



wwPDB EM Validation Summary Report ⓘ

Jun 17, 2026 – 07:39 pm BST

PDB ID : 9GHF / pdb_00009ghf
EMDB ID : EMD-51355
Title : Staphylococcus aureus FusB bound to the large subunit of the Escherichia coli
70S ribosome (FusB-70S:LSU)
Authors : Gonzalez-Lopez, A.; Selmer, M.
Deposited on : 2024-08-15
Resolution : 2.40 Å (reported)
Based on initial models : 9GHE, 8P2H

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:

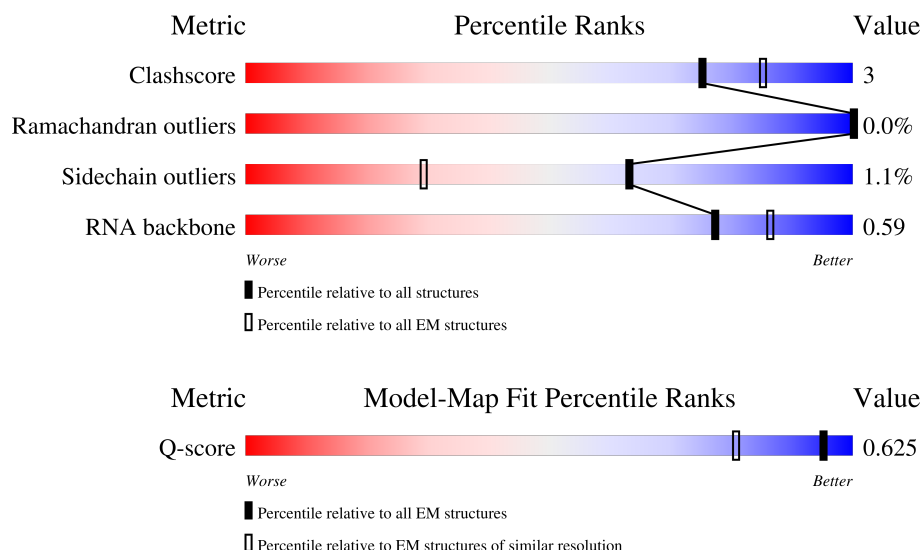
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	55	
2	1	46	
3	2	65	

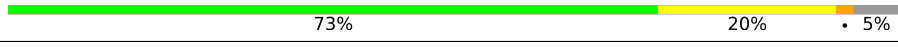
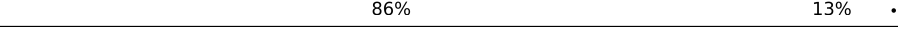
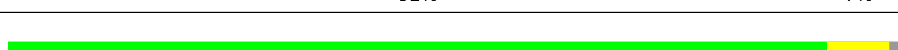
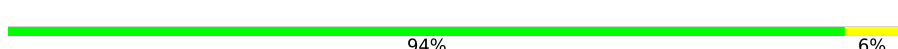
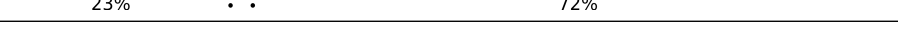
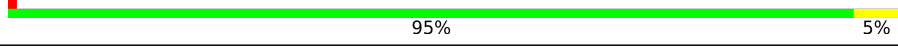
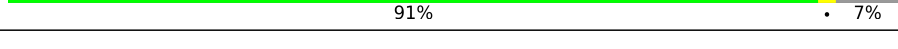
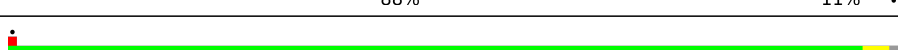
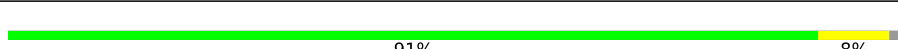
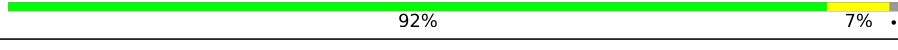
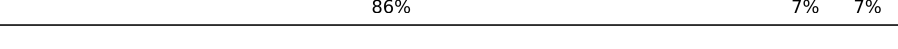
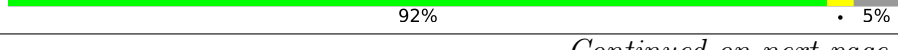
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Mol	Chain	Length	Quality of chain
4	3	38	
5	4	70	
6	9	24	
7	A	1554	
8	B	241	
9	C	233	
10	D	206	
11	E	167	
12	F	135	
13	G	179	
14	H	130	
15	I	130	
16	J	103	
17	K	129	
18	L	124	
19	M	118	
20	N	101	
21	O	89	
22	P	82	
23	Q	84	
24	R	75	
25	S	92	
26	T	87	
27	U	71	
28	V	213	

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Mol	Chain	Length	Quality of chain
29	Z	77	
30	a	2930	
31	b	119	
32	c	273	
33	d	209	
34	e	201	
35	f	179	
36	g	177	
37	h	149	
38	i	142	
39	j	123	
40	k	144	
41	l	136	
42	m	127	
43	n	117	
44	o	115	
45	p	118	
46	q	103	
47	r	110	
48	s	100	
49	t	104	
50	u	94	
51	v	85	
52	w	78	
53	x	63	

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Mol	Chain	Length	Quality of chain
54	y	59	85% 14%
55	z	57	88% 7% 5%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 141978 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 L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	50	Total	C	N	O	0	0
			413	267	75	71		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	45	Total	C	N	O	S	0	0
			367	222	88	55	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 5 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 6 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	9	10	Total	C	N	O	P	0	0
			218	98	45	65	10		

- Molecule 7 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	1514	Total	C	N	O	P	0	0
			32500	14503	5963	10520	1514		

- Molecule 8 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	222	Total	C	N	O	S	0	0
			1737	1099	312	318	8		

- Molecule 9 is a protein called 30S ribosomal protein S3.

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

- Molecule 10 is a protein called 30S ribosomal protein S4.

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

- Molecule 11 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	154	Total	C	N	O	S	0	0
			1135	706	215	208	6		

- Molecule 12 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	101	Total	C	N	O	S	0	0
			824	520	149	149	6		

- Molecule 13 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	150	Total	C	N	O	S	0	0
			1176	732	226	214	4		

- Molecule 14 is a protein called 30S ribosomal protein S8.

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

- Molecule 15 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	125	Total	C	N	O	S	0	0
			1001	622	200	176	3		

- Molecule 16 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	96	Total	C	N	O	S	0	0
			775	487	148	139	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	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	modified residue	UNP P0A7R9

- Molecule 18 is a protein called 30S ribosomal protein S12.

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

- Molecule 19 is a protein called 30S ribosomal protein S13.

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

- Molecule 20 is a protein called 30S ribosomal protein S14.

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

- Molecule 21 is a protein called 30S ribosomal protein S15.

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

- Molecule 22 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	79	Total	C	N	O	S	0	0
			629	394	124	110	1		

- Molecule 23 is a protein called 30S ribosomal protein S17.

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

- Molecule 24 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	64	Total	C	N	O	S	0	0
			524	330	99	94	1		

- Molecule 25 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 26 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 27 is a protein called 30S ribosomal protein S21.

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

- Molecule 28 is a protein called Far1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	198	Total	C	N	O	S	1	0
			1659	1075	271	306	7		

- Molecule 29 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	76	Total	C	N	O	P	0	0
			1623	723	294	530	76		

- Molecule 30 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	2782	Total	C	N	O	P	0	0
			59756	26665	11017	19292	2782		

- Molecule 31 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 32 is a protein called 50S ribosomal protein L2.

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

- Molecule 33 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	207	Total	C	N	O	S	0	0
			1552	972	286	291	3		

- Molecule 34 is a protein called 50S ribosomal protein L4.

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

- Molecule 35 is a protein called 50S ribosomal protein L5.

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

- Molecule 36 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	168	Total	C	N	O	S	0	0
			1255	791	228	234	2		

- Molecule 37 is a protein called 50S ribosomal protein L9.

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

- Molecule 38 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	141	Total	C	N	O	S	0	0
			1121	709	211	198	3		

- Molecule 39 is a protein called 50S ribosomal protein L14.

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

- Molecule 40 is a protein called 50S ribosomal protein L15.

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

- Molecule 41 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	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
l	82	MS6	MET	modified residue	UNP P0ADY7

- Molecule 42 is a protein called 50S ribosomal protein L17.

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

- Molecule 43 is a protein called 50S ribosomal protein L18.

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

- Molecule 44 is a protein called 50S ribosomal protein L19.

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

- Molecule 45 is a protein called 50S ribosomal protein L20.

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

- Molecule 46 is a protein called 50S ribosomal protein L21.

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

- Molecule 47 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	109	Total	C	N	O	S	0	0
			845	526	162	154	3		

- Molecule 48 is a protein called 50S ribosomal protein L23.

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

- Molecule 49 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	93	Total	C	N	O	S	0	0
			717	452	135	130			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	93	Total	C	N	O	S	0	0
			745	474	136	133	2		

- Molecule 51 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	75	Total	C	N	O	S	0	0
			569	353	113	102	1		

- Molecule 52 is a protein called 50S ribosomal protein L28.

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

- Molecule 53 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	60	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 54 is a protein called 50S ribosomal protein L30.

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

- Molecule 55 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	54	Total	C	N	O	S	0	0
			429	260	91	77	1		

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	3	1	Total	Zn	0
			1	1	
56	4	1	Total	Zn	0
			1	1	
56	V	1	Total	Zn	0
			1	1	

- Molecule 57 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
57	A	32	Total	K	0
			32	32	
57	F	1	Total	K	0
			1	1	
57	a	75	Total	K	0
			75	75	
57	c	3	Total	K	0
			3	3	
57	e	1	Total	K	0
			1	1	

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	A	55	Total	Mg	0
			55	55	
58	a	241	Total	Mg	0
			241	241	
58	b	3	Total	Mg	0
			3	3	

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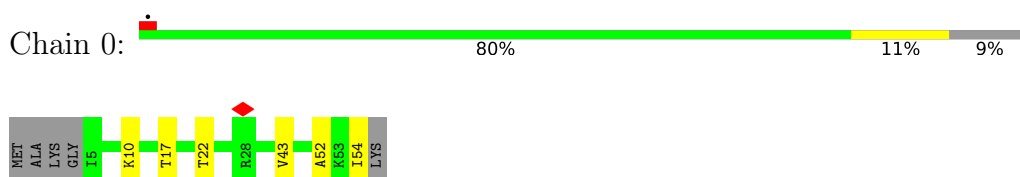
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Mol	Chain	Residues	Atoms		AltConf
58	c	2	Total 2	Mg 2	0
58	d	1	Total 1	Mg 1	0
58	z	1	Total 1	Mg 1	0

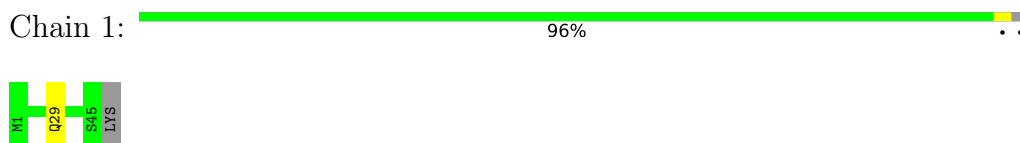
3 Residue-property plots [i](#)

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.

