



## wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 06:01 AM UTC

PDB ID : 8VS9 / pdb\_00008vs9  
EMDB ID : EMD-43490  
Title : Endogenous trans-translation complex with tmRNA\*SmpB in the P site and alanyl-tRNA in the A site and deacyl-tRNA in the E site of E. coli 70S ribosome  
Authors : Teran, D.; Zhang, Y.; Korostelev, A.A.  
Deposited on : 2024-01-23  
Resolution : 3.90 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](mailto: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>.

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

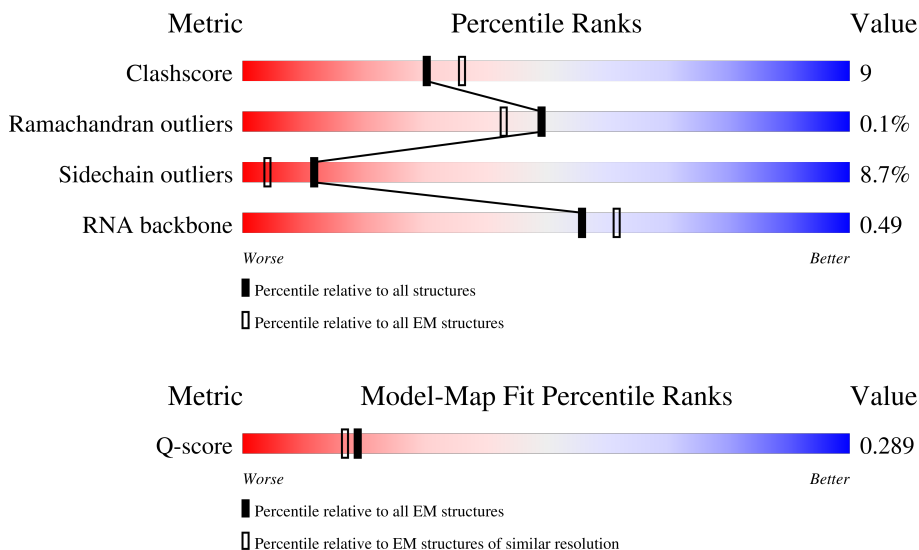
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 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 3.90 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 ( 3.40 - 4.40 )

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  $\geq 3$ , 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	16S	1539	
2	23S	2903	
3	5S	120	


























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Mol	Chain	Length	Quality of chain
4	ATRN	76	76% 24%
5	ETRN	77	70% 30%
6	L02	273	72% 25% ..
7	L03	209	73% 24% .
8	L04	201	74% 25% .
9	L05	179	68% 28% ..
10	L06	177	67% 32% ..
11	L09	149	49% 78% 19% .
12	L1	234	33% 21% 43%
13	L10	165	15% 50% 27% . 21%
14	L11	142	6% 63% 32% ..
15	L13	142	75% 23% .
16	L14	123	67% 29% ..
17	L15	144	76% 23% ..
18	L16	136	73% 24% .
19	L17	127	79% 15% . 6%
20	L18	117	74% 22% ..
21	L19	115	60% 37% ..
22	L20	118	77% 22% .
23	L21	103	67% 31% ..
24	L22	110	76% 23% .
25	L23	100	67% 24% . 7%
26	L24	104	69% 29% .
27	L25	94	65% 35%
28	L27	85	62% 24% . 12%

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Mol	Chain	Length	Quality of chain
29	L28	78	 73% 26%
30	L29	63	 68% 30%
31	L30	59	 75% 24%
32	L31	45	 53% 38% 9%
33	L32	57	 74% 19% 5%
34	L33	55	 71% 16% 9%
35	L34	46	 72% 26%
36	L35	65	 71% 26%
37	L36	38	 74% 24%
38	S02	241	 73% 18% 7%
39	S03	233	 63% 24% 12%
40	S04	206	 63% 33%
41	S05	167	 75% 17% 6%
42	S06	135	 41% 29% 26%
43	S07	179	 61% 22% 16%
44	S08	130	 70% 25% 5%
45	S09	130	 56% 37% 5%
46	S10	103	 61% 32% 5%
47	S11	129	 64% 24% 10%
48	S12	124	 67% 29%
49	S13	118	 67% 27%
50	S14	101	 66% 32%
51	S15	89	 69% 30%
52	S16	82	 65% 33%
53	S17	84	 62% 25% 8% 5%

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Mol	Chain	Length	Quality of chain
54	S18	75	<p>65% 19% 13%</p>
55	S19	92	<p>61% 22% 14%</p>
56	S20	87	<p>72% 25%</p>
57	S21	71	<p>58% 28% 6% 8%</p>
58	SMPB	150	<p>92% 6% 8%</p>
59	TMRN	363	<p>6% 57% 43%</p>

## 2 Entry composition i

There are 59 unique types of molecules in this entry. The entry contains 157472 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	16S	1539	33012	14725	6052	10697	1538	0	0

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	23S	2903	62317	27801	11468	20146	2902	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
23S	747	C	U	variant	GB 1036415628

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	5S	120	2568	1145	471	833	119	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5S	120	A	U	conflict	GB 1370526515

- Molecule 4 is a RNA chain called A-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	ATRN	76	1621	722	289	534	76	0	0

- Molecule 5 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	ETRN	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L02	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L03	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L04	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L05	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L06	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 11 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 12 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L1	134	1026	645	186	193	2	0	0

- Molecule 13 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L10	131	988	625	175	183	5	0	0

- Molecule 14 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	L11	141	1032	651	179	196	6	0	0

- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	L13	142	1129	714	212	199	4	0	0

- Molecule 16 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	L14	122	938	587	180	165	6	0	0

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	L15	143	1045	649	206	189	1	0	0

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	L16	136	1074	686	205	177	6	0	0

- Molecule 19 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	L17	120	960	593	196	166	5	0	0

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	L18	116	892	552	178	162		0	0

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	L19	114	917	574	179	163	1	0	0

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	L20	117	947	604	192	151		0	0

- Molecule 23 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	L21	103	816	516	153	145	2	0	0

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	L22	110	857	532	166	156	3	0	0

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	L23	93	738	466	139	131	2	0	0

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	L24	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L25	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L27	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 29 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L28	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L29	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 31 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L30	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 32 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	L31	45	Total	C	N	O	S	0	0
			351	219	61	65	6		

- Molecule 33 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L32	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 34 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L33	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 35 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L34	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 36 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L35	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 37 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L36	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 38 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	S02	225	Total	C	N	O	S	0	0
			1756	1111	315	322	8		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	S03	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 40 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	S04	205	1643	1026	315	298	4	0	0

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	S05	157	1156	719	218	213	6	0	0

- Molecule 42 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	S06	100	817	515	148	148	6	0	0

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	S07	151	1181	735	227	215	4	0	0

- Molecule 44 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	S08	129	979	616	173	184	6	0	0

- Molecule 45 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	S09	127	1022	634	206	179	3	0	0

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	S10	98	786	493	150	142	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	S11	116	869	535	173	158	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	S12	123	955	590	196	165	4	0	0

- Molecule 49 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	S13	114	883	546	178	156	3	0	0

- Molecule 50 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	S14	100	805	499	164	139	3	0	0

- Molecule 51 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	S15	88	714	439	144	130	1	0	0

- Molecule 52 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	S16	82	649	406	128	114	1	0	0

- Molecule 53 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	S17	80	648	411	121	113	3	0	0

- Molecule 54 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	S18	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S19	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 56 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S20	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 57 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S21	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 58 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SMPB	150	Total	C	N	O	S	0	0
			1209	763	226	216	4		

- Molecule 59 is a RNA chain called TMRN.

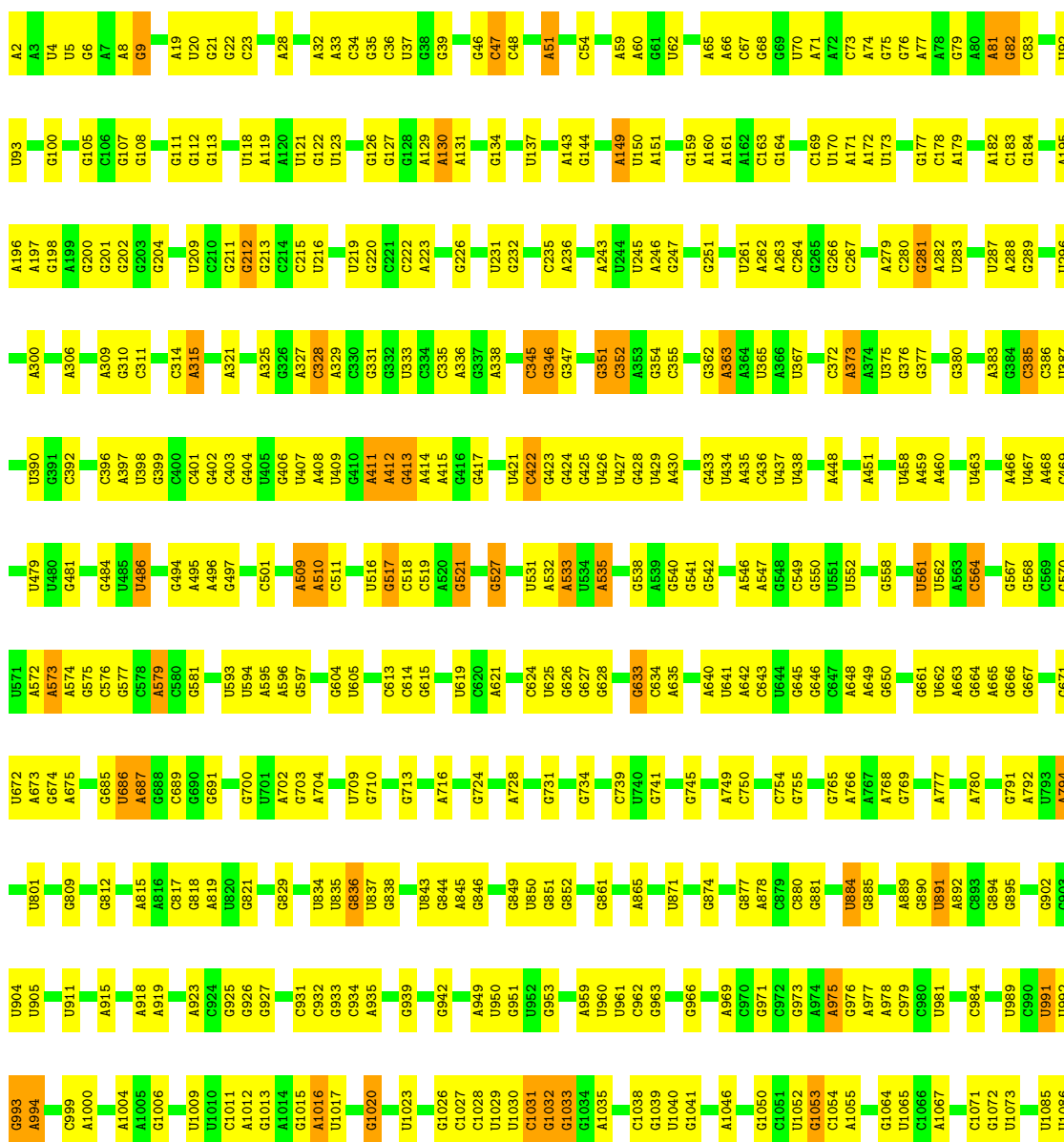
Mol	Chain	Residues	Atoms					AltConf	Trace
59	TMRN	363	Total	C	N	O	P	0	0
			7758	3465	1410	2520	363		

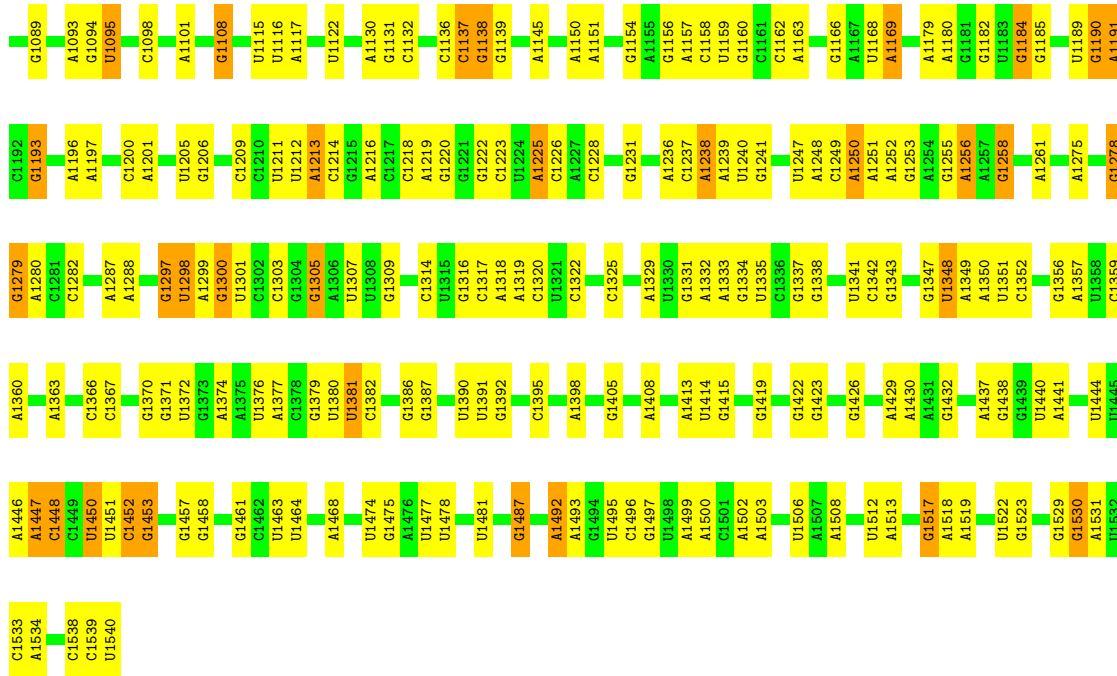
### 3 Residue-property plots [i](#)

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.

