



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 08:11 AM UTC

PDB ID : 9CLV / pdb_00009clv
EMDB ID : EMD-45731
Title : Human Kv1.3 mutant-P424G
Authors : Selvakumar, P.; Swartz, K.J.
Deposited on : 2024-07-12
Resolution : 3.18 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:

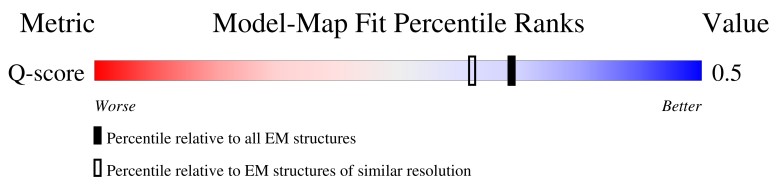
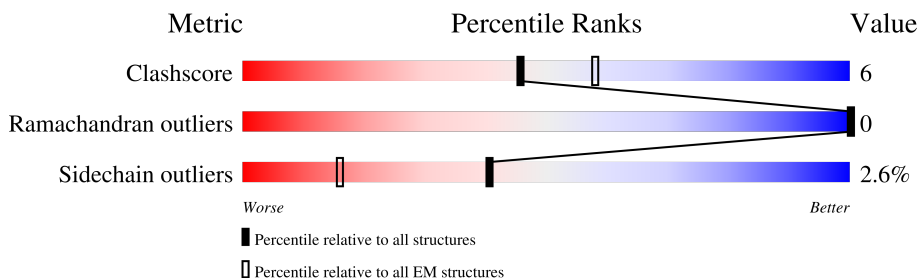
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.18 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	14470 (2.68 - 3.68)

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	856	 6% 34% 6% 60%
1	B	856	 6% 34% 6% 60%
1	C	856	 6% 34% 6% 60%
1	D	856	 6% 34% 6% 60%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11335 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 Potassium voltage-gated channel subfamily A member 3/mVenus fusion protein, Green fluorescent protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	346	Total	C	N	O	S	1	0
			2833	1864	470	488	11		
1	B	346	Total	C	N	O	S	1	0
			2833	1864	470	488	11		
1	C	346	Total	C	N	O	S	1	0
			2833	1864	470	488	11		
1	D	346	Total	C	N	O	S	1	0
			2833	1864	470	488	11		

There are 224 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	424	GLY	PRO	engineered mutation	UNP P22001
A	576	SER	-	linker	UNP P22001
A	577	LEU	-	linker	UNP P22001
A	578	GLU	-	linker	UNP P22001
A	579	VAL	-	linker	UNP P22001
A	580	LEU	-	linker	UNP P22001
A	581	PHE	-	linker	UNP P22001
A	582	GLN	-	linker	UNP P22001
A	583	GLY	-	linker	UNP P22001
A	584	PRO	-	linker	UNP P22001
A	585	ALA	-	linker	UNP P22001
A	586	ALA	-	linker	UNP P22001
A	587	ALA	-	linker	UNP P22001
A	588	MET	-	linker	UNP P22001
A	589	VAL	-	linker	UNP P22001
A	634	LEU	PHE	engineered mutation	UNP P42212
A	652	LEU	PHE	engineered mutation	UNP P42212
A	653	GLY	SER	engineered mutation	UNP P42212
A	656	LEU	VAL	engineered mutation	UNP P42212
A	660	ALA	SER	engineered mutation	UNP P42212
A	741	THR	MET	engineered mutation	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	751	ALA	VAL	engineered mutation	UNP P42212
A	763	GLY	SER	engineered mutation	UNP P42212
A	791	TYR	THR	engineered mutation	UNP P42212
A	794	LYS	ALA	engineered mutation	UNP P42212
A	819	LEU	HIS	engineered mutation	UNP P42212
A	827	SER	-	expression tag	UNP P42212
A	828	ALA	-	expression tag	UNP P42212
A	829	TRP	-	expression tag	UNP P42212
A	830	SER	-	expression tag	UNP P42212
A	831	HIS	-	expression tag	UNP P42212
A	832	PRO	-	expression tag	UNP P42212
A	833	GLN	-	expression tag	UNP P42212
A	834	PHE	-	expression tag	UNP P42212
A	835	GLU	-	expression tag	UNP P42212
A	836	LYS	-	expression tag	UNP P42212
A	837	GLY	-	expression tag	UNP P42212
A	838	GLY	-	expression tag	UNP P42212
A	839	GLY	-	expression tag	UNP P42212
A	840	SER	-	expression tag	UNP P42212
A	841	GLY	-	expression tag	UNP P42212
A	842	GLY	-	expression tag	UNP P42212
A	843	GLY	-	expression tag	UNP P42212
A	844	SER	-	expression tag	UNP P42212
A	845	GLY	-	expression tag	UNP P42212
A	846	GLY	-	expression tag	UNP P42212
A	847	GLY	-	expression tag	UNP P42212
A	848	SER	-	expression tag	UNP P42212
A	849	TRP	-	expression tag	UNP P42212
A	850	SER	-	expression tag	UNP P42212
A	851	HIS	-	expression tag	UNP P42212
A	852	PRO	-	expression tag	UNP P42212
A	853	GLN	-	expression tag	UNP P42212
A	854	PHE	-	expression tag	UNP P42212
A	855	GLU	-	expression tag	UNP P42212
A	856	LYS	-	expression tag	UNP P42212
B	424	GLY	PRO	engineered mutation	UNP P22001
B	576	SER	-	linker	UNP P22001
B	577	LEU	-	linker	UNP P22001
B	578	GLU	-	linker	UNP P22001
B	579	VAL	-	linker	UNP P22001
B	580	LEU	-	linker	UNP P22001
B	581	PHE	-	linker	UNP P22001

