



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 12:01 AM UTC

PDB ID : 9JLB / pdb_00009jlb
EMDB ID : EMD-61582
Title : Cryo-EM structure of phyB-PIF6beta complex
Authors : Jia, H.L.; Guan, Z.Y.; Ding, J.Y.; Wang, X.Y.; Ma, L.; Yin, P.
Deposited on : 2024-09-18
Resolution : 3.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

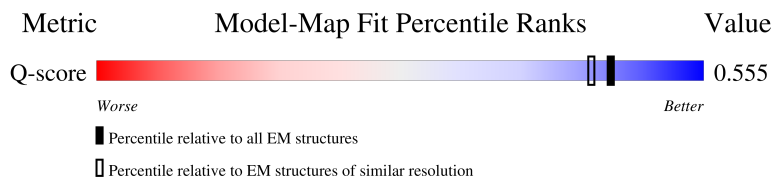
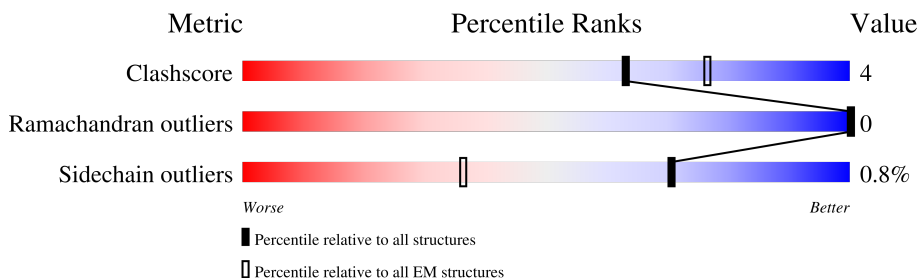
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	1226	
1	C	1226	
2	B	241	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16534 atoms, of which 8245 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 Phytochrome B.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	533	Total	C	H	N	O	S	0	0
			8271	2622	4128	718	773	30		
1	C	476	Total	C	H	N	O	S	0	0
			7393	2345	3697	640	681	30		

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	MET	-	initiating methionine	UNP P14713
A	-27	ASP	-	expression tag	UNP P14713
A	-26	TYR	-	expression tag	UNP P14713
A	-25	LYS	-	expression tag	UNP P14713
A	-24	ASP	-	expression tag	UNP P14713
A	-23	ASP	-	expression tag	UNP P14713
A	-22	ASP	-	expression tag	UNP P14713
A	-21	ASP	-	expression tag	UNP P14713
A	-20	LYS	-	expression tag	UNP P14713
A	-19	GLY	-	expression tag	UNP P14713
A	-18	ASP	-	expression tag	UNP P14713
A	-17	TYR	-	expression tag	UNP P14713
A	-16	LYS	-	expression tag	UNP P14713
A	-15	ASP	-	expression tag	UNP P14713
A	-14	ASP	-	expression tag	UNP P14713
A	-13	ASP	-	expression tag	UNP P14713
A	-12	ASP	-	expression tag	UNP P14713
A	-11	LYS	-	expression tag	UNP P14713
A	-10	ILE	-	expression tag	UNP P14713
A	-9	ASP	-	expression tag	UNP P14713
A	-8	TYR	-	expression tag	UNP P14713
A	-7	LYS	-	expression tag	UNP P14713
A	-6	ASP	-	expression tag	UNP P14713
A	-5	ASP	-	expression tag	UNP P14713
A	-4	ASP	-	expression tag	UNP P14713
A	-3	ASP	-	expression tag	UNP P14713

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	LYS	-	expression tag	UNP P14713
A	-1	GLY	-	expression tag	UNP P14713
A	0	SER	-	expression tag	UNP P14713
A	1173	LYS	-	expression tag	UNP P14713
A	1174	LEU	-	expression tag	UNP P14713
A	1175	GLY	-	expression tag	UNP P14713
A	1176	PRO	-	expression tag	UNP P14713
A	1177	GLU	-	expression tag	UNP P14713
A	1178	GLN	-	expression tag	UNP P14713
A	1179	LYS	-	expression tag	UNP P14713
A	1180	LEU	-	expression tag	UNP P14713
A	1181	ILE	-	expression tag	UNP P14713
A	1182	SER	-	expression tag	UNP P14713
A	1183	GLU	-	expression tag	UNP P14713
A	1184	GLU	-	expression tag	UNP P14713
A	1185	ASP	-	expression tag	UNP P14713
A	1186	LEU	-	expression tag	UNP P14713
A	1187	ASN	-	expression tag	UNP P14713
A	1188	SER	-	expression tag	UNP P14713
A	1189	ALA	-	expression tag	UNP P14713
A	1190	VAL	-	expression tag	UNP P14713
A	1191	ASP	-	expression tag	UNP P14713
A	1192	HIS	-	expression tag	UNP P14713
A	1193	HIS	-	expression tag	UNP P14713
A	1194	HIS	-	expression tag	UNP P14713
A	1195	HIS	-	expression tag	UNP P14713
A	1196	HIS	-	expression tag	UNP P14713
A	1197	HIS	-	expression tag	UNP P14713
C	-28	MET	-	initiating methionine	UNP P14713
C	-27	ASP	-	expression tag	UNP P14713
C	-26	TYR	-	expression tag	UNP P14713
C	-25	LYS	-	expression tag	UNP P14713
C	-24	ASP	-	expression tag	UNP P14713
C	-23	ASP	-	expression tag	UNP P14713
C	-22	ASP	-	expression tag	UNP P14713
C	-21	ASP	-	expression tag	UNP P14713
C	-20	LYS	-	expression tag	UNP P14713
C	-19	GLY	-	expression tag	UNP P14713
C	-18	ASP	-	expression tag	UNP P14713
C	-17	TYR	-	expression tag	UNP P14713
C	-16	LYS	-	expression tag	UNP P14713
C	-15	ASP	-	expression tag	UNP P14713

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-14	ASP	-	expression tag	UNP P14713
C	-13	ASP	-	expression tag	UNP P14713
C	-12	ASP	-	expression tag	UNP P14713
C	-11	LYS	-	expression tag	UNP P14713
C	-10	ILE	-	expression tag	UNP P14713
C	-9	ASP	-	expression tag	UNP P14713
C	-8	TYR	-	expression tag	UNP P14713
C	-7	LYS	-	expression tag	UNP P14713
C	-6	ASP	-	expression tag	UNP P14713
C	-5	ASP	-	expression tag	UNP P14713
C	-4	ASP	-	expression tag	UNP P14713
C	-3	ASP	-	expression tag	UNP P14713
C	-2	LYS	-	expression tag	UNP P14713
C	-1	GLY	-	expression tag	UNP P14713
C	0	SER	-	expression tag	UNP P14713
C	1173	LYS	-	expression tag	UNP P14713
C	1174	LEU	-	expression tag	UNP P14713
C	1175	GLY	-	expression tag	UNP P14713
C	1176	PRO	-	expression tag	UNP P14713
C	1177	GLU	-	expression tag	UNP P14713
C	1178	GLN	-	expression tag	UNP P14713
C	1179	LYS	-	expression tag	UNP P14713
C	1180	LEU	-	expression tag	UNP P14713
C	1181	ILE	-	expression tag	UNP P14713
C	1182	SER	-	expression tag	UNP P14713
C	1183	GLU	-	expression tag	UNP P14713
C	1184	GLU	-	expression tag	UNP P14713
C	1185	ASP	-	expression tag	UNP P14713
C	1186	LEU	-	expression tag	UNP P14713
C	1187	ASN	-	expression tag	UNP P14713
C	1188	SER	-	expression tag	UNP P14713
C	1189	ALA	-	expression tag	UNP P14713
C	1190	VAL	-	expression tag	UNP P14713
C	1191	ASP	-	expression tag	UNP P14713
C	1192	HIS	-	expression tag	UNP P14713
C	1193	HIS	-	expression tag	UNP P14713
C	1194	HIS	-	expression tag	UNP P14713
C	1195	HIS	-	expression tag	UNP P14713
C	1196	HIS	-	expression tag	UNP P14713
C	1197	HIS	-	expression tag	UNP P14713

- Molecule 2 is a protein called Transcription factor PIF6.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	43	Total	C	H	N	O	S	0	0
			712	227	348	61	73	3		

There are 58 discrepancies between the modelled and reference sequences:

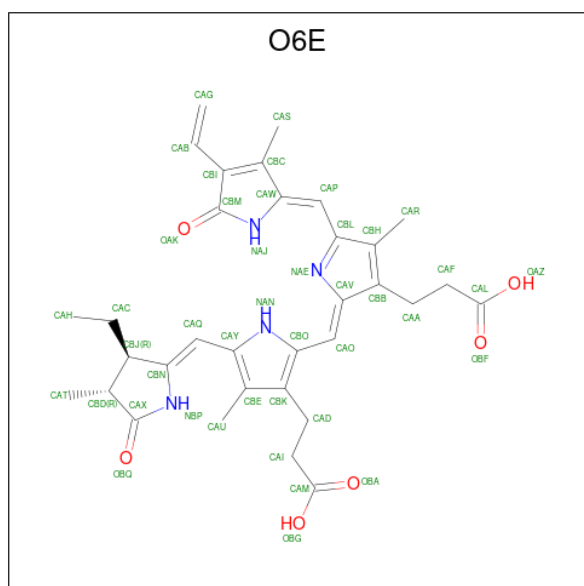
Chain	Residue	Modelled	Actual	Comment	Reference
B	-26	MET	-	initiating methionine	UNP Q8L5W7
B	-25	GLY	-	expression tag	UNP Q8L5W7
B	-24	SER	-	expression tag	UNP Q8L5W7
B	-23	SER	-	expression tag	UNP Q8L5W7
B	-22	HIS	-	expression tag	UNP Q8L5W7
B	-21	HIS	-	expression tag	UNP Q8L5W7
B	-20	HIS	-	expression tag	UNP Q8L5W7
B	-19	HIS	-	expression tag	UNP Q8L5W7
B	-18	HIS	-	expression tag	UNP Q8L5W7
B	-17	HIS	-	expression tag	UNP Q8L5W7
B	-16	SER	-	expression tag	UNP Q8L5W7
B	-15	SER	-	expression tag	UNP Q8L5W7
B	-14	GLY	-	expression tag	UNP Q8L5W7
B	-13	LEU	-	expression tag	UNP Q8L5W7
B	-12	VAL	-	expression tag	UNP Q8L5W7
B	-11	PRO	-	expression tag	UNP Q8L5W7
B	-10	ARG	-	expression tag	UNP Q8L5W7
B	-9	GLY	-	expression tag	UNP Q8L5W7
B	-8	SER	-	expression tag	UNP Q8L5W7
B	-7	HIS	-	expression tag	UNP Q8L5W7
B	-6	SER	-	expression tag	UNP Q8L5W7
B	-5	ASP	-	expression tag	UNP Q8L5W7
B	-4	GLU	-	expression tag	UNP Q8L5W7
B	-3	VAL	-	expression tag	UNP Q8L5W7
B	-2	ASP	-	expression tag	UNP Q8L5W7
B	-1	ALA	-	expression tag	UNP Q8L5W7
B	0	HIS	-	expression tag	UNP Q8L5W7
B	184	GLU	-	expression tag	UNP Q8L5W7
B	185	SER	-	expression tag	UNP Q8L5W7
B	186	ALA	-	expression tag	UNP Q8L5W7
B	187	TRP	-	expression tag	UNP Q8L5W7
B	188	SER	-	expression tag	UNP Q8L5W7
B	189	HIS	-	expression tag	UNP Q8L5W7
B	190	PRO	-	expression tag	UNP Q8L5W7
B	191	GLN	-	expression tag	UNP Q8L5W7
B	192	PHE	-	expression tag	UNP Q8L5W7
B	193	GLU	-	expression tag	UNP Q8L5W7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	194	LYS	-	expression tag	UNP Q8L5W7
B	195	GLY	-	expression tag	UNP Q8L5W7
B	196	GLY	-	expression tag	UNP Q8L5W7
B	197	GLY	-	expression tag	UNP Q8L5W7
B	198	SER	-	expression tag	UNP Q8L5W7
B	199	GLY	-	expression tag	UNP Q8L5W7
B	200	GLY	-	expression tag	UNP Q8L5W7
B	201	GLY	-	expression tag	UNP Q8L5W7
B	202	SER	-	expression tag	UNP Q8L5W7
B	203	GLY	-	expression tag	UNP Q8L5W7
B	204	GLY	-	expression tag	UNP Q8L5W7
B	205	SER	-	expression tag	UNP Q8L5W7
B	206	ALA	-	expression tag	UNP Q8L5W7
B	207	TRP	-	expression tag	UNP Q8L5W7
B	208	SER	-	expression tag	UNP Q8L5W7
B	209	HIS	-	expression tag	UNP Q8L5W7
B	210	PRO	-	expression tag	UNP Q8L5W7
B	211	GLN	-	expression tag	UNP Q8L5W7
B	212	PHE	-	expression tag	UNP Q8L5W7
B	213	GLU	-	expression tag	UNP Q8L5W7
B	214	LYS	-	expression tag	UNP Q8L5W7

- Molecule 3 is 3-[5-[[[3 {R},4 {R}]-3-ethyl-4-methyl-5-oxidanylidene-3,4-dihydropyrrol-2-yl]methyl]-2-[[5-[(4-ethyl-3-methyl-5-oxidanylidene-pyrrol-2-yl)methyl]-3-(3-hydroxy-3-oxopropyl)-4-methyl-1 {H}-pyrrol-2-yl]methyl]-4-methyl-1 {H}-pyrrol-3-yl]propanoic acid (CCD ID: O6E) (formula: C₃₃H₃₈N₄O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	H	N	O	0
			79	33	36	4	6	
3	C	1	Total	C	H	N	O	0
			79	33	36	4	6	

ASP	MET	MET	LEU	MET	MET	PRO	TYR	LYS	LEU	GLY	PRO	GLU	GLN	LYS	LEU	ILE	SER	GLU	GLU	ASP	LEU	ASN	SER	ALA	VAL	ASP	HIS	HIS	HIS	HIS	HIS	HIS
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- Molecule 1: Phytochrome B

[illegible]

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

TTR	GLY	SER	VAL	PRO	GLU	GLN	GLN	THR	ALA	TTR	LEU	LEU	ARG	ILE	ILE	GLN	ARG	G111	F117	R129	I143	M144	PRO	GLN	SER	VAL	PRO	THR	LEU	GLU	LVS	PRO	PRO	GLU	I156	G160	L166	A181	L187	N188	P189	V190	W191	I192	A203	R207	L216		
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E222	D223	L248	V261	M274	V275	Y276	D281	E282	I308	R313	K317	Q318	R322	M323	I324	V325	Q342	L346	R352	Y361	L371	G379	ASN	GLU	ASP	ASP	GLY	ASN	ASN	VAL	ALA	SER	SER	GLY	ARG	ARG	S393	W397	G398	L399	V400	M422		
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E441	R446	L450	M454	L455	L456	R457	D458	Q466	S467	P468	R468	D501	A511	D512	S513	T514	T545	R546	R547	D548	T557	E560	S585	ALA	LYS	HIS	PRO	HIS	PRO	GLU	ASP	LYS	ASP	ASP	GLY	Q577	Q597	Q611	D616	S617	F618	K619	E620	S621	GLN
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ALA ALA MET ASN SER LYS VAL VAL ASP GLY VAL VAL GLN PRO CYS ARG ASP MET ALA ALA GLY GLU GLN GLY ILE ASP LEU LEU GLY GLY VAL ALA ALA ARG GLU MET MET VAL ARG LEU ILE GLU THR THR VAL PRO PRO ILE PHE THR ALA ALA VAL ASP ALA ALA GLY GLY CYS ILE ASN TRP ASN ALA

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

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

GLY	GLN	ASP	THR	LYS	PHE	PRO	PHE	PHE	PHE	ASP	ARG	ASN	GLY	LYS	PHE	VAL	GLN	ALA	LEU	LEU	THR	ALA	ASN	LYS	ARG	VAL	SER	LEU	GLY	LYS	VAL	ILE	GLY	ALA	PHE	CYS	PHE	LEU	GLN	PRO	PRO	SER	SER	GLU	GLU	LEU	GLN	GLN	ALA	LEU	LEU	ALA	VAL	GLN	GLN	ARG	ARG	GLN	GLN	SER
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THR	GLU	CYS	PHE	THR	LYS	ALA	LYS	GLU	LEU	ALA	TYR	ILE	CYS	GLN	VAL	ILE	LYS	ASN	PRO	LEU	SER	GLY	MET	ARG	PHE	ALA	ASN	SER	LEU	LEU	GLU	ALA	THR	THR	ASP	LEU	ASN	ASP	GLU	GLN	LYS	GLN	LEU	LEU	THR	THR	SER	VAL	CYS	GLU	LYS	GLN	ILE	SER	ILE	VAL	GLY	ASP
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MET	ASP	LEU	GLU	SER	ILE	GLU	ASP	GLY	PHE	VAL	LEU	LYS	ARG	GLU	GLU	PHE	PHE	LEU	GLY	SER	SER	ILE	ASN	ALA	ILE	VAL	VAL	GLN	ALA	MET	PHE	LEU	LEU	LEU	ARG	ASP	ARG	GLY	GLN	LEU	GLN	LEU	LEU	ILE	ARG	ASP	ILE	PRO	GLU	GLU	GLY	LYS	ILE	ILE	SER	SER	ILE	GLU	VAL	PHE	GLY	ASP	GLN	TIF
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[illegible]