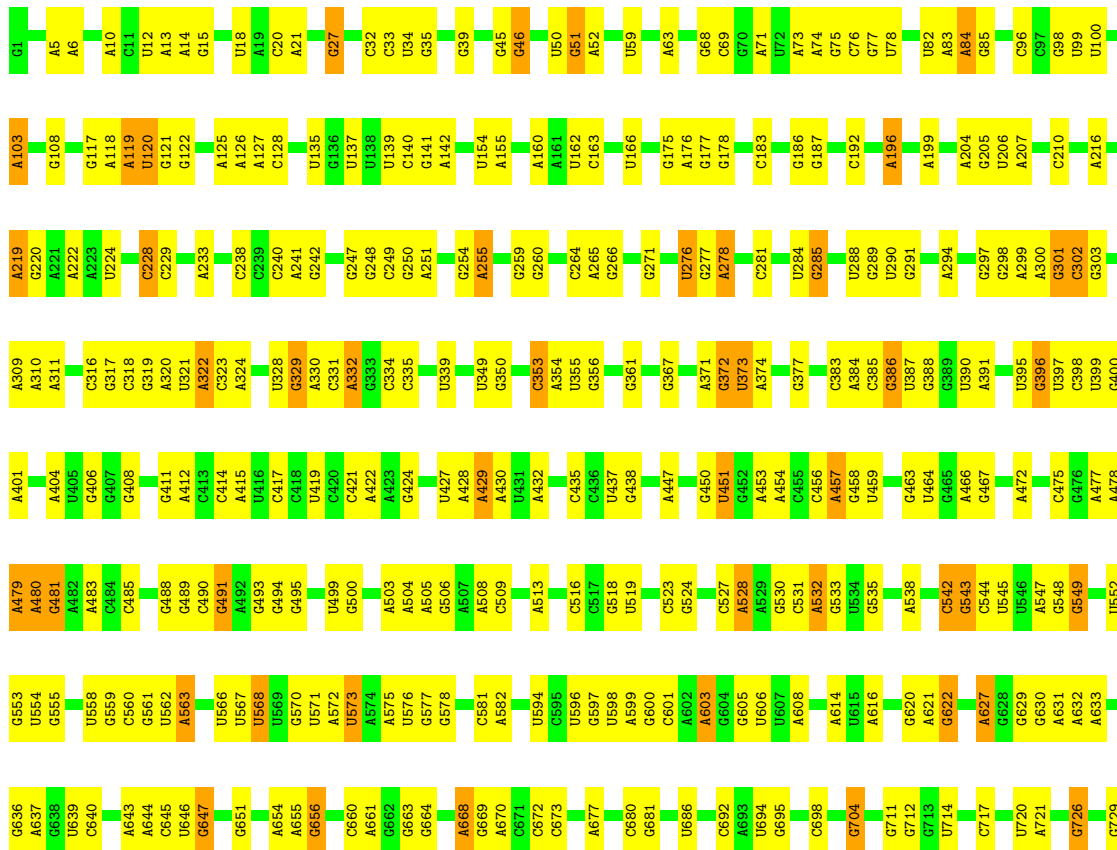
- Molecule 1: 16S ribosomal RNA

Chain 16S:  57% 37% 5%

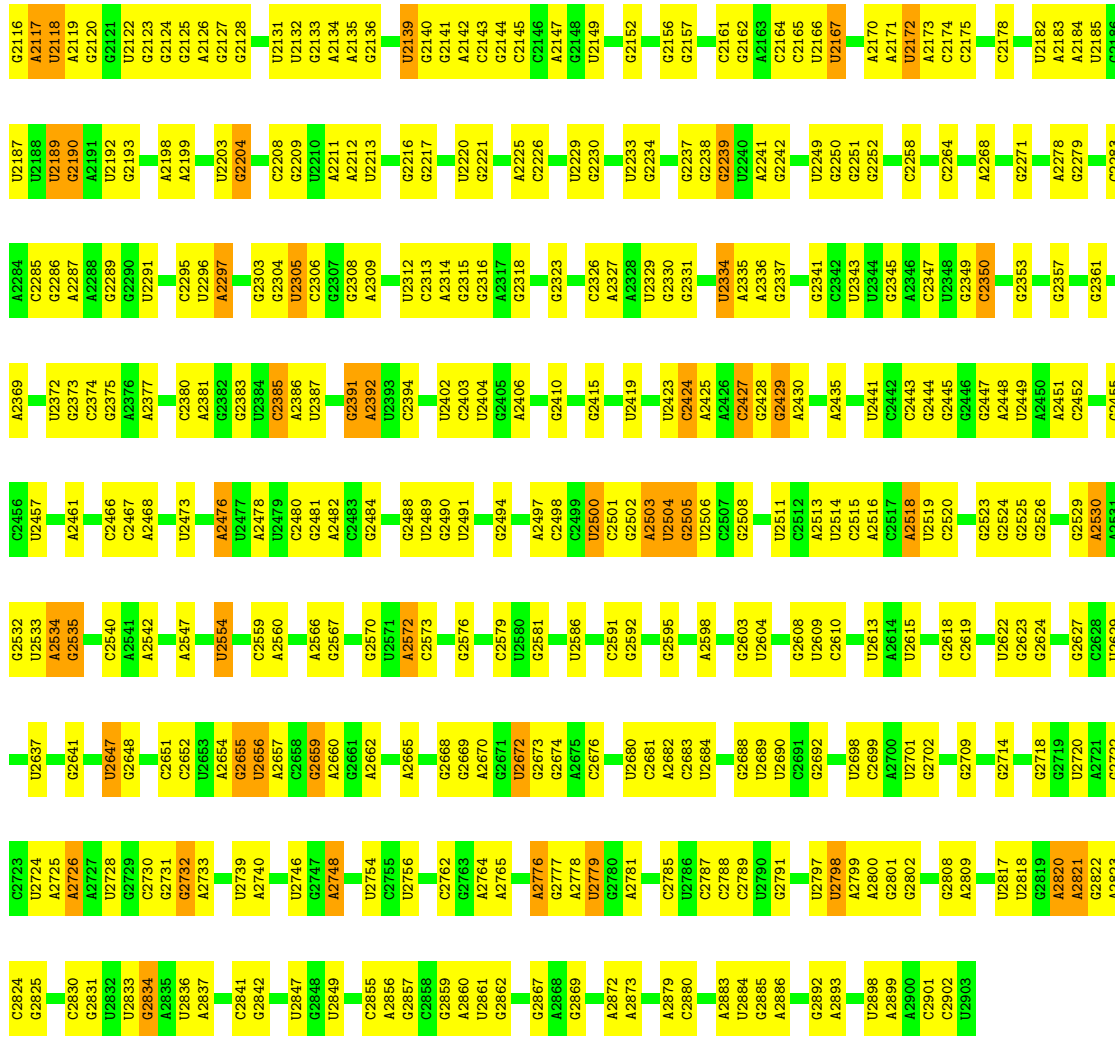




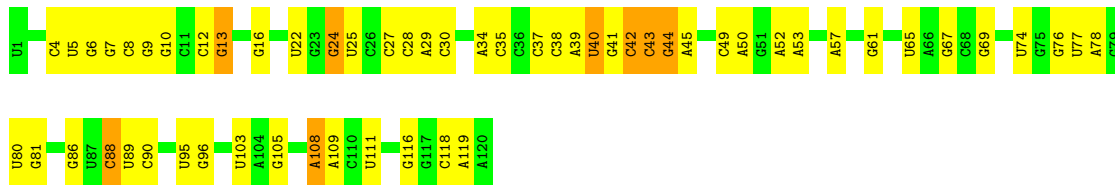
● Molecule 2: 23S ribosomal RNA



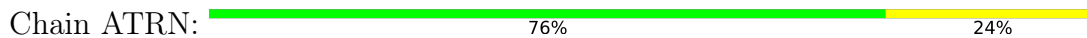




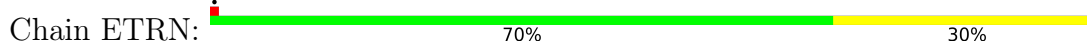
• Molecule 3: 5S ribosomal RNA



• Molecule 4: A-tRNA



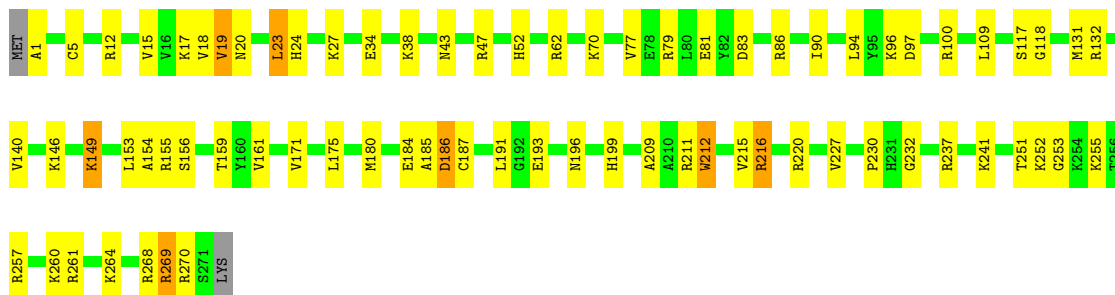
• Molecule 5: E-tRNA





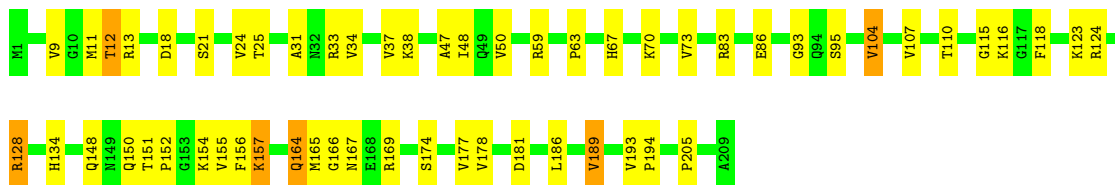
- Molecule 6: 50S ribosomal protein L2

Chain L02: 72% 25%



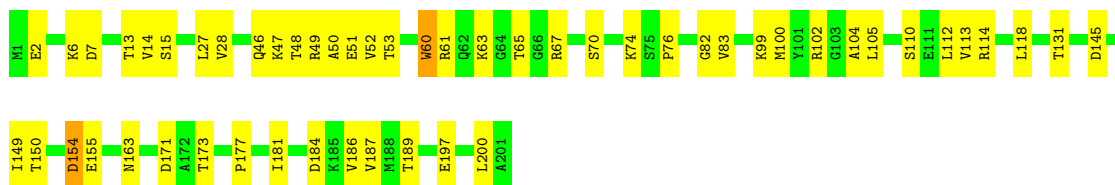
- Molecule 7: 50S ribosomal protein L3

Chain L03: 73% 24%



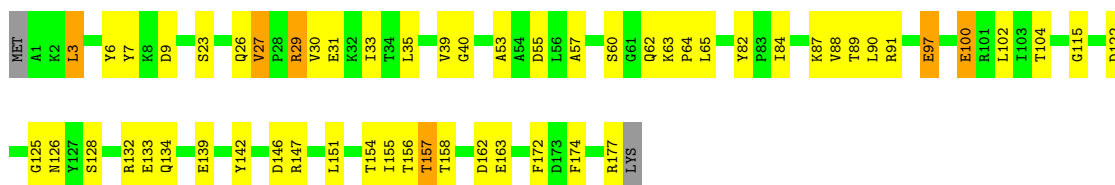
- Molecule 8: 50S ribosomal protein L4

Chain L04: 74% 25%



- Molecule 9: 50S ribosomal protein L5

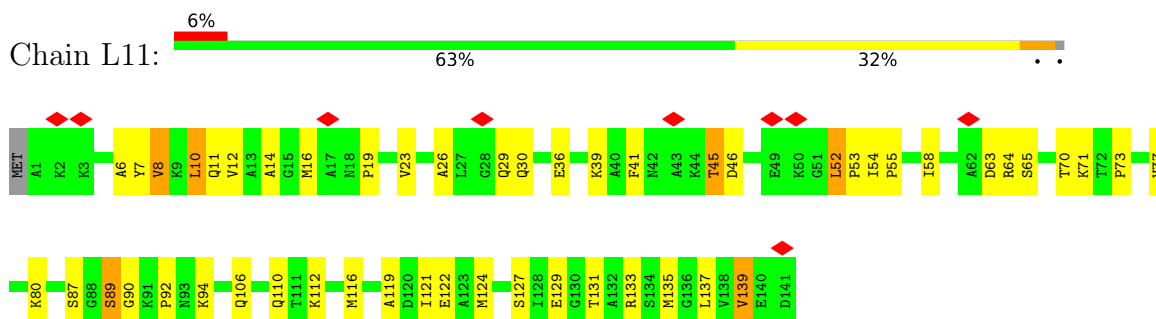
Chain L05: 68% 28%



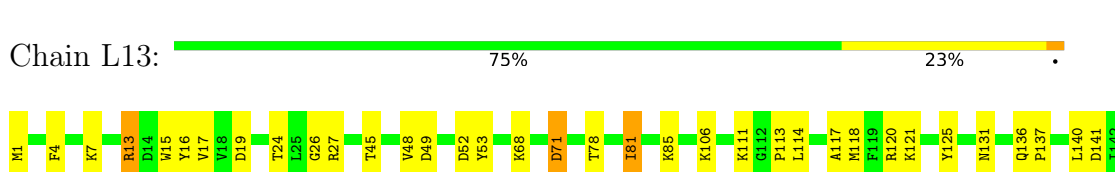
- Molecule 10: 50S ribosomal protein L6



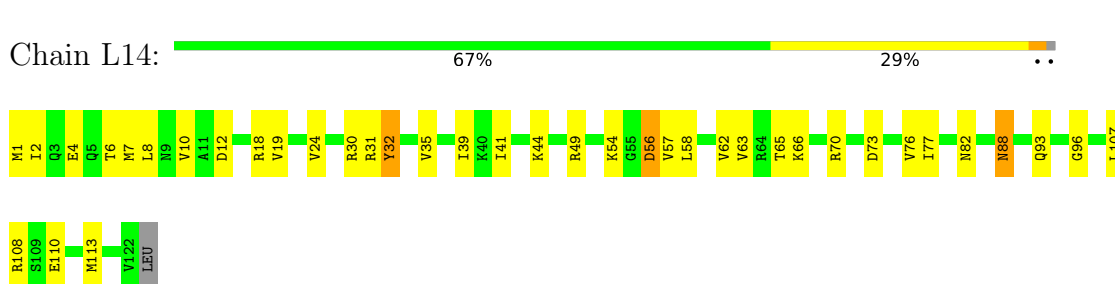
- Molecule 14: 50S ribosomal protein L11



