Full wwPDB EM Validation Report (i)

Mar 5, 2024 – 08:28 AM EST

PDB ID	:	6MHW
EMDB ID	:	EMD-9120
Title	:	Structure of human TRPV3 in the presence of 2-APB in C2 symmetry (1)
Authors	:	Zubcevic, L.; Herzik, M.A.; Wu, M.; Borschel, W.F.; Hirschi, M.; Song, A.; Lander, G.C.; Lee, S.Y.
Deposited on	:	2018-09-18
Resolution	:	4.00 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 (i) 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 (i)) were used in the production of this report:

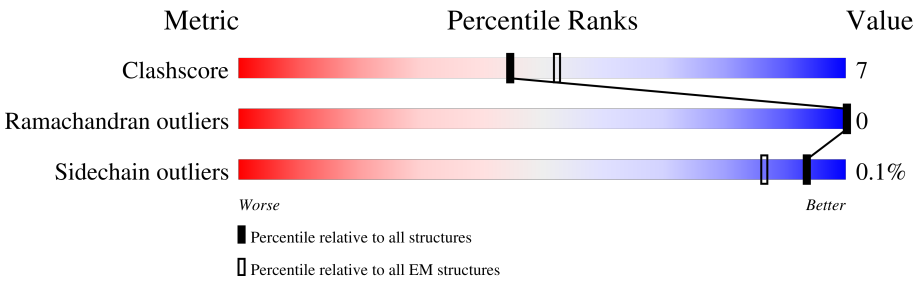
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.00 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	826	10% 63% 11% 26%
1	B	826	9% 63% 11% 26%
1	C	826	10% 63% 11% 26%
1	D	826	9% 63% 11% 26%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 34414 atoms, of which 16514 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 Transient receptor potential cation channel subfamily V member 3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	613	8634	2956	4141	753	763	21	0	0
1	B	613	8573	2933	4116	746	753	25	0	0
1	C	613	8634	2956	4141	753	763	21	0	0
1	D	613	8573	2933	4116	746	753	25	0	0

