



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2025 – 08:51 AM EDT

PDB ID : 8SYL
EMDB ID : EMD-40882
Title : Cryo-EM structure of the Escherichia coli 70S ribosome in complex with amikacin, mRNA, and A-, P-, and E-site tRNAs
Authors : Seely, S.M.; Gagnon, M.G.
Deposited on : 2023-05-25
Resolution : 2.90 Å(reported)
Based on initial model : 8EKC

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:

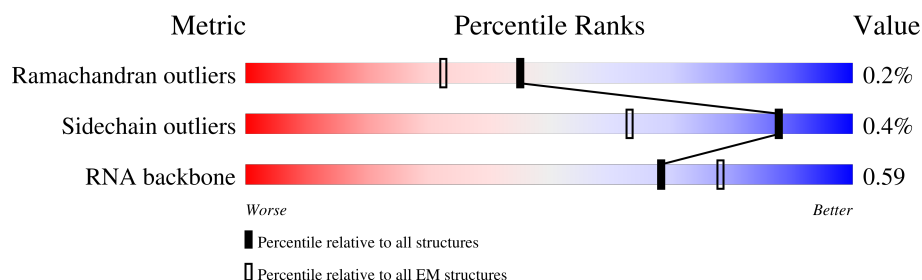
EMDB validation analysis : 0.0.1.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

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 2.90 Å.

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



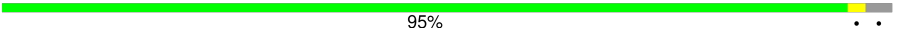


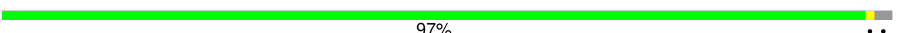

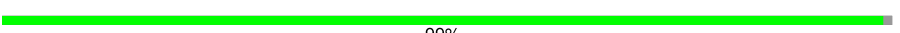














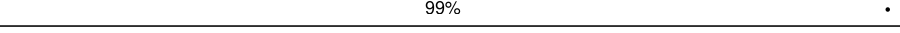
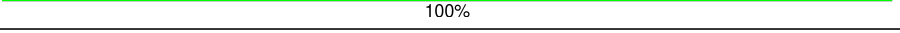
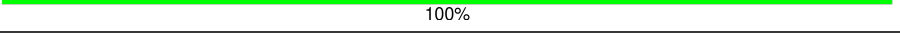
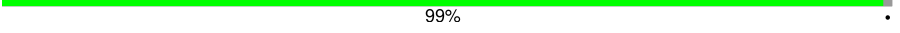
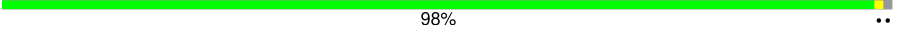
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	a	1542	
2	b	241	
3	c	233	
4	d	206	
5	e	167	
6	f	131	
7	g	156	
8	h	130	

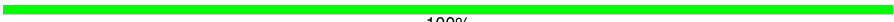










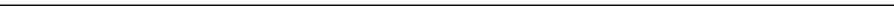


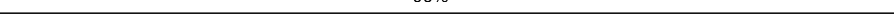
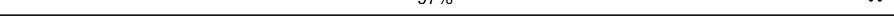
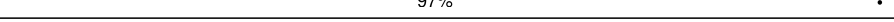
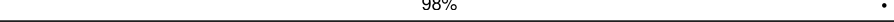

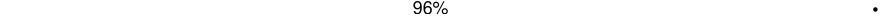

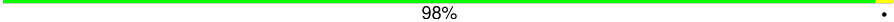
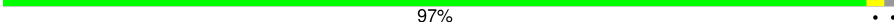
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	i	130	
10	j	103	
11	k	129	
12	l	124	
13	m	118	
14	n	101	
15	o	89	
16	p	82	
17	q	84	
18	r	75	
19	s	92	
20	t	87	
21	u	71	
22	w	76	
22	y	76	
23	x	77	
24	v	24	
25	A	2904	
26	B	120	
27	C	273	
28	D	209	
29	E	201	
30	F	179	
31	G	177	
32	H	149	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	L	142	 100%
34	M	123	 100%
35	N	144	 100%
36	O	136	 99%
37	P	127	 93% 7%
38	Q	117	 98% ..
39	R	115	 99% .
40	S	118	 99% .
41	T	103	 100%
42	U	110	 100%
43	V	100	 93% 7%
44	W	104	 98% .
45	X	94	 100%
46	Y	85	 96% ..
47	Z	78	 97% ..
48	1	63	 97% .
49	2	59	 98% .
50	3	70	 86% 14%
51	4	57	 96% .
52	5	55	 93% 7%
53	6	46	 98% .
54	7	65	 97% ..
55	8	38	 100%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 144591 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1528	Total	C	N	O	P	0	0
			32803	14637	6019	10619	1528		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	224	Total	C	N	O	S	0	0
			1514	963	279	267	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	206	Total	C	N	O	S	0	0
			1613	1023	305	282	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	156	Total	C	N	O	S	0	0
			1117	695	213	203	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	102	Total	C	N	O	S	0	0
			778	497	133	143	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	152	Total	C	N	O	S	0	0
			1054	656	204	190	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	129	Total	C	N	O	S	0	0
			969	611	169	183	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	126	Total	C	N	O	S	0	0
			937	586	183	166	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
10	j	97	Total	C	N	O	0	0
			673	428	130	115		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	117	Total	C	N	O	S	0	0
			860	531	168	158	3		

There is a discrepancy between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	121	Total	C	N	O	S	0	0
			924	570	187	162	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	113	Total	C	N	O	S	0	0
			823	510	166	145	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	100	Total	C	N	O	S	0	0
			792	492	162	135	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O	S	0	0
			703	434	141	127	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	80	Total	C	N	O	S	0	0
			613	385	123	104	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	79	Total	C	N	O	S	0	0
			630	400	116	111	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	r	54	Total	C	N	O	0	0
			441	280	83	78		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	82	Total	C	N	O	S	0	0
			641	411	120	108	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	85	Total	C	N	O	S	0	0
			648	400	134	111	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	55	Total	C	N	O	S	0	0
			373	241	72	59	1		

- Molecule 22 is a RNA chain called phenylalanine tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	w	74	Total	C	N	O	P	S	0	0
			1591	713	285	517	74	2		
22	y	74	Total	C	N	O	P	S	0	0
			1585	707	285	518	74	1		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	271	Total	C	N	O	S	0	0
			2069	1282	417	363	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	D	209	Total	C	N	O	S	0	0
			1559	976	288	292	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	E	201	Total	C	N	O	S	0	0
			1538	966	282	285	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	177	Total	C	N	O	S	0	0
			1401	895	245	255	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	175	Total	C	N	O	S	0	0
			1299	818	237	242	2		

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

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

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

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

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

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

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	N	144	Total	C	N	O	S	0	0
			1048	651	207	188	2		

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
38	Q	116	Total	C	N	O	0	0
			876	541	175	160		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R	114	Total	C	N	O	S	0	0
			913	573	178	161	1		

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

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

- Molecule 41 is a protein called Ribosomal protein L21.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	U	110	Total	C	N	O	S	0	0
			850	529	163	155	3		

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
44	W	102	Total	C	N	O	0	0
			769	486	144	139		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	X	94	Total	C	N	O	S	0	0
			750	477	137	134	2		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

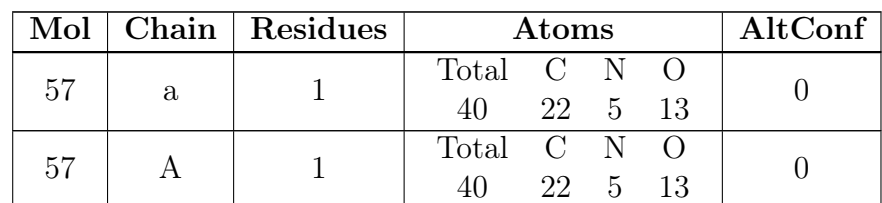
- Molecule 55 is a protein called 50S ribosomal protein L36.

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

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	a	98	Total	Mg	0
			98	98	
56	x	3	Total	Mg	0
			3	3	
56	v	1	Total	Mg	0
			1	1	
56	A	359	Total	Mg	0
			359	359	
56	B	6	Total	Mg	0
			6	6	
56	C	1	Total	Mg	0
			1	1	
56	D	1	Total	Mg	0
			1	1	
56	P	1	Total	Mg	0
			1	1	
56	S	1	Total	Mg	0
			1	1	
56	X	1	Total	Mg	0
			1	1	
56	Y	1	Total	Mg	0
			1	1	
56	4	1	Total	Mg	0
			1	1	

- Molecule 57 is (2S)-N-[(1R,2S,3S,4R,5S)-4-[(2R,3R,4S,5S,6R)-6-(aminomethyl)-3,4,5-tris(oxidanyl)oxan-2-yl]oxy-5-azanyl-2-[(2S,3R,4S,5S,6R)-4-azanyl-6-(hydroxymethyl)-3,5-bis(oxidanyl)oxan-2-yl]oxy-3-oxidanyl-cyclohexyl]-4-azanyl-2-oxidanyl-butanamide (three-letter code: AKN) (formula: C₂₂H₄₃N₅O₁₃).



-
- Chemical structure of Phenylalanine (PHE) is shown. The structure includes a benzene ring (labeled CE1, CE2, CZ, CD1, CD2, CG) attached to a chiral carbon (CA(S)). The chiral carbon is bonded to an amino group (H₂N, labeled N), a carboxyl group (COOH, labeled C, O, OH), and a hydrogen atom (H). The label PHE is positioned above the structure.

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

- 

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

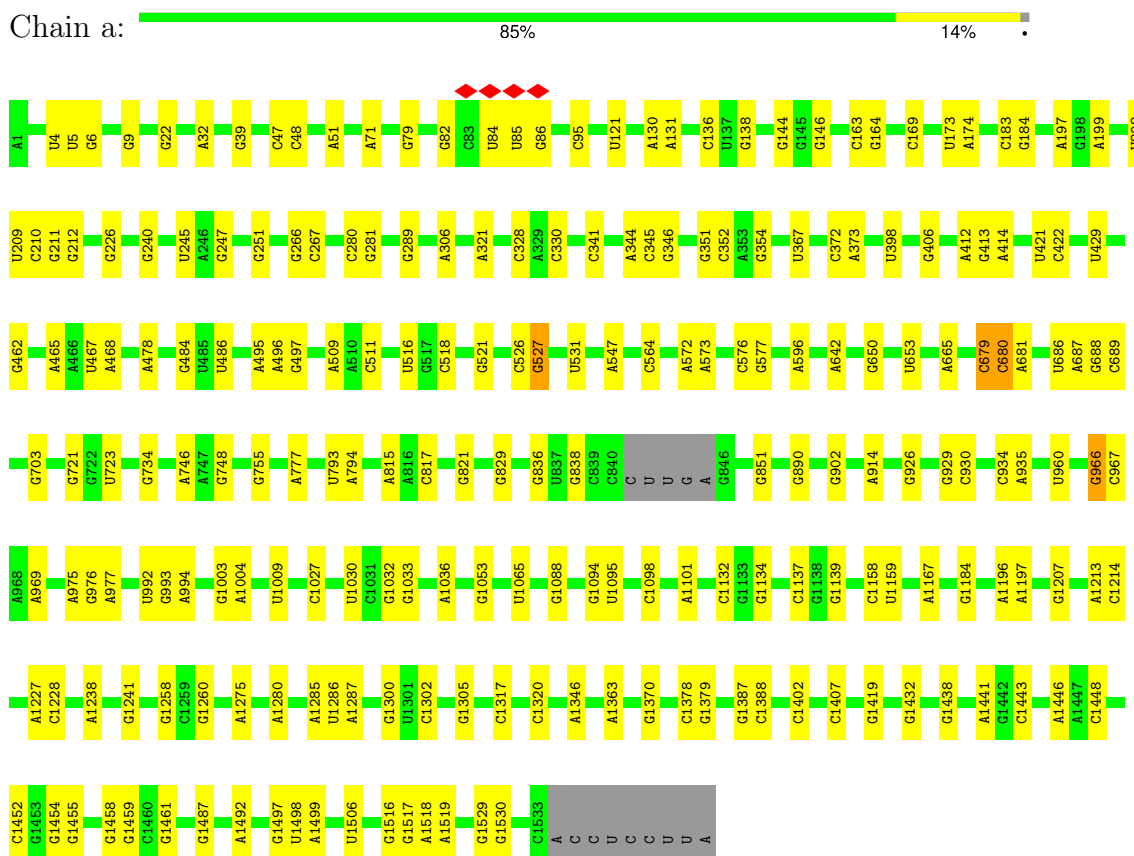
- Molecule 60 is water.

