



wwPDB EM Validation Summary Report ⓘ

Jan 30, 2025 – 12:49 PM JST

PDB ID : 8HKY
EMDB ID : EMD-34863
Title : Cryo-EM Structures and Translocation Mechanism of Crenarchaeota Ribosome
Authors : Wang, Y.H.; Zhou, J.
Deposited on : 2022-11-28
Resolution : 4.45 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.dev113
MolProbity : 4.02b-467
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) : 2.40

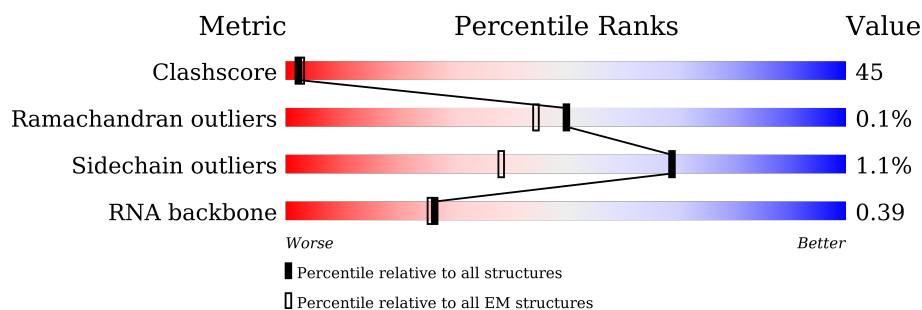
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.45 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	A23S	3022	<div> <div>5%</div> <div>59%</div> <div>37%</div> <div>..</div> </div>
2	A16S	1503	<div> <div>54%</div> <div>40%</div> <div>5%</div> <div>.</div> </div>
3	AATN	76	<div> <div>25%</div> <div>51%</div> <div>38%</div> <div>11%</div> </div>
3	AETN	76	<div> <div>89%</div> <div>50%</div> <div>45%</div> <div>5%</div> </div>
3	APTN	76	<div> <div>9%</div> <div>67%</div> <div>28%</div> <div>5%</div> </div>
4	A5S	122	<div> <div>7%</div> <div>66%</div> <div>27%</div> </div>
5	AL1P	216	<div> <div>94%</div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain	
6	AL2P	234	33%	99%
7	AL3P	339	32%	99%
8	AL4P	251	20%	99%
9	AL5P	168	40%	99%
10	AL6P	181	38%	98%
11	ALX0	76	32%	100%
12	L10E	164	20%	99%
13	L13P	140	27%	99%
14	L141	86	33%	100%
14	L142	86	42%	100%
15	L14P	134	40%	99%
16	L15E	169	30%	99%
17	L18E	112	12%	100%
18	L18P	193	26%	99%
19	L19E	144	15%	99%
20	L22P	150	34%	99%
21	L23P	81	28%	100%
22	L24E	54	26%	100%
23	L24P	122	19%	98%
24	L29P	63	16%	97%
25	L30E	94	11%	100%
26	L30P	155	27%	100%
27	L31E	75	32%	99%
28	L32E	123	35%	100%
29	L34E	77	38%	96%

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Mol	Chain	Length	Quality of chain
30	L37A	65	25% 98% .
31	L37E	54	17% 100%
32	L39E	49	16% 100%
33	L40E	55	80% 98% .
34	L44E	92	18% 100%
35	L7A1	123	41% 97% .
35	L7A2	123	46% 99% .
35	SL7A	123	86% 98% .
36	L15P	144	15% 65% 35%
37	L21E	97	28% 100%
38	L45A	101	32% 96% .
39	L46A	70	59% 99% .
40	L47A	80	92% 99% .
41	AS2P	196	59% 99% .
42	AS4E	240	30% 98% .
43	AS4P	166	27% 99% .
44	AS5P	204	27% 100%
45	AS6E	105	64% 100%
46	AS8E	126	37% 99% .
47	AS8P	130	12% 94% 5% .
48	S11P	128	38% 99% .
49	S12P	143	57% 99% .
50	S15P	149	18% 98% .
51	S17P	111	33% 97% .
52	S24E	96	48% 100%

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Mol	Chain	Length	Quality of chain
53	S27E	59	 14% 97%
54	S3AE	189	 41% 98%
55	AS3P	201	 50% 100%
56	AS7P	193	 52% 98%
57	S10P	100	 53% 99%
58	S13P	147	 44% 98%
59	S14P	52	 25% 98%
60	S17E	62	 74% 100%
61	S19E	150	 46% 99%
62	S19P	115	 30% 98%
63	AS9P	136	 38% 99%
64	S28E	63	 51% 98%
65	S27A	54	 20% 96%
66	APTP	6	 100% 100%
67	AMRN	9	 22% 89% 11%

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 169359 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A23S	2996	Total	C	N	O	P	0	0
			64357	28673	11911	20777	2996		

- Molecule 2 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A16S	1493	Total	C	N	O	P	0	0
			32063	14279	5930	10361	1493		

- Molecule 3 is a RNA chain called tRNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AATN	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		
3	APTn	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		
3	AETN	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 4 is a RNA chain called 5S rRNA (122-MER).

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

- Molecule 5 is a protein called 50S ribosomal protein L1.

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

- Molecule 6 is a protein called 50S ribosomal protein L2.

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

- Molecule 7 is a protein called 50S ribosomal protein L3.

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

- Molecule 8 is a protein called 50S ribosomal protein L4.

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

- Molecule 9 is a protein called 50S ribosomal protein L5.

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

- Molecule 10 is a protein called 50S ribosomal protein L6.

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

- Molecule 11 is a protein called 50S ribosomal protein L18Ae.

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

- Molecule 12 is a protein called 50S ribosomal protein L10e.

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

- Molecule 13 is a protein called 50S ribosomal protein L13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14e.

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

- Molecule 15 is a protein called 50S ribosomal protein L14.

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

- Molecule 16 is a protein called 50S ribosomal protein L15e.

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

- Molecule 17 is a protein called 50S ribosomal protein L18e.

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

- Molecule 18 is a protein called 50S ribosomal protein L18.

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

- Molecule 19 is a protein called 50S ribosomal protein L19e.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

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

- Molecule 22 is a protein called 50S ribosomal protein L24e.

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

- Molecule 23 is a protein called 50S ribosomal protein L24.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

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

- Molecule 25 is a protein called 50S ribosomal protein L30e.

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

- Molecule 26 is a protein called 50S ribosomal protein L30.

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

- Molecule 27 is a protein called 50S ribosomal protein L31e.

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

- Molecule 28 is a protein called 50S ribosomal protein L32e.

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

- Molecule 29 is a protein called 50S ribosomal protein L34e.

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

- Molecule 30 is a protein called 50S ribosomal protein L37Ae.

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

- Molecule 31 is a protein called 50S ribosomal protein L37e.

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

- Molecule 32 is a protein called 50S ribosomal protein L39e.

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

- Molecule 33 is a protein called 50S ribosomal protein L40E.

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

- Molecule 34 is a protein called 50S ribosomal protein L44e.

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

- Molecule 35 is a protein called 50S ribosomal protein L7Ae.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L21e.

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

- Molecule 38 is a protein called DUF2280 domain-containing protein.

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

- Molecule 39 is a protein called Conserved protein.

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

- Molecule 40 is a protein called 50S ribosomal protein L47A.

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

- Molecule 41 is a protein called 30S ribosomal protein S2.

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

- Molecule 42 is a protein called 30S ribosomal protein S4e.

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

- Molecule 43 is a protein called 30S ribosomal protein S4.

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

- Molecule 44 is a protein called 30S ribosomal protein S5.

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

- Molecule 45 is a protein called 30S ribosomal protein S6e.

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

- Molecule 46 is a protein called 30S ribosomal protein S8e.

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

- Molecule 47 is a protein called 30S ribosomal protein S8.

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

- Molecule 48 is a protein called 30S ribosomal protein S11.

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

- Molecule 49 is a protein called 30S ribosomal protein S12.

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

- Molecule 50 is a protein called 30S ribosomal protein S15.

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

- Molecule 51 is a protein called 30S ribosomal protein S17.

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

- Molecule 52 is a protein called 30S ribosomal protein S24e.

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

- Molecule 53 is a protein called 30S ribosomal protein S27e.

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

- Molecule 54 is a protein called 30S ribosomal protein S3Ae.

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

- Molecule 55 is a protein called 30S ribosomal protein S3.

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

- Molecule 56 is a protein called 30S ribosomal protein S7.

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

- Molecule 57 is a protein called 30S ribosomal protein S10.

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

- Molecule 58 is a protein called 30S ribosomal protein S13.

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

- Molecule 59 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 60 is a protein called 30S ribosomal protein S17e.

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

- Molecule 61 is a protein called 30S ribosomal protein S19e.

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

- Molecule 62 is a protein called 30S ribosomal protein S19.

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

- Molecule 63 is a protein called 30S ribosomal protein S9.

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

- Molecule 64 is a protein called 30S ribosomal protein S28e.

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

- Molecule 65 is a protein called 30S ribosomal protein S27ae.

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

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

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

- Molecule 68 is UNKNOWN LIGAND (three-letter code: UNL) (formula:) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms				AltConf
68	AS2P	33	Total	C	N	O	0
			166	99	33	34	
68	AS5P	20	Total	C	N	O	0
			100	60	20	20	

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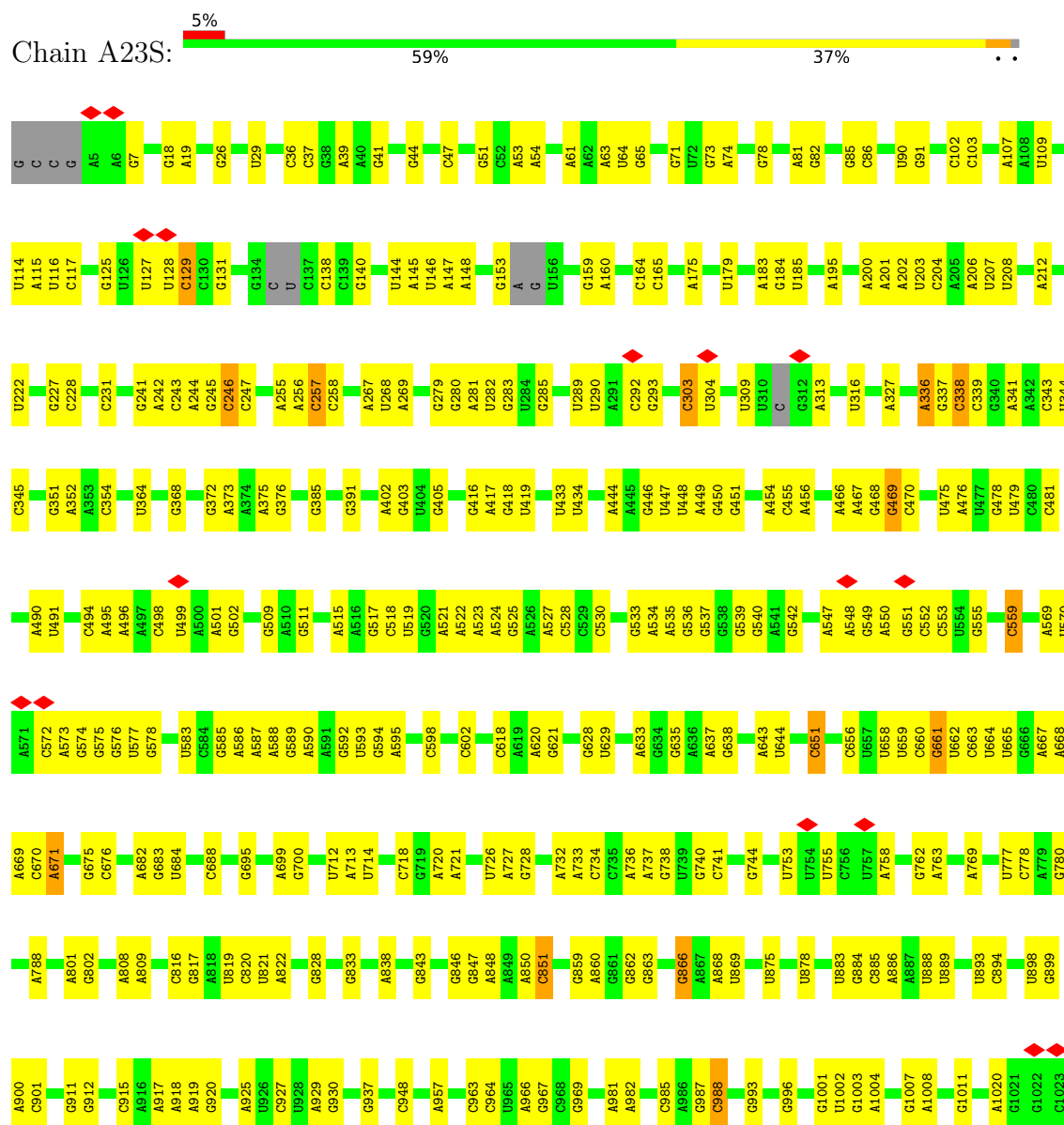
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
68	AS8P	4	20	12	4	4	0

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.

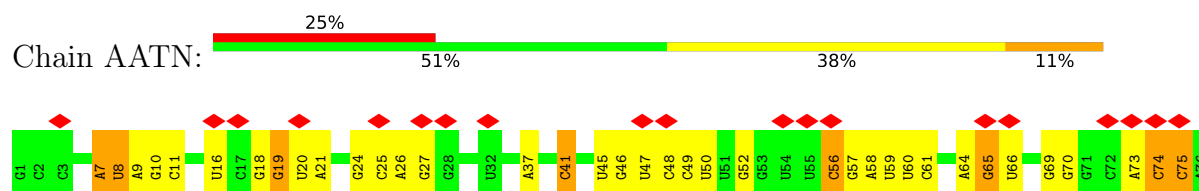
• Molecule 1: 23S rRNA



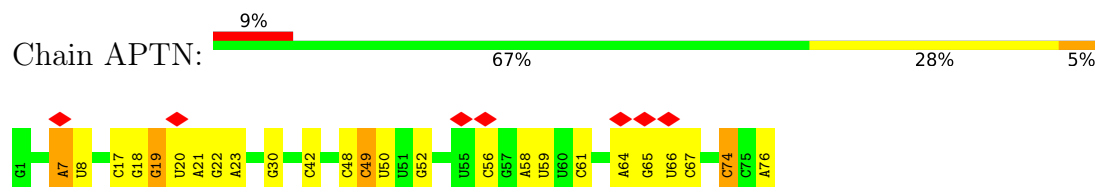




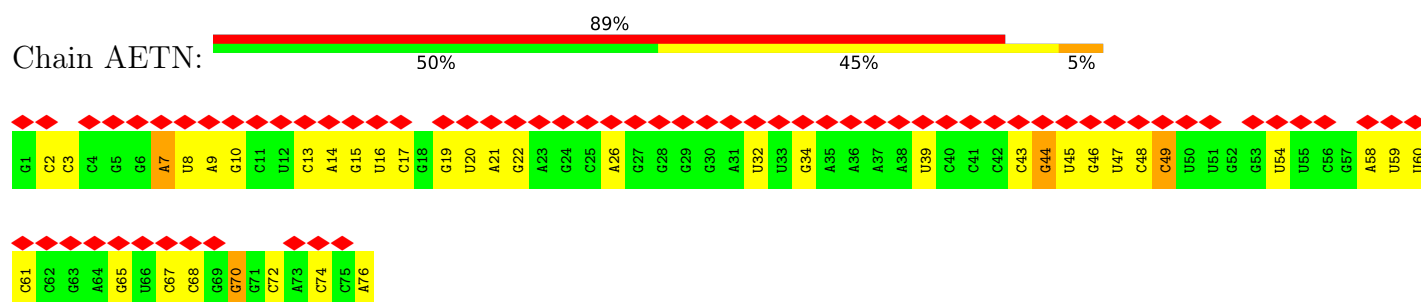
- Molecule 3: tRNA (76-MER)



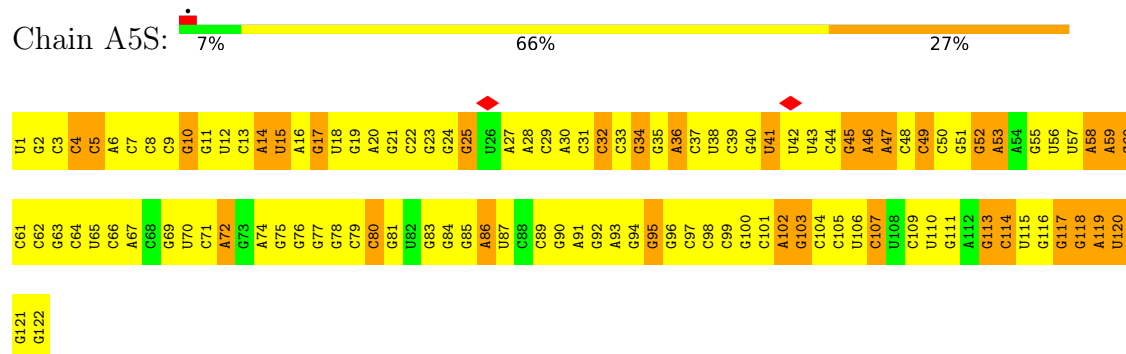
- Molecule 3: tRNA (76-MER)