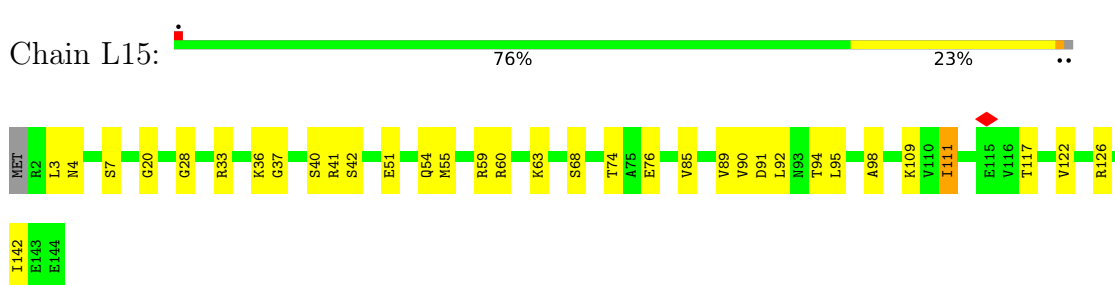
- Molecule 15: 50S ribosomal protein L13



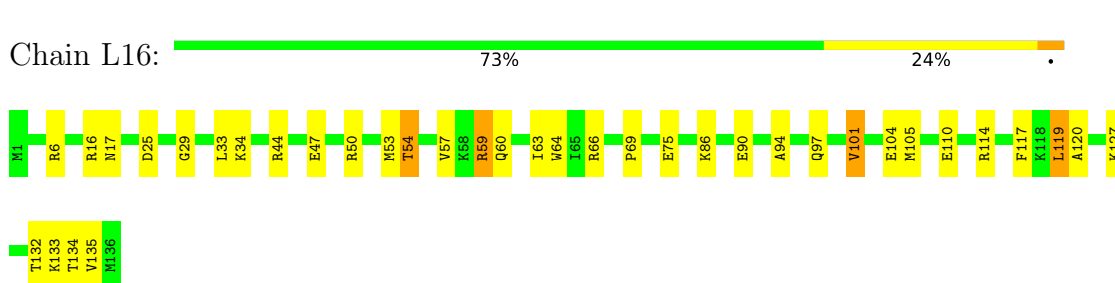
- Molecule 16: 50S ribosomal protein L14




- Molecule 17: 50S ribosomal protein L15



- Molecule 18: 50S ribosomal protein L16




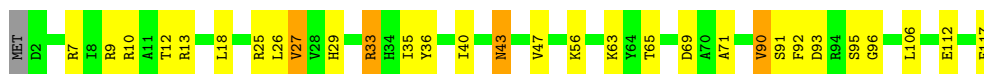
- Molecule 19: Large ribosomal subunit protein bL17

Chain L17:  79% 15% 6%



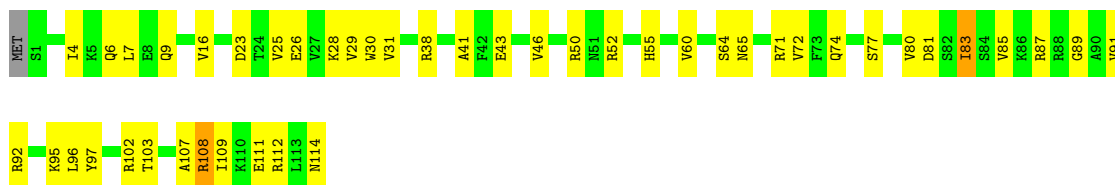
• Molecule 20: 50S ribosomal protein L18

Chain L18:  74% 22%




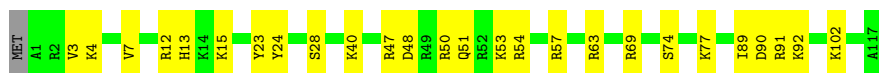
• Molecule 21: 50S ribosomal protein L19

Chain L19:  60% 37%



• Molecule 22: 50S ribosomal protein L20

Chain L20:  77% 22%




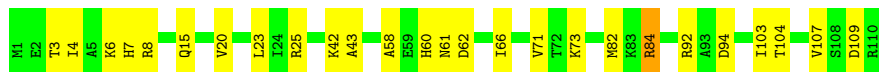
• Molecule 23: Ribosomal protein L21

Chain L21:  67% 31%



• Molecule 24: 50S ribosomal protein L22

Chain L22:  76% 23%

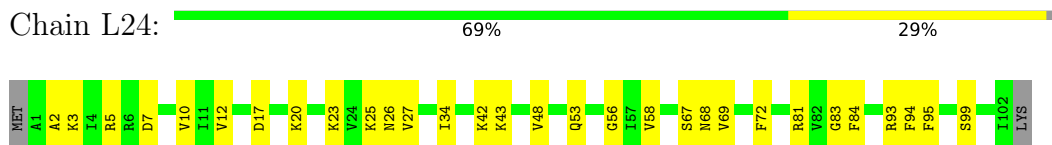


• Molecule 25: 50S ribosomal protein L23

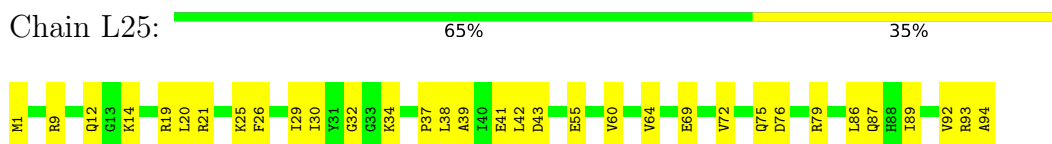
Chain L23:  67% 24% 7%



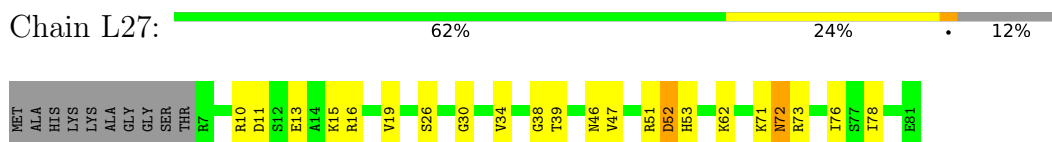
- Molecule 26: 50S ribosomal protein L24



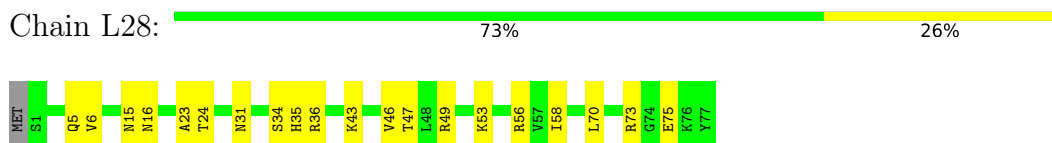
- Molecule 27: 50S ribosomal protein L25



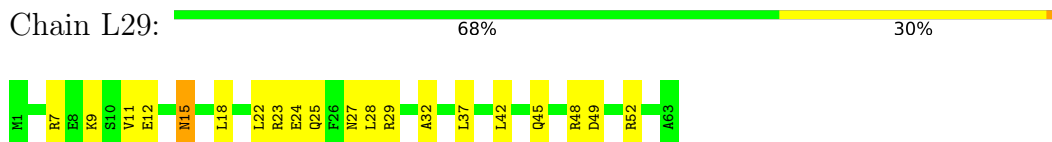
- Molecule 28: 50S ribosomal protein L27



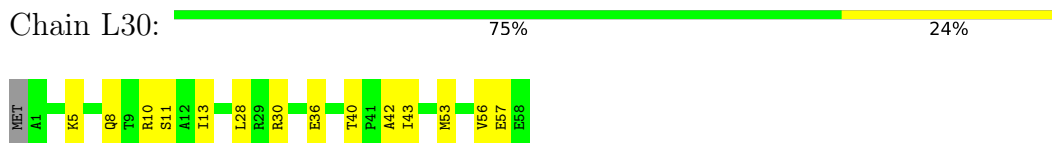
- Molecule 29: 50S ribosomal protein L28



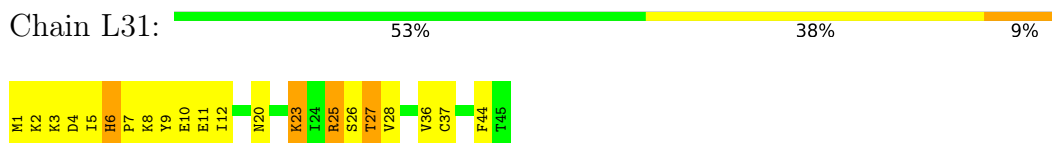
- Molecule 30: 50S ribosomal protein L29



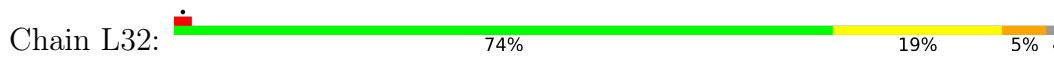
- Molecule 31: Large ribosomal subunit protein uL30



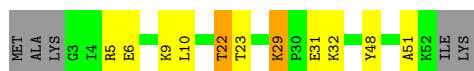
- Molecule 32: Large ribosomal subunit protein bL31



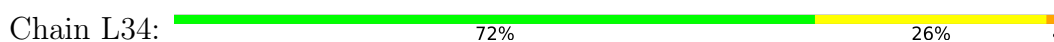
- Molecule 33: 50S ribosomal protein L32



- Molecule 34: Large ribosomal subunit protein bL33



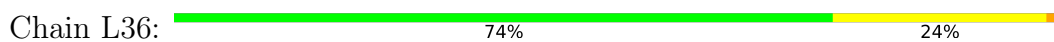
- Molecule 35: 50S ribosomal protein L34



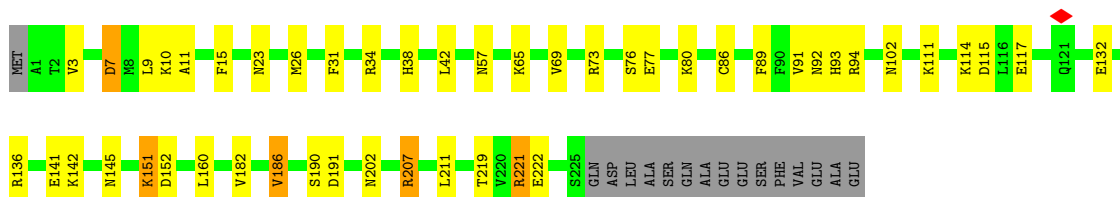
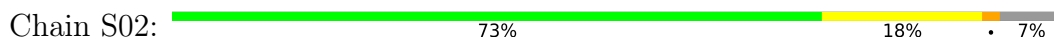
- Molecule 36: 50S ribosomal protein L35



- Molecule 37: 50S ribosomal protein L36

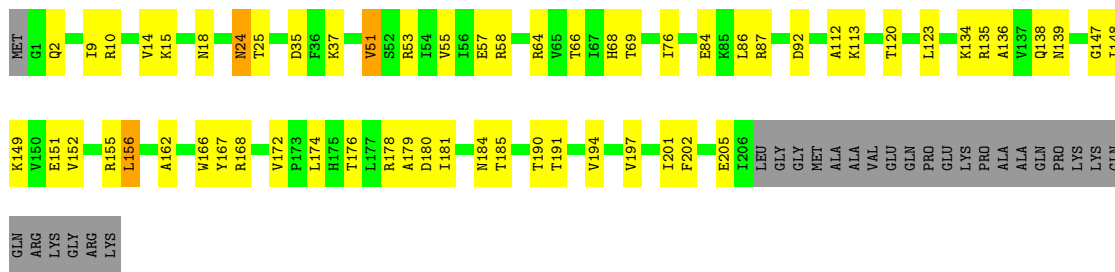


- Molecule 38: 30S ribosomal protein S2

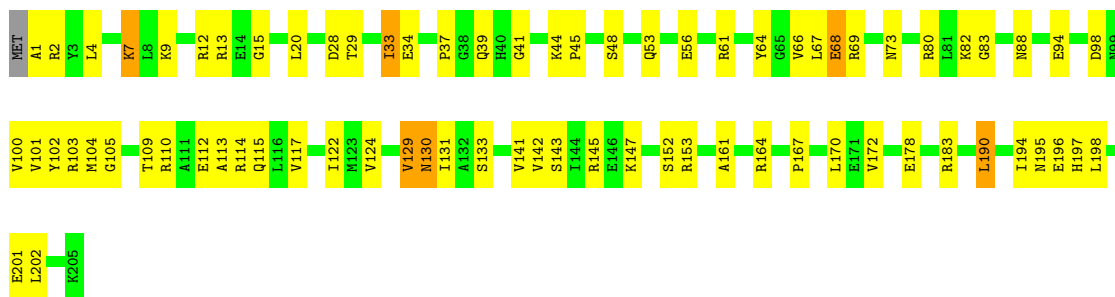


- Molecule 39: 30S ribosomal protein S3

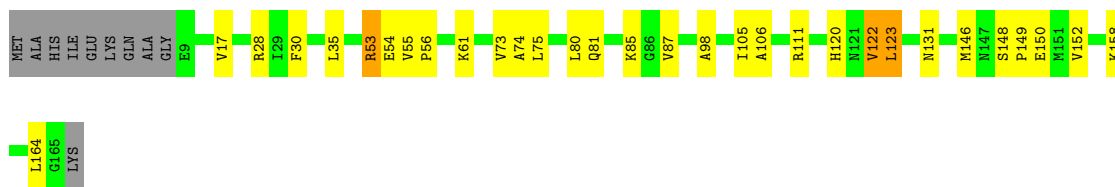
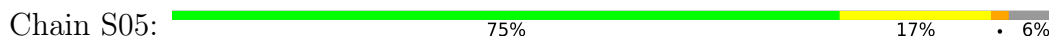