Mol	Chain	Residues	Atoms		AltConf
60	a	11	Total 11	O 11	0
60	n	1	Total 1	O 1	0
60	x	1	Total 1	O 1	0
60	A	60	Total 60	O 60	0
60	N	1	Total 1	O 1	0

3 Residue-property plots


These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

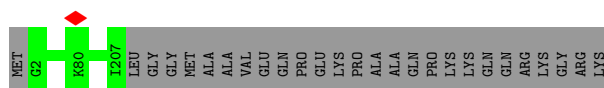
• Molecule 1: 16S Ribosomal RNA



SER
PHE
VAL
GLU
ALA
GLU

- Molecule 3: 30S ribosomal protein S3

Chain c:  88% 12%



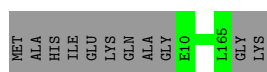
- Molecule 4: 30S ribosomal protein S4

Chain d:  98%



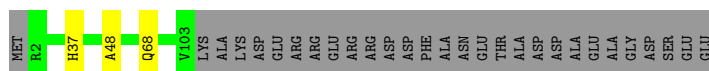
- Molecule 5: 30S ribosomal protein S5

Chain e:  93% 7%



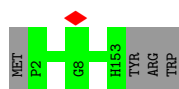
- Molecule 6: 30S ribosomal protein S6

Chain f:  76% 22%



- Molecule 7: 30S ribosomal protein S7

Chain g:  97%



- Molecule 8: 30S ribosomal protein S8

Chain h:  99%



- Molecule 9: 30S ribosomal protein S9

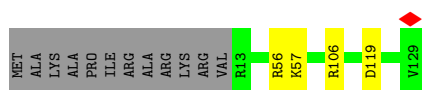
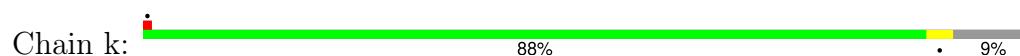
Chain i:  95%



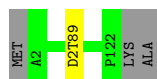
- Molecule 10: 30S ribosomal protein S10



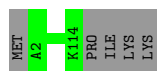
- Molecule 11: 30S ribosomal protein S11



- Molecule 12: 30S ribosomal protein S12



- Molecule 13: 30S ribosomal protein S13



- Molecule 14: 30S ribosomal protein S14

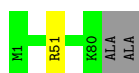


- Molecule 15: 30S ribosomal protein S15



- Molecule 16: 30S ribosomal protein S16





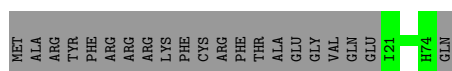
- Molecule 17: 30S ribosomal protein S17

Chain q: 92% 6%



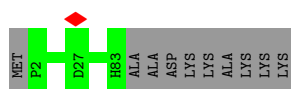
- Molecule 18: 30S ribosomal protein S18

Chain r: 72% 28%



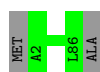
- Molecule 19: 30S ribosomal protein S19

Chain s: 89% 11%



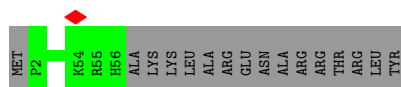
- Molecule 20: 30S ribosomal protein S20

Chain t: 98%



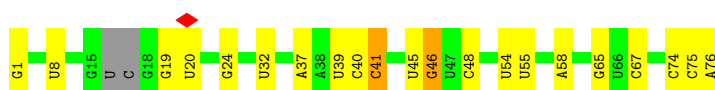
- Molecule 21: 30S ribosomal protein S21

Chain u: 77% 23%



- Molecule 22: phenylalanine tRNA

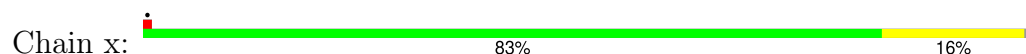
Chain w: 70% 25%



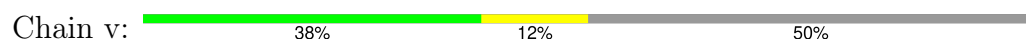
- Molecule 22: phenylalanine tRNA

Chain y: 32% 70% 24%

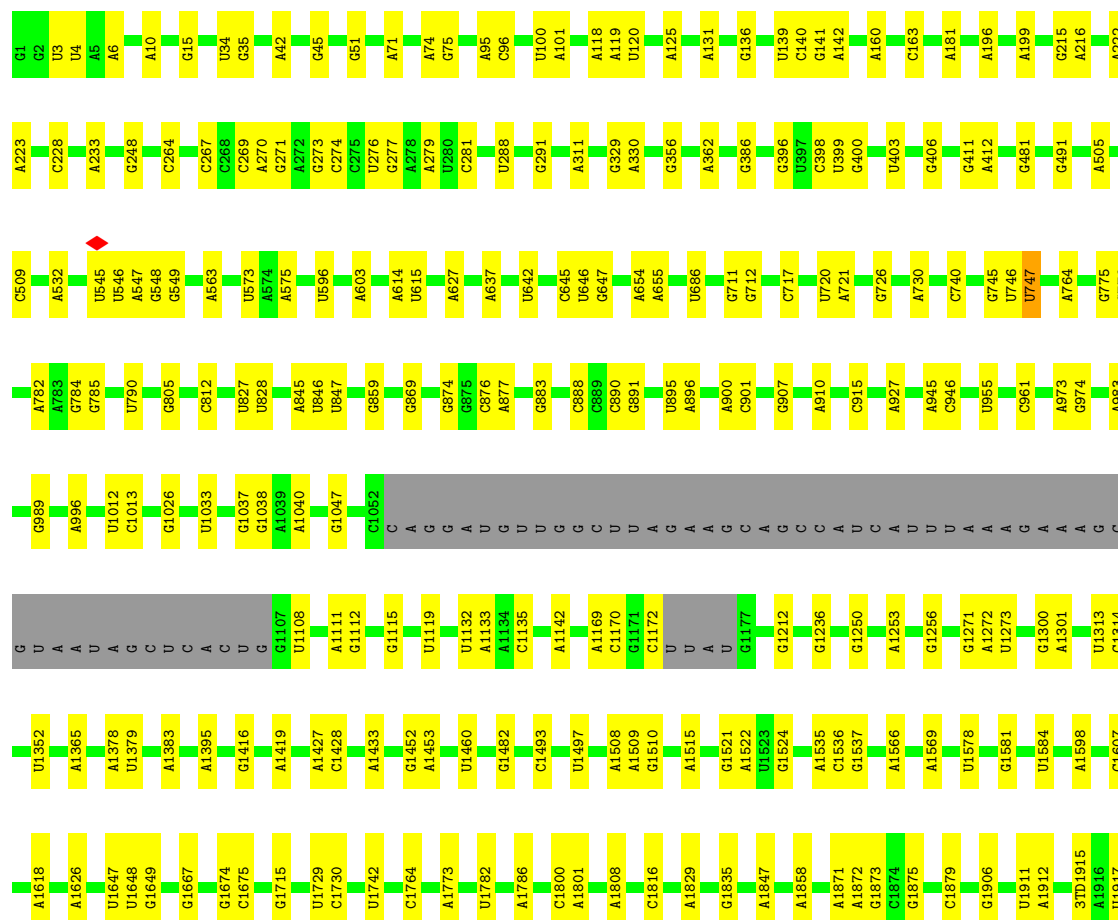
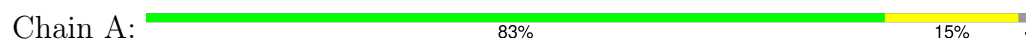
- Molecule 23: P-site initiator tRNA

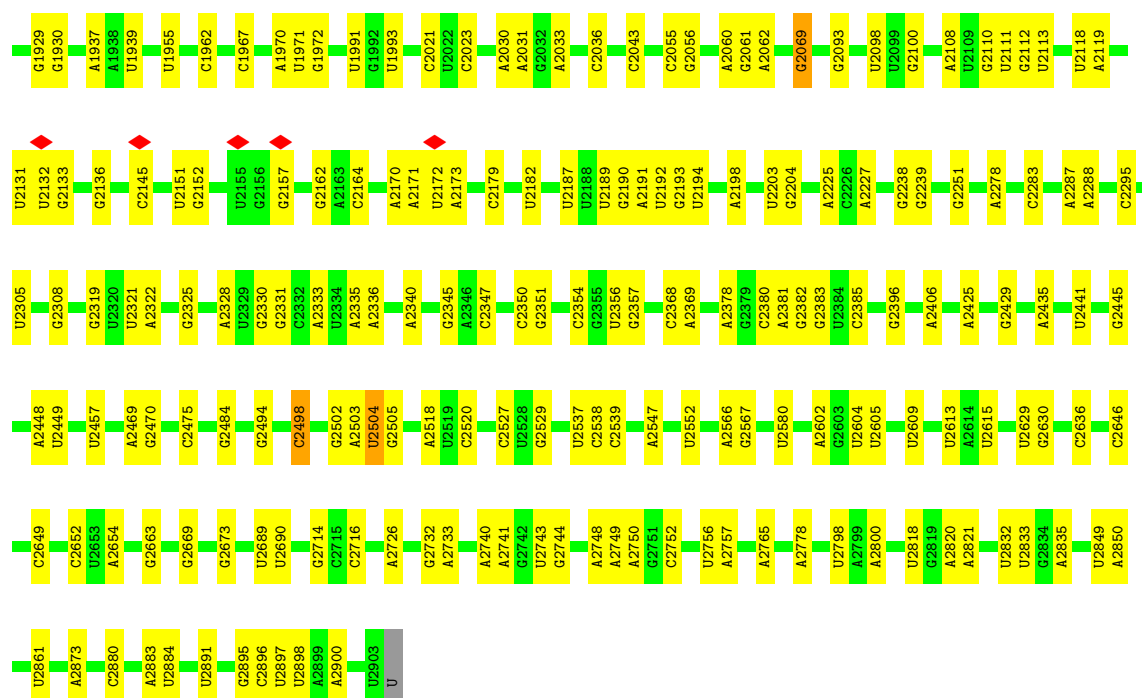


- Molecule 24: M-F-Stop mRNA



- Molecule 25: 23S Ribosomal RNA





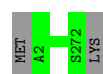
• Molecule 26: 5S Ribosomal RNA

Chain B: 87% 12%



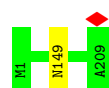
• Molecule 27: 50S ribosomal protein L2

Chain C: 99%



• Molecule 28: 50S ribosomal protein L3

Chain D: 100%



• Molecule 29: 50S ribosomal protein L4

Chain E: 100%

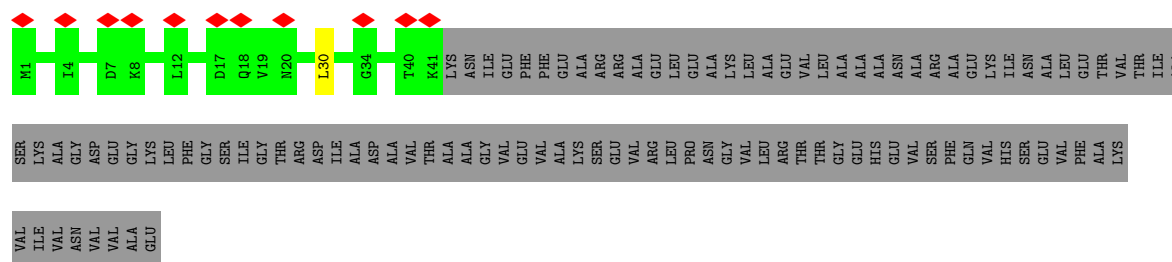
There are no outlier residues recorded for this chain.

• Molecule 30: 50S ribosomal protein L5

MET A2 R178 LYS

- MET S2 K29 K176 LYS

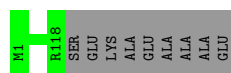
- Chain H:  7% 27% 72%



-

- 

Chain P:  93% 7%



- Molecule 38: 50S ribosomal protein L18

Chain Q:  98% ..



- Molecule 39: 50S ribosomal protein L19

Chain R:  99% .



- Molecule 40: 50S ribosomal protein L20

Chain S:  99% .



- Molecule 41: Ribosomal protein L21

Chain T:  100%

There are no outlier residues recorded for this chain.

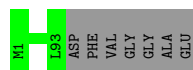
- Molecule 42: 50S ribosomal protein L22

Chain U:  100%

There are no outlier residues recorded for this chain.

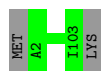
- Molecule 43: 50S ribosomal protein L23

Chain V:  93% 7%



- Molecule 44: 50S ribosomal protein L24

Chain W:  98% .



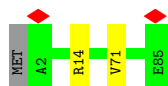
- Molecule 45: 50S ribosomal protein L25

Chain X: 100%

There are no outlier residues recorded for this chain.