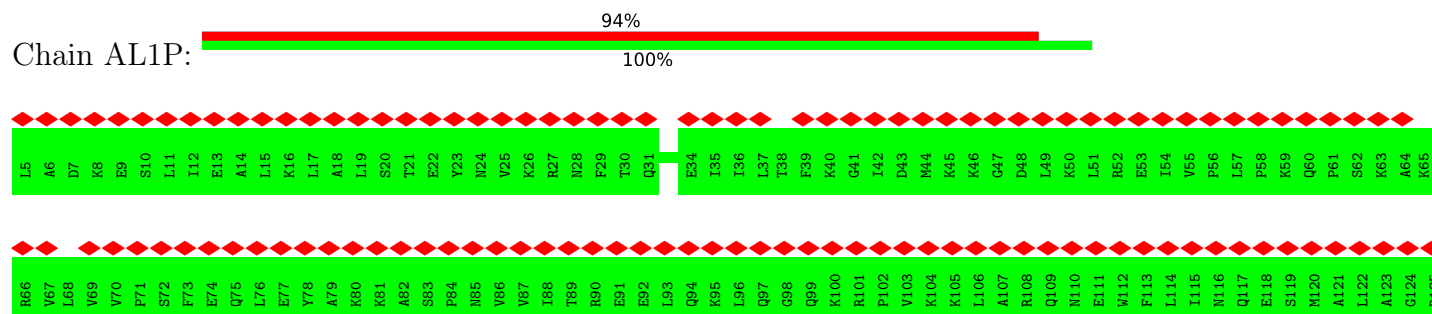
- Molecule 3: tRNA (76-MER)

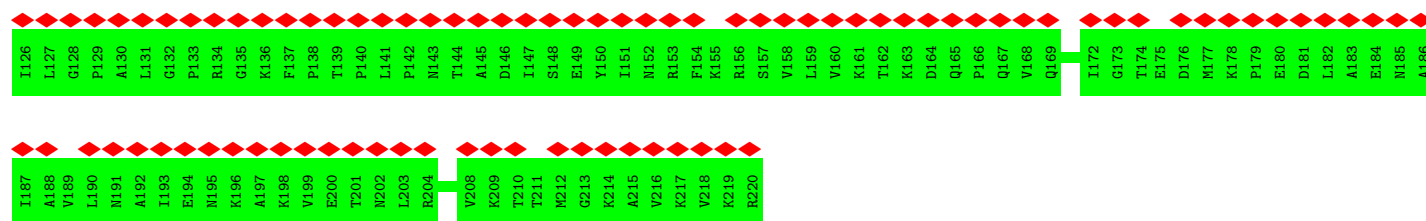


- Molecule 4: 5S rRNA (122-MER)

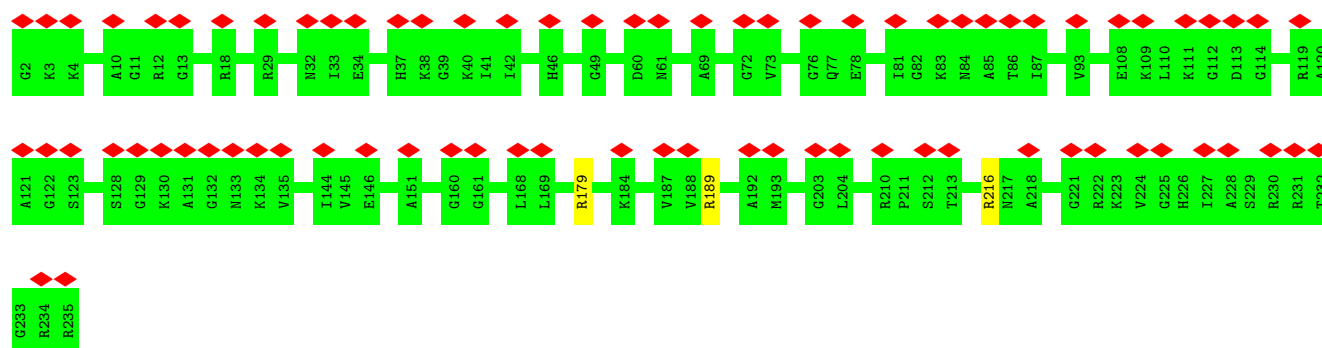


- Molecule 5: 50S ribosomal protein L1

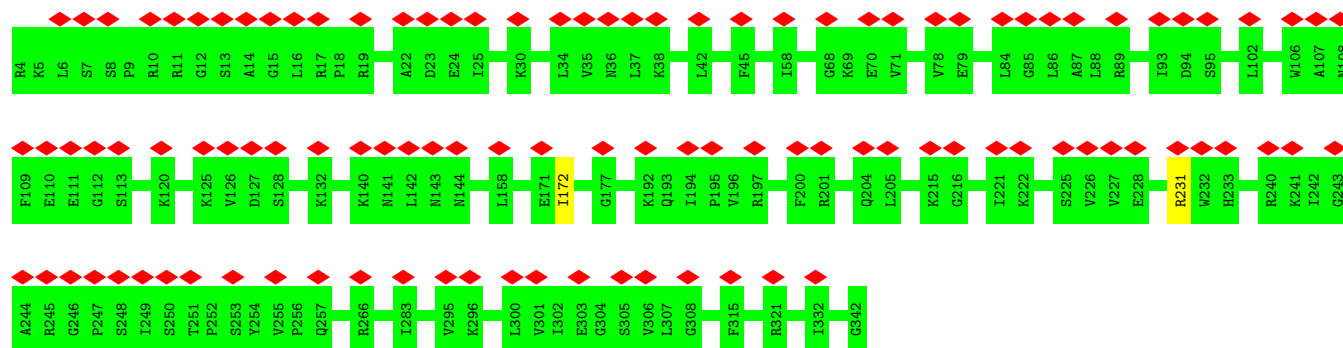




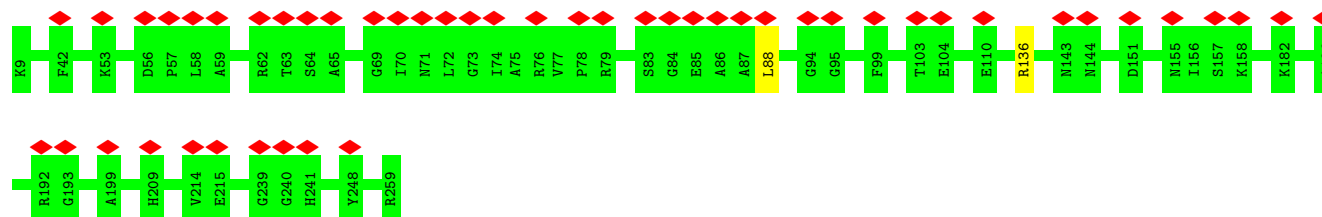
• Molecule 6: 50S ribosomal protein L2



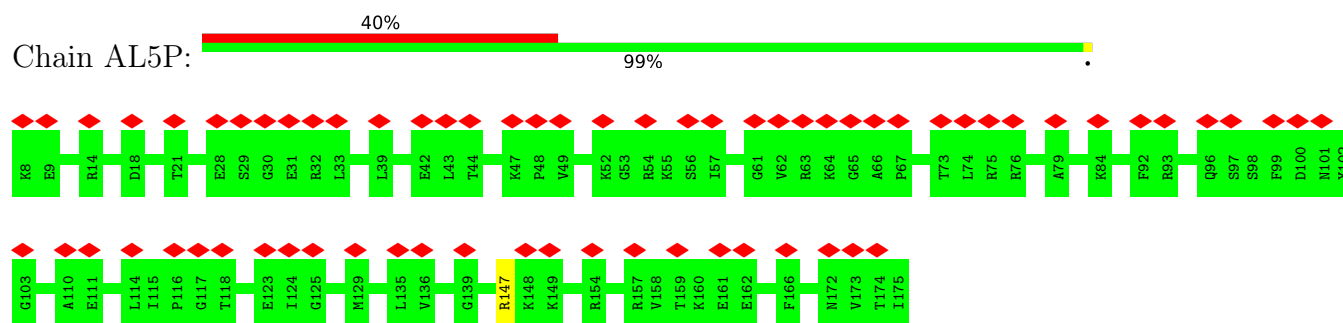
• Molecule 7: 50S ribosomal protein L3



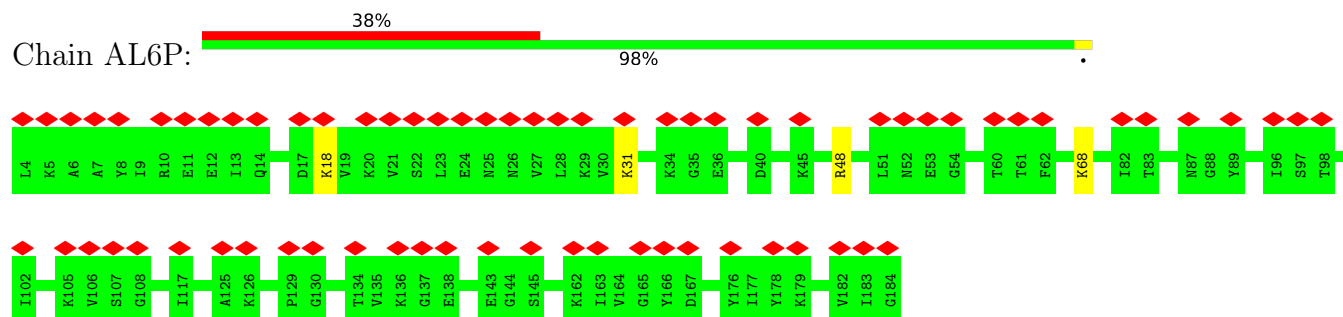
• Molecule 8: 50S ribosomal protein L4



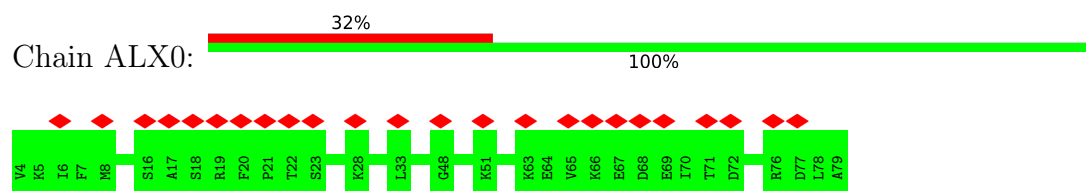
• Molecule 9: 50S ribosomal protein L5



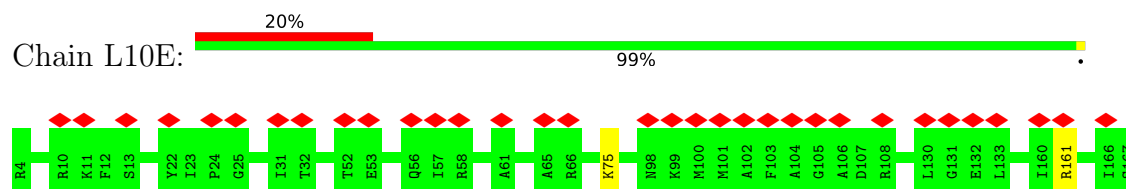
- Molecule 10: 50S ribosomal protein L6



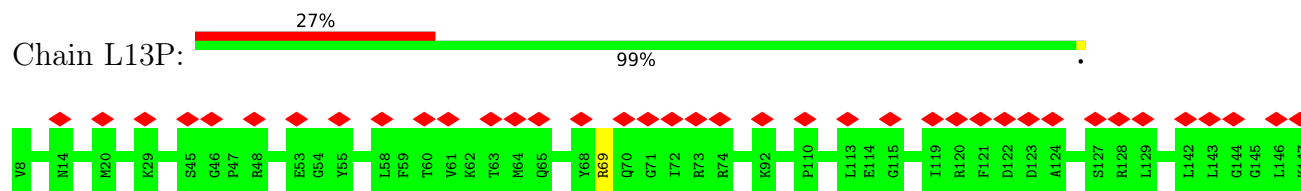
- Molecule 11: 50S ribosomal protein L18Ae



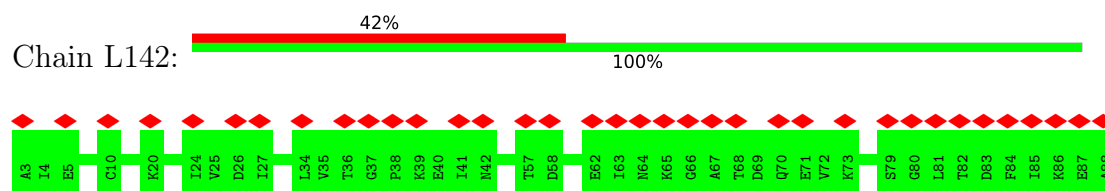
- Molecule 12: 50S ribosomal protein L10e



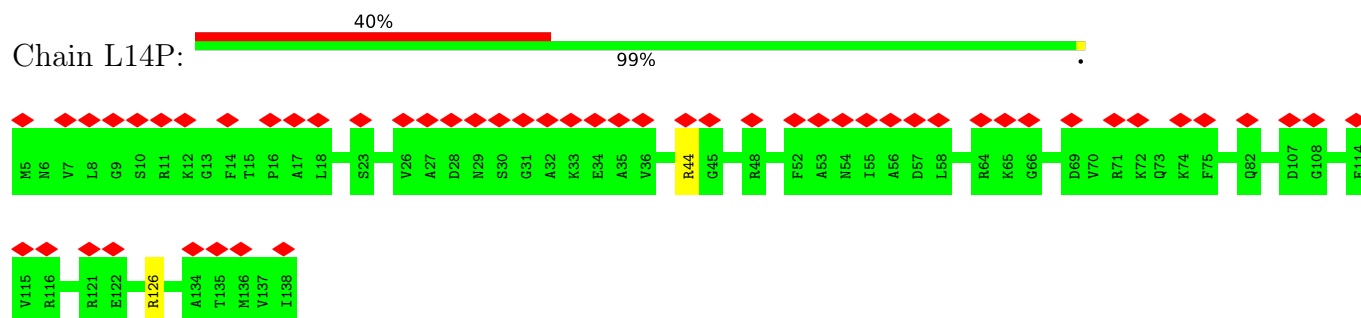
- Molecule 13: 50S ribosomal protein L13



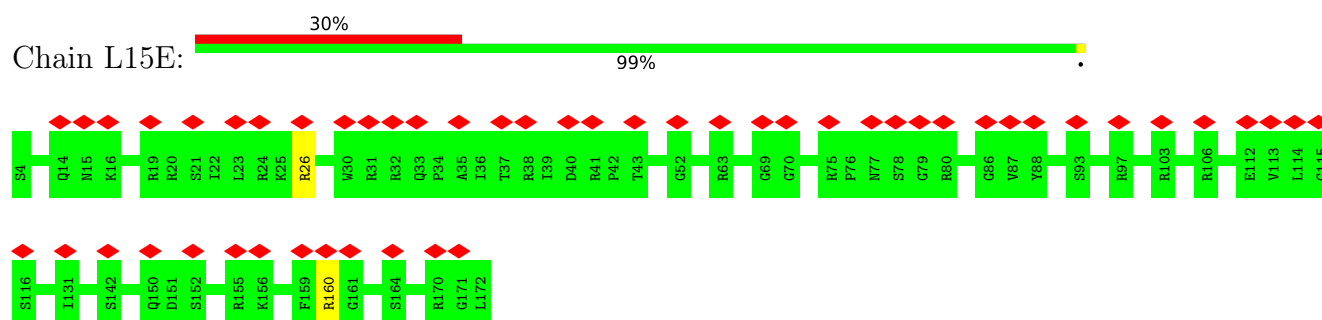
- Molecule 14: 50S ribosomal protein L14e



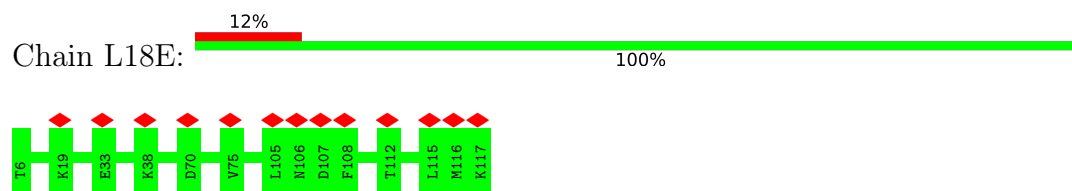
- Molecule 15: 50S ribosomal protein L14