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

SER	GLY	ASP	MET	MET	LEU	MET	MET	PRO	TYR	LYS	LEU	GLY	PRO	GLU	GLN	LYS	LEU	ILE	SER	SER	GLU	GLU	ASP	LEU	ASN	SER	ALA	VAL	ASP	HIS	HIS	HIS	HIS	HIS	HIS
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- Molecule 2: Transcription factor PIF6

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	429631	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	6.889	Depositor
Minimum map value	-4.455	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.150	Depositor
Recommended contour level	0.45	Depositor
Map size ($\text{\AA}$)	230.72, 230.72, 230.72	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.824, 0.824, 0.824	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: O6E

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	0.13	0/4225	0.27	0/5717
1	C	0.12	0/3770	0.26	0/5103
2	B	0.09	0/367	0.20	0/486
All	All	0.12	0/8362	0.26	0/11306

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4143	4128	4129	35	0
1	C	3696	3697	3696	37	0
2	B	364	348	348	5	0
3	A	43	36	0	1	0
3	C	43	36	0	1	0
All	All	8289	8245	8173	69	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 4.

The worst 5 of 69 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:C:560:GLU:OE1	1:C:597:GLN:NE2	2.02	0.92
1:C:450:LEU:O	1:C:454:MET:HE3	1.90	0.71
1:A:378:ASN:ND2	1:C:248:LEU:O	2.28	0.67
1:C:560:GLU:N	1:C:560:GLU:OE2	2.28	0.65
1:A:274:MET:HE3	1:A:276:TYR:OH	1.97	0.63

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	525/1226 (43%)	513 (98%)	12 (2%)	0	100	100
1	C	468/1226 (38%)	458 (98%)	10 (2%)	0	100	100
2	B	39/241 (16%)	39 (100%)	0	0	100	100
All	All	1032/2693 (38%)	1010 (98%)	22 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	451/1044 (43%)	446 (99%)	5 (1%)	65	83

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	402/1044 (38%)	400 (100%)	2 (0%)	81	89
2	B	39/206 (19%)	39 (100%)	0	100	100
All	All	892/2294 (39%)	885 (99%)	7 (1%)	70	86

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	416	TYR
1	A	437	LEU
1	C	318	GLN
1	C	317	LYS
1	A	274	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	328	ASN
1	C	279	HIS
1	A	577	GLN
1	A	510	HIS
1	C	235	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	O6E	C	1201	1	46,46,46	1.15	5 (10%)	62,67,67	1.65	6 (9%)
3	O6E	A	1201	1	46,46,46	1.39	8 (17%)	62,67,67	1.56	12 (19%)

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
3	O6E	C	1201	1	-	12/26/74/74	0/4/4/4
3	O6E	A	1201	1	-	9/26/74/74	0/4/4/4

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1201	O6E	CAB-CBI	-3.66	1.37	1.47
3	C	1201	O6E	CAB-CBI	-3.52	1.38	1.47
3	A	1201	O6E	CAP-CBL	-3.30	1.32	1.40
3	A	1201	O6E	OBG-CAM	-2.82	1.21	1.30
3	C	1201	O6E	CAP-CBL	-2.66	1.34	1.40

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1201	O6E	CAH-CAC-CBJ	9.55	133.68	113.41
3	A	1201	O6E	CAC-CBJ-CBN	5.39	126.50	112.67
3	A	1201	O6E	CAS-CBC-CAW	4.99	130.24	124.16
3	C	1201	O6E	CAS-CBC-CAW	3.08	127.91	124.16
3	A	1201	O6E	CBD-CBJ-CBN	3.03	105.88	101.34

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

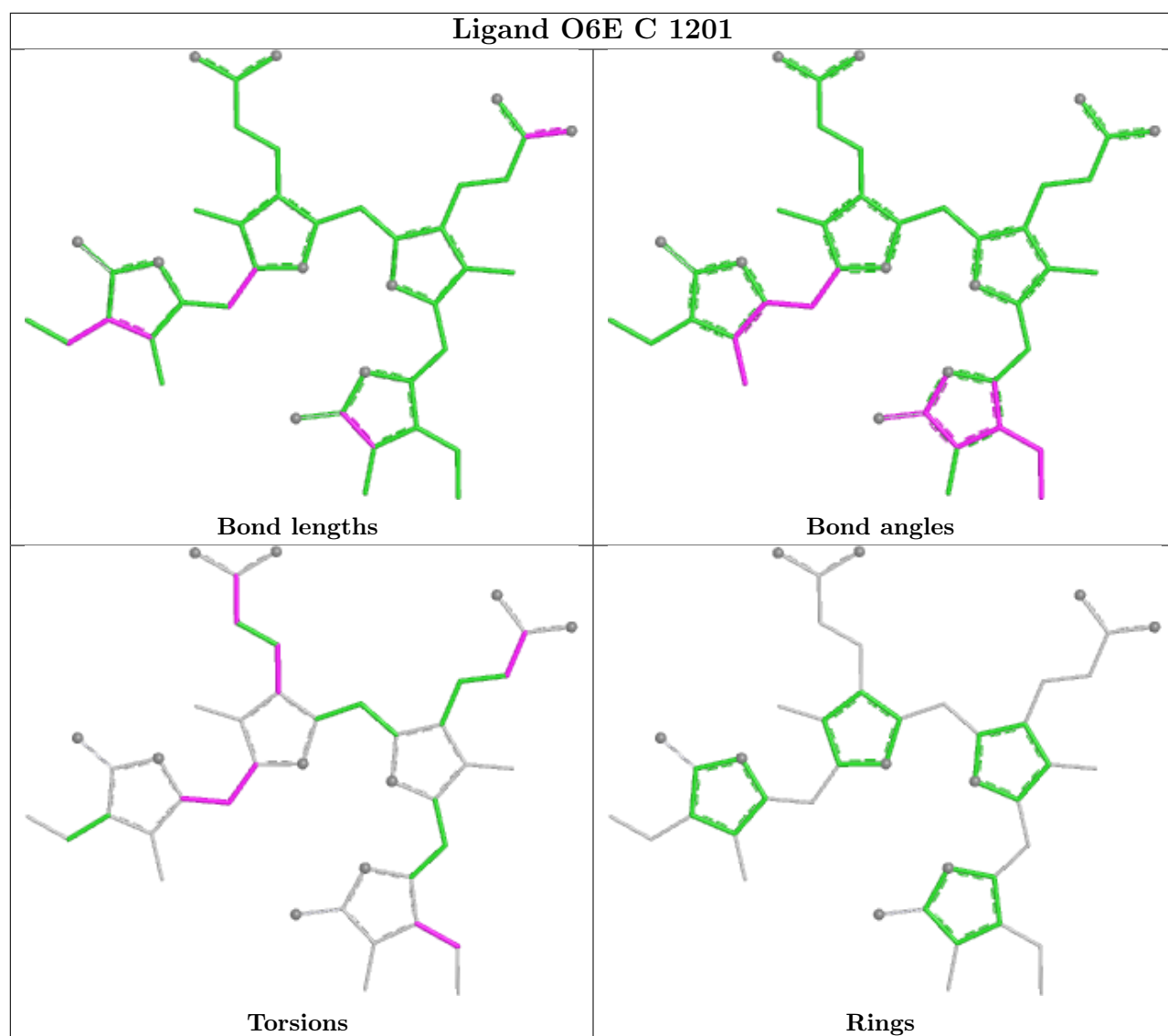
Mol	Chain	Res	Type	Atoms
3	A	1201	O6E	CAH-CAC-CBJ-CBD
3	A	1201	O6E	CAW-CAP-CBL-NAE
3	A	1201	O6E	CAW-CAP-CBL-CBH
3	C	1201	O6E	CAH-CAC-CBJ-CBD
3	C	1201	O6E	CAH-CAC-CBJ-CBN

