



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 03:57 AM UTC

PDB ID : 7SSX / pdb_00007ssx
EMDB ID : EMD-25416
Title : Structure of human Kv1.3
Authors : Meyerson, J.R.; Selvakumar, P.
Deposited on : 2021-11-11
Resolution : 2.89 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.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

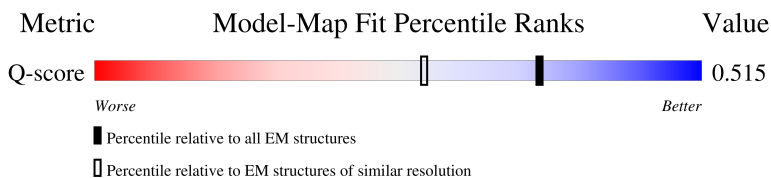
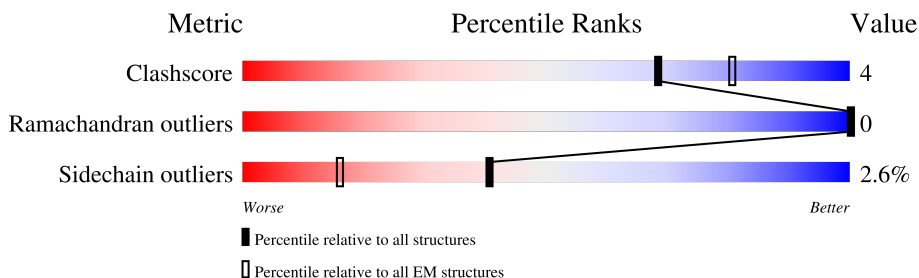
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 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	12148 (2.39 - 3.39)

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	8% 35% 5% 60%
1	B	856	8% 34% 6% 60%
1	C	856	7% 35% 6% 60%
1	D	856	7% 35% 5% 60%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11283 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, Green fluorescent protein fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	346	Total	C	N	O	S	0	0
			2820	1857	467	485	11		
1	B	346	Total	C	N	O	S	0	0
			2820	1857	467	485	11		
1	C	346	Total	C	N	O	S	0	0
			2820	1857	467	485	11		
1	D	346	Total	C	N	O	S	0	0
			2820	1857	467	485	11		

There are 220 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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	conflict	UNP P42212
A	652	LEU	PHE	conflict	UNP P42212
A	653	GLY	SER	conflict	UNP P42212
A	656	LEU	VAL	conflict	UNP P42212
A	660	ALA	SER	conflict	UNP P42212
A	741	THR	MET	conflict	UNP P42212
A	751	ALA	VAL	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	763	GLY	SER	conflict	UNP P42212
A	791	TYR	THR	conflict	UNP P42212
A	794	LYS	ALA	conflict	UNP P42212
A	819	LEU	HIS	conflict	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	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
B	582	GLN	-	linker	UNP P22001
B	583	GLY	-	linker	UNP P22001

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Chain	Residue	Modelled	Actual	Comment	Reference
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	conflict	UNP P42212
B	652	LEU	PHE	conflict	UNP P42212
B	653	GLY	SER	conflict	UNP P42212
B	656	LEU	VAL	conflict	UNP P42212
B	660	ALA	SER	conflict	UNP P42212
B	741	THR	MET	conflict	UNP P42212
B	751	ALA	VAL	conflict	UNP P42212
B	763	GLY	SER	conflict	UNP P42212
B	791	TYR	THR	conflict	UNP P42212
B	794	LYS	ALA	conflict	UNP P42212
B	819	LEU	HIS	conflict	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
B	850	SER	-	expression tag	UNP P42212
B	851	HIS	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
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	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	conflict	UNP P42212
C	652	LEU	PHE	conflict	UNP P42212
C	653	GLY	SER	conflict	UNP P42212
C	656	LEU	VAL	conflict	UNP P42212
C	660	ALA	SER	conflict	UNP P42212
C	741	THR	MET	conflict	UNP P42212
C	751	ALA	VAL	conflict	UNP P42212
C	763	GLY	SER	conflict	UNP P42212
C	791	TYR	THR	conflict	UNP P42212
C	794	LYS	ALA	conflict	UNP P42212
C	819	LEU	HIS	conflict	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
C	836	LYS	-	expression tag	UNP P42212
C	837	GLY	-	expression tag	UNP P42212
C	838	GLY	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
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	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	conflict	UNP P42212
D	652	LEU	PHE	conflict	UNP P42212
D	653	GLY	SER	conflict	UNP P42212
D	656	LEU	VAL	conflict	UNP P42212
D	660	ALA	SER	conflict	UNP P42212
D	741	THR	MET	conflict	UNP P42212
D	751	ALA	VAL	conflict	UNP P42212
D	763	GLY	SER	conflict	UNP P42212
D	791	TYR	THR	conflict	UNP P42212
D	794	LYS	ALA	conflict	UNP P42212

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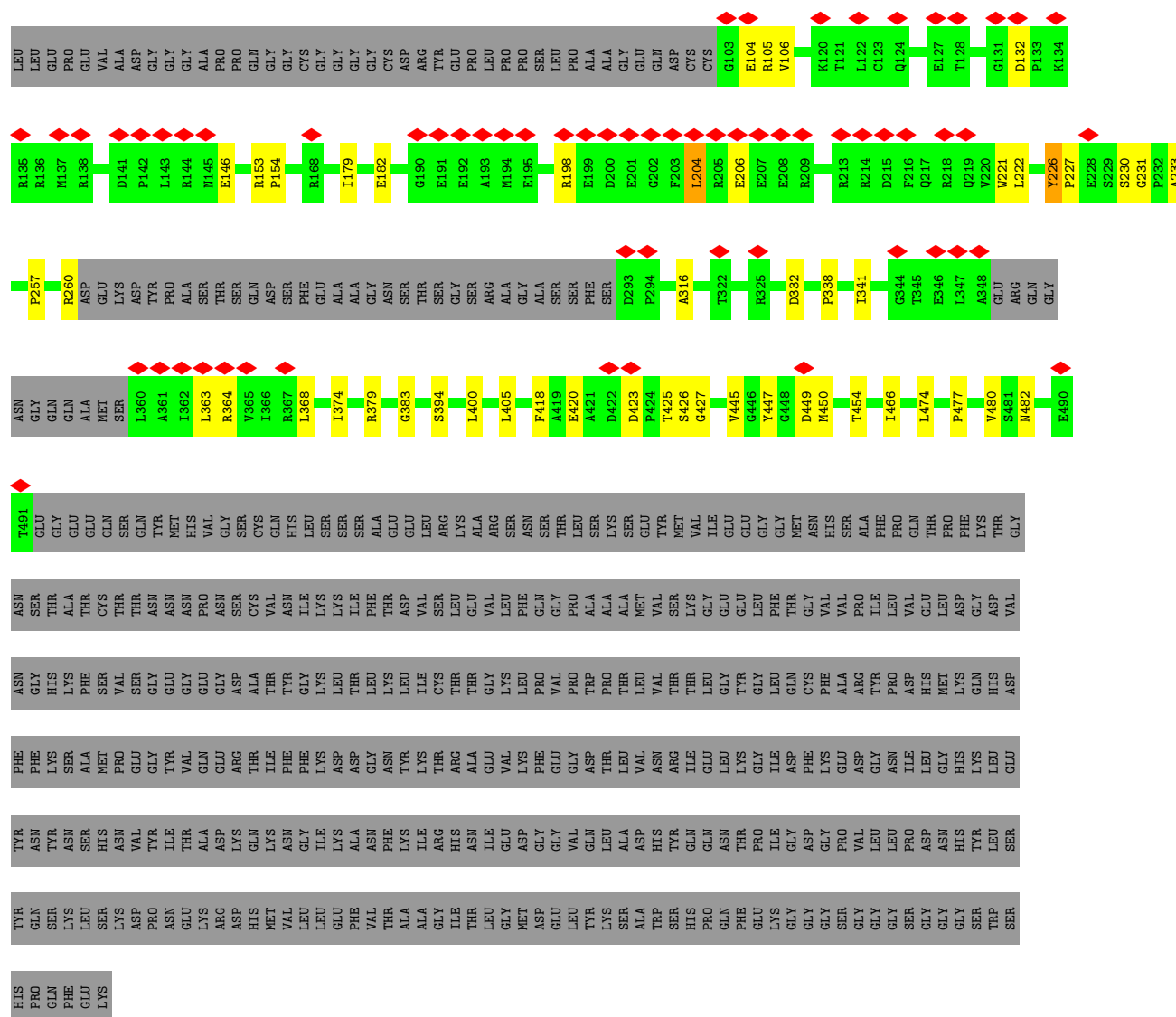
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Chain	Residue	Modelled	Actual	Comment	Reference
D	819	LEU	HIS	conflict	UNP P42212
D	827	SER	-	expression tag	UNP P42212
D	828	ALA	-	expression tag	UNP P42212
D	829	TRP	-	expression tag	UNP P42212
D	830	SER	-	expression tag	UNP P42212
D	831	HIS	-	expression 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