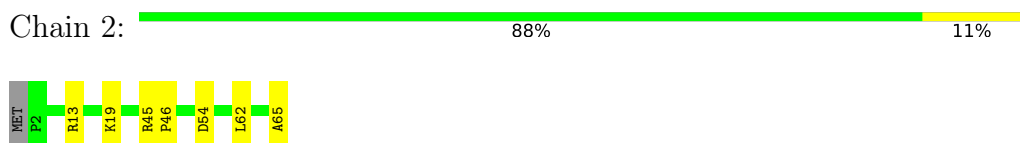
- Molecule 1: 50S ribosomal protein L33



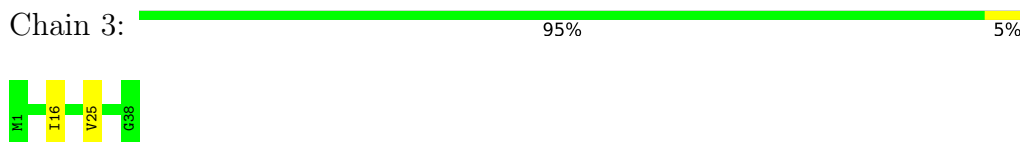
- Molecule 2: 50S ribosomal protein L34



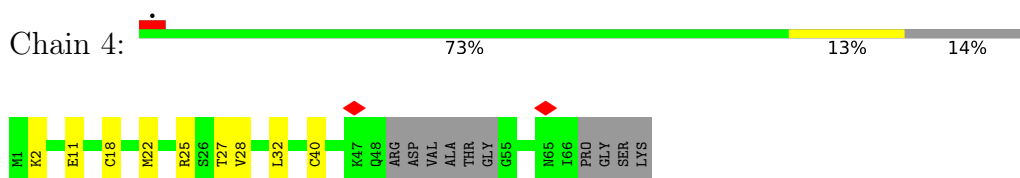
- Molecule 3: 50S ribosomal protein L35



- Molecule 4: 50S ribosomal protein L36



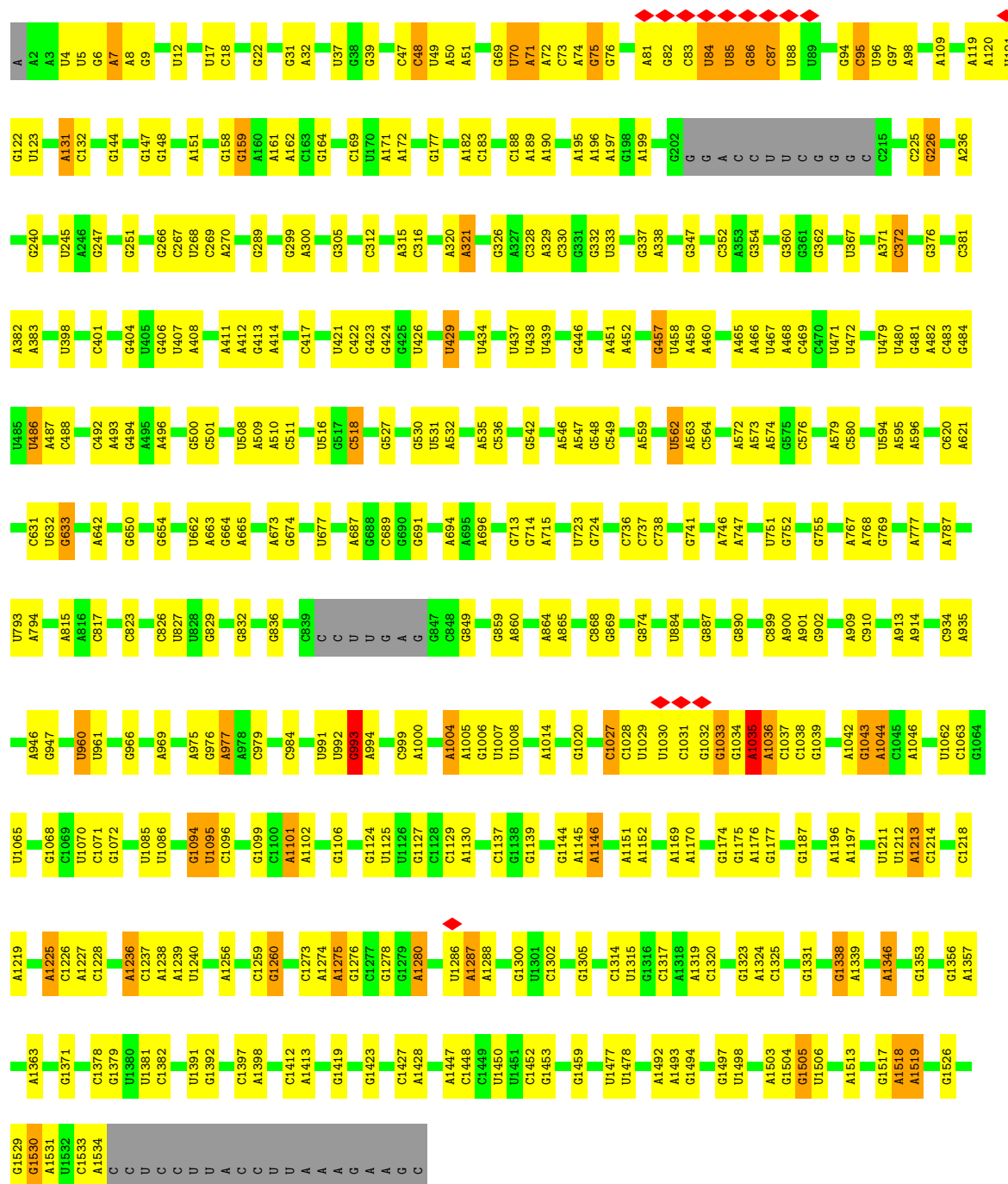
- Molecule 5: 50S ribosomal protein L31



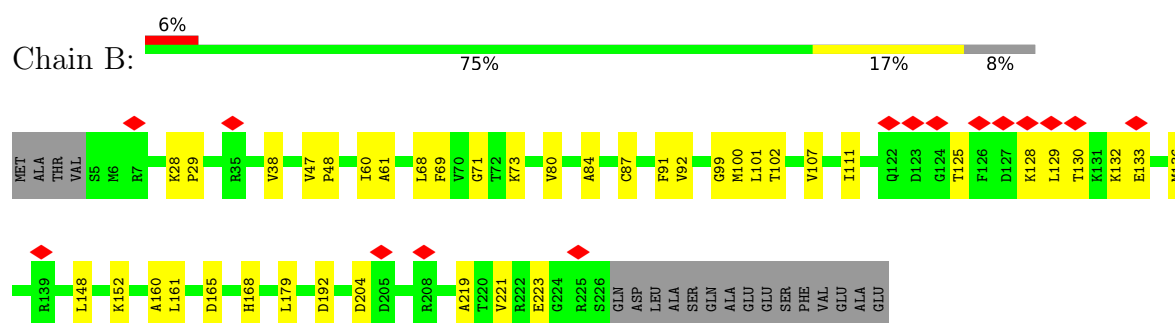
- Molecule 6: mRNA



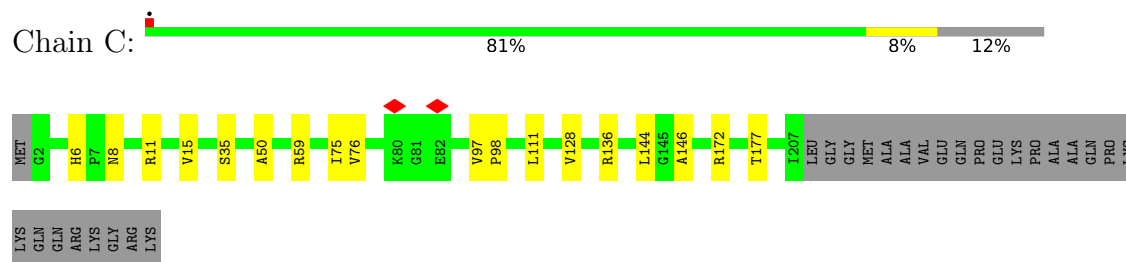
Chain A: 70% 24%



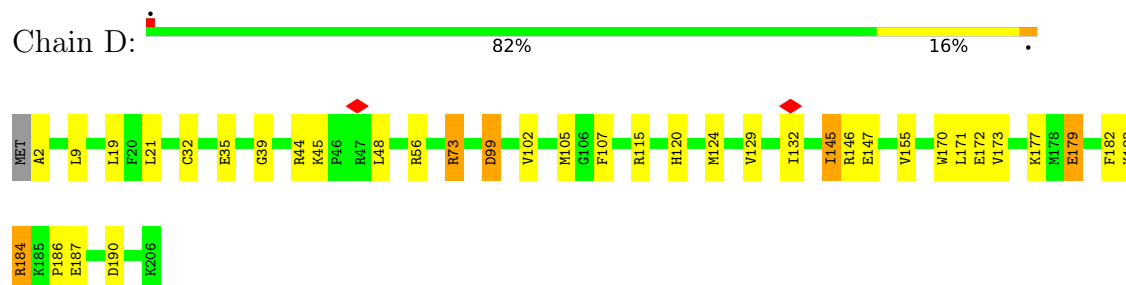
- Molecule 8: 30S ribosomal protein S2



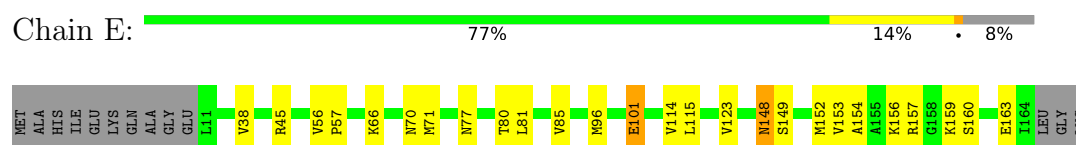
- Molecule 9: 30S ribosomal protein S3



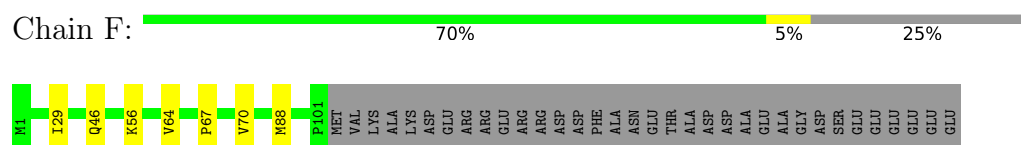
- Molecule 10: 30S ribosomal protein S4



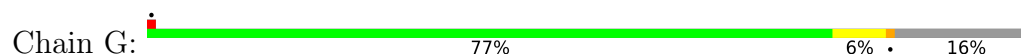
- Molecule 11: 30S ribosomal protein S5

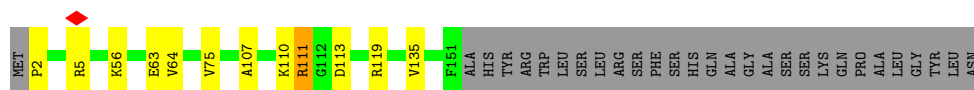


- Molecule 12: 30S ribosomal protein S6



- Molecule 13: 30S ribosomal protein S7





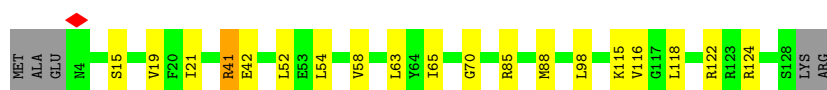
- Molecule 14: 30S ribosomal protein S8

Chain H: 88% 11%



- Molecule 15: 30S ribosomal protein S9

Chain I: 82% 14%



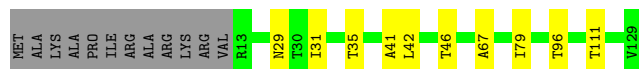
- Molecule 16: 30S ribosomal protein S10

Chain J: 5% 71% 20% 7%



- Molecule 17: Small ribosomal subunit protein uS11

Chain K: 83% 8% 9%



- Molecule 18: 30S ribosomal protein S12

Chain L: 83% 12%



- Molecule 19: 30S ribosomal protein S13

Chain M: 83% 14%



- Molecule 20: 30S ribosomal protein S14

Chain N: 94% 5%



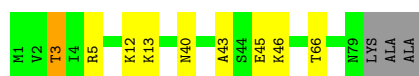
- Molecule 21: 30S ribosomal protein S15

Chain O: 98% ..



- Molecule 22: 30S ribosomal protein S16

Chain P: 85% 10% ..



- Molecule 23: 30S ribosomal protein S17

Chain Q: 77% 14% 6%



- Molecule 24: 30S ribosomal protein S18

Chain R: 76% 9% 15%



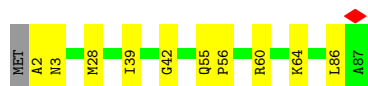
- Molecule 25: 30S ribosomal protein S19

Chain S: 82% 10% 9%



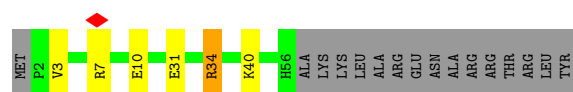
- Molecule 26: 30S ribosomal protein S20

Chain T: 87% 11%

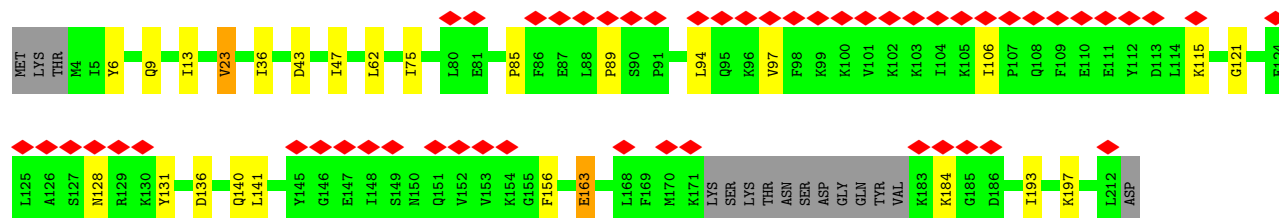
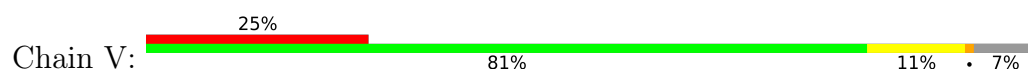


