



wwPDB EM Validation Summary Report ⓘ

Jun 24, 2026 – 02:28 AM EDT

PDB ID : 8EKC / pdb_00008ekc
EMDB ID : EMD-28197
Title : Escherichia coli 70S ribosome bound to thermorubin, deacylated P-site tRNA^fMet and aminoacylated A-site Phe-tRNA
Authors : Rybak, M.Y.; Gagnon, M.G.
Deposited on : 2022-09-20
Resolution : 2.70 Å(reported)
Based on initial model : 7K00

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

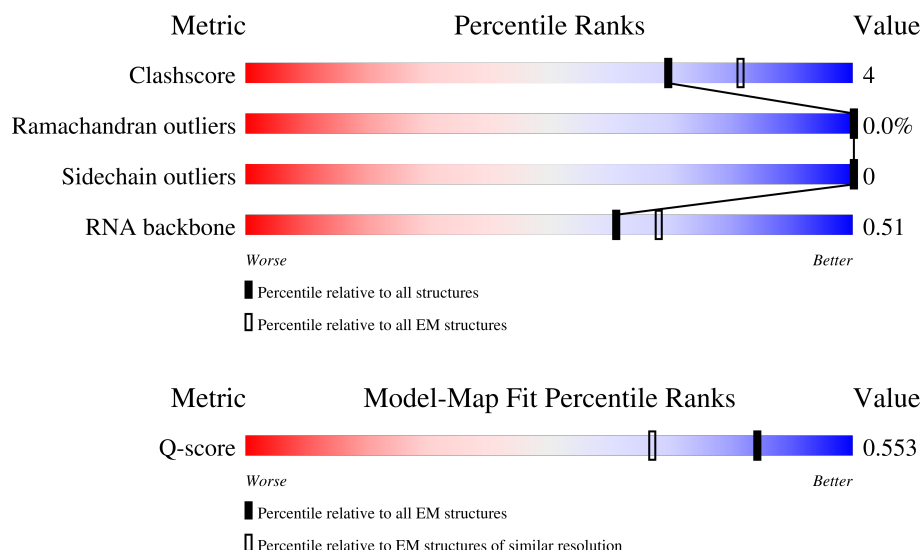
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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.



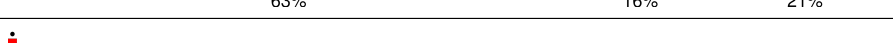
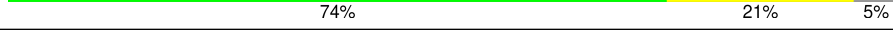
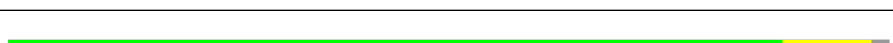
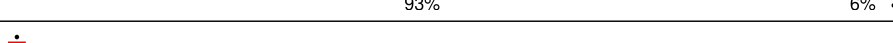
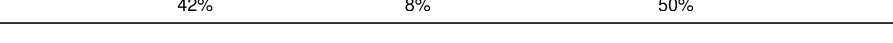
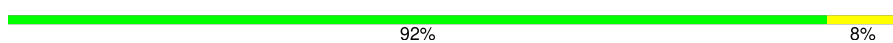
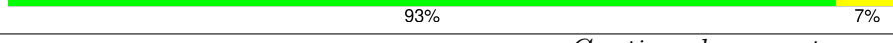
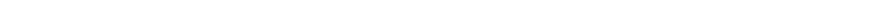
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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	a	1542	
2	b	241	
3	c	233	

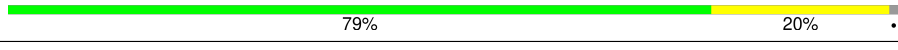
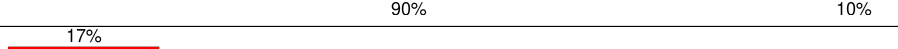
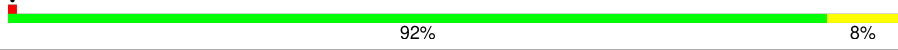
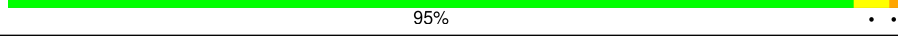
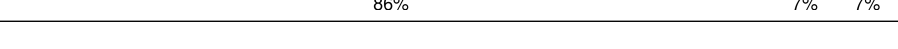
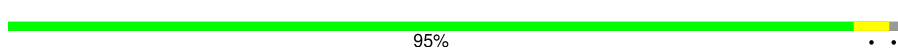
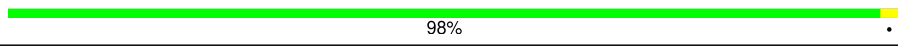
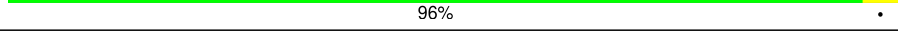
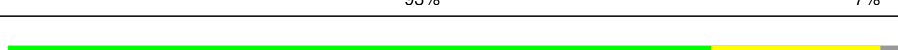
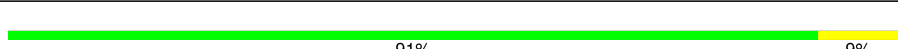
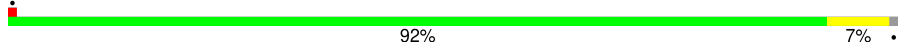
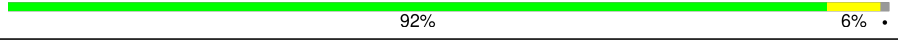
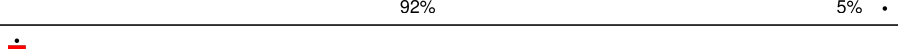
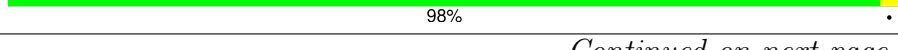
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Mol	Chain	Length	Quality of chain
4	d	206	
5	e	167	
6	f	131	
7	g	156	
8	h	130	
9	i	130	
10	j	103	
11	k	129	
12	l	124	
13	m	118	
14	n	101	
15	o	89	
16	p	82	
17	q	84	
18	r	75	
19	s	92	
20	t	87	
21	u	71	
22	w	76	
23	x	77	
24	v	24	
25	A	2904	
26	B	120	
27	C	273	
28	D	209	

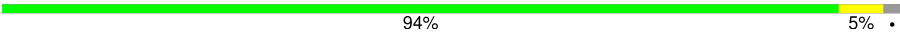
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Mol	Chain	Length	Quality of chain
29	E	201	
30	F	179	
31	G	177	
32	H	149	
33	L	142	
34	M	123	
35	N	144	
36	O	136	
37	P	127	
38	Q	117	
39	R	115	
40	S	118	
41	T	103	
42	U	110	
43	V	100	
44	W	104	
45	X	94	
46	Y	85	
47	Z	78	
48	1	63	
49	2	59	
50	3	70	
51	4	57	
52	5	55	
53	6	46	

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Mol	Chain	Length	Quality of chain
54	7	65	 94%5% •
55	8	38	 84%16%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 144543 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
1	a	1528	Total	C	N	O	P	0	0
			32803	14637	6019	10619	1528		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	224	Total	C	N	O	S	0	0
			1754	1110	315	321	8		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	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	e	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	152	Total	C	N	O	S	0	0
			1191	741	230	216	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	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	i	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	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	119	IAS	ASN	conflict	UNP A0A0H3PWX2

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	121	Total	C	N	O	S	0	0
			942	582	193	162	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	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	n	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	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	r	54	Total	C	N	O	0	0
			446	283	85	78		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	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	t	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	55	Total	C	N	O	S	0	0
			460	287	95	77	1		

- Molecule 22 is a RNA chain called A-site phenylalanine tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	w	74	Total	C	N	O	P	S	0	0
			1591	713	285	517	74	2		

- Molecule 23 is a RNA chain called P-site initiator tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	x	76	Total	C	N	O	P	S	0	0
			1625	725	294	529	76	1		

- Molecule 24 is a RNA chain called M-F-Stop mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	v	12	Total	C	N	O	P	0	0
			255	115	46	82	12		

- Molecule 25 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	2845	Total	C	N	O	P	0	0
			61097	27261	11245	19746	2845		

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

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

- Molecule 27 is a protein called 50S ribosomal protein L2.

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

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	D	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

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

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 33 is a protein called 50S ribosomal protein L13.

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

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	M	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 35 is a protein called 50S Ribosomal Protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	N	144	Total	C	N	O	S	0	0
			1052	653	207	190	2		

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	O	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	82	MS6	MET	conflict	UNP E6BI61

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	P	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 38 is a protein called 50S ribosomal protein L18.

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

- Molecule 39 is a protein called 50S ribosomal protein L19.

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

- Molecule 40 is a protein called 50S ribosomal protein L20.

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

- Molecule 41 is a protein called Ribosomal protein L21.

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

- Molecule 42 is a protein called 50S ribosomal protein L22.

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

- Molecule 43 is a protein called 50S ribosomal protein L23.

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

- Molecule 44 is a protein called 50S ribosomal protein L24.

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

- Molecule 45 is a protein called 50S ribosomal protein L25.

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

- Molecule 46 is a protein called 50S ribosomal protein L27.

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

- Molecule 47 is a protein called 50S ribosomal protein L28.

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

- Molecule 48 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 49 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	60	Total	C	N	O	S	0	0
			468	290	87	85	6		

- Molecule 51 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 52 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	5	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 54 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 55 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
56	a	132	Total	Mg	0
			132	132	
56	l	1	Total	Mg	0
			1	1	
56	n	1	Total	Mg	0
			1	1	
56	w	1	Total	Mg	0
			1	1	
56	x	2	Total	Mg	0
			2	2	
56	v	2	Total	Mg	0
			2	2	
56	A	555	Total	Mg	0
			555	555	
56	B	10	Total	Mg	0
			10	10	
56	C	3	Total	Mg	0
			3	3	
56	D	1	Total	Mg	0
			1	1	
56	N	1	Total	Mg	0
			1	1	
56	P	1	Total	Mg	0
			1	1	
56	S	1	Total	Mg	0
			1	1	
56	V	1	Total	Mg	0
			1	1	
56	4	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
56	7	1	Total Mg 1 1	0

-
- The chemical structure of T8B is a complex polycyclic molecule. It features a central benzene ring (C6-C7) fused to two other benzene rings (C8-C9 and C10-C11). The structure is substituted with several functional groups: a hydroxyl group (O7) at C16, an ester group (C12-C13-C14) at C11, a hydroxyl group (O8) at C18, an ester group (C19-C20-C21) at C20, a hydroxyl group (O9) at C23, and a complex side chain (C22-C23-C24-C25-C26) ending in a hydroxyl group (O10) and a carboxylic acid group (C27-C28-C29-C30-C31-C32). The molecule is labeled T8B.

Mol	Chain	Residues	Atoms			AltConf
57	a	1	Total	C	O	0
			44	32	12	

-
- Chemical structure of Phenylalanine (PHE) showing the amino acid backbone and the phenyl ring. The structure is labeled with various atoms and groups:
- Backbone:** The central carbon is labeled **CA(S)**. The amino group is labeled **N** and **H₂**. The carboxyl group is labeled **C**, **OH**, and **O**.
 - Side Chain:** The side chain is labeled **CB** (beta carbon) and **CG** (gamma carbon).
 - Phenyl Ring:** The phenyl ring is labeled with **CD1**, **CD2**, **CE1**, and **CE2** for the ring carbons.

Mol	Chain	Residues	Atoms				AltConf
58	w	1	Total	C	N	O	0
			11	9	1	1	

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
59	3	1	Total	Zn	0
			1	1	
59	8	1	Total	Zn	0
			1	1	

- Molecule 60 is water.

Mol	Chain	Residues	Atoms		AltConf
60	a	37	Total	O	0
			37	37	
60	n	1	Total	O	0
			1	1	
60	A	247	Total	O	0
			247	247	
60	B	4	Total	O	0
			4	4	
60	C	1	Total	O	0
			1	1	
60	D	1	Total	O	0
			1	1	
60	E	1	Total	O	0
			1	1	
60	N	1	Total	O	0
			1	1	
60	P	1	Total	O	0
			1	1	
60	R	1	Total	O	0
			1	1	
60	T	1	Total	O	0
			1	1	
60	V	1	Total	O	0
			1	1	
60	Z	1	Total	O	0
			1	1	
60	4	1	Total	O	0
			1	1	

Continued on next page...

