



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2026 – 12:39 AM EDT

PDB ID : 9N2C / pdb_00009n2c
EMDB ID : EMD-48831
Title : Impacts of ribosomal RNA sequence variation on gene expression and phenotype: Cryo-EM structure of the rrsH ribosome (HBB-70S)
Authors : Welfer, G.A.; Brady, R.A.; Natchiar, S.K.; Watson, Z.L.; Rundlet, E.J.; Alejo, J.L.; Singh, A.P.; Mishra, N.K.; Altman, R.B.; Blanchard, S.C.
Deposited on : 2025-01-28
Resolution : 2.40 Å(reported)
Based on initial model : 7N1P

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:

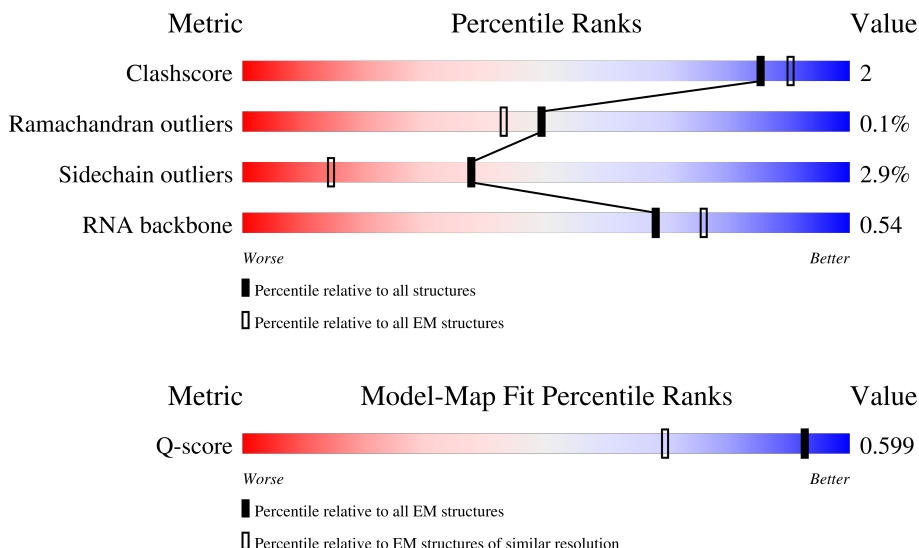
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 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.



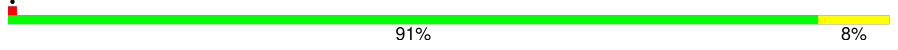
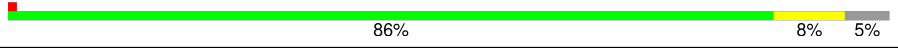
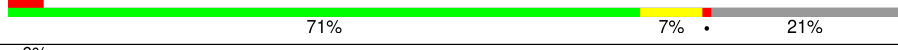
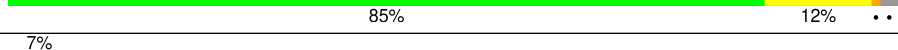
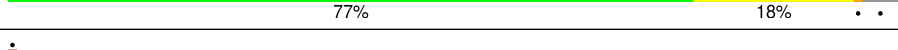
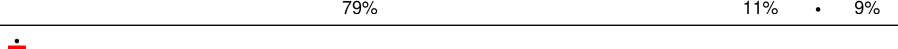
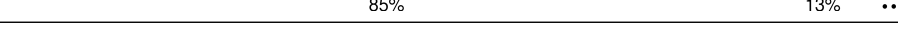
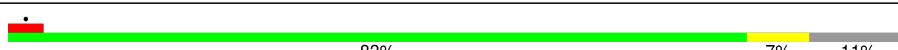
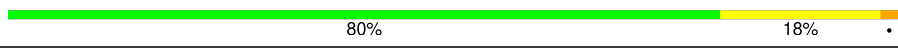
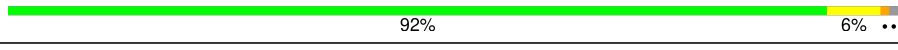
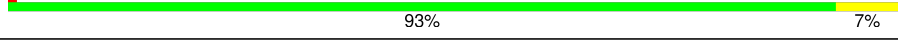
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5628 (1.90 - 2.90)

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	16	1542	 6% 78% 20% 5%
2	SB	241	 6% 83% 11% 5%

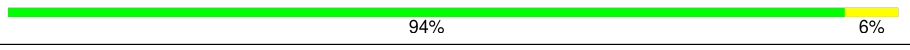
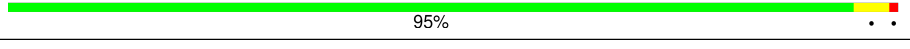
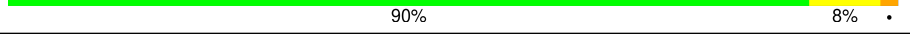
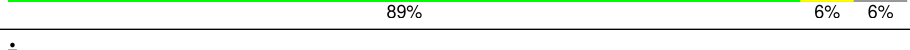
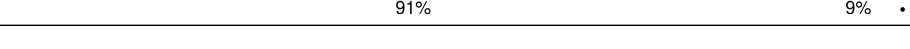
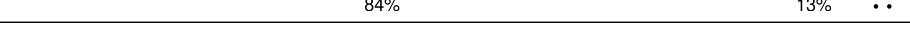
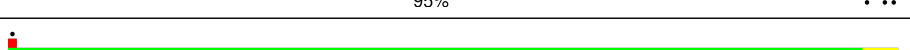
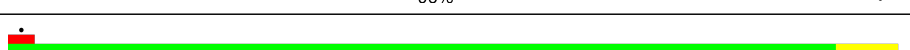
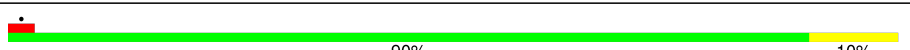
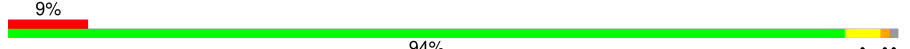
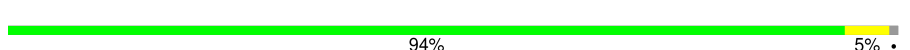
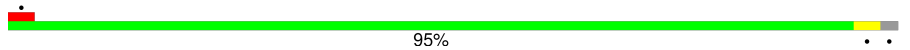
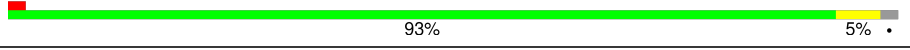
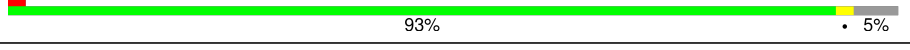
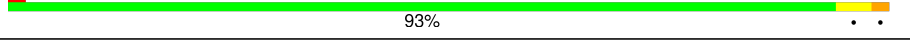
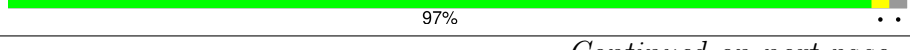
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Mol	Chain	Length	Quality of chain
3	SC	233	
4	SD	206	
5	SE	167	
6	SF	135	
7	SG	179	
8	SH	130	
9	SI	130	
10	SJ	103	
11	SK	129	
12	SL	124	
13	SM	118	
14	SN	101	
15	SO	89	
16	SP	82	
17	SQ	84	
18	SR	75	
19	SS	92	
20	ST	87	
21	SU	71	
22	mR	60	
23	23	2904	
24	5	120	
25	LB	273	
26	LC	209	
27	LD	201	

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Mol	Chain	Length	Quality of chain
28	LE	179	
29	LF	177	
30	LI	149	
31	LM	142	
32	LN	123	
33	LO	144	
34	LP	136	
35	LQ	127	
36	LR	117	
37	LS	115	
38	LT	118	
39	LU	103	
40	LV	110	
41	LW	100	
42	LX	104	
43	LY	94	
44	La	85	
45	Lb	78	
46	Lc	63	
47	Ld	59	
48	Le	70	
49	Lf	57	
50	Lg	55	
51	Lh	46	
52	Li	65	

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Mol	Chain	Length	Quality of chain
53	Lj	38	84% 16%
54	Pt	77	82% 16%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 142570 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 (rRNA) from the rrnH operon.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	16	1542	Total	C	N	O	P	0	0
			33087	14765	6058	10722	1542		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SB	229	Total	C	N	O	S	0	0
			1787	1129	320	330	8		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SC	212	Total	C	N	O	S	0	0
			1658	1049	311	294	4		

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SE	158	Total	C	N	O	S	0	0
			1166	725	220	215	6		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SF	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SG	156	Total	C	N	O	S	1	0
			1244	778	241	221	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SJ	99	Total	C	N	O	S	0	0
			795	498	152	144	1		

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SK	118	Total	C	N	O	S	1	0
			895	551	178	163	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SK	119	IAS	ASN	conflict	UNP P0A7R9

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SL	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SM	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SO	88	Total	C	N	O	S	0	0
			713	439	144	129	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called 30S ribosomal protein S17.

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

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SR	67	Total	C	N	O	S	0	0
			555	351	106	97	1		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SS	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	ST	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SU	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 22 is a RNA chain called Synthetic messenger RNA (mRNA) 60 bp in length.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	mR	18	Total	C	N	O	P	0	0
			390	174	74	124	18		

- Molecule 23 is a RNA chain called 23S ribosomal RNA (rRNA) from the rrnB operon.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	23	2768	Total	C	N	O	P	0	0
			59447	26525	10946	19208	2768		

- Molecule 24 is a RNA chain called 5S large subunit ribosomal RNA of the H operon.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	5	120	Total	C	N	O	P	0	0
			2572	1145	470	837	120		

- Molecule 25 is a protein called 50S ribosomal protein L2.

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

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LC	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 27 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LE	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LF	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 30 is a protein called 50S ribosomal protein L9.

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

- Molecule 31 is a protein called 50S ribosomal protein L13.

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

- Molecule 32 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LN	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LO	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 34 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LP	136	Total	C	N	O	S	1	0
			1085	692	209	178	6		

- Molecule 35 is a protein called 50S ribosomal protein L17.

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

- Molecule 36 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	LR	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 37 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LS	113	Total	C	N	O	S	0	0
			908	570	177	160	1		

- Molecule 38 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	LT	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 39 is a protein called 50S ribosomal protein L21.

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

- Molecule 40 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 41 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LW	95	Total	C	N	O	S	0	0
			757	479	141	135	2		

- Molecule 42 is a protein called 50S ribosomal protein L24.

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

- Molecule 43 is a protein called 50S ribosomal protein L25.

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

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	La	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 45 is a protein called 50S ribosomal protein L28.

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

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lc	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 47 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 48 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Le	68	Total	C	N	O	S	0	0
			533	330	101	96	6		

- Molecule 49 is a protein called 50S ribosomal protein L32.

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

- Molecule 50 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lg	52	Total	C	N	O	S	0	0
			426	275	78	73			

- Molecule 51 is a protein called 50S ribosomal protein L34.

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

- Molecule 52 is a protein called 50S ribosomal protein L35.

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

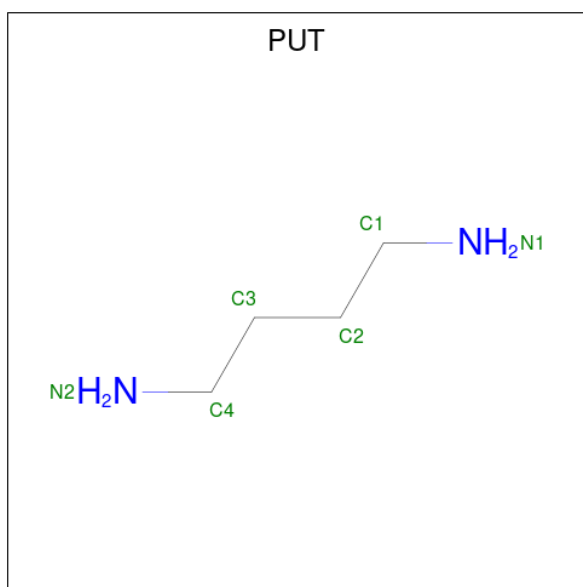
- Molecule 53 is a protein called 50S ribosomal protein L36.

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

- Molecule 54 is a RNA chain called N-formyl-methionine initiator tRNA (fMet-tRNA^{fMet}).

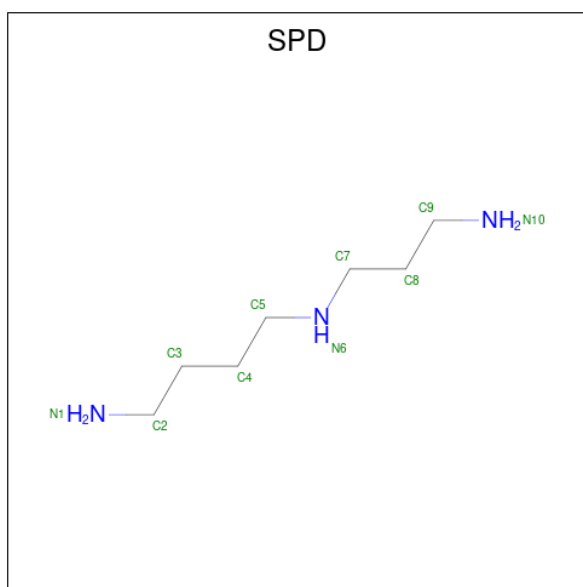
Mol	Chain	Residues	Atoms						AltConf	Trace
54	Pt	77	Total	C	N	O	P	S	0	0
			1646	734	298	536	77	1		

- Molecule 55 is 1,4-DIAMINOBTUTANE (CCD ID: PUT) (formula: C₄H₁₂N₂).



Mol	Chain	Residues	Atoms			AltConf
55	16	1	Total	C	N	0
			6	4	2	
55	23	1	Total	C	N	0
			6	4	2	
55	23	1	Total	C	N	0
			6	4	2	
55	23	1	Total	C	N	0
			6	4	2	
55	23	1	Total	C	N	0
			6	4	2	
55	23	1	Total	C	N	0
			6	4	2	
55	23	1	Total	C	N	0
			6	4	2	
55	23	1	Total	C	N	0
			6	4	2	

- Molecule 56 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms			AltConf
56	16	1	Total	C	N	0
			10	7	3	
56	23	1	Total	C	N	0
			10	7	3	
56	23	1	Total	C	N	0
			10	7	3	
56	23	1	Total	C	N	0
			10	7	3	
56	23	1	Total	C	N	0
			10	7	3	

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	16	74	Total	Mg	0
			74	74	
57	mR	2	Total	Mg	0
			2	2	
57	23	194	Total	Mg	0
			194	194	
57	5	4	Total	Mg	0
			4	4	
57	LB	3	Total	Mg	0
			3	3	
57	LD	1	Total	Mg	0
			1	1	
57	LE	1	Total	Mg	0
			1	1	

Continued on next page...