- Molecule 27: 30S ribosomal protein S21

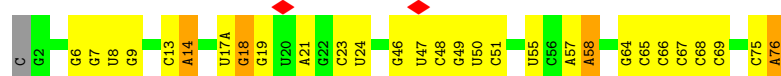
Chain U: 69% 7% 23%



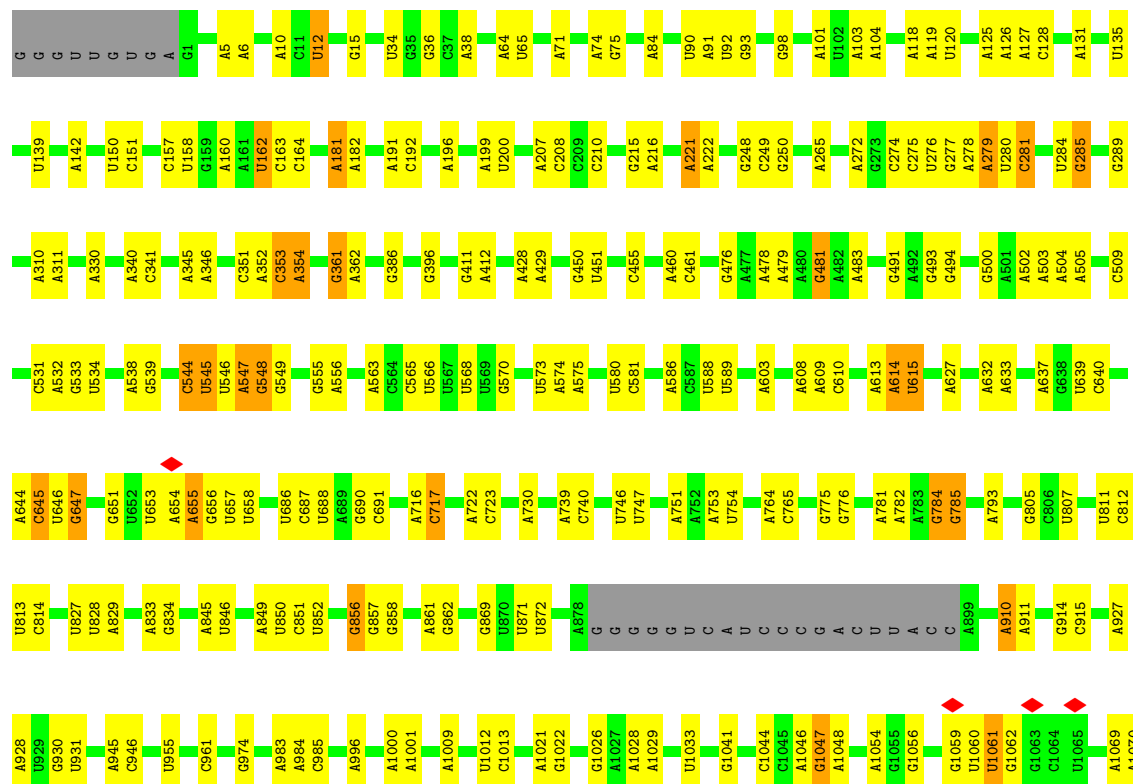
• Molecule 28: Far1

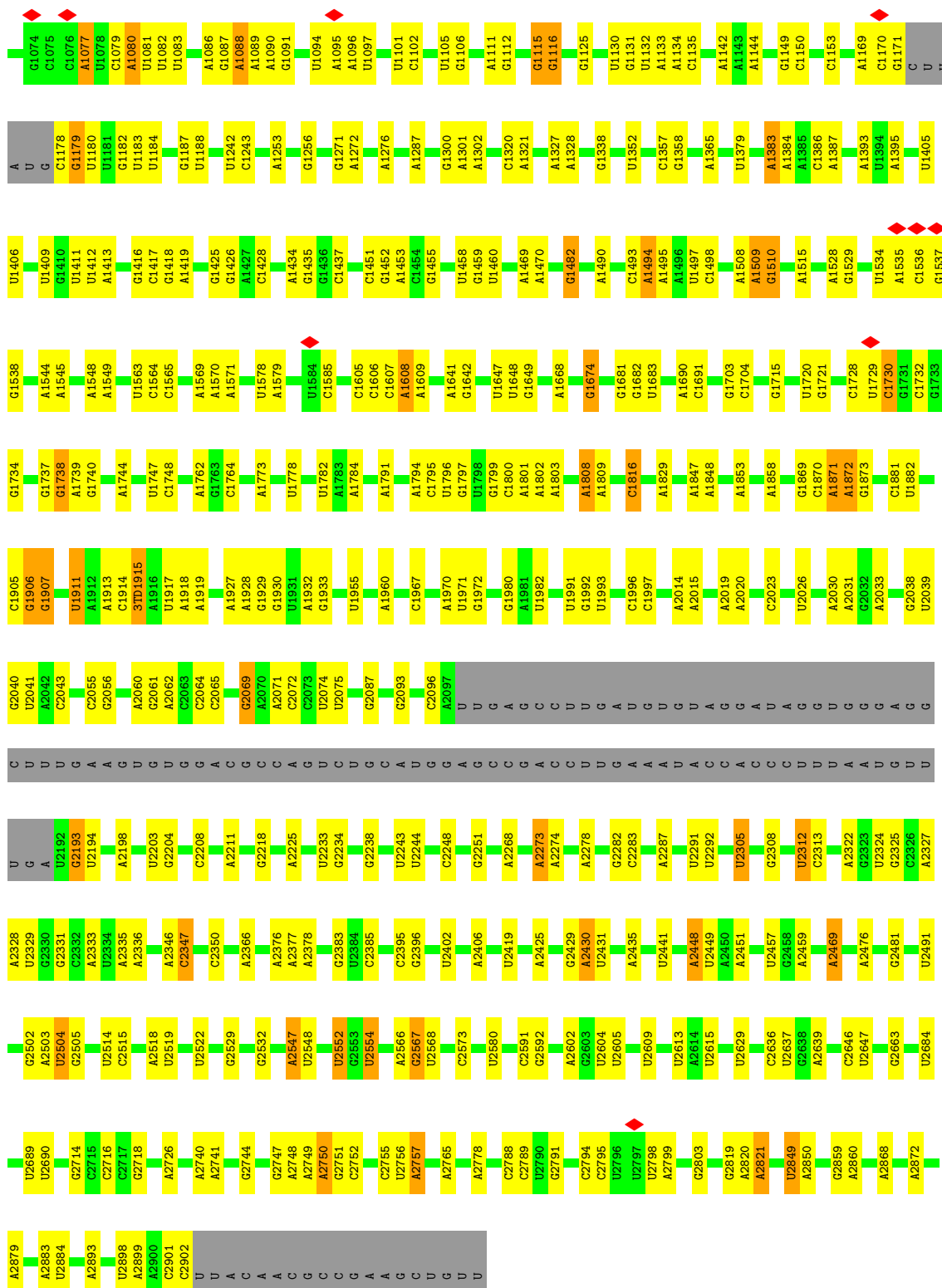


• Molecule 29: tRNA



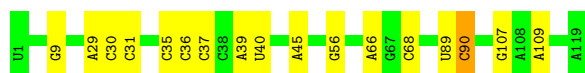
• Molecule 30: 23S rRNA





• Molecule 31: 5S rRNA

Chain b: 86% 13%



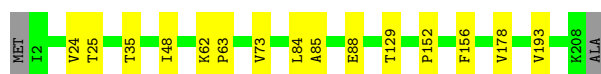
- Molecule 32: 50S ribosomal protein L2

Chain c: 92% 7% .



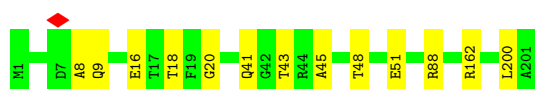
- Molecule 33: 50S ribosomal protein L3

Chain d: 92% 7% .



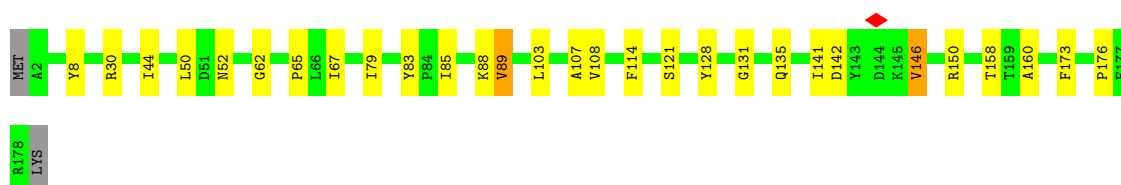
- Molecule 34: 50S ribosomal protein L4

Chain e: 94% 6%



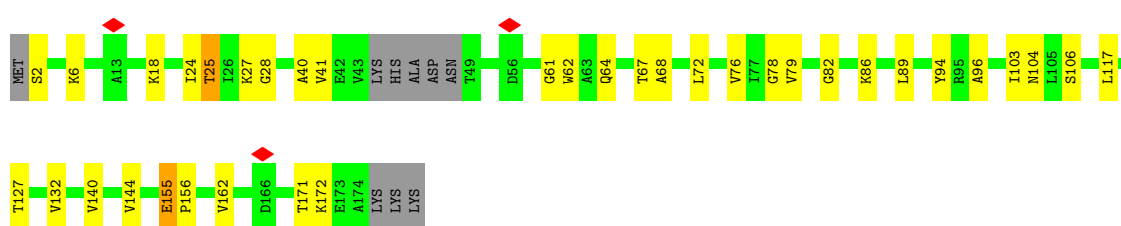
- Molecule 35: 50S ribosomal protein L5

Chain f: 83% 15% ..



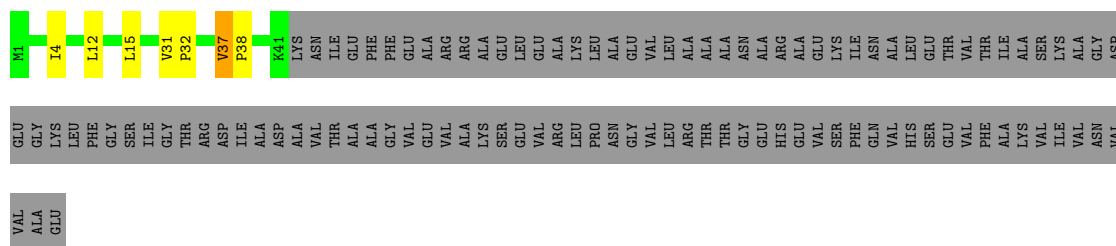
- Molecule 36: 50S ribosomal protein L6

Chain g: 75% 19% 5%



- Molecule 37: 50S ribosomal protein L9

Chain h: 23% 72%



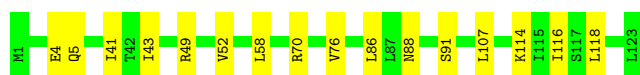
- Molecule 38: 50S ribosomal protein L13

Chain i: 89% 10% ..



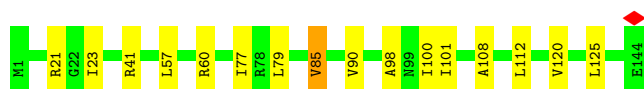
- Molecule 39: 50S ribosomal protein L14

Chain j: 87% 13%



- Molecule 40: 50S ribosomal protein L15

Chain k: 89% 10% .



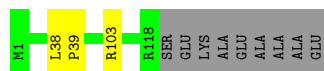
- Molecule 41: Large ribosomal subunit protein uL16

Chain l: 95% 5%



- Molecule 42: 50S ribosomal protein L17

Chain m: 91% 7%

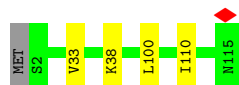


- Molecule 43: 50S ribosomal protein L18

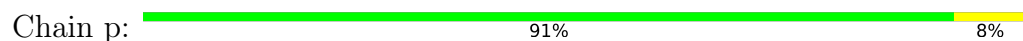
Chain n: 88% 11%



- Molecule 44: 50S ribosomal protein L19



- Molecule 45: 50S ribosomal protein L20



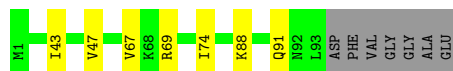
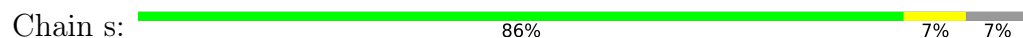
- Molecule 46: 50S ribosomal protein L21



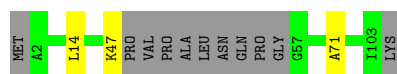
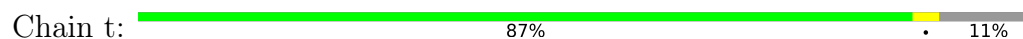
- Molecule 47: 50S ribosomal protein L22



- Molecule 48: 50S ribosomal protein L23



- Molecule 49: 50S ribosomal protein L24

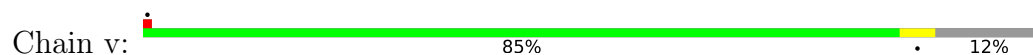


- Molecule 50: 50S ribosomal protein L25

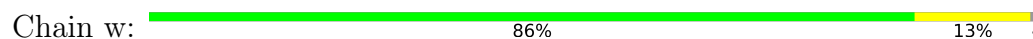




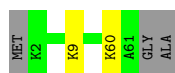
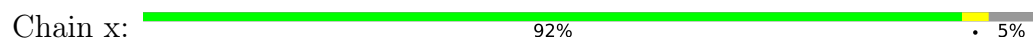
- Molecule 51: 50S ribosomal protein L27



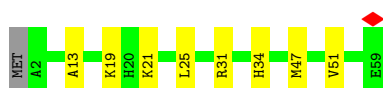
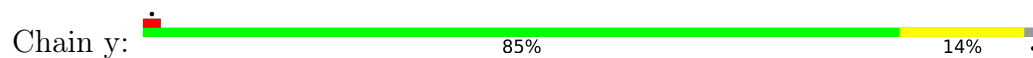
- Molecule 52: 50S ribosomal protein L28



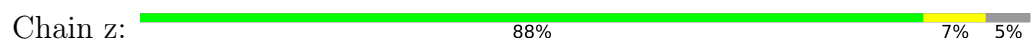
- Molecule 53: 50S ribosomal protein L29



- Molecule 54: 50S ribosomal protein L30



- Molecule 55: 50S ribosomal protein L32



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29766	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 ($e^-/\text{\AA}^2$)	45.47	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.794	Depositor
Minimum map value	-0.382	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	388.68002, 388.68002, 388.68002	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.6478, 0.6478, 0.6478	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, OMG, 6MZ, K, 2MA, MA6, IAS, PSU, H2U, MS6, 5MU, D2T, UR3, 5MC, G7M, 1MG, 3TD, 4OC, 4D4, OMU, MEQ, MG, 2MG, OMC

