



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2026 – 04:35 AM EDT

PDB ID : 8SYL / pdb_00008syl
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:

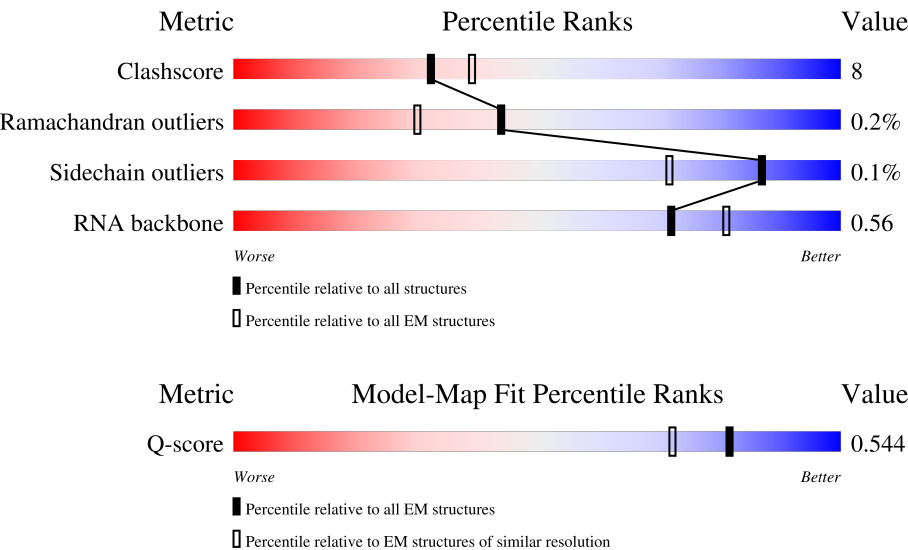
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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.



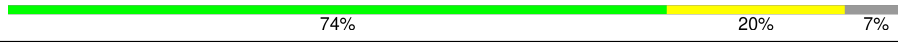
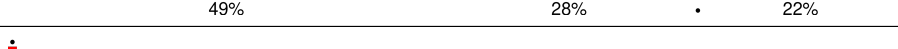
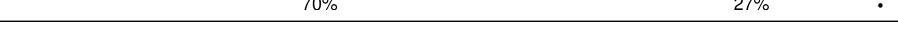
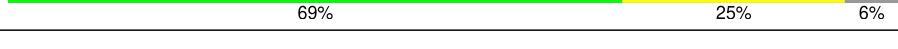
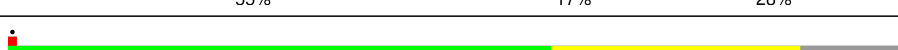
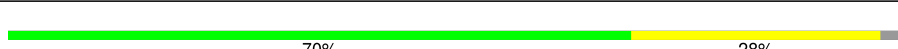
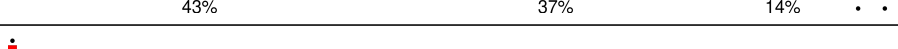
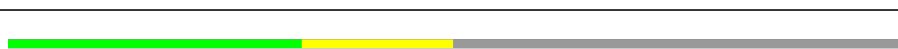
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	54% 41% . .
2	b	241	29% 76% 17% 7%
3	c	233	61% 27% 12%

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

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Mol	Chain	Length	Quality of chain
28	D	209	
29	E	201	
30	F	179	
31	G	177	
32	H	149	
33	L	142	
34	M	123	
35	N	144	
36	O	136	
37	P	127	
38	Q	117	
39	R	115	
40	S	118	
41	T	103	
42	U	110	
43	V	100	
44	W	104	
45	X	94	
46	Y	85	
47	Z	78	
48	1	63	
49	2	59	
50	3	70	
51	4	57	
52	5	55	

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Mol	Chain	Length	Quality of chain
53	6	46	83% 17%
54	7	65	85% 14%
55	8	38	82% 18%

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		

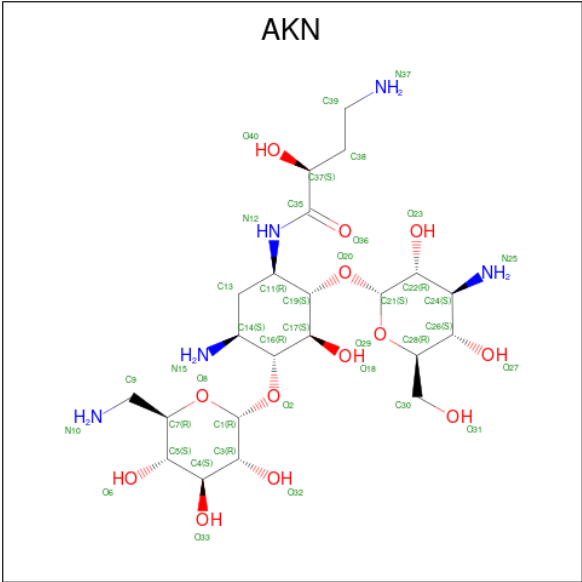
- Molecule 55 is a protein called 50S ribosomal protein L36.

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 (CCD ID: MG) (formula: Mg).

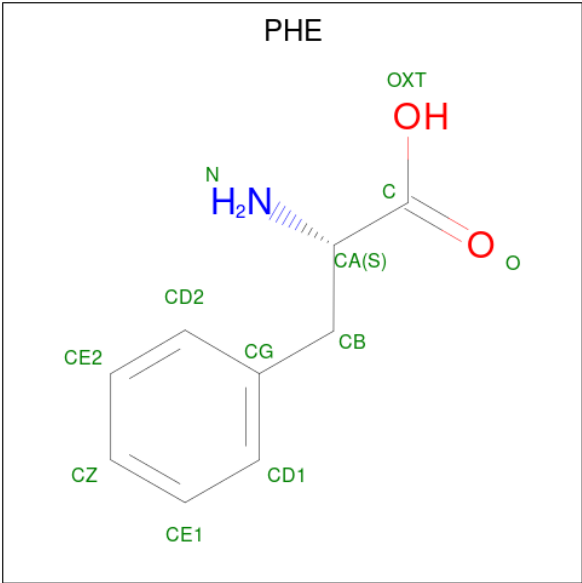
Mol	Chain	Residues	Atoms		AltConf
56	a	98	Total	Mg	0
			98	98	
56	x	3	Total	Mg	0
			3	3	
56	v	1	Total	Mg	0
			1	1	
56	A	359	Total	Mg	0
			359	359	
56	B	6	Total	Mg	0
			6	6	
56	C	1	Total	Mg	0
			1	1	
56	D	1	Total	Mg	0
			1	1	
56	P	1	Total	Mg	0
			1	1	
56	S	1	Total	Mg	0
			1	1	
56	X	1	Total	Mg	0
			1	1	
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 (CCD ID: AKN) (formula: C₂₂H₄₃N₅O₁₃).



Mol	Chain	Residues	Atoms				AltConf
57	a	1	Total	C	N	O	0
			40	22	5	13	
57	A	1	Total	C	N	O	0
			40	22	5	13	

- Molecule 58 is PHENYLALANINE (CCD ID: PHE) (formula: C₉H₁₁NO₂).



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

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

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

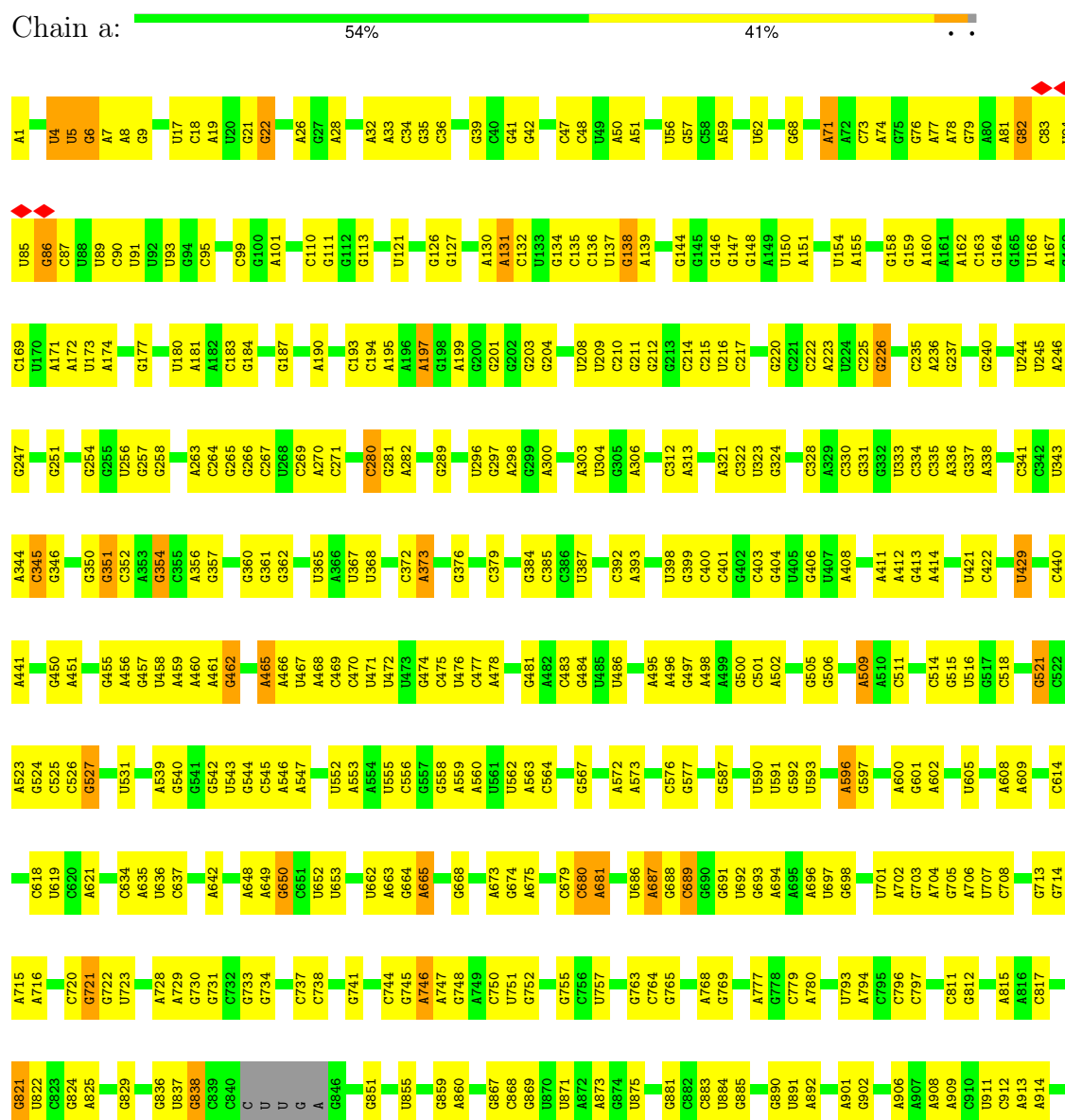
- Molecule 60 is water.

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.

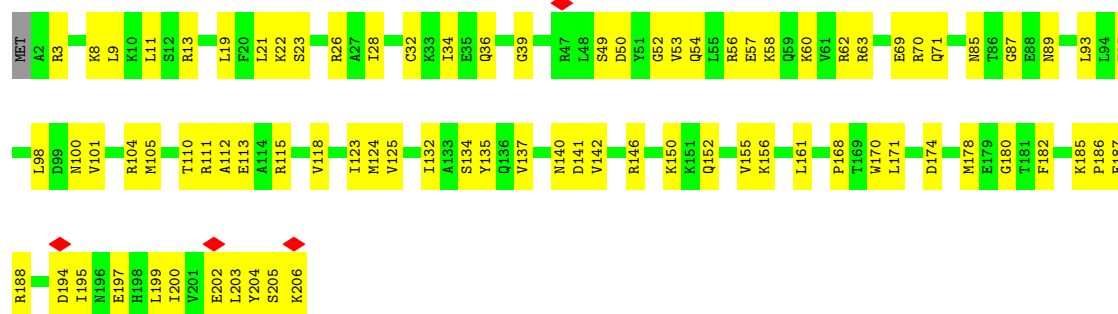
• Molecule 1: 16S Ribosomal RNA





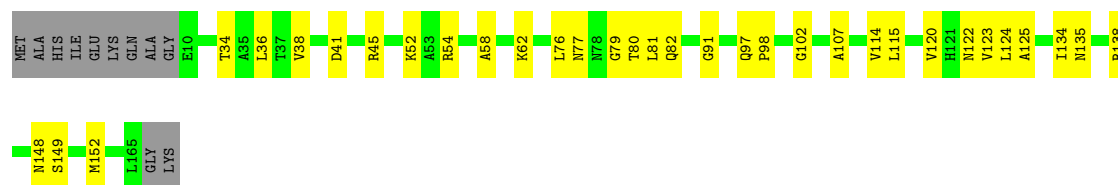
- Molecule 4: 30S ribosomal protein S4

Chain d:



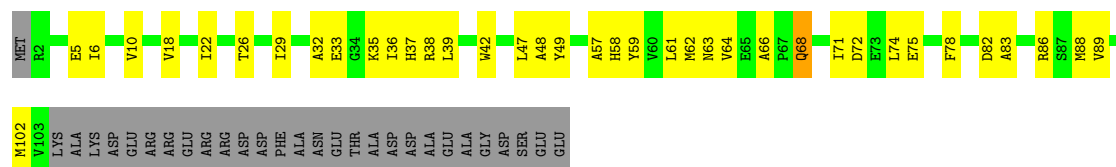
- Molecule 5: 30S ribosomal protein S5

Chain e:



- Molecule 6: 30S ribosomal protein S6

Chain f:



- Molecule 7: 30S ribosomal protein S7

Chain g:



- Molecule 8: 30S ribosomal protein S8

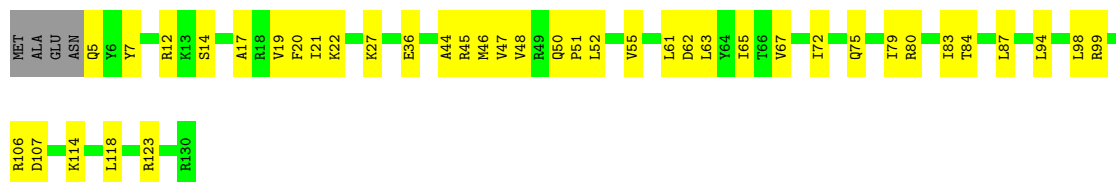
Chain h:





• Molecule 9: 30S ribosomal protein S9

Chain i: 66% 31%



• Molecule 10: 30S ribosomal protein S10

Chain j: 81% 14% 6%



• Molecule 11: 30S ribosomal protein S11

Chain k: 63% 27% 9%



• Molecule 12: 30S ribosomal protein S12

Chain l: 70% 27%



• Molecule 13: 30S ribosomal protein S13

Chain m: 78% 18%



• Molecule 14: 30S ribosomal protein S14



- | MET |
|-----|
| S2 |
| L3 |
| A7 |
| T11 |
| V12 |
| T22 |
| V29 |
| A30 |
| T33 |
| A34 |
| Q35 |
| T36 |
| L39 |
| Q40 |
| E45 |
| H46 |
| K47 |
| K48 |
| R53 |
| L56 |
| L57 |
| R58 |
| Q62 |
| R63 |
| L67 |
| D74 |
| R77 |
| L81 |
| L85 |
| R88 |
| R89 |

- | | | |
|----|----|-----|
| M1 | I4 | K12 | Q18 | V19 | V20 | A22 | R25 | I33 | E34 | R35 | R51 | L52 | W60 | I67 | R70 | I75 | V78 | N79 | X80 | A1A | A1A |
|----|----|-----|

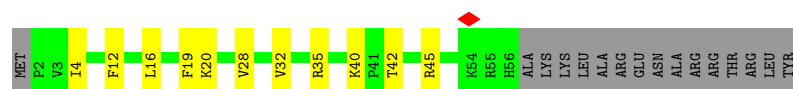
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|-----|-----|-----|----|----|----|----|----|----|-----|
| ME7 | THR | ASP | K4 | K5 | R6 | T7 | L8 | Q9 | G10 | R11 | V12 | V13 | K19 | S20 | I21 | V22 | I25 | F26 | R27 | F28 | F37 | T41 | V46 | E60 | F66 | K71 | S72 | W73 | V76 | R77 | A82 | VAL | F11 |
|-----|-----|-----|----|----|----|----|----|----|-----|

- | |
|-----|
| Met | ALA | ARG | TYR | PHE | ARG | ARG | ARG | LYS | PHE | CYS | ARG | PHE | THR | ALA | GLU | GLY | VAL | GLN | GLU | I21 | Y22 | D23 | K24 | D25 | I26 | Y32 | P41 | K50 | R53 | Q54 | L55 | Y64 | L65 | S66 | L67 | L68 | H74 | GLN |
|-----|

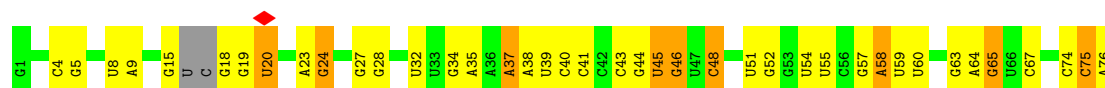
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|-----|----|-----|
| MET | P2 | F10 | H14 | H15 | L16 | K17 | K18 | V19 | E20 | D27 | P30 | L31 | R32 | R36 | R37 | S38 | T39 | M44 | L47 | T48 | T49 | A50 | R55 | S56 | H57 | E65 | K70 | L71 | G72 | R78 | T79 | H83 | ALA | ALA | ASP | LYS | LYS | ALA | LYS |
|-----|----|-----|

- | | | | | | | |
|-----|----|----|----|----|----|-----|
| ME1 | A2 | N3 | I4 | K5 | S6 | R10 | A17 | N21 | R24 | M27 | M28 | R29 | T30 | F31 | I32 | K33 | K34 | V35 | I39 | ME4 | D59 | R60 | K64 | H68 | K69 | N70 | K76 | Q82 | L86 | A18 |
|-----|----|----|----|----|----|-----|

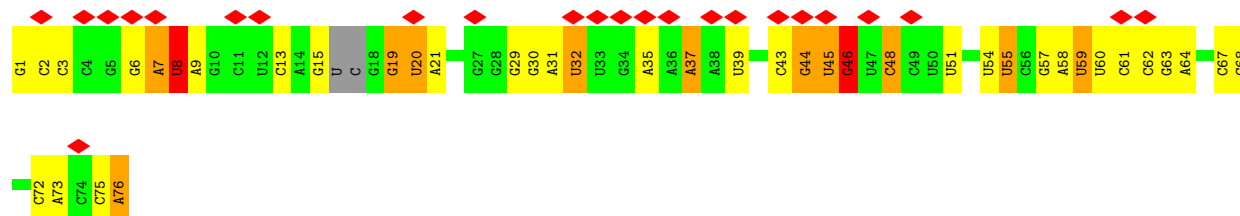
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- Molecule 22: phenylalanine tRNA



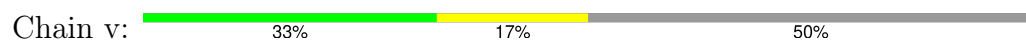
- Molecule 22: phenylalanine tRNA



- Molecule 23: P-site initiator tRNA



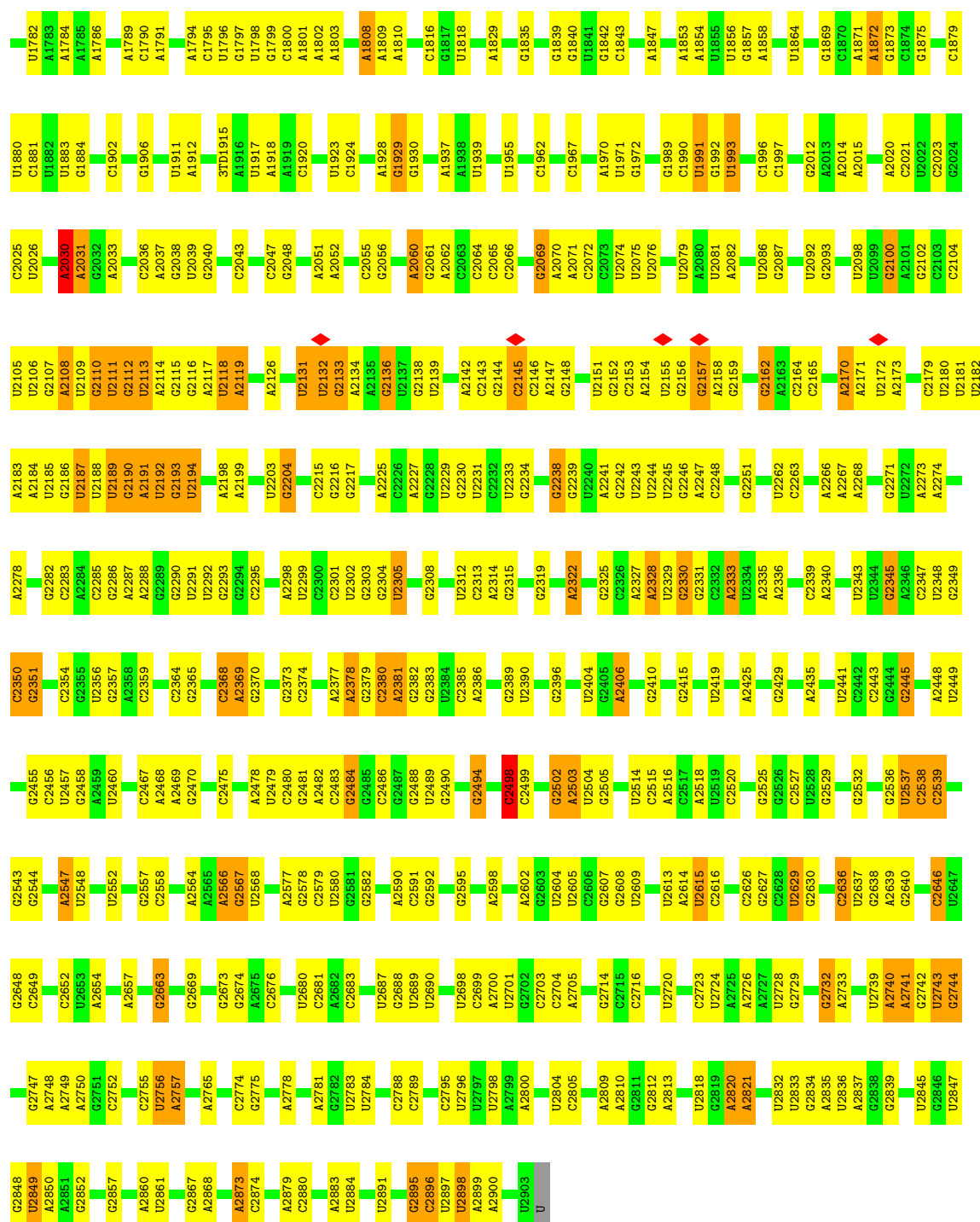
- Molecule 24: M-F-Stop mRNA



- Molecule 25: 23S Ribosomal RNA



G1667	A1549	G1462	A1353	G1239	G1125	C961	U870	A781	G659	C581	A472	A330	A219
A1668	U1563	A1453	A1354	U1240	A1126	C964	U871	A782	U667	A582	C476	A340	A222
A1669	C1564	U1460	G1360	G1248	A1127	G974	C873	A783	A668	C584	G476	A341	A223
A1672	A1565	G1469	G1361	U1249	U1130	G973	G874	G785	G871	G585	A479	C353	U224
G1673	A1566	G1470	C1362	G1250	G1131	G974	G875	G786	C672	A586	A480	A354	C225
G1674	G1567	A1470	C1363	G1251	U1132	G978	C876	A788	A675	C587	G481	U355	A226
C1675	G1568	G1475	G1364	G1252	A1133	G978	A877	A789	A676	U588	A481	G356	A227
A1676	A1569	U1476	A1365	A1253	A1134	G983	G880	C791	A677	U589	G491	G359	C228
A1677	A1570	G1478	A1378	U1254	C1135	A984	G881	A792	A678	U590	A492	U360	A233
A1678	A1571	U1479	U1379	U1255	U1141	A984	G882	A793	G682	U591	A493	G361	U234
A1679	A1572	G1482	U1379	G1256	A1142	C987	G883	G805	U686	A592	G494	A362	A244
G1681	U1573	G1483	A1383	U1263	G1149	A988	C888	G806	C687	U593	U499	G363	A244
G1682	U1578	U1484	A1384	A1264	C1150	G989	C889	U807	G697	C595	U499	G363	A244
U1682	A1579	U1485	A1385	G1265	U1150	C996	C890	G808	G698	U596	U499	G363	A244
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G1703	C1585	U1489	A1389	U1273	A1169	C999	C894	C814	G704	A603	C509	A374	A251
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G1587	G1587	U1491	A1391	A1275	G1171	A1002	C896	A819	U709	A609	G513	C383	C269
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G1710	A1591	U1493	A1393	U1277	U	G1004	C898	A821	G711	A614	A515	A386	G271
G1715	U1592	U1494	A1394	U1278	A	C1005	C899	A822	G712	A615	A516	A387	A272
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A1717	A1594	U1496	A1396	U1280	A	C1007	C901	A824	G714	A617	A518	A389	A274
U1721	A1595	U1497	U1397	G1281	G1177	A1008	C902	A825	U715	A618	A519	A390	C275
U1729	A1596	U1498	A1398	U1282	C1178	A1009	C903	A826	G716	A619	A520	A391	G276
C1730	A1600	U1499	A1399	U1283	U1179	A1010	C904	A827	G717	A620	A521	A392	U277
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G1734	A1602	U1501	A1401	U1285	U1181	C1012	C906	A829	G719	A622	A523	A394	A279
A1735	A1603	U1502	A1402	U1286	G1182	C1013	C907	A830	G720	A623	A524	A395	U280
G1738	A1604	U1503	A1403	U1287	U1183	A1014	C908	A831	G721	A624	A525	A396	C281
U1742	A1605	U1504	A1404	U1288	U1184	G1015	C909	A832	G722	A625	A526	A397	U282
G1743	A1606	U1505	A1405	U1289	U1185	A1016	C910	A833	G723	A626	A527	A398	U283
A1746	A1607	U1506	A1406	U1290	U1186	G1017	C911	A834	G724	A627	A528	A399	G291
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A1754	A1611	U1510	A1410	U1294	U1190	A1021	C915	A838	G728	A631	A532	A403	U287
C1764	A1612	U1511	A1411	U1295	U1191	A1022	C916	A839	G729	A632	A533	A404	U288
C1771	A1613	U1512	A1412	U1296	G1197	A1023	C917	A840	G730	A633	A534	A405	G292
A1772	A1614	U1513	A1413	U1297	U1198	A1024	C918	A841	A731	A634	A535	A406	U289
A1773	A1615	U1514	A1414	U1298	U1199	A1025	C919	A842	A732	A635	A536	A407	U290
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	A1619	U1518	A1418	U1302	U1203	A1029	C923	A846	A736	A639	A540	A411	G294
	A1620	U1519	A1419	U1303	U1204	A1030	C924	A847	A737	A640	A541	A412	G295
	A1621	U1520	A1420	U1304	U1205	A1031	C925	A848	A738	A641	A542	A413	U296
	A1622	U1521	A1421	U1305	U1206	A1032	C926	A849	A739	A642	A543	A414	U297
	A1623	U1522	A1422	U1306	U1207	A1033	C927	A850	A740	A643	A544	A415	U298
	A1624	U1523	A1423	U1307	U1208	A1034	C928	A851	A741	A644	A545	A416	G299
	A1625	U1524	A1424	U1308	U1209	A1035	C929	A852	A742	A645	A546	A417	A300
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	A1629	U1528	A1428	U1312	U1213	A1039	C933	A856	A746	A649	A550	A421	U306
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	A1634	U1533	A1433	U1317	U1218	A1044	C938	A861	A751	A654	A555	A426	A314
	A1635	U1534	A1434	U1318	U1219	A1045	C939	A862	A752	A655	A556	A427	A315
	A1636	U1535	A1435	U1319	U1220	A1046	C940	A863	A753	A656	A557	A428	A316
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	A1639	U1538	A1438	U1322	U1223	A1049	C943	A866	A756	A659	A560	A431	A319
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	A1641	U1540	A1440	U1324	U1225	A1051	C945	A868	A758	A661	A562	A433	A321
	A1642	U1541	A1441	U1325	U1226	A1052	C946	A869	A759	A662	A563	A434	A322
	A1643	U1542	A1442	U1326	U1227	A1053	C947	A870	A760	A663	A564	A435	A323
	A1644	U1543	A1443	U1327	U1228	A1054	C948	A871	A761	A664	A565	A436	A324
	A1645	U1544	A1444	U1328	U1229	A1055	C949	A872	A762	A665	A566	A437	A325
	A1646	U1545	A1445	U1329	U1230	A1056	C950	A873	A763	A666	A567	A438	A326
	A1647	U1546	A1446	U1330	U1231	A1057	C951	A874	A764	A667	A568	A439	A327
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	A1649	U1548	A1448	U1332	U1233	A1059	C953	A876	A766	A669	A570	A441	A329
	A1650	U1549	A1449	U1333	U1234	A1060	C954	A877	A767	A670	A571	A442	A330
	A1651	U1550	A1450	U1334	U1235	A1061	C955	A878	A768	A671	A572	A443	A331
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	A1654	U1553	A1453	U1337	U1238	A1064	C958	A881	A771	A674	A575	A446	A334
	A1655	U1554	A1454	U1338	U1239	A1065	C959	A882	A772	A675	A576	A447	A335
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	A1657	U1556	A1456	U1340	U1241	A1067	C961	A884	A774	A677	A578	A449	A337
	A1658	U1557	A1457	U1341	U1242	A1068	C962	A885	A775	A678	A579	A450	A338
	A1659	U1558	A1458	U1342	U1243	A1069	C963	A886	A776	A679	A580	A451	A339
	A1660	U1559	A1459	U1343	U1244	A1070	C964	A887	A777	A680	A581	A452	A340
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	A1662	U1561	A1461	U1345	U1246	A1072	C966	A889	A779	A682	A583	A454	A342
	A1663	U1562	A1462	U1346	U1247	A1073	C967	A890	A780	A683	A584	A455	A343
	A1664	U1563	A1463	U1347	U1248	A1074	C968	A891	A781	A684	A585	A456	A344
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	A1666	U1565	A1465	U1349	U1250	A1076	C970	A893	A783	A686	A587	A458	A346
	A1667	U1566	A1466	U1350	U1251	A1077	C971	A894	A784	A687	A588	A459	A347
	A1668	U1567	A1467	U1351	U1252	A1078	C972	A895	A785	A688	A589	A460	A348
	A1669	U1568	A1468	U1352	U1253	A1079	C973	A896	A786	A689	A590	A461	A349
	A1670	U1569	A1469	U1353	U1254	A1080	C974	A897	A787	A690	A591	A462	A350
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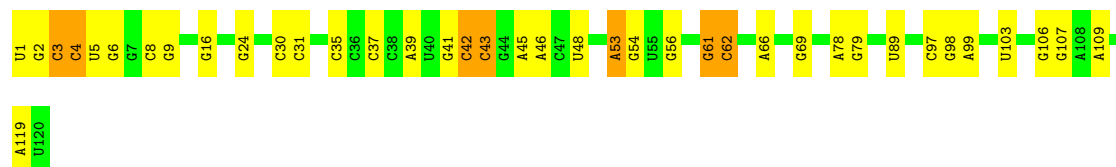