There are 148 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP Q8NET8
A	1	GLU	-	expression tag	UNP Q8NET8
A	791	VAL	-	expression tag	UNP Q8NET8
A	792	ASP	-	expression tag	UNP Q8NET8
A	793	ALA	-	expression tag	UNP Q8NET8
A	794	GLY	-	expression tag	UNP Q8NET8
A	795	LEU	-	expression tag	UNP Q8NET8
A	796	GLU	-	expression tag	UNP Q8NET8
A	797	VAL	-	expression tag	UNP Q8NET8
A	798	LEU	-	expression tag	UNP Q8NET8
A	799	PHE	-	expression tag	UNP Q8NET8
A	800	GLN	-	expression tag	UNP Q8NET8
A	801	GLY	-	expression tag	UNP Q8NET8
A	802	PRO	-	expression tag	UNP Q8NET8
A	803	ALA	-	expression tag	UNP Q8NET8
A	804	ALA	-	expression tag	UNP Q8NET8
A	805	ALA	-	expression tag	UNP Q8NET8
A	806	VAL	-	expression tag	UNP Q8NET8
A	807	ASP	-	expression tag	UNP Q8NET8
A	808	TYR	-	expression tag	UNP Q8NET8
A	809	LYS	-	expression tag	UNP Q8NET8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	810	ASP	-	expression tag	UNP Q8NET8
A	811	ASP	-	expression tag	UNP Q8NET8
A	812	ASP	-	expression tag	UNP Q8NET8
A	813	ASP	-	expression tag	UNP Q8NET8
A	814	LYS	-	expression tag	UNP Q8NET8
A	815	ALA	-	expression tag	UNP Q8NET8
A	816	HIS	-	expression tag	UNP Q8NET8
A	817	HIS	-	expression tag	UNP Q8NET8
A	818	HIS	-	expression tag	UNP Q8NET8
A	819	HIS	-	expression tag	UNP Q8NET8
A	820	HIS	-	expression tag	UNP Q8NET8
A	821	HIS	-	expression tag	UNP Q8NET8
A	822	HIS	-	expression tag	UNP Q8NET8
A	823	HIS	-	expression tag	UNP Q8NET8
A	824	HIS	-	expression tag	UNP Q8NET8
A	825	HIS	-	expression tag	UNP Q8NET8
B	0	MET	-	expression tag	UNP Q8NET8
B	1	GLU	-	expression tag	UNP Q8NET8
B	791	VAL	-	expression tag	UNP Q8NET8
B	792	ASP	-	expression tag	UNP Q8NET8
B	793	ALA	-	expression tag	UNP Q8NET8
B	794	GLY	-	expression tag	UNP Q8NET8
B	795	LEU	-	expression tag	UNP Q8NET8
B	796	GLU	-	expression tag	UNP Q8NET8
B	797	VAL	-	expression tag	UNP Q8NET8
B	798	LEU	-	expression tag	UNP Q8NET8
B	799	PHE	-	expression tag	UNP Q8NET8
B	800	GLN	-	expression tag	UNP Q8NET8
B	801	GLY	-	expression tag	UNP Q8NET8
B	802	PRO	-	expression tag	UNP Q8NET8
B	803	ALA	-	expression tag	UNP Q8NET8
B	804	ALA	-	expression tag	UNP Q8NET8
B	805	ALA	-	expression tag	UNP Q8NET8
B	806	VAL	-	expression tag	UNP Q8NET8
B	807	ASP	-	expression tag	UNP Q8NET8
B	808	TYR	-	expression tag	UNP Q8NET8
B	809	LYS	-	expression tag	UNP Q8NET8
B	810	ASP	-	expression tag	UNP Q8NET8
B	811	ASP	-	expression tag	UNP Q8NET8
B	812	ASP	-	expression tag	UNP Q8NET8
B	813	ASP	-	expression tag	UNP Q8NET8
B	814	LYS	-	expression tag	UNP Q8NET8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	815	ALA	-	expression tag	UNP Q8NET8
B	816	HIS	-	expression tag	UNP Q8NET8
B	817	HIS	-	expression tag	UNP Q8NET8
B	818	HIS	-	expression tag	UNP Q8NET8
B	819	HIS	-	expression tag	UNP Q8NET8
B	820	HIS	-	expression tag	UNP Q8NET8
B	821	HIS	-	expression tag	UNP Q8NET8
B	822	HIS	-	expression tag	UNP Q8NET8
B	823	HIS	-	expression tag	UNP Q8NET8