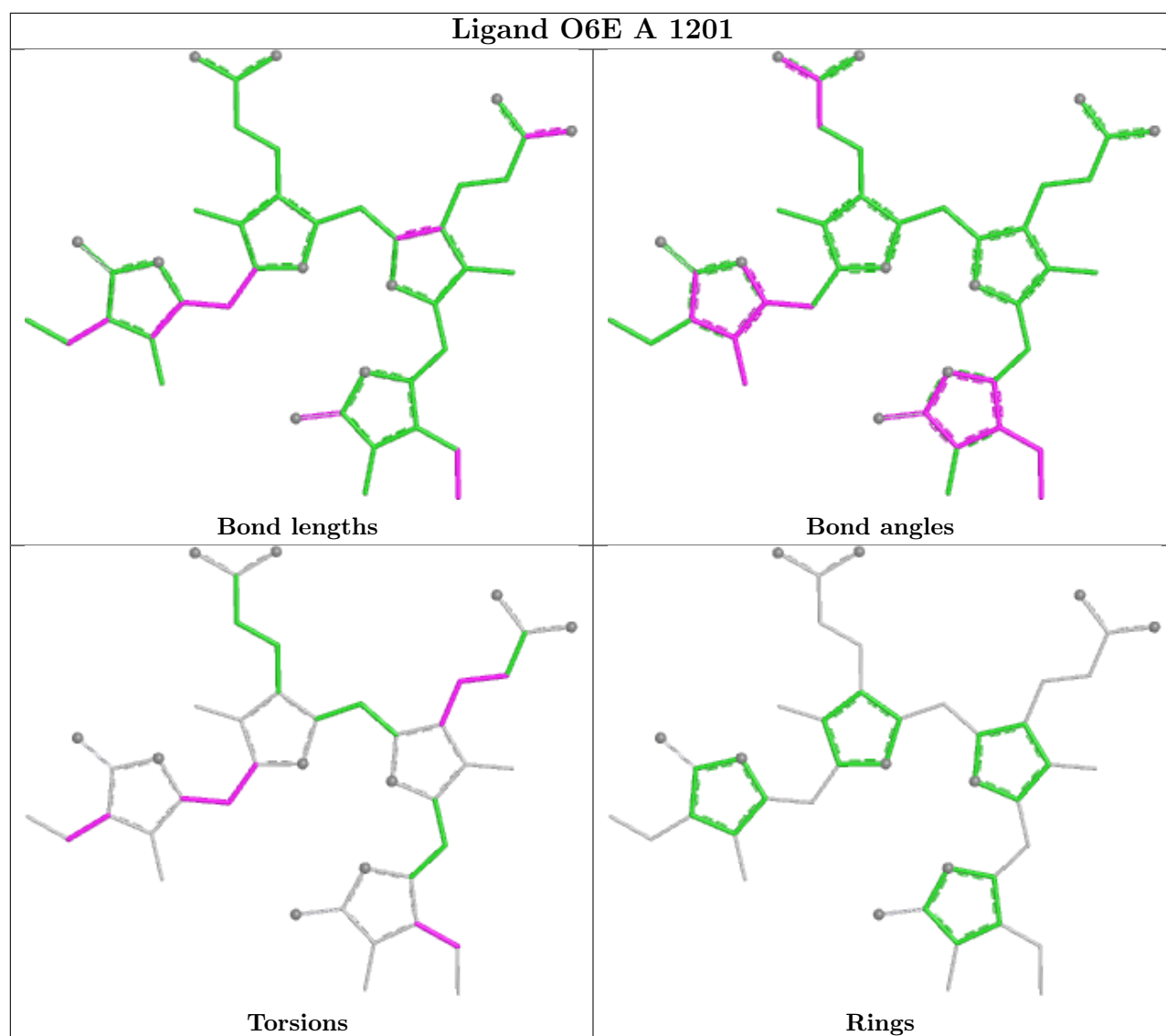
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1201	O6E	1	0
3	A	1201	O6E	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.

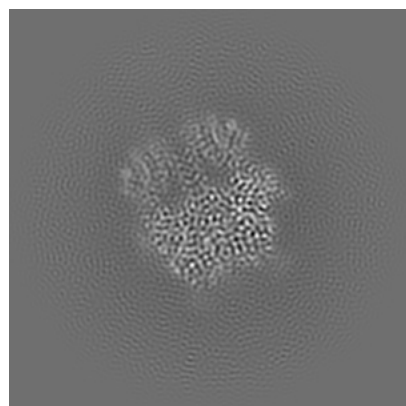
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61582. These allow visual inspection of the internal detail of the map and identification of artifacts.

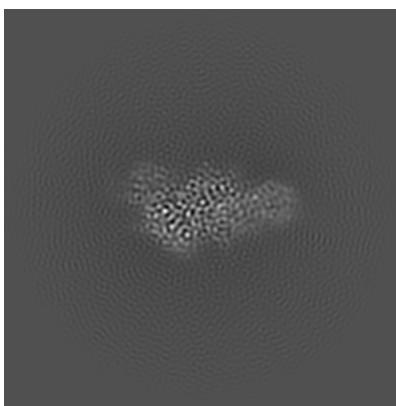
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

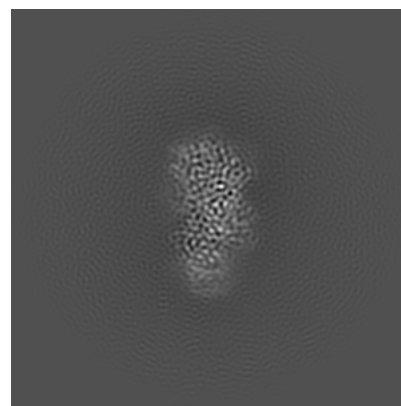
6.1.1 Primary map



X

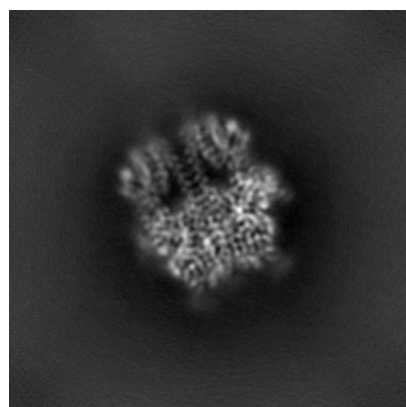


Y

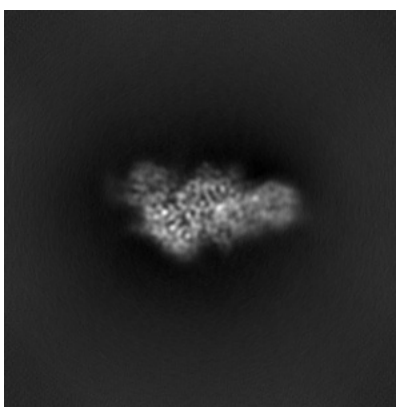


Z

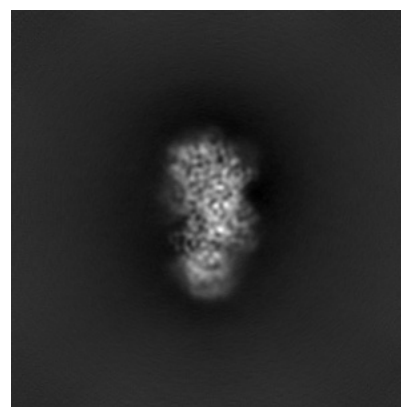
6.1.2 Raw map



X



Y

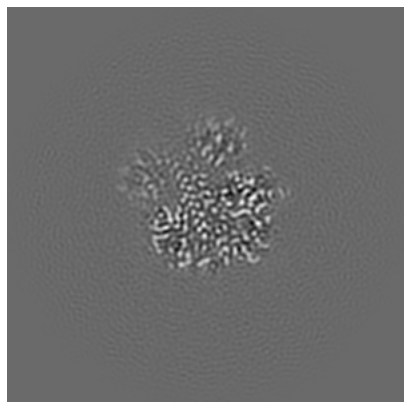


Z

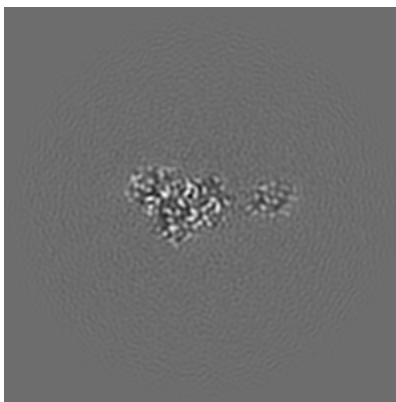
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