- Molecule 46: 50S ribosomal protein L27

Chain Y: 96%



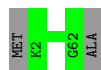
- Molecule 47: 50S ribosomal protein L28

Chain Z: 97%



- Molecule 48: 50S ribosomal protein L29

Chain 1: 97%



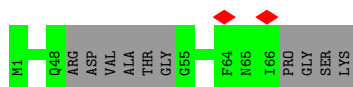
- Molecule 49: 50S ribosomal protein L30

Chain 2: 98%



- Molecule 50: 50S ribosomal protein L31

Chain 3: 86% 14%

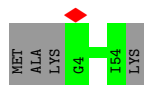


- Molecule 51: 50S ribosomal protein L32

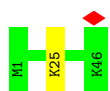
Chain 4: 96%



- Molecule 52: 50S ribosomal protein L33



- Molecule 53: 50S ribosomal protein L34



- Molecule 54: 50S ribosomal protein L35



- Molecule 55: 50S ribosomal protein L36



There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	234339	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.5852	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.699	Depositor
Minimum map value	-0.330	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, OMU, 5MC, MS6, 2MG, MIA, OMG, MA6, ZN, UR3, OMC, PSU, D2T, 4D4, 5MU, H2U, MEQ, 7MG, AKN, 3TD, 1MG, IAS, 4OC, 4SU, MG, 6MZ, G7M

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.35	0/36450	0.78	8/56856 (0.0%)
2	b	0.26	0/1542	0.47	0/2108
3	c	0.28	0/1640	0.55	0/2211
4	d	0.30	0/1665	0.60	0/2227
5	e	0.29	0/1130	0.54	0/1527
6	f	0.27	0/796	0.53	0/1086
7	g	0.26	0/1068	0.53	0/1452
8	h	0.28	0/979	0.53	0/1314
9	i	0.26	0/949	0.58	0/1276
10	j	0.26	0/682	0.51	0/933
11	k	0.33	0/867	0.57	0/1171
12	l	0.31	0/927	0.59	0/1249
13	m	0.25	0/831	0.53	0/1118
14	n	0.26	0/804	0.57	0/1072
15	o	0.27	0/711	0.58	0/952
16	p	0.28	0/623	0.59	0/842
17	q	0.29	0/639	0.53	0/859
18	r	0.28	0/447	0.55	0/601
19	s	0.26	0/658	0.54	0/889
20	t	0.26	0/654	0.52	0/871
21	u	0.27	0/380	0.54	0/518
22	w	0.59	5/1605 (0.3%)	1.16	10/2494 (0.4%)
22	y	0.32	1/1606 (0.1%)	0.77	0/2497
23	x	0.31	0/1725	0.76	0/2689
24	v	0.34	0/285	0.72	0/441
25	A	0.47	0/67852	0.78	9/105848 (0.0%)
26	B	0.42	1/2876 (0.0%)	0.81	3/4483 (0.1%)
27	C	0.33	0/2108	0.57	0/2837
28	D	0.32	0/1569	0.54	0/2111
29	E	0.29	0/1557	0.51	0/2095
30	F	0.30	0/1425	0.53	0/1915

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	G	0.28	0/1319	0.54	0/1789
32	H	0.24	0/306	0.48	0/413
33	L	0.31	0/1152	0.51	0/1551
34	M	0.31	0/955	0.57	0/1279
35	N	0.31	0/1057	0.60	0/1407
36	O	0.31	0/1073	0.55	0/1433
37	P	0.30	0/958	0.60	0/1281
38	Q	0.27	0/886	0.55	0/1192
39	R	0.31	0/925	0.54	0/1238
40	S	0.33	0/960	0.52	0/1278
41	T	0.32	0/829	0.55	0/1107
42	U	0.29	0/857	0.52	0/1149
43	V	0.27	0/744	0.51	0/994
44	W	0.30	0/777	0.53	0/1038
45	X	0.31	0/763	0.54	0/1022
46	Y	0.30	0/642	0.55	0/848
47	Z	0.29	0/635	0.55	0/848
48	1	0.25	0/496	0.53	0/660
49	2	0.28	0/453	0.56	0/605
50	3	0.25	0/475	0.47	0/633
51	4	0.30	0/440	0.56	0/588
52	5	0.29	0/424	0.52	0/565
53	6	0.29	0/380	0.64	0/498
54	7	0.28	0/513	0.56	0/676
55	8	0.32	0/303	0.60	0/397
All	All	0.40	7/155372 (0.0%)	0.74	30/233031 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
36	O	0	1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	w	76	A	N7-C5	-12.11	1.31	1.39
22	w	1	G	OP3-P	-10.68	1.48	1.61
22	y	1	G	OP3-P	-10.62	1.48	1.61
26	B	1	U	OP3-P	-10.57	1.48	1.61

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	w	76	A	C5-C6	-8.46	1.33	1.41

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	w	75	C	OP1-P-O3'	19.06	147.14	105.20
22	w	76	A	C2-N3-C4	18.68	119.94	110.60
22	w	76	A	N1-C2-N3	-18.64	119.98	129.30
22	w	76	A	N3-C4-C5	-9.99	119.81	126.80
22	w	76	A	N7-C8-N9	-9.31	109.14	113.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	O	81	4D4	Mainchain

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	222/241 (92%)	206 (93%)	16 (7%)	0	100	100
3	c	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
4	d	203/206 (98%)	200 (98%)	3 (2%)	0	100	100
5	e	154/167 (92%)	149 (97%)	5 (3%)	0	100	100
6	f	100/131 (76%)	83 (83%)	14 (14%)	3 (3%)	3	15

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	g	150/156 (96%)	143 (95%)	7 (5%)	0	100	100
8	h	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
9	i	124/130 (95%)	118 (95%)	6 (5%)	0	100	100
10	j	95/103 (92%)	90 (95%)	4 (4%)	1 (1%)	12	37
11	k	113/129 (88%)	106 (94%)	7 (6%)	0	100	100
12	l	118/124 (95%)	111 (94%)	7 (6%)	0	100	100
13	m	111/118 (94%)	107 (96%)	4 (4%)	0	100	100
14	n	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
15	o	86/89 (97%)	86 (100%)	0	0	100	100
16	p	78/82 (95%)	75 (96%)	3 (4%)	0	100	100
17	q	77/84 (92%)	75 (97%)	2 (3%)	0	100	100
18	r	52/75 (69%)	51 (98%)	1 (2%)	0	100	100
19	s	80/92 (87%)	76 (95%)	4 (5%)	0	100	100
20	t	83/87 (95%)	80 (96%)	3 (4%)	0	100	100
21	u	53/71 (75%)	53 (100%)	0	0	100	100
27	C	269/273 (98%)	261 (97%)	8 (3%)	0	100	100
28	D	206/209 (99%)	200 (97%)	5 (2%)	1 (0%)	25	56
29	E	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
30	F	175/179 (98%)	163 (93%)	12 (7%)	0	100	100
31	G	173/177 (98%)	152 (88%)	21 (12%)	0	100	100
32	H	39/149 (26%)	36 (92%)	2 (5%)	1 (3%)	4	17
33	L	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
34	M	121/123 (98%)	120 (99%)	1 (1%)	0	100	100
35	N	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
36	O	132/136 (97%)	129 (98%)	3 (2%)	0	100	100
37	P	116/127 (91%)	112 (97%)	4 (3%)	0	100	100
38	Q	114/117 (97%)	102 (90%)	11 (10%)	1 (1%)	14	43
39	R	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
40	S	115/118 (98%)	115 (100%)	0	0	100	100
41	T	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
42	U	108/110 (98%)	107 (99%)	1 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	V	91/100 (91%)	83 (91%)	8 (9%)	0	100	100
44	W	100/104 (96%)	94 (94%)	6 (6%)	0	100	100
45	X	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
46	Y	82/85 (96%)	78 (95%)	3 (4%)	1 (1%)	11	35
47	Z	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
48	1	59/63 (94%)	57 (97%)	2 (3%)	0	100	100
49	2	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
50	3	56/70 (80%)	52 (93%)	4 (7%)	0	100	100
51	4	53/57 (93%)	53 (100%)	0	0	100	100
52	5	49/55 (89%)	49 (100%)	0	0	100	100
53	6	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	7	62/65 (95%)	59 (95%)	2 (3%)	1 (2%)	8	28
55	8	36/38 (95%)	36 (100%)	0	0	100	100
All	All	5445/5886 (92%)	5219 (96%)	217 (4%)	9 (0%)	45	73

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	f	37	HIS
6	f	68	GLN
38	Q	90	VAL
10	j	57	VAL
28	D	149	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	b	115/199 (58%)	115 (100%)	0	100	100
3	c	167/190 (88%)	167 (100%)	0	100	100
4	d	172/173 (99%)	169 (98%)	3 (2%)	56	83

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	e	110/126 (87%)	110 (100%)	0	100	100
6	f	77/112 (69%)	77 (100%)	0	100	100
7	g	89/129 (69%)	89 (100%)	0	100	100
8	h	102/105 (97%)	102 (100%)	0	100	100
9	i	87/107 (81%)	84 (97%)	3 (3%)	32	67
10	j	55/90 (61%)	55 (100%)	0	100	100
11	k	85/98 (87%)	82 (96%)	3 (4%)	31	66
12	l	97/103 (94%)	97 (100%)	0	100	100
13	m	78/96 (81%)	78 (100%)	0	100	100
14	n	78/84 (93%)	78 (100%)	0	100	100
15	o	74/77 (96%)	73 (99%)	1 (1%)	62	86
16	p	58/65 (89%)	57 (98%)	1 (2%)	56	83
17	q	70/78 (90%)	68 (97%)	2 (3%)	37	72
18	r	46/65 (71%)	46 (100%)	0	100	100
19	s	68/79 (86%)	68 (100%)	0	100	100
20	t	61/66 (92%)	61 (100%)	0	100	100
21	u	28/61 (46%)	28 (100%)	0	100	100
27	C	213/218 (98%)	213 (100%)	0	100	100
28	D	161/163 (99%)	161 (100%)	0	100	100
29	E	161/165 (98%)	161 (100%)	0	100	100
30	F	146/150 (97%)	146 (100%)	0	100	100
31	G	133/138 (96%)	132 (99%)	1 (1%)	79	93
32	H	32/114 (28%)	32 (100%)	0	100	100
33	L	116/116 (100%)	116 (100%)	0	100	100
34	M	104/104 (100%)	104 (100%)	0	100	100
35	N	102/103 (99%)	102 (100%)	0	100	100
36	O	107/107 (100%)	107 (100%)	0	100	100
37	P	98/103 (95%)	98 (100%)	0	100	100
38	Q	82/87 (94%)	82 (100%)	0	100	100
39	R	98/100 (98%)	98 (100%)	0	100	100
40	S	89/90 (99%)	89 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	T	84/84 (100%)	84 (100%)	0	100	100
42	U	92/93 (99%)	92 (100%)	0	100	100
43	V	80/84 (95%)	80 (100%)	0	100	100
44	W	80/85 (94%)	80 (100%)	0	100	100
45	X	77/78 (99%)	77 (100%)	0	100	100
46	Y	62/63 (98%)	61 (98%)	1 (2%)	58	84
47	Z	67/68 (98%)	66 (98%)	1 (2%)	60	85
48	1	54/55 (98%)	54 (100%)	0	100	100
49	2	48/49 (98%)	48 (100%)	0	100	100
50	3	53/62 (86%)	53 (100%)	0	100	100
51	4	46/48 (96%)	46 (100%)	0	100	100
52	5	46/49 (94%)	46 (100%)	0	100	100
53	6	38/38 (100%)	37 (97%)	1 (3%)	41	74
54	7	51/52 (98%)	51 (100%)	0	100	100
55	8	34/34 (100%)	34 (100%)	0	100	100
All	All	4271/4803 (89%)	4254 (100%)	17 (0%)	88	97

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	Y	14	ARG
53	6	25	LYS
11	k	57	LYS
11	k	106	ARG
15	o	58	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
36	O	22	GLN
43	V	28	ASN
37	P	23	ASN
40	S	44	GLN
47	Z	23	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1523/1542 (98%)	206 (13%)	0
22	w	71/76 (93%)	12 (16%)	0
22	y	71/76 (93%)	16 (22%)	0
23	x	75/77 (97%)	8 (10%)	0
24	v	11/24 (45%)	3 (27%)	0
25	A	2838/2904 (97%)	399 (14%)	11 (0%)
26	B	119/120 (99%)	12 (10%)	3 (2%)
All	All	4708/4819 (97%)	656 (13%)	14 (0%)

5 of 656 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	4	U
1	a	5	U
1	a	6	G
1	a	9	G
1	a	22	G

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	2538	C
25	A	2756	U
26	B	61	G
26	B	3	C
26	B	42	C