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	0	0.47	0/420	0.82	0/560
2	1	0.47	0/370	0.88	0/487
3	2	0.50	0/513	0.86	0/676
4	3	0.48	0/303	0.74	0/397
5	4	0.47	0/488	0.87	0/649
6	9	0.54	0/245	0.79	0/380
7	A	0.52	0/36110	0.77	3/56322 (0.0%)
8	B	0.46	0/1768	0.93	0/2381
9	C	0.47	0/1651	0.82	0/2225
10	D	0.45	0/1665	0.89	0/2227
11	E	0.48	0/1148	0.83	0/1545
12	F	0.45	0/843	0.80	0/1140
13	G	0.46	0/1190	0.89	0/1595
14	H	0.48	0/989	0.84	0/1326
15	I	0.45	0/1013	0.84	0/1350
16	J	0.47	0/784	0.85	0/1059
17	K	0.52	0/884	0.83	0/1191
18	L	0.47	0/945	0.80	0/1268
19	M	0.48	0/900	0.91	0/1204
20	N	0.47	0/817	0.87	0/1088
21	O	0.44	0/722	0.91	0/964
22	P	0.45	0/639	0.82	0/859
23	Q	0.46	0/650	0.75	0/871
24	R	0.45	0/532	0.91	0/715
25	S	0.50	0/685	0.86	0/922
26	T	0.47	0/676	0.93	0/895
27	U	0.47	0/467	0.90	0/620
28	V	0.43	0/1693	0.84	0/2274
29	Z	0.55	0/1813	0.75	0/2825
30	a	0.51	1/66355 (0.0%)	0.78	4/103511 (0.0%)
31	b	0.53	0/2850	0.77	0/4444

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	c	0.49	0/2121	0.80	0/2852
33	d	0.47	0/1562	0.79	0/2102
34	e	0.45	0/1571	0.86	0/2113
35	f	0.46	0/1434	0.90	0/1926
36	g	0.48	0/1273	0.84	1/1725 (0.1%)
37	h	0.49	0/306	0.85	0/413
38	i	0.46	0/1144	0.83	0/1541
39	j	0.46	0/955	0.81	0/1279
40	k	0.47	0/1062	0.84	0/1413
41	l	0.47	0/1073	0.82	0/1433
42	m	0.46	0/958	0.85	0/1281
43	n	0.48	0/902	0.88	0/1209
44	o	0.47	0/929	0.75	0/1242
45	p	0.45	0/960	0.88	0/1278
46	q	0.46	0/829	0.73	0/1107
47	r	0.46	0/852	0.82	0/1142
48	s	0.45	0/744	0.81	0/994
49	t	0.46	0/721	0.78	0/956
50	u	0.46	0/758	0.79	0/1015
51	v	0.47	0/576	0.76	0/762
52	w	0.46	0/635	0.82	0/848
53	x	0.41	0/492	0.90	0/655
54	y	0.46	0/453	0.82	0/605
55	z	0.47	0/435	0.84	0/581
All	All	0.50	1/152873 (0.0%)	0.79	8/228442 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	2	0	1
10	D	0	2
13	G	0	1
15	I	0	1
16	J	0	1
21	O	0	1
23	Q	0	1
27	U	0	1
52	w	0	1
All	All	0	10

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	2552	OMU	O3'-P	5.18	1.61	1.56

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	781	A	O3'-P-O5'	-6.71	93.94	104.00
30	a	2519	U	O3'-P-O5'	-6.35	94.48	104.00
30	a	2879	A	O3'-P-O5'	-5.81	95.28	104.00
7	A	1035	A	C2'-C3'-O3'	5.40	117.61	109.50
7	A	993	G	O3'-P-O5'	-5.39	95.91	104.00

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	2	13	ARG	Sidechain
10	D	184	ARG	Sidechain
10	D	73	ARG	Sidechain
13	G	111	ARG	Sidechain
15	I	41	ARG	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	413	0	448	5	0
2	1	367	0	405	1	0
3	2	504	0	572	4	0
4	3	302	0	340	1	0
5	4	480	0	478	6	0
6	9	218	0	110	0	0
7	A	32500	0	16368	171	0
8	B	1737	0	1763	20	0
9	C	1624	0	1696	11	0
10	D	1643	0	1707	24	0
11	E	1135	0	1179	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	F	824	0	815	4	0
13	G	1176	0	1233	6	0
14	H	979	0	1031	9	0
15	I	1001	0	1044	11	0
16	J	775	0	817	16	0
17	K	877	0	884	6	0
18	L	942	0	999	13	0
19	M	891	0	952	10	0
20	N	805	0	844	5	0
21	O	714	0	734	0	0
22	P	629	0	643	6	0
23	Q	641	0	682	8	0
24	R	524	0	543	3	0
25	S	668	0	693	5	0
26	T	670	0	719	7	0
27	U	460	0	486	5	0
28	V	1659	0	1689	15	0
29	Z	1623	0	825	6	0
30	a	59756	0	30055	230	0
31	b	2549	0	1291	9	0
32	c	2082	0	2153	12	0
33	d	1552	0	1601	9	0
34	e	1552	0	1619	9	0
35	f	1410	0	1444	21	0
36	g	1255	0	1296	17	0
37	h	303	0	327	3	0
38	i	1121	0	1150	8	0
39	j	946	0	1023	11	0
40	k	1053	0	1129	10	0
41	l	1075	0	1145	4	0
42	m	945	0	989	2	0
43	n	892	0	923	6	0
44	o	917	0	962	2	0
45	p	947	0	1019	9	0
46	q	816	0	839	9	0
47	r	845	0	909	5	0
48	s	738	0	807	4	0
49	t	717	0	766	2	0
50	u	745	0	768	2	0
51	v	569	0	581	2	0
52	w	625	0	652	5	0
53	x	491	0	523	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	y	449	0	488	5	0
55	z	429	0	440	3	0
56	3	1	0	0	0	0
56	4	1	0	0	0	0
56	V	1	0	0	0	0
57	A	32	0	0	0	0
57	F	1	0	0	0	0
57	a	75	0	0	0	0
57	c	3	0	0	0	0
57	e	1	0	0	0	0
58	A	55	0	0	0	0
58	a	241	0	0	0	0
58	b	3	0	0	0	0
58	c	2	0	0	0	0
58	d	1	0	0	0	0
58	z	1	0	0	0	0
All	All	141978	0	95598	728	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 3.

The worst 5 of 728 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)
7:A:1035:A:O2'	7:A:1036:A:H5''	1.32	1.26
7:A:1035:A:O2'	7:A:1036:A:C5'	2.20	0.90
7:A:1043:G:O2'	7:A:1044:A:O5'	1.92	0.88
7:A:158:G:C2'	7:A:159:G:H5''	2.06	0.86
7:A:225:C:H2'	7:A:226:G:H5''	1.58	0.85

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	48/55 (87%)	48 (100%)	0	0	100	100
2	1	43/46 (94%)	43 (100%)	0	0	100	100
3	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
4	3	36/38 (95%)	36 (100%)	0	0	100	100
5	4	56/70 (80%)	55 (98%)	1 (2%)	0	100	100
8	B	220/241 (91%)	214 (97%)	5 (2%)	1 (0%)	24	37
9	C	204/233 (88%)	199 (98%)	5 (2%)	0	100	100
10	D	203/206 (98%)	202 (100%)	1 (0%)	0	100	100
11	E	152/167 (91%)	150 (99%)	2 (1%)	0	100	100
12	F	99/135 (73%)	99 (100%)	0	0	100	100
13	G	148/179 (83%)	147 (99%)	1 (1%)	0	100	100
14	H	127/130 (98%)	127 (100%)	0	0	100	100
15	I	123/130 (95%)	120 (98%)	3 (2%)	0	100	100
16	J	92/103 (89%)	88 (96%)	3 (3%)	1 (1%)	11	18
17	K	113/129 (88%)	111 (98%)	2 (2%)	0	100	100
18	L	118/124 (95%)	114 (97%)	4 (3%)	0	100	100
19	M	113/118 (96%)	111 (98%)	2 (2%)	0	100	100
20	N	98/101 (97%)	98 (100%)	0	0	100	100
21	O	86/89 (97%)	86 (100%)	0	0	100	100
22	P	77/82 (94%)	75 (97%)	2 (3%)	0	100	100
23	Q	77/84 (92%)	77 (100%)	0	0	100	100
24	R	62/75 (83%)	62 (100%)	0	0	100	100
25	S	82/92 (89%)	81 (99%)	1 (1%)	0	100	100
26	T	84/87 (97%)	84 (100%)	0	0	100	100
27	U	53/71 (75%)	53 (100%)	0	0	100	100
28	V	195/213 (92%)	192 (98%)	3 (2%)	0	100	100
32	c	269/273 (98%)	263 (98%)	6 (2%)	0	100	100
33	d	204/209 (98%)	200 (98%)	4 (2%)	0	100	100
34	e	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
35	f	175/179 (98%)	173 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	g	164/177 (93%)	163 (99%)	1 (1%)	0	100	100
37	h	39/149 (26%)	37 (95%)	2 (5%)	0	100	100
38	i	139/142 (98%)	139 (100%)	0	0	100	100
39	j	121/123 (98%)	120 (99%)	1 (1%)	0	100	100
40	k	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
41	l	132/136 (97%)	130 (98%)	2 (2%)	0	100	100
42	m	116/127 (91%)	114 (98%)	2 (2%)	0	100	100
43	n	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
44	o	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
45	p	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
46	q	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
47	r	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
48	s	91/100 (91%)	90 (99%)	1 (1%)	0	100	100
49	t	89/104 (86%)	89 (100%)	0	0	100	100
50	u	91/94 (97%)	91 (100%)	0	0	100	100
51	v	73/85 (86%)	72 (99%)	1 (1%)	0	100	100
52	w	75/78 (96%)	75 (100%)	0	0	100	100
53	x	58/63 (92%)	58 (100%)	0	0	100	100
54	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
55	z	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
All	All	5605/6126 (92%)	5529 (99%)	74 (1%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	J	57	VAL
8	B	165	ASP

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	
1	0	46/49 (94%)	46 (100%)	0	100	100
2	1	37/38 (97%)	37 (100%)	0	100	100
3	2	51/52 (98%)	51 (100%)	0	100	100
4	3	34/34 (100%)	34 (100%)	0	100	100
5	4	55/62 (89%)	54 (98%)	1 (2%)	51	73
8	B	184/199 (92%)	180 (98%)	4 (2%)	45	67
9	C	170/190 (90%)	169 (99%)	1 (1%)	78	89
10	D	172/173 (99%)	165 (96%)	7 (4%)	27	46
11	E	117/126 (93%)	115 (98%)	2 (2%)	53	74
12	F	88/116 (76%)	88 (100%)	0	100	100
13	G	124/147 (84%)	121 (98%)	3 (2%)	43	65
14	H	104/105 (99%)	104 (100%)	0	100	100
15	I	103/107 (96%)	101 (98%)	2 (2%)	50	71
16	J	85/90 (94%)	84 (99%)	1 (1%)	63	81
17	K	89/98 (91%)	89 (100%)	0	100	100
18	L	101/103 (98%)	99 (98%)	2 (2%)	48	70
19	M	93/96 (97%)	93 (100%)	0	100	100
20	N	83/84 (99%)	83 (100%)	0	100	100
21	O	76/77 (99%)	76 (100%)	0	100	100
22	P	64/65 (98%)	63 (98%)	1 (2%)	55	76
23	Q	73/78 (94%)	70 (96%)	3 (4%)	27	46
24	R	55/65 (85%)	54 (98%)	1 (2%)	51	73
25	S	72/79 (91%)	72 (100%)	0	100	100
26	T	65/66 (98%)	65 (100%)	0	100	100
27	U	48/61 (79%)	48 (100%)	0	100	100
28	V	191/204 (94%)	188 (98%)	3 (2%)	55	76
32	c	216/218 (99%)	215 (100%)	1 (0%)	81	91
33	d	162/163 (99%)	162 (100%)	0	100	100
34	e	165/165 (100%)	165 (100%)	0	100	100
35	f	148/150 (99%)	146 (99%)	2 (1%)	59	79
36	g	130/138 (94%)	124 (95%)	6 (5%)	24	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	h	32/114 (28%)	29 (91%)	3 (9%)	8	13
38	i	115/116 (99%)	113 (98%)	2 (2%)	53	74
39	j	104/104 (100%)	104 (100%)	0	100	100
40	k	103/103 (100%)	101 (98%)	2 (2%)	50	71
41	l	107/107 (100%)	104 (97%)	3 (3%)	38	60
42	m	98/103 (95%)	98 (100%)	0	100	100
43	n	86/87 (99%)	84 (98%)	2 (2%)	44	66
44	o	99/100 (99%)	99 (100%)	0	100	100
45	p	89/90 (99%)	89 (100%)	0	100	100
46	q	84/84 (100%)	84 (100%)	0	100	100
47	r	92/93 (99%)	92 (100%)	0	100	100
48	s	80/84 (95%)	80 (100%)	0	100	100
49	t	76/85 (89%)	76 (100%)	0	100	100
50	u	77/78 (99%)	77 (100%)	0	100	100
51	v	56/63 (89%)	56 (100%)	0	100	100
52	w	67/68 (98%)	67 (100%)	0	100	100
53	x	54/55 (98%)	54 (100%)	0	100	100
54	y	48/49 (98%)	48 (100%)	0	100	100
55	z	46/48 (96%)	46 (100%)	0	100	100
All	All	4714/5029 (94%)	4662 (99%)	52 (1%)	63	82

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	V	23	VAL
36	g	27	LYS
41	l	36	VAL
28	V	163	GLU
35	f	89	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
38	i	136	GLN