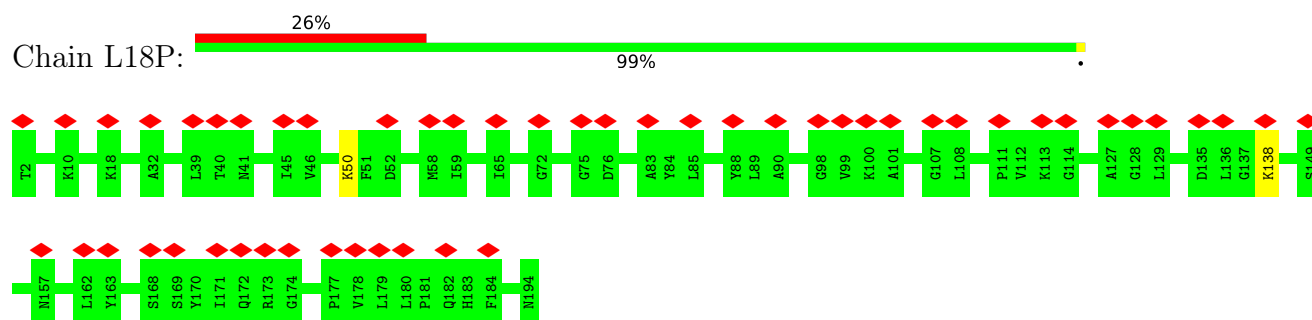
- Molecule 16: 50S ribosomal protein L15e



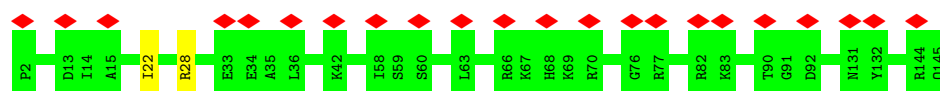
- Molecule 17: 50S ribosomal protein L18e



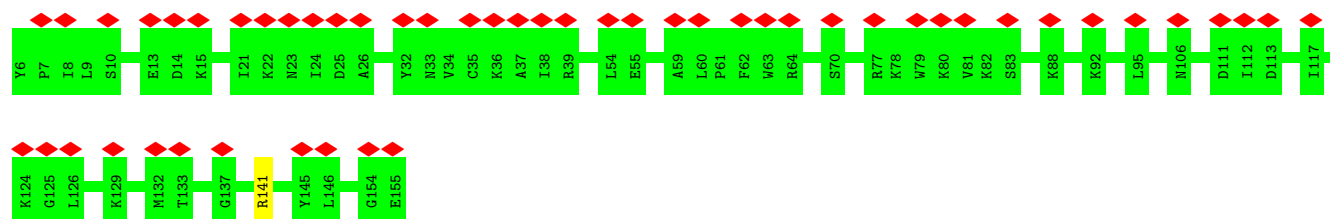
- Molecule 18: 50S ribosomal protein L18



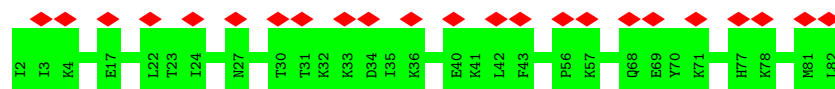
- Molecule 19: 50S ribosomal protein L19e



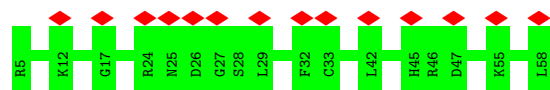
• Molecule 20: 50S ribosomal protein L22



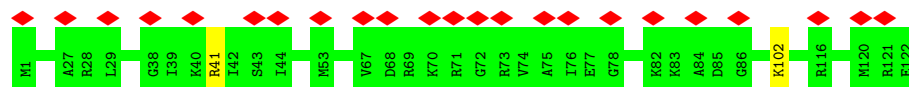
• Molecule 21: 50S ribosomal protein L23



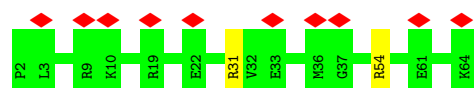
• Molecule 22: 50S ribosomal protein L24e



• Molecule 23: 50S ribosomal protein L24

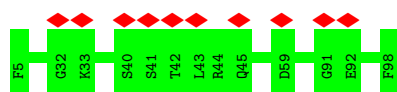


• Molecule 24: 50S ribosomal protein L29

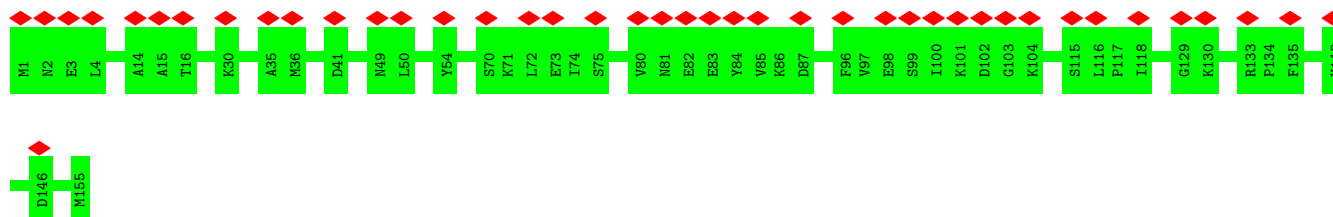


• Molecule 25: 50S ribosomal protein L30e

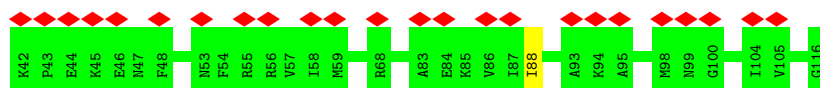




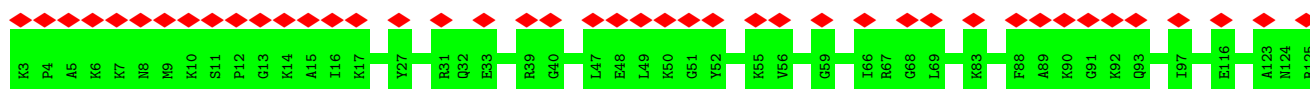
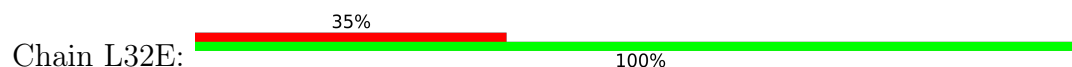
- Molecule 26: 50S ribosomal protein L30



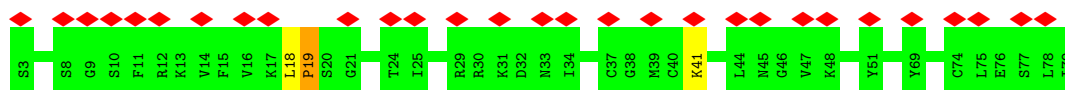
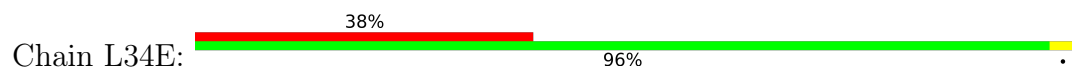
- Molecule 27: 50S ribosomal protein L31e



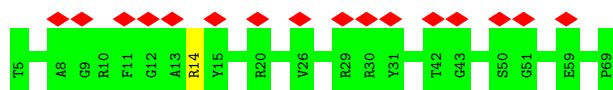
- Molecule 28: 50S ribosomal protein L32e



- Molecule 29: 50S ribosomal protein L34e

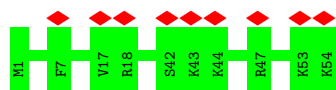


- Molecule 30: 50S ribosomal protein L37Ae

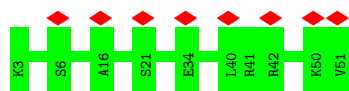


- Molecule 31: 50S ribosomal protein L37e

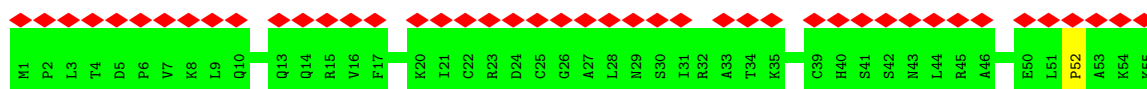
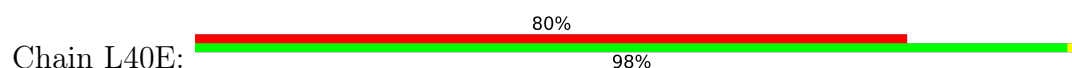




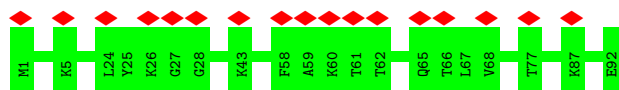
- Molecule 32: 50S ribosomal protein L39e



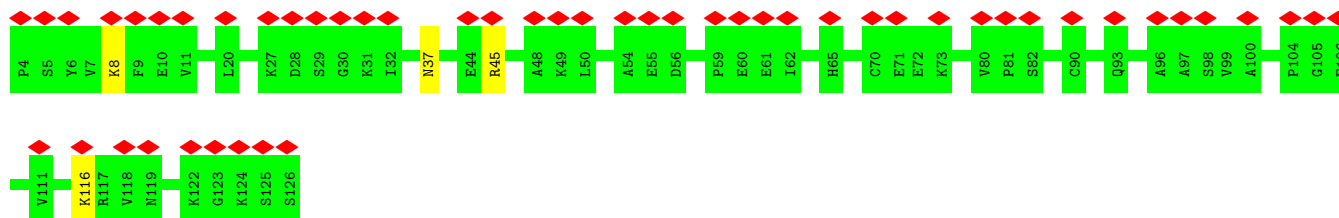
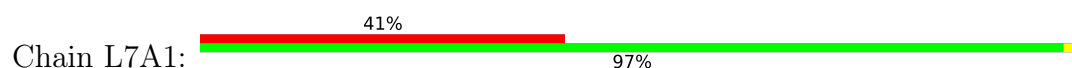
- Molecule 33: 50S ribosomal protein L40E



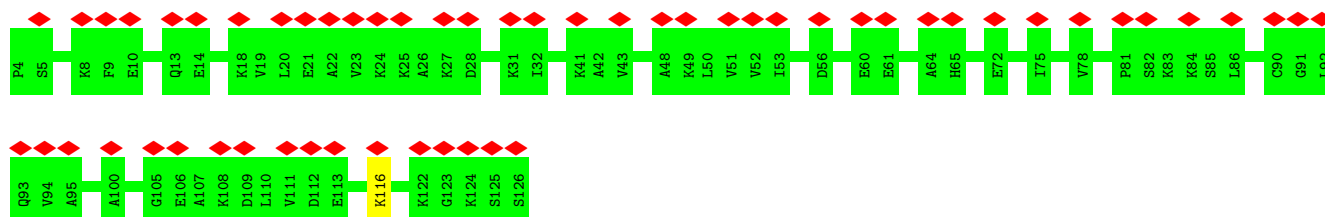
- Molecule 34: 50S ribosomal protein L44e



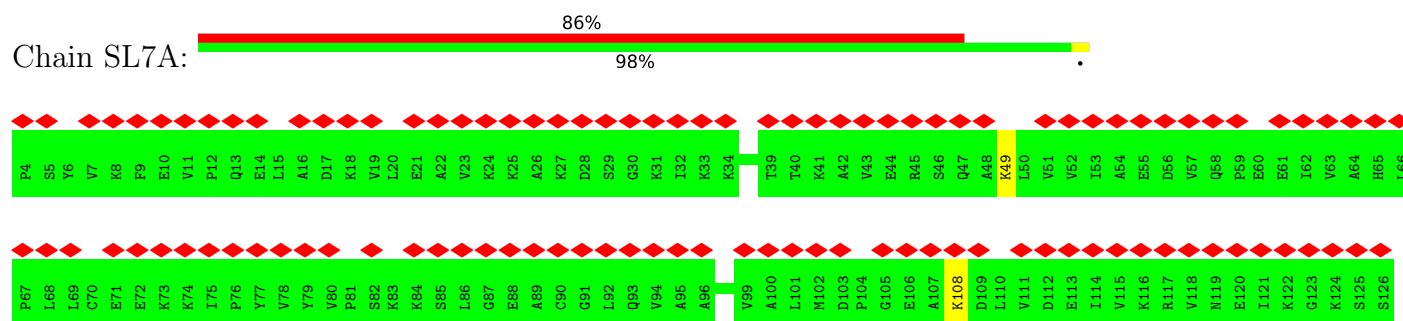
- Molecule 35: 50S ribosomal protein L7Ae



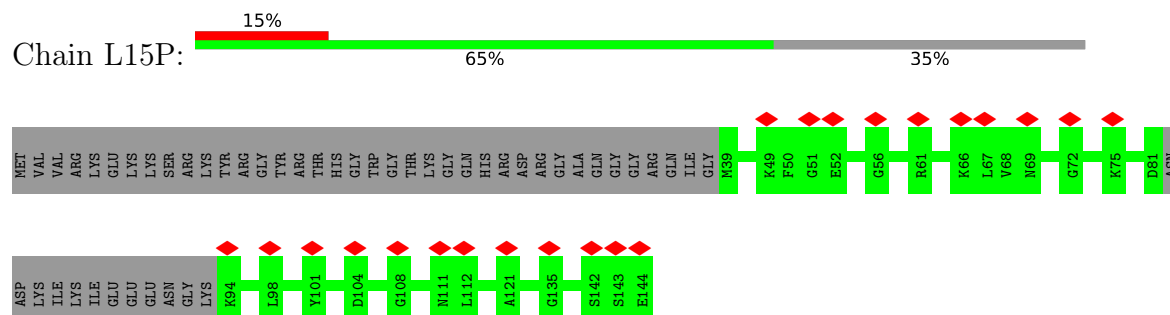
- Molecule 35: 50S ribosomal protein L7Ae



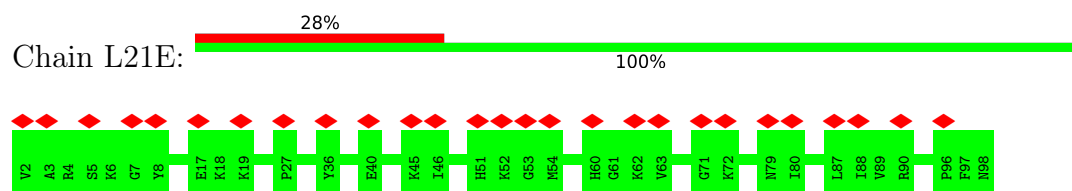
- Molecule 35: 50S ribosomal protein L7Ae



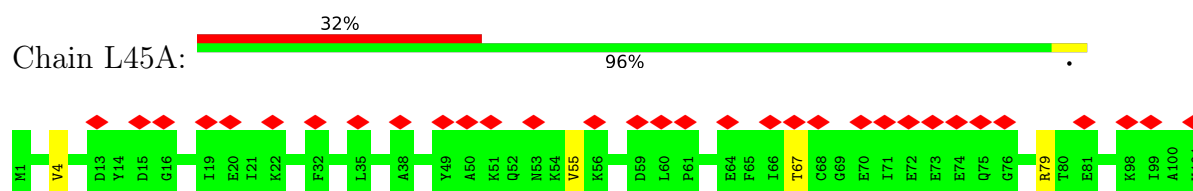
- Molecule 36: 50S ribosomal protein L15



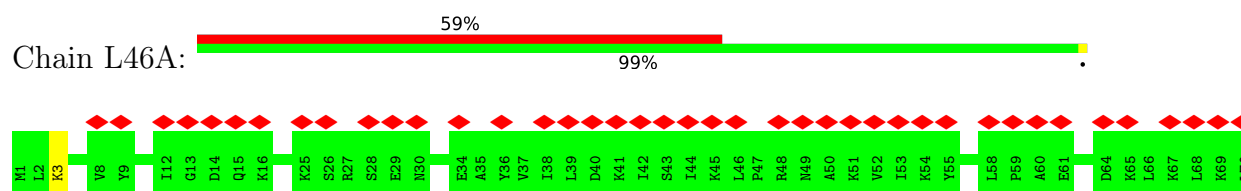
- Molecule 37: 50S ribosomal protein L21e



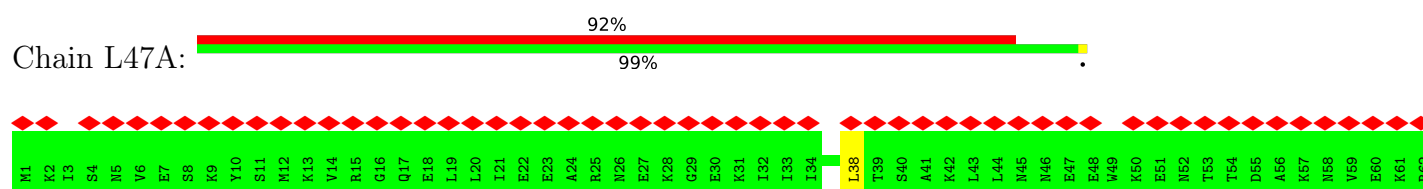
- Molecule 38: DUF2280 domain-containing protein