B	824	HIS	-	expression tag	UNP Q8NET8
B	825	HIS	-	expression tag	UNP Q8NET8
C	0	MET	-	expression tag	UNP Q8NET8
C	1	GLU	-	expression tag	UNP Q8NET8
C	791	VAL	-	expression tag	UNP Q8NET8
C	792	ASP	-	expression tag	UNP Q8NET8
C	793	ALA	-	expression tag	UNP Q8NET8
C	794	GLY	-	expression tag	UNP Q8NET8
C	795	LEU	-	expression tag	UNP Q8NET8
C	796	GLU	-	expression tag	UNP Q8NET8
C	797	VAL	-	expression tag	UNP Q8NET8
C	798	LEU	-	expression tag	UNP Q8NET8
C	799	PHE	-	expression tag	UNP Q8NET8
C	800	GLN	-	expression tag	UNP Q8NET8
C	801	GLY	-	expression tag	UNP Q8NET8
C	802	PRO	-	expression tag	UNP Q8NET8
C	803	ALA	-	expression tag	UNP Q8NET8
C	804	ALA	-	expression tag	UNP Q8NET8
C	805	ALA	-	expression tag	UNP Q8NET8
C	806	VAL	-	expression tag	UNP Q8NET8
C	807	ASP	-	expression tag	UNP Q8NET8
C	808	TYR	-	expression tag	UNP Q8NET8
C	809	LYS	-	expression tag	UNP Q8NET8
C	810	ASP	-	expression tag	UNP Q8NET8
C	811	ASP	-	expression tag	UNP Q8NET8
C	812	ASP	-	expression tag	UNP Q8NET8
C	813	ASP	-	expression tag	UNP Q8NET8
C	814	LYS	-	expression tag	UNP Q8NET8
C	815	ALA	-	expression tag	UNP Q8NET8
C	816	HIS	-	expression tag	UNP Q8NET8
C	817	HIS	-	expression tag	UNP Q8NET8
C	818	HIS	-	expression tag	UNP Q8NET8
C	819	HIS	-	expression tag	UNP Q8NET8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	820	HIS	-	expression tag	UNP Q8NET8
C	821	HIS	-	expression tag	UNP Q8NET8
C	822	HIS	-	expression tag	UNP Q8NET8
C	823	HIS	-	expression tag	UNP Q8NET8
C	824	HIS	-	expression tag	UNP Q8NET8
C	825	HIS	-	expression tag	UNP Q8NET8
D	0	MET	-	expression tag	UNP Q8NET8
D	1	GLU	-	expression tag	UNP Q8NET8
D	791	VAL	-	expression tag	UNP Q8NET8
D	792	ASP	-	expression tag	UNP Q8NET8
D	793	ALA	-	expression tag	UNP Q8NET8
D	794	GLY	-	expression tag	UNP Q8NET8
D	795	LEU	-	expression tag	UNP Q8NET8
D	796	GLU	-	expression tag	UNP Q8NET8
D	797	VAL	-	expression tag	UNP Q8NET8
D	798	LEU	-	expression tag	UNP Q8NET8
D	799	PHE	-	expression tag	UNP Q8NET8
D	800	GLN	-	expression tag	UNP Q8NET8
D	801	GLY	-	expression tag	UNP Q8NET8
D	802	PRO	-	expression tag	UNP Q8NET8
D	803	ALA	-	expression tag	UNP Q8NET8
D	804	ALA	-	expression tag	UNP Q8NET8
D	805	ALA	-	expression tag	UNP Q8NET8
D	806	VAL	-	expression tag	UNP Q8NET8
D	807	ASP	-	expression tag	UNP Q8NET8
D	808	TYR	-	expression tag	UNP Q8NET8
D	809	LYS	-	expression tag	UNP Q8NET8
D	810	ASP	-	expression tag	UNP Q8NET8
D	811	ASP	-	expression tag	UNP Q8NET8
D	812	ASP	-	expression tag	UNP Q8NET8
D	813	ASP	-	expression tag	UNP Q8NET8
D	814	LYS	-	expression tag	UNP Q8NET8
D	815	ALA	-	expression tag	UNP Q8NET8
D	816	HIS	-	expression tag	UNP Q8NET8
D	817	HIS	-	expression tag	UNP Q8NET8
D	818	HIS	-	expression tag	UNP Q8NET8
D	819	HIS	-	expression tag	UNP Q8NET8
D	820	HIS	-	expression tag	UNP Q8NET8
D	821	HIS	-	expression tag	UNP Q8NET8
D	822	HIS	-	expression tag	UNP Q8NET8
D	823	HIS	-	expression tag	UNP Q8NET8
D	824	HIS	-	expression tag	UNP Q8NET8