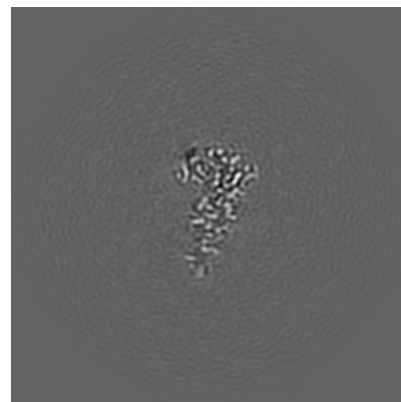
6.2.1 Primary map



X Index: 140

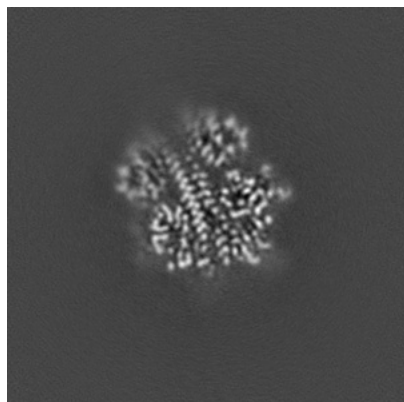


Y Index: 140

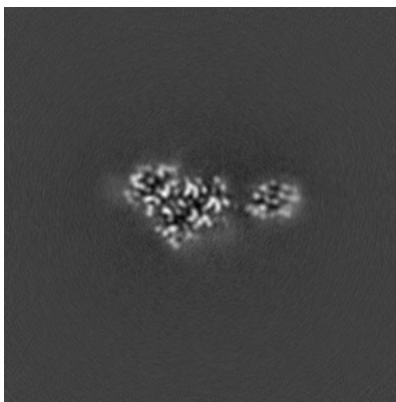


Z Index: 140

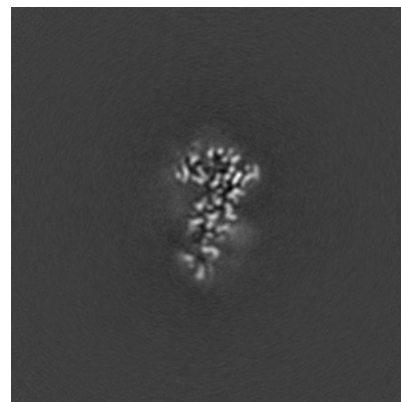
6.2.2 Raw map



X Index: 140



Y Index: 140

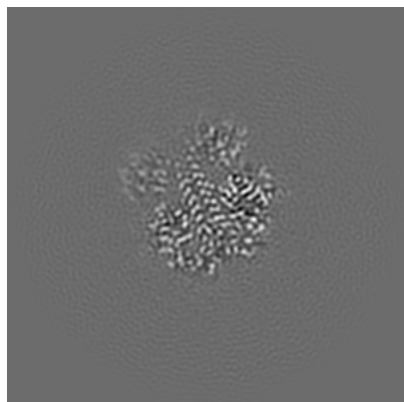


Z Index: 140

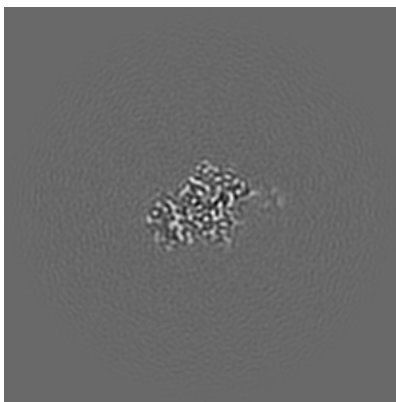
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

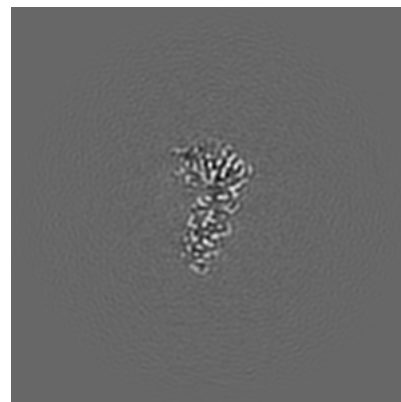
6.3.1 Primary map



X Index: 142

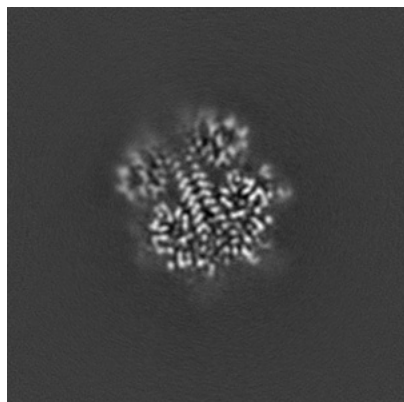


Y Index: 167

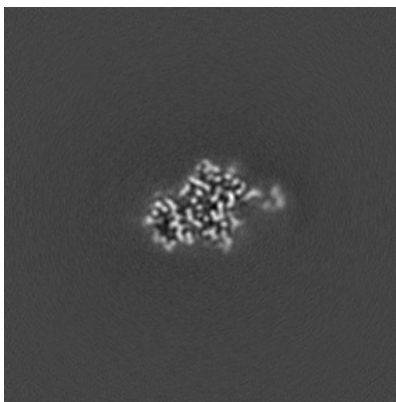


Z Index: 135

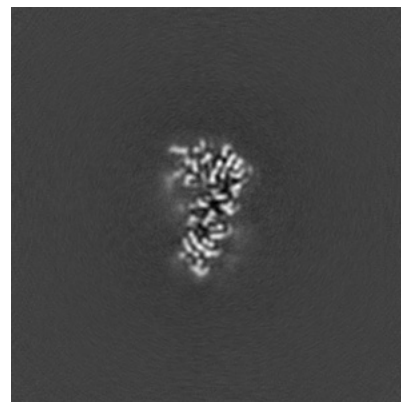
6.3.2 Raw map



X Index: 141



Y Index: 167

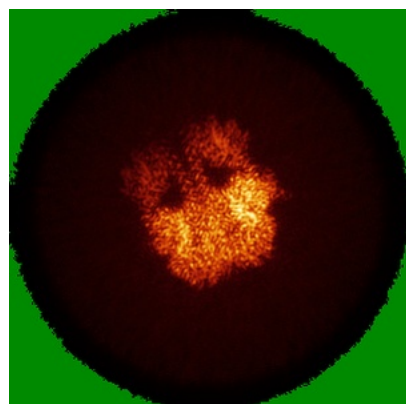


Z Index: 134

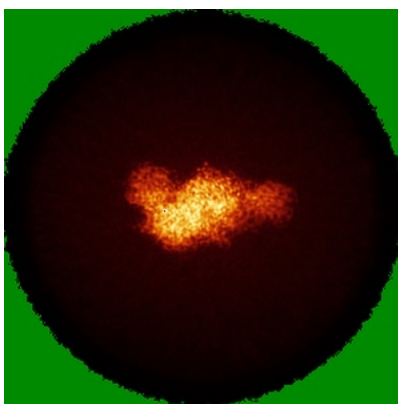
The images above show the largest variance slices of the map in three orthogonal directions.

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

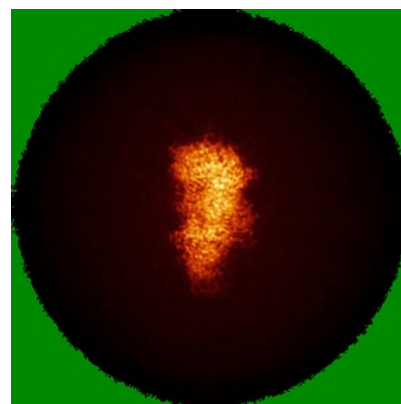
6.4.1 Primary map



X



Y

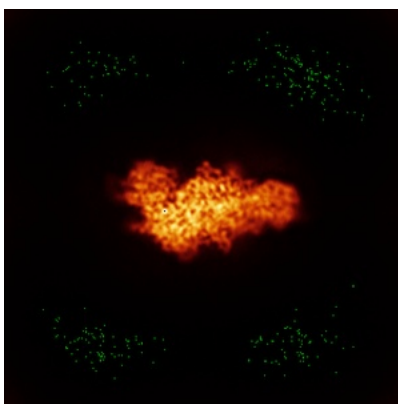


Z

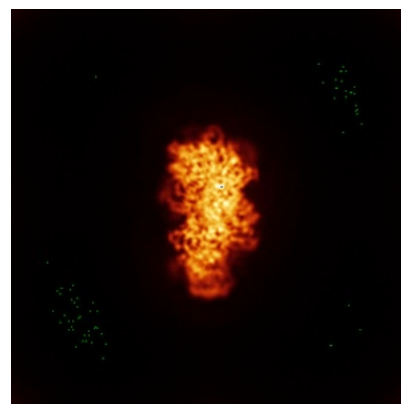
6.4.2 Raw map



X



Y

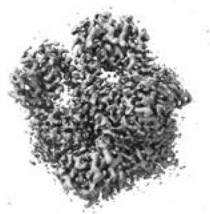


Z

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



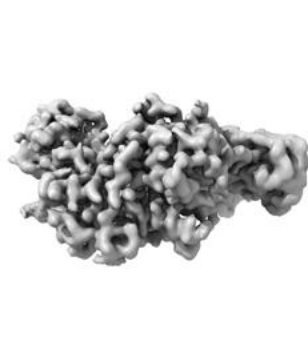
Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. 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.