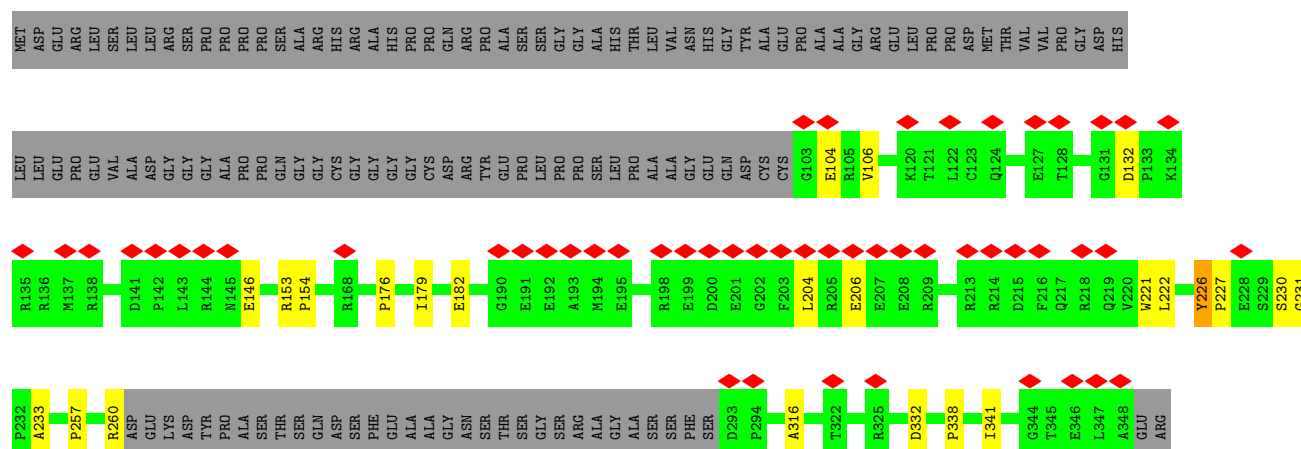
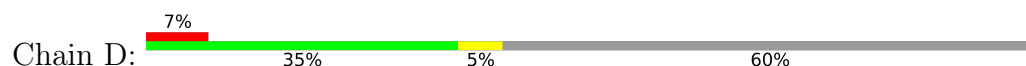
- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
2	A	3	Total K 3 3	0

MET	ASP	GLU	GLU	ARG	LEU	SER	LEU	LEU	ARG	SER	PRO	PRO	PRO	PRO	PRO	GLN	ARG	GLN	PRO	PRO	ALA	ALA	SER	SER	GLY	GLY	ALA	HIS	HIS	THR	LEU	VAL	ASN	GLY	HIS	GLY	TYR	ALA	ALA	GLU	PRO	ALA	ALA	GLY	GLY	ARG	GLU	LEU	LEU	PRO	PRO	ASP	MET	THR	VAL	VAL	VAL	PRO	GLY	GLY	ASP
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- Molecule 1: Potassium voltage-gated channel subfamily A member 3, Green fluorescent protein fusion



GLN	GLY	GLN	GLY	ASN	GLY	GLN	GLN	ALA	MET	SER	L360	A361	I362	L363	R364	V365	I366	R367	L368	I374	R379	G383	S394	L405	F418	A419	E420	A421	D422	D423	P424	T425	S426	G427	V445	G446	Y447	G448	D449	M450	T454	I466	P477	V480	S481	M482	E490	T491	GLU						
THR	ALA	THR	CYS	THR	THR	ASN	ASN	ASN	PRO	VAL	GLY	ASN	SER	CYS	GLN	HIS	LEU	SER	ALA	THR	ASP	GLU	LEU	PHE	ASN	GLN	ALA	SER	LYS	ALA	VAL	THR	LYS	GLY	GLU	GLY	THR	MET	ASN	HIS	VAL	PRO	ALA	ILE	PHE	PRO	GLN	THR	PRO	PHE	LYS	THR	GLY	ASN	SER
HIS	LYS	PHE	SER	VAL	SER	GLY	GLY	GLY	GLU	GLY	GLY	ASP	ASP	ALA	THR	TYR	GLY	LYS	THR	ILE	VAL	GLY	VAL	LEU	PHE	GLY	ALA	LYS	PRO	VAL	VAL	THR	LYS	GLY	GLU	GLY	THR	PHE	GLY	GLY	VAL	VAL	PRO	ILE	THR	LEU	VAL	GLU	THR	PRO	PHE	GLY	ASN	SER	
LYS	SER	ALA	MET	PRO	GLU	GLY	TYR	VAL	GLN	GLY	GLY	GLY	ASP	THR	ALA	THR	LEU	THR	THR	ASP	GLY	LYS	LEU	TYR	LYS	ILE	VAL	PRO	GLY	VAL	ASN	THR	ILE	GLY	GLY	GLY	THR	GLN	CYS	PHE	ALA	ARG	ASP	TYR	LEU	HIS	ASP	PHE	ASN	GLY	THR	PHE			
TYR	ASN	SER	HIS	ASN	VAL	TYR	ILE	THR	ALA	LYS	PHE	PHE	LYS	ILE	GLY	LYS	GLY	ASP	GLY	ASN	PHE	LYS	TYR	LYS	ARG	THR	GLY	GLY	VAL	GLY	ASN	ARG	ILE	GLY	GLY	ASP	PHE	GLY	GLY	LYS	PRO	VAL	GLY	ASN	ILE	PRO	ASP	GLY	THR	ASN	PHE				
SER	LYS	LEU	SER	LYS	ASP	PRO	ASN	GLU	LYS	ARG	GLY	ASN	HIS	MET	VAL	LEU	LEU	PHE	VAL	THR	ALA	LYS	ILE	ARG	ILE	HIS	ASN	ILE	GLY	GLY	ASN	TRP	HIS	GLN	GLN	ILE	GLY	GLY	ASP	PHE	GLY	GLY	PRO	VAL	GLY	LEU	PRO	ASP	GLY	THR	ASN	GLN			
GLN	PHE	GLU	LYS																																																				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	190793	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	6.013	Depositor
Minimum map value	-4.621	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.52	Depositor
Map size (Å)	272.64, 272.64, 272.64	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85200006, 0.85200006, 0.85200006	Depositor