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Mol	Chain	Res	Type
51	v	57	HIS
40	k	104	GLN
45	p	81	ASN
53	x	39	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	Z	75/77 (97%)	22 (29%)	2 (2%)
30	a	2778/2930 (94%)	329 (11%)	0
31	b	118/119 (99%)	9 (7%)	0
6	9	9/24 (37%)	4 (44%)	1 (11%)
7	A	1511/1554 (97%)	193 (12%)	44 (2%)
All	All	4491/4704 (95%)	557 (12%)	47 (1%)

5 of 557 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	9	19	G
6	9	20	C
6	9	21	A
6	9	22	A
7	A	4	U

5 of 47 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	1094	G
7	A	1225	A
7	A	1124	G
7	A	1187	G
7	A	1275	A

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	MA6	A	1518	7	23,26,27	0.26	0	34,38,41	0.66	1 (2%)
7	2MG	A	1207	7,57	23,26,27	0.38	0	32,38,41	0.41	0
30	5MC	a	1962	30	18,22,23	0.31	0	26,32,35	0.50	0
7	4OC	A	1402	7	20,23,24	0.37	0	26,32,35	0.43	0
30	PSU	a	1917	30	18,21,22	0.91	1 (5%)	22,30,33	0.55	0
30	PSU	a	2605	30	18,21,22	0.95	1 (5%)	22,30,33	0.69	0
30	PSU	a	746	30,58	18,21,22	0.90	1 (5%)	22,30,33	0.62	0
30	G7M	a	2069	30	23,26,27	0.71	1 (4%)	35,39,42	0.61	0
30	OMU	a	2552	30	19,22,23	0.20	0	26,31,34	0.41	0
30	6MZ	a	2030	30	22,25,26	0.29	0	30,36,39	0.63	0
30	2MG	a	1835	30	23,26,27	0.37	0	32,38,41	0.35	0
30	OMG	a	2251	30,57,29	23,26,27	0.33	0	33,38,41	0.48	0
7	5MC	A	967	7	18,22,23	0.32	0	26,32,35	0.51	0
30	3TD	a	1915	30	18,22,23	0.96	1 (5%)	22,32,35	0.63	0
7	5MC	A	1407	7	18,22,23	0.32	0	26,32,35	0.57	0
7	G7M	A	527	7	23,26,27	0.71	1 (4%)	35,39,42	0.59	0
7	2MG	A	966	7	23,26,27	0.38	0	32,38,41	0.38	0
30	PSU	a	2580	30,57	18,21,22	0.92	1 (5%)	22,30,33	0.73	1 (4%)
7	2MG	A	1516	7	23,26,27	0.39	0	32,38,41	0.46	0
30	2MA	a	2503	30,57,58	22,25,26	0.96	2 (9%)	33,37,40	1.06	4 (12%)
30	PSU	a	1911	30	18,21,22	0.88	1 (5%)	22,30,33	0.69	0
41	MS6	l	82	41	5,7,8	0.22	0	2,7,9	0.09	0
33	MEQ	d	150	33	8,9,10	0.42	0	5,10,12	0.60	0
17	IAS	K	119	17	6,7,8	0.91	0	6,8,10	1.01	0
30	6MZ	a	1618	30	22,25,26	0.39	0	30,36,39	0.53	0
30	PSU	a	2604	30	18,21,22	0.89	1 (5%)	22,30,33	0.82	1 (4%)
30	OMC	a	2498	30,58	19,22,23	0.28	0	26,31,34	0.45	0
30	5MU	a	747	30	19,22,23	0.25	0	28,32,35	0.31	0
18	D2T	L	89	18	7,9,10	0.95	0	6,11,13	2.54	4 (66%)
30	2MG	a	2445	30	23,26,27	0.41	0	32,38,41	0.38	0
30	5MU	a	1939	30,57	19,22,23	0.30	0	28,32,35	0.35	0
7	PSU	A	516	7,58	18,21,22	0.91	1 (5%)	22,30,33	0.64	0
41	4D4	l	81	41	9,11,12	0.48	0	8,13,15	0.71	0
30	PSU	a	2504	30,57	18,21,22	0.91	1 (5%)	22,30,33	0.69	0
30	PSU	a	955	30	18,21,22	0.89	1 (5%)	22,30,33	0.65	0
30	H2U	a	2449	30	18,21,22	0.56	0	21,30,33	0.78	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
30	PSU	a	2457	30	18,21,22	0.88	1 (5%)	22,30,33	0.65	0
30	1MG	a	745	30	22,26,27	0.52	0	33,39,42	0.49	0
7	UR3	A	1498	7	19,22,23	0.25	0	26,32,35	0.63	0
7	MA6	A	1519	7	23,26,27	0.25	0	34,38,41	0.72	1 (2%)

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
7	MA6	A	1518	7	-	0/11/29/30	0/3/3/3
7	2MG	A	1207	7,57	-	0/9/27/28	0/3/3/3
30	5MC	a	1962	30	-	2/7/25/26	0/2/2/2
7	4OC	A	1402	7	-	0/9/29/30	0/2/2/2
30	PSU	a	1917	30	-	0/7/25/26	0/2/2/2
30	PSU	a	2605	30	-	0/7/25/26	0/2/2/2
30	PSU	a	746	30,58	-	4/7/25/26	0/2/2/2
30	G7M	a	2069	30	-	2/7/25/26	0/3/3/3
30	OMU	a	2552	30	-	0/9/27/28	0/2/2/2
30	6MZ	a	2030	30	-	2/9/27/28	0/3/3/3
30	2MG	a	1835	30	-	0/9/27/28	0/3/3/3
30	OMG	a	2251	30,57,29	-	1/9/27/28	0/3/3/3
7	5MC	A	967	7	-	0/7/25/26	0/2/2/2
30	3TD	a	1915	30	-	2/7/25/26	0/2/2/2
7	5MC	A	1407	7	-	0/7/25/26	0/2/2/2
7	G7M	A	527	7	-	1/7/25/26	0/3/3/3
7	2MG	A	966	7	-	0/9/27/28	0/3/3/3
30	PSU	a	2580	30,57	-	0/7/25/26	0/2/2/2
7	2MG	A	1516	7	-	0/9/27/28	0/3/3/3
30	2MA	a	2503	30,57,58	-	2/7/25/26	0/3/3/3
30	PSU	a	1911	30	-	2/7/25/26	0/2/2/2
41	MS6	l	82	41	-	1/4/6/8	-
33	MEQ	d	150	33	-	2/8/9/11	-
17	IAS	K	119	17	-	1/7/7/8	-
30	6MZ	a	1618	30	-	0/9/27/28	0/3/3/3
30	PSU	a	2604	30	-	0/7/25/26	0/2/2/2
30	OMC	a	2498	30,58	-	0/9/27/28	0/2/2/2
30	5MU	a	747	30	-	0/7/25/26	0/2/2/2
18	D2T	L	89	18	-	2/7/12/14	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	2MG	a	2445	30	-	0/9/27/28	0/3/3/3
30	5MU	a	1939	30,57	-	0/7/25/26	0/2/2/2
7	PSU	A	516	7,58	-	0/7/25/26	0/2/2/2
41	4D4	l	81	41	-	2/11/12/14	-
30	PSU	a	2504	30,57	-	0/7/25/26	0/2/2/2
30	PSU	a	955	30	-	0/7/25/26	0/2/2/2
30	H2U	a	2449	30	-	0/7/38/39	0/2/2/2
30	PSU	a	2457	30	-	0/7/25/26	0/2/2/2
30	1MG	a	745	30	-	0/7/25/26	0/3/3/3
7	UR3	A	1498	7	-	0/7/25/26	0/2/2/2
7	MA6	A	1519	7	-	0/11/29/30	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	2605	PSU	C6-C5	3.72	1.39	1.35
30	a	2504	PSU	C6-C5	3.61	1.39	1.35
30	a	1915	3TD	C6-C5	3.60	1.39	1.35
7	A	516	PSU	C6-C5	3.58	1.39	1.35
30	a	1917	PSU	C6-C5	3.57	1.39	1.35

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	L	89	D2T	CB-CA-N	4.81	119.34	109.10
7	A	1519	MA6	C2-N1-C6	2.99	118.81	111.75
7	A	1518	MA6	C2-N1-C6	2.91	118.63	111.75
30	a	2503	2MA	C5-C4-N3	-2.84	123.99	127.19
30	a	2503	2MA	CM2-C2-N1	2.59	121.19	117.15

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
30	a	746	PSU	C2'-C1'-C5-C4
30	a	746	PSU	C2'-C1'-C5-C6
30	a	746	PSU	O4'-C1'-C5-C6
30	a	1911	PSU	O4'-C1'-C5-C4
30	a	1911	PSU	O4'-C1'-C5-C6

There are no ring outliers.

9 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1518	MA6	1	0
30	a	2552	OMU	2	0
30	a	2030	6MZ	2	0
30	a	2251	OMG	1	0
30	a	1911	PSU	1	0
18	L	89	D2T	3	0
30	a	2504	PSU	1	0
7	A	1498	UR3	1	0
7	A	1519	MA6	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 418 ligands modelled in this entry, 418 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

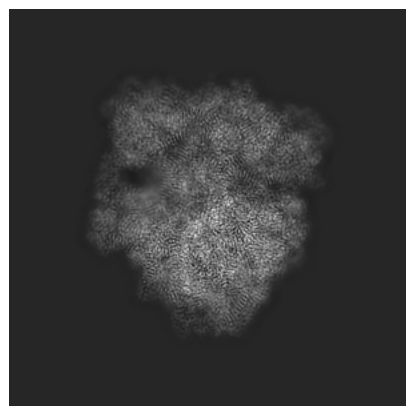
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51355. These allow visual inspection of the internal detail of the map and identification of artifacts.

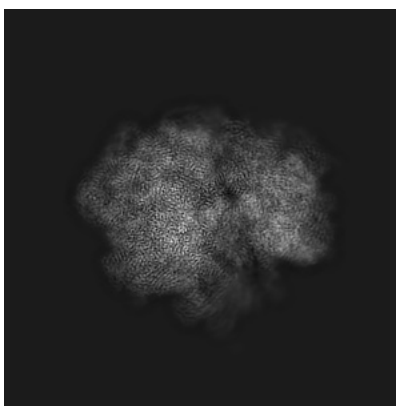
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

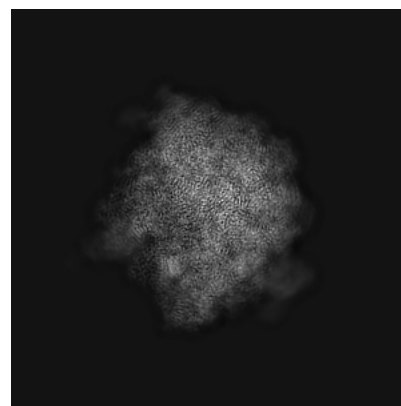
6.1.1 Primary map



X

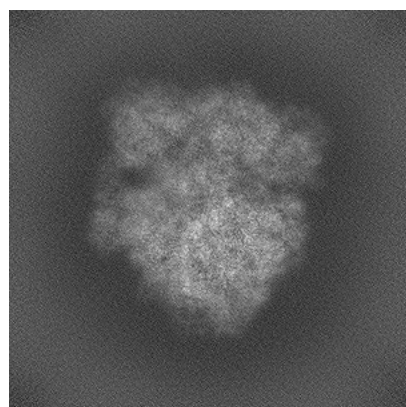


Y

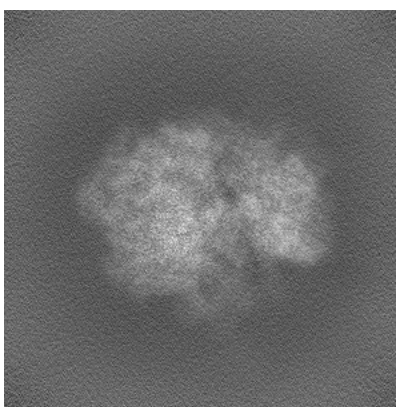


Z

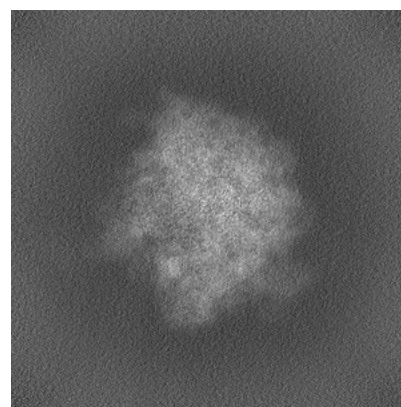
6.1.2 Raw map



X



Y

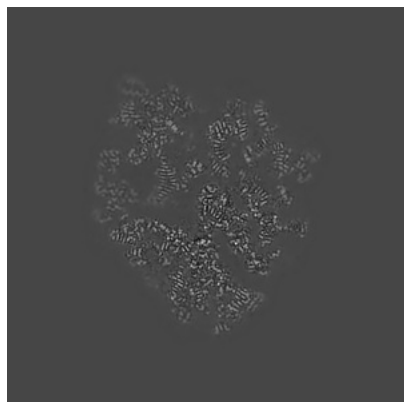


Z

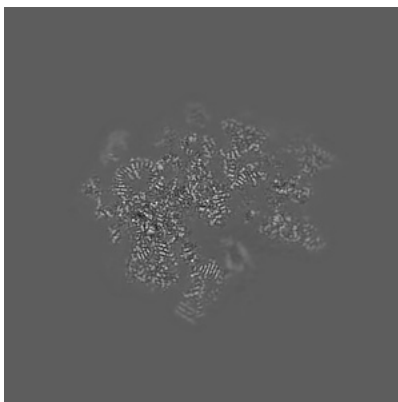
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