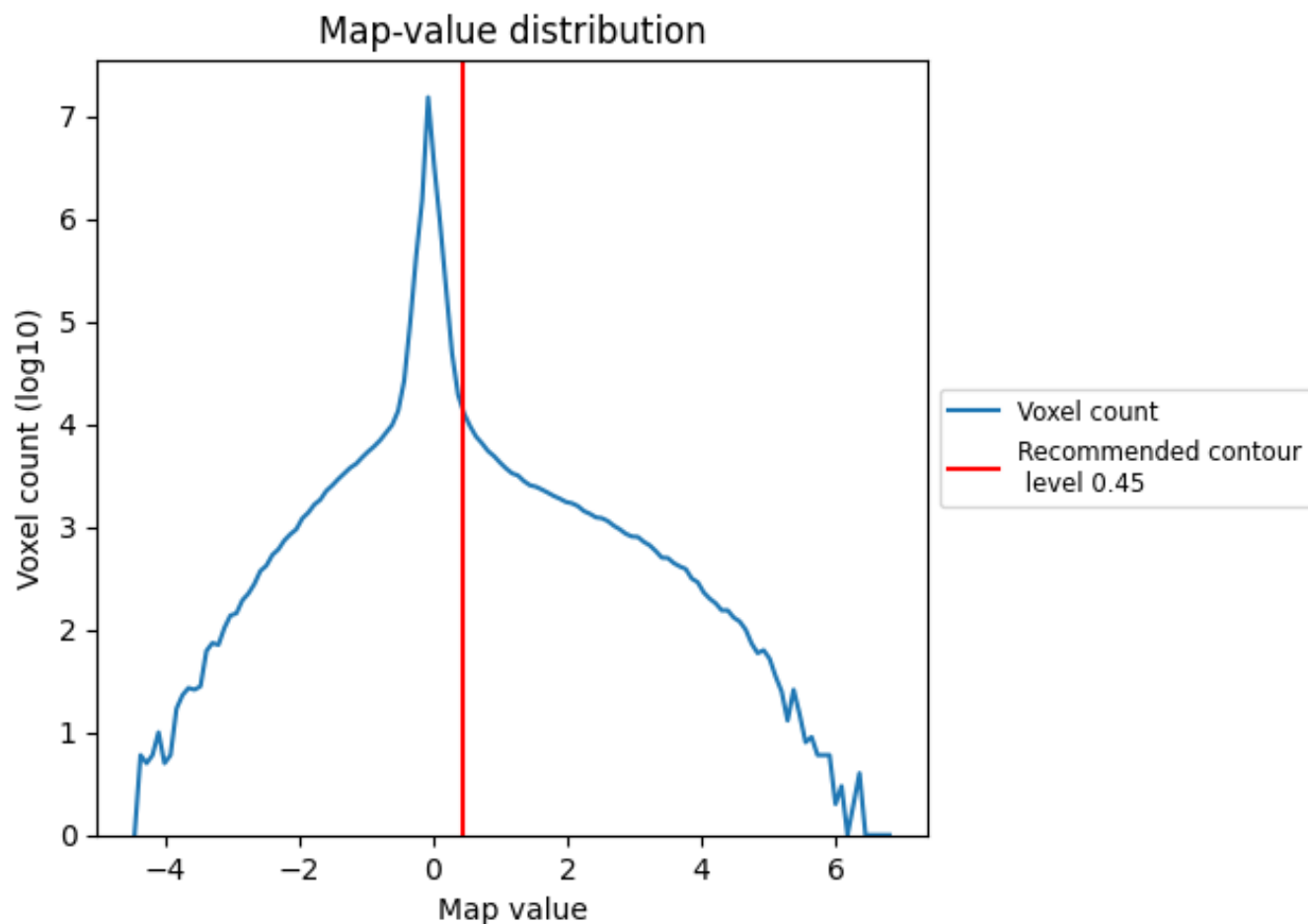
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

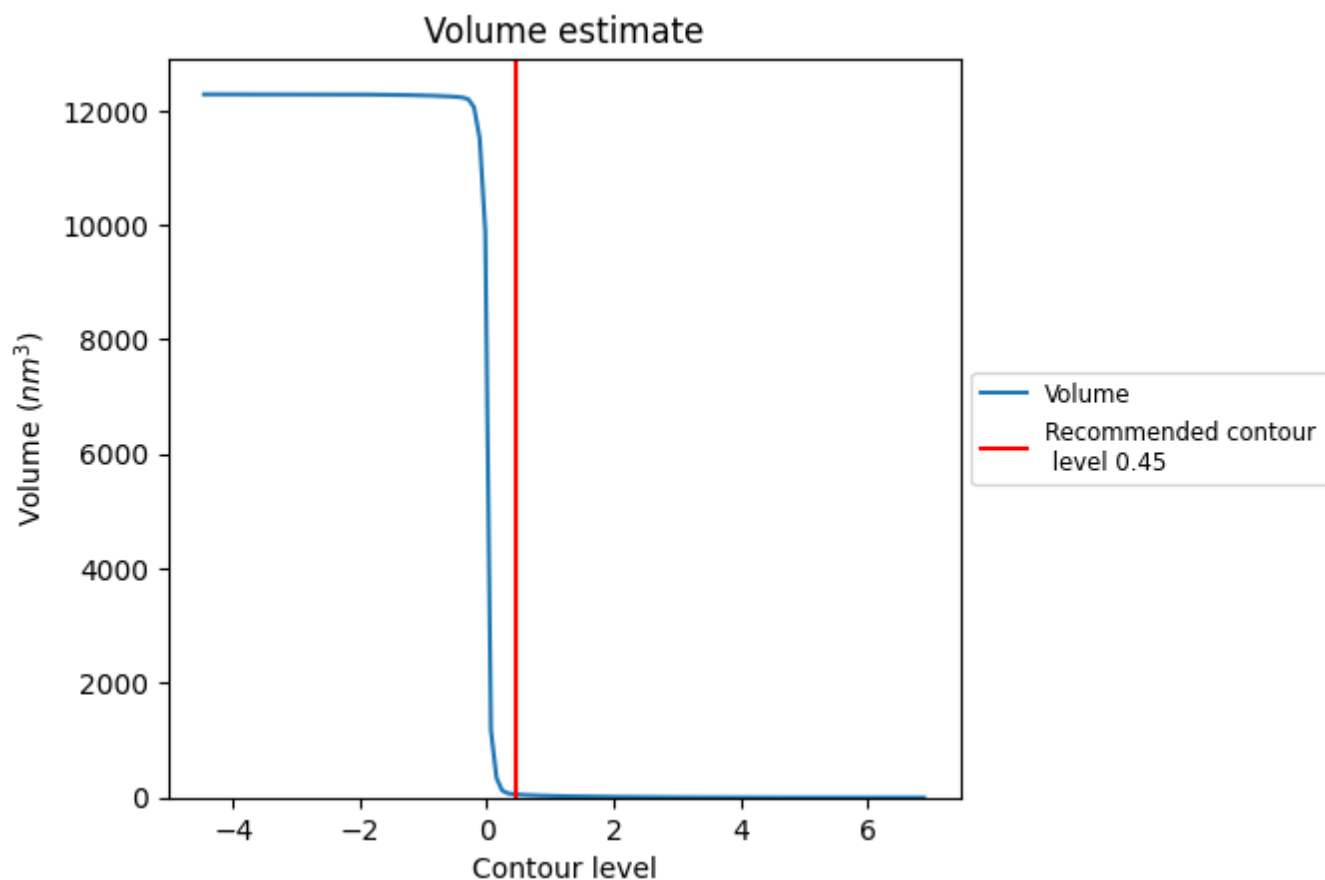
This section contains the results of statistical analysis of the map.

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.