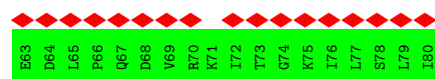


- Molecule 39: Conserved protein

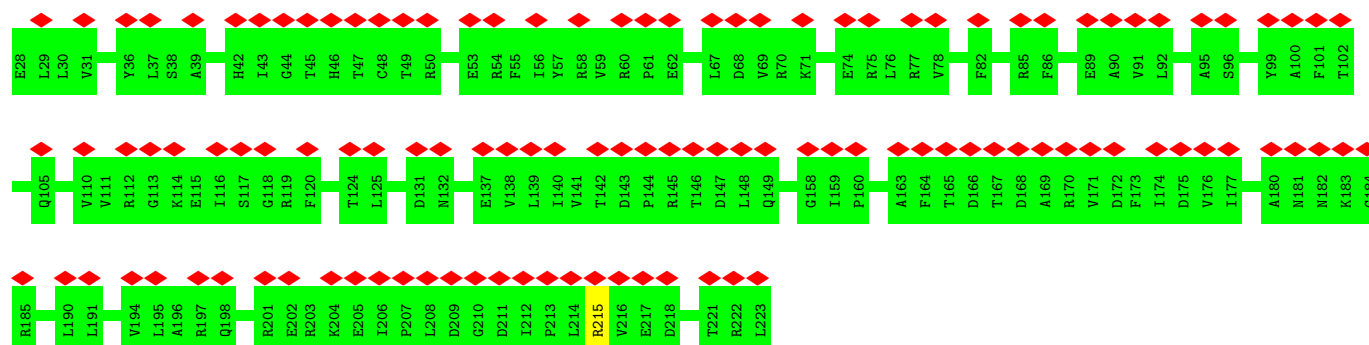


- Molecule 40: 50S ribosomal protein L47A

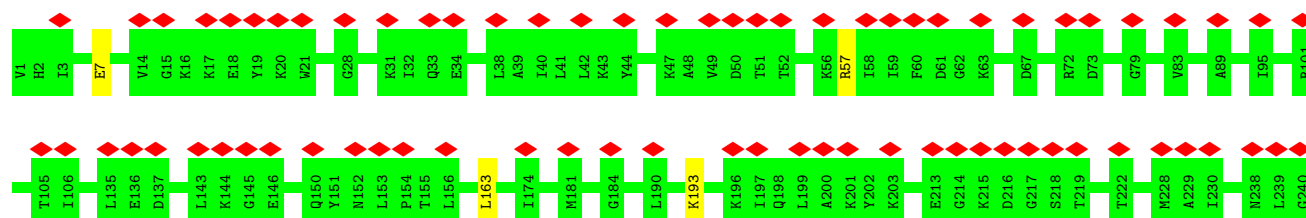




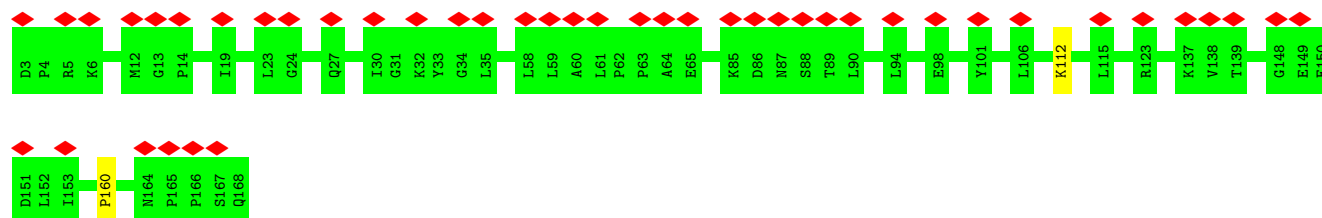
- Molecule 41: 30S ribosomal protein S2



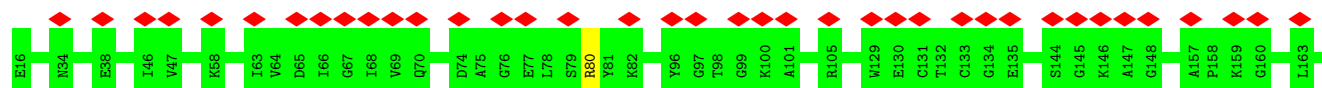
- Molecule 42: 30S ribosomal protein S4e

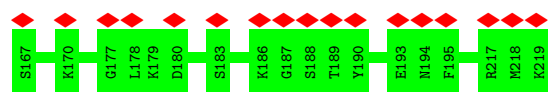


- Molecule 43: 30S ribosomal protein S4

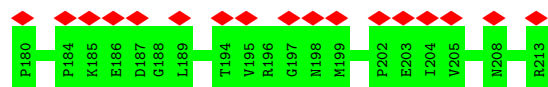
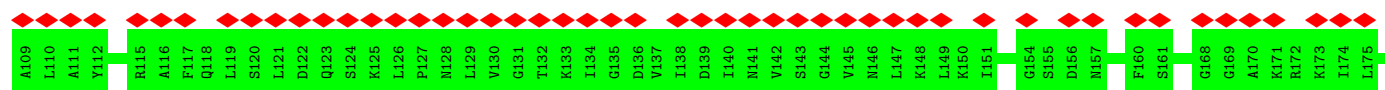


- Molecule 44: 30S ribosomal protein S5

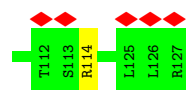
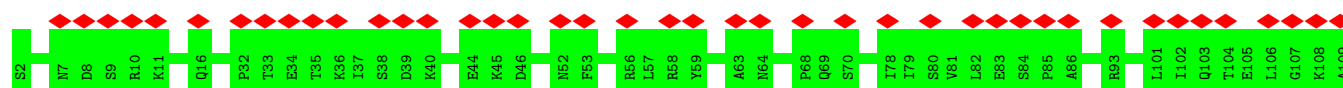
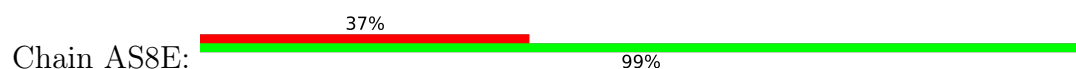




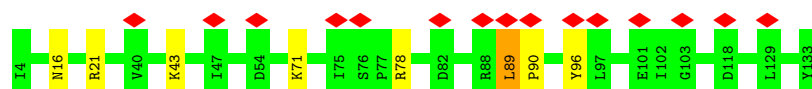
- Molecule 45: 30S ribosomal protein S6e



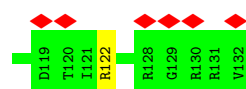
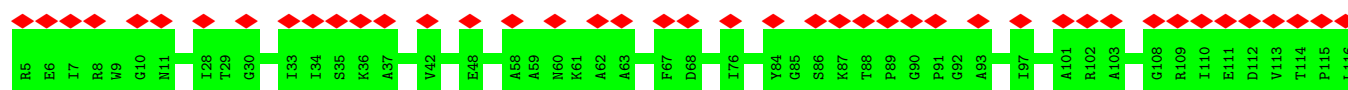
- Molecule 46: 30S ribosomal protein S8e



- Molecule 47: 30S ribosomal protein S8



- Molecule 48: 30S ribosomal protein S11



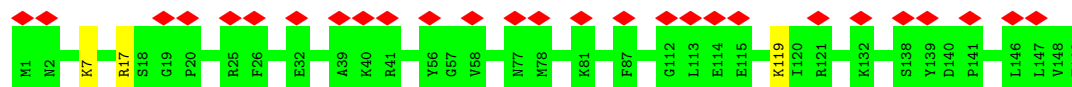
- Molecule 49: 30S ribosomal protein S12





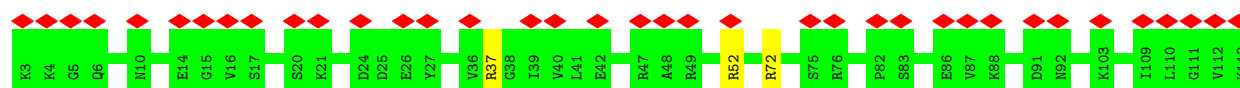
- Molecule 50: 30S ribosomal protein S15

Chain S15P: 18% 98%



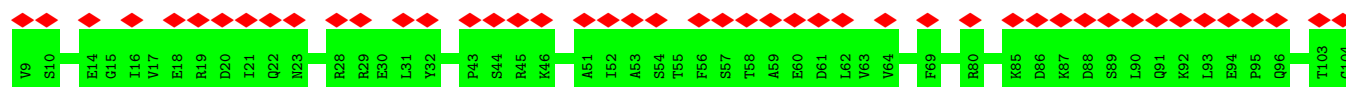
- Molecule 51: 30S ribosomal protein S17

Chain S17P: 33% 97%



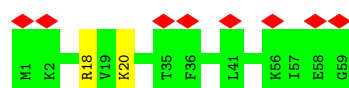
- Molecule 52: 30S ribosomal protein S24e

Chain S24E: 48% 100%



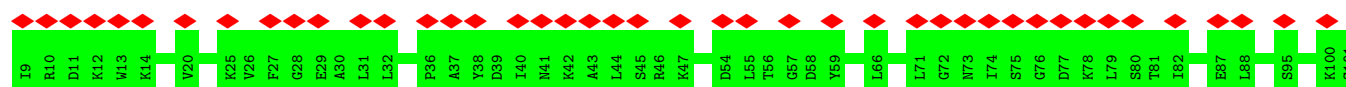
- Molecule 53: 30S ribosomal protein S27e

Chain S27E: 14% 97%

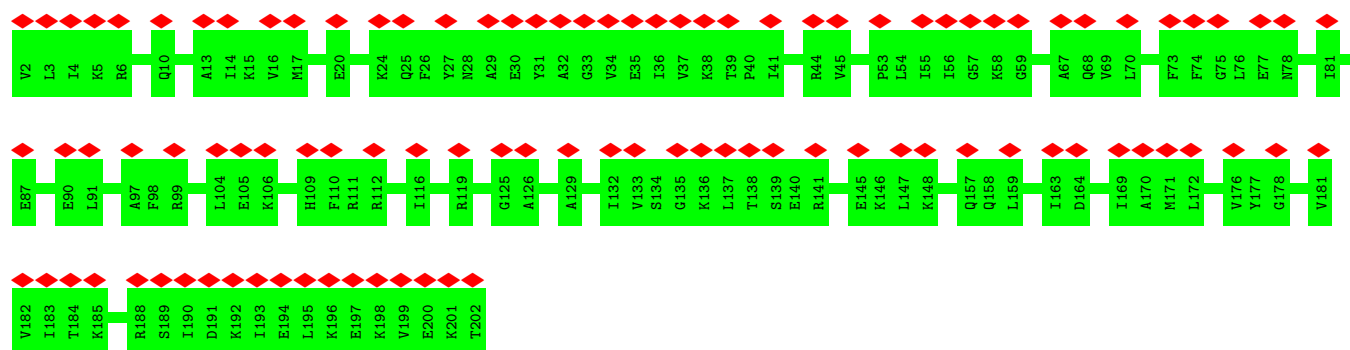


- Molecule 54: 30S ribosomal protein S3Ae

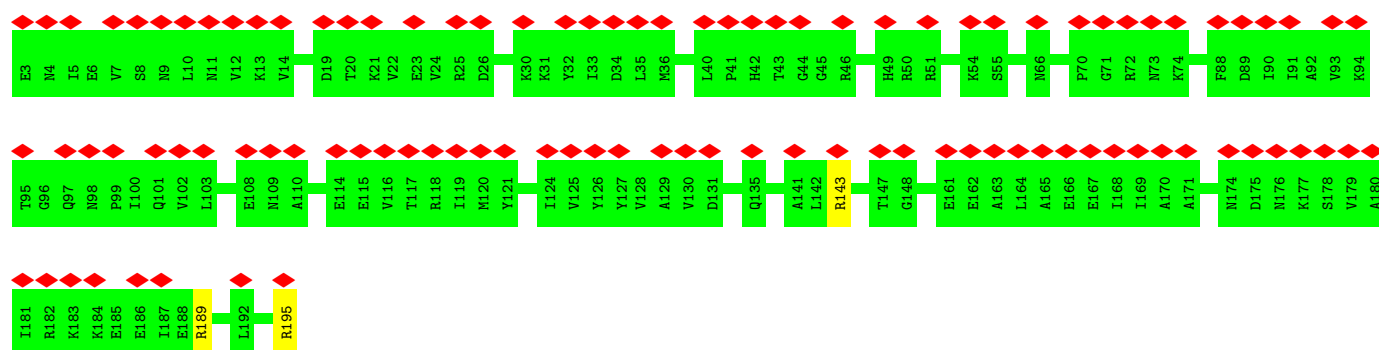
Chain S3AE: 41% 98%



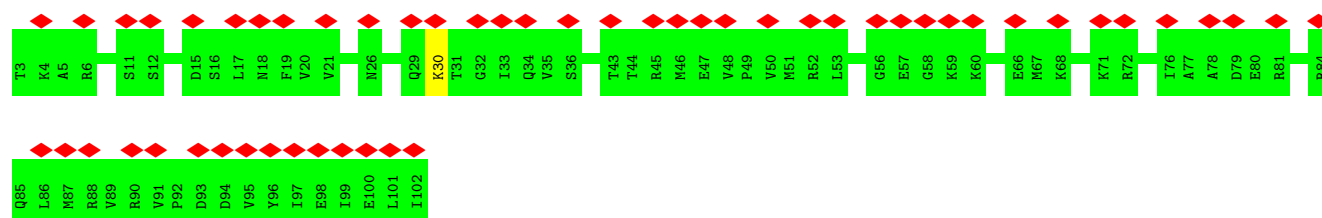
- Molecule 55: 30S ribosomal protein S3



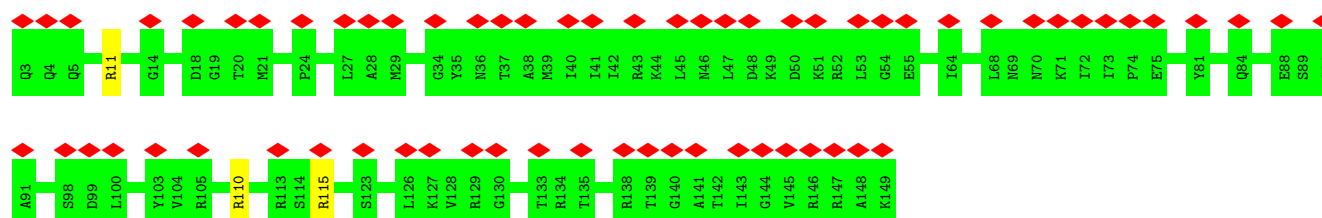
• Molecule 56: 30S ribosomal protein S7



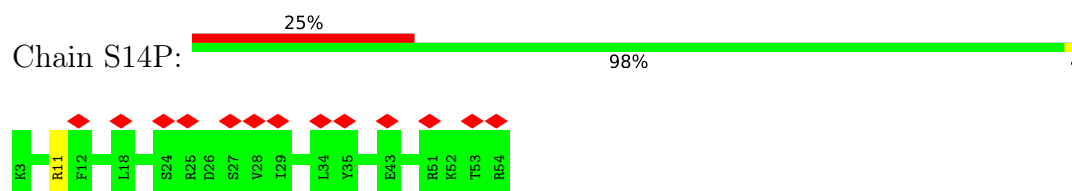
• Molecule 57: 30S ribosomal protein S10



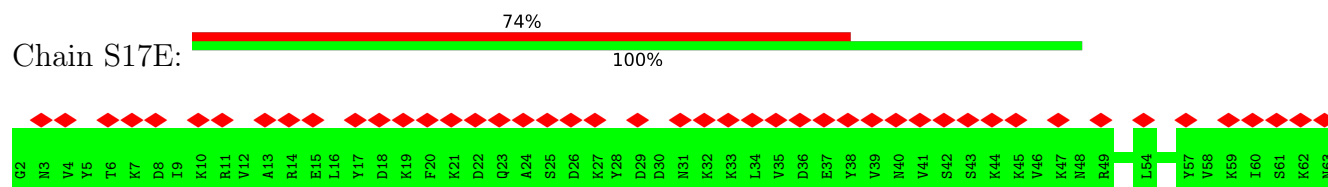
• Molecule 58: 30S ribosomal protein S13



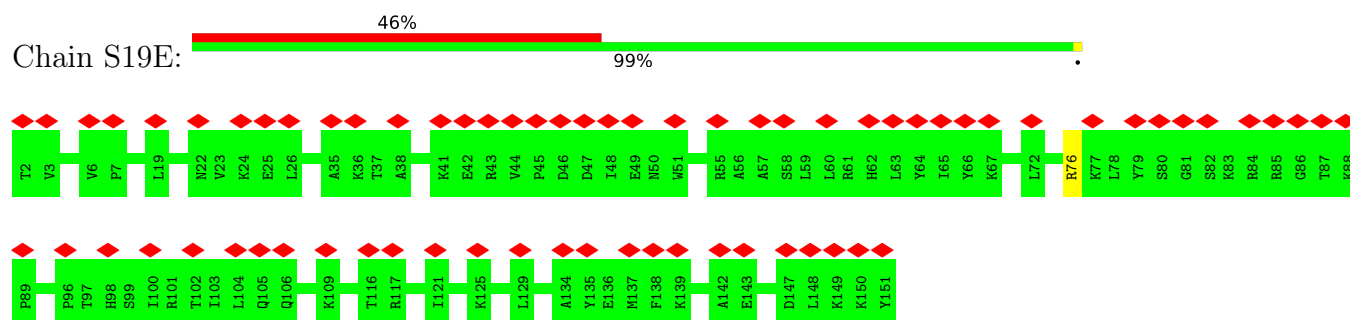
- Molecule 59: 30S ribosomal protein S14 type Z



