



Full wwPDB EM Validation Report ⓘ

Aug 20, 2026 – 03:04 PM EDT

PDB ID : 9EJA / pdb_00009eja
EMDB ID : EMD-48098
Title : Human FANCI helicase bound to a fork DNA in the closed state
Authors : You, Q.; Li, H.
Deposited on : 2024-11-27
Resolution : 3.30 Å (reported)

This is a Full wwPDB EM Validation 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.dev133
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) : 2.50

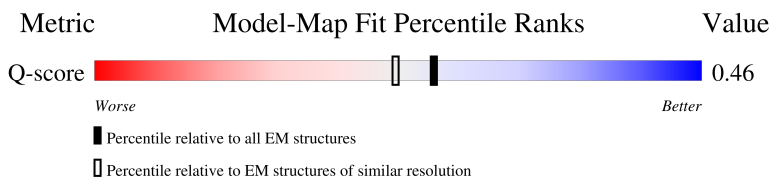
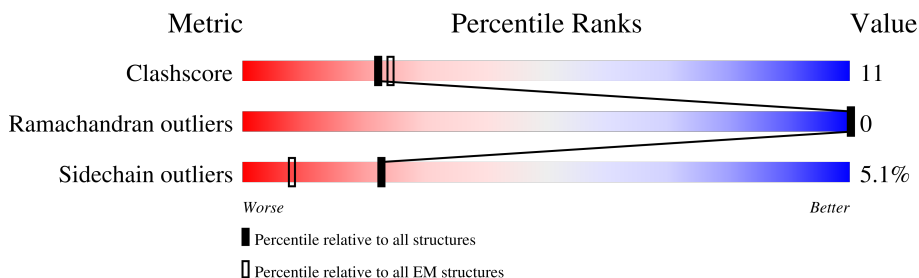
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	1271	
2	B	44	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	SF4	A	1303	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5626 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Fanconi anemia group J protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	676	Total	C	N	O	S	0	0
			5403	3435	936	1001	31		

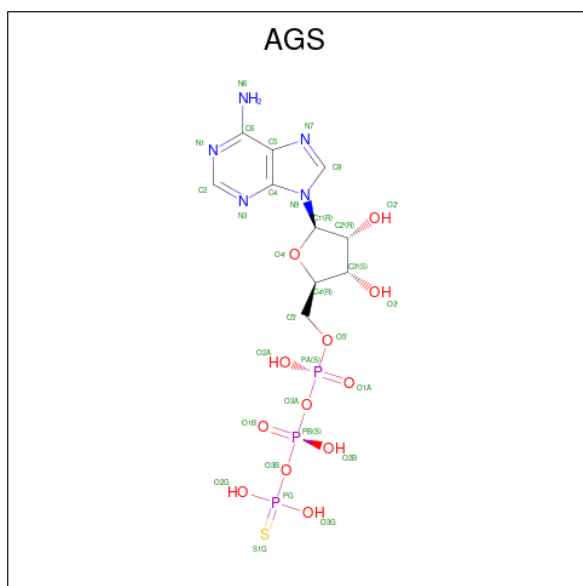
There are 22 discrepancies between the modelled and reference sequences:

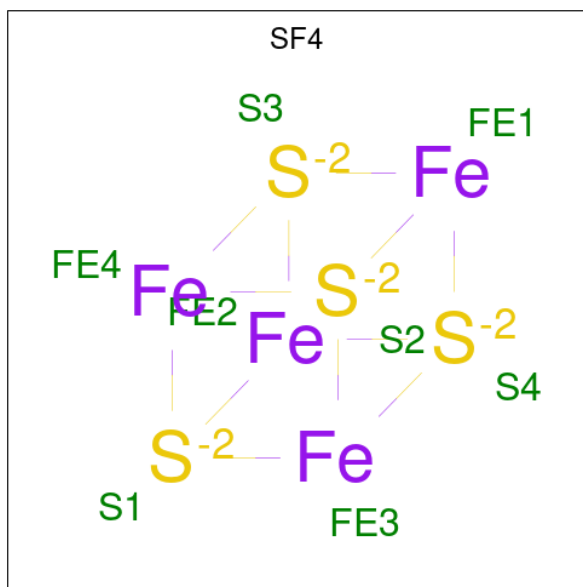
Chain	Residue	Modelled	Actual	Comment	Reference
A	1250	ASP	-	expression tag	UNP Q9BX63
A	1251	TYR	-	expression tag	UNP Q9BX63
A	1252	LYS	-	expression tag	UNP Q9BX63
A	1253	ASP	-	expression tag	UNP Q9BX63
A	1254	HIS	-	expression tag	UNP Q9BX63
A	1255	ASP	-	expression tag	UNP Q9BX63
A	1256	GLY	-	expression tag	UNP Q9BX63
A	1257	ASP	-	expression tag	UNP Q9BX63
A	1258	TYR	-	expression tag	UNP Q9BX63
A	1259	LYS	-	expression tag	UNP Q9BX63
A	1260	ASP	-	expression tag	UNP Q9BX63
A	1261	HIS	-	expression tag	UNP Q9BX63
A	1262	ASP	-	expression tag	UNP Q9BX63
A	1263	ILE	-	expression tag	UNP Q9BX63
A	1264	ASP	-	expression tag	UNP Q9BX63
A	1265	TYR	-	expression tag	UNP Q9BX63
A	1266	LYS	-	expression tag	UNP Q9BX63
A	1267	ASP	-	expression tag	UNP Q9BX63
A	1268	ASP	-	expression tag	UNP Q9BX63
A	1269	ASP	-	expression tag	UNP Q9BX63
A	1270	ASP	-	expression tag	UNP Q9BX63
A	1271	LYS	-	expression tag	UNP Q9BX63

- Molecule 2 is a DNA chain called DNA (5'-D(P*GP*AP*AP*AP*AP*CP*CP*CP*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	9	Total	C	N	O	P	0	0
			183	87	36	51	9		

- Molecule 3 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$) (labeled as "Ligand of Interest" by depositor).

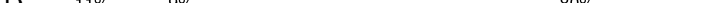


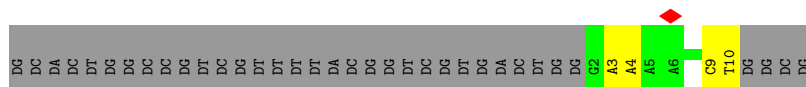


Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
5	A	1	8	4	4	0

HIS	ASP	ILE	ASP	THR	ALA	PRO	SER	ASN
	ILE	GLU	THR	THR	THR	GLU	ILE	ILE
	ASP	GLU	ASP	LEU	LEU	GLN	GLN	GLN
	TYR	SER	GLU	THR	GLY	SER	SER	ASP
	LYS	LYS	GLU	ARG	SER	LYS	LYS	GLU
	ASP	ASN	LYS	LYS	SER	GLU	GLY	SER
	ASP	ASN	ASN	ASN	ASN	ASN	LYS	THR
	ASP	ILE	LEU	SER	GLU	ALA	ASP	GLU
	ASP	ASP	ALA	GLU	ALA	GLU	ASP	GLU
	LYS	GLY	GLU	HIS	HIS	SER	PRO	VAL
LYS	ASN	VAL	THR	THR	PRO	SER	VAL	THR
	LYS	LYS	ARG	CYS	PRO	ARG	LEU	LEU
	THR	THR	GLY	SER	ARG	PHE	GLU	GLU
	THR	THR	ARG	GLU	GLU	THR	ALA	SER
	ILE	ILE	LEU	ALA	THR	THR	GLY	THR
	ASN	ALA	LEU	LEU	GLU	LYS	LYS	SER
	GLU	GLU	ASN	ASP	LYS	ALA	ALA	PRO
	LEU	LEU	ASN	PRO	ASN	GLU	GLU	TYR
	GLU	SER	ASP	ASP	GLU	LYS	LYS	LEU
	GLY	CYS	ILE	ILE	GLU	SER	VAL	GLU
LYS	LYS	ILE	ILE	LEU	LEU	THR	ILE	ALA
	THR	THR	LEU	ALA	SER	VAL	ARG	SER
	HIS	HIS	ALA	LEU	LEU	PRO	THR	HIS
	GLU	GLU	LYS	VAL	GLU	PHE	SER	LEU
	ILE	ILE	ASP	SER	SER	PHE	THR	SER
	GLU	LEU	LEU	GLU	GLU	THR	SER	SER
	ILE	PHE	GLU	GLU	ASP	PRO	THR	PRO
	LYS	ASN	ILE	ASP	CYS	LYS	PHE	GLU
	ASN	PHE	ARG	GLN	GLU	ASN	ASN	PHE
	LYS	LYS	THR	SER	SER	LYS	VAL	VAL
LYS	PRO	PRO	ILE	THR	SER	SER	GLN	GLU
	SER	LYS	THR	SER	LYS	SER	THR	ASP
	PRO	PRO	GLU	ASN	LEU	LYS	GLU	GLU
	PRO	VAL	VAL	ARG	THR	ARG	ALA	ALA
	LYS	LYS	ASP	ASP	VAL	VAL	VAL	LYS
	ASN	SER	SER	PHE	ASN	SER	SER	ILE
	LYS	ALA	ALA	GLU	THR	TRP	CYS	VAL
	GLY	ARG	GLU	THR	SER	SER	GLN	SER
	PHE	VAL	VAL	ALA	GLY	PHE	GLU	GLU
	LYS	PRO	LYS	GLU	SER	ASN	GLN	CYS
LYS	PHE	GLU	GLU	ASP	PRO	LEU	LEU	CYS
	LYS	ASP	ASP	GLN	GLN	GLY	GLY	PRO
	ASP	ASP	CYS	ILE	SER	GLN	GLN	LYS
	TYR	TYR	ILE	TYR	GLU	THR	THR	ILE
	LYS	LYS	THR	PHE	ILE	GLY	GLY	LYS
	ASP	ASP	THR	THR	THR	THR	THR	THR
	HIS	HIS	LYS	PRO	ILE	ILE	ILE	LYS
	ASP	ASP	LEU	GLU	SER	LYS	LYS	ASN
	GLY	GLY	ASN	LEU	SER	ILE	ILE	ASN
	ASP	ASP	GLY	TYR	LEU	PRO	PRO	PRO
LYS	TYR	TYR	ILE	ASP	LYS	LYS	LYS	LEU
	LYS	LYS	THR	THR	ILE	THR	THR	THR
	ASP	ASP	PRO	ASP	THR	THR	THR	THR
	HIS	HIS	PRO	PRO	ILE	ILE	GLY	LYS
	ASP	ASP	GLU	GLU	SER	LYS	LYS	ASN
	GLY	GLY	LEU	LEU	THR	THR	THR	THR
	ASP	ASP	THR	THR	THR	THR	THR	THR
	ILE	ILE	THR	THR	THR	THR	THR	THR
	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP

- Molecule 2: DNA (5'-D(P*GP*AP*AP*AP*AP*CP*CP*CP*T)-3')

Chain B:  11% 9% 80%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	278584	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.545	Depositor
Minimum map value	-1.221	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.134	Depositor
Map size (Å)	298.08002, 298.08002, 298.08002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82800007, 0.82800007, 0.82800007	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SF4, AGS

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	0.28	1/5515 (0.0%)	0.49	3/7454 (0.0%)
2	B	0.24	0/205	0.37	0/313
All	All	0.28	1/5720 (0.0%)	0.48	3/7767 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	276	LEU	C-N	11.13	1.46	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	719	LEU	CA-C-N	-5.49	116.10	122.63
1	A	719	LEU	C-N-CA	-5.49	116.10	122.63
1	A	603	ILE	N-CA-C	-5.41	108.57	113.71

There are no chirality outliers.

There are no planarity outliers.

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	5403	0	5383	125	0
2	B	183	0	101	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	31	0	12	3	0
4	A	1	0	0	0	0
5	A	8	0	0	6	0
All	All	5626	0	5496	127	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 11.

All (127) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:CYS:SG	5:A:1303:SF4:FE3	1.40	1.12
1:A:310:CYS:SG	5:A:1303:SF4:FE2	1.62	0.91
1:A:283:CYS:HB3	1:A:294:ARG:HH11	1.41	0.84
1:A:45:GLU:HB3	1:A:636:GLU:HA	1.68	0.75
1:A:310:CYS:HG	5:A:1303:SF4:FE2	0.47	0.73
1:A:274:THR:HB	1:A:365:ILE:HG12	1.72	0.72
1:A:499:GLN:HE22	1:A:502:GLU:HG3	1.57	0.69
1:A:614:SER:HB3	1:A:617:LEU:HB2	1.74	0.69
1:A:43:LEU:HD22	1:A:617:LEU:HD21	1.74	0.69
1:A:853:PRO:O	1:A:857:ILE:HB	1.91	0.68
1:A:830:GLY:O	1:A:834:ARG:NH1	2.27	0.68
1:A:258:GLN:NE2	1:A:770:ASP:OD2	2.28	0.67
1:A:298:CYS:SG	5:A:1303:SF4:S1	2.93	0.66
1:A:279:ARG:NH2	1:A:352:TYR:HE2	1.94	0.65
1:A:721:LYS:NZ	1:A:753:ASP:O	2.29	0.65
1:A:57:LEU:HD11	1:A:263:LEU:HD12	1.80	0.63
1:A:64:GLN:NE2	1:A:244:PRO:O	2.33	0.61
1:A:693:CYS:HB3	1:A:758:VAL:HG13	1.83	0.60
1:A:279:ARG:NH2	1:A:352:TYR:CE2	2.69	0.60
1:A:310:CYS:SG	1:A:312:PHE:HB2	2.42	0.60
1:A:646:VAL:HG11	1:A:863:TRP:HZ3	1.67	0.58
1:A:369:TYR:HB3	1:A:373:LEU:HD13	1.85	0.58
1:A:422:LEU:O	1:A:426:VAL:HG23	2.04	0.58
1:A:29:MET:HG2	1:A:59:SER:HB2	1.87	0.57
1:A:500:LYS:NZ	1:A:516:VAL:O	2.37	0.56
1:A:253:HIS:NE2	2:B:9:DC:OP1	2.36	0.56
1:A:495:SER:HA	1:A:498:LEU:HD12	1.88	0.56
1:A:547:ASP:OD2	1:A:595:ASN:ND2	2.38	0.56
1:A:251:ARG:HH11	1:A:767:GLU:HG2	1.70	0.55
1:A:827:GLN:O	1:A:831:ARG:NH1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:ASP:OD1	1:A:403:ARG:NH1	2.39	0.55
1:A:858:SER:O	1:A:865:ARG:NH1	2.39	0.55
1:A:654:GLY:N	1:A:658:ARG:O	2.32	0.55
1:A:831:ARG:HH21	1:A:834:ARG:HH12	1.54	0.54
1:A:869:GLN:HB2	1:A:871:HIS:HE1	1.72	0.54
1:A:822:TYR:O	1:A:826:ASN:ND2	2.41	0.54
1:A:278:SER:O	1:A:282:THR:OG1	2.26	0.53
1:A:651:ILE:HG21	1:A:874:PHE:HD1	1.73	0.53
1:A:369:TYR:OH	1:A:393:ASP:O	2.22	0.53
1:A:795:GLU:O	1:A:799:GLN:HG2	2.09	0.53
1:A:24:SER:HB3	1:A:637:ALA:HB1	1.90	0.52
1:A:648:VAL:HG11	1:A:864:VAL:HG13	1.92	0.52
1:A:642:LYS:HG3	1:A:645:GLN:HG3	1.92	0.52
1:A:643:ASN:HA	1:A:867:GLN:HE22	1.75	0.52
1:A:862:LYS:HA	1:A:865:ARG:HE	1.73	0.52
1:A:539:ARG:HG2	1:A:540:GLN:HG3	1.91	0.51
1:A:297:LYS:O	1:A:301:LEU:HB2	2.11	0.51
1:A:856:TYR:OH	2:B:3:DA:OP1	2.22	0.51
1:A:279:ARG:CZ	1:A:352:TYR:CE2	2.94	0.50
1:A:14:LYS:HE3	1:A:14:LYS:HA	1.93	0.50
1:A:277:SER:O	1:A:371:TYR:OH	2.30	0.50
1:A:260:THR:HG21	1:A:275:ILE:HD11	1.93	0.49
1:A:656:LYS:NZ	1:A:675:GLU:OE2	2.43	0.49
1:A:725:VAL:HG22	1:A:758:VAL:HB	1.94	0.49
1:A:266:THR:OG1	1:A:267:ALA:N	2.46	0.49
1:A:276:LEU:HD11	1:A:359:ILE:HD11	1.95	0.49
1:A:786:PHE:HB3	1:A:817:TYR:HE1	1.77	0.49
1:A:477:LEU:HD22	1:A:534:LEU:HD21	1.95	0.49
1:A:298:CYS:SG	5:A:1303:SF4:S2	3.11	0.48
1:A:6:SER:OG	1:A:17:PHE:O	2.23	0.48
1:A:283:CYS:HB3	1:A:294:ARG:NH1	2.20	0.48
1:A:696:PRO:HB3	1:A:785:PRO:HA	1.96	0.48
1:A:456:LEU:HD12	1:A:554:GLN:HB2	1.96	0.48
1:A:298:CYS:HG	5:A:1303:SF4:FE3	0.24	0.47
1:A:299:MET:O	1:A:299:MET:HE3	2.13	0.47
2:B:3:DA:H2"	2:B:4:DA:H5"	1.97	0.47
1:A:47:PRO:O	1:A:52:LYS:NZ	2.46	0.47
1:A:272:PRO:HB2	1:A:362:ALA:HA	1.96	0.47
1:A:256:ILE:O	1:A:260:THR:HG23	2.16	0.46
1:A:791:ASP:HB3	1:A:794:VAL:HB	1.97	0.46
1:A:381:MET:HG3	1:A:383:LEU:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:PRO:HG3	1:A:267:ALA:HB2	1.96	0.46
1:A:473:MET:HE2	1:A:550:ILE:HG21	1.96	0.46
1:A:608:GLN:HG2	1:A:609:THR:HG23	1.95	0.46
1:A:353:TYR:O	1:A:357:GLU:HG2	2.15	0.46
1:A:612:LEU:HD13	1:A:631:PHE:HZ	1.80	0.46
1:A:656:LYS:HG3	1:A:657:GLY:H	1.81	0.46
1:A:692:LEU:HD23	1:A:757:LEU:HD23	1.96	0.46
1:A:312:PHE:HA	1:A:348:LYS:O	2.16	0.46
1:A:834:ARG:NH2	3:A:1301:AGS:O1B	2.46	0.46
1:A:252:THR:HG22	1:A:254:LYS:H	1.82	0.46
1:A:804:HIS:HB3	1:A:808:ARG:HG3	1.98	0.46
1:A:848:ARG:HA	1:A:851:ASN:HB3	1.98	0.46
3:A:1301:AGS:O1B	3:A:1301:AGS:O2G	2.34	0.46
1:A:831:ARG:HH21	1:A:834:ARG:NH1	2.13	0.45
1:A:470:GLY:HA3	1:A:545:ALA:O	2.17	0.45
1:A:604:ASN:HA	1:A:610:ILE:HD11	1.97	0.45
1:A:749:LYS:HD2	1:A:753:ASP:HA	1.98	0.45
1:A:276:LEU:HB2	1:A:367:CYS:HB3	1.99	0.44
1:A:658:ARG:HG2	1:A:675:GLU:HG3	1.98	0.44
1:A:46:SER:C	1:A:52:LYS:HZ2	2.26	0.44
1:A:471:ASN:O	1:A:475:LEU:HG	2.18	0.44
1:A:652:GLY:H	1:A:850:ARG:HH12	1.65	0.44
1:A:369:TYR:HB2	1:A:401:CYS:SG	2.58	0.44
1:A:28:MET:HE2	1:A:44:LEU:HD12	2.00	0.44
1:A:323:HIS:O	1:A:327:THR:OG1	2.25	0.43
1:A:466:LYS:HA	1:A:466:LYS:HE2	1.99	0.43
1:A:642:LYS:H	1:A:642:LYS:HG2	1.70	0.43
1:A:244:PRO:HB3	1:A:388:GLN:HA	2.00	0.43
1:A:394:GLU:OE2	3:A:1301:AGS:O3G	2.37	0.43
1:A:47:PRO:HG2	1:A:639:HIS:H	1.83	0.43
1:A:549:LYS:HA	1:A:549:LYS:HD3	1.72	0.43
1:A:251:ARG:HD3	1:A:767:GLU:HG2	2.00	0.43
1:A:398:ILE:HA	1:A:398:ILE:HD13	1.84	0.43
1:A:829:LEU:HD23	1:A:829:LEU:HA	1.87	0.42
1:A:735:PHE:HE2	1:A:764:LYS:HB2	1.85	0.42
1:A:431:ARG:NH1	1:A:499:GLN:O	2.52	0.42
1:A:474:LEU:HD21	1:A:537:LEU:HD22	2.02	0.42
1:A:25:GLN:HE21	1:A:51:GLY:HA3	1.85	0.42
1:A:305:LYS:HD3	1:A:305:LYS:HA	1.92	0.41
1:A:757:LEU:HD21	1:A:765:VAL:HG21	2.02	0.41
1:A:816:TRP:O	1:A:820:GLN:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:LEU:HD13	1:A:63:TRP:CD2	2.56	0.41
1:A:648:VAL:HG22	1:A:842:LEU:HD12	2.01	0.41
1:A:779:VAL:HG12	1:A:779:VAL:O	2.20	0.41
1:A:33:LEU:HD13	1:A:33:LEU:HA	1.92	0.41
1:A:652:GLY:N	1:A:850:ARG:HH12	2.18	0.41
1:A:658:ARG:HA	1:A:658:ARG:HD3	1.93	0.41
1:A:242:LYS:HG3	1:A:243:ILE:H	1.86	0.41
1:A:739:LEU:O	1:A:743:TYR:HD2	2.03	0.41
1:A:371:TYR:OH	2:B:10:DT:OP1	2.35	0.41
1:A:640:ILE:HD13	1:A:640:ILE:HA	1.90	0.41
1:A:811:LEU:HD22	1:A:815:GLN:HG3	2.01	0.41
1:A:621:LYS:HB2	1:A:621:LYS:HE2	1.80	0.41
1:A:724:ILE:HG22	1:A:724:ILE:O	2.22	0.40
1:A:726:GLU:HA	1:A:727:PRO:HD3	1.86	0.40
1:A:20:LYS:HA	1:A:20:LYS:HD2	1.89	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	668/1271 (53%)	629 (94%)	39 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	594/1143 (52%)	564 (95%)	30 (5%)	21	50