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Chain	Residue	Modelled	Actual	Comment	Reference
B	582	GLN	-	linker	UNP P22001
B	583	GLY	-	linker	UNP P22001
B	584	PRO	-	linker	UNP P22001
B	585	ALA	-	linker	UNP P22001
B	586	ALA	-	linker	UNP P22001
B	587	ALA	-	linker	UNP P22001
B	588	MET	-	linker	UNP P22001
B	589	VAL	-	linker	UNP P22001
B	634	LEU	PHE	engineered mutation	UNP P42212
B	652	LEU	PHE	engineered mutation	UNP P42212
B	653	GLY	SER	engineered mutation	UNP P42212
B	656	LEU	VAL	engineered mutation	UNP P42212
B	660	ALA	SER	engineered mutation	UNP P42212
B	741	THR	MET	engineered mutation	UNP P42212
B	751	ALA	VAL	engineered mutation	UNP P42212
B	763	GLY	SER	engineered mutation	UNP P42212
B	791	TYR	THR	engineered mutation	UNP P42212
B	794	LYS	ALA	engineered mutation	UNP P42212
B	819	LEU	HIS	engineered mutation	UNP P42212
B	827	SER	-	expression tag	UNP P42212
B	828	ALA	-	expression tag	UNP P42212
B	829	TRP	-	expression tag	UNP P42212
B	830	SER	-	expression tag	UNP P42212
B	831	HIS	-	expression tag	UNP P42212
B	832	PRO	-	expression tag	UNP P42212
B	833	GLN	-	expression tag	UNP P42212
B	834	PHE	-	expression tag	UNP P42212
B	835	GLU	-	expression tag	UNP P42212
B	836	LYS	-	expression tag	UNP P42212
B	837	GLY	-	expression tag	UNP P42212
B	838	GLY	-	expression tag	UNP P42212
B	839	GLY	-	expression tag	UNP P42212
B	840	SER	-	expression tag	UNP P42212
B	841	GLY	-	expression tag	UNP P42212
B	842	GLY	-	expression tag	UNP P42212
B	843	GLY	-	expression tag	UNP P42212
B	844	SER	-	expression tag	UNP P42212
B	845	GLY	-	expression tag	UNP P42212
B	846	GLY	-	expression tag	UNP P42212
B	847	GLY	-	expression tag	UNP P42212
B	848	SER	-	expression tag	UNP P42212
B	849	TRP	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	850	SER	-	expression tag	UNP P42212
B	851	HIS	-	expression tag	UNP P42212
B	852	PRO	-	expression tag	UNP P42212
B	853	GLN	-	expression tag	UNP P42212
B	854	PHE	-	expression tag	UNP P42212
B	855	GLU	-	expression tag	UNP P42212
B	856	LYS	-	expression tag	UNP P42212
C	424	GLY	PRO	engineered mutation	UNP P22001
C	576	SER	-	linker	UNP P22001
C	577	LEU	-	linker	UNP P22001
C	578	GLU	-	linker	UNP P22001
C	579	VAL	-	linker	UNP P22001
C	580	LEU	-	linker	UNP P22001
C	581	PHE	-	linker	UNP P22001
C	582	GLN	-	linker	UNP P22001
C	583	GLY	-	linker	UNP P22001
C	584	PRO	-	linker	UNP P22001
C	585	ALA	-	linker	UNP P22001
C	586	ALA	-	linker	UNP P22001
C	587	ALA	-	linker	UNP P22001
C	588	MET	-	linker	UNP P22001
C	589	VAL	-	linker	UNP P22001
C	634	LEU	PHE	engineered mutation	UNP P42212
C	652	LEU	PHE	engineered mutation	UNP P42212
C	653	GLY	SER	engineered mutation	UNP P42212
C	656	LEU	VAL	engineered mutation	UNP P42212
C	660	ALA	SER	engineered mutation	UNP P42212
C	741	THR	MET	engineered mutation	UNP P42212
C	751	ALA	VAL	engineered mutation	UNP P42212
C	763	GLY	SER	engineered mutation	UNP P42212
C	791	TYR	THR	engineered mutation	UNP P42212
C	794	LYS	ALA	engineered mutation	UNP P42212
C	819	LEU	HIS	engineered mutation	UNP P42212
C	827	SER	-	expression tag	UNP P42212
C	828	ALA	-	expression tag	UNP P42212
C	829	TRP	-	expression tag	UNP P42212
C	830	SER	-	expression tag	UNP P42212
C	831	HIS	-	expression tag	UNP P42212
C	832	PRO	-	expression tag	UNP P42212
C	833	GLN	-	expression tag	UNP P42212
C	834	PHE	-	expression tag	UNP P42212
C	835	GLU	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
C	836	LYS	-	expression tag	UNP P42212
C	837	GLY	-	expression tag	UNP P42212
C	838	GLY	-	expression tag	UNP P42212
C	839	GLY	-	expression tag	UNP P42212
C	840	SER	-	expression tag	UNP P42212
C	841	GLY	-	expression tag	UNP P42212
C	842	GLY	-	expression tag	UNP P42212
C	843	GLY	-	expression tag	UNP P42212
C	844	SER	-	expression tag	UNP P42212
C	845	GLY	-	expression tag	UNP P42212
C	846	GLY	-	expression tag	UNP P42212
C	847	GLY	-	expression tag	UNP P42212
C	848	SER	-	expression tag	UNP P42212
C	849	TRP	-	expression tag	UNP P42212
C	850	SER	-	expression tag	UNP P42212
C	851	HIS	-	expression tag	UNP P42212
C	852	PRO	-	expression tag	UNP P42212
C	853	GLN	-	expression tag	UNP P42212
C	854	PHE	-	expression tag	UNP P42212
C	855	GLU	-	expression tag	UNP P42212
C	856	LYS	-	expression tag	UNP P42212
D	424	GLY	PRO	engineered mutation	UNP P22001
D	576	SER	-	linker	UNP P22001
D	577	LEU	-	linker	UNP P22001
D	578	GLU	-	linker	UNP P22001
D	579	VAL	-	linker	UNP P22001
D	580	LEU	-	linker	UNP P22001
D	581	PHE	-	linker	UNP P22001
D	582	GLN	-	linker	UNP P22001
D	583	GLY	-	linker	UNP P22001
D	584	PRO	-	linker	UNP P22001
D	585	ALA	-	linker	UNP P22001
D	586	ALA	-	linker	UNP P22001
D	587	ALA	-	linker	UNP P22001
D	588	MET	-	linker	UNP P22001
D	589	VAL	-	linker	UNP P22001
D	634	LEU	PHE	engineered mutation	UNP P42212
D	652	LEU	PHE	engineered mutation	UNP P42212
D	653	GLY	SER	engineered mutation	UNP P42212
D	656	LEU	VAL	engineered mutation	UNP P42212
D	660	ALA	SER	engineered mutation	UNP P42212
D	741	THR	MET	engineered mutation	UNP P42212

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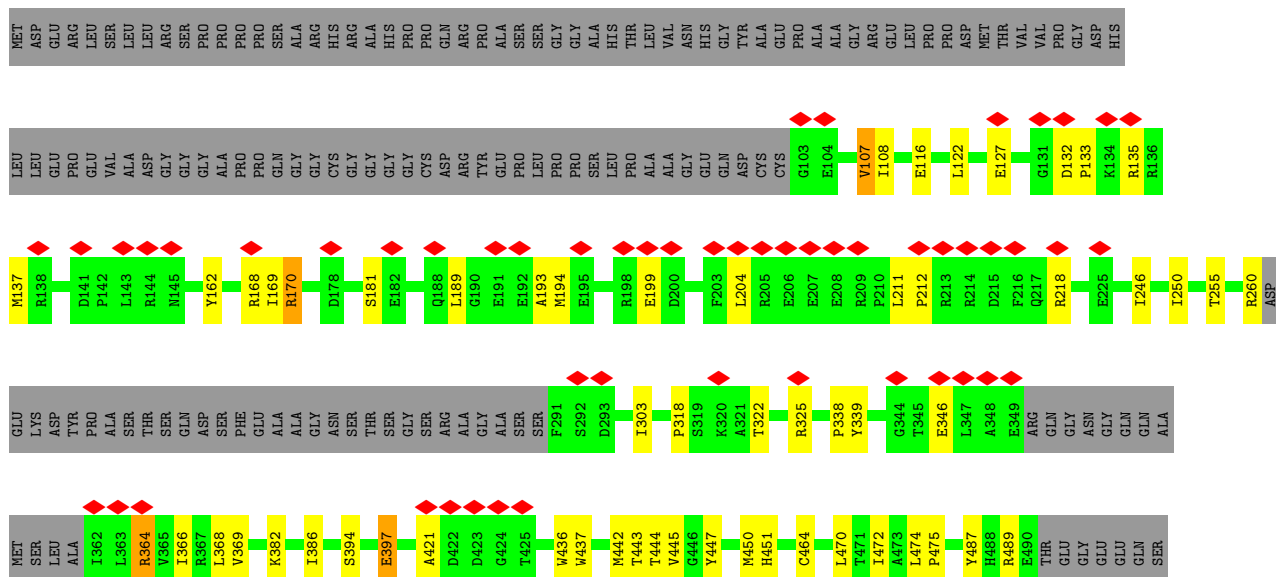
Chain	Residue	Modelled	Actual	Comment	Reference
D	751	ALA	VAL	engineered mutation	UNP P42212
D	763	GLY	SER	engineered mutation	UNP P42212
D	791	TYR	THR	engineered mutation	UNP P42212
D	794	LYS	ALA	engineered mutation	UNP P42212
D	819	LEU	HIS	engineered mutation	UNP P42212
D	827	SER	-	expression tag	UNP P42212
D	828	ALA	-	expression tag	UNP P42212
D	829	TRP	-	expression tag	UNP P42212
D	830	SER	-	expression tag	UNP P42212
D	831	HIS	-	expression tag	UNP P42212
D	832	PRO	-	expression tag	UNP P42212
D	833	GLN	-	expression tag	UNP P42212
D	834	PHE	-	expression tag	UNP P42212
D	835	GLU	-	expression tag	UNP P42212
D	836	LYS	-	expression tag	UNP P42212
D	837	GLY	-	expression tag	UNP P42212
D	838	GLY	-	expression tag	UNP P42212
D	839	GLY	-	expression tag	UNP P42212
D	840	SER	-	expression tag	UNP P42212
D	841	GLY	-	expression tag	UNP P42212
D	842	GLY	-	expression tag	UNP P42212
D	843	GLY	-	expression tag	UNP P42212
D	844	SER	-	expression tag	UNP P42212
D	845	GLY	-	expression tag	UNP P42212
D	846	GLY	-	expression tag	UNP P42212
D	847	GLY	-	expression tag	UNP P42212
D	848	SER	-	expression tag	UNP P42212
D	849	TRP	-	expression tag	UNP P42212
D	850	SER	-	expression tag	UNP P42212
D	851	HIS	-	expression tag	UNP P42212
D	852	PRO	-	expression tag	UNP P42212
D	853	GLN	-	expression tag	UNP P42212
D	854	PHE	-	expression tag	UNP P42212
D	855	GLU	-	expression tag	UNP P42212
D	856	LYS	-	expression tag	UNP P42212

- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
2	A	2	Total K 2 2	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		AltConf
3	D	1	Total	O	0
			1	1	



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	109882	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 ($e^-/\text{\AA}^2$)	51.8	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.998	Depositor
Minimum map value	-1.429	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	264.0, 264.0, 264.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	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: K

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	0.18	0/2906	0.34	0/3936
1	B	0.18	0/2906	0.34	0/3936
1	C	0.18	0/2906	0.34	0/3936
1	D	0.18	0/2906	0.34	0/3936
All	All	0.18	0/11624	0.34	0/15744

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	2833	0	2858	40	0
1	B	2833	0	2858	37	0
1	C	2833	0	2858	40	0
1	D	2833	0	2858	38	0
2	A	2	0	0	0	0
3	D	1	0	0	0	0
All	All	11335	0	11432	140	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 6.

The worst 5 of 140 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:421:ALA:HB3	1:D:364:ARG:HH21	1.57	0.68
1:B:421:ALA:HB3	1:C:364:ARG:HH21	1.59	0.67
1:A:421:ALA:HB3	1:B:364:ARG:HH21	1.60	0.66
1:C:168:ARG:HG2	1:C:170:ARG:HD3	1.79	0.65
1:B:168:ARG:HG2	1:B:170:ARG:HD3	1.79	0.65

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	341/856 (40%)	336 (98%)	5 (2%)	0	100	100
1	B	341/856 (40%)	336 (98%)	5 (2%)	0	100	100
1	C	341/856 (40%)	336 (98%)	5 (2%)	0	100	100
1	D	341/856 (40%)	336 (98%)	5 (2%)	0	100	100
All	All	1364/3424 (40%)	1344 (98%)	20 (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	308/723 (43%)	300 (97%)	8 (3%)	40	66
1	B	308/723 (43%)	300 (97%)	8 (3%)	40	66
1	C	308/723 (43%)	300 (97%)	8 (3%)	40	66
1	D	308/723 (43%)	300 (97%)	8 (3%)	40	66
All	All	1232/2892 (43%)	1200 (97%)	32 (3%)	41	66

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	364	ARG
1	D	382	LYS
1	B	364	ARG
1	B	346	GLU
1	D	397	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	380	HIS
1	C	389	GLN
1	D	389	GLN
1	D	217	GLN
1	B	217	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

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

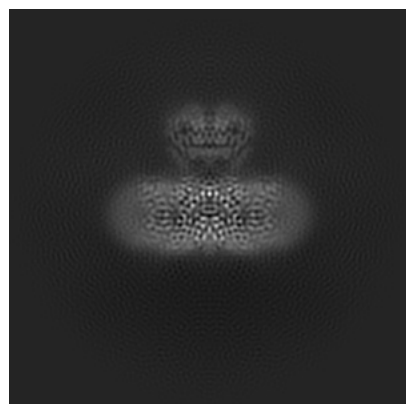
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45731. These allow visual inspection of the internal detail of the map and identification of artifacts.

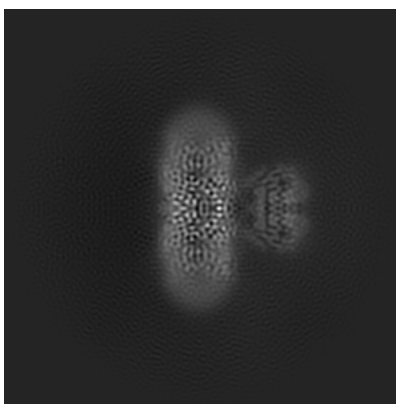
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

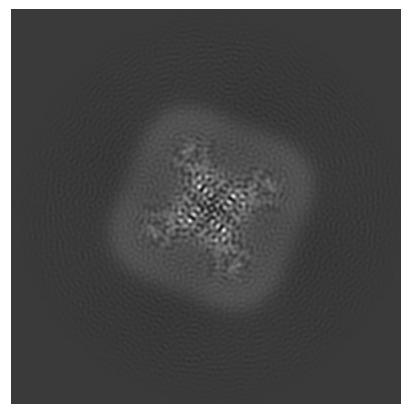
6.1.1 Primary map



X

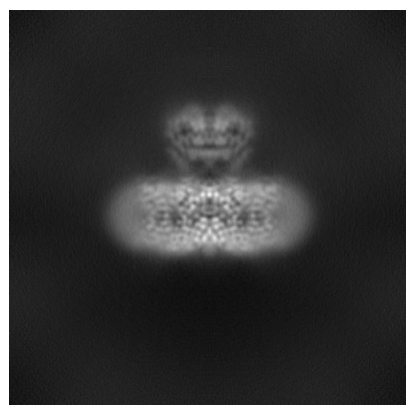


Y

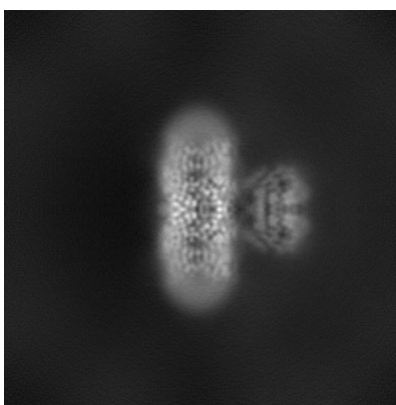


Z

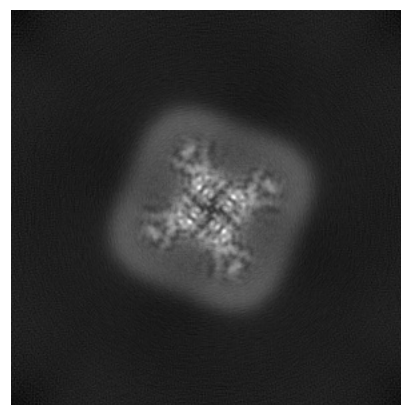
6.1.2 Raw map



X



Y

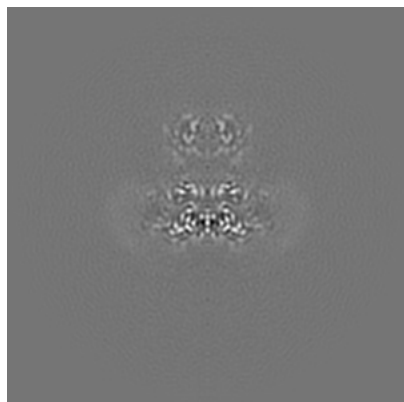


Z

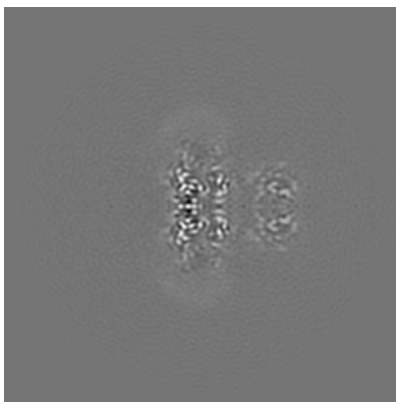
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

