



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 03:11 PM UTC

PDB ID : 8VRL / pdb_00008vrl
EMDB ID : EMD-43484
Title : Structure of Mycobacterium smegmatis 50S ribosomal subunit bound to HflX and chloramphenicol:50S-HflX-A-Clm
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.; Agrawal, R.K.
Deposited on : 2024-01-22
Resolution : 3.33 Å (reported)
Based on initial models : 5O61, 6DZI

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:

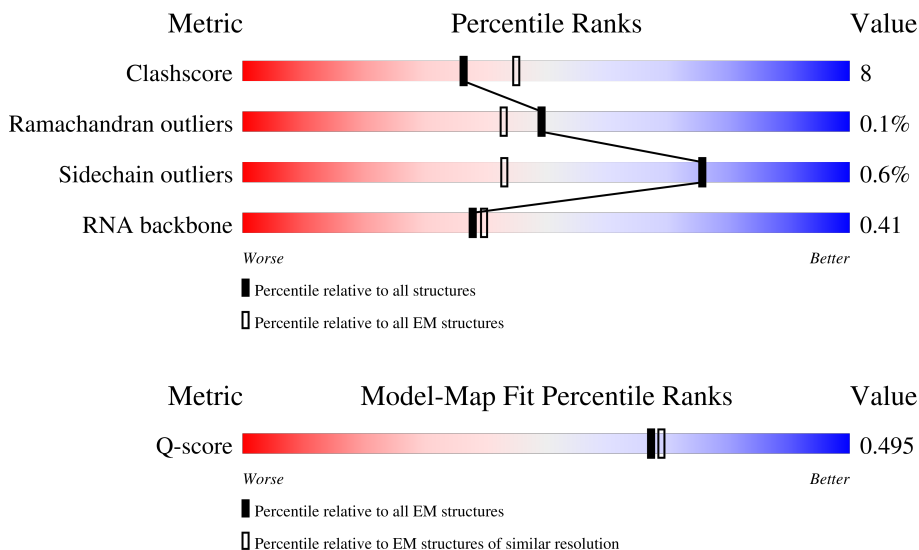
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.33 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.



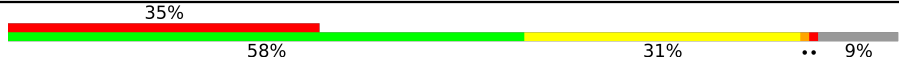

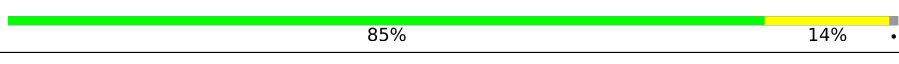


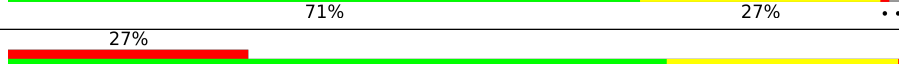
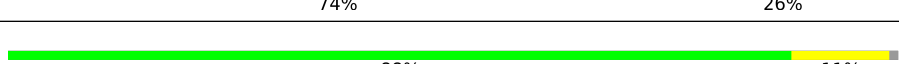
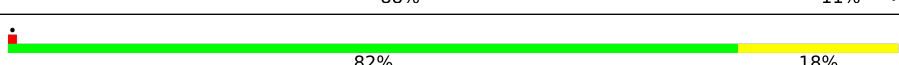
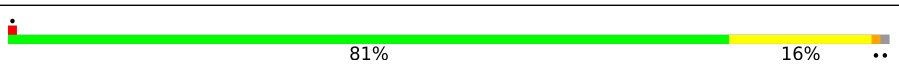

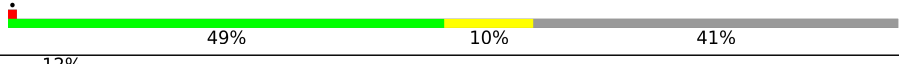
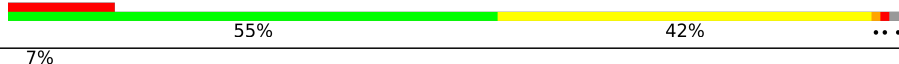
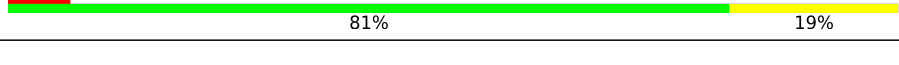

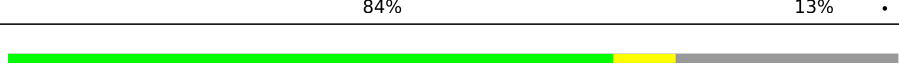


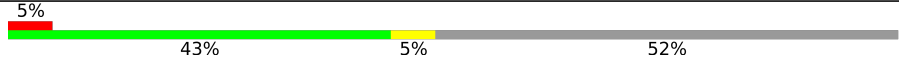







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14484 (2.83 - 3.83)

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	2	61	
2	3	24	

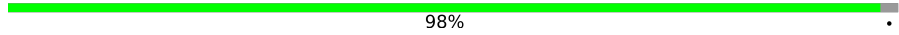
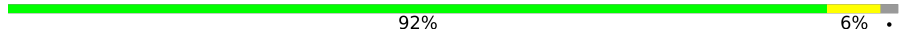

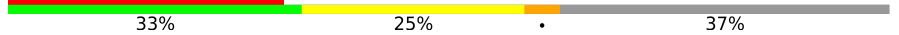

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Mol	Chain	Length	Quality of chain
3	4	470	
4	B	118	
5	C	278	
6	D	217	
7	E	215	
8	G	179	
9	H	151	
10	K	147	
11	L	122	
12	M	147	
13	N	138	
14	O	199	
15	P	127	
16	Q	113	
17	R	129	
18	S	103	
19	T	153	
20	U	100	
21	V	105	
22	W	215	
23	X	88	
24	Y	64	
25	Z	77	
26	b	57	
27	c	55	

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Mol	Chain	Length	Quality of chain
28	d	47	 98%
29	e	64	 92% 6%
30	f	37	 89% 11%
31	g	75	 31% 33% 25% 37%
32	A	3120	 10% 63% 27% 9%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
33	GCP	4	501	-	-	X	-
34	CLM	A	3201	-	X	-	-

2 Entry composition [i](#)

There are 34 unique types of molecules in this entry. The entry contains 96921 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 protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	2	59	474	292	95	87	0	0

- Molecule 2 is a protein called 50S Ribosomal Protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	3	23	189	111	50	28	0	0

- Molecule 3 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	4	426	3228	1997	599	625	7	0	0

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	B	118	2522	1126	468	810	118	0	0

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	275	2110	1298	438	370	4	0	0

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	D	214	1587	982	310	290	5	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	E	209	1569	969	295	303	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	176	1348	845	249	253	1	0	0

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	H	151	1018	635	188	194	1	0	0

- Molecule 10 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	K	146	1130	722	207	200	1	0	0

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	122	938	586	179	170	3	0	0

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	145	1078	676	205	194	3	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	136	1092	690	213	187	2	0	0

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 15 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	125	Total	C	N	O	S	0	0
			943	579	195	169			

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 17 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	124	Total	C	N	O	S	0	0
			988	613	203	172			

- Molecule 18 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	100	Total	C	N	O	S	0	0
			754	478	137	139			

- Molecule 19 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	114	Total	C	N	O	S	0	0
			873	543	171	159			

- Molecule 20 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	97	Total	C	N	O	S	0	0
			756	479	138	139			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	V	97	732	456	137	137	2	0	0

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	W	103	785	481	158	146		0	0

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	X	79	586	361	123	102		0	0

- Molecule 24 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Y	63	470	283	103	80	4	0	0

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Z	64	531	324	103	103	1	0	0

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	b	54	423	260	93	69	1	0	0

- Molecule 27 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	c	49	405	248	82	71	4	0	0

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	d	46	377	225	97	54	1	0	0

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	e	63	502	302	115	85	0	0

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	f	37	299	181	66	47	5	0	0

- Molecule 31 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	g	47	346	210	62	69	5	0	0

- Molecule 32 is a RNA chain called 23S ribosomal RNA.


Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
32	A	3119	66981	29854	12313	21695	3119	0	0