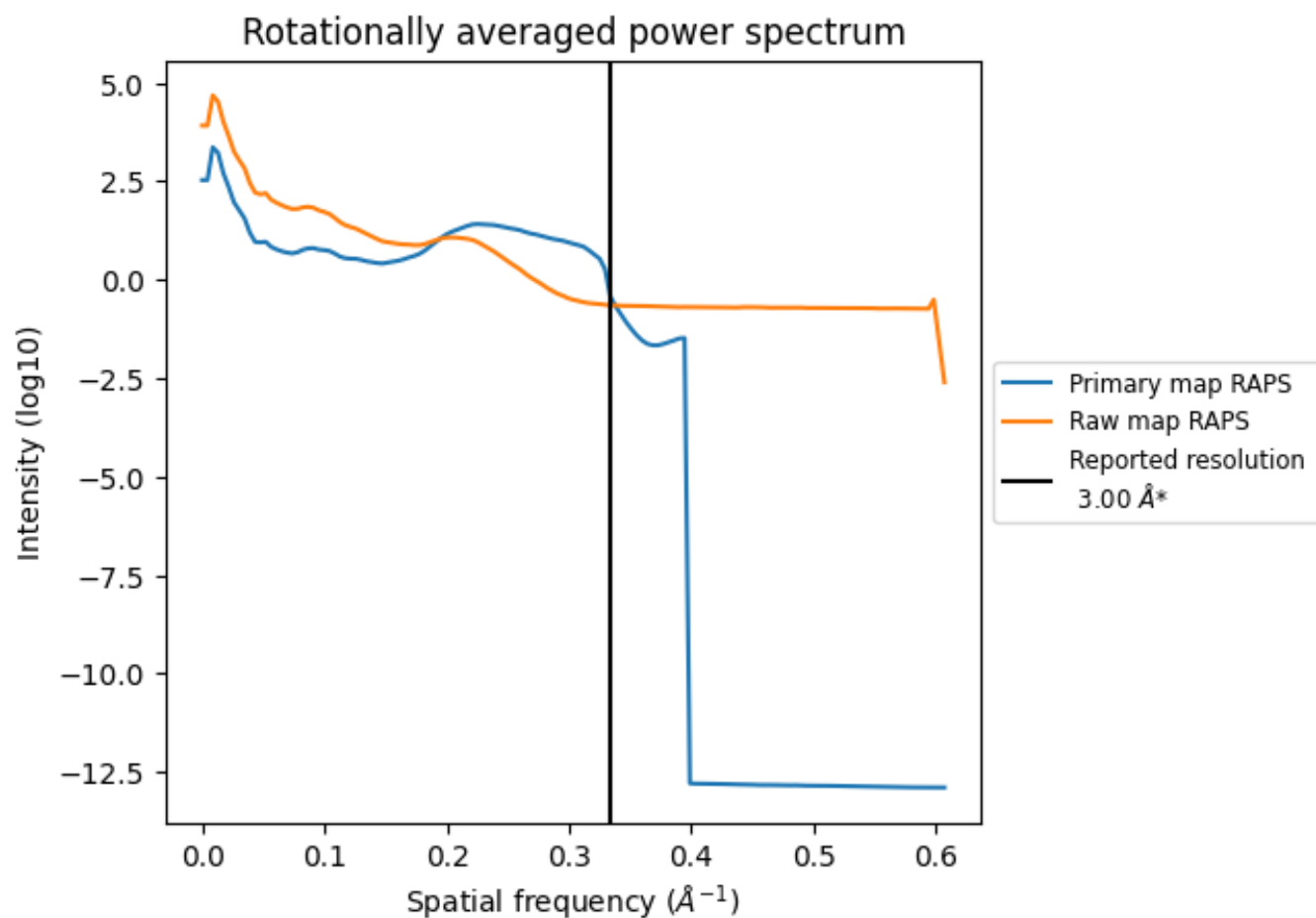
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 57 nm³; this corresponds to an approximate mass of 51 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 ⓘ

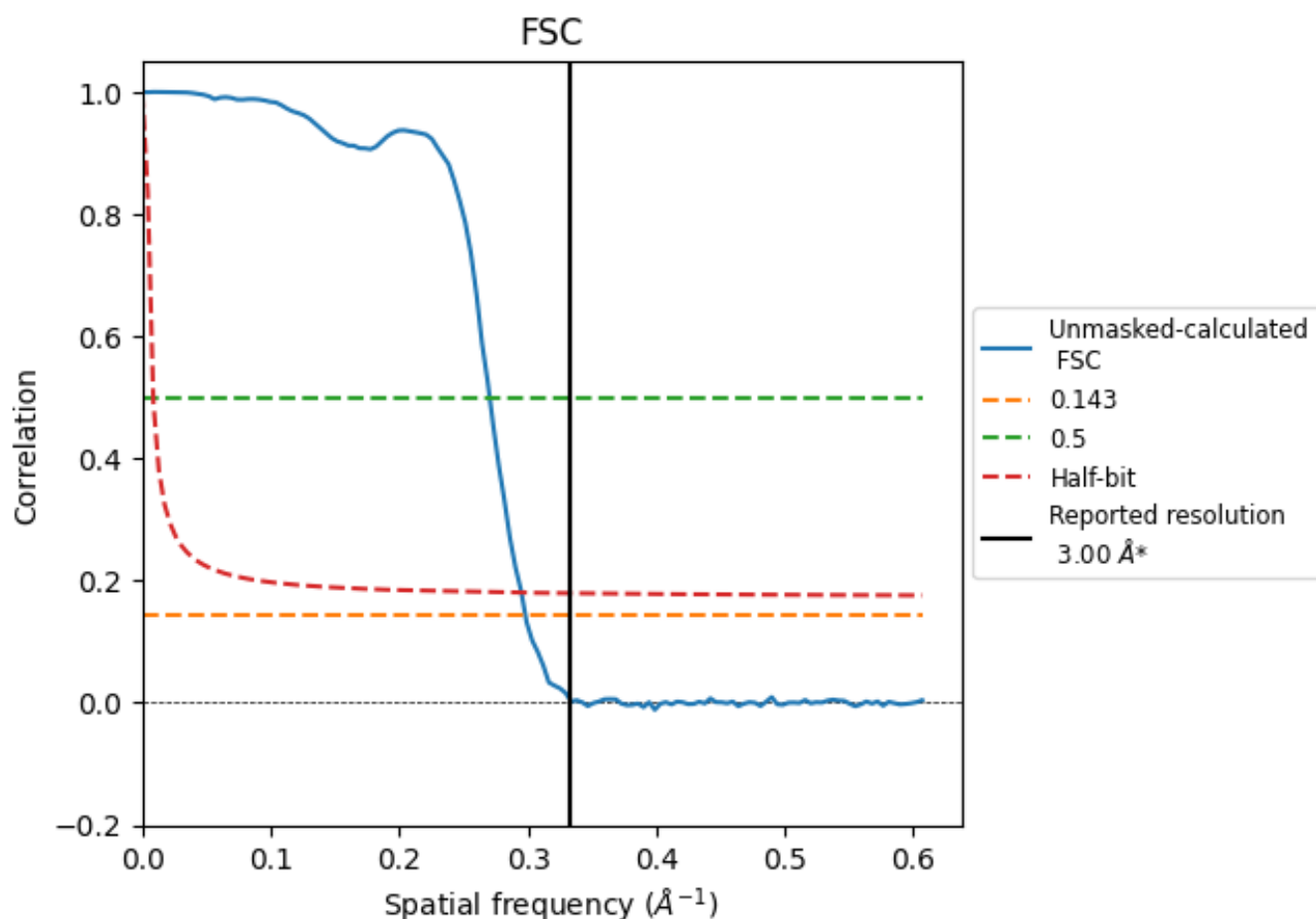


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

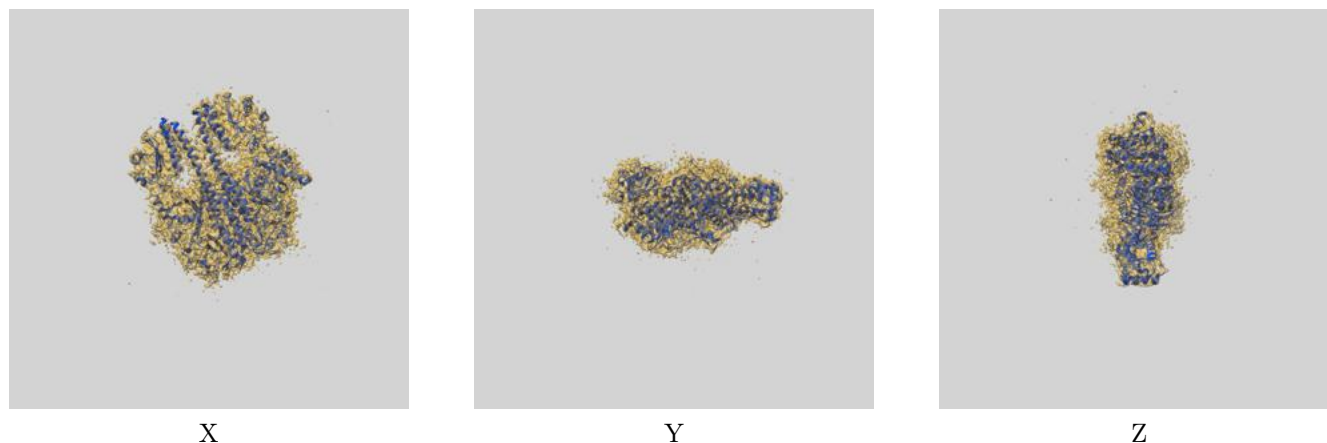
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.35	3.70	3.39

