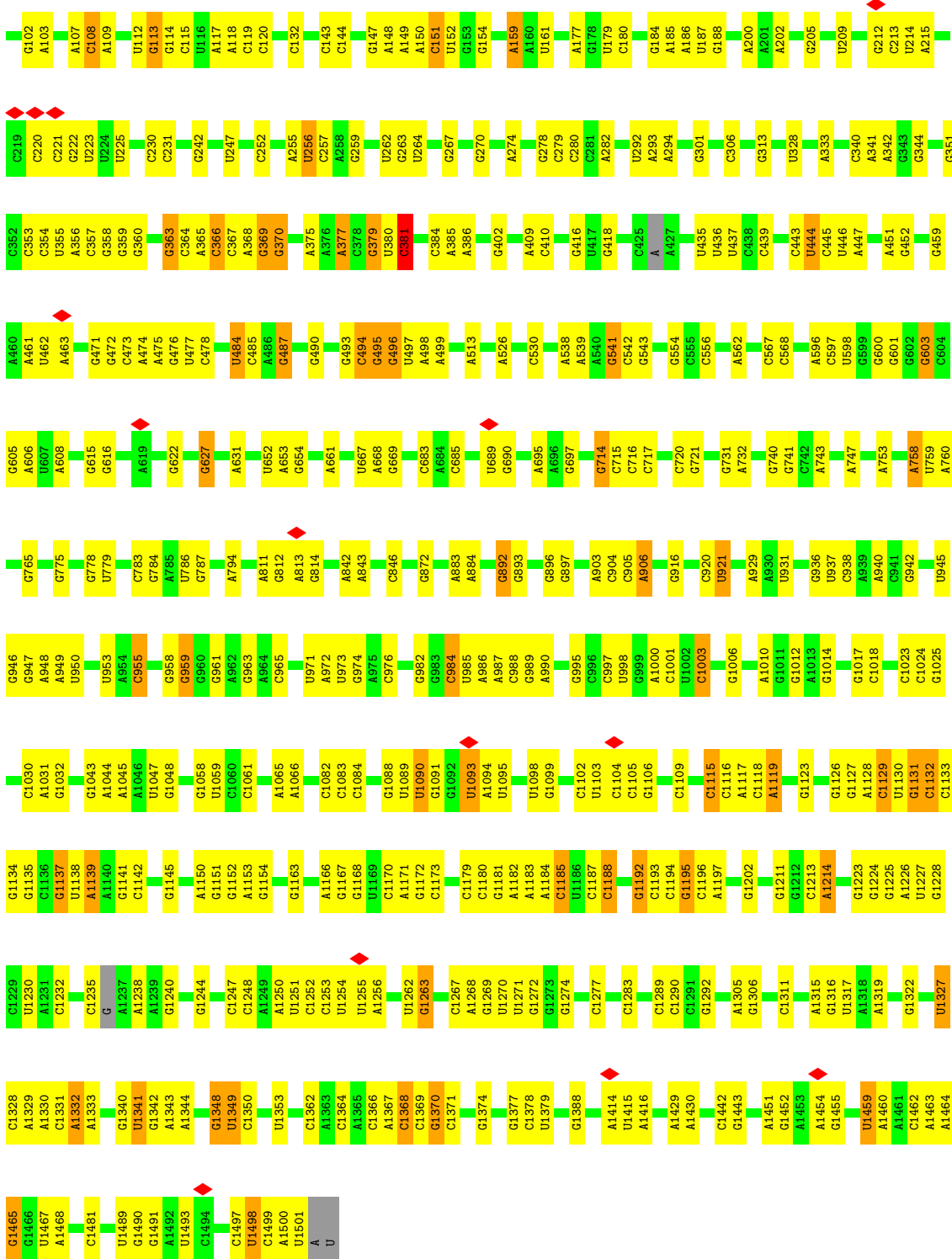
- Molecule 1: 23s rRNA (3000-MER)





● Molecule 2: 16s rRNA (1493-MER)



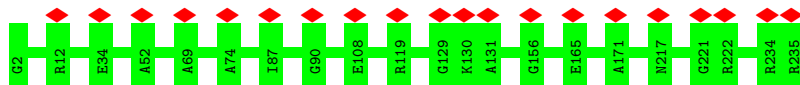


● Molecule 3: 5s rRNA (122-MER)

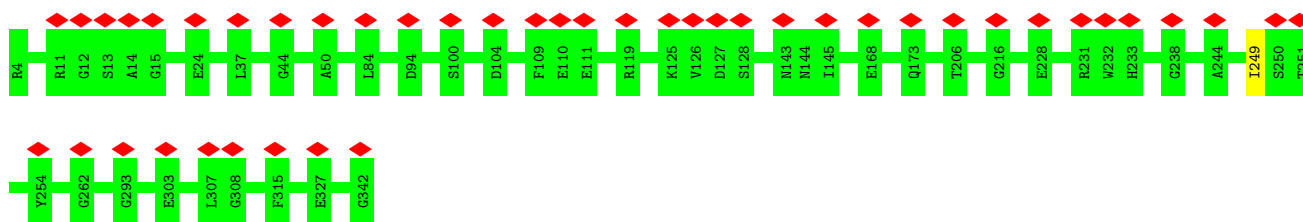




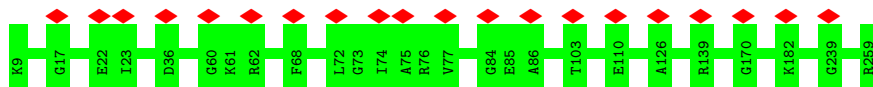
- Molecule 4: 50S ribosomal protein L2



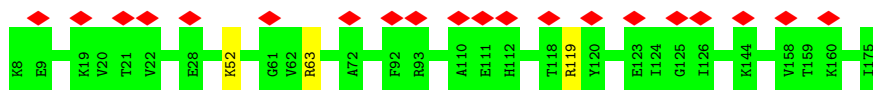
- Molecule 5: 50S ribosomal protein L3



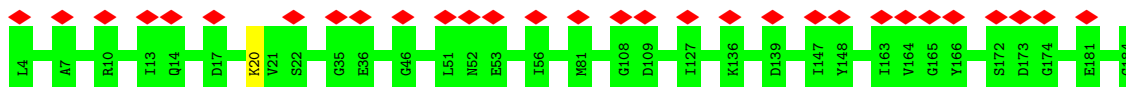
- Molecule 6: 50S ribosomal protein L4



- Molecule 7: 50S ribosomal protein L5

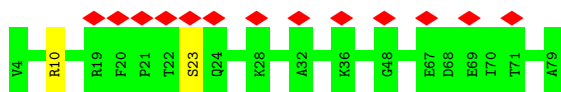


- Molecule 8: 50S ribosomal protein L6

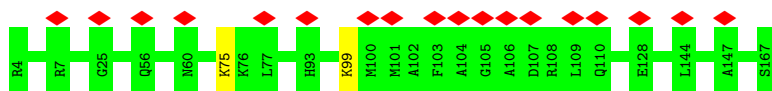


- Molecule 9: 50S ribosomal protein L18Ae

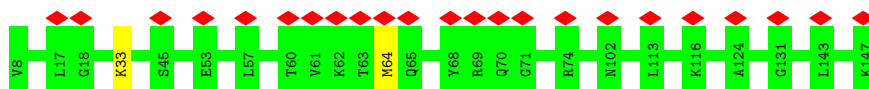




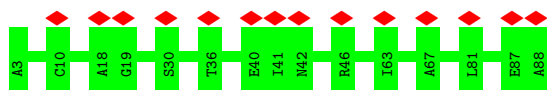
- Molecule 10: 50S ribosomal protein L10e



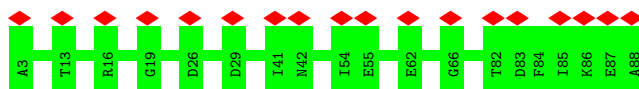
- Molecule 11: 50S ribosomal protein L13



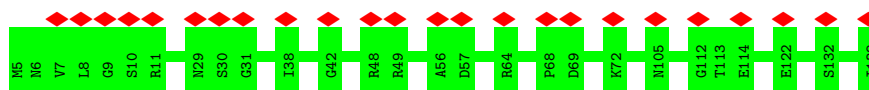
- Molecule 12: 50S ribosomal protein L14e



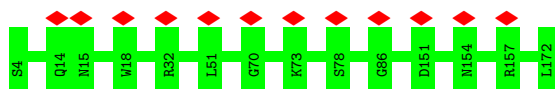
- Molecule 12: 50S ribosomal protein L14e



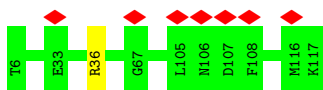
- Molecule 13: 50S ribosomal protein L14



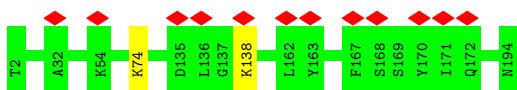
- Molecule 14: 50S ribosomal protein L15e



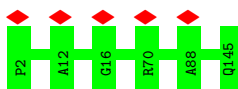
- Molecule 15: 50S ribosomal protein L18e



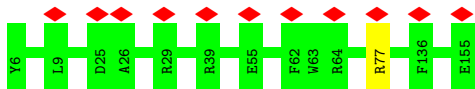
- Molecule 16: 50S ribosomal protein L18



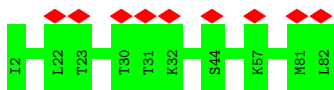
- Molecule 17: 50S ribosomal protein L19e



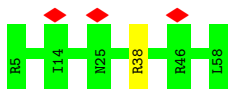
- Molecule 18: 50S ribosomal protein L22



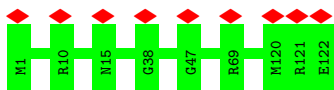
- Molecule 19: 50S ribosomal protein L23



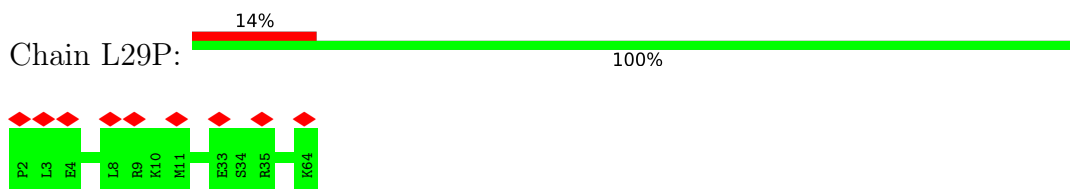
- Molecule 20: 50S ribosomal protein L24e



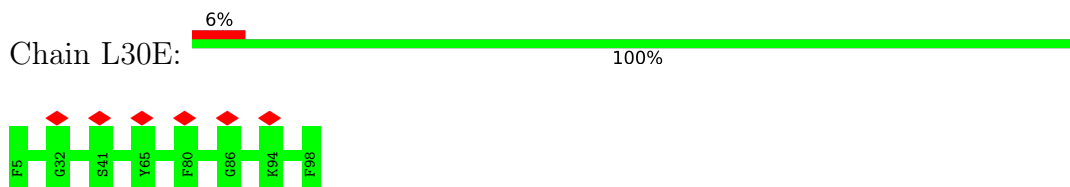
- Molecule 21: 50S ribosomal protein L24



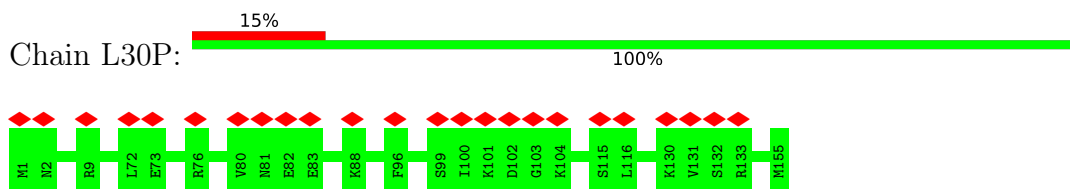
- Molecule 22: 50S ribosomal protein L29



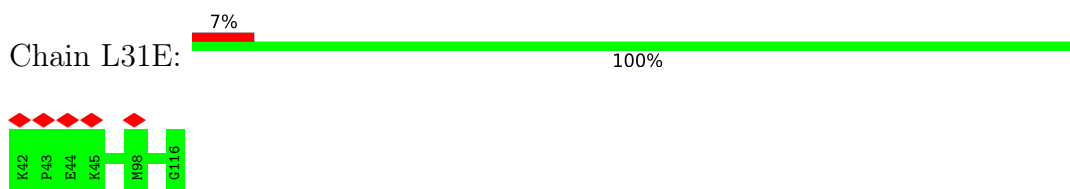
- Molecule 23: 50S ribosomal protein L30e



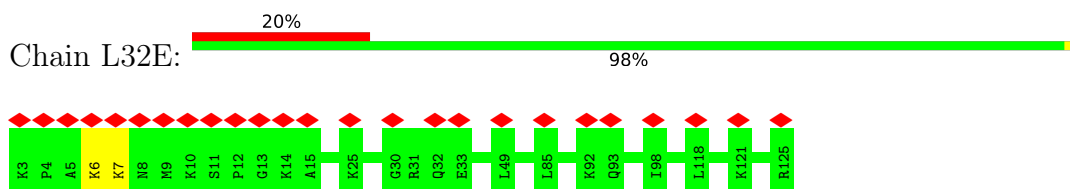
- Molecule 24: 50S ribosomal protein L30



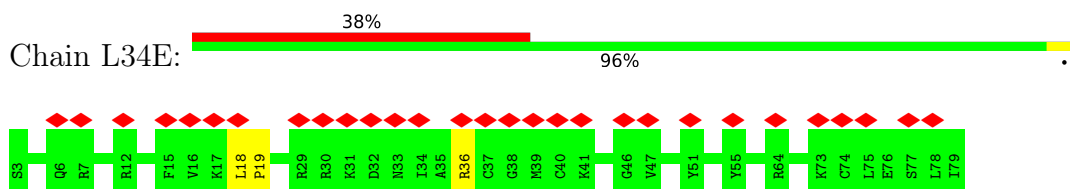
- Molecule 25: 50S ribosomal protein L31e