- Molecule 33 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

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: 50S ribosomal protein L30

Chain 2:  89% 8%



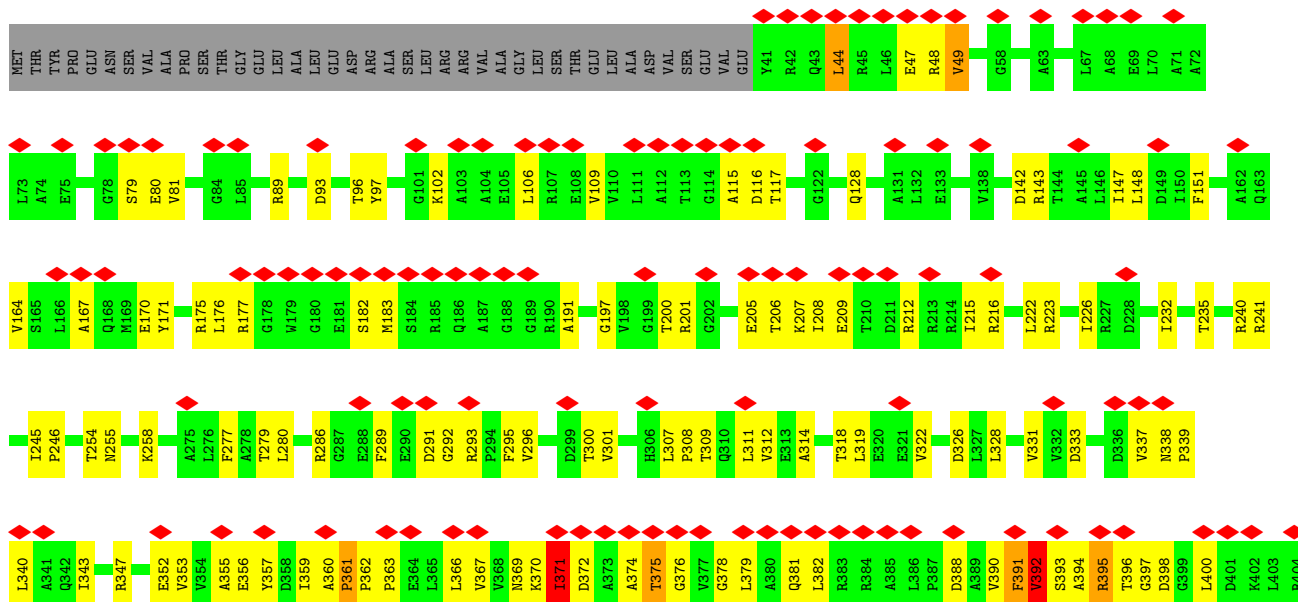
- Molecule 2: 50S Ribosomal Protein L27

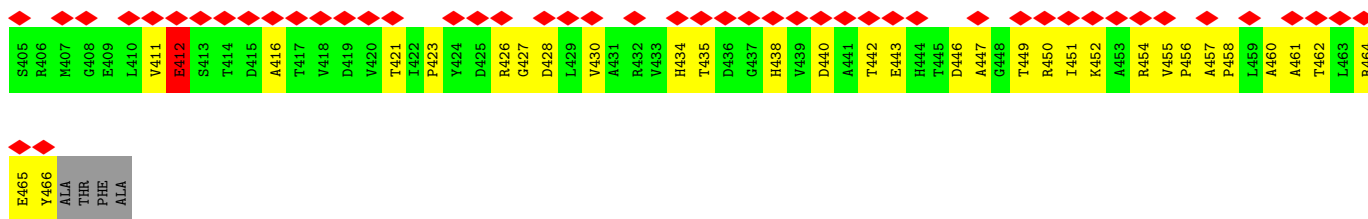
Chain 3:  88% 8%



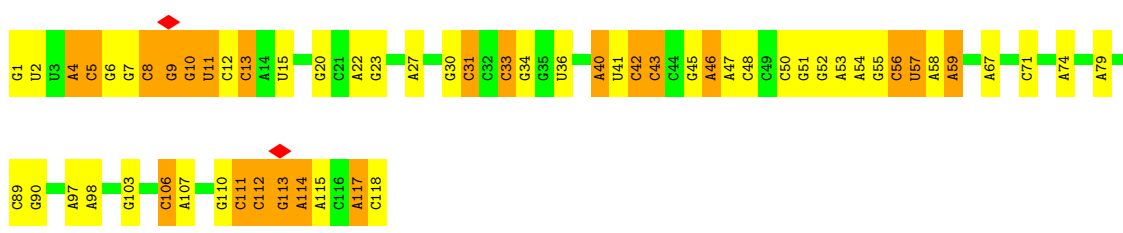
- Molecule 3: GTPase HflX

Chain 4:  35% 58% 31% 9%

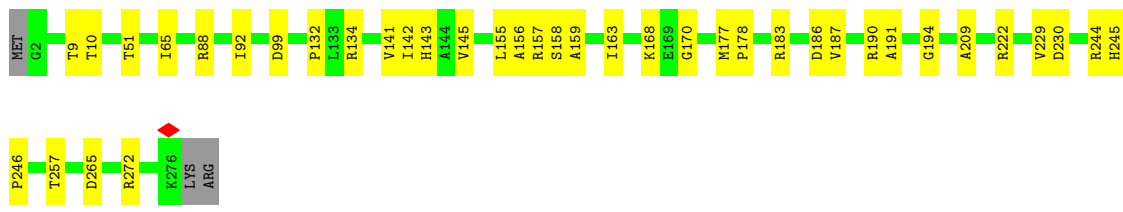
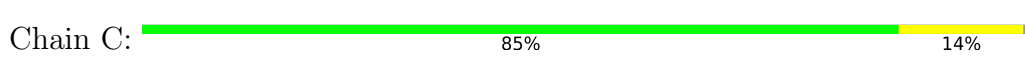




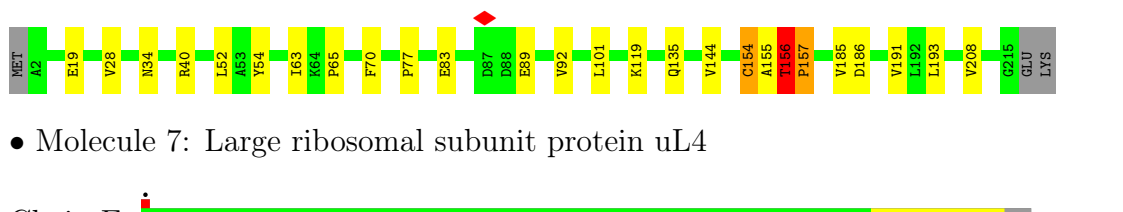
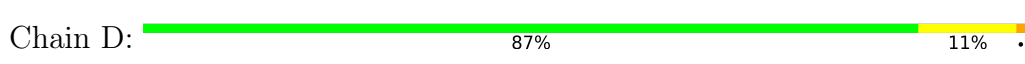
• Molecule 4: 5S ribosomal RNA



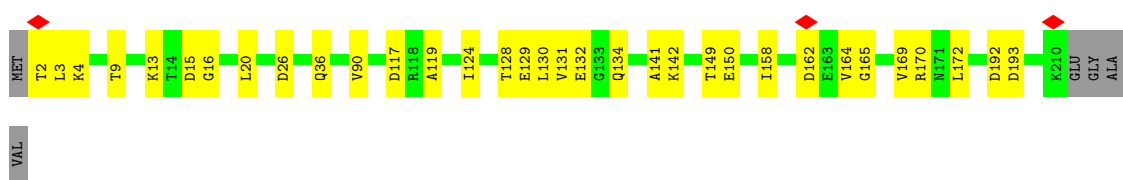
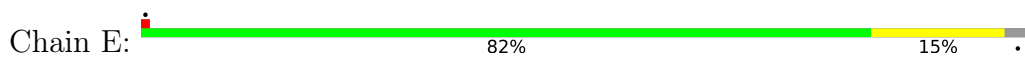
• Molecule 5: 50S ribosomal protein L2



• Molecule 6: 50S ribosomal protein L3

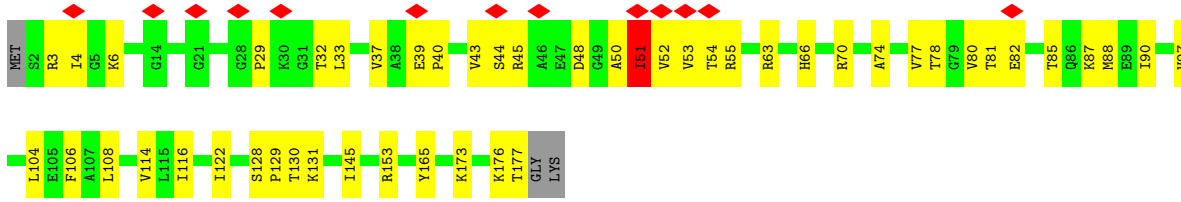


• Molecule 7: Large ribosomal subunit protein uL4

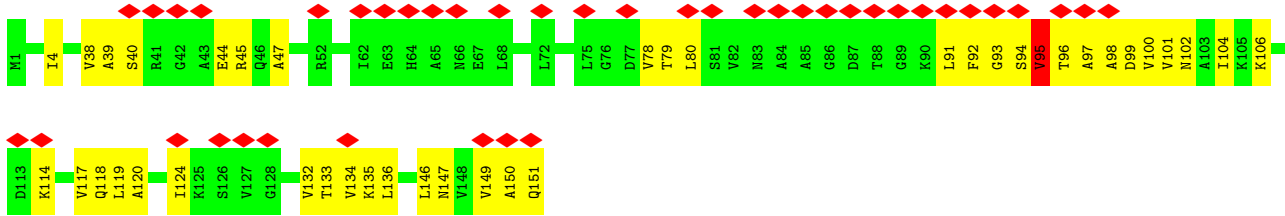
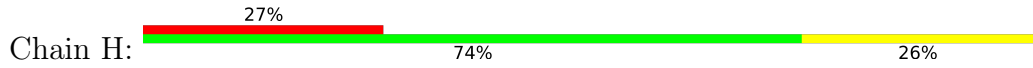


• Molecule 8: 50S ribosomal protein L6

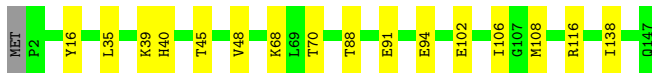
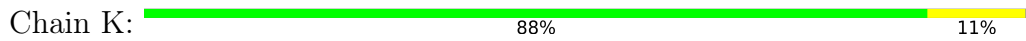




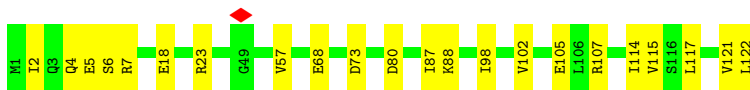
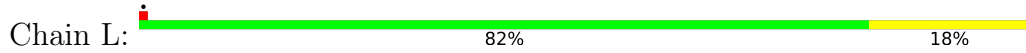
- Molecule 9: 50S ribosomal protein L9



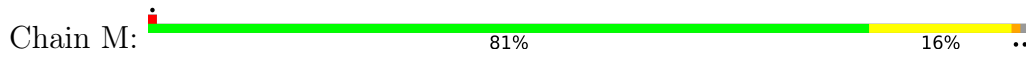
- Molecule 10: Large ribosomal subunit protein uL13



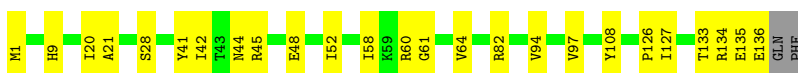
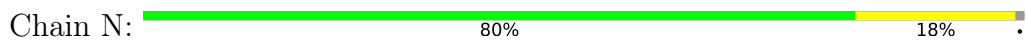
- Molecule 11: 50S ribosomal protein L14



- Molecule 12: 50S ribosomal protein L15

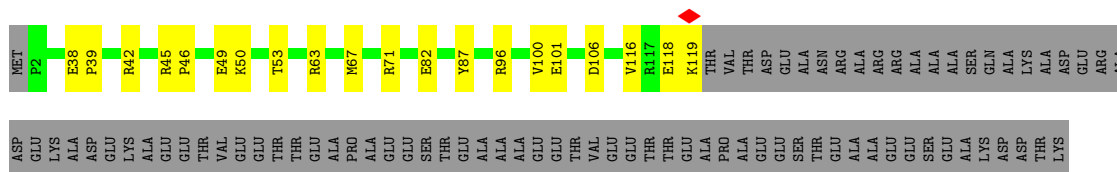


- Molecule 13: Large ribosomal subunit protein uL16

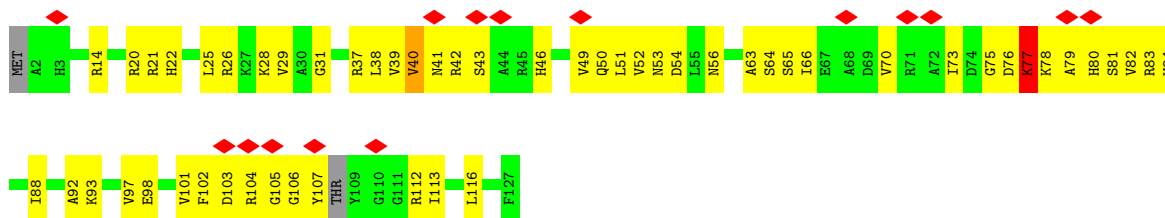


- Molecule 14: 50S ribosomal protein L17

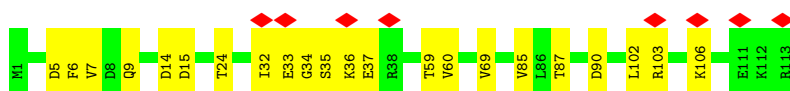
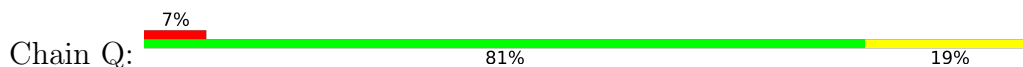




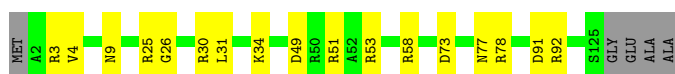
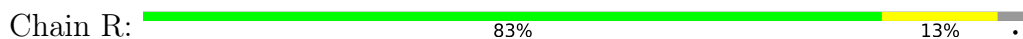
• Molecule 15: Large ribosomal subunit protein uL18



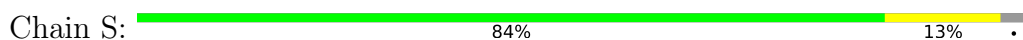
• Molecule 16: 50S ribosomal protein L19



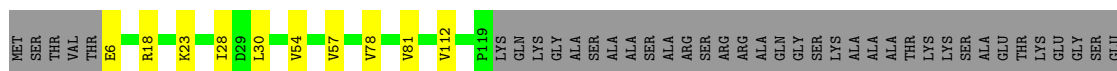
• Molecule 17: Large ribosomal subunit protein bL20



• Molecule 18: Large ribosomal subunit protein bL21

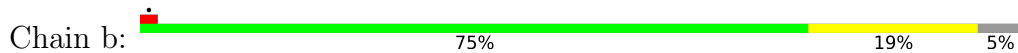


• Molecule 19: Large ribosomal subunit protein uL22

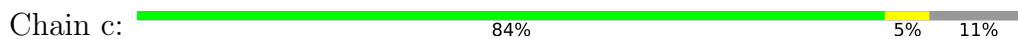


• Molecule 20: Large ribosomal subunit protein uL23





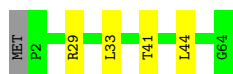
• Molecule 27: 50S Ribosomal Protein L33