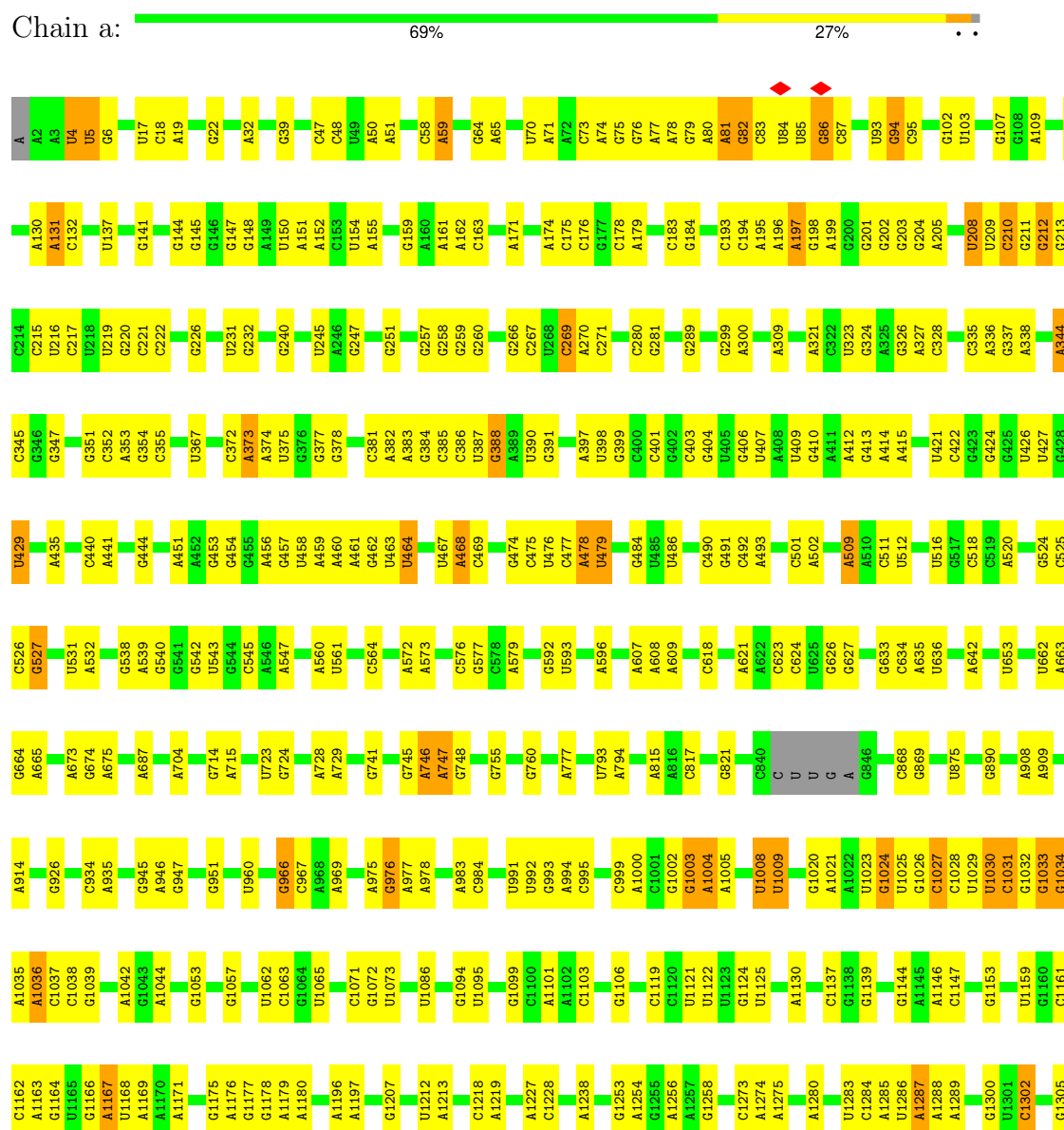
Continued from previous page...

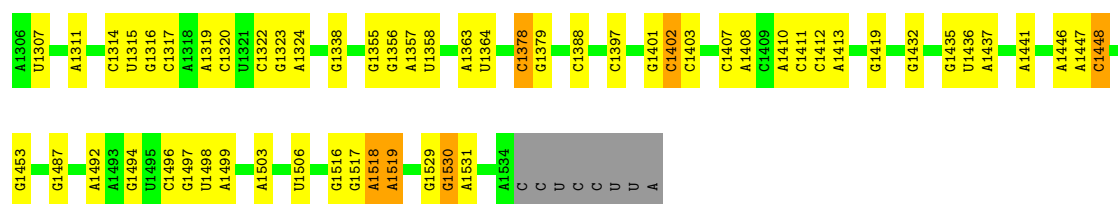
Mol	Chain	Residues	Atoms		AltConf
60	8	1	Total	O	0
			1	1	

3 Residue-property plots [i](#)

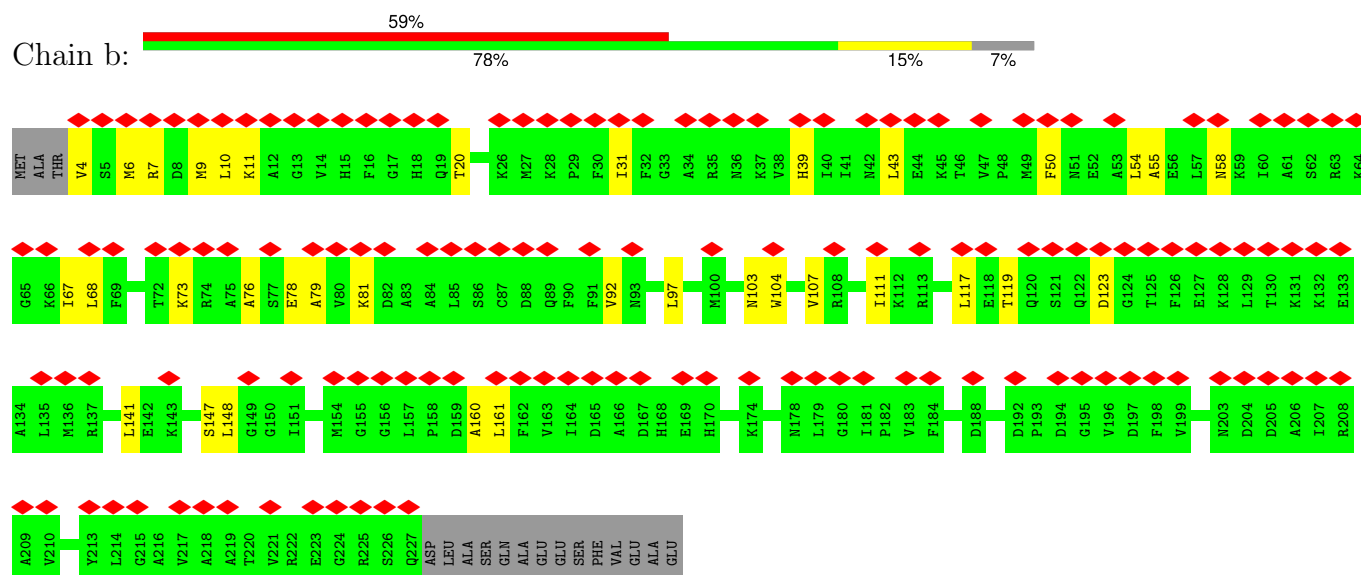
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

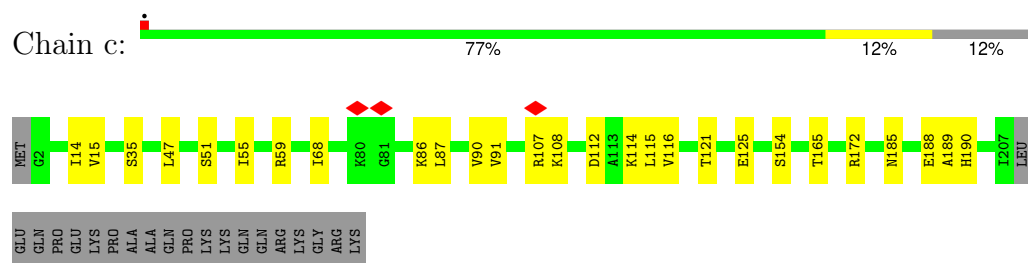




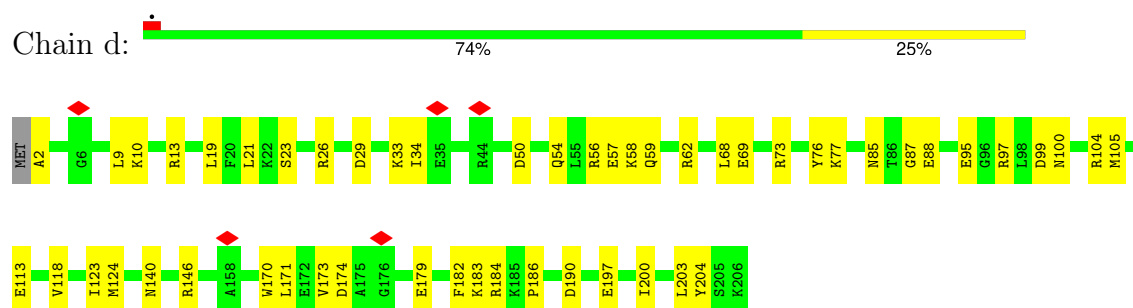
• Molecule 2: 30S ribosomal protein S2



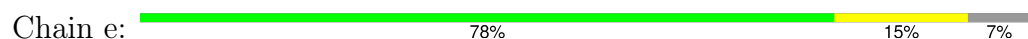
• Molecule 3: 30S ribosomal protein S3



• Molecule 4: 30S ribosomal protein S4

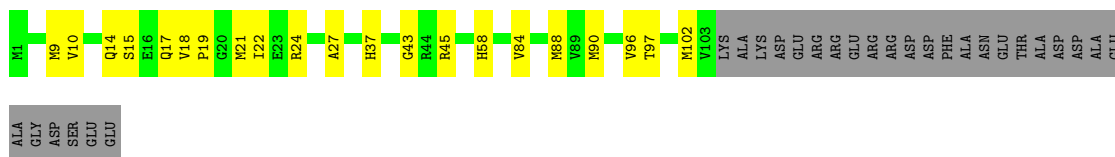


• Molecule 5: 30S ribosomal protein S5

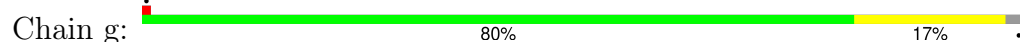




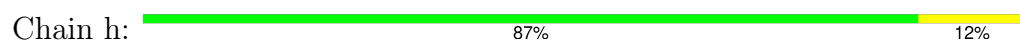
- Molecule 6: 30S ribosomal protein S6



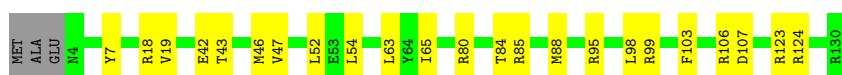
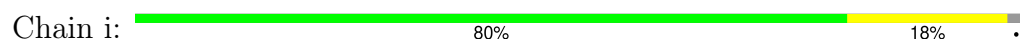
- Molecule 7: 30S ribosomal protein S7



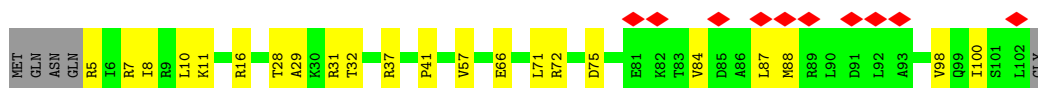
- Molecule 8: 30S ribosomal protein S8



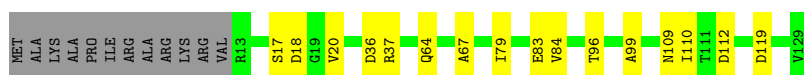
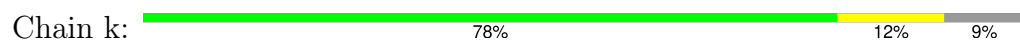
- Molecule 9: 30S ribosomal protein S9



- Molecule 10: 30S ribosomal protein S10

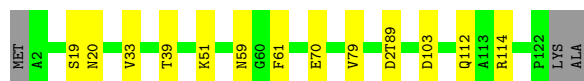


- Molecule 11: 30S ribosomal protein S11



- Molecule 12: 30S ribosomal protein S12

Chain l:  87% 10%



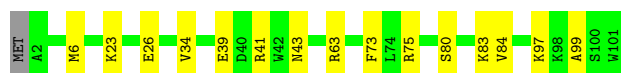
- Molecule 13: 30S ribosomal protein S13

Chain m:  88% 9%

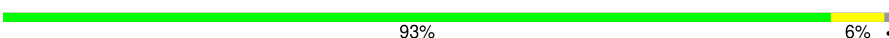


- Molecule 14: 30S ribosomal protein S14

Chain n:  84% 15%



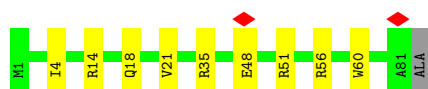
- Molecule 15: 30S ribosomal protein S15

Chain o:  93% 6%



- Molecule 16: 30S ribosomal protein S16

Chain p:  88% 11%



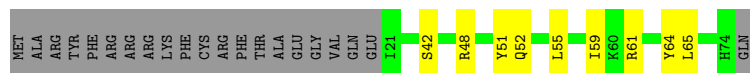
- Molecule 17: 30S ribosomal protein S17

Chain q:  86% 8% 6%

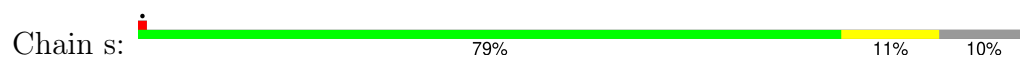


- Molecule 18: 30S ribosomal protein S18

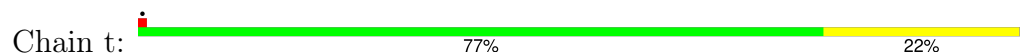
Chain r:  60% 12% 28%



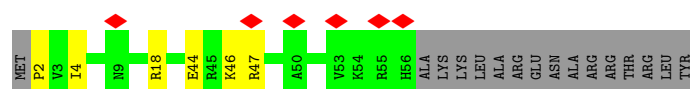
- Molecule 19: 30S ribosomal protein S19