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Mol	Chain	Residues	Atoms		AltConf
57	LO	1	Total 1	Mg 1	0
57	LT	1	Total 1	Mg 1	0
57	Lf	1	Total 1	Mg 1	0
57	Pt	1	Total 1	Mg 1	0

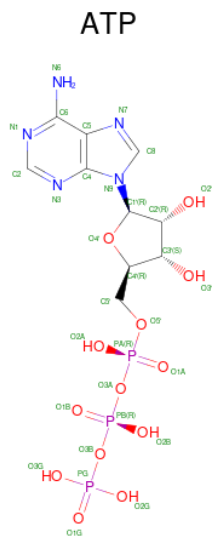
- Molecule 58 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
58	16	9	Total 9	K 9	0
58	23	39	Total 39	K 39	0
58	LB	1	Total 1	K 1	0

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

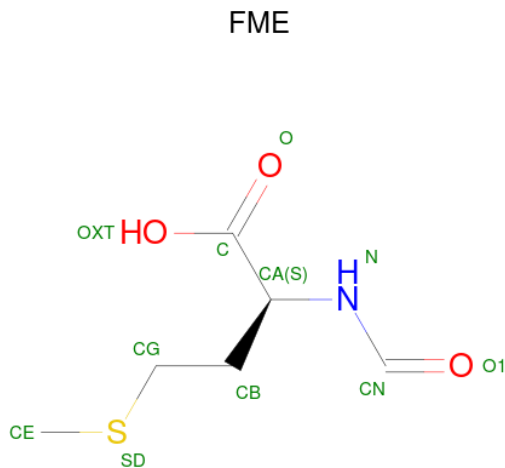
Mol	Chain	Residues	Atoms		AltConf
59	SB	1	Total 1	Zn 1	0
59	Le	1	Total 1	Zn 1	0
59	Lj	1	Total 1	Zn 1	0

- Molecule 60 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					AltConf
60	23	1	Total 31	C 10	N 5	O 13	P 3	0
60	23	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 61 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $\text{C}_6\text{H}_{11}\text{NO}_3\text{S}$).

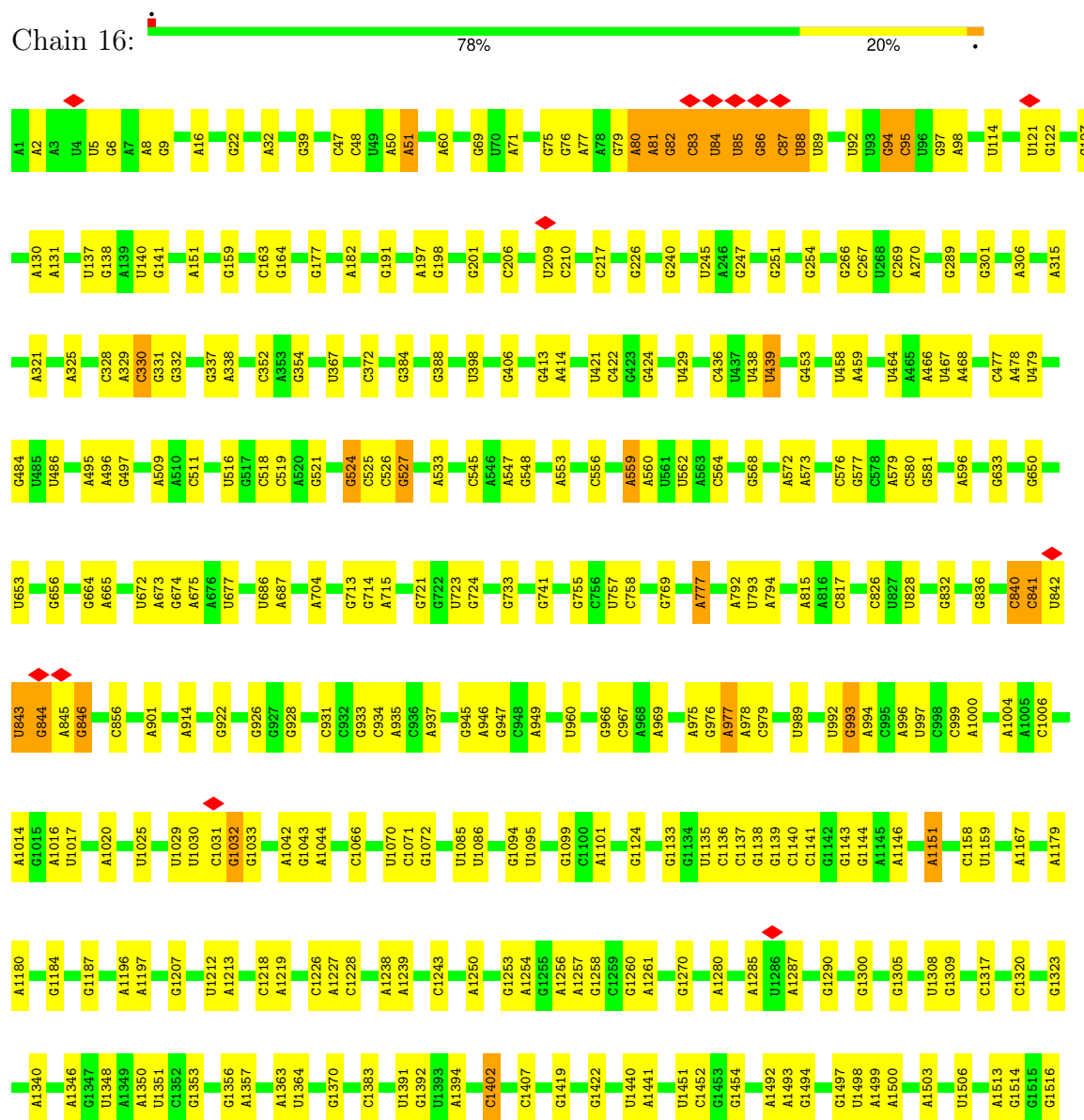


Mol	Chain	Residues	Atoms					AltConf
61	Pt	1	Total	C	N	O	S	0
			10	6	1	2	1	

3 Residue-property plots

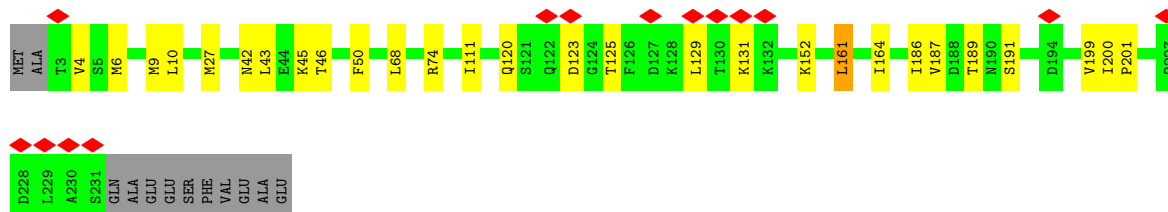
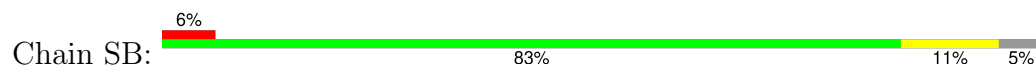
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S ribosomal RNA (rRNA) from the rrnH operon

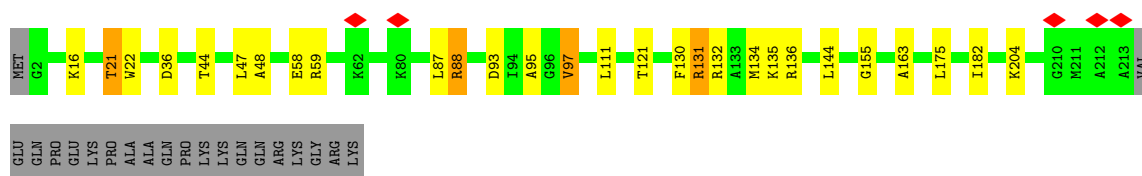
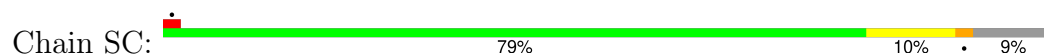




- Molecule 2: 30S ribosomal protein S2



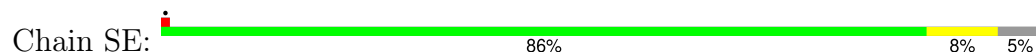
- Molecule 3: 30S ribosomal protein S3



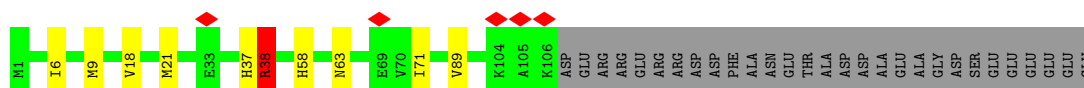
- Molecule 4: 30S ribosomal protein S4



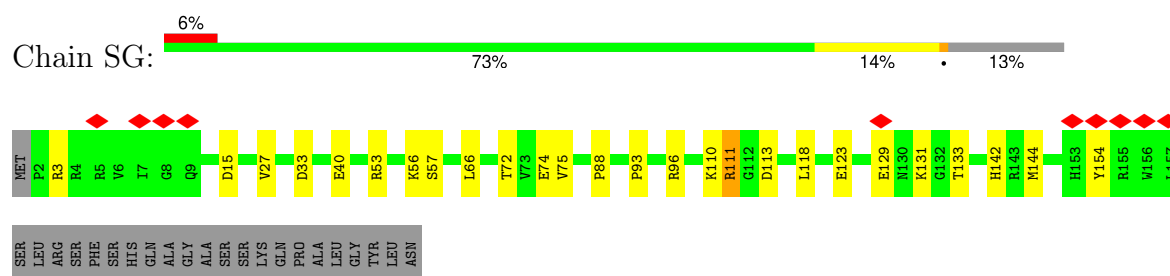
- Molecule 5: 30S ribosomal protein S5



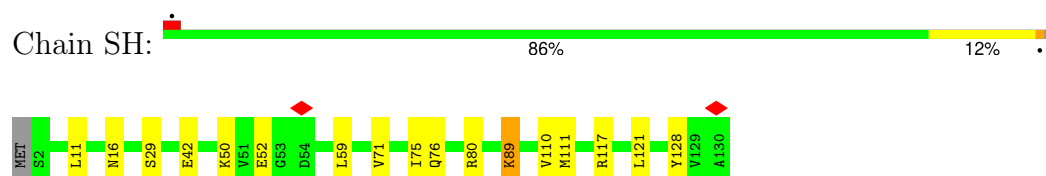
- Molecule 6: 30S ribosomal protein S6



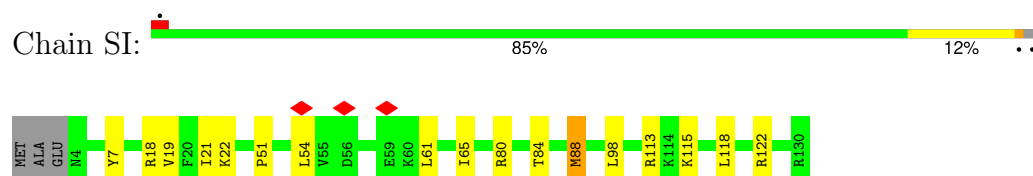
- Molecule 7: 30S ribosomal protein S7



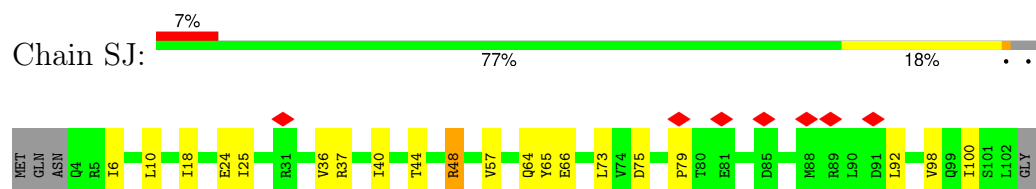
- Molecule 8: 30S ribosomal protein S8



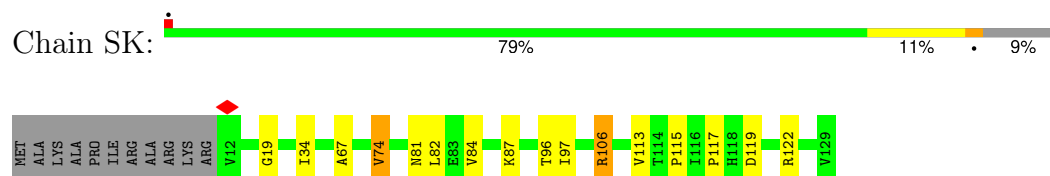
- Molecule 9: 30S ribosomal protein S9



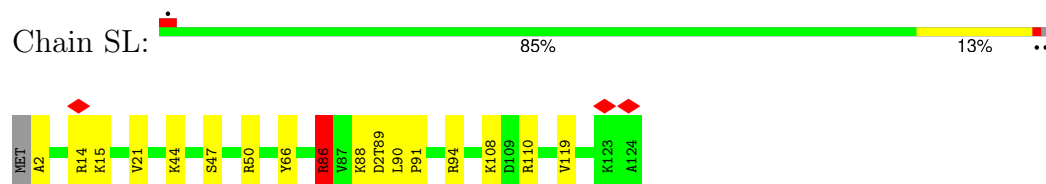
- Molecule 10: 30S ribosomal protein S10



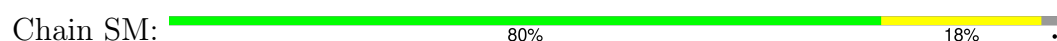
- Molecule 11: Small ribosomal subunit protein uS11

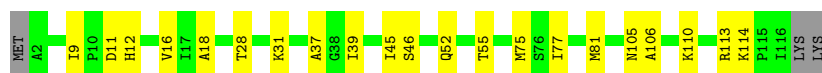


- Molecule 12: Small ribosomal subunit protein uS12

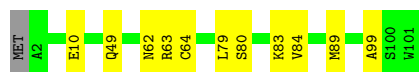


- Molecule 13: 30S ribosomal protein S13





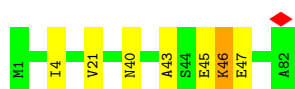
- Molecule 14: 30S ribosomal protein S14



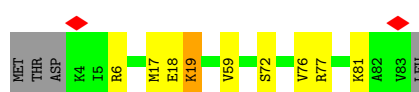
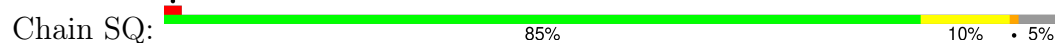
- Molecule 15: 30S ribosomal protein S15



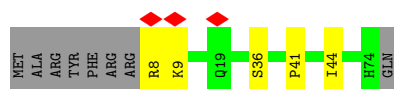
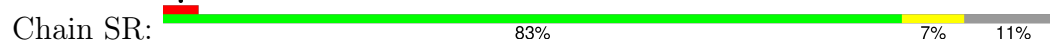
- Molecule 16: 30S ribosomal protein S16



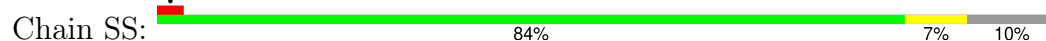
- Molecule 17: 30S ribosomal protein S17



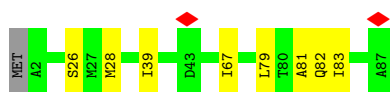
- Molecule 18: 30S ribosomal protein S18

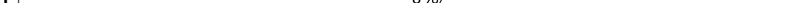


- Molecule 19: 30S ribosomal protein S19

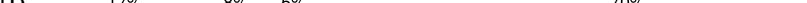


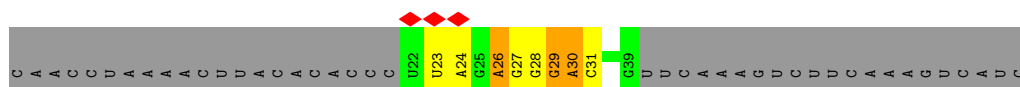
- Molecule 20: 30S ribosomal protein S20