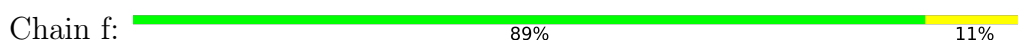
• Molecule 28: 50S ribosomal protein L34



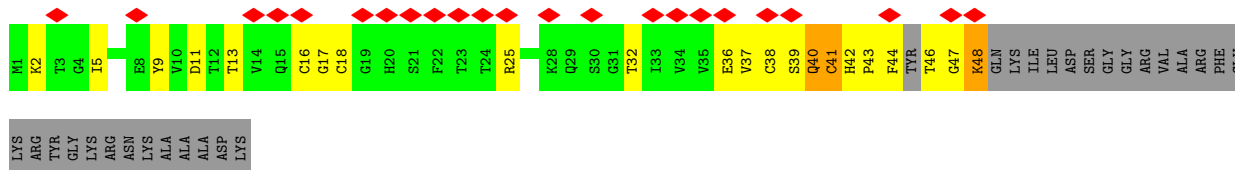
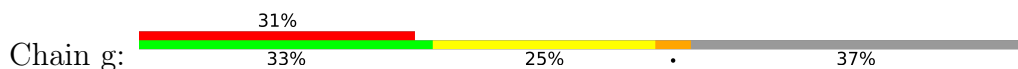
• Molecule 29: 50S ribosomal protein L35



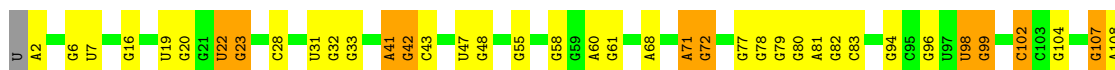
• Molecule 30: 50S ribosomal protein L36

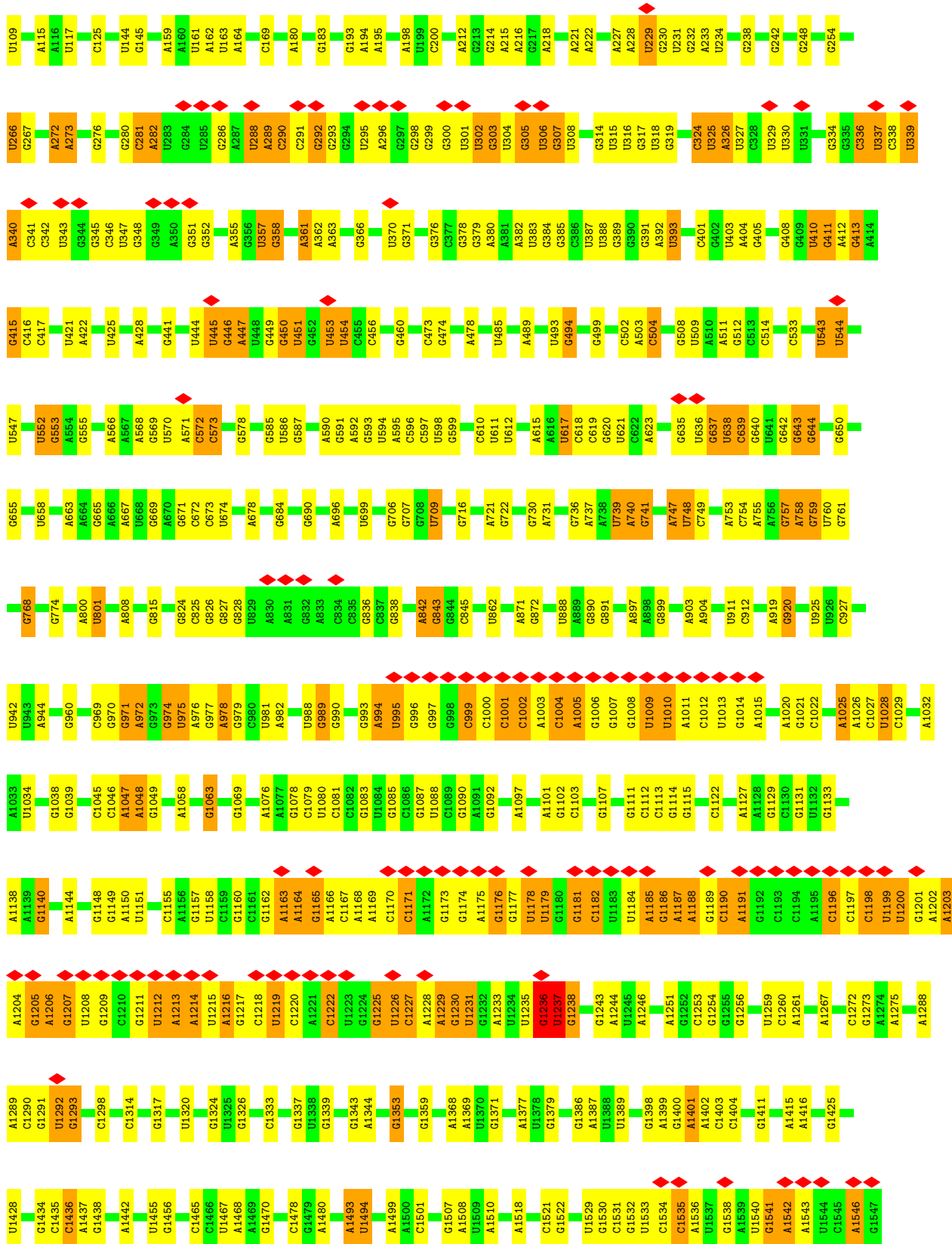


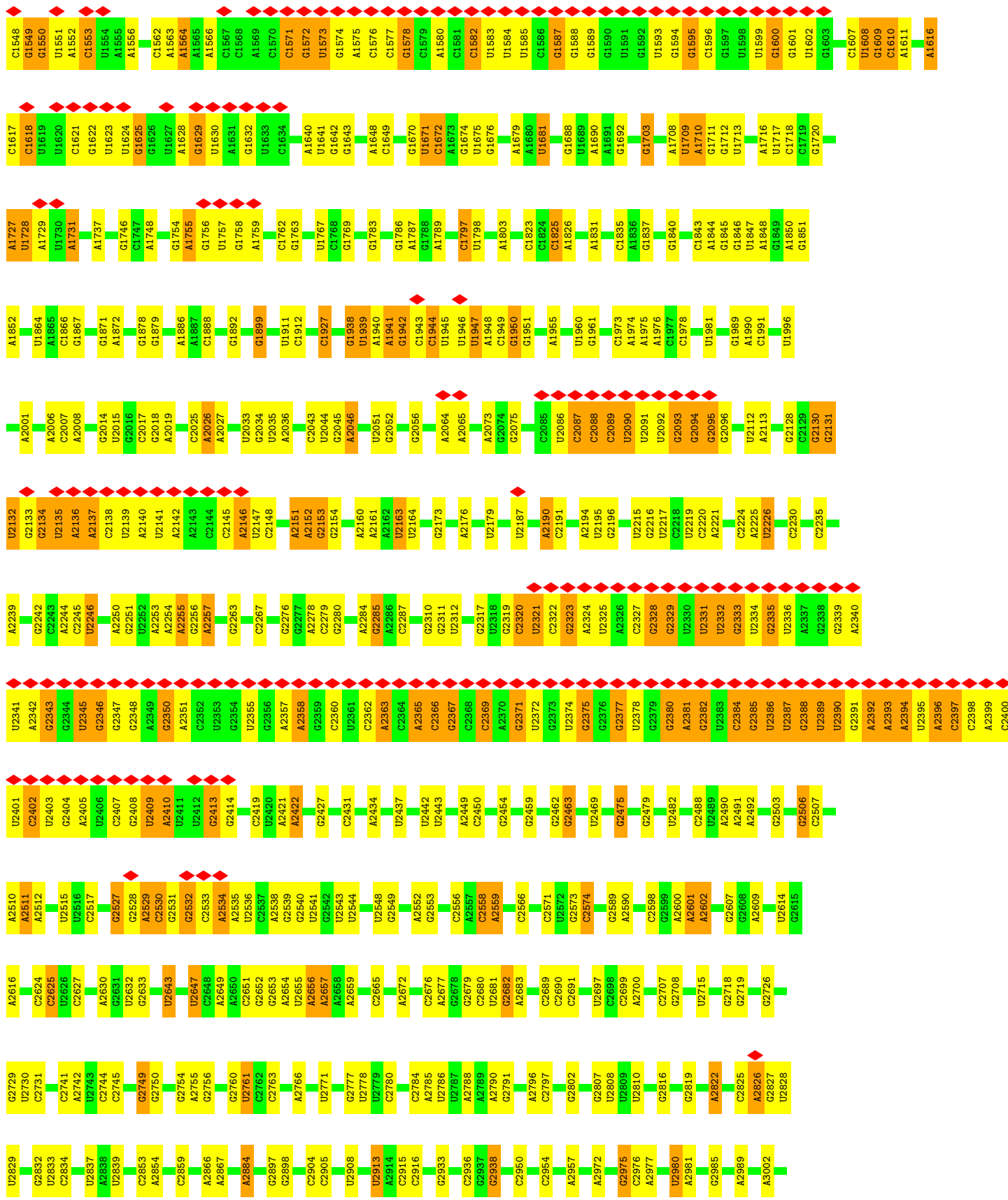
• Molecule 31: 50S Ribosomal Protein L31

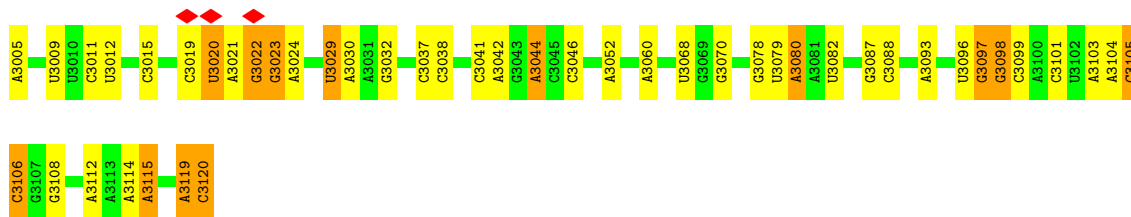


• Molecule 32: 23S ribosomal RNA









4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	65766	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 ($e^-/\text{\AA}^2$)	70.14	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.438	Depositor
Minimum map value	-0.931	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.17	Depositor
Map size (Å)	432.2816, 432.2816, 432.2816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8443, 0.8443, 0.8443	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	2	0.34	0/477	0.42	0/640
2	3	0.33	0/191	0.45	0/247
3	4	0.32	0/3268	0.60	7/4428 (0.2%)
4	B	0.28	0/2821	0.36	0/4396
5	C	0.35	0/2153	0.48	0/2895
6	D	0.46	0/1609	0.66	4/2165 (0.2%)
7	E	0.32	0/1592	0.47	0/2153
8	G	0.26	0/1369	0.53	1/1848 (0.1%)
9	H	0.40	0/1027	0.67	2/1398 (0.1%)
10	K	0.32	0/1157	0.44	0/1567
11	L	0.33	0/946	0.47	0/1268
12	M	0.54	1/1091 (0.1%)	0.69	3/1457 (0.2%)
13	N	0.30	0/1118	0.41	0/1506
14	O	0.35	0/945	0.49	0/1267
15	P	0.39	0/952	0.79	5/1278 (0.4%)
16	Q	0.32	0/921	0.48	0/1236
17	R	0.36	0/1000	0.46	0/1341
18	S	0.30	0/764	0.42	0/1030
19	T	0.32	0/887	0.46	0/1204
20	U	0.30	0/766	0.43	0/1030
21	V	0.28	0/738	0.47	0/987
22	W	0.24	0/794	0.44	0/1074
23	X	0.47	0/595	0.53	0/798
24	Y	0.34	0/478	0.53	0/641
25	Z	0.29	0/534	0.45	0/713
26	b	0.33	0/427	0.47	0/572
27	c	0.30	0/413	0.46	0/553
28	d	0.34	0/380	0.36	0/500
29	e	0.33	0/507	0.44	0/672
30	f	0.31	0/303	0.45	0/401
31	g	0.30	0/351	0.56	0/473
32	A	0.32	0/75001	0.35	3/117027 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.33	1/105575 (0.0%)	0.40	25/158765 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	M	31	LYS	CA-C	-5.74	1.45	1.52

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	A	1237	U	O5'-P-OP1	-24.60	34.21	108.00
12	M	30	GLY	N-CA-C	11.79	141.13	113.18
32	A	1236	G	O3'-P-O5'	-9.02	90.47	104.00
15	P	40	VAL	CA-C-N	-8.82	108.86	123.33
15	P	40	VAL	C-N-CA	-8.82	108.86	123.33

There are no chirality outliers.