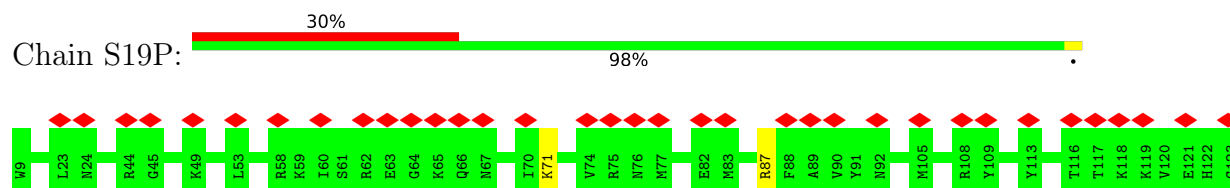
- Molecule 60: 30S ribosomal protein S17e



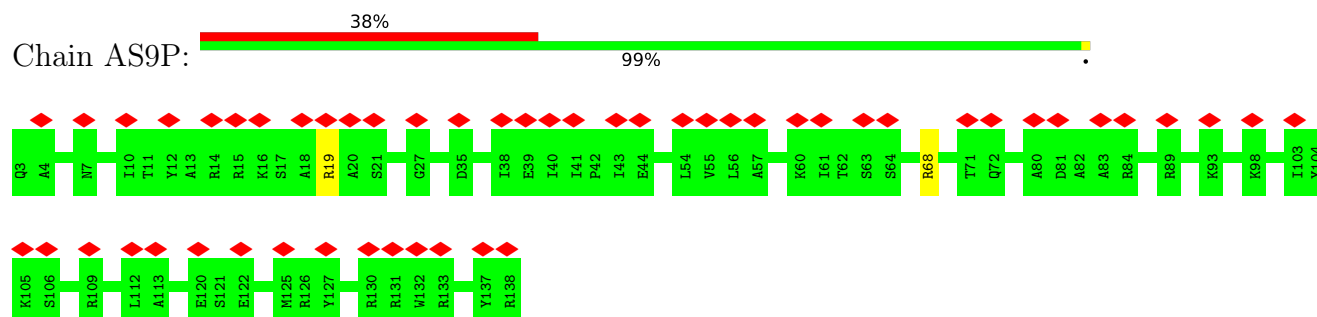
- Molecule 61: 30S ribosomal protein S19e



- Molecule 62: 30S ribosomal protein S19

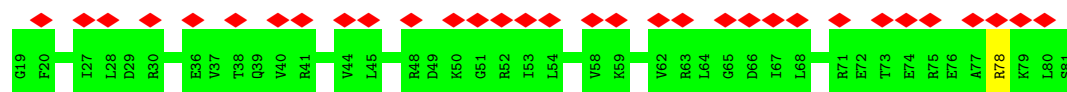


- Molecule 63: 30S ribosomal protein S9

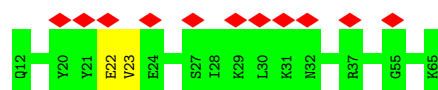


- Molecule 64: 30S ribosomal protein S28e

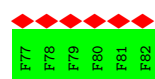




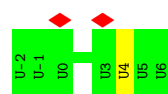
- Molecule 65: 30S ribosomal protein S27ae



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



- Molecule 67: mRNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*U)-3')



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5781	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	1.201	Depositor
Minimum map value	-0.533	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.33	Depositor
Map size (Å)	413.06, 413.06, 413.06	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.087, 1.087, 1.087	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.71	59/72048 (0.1%)	1.25	448/112407 (0.4%)
2	A16S	0.74	51/35889 (0.1%)	1.34	477/56002 (0.9%)
3	AATN	0.81	7/1809 (0.4%)	2.17	39/2819 (1.4%)
3	AETN	0.49	1/1809 (0.1%)	1.23	21/2819 (0.7%)
3	APTN	0.63	2/1809 (0.1%)	1.56	29/2819 (1.0%)
4	A5S	0.54	0/2917	0.88	1/4549 (0.0%)
5	AL1P	0.27	0/1739	0.54	0/2338
6	AL2P	0.35	0/1787	0.59	0/2409
7	AL3P	0.34	0/2758	0.59	0/3727
8	AL4P	0.32	0/1956	0.57	1/2635 (0.0%)
9	AL5P	0.33	0/1364	0.61	0/1827
10	AL6P	0.31	0/1450	0.53	0/1949
11	ALX0	0.35	0/638	0.62	0/851
12	L10E	0.34	0/1334	0.60	0/1787
13	L13P	0.32	0/1123	0.59	0/1502
14	L141	0.29	0/673	0.55	0/900
14	L142	0.30	0/673	0.53	0/900
15	L14P	0.36	0/1054	0.63	0/1425
16	L15E	0.36	0/1458	0.64	0/1956
17	L18E	0.31	0/907	0.57	0/1214
18	L18P	0.34	0/1570	0.56	0/2115
19	L19E	0.33	0/1223	0.59	0/1622
20	L22P	0.31	0/1246	0.57	0/1671
21	L23P	0.33	0/655	0.49	0/874
22	L24E	0.35	0/451	0.53	0/599
23	L24P	0.33	0/1000	0.59	0/1329
24	L29P	0.27	0/513	0.61	0/678
25	L30E	0.35	0/738	0.52	0/985
26	L30P	0.40	0/1278	0.61	0/1713
27	L31E	0.34	0/632	0.67	0/837
28	L32E	0.33	0/1027	0.61	0/1366
29	L34E	0.44	0/642	0.82	4/854 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	L37A	0.40	0/542	0.63	0/726
31	L37E	0.39	0/445	0.69	0/585
32	L39E	0.32	0/422	0.69	0/562
33	L40E	0.28	0/443	0.63	0/587
34	L44E	0.32	0/763	0.57	0/1008
35	L7A1	0.30	0/946	0.46	0/1272
35	L7A2	0.29	0/946	0.45	0/1272
35	SL7A	0.28	0/946	0.48	0/1272
36	L15P	0.33	0/766	0.53	0/1023
37	L21E	0.33	0/800	0.57	0/1067
38	L45A	0.32	0/824	0.56	0/1094
39	L46A	0.30	0/595	0.57	0/793
40	L47A	0.28	0/652	0.55	0/870
41	AS2P	0.31	0/1621	0.57	0/2202
42	AS4E	0.31	0/1956	0.61	1/2635 (0.0%)
43	AS4P	0.32	0/1399	0.57	0/1883
44	AS5P	0.34	0/1631	0.57	0/2200
45	AS6E	0.30	0/815	0.62	0/1093
46	AS8E	0.30	0/1005	0.58	0/1342
47	AS8P	0.34	0/1046	0.60	0/1410
48	S11P	0.29	0/976	0.63	0/1315
49	S12P	0.32	0/1120	0.61	0/1495
50	S15P	0.33	0/1250	0.59	0/1677
51	S17P	0.31	0/899	0.57	0/1203
52	S24E	0.29	0/769	0.54	0/1034
53	S27E	0.30	0/465	0.53	0/618
54	S3AE	0.30	0/1573	0.57	0/2115
55	AS3P	0.32	0/1599	0.55	0/2147
56	AS7P	0.30	0/1561	0.59	0/2105
57	S10P	0.31	0/840	0.56	0/1132
58	S13P	0.31	0/1221	0.62	0/1634
59	S14P	0.37	0/441	0.63	0/583
60	S17E	0.30	0/523	0.49	0/696
61	S19E	0.30	0/1267	0.55	0/1705
62	S19P	0.31	0/985	0.57	0/1310
63	AS9P	0.31	0/1115	0.59	0/1496
64	S28E	0.27	0/500	0.67	0/669
65	S27A	0.36	0/444	0.66	0/590
66	APTP	0.33	0/72	0.37	0/93
67	AMRN	0.39	0/197	0.88	0/302
All	All	0.60	120/182550 (0.1%)	1.11	1021/270293 (0.4%)

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
13	L13P	0	1
42	AS4E	0	1
43	AS4P	0	1
44	AS5P	0	1
47	AS8P	0	2
50	S15P	0	1
65	S27A	0	2
All	All	0	10

The worst 5 of 120 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A16S	381	C	C2-O2	-16.49	1.09	1.24
2	A16S	381	C	N1-C6	-15.77	1.27	1.37
3	AATN	75	C	N3-C4	-14.54	1.23	1.33
3	AATN	75	C	C2-N3	-12.52	1.25	1.35
1	A23S	2677	G	C6-N1	-11.78	1.31	1.39

The worst 5 of 1021 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A23S	2677	G	N1-C6-O6	-107.85	55.19	119.90
1	A23S	2677	G	N1-C2-N2	-77.05	46.86	116.20
2	A16S	381	C	N1-C2-O2	-58.44	83.84	118.90
1	A23S	2677	G	C6-N1-C2	54.20	157.62	125.10
1	A23S	1626	C	C6-N1-C2	-52.23	99.41	120.30

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A16S	381	C	Sidechain
42	AS4E	163	LEU	Peptide
43	AS4P	160	PRO	Peptide
44	AS5P	80	ARG	Sidechain
13	L13P	69	ARG	Sidechain

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	64357	0	0	0	0
2	A16S	32063	0	0	0	0
3	AATN	1619	0	0	0	0
3	AETN	1619	0	0	0	0
3	APTN	1619	0	0	0	0
4	A5S	2609	0	1324	150	0
5	AL1P	1715	0	0	0	0
6	AL2P	1754	0	0	0	0
7	AL3P	2695	0	0	0	0
8	AL4P	1926	0	0	0	0
9	AL5P	1343	0	0	0	0
10	AL6P	1431	0	0	0	0
11	ALX0	629	0	0	0	0
12	L10E	1310	0	0	0	0
13	L13P	1109	0	0	0	0
14	L141	669	0	0	0	0
14	L142	669	0	0	0	0
15	L14P	1034	0	0	0	0
16	L15E	1423	0	0	0	0
17	L18E	895	0	0	0	0
18	L18P	1539	0	0	0	0
19	L19E	1206	0	0	0	0
20	L22P	1223	0	0	0	0
21	L23P	650	0	0	0	0
22	L24E	441	0	0	0	0
23	L24P	989	0	0	0	0
24	L29P	513	0	0	0	0
25	L30E	729	0	0	0	0
26	L30P	1254	0	0	0	0
27	L31E	625	0	0	0	0
28	L32E	1010	0	0	0	0
29	L34E	629	0	0	0	0
30	L37A	527	0	0	0	0
31	L37E	436	0	0	0	0
32	L39E	414	0	0	0	0
33	L40E	439	0	0	0	0
34	L44E	753	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	L7A1	935	0	0	0	0
35	L7A2	935	0	0	0	0
35	SL7A	935	0	0	0	0
36	L15P	752	0	0	0	0
37	L21E	785	0	0	0	0
38	L45A	816	0	0	0	0
39	L46A	586	0	0	0	0
40	L47A	648	0	0	0	0
41	AS2P	1587	0	0	0	0
42	AS4E	1925	0	0	0	0
43	AS4P	1370	0	0	0	0
44	AS5P	1600	0	0	0	0
45	AS6E	805	0	0	0	0
46	AS8E	993	0	0	0	0
47	AS8P	1028	0	0	0	0
48	S11P	960	0	0	0	0
49	S12P	1103	0	0	0	0
50	S15P	1225	0	0	0	0
51	S17P	885	0	0	0	0
52	S24E	759	0	0	0	0
53	S27E	458	0	0	0	0
54	S3AE	1545	0	0	0	0
55	AS3P	1576	0	0	0	0
56	AS7P	1537	0	0	0	0
57	S10P	824	0	0	0	0
58	S13P	1204	0	0	0	0
59	S14P	432	0	0	0	0
60	S17E	517	0	0	0	0
61	S19E	1239	0	0	0	0
62	S19P	968	0	0	0	0
63	AS9P	1096	0	0	0	0
64	S28E	498	0	0	0	0
65	S27A	435	0	0	0	0
66	APTP	67	0	0	0	0
67	AMRN	180	0	0	0	0
68	AS2P	166	0	0	0	0
68	AS5P	100	0	0	0	0
68	AS8P	20	0	0	0	0
All	All	169359	0	1324	150	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 45.

The worst 5 of 150 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)
4:A5S:76:G:N1	4:A5S:106:U:O2	2.06	0.89
4:A5S:32:C:N3	4:A5S:52:G:N2	2.21	0.88
4:A5S:10:G:H1	4:A5S:115:U:H3	1.14	0.87
4:A5S:35:G:N1	4:A5S:49:C:N3	2.23	0.84
4:A5S:4:C:N3	4:A5S:121:G:N1	2.24	0.84

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	AL1P	214/216 (99%)	190 (89%)	24 (11%)	0	100	100
6	AL2P	232/234 (99%)	205 (88%)	27 (12%)	0	100	100
7	AL3P	337/339 (99%)	287 (85%)	49 (14%)	1 (0%)	37	72
8	AL4P	249/251 (99%)	229 (92%)	20 (8%)	0	100	100
9	AL5P	166/168 (99%)	153 (92%)	13 (8%)	0	100	100
10	AL6P	179/181 (99%)	156 (87%)	23 (13%)	0	100	100
11	ALX0	74/76 (97%)	63 (85%)	11 (15%)	0	100	100
12	L10E	162/164 (99%)	136 (84%)	26 (16%)	0	100	100
13	L13P	138/140 (99%)	127 (92%)	11 (8%)	0	100	100
14	L141	84/86 (98%)	67 (80%)	17 (20%)	0	100	100
14	L142	84/86 (98%)	75 (89%)	9 (11%)	0	100	100
15	L14P	132/134 (98%)	112 (85%)	20 (15%)	0	100	100
16	L15E	167/169 (99%)	155 (93%)	12 (7%)	0	100	100
17	L18E	110/112 (98%)	105 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	L18P	191/193 (99%)	165 (86%)	26 (14%)	0	100	100
19	L19E	142/144 (99%)	132 (93%)	10 (7%)	0	100	100
20	L22P	148/150 (99%)	131 (88%)	17 (12%)	0	100	100
21	L23P	79/81 (98%)	70 (89%)	9 (11%)	0	100	100
22	L24E	52/54 (96%)	44 (85%)	8 (15%)	0	100	100
23	L24P	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
24	L29P	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
25	L30E	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
26	L30P	153/155 (99%)	123 (80%)	30 (20%)	0	100	100
27	L31E	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
28	L32E	121/123 (98%)	106 (88%)	15 (12%)	0	100	100
29	L34E	75/77 (97%)	58 (77%)	16 (21%)	1 (1%)	10	42
30	L37A	63/65 (97%)	53 (84%)	10 (16%)	0	100	100
31	L37E	52/54 (96%)	41 (79%)	11 (21%)	0	100	100
32	L39E	47/49 (96%)	39 (83%)	8 (17%)	0	100	100
33	L40E	53/55 (96%)	43 (81%)	9 (17%)	1 (2%)	6	33
34	L44E	90/92 (98%)	83 (92%)	7 (8%)	0	100	100
35	L7A1	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
35	L7A2	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
35	SL7A	121/123 (98%)	109 (90%)	12 (10%)	0	100	100
36	L15P	90/144 (62%)	79 (88%)	11 (12%)	0	100	100
37	L21E	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
38	L45A	99/101 (98%)	74 (75%)	22 (22%)	3 (3%)	3	23
39	L46A	68/70 (97%)	57 (84%)	11 (16%)	0	100	100
40	L47A	78/80 (98%)	70 (90%)	7 (9%)	1 (1%)	10	42
41	AS2P	194/196 (99%)	182 (94%)	12 (6%)	0	100	100
42	AS4E	238/240 (99%)	207 (87%)	31 (13%)	0	100	100
43	AS4P	164/166 (99%)	135 (82%)	29 (18%)	0	100	100
44	AS5P	202/204 (99%)	180 (89%)	22 (11%)	0	100	100
45	AS6E	103/105 (98%)	89 (86%)	14 (14%)	0	100	100
46	AS8E	124/126 (98%)	102 (82%)	22 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	AS8P	128/130 (98%)	113 (88%)	13 (10%)	2 (2%)	8	38
48	S11P	126/128 (98%)	105 (83%)	21 (17%)	0	100	100
49	S12P	141/143 (99%)	117 (83%)	24 (17%)	0	100	100
50	S15P	147/149 (99%)	125 (85%)	22 (15%)	0	100	100
51	S17P	109/111 (98%)	99 (91%)	10 (9%)	0	100	100
52	S24E	94/96 (98%)	81 (86%)	13 (14%)	0	100	100
53	S27E	57/59 (97%)	46 (81%)	11 (19%)	0	100	100
54	S3AE	187/189 (99%)	157 (84%)	30 (16%)	0	100	100
55	AS3P	199/201 (99%)	185 (93%)	14 (7%)	0	100	100
56	AS7P	191/193 (99%)	154 (81%)	37 (19%)	0	100	100
57	S10P	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
58	S13P	145/147 (99%)	123 (85%)	22 (15%)	0	100	100
59	S14P	50/52 (96%)	36 (72%)	14 (28%)	0	100	100
60	S17E	60/62 (97%)	54 (90%)	6 (10%)	0	100	100
61	S19E	148/150 (99%)	127 (86%)	21 (14%)	0	100	100
62	S19P	113/115 (98%)	96 (85%)	17 (15%)	0	100	100
63	AS9P	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
64	S28E	61/63 (97%)	52 (85%)	9 (15%)	0	100	100
65	S27A	52/54 (96%)	39 (75%)	13 (25%)	0	100	100
66	APTP	4/6 (67%)	2 (50%)	2 (50%)	0	100	100
All	All	8002/8184 (98%)	6995 (87%)	998 (12%)	9 (0%)	50	83