*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 3.35 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

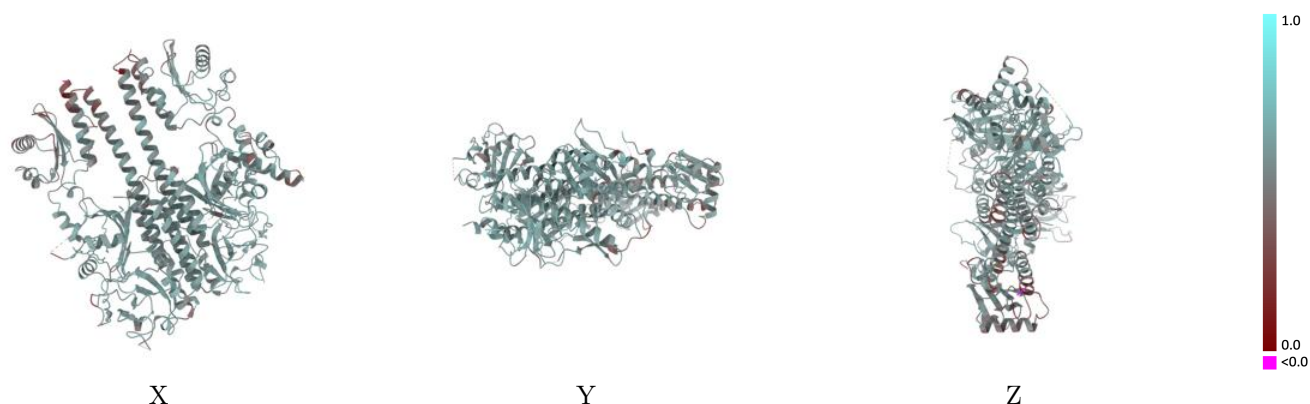
This section contains information regarding the fit between EMDB map EMD-61582 and PDB model 9JLB. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



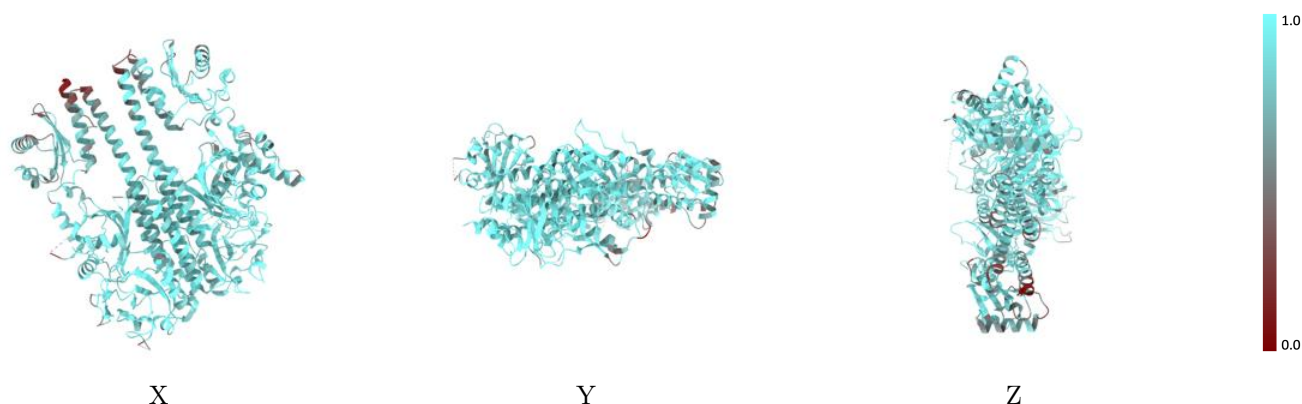
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



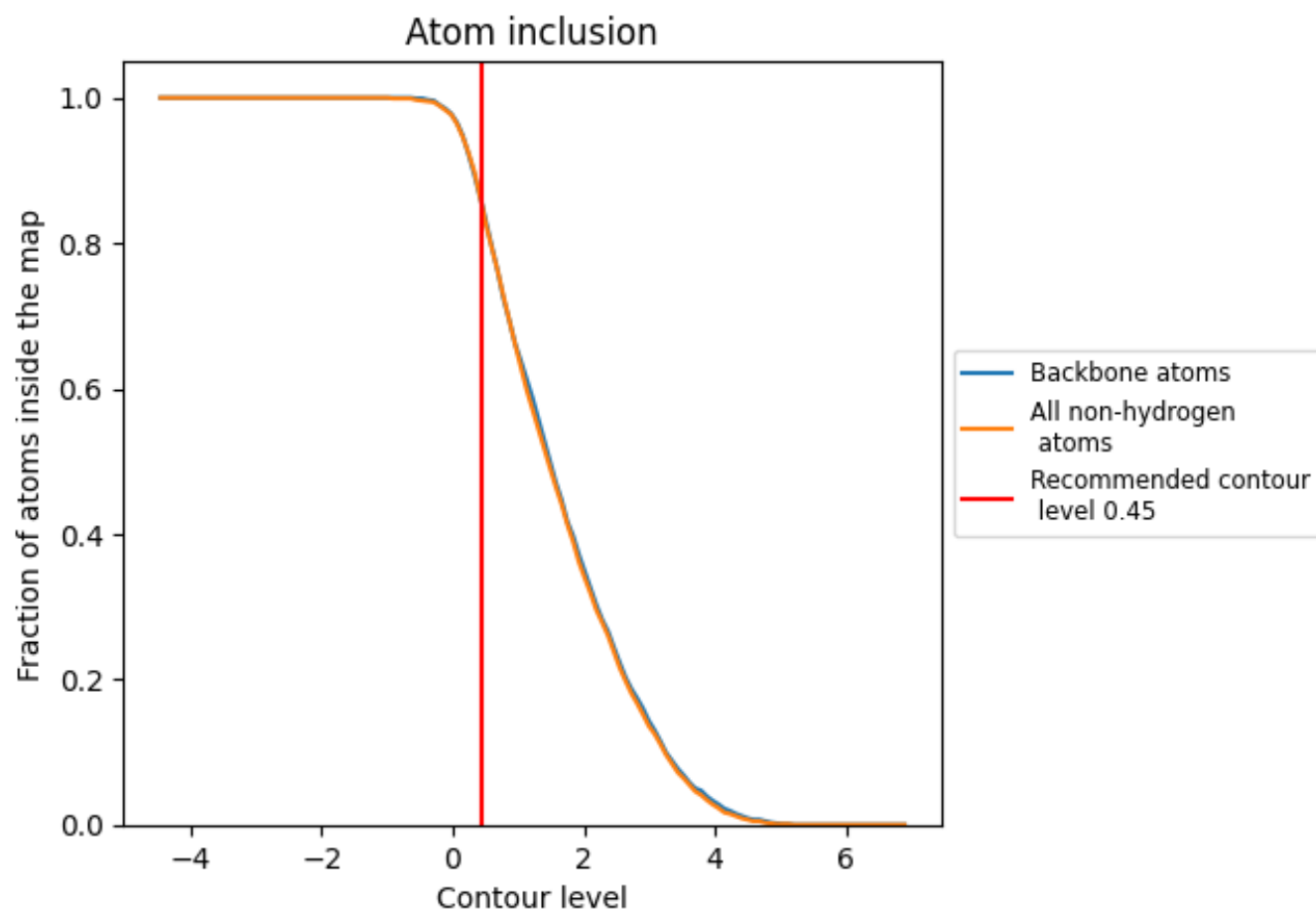
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 85% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8510	0.5550
A	0.8730	0.5620
B	0.8700	0.5690
C	0.8340	0.5450