5 Model quality

5.1 Standard geometry

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	0.74	0/2892	0.97	5/3919 (0.1%)
1	B	0.74	0/2892	0.97	5/3919 (0.1%)
1	C	0.74	0/2892	0.97	5/3919 (0.1%)
1	D	0.74	0/2892	0.97	5/3919 (0.1%)
All	All	0.74	0/11568	0.97	20/15676 (0.1%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	445	VAL	N-CA-C	-9.34	101.09	110.62
1	C	445	VAL	N-CA-C	-9.30	101.13	110.62
1	A	445	VAL	N-CA-C	-9.29	101.14	110.62
1	D	445	VAL	N-CA-C	-9.29	101.14	110.62
1	B	447	TYR	CB-CA-C	-6.34	101.20	110.96
1	C	447	TYR	CB-CA-C	-6.34	101.20	110.96
1	A	447	TYR	CB-CA-C	-6.33	101.21	110.96
1	D	447	TYR	CB-CA-C	-6.32	101.22	110.96
1	B	132	ASP	CB-CA-C	5.53	117.32	109.08
1	A	132	ASP	CB-CA-C	5.50	117.27	109.08
1	C	132	ASP	CB-CA-C	5.49	117.26	109.08
1	D	132	ASP	CB-CA-C	5.47	117.24	109.08
1	B	226	TYR	CB-CA-C	5.37	115.81	110.33
1	A	226	TYR	CB-CA-C	5.32	115.75	110.33
1	C	226	TYR	CB-CA-C	5.29	115.73	110.33
1	D	226	TYR	CB-CA-C	5.26	115.70	110.33
1	A	449	ASP	N-CA-C	-5.11	105.71	111.28
1	C	449	ASP	N-CA-C	-5.11	105.71	111.28
1	D	449	ASP	N-CA-C	-5.11	105.71	111.28
1	B	449	ASP	N-CA-C	-5.11	105.71	111.28

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	2820	0	2858	24	0
1	B	2820	0	2858	30	0
1	C	2820	0	2858	27	0
1	D	2820	0	2858	22	0
2	A	3	0	0	0	0
All	All	11283	0	11432	84	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.

All (84) 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:105:ARG:NH1	1:B:146:GLU:OE2	2.25	0.69
1:A:466:ILE:HD11	1:B:405:LEU:HD22	1.84	0.59
1:C:418:PHE:HD2	1:D:368:LEU:HD13	1.69	0.56
1:C:230:SER:OG	1:C:231:GLY:N	2.38	0.56
1:D:230:SER:OG	1:D:231:GLY:N	2.38	0.56
1:A:418:PHE:HD2	1:B:368:LEU:HD13	1.71	0.56
1:B:105:ARG:NH1	1:C:146:GLU:OE2	2.37	0.56
1:B:418:PHE:HD2	1:C:368:LEU:HD13	1.70	0.56
1:A:230:SER:OG	1:A:231:GLY:N	2.38	0.56
1:D:227:PRO:HA	1:D:233:ALA:HB1	1.89	0.55
1:A:227:PRO:HA	1:A:233:ALA:HB1	1.89	0.55
1:C:227:PRO:HA	1:C:233:ALA:HB1	1.89	0.55
1:C:466:ILE:HD11	1:D:405:LEU:HD22	1.89	0.55
1:B:227:PRO:HA	1:B:233:ALA:HB1	1.89	0.54
1:B:230:SER:OG	1:B:231:GLY:N	2.38	0.54
1:A:405:LEU:HD22	1:D:466:ILE:HD11	1.89	0.54
1:B:466:ILE:HD11	1:C:405:LEU:HD22	1.89	0.54
1:C:257:PRO:HA	1:C:260:ARG:HG2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:257:PRO:HA	1:D:260:ARG:HG2	1.90	0.53
1:B:257:PRO:HA	1:B:260:ARG:HG2	1.90	0.52
1:A:257:PRO:HA	1:A:260:ARG:HG2	1.90	0.52
1:B:332:ASP:OD2	1:B:379:ARG:NH2	2.43	0.51
1:D:332:ASP:OD2	1:D:379:ARG:NH2	2.43	0.51
1:B:222:LEU:HA	1:B:226:TYR:HD2	1.76	0.51
1:C:332:ASP:OD2	1:C:379:ARG:NH2	2.43	0.51
1:A:222:LEU:HA	1:A:226:TYR:HD2	1.76	0.51
1:A:368:LEU:HD13	1:D:418:PHE:HD2	1.75	0.51
1:A:332:ASP:OD2	1:A:379:ARG:NH2	2.43	0.51
1:C:222:LEU:HA	1:C:226:TYR:HD2	1.75	0.50
1:D:222:LEU:HA	1:D:226:TYR:HD2	1.75	0.50
1:C:105:ARG:NH1	1:D:146:GLU:OE2	2.39	0.49
1:A:338:PRO:HA	1:A:341:ILE:HG12	1.96	0.48
1:C:338:PRO:HA	1:C:341:ILE:HG12	1.96	0.47
1:D:338:PRO:HA	1:D:341:ILE:HG12	1.96	0.47
1:B:420:GLU:HB3	1:B:426:SER:HB2	1.97	0.47
1:B:338:PRO:HA	1:B:341:ILE:HG12	1.96	0.46
1:A:400:LEU:HD21	1:B:383:GLY:HA3	1.96	0.46
1:B:477:PRO:HA	1:B:480:VAL:HG22	1.98	0.46
1:C:420:GLU:HB3	1:C:426:SER:HB2	1.97	0.46
1:A:420:GLU:HB3	1:A:426:SER:HB2	1.97	0.45
1:B:427:GLY:HA3	1:B:450:MET:HG2	1.98	0.45
1:C:477:PRO:HA	1:C:480:VAL:HG22	1.98	0.45
1:A:221:TRP:HB2	1:A:316:ALA:O	2.17	0.45
1:A:427:GLY:HA3	1:A:450:MET:HG2	1.98	0.45
1:D:427:GLY:HA3	1:D:450:MET:HG2	1.98	0.45
1:D:221:TRP:HB2	1:D:316:ALA:O	2.17	0.45
1:B:221:TRP:HB2	1:B:316:ALA:O	2.17	0.45
1:A:192:GLU:H	1:A:192:GLU:HG3	1.57	0.45
1:A:477:PRO:HA	1:A:480:VAL:HG22	1.98	0.45
1:C:221:TRP:HB2	1:C:316:ALA:O	2.17	0.45
1:C:427:GLY:HA3	1:C:450:MET:HG2	1.98	0.45
1:D:420:GLU:HB3	1:D:426:SER:HB2	1.97	0.45
1:A:157:ASP:OD1	1:B:153:ARG:HD3	2.17	0.44
1:D:477:PRO:HA	1:D:480:VAL:HG22	1.98	0.44
1:D:179:ILE:O	1:D:182:GLU:HG2	2.18	0.43
1:C:179:ILE:O	1:C:182:GLU:HG2	2.18	0.43
1:C:394:SER:OG	1:C:482:ASN:ND2	2.45	0.43
1:C:204:LEU:H	1:C:204:LEU:HG	1.61	0.43
1:A:179:ILE:O	1:A:182:GLU:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:LEU:HD23	1:A:363:LEU:HA	1.85	0.43
1:A:474:LEU:HD23	1:B:480:VAL:HG12	2.01	0.43
1:C:198:ARG:HD3	1:C:198:ARG:HA	1.84	0.43
1:B:394:SER:OG	1:B:482:ASN:ND2	2.45	0.42
1:D:394:SER:OG	1:D:482:ASN:ND2	2.45	0.42
1:B:179:ILE:O	1:B:182:GLU:HG2	2.18	0.42
1:B:400:LEU:HD23	1:B:400:LEU:HA	1.92	0.41
1:B:400:LEU:HD21	1:C:383:GLY:HA3	2.02	0.41
1:A:153:ARG:N	1:A:154:PRO:HD2	2.35	0.41
1:C:363:LEU:HD23	1:C:363:LEU:HA	1.86	0.41
1:B:153:ARG:N	1:B:154:PRO:HD2	2.35	0.41
1:C:153:ARG:N	1:C:154:PRO:HD2	2.35	0.41
1:D:153:ARG:N	1:D:154:PRO:HD2	2.35	0.41
1:B:474:LEU:HD23	1:C:480:VAL:HG12	2.02	0.41
1:B:422:ASP:OD1	1:C:364:ARG:NH2	2.54	0.41
1:C:400:LEU:HD21	1:D:383:GLY:HA3	2.01	0.41
1:A:204:LEU:H	1:A:204:LEU:HG	1.61	0.40
1:B:242:LEU:HD23	1:B:242:LEU:HA	1.91	0.40
1:C:474:LEU:HD23	1:D:480:VAL:HG12	2.03	0.40
1:D:363:LEU:HD23	1:D:363:LEU:HA	1.85	0.40
1:B:120:LYS:HE3	1:B:120:LYS:HB3	1.97	0.40
1:B:192:GLU:H	1:B:192:GLU:HG3	1.57	0.40
1:B:378:SER:O	1:B:385:GLN:NE2	2.51	0.40
1:A:176:PRO:HD2	1:A:179:ILE:HD12	2.04	0.40
1:D:176:PRO:HD2	1:D:179:ILE:HD12	2.04	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	340/856 (40%)	323 (95%)	17 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	340/856 (40%)	323 (95%)	17 (5%)	0	100	100
1	C	340/856 (40%)	323 (95%)	17 (5%)	0	100	100
1	D	340/856 (40%)	323 (95%)	17 (5%)	0	100	100
All	All	1360/3424 (40%)	1292 (95%)	68 (5%)	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	307/724 (42%)	299 (97%)	8 (3%)	40	73
1	B	307/724 (42%)	299 (97%)	8 (3%)	40	73
1	C	307/724 (42%)	299 (97%)	8 (3%)	40	73
1	D	307/724 (42%)	299 (97%)	8 (3%)	40	73
All	All	1228/2896 (42%)	1196 (97%)	32 (3%)	41	73