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	SER
1	A	19	TYR
1	A	42	CYS
1	A	52	LYS
1	A	66	SER
1	A	67	LEU
1	A	250	THR
1	A	273	MET
1	A	278	SER
1	A	282	THR
1	A	285	HIS
1	A	301	LEU
1	A	319	ILE
1	A	364	ILE
1	A	465	CYS
1	A	528	LYS
1	A	546	ASP
1	A	552	ILE
1	A	588	VAL
1	A	622	SER
1	A	630	THR
1	A	641	ILE
1	A	713	LEU
1	A	737	GLU
1	A	842	LEU
1	A	857	ILE
1	A	868	ILE
1	A	871	HIS
1	A	873	THR
1	A	888	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	255	GLN

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Mol	Chain	Res	Type
1	A	285	HIS
1	A	293	ASN
1	A	323	HIS
1	A	414	GLN
1	A	452	ASN
1	A	524	GLN
1	A	554	GLN
1	A	638	ASN
1	A	715	HIS
1	A	799	GLN
1	A	826	ASN
1	A	851	ASN
1	A	867	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	SF4	A	1303	1	0,12,12	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AGS	A	1301	4	32,33,33	0.61	1 (3%)	45,52,52	0.72	1 (2%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	SF4	A	1303	1	-	-	0/6/5/5
3	AGS	A	1301	4	-	2/21/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1301	AGS	PG-S1G	2.09	1.95	1.90

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1301	AGS	PB-O3B-PG	-3.78	119.35	133.17

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1301	AGS	PB-O3A-PA-O1A
3	A	1301	AGS	PB-O3A-PA-O2A

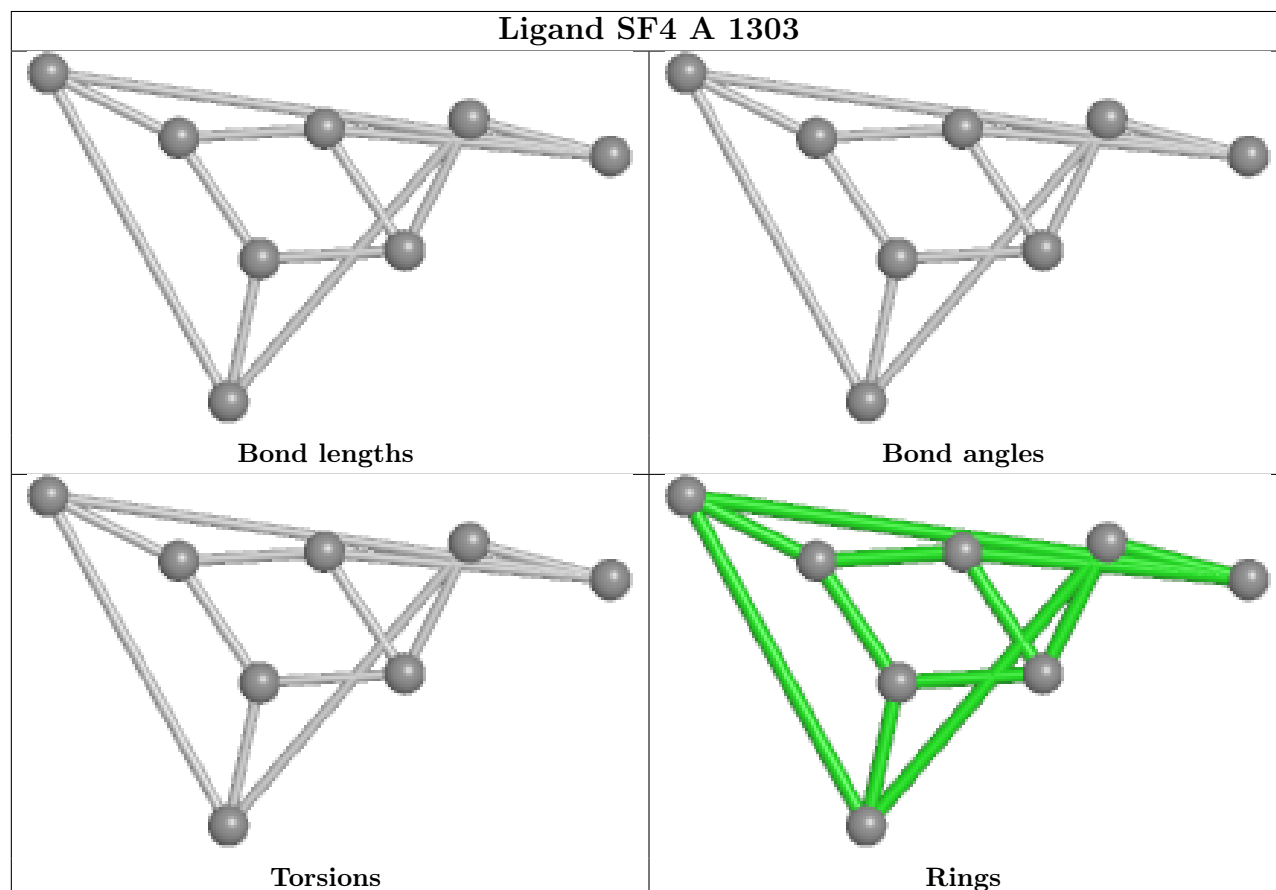
There are no ring outliers.