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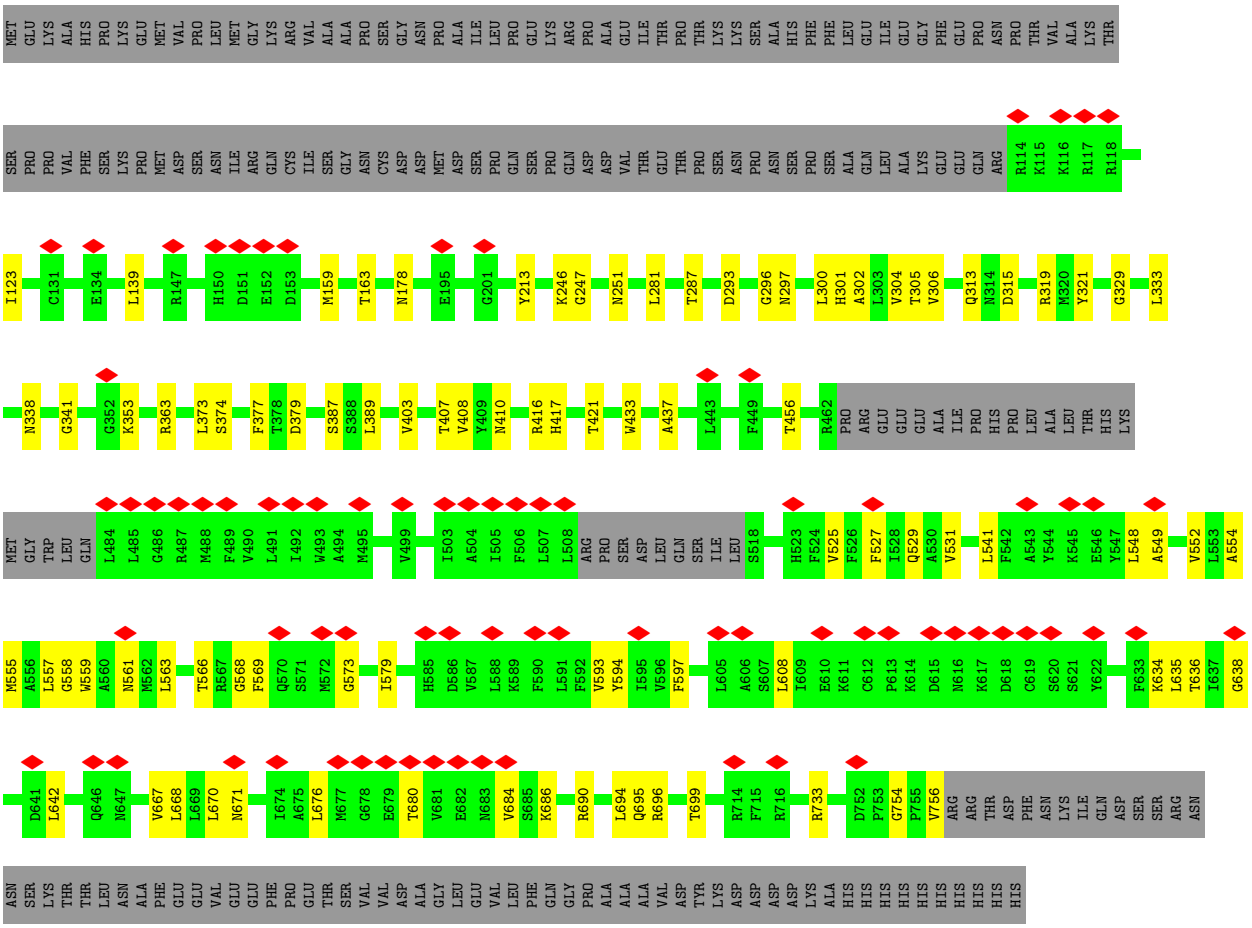
Chain	Residue	Modelled	Actual	Comment	Reference
D	825	HIS	-	expression tag	UNP Q8NET8