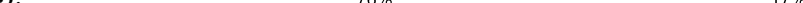


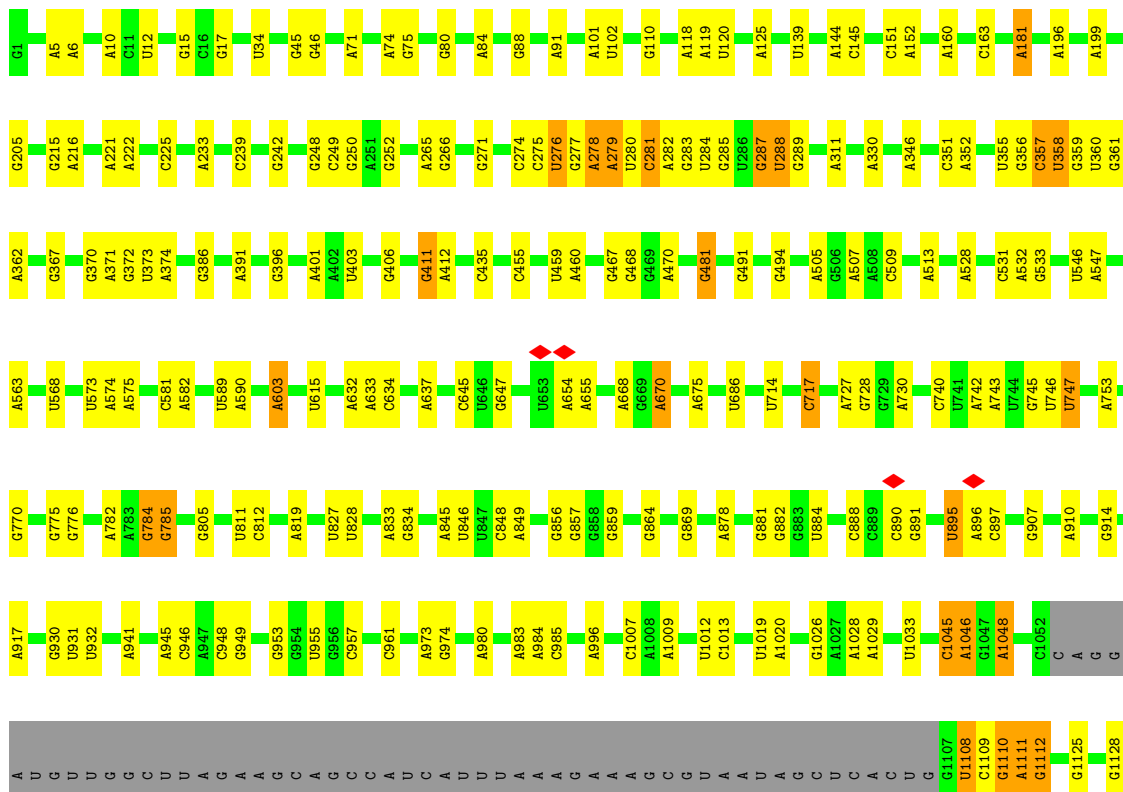
- Chain SU: 

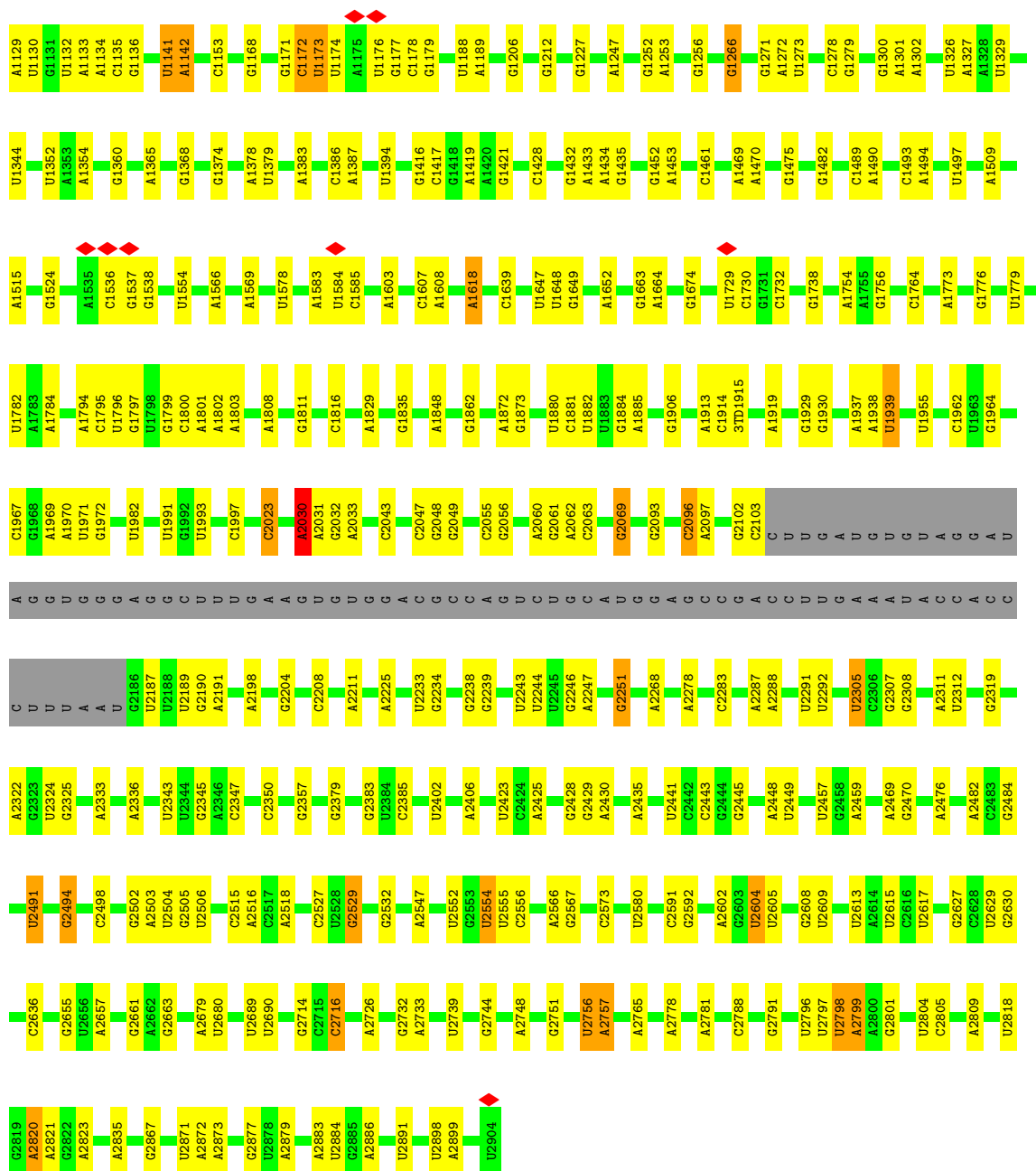


- Chain mR: 



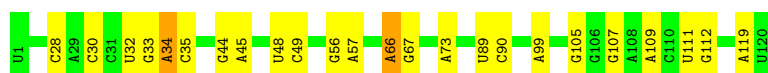
- Chain 23:  76% 17% • 5%





- Molecule 24: 5S large subunit ribosomal RNA of the H operon

Chain 5: 80% 18%



- Molecule 25: 50S ribosomal protein L2

Chain LB: 92% 6%



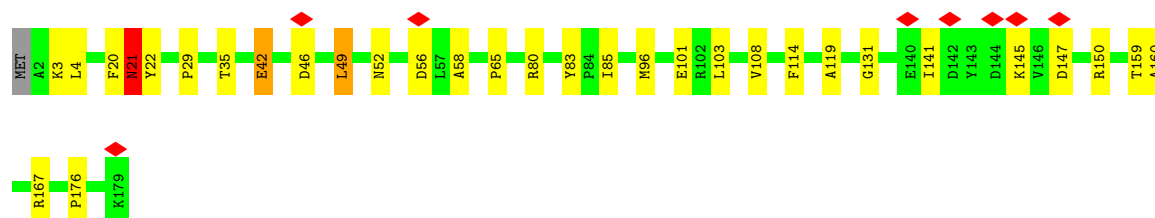
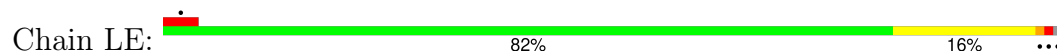
- Molecule 26: 50S ribosomal protein L3



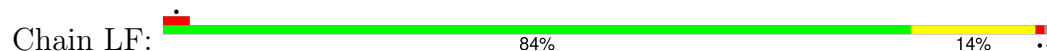
- Molecule 27: Large ribosomal subunit protein uL4



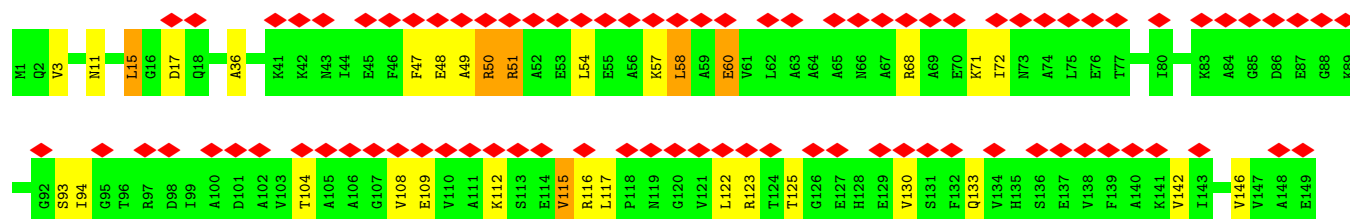
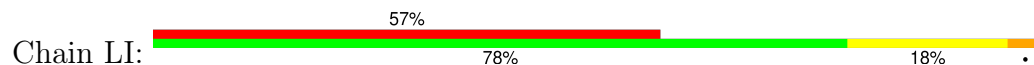
- Molecule 28: 50S ribosomal protein L5



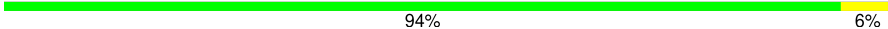
- Molecule 29: 50S ribosomal protein L6



- Molecule 30: 50S ribosomal protein L9



- Molecule 31: 50S ribosomal protein L13

Chain LM:  94% 6%



- Molecule 32: 50S ribosomal protein L14

Chain LN:  95% ..



- Molecule 33: 50S ribosomal protein L15

Chain LO:  85% 14% .



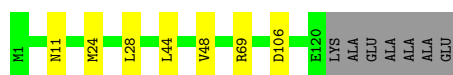
- Molecule 34: 50S ribosomal protein L16

Chain LP:  90% 8% .



- Molecule 35: 50S ribosomal protein L17

Chain LQ:  89% 6% 6%



- Molecule 36: 50S ribosomal protein L18

Chain LR:  91% 9% .

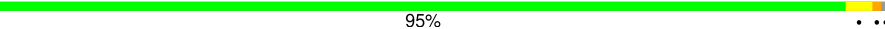


- Molecule 37: 50S ribosomal protein L19

Chain LS:  84% 13% ..



- Molecule 38: 50S ribosomal protein L20

Chain LT:  95% ..



- Molecule 39: 50S ribosomal protein L21

Chain LU:  96% .



- Molecule 40: Large ribosomal subunit protein uL22

Chain LV:  93% 7%



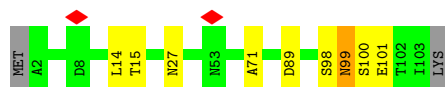
- Molecule 41: 50S ribosomal protein L23

Chain LW:  83% 11% 5%



- Molecule 42: 50S ribosomal protein L24

Chain LX:  89% 8% ..



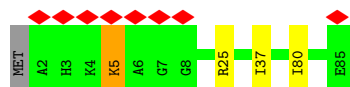
- Molecule 43: 50S ribosomal protein L25

Chain LY:  90% 10%



- Molecule 44: 50S ribosomal protein L27

Chain La:  9% 94% ..

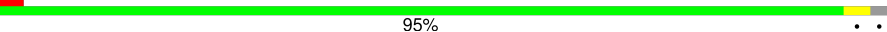


- Molecule 45: 50S ribosomal protein L28

Chain Lb:  94% 5%



- Molecule 46: 50S ribosomal protein L29

Chain Lc:  95%



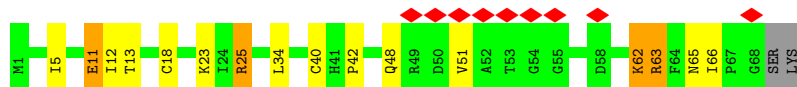
- Molecule 47: Large ribosomal subunit protein uL30

Chain Ld:  73% 19% 7%



- Molecule 48: 50S ribosomal protein L31

Chain Le:  13% 74% 17% 6%

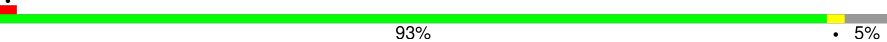


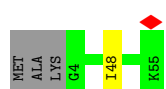
- Molecule 49: 50S ribosomal protein L32

Chain Lf:  93% 5%



- Molecule 50: 50S ribosomal protein L33

Chain Lg:  93% 5%



- Molecule 51: 50S ribosomal protein L34

Chain Lh:  93% 5%



- Molecule 52: 50S ribosomal protein L35

Chain Li: 97%



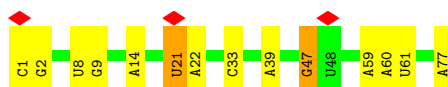
- Molecule 53: 50S ribosomal protein L36

Chain Lj: 84% 16%



- Molecule 54: N-formyl-methionine initiator tRNA (fMet-tRNA^{fMet})

Chain Pt: 82% 16%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	417599	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.45	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.087	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	342.40002, 342.40002, 342.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 4D4, UR3, ZN, OMC, G7M, 3TD, ATP, 1MG, 2MA, 6MZ, 4OC, PUT, H2U, 2MG, 4SU, 5MC, IAS, 5MU, K, MG, PSU, OMG, MA6, OMU, FME, D2T, SPD

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	16	0.33	0/36765	0.48	0/57346
2	SB	0.37	0/1818	0.71	0/2450
3	SC	0.40	0/1685	0.67	0/2270
4	SD	0.30	0/1665	0.56	0/2227
5	SE	0.37	0/1179	0.65	0/1584
6	SF	0.42	2/881 (0.2%)	0.68	0/1189
7	SG	0.30	0/1265	0.57	0/1697
8	SH	0.26	0/989	0.51	0/1326
9	SI	0.38	0/1034	0.69	0/1375
10	SJ	0.52	0/805	0.79	0/1089
11	SK	0.46	0/902	0.67	1/1215 (0.1%)
12	SL	0.37	0/960	0.61	0/1286
13	SM	0.29	0/900	0.62	0/1204
14	SN	0.26	0/817	0.47	0/1088
15	SO	0.27	0/721	0.50	0/964
16	SP	0.34	0/659	0.60	0/884
17	SQ	0.37	0/657	0.59	0/881
18	SR	0.24	0/564	0.56	0/756
19	SS	0.22	0/680	0.47	0/915
20	ST	0.50	2/675 (0.3%)	0.61	1/895 (0.1%)
21	SU	0.25	0/598	0.54	0/792
22	mR	0.45	0/437	0.61	0/680
23	23	0.36	0/66049	0.54	2/103033 (0.0%)
24	5	0.36	0/2876	0.51	1/4483 (0.0%)
25	LB	0.37	1/2121 (0.0%)	0.59	2/2852 (0.1%)
26	LC	0.33	0/1585	0.61	0/2134
27	LD	0.31	0/1571	0.59	1/2113 (0.0%)
28	LE	0.37	0/1444	0.70	0/1937
29	LF	0.41	1/1333 (0.1%)	0.61	1/1805 (0.1%)
30	LI	0.53	1/1122 (0.1%)	0.78	0/1515
31	LM	0.30	0/1152	0.55	0/1551