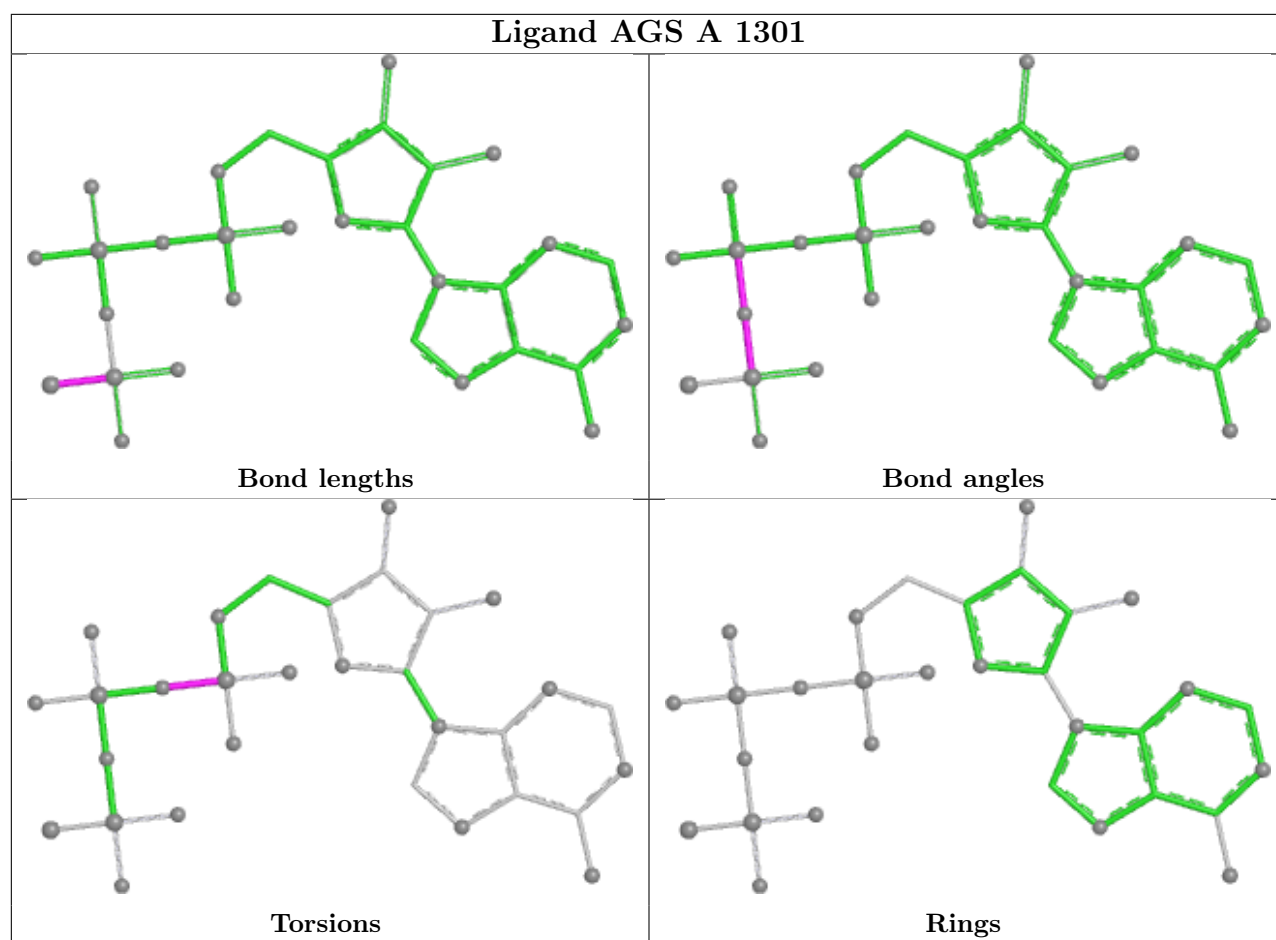
2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1303	SF4	6	0
3	A	1301	AGS	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

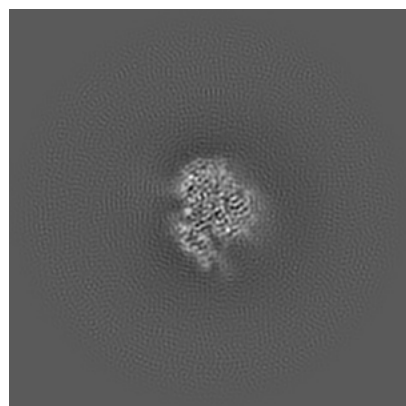
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48098. These allow visual inspection of the internal detail of the map and identification of artifacts.

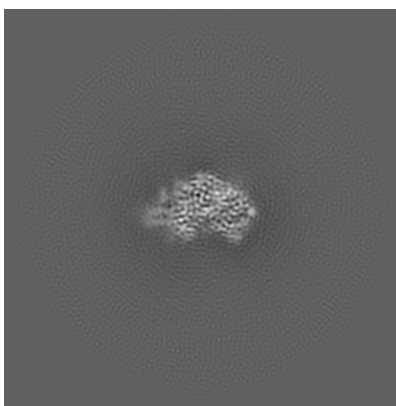
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

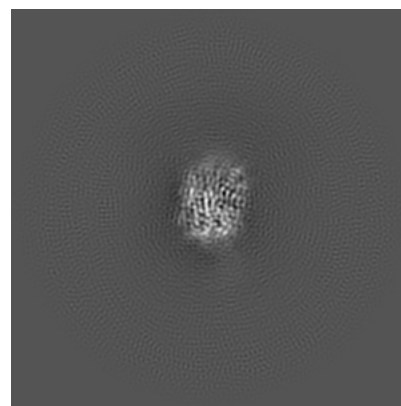
6.1.1 Primary map



X

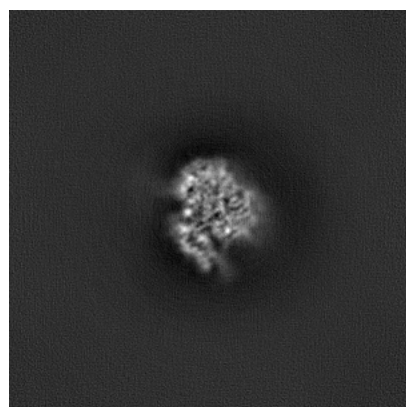


Y

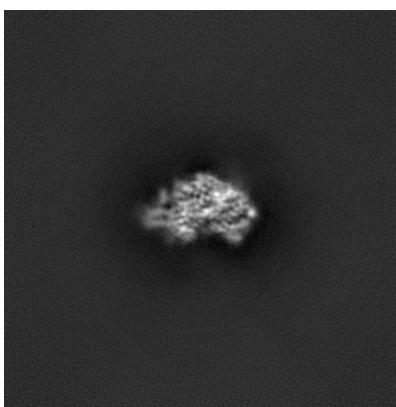


Z

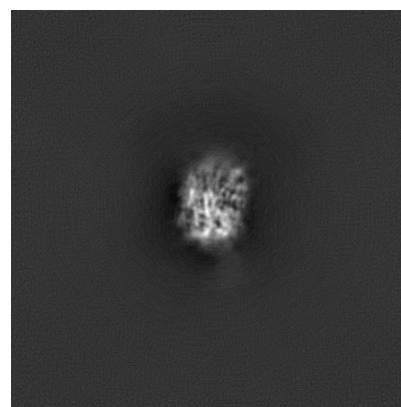
6.1.2 Raw map



X



Y

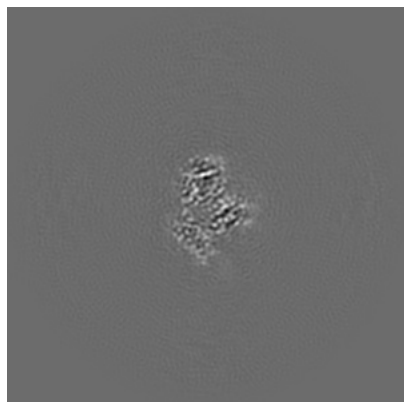


Z

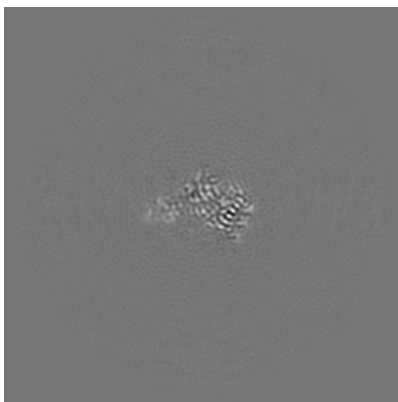
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