- Molecule 20: 30S ribosomal protein S20



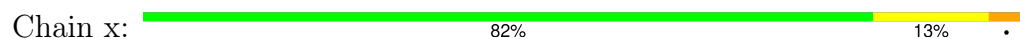
- Molecule 21: 30S ribosomal protein S21



- Molecule 22: A-site phenylalanine tRNA



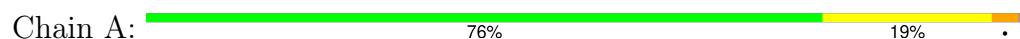
- Molecule 23: P-site initiator tRNA



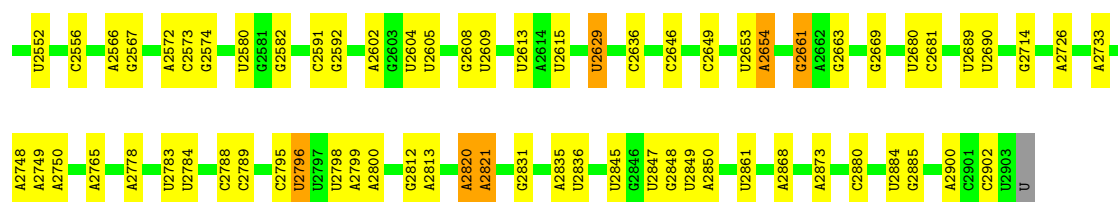
- Molecule 24: M-F-Stop mRNA



- Molecule 25: 23S Ribosomal RNA



U2402	G2204	G2127	C2036	A1872	G1649	G1452	A1241	A	C1007	A849	U710	C544	A354	A161
A2406	A2211	U2131	A2037	C1879	G1673	A1453	G1260	A	A1009	U850	G713	U545	U355	G186
G2410	A2225	U2132	G2038	U1883	G1674	A1469	A1263	A	A1009	G856	A716	U547	G356	G186
U2419	A2239	G2133	U2039	U1884	G1682	A1470	G1266	A	U1012	G858	C717	G548	U357	A191
A2425	G2238	A2134	C2043	A1889	U1683	G1482	G1267	C	C1013	G859	A718	C550	U359	C192
G2428	A2135	G2136	C2055	A1890	G1715	G1483	U1263	C	G1026	A866	A721	U558	U360	A196
G2430	G2239	G2137	G2056	A1905	U1720	A1493	U1263	U	A1027	A362	A722	A362	A362	A199
A2435	U2243	G2144	A2060	G1905	G1721	A1495	G1266	A	A1028	A877	G725	A563	G363	A199
U2441	G2251	C2145	A2062	U1911	U1729	A1496	U1267	U	C1030	G881	G726	U573	U364	G215
G2445	U2259	C2146	C2063	A1912	C1730	A1508	A1268	A	G1031	G882	A730	A574	U365	A216
U2448	C2268	C2147	C2065	3TD1915	G1731	A1509	G1271	G	A1032	U884	C	U576	G366	A221
U2457	A2268	G2148	G2069	A1916	C1732	G1510	U1272	U	U1033	U884	C736	U577	G367	A222
A2469	A2273	G2152	A2070	U1917	G1738	A1515	U1273	C	G1036	C888	G745	A586	G366	A223
U2473	A2274	C2153	A2071	G1929	A1739	G1524	C1289	A	G1037	C889	U746	A586	G366	U224
U2478	C2283	A2154	C2072	G1930	G1743	G1529	U1294	C	G1038	C890	U747	A592	A404	A233
U2488	A2287	U2155	U2074	A1937	A1744	U1534	G1300	G	A1039	C891	C758	U593	G411	G248
A2489	U2291	C2156	U2075	A1938	A1745	A1535	A1301	G	C1045	U895	A764	A603	A412	C249
U2474	U2292	G2157	U2076	U1939	U1747	C1536	A1321	U	G1047	U896	G775	A608	C414	G250
C2475	C2295	G2158	A2097	C1941	C1764	G1537	U1352	C	C1052	A900	G776	A609	A415	A251
A2476	U2305	C2163	U2098	U1955	C1771	A1542	U1352	A	C	A910	A782	A608	A415	C264
U2477	C2308	A2168	U2099	C1962	A1772	A1544	A1354	G	A	G914	A783	A612	A422	C269
A2478	A2322	A2169	A2101	U1963	A1773	A1545	C1357	G	G	C915	G784	A613	A428	A270
G2494	A2322	A2170	C2103	G1964	A1786	G1546	G1358	U	A	U927	G785	U615	A456	A271
G2488	G2325	A2171	C2104	C1967	C1800	A1566	A1365	U	U	U931	A789	G618	A479	C272
C2498	C2326	U2172	U2105	A1970	A1801	A1569	U1379	U	G	A627	A792	A627	A480	C273
C2499	A2327	C2176	U2106	U1971	A1802	U1578	A1383	C	C	C946	A793	A627	G481	U276
G2502	A2328	C2177	G2107	G1972	A1803	A1583	A1386	U	U	A947	A794	C634	A491	A277
U2503	U2329	C2178	A2108	U1991	A1808	U1584	A1387	A	U	C948	G798	C635	A504	U280
U2504	A2333	C2179	G2110	G1992	C1816	C1585	A1395	C	A	U955	G805	A637	A505	C281
G2505	U2334	U2180	U2111	U1993	A1587	A1586	U1405	G	A	U958	C806	U639	A508	A282
A2518	C2339	U2181	G2112	C2006	G1587	A1587	U1406	A	A	C961	U807	C640	C509	G283
C2519	A2350	A2182	U2113	G2012	A1590	A1591	U1416	C	C	C968	C812	C645	A508	U284
C2520	G2361	A2183	G2114	G2012	A1591	A1609	G1417	U	A	G974	C814	U646	C509	G285
G2529	A2377	U2186	A2117	A2020	A1618	A1618	C1417	A	C	U827	U828	G647	G512	U286
G2535	U2188	U2187	U2118	C2023	A1618	A1618	A1420	C	C	A983	U832	U653	G530	U287
G2538	U2189	U2188	A2119	G2027	U1856	A1632	C1428	A	A	A984	A833	A655	C631	G288
C2539	G2190	G2190	G2120	G2027	A1857	A1632	G1429	C	C	C985	A845	U653	G532	U289
U2547	A2191	U2192	G2123	A2030	A1858	G1645	A1434	A	U	A996	U846	U653	G532	G307
U2548	U2192	U2192	G2124	A2031	U1864	C1646	G1435	U	U	A1000	U847	U653	G532	A310
	U2194	U2194	G2125	A2033	U1647	U1647	G1435	U	U	A1000	C848	U653	G532	A311
	A2198	A2198	A2126	A2033	U1648	U1648	G1435	A	A	A1001		U709	U653	G329



• Molecule 26: 5S Ribosomal RNA

Chain B: 78% 18%



• Molecule 27: 50S ribosomal protein L2

Chain C: 92% 8%



• Molecule 28: 50S ribosomal protein L3

Chain D: 93% 7%



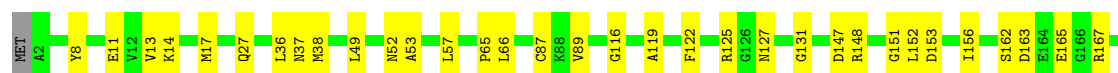
• Molecule 29: 50S ribosomal protein L4

Chain E: 91% 9%



• Molecule 30: 50S ribosomal protein L5

Chain F: 79% 20%



• Molecule 31: 50S ribosomal protein L6

Chain G: 90% 10%





- Molecule 38: 50S ribosomal protein L18

Chain Q: 93% 6%



- Molecule 39: 50S ribosomal protein L19

Chain R: 90% 9%



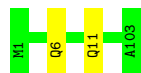
- Molecule 40: 50S ribosomal protein L20

Chain S: 95% 2%



- Molecule 41: Ribosomal protein L21

Chain T: 98% 2%



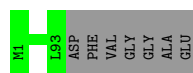
- Molecule 42: 50S ribosomal protein L22

Chain U: 96% 2%



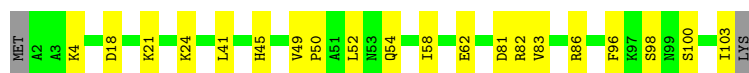
- Molecule 43: 50S ribosomal protein L23

Chain V: 93% 7%



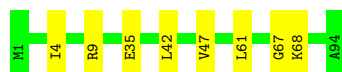
- Molecule 44: 50S ribosomal protein L24

Chain W: 79% 19%



- Molecule 45: 50S ribosomal protein L25

Chain X: 91% 9%



- Molecule 46: 50S ribosomal protein L27

Chain Y: 92% 7%



- Molecule 47: 50S ribosomal protein L28

Chain Z: 92% 6%



- Molecule 48: 50S ribosomal protein L29

Chain 1: 92% 5%



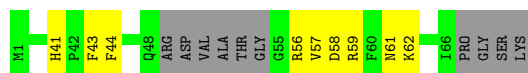
- Molecule 49: 50S ribosomal protein L30

Chain 2: 85% 14%



- Molecule 50: 50S ribosomal protein L31

Chain 3: 73% 13% 14%



- Molecule 51: 50S ribosomal protein L32

Chain 4: 88% 9%



- Molecule 52: 50S ribosomal protein L33

Chain 5: 89% 7%



- Molecule 53: 50S ribosomal protein L34

Chain 6: 98%



- Molecule 54: 50S ribosomal protein L35

Chain 7: 94% 5%



- Molecule 55: 50S ribosomal protein L36

Chain 8: 84% 16%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	310702	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.941	Depositor
Minimum map value	-0.713	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.085	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	440.32, 440.32, 440.32	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	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, MS6, MIA, MEQ, IAS, UR3, 6MZ, H2U, 5MU, T8B, OMG, PSU, 4OC, G7M, 3TD, 5MC, MA6, D2T, 2MA, 2MG, MG, 1MG, OMU, OMC, 4SU, ZN

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	a	0.26	0/36450	0.32	0/56856
2	b	0.14	0/1785	0.35	0/2404
3	c	0.18	0/1651	0.36	0/2225
4	d	0.18	0/1665	0.39	0/2227
5	e	0.24	0/1165	0.39	0/1568
6	f	0.23	0/858	0.44	0/1160
7	g	0.18	0/1206	0.40	0/1617
8	h	0.23	0/989	0.36	0/1326
9	i	0.18	0/1034	0.33	0/1375
10	j	0.17	0/796	0.42	0/1077
11	k	0.22	0/884	0.35	0/1191
12	l	0.23	0/945	0.43	0/1268
13	m	0.19	0/900	0.31	0/1204
14	n	0.17	0/817	0.29	0/1088
15	o	0.24	0/722	0.36	0/964
16	p	0.17	0/653	0.39	0/877
17	q	0.21	0/650	0.39	0/871
18	r	0.23	0/453	0.34	0/609
19	s	0.17	0/680	0.31	0/915
20	t	0.24	0/676	0.49	0/895
21	u	0.15	0/467	0.25	0/620
22	w	0.33	0/1605	0.39	0/2494
23	x	0.27	0/1725	0.31	0/2689
24	v	0.27	0/285	0.25	0/441
25	A	0.39	0/67852	0.40	1/105848 (0.0%)
26	B	0.30	0/2876	0.35	0/4483
27	C	0.32	0/2121	0.41	0/2852
28	D	0.34	0/1576	0.44	0/2119
29	E	0.29	0/1571	0.37	0/2113
30	F	0.22	0/1434	0.34	0/1926
31	G	0.23	0/1343	0.39	0/1816

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	H	0.15	0/306	0.44	0/413
33	L	0.32	0/1152	0.37	0/1551
34	M	0.32	0/955	0.41	0/1279
35	N	0.31	0/1061	0.38	0/1412
36	O	0.31	0/1073	0.42	0/1433
37	P	0.35	0/958	0.45	0/1281
38	Q	0.25	0/902	0.36	0/1209
39	R	0.32	0/929	0.36	0/1242
40	S	0.36	0/960	0.36	0/1278
41	T	0.31	0/829	0.38	0/1107
42	U	0.31	0/864	0.32	0/1156
43	V	0.29	0/744	0.38	0/994
44	W	0.27	0/787	0.43	0/1051
45	X	0.27	0/766	0.35	0/1025
46	Y	0.31	0/642	0.44	0/848
47	Z	0.29	0/635	0.36	0/848
48	1	0.25	0/496	0.29	0/660
49	2	0.30	0/453	0.37	0/605
50	3	0.14	0/475	0.28	0/633
51	4	0.34	0/440	0.38	0/588
52	5	0.25	0/424	0.41	0/565
53	6	0.36	0/380	0.37	0/498
54	7	0.33	0/513	0.37	0/676
55	8	0.30	0/303	0.37	0/397
All	All	0.33	0/154881	0.37	1/231867 (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
36	O	0	1
54	7	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	512	G	O4'-C1'-N9	5.47	116.41	108.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
54	7	30	ARG	Peptide
36	O	81	4D4	Mainchain