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LN	0.29	0/956	0.62	0/1279
33	LO	0.33	0/1062	0.58	0/1413
34	LP	0.36	0/1091	0.63	1/1457 (0.1%)
35	LQ	0.34	0/973	0.63	0/1301
36	LR	0.34	0/902	0.73	1/1209 (0.1%)
37	LS	0.58	3/920 (0.3%)	0.66	3/1231 (0.2%)
38	LT	0.35	0/960	0.64	0/1278
39	LU	0.26	0/829	0.61	0/1107
40	LV	0.27	0/864	0.55	0/1156
41	LW	0.31	0/764	0.62	1/1021 (0.1%)
42	LX	0.30	0/787	0.61	0/1051
43	LY	0.40	0/766	0.61	0/1025
44	La	0.30	0/642	0.60	0/848
45	Lb	0.36	0/635	0.61	0/848
46	Lc	0.28	0/502	0.54	0/667
47	Ld	0.55	0/453	0.87	0/605
48	Le	0.51	0/543	0.80	0/726
49	Lf	0.26	0/450	0.54	0/599
50	Lg	0.26	0/433	0.51	0/576
51	Lh	0.51	0/380	0.61	0/498
52	Li	0.38	0/513	0.66	0/676
53	Lj	0.50	0/303	0.68	0/397
54	Pt	0.40	1/1744 (0.1%)	0.54	0/2716
All	All	0.36	11/153381 (0.0%)	0.55	15/229220 (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
3	SC	0	3
5	SE	0	1
6	SF	0	1
7	SG	0	1
10	SJ	0	1
11	SK	0	2
12	SL	0	2
30	LI	0	2
32	LN	0	1
33	LO	0	1
34	LP	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
36	LR	0	1
37	LS	0	2
38	LT	0	1
47	Ld	0	1
48	Le	0	1
49	Lf	0	1
51	Lh	0	2
53	Lj	0	1
All	All	0	26

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	LS	88	ARG	C-N	9.71	1.47	1.33
37	LS	89	ARG	C-N	8.49	1.45	1.33
20	ST	81	ALA	C-N	-6.86	1.24	1.33
30	LI	115	VAL	C-N	6.67	1.43	1.33
6	SF	38	ARG	C-N	-6.34	1.25	1.33

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	5	34	A	O3'-P-O5'	-6.17	94.75	104.00
36	LR	61	GLN	N-CA-C	-6.07	105.74	113.02
37	LS	88	ARG	O-C-N	5.91	130.32	123.41
34	LP	85	GLY	CA-C-O	-5.83	118.11	122.37
37	LS	89	ARG	CA-C-N	-5.71	116.21	122.38

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	SC	132	ARG	Sidechain
3	SC	136	ARG	Sidechain
3	SC	88	ARG	Sidechain
5	SE	29	ARG	Sidechain
6	SF	38	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	16	33087	0	16672	81	0
2	SB	1787	0	1812	17	0
3	SC	1658	0	1732	13	0
4	SD	1643	0	1707	14	0
5	SE	1166	0	1212	8	0
6	SF	862	0	864	5	0
7	SG	1244	0	1301	13	0
8	SH	979	0	1031	8	0
9	SI	1022	0	1070	10	0
10	SJ	795	0	836	10	0
11	SK	895	0	905	6	0
12	SL	957	0	1017	12	0
13	SM	891	0	952	13	0
14	SN	805	0	844	8	0
15	SO	713	0	734	5	0
16	SP	649	0	666	3	0
17	SQ	648	0	691	5	0
18	SR	555	0	578	3	0
19	SS	663	0	688	6	0
20	ST	669	0	719	3	0
21	SU	590	0	629	6	0
22	mR	390	0	195	5	0
23	23	59447	0	29919	127	0
24	5	2572	0	1301	5	0
25	LB	2082	0	2153	9	0
26	LC	1564	0	1616	9	0
27	LD	1552	0	1619	12	0
28	LE	1420	0	1457	18	0
29	LF	1313	0	1358	12	0
30	LI	1111	0	1148	14	0
31	LM	1129	0	1162	6	0
32	LN	947	0	1023	3	0
33	LO	1053	0	1128	11	0
34	LP	1085	0	1166	9	0
35	LQ	960	0	1000	5	0
36	LR	892	0	923	4	0
37	LS	908	0	956	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	LT	947	0	1019	3	0
39	LU	816	0	839	2	0
40	LV	857	0	922	6	0
41	LW	757	0	820	5	0
42	LX	779	0	831	3	0
43	LY	753	0	780	7	0
44	La	634	0	653	4	0
45	Lb	625	0	652	2	0
46	Lc	501	0	531	1	0
47	Ld	449	0	488	7	0
48	Le	533	0	530	7	0
49	Lf	444	0	458	1	0
50	Lg	426	0	464	0	0
51	Lh	377	0	418	1	0
52	Li	504	0	572	1	0
53	Lj	302	0	340	4	0
54	Pt	1646	0	843	2	0
55	16	6	0	12	1	0
55	23	54	0	108	2	0
56	16	10	0	19	0	0
56	23	40	0	76	2	0
57	16	74	0	0	0	0
57	23	194	0	0	0	0
57	5	4	0	0	0	0
57	LB	3	0	0	0	0
57	LD	1	0	0	0	0
57	LE	1	0	0	0	0
57	LO	1	0	0	0	0
57	LT	1	0	0	0	0
57	Lf	1	0	0	0	0
57	Pt	1	0	0	0	0
57	mR	2	0	0	0	0
58	16	9	0	0	0	0
58	23	39	0	0	0	0
58	LB	1	0	0	0	0
59	Le	1	0	0	0	0
59	Lj	1	0	0	0	0
59	SB	1	0	0	0	0
60	23	62	0	24	0	0
61	Pt	10	0	10	0	0
All	All	142570	0	96193	502	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 2.

The worst 5 of 502 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)
23:23:881:G:H1	23:23:895:U:H3	0.92	0.91
23:23:17:G:H4'	38:LT:25:TYR:HE1	1.44	0.82
23:23:2494:G:O2'	34:LP:79:ALA:HA	1.81	0.81
12:SL:50:ARG:HB3	12:SL:66:TYR:HE1	1.52	0.75
1:16:1402:4OC:H5	1:16:1500:A:H61	1.52	0.74

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	
2	SB	227/241 (94%)	216 (95%)	10 (4%)	1 (0%)	30	43
3	SC	210/233 (90%)	205 (98%)	5 (2%)	0	100	100
4	SD	203/206 (98%)	203 (100%)	0	0	100	100
5	SE	156/167 (93%)	154 (99%)	2 (1%)	0	100	100
6	SF	104/135 (77%)	102 (98%)	2 (2%)	0	100	100
7	SG	155/179 (87%)	152 (98%)	3 (2%)	0	100	100
8	SH	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
9	SI	125/130 (96%)	121 (97%)	4 (3%)	0	100	100
10	SJ	97/103 (94%)	92 (95%)	4 (4%)	1 (1%)	12	20
11	SK	115/129 (89%)	110 (96%)	5 (4%)	0	100	100
12	SL	120/124 (97%)	116 (97%)	4 (3%)	0	100	100
13	SM	113/118 (96%)	108 (96%)	5 (4%)	0	100	100
14	SN	98/101 (97%)	98 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	SO	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
16	SP	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
17	SQ	78/84 (93%)	75 (96%)	3 (4%)	0	100	100
18	SR	65/75 (87%)	61 (94%)	4 (6%)	0	100	100
19	SS	81/92 (88%)	79 (98%)	2 (2%)	0	100	100
20	ST	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
21	SU	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
25	LB	269/273 (98%)	263 (98%)	6 (2%)	0	100	100
26	LC	207/209 (99%)	201 (97%)	6 (3%)	0	100	100
27	LD	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
28	LE	176/179 (98%)	168 (96%)	7 (4%)	1 (1%)	21	32
29	LF	173/177 (98%)	165 (95%)	8 (5%)	0	100	100
30	LI	147/149 (99%)	134 (91%)	13 (9%)	0	100	100
31	LM	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
32	LN	121/123 (98%)	119 (98%)	2 (2%)	0	100	100
33	LO	142/144 (99%)	140 (99%)	2 (1%)	0	100	100
34	LP	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
35	LQ	118/127 (93%)	116 (98%)	2 (2%)	0	100	100
36	LR	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
37	LS	111/115 (96%)	109 (98%)	2 (2%)	0	100	100
38	LT	115/118 (98%)	115 (100%)	0	0	100	100
39	LU	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
40	LV	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
41	LW	93/100 (93%)	92 (99%)	0	1 (1%)	11	18
42	LX	100/104 (96%)	92 (92%)	6 (6%)	2 (2%)	6	7
43	LY	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
44	La	82/85 (96%)	79 (96%)	3 (4%)	0	100	100
45	Lb	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
46	Lc	60/63 (95%)	60 (100%)	0	0	100	100
47	Ld	56/59 (95%)	56 (100%)	0	0	100	100
48	Le	66/70 (94%)	61 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	Lf	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
50	Lg	50/55 (91%)	48 (96%)	2 (4%)	0	100	100
51	Lh	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	Li	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
53	Lj	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
All	All	5637/5913 (95%)	5473 (97%)	158 (3%)	6 (0%)	49	64

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	SB	164	ILE
28	LE	21	ASN
42	LX	98	SER
42	LX	100	SER
10	SJ	57	VAL

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	
2	SB	190/199 (96%)	188 (99%)	2 (1%)	65	82
3	SC	172/190 (90%)	162 (94%)	10 (6%)	18	32
4	SD	172/173 (99%)	170 (99%)	2 (1%)	63	81
5	SE	120/126 (95%)	118 (98%)	2 (2%)	53	74
6	SF	92/116 (79%)	92 (100%)	0	100	100
7	SG	130/147 (88%)	125 (96%)	5 (4%)	29	49
8	SH	104/105 (99%)	98 (94%)	6 (6%)	18	32
9	SI	105/107 (98%)	102 (97%)	3 (3%)	37	60
10	SJ	87/90 (97%)	82 (94%)	5 (6%)	18	33
11	SK	91/98 (93%)	88 (97%)	3 (3%)	33	55
12	SL	102/103 (99%)	100 (98%)	2 (2%)	48	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	SM	93/96 (97%)	88 (95%)	5 (5%)	20	35
14	SN	83/84 (99%)	83 (100%)	0	100	100
15	SO	76/77 (99%)	74 (97%)	2 (3%)	40	63
16	SP	65/65 (100%)	63 (97%)	2 (3%)	35	57
17	SQ	74/78 (95%)	70 (95%)	4 (5%)	20	35
18	SR	58/65 (89%)	57 (98%)	1 (2%)	53	74
19	SS	72/79 (91%)	72 (100%)	0	100	100
20	ST	65/66 (98%)	64 (98%)	1 (2%)	57	77
21	SU	60/61 (98%)	60 (100%)	0	100	100
25	LB	216/218 (99%)	212 (98%)	4 (2%)	50	71
26	LC	164/164 (100%)	160 (98%)	4 (2%)	43	65
27	LD	165/165 (100%)	163 (99%)	2 (1%)	63	81
28	LE	149/150 (99%)	141 (95%)	8 (5%)	20	35
29	LF	136/138 (99%)	127 (93%)	9 (7%)	15	26
30	LI	114/114 (100%)	102 (90%)	12 (10%)	6	10
31	LM	116/116 (100%)	116 (100%)	0	100	100
32	LN	104/104 (100%)	102 (98%)	2 (2%)	50	71
33	LO	103/103 (100%)	98 (95%)	5 (5%)	22	39
34	LP	109/108 (101%)	105 (96%)	4 (4%)	30	51
35	LQ	100/103 (97%)	100 (100%)	0	100	100
36	LR	86/87 (99%)	85 (99%)	1 (1%)	63	81
37	LS	98/100 (98%)	97 (99%)	1 (1%)	68	84
38	LT	89/90 (99%)	87 (98%)	2 (2%)	45	67
39	LU	84/84 (100%)	83 (99%)	1 (1%)	63	81
40	LV	93/93 (100%)	93 (100%)	0	100	100
41	LW	82/84 (98%)	79 (96%)	3 (4%)	30	51
42	LX	83/85 (98%)	80 (96%)	3 (4%)	31	52
43	LY	78/78 (100%)	78 (100%)	0	100	100
44	La	62/63 (98%)	61 (98%)	1 (2%)	55	76
45	Lb	67/68 (98%)	67 (100%)	0	100	100
46	Lc	54/55 (98%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	Ld	48/49 (98%)	41 (85%)	7 (15%)	3	4
48	Le	60/62 (97%)	50 (83%)	10 (17%)	2	3
49	Lf	47/48 (98%)	47 (100%)	0	100	100
50	Lg	47/49 (96%)	46 (98%)	1 (2%)	47	69
51	Lh	38/38 (100%)	38 (100%)	0	100	100
52	Li	51/52 (98%)	51 (100%)	0	100	100
53	Lj	34/34 (100%)	34 (100%)	0	100	100
All	All	4688/4827 (97%)	4553 (97%)	135 (3%)	38	60

5 of 135 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	LX	99	ASN
47	Ld	6	LYS
48	Le	51	VAL
16	SP	46	LYS
16	SP	45	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 122 such sidechains are listed below:

Mol	Chain	Res	Type
25	LB	86	ASN
46	Lc	20	ASN
29	LF	139	GLN
46	Lc	15	ASN
52	Li	31	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	16	1541/1542 (99%)	248 (16%)	6 (0%)
22	mR	17/60 (28%)	6 (35%)	0
23	23	2765/2904 (95%)	390 (14%)	20 (0%)
24	5	119/120 (99%)	16 (13%)	1 (0%)
54	Pt	76/77 (98%)	8 (10%)	0
All	All	4518/4703 (96%)	668 (14%)	27 (0%)

5 of 668 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	16	2	A
1	16	5	U
1	16	6	G
1	16	9	G
1	16	16	A

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	23	984	A
23	23	1141	U
23	23	2798	U
23	23	1111	A
23	23	1489	C