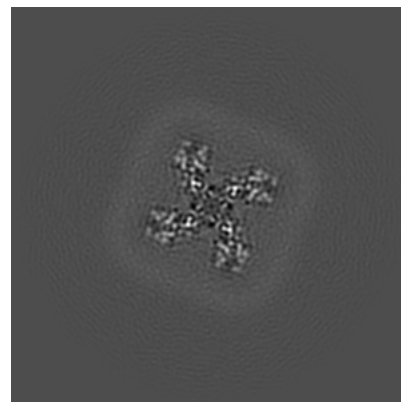
6.2.1 Primary map



X Index: 160

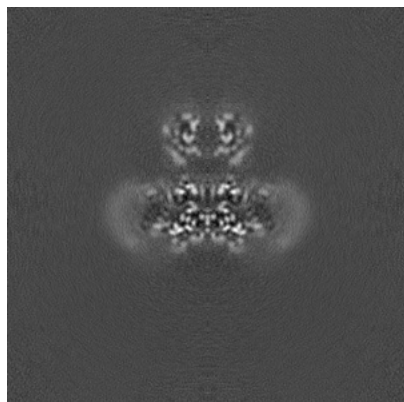


Y Index: 160

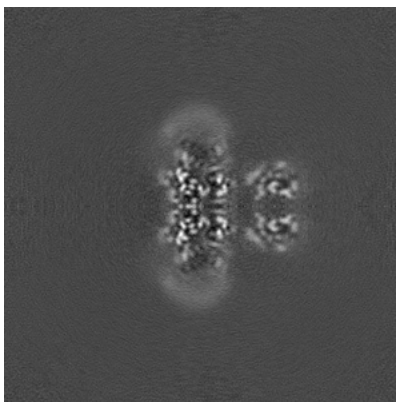


Z Index: 160

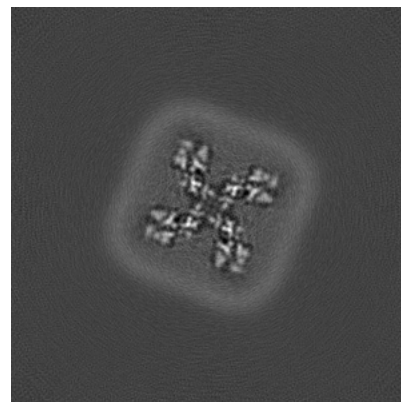
6.2.2 Raw map



X Index: 160



Y Index: 160

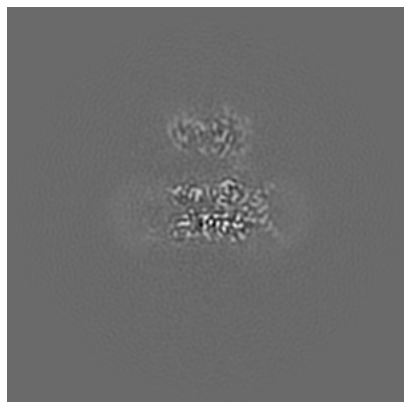


Z Index: 160

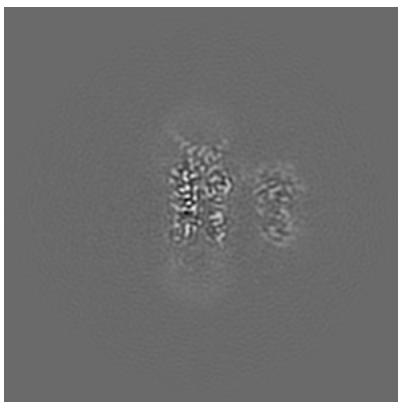
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

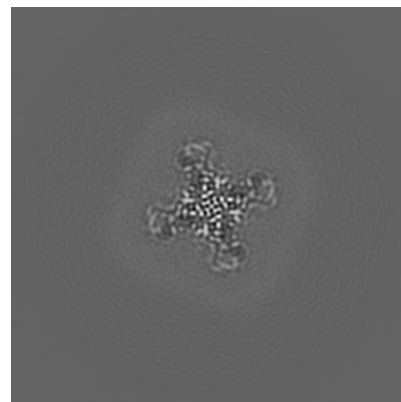
6.3.1 Primary map



X Index: 155

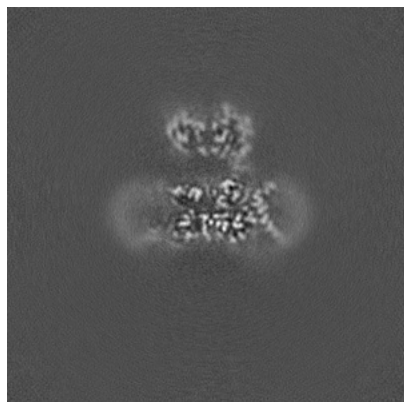


Y Index: 165

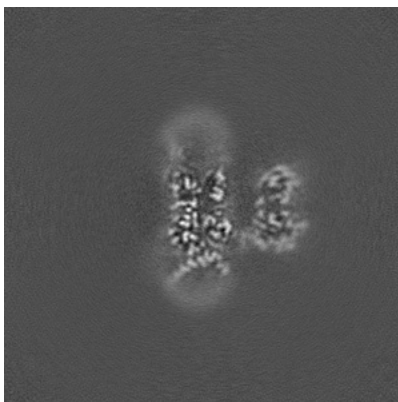


Z Index: 146

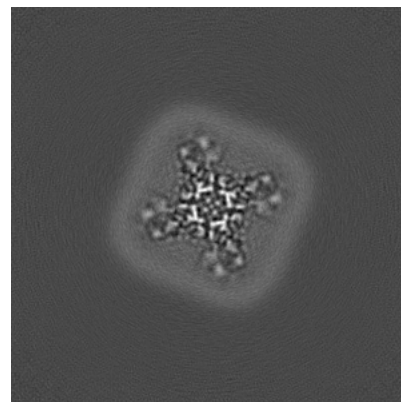
6.3.2 Raw map



X Index: 155



Y Index: 155

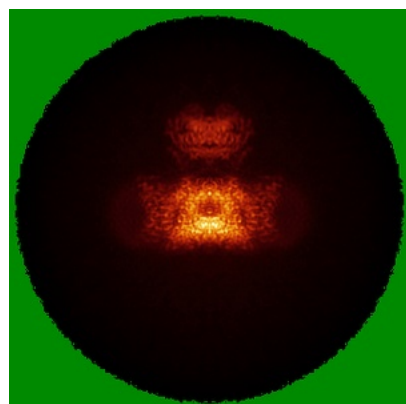


Z Index: 142

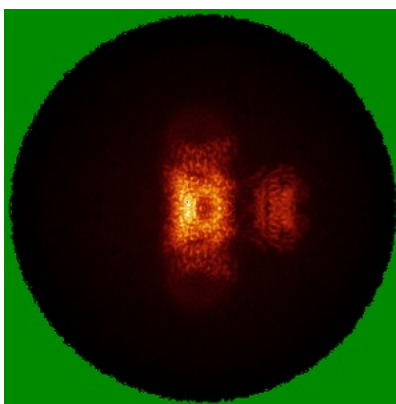
The images above show the largest variance slices of the map in three orthogonal directions.