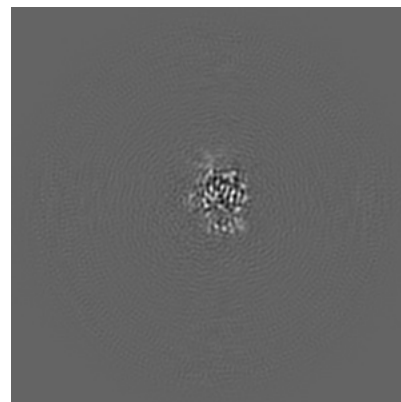
6.2.1 Primary map



X Index: 180

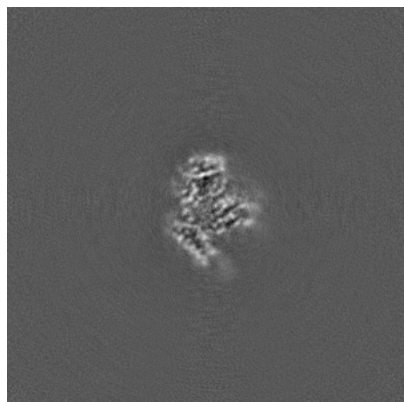


Y Index: 180

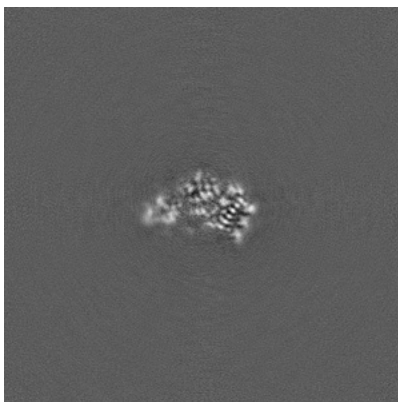


Z Index: 180

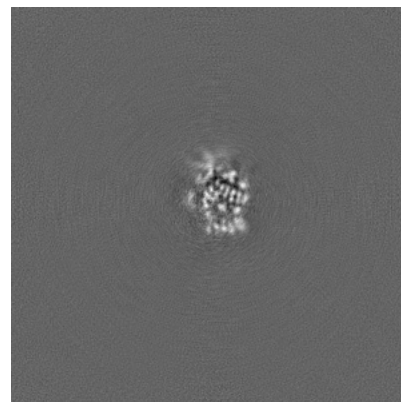
6.2.2 Raw map



X Index: 180



Y Index: 180

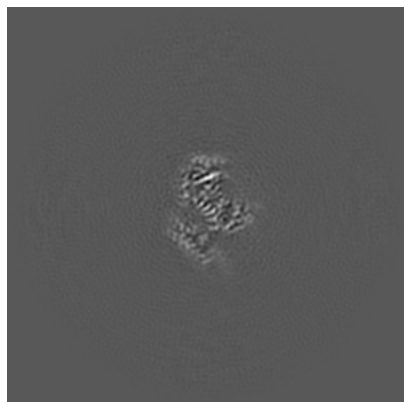


Z Index: 180

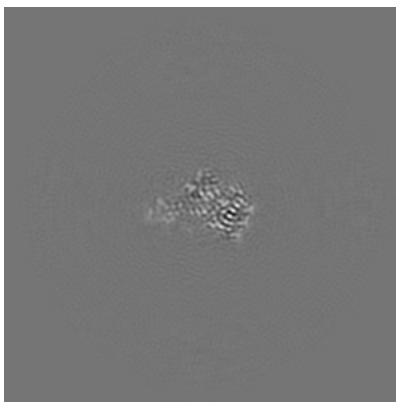
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

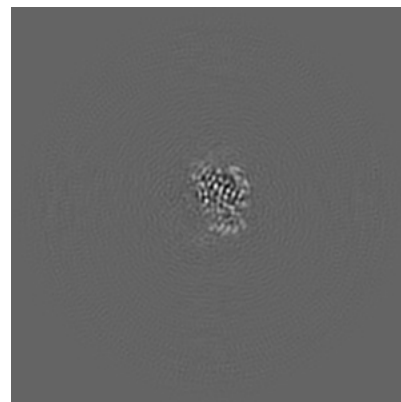
6.3.1 Primary map



X Index: 176

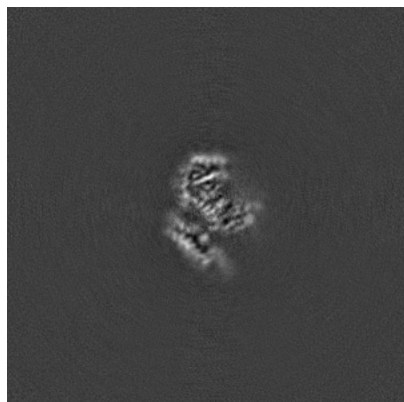


Y Index: 181

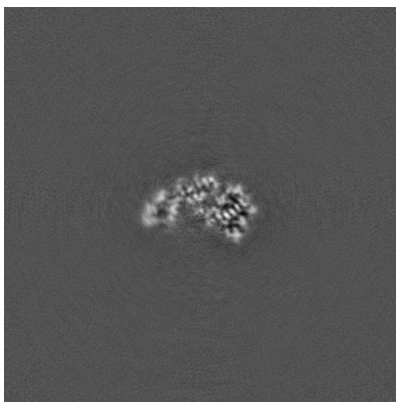


Z Index: 176

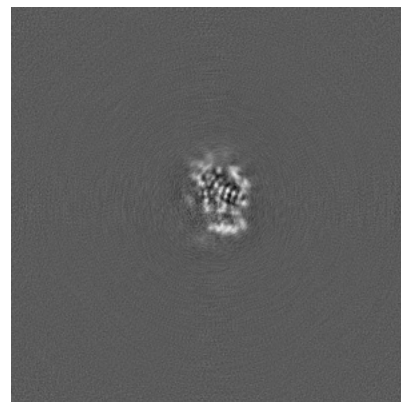
6.3.2 Raw map



X Index: 176



Y Index: 177

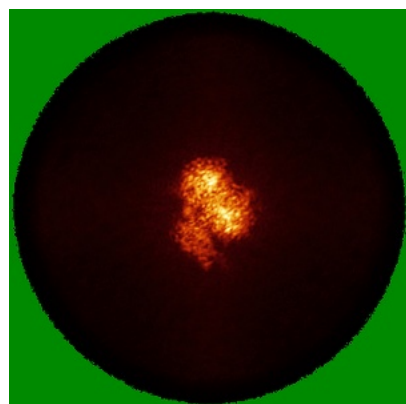


Z Index: 177

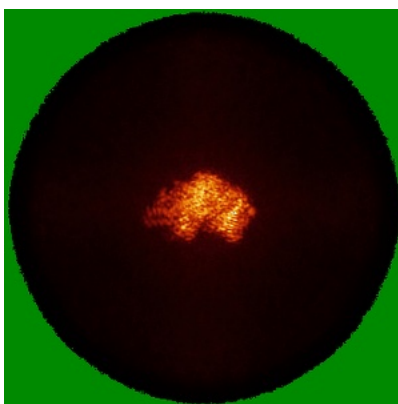
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