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MA6	a	1519	1	19,26,27	0.95	1 (5%)	18,38,41	2.32	7 (38%)
25	3TD	A	1915	25	19,22,23	4.22	7 (36%)	23,32,35	1.83	4 (17%)
36	4D4	O	81	36	9,11,12	2.72	3 (33%)	7,13,15	0.81	0
1	G7M	a	527	1	20,26,27	1.18	2 (10%)	16,39,42	0.54	0
25	PSU	A	2504	25	18,21,22	1.41	4 (22%)	21,30,33	2.04	3 (14%)
23	5MC	x	32	23	19,22,23	1.46	3 (15%)	26,32,35	1.23	3 (11%)
25	PSU	A	2457	25	18,21,22	1.42	4 (22%)	21,30,33	2.10	5 (23%)
1	2MG	a	1207	1	18,26,27	0.91	1 (5%)	16,38,41	1.23	2 (12%)
25	OMU	A	2552	25	19,22,23	1.26	3 (15%)	25,31,34	1.82	5 (20%)
1	PSU	a	516	1	18,21,22	1.37	2 (11%)	21,30,33	2.05	4 (19%)
22	MIA	y	37	22	17,24,32	0.92	1 (5%)	16,35,47	1.27	2 (12%)
1	5MC	a	1407	1	19,22,23	1.47	3 (15%)	26,32,35	1.13	3 (11%)
11	IAS	k	119	11	6,7,8	0.97	0	3,8,10	1.45	1 (33%)
25	PSU	A	2580	25	18,21,22	1.44	5 (27%)	21,30,33	2.17	4 (19%)
25	G7M	A	2069	25	20,26,27	1.15	2 (10%)	16,39,42	0.64	0
22	4SU	y	8	22	18,21,22	1.83	4 (22%)	25,30,33	2.34	5 (20%)
25	5MU	A	747	25	19,22,23	1.38	4 (21%)	27,32,35	2.20	6 (22%)
12	D2T	l	89	12	8,9,10	1.98	1 (12%)	6,11,13	2.56	2 (33%)
22	7MG	y	46	22	23,26,27	1.31	3 (13%)	27,39,42	2.59	6 (22%)
25	2MG	A	2445	25	18,26,27	0.93	1 (5%)	16,38,41	1.45	5 (31%)
1	UR3	a	1498	1	19,22,23	0.95	0	26,32,35	1.72	2 (7%)
22	4SU	w	8	22	18,21,22	1.90	4 (22%)	25,30,33	2.10	4 (16%)
25	PSU	A	955	25	18,21,22	1.42	4 (22%)	21,30,33	2.08	3 (14%)
1	4OC	a	1402	1	20,23,24	0.75	0	25,32,35	0.95	1 (4%)
22	PSU	y	32	22	18,21,22	1.36	2 (11%)	21,30,33	2.00	3 (14%)
22	PSU	w	55	22	18,21,22	1.36	2 (11%)	21,30,33	2.02	3 (14%)
22	5MU	w	54	22	19,22,23	1.40	5 (26%)	27,32,35	1.94	5 (18%)
25	PSU	A	746	25,56	18,21,22	1.40	3 (16%)	21,30,33	2.02	4 (19%)
25	PSU	A	2604	25	18,21,22	1.41	3 (16%)	21,30,33	2.08	4 (19%)
23	4SU	x	8	23	18,21,22	1.86	4 (22%)	25,30,33	2.29	5 (20%)
22	PSU	w	39	22	18,21,22	1.29	2 (11%)	21,30,33	2.26	3 (14%)
23	5MU	x	54	23	19,22,23	1.36	5 (26%)	27,32,35	2.13	6 (22%)
25	2MG	A	1835	25	18,26,27	0.89	1 (5%)	16,38,41	1.46	5 (31%)
25	5MU	A	1939	25	19,22,23	1.39	4 (21%)	27,32,35	2.15	6 (22%)
23	PSU	x	55	23	18,21,22	1.37	2 (11%)	21,30,33	2.06	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	6MZ	A	2030	25	17,25,26	0.86	1 (5%)	15,36,39	2.57	4 (26%)
25	PSU	A	1911	25	18,21,22	1.40	3 (16%)	21,30,33	2.06	3 (14%)
25	OMC	A	2498	25,56	19,22,23	0.82	0	25,31,34	0.95	1 (4%)
22	PSU	w	32	22	18,21,22	1.37	2 (11%)	21,30,33	2.03	4 (19%)
25	6MZ	A	1618	25	17,25,26	0.89	1 (5%)	15,36,39	2.35	4 (26%)
25	PSU	A	2605	25	18,21,22	1.40	3 (16%)	21,30,33	2.09	4 (19%)
1	MA6	a	1518	1	19,26,27	0.96	1 (5%)	18,38,41	2.28	7 (38%)
25	H2U	A	2449	25	18,21,22	1.11	3 (16%)	19,30,33	1.11	2 (10%)
25	OMG	A	2251	25,23	19,26,27	0.91	1 (5%)	21,38,41	1.03	2 (9%)
22	5MU	y	54	22	19,22,23	1.38	6 (31%)	27,32,35	2.07	6 (22%)
25	1MG	A	745	25	19,26,27	0.87	1 (5%)	18,39,42	1.19	2 (11%)
1	2MG	a	1516	1	18,26,27	0.89	1 (5%)	16,38,41	1.53	5 (31%)
22	PSU	y	39	22	18,21,22	1.36	2 (11%)	21,30,33	2.00	3 (14%)
25	5MC	A	1962	25	19,22,23	1.41	3 (15%)	26,32,35	1.09	2 (7%)
28	MEQ	D	150	28	8,9,10	0.51	0	5,10,12	0.34	0
25	PSU	A	1917	25	18,21,22	1.42	3 (16%)	21,30,33	2.01	3 (14%)
22	PSU	y	55	22	18,21,22	1.37	2 (11%)	21,30,33	2.04	3 (14%)
25	2MA	A	2503	25,56	18,25,26	0.67	0	20,37,40	2.05	4 (20%)
22	MIA	w	37	22	24,31,32	2.22	3 (12%)	22,44,47	2.64	7 (31%)
1	2MG	a	966	1	18,26,27	0.92	1 (5%)	16,38,41	1.21	2 (12%)
22	7MG	w	46	22	23,26,27	1.31	3 (13%)	27,39,42	2.62	6 (22%)
1	5MC	a	967	1	19,22,23	1.52	3 (15%)	26,32,35	1.11	2 (7%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MA6	a	1519	1	-	4/7/29/30	0/3/3/3
25	3TD	A	1915	25	-	0/7/25/26	0/2/2/2
36	4D4	O	81	36	-	2/11/12/14	-
1	G7M	a	527	1	-	2/3/25/26	0/3/3/3
25	PSU	A	2504	25	-	1/7/25/26	0/2/2/2
23	5MC	x	32	23	-	0/7/25/26	0/2/2/2
25	PSU	A	2457	25	-	0/7/25/26	0/2/2/2
1	2MG	a	1207	1	-	0/5/27/28	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	OMU	A	2552	25	-	0/9/27/28	0/2/2/2
1	PSU	a	516	1	-	0/7/25/26	0/2/2/2
22	MIA	y	37	22	-	2/3/25/34	0/3/3/3
1	5MC	a	1407	1	-	0/7/25/26	0/2/2/2
11	IAS	k	119	11	-	3/7/7/8	-
25	PSU	A	2580	25	-	0/7/25/26	0/2/2/2
25	G7M	A	2069	25	-	0/3/25/26	0/3/3/3
22	4SU	y	8	22	-	2/7/25/26	0/2/2/2
25	5MU	A	747	25	-	0/7/25/26	0/2/2/2
12	D2T	l	89	12	-	1/7/12/14	-
22	7MG	y	46	22	-	6/7/37/38	0/3/3/3
25	2MG	A	2445	25	-	0/5/27/28	0/3/3/3
1	UR3	a	1498	1	-	0/7/25/26	0/2/2/2
22	4SU	w	8	22	-	0/7/25/26	0/2/2/2
25	PSU	A	955	25	-	0/7/25/26	0/2/2/2
1	4OC	a	1402	1	-	1/9/29/30	0/2/2/2
22	PSU	y	32	22	-	0/7/25/26	0/2/2/2
22	PSU	w	55	22	-	0/7/25/26	0/2/2/2
22	5MU	w	54	22	-	0/7/25/26	0/2/2/2
25	PSU	A	746	25,56	-	2/7/25/26	0/2/2/2
25	PSU	A	2604	25	-	0/7/25/26	0/2/2/2
23	4SU	x	8	23	-	0/7/25/26	0/2/2/2
22	PSU	w	39	22	-	0/7/25/26	0/2/2/2
23	5MU	x	54	23	-	0/7/25/26	0/2/2/2
25	2MG	A	1835	25	-	0/5/27/28	0/3/3/3
25	5MU	A	1939	25	-	0/7/25/26	0/2/2/2
23	PSU	x	55	23	-	0/7/25/26	0/2/2/2
25	6MZ	A	2030	25	-	2/5/27/28	0/3/3/3
25	PSU	A	1911	25	-	0/7/25/26	0/2/2/2
25	OMC	A	2498	25,56	-	1/9/27/28	0/2/2/2
22	PSU	w	32	22	-	0/7/25/26	0/2/2/2
25	6MZ	A	1618	25	-	0/5/27/28	0/3/3/3
25	PSU	A	2605	25	-	0/7/25/26	0/2/2/2
1	MA6	a	1518	1	-	1/7/29/30	0/3/3/3
25	H2U	A	2449	25	-	0/7/38/39	0/2/2/2
25	OMG	A	2251	25,23	-	0/5/27/28	0/3/3/3
22	5MU	y	54	22	-	0/7/25/26	0/2/2/2
25	1MG	A	745	25	-	0/3/25/26	0/3/3/3
1	2MG	a	1516	1	-	0/5/27/28	0/3/3/3
22	PSU	y	39	22	-	0/7/25/26	0/2/2/2
25	5MC	A	1962	25	-	0/7/25/26	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	MEQ	D	150	28	-	2/8/9/11	-
25	PSU	A	1917	25	-	2/7/25/26	0/2/2/2
22	PSU	y	55	22	-	3/7/25/26	0/2/2/2
25	2MA	A	2503	25,56	-	0/3/25/26	0/3/3/3
22	MIA	w	37	22	-	2/11/33/34	0/3/3/3
1	2MG	a	966	1	-	0/5/27/28	0/3/3/3
22	7MG	w	46	22	-	2/7/37/38	0/3/3/3
1	5MC	a	967	1	-	0/7/25/26	0/2/2/2

The worst 5 of 138 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	1915	3TD	C6-C5	12.56	1.49	1.35
25	A	1915	3TD	C2-N1	9.74	1.49	1.37
22	w	37	MIA	C2-S10	-7.36	1.69	1.75
22	w	37	MIA	C13-C14	6.73	1.52	1.32
36	O	81	4D4	CZ-NE	6.33	1.45	1.33

The worst 5 of 201 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	w	37	MIA	C12-C13-C14	-9.20	110.50	127.01
22	w	46	7MG	N9-C4-N3	8.88	138.48	125.46
22	y	46	7MG	N9-C4-N3	8.75	138.28	125.46
22	y	8	4SU	C4-N3-C2	-7.21	120.40	127.31
25	A	2503	2MA	C2-N3-C4	7.16	121.24	115.46

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	a	1519	MA6	O4'-C4'-C5'-O5'
1	a	1519	MA6	C5-C6-N6-C9
22	w	37	MIA	C12-C13-C14-C16
22	y	55	PSU	C2'-C1'-C5-C4
1	a	527	G7M	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 479 ligands modelled in this entry, 476 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
58	PHE	w	101	22	10,11,12	1.70	1 (10%)	8,13,15	0.58	0
57	AKN	a	3099	-	41,42,42	2.02	10 (24%)	55,61,61	1.22	6 (10%)
57	AKN	A	3360	-	41,42,42	1.96	11 (26%)	55,61,61	1.09	3 (5%)

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
58	PHE	w	101	22	-	3/5/6/8	0/1/1/1
57	AKN	a	3099	-	-	3/23/83/83	0/3/3/3
57	AKN	A	3360	-	-	6/23/83/83	0/3/3/3

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	A	3360	AKN	C35-N12	5.87	1.46	1.34
57	a	3099	AKN	C35-N12	5.72	1.46	1.34
57	a	3099	AKN	C22-C24	-5.40	1.46	1.53
58	w	101	PHE	CB-CG	-5.21	1.39	1.51
57	A	3360	AKN	C22-C24	-5.06	1.47	1.53

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	a	3099	AKN	C13-C11-N12	-3.36	105.65	110.78
57	a	3099	AKN	C21-O20-C19	-3.00	110.86	117.98
57	A	3360	AKN	C21-O20-C19	-2.73	111.52	117.98
57	a	3099	AKN	C11-N12-C35	-2.69	118.57	123.25
57	a	3099	AKN	C19-C17-C16	2.59	114.35	109.11

There are no chirality outliers.