Chain B:

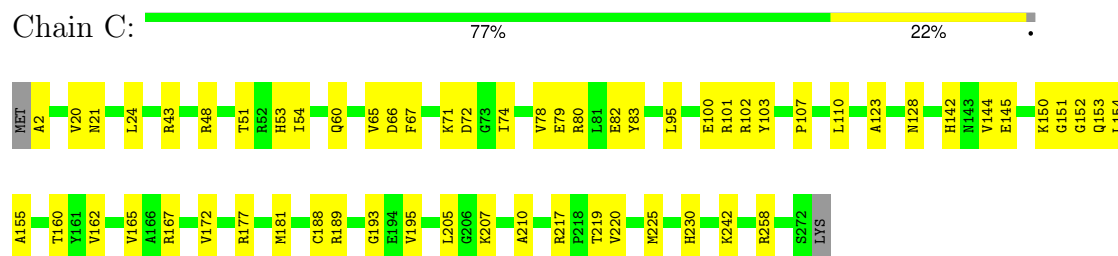
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27%

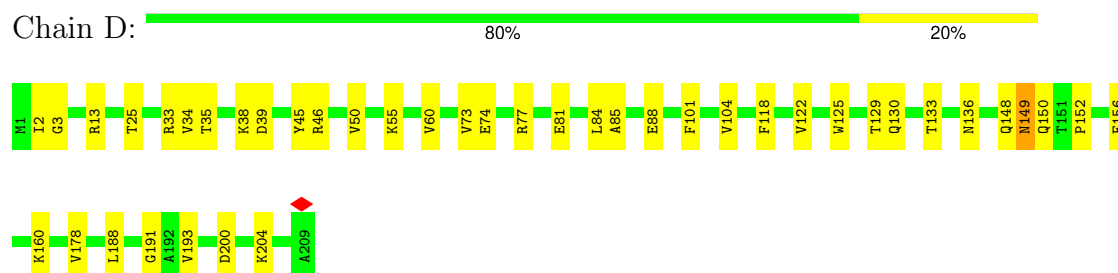
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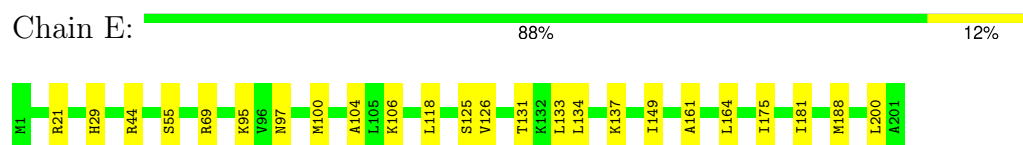
- Molecule 27: 50S ribosomal protein L2



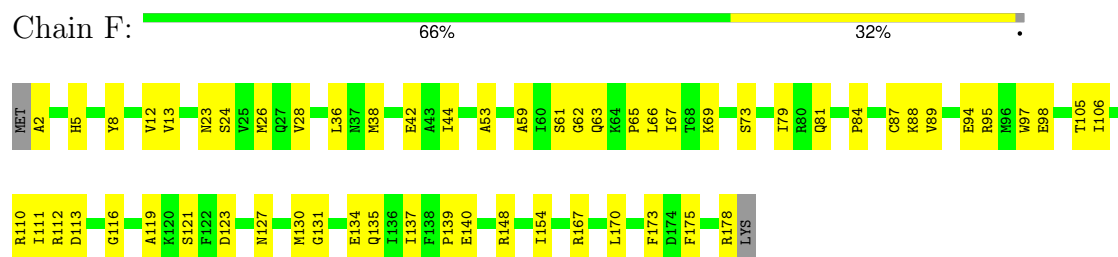
- Molecule 28: 50S ribosomal protein L3



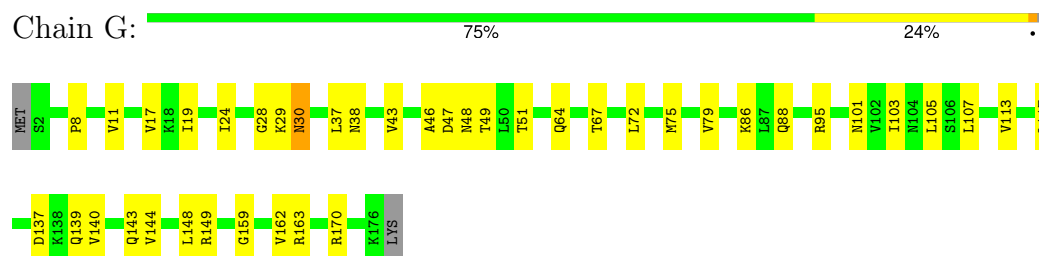
- Molecule 29: 50S ribosomal protein L4



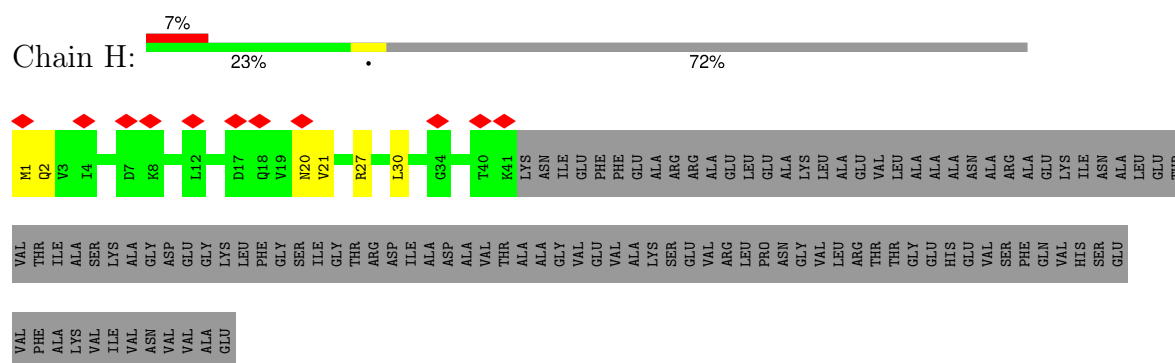
- Molecule 30: 50S ribosomal protein L5



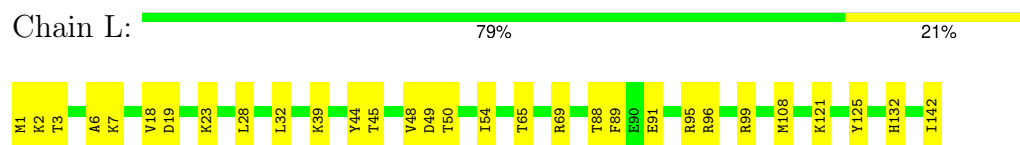
- Molecule 31: 50S ribosomal protein L6



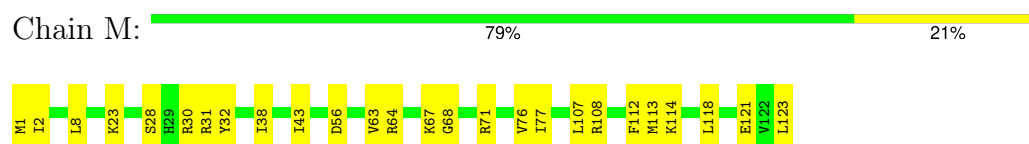
- Molecule 32: 50S ribosomal protein L9



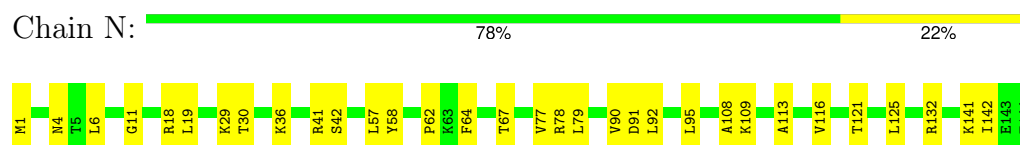
- Molecule 33: 50S ribosomal protein L13



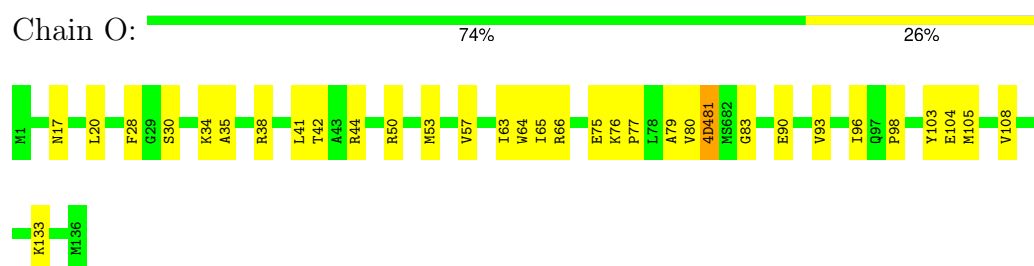
- Molecule 34: 50S ribosomal protein L14



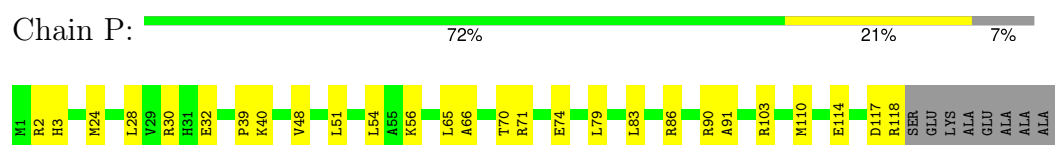
- Molecule 35: 50S ribosomal protein L15



- Molecule 36: 50S ribosomal protein L16



- Molecule 37: 50S ribosomal protein L17



- Molecule 38: 50S ribosomal protein L18

Chain Q:  74% 26%



- Molecule 39: 50S ribosomal protein L19

Chain R:  83% 17%



- Molecule 40: 50S ribosomal protein L20

Chain S:  83% 16%



- Molecule 41: Ribosomal protein L21

Chain T:  89% 11%



- Molecule 42: 50S ribosomal protein L22

Chain U:  79% 21%



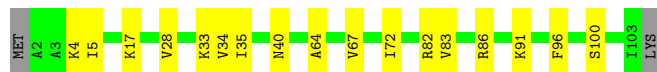
- Molecule 43: 50S ribosomal protein L23

Chain V:  77% 16% 7%



- Molecule 44: 50S ribosomal protein L24

Chain W:  82% 16%



- Molecule 45: 50S ribosomal protein L25

Chain X:  71% 29%



- Molecule 46: 50S ribosomal protein L27

Chain Y:  84% 14%



- Molecule 47: 50S ribosomal protein L28

Chain Z:  79% 19%



- Molecule 48: 50S ribosomal protein L29

Chain 1:  70% 27%



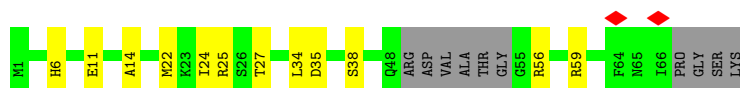
- Molecule 49: 50S ribosomal protein L30