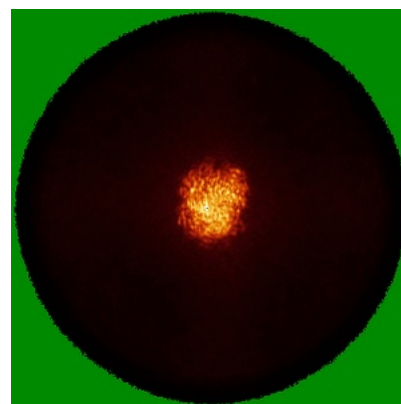
6.4.1 Primary map



X

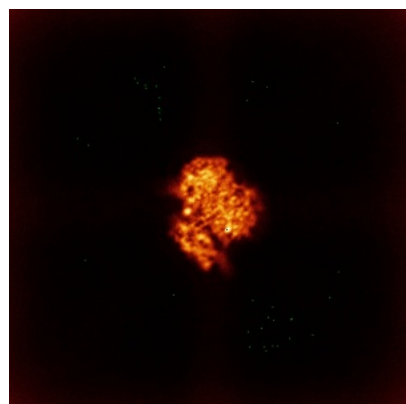


Y

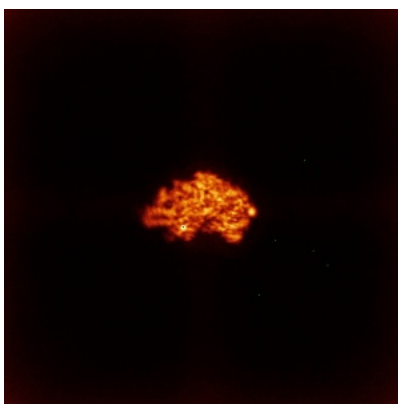


Z

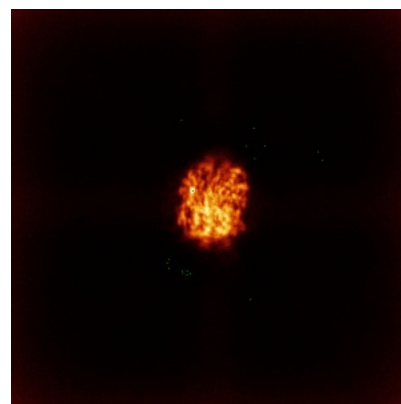
6.4.2 Raw map



X



Y

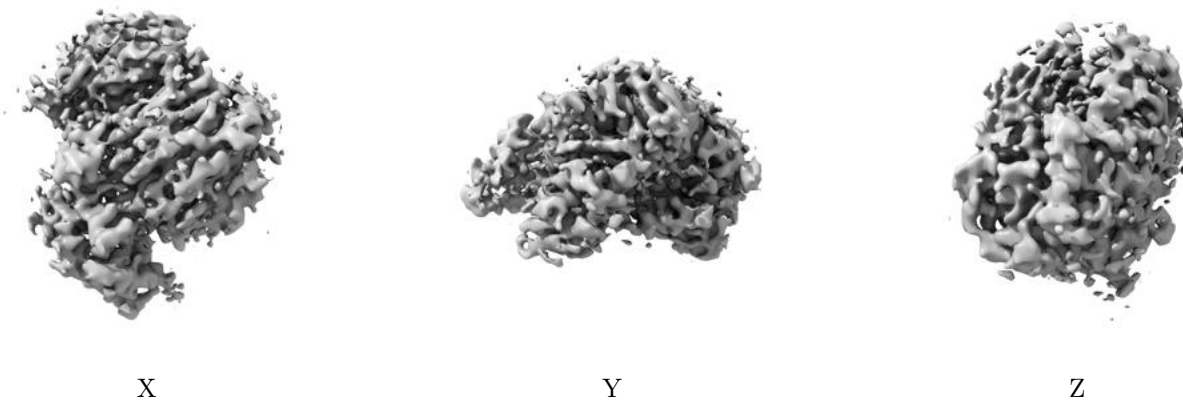


Z

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

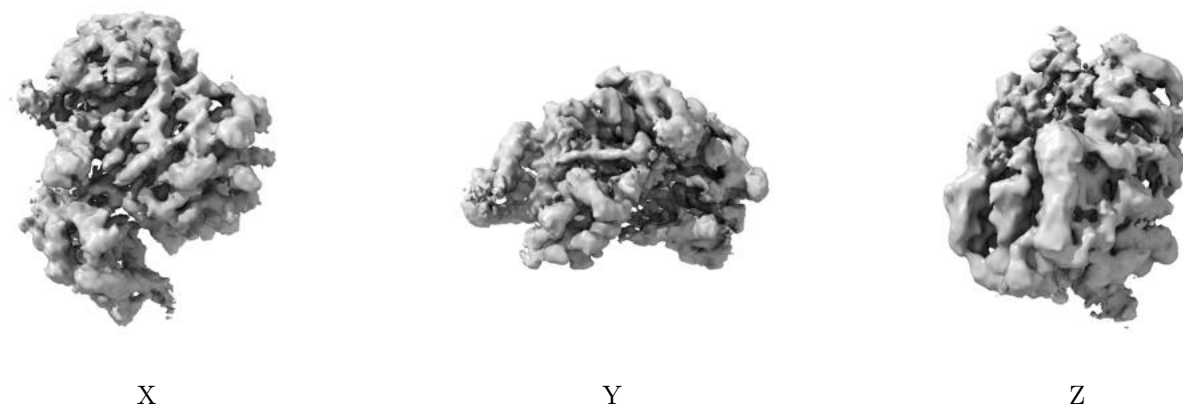
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.134. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

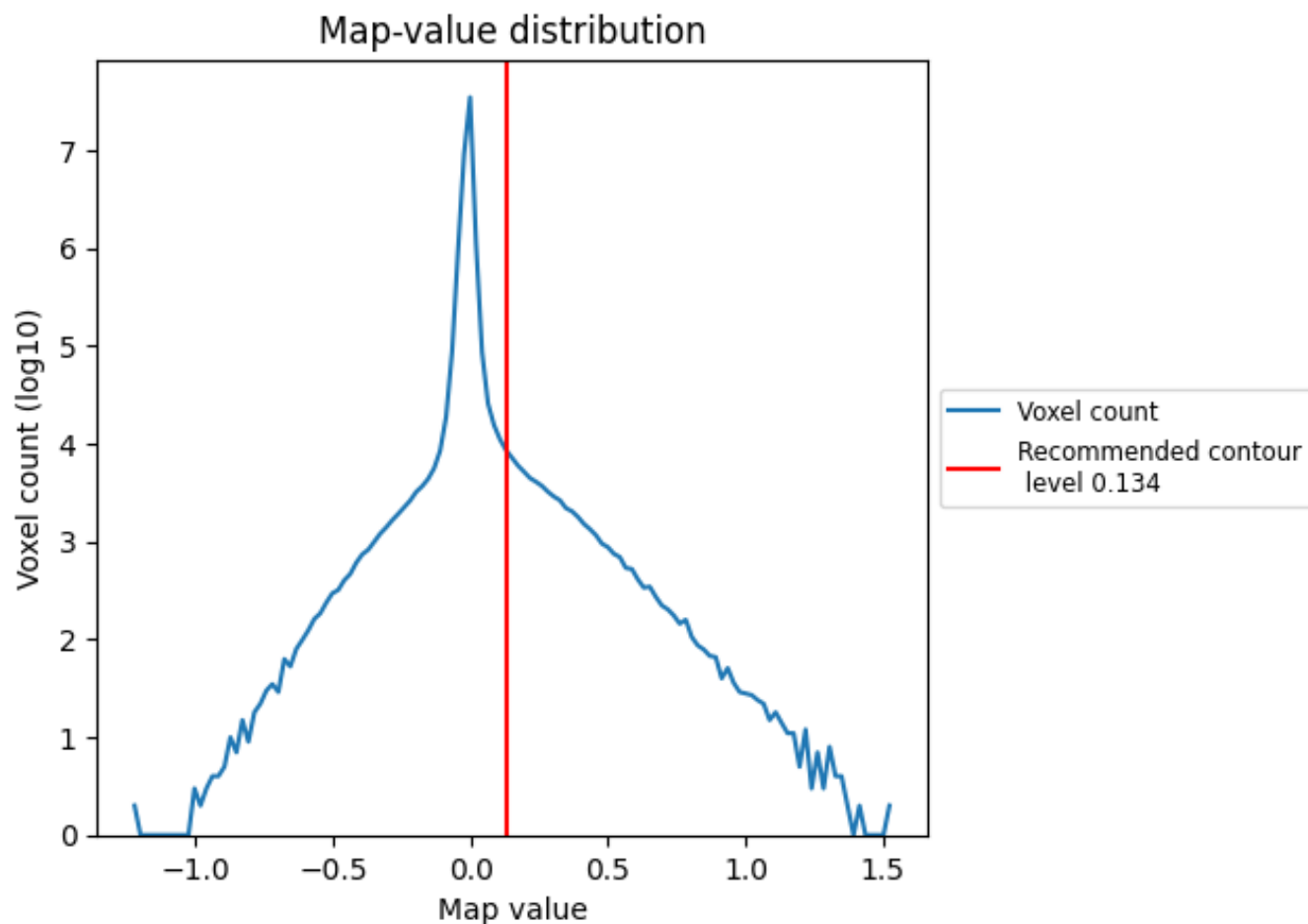
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

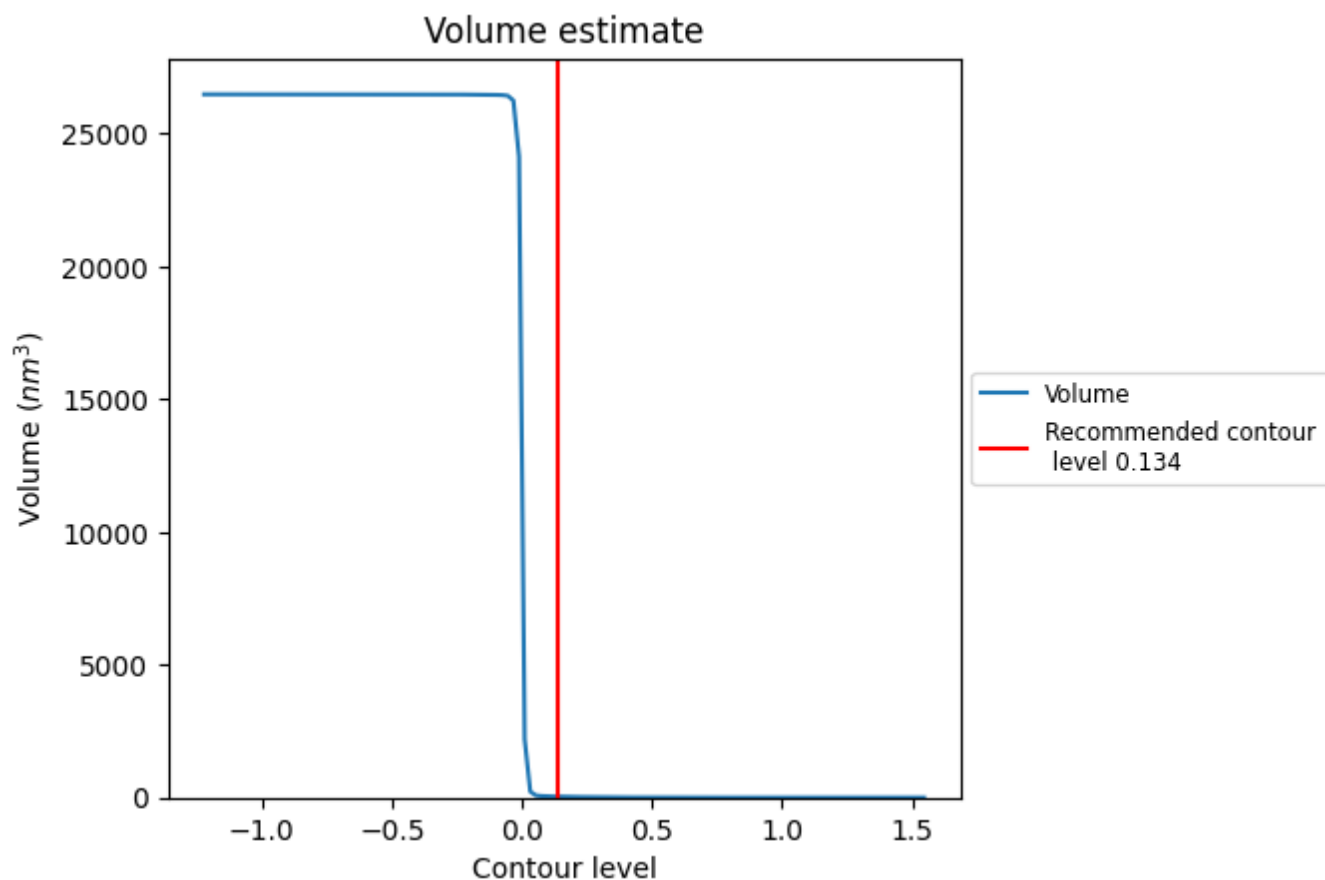
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