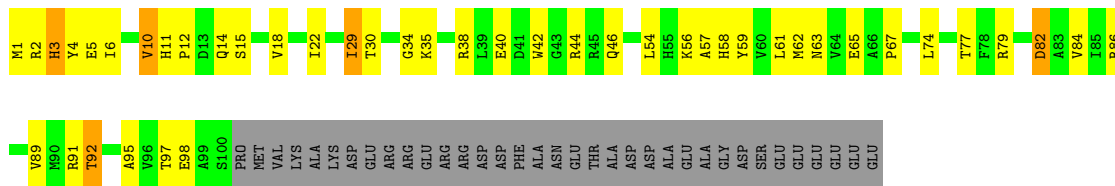
• Molecule 40: 30S ribosomal protein S4



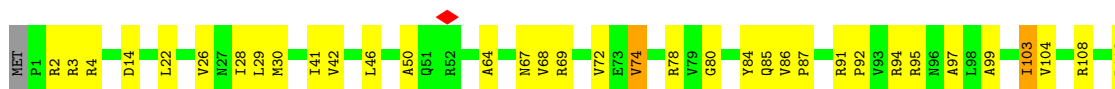
• Molecule 41: 30S ribosomal protein S5

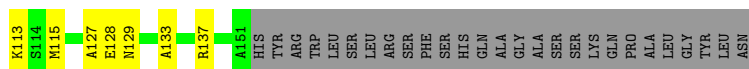


• Molecule 42: 30S ribosomal protein S6

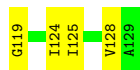
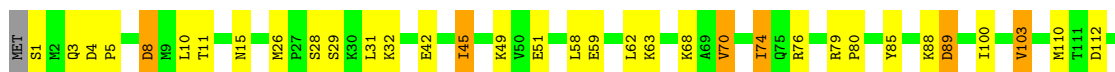


• Molecule 43: 30S ribosomal protein S7

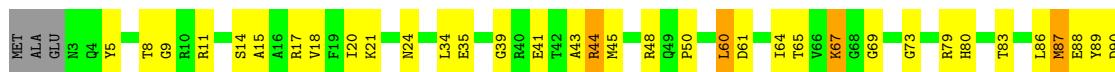




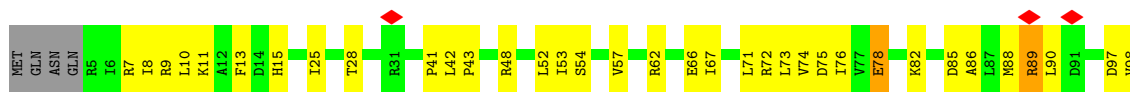
• Molecule 44: 30S ribosomal protein S8



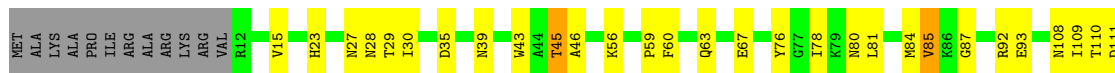
• Molecule 45: Small ribosomal subunit protein uS9



• Molecule 46: 30S ribosomal protein S10

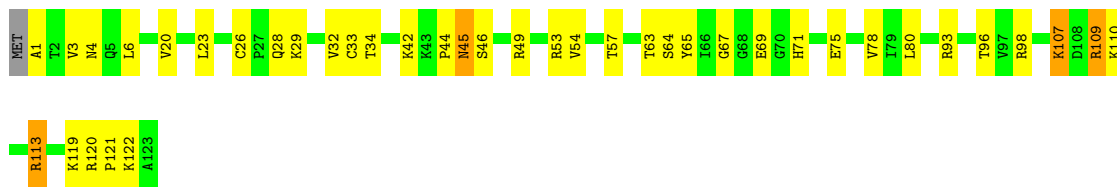


• Molecule 47: 30S ribosomal protein S11

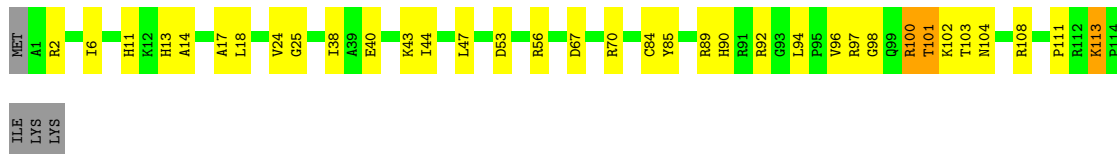


• Molecule 48: 30S ribosomal protein S12





• Molecule 49: 30S ribosomal protein S13



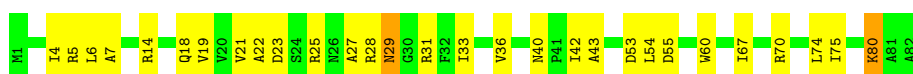
• Molecule 50: Small ribosomal subunit protein uS14



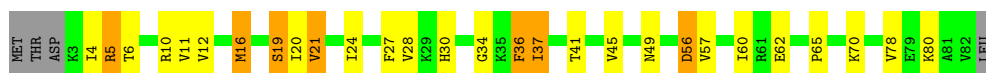
• Molecule 51: Small ribosomal subunit protein uS15



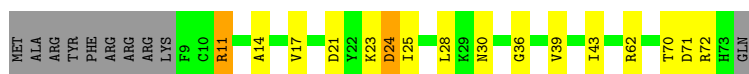
• Molecule 52: 30S ribosomal protein S16



• Molecule 53: Small ribosomal subunit protein uS17



• Molecule 54: 30S ribosomal protein S18



• Molecule 55: 30S ribosomal protein S19



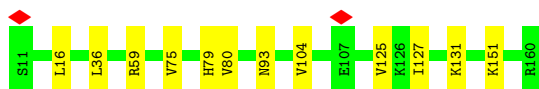
• Molecule 56: 30S ribosomal protein S20



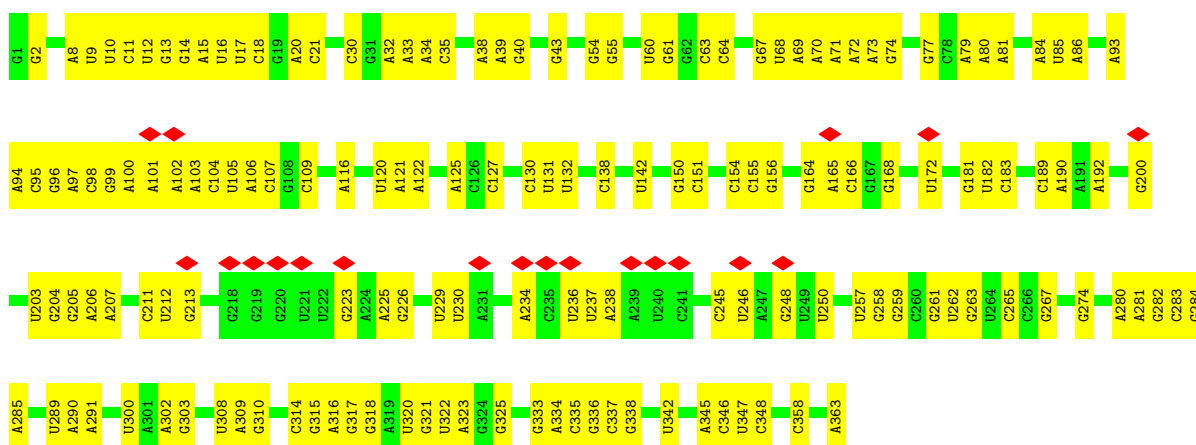
• Molecule 57: 30S ribosomal protein S21



• Molecule 58: SsrA-binding protein



• Molecule 59: TMRN



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	4215	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	29.9	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1100	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	24.205	Depositor
Minimum map value	-12.008	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.736	Depositor
Recommended contour level	3	Depositor
Map size ( $\text{\AA}$ )	487.2, 487.2, 487.2	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.87, 0.87, 0.87	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	16S	0.13	0/36963	0.25	0/57662
2	23S	0.15	0/69796	0.26	0/108888
3	5S	0.14	0/2872	0.28	0/4479
4	ATRN	0.14	0/1810	0.25	0/2820
5	ETRN	0.12	0/1832	0.25	0/2855
6	L02	0.15	0/2121	0.37	2/2852 (0.1%)
7	L03	0.14	0/1586	0.35	0/2134
8	L04	0.12	0/1571	0.31	0/2113
9	L05	0.16	0/1434	0.40	0/1926
10	L06	0.12	0/1343	0.33	0/1816
11	L09	0.14	0/1122	0.36	0/1515
12	L1	0.12	0/1033	0.31	0/1387
13	L10	0.21	0/1001	0.55	3/1350 (0.2%)
14	L11	0.16	0/1046	0.39	0/1410
15	L13	0.13	0/1152	0.28	0/1551
16	L14	0.14	0/947	0.38	0/1268
17	L15	0.14	0/1054	0.40	0/1403
18	L16	0.16	0/1093	0.41	0/1460
19	L17	0.15	0/973	0.43	0/1301
20	L18	0.12	0/902	0.35	0/1209
21	L19	0.13	0/929	0.30	0/1242
22	L20	0.10	0/960	0.26	0/1278
23	L21	0.14	0/829	0.34	0/1107
24	L22	0.12	0/864	0.32	0/1156
25	L23	0.12	0/744	0.30	0/994
26	L24	0.13	0/787	0.39	0/1051
27	L25	0.13	0/766	0.31	0/1025
28	L27	0.12	0/582	0.30	0/769
29	L28	0.12	0/635	0.28	0/848
30	L29	0.10	0/510	0.31	0/677
31	L30	0.12	0/453	0.26	0/605
32	L31	0.24	0/358	0.61	0/480
33	L32	0.13	0/450	0.35	0/599
34	L33	0.13	0/416	0.30	0/554

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	L34	0.11	0/380	0.26	0/498
36	L35	0.17	0/513	0.41	0/676
37	L36	0.11	0/303	0.31	0/397
38	S02	0.13	0/1787	0.32	0/2408
39	S03	0.11	0/1651	0.30	0/2225
40	S04	0.14	0/1665	0.41	0/2227
41	S05	0.17	0/1169	0.46	0/1573
42	S06	0.15	0/835	0.46	0/1128
43	S07	0.13	0/1195	0.38	0/1602
44	S08	0.13	0/989	0.33	0/1326
45	S09	0.14	0/1034	0.41	0/1375
46	S10	0.14	0/796	0.40	0/1077
47	S11	0.14	0/885	0.39	0/1195
48	S12	0.17	0/969	0.45	0/1300
49	S13	0.12	0/892	0.42	0/1193
50	S14	0.14	0/817	0.37	0/1088
51	S15	0.12	0/722	0.39	0/964
52	S16	0.12	0/659	0.34	0/884
53	S17	0.13	0/657	0.38	0/881
54	S18	0.10	0/544	0.30	0/731
55	S19	0.13	0/652	0.33	0/877
56	S20	0.13	0/671	0.35	0/888
57	S21	0.22	0/550	0.61	0/728
58	SMPB	0.15	0/1231	0.41	0/1655
59	TMRN	0.14	0/8681	0.31	0/13532
All	All	0.14	0/171181	0.29	5/256212 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
41	S05	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	L10	54	VAL	N-CA-C	-7.23	105.48	111.91
13	L10	117	LEU	CA-C-N	6.52	134.19	122.13
13	L10	117	LEU	C-N-CA	6.52	134.19	122.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L02	232	GLY	CA-C-N	5.16	131.53	121.41
6	L02	232	GLY	C-N-CA	5.16	131.53	121.41

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
41	S05	120	HIS	Peptide

## 5.2 Too-close contacts [i](#)

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	16S	33012	0	16618	421	0
2	23S	62317	0	31346	767	0
3	5S	2568	0	1303	34	0
4	ATRN	1621	0	0	0	0
5	ETRN	1640	0	0	0	0
6	L02	2082	0	2157	52	0
7	L03	1565	0	1616	44	0
8	L04	1552	0	1619	30	0
9	L05	1410	0	1447	31	0
10	L06	1323	0	1374	27	0
11	L09	1111	0	1148	15	0
12	L1	1026	0	1092	29	0
13	L10	988	0	1025	26	0
14	L11	1032	0	1088	33	0
15	L13	1129	0	1162	27	0
16	L14	938	0	1012	23	0
17	L15	1045	0	1117	22	0
18	L16	1074	0	1157	28	0
19	L17	960	0	1000	14	0
20	L18	892	0	923	20	0
21	L19	917	0	965	33	0
22	L20	947	0	1022	23	0
23	L21	816	0	839	20	0
24	L22	857	0	922	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	L23	738	0	807	10	0
26	L24	779	0	834	19	0
27	L25	753	0	780	18	0
28	L27	575	0	592	15	0
29	L28	625	0	655	11	0
30	L29	509	0	543	14	0
31	L30	449	0	491	8	0
32	L31	351	0	350	15	0
33	L32	444	0	461	10	0
34	L33	409	0	440	5	0
35	L34	377	0	418	10	0
36	L35	504	0	574	13	0
37	L36	302	0	343	7	0
38	S02	1756	0	1787	25	0
39	S03	1624	0	1699	32	0
40	S04	1643	0	1710	50	0
41	S05	1156	0	1199	15	0
42	S06	817	0	808	27	0
43	S07	1181	0	1240	20	0
44	S08	979	0	1034	26	0
45	S09	1022	0	1070	37	0
46	S10	786	0	828	20	0
47	S11	869	0	878	17	0
48	S12	955	0	1019	29	0
49	S13	883	0	944	20	0
50	S14	805	0	847	28	0
51	S15	714	0	737	18	0
52	S16	649	0	666	17	0
53	S17	648	0	691	17	0
54	S18	535	0	552	10	0
55	S19	637	0	665	13	0
56	S20	665	0	714	17	0
57	S21	544	0	579	14	0
58	SMPB	1209	0	0	0	0
59	TMRN	7758	0	0	0	0
All	All	157472	0	98907	1997	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 9.