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

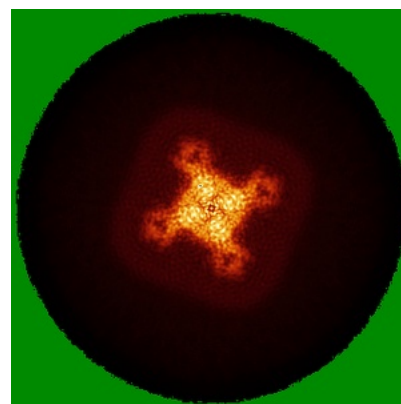
6.4.1 Primary map



X

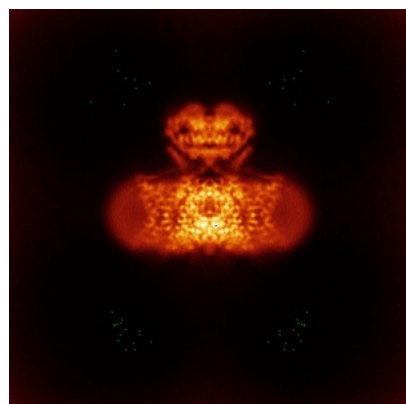


Y

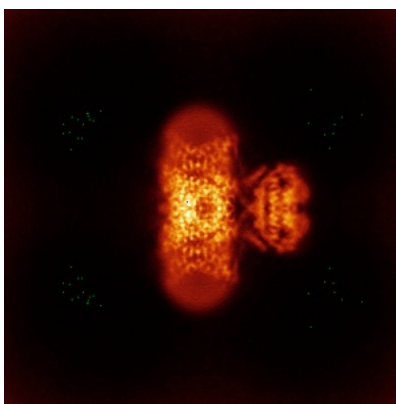


Z

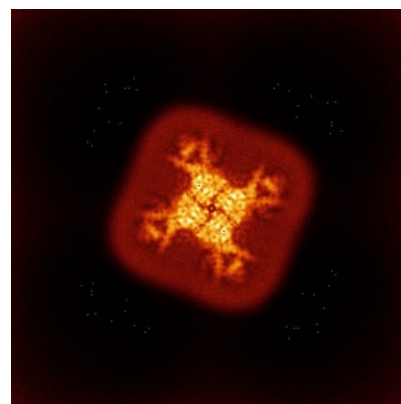
6.4.2 Raw map



X



Y

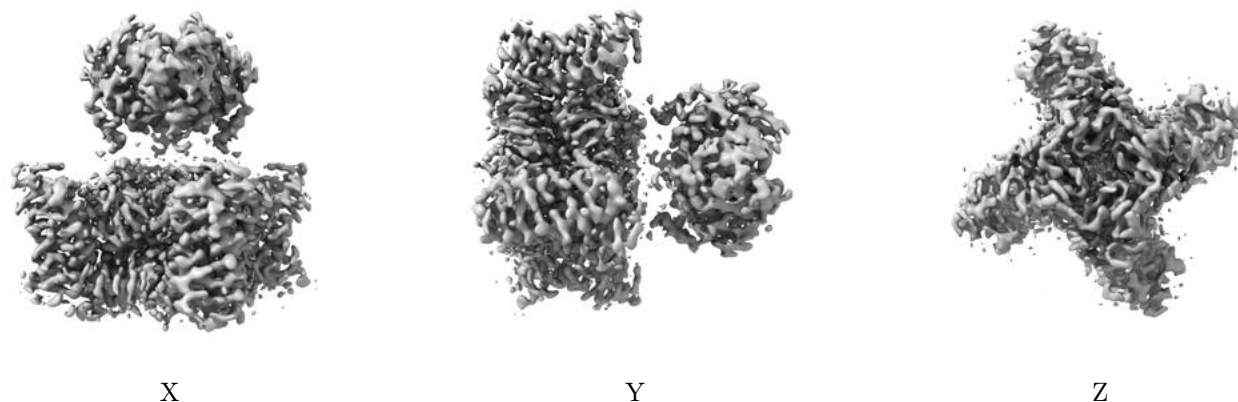


Z

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

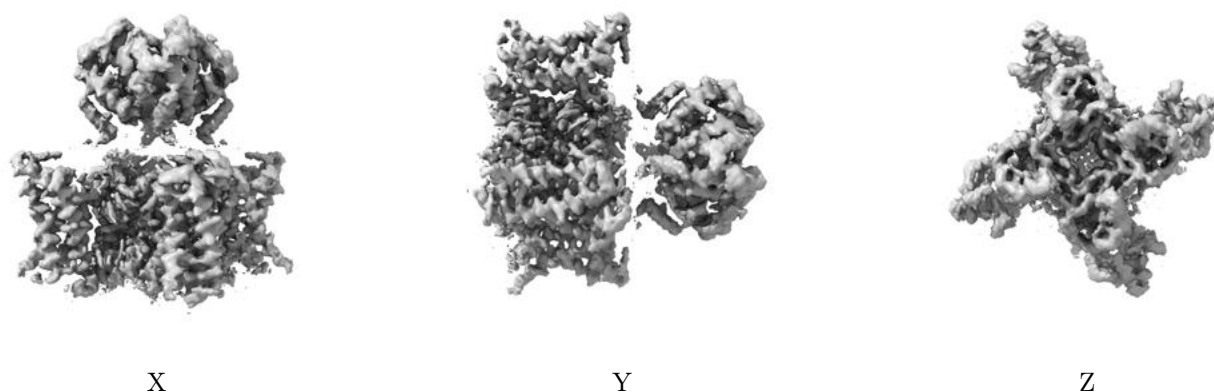
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

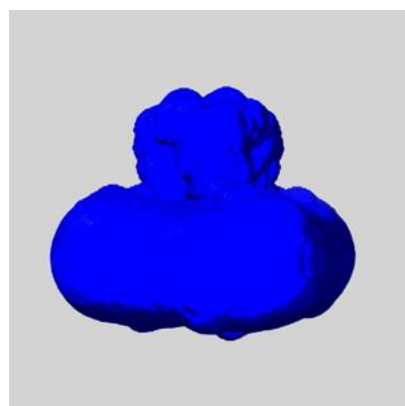
6.6 Mask visualisation [i](#)

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

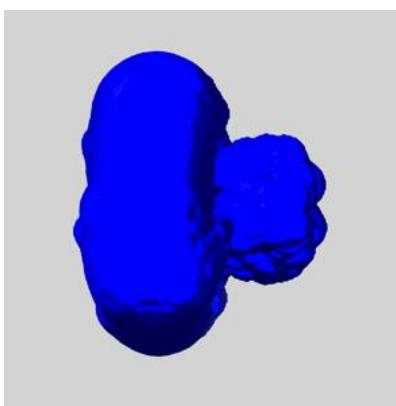
A mask typically either:

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

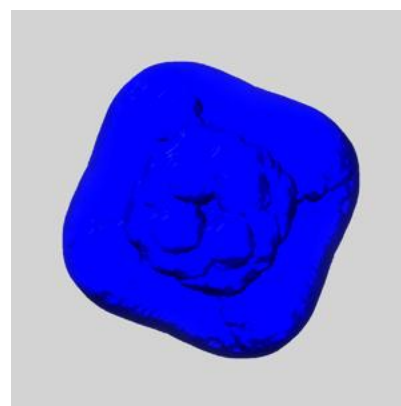
6.6.1 emd_45731_msk_1.map [i](#)