Chain 2:  78% 20%



- Molecule 50: 50S ribosomal protein L31

Chain 3:  69% 17% 14%



- Molecule 51: 50S ribosomal protein L32

Chain 4:  70% 26%



- Molecule 52: 50S ribosomal protein L33

Chain 5:  76% 16% 7%



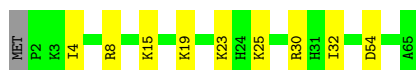
- Molecule 53: 50S ribosomal protein L34

Chain 6:  83% 17%



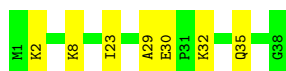
- Molecule 54: 50S ribosomal protein L35

Chain 7:  85% 14%



- Molecule 55: 50S ribosomal protein L36

Chain 8:  82% 18%



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: MIA, 3TD, 5MU, 6MZ, OMC, 4OC, ZN, IAS, MS6, 4D4, AKN, G7M, OMG, 5MC, 4SU, MG, D2T, 2MA, H2U, 2MG, 7MG, MA6, MEQ, 1MG, OMU, UR3, PSU

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	0.17	0/36450	0.26	0/56856
2	b	0.13	0/1542	0.32	0/2108
3	c	0.17	0/1640	0.34	0/2211
4	d	0.18	0/1665	0.40	0/2227
5	e	0.19	0/1130	0.35	0/1527
6	f	0.16	0/796	0.43	0/1086
7	g	0.15	0/1068	0.32	0/1452
8	h	0.17	0/979	0.33	0/1314
9	i	0.15	0/949	0.37	0/1276
10	j	0.14	0/682	0.31	0/933
11	k	0.34	0/867	0.50	0/1171
12	l	0.18	0/927	0.33	0/1249
13	m	0.12	0/831	0.28	0/1118
14	n	0.15	0/804	0.31	0/1072
15	o	0.18	0/711	0.32	0/952
16	p	0.15	0/623	0.33	0/842
17	q	0.17	0/639	0.39	0/859
18	r	0.15	0/447	0.26	0/601
19	s	0.14	0/658	0.33	0/889
20	t	0.19	0/654	0.36	0/871
21	u	0.12	0/380	0.37	0/518
22	w	0.24	0/1605	0.40	1/2494 (0.0%)
22	y	0.15	0/1606	0.24	0/2497
23	x	0.19	0/1725	0.24	0/2689
24	v	0.18	0/285	0.18	0/441
25	A	0.23	0/67852	0.28	0/105848
26	B	0.19	0/2876	0.28	0/4483
27	C	0.23	0/2108	0.32	0/2837
28	D	0.22	0/1569	0.32	0/2111
29	E	0.19	0/1557	0.28	0/2095
30	F	0.17	0/1425	0.32	0/1915

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	G	0.16	0/1319	0.37	1/1789 (0.1%)
32	H	0.10	0/306	0.29	0/413
33	L	0.21	0/1152	0.28	0/1551
34	M	0.21	0/955	0.29	0/1279
35	N	0.21	0/1057	0.32	0/1407
36	O	0.21	0/1073	0.29	0/1433
37	P	0.22	0/958	0.35	0/1281
38	Q	0.16	0/886	0.35	0/1192
39	R	0.20	0/925	0.27	0/1238
40	S	0.23	0/960	0.28	0/1278
41	T	0.21	0/829	0.31	0/1107
42	U	0.21	0/857	0.27	0/1149
43	V	0.17	0/744	0.27	0/994
44	W	0.18	0/777	0.33	0/1038
45	X	0.18	0/763	0.35	0/1022
46	Y	0.19	0/642	0.31	0/848
47	Z	0.20	0/635	0.24	0/848
48	1	0.17	0/496	0.31	0/660
49	2	0.21	0/453	0.26	0/605
50	3	0.10	0/475	0.22	0/633
51	4	0.21	0/440	0.28	0/588
52	5	0.16	0/424	0.27	0/565
53	6	0.22	0/380	0.29	0/498
54	7	0.20	0/513	0.31	0/676
55	8	0.22	0/303	0.31	0/397
All	All	0.20	0/155372	0.29	2/233031 (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

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	w	75	C	OP1-P-O3'	13.05	147.14	108.00
31	G	30	ASN	N-CA-C	-6.15	106.75	114.56

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 ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32803	0	16528	474	0
2	b	1514	0	1322	27	0
3	c	1613	0	1686	43	0
4	d	1643	0	1707	73	0
5	e	1117	0	1132	23	0
6	f	778	0	731	26	0
7	g	1054	0	979	14	0
8	h	969	0	1014	22	0
9	i	937	0	921	35	0
10	j	673	0	628	12	0
11	k	860	0	854	28	0
12	l	924	0	955	23	0
13	m	823	0	838	15	0
14	n	792	0	817	21	0
15	o	703	0	719	19	0
16	p	613	0	608	21	0
17	q	630	0	657	17	0
18	r	441	0	467	13	0
19	s	641	0	648	20	0
20	t	648	0	677	20	0
21	u	373	0	339	11	0
22	w	1591	0	818	25	0
22	y	1585	0	804	26	0
23	x	1625	0	829	14	0
24	v	255	0	129	1	0
25	A	61097	0	30754	680	0
26	B	2572	0	1301	34	0
27	C	2069	0	2129	41	0
28	D	1559	0	1607	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	E	1538	0	1598	18	0
30	F	1401	0	1429	47	0
31	G	1299	0	1332	31	0
32	H	303	0	327	3	0
33	L	1129	0	1162	21	0
34	M	946	0	1023	18	0
35	N	1048	0	1123	27	0
36	O	1075	0	1146	25	0
37	P	945	0	989	19	0
38	Q	876	0	886	21	0
39	R	913	0	958	19	0
40	S	947	0	1019	18	0
41	T	816	0	839	9	0
42	U	850	0	911	15	0
43	V	738	0	807	10	0
44	W	769	0	812	14	0
45	X	750	0	773	20	0
46	Y	634	0	653	10	0
47	Z	625	0	652	12	0
48	1	495	0	526	15	0
49	2	449	0	488	11	0
50	3	468	0	460	11	0
51	4	434	0	445	12	0
52	5	417	0	451	7	0
53	6	377	0	418	8	0
54	7	504	0	572	8	0
55	8	302	0	340	7	0
56	4	1	0	0	0	0
56	A	359	0	0	0	0
56	B	6	0	0	0	0
56	C	1	0	0	0	0
56	D	1	0	0	0	0
56	P	1	0	0	0	0
56	S	1	0	0	0	0
56	X	1	0	0	0	0
56	Y	1	0	0	0	0
56	a	98	0	0	0	0
56	v	1	0	0	0	0
56	x	3	0	0	0	0
57	A	40	0	43	0	0
57	a	40	0	43	1	0
58	w	11	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	3	1	0	0	0	0
59	8	1	0	0	0	0
60	A	60	0	0	1	0
60	N	1	0	0	0	0
60	a	11	0	0	0	0
60	n	1	0	0	0	0
60	x	1	0	0	0	0
All	All	144591	0	94831	1966	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 1966 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)
25:A:1047:G:HO2'	25:A:1110:G:H1	1.10	0.99
1:a:180:U:H3	1:a:195:A:H62	1.00	0.96
27:C:71:LYS:HD3	27:C:74:ILE:HD11	1.48	0.94
22:y:15:G:H22	22:y:48:C:H42	1.15	0.93
25:A:881:G:H1	25:A:895:U:H3	0.98	0.91

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	f	100/131 (76%)	83 (83%)	14 (14%)	3 (3%)	3	14
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%)	11	36
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%)	24	54
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	41
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	U	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
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%)	10	34
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%)	7	27
55	8	36/38 (95%)	36 (100%)	0	0	100	100
All	All	5445/5886 (92%)	5219 (96%)	217 (4%)	9 (0%)	44	72

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	d	172/173 (99%)	172 (100%)	0	100	100
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%)	87 (100%)	0	100	100
10	j	55/90 (61%)	55 (100%)	0	100	100
11	k	85/98 (87%)	82 (96%)	3 (4%)	32	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%)	74 (100%)	0	100	100
16	p	58/65 (89%)	58 (100%)	0	100	100
17	q	70/78 (90%)	70 (100%)	0	100	100
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%)	133 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	S	89/90 (99%)	89 (100%)	0	100	100
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%)	62 (100%)	0	100	100
47	Z	67/68 (98%)	67 (100%)	0	100	100
48	1	54/55 (98%)	54 (100%)	0	100	100
49	2	48/49 (98%)	48 (100%)	0	100	100
50	3	53/62 (86%)	53 (100%)	0	100	100
51	4	46/48 (96%)	46 (100%)	0	100	100
52	5	46/49 (94%)	46 (100%)	0	100	100
53	6	38/38 (100%)	38 (100%)	0	100	100
54	7	51/52 (98%)	51 (100%)	0	100	100
55	8	34/34 (100%)	34 (100%)	0	100	100
All	All	4271/4803 (89%)	4268 (100%)	3 (0%)	87	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	k	56	ARG
11	k	57	LYS
11	k	59	THR

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

Mol	Chain	Res	Type
33	L	131	ASN
41	T	89	HIS
34	M	89	ASN
38	Q	38	GLN
46	Y	57	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1526/1542 (98%)	207 (13%)	0
22	w	72/76 (94%)	12 (16%)	0
22	y	72/76 (94%)	17 (23%)	0
23	x	75/77 (97%)	8 (10%)	0
24	v	11/24 (45%)	3 (27%)	0
25	A	2842/2904 (97%)	399 (14%)	11 (0%)
26	B	119/120 (99%)	12 (10%)	3 (2%)
All	All	4717/4819 (97%)	658 (13%)	14 (0%)

5 of 658 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 ⓘ

58 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	PSU	a	516	1	18,21,22	1.37	2 (11%)	21,30,33	2.05	4 (19%)
25	PSU	A	746	25,56	18,21,22	1.40	3 (16%)	21,30,33	2.02	4 (19%)
1	UR3	a	1498	1	19,22,23	0.95	0	26,32,35	1.72	2 (7%)
25	5MC	A	1962	25	19,22,23	1.41	3 (15%)	26,32,35	1.09	2 (7%)
22	5MU	w	54	22	19,22,23	1.40	5 (26%)	27,32,35	1.94	5 (18%)
12	D2T	l	89	12	8,9,10	1.98	1 (12%)	6,11,13	2.56	2 (33%)
36	MS6	O	82	36	5,7,8	0.56	0	2,7,9	1.24	0
22	PSU	y	55	22	18,21,22	1.37	2 (11%)	21,30,33	2.04	3 (14%)
25	H2U	A	2449	25	18,21,22	1.11	3 (16%)	19,30,33	1.11	2 (10%)
1	MA6	a	1519	1	23,26,27	1.47	5 (21%)	33,38,41	2.43	13 (39%)
23	5MC	x	32	23	19,22,23	1.46	3 (15%)	26,32,35	1.23	3 (11%)
25	PSU	A	1911	25	18,21,22	1.40	3 (16%)	21,30,33	2.06	3 (14%)
25	PSU	A	2504	25	18,21,22	1.41	4 (22%)	21,30,33	2.04	3 (14%)
25	3TD	A	1915	25	19,22,23	4.22	7 (36%)	23,32,35	1.83	4 (17%)
25	PSU	A	2457	25	18,21,22	1.42	4 (22%)	21,30,33	2.10	5 (23%)
25	PSU	A	2604	25	18,21,22	1.41	3 (16%)	21,30,33	2.08	4 (19%)
1	2MG	a	966	1	23,26,27	1.29	4 (17%)	33,38,41	2.21	7 (21%)
22	PSU	y	39	22	18,21,22	1.36	2 (11%)	21,30,33	2.00	3 (14%)
25	1MG	A	745	25	23,26,27	1.17	3 (13%)	33,39,42	1.77	5 (15%)
28	MEQ	D	150	28	8,9,10	0.51	0	5,10,12	0.34	0
1	5MC	a	967	1	19,22,23	1.52	3 (15%)	26,32,35	1.11	2 (7%)
1	4OC	a	1402	1	20,23,24	0.75	0	25,32,35	0.95	1 (4%)
22	4SU	w	8	22	18,21,22	1.90	4 (22%)	25,30,33	2.10	4 (16%)
25	6MZ	A	1618	25	22,25,26	1.44	5 (22%)	29,36,39	2.21	10 (34%)
23	PSU	x	55	23	18,21,22	1.37	2 (11%)	21,30,33	2.06	4 (19%)
22	PSU	w	55	22	18,21,22	1.36	2 (11%)	21,30,33	2.02	3 (14%)
22	MIA	w	37	22	28,31,32	2.33	6 (21%)	38,44,47	2.83	14 (36%)
1	2MG	a	1516	1	23,26,27	1.23	4 (17%)	33,38,41	2.26	9 (27%)
23	4SU	x	8	23	18,21,22	1.86	4 (22%)	25,30,33	2.29	5 (20%)
25	2MG	A	1835	25	23,26,27	1.25	3 (13%)	33,38,41	2.27	9 (27%)
22	4SU	y	8	22	18,21,22	1.83	4 (22%)	25,30,33	2.34	5 (20%)
23	5MU	x	54	23	19,22,23	1.36	5 (26%)	27,32,35	2.13	6 (22%)
25	PSU	A	2605	25	18,21,22	1.40	3 (16%)	21,30,33	2.09	4 (19%)
25	PSU	A	2580	25	18,21,22	1.44	5 (27%)	21,30,33	2.17	4 (19%)
25	2MG	A	2445	25	23,26,27	1.27	3 (13%)	33,38,41	2.23	9 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	a	1407	1	19,22,23	1.47	3 (15%)	26,32,35	1.13	3 (11%)
25	OMC	A	2498	25,56	19,22,23	0.82	0	25,31,34	0.95	1 (4%)
22	MIA	y	37	22	21,24,32	1.56	4 (19%)	30,35,47	2.02	7 (23%)
25	2MA	A	2503	25,56	22,25,26	1.46	5 (22%)	32,37,40	2.28	9 (28%)
36	4D4	O	81	36	9,11,12	2.72	3 (33%)	7,13,15	0.81	0
22	7MG	w	46	22	23,26,27	1.31	3 (13%)	27,39,42	2.62	6 (22%)
25	PSU	A	955	25	18,21,22	1.42	4 (22%)	21,30,33	2.08	3 (14%)
25	G7M	A	2069	25	23,26,27	1.56	4 (17%)	34,39,42	1.68	5 (14%)
1	2MG	a	1207	1	23,26,27	1.27	4 (17%)	33,38,41	2.20	7 (21%)
1	MA6	a	1518	1	23,26,27	1.48	5 (21%)	33,38,41	2.39	13 (39%)
22	PSU	w	39	22	18,21,22	1.29	2 (11%)	21,30,33	2.26	3 (14%)
22	5MU	y	54	22	19,22,23	1.38	6 (31%)	27,32,35	2.07	6 (22%)
11	IAS	k	119	11	6,7,8	0.97	0	3,8,10	1.45	1 (33%)
25	5MU	A	747	25	19,22,23	1.38	4 (21%)	27,32,35	2.20	6 (22%)
22	PSU	w	32	22	18,21,22	1.37	2 (11%)	21,30,33	2.03	4 (19%)
1	G7M	a	527	1	23,26,27	1.59	3 (13%)	34,39,42	1.78	5 (14%)
25	5MU	A	1939	25	19,22,23	1.39	4 (21%)	27,32,35	2.15	6 (22%)
25	PSU	A	1917	25	18,21,22	1.42	3 (16%)	21,30,33	2.01	3 (14%)
25	OMG	A	2251	25,23	23,26,27	1.22	3 (13%)	32,38,41	1.97	6 (18%)
25	6MZ	A	2030	25	22,25,26	1.45	5 (22%)	29,36,39	2.32	11 (37%)
22	7MG	y	46	22	23,26,27	1.31	3 (13%)	27,39,42	2.59	6 (22%)
22	PSU	y	32	22	18,21,22	1.36	2 (11%)	21,30,33	2.00	3 (14%)
25	OMU	A	2552	25	19,22,23	1.26	3 (15%)	25,31,34	1.82	5 (20%)