There are no planarity outliers.

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	2	474	0	500	4	0
2	3	189	0	205	2	0
3	4	3228	0	3285	149	0
4	B	2522	0	1285	51	0
5	C	2110	0	2165	31	0
6	D	1587	0	1630	22	0
7	E	1569	0	1607	29	0
8	G	1348	0	1399	44	0
9	H	1018	0	988	51	0
10	K	1130	0	1167	11	0
11	L	938	0	1000	17	0
12	M	1078	0	1151	25	0
13	N	1092	0	1128	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	O	928	0	972	16	0
15	P	943	0	972	80	0
16	Q	907	0	938	16	0
17	R	988	0	1038	18	0
18	S	754	0	802	11	0
19	T	873	0	909	8	0
20	U	756	0	802	6	0
21	V	732	0	782	15	0
22	W	785	0	800	10	0
23	X	586	0	601	13	0
24	Y	470	0	481	5	0
25	Z	531	0	541	7	0
26	b	423	0	463	10	0
27	c	405	0	411	3	0
28	d	377	0	411	0	0
29	e	502	0	541	3	0
30	f	299	0	324	4	0
31	g	346	0	335	20	0
32	A	66981	0	33700	621	0
33	4	32	0	14	11	0
34	A	20	0	8	3	0
All	All	96921	0	63355	1207	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 8.

The worst 5 of 1207 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:47:GLU:HA	3:4:80:GLU:H	1.15	1.07
15:P:76:ASP:HB3	15:P:78:LYS:HG2	1.35	1.04
4:B:10:G:O2'	4:B:11:U:OP2	1.77	1.00
9:H:95:VAL:HG23	9:H:124:ILE:HG21	1.41	1.00
32:A:2320:C:O2'	32:A:2321:U:OP1	1.81	0.99

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	
1	2	57/61 (93%)	56 (98%)	1 (2%)	0	100	100
2	3	21/24 (88%)	21 (100%)	0	0	100	100
3	4	424/470 (90%)	348 (82%)	75 (18%)	1 (0%)	43	71
5	C	273/278 (98%)	248 (91%)	25 (9%)	0	100	100
6	D	212/217 (98%)	202 (95%)	9 (4%)	1 (0%)	24	55
7	E	207/215 (96%)	193 (93%)	14 (7%)	0	100	100
8	G	174/179 (97%)	153 (88%)	21 (12%)	0	100	100
9	H	149/151 (99%)	120 (80%)	29 (20%)	0	100	100
10	K	144/147 (98%)	139 (96%)	5 (4%)	0	100	100
11	L	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
12	M	143/147 (97%)	135 (94%)	8 (6%)	0	100	100
13	N	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
14	O	116/199 (58%)	109 (94%)	7 (6%)	0	100	100
15	P	121/127 (95%)	95 (78%)	26 (22%)	0	100	100
16	Q	111/113 (98%)	96 (86%)	15 (14%)	0	100	100
17	R	122/129 (95%)	119 (98%)	3 (2%)	0	100	100
18	S	98/103 (95%)	91 (93%)	7 (7%)	0	100	100
19	T	112/153 (73%)	110 (98%)	2 (2%)	0	100	100
20	U	95/100 (95%)	86 (90%)	9 (10%)	0	100	100
21	V	93/105 (89%)	82 (88%)	11 (12%)	0	100	100
22	W	99/215 (46%)	95 (96%)	4 (4%)	0	100	100
23	X	77/88 (88%)	67 (87%)	10 (13%)	0	100	100
24	Y	61/64 (95%)	52 (85%)	9 (15%)	0	100	100
25	Z	62/77 (80%)	61 (98%)	1 (2%)	0	100	100
26	b	52/57 (91%)	52 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	c	47/55 (86%)	44 (94%)	3 (6%)	0	100	100
28	d	44/47 (94%)	44 (100%)	0	0	100	100
29	e	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
30	f	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
31	g	43/75 (57%)	35 (81%)	8 (19%)	0	100	100
All	All	3507/3957 (89%)	3179 (91%)	326 (9%)	2 (0%)	49	76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	D	156	THR
3	4	361	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2	52/54 (96%)	52 (100%)	0	100	100
2	3	18/19 (95%)	18 (100%)	0	100	100
3	4	337/372 (91%)	331 (98%)	6 (2%)	51	69
5	C	215/218 (99%)	215 (100%)	0	100	100
6	D	160/163 (98%)	159 (99%)	1 (1%)	78	81
7	E	169/173 (98%)	169 (100%)	0	100	100
8	G	148/150 (99%)	147 (99%)	1 (1%)	76	79
9	H	90/116 (78%)	87 (97%)	3 (3%)	33	59
10	K	119/120 (99%)	119 (100%)	0	100	100
11	L	100/100 (100%)	100 (100%)	0	100	100
12	M	112/114 (98%)	112 (100%)	0	100	100
13	N	114/116 (98%)	114 (100%)	0	100	100
14	O	97/158 (61%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	P	91/94 (97%)	89 (98%)	2 (2%)	45	65
16	Q	100/100 (100%)	100 (100%)	0	100	100
17	R	97/99 (98%)	97 (100%)	0	100	100
18	S	81/83 (98%)	81 (100%)	0	100	100
19	T	90/117 (77%)	90 (100%)	0	100	100
20	U	83/85 (98%)	83 (100%)	0	100	100
21	V	81/86 (94%)	81 (100%)	0	100	100
22	W	81/168 (48%)	81 (100%)	0	100	100
23	X	58/63 (92%)	58 (100%)	0	100	100
24	Y	50/51 (98%)	50 (100%)	0	100	100
25	Z	58/66 (88%)	58 (100%)	0	100	100
26	b	43/46 (94%)	43 (100%)	0	100	100
27	c	47/52 (90%)	47 (100%)	0	100	100
28	d	35/36 (97%)	35 (100%)	0	100	100
29	e	53/54 (98%)	53 (100%)	0	100	100
30	f	35/35 (100%)	35 (100%)	0	100	100
31	g	41/63 (65%)	38 (93%)	3 (7%)	13	39
All	All	2855/3171 (90%)	2839 (99%)	16 (1%)	76	81

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	g	41	CYS
31	g	40	GLN
9	H	91	LEU
15	P	83	ARG
8	G	51	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
13	N	14	HIS
18	S	47	ASN
27	c	20	HIS
13	N	57	HIS

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Mol	Chain	Res	Type
21	V	67	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	A	3118/3120 (99%)	700 (22%)	33 (1%)
4	B	117/118 (99%)	36 (30%)	3 (2%)
All	All	3235/3238 (99%)	736 (22%)	36 (1%)

5 of 736 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	B	4	A
4	B	5	C
4	B	8	C
4	B	9	G
4	B	10	G

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
32	A	2328	G
32	A	3097	G
32	A	2331	U
32	A	2396	A
32	A	643	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands 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
33	GCP	4	501	-	32,34,34	1.40	5 (15%)	49,54,54	1.86	10 (20%)
34	CLM	A	3201	-	20,20,20	4.98	12 (60%)	23,27,27	3.76	13 (56%)

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
33	GCP	4	501	-	-	4/19/38/38	0/3/3/3
34	CLM	A	3201	-	-	6/20/22/22	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	A	3201	CLM	C8-C9	-9.52	1.21	1.38
34	A	3201	CLM	C10-C9	-8.30	1.23	1.38
34	A	3201	CLM	C5-C3	-7.79	1.44	1.53
34	A	3201	CLM	C11-C6	-7.08	1.28	1.39
34	A	3201	CLM	C3-N2	-6.73	1.35	1.46

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	A	3201	CLM	C3-N2-C2	8.43	137.91	123.25
34	A	3201	CLM	C11-C6-C7	-7.21	109.36	118.30
34	A	3201	CLM	C8-C7-C6	6.78	127.95	121.18
33	4	501	GCP	C5-C4-N3	-6.63	117.84	128.39
34	A	3201	CLM	O9B-N9-C9	5.67	126.61	118.82

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

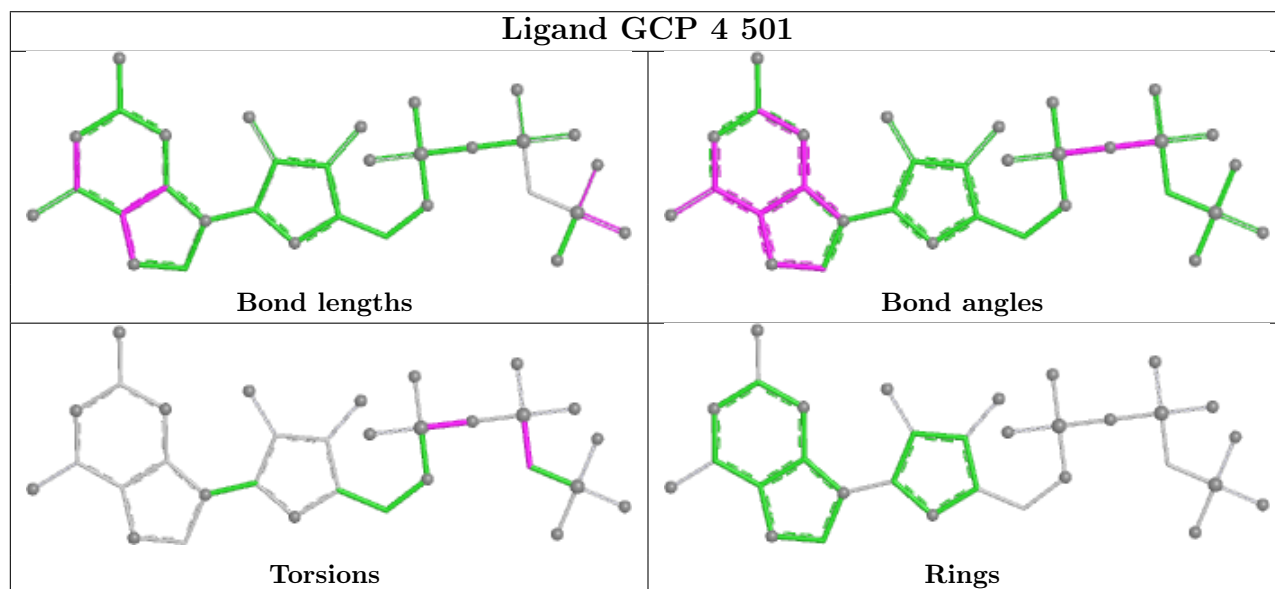
Mol	Chain	Res	Type	Atoms
33	4	501	GCP	PG-C3B-PB-O1B
33	4	501	GCP	PG-C3B-PB-O2B
33	4	501	GCP	PG-C3B-PB-O3A
34	A	3201	CLM	CL1-C1-C2-N2
34	A	3201	CLM	C4-C3-N2-C2