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

40 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	D2T	SL	89	12	8,9,10	7.08	2 (25%)	6,11,13	2.60	3 (50%)
23	PSU	23	2504	58,23	18,21,22	0.91	1 (5%)	21,30,33	0.74	0
1	MA6	16	1518	1	23,26,27	1.57	5 (21%)	33,38,41	2.24	10 (30%)
1	2MG	16	966	1	23,26,27	1.28	4 (17%)	33,38,41	2.10	6 (18%)
1	PSU	16	516	57,1	18,21,22	1.43	4 (22%)	21,30,33	2.04	4 (19%)
1	4OC	16	1402	57,1	20,23,24	0.78	0	25,32,35	2.15	7 (28%)
23	6MZ	23	2030	23	22,25,26	1.50	5 (22%)	29,36,39	2.47	11 (37%)
1	G7M	16	527	1	23,26,27	0.71	1 (4%)	34,39,42	0.62	1 (2%)
23	PSU	23	746	57,23	18,21,22	1.45	3 (16%)	21,30,33	2.16	5 (23%)
34	4D4	LP	81	34	9,11,12	2.03	2 (22%)	7,13,15	1.78	3 (42%)
23	PSU	23	2580	23	18,21,22	1.40	3 (16%)	21,30,33	2.28	4 (19%)
23	5MU	23	747	23	19,22,23	1.42	6 (31%)	27,32,35	2.05	10 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
54	H2U	Pt	21	54	18,21,22	0.93	2 (11%)	19,30,33	0.94	0
23	H2U	23	2449	23	18,21,22	1.10	2 (11%)	19,30,33	1.07	1 (5%)
23	PSU	23	2604	23	18,21,22	1.43	3 (16%)	21,30,33	2.13	3 (14%)
23	5MU	23	1939	58,23	19,22,23	1.37	5 (26%)	27,32,35	2.31	6 (22%)
23	2MA	23	2503	58,57,23	22,25,26	0.84	1 (4%)	32,37,40	1.20	4 (12%)
23	3TD	23	1915	23	19,22,23	1.26	2 (10%)	23,32,35	2.02	3 (13%)
54	OMC	Pt	33	54	19,22,23	0.85	0	25,31,34	1.29	3 (12%)
23	2MG	23	2445	23	23,26,27	1.29	3 (13%)	33,38,41	2.27	5 (15%)
23	PSU	23	2457	23	18,21,22	1.42	3 (16%)	21,30,33	2.05	5 (23%)
23	OMC	23	2498	57,23	19,22,23	0.84	0	25,31,34	1.13	2 (8%)
23	OMU	23	2552	23	19,22,23	1.17	3 (15%)	25,31,34	1.88	6 (24%)
11	IAS	SK	119	11	6,7,8	1.33	1 (16%)	3,8,10	0.65	0
1	5MC	16	1407	1	19,22,23	1.38	2 (10%)	26,32,35	1.41	3 (11%)
1	2MG	16	1207	1	23,26,27	1.27	3 (13%)	33,38,41	2.20	5 (15%)
1	5MC	16	967	1	19,22,23	1.50	3 (15%)	26,32,35	1.10	2 (7%)
23	PSU	23	2605	23	18,21,22	1.47	3 (16%)	21,30,33	2.07	5 (23%)
1	2MG	16	1516	1	23,26,27	1.22	4 (17%)	33,38,41	2.26	8 (24%)
23	6MZ	23	1618	23	22,25,26	1.43	3 (13%)	29,36,39	2.28	10 (34%)
23	OMG	23	2251	54,23	23,26,27	1.23	3 (13%)	32,38,41	2.00	5 (15%)
23	G7M	23	2069	23	23,26,27	0.71	1 (4%)	34,39,42	0.67	1 (2%)
1	UR3	16	1498	1	19,22,23	0.89	0	26,32,35	1.81	4 (15%)
23	5MC	23	1962	58,23	19,22,23	1.54	3 (15%)	26,32,35	0.98	2 (7%)
54	G7M	Pt	47	54	23,26,27	2.38	5 (21%)	34,39,42	3.13	11 (32%)
23	PSU	23	955	23	18,21,22	1.38	4 (22%)	21,30,33	2.07	3 (14%)
23	2MG	23	1835	23	23,26,27	1.24	3 (13%)	33,38,41	2.44	9 (27%)
54	4SU	Pt	8	54	18,21,22	1.86	4 (22%)	25,30,33	2.32	5 (20%)
1	MA6	16	1519	1	23,26,27	1.53	5 (21%)	33,38,41	2.17	10 (30%)
23	1MG	23	745	23	23,26,27	1.18	4 (17%)	33,39,42	1.79	5 (15%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	D2T	SL	89	12	-	4/7/12/14	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	PSU	23	2504	58,23	-	0/7/25/26	0/2/2/2
1	MA6	16	1518	1	-	0/11/29/30	0/3/3/3
1	2MG	16	966	1	-	0/9/27/28	0/3/3/3
1	PSU	16	516	57,1	-	0/7/25/26	0/2/2/2
1	4OC	16	1402	57,1	-	2/9/29/30	0/2/2/2
23	6MZ	23	2030	23	-	2/9/27/28	0/3/3/3
1	G7M	16	527	1	-	2/7/25/26	0/3/3/3
23	PSU	23	746	57,23	-	1/7/25/26	0/2/2/2
34	4D4	LP	81	34	-	2/11/12/14	-
23	PSU	23	2580	23	-	0/7/25/26	0/2/2/2
23	5MU	23	747	23	-	0/7/25/26	0/2/2/2
54	H2U	Pt	21	54	-	2/7/38/39	0/2/2/2
23	H2U	23	2449	23	-	0/7/38/39	0/2/2/2
23	PSU	23	2604	23	-	0/7/25/26	0/2/2/2
23	5MU	23	1939	58,23	-	0/7/25/26	0/2/2/2
23	2MA	23	2503	58,57,23	-	1/7/25/26	0/3/3/3
23	3TD	23	1915	23	-	0/7/25/26	0/2/2/2
54	OMC	Pt	33	54	-	0/9/27/28	0/2/2/2
23	2MG	23	2445	23	-	1/9/27/28	0/3/3/3
23	PSU	23	2457	23	-	0/7/25/26	0/2/2/2
23	OMC	23	2498	57,23	-	0/9/27/28	0/2/2/2
23	OMU	23	2552	23	-	0/9/27/28	0/2/2/2
11	IAS	SK	119	11	-	0/7/7/8	-
1	5MC	16	1407	1	-	0/7/25/26	0/2/2/2
1	2MG	16	1207	1	-	0/9/27/28	0/3/3/3
1	5MC	16	967	1	-	0/7/25/26	0/2/2/2
23	PSU	23	2605	23	-	0/7/25/26	0/2/2/2
1	2MG	16	1516	1	-	0/9/27/28	0/3/3/3
23	6MZ	23	1618	23	-	4/9/27/28	0/3/3/3
23	OMG	23	2251	54,23	-	1/9/27/28	0/3/3/3
23	G7M	23	2069	23	-	0/7/25/26	0/3/3/3
1	UR3	16	1498	1	-	0/7/25/26	0/2/2/2
23	5MC	23	1962	58,23	-	0/7/25/26	0/2/2/2
54	G7M	Pt	47	54	-	2/7/25/26	0/3/3/3
23	PSU	23	955	23	-	0/7/25/26	0/2/2/2
23	2MG	23	1835	23	-	0/9/27/28	0/3/3/3
54	4SU	Pt	8	54	-	0/7/25/26	0/2/2/2
1	MA6	16	1519	1	-	3/11/29/30	0/3/3/3
23	1MG	23	745	23	-	0/7/25/26	0/3/3/3

The worst 5 of 111 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	SL	89	D2T	CB-CA	-19.05	1.48	1.54
54	Pt	47	G7M	C8-N7	7.54	1.45	1.33
23	23	1962	5MC	C5-C4	5.55	1.48	1.44
1	16	967	5MC	C5-C4	5.36	1.48	1.44
54	Pt	8	4SU	C4-S4	-5.13	1.59	1.68

The worst 5 of 190 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	23	1835	2MG	C2-N3-C4	8.35	122.44	112.00
54	Pt	47	G7M	CN7-N7-C8	-8.07	112.57	124.79
23	23	2445	2MG	C2-N3-C4	7.77	121.72	112.00
1	16	1207	2MG	C2-N3-C4	7.42	121.28	112.00
1	16	1516	2MG	C2-N3-C4	7.32	121.16	112.00

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	16	1402	4OC	O4'-C1'-N1-C2
1	16	1402	4OC	O4'-C1'-N1-C6
12	SL	89	D2T	CA-CB-CG-OD1
12	SL	89	D2T	CA-CB-CG-OD2
23	23	1618	6MZ	O4'-C4'-C5'-O5'

There are no ring outliers.

5 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	16	1402	4OC	1	0
23	23	2030	6MZ	1	0
23	23	2604	PSU	1	0
23	23	1939	5MU	1	0
23	23	2251	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 353 ligands modelled in this entry, 335 are monoatomic - leaving 18 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
55	PUT	23	3004	-	5,5,5	0.08	0	4,4,4	0.32	0
61	FME	Pt	101	54	8,9,10	0.61	0	8,9,11	1.14	1 (12%)
55	PUT	23	3011	-	5,5,5	0.14	0	4,4,4	0.16	0
55	PUT	23	3006	-	5,5,5	0.09	0	4,4,4	0.25	0
56	SPD	23	3015	-	9,9,9	0.32	0	8,8,8	0.45	0
60	ATP	23	3001	-	32,33,33	0.28	0	48,52,52	0.33	0
56	SPD	23	3013	-	9,9,9	0.15	0	8,8,8	0.18	0
55	PUT	23	3003	-	5,5,5	0.12	0	4,4,4	0.20	0
55	PUT	23	3009	-	5,5,5	0.10	0	4,4,4	0.23	0
55	PUT	23	3007	-	5,5,5	0.13	0	4,4,4	0.14	0
55	PUT	16	1601	-	5,5,5	0.11	0	4,4,4	0.21	0
55	PUT	23	3010	-	5,5,5	0.12	0	4,4,4	0.19	0
56	SPD	16	1602	-	9,9,9	0.30	0	8,8,8	0.46	0
56	SPD	23	3012	-	9,9,9	0.30	0	8,8,8	0.47	0
56	SPD	23	3014	-	9,9,9	0.15	0	8,8,8	0.21	0
60	ATP	23	3002	-	32,33,33	0.29	0	48,52,52	0.39	0
55	PUT	23	3008	-	5,5,5	0.15	0	4,4,4	0.19	0
55	PUT	23	3005	-	5,5,5	0.12	0	4,4,4	0.19	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	PUT	23	3004	-	-	1/3/3/3	-
61	FME	Pt	101	54	-	5/7/9/11	-
55	PUT	23	3011	-	-	0/3/3/3	-
55	PUT	23	3006	-	-	1/3/3/3	-
56	SPD	23	3015	-	-	4/7/7/7	-
60	ATP	23	3001	-	-	3/22/38/38	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	SPD	23	3013	-	-	6/7/7/7	-
55	PUT	23	3003	-	-	1/3/3/3	-
55	PUT	23	3009	-	-	0/3/3/3	-
55	PUT	23	3007	-	-	2/3/3/3	-
55	PUT	16	1601	-	-	0/3/3/3	-
55	PUT	23	3010	-	-	0/3/3/3	-
56	SPD	16	1602	-	-	5/7/7/7	-
56	SPD	23	3012	-	-	4/7/7/7	-
56	SPD	23	3014	-	-	2/7/7/7	-
60	ATP	23	3002	-	-	2/22/38/38	0/3/3/3
55	PUT	23	3008	-	-	1/3/3/3	-
55	PUT	23	3005	-	-	1/3/3/3	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	Pt	101	FME	O-C-CA	-2.85	117.43	124.77

There are no chirality outliers.

5 of 38 torsion outliers are listed below:

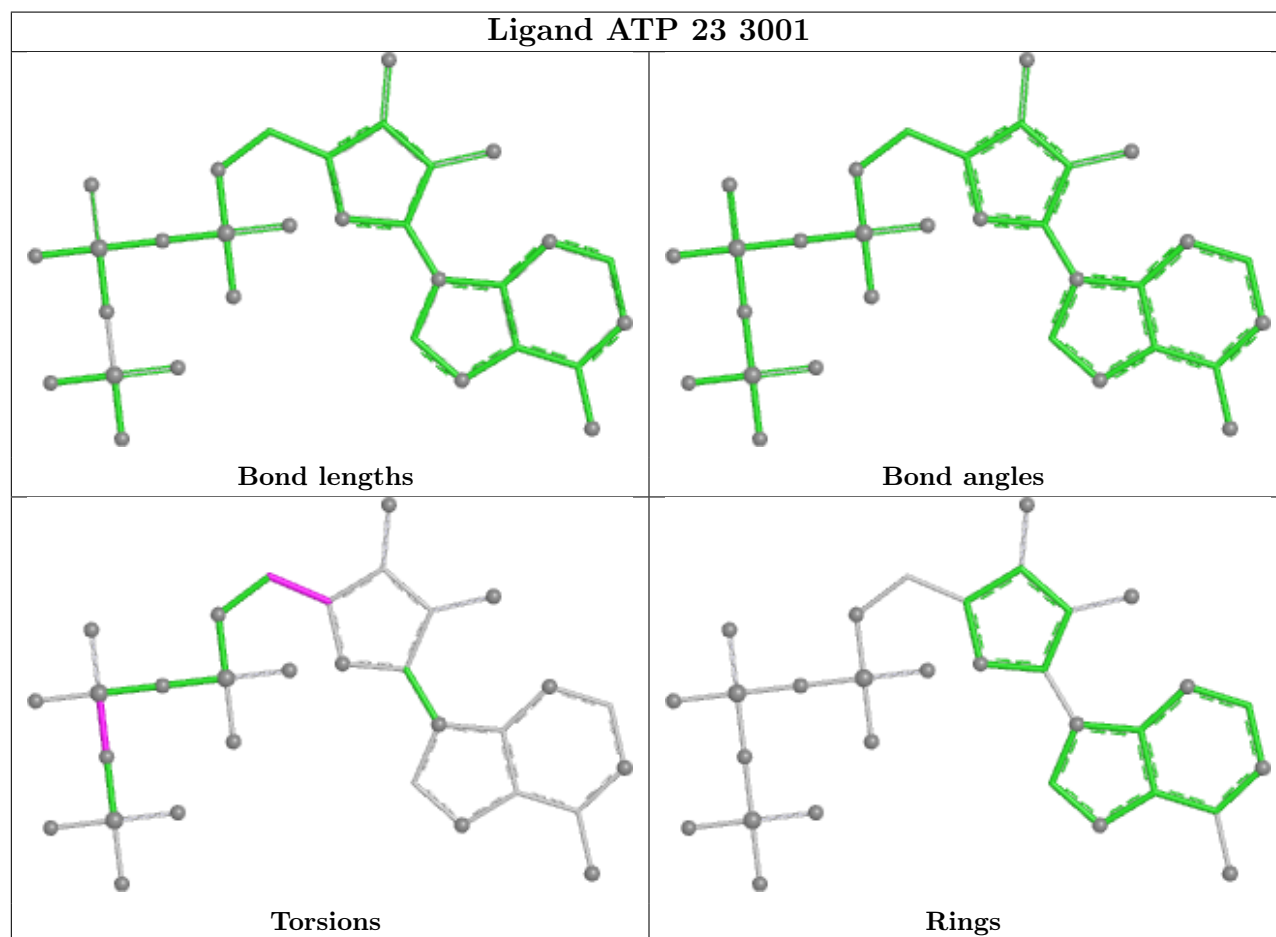
Mol	Chain	Res	Type	Atoms
61	Pt	101	FME	O1-CN-N-CA
61	Pt	101	FME	N-CA-CB-CG
60	23	3001	ATP	C3'-C4'-C5'-O5'
61	Pt	101	FME	CA-CB-CG-SD
60	23	3001	ATP	O4'-C4'-C5'-O5'

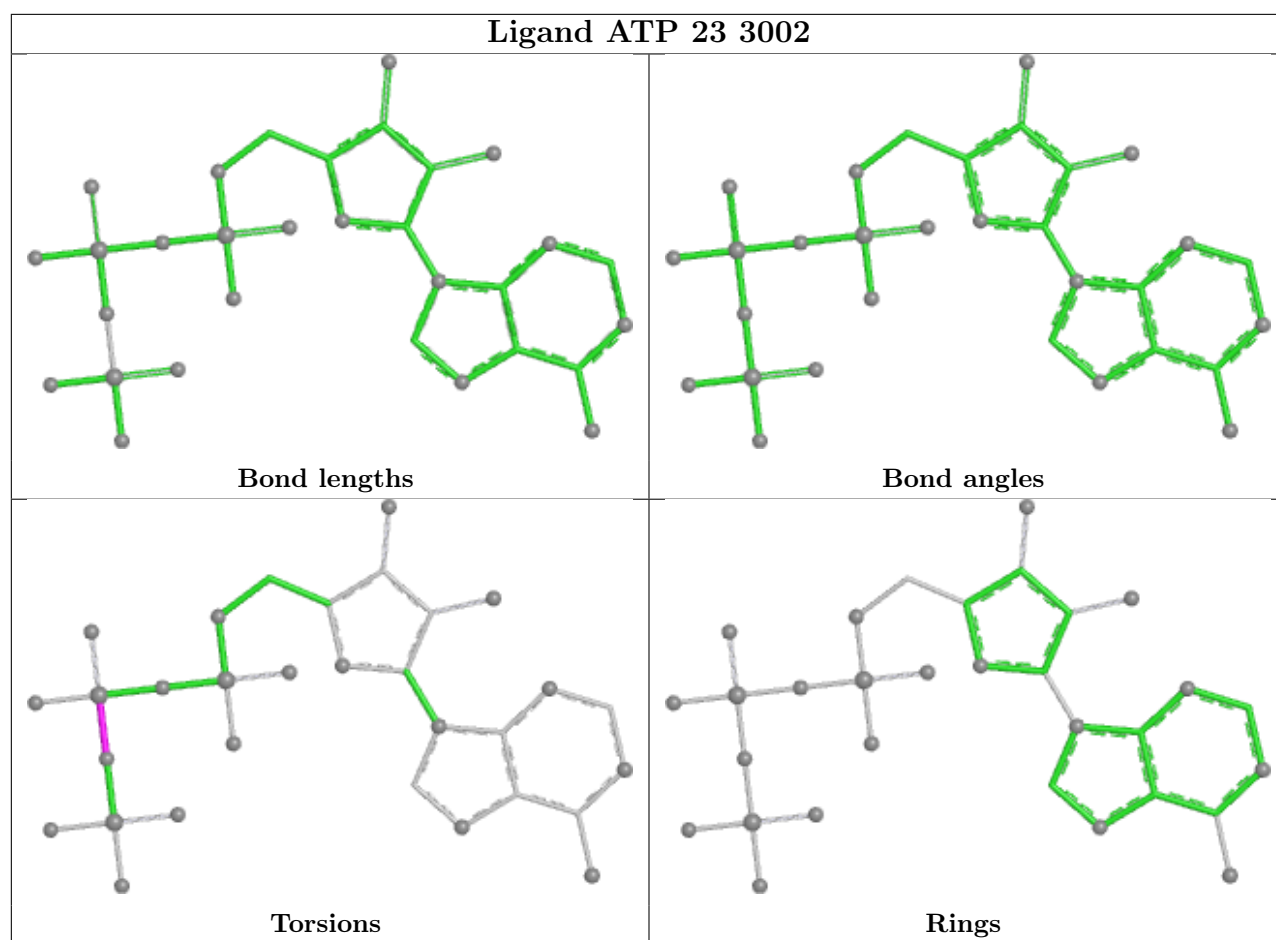
There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	23	3015	SPD	1	0
55	23	3003	PUT	1	0
55	23	3007	PUT	1	0
55	16	1601	PUT	1	0
56	23	3012	SPD	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