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	PSU	a	516	1	-	0/7/25/26	0/2/2/2
25	PSU	A	746	25,56	-	2/7/25/26	0/2/2/2
1	UR3	a	1498	1	-	0/7/25/26	0/2/2/2
25	5MC	A	1962	25	-	0/7/25/26	0/2/2/2
22	5MU	w	54	22	-	0/7/25/26	0/2/2/2
12	D2T	l	89	12	-	1/7/12/14	-
36	MS6	O	82	36	-	4/4/6/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	PSU	y	55	22	-	3/7/25/26	0/2/2/2
25	H2U	A	2449	25	-	0/7/38/39	0/2/2/2
1	MA6	a	1519	1	-	4/11/29/30	0/3/3/3
23	5MC	x	32	23	-	0/7/25/26	0/2/2/2
25	PSU	A	1911	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2504	25	-	1/7/25/26	0/2/2/2
25	3TD	A	1915	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2457	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2604	25	-	0/7/25/26	0/2/2/2
1	2MG	a	966	1	-	0/9/27/28	0/3/3/3
22	PSU	y	39	22	-	0/7/25/26	0/2/2/2
25	1MG	A	745	25	-	0/7/25/26	0/3/3/3
28	MEQ	D	150	28	-	2/8/9/11	-
1	5MC	a	967	1	-	0/7/25/26	0/2/2/2
1	4OC	a	1402	1	-	1/9/29/30	0/2/2/2
22	4SU	w	8	22	-	0/7/25/26	0/2/2/2
25	6MZ	A	1618	25	-	0/9/27/28	0/3/3/3
23	PSU	x	55	23	-	0/7/25/26	0/2/2/2
22	PSU	w	55	22	-	0/7/25/26	0/2/2/2
22	MIA	w	37	22	-	2/15/33/34	0/3/3/3
1	2MG	a	1516	1	-	0/9/27/28	0/3/3/3
23	4SU	x	8	23	-	0/7/25/26	0/2/2/2
25	2MG	A	1835	25	-	0/9/27/28	0/3/3/3
22	4SU	y	8	22	-	2/7/25/26	0/2/2/2
23	5MU	x	54	23	-	0/7/25/26	0/2/2/2
25	PSU	A	2605	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2580	25	-	0/7/25/26	0/2/2/2
25	2MG	A	2445	25	-	0/9/27/28	0/3/3/3
1	5MC	a	1407	1	-	0/7/25/26	0/2/2/2
25	OMC	A	2498	25,56	-	1/9/27/28	0/2/2/2
22	MIA	y	37	22	-	2/7/25/34	0/3/3/3
25	2MA	A	2503	25,56	-	0/7/25/26	0/3/3/3
36	4D4	O	81	36	-	2/11/12/14	-
22	7MG	w	46	22	-	2/7/37/38	0/3/3/3
25	PSU	A	955	25	-	0/7/25/26	0/2/2/2
25	G7M	A	2069	25	-	0/7/25/26	0/3/3/3
1	2MG	a	1207	1	-	0/9/27/28	0/3/3/3
1	MA6	a	1518	1	-	2/11/29/30	0/3/3/3
22	PSU	w	39	22	-	0/7/25/26	0/2/2/2
22	5MU	y	54	22	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	IAS	k	119	11	-	3/7/7/8	-
25	5MU	A	747	25	-	0/7/25/26	0/2/2/2
22	PSU	w	32	22	-	0/7/25/26	0/2/2/2
1	G7M	a	527	1	-	2/7/25/26	0/3/3/3
25	5MU	A	1939	25	-	0/7/25/26	0/2/2/2
25	PSU	A	1917	25	-	2/7/25/26	0/2/2/2
25	OMG	A	2251	25,23	-	0/9/27/28	0/3/3/3
25	6MZ	A	2030	25	-	2/9/27/28	0/3/3/3
22	7MG	y	46	22	-	6/7/37/38	0/3/3/3
22	PSU	y	32	22	-	0/7/25/26	0/2/2/2
25	OMU	A	2552	25	-	0/9/27/28	0/2/2/2

The worst 5 of 185 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 282 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
25	A	2503	2MA	C5-C4-N3	-8.00	118.75	127.18
22	w	37	MIA	C5-C4-N3	-7.93	118.83	127.18

There are no chirality outliers.

5 of 46 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
36	O	82	MS6	CA-CB-CG-SD

There are no ring outliers.

14 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	a	1519	MA6	2	0
1	a	966	2MG	2	0
28	D	150	MEQ	1	0
1	a	967	5MC	1	0
1	a	1402	4OC	2	0
22	w	37	MIA	2	0
22	y	8	4SU	2	0
25	A	2445	2MG	1	0
25	A	2498	OMC	2	0
25	A	2503	2MA	1	0
1	a	1518	MA6	3	0
25	A	2030	6MZ	3	0
22	y	46	7MG	1	0
22	y	32	PSU	2	0

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:

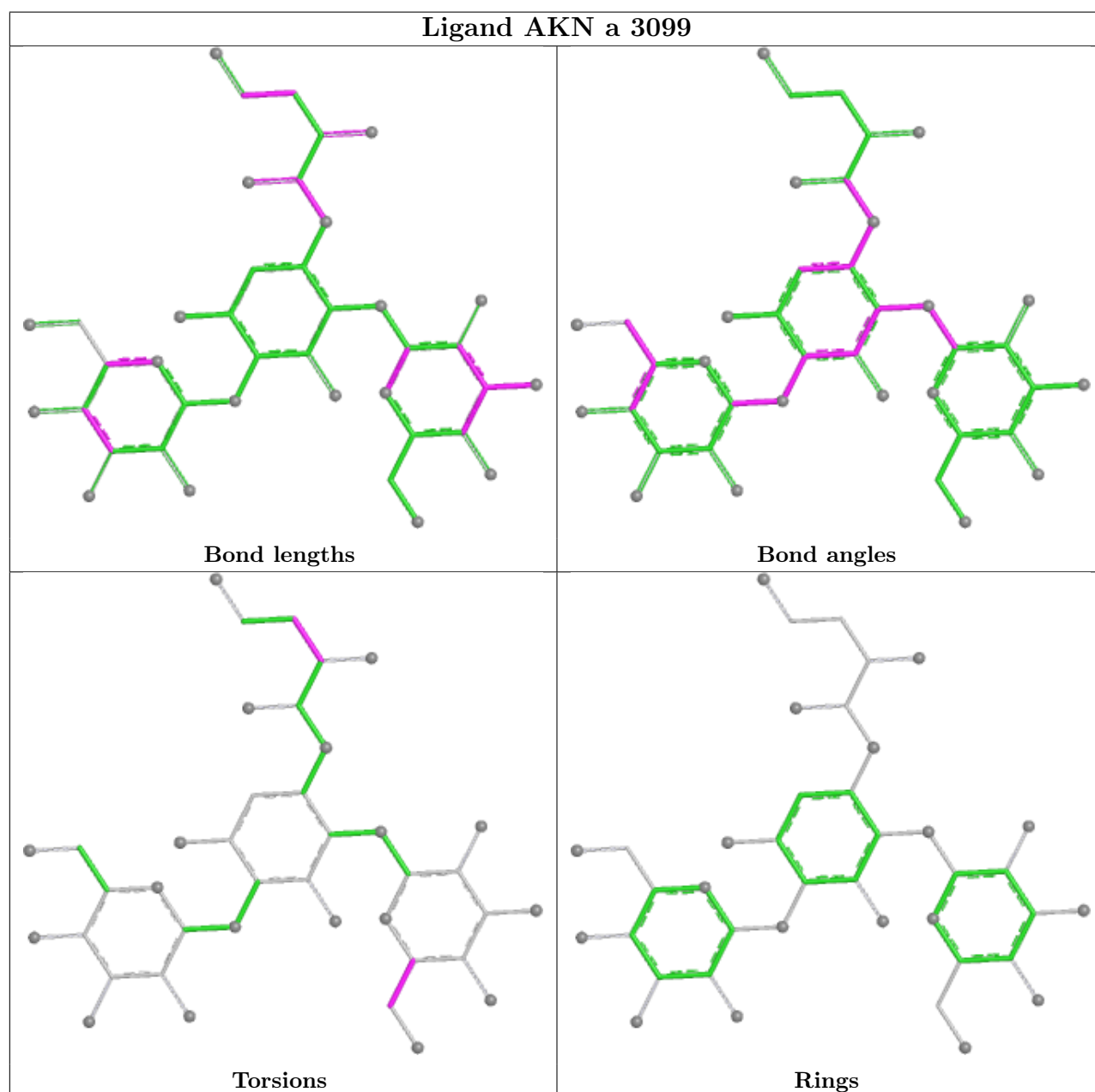
Mol	Chain	Res	Type	Atoms
57	A	3360	AKN	C14-C16-O2-C1
57	A	3360	AKN	C35-C37-C38-C39
57	A	3360	AKN	O40-C37-C38-C39
58	w	101	PHE	O-C-CA-CB
58	w	101	PHE	C-CA-CB-CG

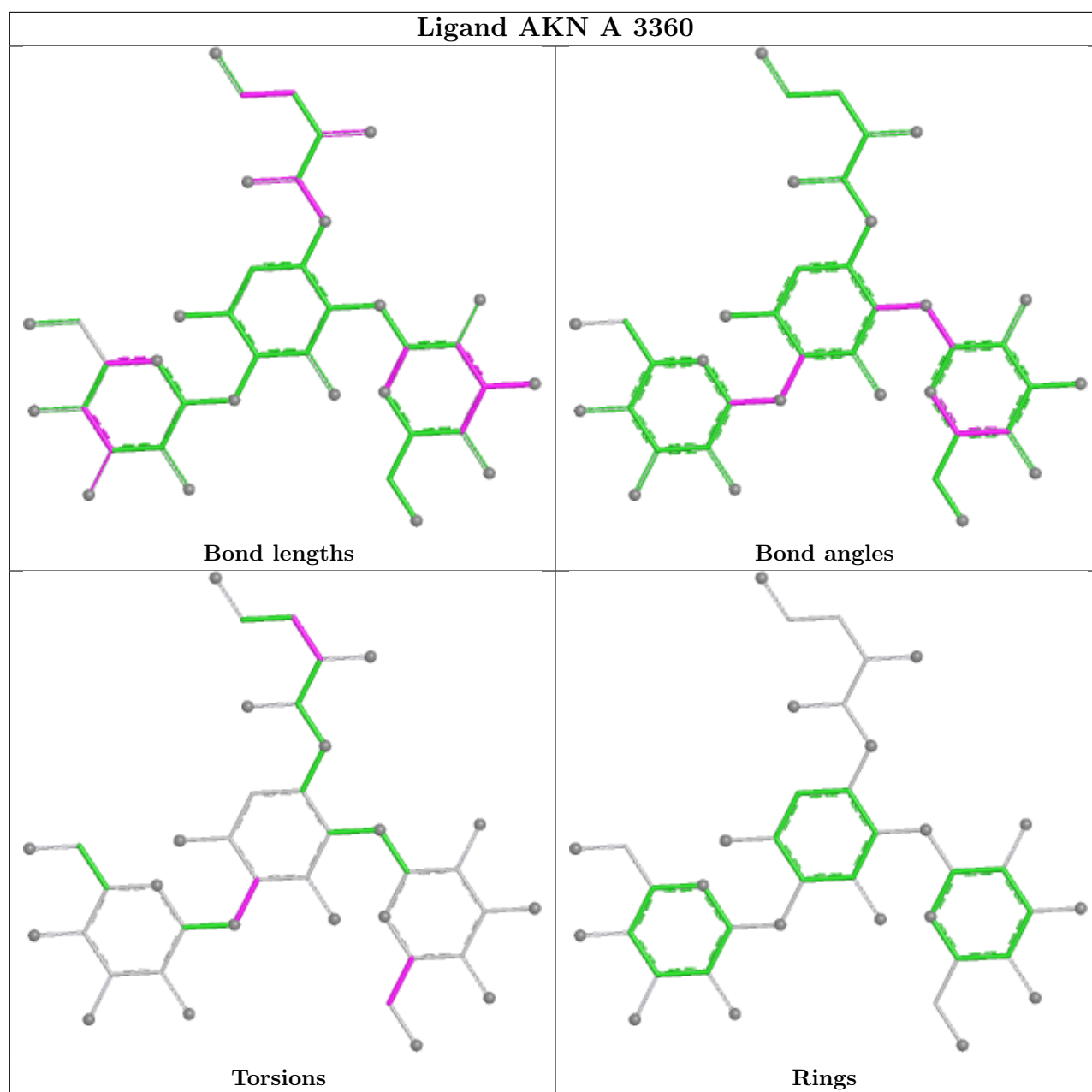
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	w	101	PHE	1	0
57	a	3099	AKN	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