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	L45A	4	VAL
38	L45A	67	THR
7	AL3P	231	ARG
38	L45A	55	VAL
29	L34E	19	PRO

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	AL1P	189/190 (100%)	189 (100%)	0	100	100
6	AL2P	181/181 (100%)	178 (98%)	3 (2%)	56	72
7	AL3P	297/297 (100%)	296 (100%)	1 (0%)	91	91
8	AL4P	212/212 (100%)	211 (100%)	1 (0%)	86	89
9	AL5P	144/144 (100%)	143 (99%)	1 (1%)	81	87
10	AL6P	157/157 (100%)	153 (98%)	4 (2%)	42	62
11	ALX0	68/68 (100%)	68 (100%)	0	100	100
12	L10E	137/137 (100%)	135 (98%)	2 (2%)	60	75
13	L13P	121/121 (100%)	121 (100%)	0	100	100
14	L141	74/74 (100%)	74 (100%)	0	100	100
14	L142	74/74 (100%)	74 (100%)	0	100	100
15	L14P	110/110 (100%)	108 (98%)	2 (2%)	54	71
16	L15E	146/146 (100%)	144 (99%)	2 (1%)	62	75
17	L18E	98/98 (100%)	98 (100%)	0	100	100
18	L18P	162/162 (100%)	160 (99%)	2 (1%)	67	79
19	L19E	126/126 (100%)	124 (98%)	2 (2%)	58	74
20	L22P	131/131 (100%)	130 (99%)	1 (1%)	79	84
21	L23P	74/74 (100%)	74 (100%)	0	100	100
22	L24E	50/50 (100%)	50 (100%)	0	100	100
23	L24P	108/108 (100%)	106 (98%)	2 (2%)	52	69
24	L29P	59/59 (100%)	57 (97%)	2 (3%)	32	53
25	L30E	83/83 (100%)	83 (100%)	0	100	100
26	L30P	136/136 (100%)	136 (100%)	0	100	100
27	L31E	66/66 (100%)	65 (98%)	1 (2%)	60	75
28	L32E	106/106 (100%)	106 (100%)	0	100	100
29	L34E	70/70 (100%)	69 (99%)	1 (1%)	62	75
30	L37A	53/53 (100%)	52 (98%)	1 (2%)	52	69
31	L37E	45/45 (100%)	45 (100%)	0	100	100
32	L39E	44/44 (100%)	44 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	L40E	50/50 (100%)	50 (100%)	0	100	100
34	L44E	84/84 (100%)	84 (100%)	0	100	100
35	L7A1	104/104 (100%)	100 (96%)	4 (4%)	28	50
35	L7A2	104/104 (100%)	103 (99%)	1 (1%)	73	81
35	SL7A	104/104 (100%)	102 (98%)	2 (2%)	52	69
36	L15P	78/118 (66%)	78 (100%)	0	100	100
37	L21E	85/85 (100%)	85 (100%)	0	100	100
38	L45A	91/91 (100%)	90 (99%)	1 (1%)	70	80
39	L46A	66/66 (100%)	65 (98%)	1 (2%)	60	75
40	L47A	74/74 (100%)	74 (100%)	0	100	100
41	AS2P	174/174 (100%)	173 (99%)	1 (1%)	84	88
42	AS4E	210/210 (100%)	208 (99%)	2 (1%)	73	81
43	AS4P	149/149 (100%)	148 (99%)	1 (1%)	81	87
44	AS5P	174/174 (100%)	174 (100%)	0	100	100
45	AS6E	88/88 (100%)	88 (100%)	0	100	100
46	AS8E	106/106 (100%)	105 (99%)	1 (1%)	75	83
47	AS8P	111/111 (100%)	106 (96%)	5 (4%)	23	46
48	S11P	94/94 (100%)	93 (99%)	1 (1%)	70	80
49	S12P	116/116 (100%)	114 (98%)	2 (2%)	56	72
50	S15P	133/133 (100%)	131 (98%)	2 (2%)	60	75
51	S17P	97/97 (100%)	94 (97%)	3 (3%)	35	55
52	S24E	84/84 (100%)	84 (100%)	0	100	100
53	S27E	51/51 (100%)	49 (96%)	2 (4%)	27	49
54	S3AE	170/170 (100%)	167 (98%)	3 (2%)	54	71
55	AS3P	165/165 (100%)	165 (100%)	0	100	100
56	AS7P	166/166 (100%)	163 (98%)	3 (2%)	54	71
57	S10P	92/92 (100%)	91 (99%)	1 (1%)	70	80
58	S13P	129/129 (100%)	126 (98%)	3 (2%)	45	64
59	S14P	45/45 (100%)	44 (98%)	1 (2%)	47	65
60	S17E	57/57 (100%)	57 (100%)	0	100	100
61	S19E	134/134 (100%)	133 (99%)	1 (1%)	81	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	S19P	106/106 (100%)	104 (98%)	2 (2%)	52	69
63	AS9P	113/113 (100%)	111 (98%)	2 (2%)	54	71
64	S28E	54/54 (100%)	53 (98%)	1 (2%)	52	69
65	S27A	47/47 (100%)	47 (100%)	0	100	100
66	APTP	6/6 (100%)	6 (100%)	0	100	100
All	All	7032/7073 (99%)	6958 (99%)	74 (1%)	69	80

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	S3AE	176	LYS
64	S28E	78	ARG
56	AS7P	189	ARG
59	S14P	11	ARG
24	L29P	54	ARG

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

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A23S	2986/3022 (98%)	1128 (37%)	61 (2%)
2	A16S	1491/1503 (99%)	606 (40%)	51 (3%)
3	AATN	75/76 (98%)	33 (44%)	4 (5%)
3	AETN	75/76 (98%)	36 (48%)	5 (6%)
3	APTN	75/76 (98%)	24 (32%)	1 (1%)
4	A5S	121/122 (99%)	38 (31%)	2 (1%)
67	AMRN	8/9 (88%)	1 (12%)	0
All	All	4831/4884 (98%)	1866 (38%)	124 (2%)

5 of 1866 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A23S	7	G
1	A23S	18	G
1	A23S	19	A
1	A23S	26	G
1	A23S	29	U

5 of 124 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A23S	2732	G
2	A16S	1478	G
2	A16S	220	C
2	A16S	1351	C
3	APTN	19	G

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 57 ligands modelled in this entry, 57 are unknown - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

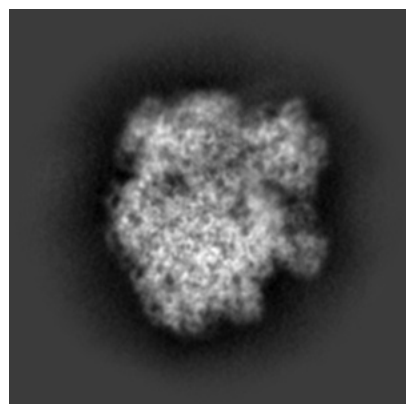
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34863. These allow visual inspection of the internal detail of the map and identification of artifacts.

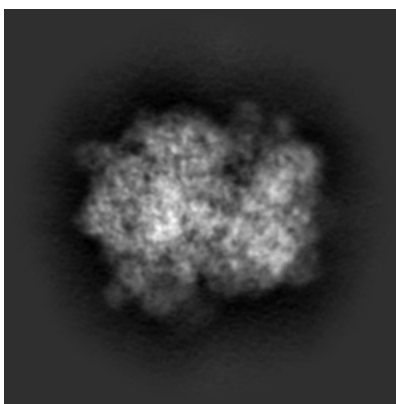
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

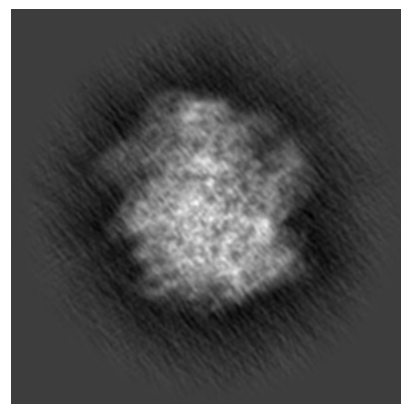
6.1.1 Primary map



X

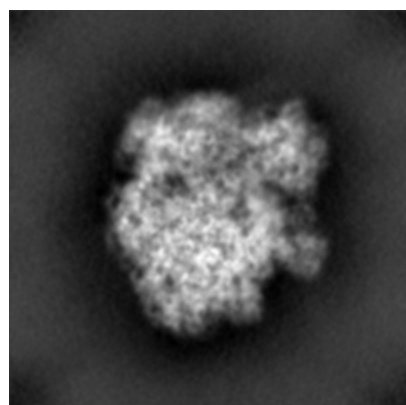


Y

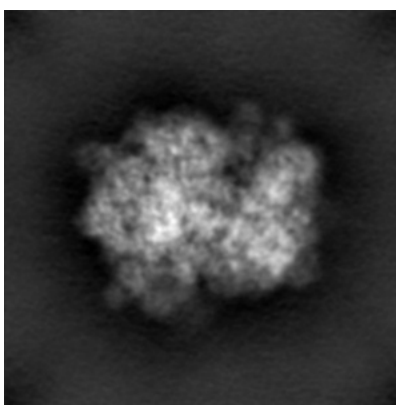


Z

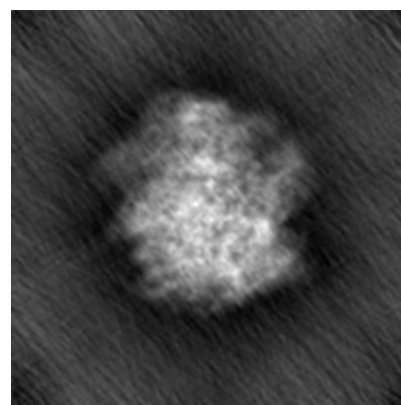
6.1.2 Raw map



X



Y

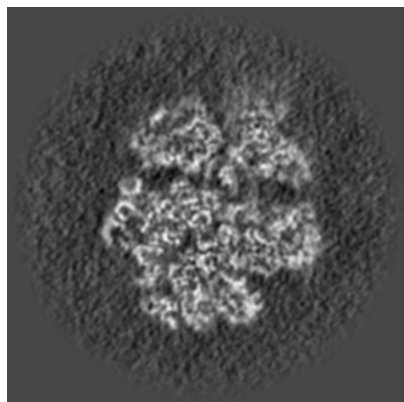


Z

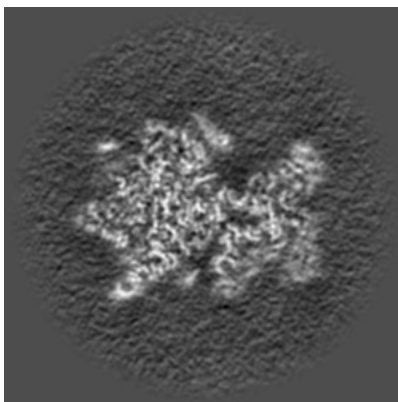
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

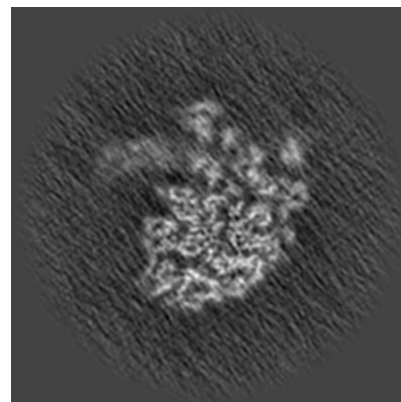
6.2.1 Primary map



X Index: 190

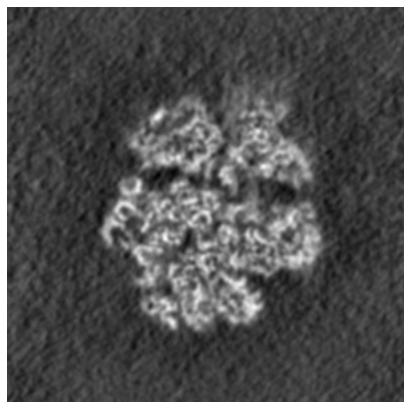


Y Index: 190

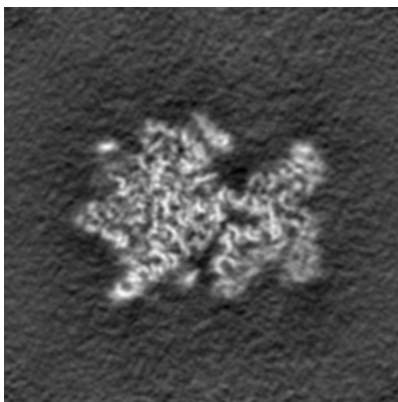


Z Index: 190

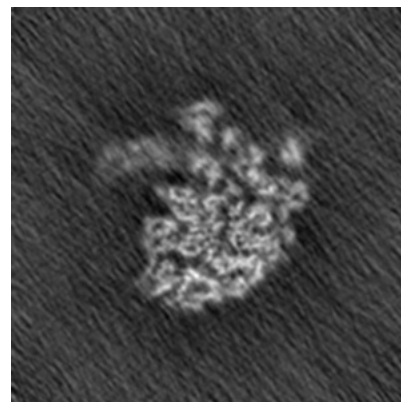
6.2.2 Raw map



X Index: 190



Y Index: 190

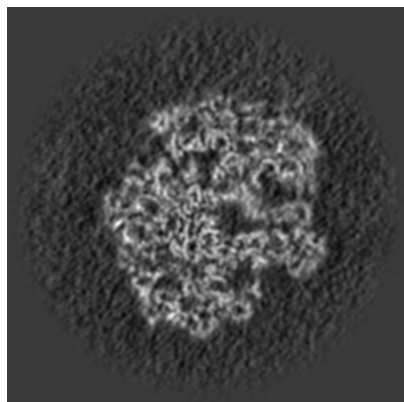


Z Index: 190

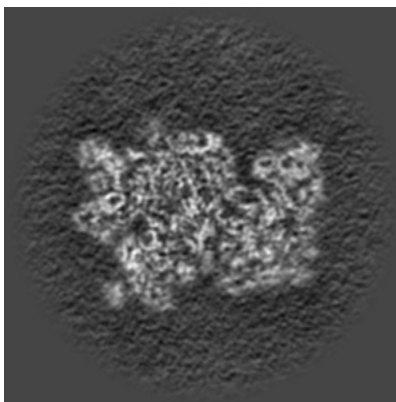
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

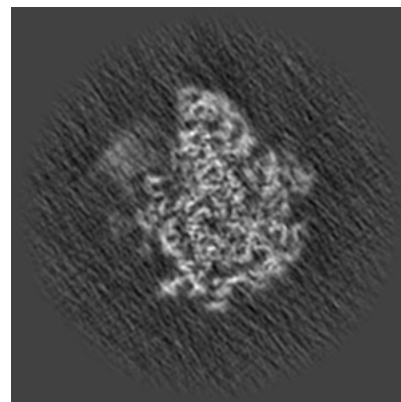
6.3.1 Primary map



X Index: 176

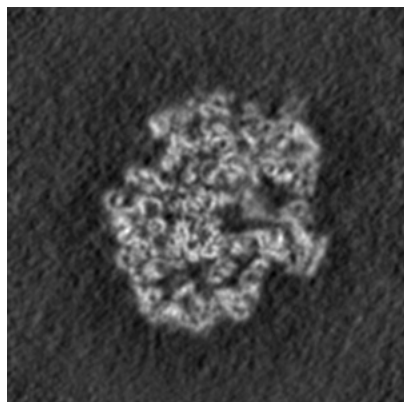


Y Index: 178

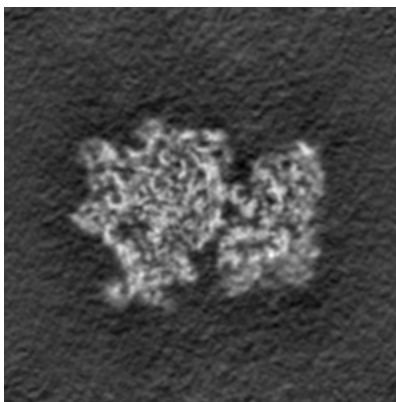


Z Index: 159

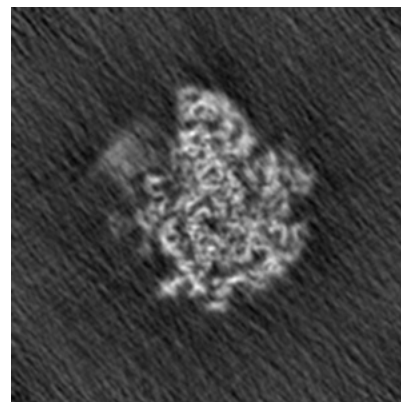
6.3.2 Raw map



X Index: 172



Y Index: 182

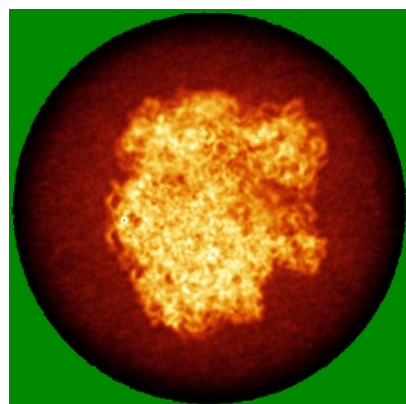


Z Index: 159

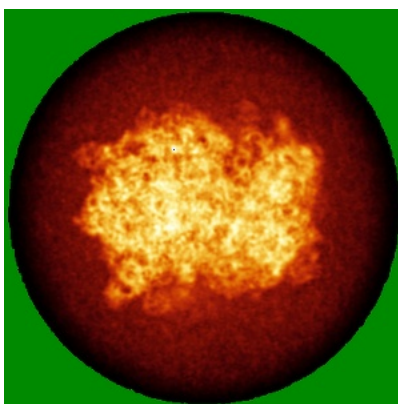
The images above show the largest variance slices of the map in three orthogonal directions.