The worst 5 of 1997 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)
1:16S:978:A:C2	1:16S:1316:G:N2	2.23	1.06
2:23S:1072:C:H42	2:23S:1093:G:N2	1.54	1.04
2:23S:881:G:H1	2:23S:895:U:H3	1.04	0.99
2:23S:2834:G:H21	2:23S:2883:A:N6	1.61	0.99
2:23S:1035:U:H3	2:23S:1120:G:H1	1.09	0.98

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	
6	L02	269/273 (98%)	247 (92%)	22 (8%)	0	100	100
7	L03	207/209 (99%)	196 (95%)	11 (5%)	0	100	100
8	L04	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	59
9	L05	175/179 (98%)	160 (91%)	15 (9%)	0	100	100
10	L06	174/177 (98%)	165 (95%)	9 (5%)	0	100	100
11	L09	147/149 (99%)	132 (90%)	14 (10%)	1 (1%)	18	53
12	L1	130/234 (56%)	123 (95%)	7 (5%)	0	100	100
13	L10	129/165 (78%)	111 (86%)	17 (13%)	1 (1%)	16	50
14	L11	139/142 (98%)	123 (88%)	16 (12%)	0	100	100
15	L13	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
16	L14	120/123 (98%)	111 (92%)	9 (8%)	0	100	100
17	L15	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
18	L16	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
19	L17	118/127 (93%)	104 (88%)	14 (12%)	0	100	100
20	L18	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
21	L19	112/115 (97%)	104 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	L20	115/118 (98%)	115 (100%)	0	0	100	100
23	L21	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	12	45
24	L22	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
25	L23	91/100 (91%)	84 (92%)	7 (8%)	0	100	100
26	L24	100/104 (96%)	89 (89%)	11 (11%)	0	100	100
27	L25	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
28	L27	73/85 (86%)	70 (96%)	3 (4%)	0	100	100
29	L28	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
30	L29	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
31	L30	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
32	L31	43/45 (96%)	35 (81%)	8 (19%)	0	100	100
33	L32	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
34	L33	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
35	L34	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
36	L35	62/65 (95%)	56 (90%)	6 (10%)	0	100	100
37	L36	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
38	S02	223/241 (92%)	215 (96%)	8 (4%)	0	100	100
39	S03	204/233 (88%)	195 (96%)	9 (4%)	0	100	100
40	S04	203/206 (98%)	182 (90%)	21 (10%)	0	100	100
41	S05	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
42	S06	98/135 (73%)	84 (86%)	14 (14%)	0	100	100
43	S07	149/179 (83%)	142 (95%)	7 (5%)	0	100	100
44	S08	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
45	S09	125/130 (96%)	113 (90%)	12 (10%)	0	100	100
46	S10	96/103 (93%)	86 (90%)	10 (10%)	0	100	100
47	S11	114/129 (88%)	107 (94%)	7 (6%)	0	100	100
48	S12	121/124 (98%)	103 (85%)	18 (15%)	0	100	100
49	S13	112/118 (95%)	104 (93%)	8 (7%)	0	100	100
50	S14	98/101 (97%)	92 (94%)	6 (6%)	0	100	100
51	S15	86/89 (97%)	76 (88%)	10 (12%)	0	100	100
52	S16	80/82 (98%)	73 (91%)	7 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	S17	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
54	S18	63/75 (84%)	62 (98%)	1 (2%)	0	100	100
55	S19	77/92 (84%)	70 (91%)	7 (9%)	0	100	100
56	S20	83/87 (95%)	82 (99%)	1 (1%)	0	100	100
57	S21	63/71 (89%)	45 (71%)	18 (29%)	0	100	100
58	SMPB	148/150 (99%)	125 (84%)	22 (15%)	1 (1%)	18	53
All	All	6110/6579 (93%)	5629 (92%)	476 (8%)	5 (0%)	49	80

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	L10	118	ILE
23	L21	54	VAL
8	L04	83	VAL
58	SMPB	79	HIS
11	L09	9	VAL

### 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	
6	L02	216/218 (99%)	204 (94%)	12 (6%)	19	45
7	L03	164/164 (100%)	155 (94%)	9 (6%)	19	45
8	L04	165/165 (100%)	155 (94%)	10 (6%)	17	43
9	L05	148/150 (99%)	127 (86%)	21 (14%)	3	17
10	L06	137/138 (99%)	124 (90%)	13 (10%)	8	29
11	L09	114/114 (100%)	101 (89%)	13 (11%)	5	22
12	L1	110/181 (61%)	89 (81%)	21 (19%)	1	10
13	L10	100/123 (81%)	90 (90%)	10 (10%)	7	27
14	L11	109/110 (99%)	96 (88%)	13 (12%)	5	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	L13	116/116 (100%)	112 (97%)	4 (3%)	32	55
16	L14	103/104 (99%)	90 (87%)	13 (13%)	4	20
17	L15	102/103 (99%)	96 (94%)	6 (6%)	18	44
18	L16	109/109 (100%)	103 (94%)	6 (6%)	19	45
19	L17	100/103 (97%)	97 (97%)	3 (3%)	36	57
20	L18	86/87 (99%)	78 (91%)	8 (9%)	8	30
21	L19	99/100 (99%)	95 (96%)	4 (4%)	28	51
22	L20	89/90 (99%)	87 (98%)	2 (2%)	45	64
23	L21	84/84 (100%)	73 (87%)	11 (13%)	4	19
24	L22	93/93 (100%)	90 (97%)	3 (3%)	34	56
25	L23	80/84 (95%)	69 (86%)	11 (14%)	3	18
26	L24	83/85 (98%)	78 (94%)	5 (6%)	17	44
27	L25	78/78 (100%)	69 (88%)	9 (12%)	5	22
28	L27	57/63 (90%)	54 (95%)	3 (5%)	20	46
29	L28	67/68 (98%)	63 (94%)	4 (6%)	17	44
30	L29	55/55 (100%)	52 (94%)	3 (6%)	19	45
31	L30	48/49 (98%)	44 (92%)	4 (8%)	10	34
32	L31	42/42 (100%)	34 (81%)	8 (19%)	1	10
33	L32	47/48 (98%)	40 (85%)	7 (15%)	3	16
34	L33	45/49 (92%)	41 (91%)	4 (9%)	9	32
35	L34	38/38 (100%)	36 (95%)	2 (5%)	20	46
36	L35	51/52 (98%)	49 (96%)	2 (4%)	28	52
37	L36	34/34 (100%)	32 (94%)	2 (6%)	18	44
38	S02	186/199 (94%)	171 (92%)	15 (8%)	11	35
39	S03	170/190 (90%)	156 (92%)	14 (8%)	10	34
40	S04	172/173 (99%)	155 (90%)	17 (10%)	7	28
41	S05	119/126 (94%)	106 (89%)	13 (11%)	6	24
42	S06	87/116 (75%)	78 (90%)	9 (10%)	7	26
43	S07	124/147 (84%)	112 (90%)	12 (10%)	8	28
44	S08	104/105 (99%)	97 (93%)	7 (7%)	15	41
45	S09	105/107 (98%)	95 (90%)	10 (10%)	8	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	S10	86/90 (96%)	76 (88%)	10 (12%)	5	22
47	S11	89/99 (90%)	77 (86%)	12 (14%)	4	18
48	S12	103/104 (99%)	96 (93%)	7 (7%)	14	41
49	S13	92/96 (96%)	84 (91%)	8 (9%)	9	33
50	S14	83/84 (99%)	79 (95%)	4 (5%)	23	48
51	S15	76/77 (99%)	73 (96%)	3 (4%)	28	52
52	S16	65/65 (100%)	57 (88%)	8 (12%)	4	20
53	S17	74/78 (95%)	64 (86%)	10 (14%)	4	18
54	S18	56/65 (86%)	50 (89%)	6 (11%)	6	24
55	S19	70/79 (89%)	61 (87%)	9 (13%)	4	20
56	S20	65/66 (98%)	62 (95%)	3 (5%)	24	48
57	S21	55/61 (90%)	48 (87%)	7 (13%)	4	20
58	SMPB	125/125 (100%)	114 (91%)	11 (9%)	9	32
All	All	5075/5349 (95%)	4634 (91%)	441 (9%)	12	33

5 of 441 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	L32	21	LEU
40	S04	141	VAL
58	SMPB	127	ILE
53	S17	21	VAL
34	L33	29	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
12	L1	57	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	16S	1538/1539 (99%)	251 (16%)	5 (0%)
2	23S	2902/2903 (99%)	561 (19%)	12 (0%)
3	5S	119/120 (99%)	22 (18%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	ATRN	75/76 (98%)	18 (24%)	1 (1%)
5	ETRN	76/77 (98%)	23 (30%)	0
59	TMRN	362/363 (99%)	150 (41%)	13 (3%)
All	All	5072/5078 (99%)	1025 (20%)	32 (0%)

5 of 1025 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	16S	4	U
1	16S	6	G
1	16S	9	G
1	16S	22	G
1	16S	32	A

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
59	TMRN	308	U
59	TMRN	314	C
2	23S	1730	C
2	23S	1020	A
59	TMRN	322	U

#### 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](#)

There are no ligands in this entry.

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

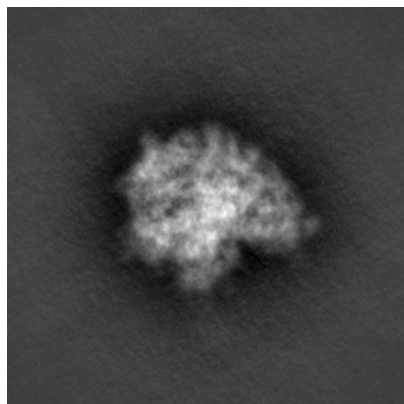
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43490. These allow visual inspection of the internal detail of the map and identification of artifacts.

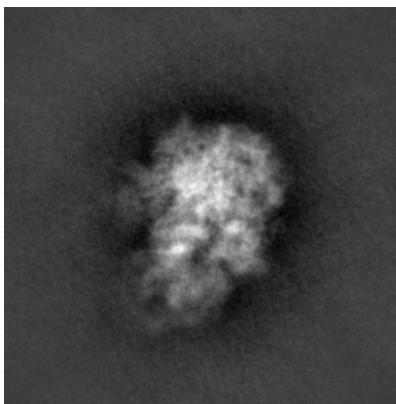
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

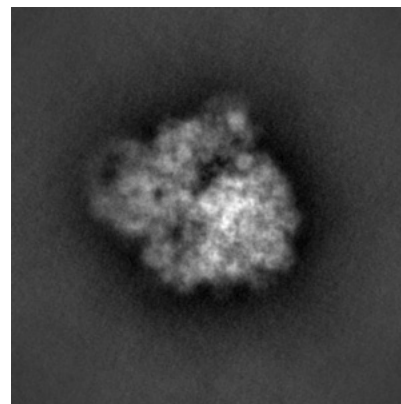
#### 6.1.1 Primary map



X

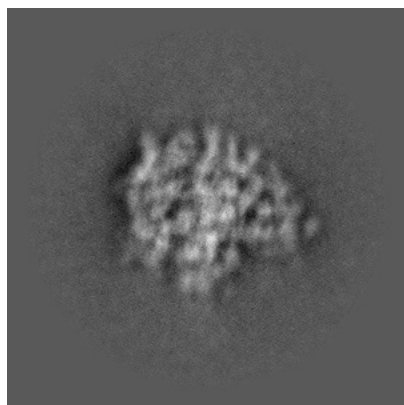


Y

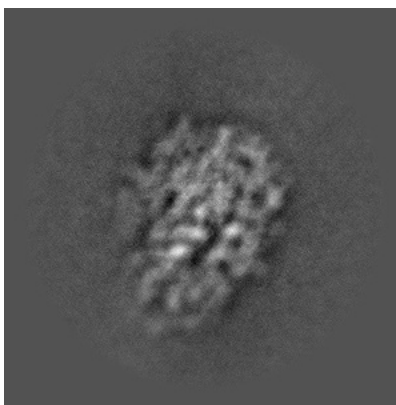


Z

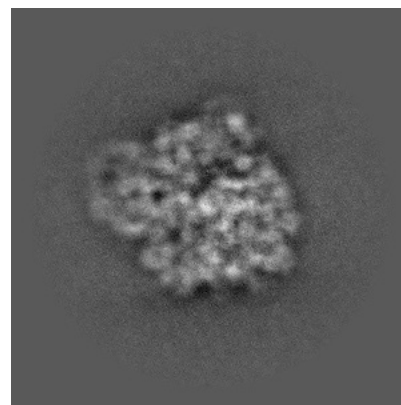
#### 6.1.2 Raw map



X



Y

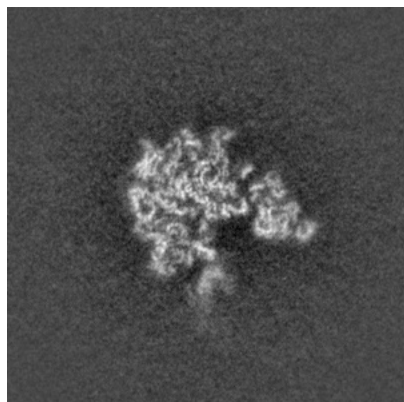


Z

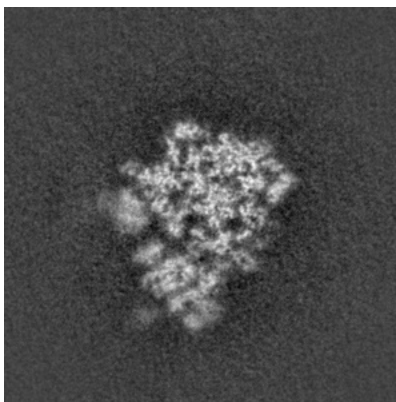
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