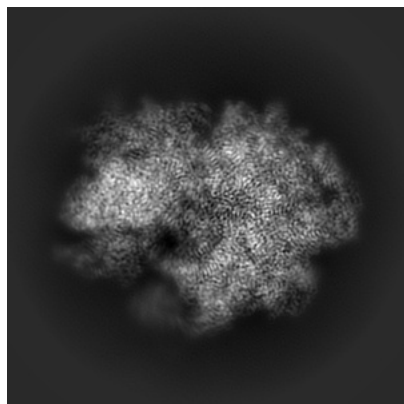
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48831. These allow visual inspection of the internal detail of the map and identification of artifacts.

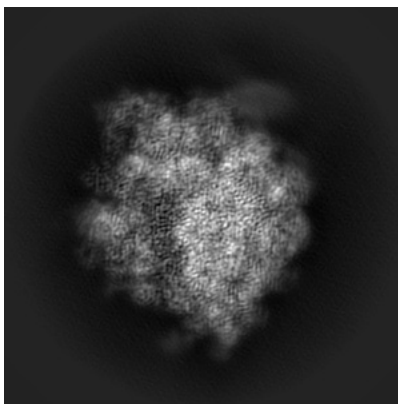
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

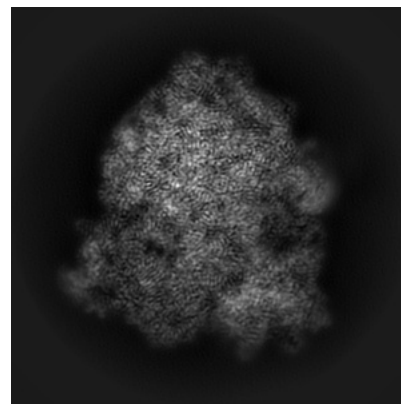
6.1.1 Primary map



X

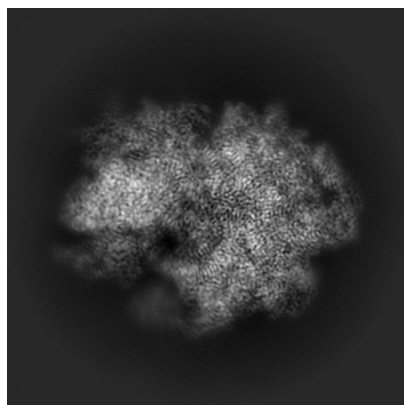


Y

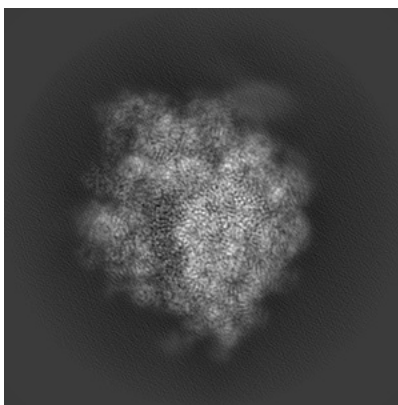


Z

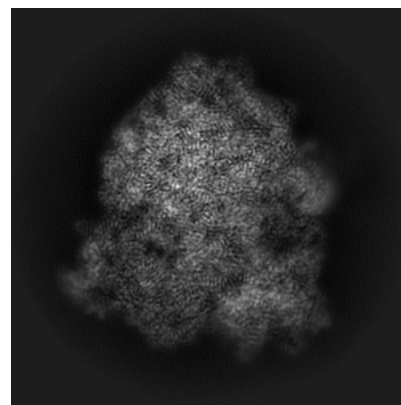
6.1.2 Raw map



X



Y

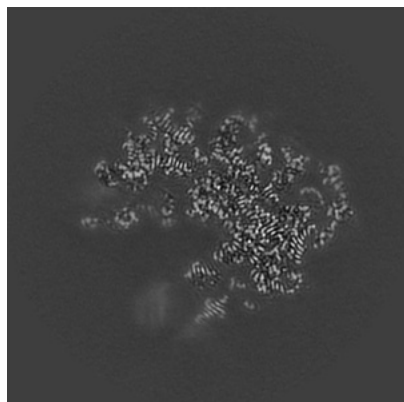


Z

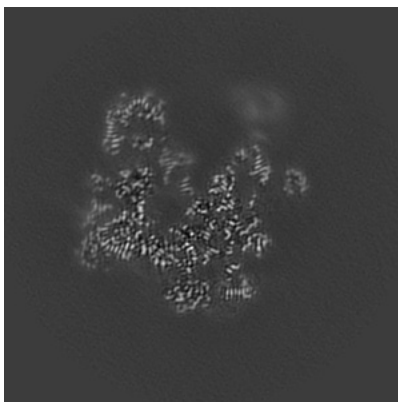
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

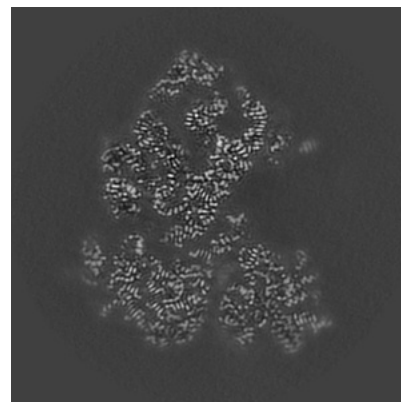
6.2.1 Primary map



X Index: 160

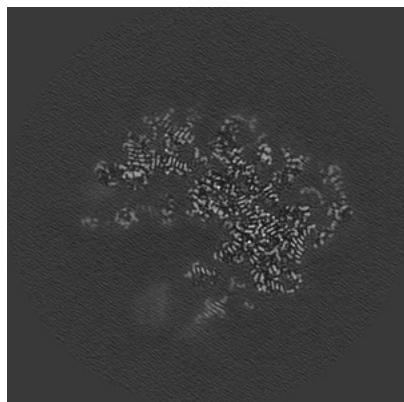


Y Index: 160

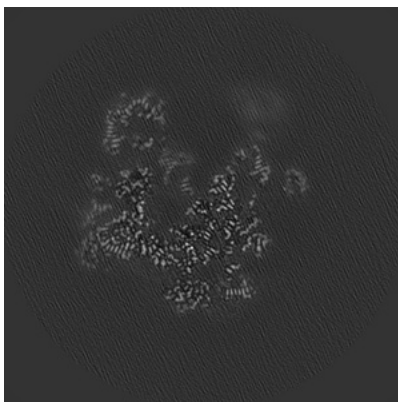


Z Index: 160

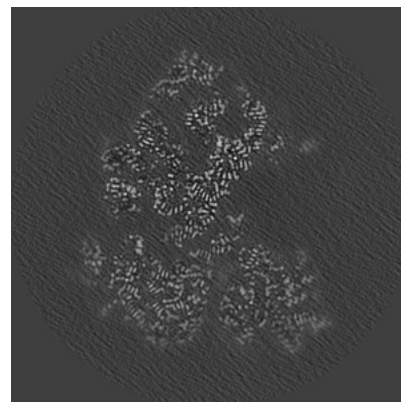
6.2.2 Raw map



X Index: 160



Y Index: 160

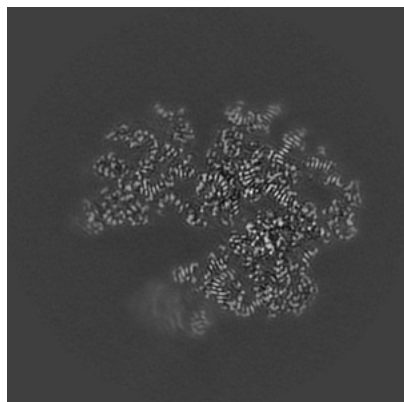


Z Index: 160

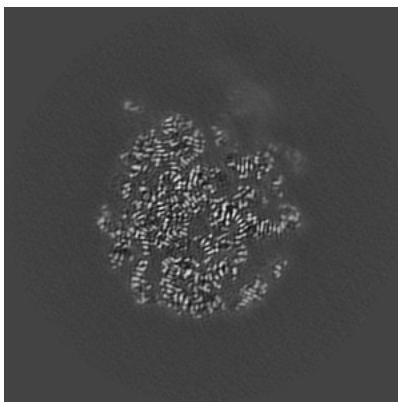
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

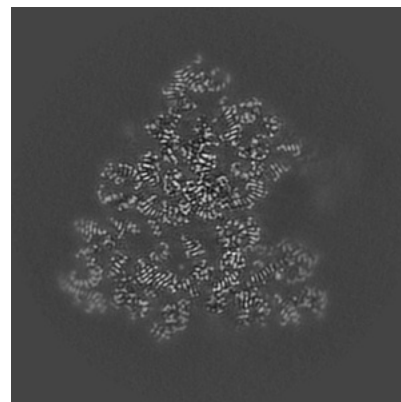
6.3.1 Primary map



X Index: 149

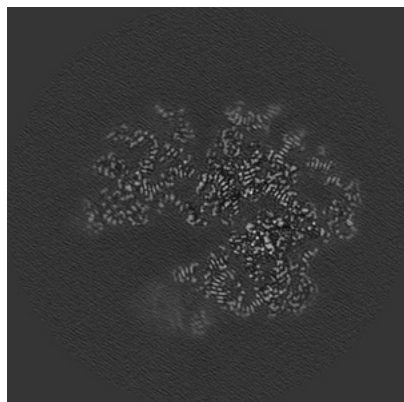


Y Index: 196

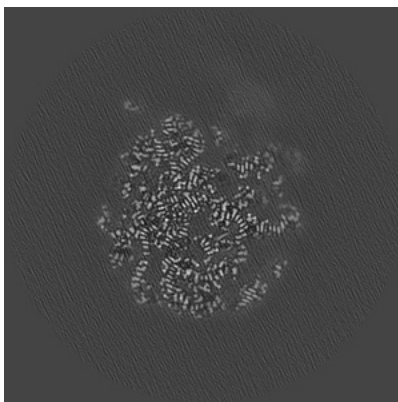


Z Index: 179

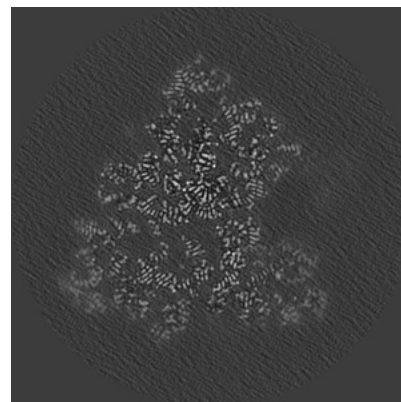
6.3.2 Raw map



X Index: 149



Y Index: 196

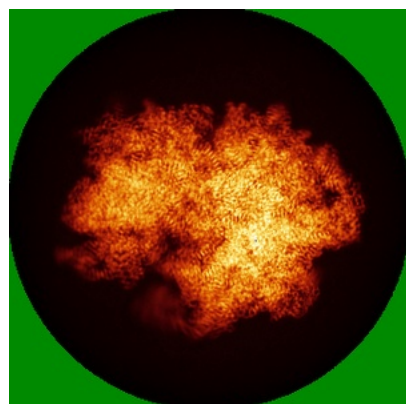


Z Index: 179

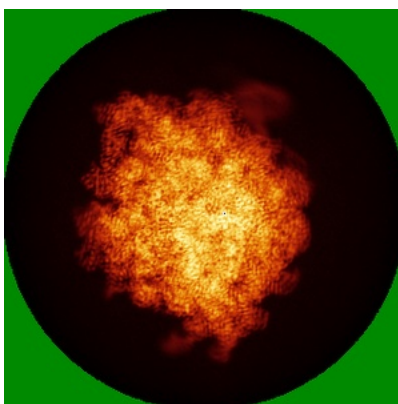
The images above show the largest variance slices of the map in three orthogonal directions.

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

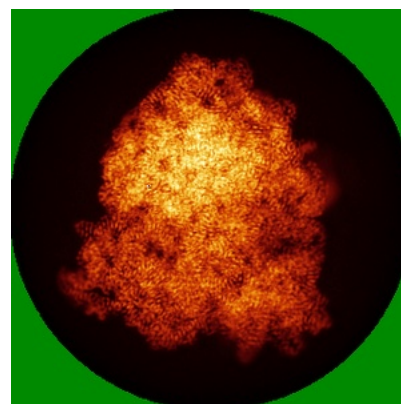
6.4.1 Primary map



X

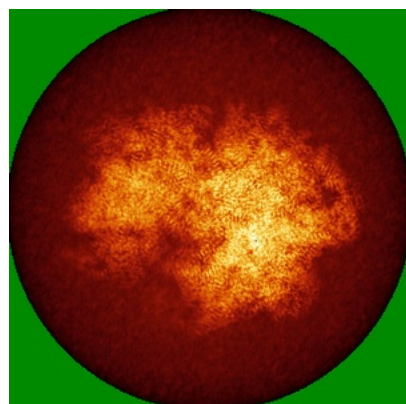


Y

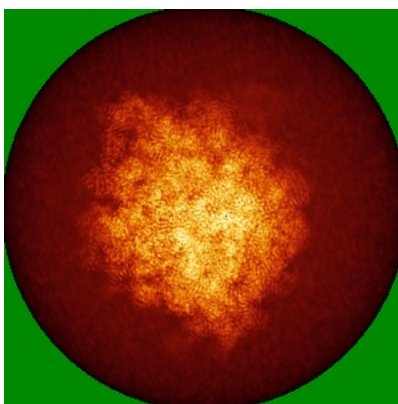


Z

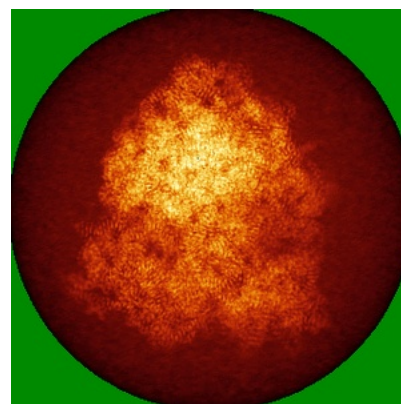
6.4.2 Raw map



X



Y

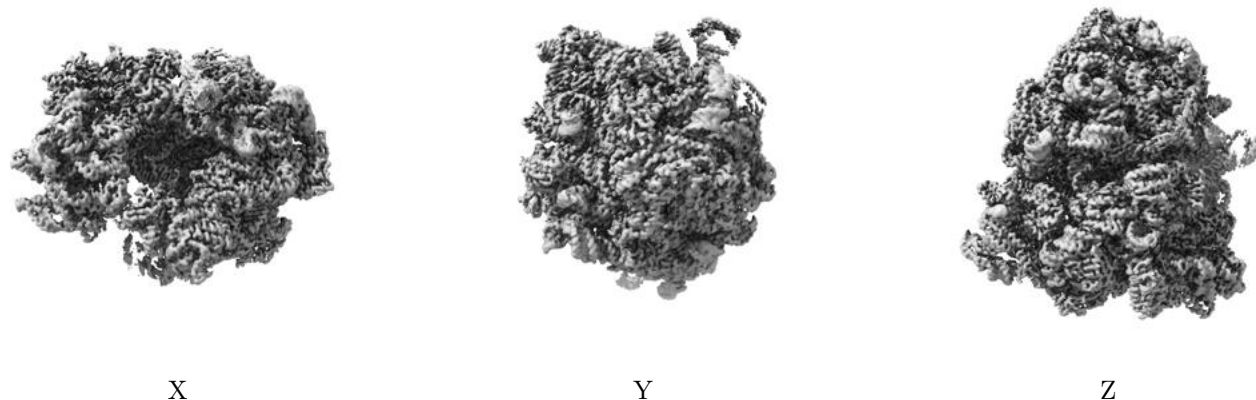


Z

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.