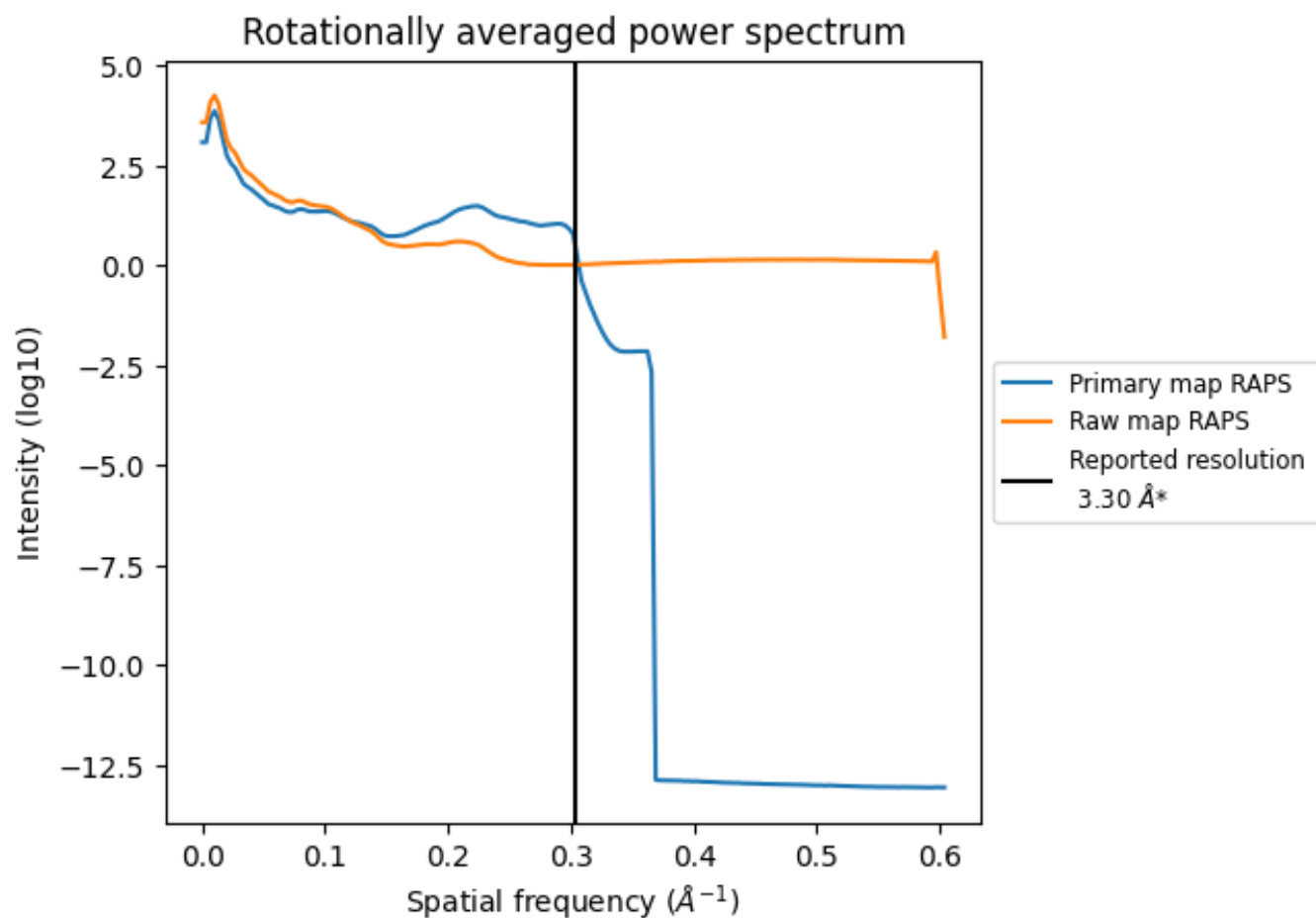
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 36 nm³; this corresponds to an approximate mass of 33 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 ⓘ

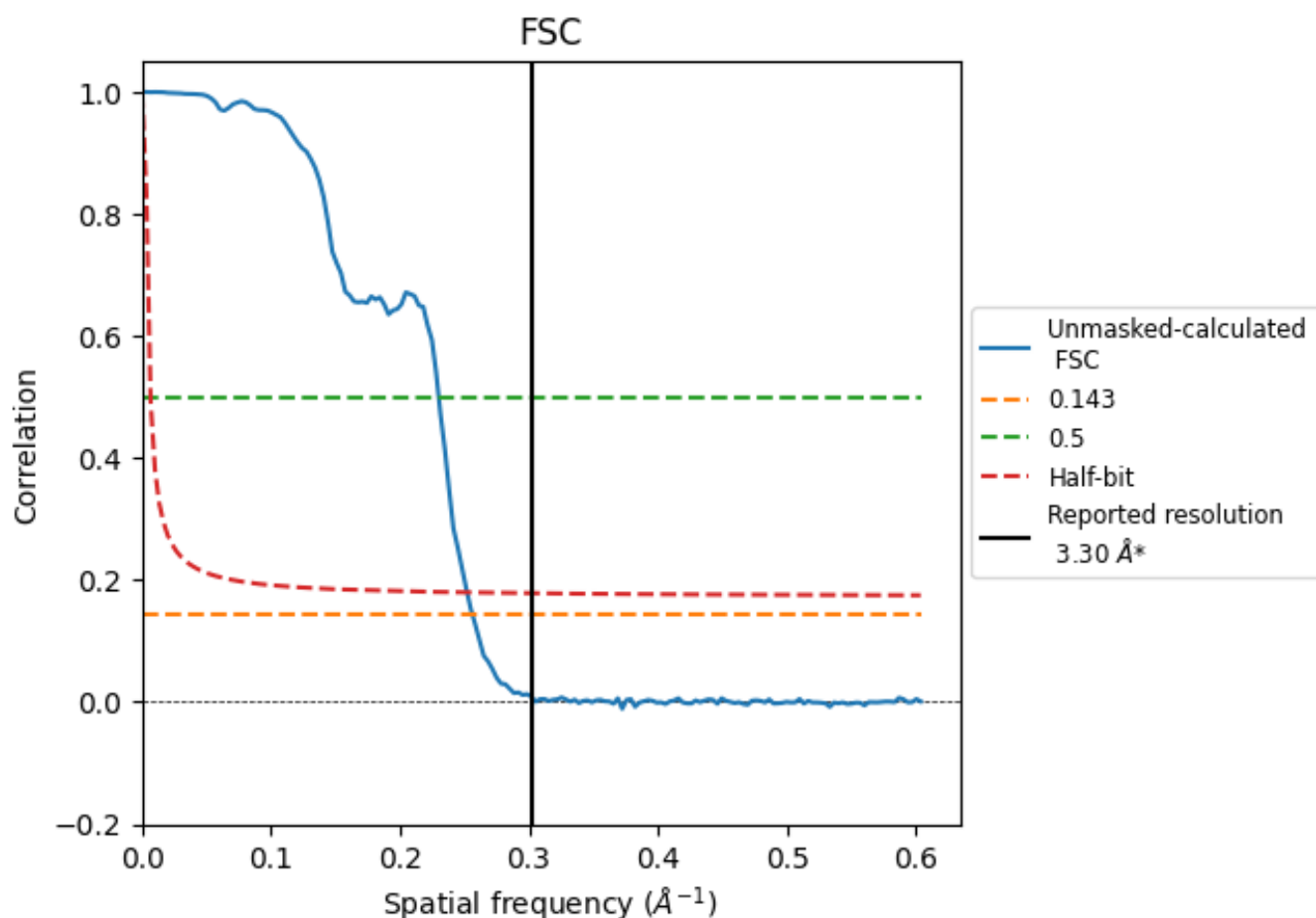


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

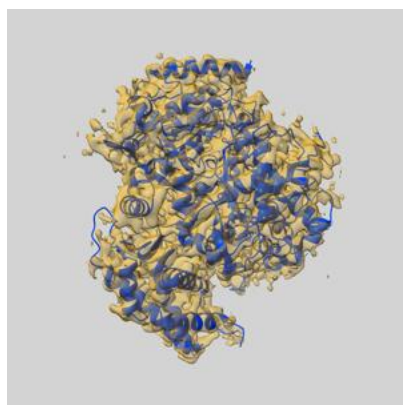
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.90	4.35	3.97