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	a	32803	0	16528	242	0
2	b	1754	0	1782	28	0
3	c	1624	0	1696	17	0
4	d	1643	0	1707	40	0
5	e	1152	0	1196	17	0
6	f	839	0	833	16	0
7	g	1191	0	1245	15	0
8	h	979	0	1031	11	0
9	i	1022	0	1070	19	0
10	j	786	0	828	13	0
11	k	877	0	884	9	0
12	l	942	0	999	8	0
13	m	891	0	952	9	0
14	n	805	0	844	9	0
15	o	714	0	734	3	0
16	p	643	0	661	7	0
17	q	641	0	682	4	0
18	r	446	0	472	6	0
19	s	663	0	688	8	0
20	t	670	0	719	15	0
21	u	460	0	486	5	0
22	w	1591	0	817	8	0
23	x	1625	0	829	2	0
24	v	255	0	129	0	0
25	A	61097	0	30752	210	0
26	B	2572	0	1301	11	0
27	C	2082	0	2154	14	0
28	D	1566	0	1618	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	E	1552	0	1619	11	0
30	F	1410	0	1444	28	0
31	G	1323	0	1371	9	0
32	H	303	0	327	5	0
33	L	1129	0	1162	9	0
34	M	946	0	1023	9	0
35	N	1052	0	1127	8	0
36	O	1075	0	1146	4	0
37	P	945	0	989	6	0
38	Q	892	0	923	5	0
39	R	917	0	962	6	0
40	S	947	0	1019	4	0
41	T	816	0	839	1	0
42	U	857	0	922	2	0
43	V	738	0	807	0	0
44	W	779	0	831	11	0
45	X	753	0	780	5	0
46	Y	634	0	653	3	0
47	Z	625	0	652	3	0
48	1	495	0	526	2	0
49	2	449	0	488	4	0
50	3	468	0	460	6	0
51	4	434	0	445	4	0
52	5	417	0	451	1	0
53	6	377	0	418	1	0
54	7	504	0	572	1	0
55	8	302	0	340	4	0
56	4	1	0	0	0	0
56	7	1	0	0	0	0
56	A	555	0	0	0	0
56	B	10	0	0	0	0
56	C	3	0	0	0	0
56	D	1	0	0	0	0
56	N	1	0	0	0	0
56	P	1	0	0	0	0
56	S	1	0	0	0	0
56	V	1	0	0	0	0
56	a	132	0	0	0	0
56	l	1	0	0	0	0
56	n	1	0	0	0	0
56	v	2	0	0	0	0
56	w	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	x	2	0	0	0	0
57	a	44	0	20	3	0
58	w	11	0	8	0	0
59	3	1	0	0	0	0
59	8	1	0	0	0	0
60	4	1	0	0	0	0
60	8	1	0	0	1	0
60	A	247	0	0	2	0
60	B	4	0	0	0	0
60	C	1	0	0	0	0
60	D	1	0	0	0	0
60	E	1	0	0	1	0
60	N	1	0	0	0	0
60	P	1	0	0	0	0
60	R	1	0	0	0	0
60	T	1	0	0	0	0
60	V	1	0	0	0	0
60	Z	1	0	0	1	0
60	a	37	0	0	0	0
60	n	1	0	0	0	0
All	All	144543	0	95961	826	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 4.

The worst 5 of 826 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:a:1009:U:H3	1:a:1020:G:H1	0.98	0.96
25:A:544:C:O2	25:A:549:G:N2	2.01	0.94
25:A:284:U:H3	25:A:356:G:H1	1.18	0.90
1:a:137:U:H3	1:a:226:G:H1	1.19	0.87
4:d:58:LYS:NZ	4:d:69:GLU:OE2	2.09	0.85

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	b	222/241 (92%)	205 (92%)	17 (8%)	0	100	100
3	c	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
4	d	203/206 (98%)	197 (97%)	6 (3%)	0	100	100
5	e	154/167 (92%)	149 (97%)	5 (3%)	0	100	100
6	f	101/131 (77%)	92 (91%)	9 (9%)	0	100	100
7	g	150/156 (96%)	141 (94%)	9 (6%)	0	100	100
8	h	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
9	i	125/130 (96%)	121 (97%)	4 (3%)	0	100	100
10	j	96/103 (93%)	92 (96%)	3 (3%)	1 (1%)	12	32
11	k	113/129 (88%)	103 (91%)	10 (9%)	0	100	100
12	l	118/124 (95%)	113 (96%)	5 (4%)	0	100	100
13	m	113/118 (96%)	107 (95%)	6 (5%)	0	100	100
14	n	98/101 (97%)	98 (100%)	0	0	100	100
15	o	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
16	p	79/82 (96%)	70 (89%)	9 (11%)	0	100	100
17	q	77/84 (92%)	73 (95%)	4 (5%)	0	100	100
18	r	52/75 (69%)	49 (94%)	3 (6%)	0	100	100
19	s	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
20	t	84/87 (97%)	81 (96%)	3 (4%)	0	100	100
21	u	53/71 (75%)	51 (96%)	2 (4%)	0	100	100
27	C	269/273 (98%)	262 (97%)	7 (3%)	0	100	100
28	D	206/209 (99%)	196 (95%)	9 (4%)	1 (0%)	24	48
29	E	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
30	F	175/179 (98%)	163 (93%)	12 (7%)	0	100	100
31	G	174/177 (98%)	164 (94%)	10 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	H	39/149 (26%)	34 (87%)	5 (13%)	0	100	100
33	L	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
34	M	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
35	N	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
36	O	132/136 (97%)	127 (96%)	5 (4%)	0	100	100
37	P	116/127 (91%)	112 (97%)	4 (3%)	0	100	100
38	Q	114/117 (97%)	111 (97%)	3 (3%)	0	100	100
39	R	112/115 (97%)	109 (97%)	3 (3%)	0	100	100
40	S	115/118 (98%)	115 (100%)	0	0	100	100
41	T	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
42	U	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
43	V	91/100 (91%)	86 (94%)	5 (6%)	0	100	100
44	W	100/104 (96%)	95 (95%)	5 (5%)	0	100	100
45	X	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
46	Y	82/85 (96%)	81 (99%)	1 (1%)	0	100	100
47	Z	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
48	1	59/63 (94%)	57 (97%)	2 (3%)	0	100	100
49	2	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
50	3	56/70 (80%)	51 (91%)	5 (9%)	0	100	100
51	4	53/57 (93%)	53 (100%)	0	0	100	100
52	5	49/55 (89%)	46 (94%)	3 (6%)	0	100	100
53	6	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	7	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
55	8	36/38 (95%)	36 (100%)	0	0	100	100
All	All	5454/5886 (93%)	5227 (96%)	225 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
28	D	149	ASN
10	j	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	b	186/199 (94%)	186 (100%)	0	100	100
3	c	170/190 (90%)	170 (100%)	0	100	100
4	d	172/173 (99%)	172 (100%)	0	100	100
5	e	119/126 (94%)	119 (100%)	0	100	100
6	f	90/112 (80%)	90 (100%)	0	100	100
7	g	125/129 (97%)	125 (100%)	0	100	100
8	h	104/105 (99%)	104 (100%)	0	100	100
9	i	105/107 (98%)	105 (100%)	0	100	100
10	j	86/90 (96%)	86 (100%)	0	100	100
11	k	89/98 (91%)	89 (100%)	0	100	100
12	l	101/103 (98%)	101 (100%)	0	100	100
13	m	93/96 (97%)	93 (100%)	0	100	100
14	n	83/84 (99%)	83 (100%)	0	100	100
15	o	76/77 (99%)	76 (100%)	0	100	100
16	p	65/65 (100%)	65 (100%)	0	100	100
17	q	73/78 (94%)	73 (100%)	0	100	100
18	r	47/65 (72%)	47 (100%)	0	100	100
19	s	72/79 (91%)	72 (100%)	0	100	100
20	t	65/66 (98%)	65 (100%)	0	100	100
21	u	48/61 (79%)	48 (100%)	0	100	100
27	C	216/218 (99%)	216 (100%)	0	100	100
28	D	163/163 (100%)	163 (100%)	0	100	100
29	E	165/165 (100%)	165 (100%)	0	100	100
30	F	148/150 (99%)	148 (100%)	0	100	100
31	G	137/138 (99%)	137 (100%)	0	100	100
32	H	32/114 (28%)	32 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	L	116/116 (100%)	116 (100%)	0	100	100
34	M	104/104 (100%)	104 (100%)	0	100	100
35	N	103/103 (100%)	103 (100%)	0	100	100
36	O	107/107 (100%)	107 (100%)	0	100	100
37	P	98/103 (95%)	98 (100%)	0	100	100
38	Q	86/87 (99%)	86 (100%)	0	100	100
39	R	99/100 (99%)	99 (100%)	0	100	100
40	S	89/90 (99%)	89 (100%)	0	100	100
41	T	84/84 (100%)	84 (100%)	0	100	100
42	U	93/93 (100%)	93 (100%)	0	100	100
43	V	80/84 (95%)	80 (100%)	0	100	100
44	W	83/85 (98%)	83 (100%)	0	100	100
45	X	78/78 (100%)	78 (100%)	0	100	100
46	Y	62/63 (98%)	62 (100%)	0	100	100
47	Z	67/68 (98%)	67 (100%)	0	100	100
48	1	54/55 (98%)	54 (100%)	0	100	100
49	2	48/49 (98%)	48 (100%)	0	100	100
50	3	53/62 (86%)	53 (100%)	0	100	100
51	4	46/48 (96%)	46 (100%)	0	100	100
52	5	46/49 (94%)	46 (100%)	0	100	100
53	6	38/38 (100%)	38 (100%)	0	100	100
54	7	51/52 (98%)	51 (100%)	0	100	100
55	8	34/34 (100%)	34 (100%)	0	100	100
All	All	4549/4803 (95%)	4549 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
33	L	40	HIS
42	U	7	HIS
36	O	22	GLN
38	Q	100	HIS

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Mol	Chain	Res	Type
44	W	66	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1526/1542 (98%)	194 (12%)	0
22	w	72/76 (94%)	16 (22%)	0
23	x	75/77 (97%)	8 (10%)	0
24	v	11/24 (45%)	2 (18%)	0
25	A	2842/2904 (97%)	397 (13%)	14 (0%)
26	B	119/120 (99%)	15 (12%)	2 (1%)
All	All	4645/4743 (97%)	632 (13%)	16 (0%)

5 of 632 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	4	U
1	a	5	U
1	a	6	G
1	a	19	A
1	a	22	G

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	B	3	C
25	A	2799	A
25	A	2189	U
25	A	2538	C
25	A	2097	A

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

51 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
1	2MG	a	1516	1	23,26,27	1.27	4 (17%)	33,38,41	2.33	10 (30%)
1	MA6	a	1519	1	23,26,27	1.47	5 (21%)	33,38,41	2.49	13 (39%)
23	4SU	x	8	23	18,21,22	1.87	4 (22%)	25,30,33	2.27	5 (20%)
1	4OC	a	1402	56,1	20,23,24	0.76	1 (5%)	25,32,35	1.01	2 (8%)
25	5MU	A	1939	25	19,22,23	1.45	4 (21%)	27,32,35	2.30	6 (22%)
25	H2U	A	2449	25	18,21,22	1.22	2 (11%)	19,30,33	1.05	2 (10%)
25	PSU	A	2604	25	18,21,22	1.51	4 (22%)	21,30,33	2.20	5 (23%)
12	D2T	l	89	12	8,9,10	1.78	1 (12%)	6,11,13	2.69	3 (50%)
25	2MA	A	2503	56,25	22,25,26	1.41	5 (22%)	32,37,40	2.33	9 (28%)
25	2MG	A	2445	56,25	23,26,27	1.36	5 (21%)	33,38,41	2.29	7 (21%)
25	PSU	A	955	25	18,21,22	1.53	4 (22%)	21,30,33	2.20	5 (23%)
22	PSU	w	55	22	18,21,22	1.44	4 (22%)	21,30,33	2.17	3 (14%)
25	OMG	A	2251	56,25,23	23,26,27	1.29	3 (13%)	32,38,41	2.16	6 (18%)
25	PSU	A	2580	56,25	18,21,22	1.59	6 (33%)	21,30,33	2.06	5 (23%)
25	PSU	A	1911	25	18,21,22	1.49	4 (22%)	21,30,33	2.17	5 (23%)
28	MEQ	D	150	28	8,9,10	0.51	0	5,10,12	0.43	0
25	OMU	A	2552	25	19,22,23	1.39	3 (15%)	25,31,34	2.01	5 (20%)
11	IAS	k	119	11	6,7,8	0.99	0	3,8,10	1.32	1 (33%)
25	5MU	A	747	25	19,22,23	1.41	5 (26%)	27,32,35	2.23	9 (33%)
36	MS6	O	82	36	5,7,8	0.57	0	2,7,9	0.99	0
25	6MZ	A	2030	25	22,25,26	1.43	4 (18%)	29,36,39	2.25	9 (31%)
25	PSU	A	746	56,25	18,21,22	1.54	4 (22%)	21,30,33	2.03	4 (19%)
22	PSU	w	39	22	18,21,22	1.26	3 (16%)	21,30,33	2.37	4 (19%)
1	5MC	a	1407	1	19,22,23	1.42	3 (15%)	26,32,35	1.18	3 (11%)
25	PSU	A	2504	25	18,21,22	1.51	4 (22%)	21,30,33	2.08	3 (14%)
23	5MC	x	32	23	19,22,23	1.45	3 (15%)	26,32,35	1.24	3 (11%)
25	PSU	A	2605	25	18,21,22	1.53	4 (22%)	21,30,33	2.12	4 (19%)
25	3TD	A	1915	56,25	19,22,23	4.10	7 (36%)	23,32,35	1.86	3 (13%)
1	UR3	a	1498	1	19,22,23	0.93	1 (5%)	26,32,35	1.80	5 (19%)
22	G7M	w	46	22	23,26,27	2.40	5 (21%)	34,39,42	3.00	10 (29%)
25	5MC	A	1962	25	19,22,23	1.33	3 (15%)	26,32,35	1.17	3 (11%)
25	PSU	A	2457	25	18,21,22	1.61	5 (27%)	21,30,33	2.29	6 (28%)
1	2MG	a	1207	1	23,26,27	1.28	3 (13%)	33,38,41	2.16	5 (15%)
25	2MG	A	1835	25	23,26,27	1.34	4 (17%)	33,38,41	2.19	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	G7M	A	2069	56,25	23,26,27	1.58	4 (17%)	34,39,42	1.79	5 (14%)
1	G7M	a	527	1	23,26,27	1.56	3 (13%)	34,39,42	1.76	5 (14%)
22	5MU	w	54	22	19,22,23	1.39	4 (21%)	27,32,35	2.05	6 (22%)
22	PSU	w	32	22	18,21,22	1.41	4 (22%)	21,30,33	2.07	4 (19%)
22	MIA	w	37	22	28,31,32	2.33	7 (25%)	38,44,47	2.82	14 (36%)
25	OMC	A	2498	56,25	19,22,23	0.85	1 (5%)	25,31,34	1.15	1 (4%)
1	5MC	a	967	1	19,22,23	1.47	3 (15%)	26,32,35	1.16	2 (7%)
25	1MG	A	745	25	23,26,27	1.11	2 (8%)	33,39,42	1.76	5 (15%)
22	4SU	w	8	22	18,21,22	1.96	4 (22%)	25,30,33	1.86	4 (16%)
1	PSU	a	516	56,1	18,21,22	1.41	5 (27%)	21,30,33	2.05	4 (19%)
25	6MZ	A	1618	25	22,25,26	1.42	5 (22%)	29,36,39	2.25	9 (31%)
36	4D4	O	81	36	9,11,12	2.56	3 (33%)	7,13,15	1.02	0
1	MA6	a	1518	1	23,26,27	1.42	5 (21%)	33,38,41	2.48	13 (39%)
23	5MU	x	54	23	19,22,23	1.39	5 (26%)	27,32,35	2.23	6 (22%)
25	PSU	A	1917	25	18,21,22	1.52	4 (22%)	21,30,33	2.10	4 (19%)
23	PSU	x	55	23	18,21,22	1.35	3 (16%)	21,30,33	2.04	4 (19%)
1	2MG	a	966	1	23,26,27	1.32	4 (17%)	33,38,41	2.22	7 (21%)