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	104	GLU
1	A	106	VAL
1	A	204	LEU
1	A	206	GLU
1	A	374	ILE
1	A	423	ASP
1	A	425	THR
1	A	454	THR
1	B	104	GLU
1	B	106	VAL
1	B	204	LEU
1	B	206	GLU
1	B	374	ILE

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Mol	Chain	Res	Type
1	B	423	ASP
1	B	425	THR
1	B	454	THR
1	C	104	GLU
1	C	106	VAL
1	C	204	LEU
1	C	206	GLU
1	C	374	ILE
1	C	423	ASP
1	C	425	THR
1	C	454	THR
1	D	104	GLU
1	D	106	VAL
1	D	204	LEU
1	D	206	GLU
1	D	374	ILE
1	D	423	ASP
1	D	425	THR
1	D	454	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	124	GLN
1	A	145	ASN
1	B	124	GLN
1	B	145	ASN
1	C	124	GLN
1	C	145	ASN
1	D	124	GLN
1	D	145	ASN
1	D	389	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

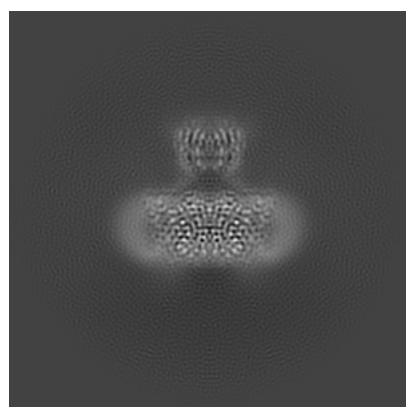
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25416. These allow visual inspection of the internal detail of the map and identification of artifacts.

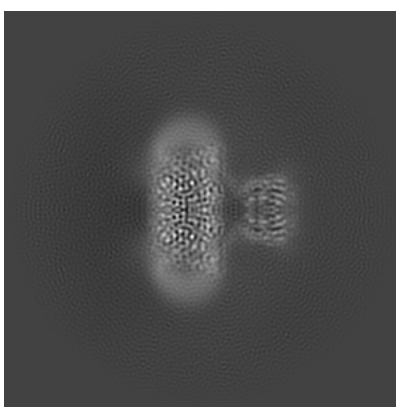
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

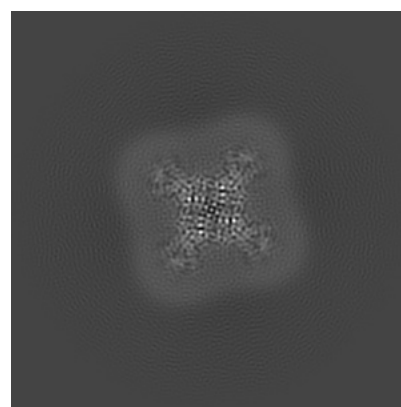
6.1.1 Primary map



X



Y

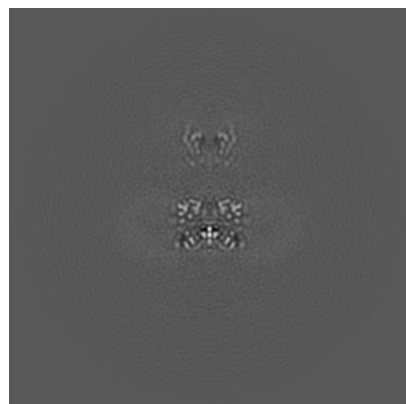


Z

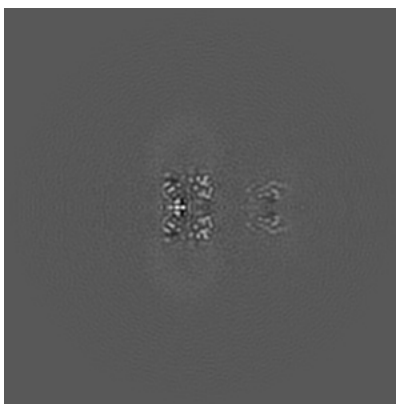
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