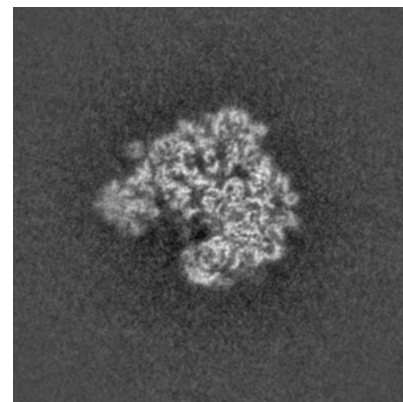
### 6.2.1 Primary map



X Index: 280

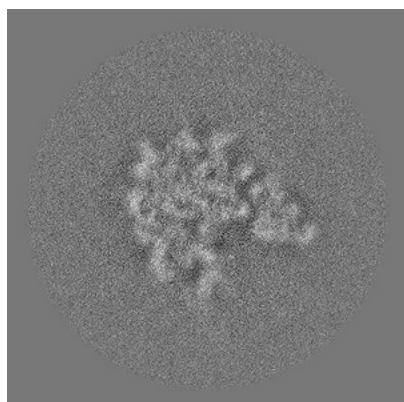


Y Index: 280

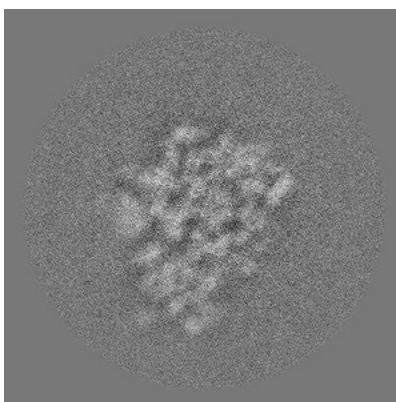


Z Index: 280

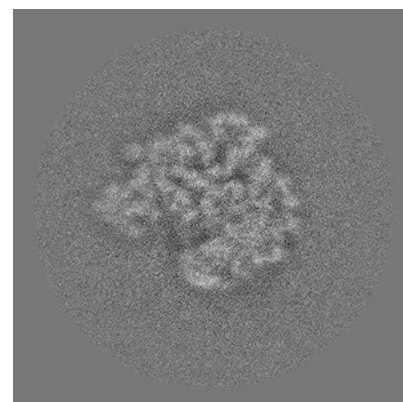
### 6.2.2 Raw map



X Index: 280



Y Index: 280

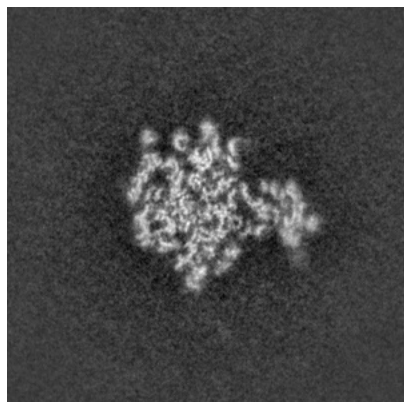


Z Index: 280

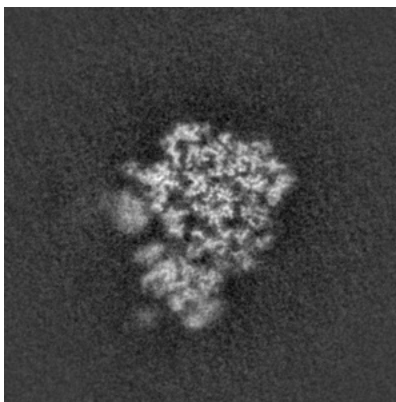
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

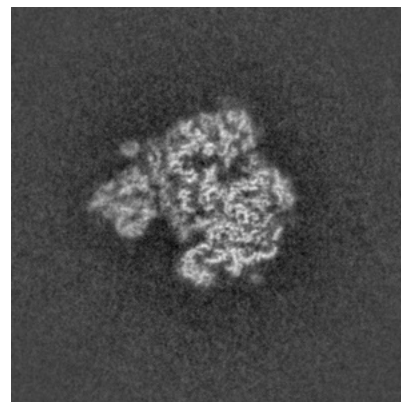
### 6.3.1 Primary map



X Index: 309

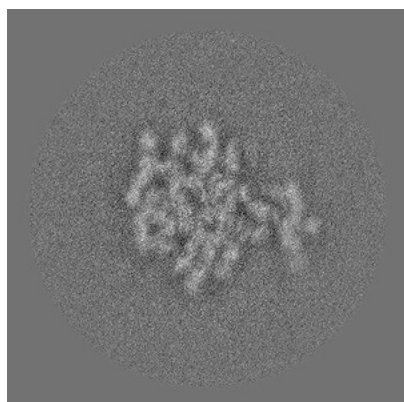


Y Index: 283

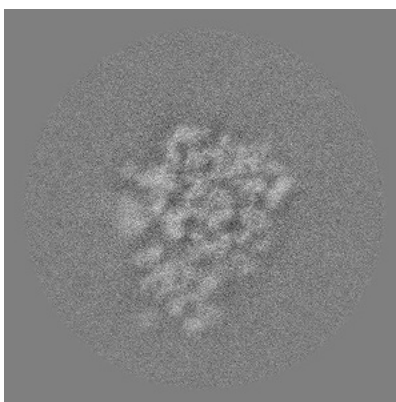


Z Index: 273

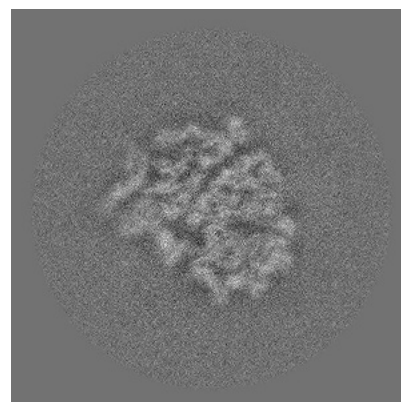
### 6.3.2 Raw map



X Index: 310



Y Index: 281

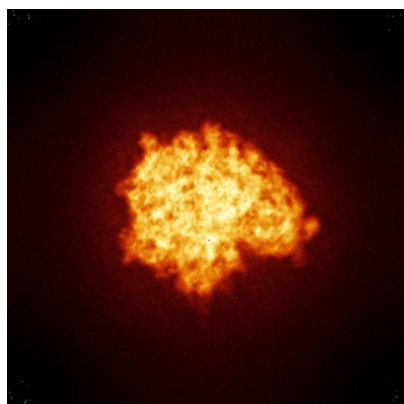


Z Index: 301

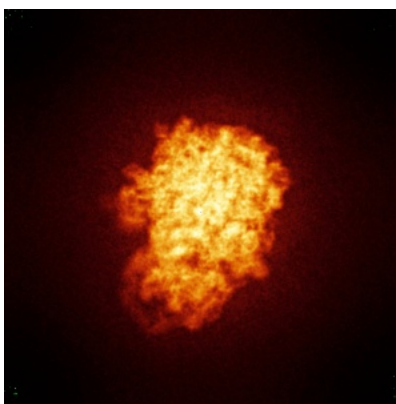
The images above show the largest variance slices of the map in three orthogonal directions.

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

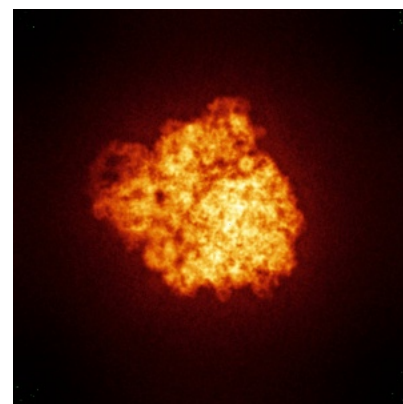
### 6.4.1 Primary map



X

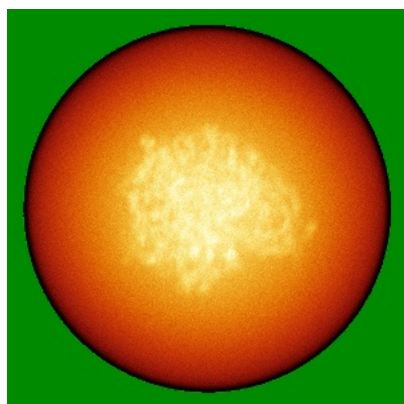


Y

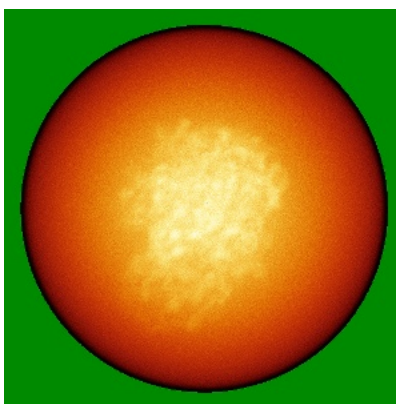


Z

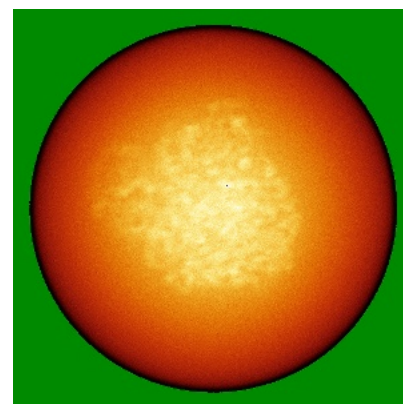
### 6.4.2 Raw map



X



Y

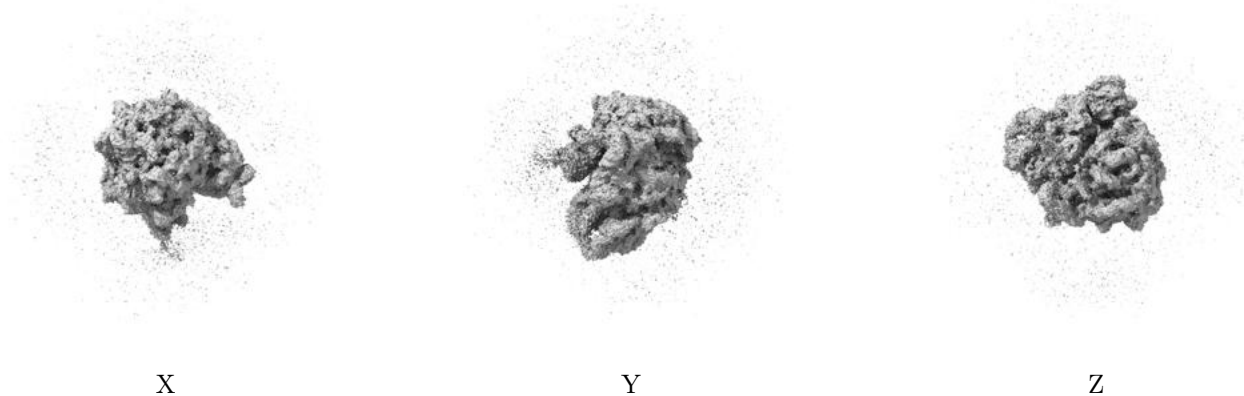


Z

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.