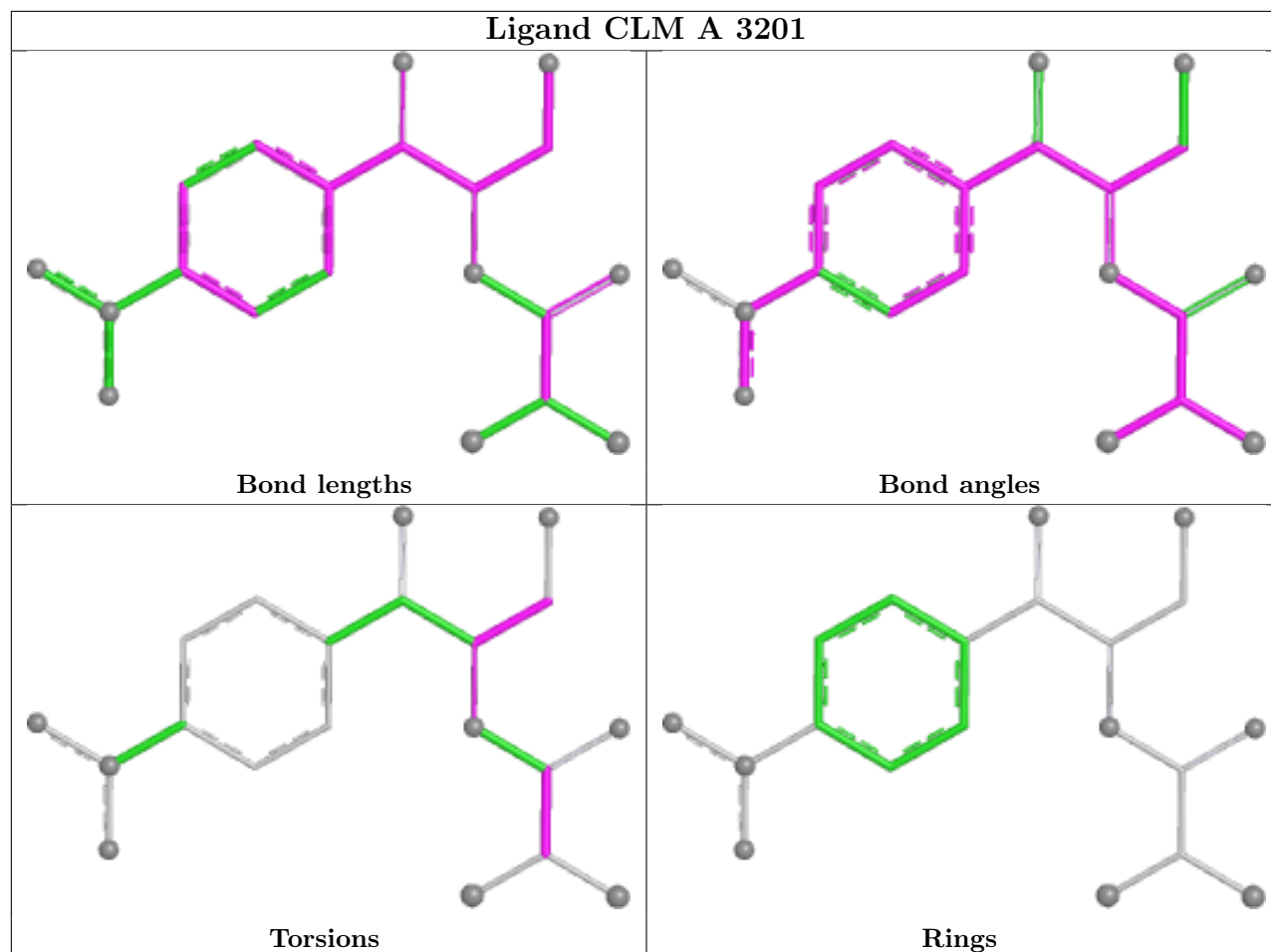
There are no ring outliers.

2 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	4	501	GCP	11	0
34	A	3201	CLM	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.

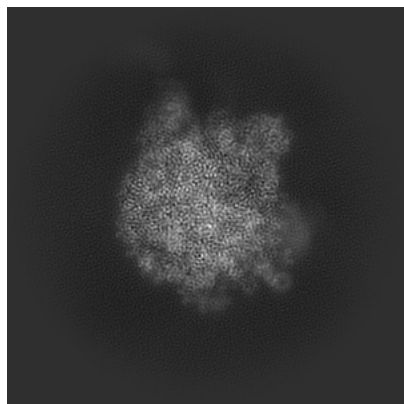
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43484. These allow visual inspection of the internal detail of the map and identification of artifacts.

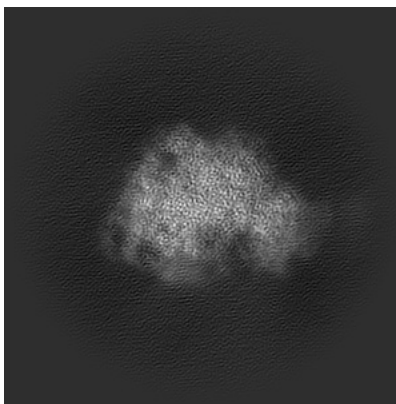
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

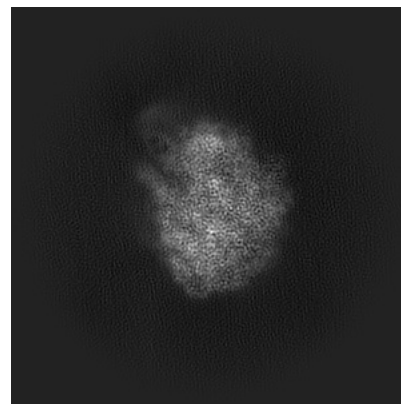
6.1.1 Primary map



X

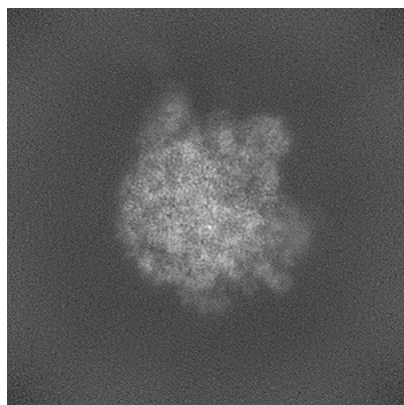


Y

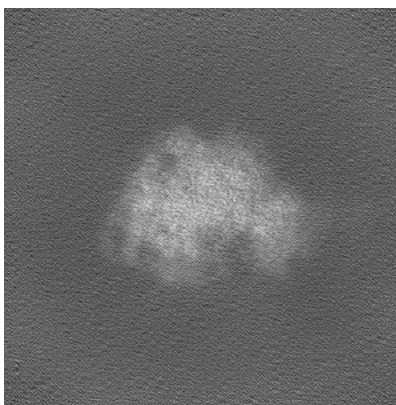


Z

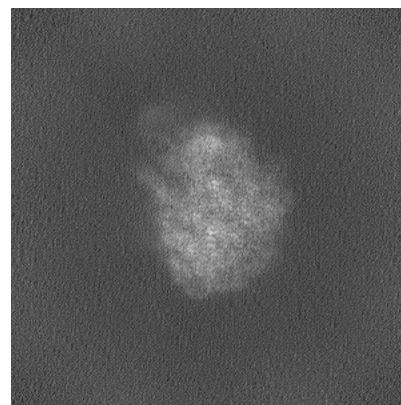
6.1.2 Raw map



X



Y

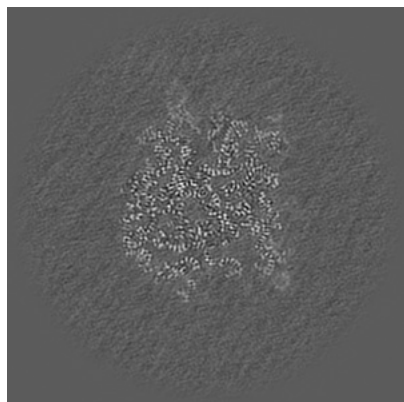


Z

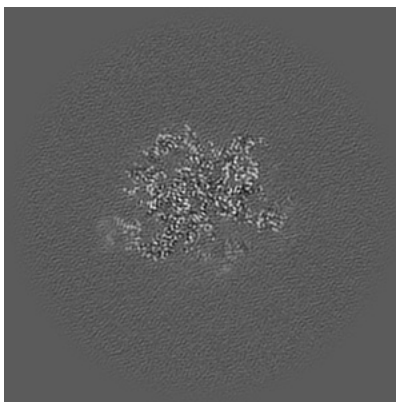
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

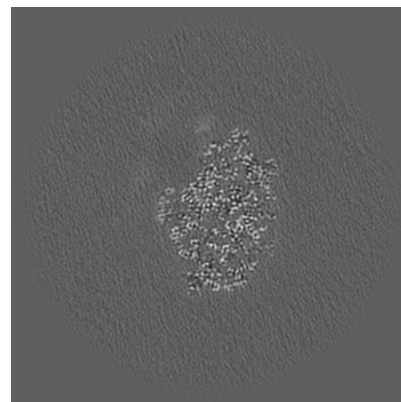
6.2.1 Primary map



X Index: 256

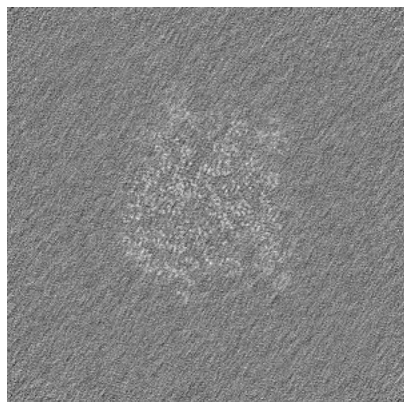


Y Index: 256

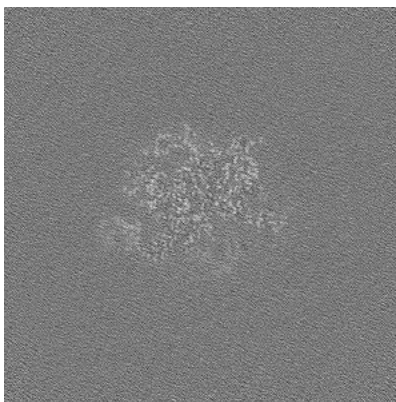


Z Index: 256

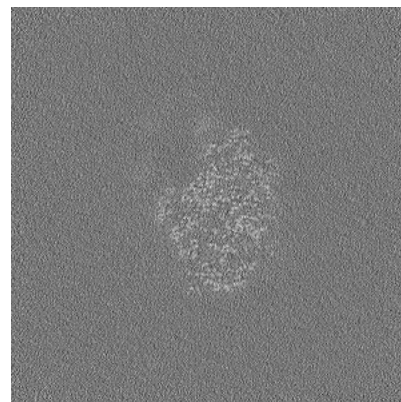
6.2.2 Raw map



X Index: 256



Y Index: 256

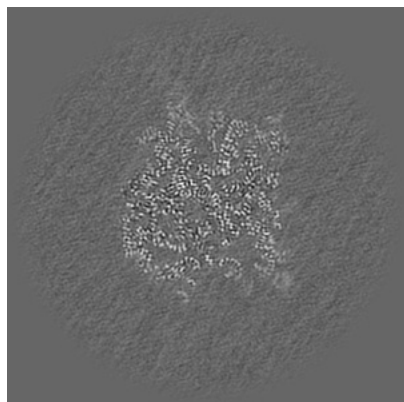


Z Index: 256

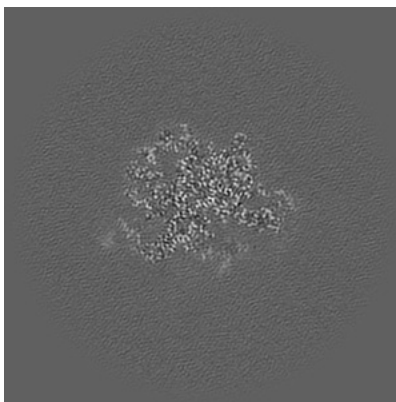
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