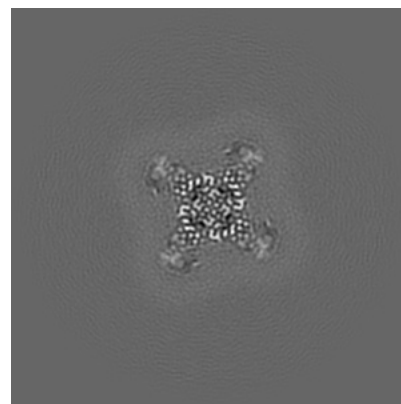
6.2.1 Primary map



X Index: 160



Y Index: 160

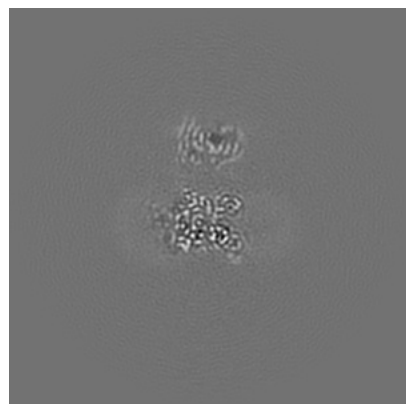


Z Index: 160

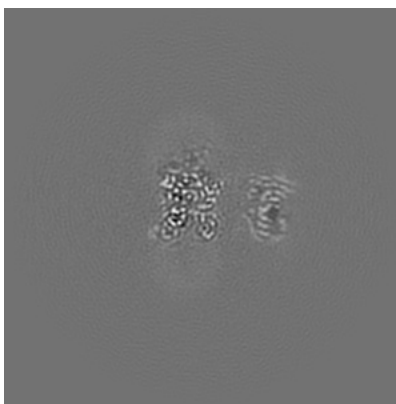
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

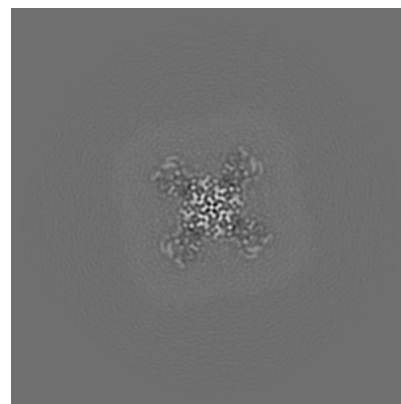
6.3.1 Primary map



X Index: 150



Y Index: 150

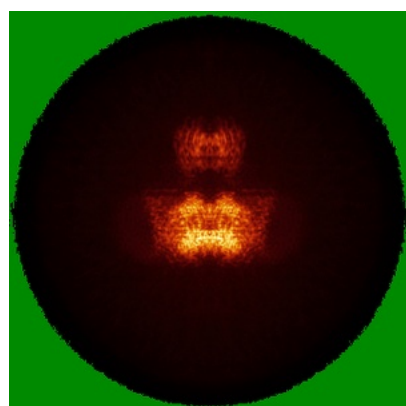


Z Index: 138

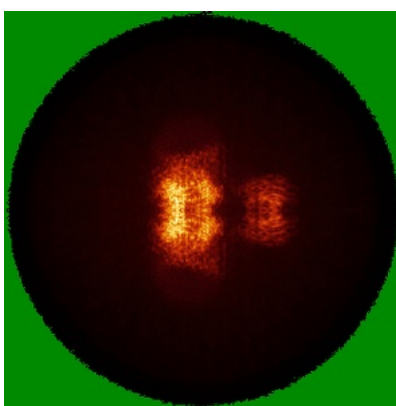
The images above show the largest variance slices of the map in three orthogonal directions.

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

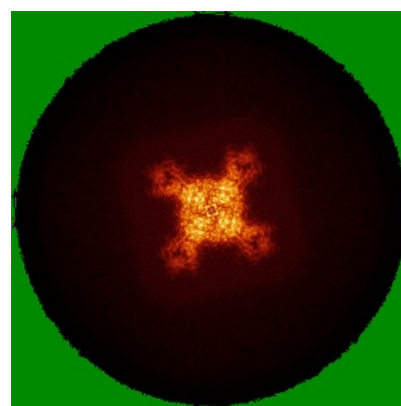
6.4.1 Primary map



X



Y

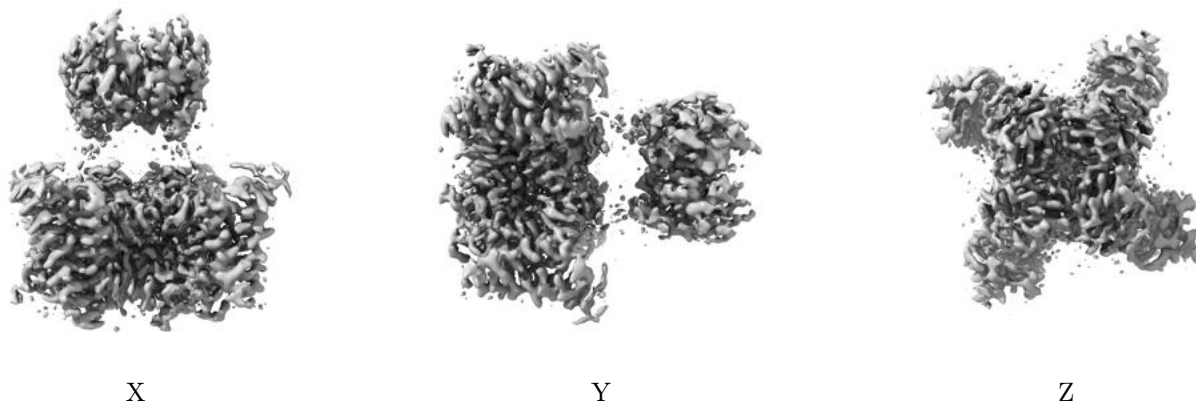


Z

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 0.52. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