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

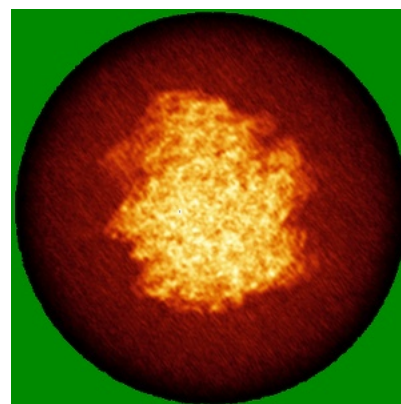
6.4.1 Primary map



X

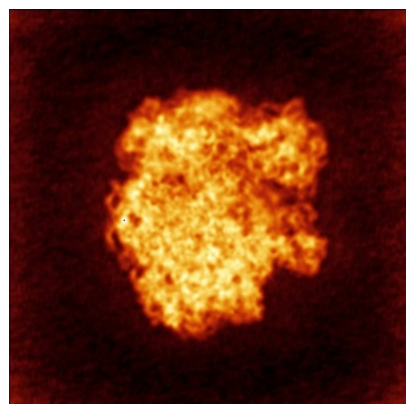


Y

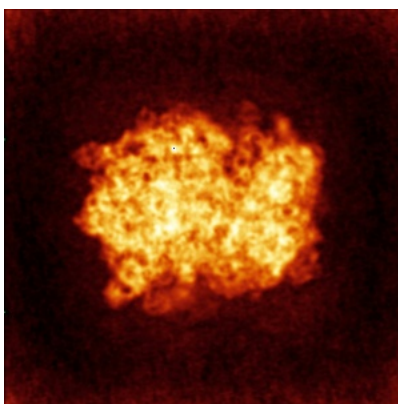


Z

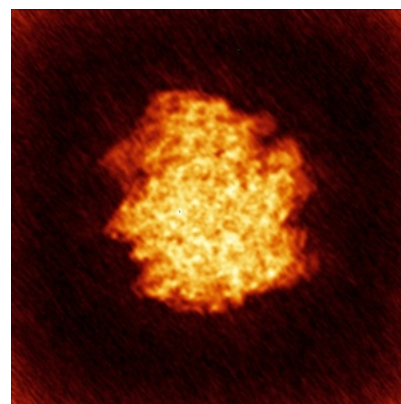
6.4.2 Raw map



X



Y

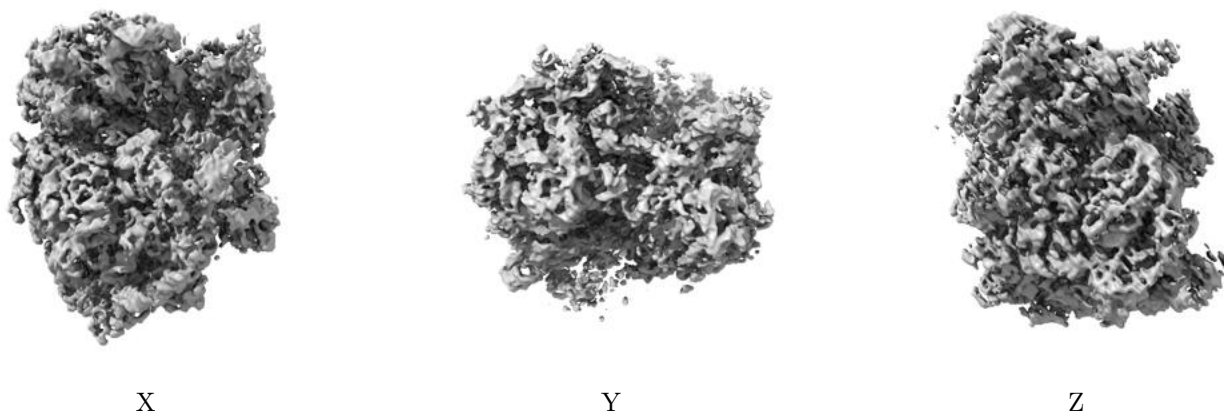


Z

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.

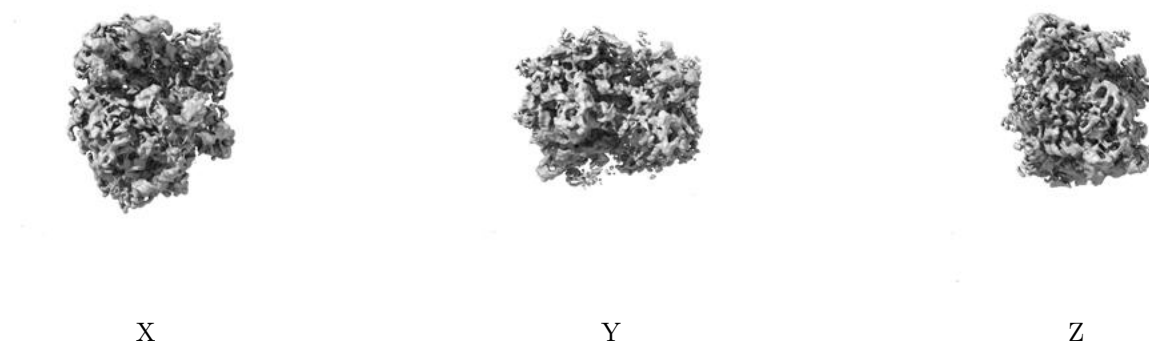
6.5 Orthogonal surface views [i](#)

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.

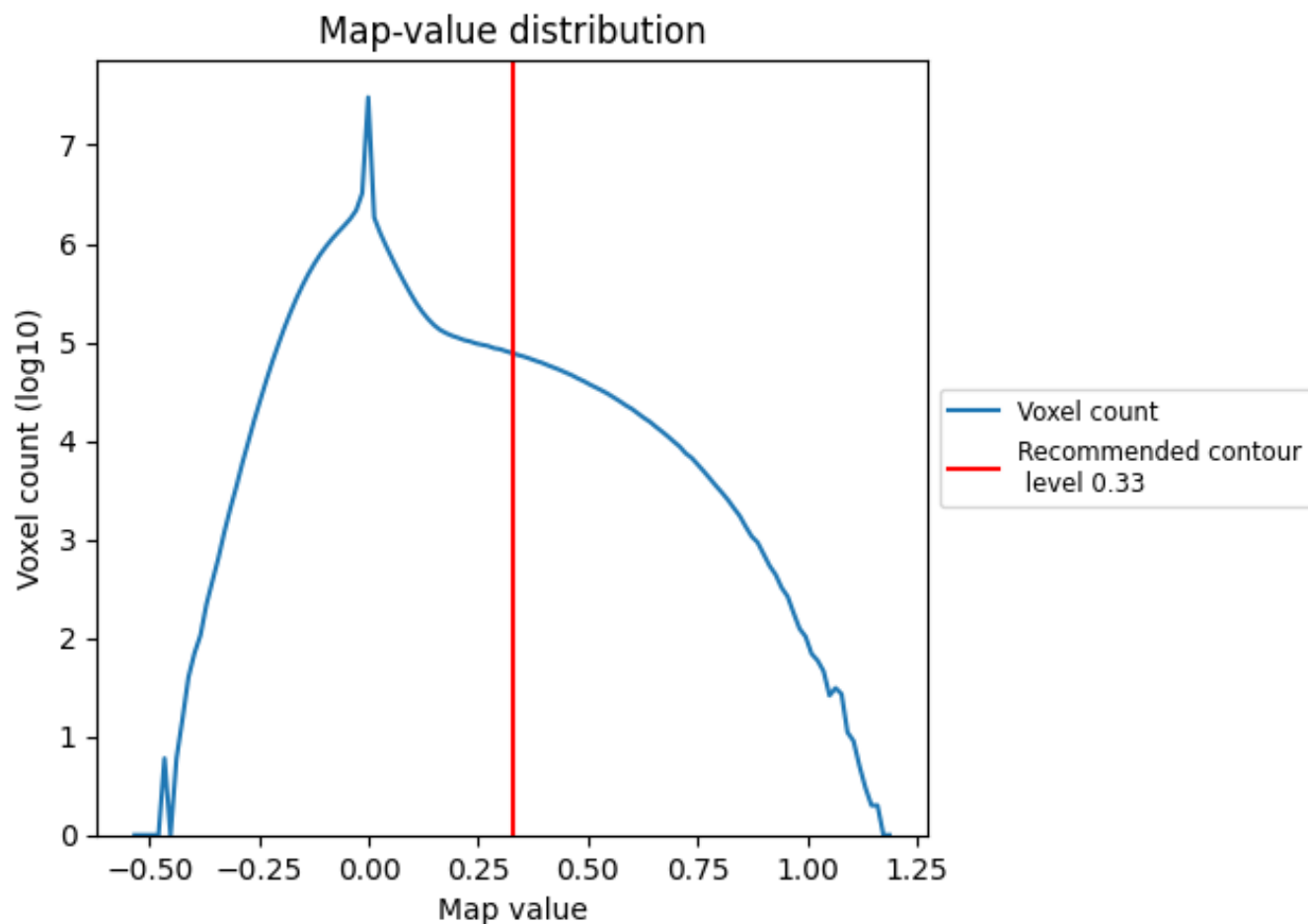
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

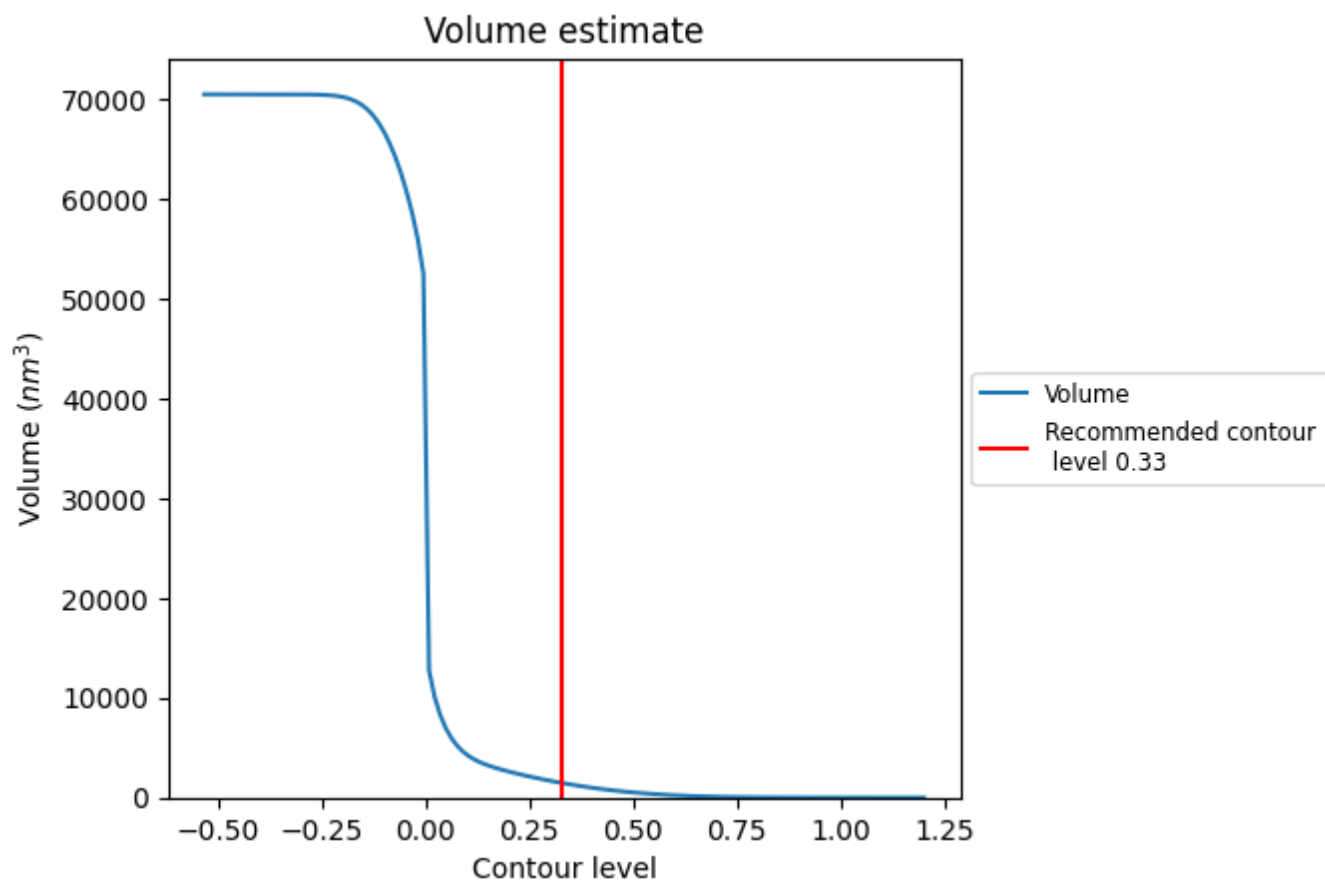
This section contains the results of statistical analysis of the map.

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.

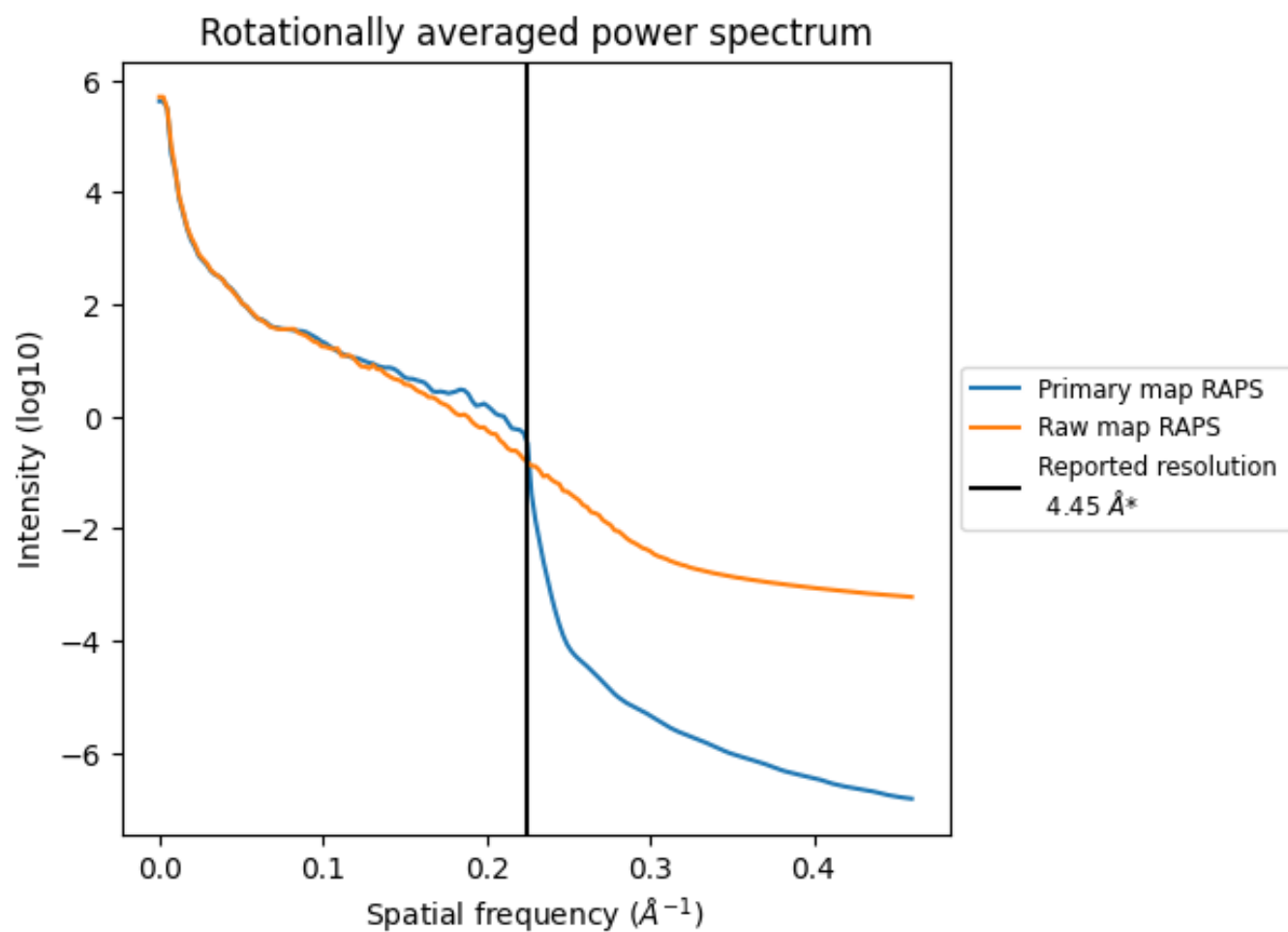
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1452 nm³; this corresponds to an approximate mass of 1311 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 ⓘ