- Molecule 26: 50S ribosomal protein L32e

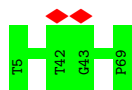


- Molecule 27: 50S ribosomal protein L34e

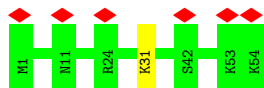


- Molecule 28: 50S ribosomal protein L37Ae

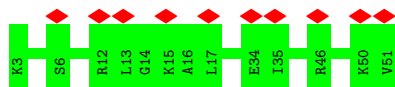




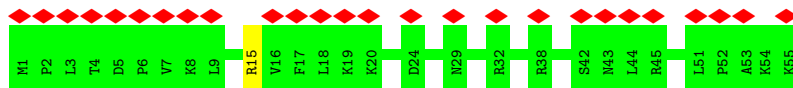
- Molecule 29: 50S ribosomal protein L37e



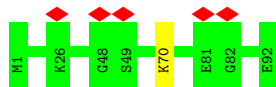
- Molecule 30: 50S ribosomal protein L39e



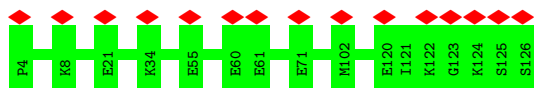
- Molecule 31: 50S ribosomal protein L40E



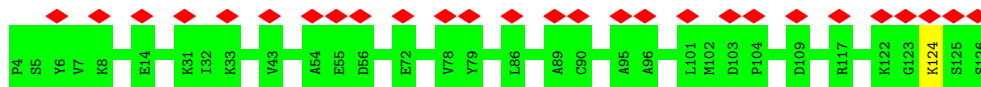
- Molecule 32: 50S ribosomal protein L44e



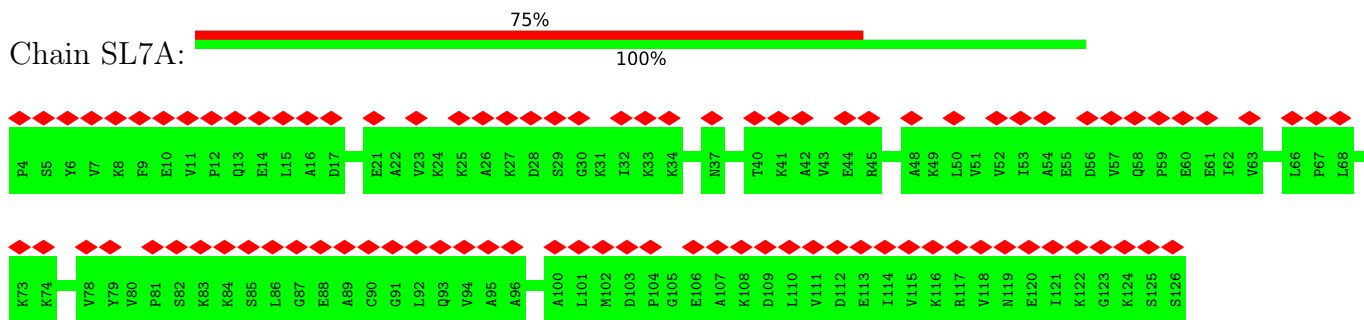
- Molecule 33: 50S ribosomal protein L7Ae



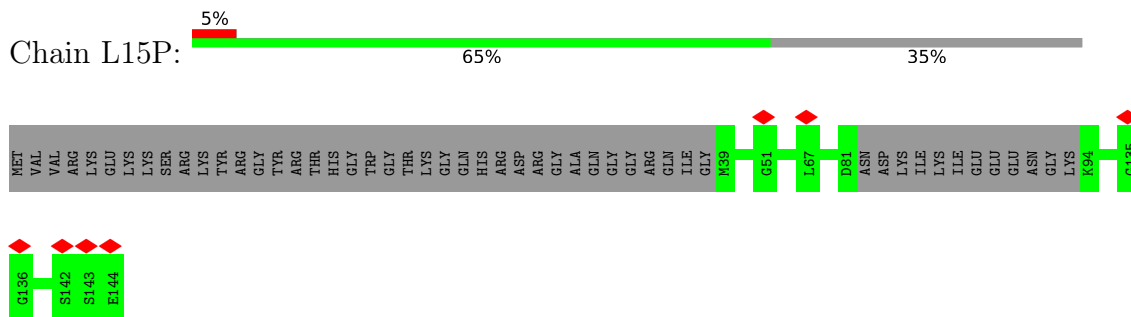
- Molecule 33: 50S ribosomal protein L7Ae



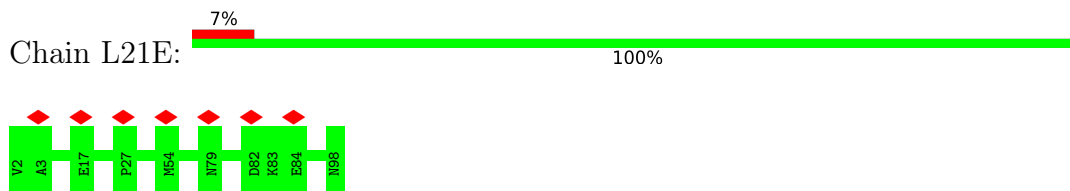
- Molecule 33: 50S ribosomal protein L7Ae



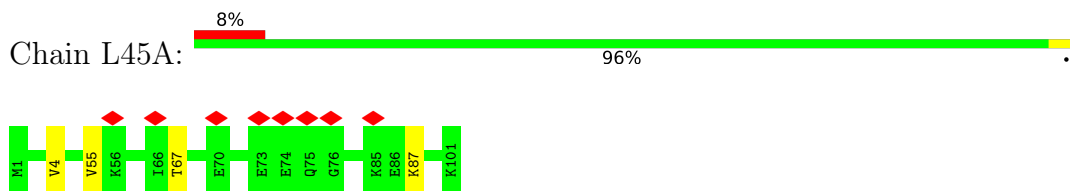
• Molecule 34: 50S ribosomal protein L15



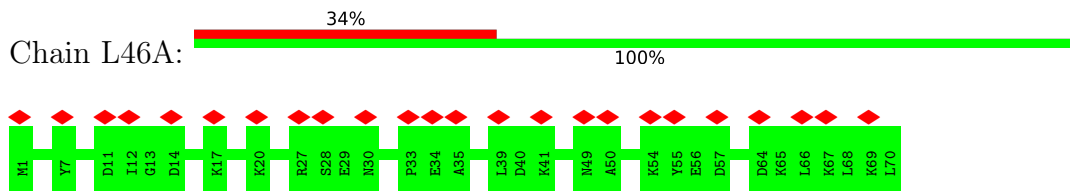
• Molecule 35: 50S ribosomal protein L21e



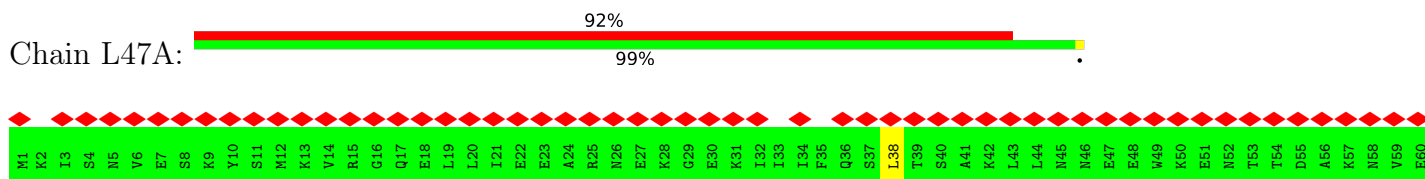
• Molecule 36: DUF2280 domain-containing protein

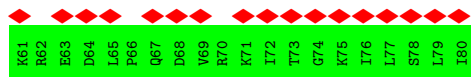


• Molecule 37: Conserved protein

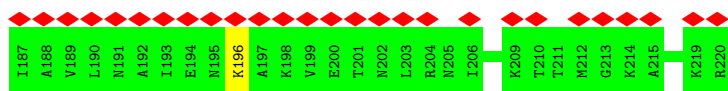
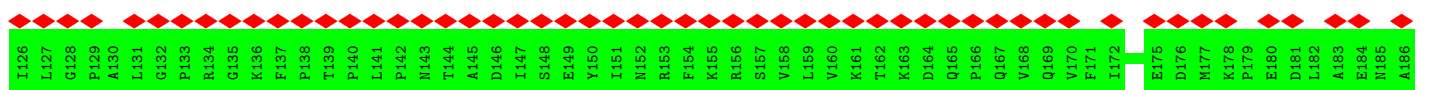
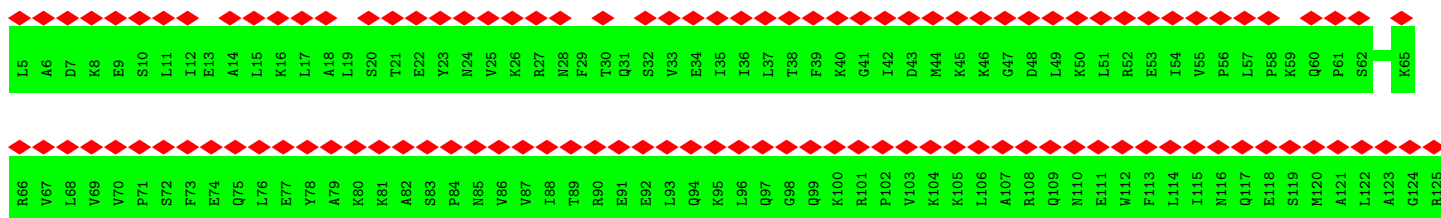


• Molecule 38: 50S ribosomal protein L47A

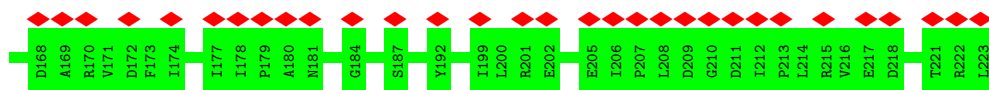
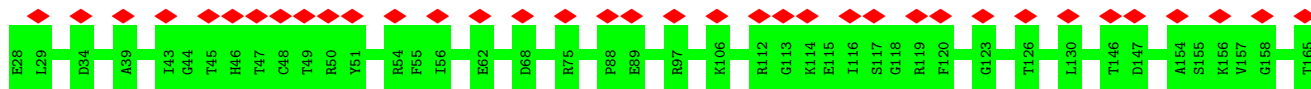




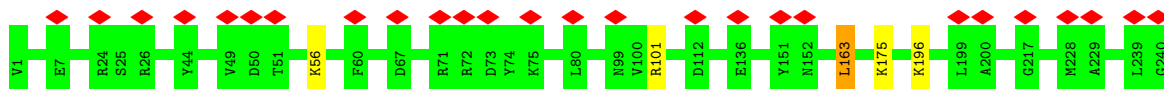
• Molecule 39: 50S ribosomal protein L1



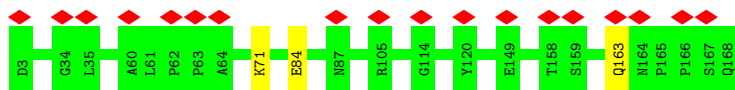
• Molecule 40: 30S ribosomal protein S2



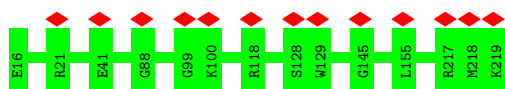
• Molecule 41: 30S ribosomal protein S4e



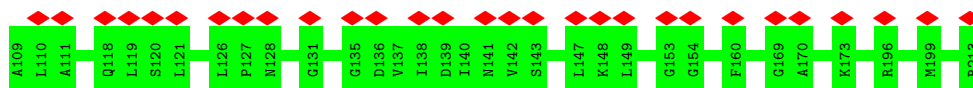
• Molecule 42: 30S ribosomal protein S4



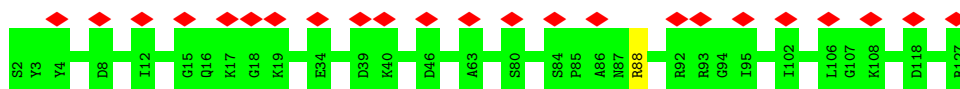
• Molecule 43: 30S ribosomal protein S5



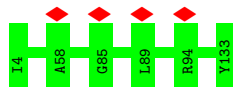
- Molecule 44: 30S ribosomal protein S6e



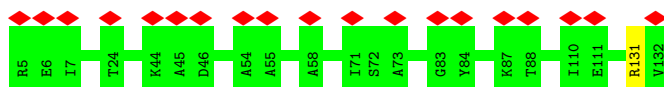
- Molecule 45: 30S ribosomal protein S8e



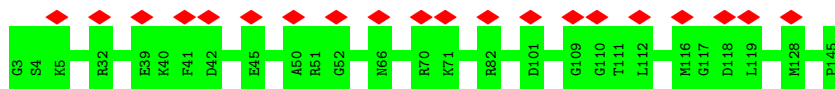
- Molecule 46: Small ribosomal subunit protein uS8



- Molecule 47: 30S ribosomal protein S11



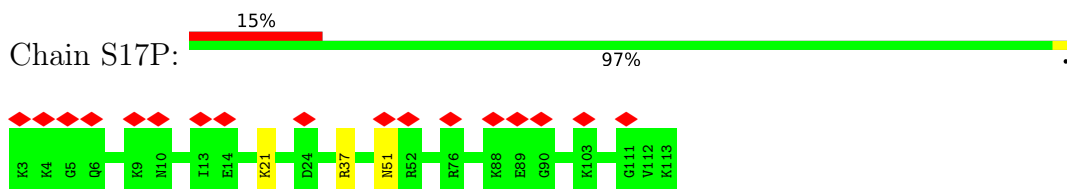
- Molecule 48: 30S ribosomal protein S12