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
1	2MG	a	1516	1	-	0/9/27/28	0/3/3/3
1	MA6	a	1519	1	-	3/11/29/30	0/3/3/3
23	4SU	x	8	23	-	0/7/25/26	0/2/2/2
1	4OC	a	1402	56,1	-	3/9/29/30	0/2/2/2
25	5MU	A	1939	25	-	0/7/25/26	0/2/2/2
25	H2U	A	2449	25	-	0/7/38/39	0/2/2/2
25	PSU	A	2604	25	-	0/7/25/26	0/2/2/2
12	D2T	l	89	12	-	4/7/12/14	-
25	2MA	A	2503	56,25	-	0/7/25/26	0/3/3/3
25	2MG	A	2445	56,25	-	0/9/27/28	0/3/3/3
25	PSU	A	955	25	-	0/7/25/26	0/2/2/2
22	PSU	w	55	22	-	1/7/25/26	0/2/2/2
25	OMG	A	2251	56,25,23	-	0/9/27/28	0/3/3/3
25	PSU	A	2580	56,25	-	1/7/25/26	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	PSU	A	1911	25	-	0/7/25/26	0/2/2/2
28	MEQ	D	150	28	-	2/8/9/11	-
25	OMU	A	2552	25	-	0/9/27/28	0/2/2/2
11	IAS	k	119	11	-	0/7/7/8	-
25	5MU	A	747	25	-	0/7/25/26	0/2/2/2
36	MS6	O	82	36	-	2/4/6/8	-
25	6MZ	A	2030	25	-	2/9/27/28	0/3/3/3
25	PSU	A	746	56,25	-	2/7/25/26	0/2/2/2
22	PSU	w	39	22	-	0/7/25/26	0/2/2/2
1	5MC	a	1407	1	-	0/7/25/26	0/2/2/2
25	PSU	A	2504	25	-	1/7/25/26	0/2/2/2
23	5MC	x	32	23	-	0/7/25/26	0/2/2/2
25	PSU	A	2605	25	-	0/7/25/26	0/2/2/2
25	3TD	A	1915	56,25	-	2/7/25/26	0/2/2/2
1	UR3	a	1498	1	-	0/7/25/26	0/2/2/2
22	G7M	w	46	22	-	0/7/25/26	0/3/3/3
25	5MC	A	1962	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2457	25	-	0/7/25/26	0/2/2/2
1	2MG	a	1207	1	-	0/9/27/28	0/3/3/3
25	2MG	A	1835	25	-	0/9/27/28	0/3/3/3
25	G7M	A	2069	56,25	-	0/7/25/26	0/3/3/3
1	G7M	a	527	1	-	2/7/25/26	0/3/3/3
22	5MU	w	54	22	-	0/7/25/26	0/2/2/2
22	PSU	w	32	22	-	0/7/25/26	0/2/2/2
22	MIA	w	37	22	-	2/15/33/34	0/3/3/3
25	OMC	A	2498	56,25	-	1/9/27/28	0/2/2/2
1	5MC	a	967	1	-	0/7/25/26	0/2/2/2
25	1MG	A	745	25	-	0/7/25/26	0/3/3/3
22	4SU	w	8	22	-	0/7/25/26	0/2/2/2
1	PSU	a	516	56,1	-	0/7/25/26	0/2/2/2
25	6MZ	A	1618	25	-	0/9/27/28	0/3/3/3
36	4D4	O	81	36	-	3/11/12/14	-
1	MA6	a	1518	1	-	2/11/29/30	0/3/3/3
23	5MU	x	54	23	-	0/7/25/26	0/2/2/2
25	PSU	A	1917	25	-	2/7/25/26	0/2/2/2
23	PSU	x	55	23	-	0/7/25/26	0/2/2/2
1	2MG	a	966	1	-	0/9/27/28	0/3/3/3

The worst 5 of 183 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	1915	3TD	C6-C5	12.38	1.49	1.35
25	A	1915	3TD	C2-N1	9.34	1.48	1.37
22	w	46	G7M	C8-N7	7.79	1.46	1.33
22	w	37	MIA	C2-S10	-7.79	1.69	1.75
22	w	37	MIA	C13-C14	6.71	1.52	1.32

The worst 5 of 262 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	w	37	MIA	C12-C13-C14	-9.62	109.74	127.01
25	A	2503	2MA	C5-C4-N3	-8.46	118.27	127.18
22	w	37	MIA	C5-C4-N3	-7.74	119.03	127.18
22	w	46	G7M	CN7-N7-C8	-7.63	113.24	124.79
25	A	2445	2MG	C2-N3-C4	7.59	121.49	112.00

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	a	527	G7M	O4'-C4'-C5'-O5'
1	a	1518	MA6	C5-C6-N6-C9
1	a	1519	MA6	C5-C6-N6-C9
12	l	89	D2T	CA-CB-CG-OD1
12	l	89	D2T	CA-CB-CG-OD2

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	a	1519	MA6	2	0
1	a	1402	4OC	1	0
25	A	2498	OMC	1	0
1	a	1518	MA6	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 718 ligands modelled in this entry, 716 are monoatomic - leaving 2 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$
57	T8B	a	3133	-	48,48,48	2.73	10 (20%)	63,71,71	1.73	17 (26%)
58	PHE	w	102	22	10,11,12	1.66	1 (10%)	8,13,15	0.55	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
57	T8B	a	3133	-	-	0/26/26/26	0/5/5/5
58	PHE	w	102	22	-	0/5/6/8	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	a	3133	T8B	C27-C26	-10.06	1.40	1.48
57	a	3133	T8B	C2-C3	-8.83	1.39	1.51
57	a	3133	T8B	C25-C26	7.67	1.52	1.38
58	w	102	PHE	CB-CG	-5.08	1.39	1.51
57	a	3133	T8B	C10-C11	4.57	1.38	1.33

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	a	3133	T8B	O5-C14-O6	4.74	122.11	116.45
57	a	3133	T8B	C21-C23-C24	-4.44	120.00	125.09
57	a	3133	T8B	C13-O4-C12	-3.69	109.01	115.85
57	a	3133	T8B	O11-C26-C27	3.37	118.98	113.95
57	a	3133	T8B	C26-C25-C24	-3.25	116.24	120.81

There are no chirality outliers.

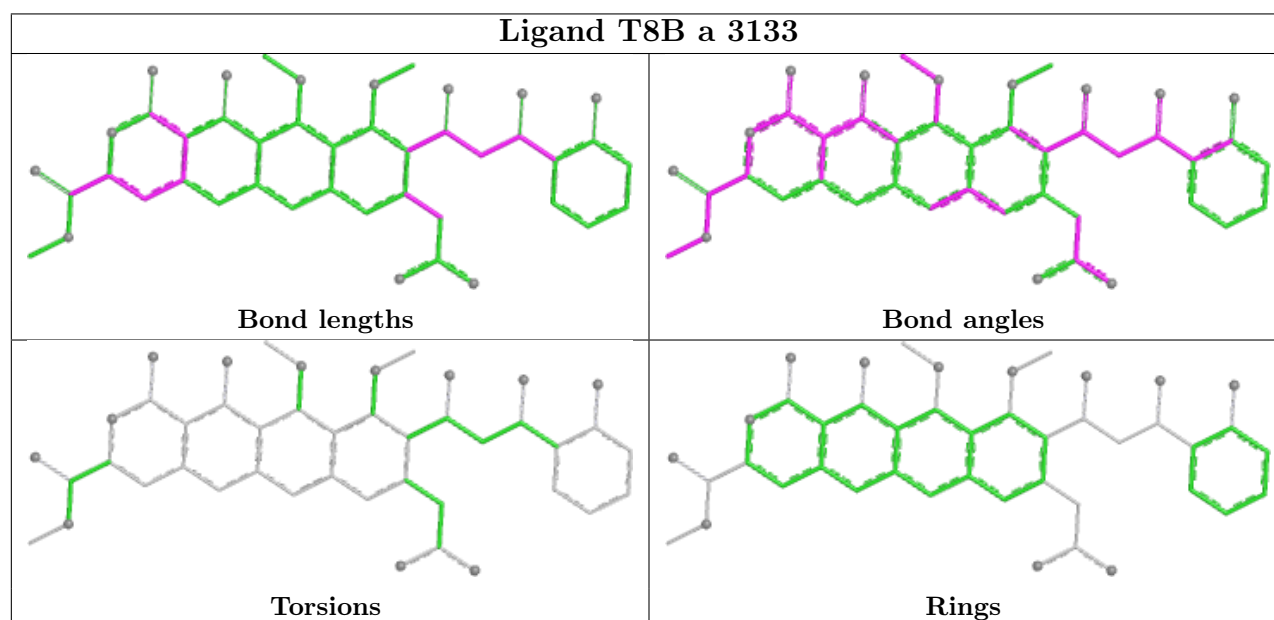
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	a	3133	T8B	3	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.

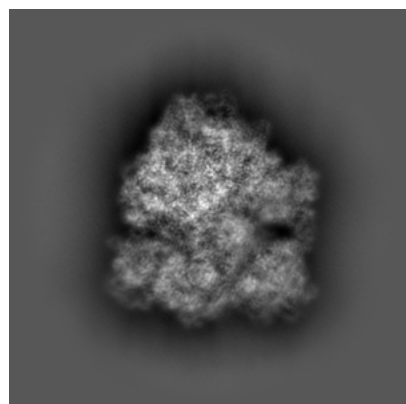
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28197. These allow visual inspection of the internal detail of the map and identification of artifacts.