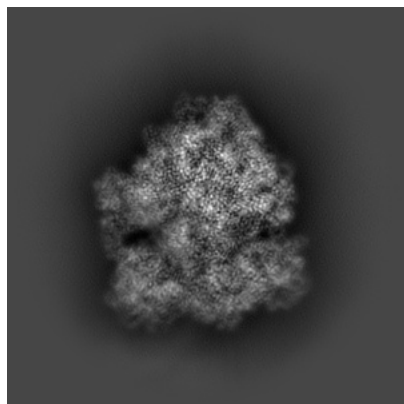
6 Map visualisation [i](#)

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

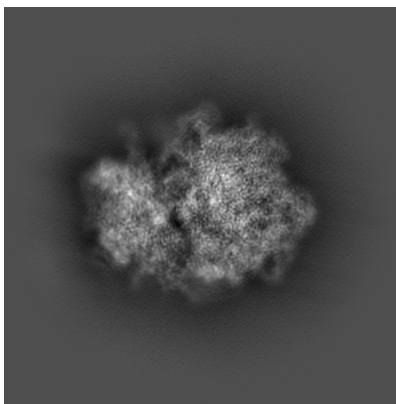
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

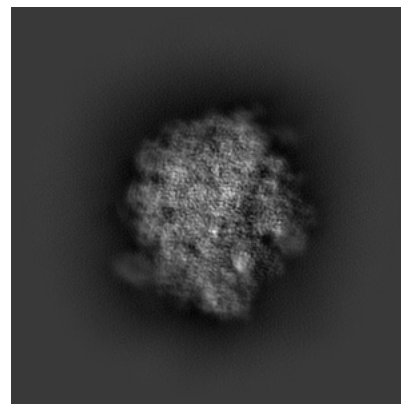
6.1.1 Primary map



X

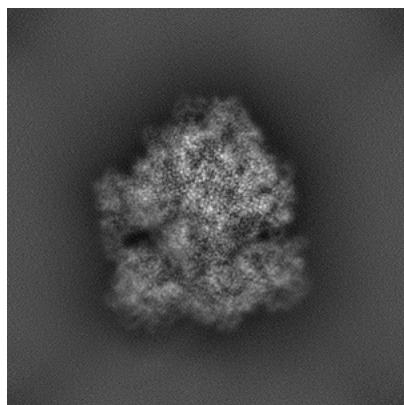


Y

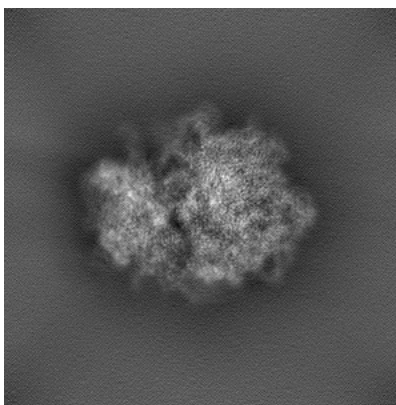


Z

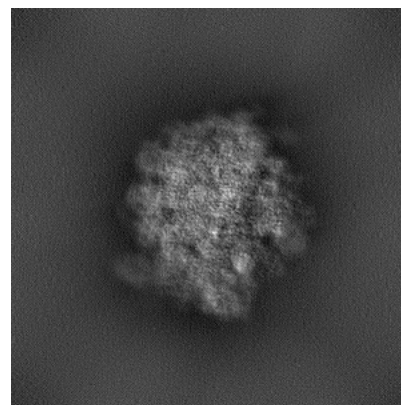
6.1.2 Raw map



X



Y

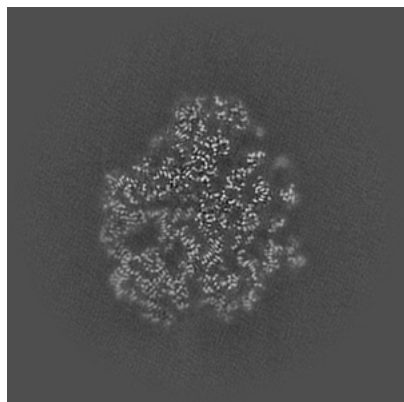


Z

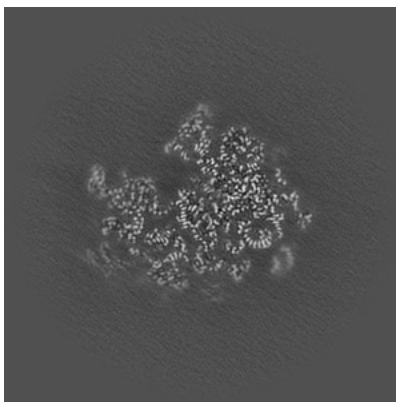
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

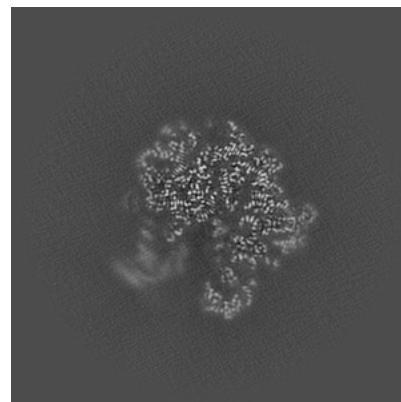
6.2.1 Primary map



X Index: 256

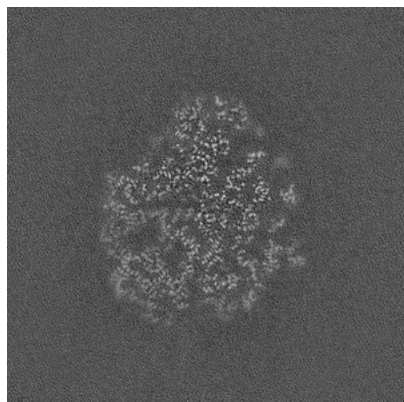


Y Index: 256

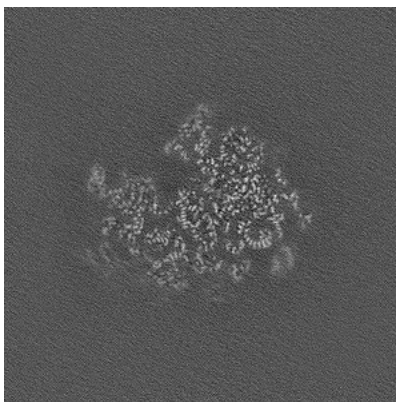


Z Index: 256

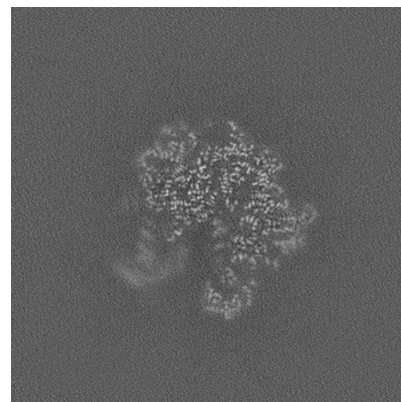
6.2.2 Raw map



X Index: 256



Y Index: 256

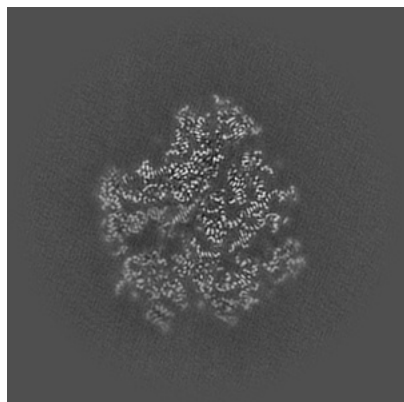


Z Index: 256

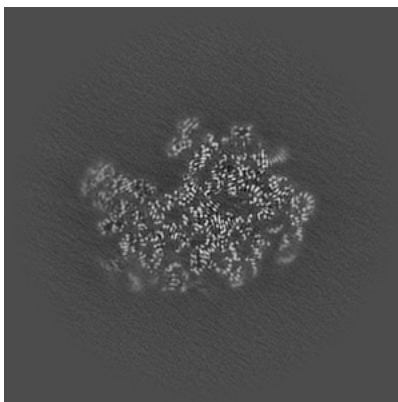
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

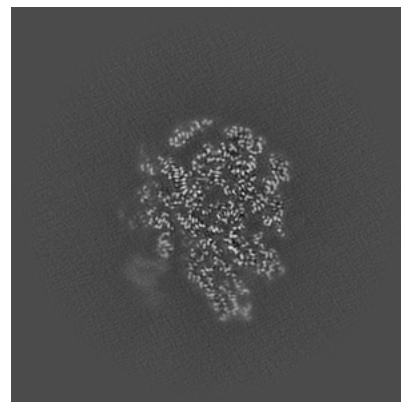
6.3.1 Primary map



X Index: 262

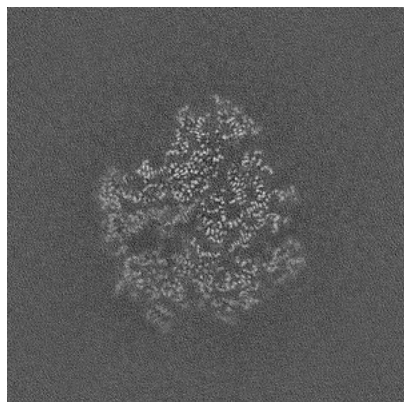


Y Index: 270

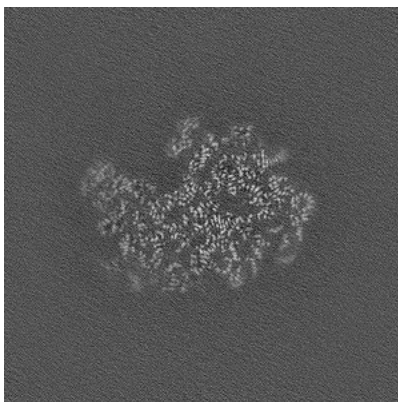


Z Index: 284

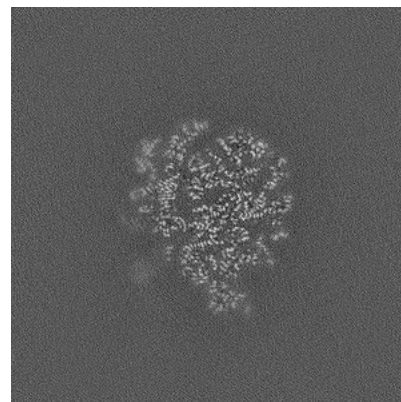
6.3.2 Raw map



X Index: 262



Y Index: 270

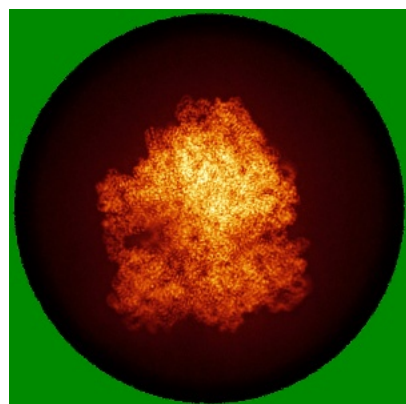


Z Index: 293

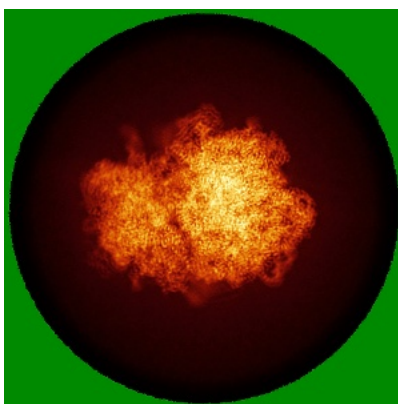
The images above show the largest variance slices of the map in three orthogonal directions.

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

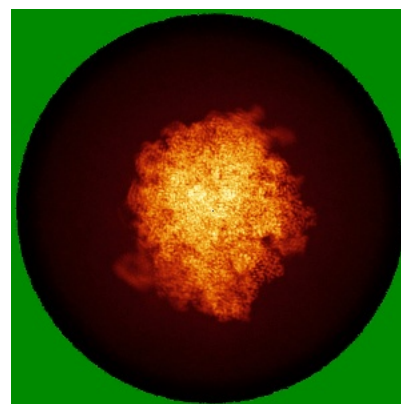
6.4.1 Primary map



X

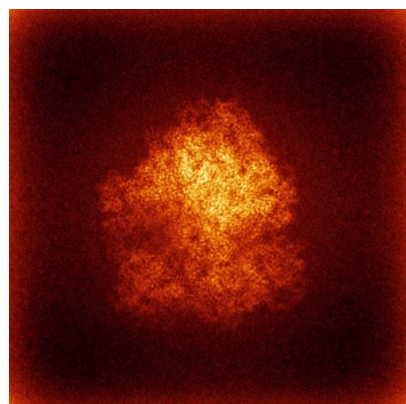


Y

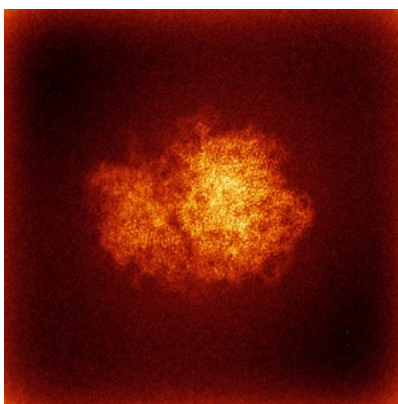


Z

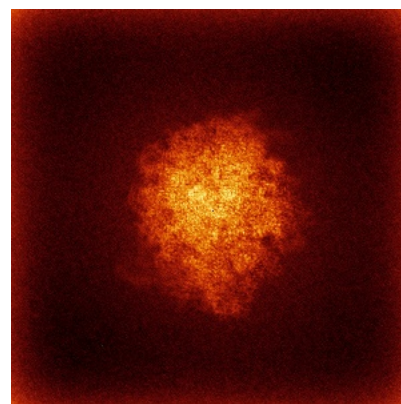
6.4.2 Raw map



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



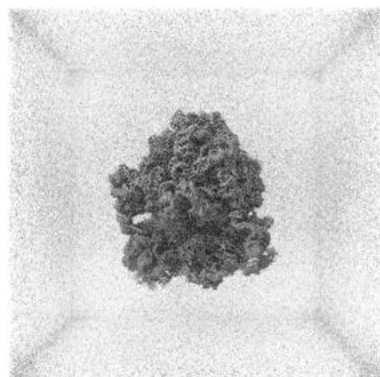
Y



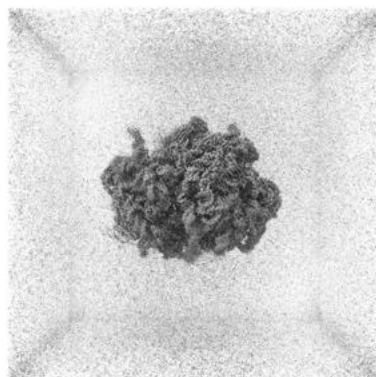
Z

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.