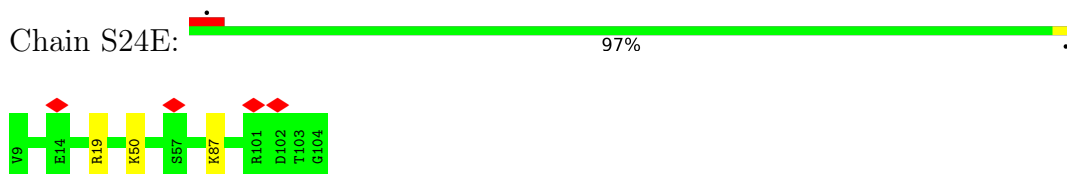
- Molecule 49: 30S ribosomal protein S15



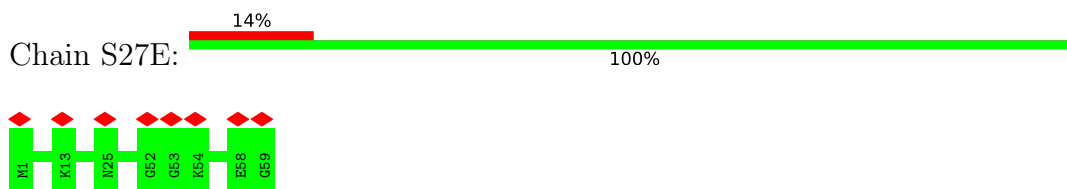
- Molecule 50: 30S ribosomal protein S17



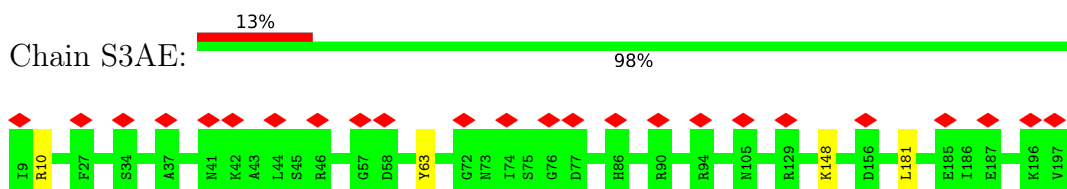
- Molecule 51: 30S ribosomal protein S24e



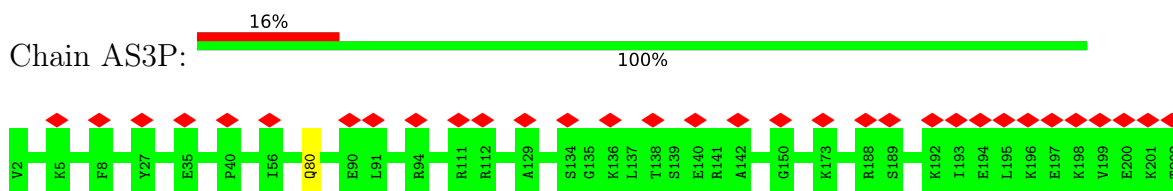
- Molecule 52: 30S ribosomal protein S27e



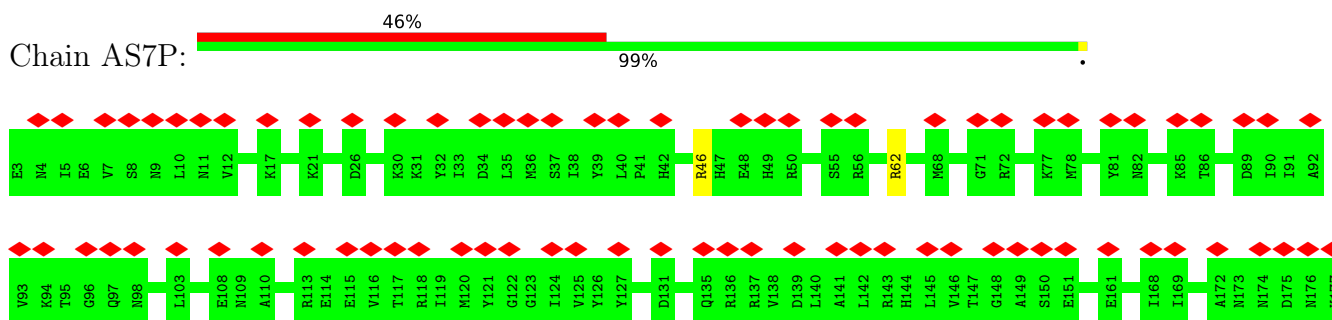
- Molecule 53: 30S ribosomal protein S3Ae

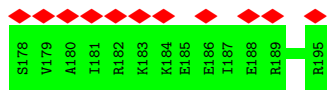


- Molecule 54: 30S ribosomal protein S3

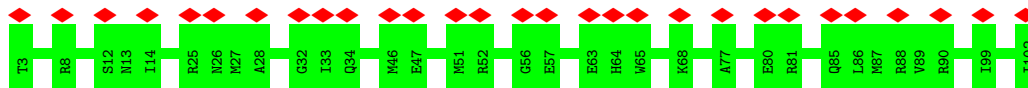


- Molecule 55: 30S ribosomal protein S7

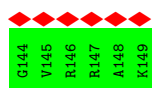
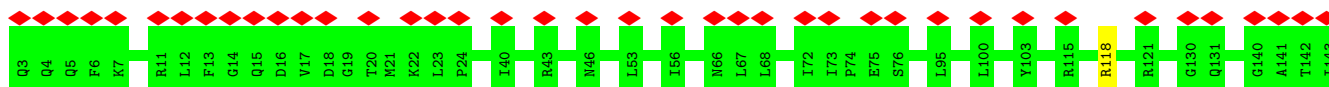




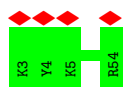
- Molecule 56: 30S ribosomal protein S10



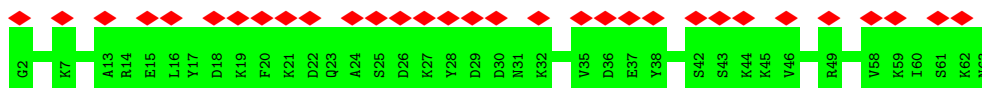
- Molecule 57: 30S ribosomal protein S13



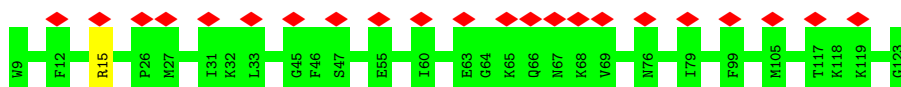
- Molecule 58: 30S ribosomal protein S14 type Z



- Molecule 59: 30S ribosomal protein S17e

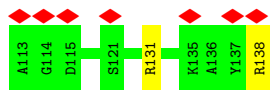
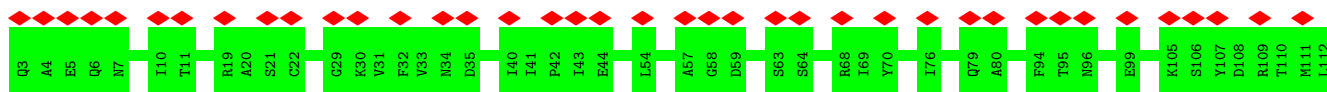


- Molecule 60: 30S ribosomal protein S19



- Molecule 61: 30S ribosomal protein S9

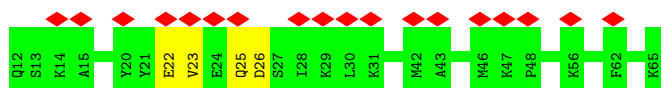




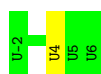
- Molecule 62: 30S ribosomal protein S28e



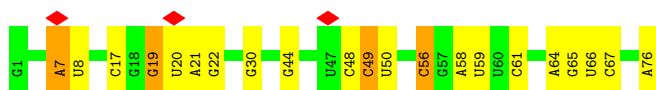
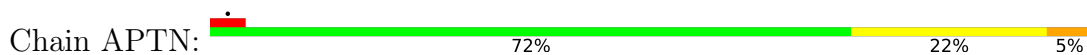
- Molecule 63: 30S ribosomal protein S27ae



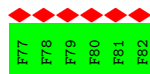
- Molecule 64: mRNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*U)-3')



- Molecule 65: tRNA (76-MER)

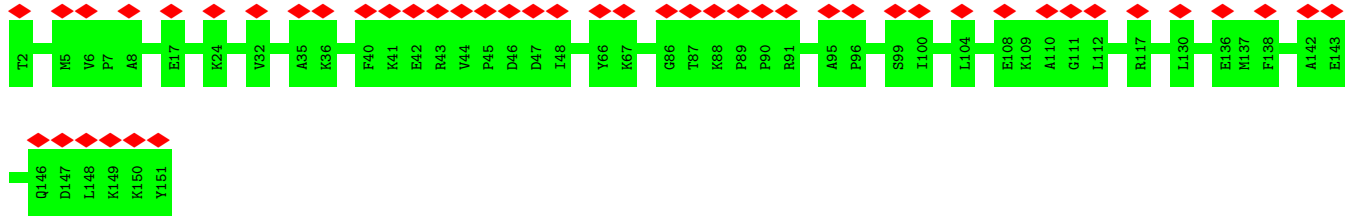


- Molecule 66: PHE-PHE-PHE-PHE-PHE-PHE

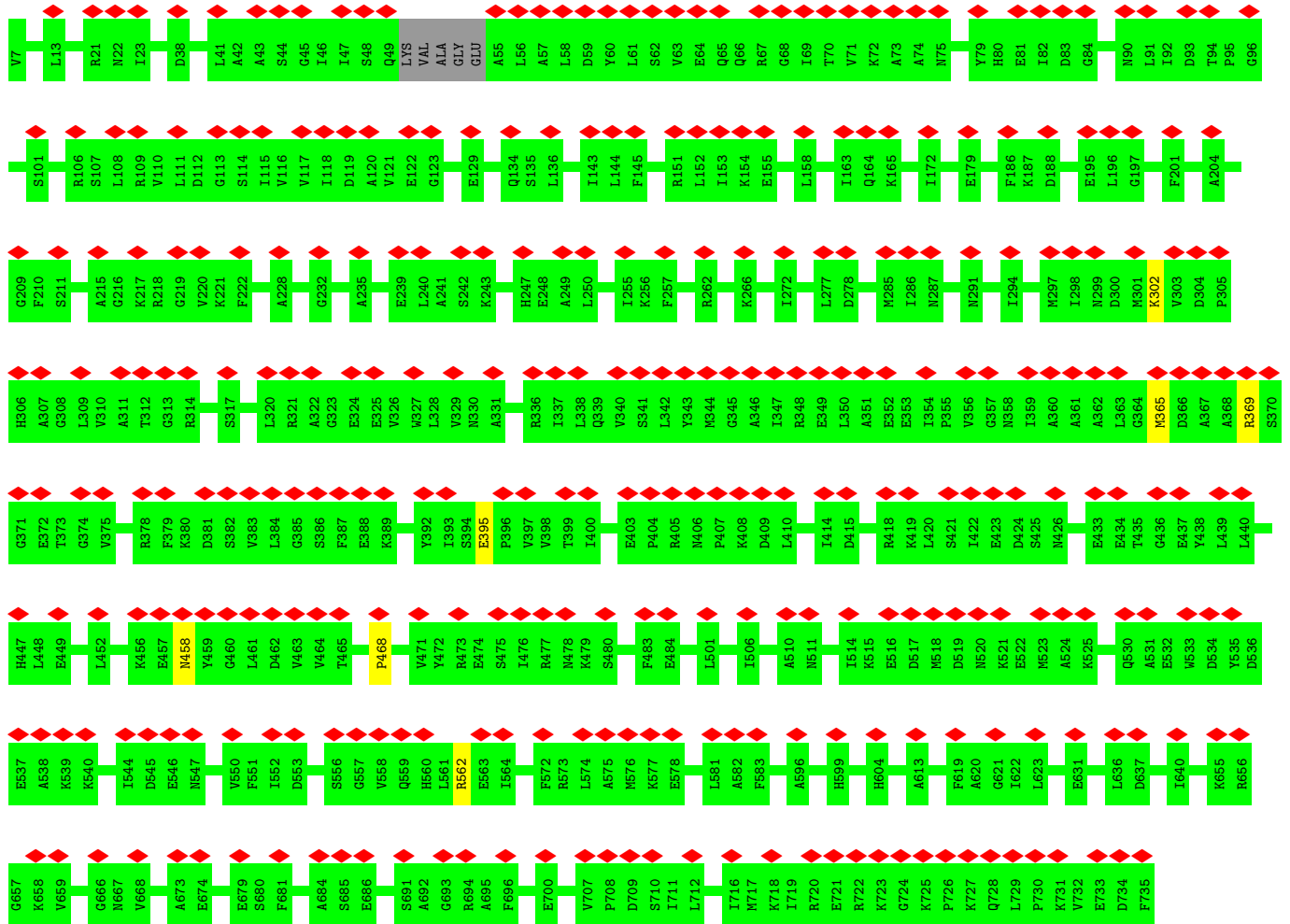


- Molecule 67: 30S ribosomal protein S19e





• Molecule 68: Elongation factor 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5357	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 ($e^-/\text{\AA}^2$)	26.7	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.457	Depositor
Minimum map value	-0.621	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.104	Depositor
Recommended contour level	0.33	Depositor
Map size (\AA)	413.06, 413.06, 413.06	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.087, 1.087, 1.087	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GNP