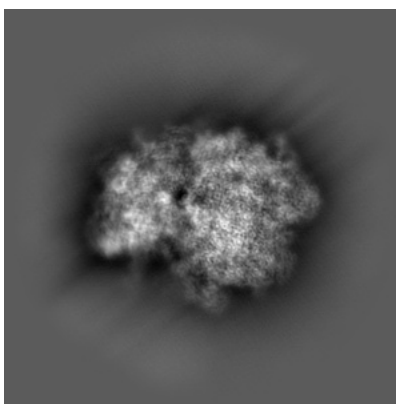
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

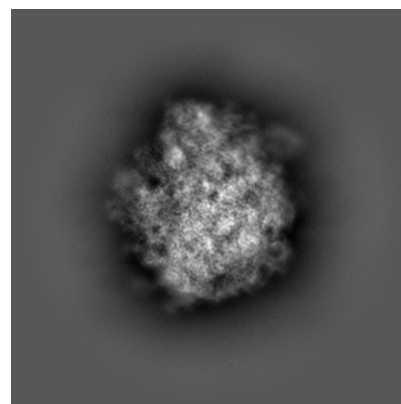
6.1.1 Primary map



X

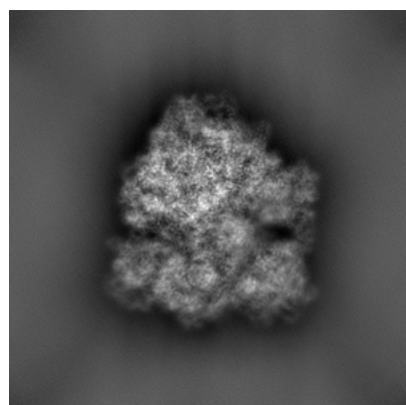


Y

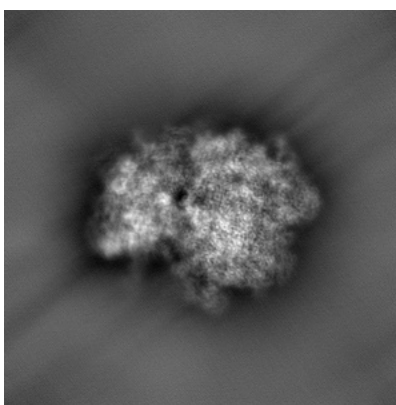


Z

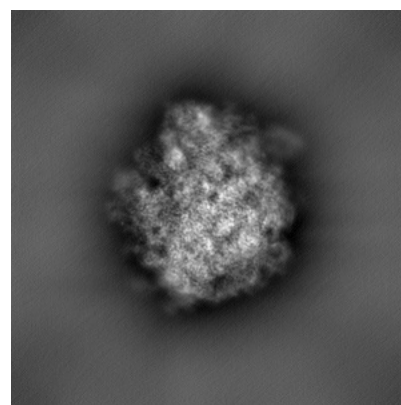
6.1.2 Raw map



X



Y

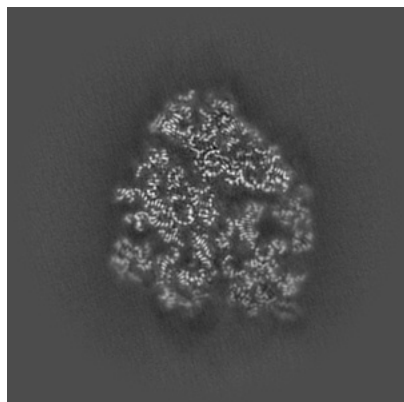


Z

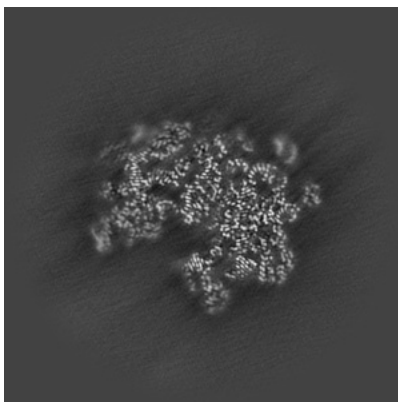
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

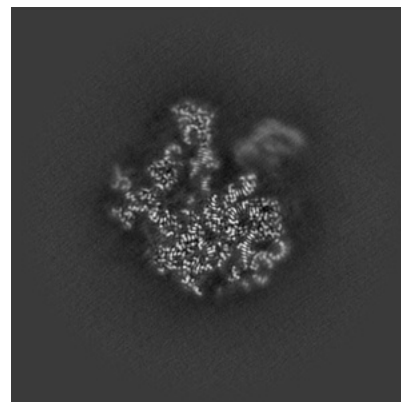
6.2.1 Primary map



X Index: 256

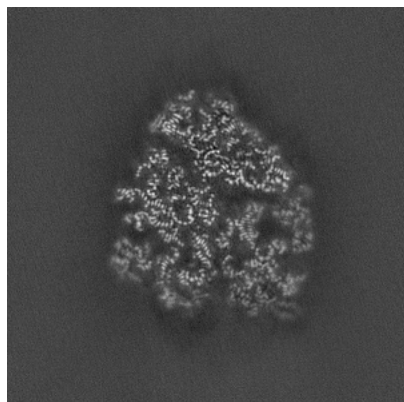


Y Index: 256

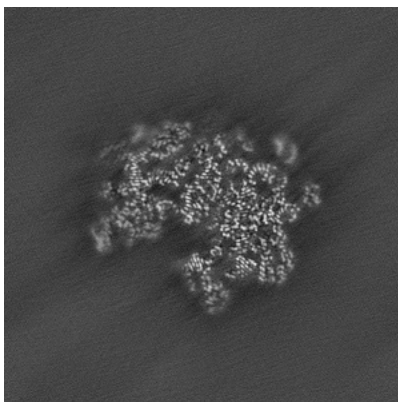


Z Index: 256

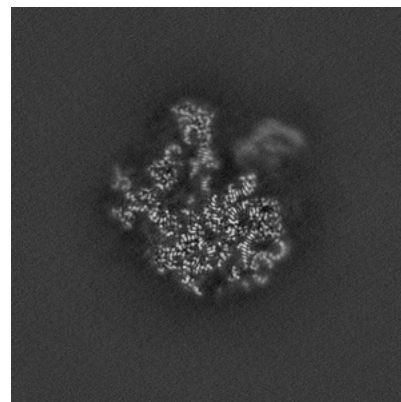
6.2.2 Raw map



X Index: 256



Y Index: 256

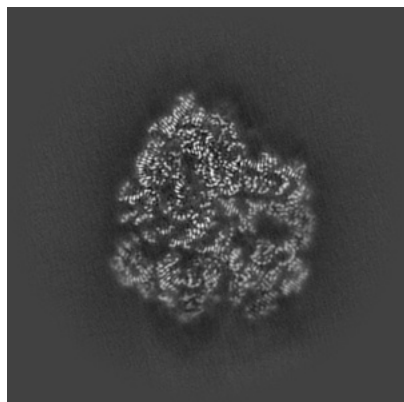


Z Index: 256

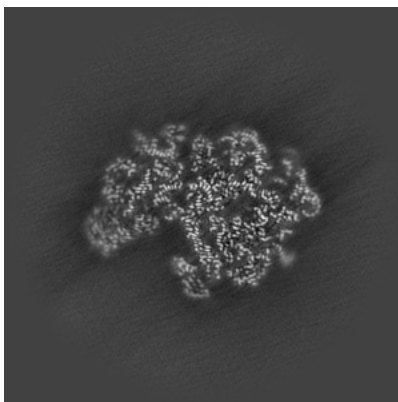
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

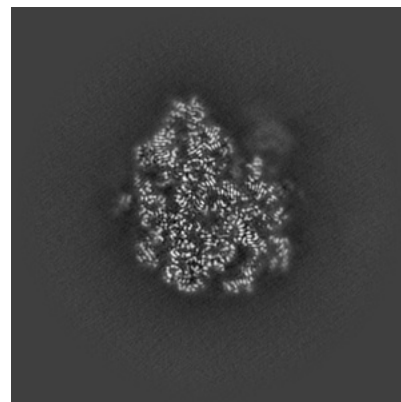
6.3.1 Primary map



X Index: 247

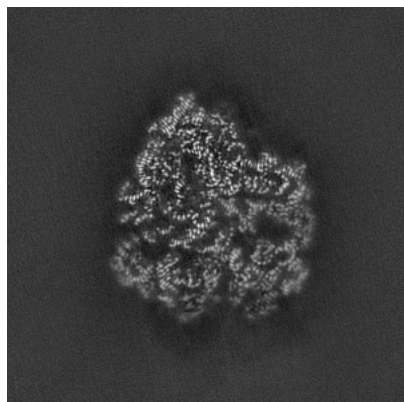


Y Index: 237

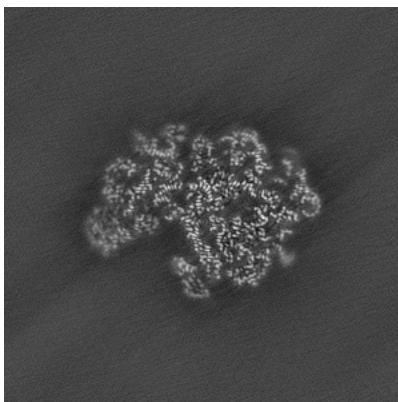


Z Index: 288

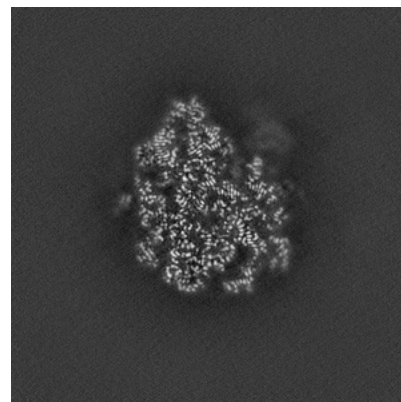
6.3.2 Raw map



X Index: 247



Y Index: 237

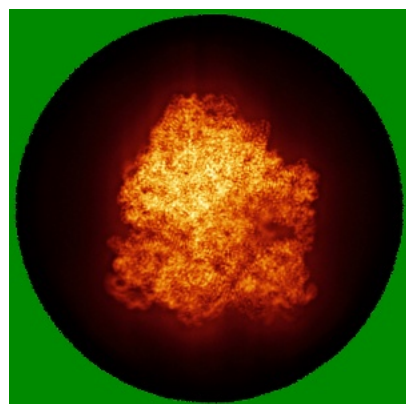


Z Index: 288

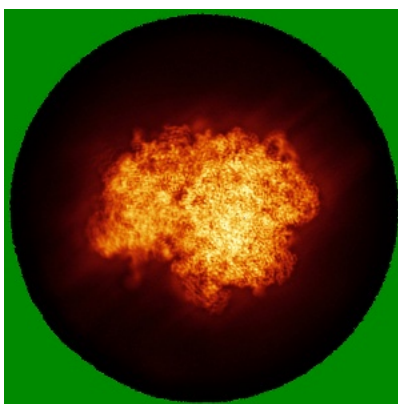
The images above show the largest variance slices of the map in three orthogonal directions.

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

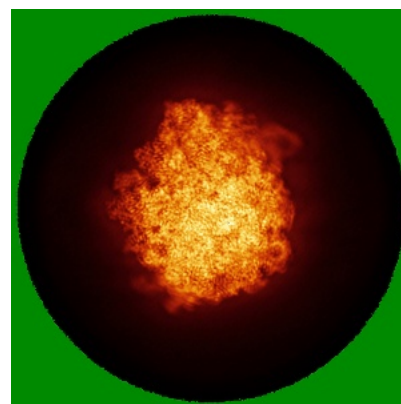
6.4.1 Primary map



X

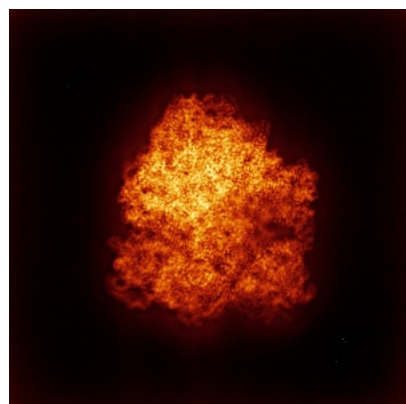


Y

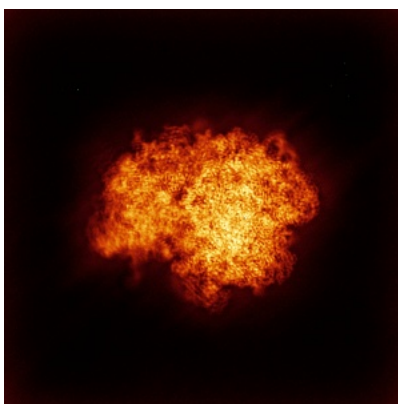


Z

6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

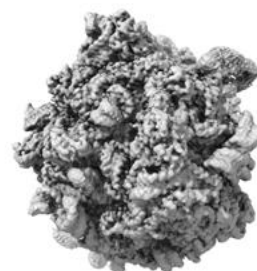
6.5.1 Primary map



X



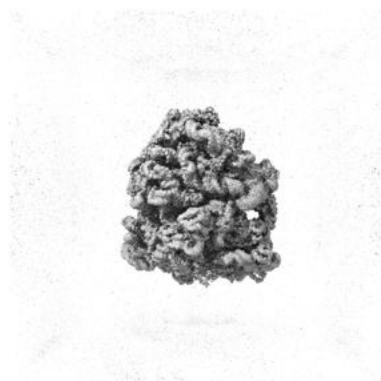
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

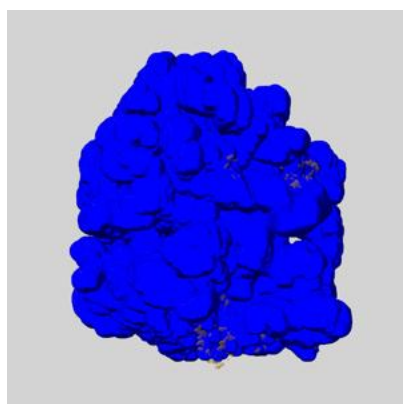
6.6 Mask visualisation [i](#)

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

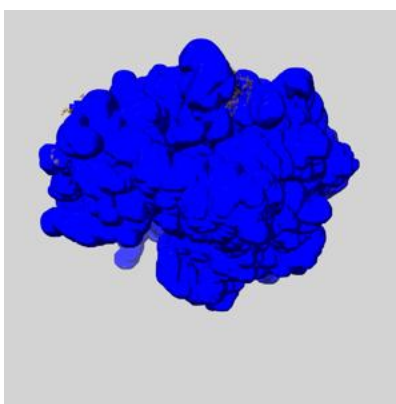
A mask typically either:

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

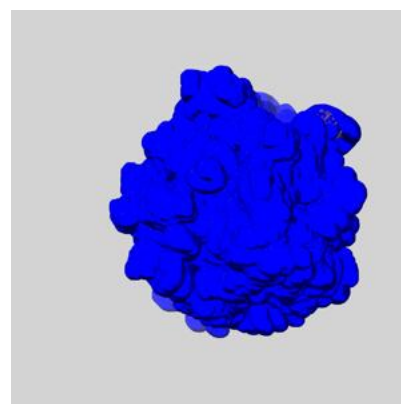
6.6.1 emd_28197_msk_1.map [i](#)



X



Y

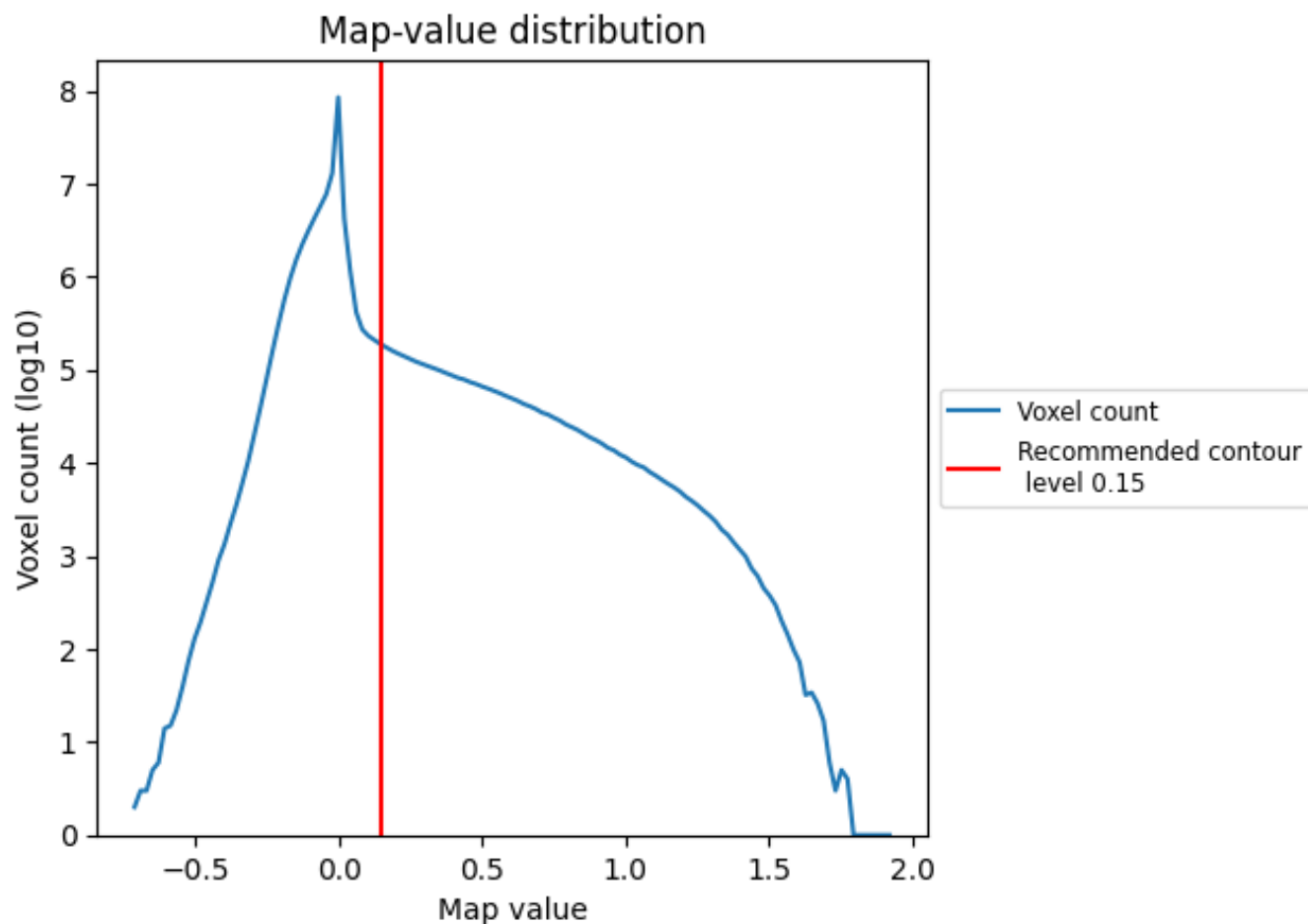


Z

7 Map analysis [i](#)

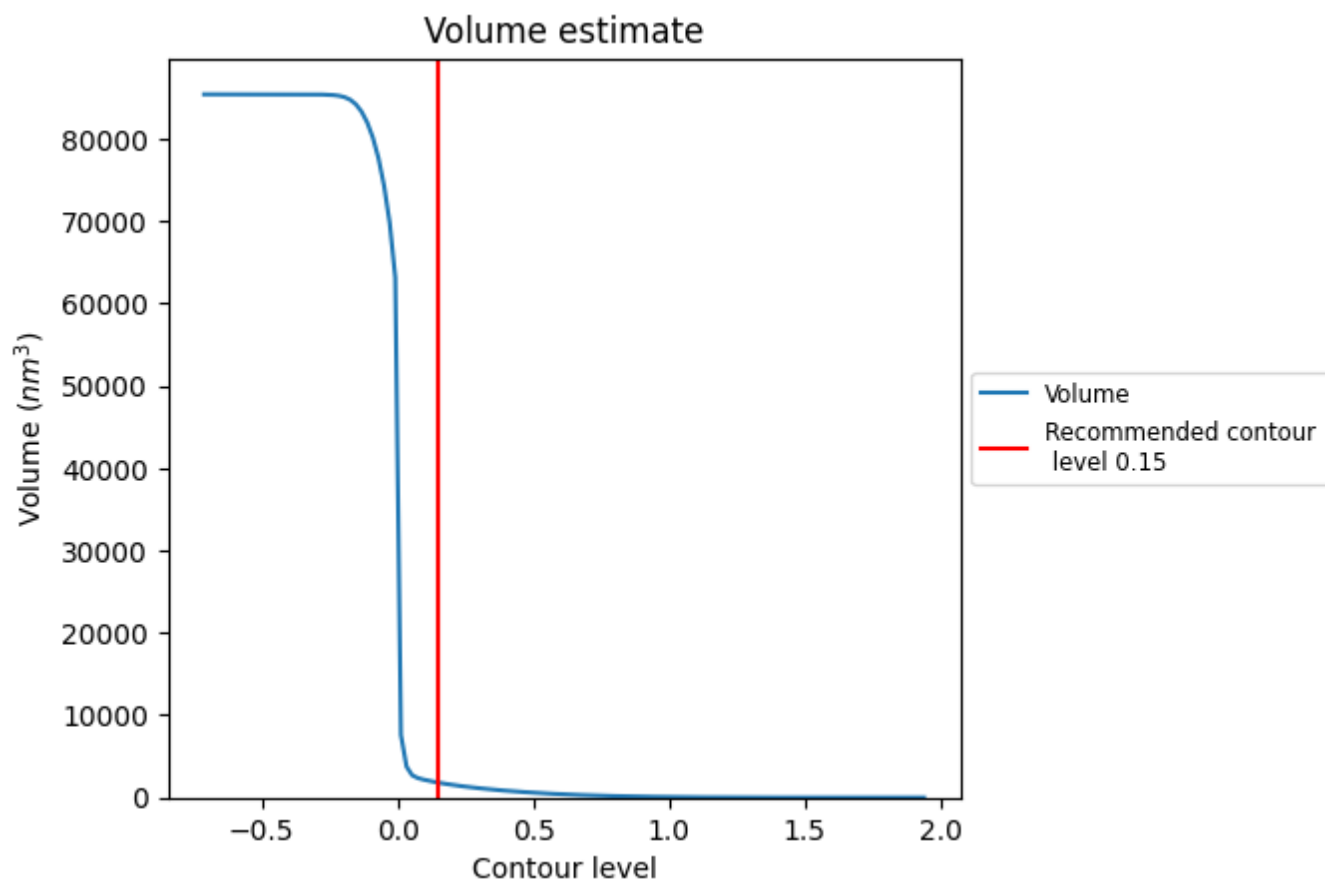
This section contains the results of statistical analysis of the map.

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.

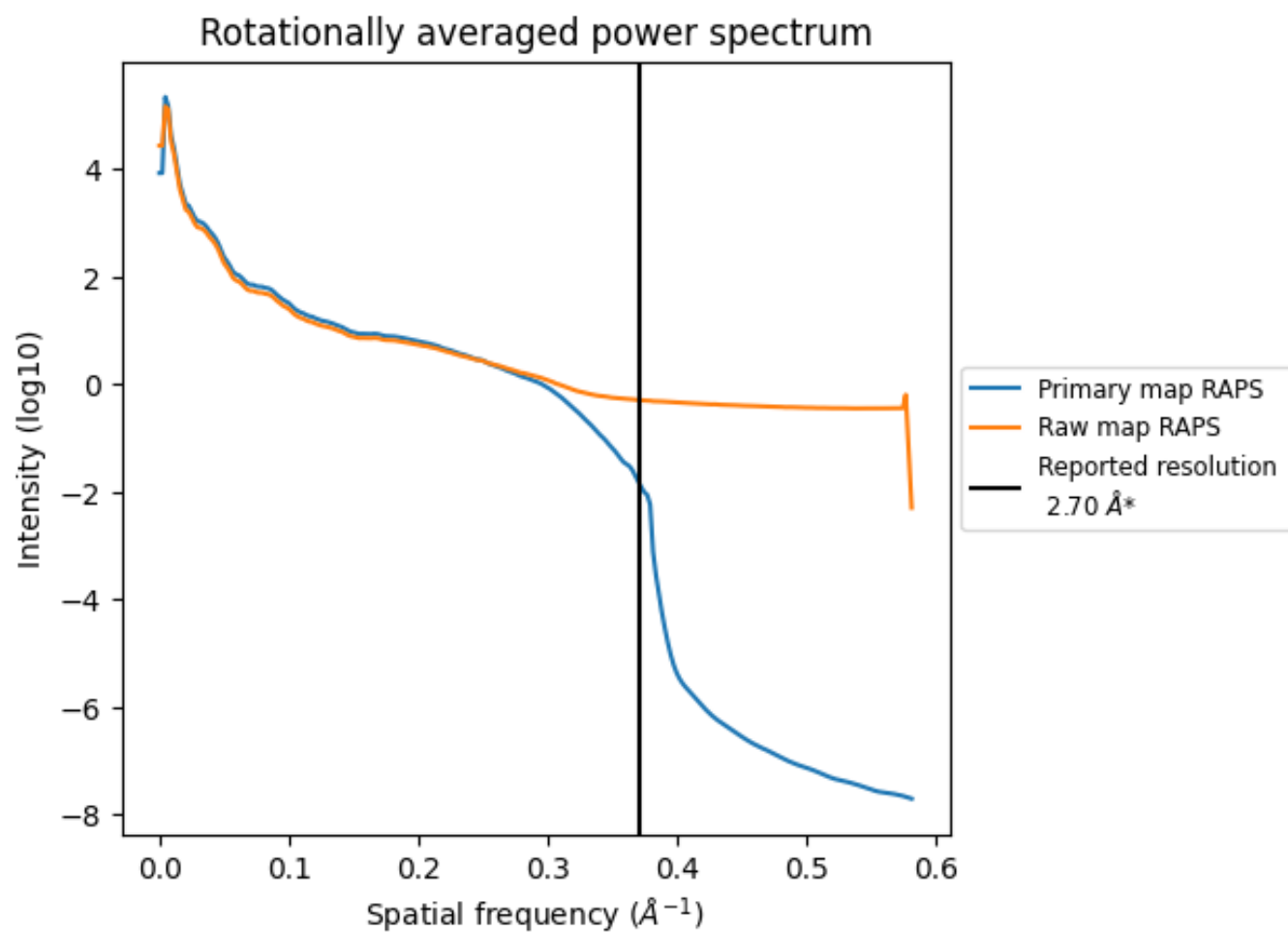
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1815 nm^3 ; this corresponds to an approximate mass of 1640 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 ⓘ