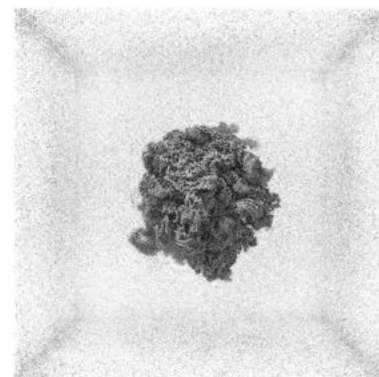
6.5.2 Raw map



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.

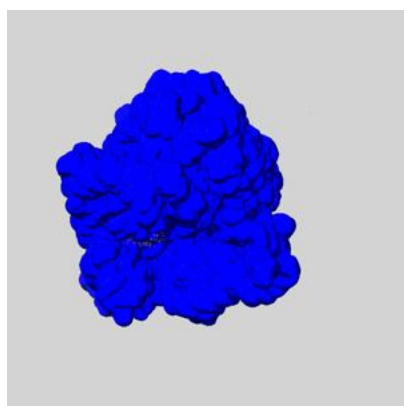
6.6 Mask visualisation [i](#)

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

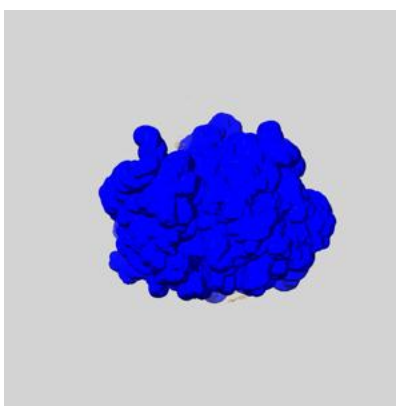
A mask typically either:

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

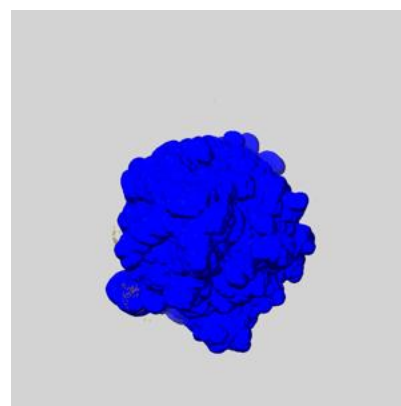
6.6.1 emd_40882_msk_1.map [i](#)



X



Y

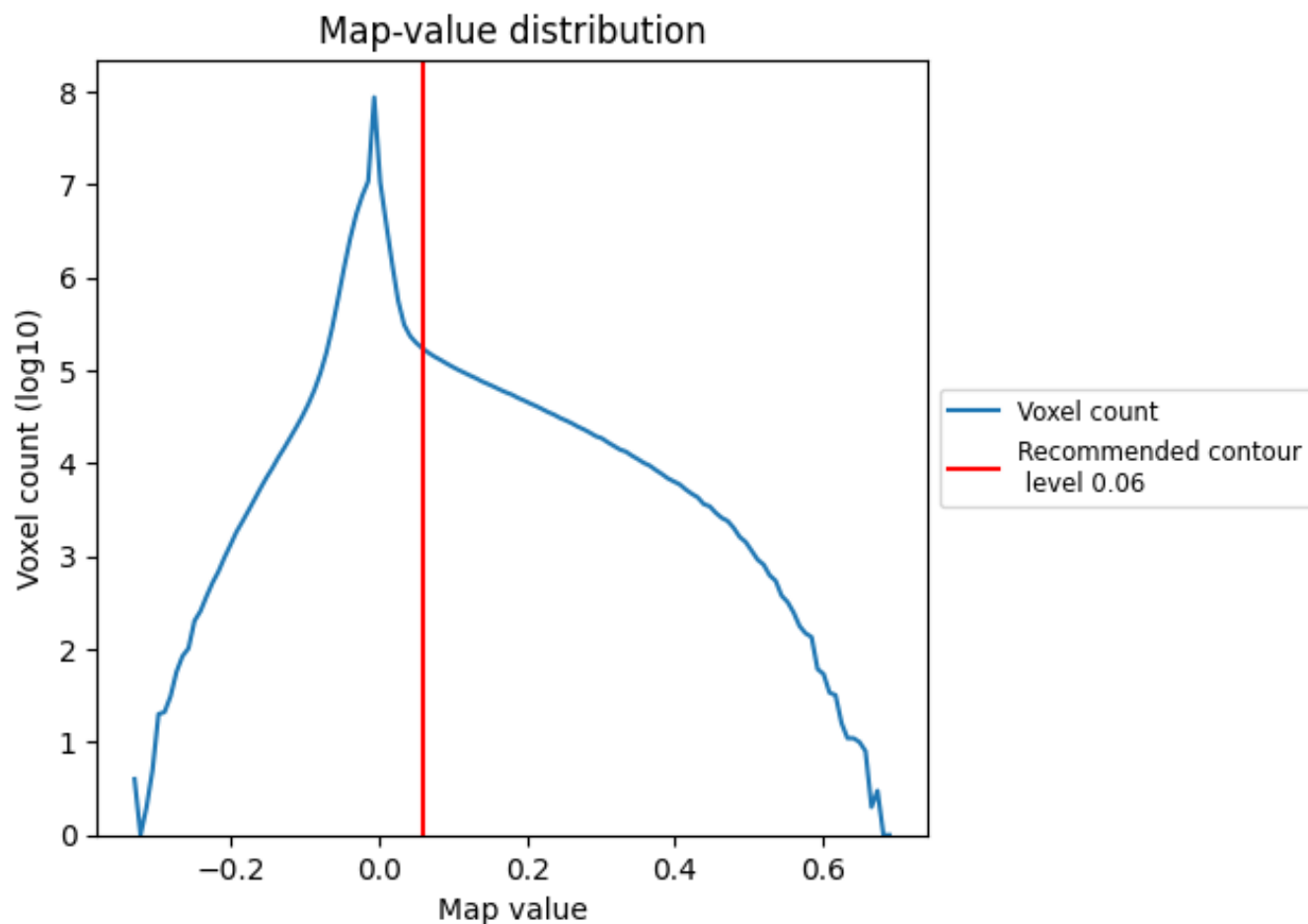


Z

7 Map analysis [i](#)

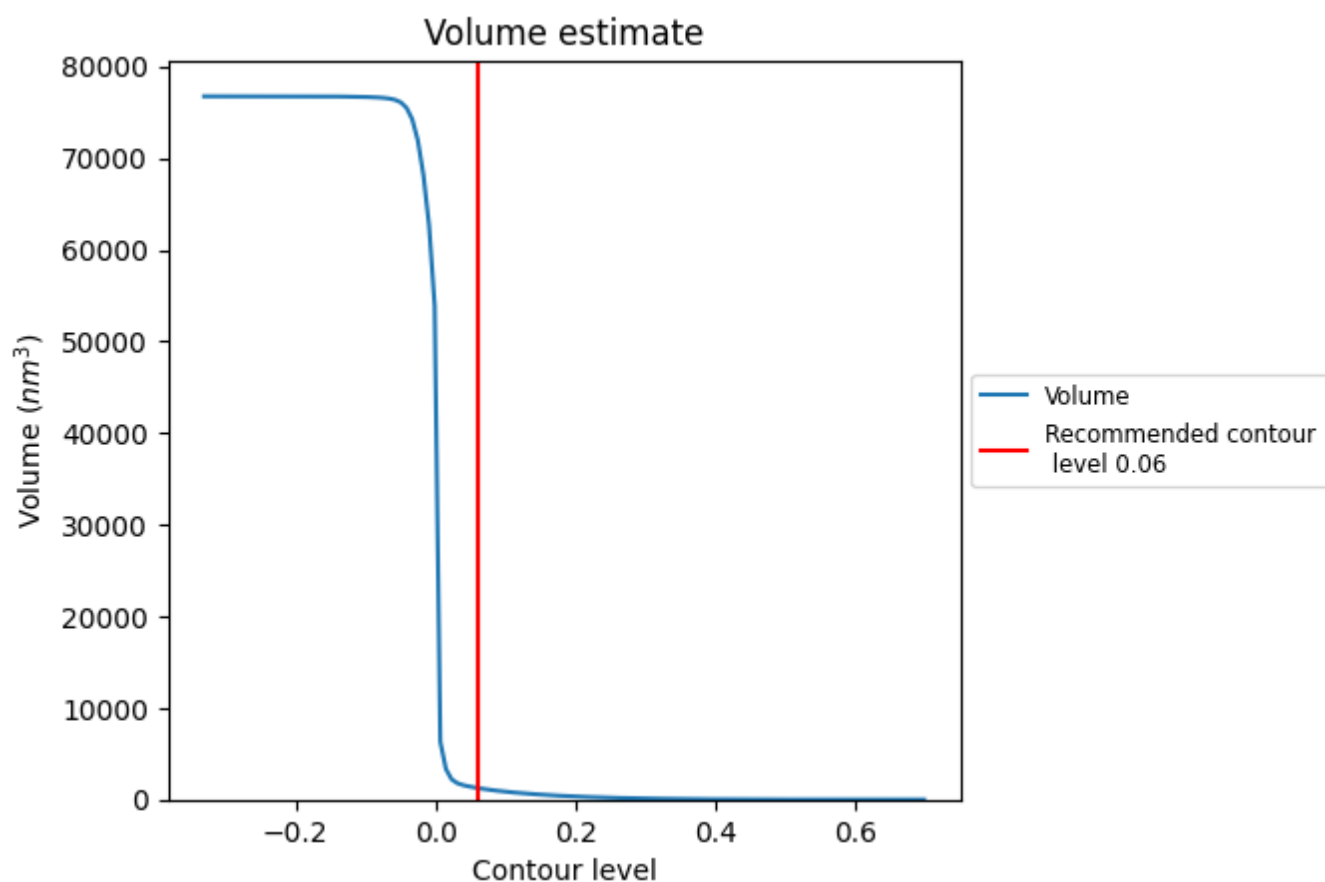
This section contains the results of statistical analysis of the map.

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.

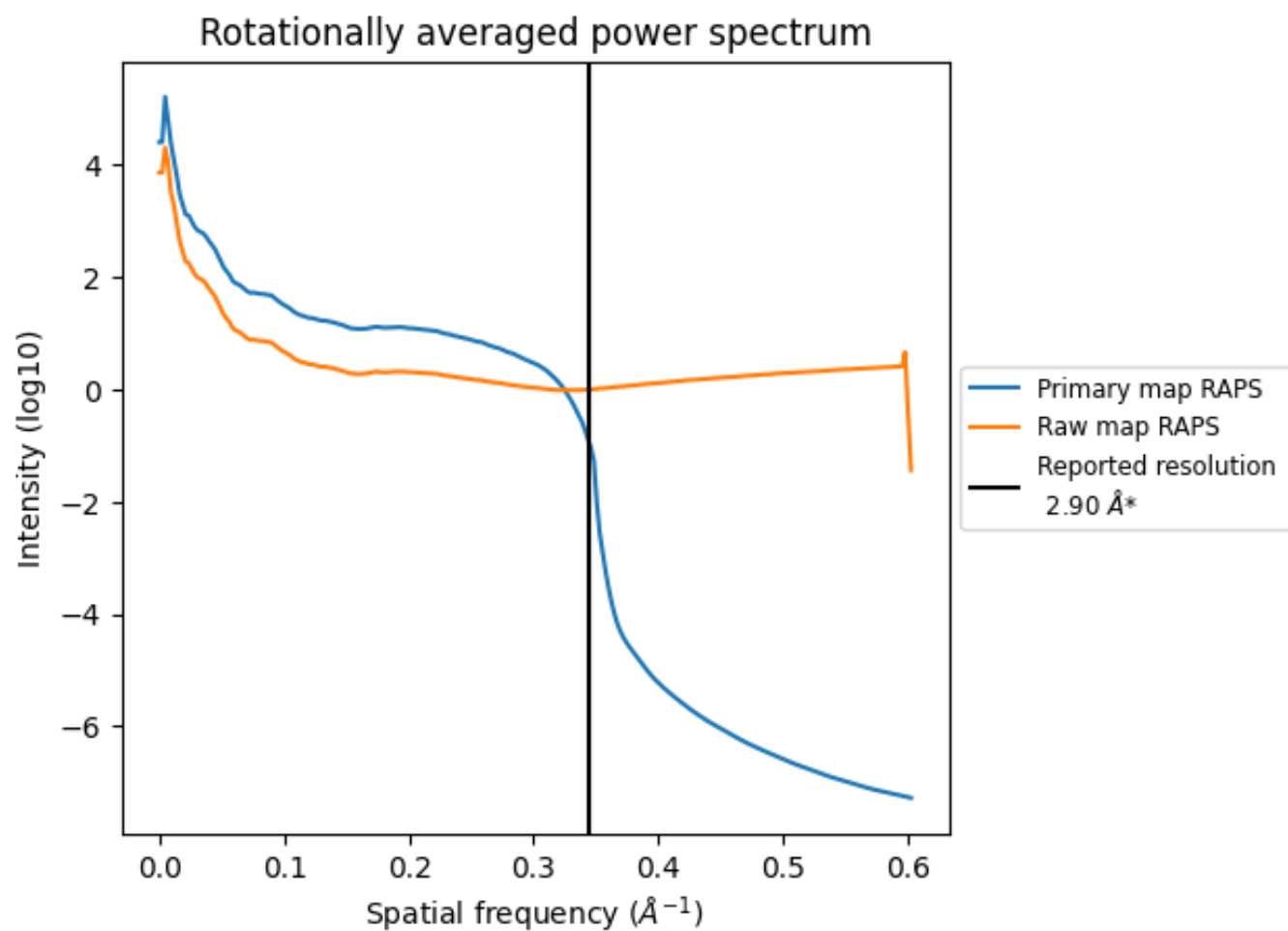
7.2 Volume estimate [i](#)