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	A23S	0.42	48/72029 (0.1%)	1.00	375/112378 (0.3%)
2	A16S	0.53	44/35862 (0.1%)	1.21	437/55957 (0.8%)
3	A5S	0.26	0/2917	0.71	0/4549
4	AL2P	0.27	0/1787	0.54	0/2409
5	AL3P	0.26	0/2758	0.53	0/3727
6	AL4P	0.25	0/1956	0.51	0/2635
7	AL5P	0.26	0/1364	0.56	0/1827
8	AL6P	0.26	0/1450	0.49	0/1949
9	ALX0	0.34	0/638	0.63	0/851
10	L10E	0.26	0/1334	0.53	0/1787
11	L13P	0.26	0/1123	0.56	0/1502
12	L141	0.25	0/673	0.52	0/900
12	L142	0.25	0/673	0.54	0/900
13	L14P	0.26	0/1054	0.55	0/1425
14	L15E	0.27	0/1458	0.57	0/1956
15	L18E	0.25	0/907	0.51	0/1214
16	L18P	0.26	0/1570	0.51	0/2115
17	L19E	0.24	0/1223	0.53	0/1622
18	L22P	0.27	0/1246	0.50	0/1671
19	L23P	0.26	0/655	0.47	0/874
20	L24E	0.25	0/451	0.49	0/599
21	L24P	0.25	0/1000	0.55	0/1329
22	L29P	0.24	0/513	0.54	0/678
23	L30E	0.26	0/738	0.48	0/985
24	L30P	0.27	0/1278	0.53	0/1713
25	L31E	0.25	0/632	0.60	0/837
26	L32E	0.26	0/1027	0.54	0/1366
27	L34E	0.33	0/642	0.89	4/854 (0.5%)
28	L37A	0.28	0/542	0.61	0/726
29	L37E	0.27	0/445	0.57	0/585
30	L39E	0.25	0/422	0.64	0/562
31	L40E	0.25	0/443	0.58	0/587

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	L44E	0.26	0/763	0.54	0/1008
33	L7A1	0.24	0/946	0.40	0/1272
33	L7A2	0.24	0/946	0.43	0/1272
33	SL7A	0.25	0/946	0.46	0/1272
34	L15P	0.25	0/766	0.49	0/1023
35	L21E	0.26	0/800	0.51	0/1067
36	L45A	0.27	0/824	0.56	0/1094
37	L46A	0.25	0/595	0.49	0/793
38	L47A	0.23	0/652	0.49	0/870
39	AL1P	0.24	0/1739	0.50	0/2338
40	AS2P	0.26	0/1621	0.53	0/2202
41	AS4E	0.25	0/1956	0.57	1/2635 (0.0%)
42	AS4P	0.25	0/1399	0.53	0/1883
43	AS5P	0.26	0/1631	0.50	0/2200
44	AS6E	0.27	0/815	0.58	0/1093
45	AS8E	0.25	0/1005	0.54	0/1342
46	AS8P	0.27	0/1046	0.53	0/1410
47	S11P	0.25	0/976	0.58	0/1315
48	S12P	0.26	0/1120	0.56	0/1495
49	S15P	0.25	0/1250	0.53	0/1677
50	S17P	0.26	0/899	0.53	0/1203
51	S24E	0.26	0/769	0.51	0/1034
52	S27E	0.26	0/465	0.49	0/618
53	S3AE	0.26	0/1573	0.54	0/2115
54	AS3P	0.26	0/1599	0.49	0/2147
55	AS7P	0.25	0/1561	0.56	0/2105
56	S10P	0.27	0/840	0.57	0/1132
57	S13P	0.25	0/1221	0.57	0/1634
58	S14P	0.28	0/441	0.61	0/583
59	S17E	0.23	0/523	0.46	0/696
60	S19P	0.26	0/985	0.54	0/1310
61	AS9P	0.26	0/1115	0.58	0/1496
62	S28E	0.24	0/500	0.59	0/669
63	S27A	0.33	0/444	0.71	0/590
64	AMRN	0.17	0/197	0.69	0/302
65	APTN	0.39	1/1809 (0.1%)	1.26	17/2819 (0.6%)
66	APTP	0.37	0/72	0.47	0/93
67	S19E	0.26	0/1267	0.52	0/1705
68	AEFG	0.25	0/5762	0.50	0/7796
All	All	0.39	93/184648 (0.1%)	0.92	834/272377 (0.3%)

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
2	A16S	0	1
9	ALX0	0	1
27	L34E	0	1
41	AS4E	0	1
42	AS4P	0	2
49	S15P	0	2
53	S3AE	0	1
63	S27A	0	3
All	All	0	12

The worst 5 of 93 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A16S	381	C	C2-O2	-16.03	1.10	1.24
2	A16S	381	C	N1-C6	-14.97	1.28	1.37
2	A16S	381	C	C4-C5	-9.14	1.35	1.43
1	A23S	1626	C	C2-O2	-9.04	1.16	1.24
1	A23S	1626	C	C4-C5	-9.01	1.35	1.43

The worst 5 of 834 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A16S	381	C	N1-C2-O2	-57.68	84.30	118.90
1	A23S	1626	C	C6-N1-C2	-51.19	99.83	120.30
1	A23S	1626	C	C5-C6-N1	36.07	139.03	121.00
2	A16S	381	C	N3-C2-O2	33.85	145.59	121.90
1	A23S	1626	C	N3-C4-C5	-30.82	109.57	121.90

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A16S	381	C	Sidechain
9	ALX0	23	SER	Peptide
41	AS4E	163	LEU	Peptide
42	AS4P	84	GLU	Peptide
27	L34E	36	ARG	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	A23S	64339	0	0	0	0
2	A16S	32040	0	0	0	0
3	A5S	2609	0	1324	43	0
4	AL2P	1754	0	0	0	0
5	AL3P	2695	0	0	0	0
6	AL4P	1926	0	0	0	0
7	AL5P	1343	0	0	0	0
8	AL6P	1431	0	0	0	0
9	ALX0	629	0	0	0	0
10	L10E	1310	0	0	0	0
11	L13P	1109	0	0	0	0
12	L141	669	0	0	0	0
12	L142	669	0	0	0	0
13	L14P	1034	0	0	0	0
14	L15E	1423	0	0	0	0
15	L18E	895	0	0	0	0
16	L18P	1539	0	0	0	0
17	L19E	1206	0	0	0	0
18	L22P	1223	0	0	0	0
19	L23P	650	0	0	0	0
20	L24E	441	0	0	0	0
21	L24P	989	0	0	0	0
22	L29P	513	0	0	0	0
23	L30E	729	0	0	0	0
24	L30P	1254	0	0	0	0
25	L31E	625	0	0	0	0
26	L32E	1010	0	0	0	0
27	L34E	629	0	0	0	0
28	L37A	527	0	0	0	0
29	L37E	436	0	0	0	0
30	L39E	414	0	0	0	0
31	L40E	439	0	0	0	0
32	L44E	753	0	0	0	0
33	L7A1	935	0	0	0	0
33	L7A2	935	0	0	0	0
33	SL7A	935	0	0	0	0
34	L15P	752	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	L21E	785	0	0	0	0
36	L45A	816	0	0	0	0
37	L46A	586	0	0	0	0
38	L47A	648	0	0	0	0
39	AL1P	1715	0	0	0	0
40	AS2P	1587	0	0	0	0
41	AS4E	1925	0	0	0	0
42	AS4P	1370	0	0	0	0
43	AS5P	1600	0	0	0	0
44	AS6E	805	0	0	0	0
45	AS8E	993	0	0	0	0
46	AS8P	1028	0	0	0	0
47	S11P	960	0	0	0	0
48	S12P	1103	0	0	0	0
49	S15P	1225	0	0	0	0
50	S17P	885	0	0	0	0
51	S24E	759	0	0	0	0
52	S27E	458	0	0	0	0
53	S3AE	1545	0	0	0	0
54	AS3P	1576	0	0	0	0
55	AS7P	1537	0	0	0	0
56	S10P	824	0	0	0	0
57	S13P	1204	0	0	0	0
58	S14P	432	0	0	0	0
59	S17E	517	0	0	0	0
60	S19P	968	0	0	0	0
61	AS9P	1096	0	0	0	0
62	S28E	498	0	0	0	0
63	S27A	435	0	0	0	0
64	AMRN	180	0	0	0	0
65	APTN	1619	0	0	0	0
66	APTP	67	0	0	0	0
67	S19E	1239	0	0	0	0
68	AEFG	5668	0	0	0	0
69	AS2P	186	0	0	0	0
69	AS5P	65	0	0	0	0
69	AS8P	35	0	0	0	0
70	AEFG	32	0	0	0	0
All	All	171780	0	1324	43	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 25.

The worst 5 of 43 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)
3:A5S:25:G:O2'	3:A5S:28:A:N6	2.28	0.67
3:A5S:40:G:O2'	3:A5S:47:A:N1	2.29	0.66
3:A5S:5:C:H2'	3:A5S:6:A:C8	2.31	0.66
3:A5S:53:A:HO2'	3:A5S:54:A:H8	1.53	0.57
3:A5S:115:U:H2'	3:A5S:116:G:H8	1.70	0.57

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	
4	AL2P	232/234 (99%)	221 (95%)	11 (5%)	0	100	100
5	AL3P	337/339 (99%)	304 (90%)	33 (10%)	0	100	100
6	AL4P	249/251 (99%)	239 (96%)	10 (4%)	0	100	100
7	AL5P	166/168 (99%)	146 (88%)	20 (12%)	0	100	100
8	AL6P	179/181 (99%)	166 (93%)	13 (7%)	0	100	100
9	ALX0	74/76 (97%)	66 (89%)	8 (11%)	0	100	100
10	L10E	162/164 (99%)	150 (93%)	12 (7%)	0	100	100
11	L13P	138/140 (99%)	127 (92%)	11 (8%)	0	100	100
12	L141	84/86 (98%)	78 (93%)	6 (7%)	0	100	100
12	L142	84/86 (98%)	75 (89%)	9 (11%)	0	100	100
13	L14P	132/134 (98%)	119 (90%)	13 (10%)	0	100	100
14	L15E	167/169 (99%)	159 (95%)	8 (5%)	0	100	100
15	L18E	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
16	L18P	191/193 (99%)	178 (93%)	13 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	L19E	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
18	L22P	148/150 (99%)	138 (93%)	10 (7%)	0	100	100
19	L23P	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
20	L24E	52/54 (96%)	50 (96%)	2 (4%)	0	100	100
21	L24P	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
22	L29P	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
23	L30E	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
24	L30P	153/155 (99%)	134 (88%)	19 (12%)	0	100	100
25	L31E	73/75 (97%)	69 (94%)	4 (6%)	0	100	100
26	L32E	121/123 (98%)	112 (93%)	9 (7%)	0	100	100
27	L34E	75/77 (97%)	47 (63%)	28 (37%)	0	100	100
28	L37A	63/65 (97%)	53 (84%)	10 (16%)	0	100	100
29	L37E	52/54 (96%)	51 (98%)	1 (2%)	0	100	100
30	L39E	47/49 (96%)	38 (81%)	9 (19%)	0	100	100
31	L40E	53/55 (96%)	38 (72%)	15 (28%)	0	100	100
32	L44E	90/92 (98%)	80 (89%)	10 (11%)	0	100	100
33	L7A1	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
33	L7A2	121/123 (98%)	121 (100%)	0	0	100	100
33	SL7A	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
34	L15P	90/144 (62%)	85 (94%)	5 (6%)	0	100	100
35	L21E	95/97 (98%)	88 (93%)	7 (7%)	0	100	100
36	L45A	99/101 (98%)	81 (82%)	15 (15%)	3 (3%)	4	31
37	L46A	68/70 (97%)	64 (94%)	4 (6%)	0	100	100
38	L47A	78/80 (98%)	72 (92%)	5 (6%)	1 (1%)	12	48
39	AL1P	214/216 (99%)	199 (93%)	15 (7%)	0	100	100
40	AS2P	194/196 (99%)	181 (93%)	13 (7%)	0	100	100
41	AS4E	238/240 (99%)	213 (90%)	25 (10%)	0	100	100
42	AS4P	164/166 (99%)	136 (83%)	28 (17%)	0	100	100
43	AS5P	202/204 (99%)	186 (92%)	16 (8%)	0	100	100
44	AS6E	103/105 (98%)	89 (86%)	14 (14%)	0	100	100
45	AS8E	124/126 (98%)	111 (90%)	13 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	AS8P	128/130 (98%)	122 (95%)	6 (5%)	0	100	100
47	S11P	126/128 (98%)	109 (86%)	17 (14%)	0	100	100
48	S12P	141/143 (99%)	122 (86%)	19 (14%)	0	100	100
49	S15P	147/149 (99%)	126 (86%)	21 (14%)	0	100	100
50	S17P	109/111 (98%)	102 (94%)	7 (6%)	0	100	100
51	S24E	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
52	S27E	57/59 (97%)	50 (88%)	7 (12%)	0	100	100
53	S3AE	187/189 (99%)	159 (85%)	27 (14%)	1 (0%)	29	68
54	AS3P	199/201 (99%)	187 (94%)	12 (6%)	0	100	100
55	AS7P	191/193 (99%)	169 (88%)	22 (12%)	0	100	100
56	S10P	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
57	S13P	145/147 (99%)	132 (91%)	13 (9%)	0	100	100
58	S14P	50/52 (96%)	43 (86%)	7 (14%)	0	100	100
59	S17E	60/62 (97%)	52 (87%)	8 (13%)	0	100	100
60	S19P	113/115 (98%)	101 (89%)	12 (11%)	0	100	100
61	AS9P	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
62	S28E	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
63	S27A	52/54 (96%)	39 (75%)	12 (23%)	1 (2%)	8	40
66	AFTP	4/6 (67%)	3 (75%)	1 (25%)	0	100	100
67	S19E	148/150 (99%)	134 (90%)	14 (10%)	0	100	100
68	AEFG	720/729 (99%)	679 (94%)	39 (5%)	2 (0%)	41	76
All	All	8722/8913 (98%)	7963 (91%)	751 (9%)	8 (0%)	54	85

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
36	L45A	4	VAL
36	L45A	55	VAL
68	AEFG	468	PRO
36	L45A	67	THR
53	S3AE	63	TYR