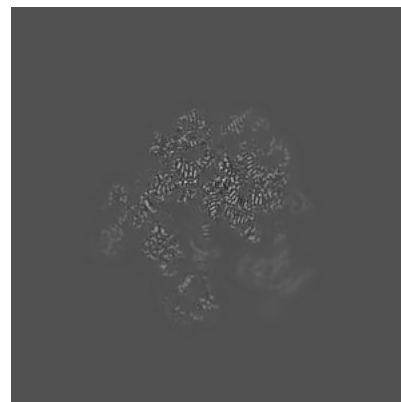
6.2.1 Primary map



X Index: 300

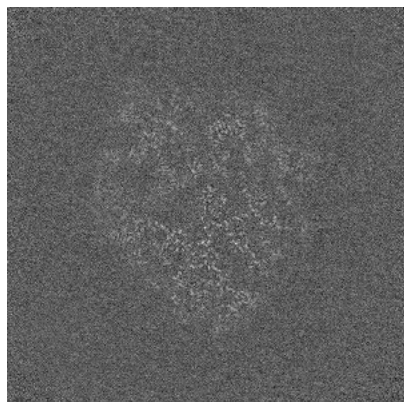


Y Index: 300

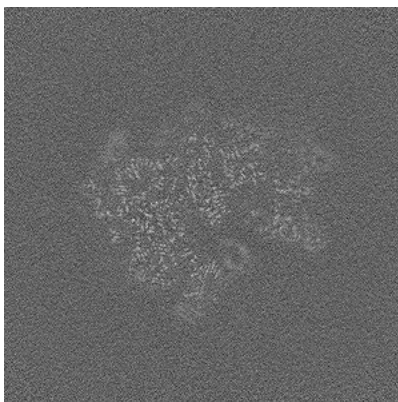


Z Index: 300

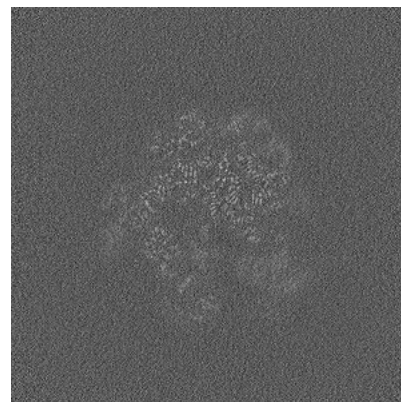
6.2.2 Raw map



X Index: 300



Y Index: 300



Z Index: 300

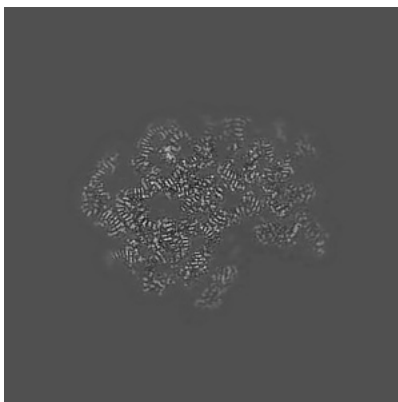
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

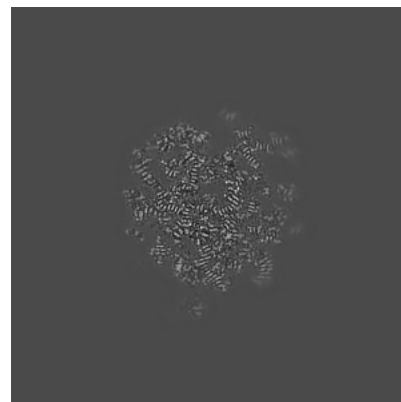
6.3.1 Primary map



X Index: 290

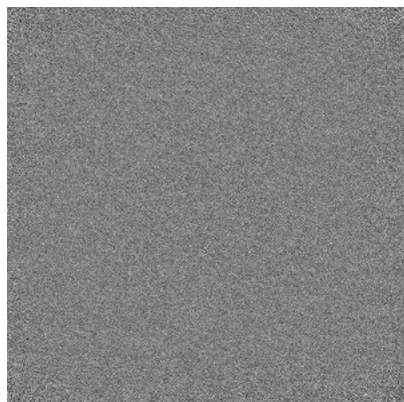


Y Index: 322

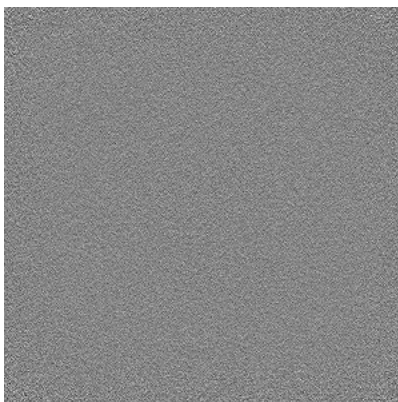


Z Index: 235

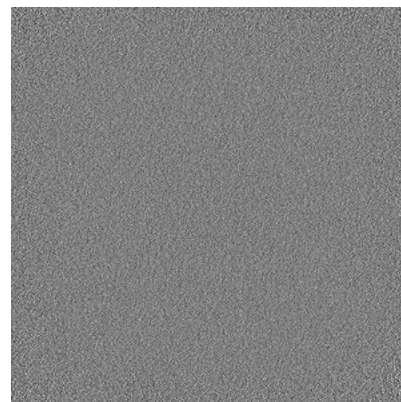
6.3.2 Raw map



X Index: 0



Y Index: 0

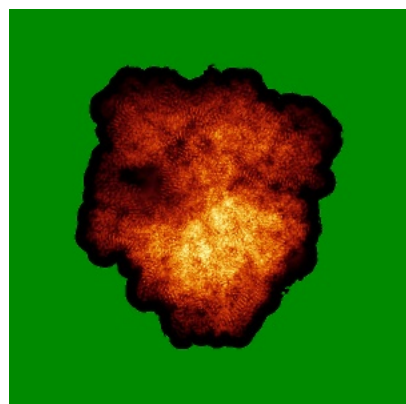


Z Index: 0

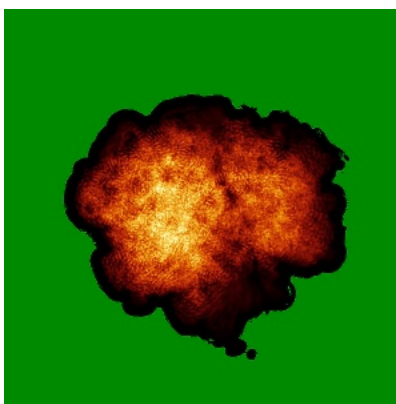
The images above show the largest variance slices of the map in three orthogonal directions.

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

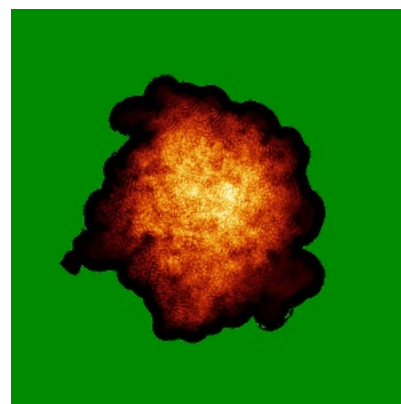
6.4.1 Primary map



X

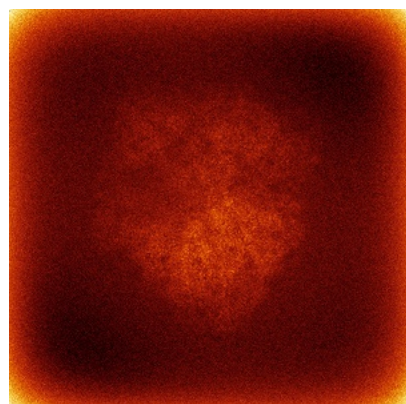


Y

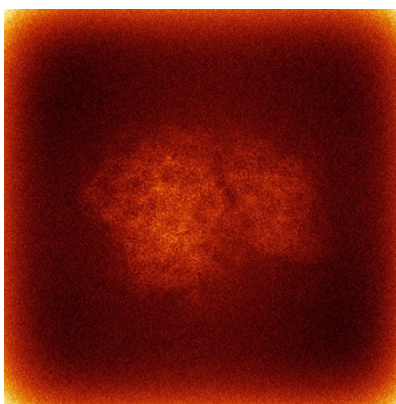


Z

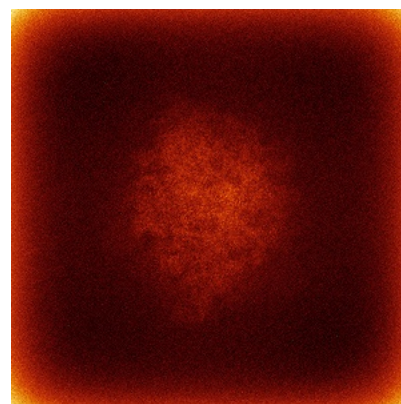
6.4.2 Raw map



X



Y

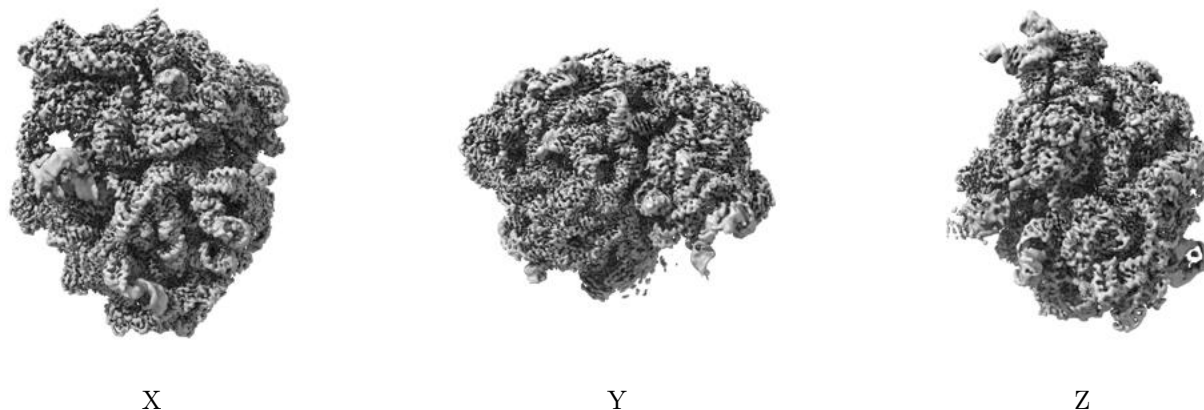


Z

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.

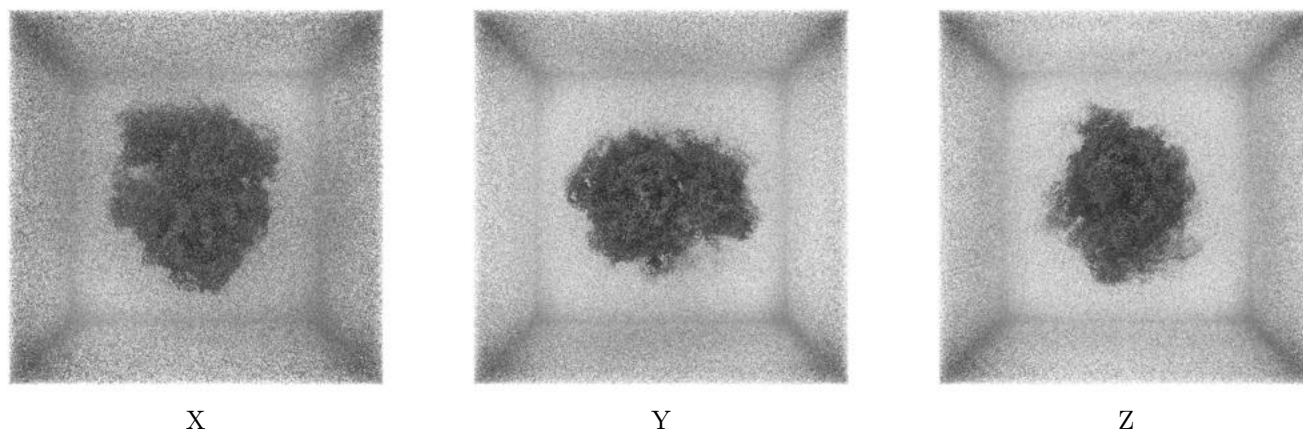
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

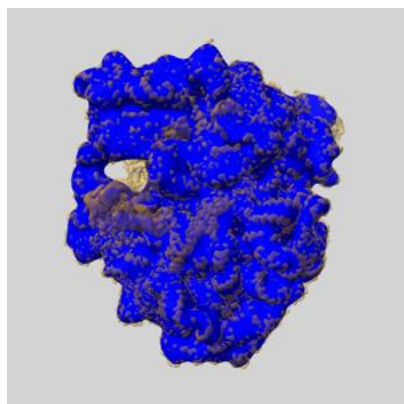
6.6 Mask visualisation [i](#)

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

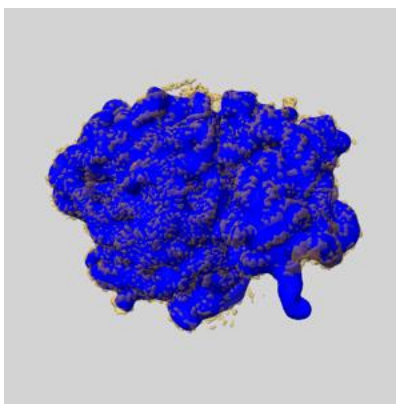
A mask typically either:

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

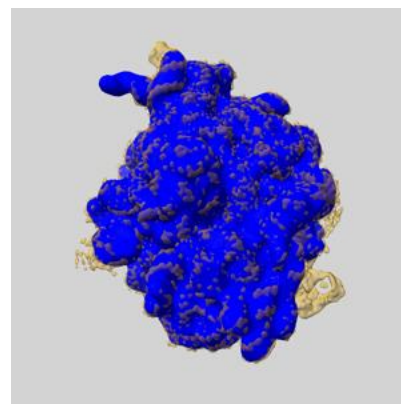
6.6.1 emd_51355_msk_1.map [i](#)



X



Y

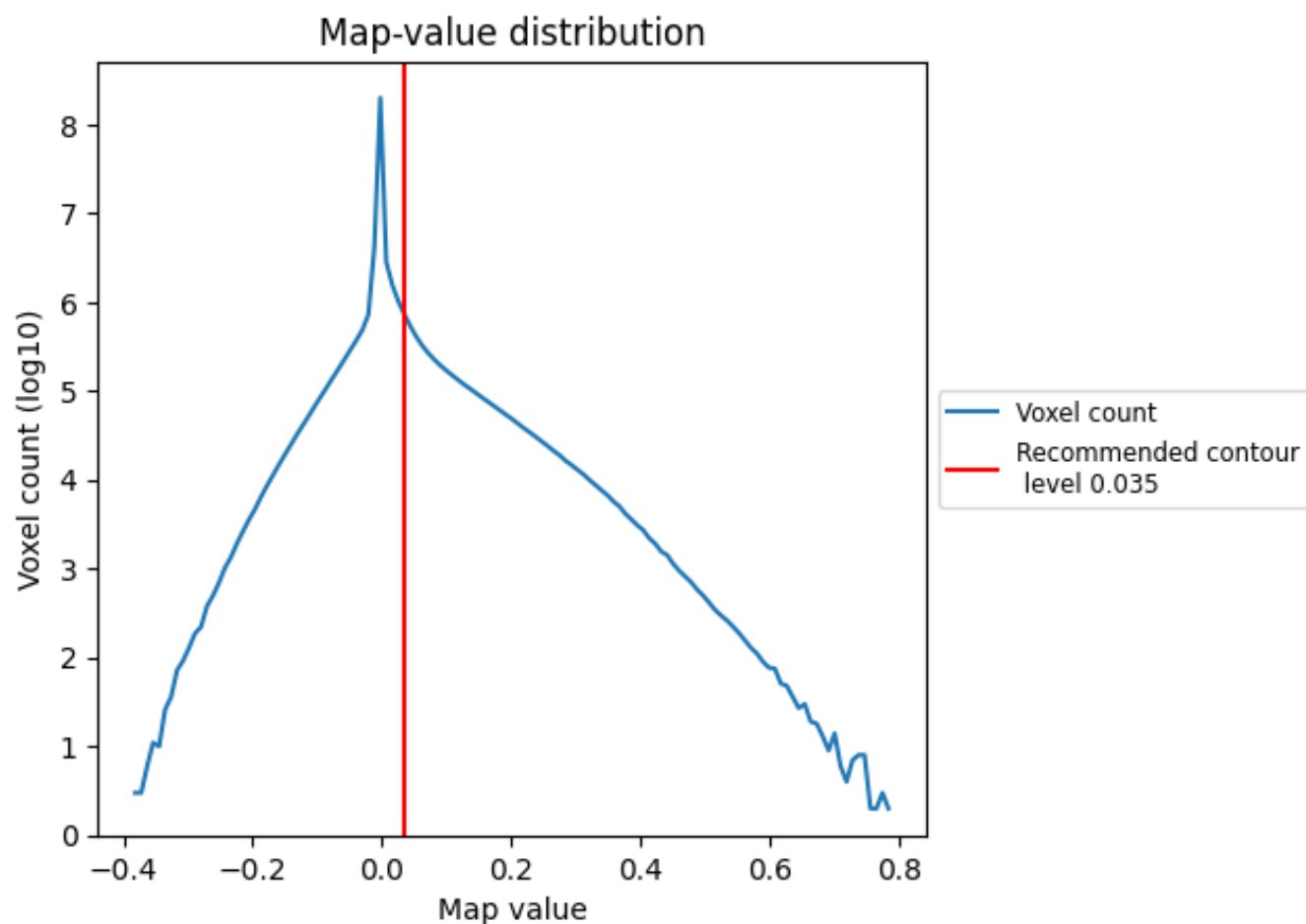


Z

7 Map analysis [i](#)

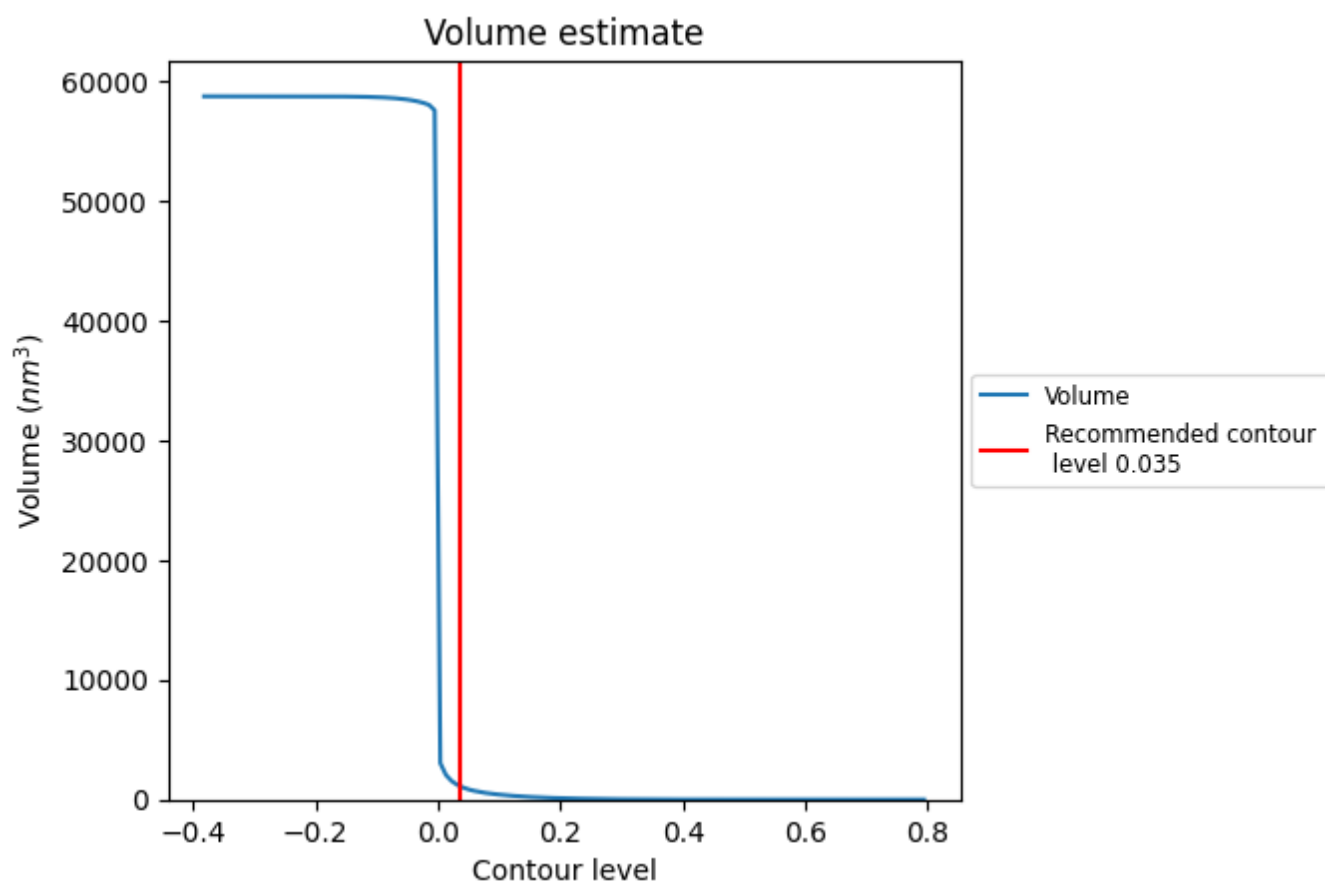
This section contains the results of statistical analysis of the map.

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.

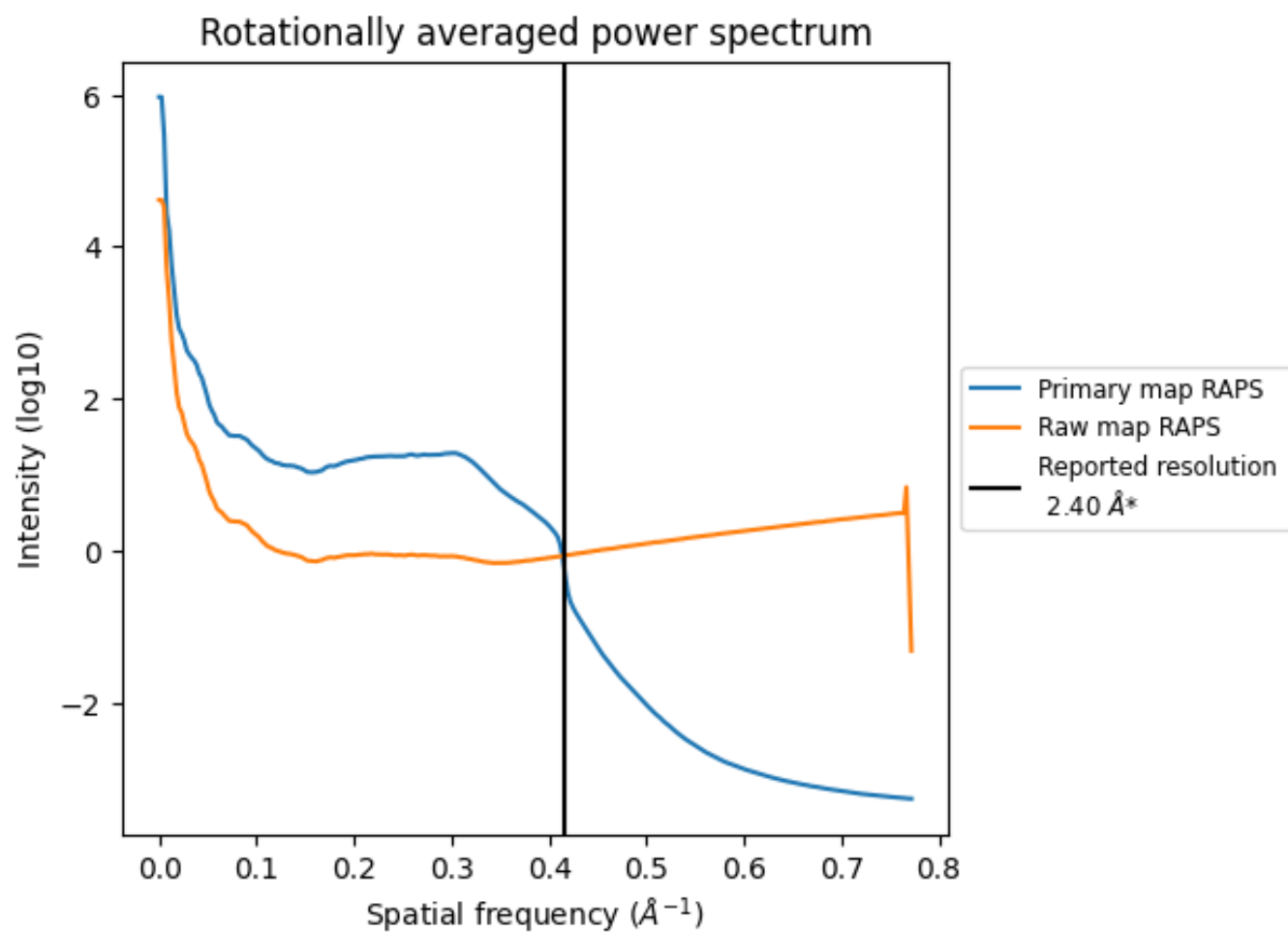
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1148 nm^3 ; this corresponds to an approximate mass of 1037 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