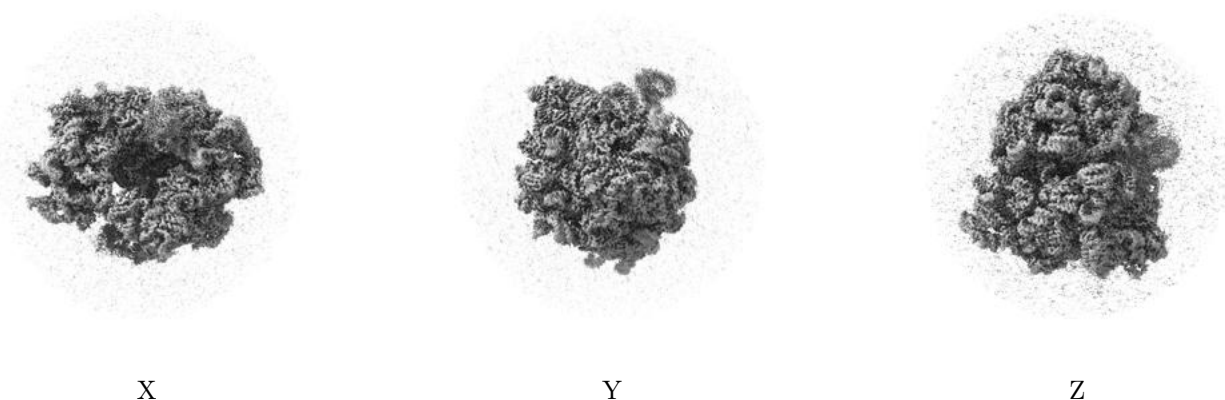
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. 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.

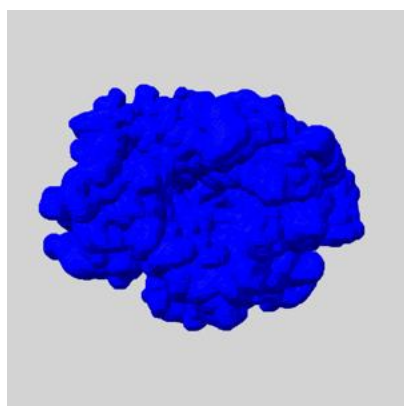
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

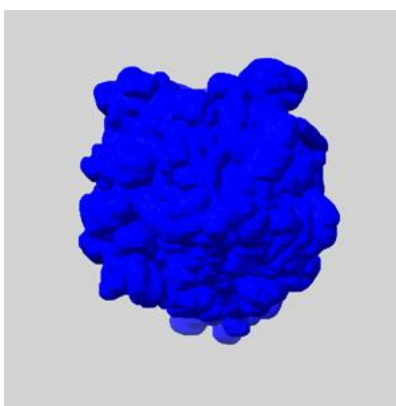
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

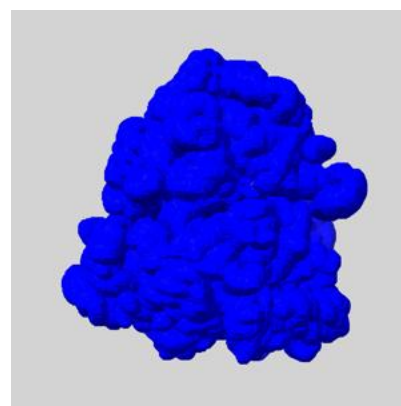
6.6.1 emd_48831_msk_1.map [i](#)



X



Y

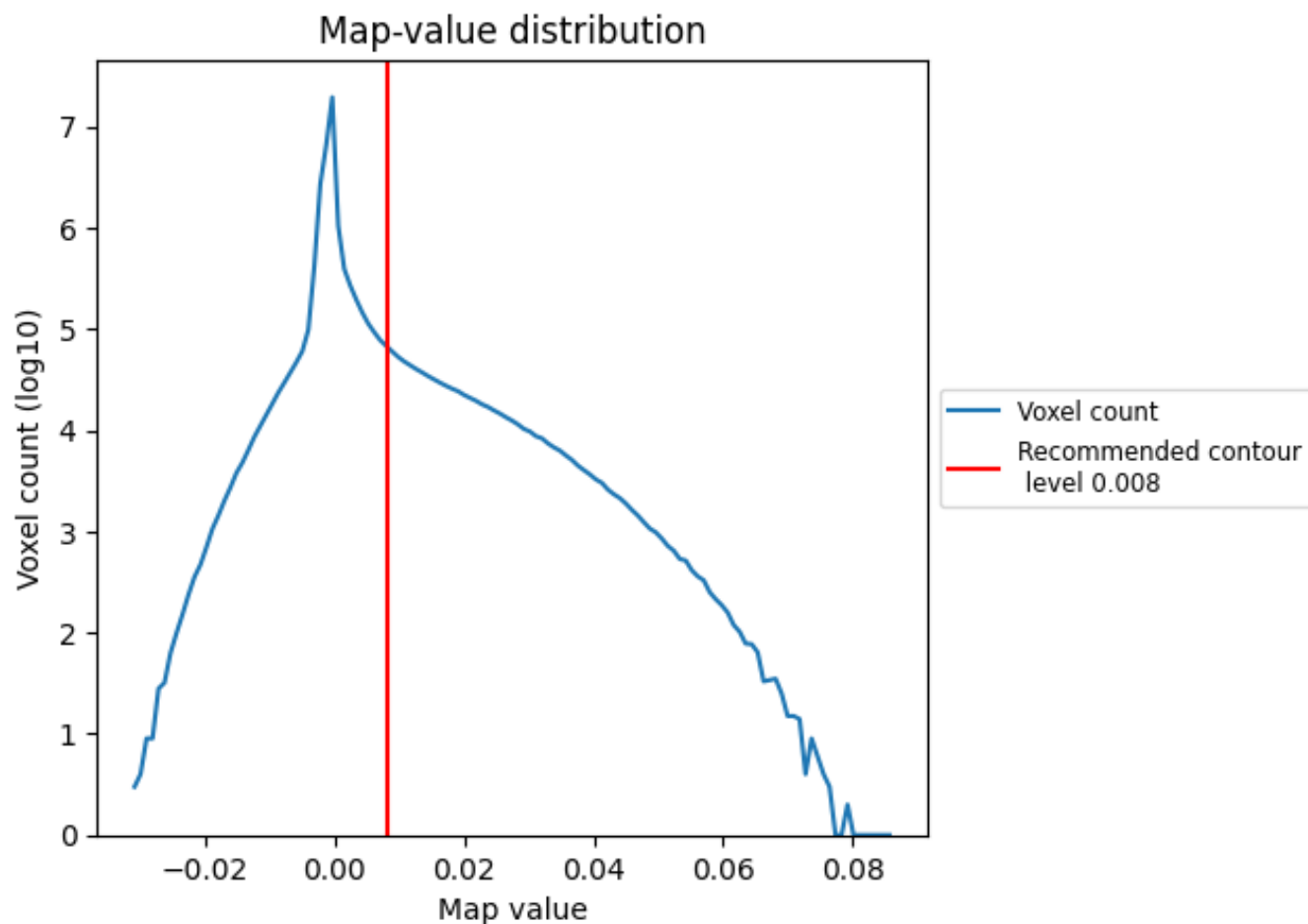


Z

7 Map analysis [i](#)

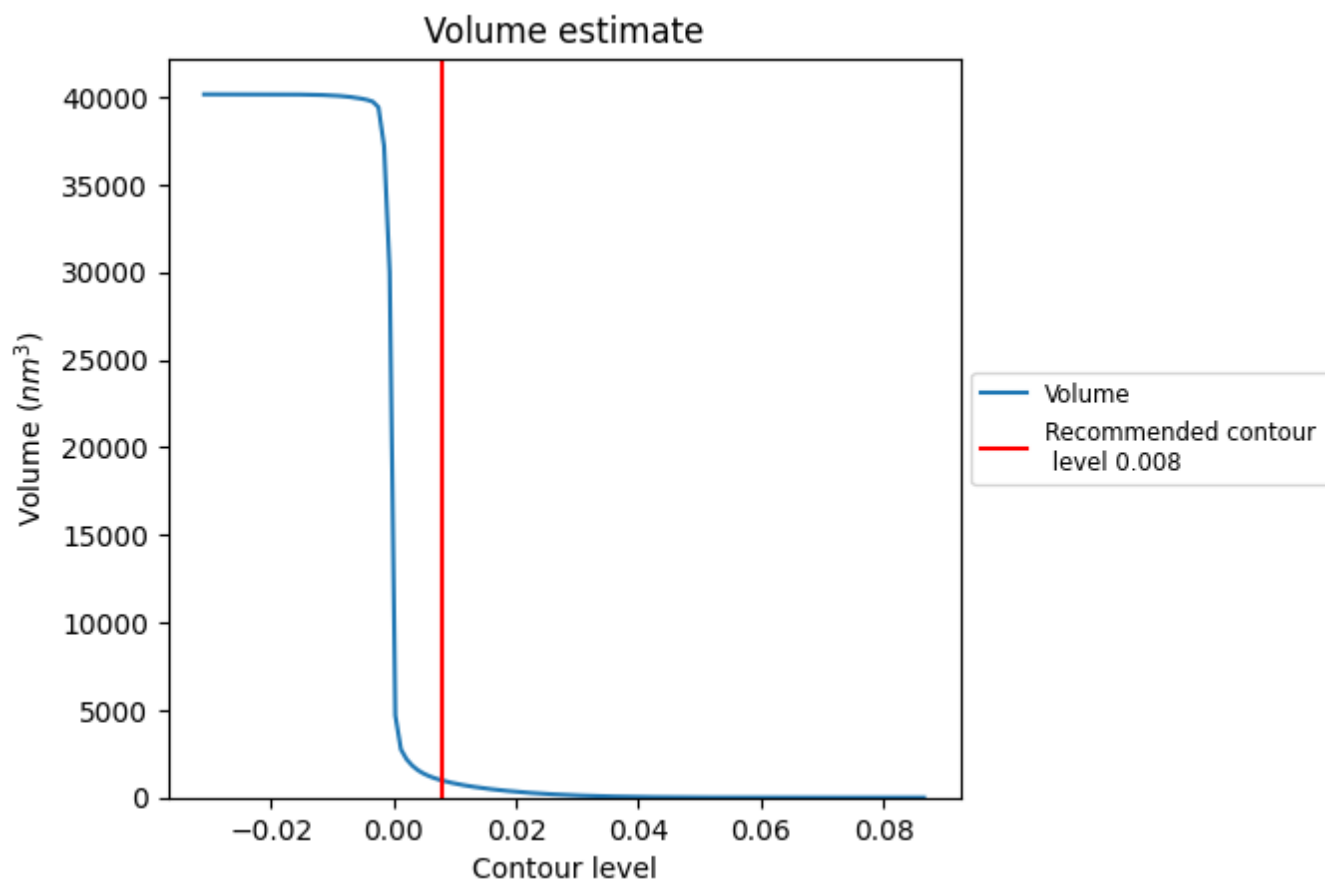
This section contains the results of statistical analysis of the map.

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.

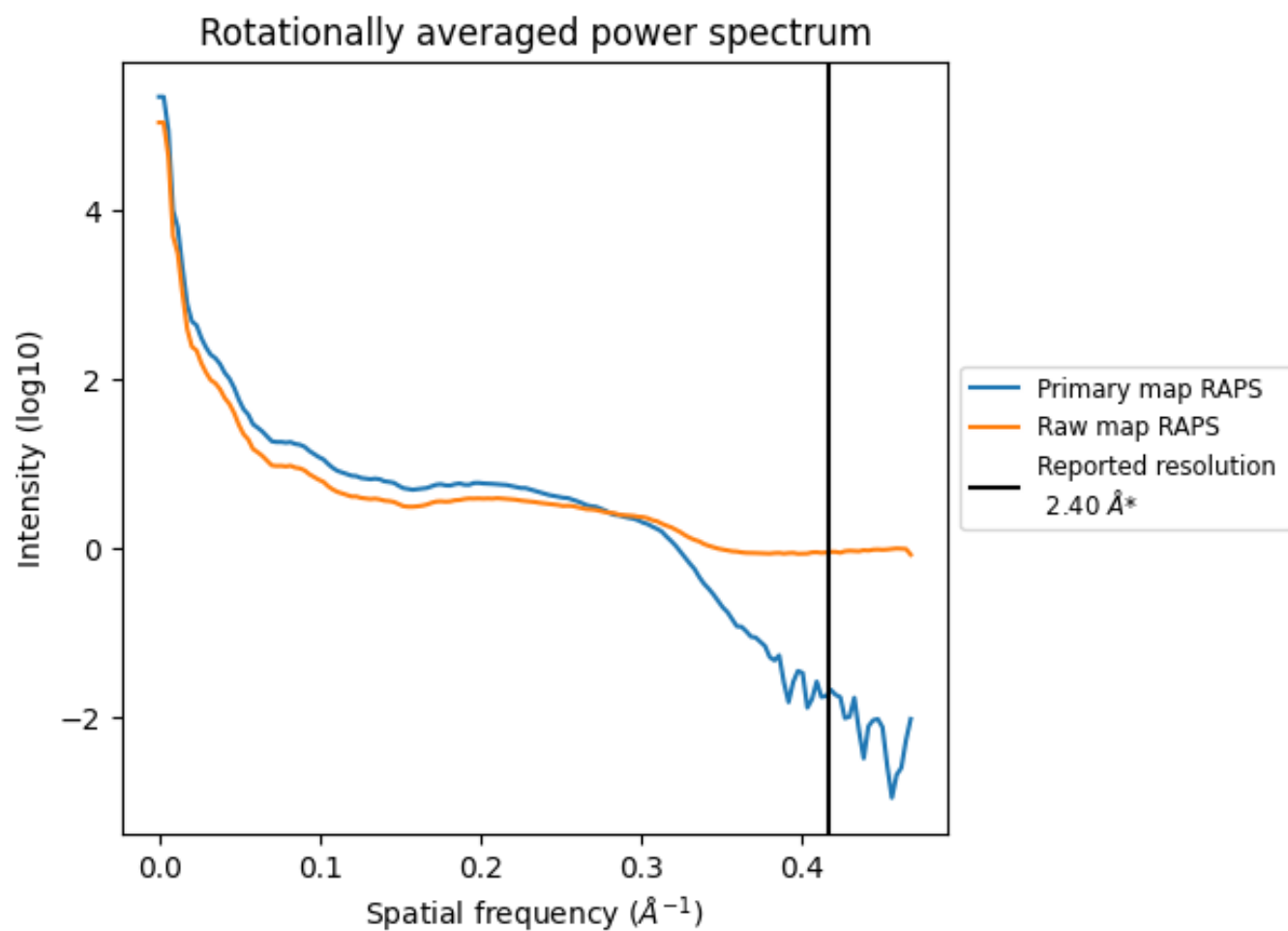
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 972 nm^3 ; this corresponds to an approximate mass of 878 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 ⓘ