5.3.2 Protein sidechains [i](#)

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	
4	AL2P	181/181 (100%)	181 (100%)	0	100	100
5	AL3P	297/297 (100%)	296 (100%)	1 (0%)	92	95
6	AL4P	212/212 (100%)	212 (100%)	0	100	100
7	AL5P	144/144 (100%)	141 (98%)	3 (2%)	53	72
8	AL6P	157/157 (100%)	156 (99%)	1 (1%)	86	92
9	ALX0	68/68 (100%)	67 (98%)	1 (2%)	65	80
10	L10E	137/137 (100%)	135 (98%)	2 (2%)	65	80
11	L13P	121/121 (100%)	119 (98%)	2 (2%)	60	78
12	L141	74/74 (100%)	74 (100%)	0	100	100
12	L142	74/74 (100%)	74 (100%)	0	100	100
13	L14P	110/110 (100%)	110 (100%)	0	100	100
14	L15E	146/146 (100%)	146 (100%)	0	100	100
15	L18E	98/98 (100%)	97 (99%)	1 (1%)	76	86
16	L18P	162/162 (100%)	160 (99%)	2 (1%)	71	84
17	L19E	126/126 (100%)	126 (100%)	0	100	100
18	L22P	131/131 (100%)	130 (99%)	1 (1%)	81	89
19	L23P	74/74 (100%)	74 (100%)	0	100	100
20	L24E	50/50 (100%)	49 (98%)	1 (2%)	55	73
21	L24P	108/108 (100%)	108 (100%)	0	100	100
22	L29P	59/59 (100%)	59 (100%)	0	100	100
23	L30E	83/83 (100%)	83 (100%)	0	100	100
24	L30P	136/136 (100%)	136 (100%)	0	100	100
25	L31E	66/66 (100%)	66 (100%)	0	100	100
26	L32E	106/106 (100%)	104 (98%)	2 (2%)	57	75
27	L34E	70/70 (100%)	70 (100%)	0	100	100
28	L37A	53/53 (100%)	53 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	L37E	45/45 (100%)	44 (98%)	1 (2%)	52	71
30	L39E	44/44 (100%)	44 (100%)	0	100	100
31	L40E	50/50 (100%)	49 (98%)	1 (2%)	55	73
32	L44E	84/84 (100%)	83 (99%)	1 (1%)	71	84
33	L7A1	104/104 (100%)	104 (100%)	0	100	100
33	L7A2	104/104 (100%)	103 (99%)	1 (1%)	76	86
33	SL7A	104/104 (100%)	104 (100%)	0	100	100
34	L15P	78/118 (66%)	78 (100%)	0	100	100
35	L21E	85/85 (100%)	85 (100%)	0	100	100
36	L45A	91/91 (100%)	90 (99%)	1 (1%)	73	85
37	L46A	66/66 (100%)	66 (100%)	0	100	100
38	L47A	74/74 (100%)	74 (100%)	0	100	100
39	AL1P	189/190 (100%)	188 (100%)	1 (0%)	88	93
40	AS2P	174/174 (100%)	174 (100%)	0	100	100
41	AS4E	210/210 (100%)	206 (98%)	4 (2%)	57	75
42	AS4P	149/149 (100%)	148 (99%)	1 (1%)	84	90
43	AS5P	174/174 (100%)	174 (100%)	0	100	100
44	AS6E	88/88 (100%)	88 (100%)	0	100	100
45	AS8E	106/106 (100%)	105 (99%)	1 (1%)	78	87
46	AS8P	111/111 (100%)	111 (100%)	0	100	100
47	S11P	94/94 (100%)	93 (99%)	1 (1%)	73	85
48	S12P	116/116 (100%)	116 (100%)	0	100	100
49	S15P	133/133 (100%)	132 (99%)	1 (1%)	81	89
50	S17P	97/97 (100%)	94 (97%)	3 (3%)	40	62
51	S24E	84/84 (100%)	81 (96%)	3 (4%)	35	59
52	S27E	51/51 (100%)	51 (100%)	0	100	100
53	S3AE	170/170 (100%)	168 (99%)	2 (1%)	71	84
54	AS3P	165/165 (100%)	164 (99%)	1 (1%)	86	92
55	AS7P	166/166 (100%)	164 (99%)	2 (1%)	71	84
56	S10P	92/92 (100%)	92 (100%)	0	100	100
57	S13P	129/129 (100%)	128 (99%)	1 (1%)	81	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	S14P	45/45 (100%)	45 (100%)	0	100	100
59	S17E	57/57 (100%)	57 (100%)	0	100	100
60	S19P	106/106 (100%)	105 (99%)	1 (1%)	78	87
61	AS9P	113/113 (100%)	111 (98%)	2 (2%)	59	77
62	S28E	54/54 (100%)	54 (100%)	0	100	100
63	S27A	47/47 (100%)	47 (100%)	0	100	100
66	APTP	6/6 (100%)	6 (100%)	0	100	100
67	S19E	134/134 (100%)	134 (100%)	0	100	100
68	AEFG	624/627 (100%)	619 (99%)	5 (1%)	81	89
All	All	7656/7700 (99%)	7605 (99%)	51 (1%)	84	90

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	AS8E	88	ARG
51	S24E	50	LYS
68	AEFG	458	ASN
47	S11P	131	ARG
50	S17P	37	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A23S	2985/3022 (98%)	662 (22%)	32 (1%)
2	A16S	1489/1503 (99%)	412 (27%)	48 (3%)
3	A5S	121/122 (99%)	21 (17%)	1 (0%)
64	AMRN	8/9 (88%)	1 (12%)	0
65	APTN	75/76 (98%)	20 (26%)	2 (2%)
All	All	4678/4732 (98%)	1116 (23%)	83 (1%)

5 of 1116 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A23S	18	G
1	A23S	19	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A23S	25	C
1	A23S	30	C
1	A23S	31	G

5 of 83 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A16S	972	A
2	A16S	1316	G
2	A16S	989	G
2	A16S	1152	G
2	A16S	1429	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 58 ligands modelled in this entry, 57 are unknown - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
70	GNP	AEFG	801	68	29,34,34	1.61	7 (24%)	33,54,54	2.15	6 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
70	GNP	AEFG	801	68	-	4/14/38/38	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
70	AEFG	801	GNP	PB-O3A	4.45	1.64	1.59
70	AEFG	801	GNP	C6-N1	3.19	1.38	1.33
70	AEFG	801	GNP	PG-N3B	3.15	1.71	1.63
70	AEFG	801	GNP	PB-O1B	2.83	1.50	1.46
70	AEFG	801	GNP	PG-O1G	2.61	1.50	1.46

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
70	AEFG	801	GNP	C5-C6-N1	-8.33	112.03	123.43
70	AEFG	801	GNP	C2-N1-C6	5.71	125.00	115.93
70	AEFG	801	GNP	PB-O3A-PA	-3.22	121.26	132.62
70	AEFG	801	GNP	N3-C2-N1	-2.75	123.55	127.22
70	AEFG	801	GNP	C4-C5-C6	-2.51	118.40	120.80

There are no chirality outliers.

All (4) torsion outliers are listed below:

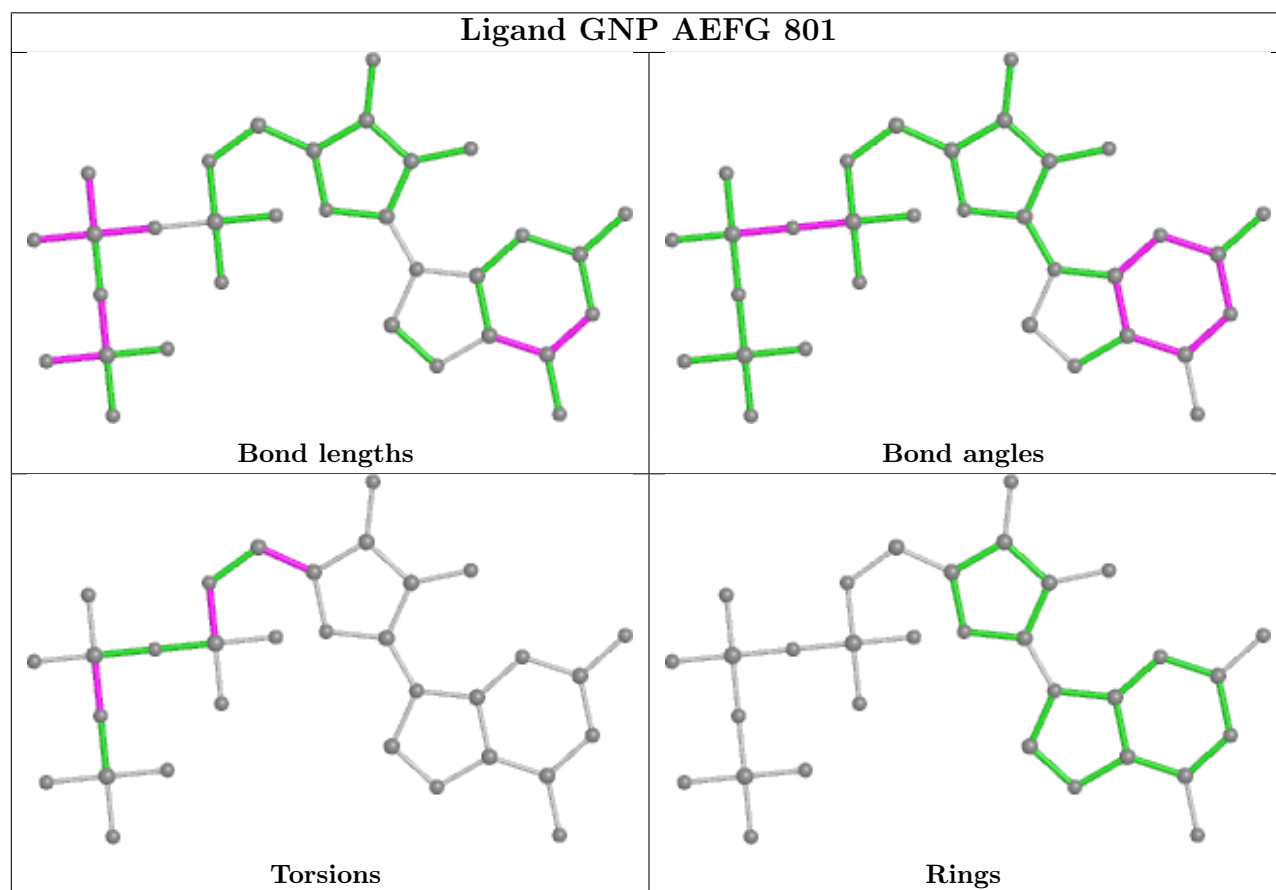
Mol	Chain	Res	Type	Atoms
70	AEFG	801	GNP	PG-N3B-PB-O1B
70	AEFG	801	GNP	C5'-O5'-PA-O3A
70	AEFG	801	GNP	C5'-O5'-PA-O1A
70	AEFG	801	GNP	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

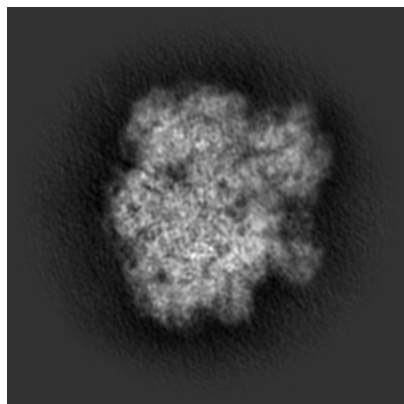
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34869. These allow visual inspection of the internal detail of the map and identification of artifacts.

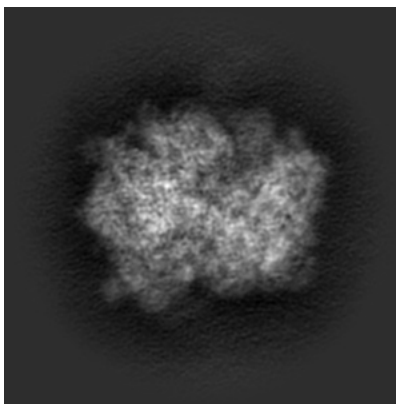
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

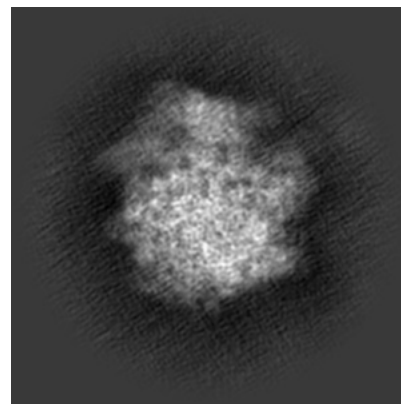
6.1.1 Primary map



X

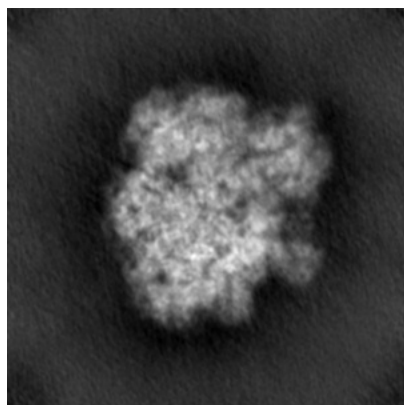


Y

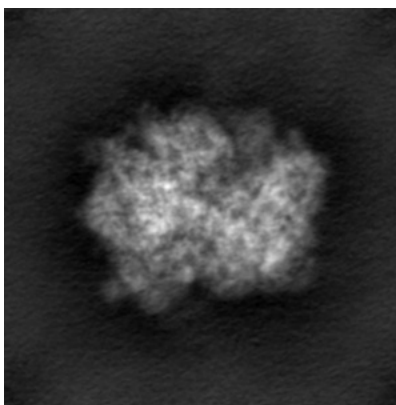


Z

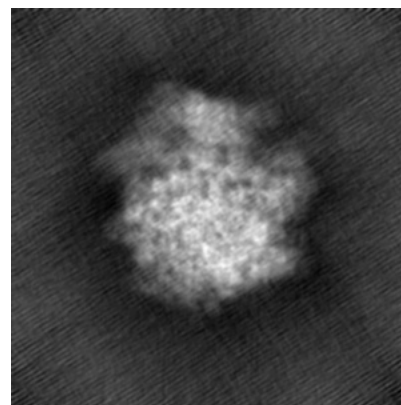
6.1.2 Raw map



X



Y

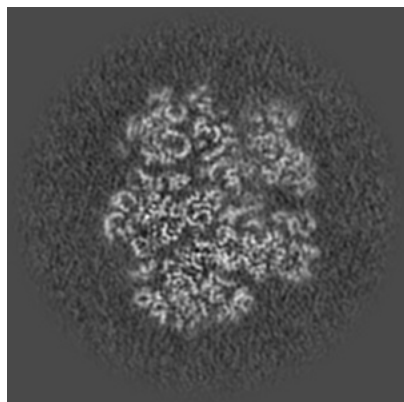


Z

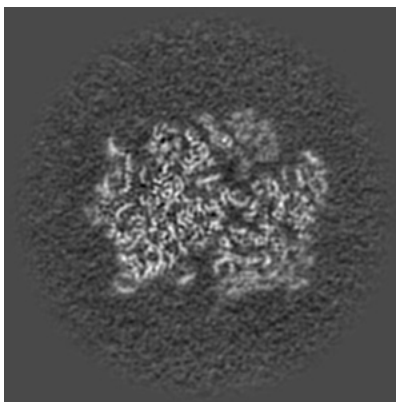
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