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 ⓘ

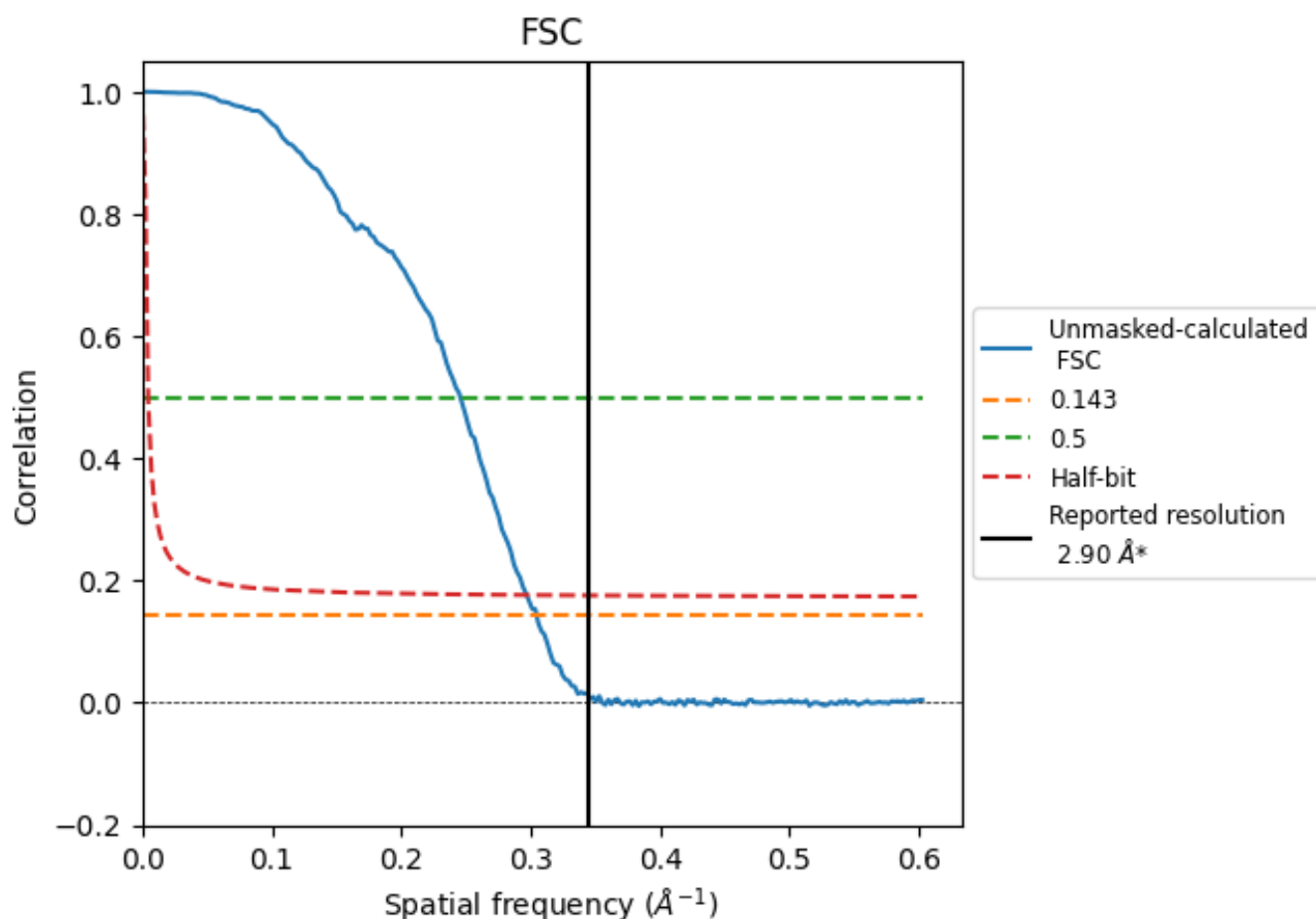


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

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](#)

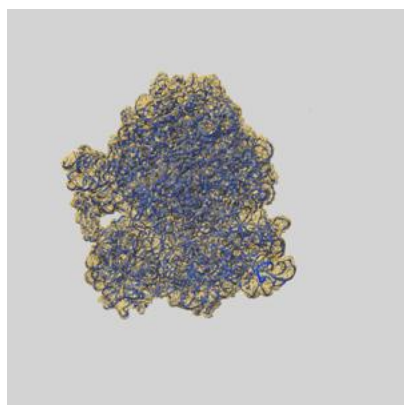
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.28	4.07	3.37

*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 %

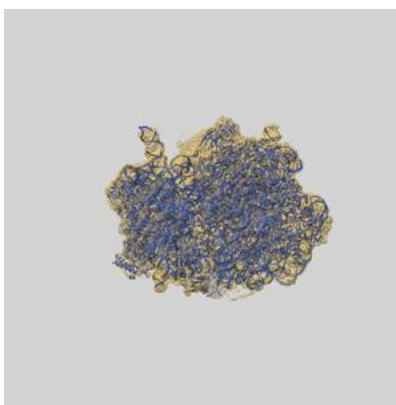
9 Map-model fit [i](#)

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 [17](#).

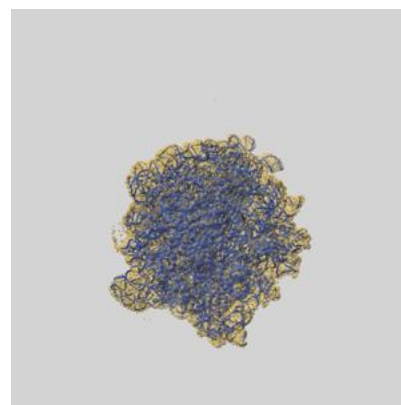
9.1 Map-model overlay [i](#)



X



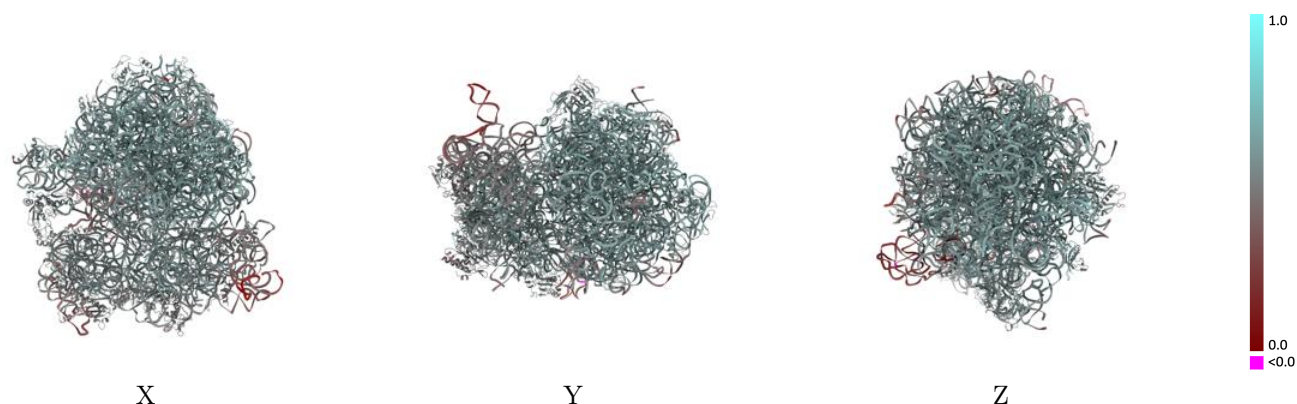
Y



Z

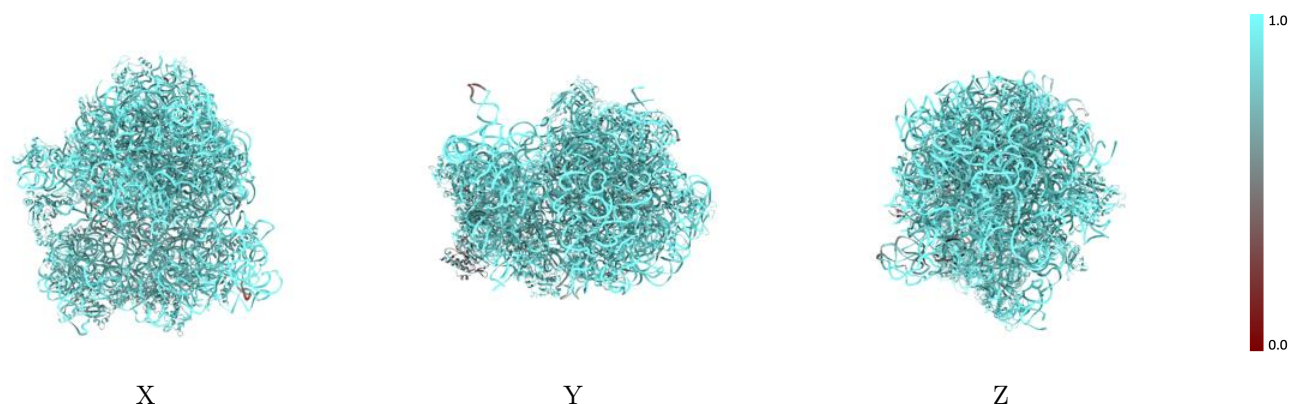
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



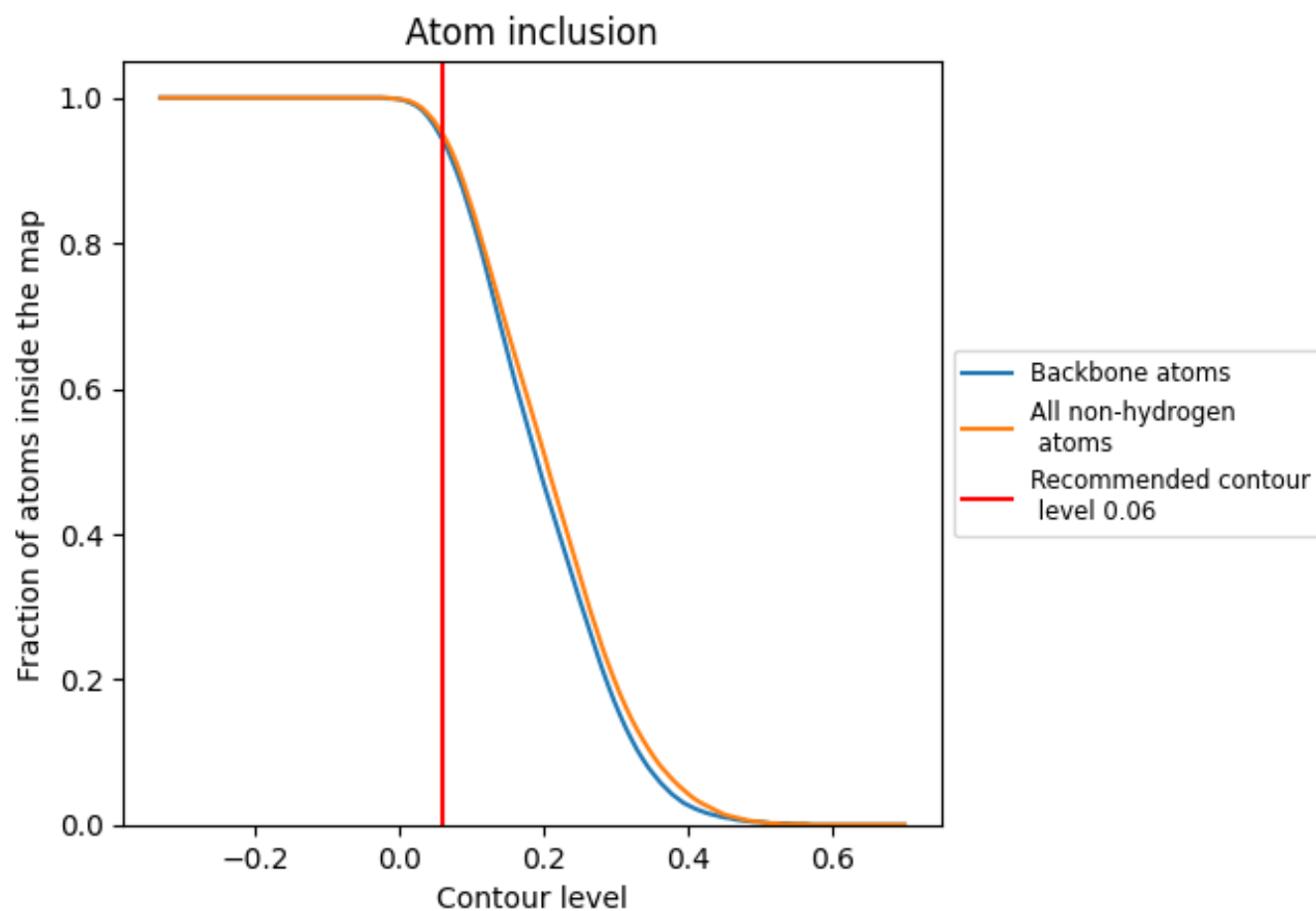
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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



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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