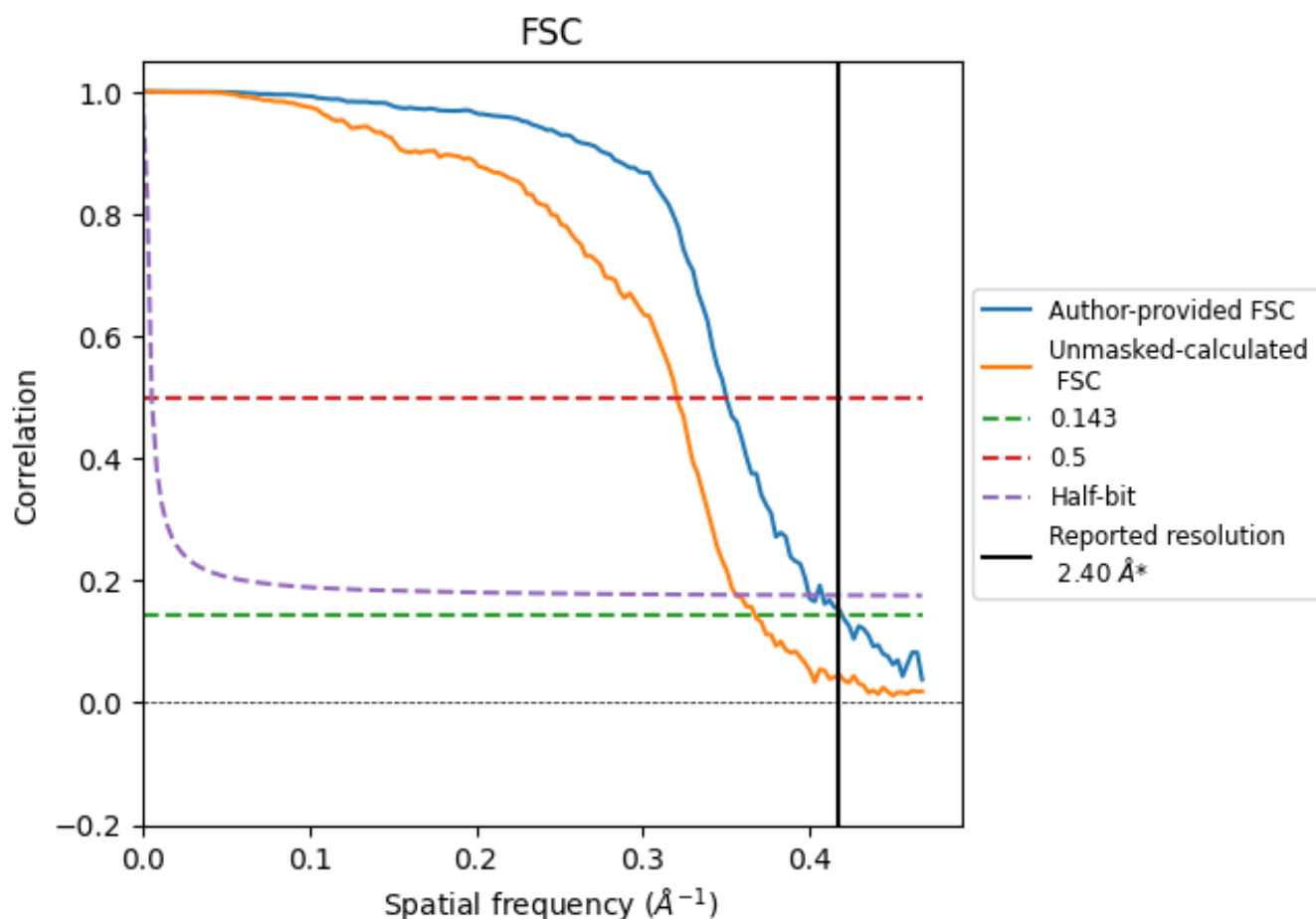


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8.2 Resolution estimates [i](#)

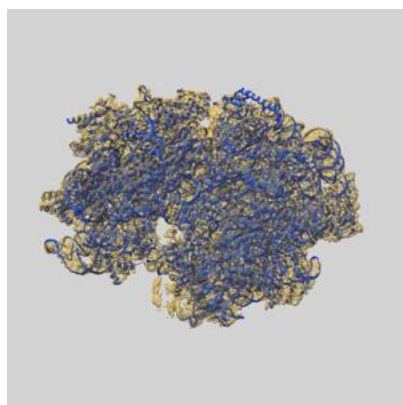
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.38	2.86	2.50
Unmasked-calculated*	2.72	3.12	2.81

*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 2.72 differs from the reported value 2.4 by more than 10 %

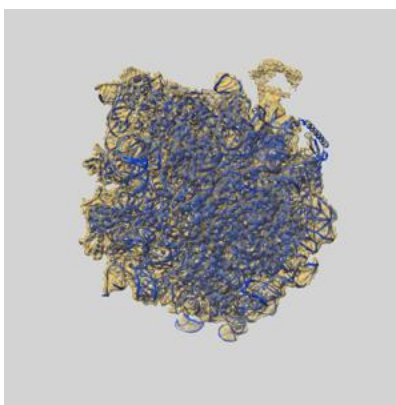
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48831 and PDB model 9N2C. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

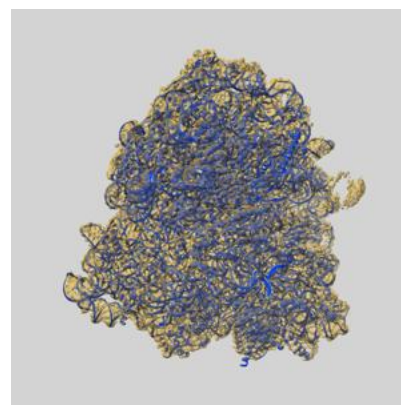
9.1 Map-model overlay [i](#)



X



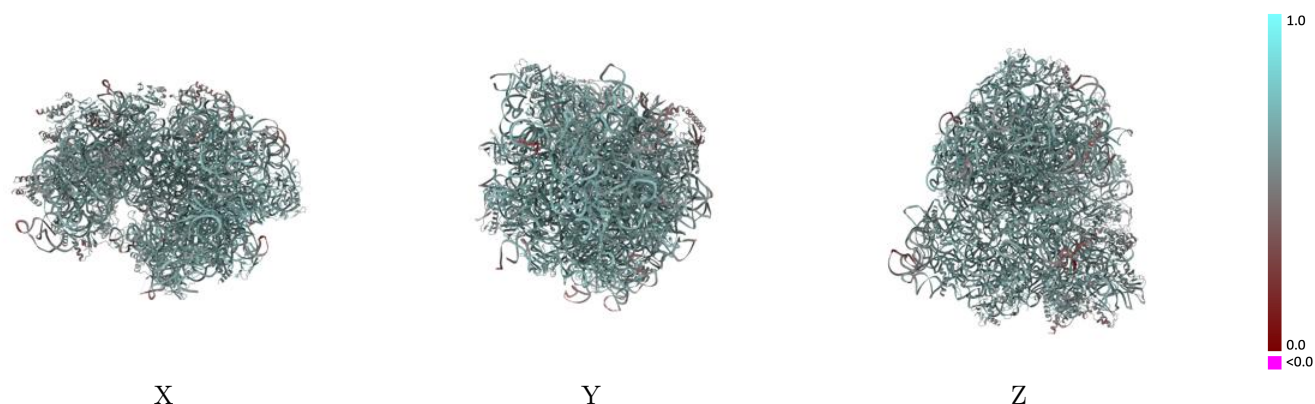
Y



Z

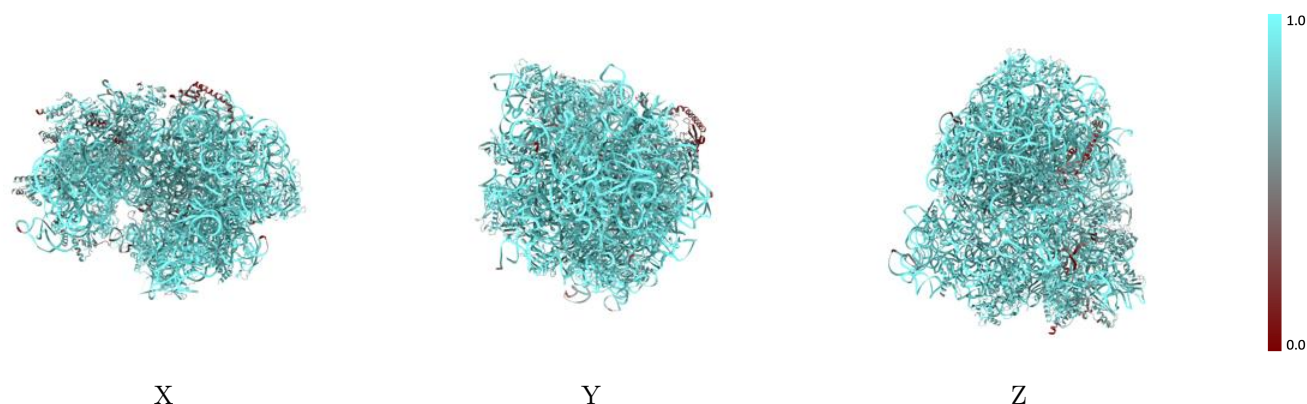
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



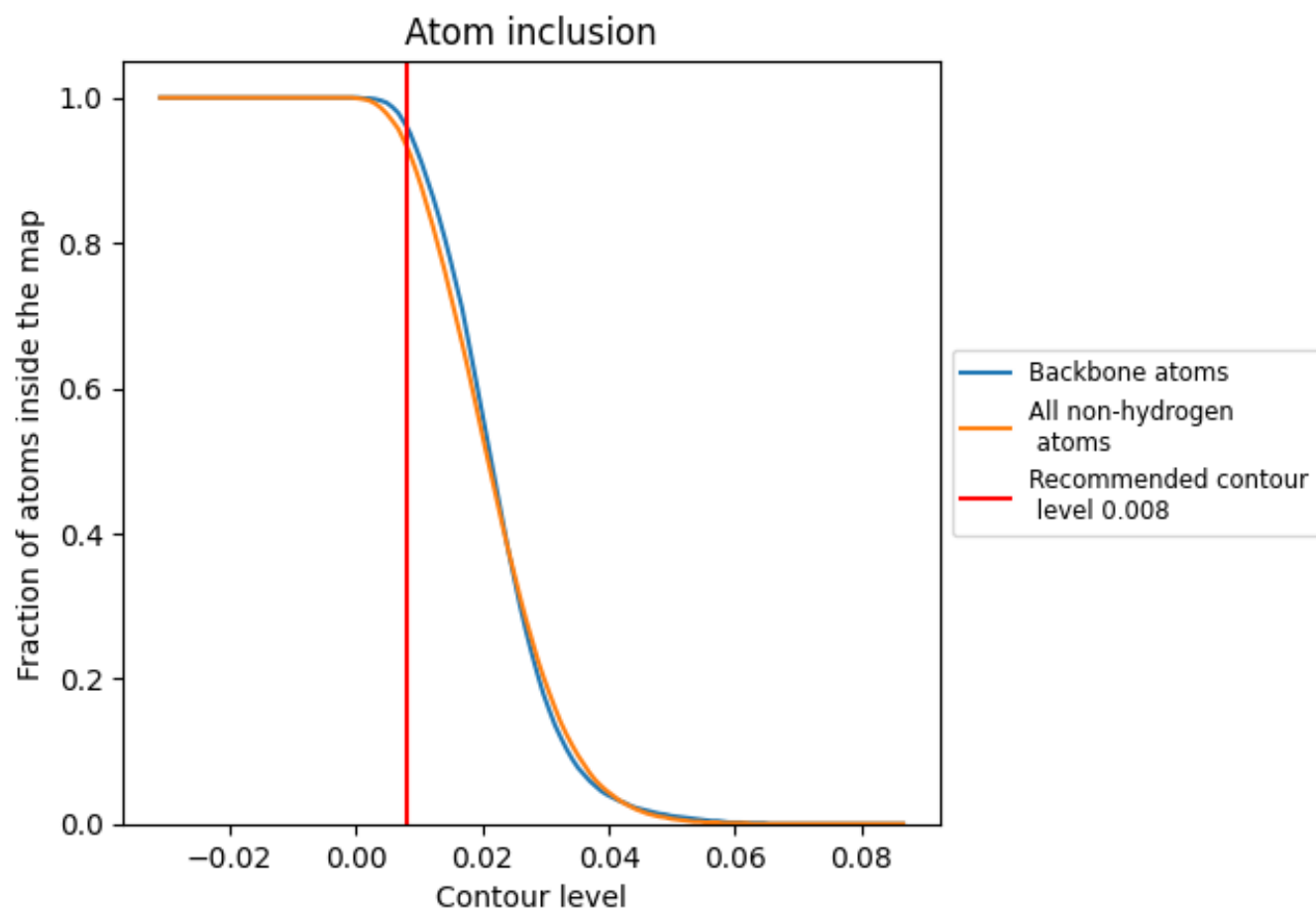
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 93% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9340	 0.5990
16	 0.9680	 0.5900
23	 0.9780	 0.6150
5	 0.9720	 0.5990
LB	 0.9350	 0.6350
LC	 0.9190	 0.6200
LD	 0.8920	 0.6060
LE	 0.7920	 0.5550
LF	 0.7850	 0.5390
LI	 0.3920	 0.4690
LM	 0.9240	 0.6180
LN	 0.9020	 0.6220
LO	 0.9090	 0.6120
LP	 0.9100	 0.6190
LQ	 0.9510	 0.6310
LR	 0.8750	 0.5730
LS	 0.8960	 0.6190
LT	 0.9450	 0.6290
LU	 0.9000	 0.6080
LV	 0.8990	 0.6140
LW	 0.8560	 0.5980
LX	 0.8790	 0.5870
LY	 0.8550	 0.5870
La	 0.8450	 0.6150
Lb	 0.9070	 0.6210
Lc	 0.8570	 0.5690
Ld	 0.8990	 0.6110
Le	 0.6810	 0.5120
Lf	 0.9040	 0.6250
Lg	 0.8570	 0.6060
Lh	 0.9490	 0.6460
Li	 0.9490	 0.6420
Lj	 0.9350	 0.6220
Pt	 0.8910	 0.5800
SB	 0.7560	 0.5360



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Chain	Atom inclusion	Q-score
SC	 0.8380	 0.5750
SD	 0.8500	 0.5770
SE	 0.8830	 0.5960
SF	 0.7980	 0.5510
SG	 0.7110	 0.5200
SH	 0.8870	 0.6040
SI	 0.8460	 0.5680
SJ	 0.7640	 0.5240
SK	 0.8640	 0.5760
SL	 0.8780	 0.6070
SM	 0.8310	 0.5640
SN	 0.8610	 0.5770
SO	 0.8840	 0.5890
SP	 0.8800	 0.5870
SQ	 0.8170	 0.5690
SR	 0.8440	 0.5690
SS	 0.8420	 0.5600
ST	 0.8850	 0.5820
SU	 0.6980	 0.5210
mR	 0.6990	 0.5100