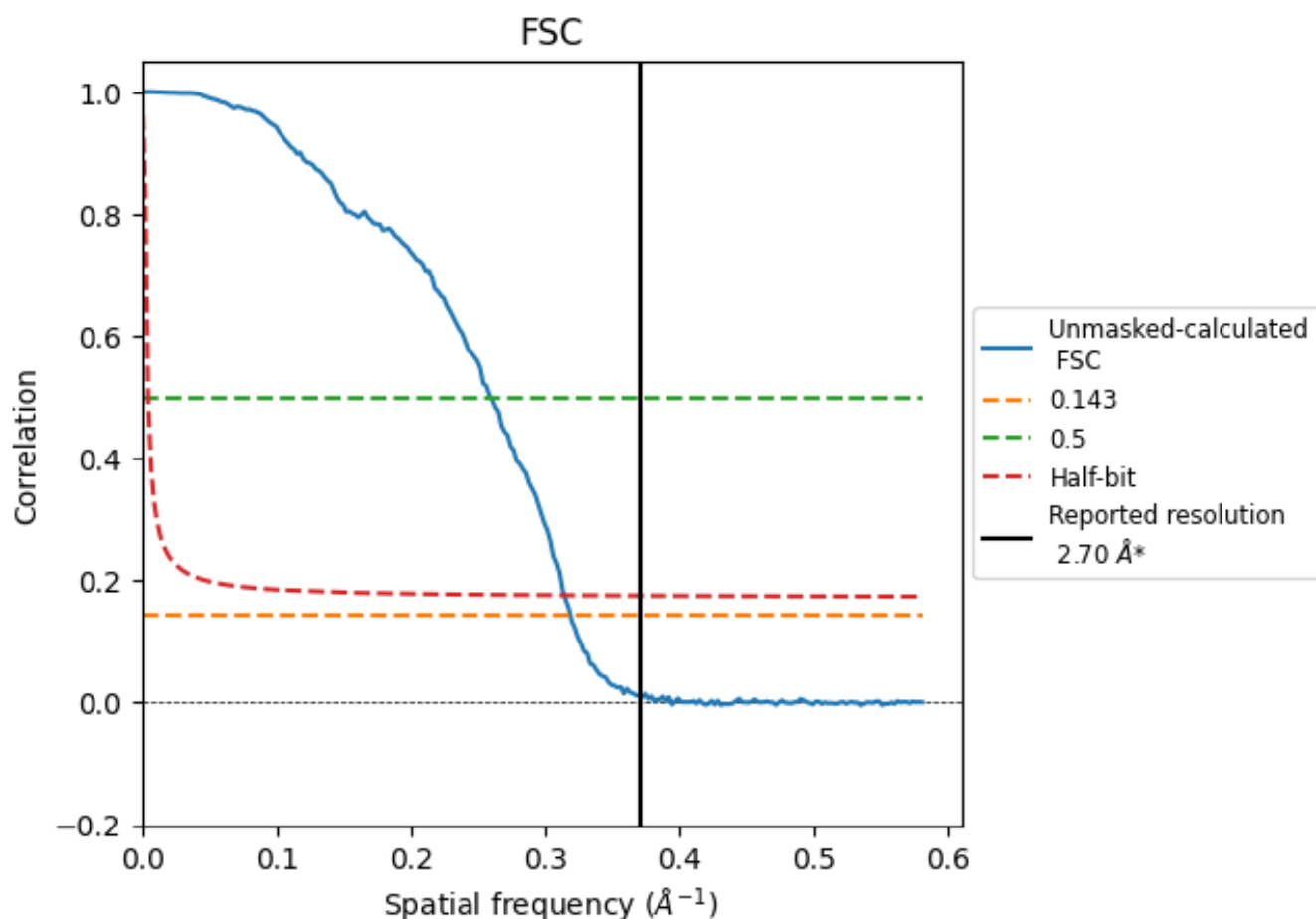


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 Å⁻¹

8.2 Resolution estimates [i](#)

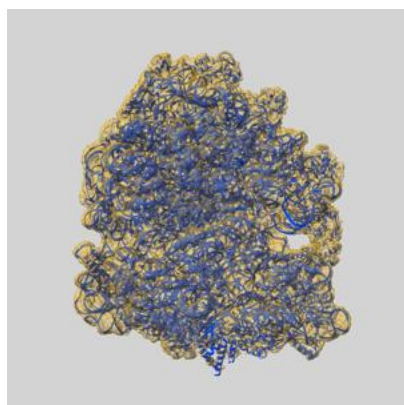
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.13	3.85	3.18

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.13 differs from the reported value 2.7 by more than 10 %

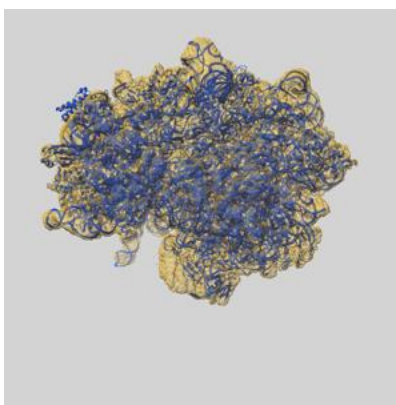
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-28197 and PDB model 8EKC. Per-residue inclusion information can be found in section 3 on page 18.

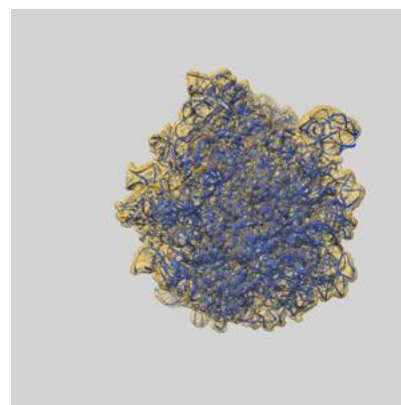
9.1 Map-model overlay [i](#)



X



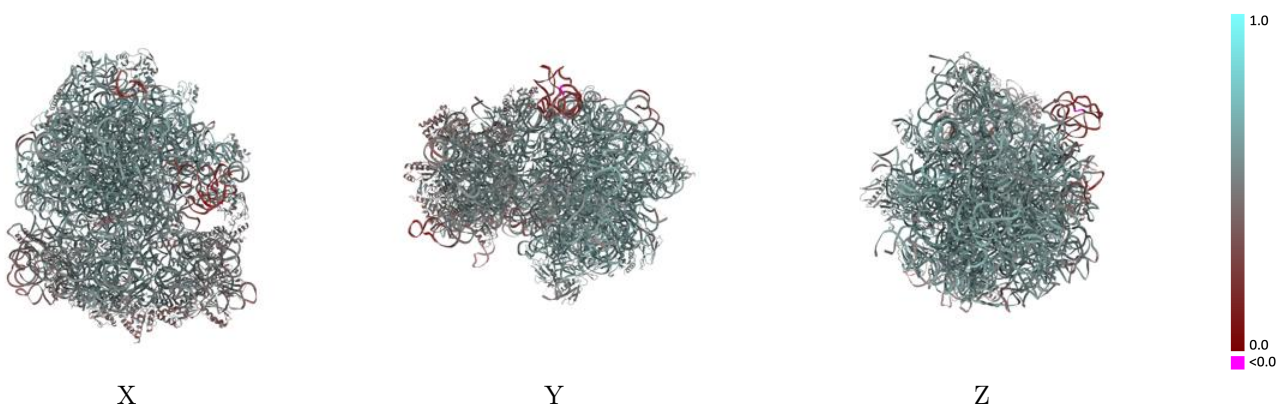
Y



Z

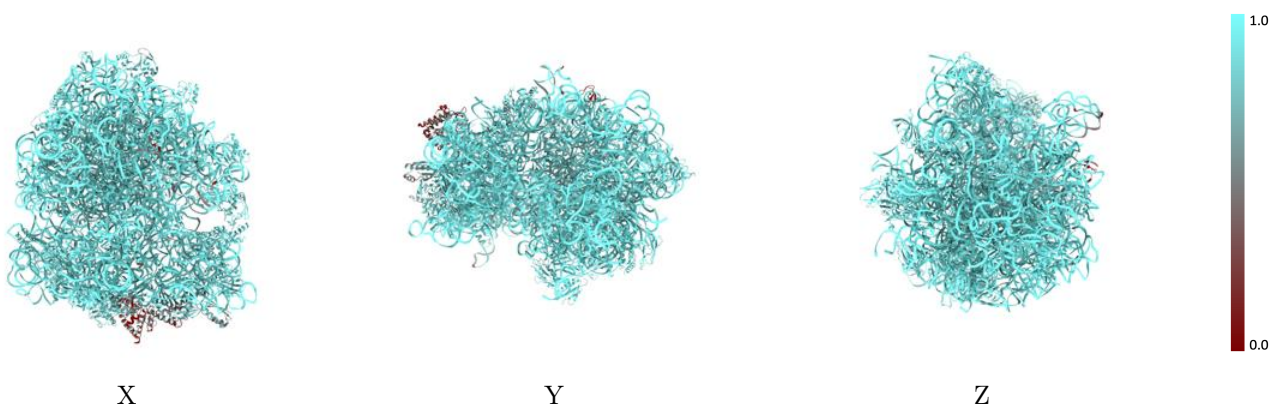
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



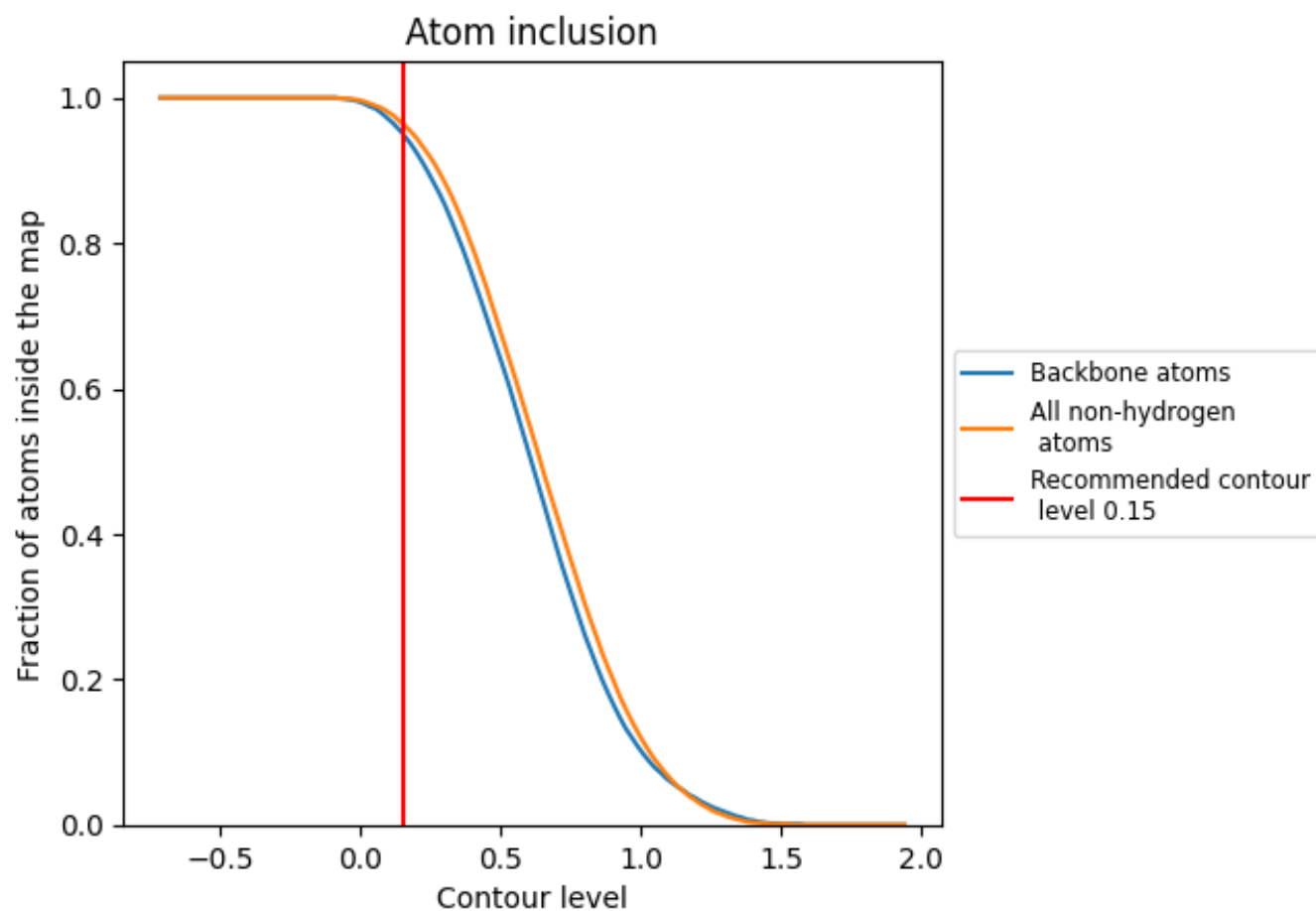
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 96% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9640	 0.5530
1	 0.9380	 0.5330
2	 0.9660	 0.5820
3	 0.8810	 0.4830
4	 0.9710	 0.6010
5	 0.9410	 0.5680
6	 0.9780	 0.6150
7	 0.9740	 0.6120
8	 0.9690	 0.6010
A	 0.9920	 0.5800
B	 0.9980	 0.5580
C	 0.9720	 0.6060
D	 0.9760	 0.5990
E	 0.9350	 0.5670
F	 0.9520	 0.5160
G	 0.9340	 0.5210
H	 0.2870	 0.4390
L	 0.9760	 0.5970
M	 0.9730	 0.5960
N	 0.9530	 0.5880
O	 0.9670	 0.5960
P	 0.9890	 0.6060
Q	 0.9660	 0.5500
R	 0.9540	 0.5880
S	 0.9860	 0.6030
T	 0.9500	 0.5820
U	 0.9570	 0.5950
V	 0.9360	 0.5650
W	 0.9530	 0.5450
X	 0.9540	 0.5630
Y	 0.9530	 0.5960
Z	 0.9680	 0.5930
a	 0.9930	 0.5200
b	 0.3340	 0.4180
c	 0.8060	 0.5120



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Chain	Atom inclusion	Q-score
d	 0.8690	 0.4470
e	 0.9410	 0.5460
f	 0.9020	 0.4790
g	 0.8730	 0.4640
h	 0.9540	 0.5480
i	 0.9140	 0.4820
j	 0.7150	 0.4530
k	 0.9450	 0.5230
l	 0.9450	 0.5550
m	 0.9420	 0.5000
n	 0.8620	 0.5050
o	 0.9520	 0.5190
p	 0.9020	 0.4690
q	 0.9390	 0.5030
r	 0.9600	 0.5300
s	 0.9160	 0.4810
t	 0.9160	 0.4550
u	 0.6900	 0.4750
v	 0.9960	 0.5750
w	 0.9920	 0.5330
x	 0.9930	 0.5580