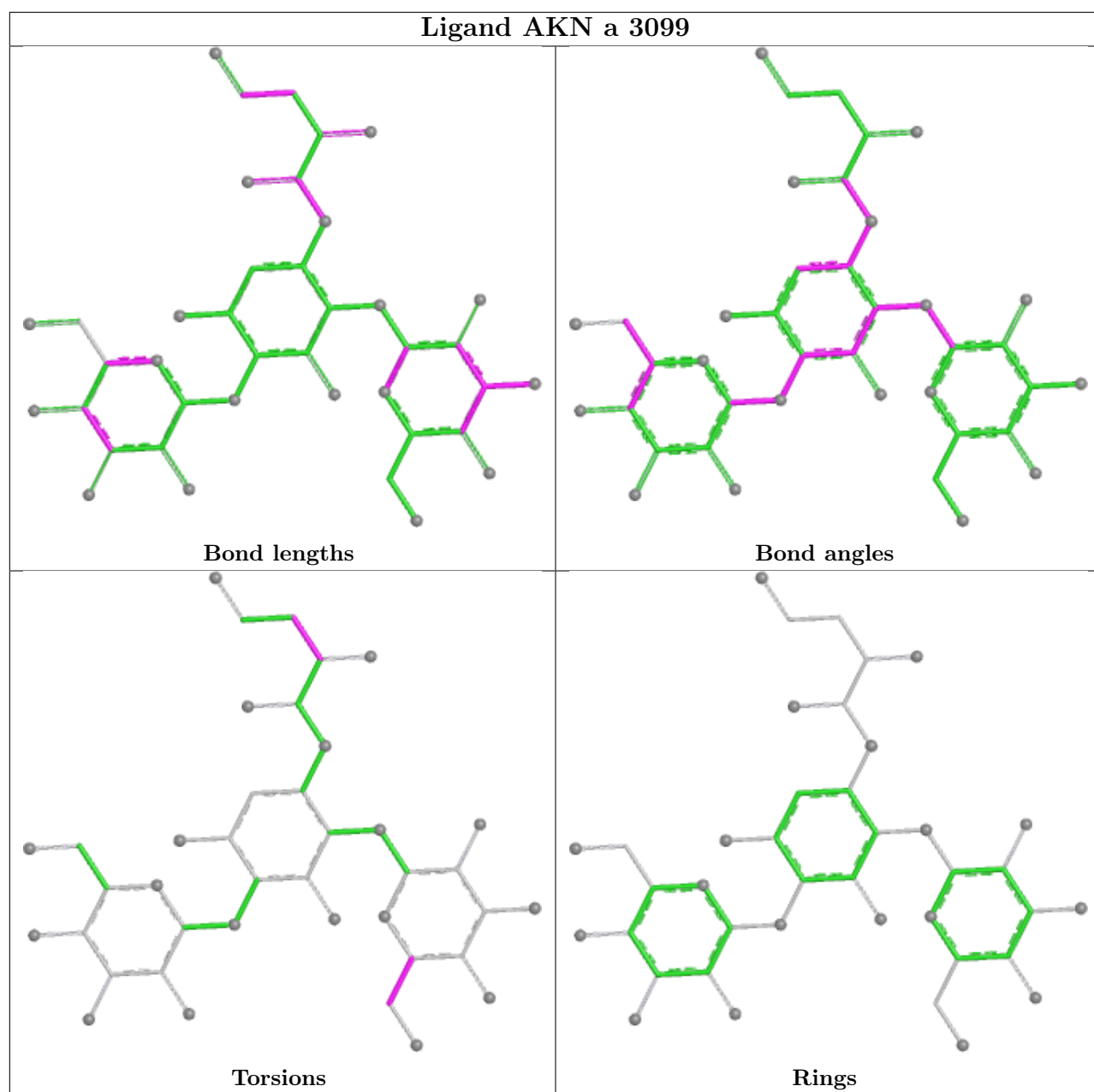
5 of 12 torsion outliers are listed below:

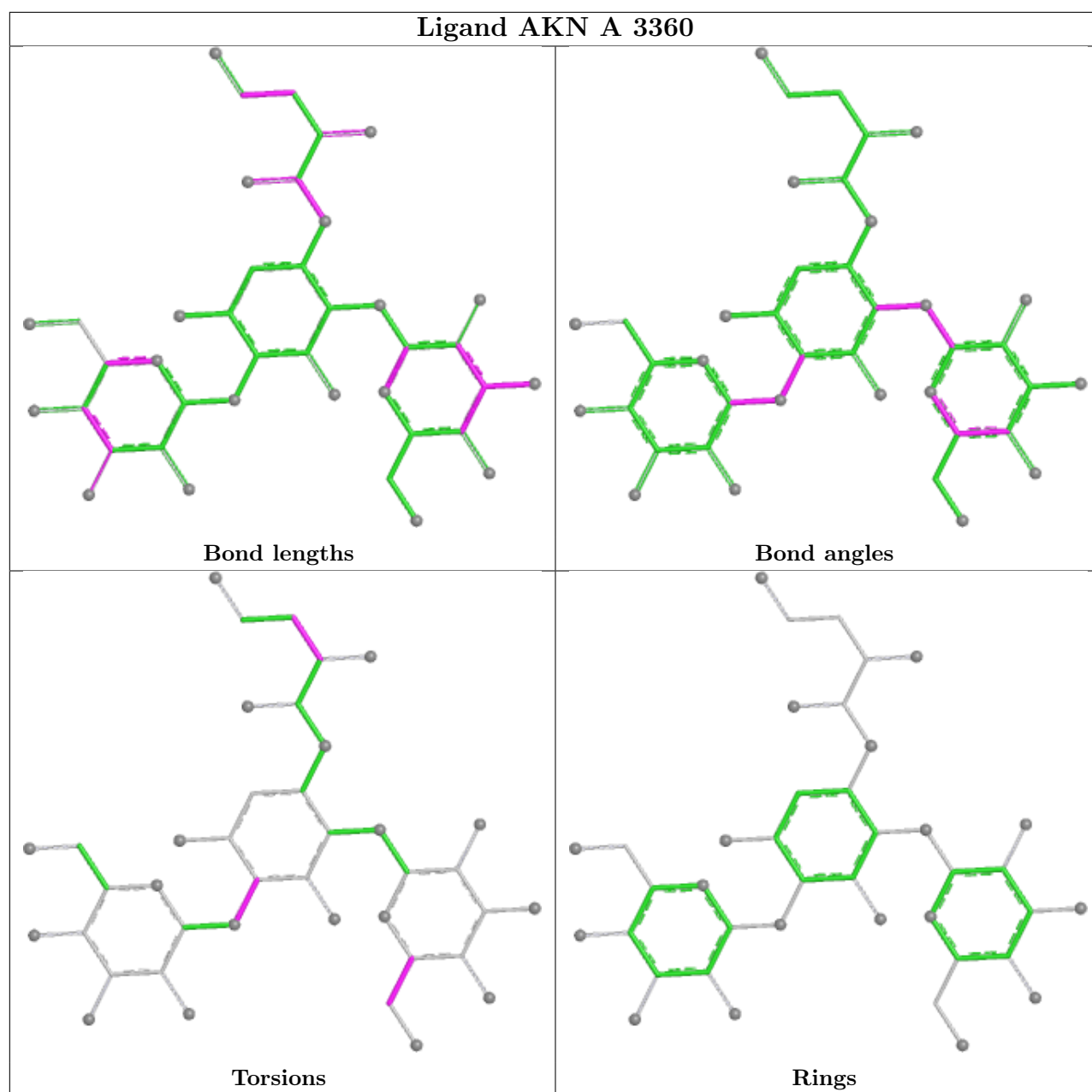
Mol	Chain	Res	Type	Atoms
57	A	3360	AKN	C14-C16-O2-C1
57	A	3360	AKN	C35-C37-C38-C39
57	A	3360	AKN	O40-C37-C38-C39
58	w	101	PHE	O-C-CA-CB
58	w	101	PHE	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

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.

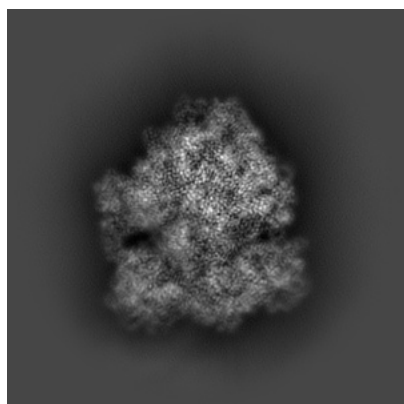
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40882. These allow visual inspection of the internal detail of the map and identification of artifacts.

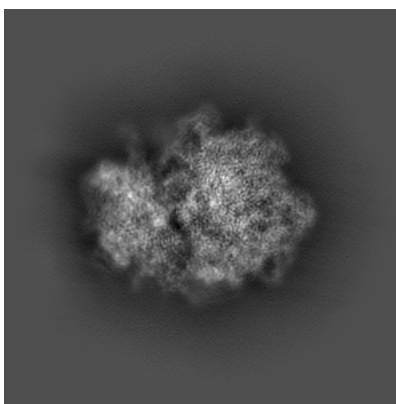
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

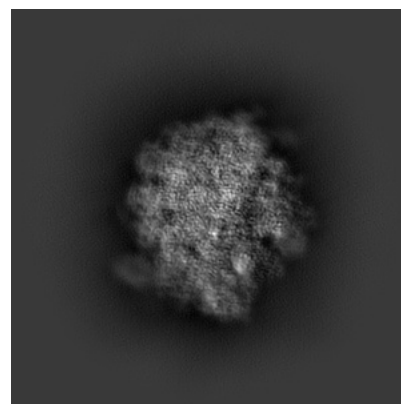
6.1.1 Primary map



X

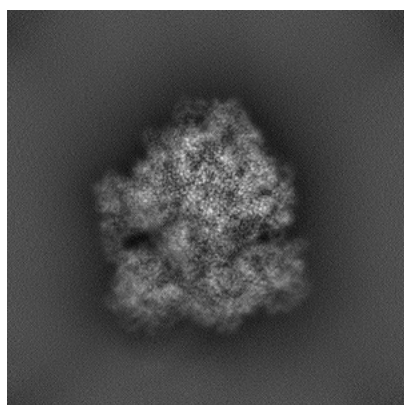


Y

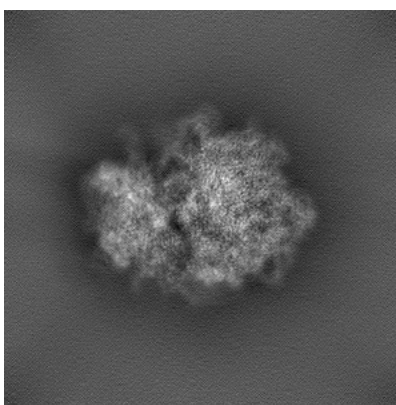


Z

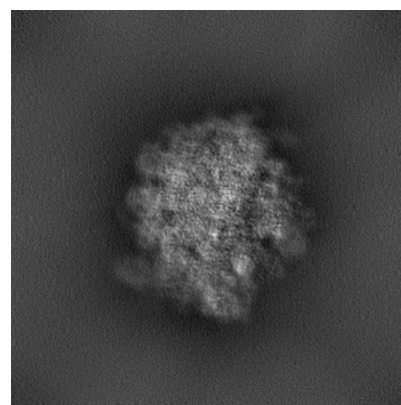
6.1.2 Raw map



X



Y

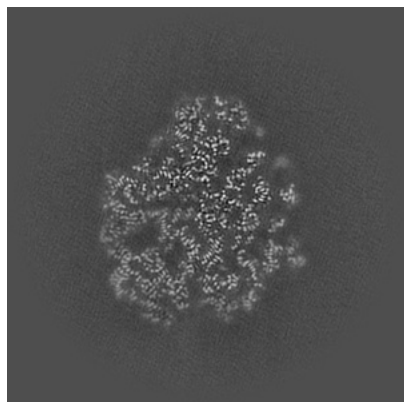


Z

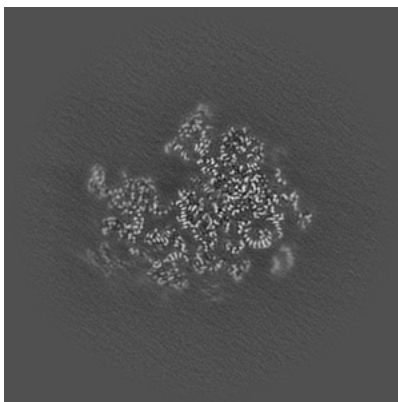
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