X



Y

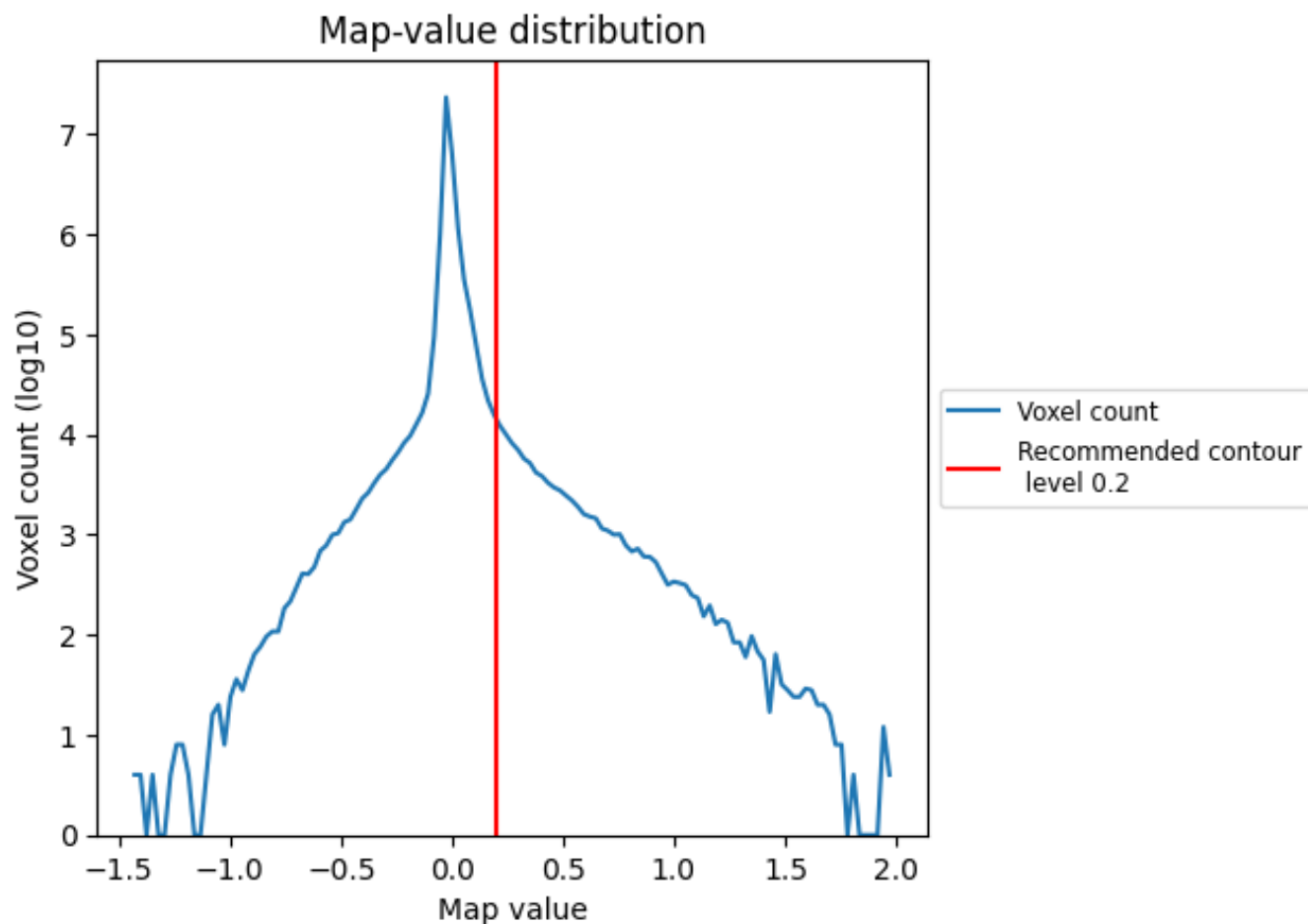


Z

7 Map analysis [i](#)

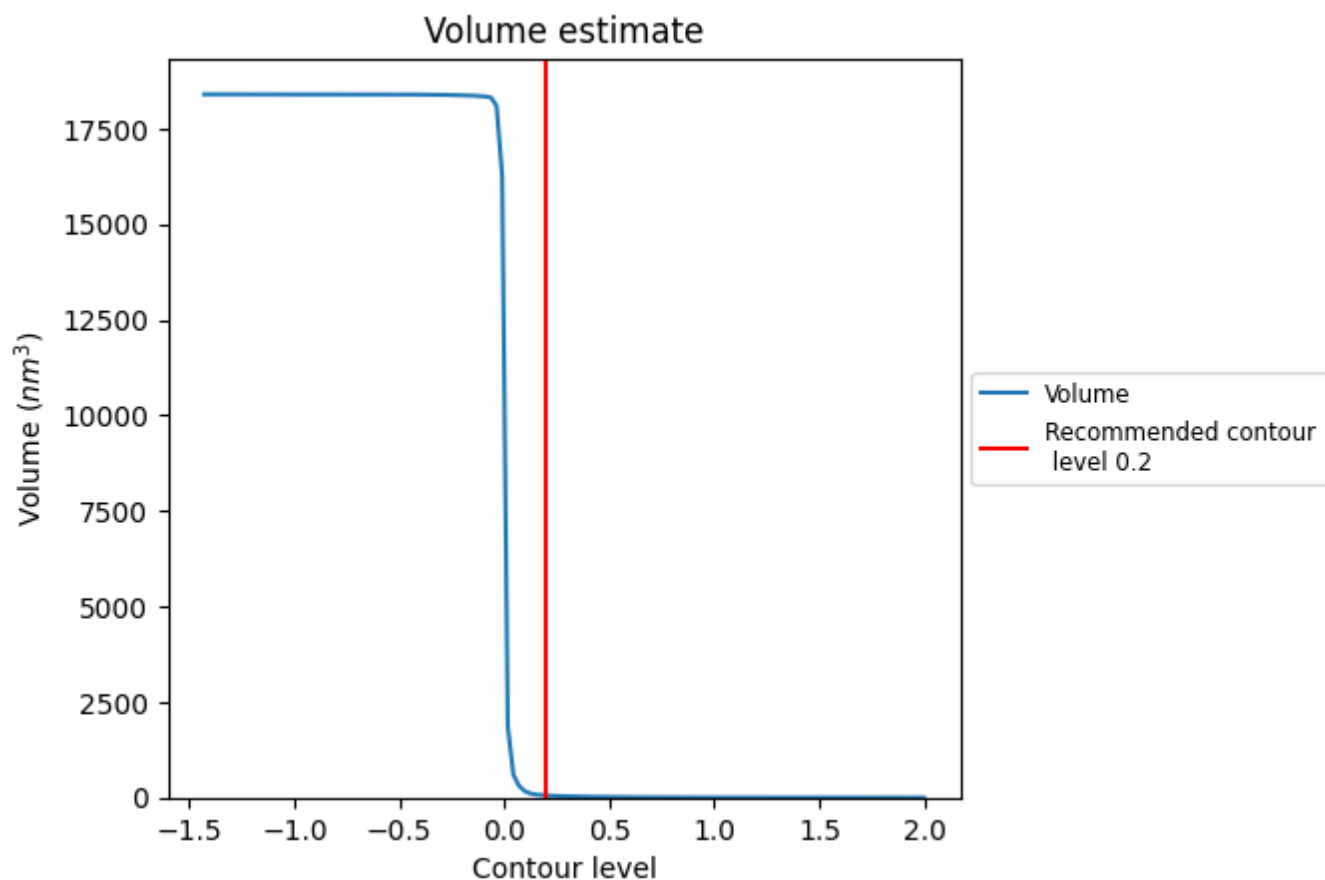
This section contains the results of statistical analysis of the map.

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.