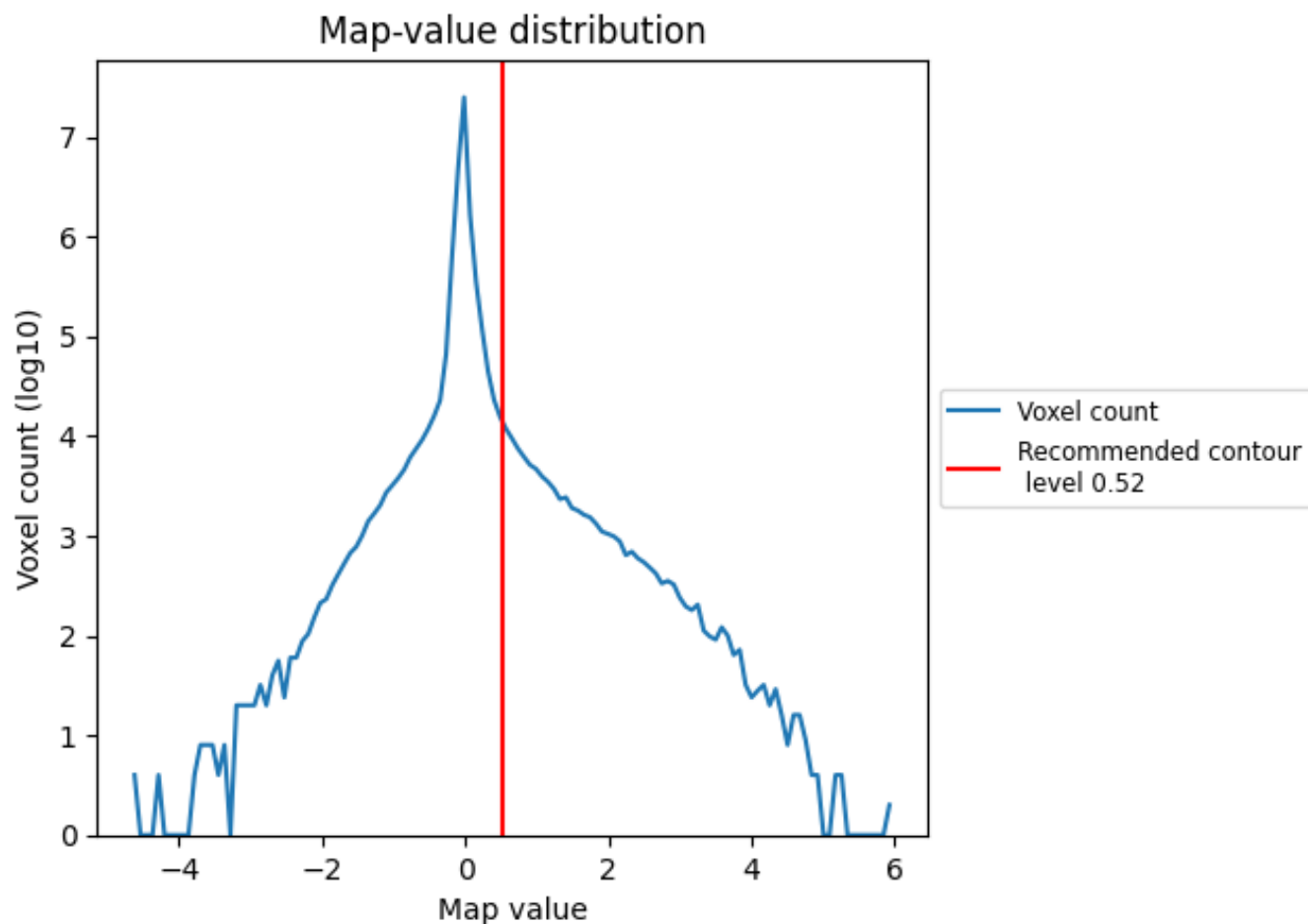
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

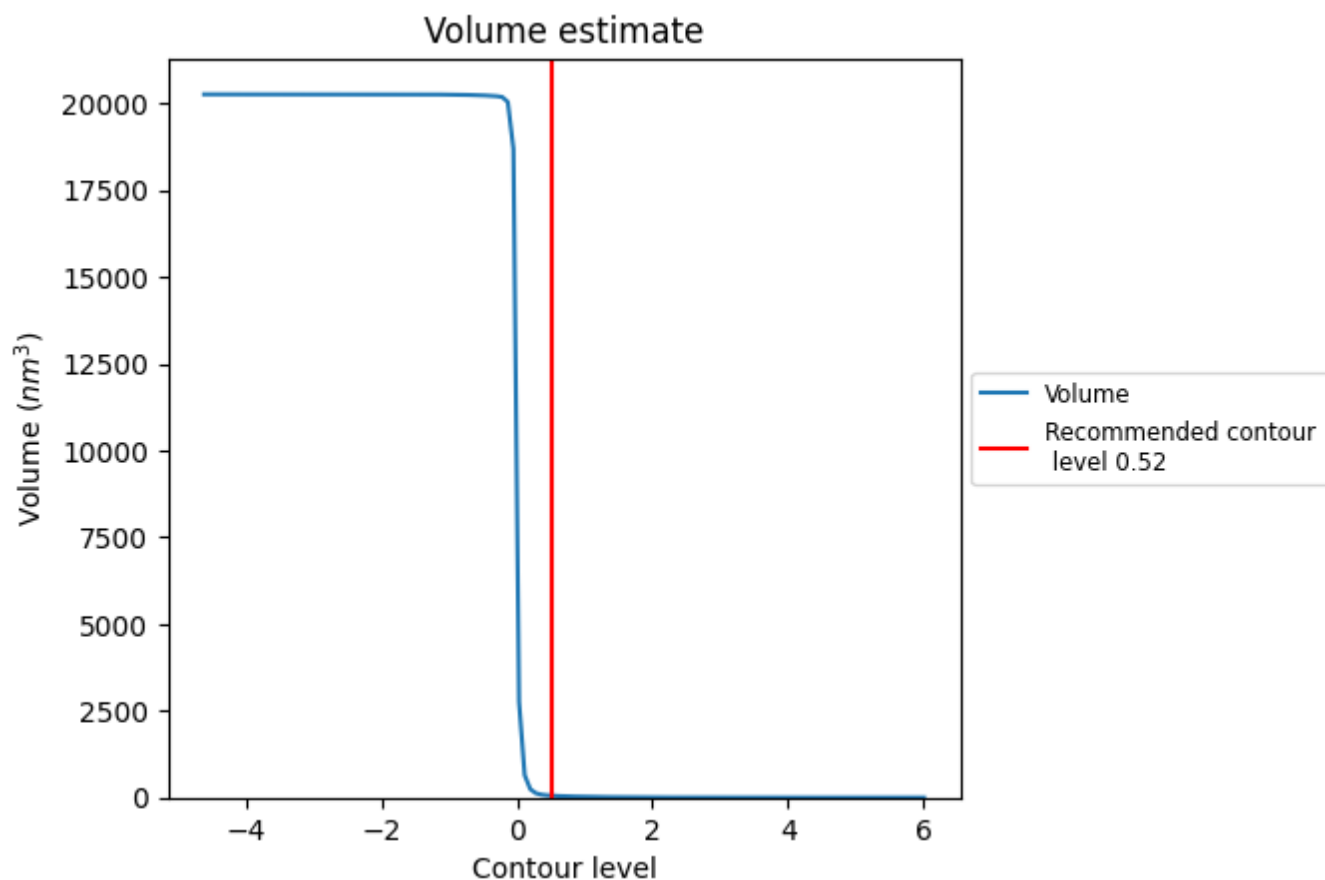
This section contains the results of statistical analysis of the map.

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.