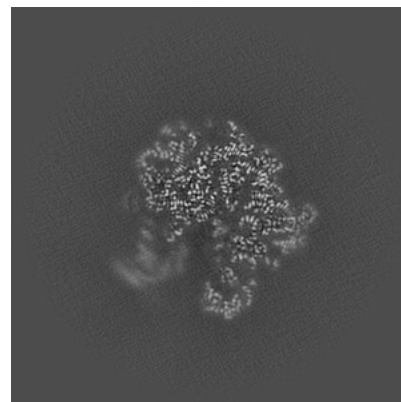
6.2.1 Primary map



X Index: 256

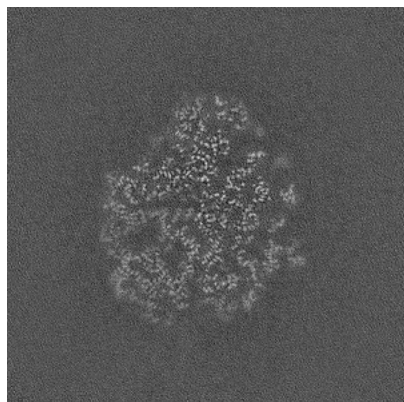


Y Index: 256

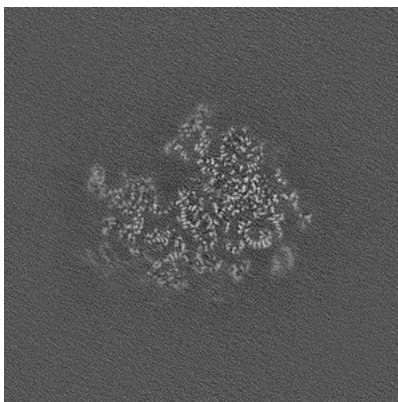


Z Index: 256

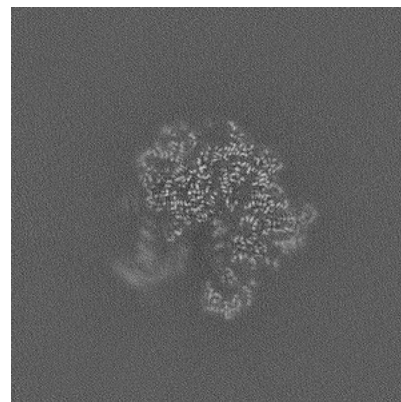
6.2.2 Raw map



X Index: 256



Y Index: 256

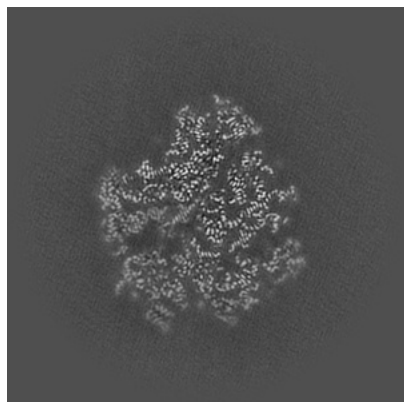


Z Index: 256

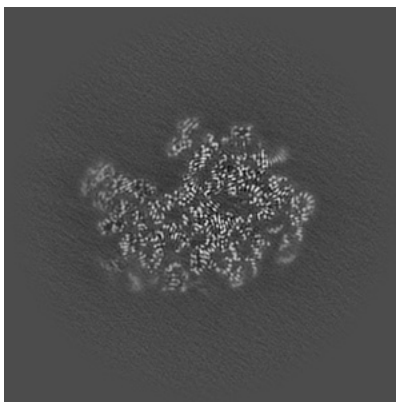
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

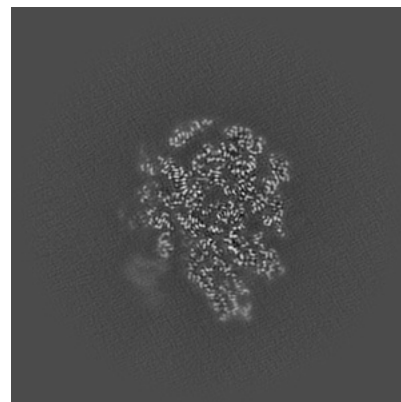
6.3.1 Primary map



X Index: 262

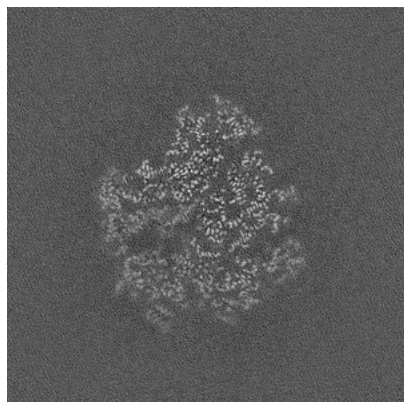


Y Index: 270

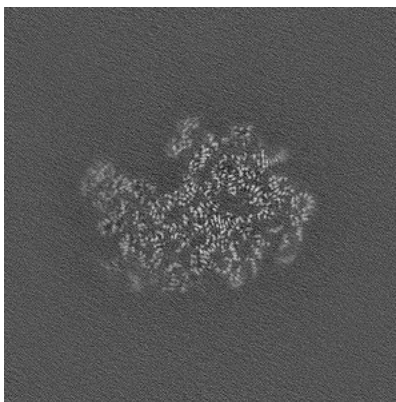


Z Index: 284

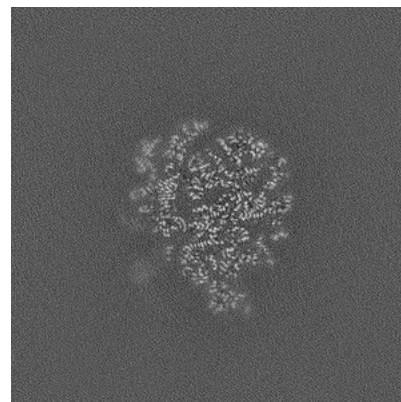
6.3.2 Raw map



X Index: 262



Y Index: 270

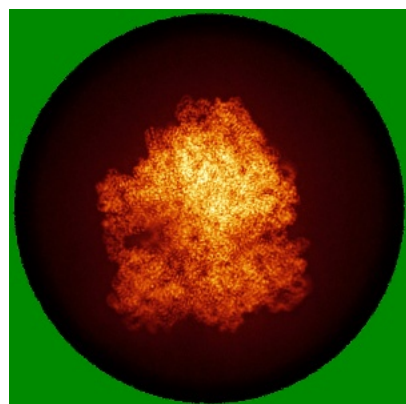


Z Index: 293

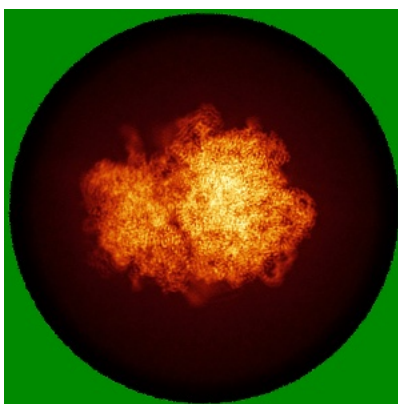
The images above show the largest variance slices of the map in three orthogonal directions.

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

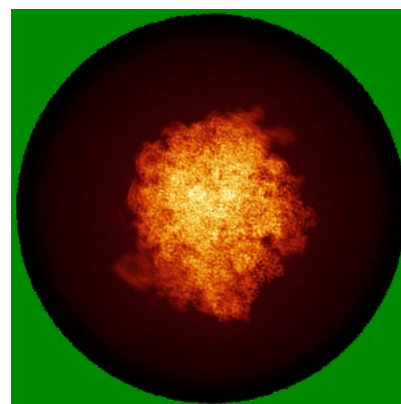
6.4.1 Primary map



X

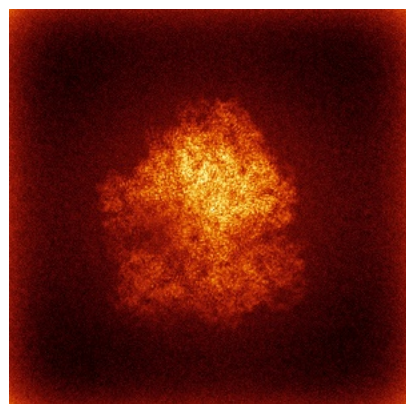


Y

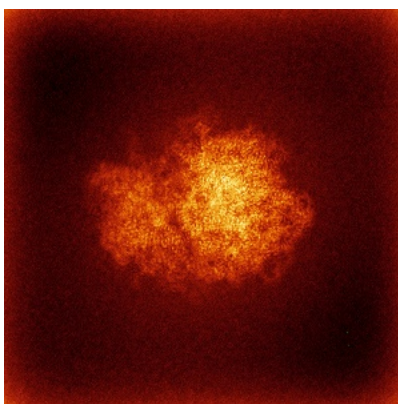


Z

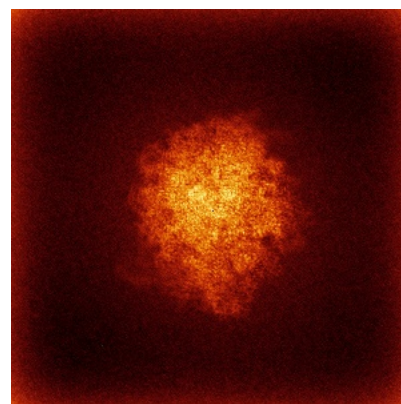
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



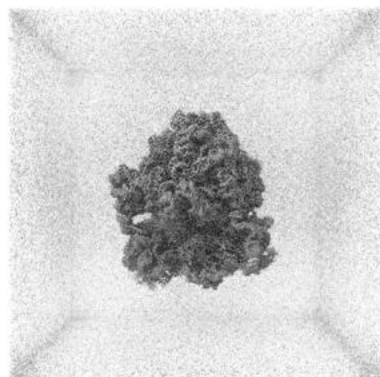
Y



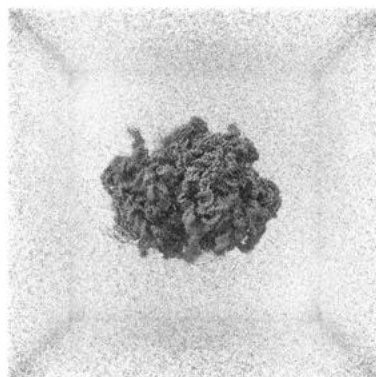
Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

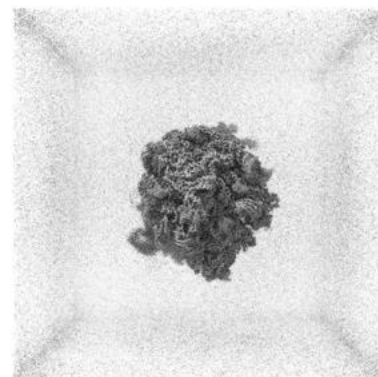
6.5.2 Raw map



X



Y



Z

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

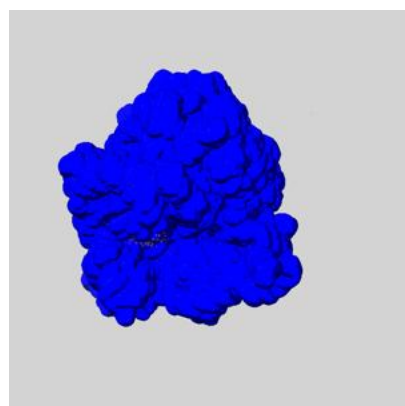
6.6 Mask visualisation [i](#)

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

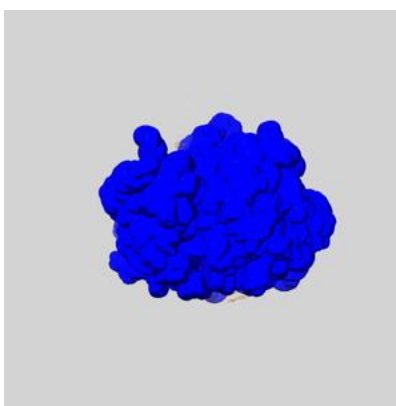
A mask typically either:

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

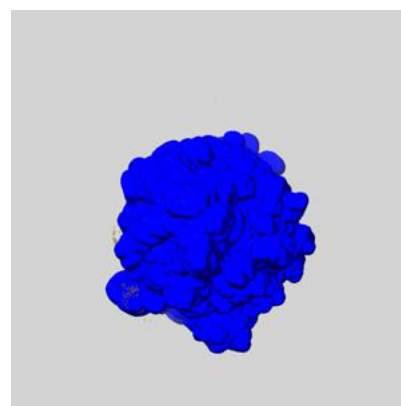
6.6.1 emd_40882_msk_1.map [i](#)