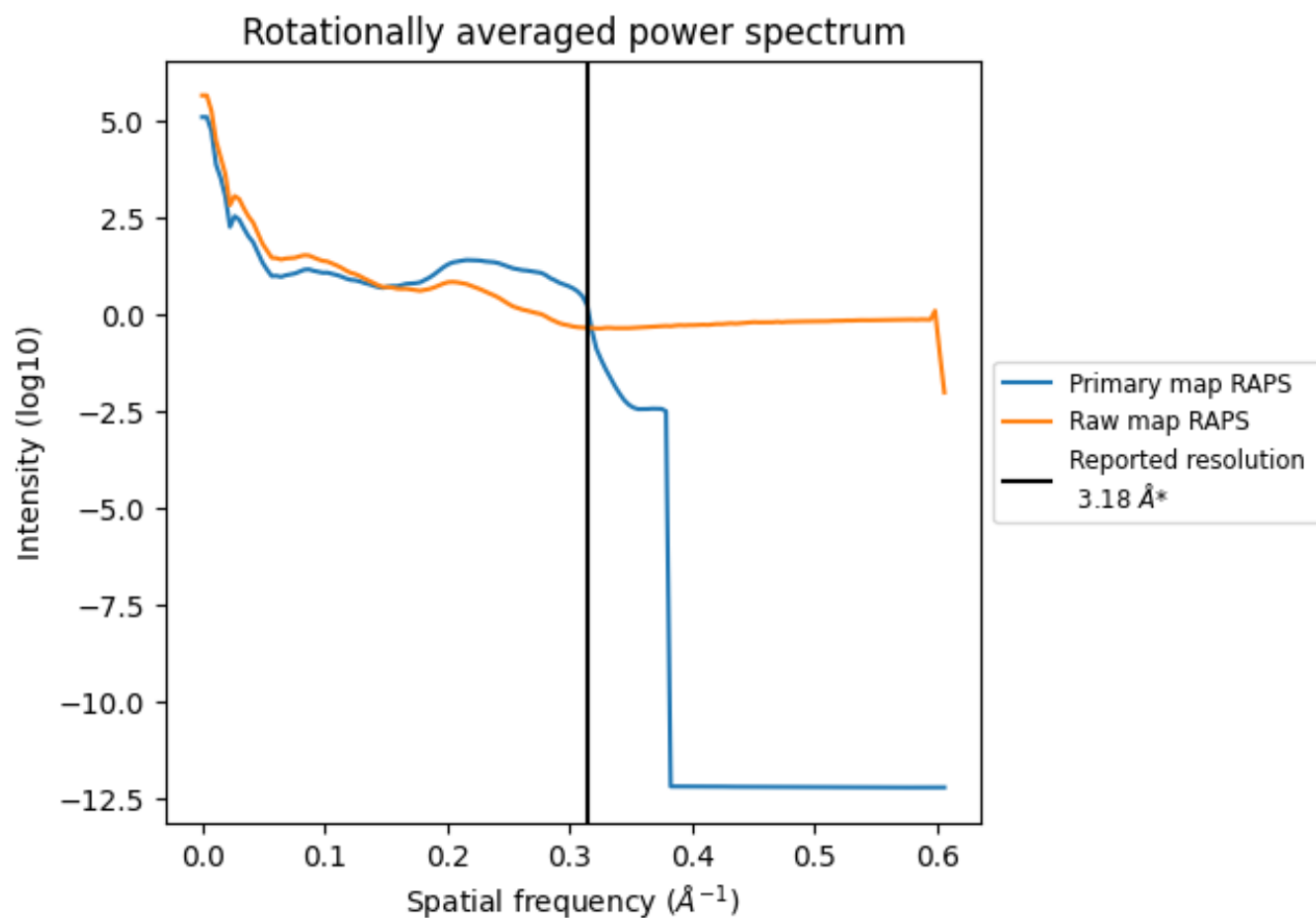
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 55 nm^3 ; this corresponds to an approximate mass of 50 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 ⓘ

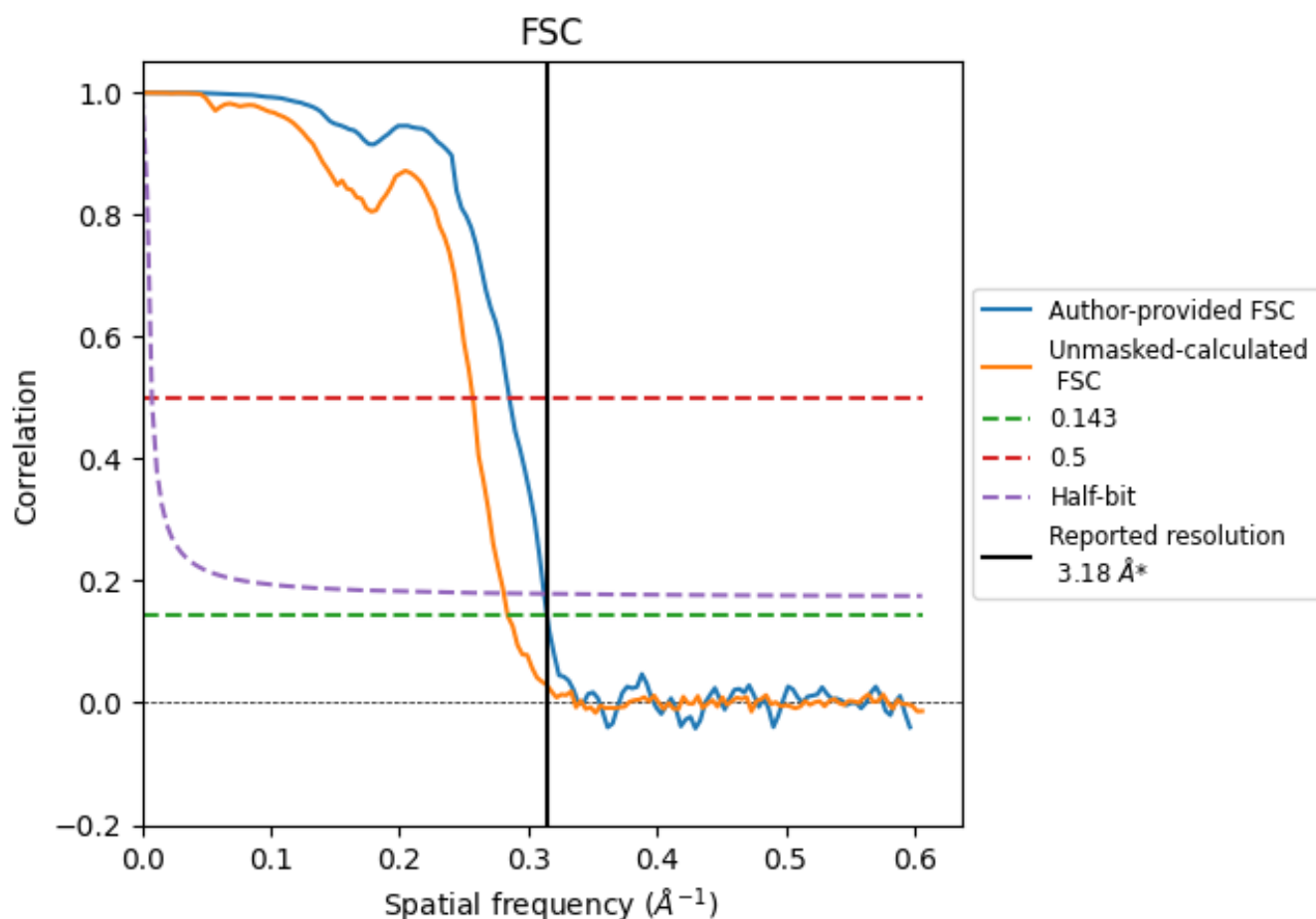


*Reported resolution corresponds to spatial frequency of 0.314 Å⁻¹

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 0.314 \AA^{-1}

8.2 Resolution estimates [i](#)

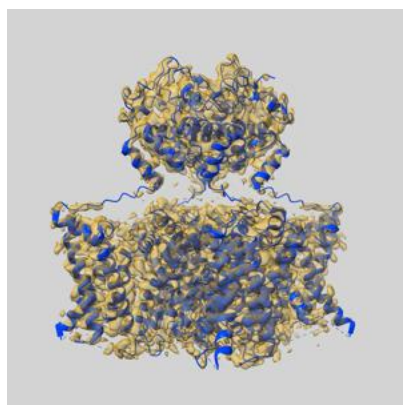
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.18	-	-
Author-provided FSC curve	3.18	3.51	3.20
Unmasked-calculated*	3.52	3.89	3.56

*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 3.52 differs from the reported value 3.18 by more than 10 %

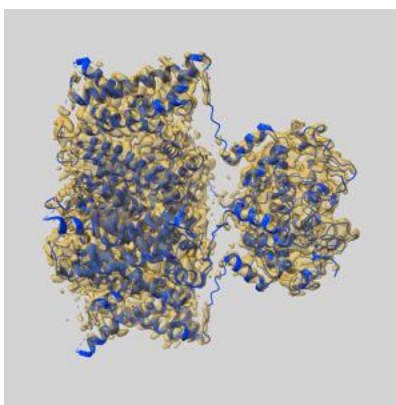
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45731 and PDB model 9CLV. Per-residue inclusion information can be found in section [3](#) on page [10](#).