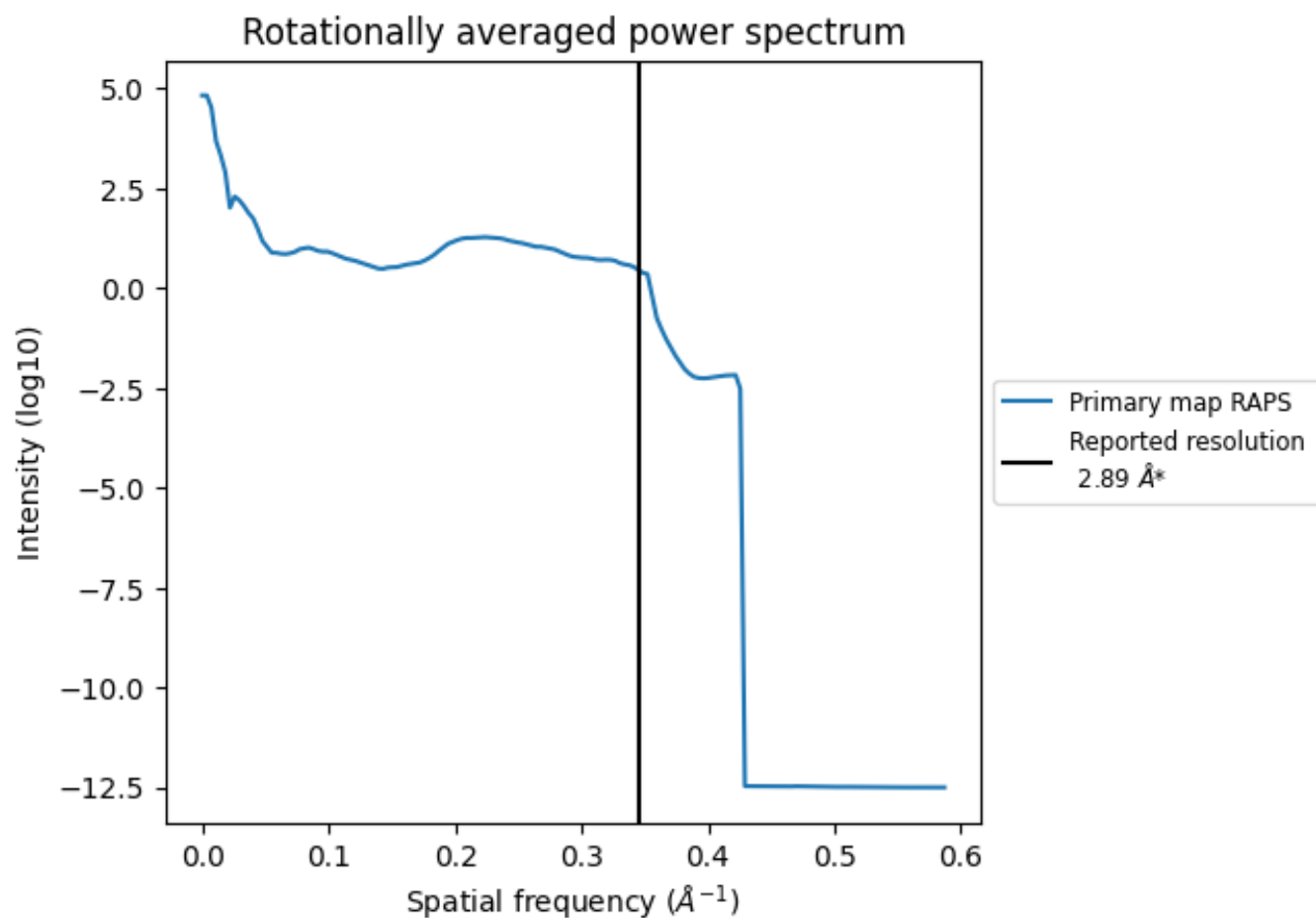
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 54 nm³; this corresponds to an approximate mass of 49 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 ⓘ

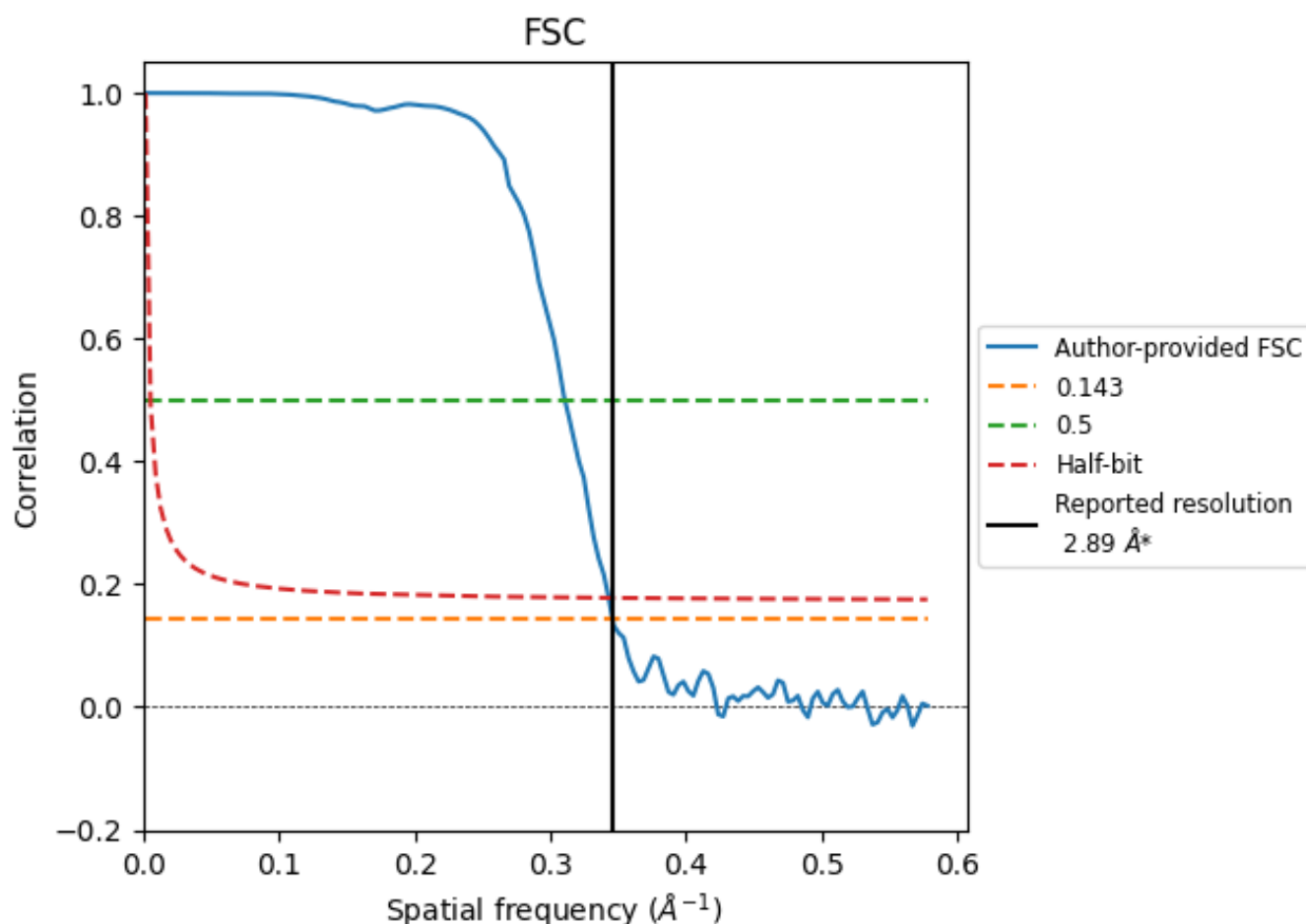


*Reported resolution corresponds to spatial frequency of 0.346 Å⁻¹

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 0.346 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	2.89	3.22	2.92
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