X



Y

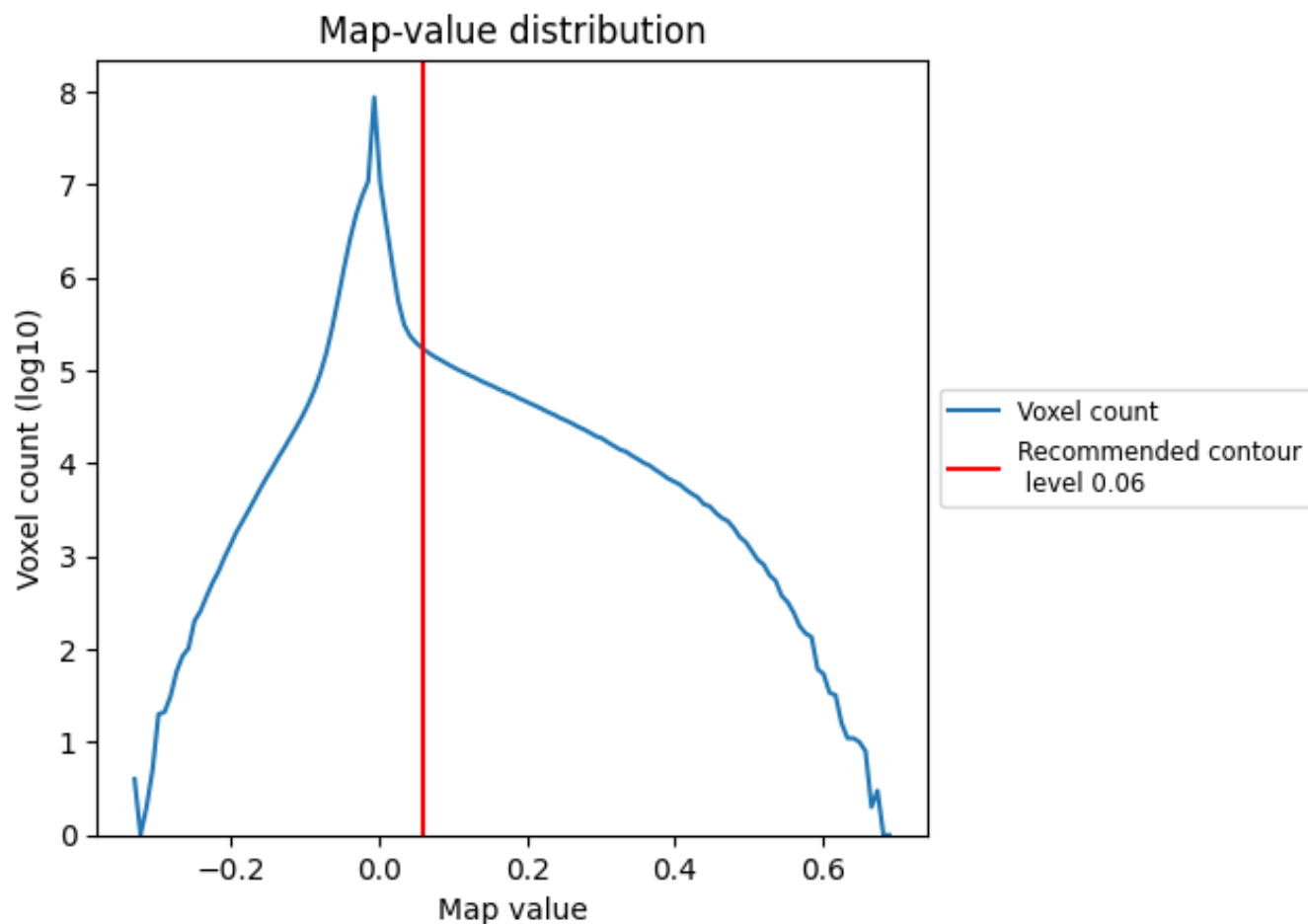


Z

7 Map analysis [i](#)

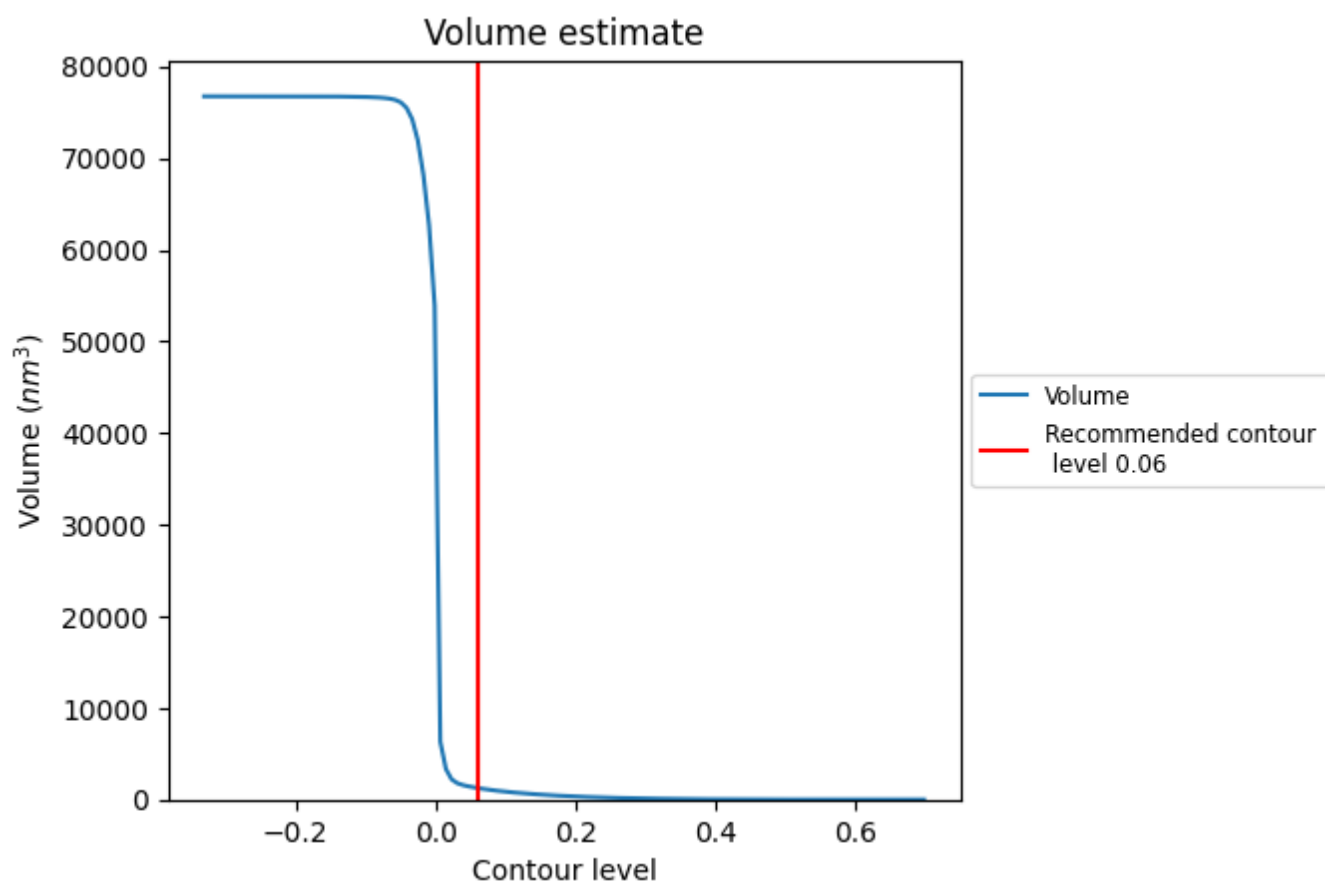
This section contains the results of statistical analysis of the map.

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.

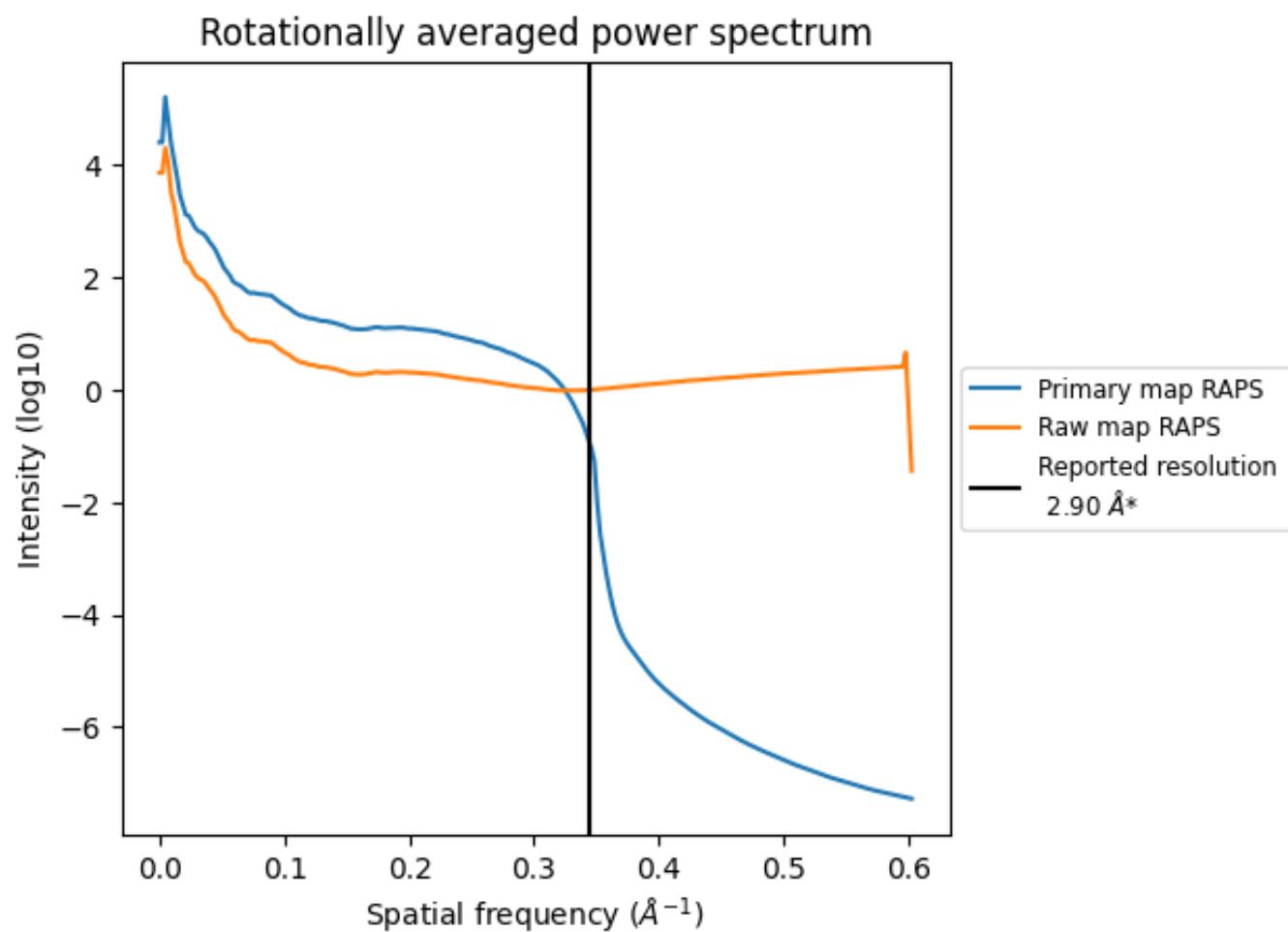
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1266 nm³; this corresponds to an approximate mass of 1144 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 ⓘ