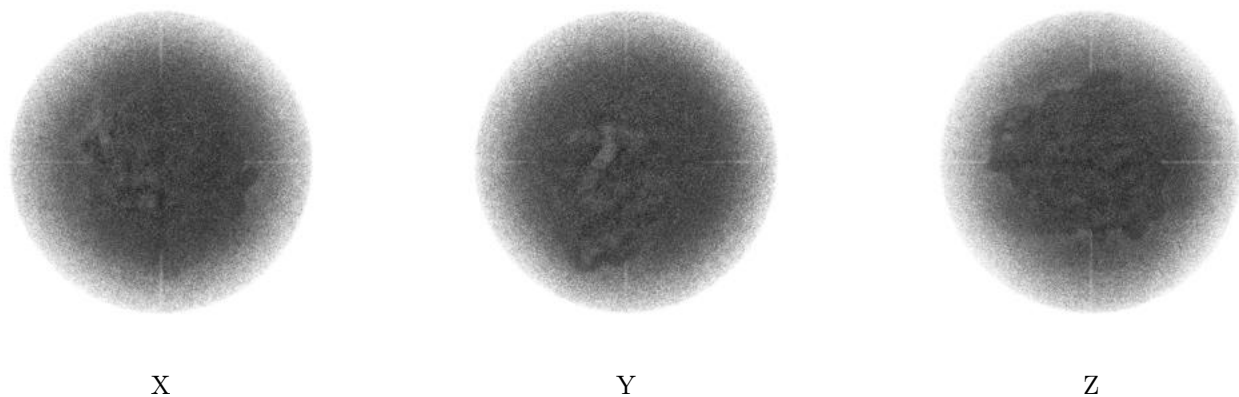
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

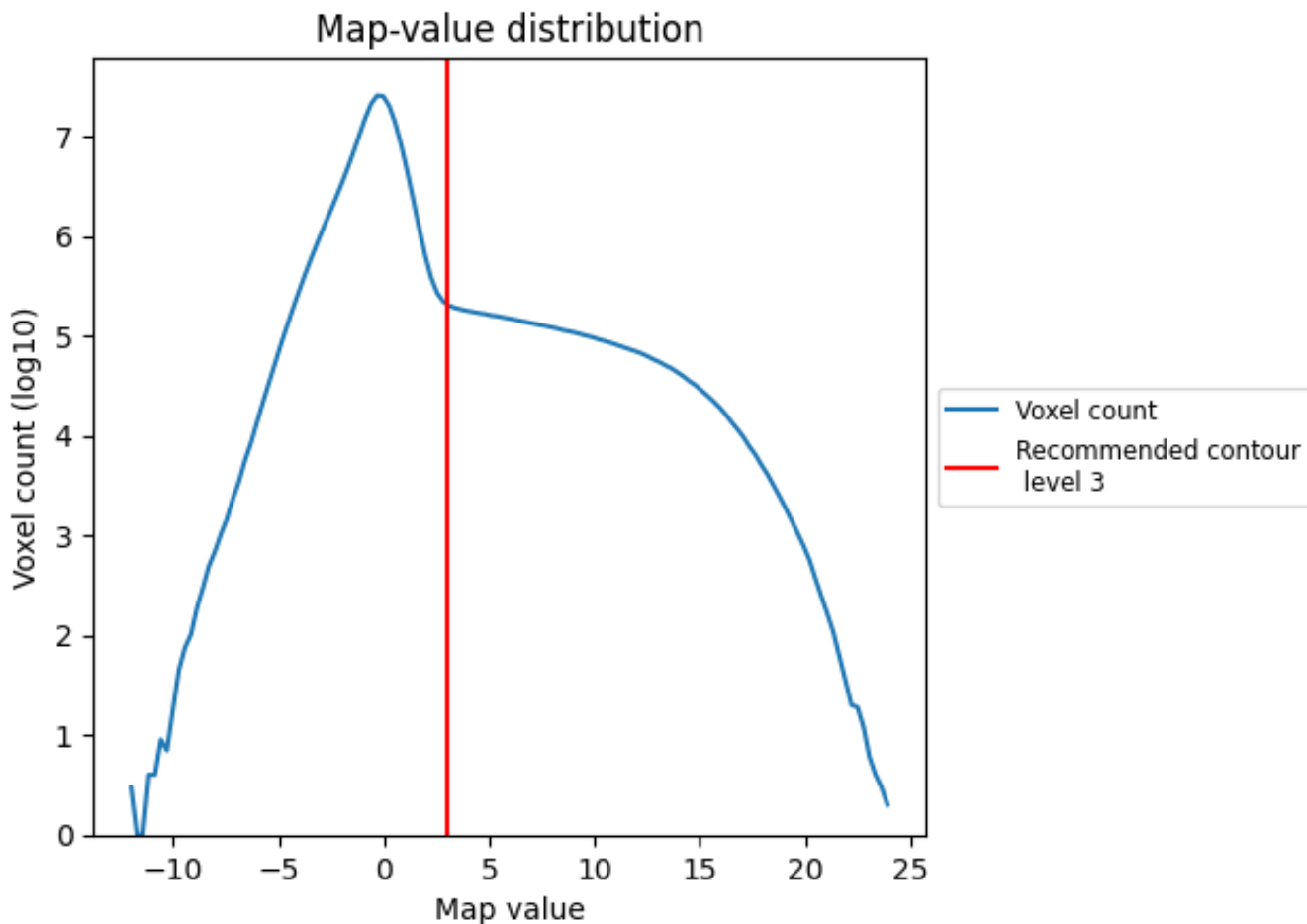
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

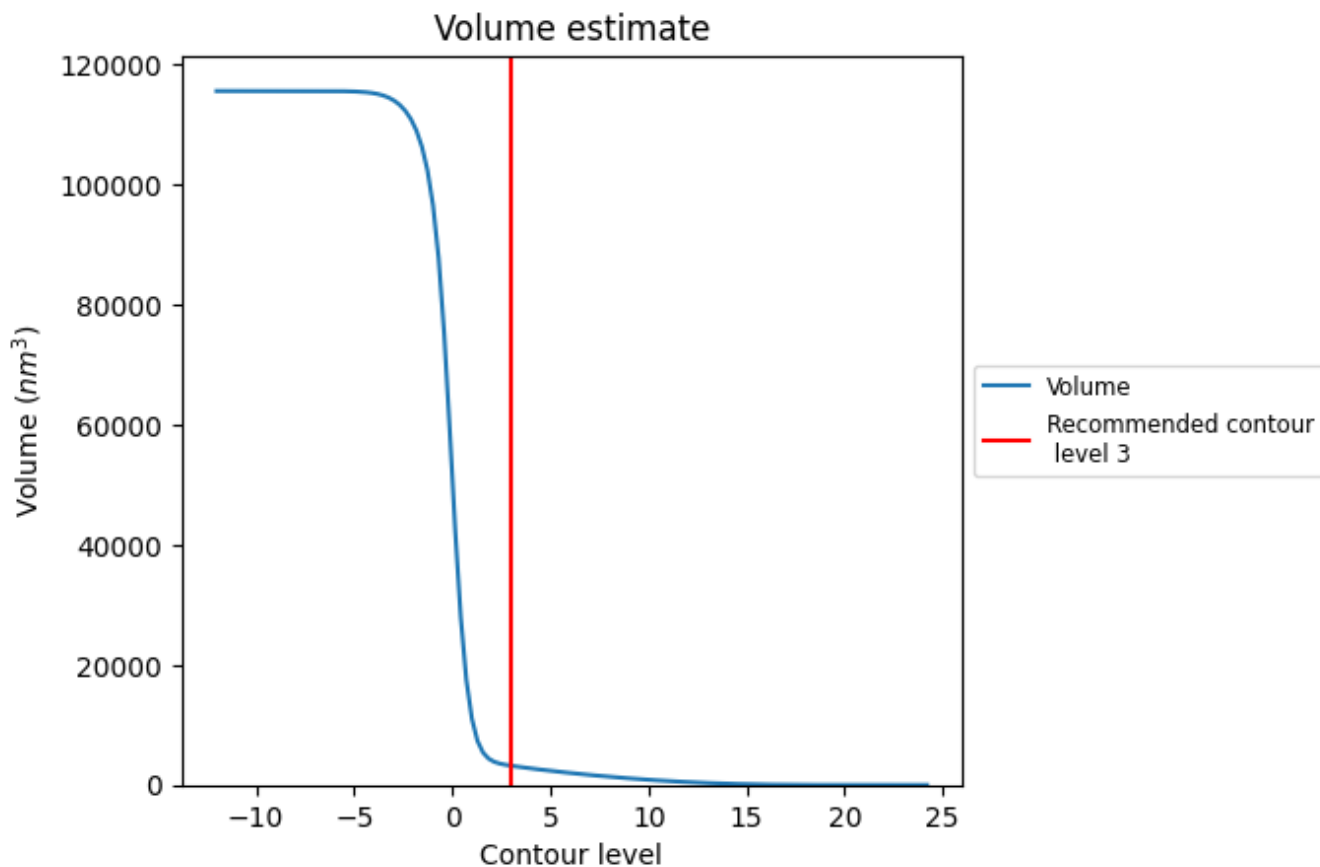
This section contains the results of statistical analysis of the map.

### 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.

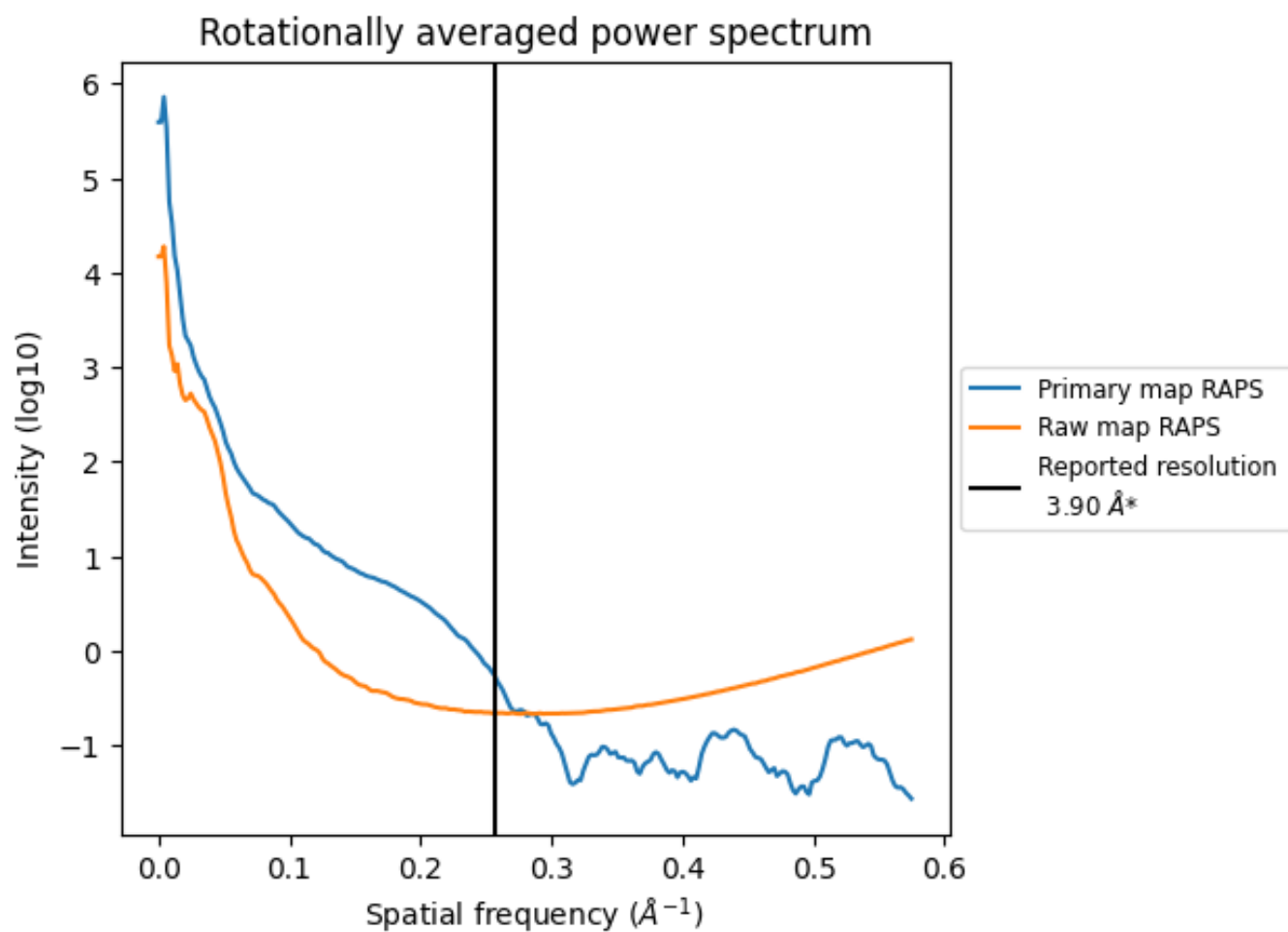
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 3206  $\text{nm}^3$ ; this corresponds to an approximate mass of 2896 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