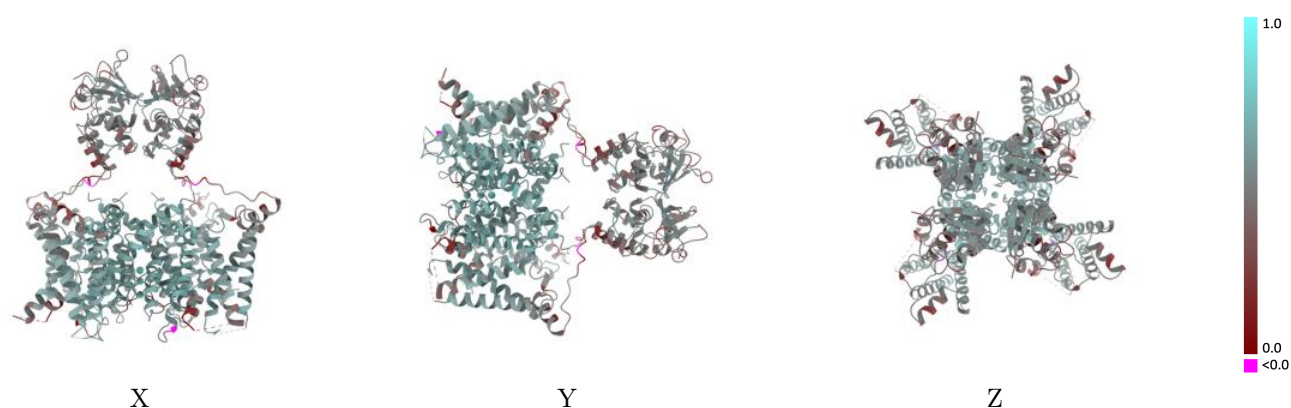
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25416 and PDB model 7SSX. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

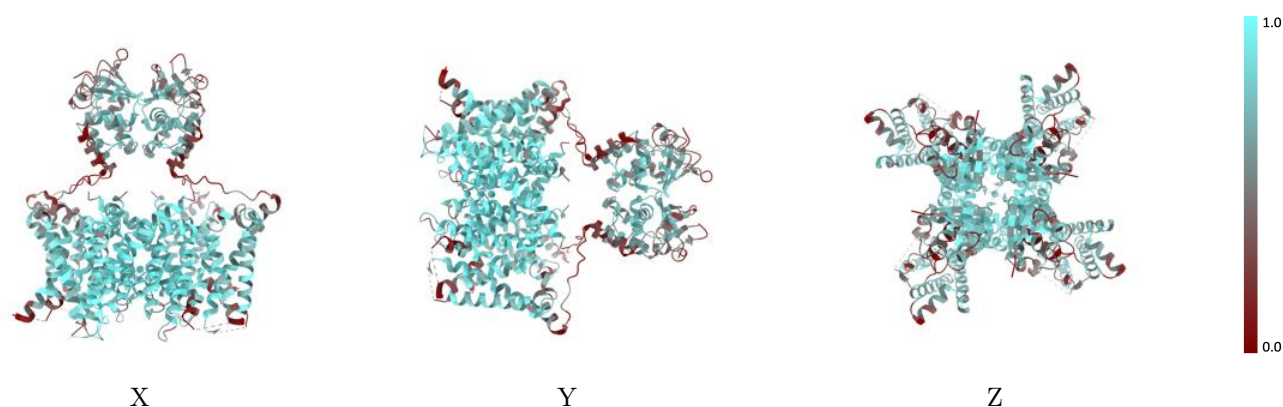
This section was not generated.

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



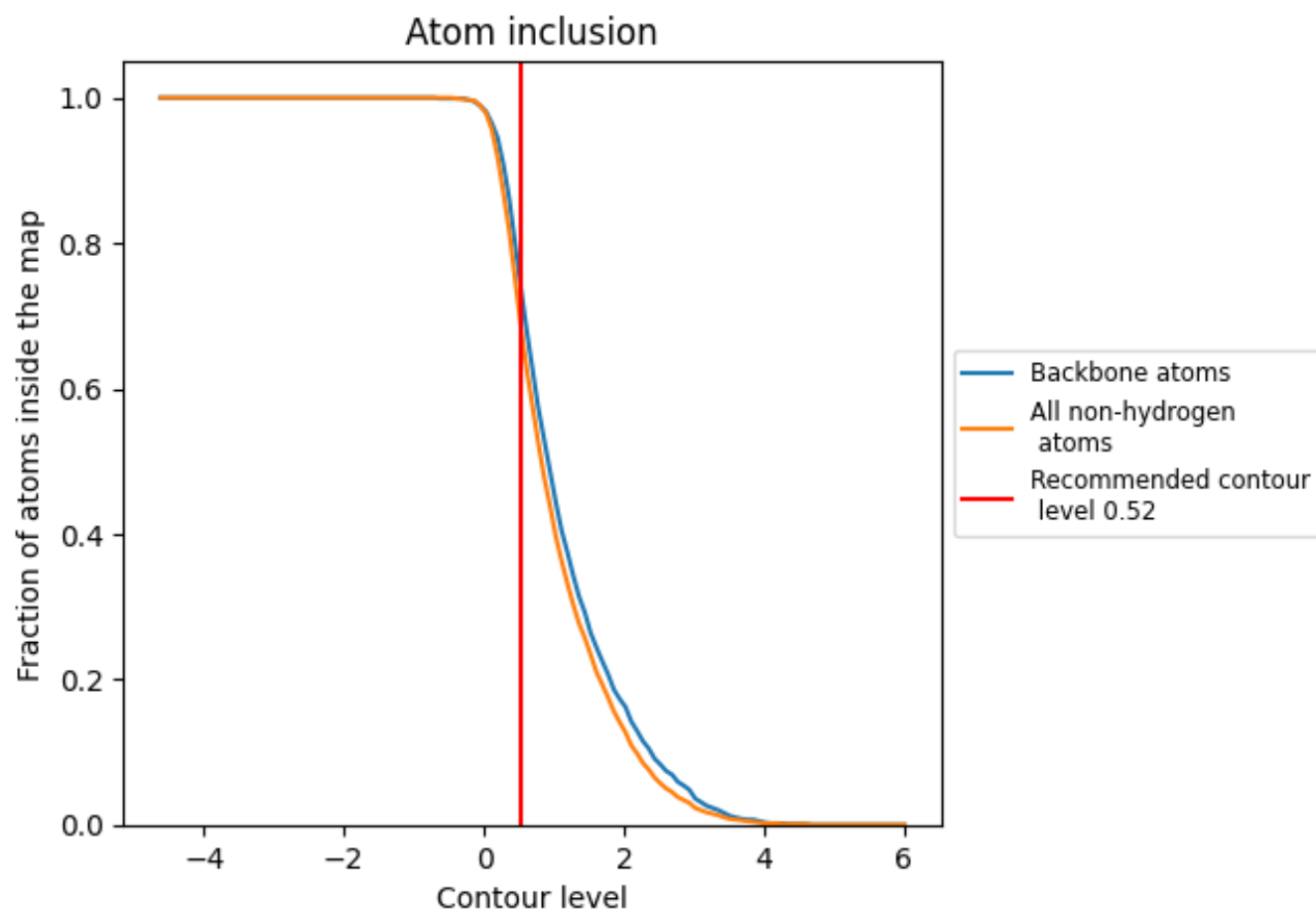
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.52).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 69% 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 (0.52) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6930	0.5150
A	0.6890	0.5130
B	0.6940	0.5160
C	0.6940	0.5160
D	0.6930	0.5160