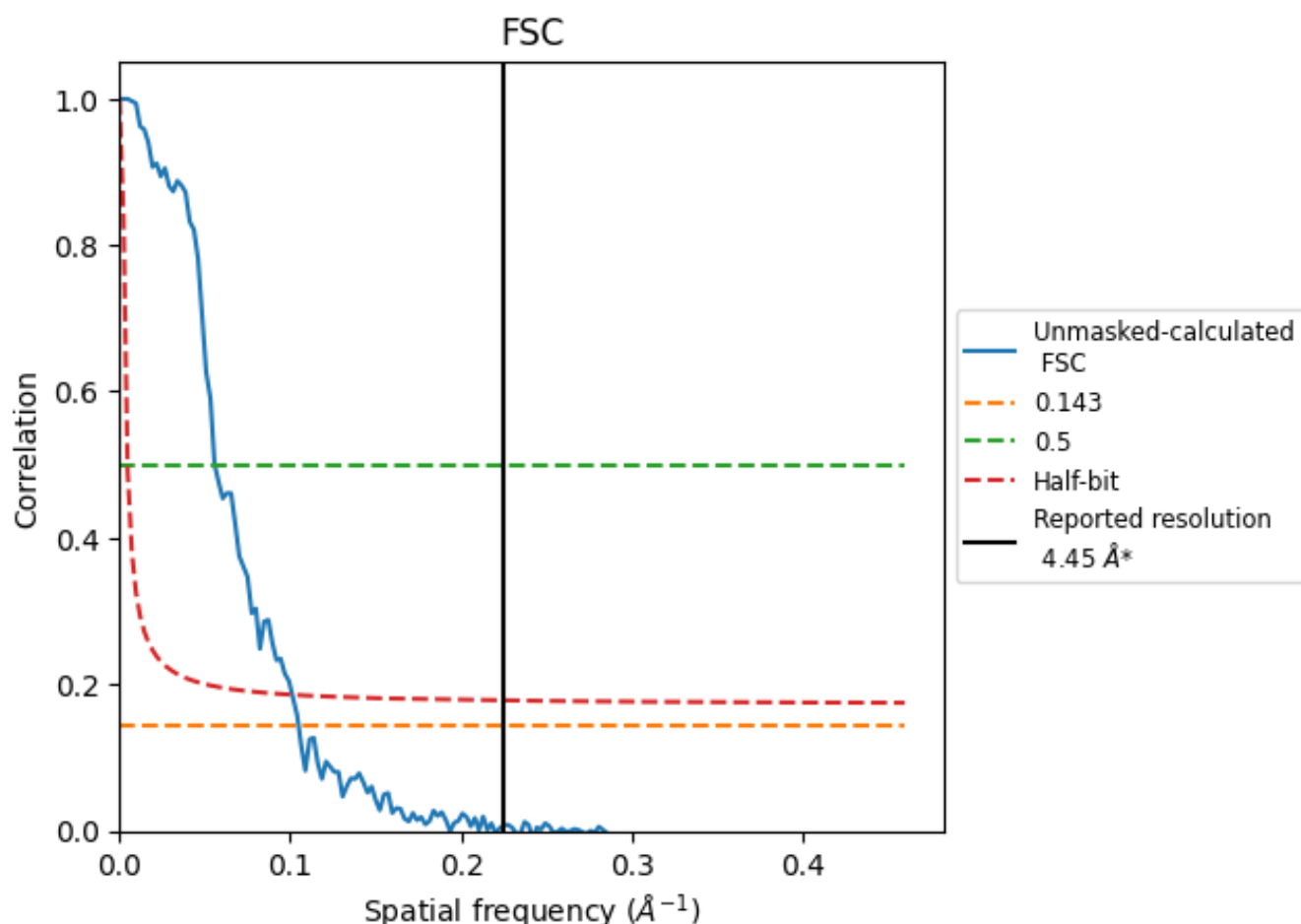


*Reported resolution corresponds to spatial frequency of 0.225 \AA^{-1}

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 0.225 Å⁻¹

8.2 Resolution estimates [i](#)

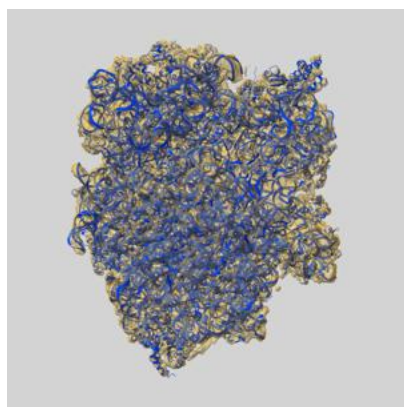
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.45	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.53	17.95	9.88

*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 9.53 differs from the reported value 4.45 by more than 10 %

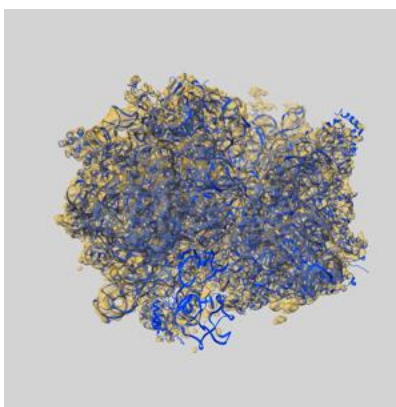
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34863 and PDB model 8HKY. Per-residue inclusion information can be found in section [3](#) on page [17](#).

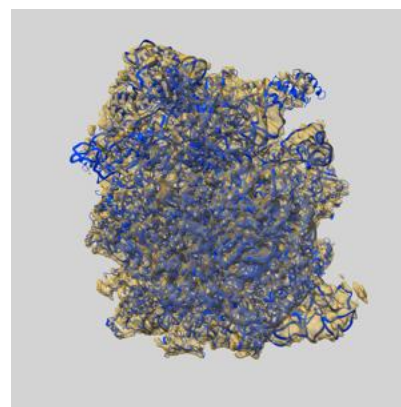
9.1 Map-model overlay [i](#)



X



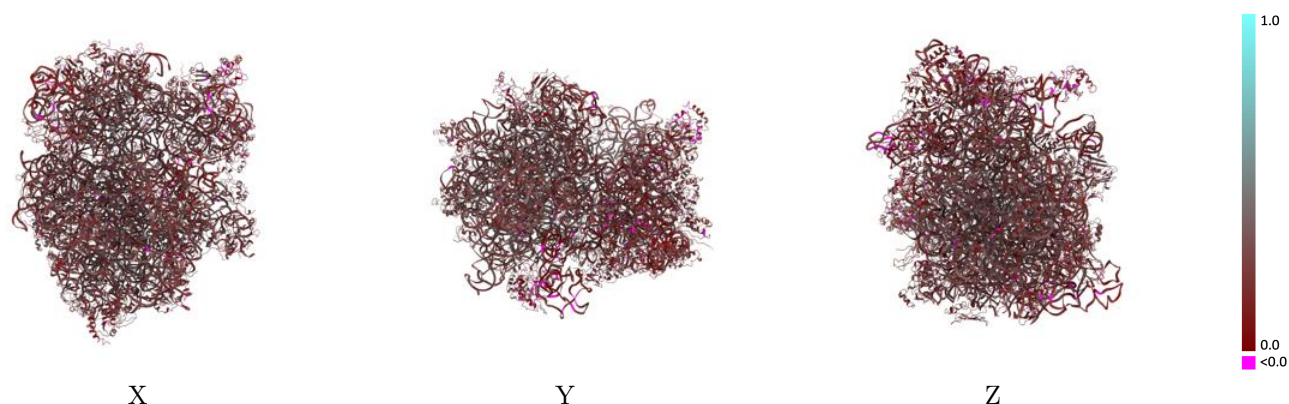
Y



Z

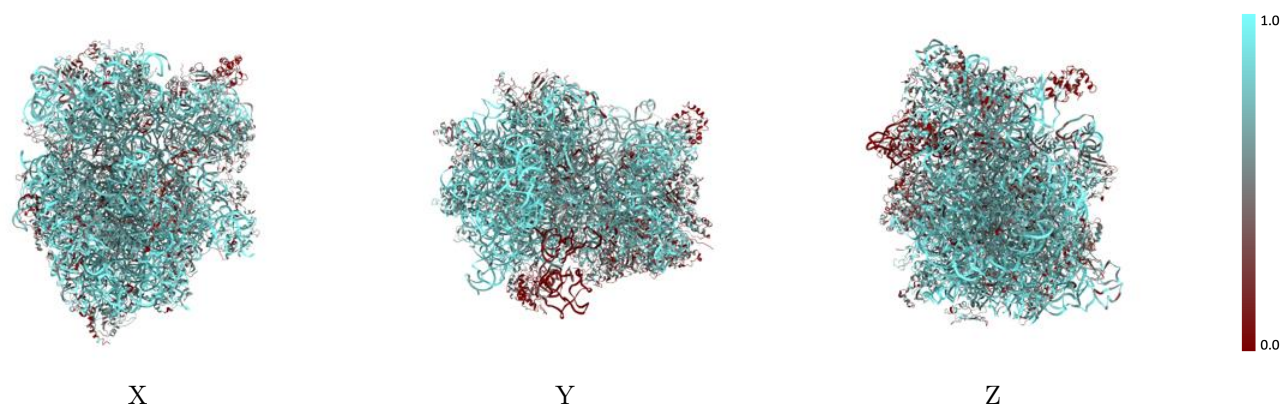
The images above show the 3D surface view of the map at the recommended contour level 0.33 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



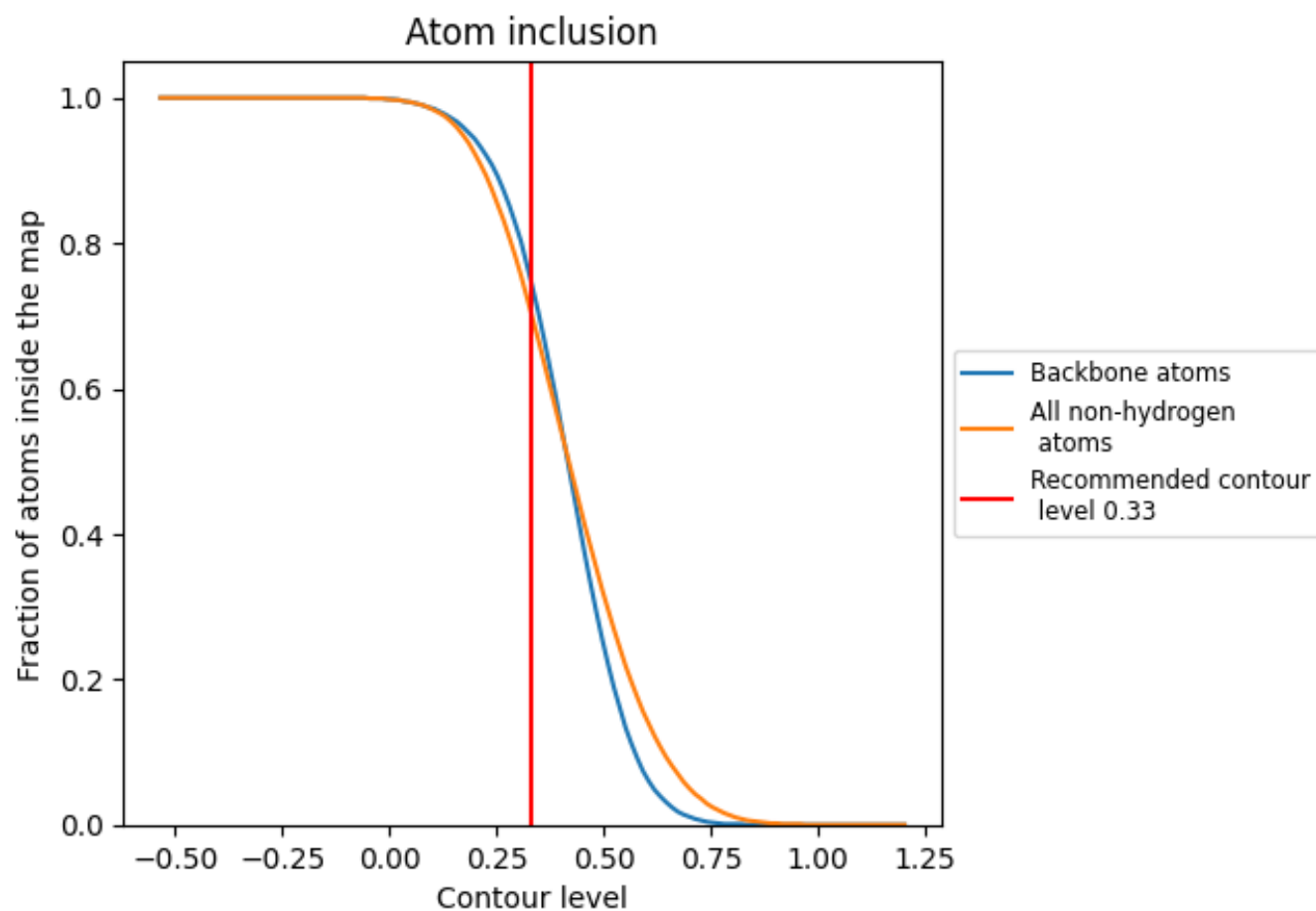
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 75% of all backbone atoms, 70% 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	 0.7050	 0.2700
A16S	 0.8390	 0.2620
A23S	 0.8540	 0.2930
A5S	 0.9230	 0.2840
AATN	 0.6020	 0.2530
AETN	 0.1230	 0.1350
AL1P	 0.0780	 0.1850
AL2P	 0.5090	 0.3170
AL3P	 0.5220	 0.2660
AL4P	 0.6140	 0.3010
AL5P	 0.5130	 0.2590
AL6P	 0.4860	 0.2600
ALX0	 0.5740	 0.2380
AMRN	 0.7390	 0.3130
APTN	 0.7230	 0.2360
APTP	 0.0300	 0.1860
AS2P	 0.3820	 0.2380
AS3P	 0.3950	 0.2640
AS4E	 0.5590	 0.2280
AS4P	 0.5700	 0.2480
AS5P	 0.5710	 0.2970
AS6E	 0.3180	 0.2040
AS7P	 0.4060	 0.2410
AS8E	 0.4930	 0.2440
AS8P	 0.6580	 0.2720
AS9P	 0.5260	 0.2330
L10E	 0.5900	 0.2860
L13P	 0.5410	 0.2450
L141	 0.5100	 0.2630
L142	 0.4660	 0.2270
L14P	 0.4670	 0.2940
L15E	 0.5500	 0.2900
L15P	 0.5890	 0.2770
L18E	 0.6540	 0.2840
L18P	 0.5990	 0.2580



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Chain	Atom inclusion	Q-score
L19E	 0.6350	 0.2780
L21E	 0.5350	 0.2860
L22P	 0.5260	 0.3020
L23P	 0.5510	 0.2710
L24E	 0.5920	 0.2720
L24P	 0.6610	 0.2730
L29P	 0.5950	 0.2620
L30E	 0.6670	 0.2800
L30P	 0.5830	 0.2520
L31E	 0.5430	 0.2780
L32E	 0.4760	 0.2850
L34E	 0.5190	 0.2350
L37A	 0.5960	 0.2930
L37E	 0.6140	 0.3100
L39E	 0.6560	 0.2590
L40E	 0.1760	 0.2080
L44E	 0.6320	 0.2940
L45A	 0.5390	 0.2680
L46A	 0.3980	 0.2810
L47A	 0.0780	 0.1970
L7A1	 0.4230	 0.2670
L7A2	 0.4470	 0.2280
S10P	 0.3930	 0.2280
S11P	 0.4700	 0.2580
S12P	 0.3550	 0.2790
S13P	 0.4330	 0.2080
S14P	 0.5480	 0.2500
S15P	 0.6190	 0.2460
S17E	 0.2460	 0.2090
S17P	 0.5450	 0.2850
S19E	 0.4350	 0.1840
S19P	 0.5930	 0.2320
S24E	 0.4530	 0.2430
S27A	 0.6680	 0.1690
S27E	 0.6440	 0.2390
S28E	 0.3540	 0.2380
S3AE	 0.4420	 0.2370
SL7A	 0.1520	 0.1760