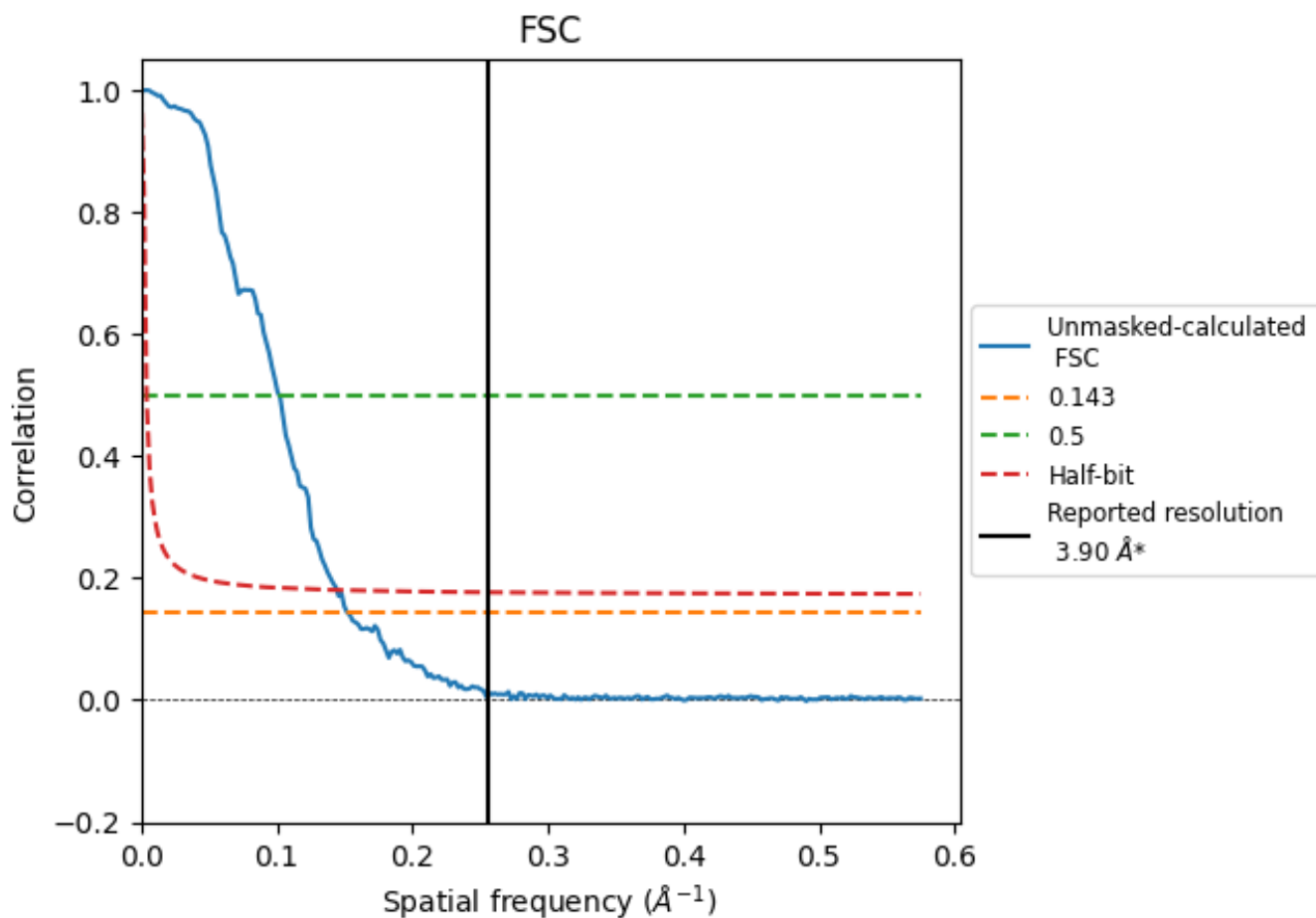


\*Reported resolution corresponds to spatial frequency of 0.256 Å<sup>-1</sup>

## 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 0.256 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

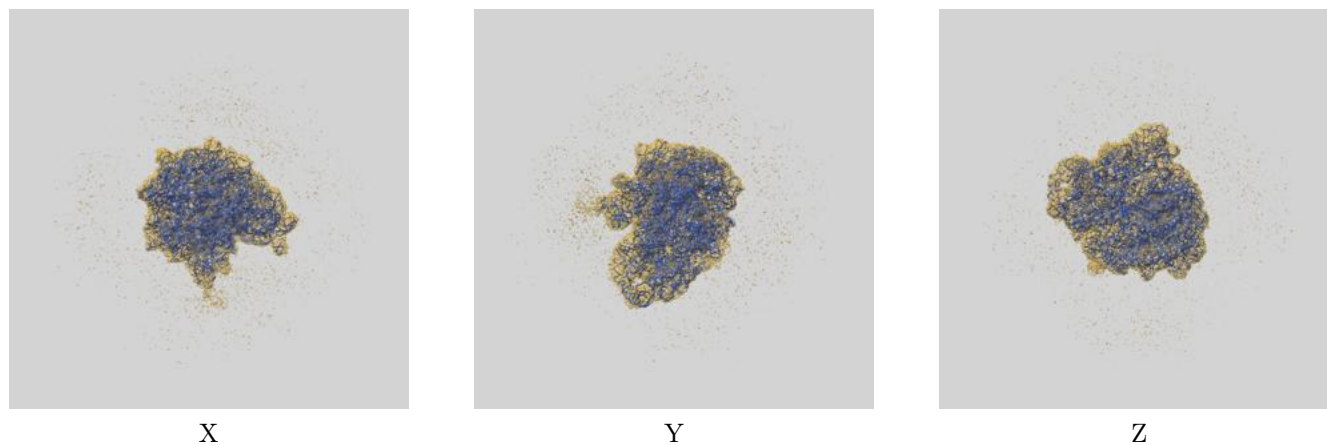
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.58	9.84	6.93

\*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 6.58 differs from the reported value 3.9 by more than 10 %

## 9 Map-model fit [i](#)

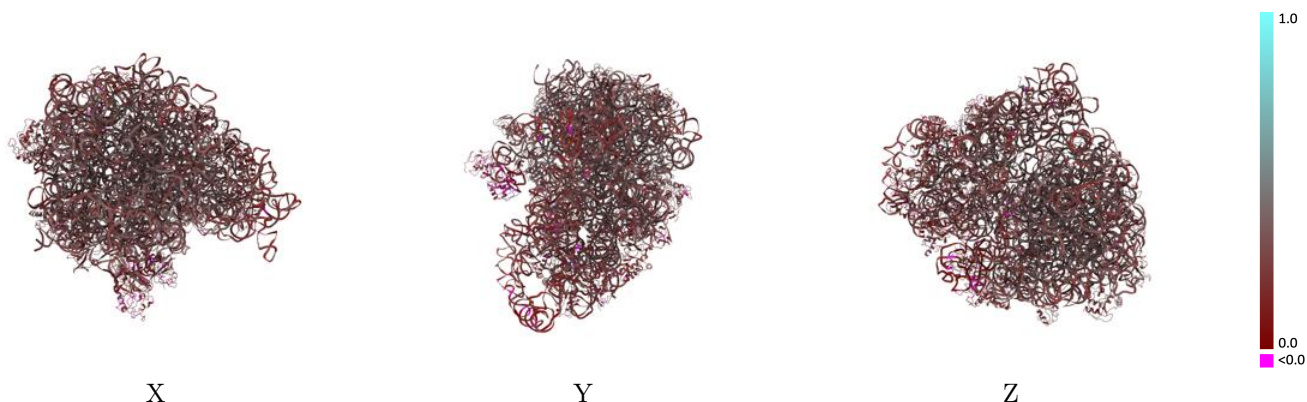
This section contains information regarding the fit between EMDB map EMD-43490 and PDB model 8VS9. Per-residue inclusion information can be found in section [3](#) on page [15](#).

### 9.1 Map-model overlay [i](#)



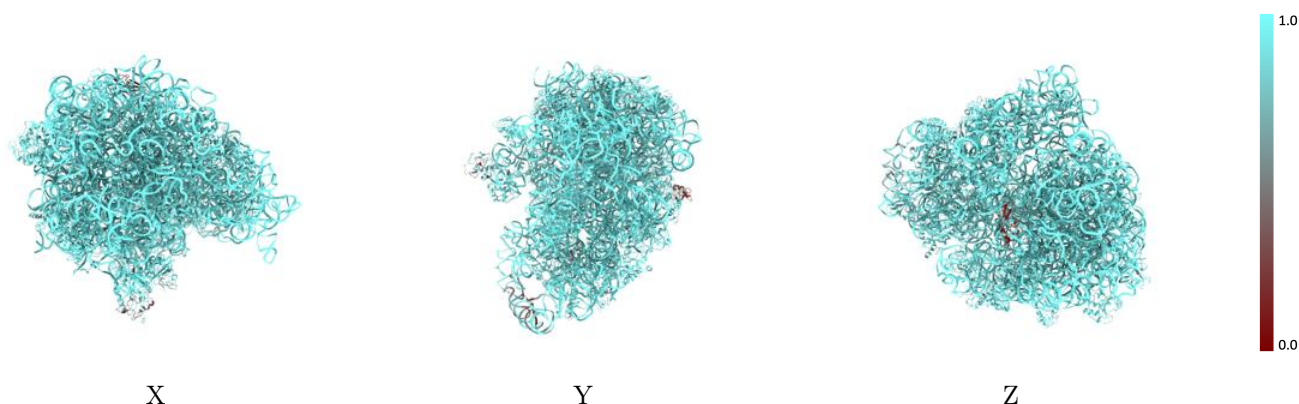
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



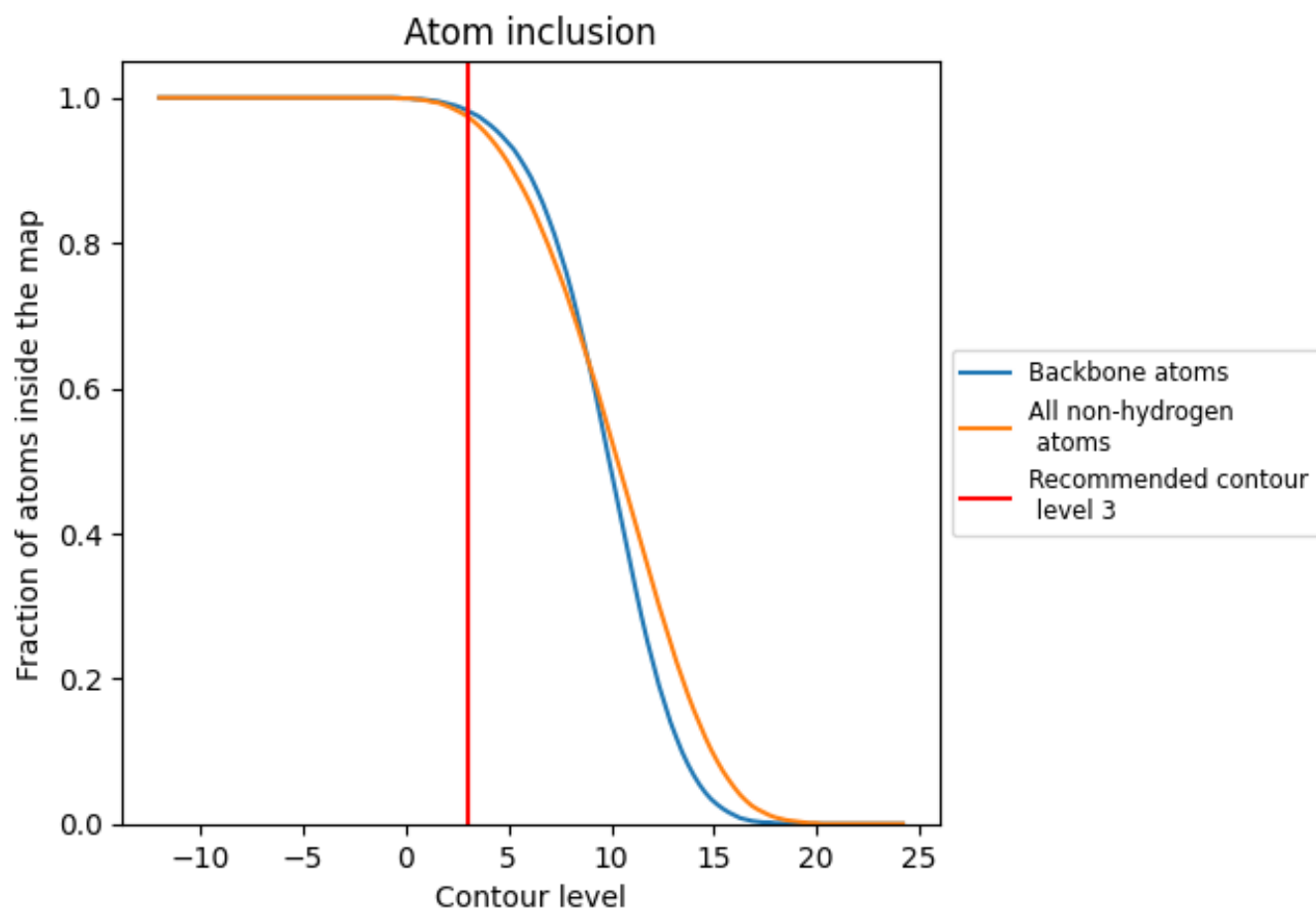
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9740	 0.2890
16S	 0.9980	 0.2900
23S	 0.9980	 0.3210
5S	 0.9980	 0.2870
ATRN	 0.9920	 0.2820
ETRN	 0.9500	 0.1740
L02	 0.9720	 0.3340
L03	 0.9770	 0.3090
L04	 0.9590	 0.2930
L05	 0.9640	 0.2280
L06	 0.9740	 0.2880
L09	 0.4580	 0.2230
L1	 0.9010	 0.1460
L10	 0.7180	 0.1410
L11	 0.8470	 0.1360
L13	 0.9760	 0.3180
L14	 0.9320	 0.3300
L15	 0.9680	 0.3120
L16	 0.9620	 0.3090
L17	 0.9760	 0.2980
L18	 0.9880	 0.2670
L19	 0.9480	 0.3130
L20	 0.9800	 0.3000
L21	 0.9720	 0.3070
L22	 0.9430	 0.3060
L23	 0.9560	 0.2980
L24	 0.9540	 0.2860
L25	 0.9730	 0.2880
L27	 0.9890	 0.3040
L28	 0.9670	 0.3000
L29	 0.9800	 0.2510
L30	 0.9680	 0.3120
L31	 0.9430	 0.1960
L32	 0.9490	 0.3250
L33	 0.9650	 0.2830



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Chain	Atom inclusion	Q-score
L34	 0.9860	 0.3280
L35	 0.9820	 0.3160
L36	 0.9970	 0.3060
S02	 0.9220	 0.2510
S03	 0.9530	 0.2710
S04	 0.9740	 0.2180
S05	 0.9670	 0.3000
S06	 0.9360	 0.2690
S07	 0.9150	 0.2310
S08	 0.9640	 0.2840
S09	 0.9630	 0.2210
S10	 0.9150	 0.2380
S11	 0.9460	 0.2980
S12	 0.9490	 0.2890
S13	 0.9510	 0.2110
S14	 0.9770	 0.2270
S15	 0.9740	 0.2700
S16	 0.9830	 0.2650
S17	 0.9640	 0.2630
S18	 0.9770	 0.2760
S19	 0.9920	 0.2220
S20	 0.9890	 0.2310
S21	 0.9070	 0.2460
SMPB	 0.8990	 0.2520
TMRN	 0.8820	 0.1840