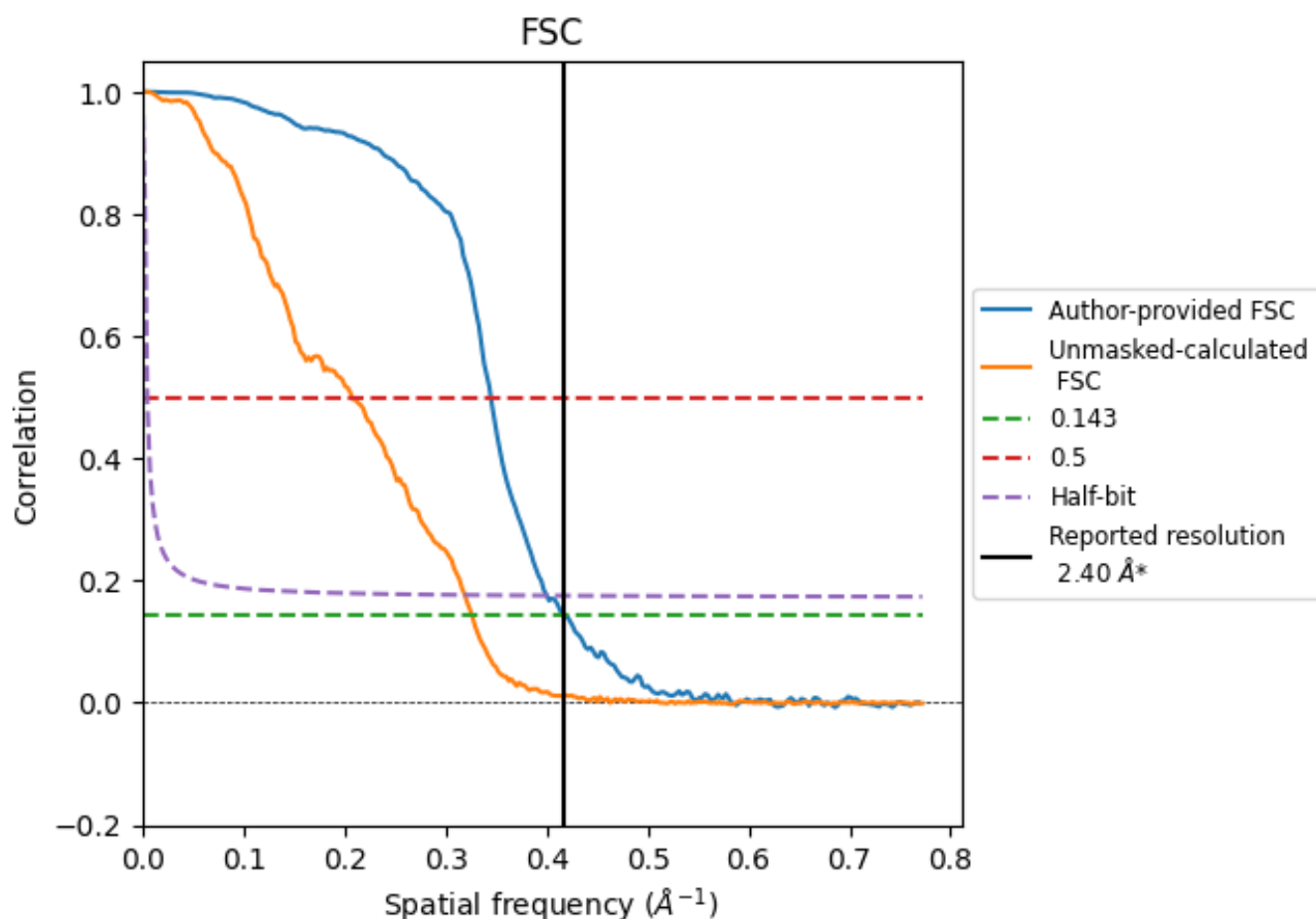


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.417 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

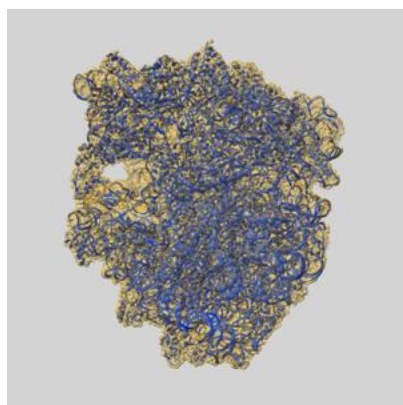
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.40	2.90	2.50
Unmasked-calculated*	3.06	4.81	3.13

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

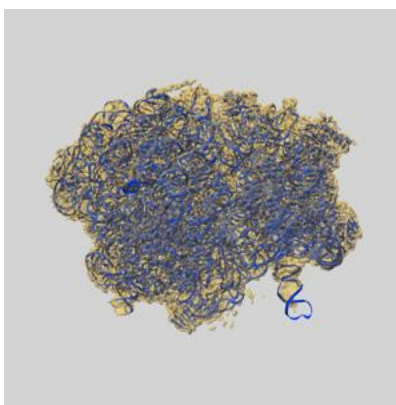
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51355 and PDB model 9GHF. Per-residue inclusion information can be found in section 3 on page 16.

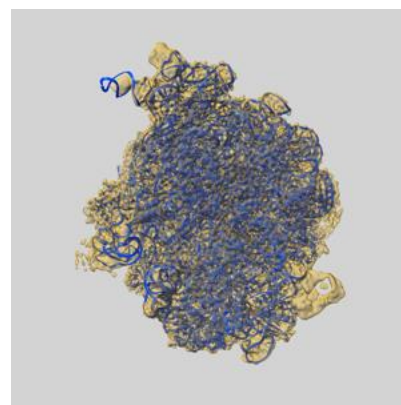
9.1 Map-model overlay [i](#)



X



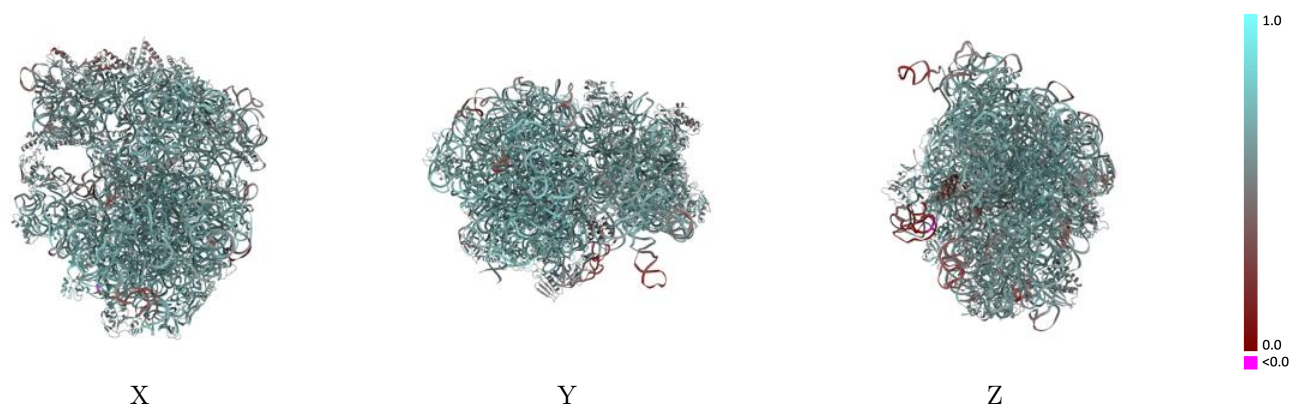
Y



Z

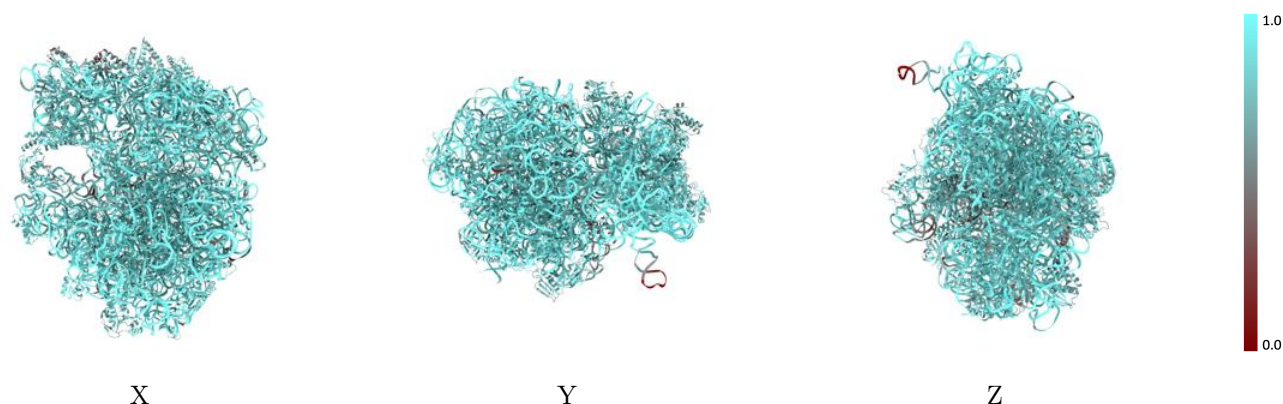
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



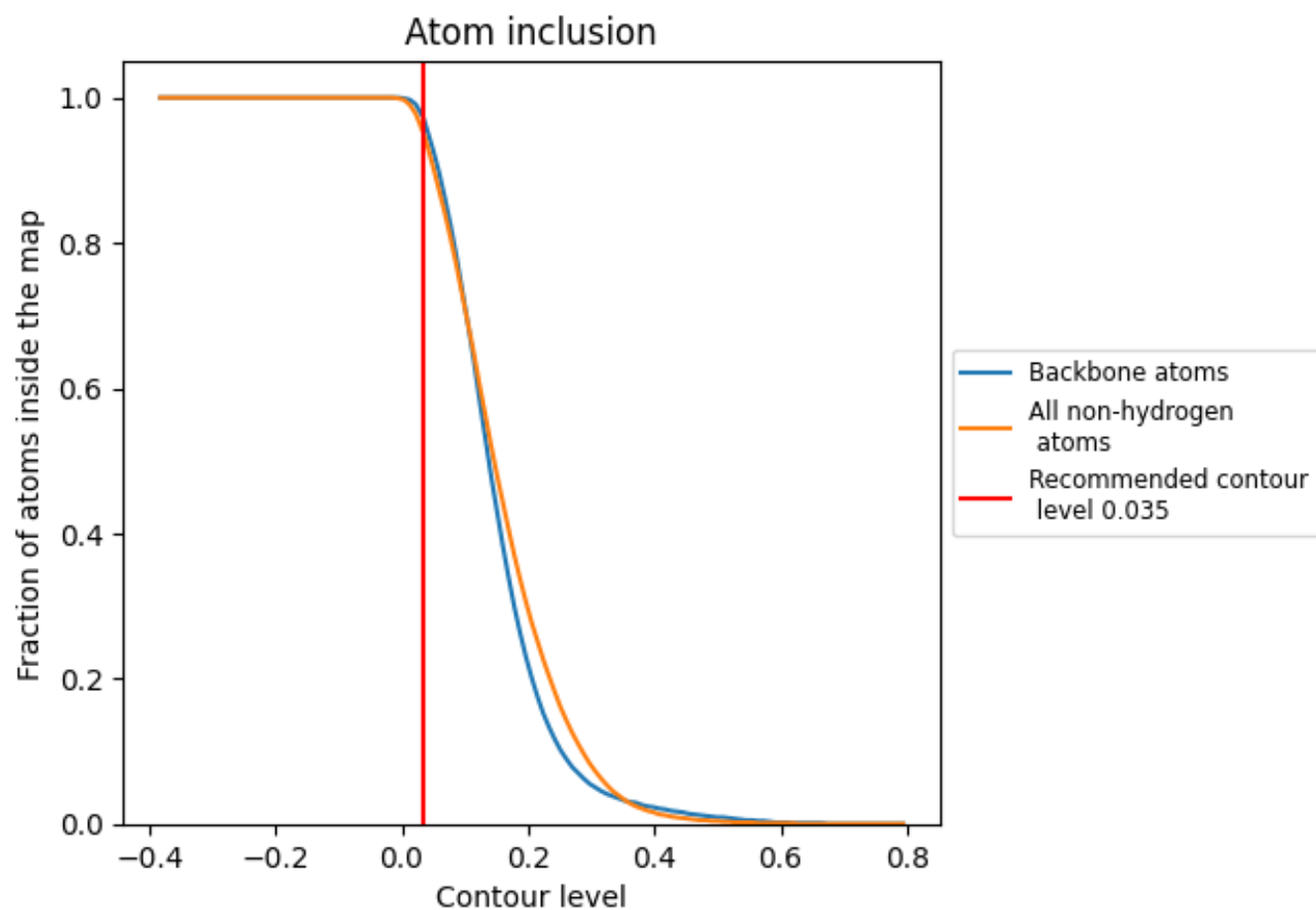
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 95% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9500	 0.6250
0	 0.9210	 0.6210
1	 1.0000	 0.7090
2	 0.9940	 0.6900
3	 0.9420	 0.6350
4	 0.7900	 0.4830
9	 0.7750	 0.4820
A	 0.9740	 0.6210
B	 0.7540	 0.4970
C	 0.8720	 0.5660
D	 0.8790	 0.5680
E	 0.9410	 0.6160
F	 0.8680	 0.5530
G	 0.8350	 0.5340
H	 0.9310	 0.6130
I	 0.8580	 0.5440
J	 0.7800	 0.5060
K	 0.9070	 0.5990
L	 0.9200	 0.6100
M	 0.8670	 0.5620
N	 0.8950	 0.5720
O	 0.9200	 0.6010
P	 0.9240	 0.6050
Q	 0.8910	 0.5660
R	 0.9030	 0.5870
S	 0.8370	 0.5320
T	 0.9040	 0.5910
U	 0.8110	 0.5330
V	 0.5260	 0.3460
Z	 0.8910	 0.5470
a	 0.9800	 0.6520
b	 0.9840	 0.6280
c	 0.9770	 0.6800
d	 0.9590	 0.6670
e	 0.9210	 0.6280



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Chain	Atom inclusion	Q-score
f	 0.8380	 0.5390
g	 0.8370	 0.5260
h	 0.8700	 0.5530
i	 0.9670	 0.6590
j	 0.9410	 0.6480
k	 0.9540	 0.6550
l	 0.9530	 0.6530
m	 0.9860	 0.6830
n	 0.9210	 0.6040
o	 0.9320	 0.6460
p	 0.9780	 0.6920
q	 0.9330	 0.6410
r	 0.9540	 0.6580
s	 0.9200	 0.6060
t	 0.9400	 0.6120
u	 0.9030	 0.5940
v	 0.9620	 0.6600
w	 0.9620	 0.6570
x	 0.8930	 0.5750
y	 0.9410	 0.6480
z	 0.9660	 0.6730