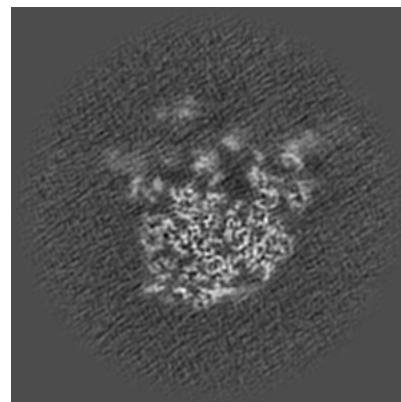
6.2.1 Primary map



X Index: 190

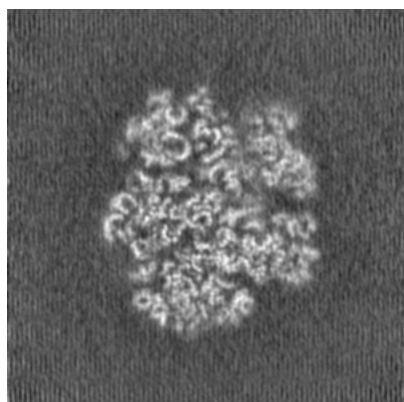


Y Index: 190

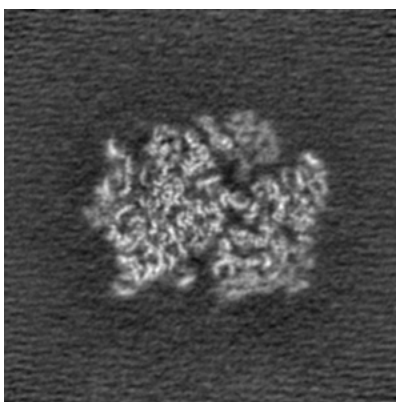


Z Index: 190

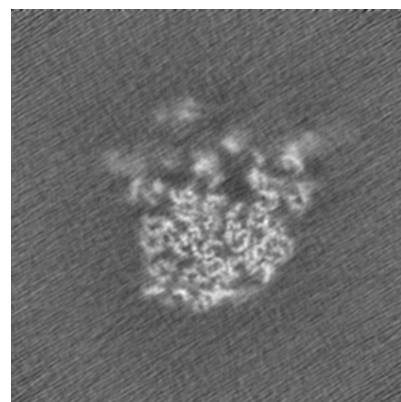
6.2.2 Raw map



X Index: 190



Y Index: 190

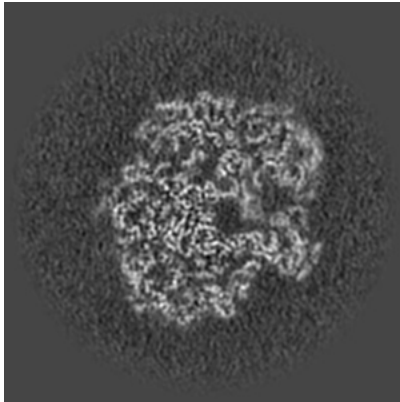


Z Index: 190

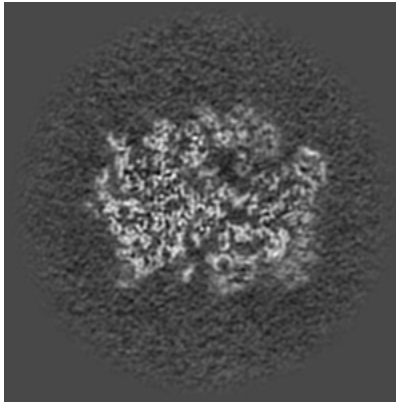
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

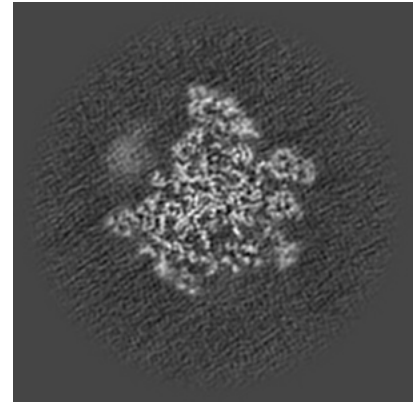
6.3.1 Primary map



X Index: 177

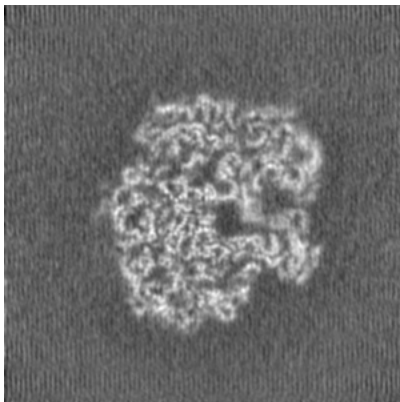


Y Index: 193

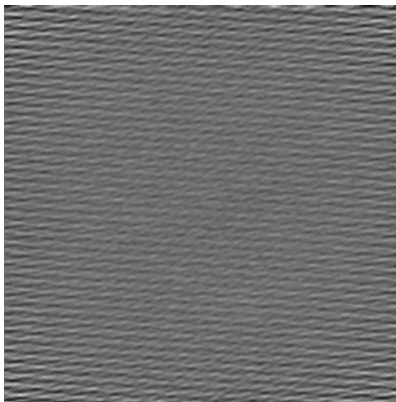


Z Index: 144

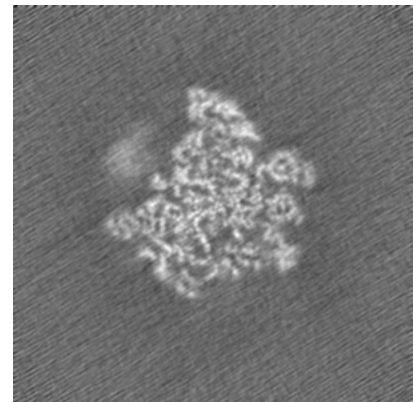
6.3.2 Raw map



X Index: 178



Y Index: 0

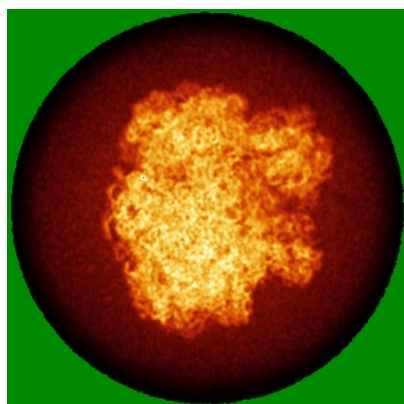


Z Index: 145

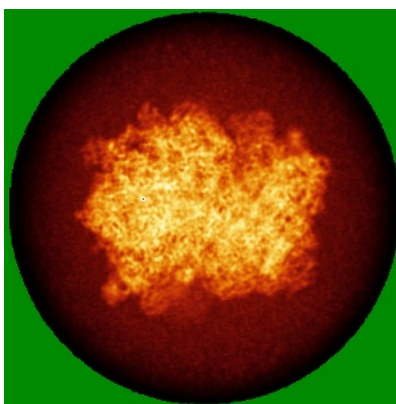
The images above show the largest variance slices of the map in three orthogonal directions.

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

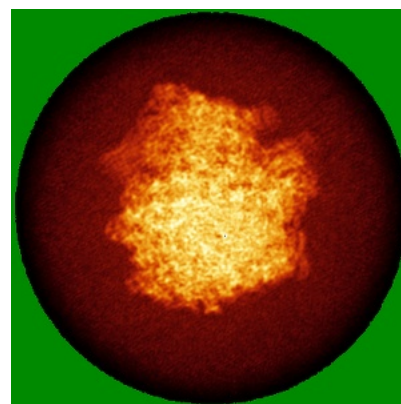
6.4.1 Primary map



X

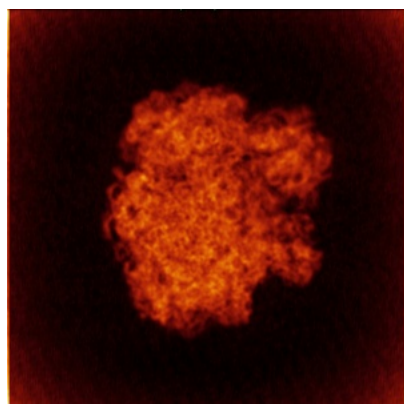


Y

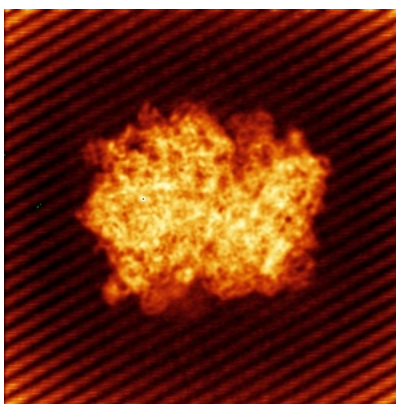


Z

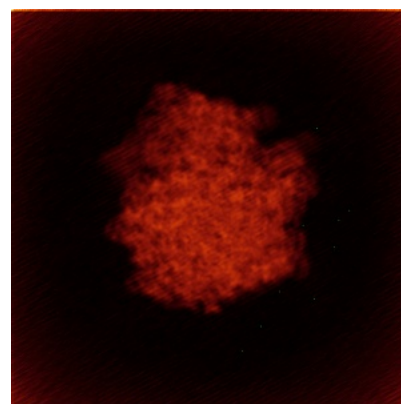
6.4.2 Raw map



X



Y

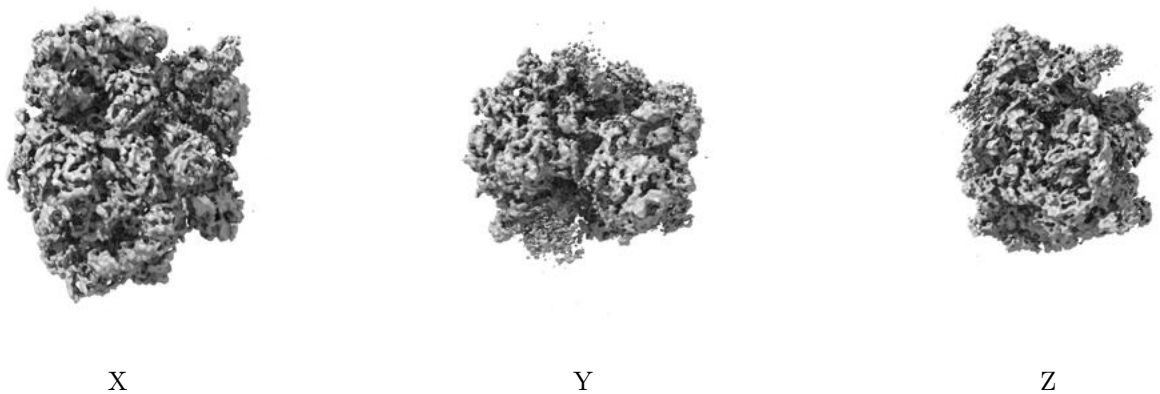


Z

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.

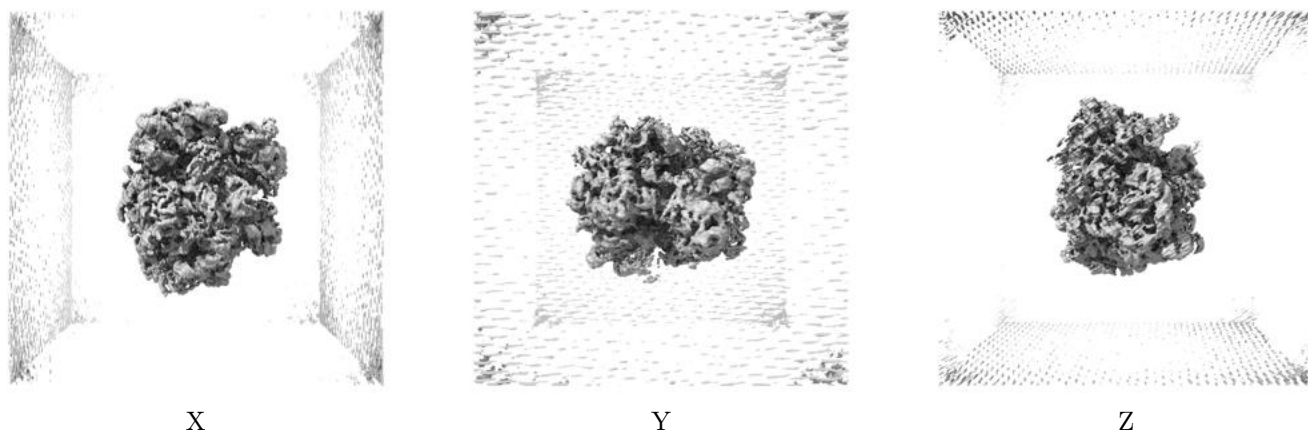
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.33. 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



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.