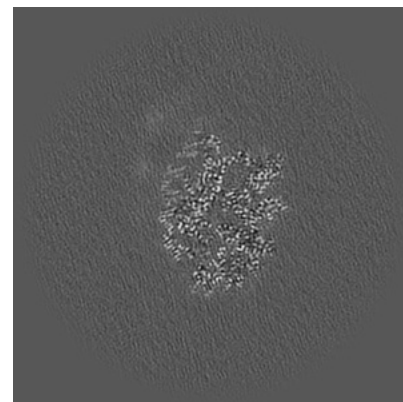
6.3.1 Primary map



X Index: 255

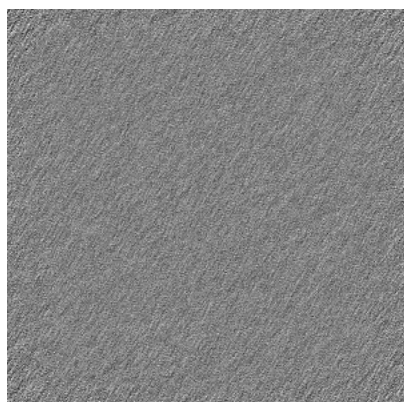


Y Index: 260

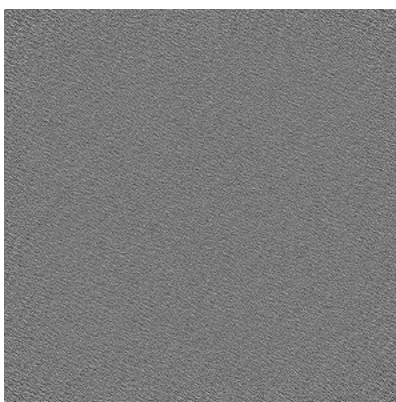


Z Index: 244

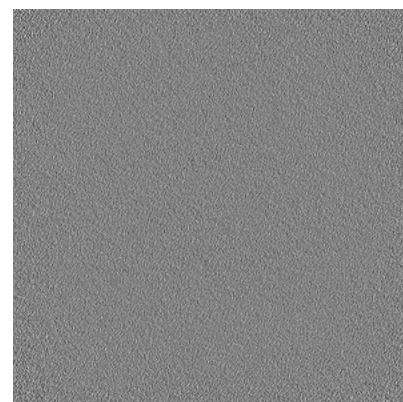
6.3.2 Raw map



X Index: 0



Y Index: 0

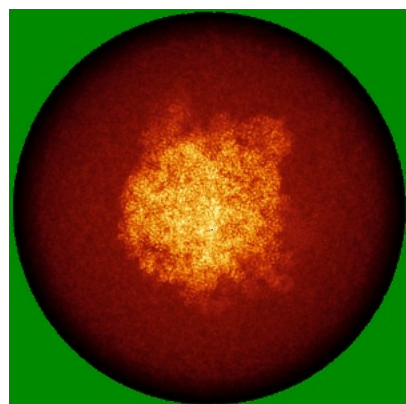


Z Index: 0

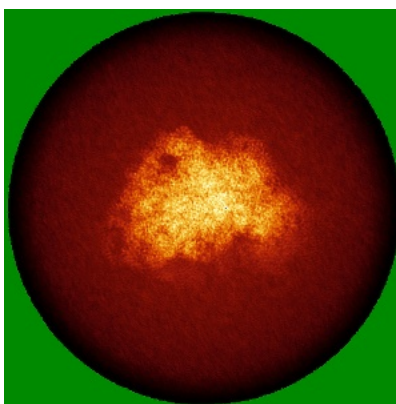
The images above show the largest variance slices of the map in three orthogonal directions.

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

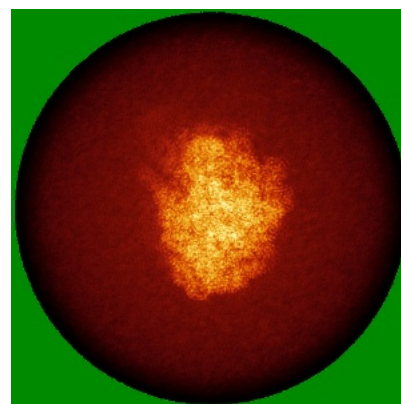
6.4.1 Primary map



X

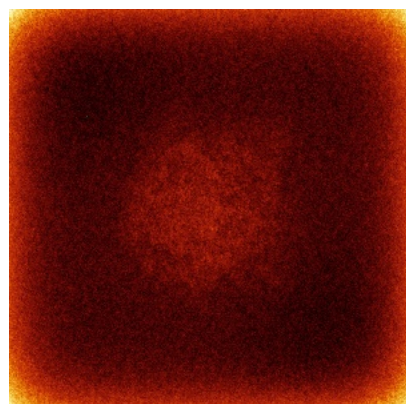


Y

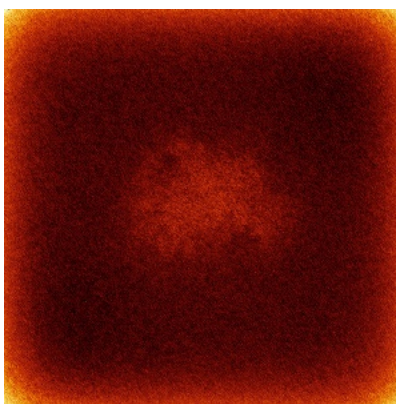


Z

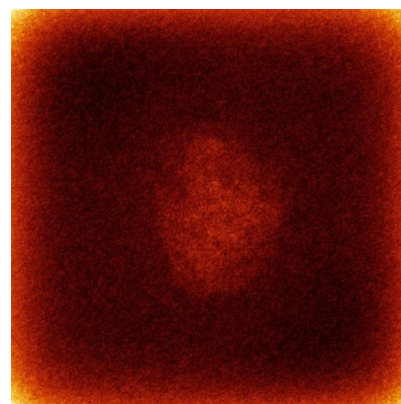
6.4.2 Raw map



X



Y

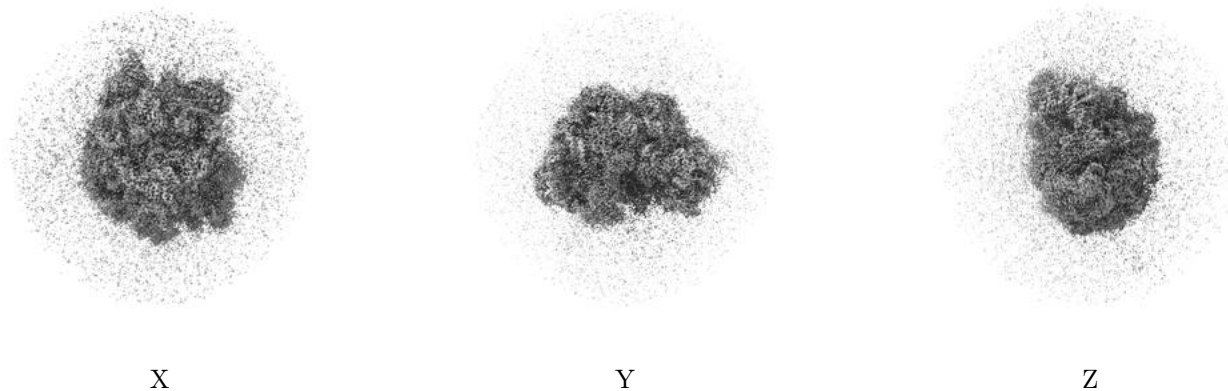


Z

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.

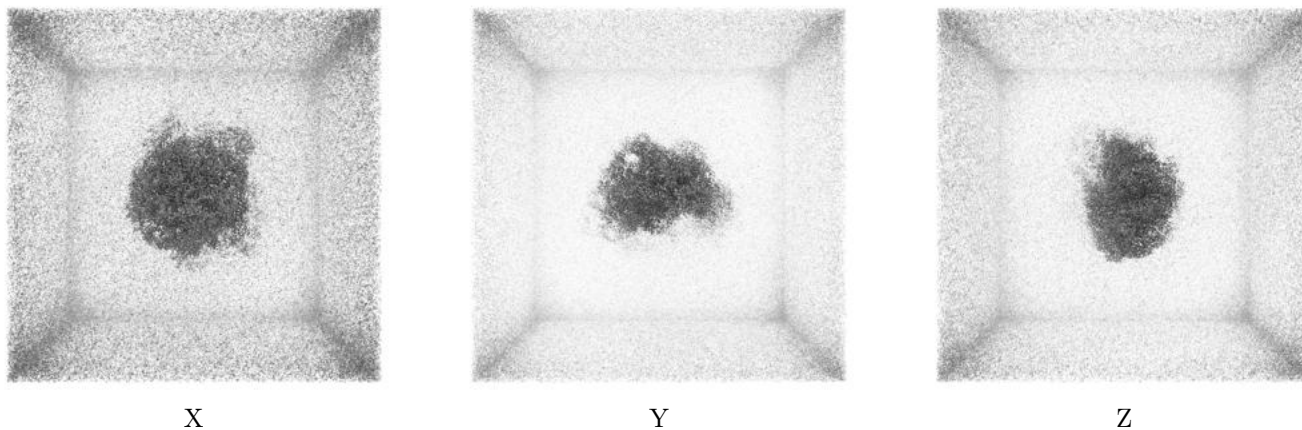
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.17. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

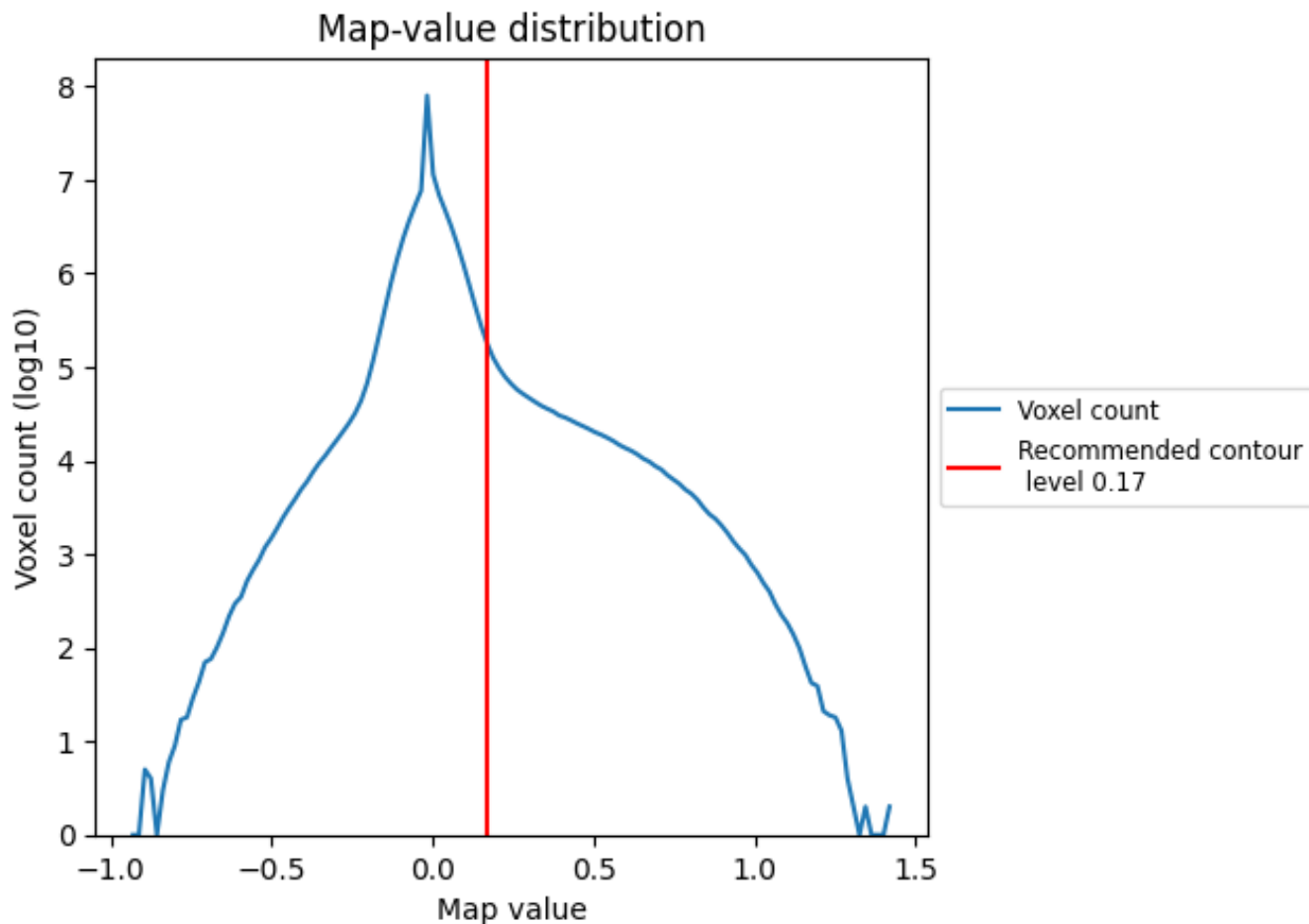
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