*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 3.90 differs from the reported value 3.3 by more than 10 %

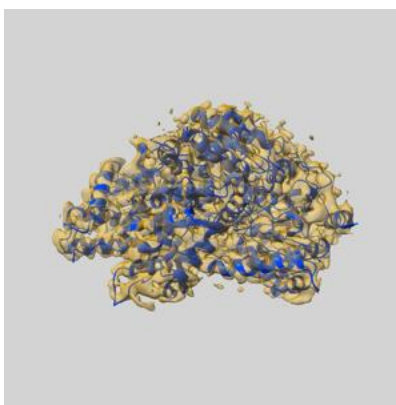
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48098 and PDB model 9EJA. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

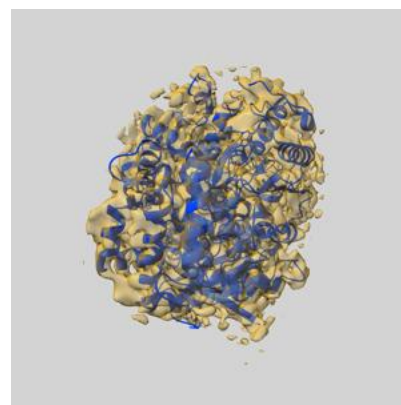
9.1 Map-model overlay [i](#)



X



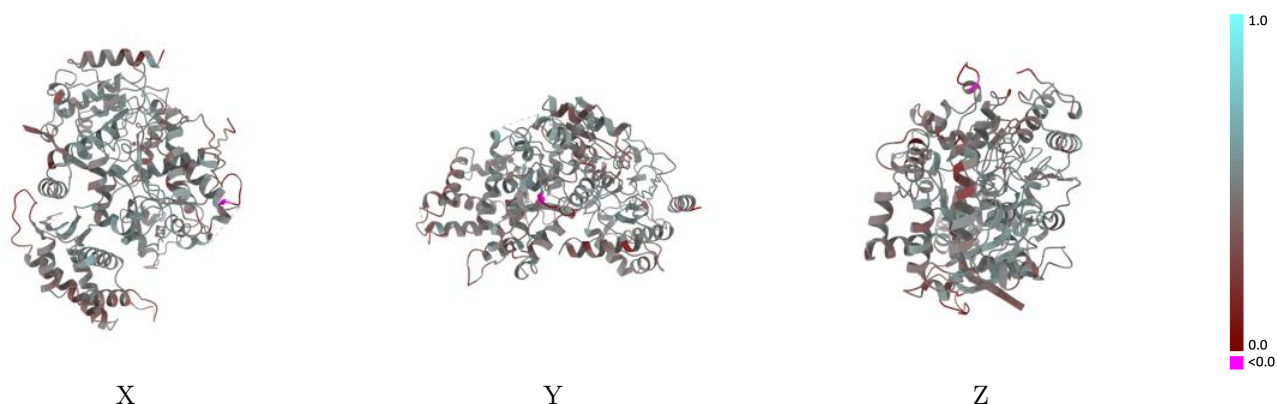
Y



Z

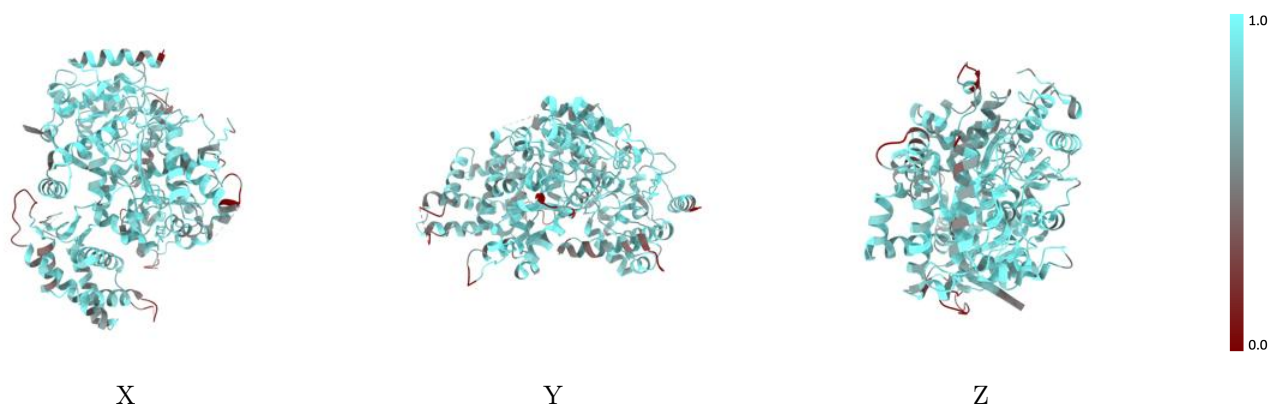
The images above show the 3D surface view of the map at the recommended contour level 0.134 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



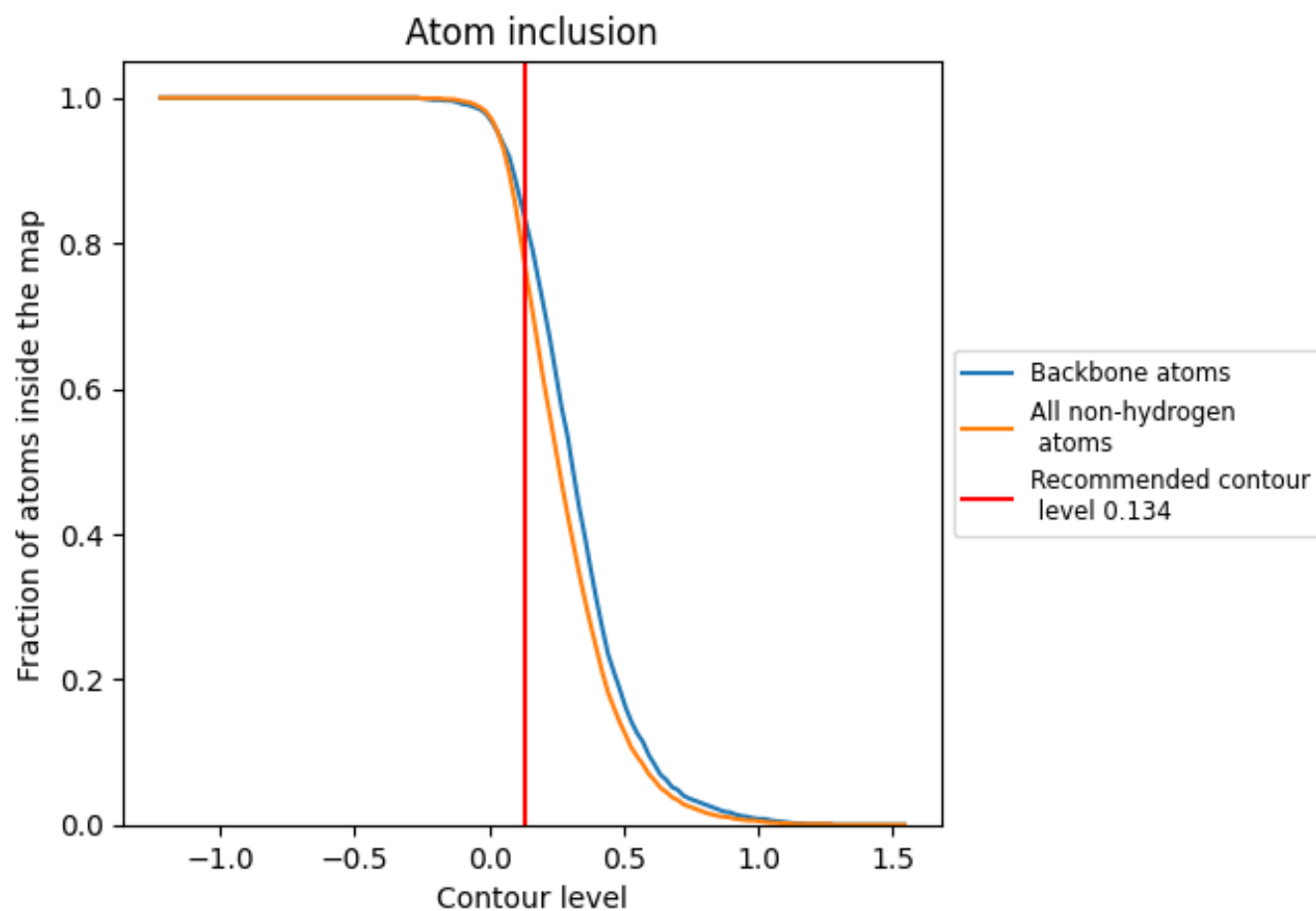
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.134).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 77% 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 (0.134) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7670	0.4600
A	0.7680	0.4600
B	0.7320	0.4360