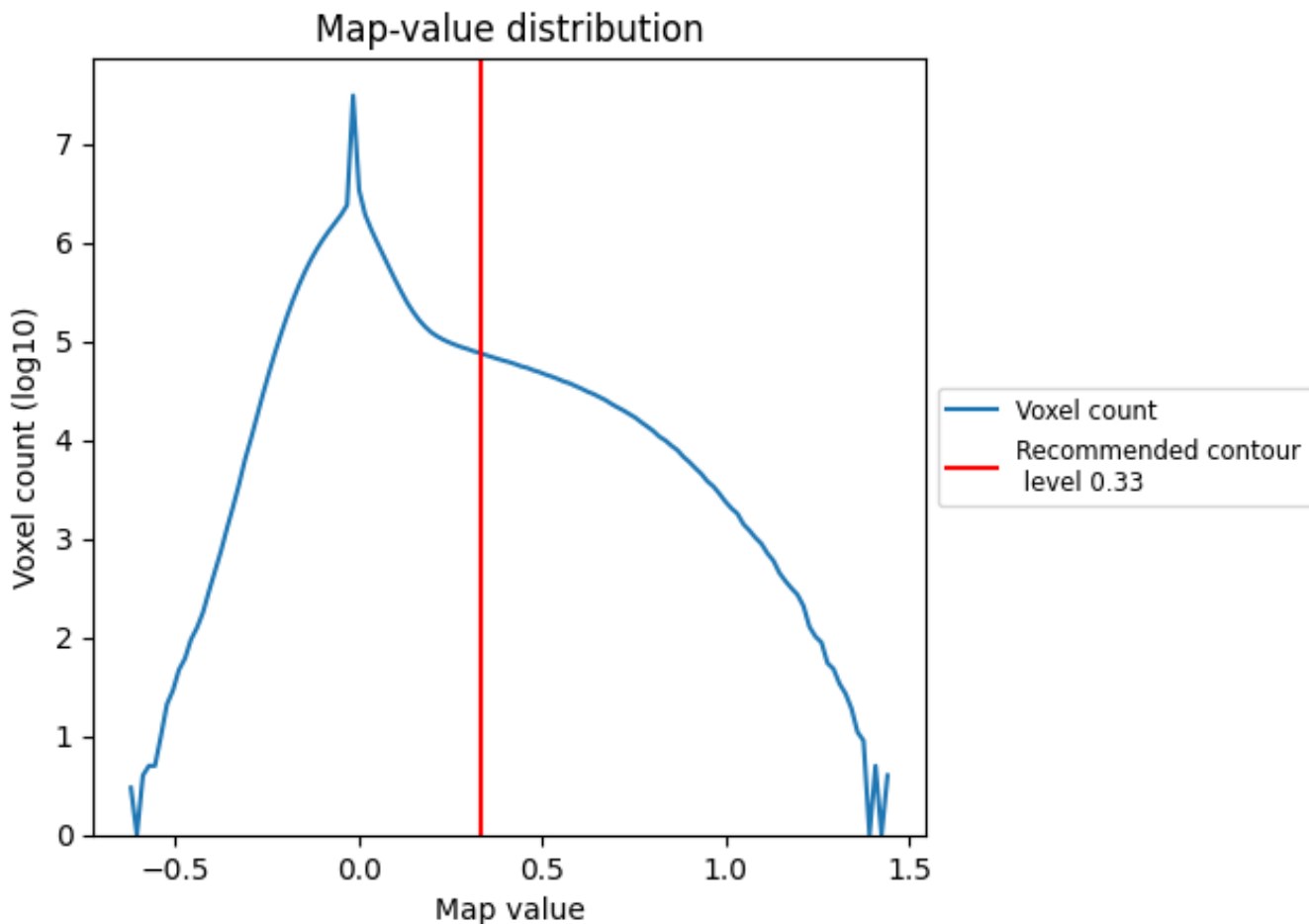
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

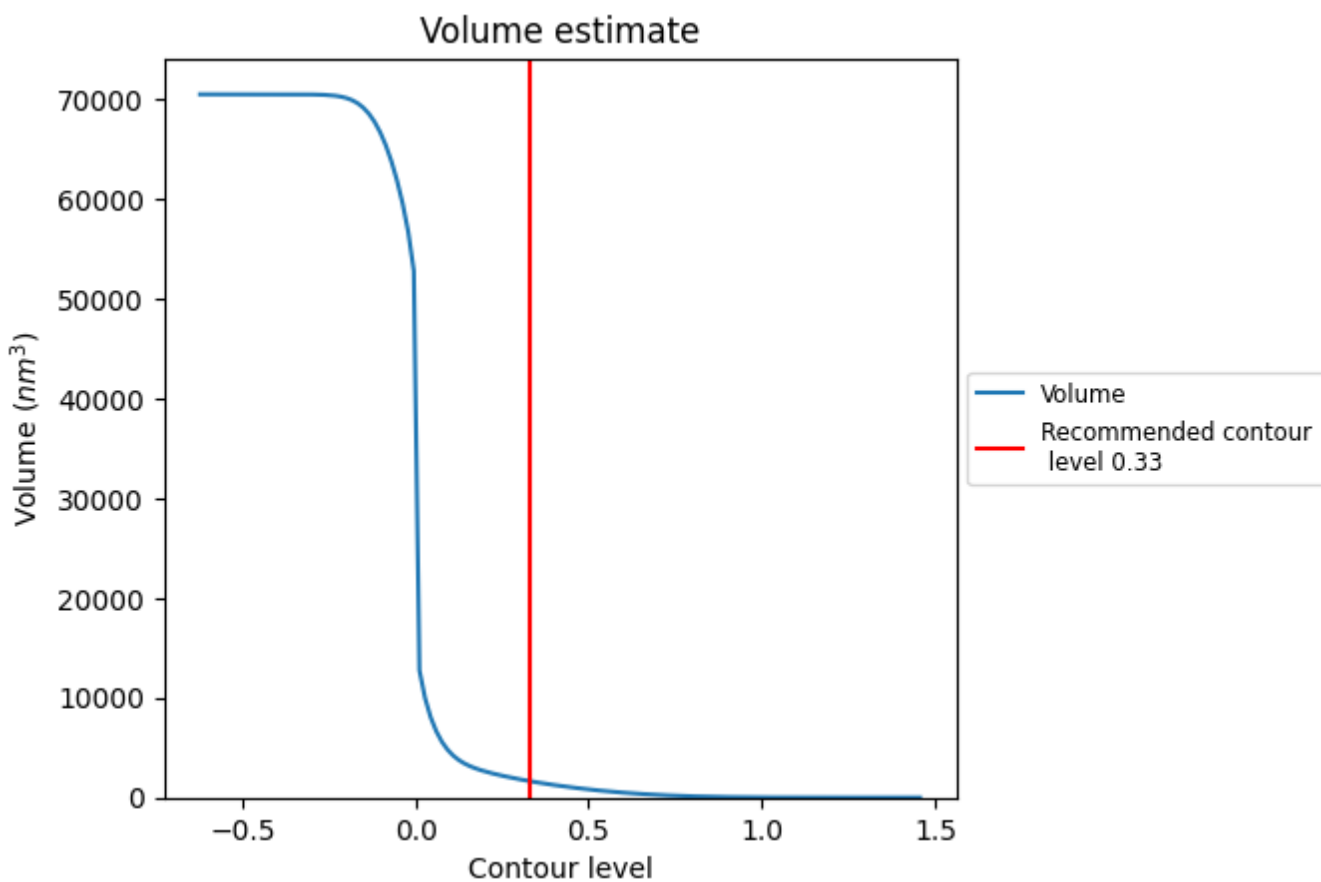
This section contains the results of statistical analysis of the map.

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.

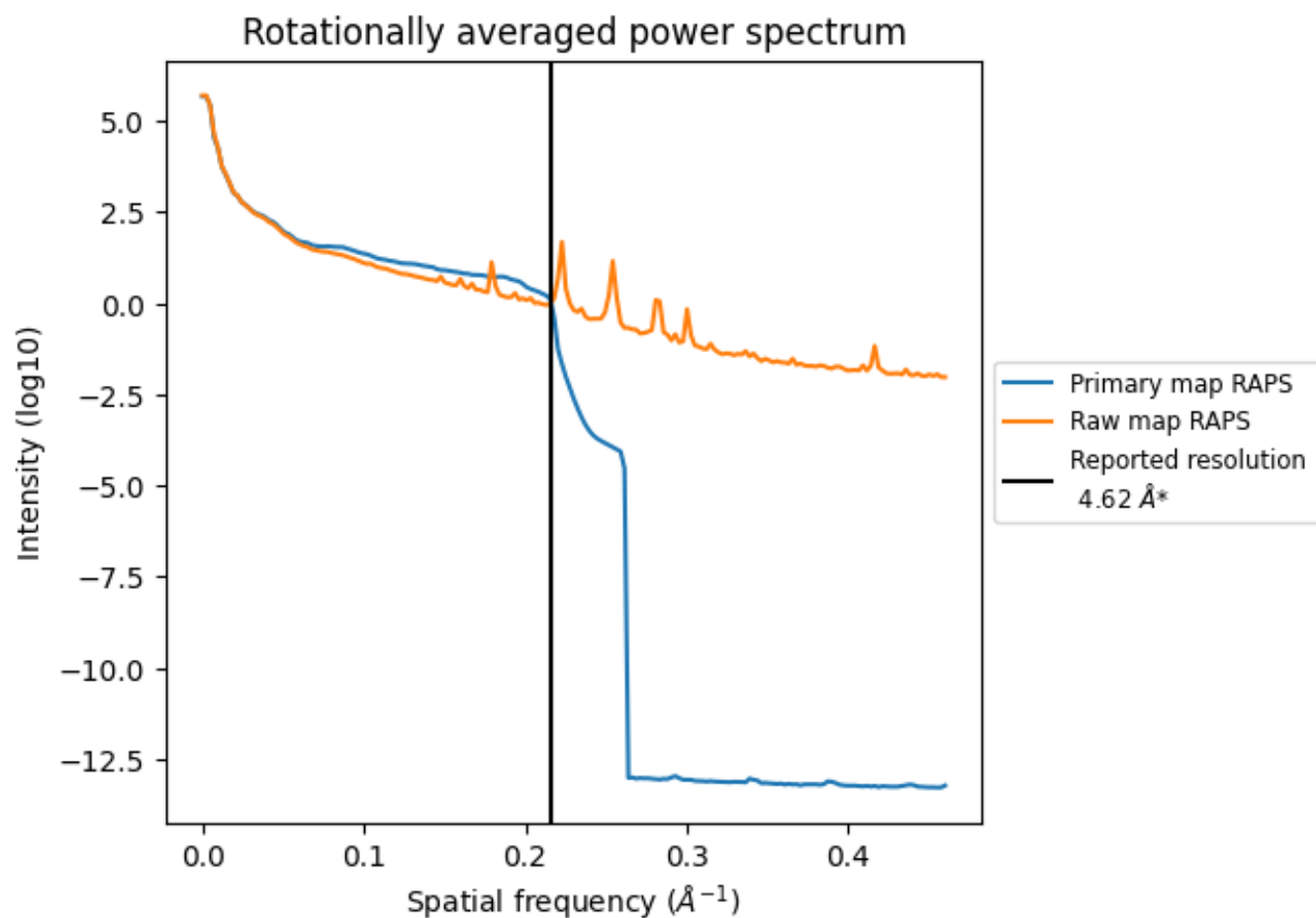
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1650 nm³; this corresponds to an approximate mass of 1490 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 i