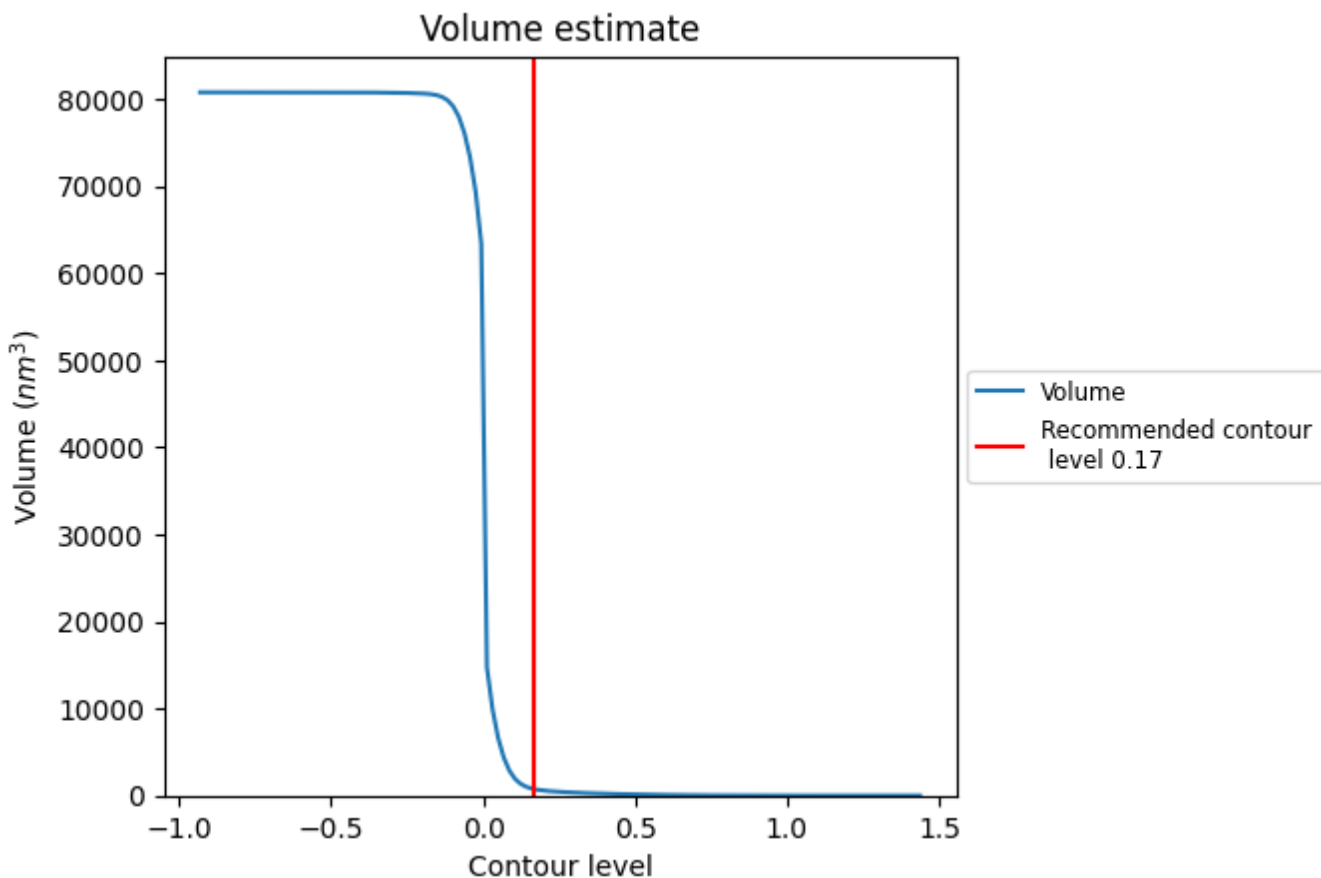
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

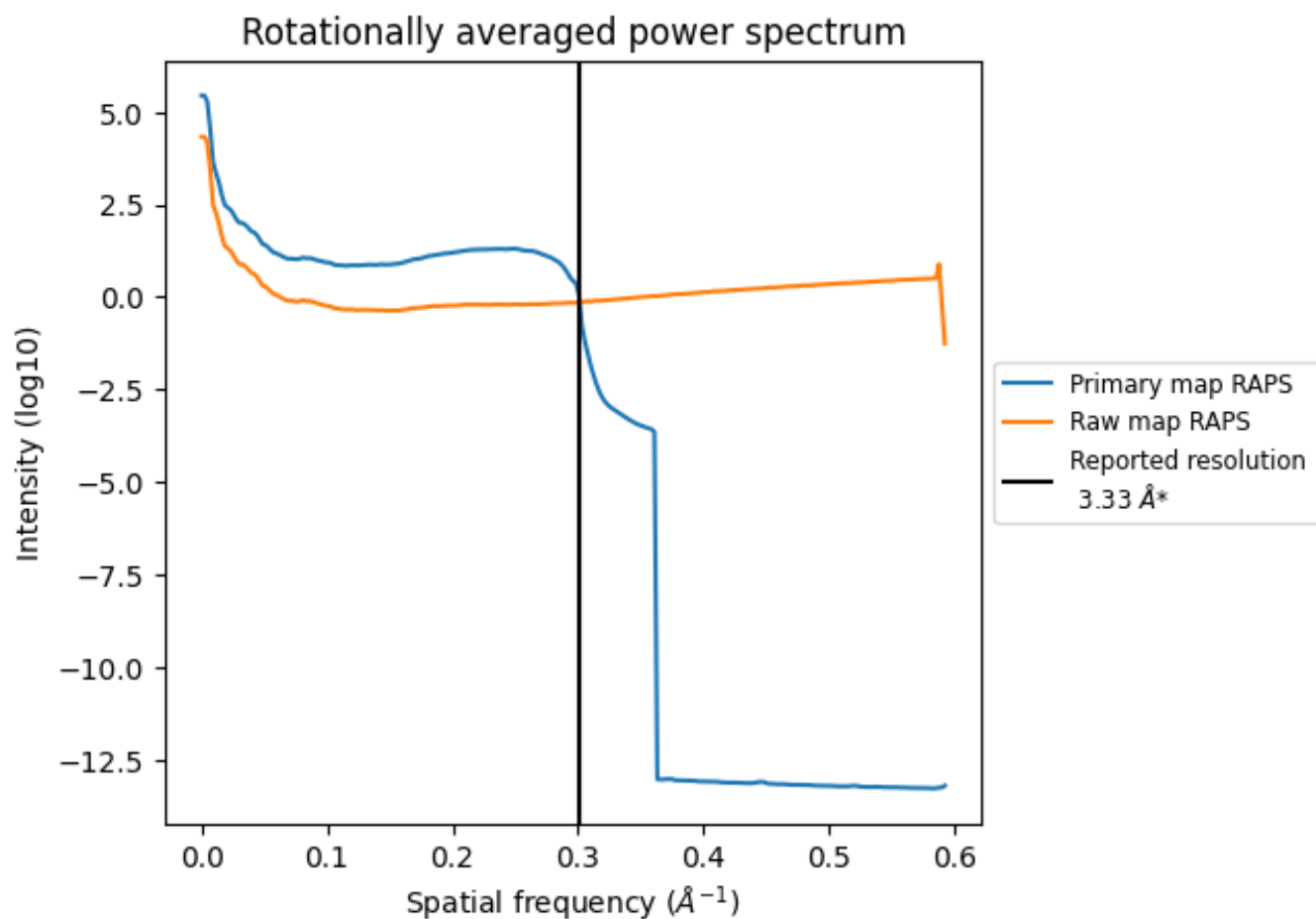
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 735 nm³; this corresponds to an approximate mass of 664 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