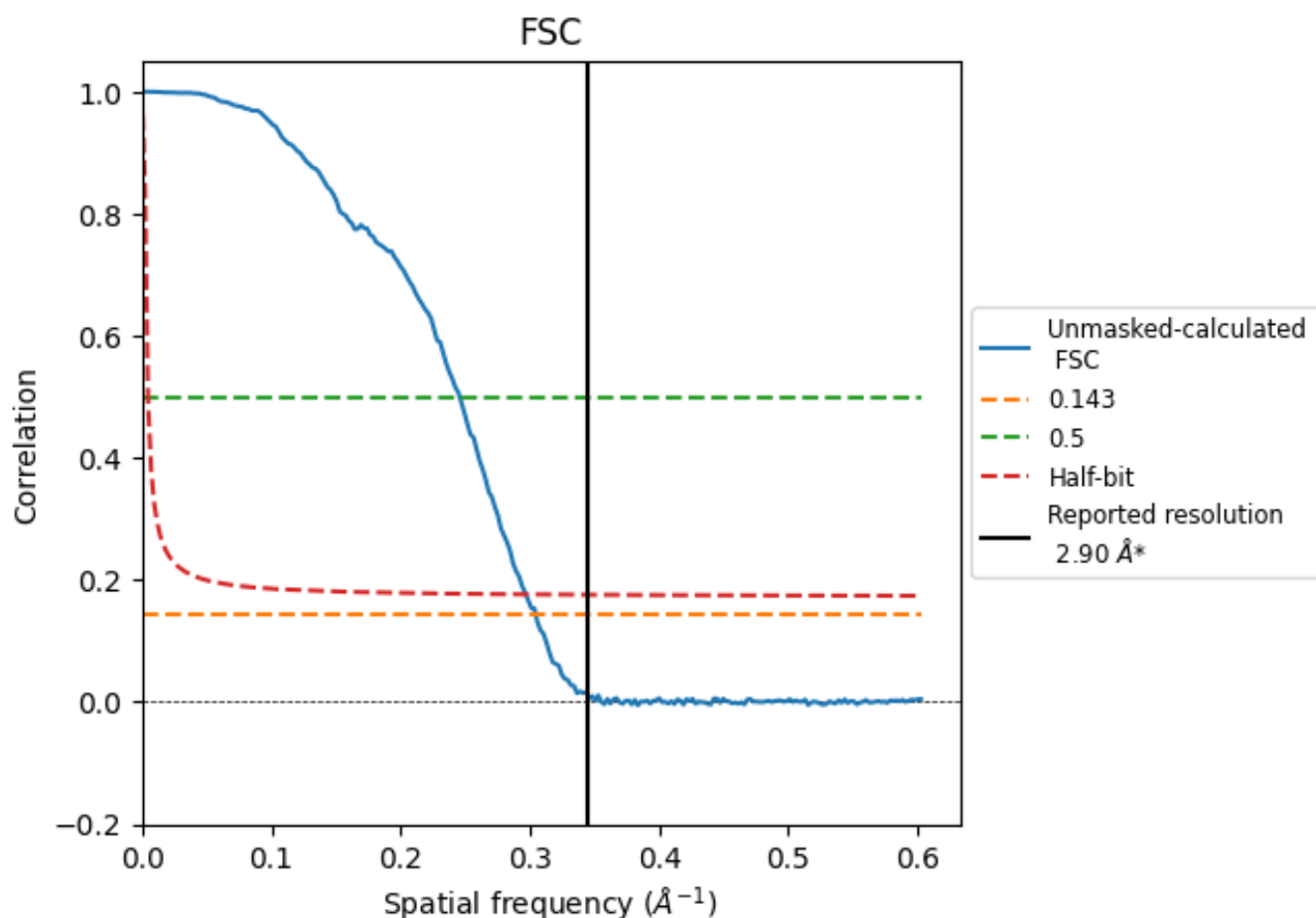


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

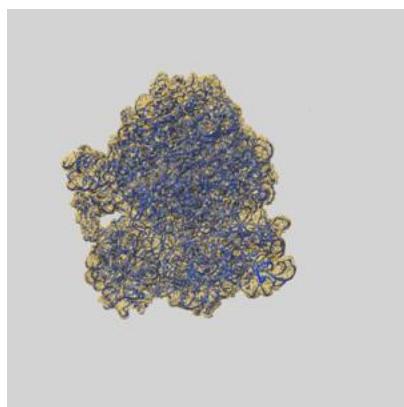
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.28	4.07	3.37

*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 3.28 differs from the reported value 2.9 by more than 10 %

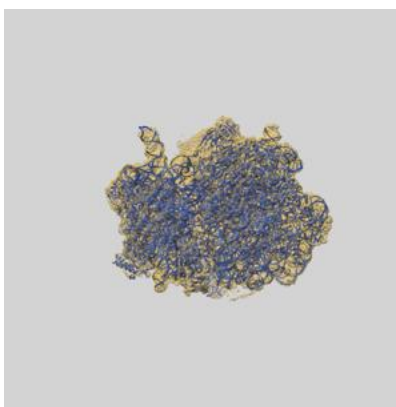
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40882 and PDB model 8SYL. Per-residue inclusion information can be found in section [3](#) on page [16](#).

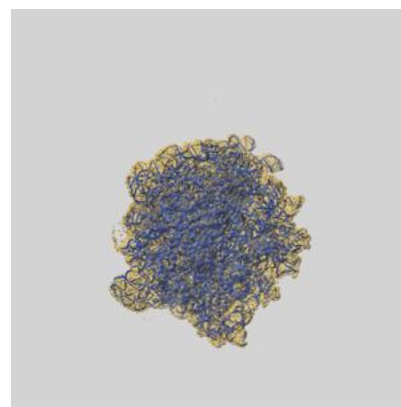
9.1 Map-model overlay [i](#)



X



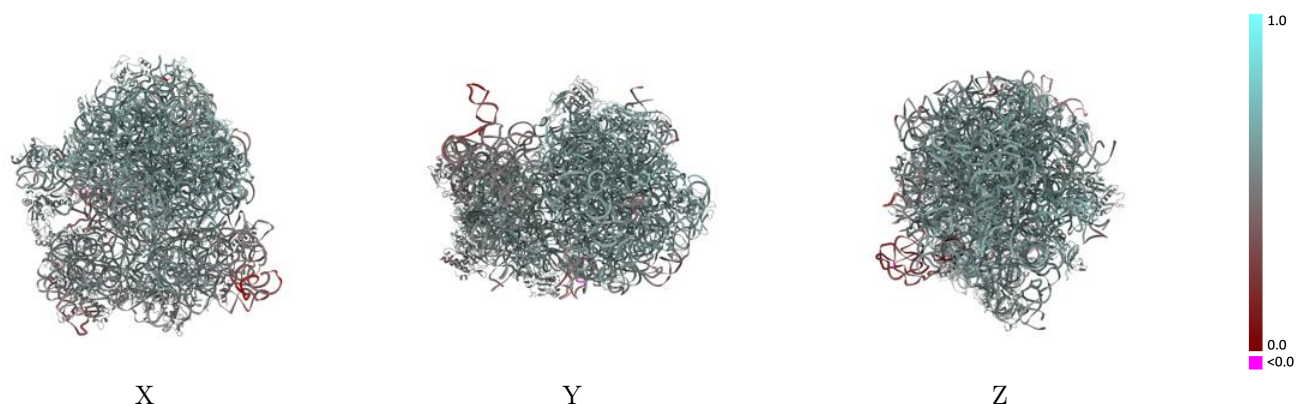
Y



Z

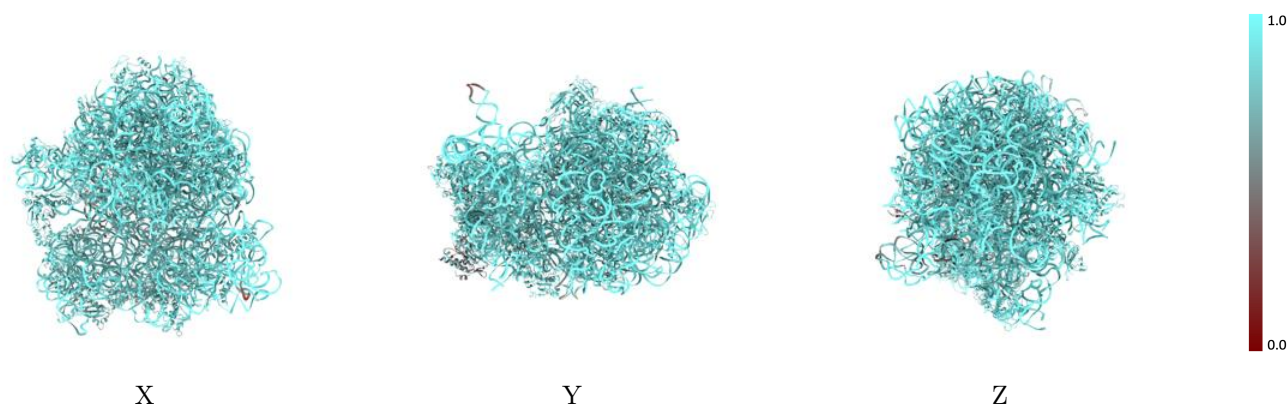
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



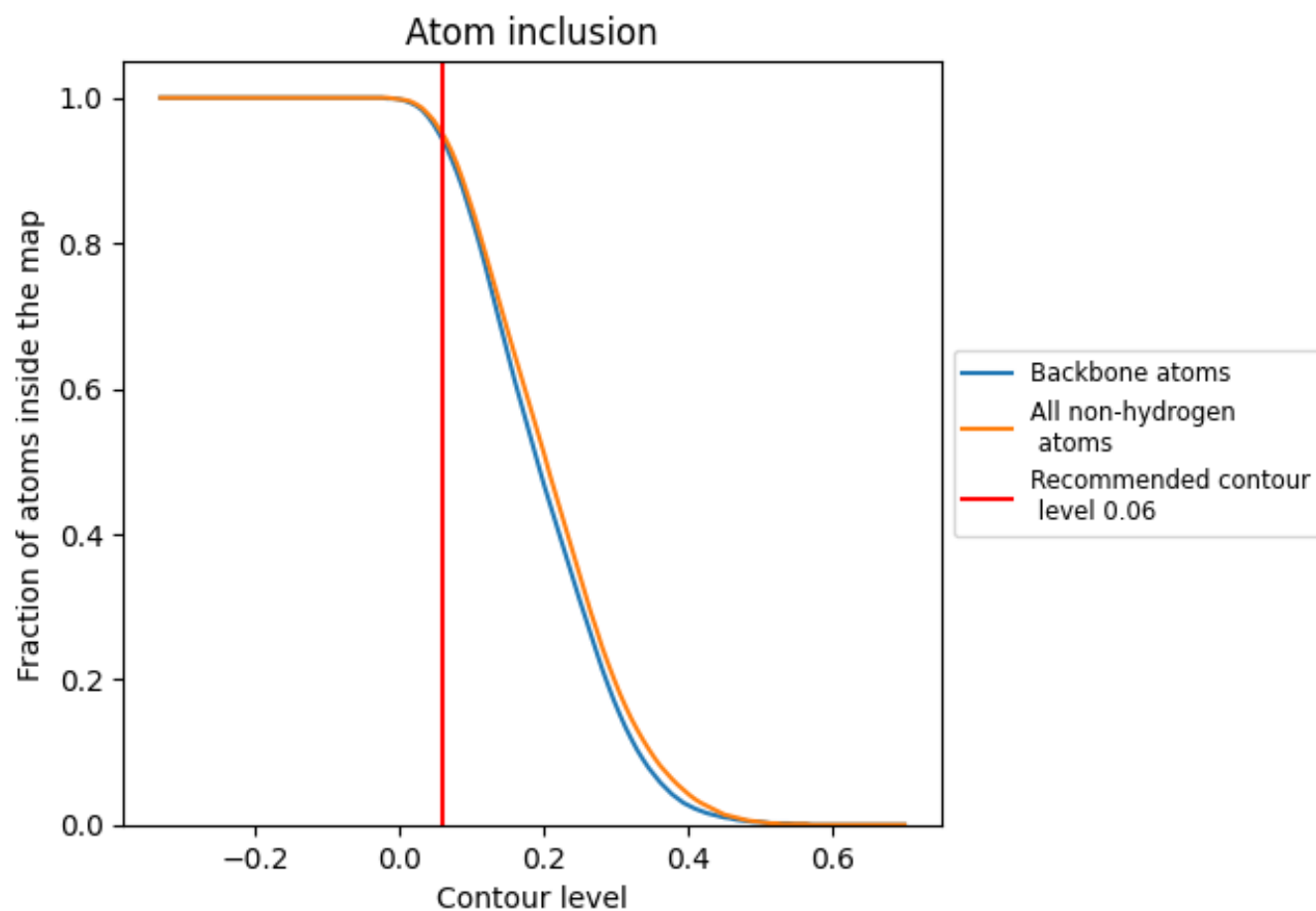
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9500	 0.5440
1	 0.9380	 0.5210
2	 0.9450	 0.5780
3	 0.8250	 0.4950
4	 0.9620	 0.5920
5	 0.8730	 0.5670
6	 0.9610	 0.6030
7	 0.9630	 0.6060
8	 0.9420	 0.5770
A	 0.9850	 0.5650
B	 0.9890	 0.5450
C	 0.9520	 0.5930
D	 0.9570	 0.5890
E	 0.9460	 0.5760
F	 0.8870	 0.5130
G	 0.9170	 0.5230
H	 0.5530	 0.5060
L	 0.9540	 0.5890
M	 0.9380	 0.5900
N	 0.9530	 0.5790
O	 0.9440	 0.5880
P	 0.9780	 0.5990
Q	 0.9540	 0.5430
R	 0.9230	 0.5840
S	 0.9780	 0.5990
T	 0.9520	 0.5820
U	 0.9510	 0.5910
V	 0.9150	 0.5580
W	 0.9430	 0.5520
X	 0.9240	 0.5600
Y	 0.9210	 0.5870
Z	 0.9580	 0.5880
a	 0.9780	 0.5190
b	 0.5300	 0.4590
c	 0.8340	 0.5230



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
d	 0.8450	 0.4770
e	 0.9170	 0.5530
f	 0.8910	 0.5000
g	 0.9020	 0.5020
h	 0.9050	 0.5360
i	 0.9070	 0.5050
j	 0.8500	 0.5110
k	 0.8940	 0.5350
l	 0.9210	 0.5660
m	 0.9100	 0.5190
n	 0.8630	 0.5180
o	 0.9130	 0.5340
p	 0.9200	 0.5050
q	 0.8980	 0.5270
r	 0.9030	 0.5300
s	 0.8790	 0.5050
t	 0.8990	 0.5000
u	 0.7310	 0.5210
v	 0.9610	 0.5640
w	 0.8730	 0.4950
x	 0.9410	 0.5370
y	 0.5170	 0.2430