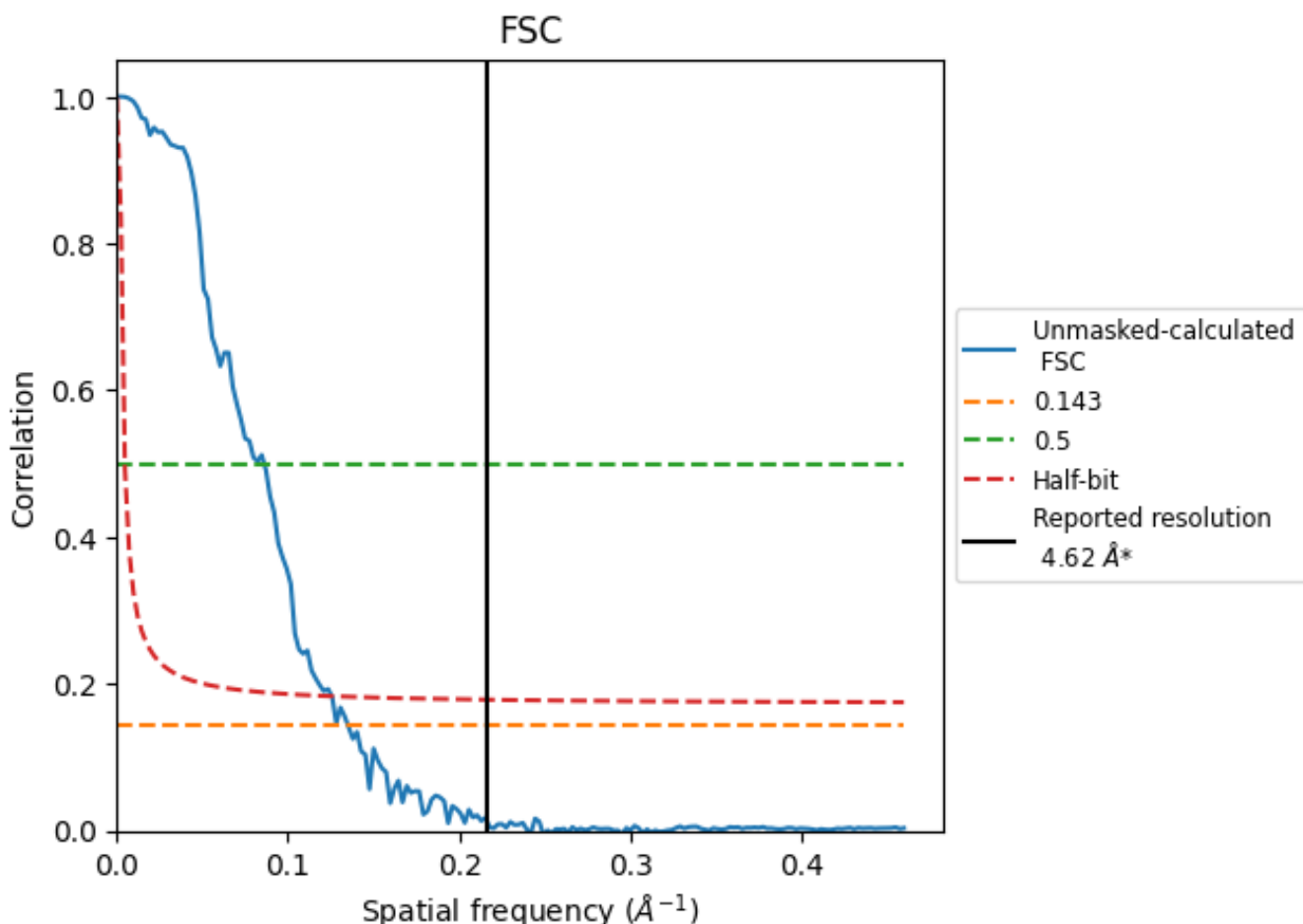


*Reported resolution corresponds to spatial frequency of 0.216 Å⁻¹

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 0.216 Å⁻¹

8.2 Resolution estimates [i](#)

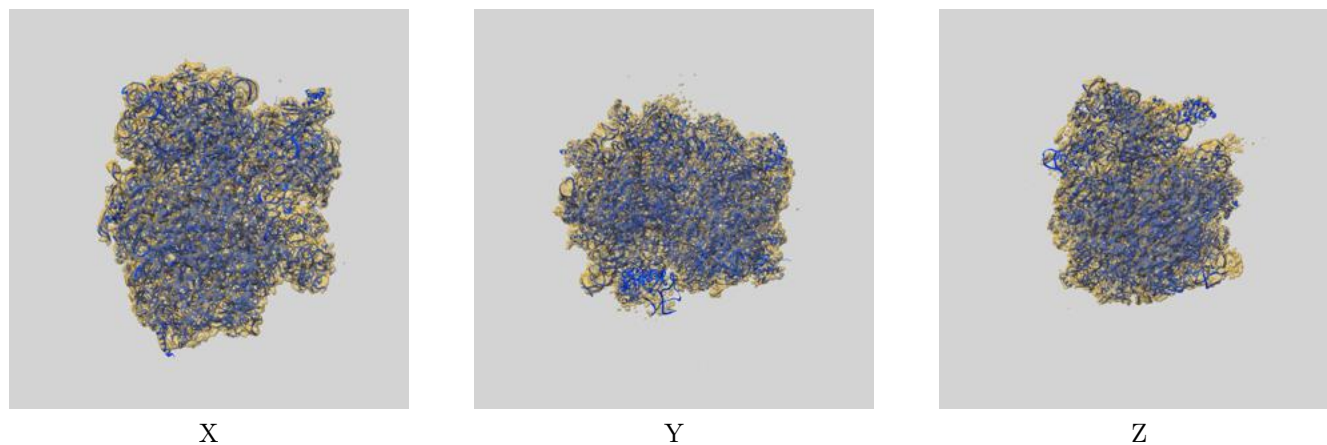
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.62	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.40	11.61	7.96

*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 7.40 differs from the reported value 4.62 by more than 10 %

9 Map-model fit [i](#)

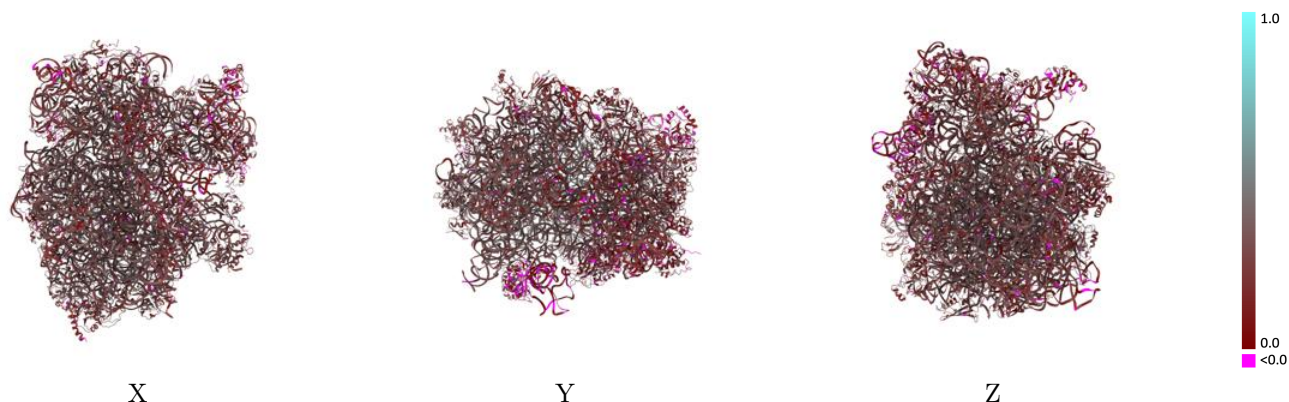
This section contains information regarding the fit between EMDB map EMD-34869 and PDB model 8HL4. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



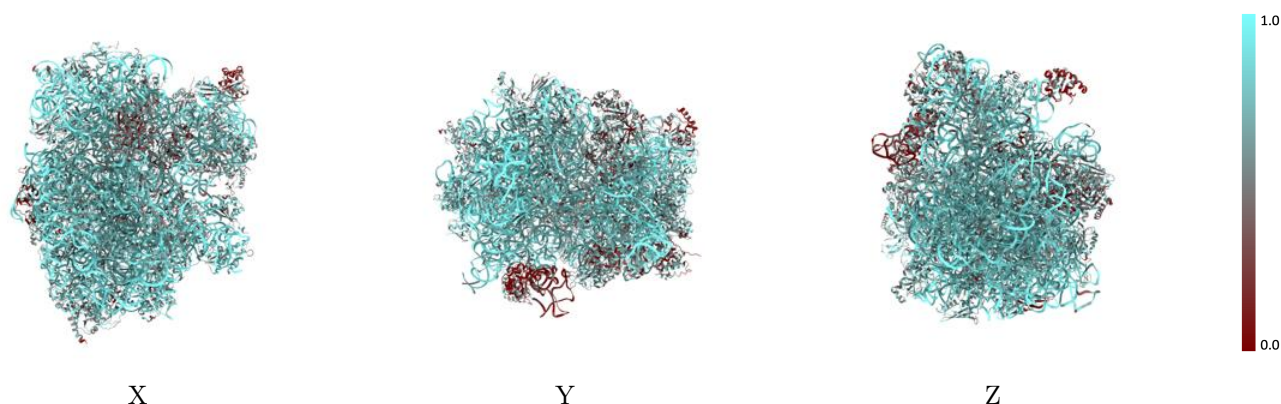
The images above show the 3D surface view of the map at the recommended contour level 0.33 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



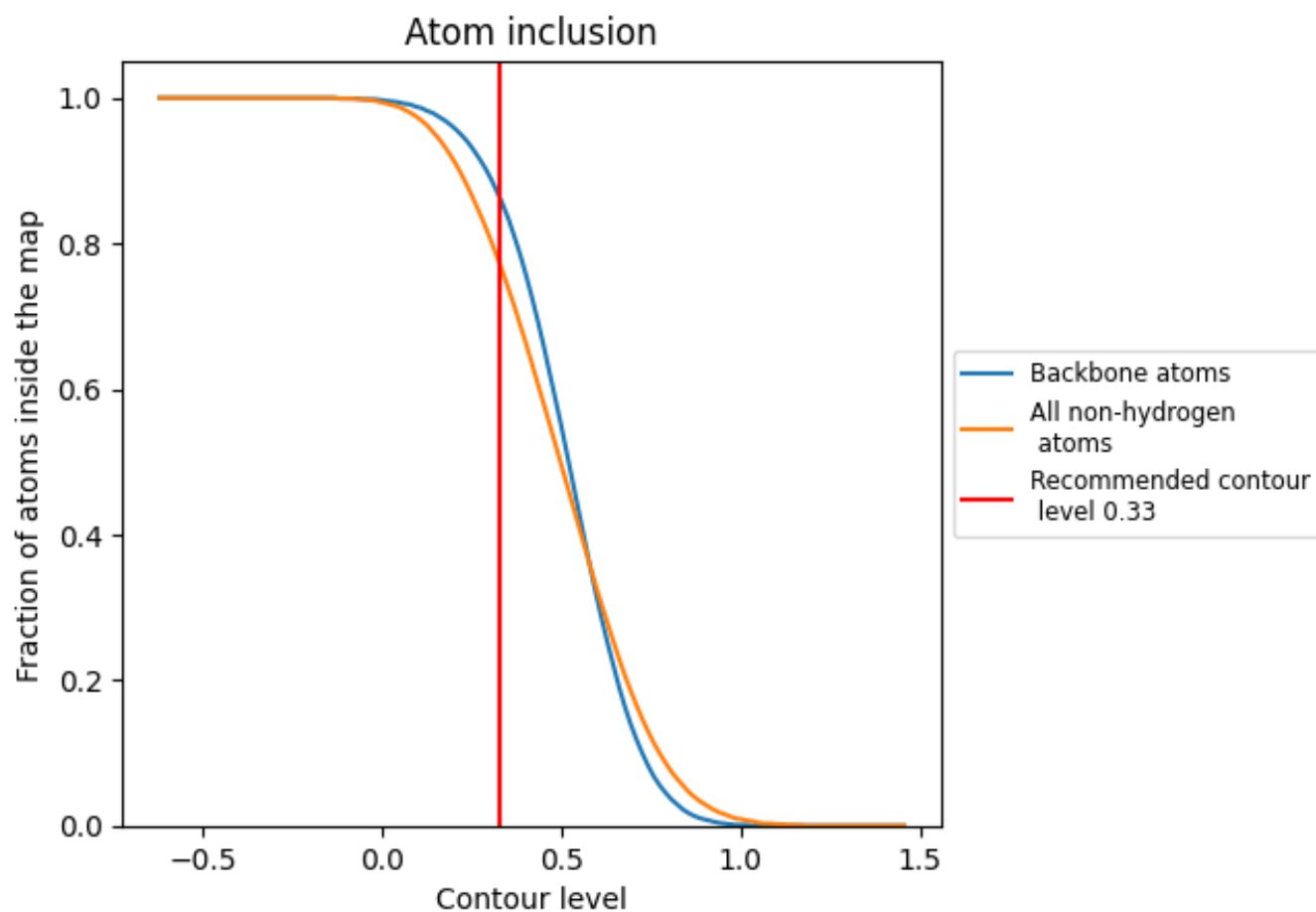
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.33).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 77% 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 (0.33) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7690	 0.2790
A16S	 0.8970	 0.2860
A23S	 0.8910	 0.3160
A5S	 0.9550	 0.3060
AEFG	 0.4250	 0.2350
AL1P	 0.1060	 0.0690
AL2P	 0.6540	 0.3130
AL3P	 0.6580	 0.2830
AL4P	 0.6820	 0.3050
AL5P	 0.6560	 0.2510
AL6P	 0.6190	 0.2480
ALX0	 0.6360	 0.2120
AMRN	 0.7390	 0.3240
APTN	 0.8460	 0.2440
APTP	 0.1790	 0.0700
AS2P	 0.5210	 0.2180
AS3P	 0.5910	 0.2410
AS4E	 0.6630	 0.2330
AS4P	 0.6690	 0.2400
AS5P	 0.6720	 0.2810
AS6E	 0.5520	 0.2020
AS7P	 0.4500	 0.1690
AS8E	 0.6060	 0.2380
AS8P	 0.7590	 0.2800
AS9P	 0.5130	 0.1880
L10E	 0.6610	 0.2750
L13P	 0.6170	 0.2370
L141	 0.6150	 0.2180
L142	 0.6240	 0.2270
L14P	 0.5920	 0.3040
L15E	 0.6800	 0.2950
L15P	 0.6990	 0.2860
L18E	 0.7210	 0.2950
L18P	 0.7260	 0.2480
L19E	 0.7160	 0.3010



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Chain	Atom inclusion	Q-score
L21E	 0.7020	 0.3200
L22P	 0.6670	 0.2980
L23P	 0.6130	 0.2600
L24E	 0.6900	 0.3030
L24P	 0.6970	 0.2730
L29P	 0.6250	 0.2260
L30E	 0.6820	 0.2770
L30P	 0.6540	 0.2450
L31E	 0.6490	 0.2810
L32E	 0.5960	 0.2930
L34E	 0.5270	 0.2260
L37A	 0.7410	 0.3130
L37E	 0.6350	 0.2590
L39E	 0.6180	 0.2650
L40E	 0.4310	 0.1740
L44E	 0.7250	 0.2980
L45A	 0.6310	 0.2500
L46A	 0.5070	 0.2840
L47A	 0.0720	 0.1820
L7A1	 0.6340	 0.2410
L7A2	 0.5430	 0.2190
S10P	 0.5450	 0.2080
S11P	 0.6350	 0.2690
S12P	 0.6110	 0.3000
S13P	 0.5050	 0.1680
S14P	 0.6890	 0.2500
S15P	 0.6860	 0.2410
S17E	 0.3860	 0.1440
S17P	 0.6490	 0.2900
S19E	 0.5360	 0.1580
S19P	 0.6170	 0.1910
S24E	 0.6860	 0.2340
S27A	 0.5840	 0.0860
S27E	 0.6930	 0.2530
S28E	 0.4060	 0.1780
S3AE	 0.6370	 0.2320
SL7A	 0.2410	 0.0940