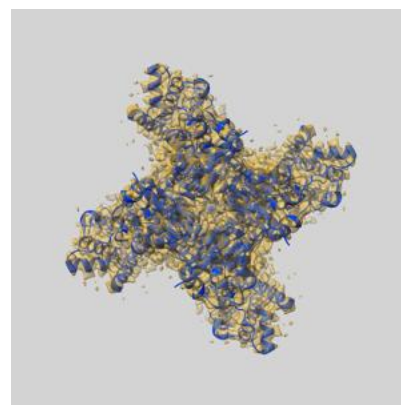
9.1 Map-model overlay [i](#)



X



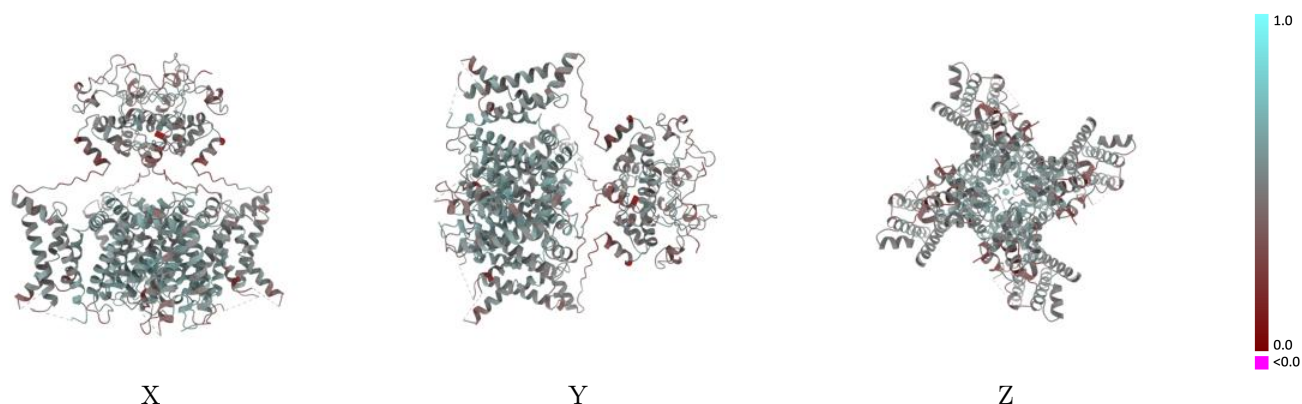
Y



Z

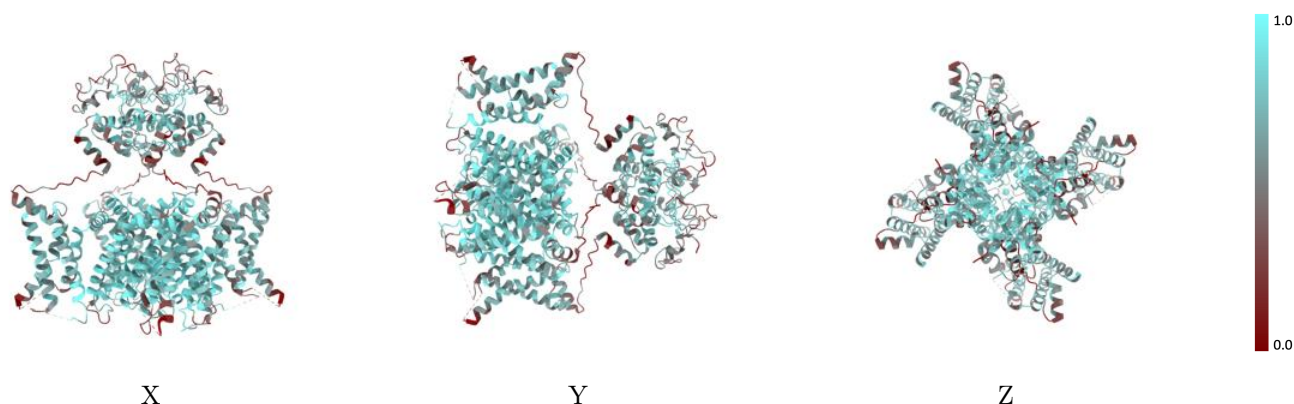
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



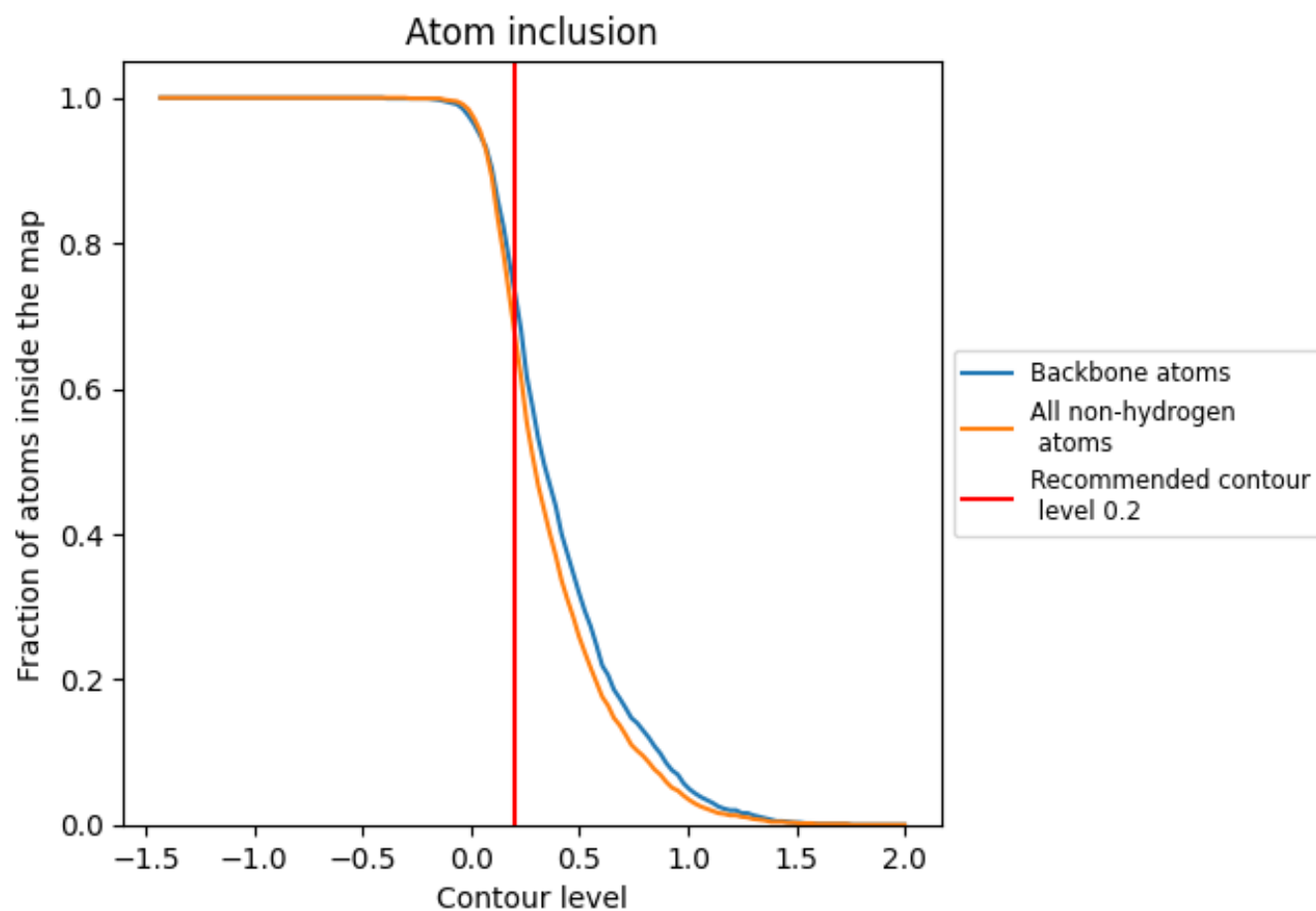
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 68% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6800	<div></div> 0.5000
A	<div></div> 0.6800	<div></div> 0.5000
B	<div></div> 0.6790	<div></div> 0.5000
C	<div></div> 0.6810	<div></div> 0.4990
D	<div></div> 0.6790	<div></div> 0.4990