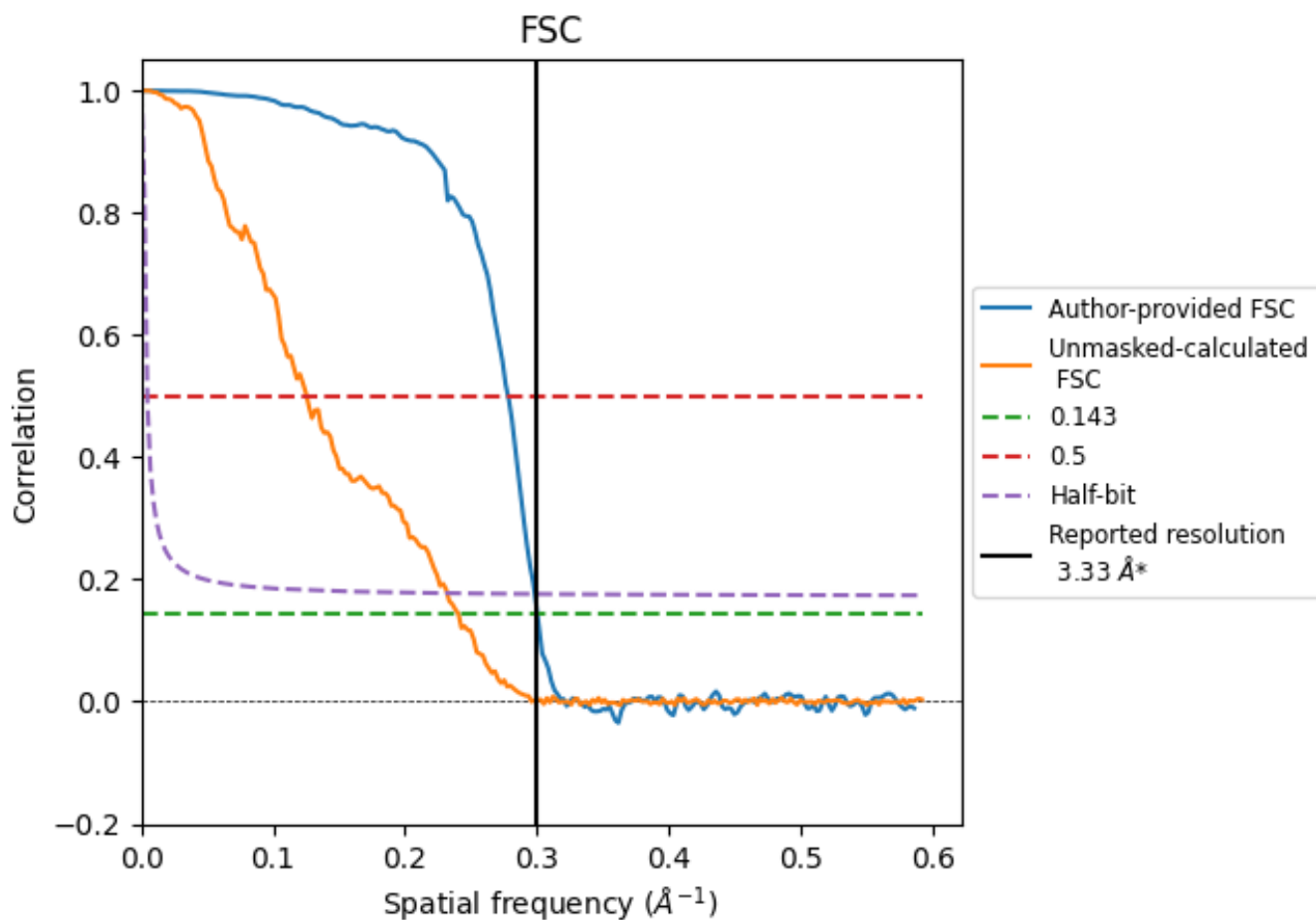


*Reported resolution corresponds to spatial frequency of 0.300 Å⁻¹

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 0.300 Å⁻¹

8.2 Resolution estimates [i](#)

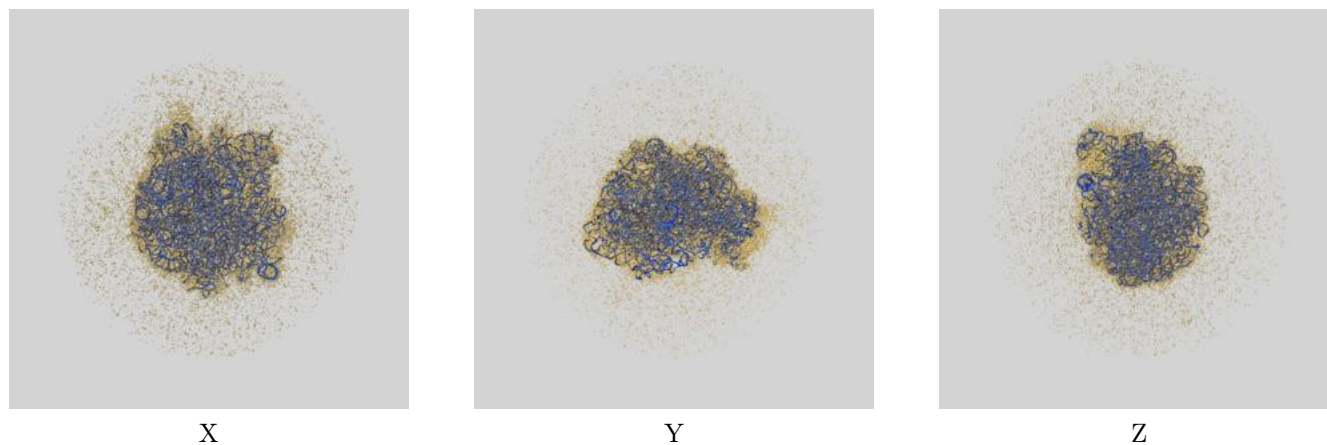
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.33	-	-
Author-provided FSC curve	3.33	3.59	3.35
Unmasked-calculated*	4.16	7.97	4.31

*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 4.16 differs from the reported value 3.33 by more than 10 %

9 Map-model fit [i](#)

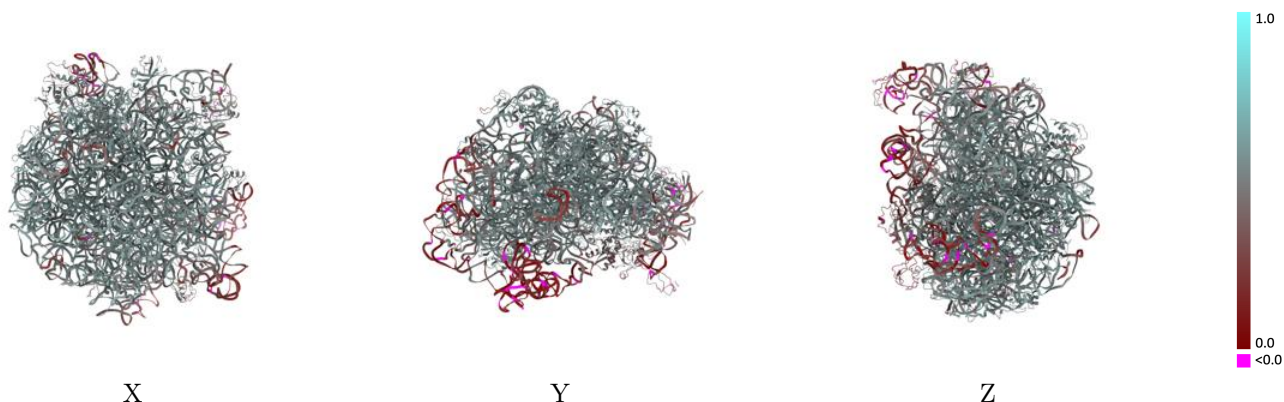
This section contains information regarding the fit between EMDB map EMD-43484 and PDB model 8VRL. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



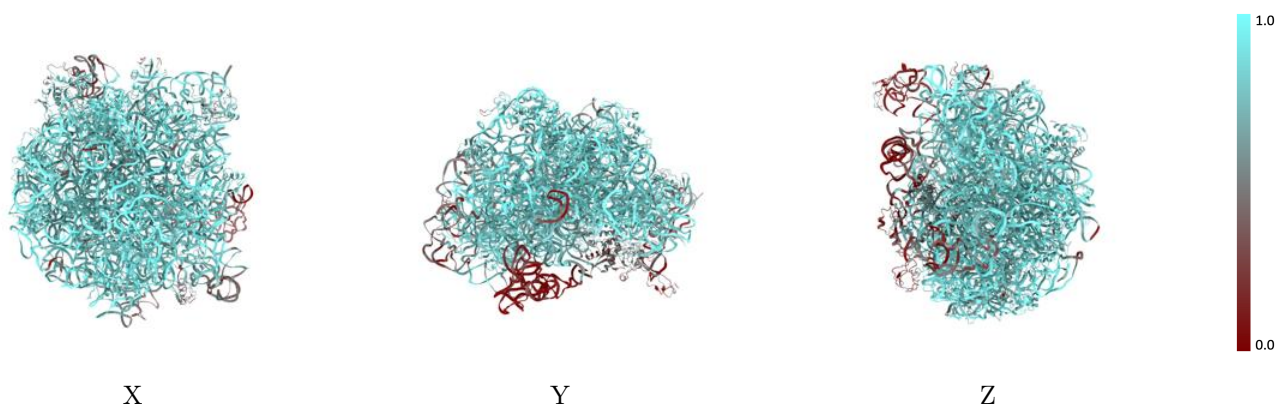
The images above show the 3D surface view of the map at the recommended contour level 0.17 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



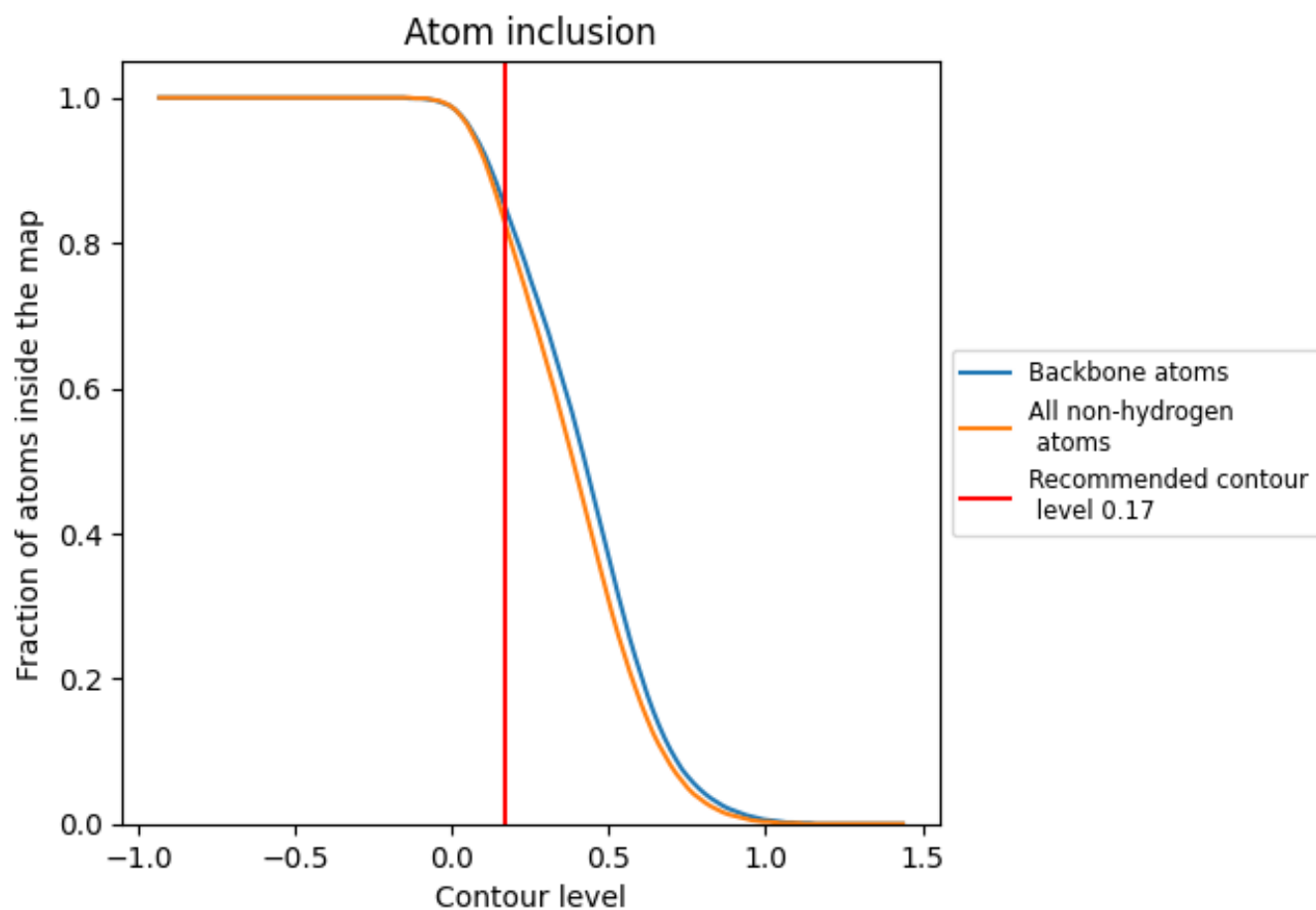
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.17).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 83% 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 (0.17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8270	 0.4950
2	 0.8890	 0.5560
3	 0.9330	 0.5840
4	 0.4760	 0.4020
A	 0.8390	 0.4850
B	 0.8500	 0.4790
C	 0.8830	 0.5620
D	 0.8880	 0.5630
E	 0.8620	 0.5440
G	 0.7240	 0.4820
H	 0.6040	 0.4470
K	 0.9060	 0.5710
L	 0.8630	 0.5500
M	 0.8860	 0.5570
N	 0.8860	 0.5650
O	 0.8880	 0.5580
P	 0.7200	 0.4230
Q	 0.8140	 0.5130
R	 0.9040	 0.5640
S	 0.8940	 0.5680
T	 0.8860	 0.5570
U	 0.8350	 0.5300
V	 0.7870	 0.4990
W	 0.7450	 0.5170
X	 0.8680	 0.5440
Y	 0.9010	 0.5560
Z	 0.8330	 0.5340
b	 0.8660	 0.5480
c	 0.8710	 0.5660
d	 0.9280	 0.5870
e	 0.9230	 0.5810
f	 0.8990	 0.5630
g	 0.3970	 0.3440