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

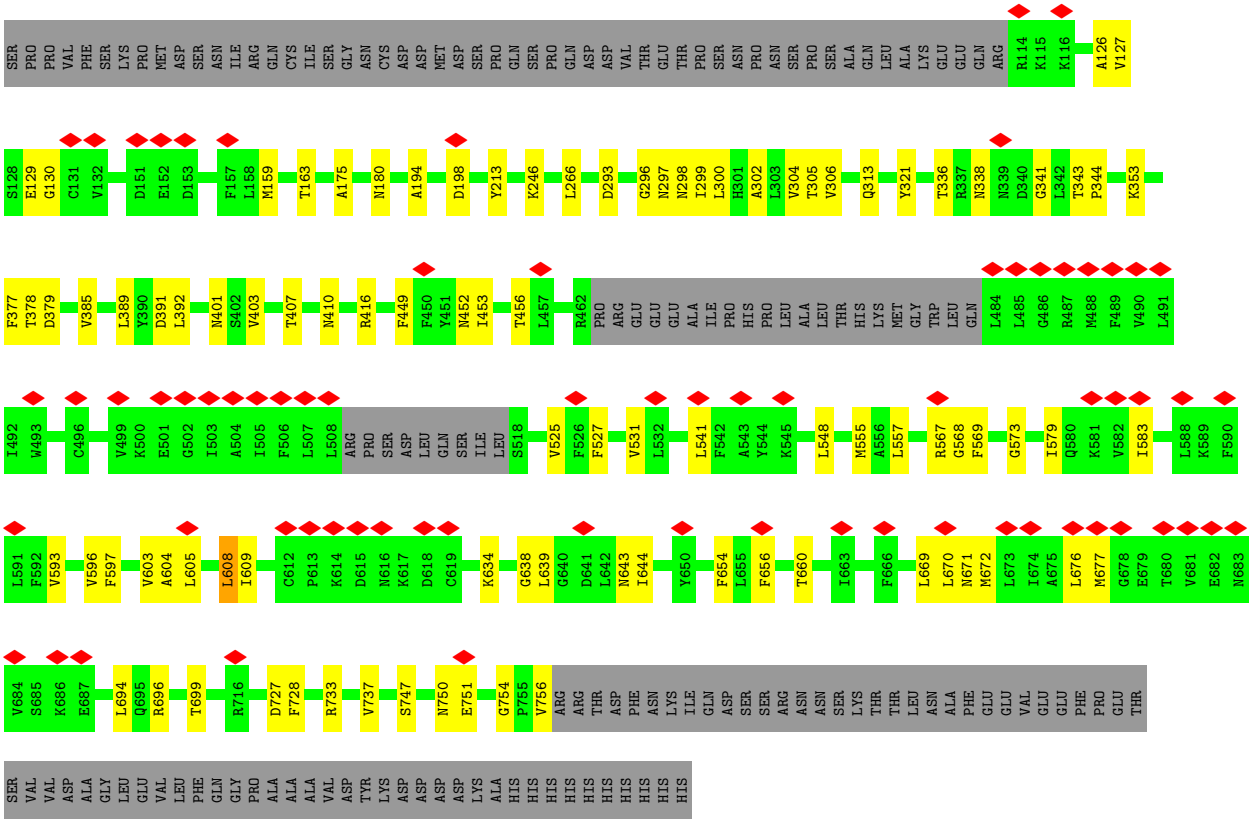
• Molecule 1: Transient receptor potential cation channel subfamily V member 3

Chain A:



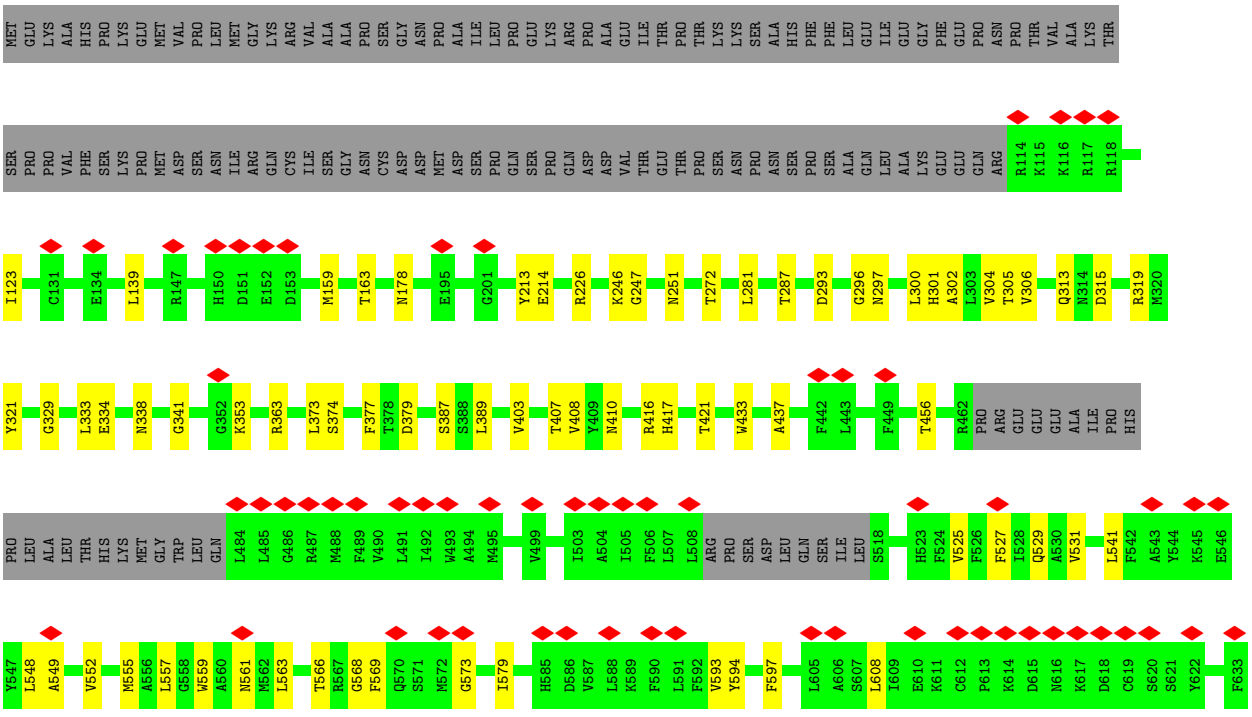
• Molecule 1: Transient receptor potential cation channel subfamily V member 3

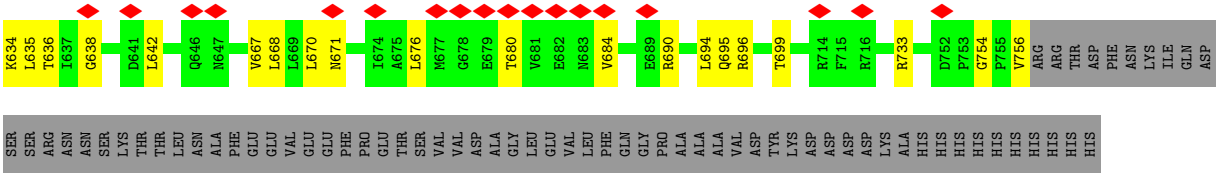
Chain B:



• Molecule 1: Transient receptor potential cation channel subfamily V member 3

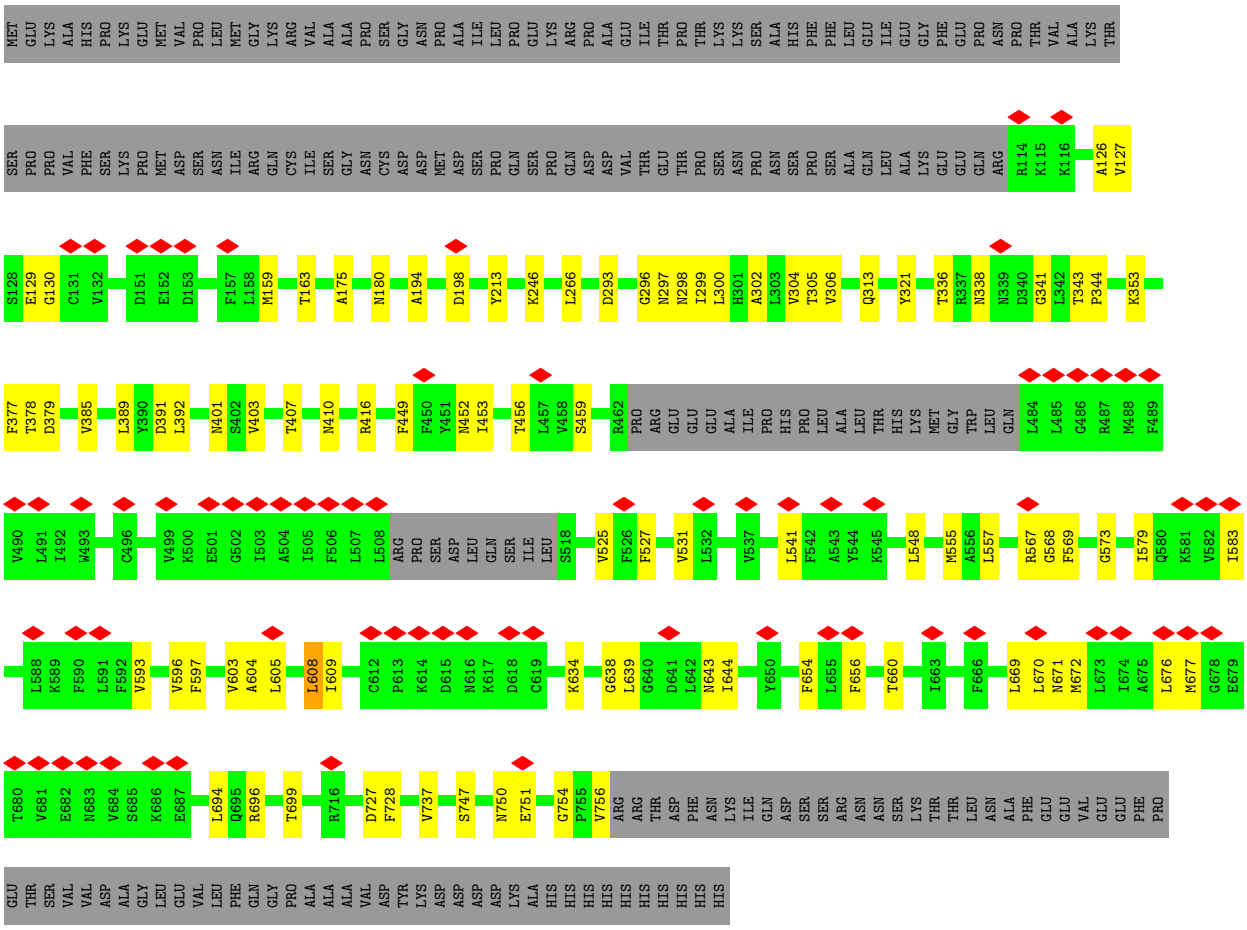
Chain C:





• Molecule 1: Transient receptor potential cation channel subfamily V member 3

Chain D:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	61292	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	60.0	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.311	Depositor
Minimum map value	-0.158	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.065	Depositor
Map size (Å)	331.19998, 331.19998, 331.19998	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.15, 1.15, 1.15	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	A	0.28	0/4593	0.45	7/6278 (0.1%)
1	B	0.28	0/4554	0.45	6/6223 (0.1%)
1	C	0.28	0/4593	0.45	7/6278 (0.1%)
1	D	0.28	0/4554	0.45	7/6223 (0.1%)
All	All	0.28	0/18294	0.45	27/25002 (0.1%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	756	VAL	CG1-CB-CG2	7.27	122.54	110.90
1	C	756	VAL	CG1-CB-CG2	7.26	122.52	110.90
1	B	756	VAL	CG1-CB-CG2	7.21	122.44	110.90
1	D	756	VAL	CG1-CB-CG2	7.17	122.37	110.90
1	C	541	LEU	CB-CG-CD2	6.64	122.28	111.00
1	A	541	LEU	CB-CG-CD2	6.61	122.23	111.00
1	B	548	LEU	CB-CG-CD2	6.38	121.85	111.00
1	D	548	LEU	CB-CG-CD2	6.36	121.81	111.00
1	B	541	LEU	CB-CG-CD2	6.33	121.76	111.00
1	D	541	LEU	CB-CG-CD2	6.31	121.72	111.00
1	C	548	LEU	CB-CG-CD2	6.21	121.56	111.00
1	A	548	LEU	CB-CG-CD2	6.21	121.55	111.00
1	D	608	LEU	CB-CG-CD2	5.88	120.99	111.00
1	A	608	LEU	CB-CG-CD2	5.84	120.94	111.00
1	B	608	LEU	CB-CG-CD2	5.84	120.93	111.00
1	C	608	LEU	CB-CG-CD2	5.77	120.81	111.00
1	D	541	LEU	CB-CG-CD1	5.60	120.51	111.00
1	B	541	LEU	CB-CG-CD1	5.57	120.46	111.00
1	D	548	LEU	CB-CG-CD1	5.41	120.20	111.00
1	B	548	LEU	CB-CG-CD1	5.37	120.13	111.00
1	C	608	LEU	CB-CG-CD1	5.37	120.12	111.00
1	A	541	LEU	CB-CG-CD1	5.33	120.06	111.00
1	C	541	LEU	CB-CG-CD1	5.28	119.98	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	548	LEU	CB-CG-CD1	5.24	119.91	111.00
1	A	548	LEU	CB-CG-CD1	5.24	119.90	111.00
1	A	608	LEU	CB-CG-CD1	5.21	119.86	111.00
1	D	608	LEU	CB-CG-CD1	5.04	119.57	111.00

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	4493	4141	4204	67	0
1	B	4457	4116	4166	67	0
1	C	4493	4141	4204	69	0
1	D	4457	4116	4166	64	0
All	All	17900	16514	16740	234	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 7.

All (234) 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:B:583:ILE:HG21	1:C:667:VAL:CG1	1.94	0.97
1:A:667:VAL:CG1	1:D:583:ILE:HG21	1.97	0.95
1:B:583:ILE:HG21	1:C:667:VAL:HG13	1.53	0.89
1:A:667:VAL:HG13	1:D:583:ILE:HG21	1.52	0.89
1:C:379:ASP:OD1	1:C:387:SER:OG	1.93	0.86
1:A:379:ASP:OD1	1:A:387:SER:OG	1.93	0.84
1:C:304:VAL:O	1:C:353:LYS:NZ	2.13	0.81
1:A:304:VAL:O	1:A:353:LYS:NZ	2.13	0.81
1:B:304:VAL:O	1:B:353:LYS:NZ	2.15	0.80
1:D:304:VAL:O	1:D:353:LYS:NZ	2.15	0.80
1:C:529:GLN:OE1	1:C:561:ASN:ND2	2.23	0.72
1:A:377:PHE:O	1:A:389:LEU:N	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:377:PHE:O	1:C:389:LEU:N	2.23	0.71
1:A:529:GLN:OE1	1:A:561:ASN:ND2	2.23	0.71
1:B:583:ILE:HD11	1:C:671:ASN:HB2	1.72	0.71
1:A:671:ASN:HB2	1:D:583:ILE:HD11	1.73	0.70
1:A:159:MET:O	1:A:163:THR:N	2.26	0.69
1:B:583:ILE:CG2	1:C:667:VAL:HG13	2.23	0.68
1:B:302:ALA:O	1:B:305:THR:OG1	2.10	0.68
1:A:568:GLY:O	1:A:696:ARG:NH1	2.27	0.68
1:C:159:MET:O	1:C:163:THR:N	2.26	0.68
1:C:563:LEU:O	1:C:566:THR:OG1	2.09	0.67
1:C:568:GLY:O	1:C:696:ARG:NH1	2.27	0.67
1:D:302:ALA:O	1:D:305:THR:OG1	2.10	0.67
1:A:213:TYR:OH	1:D:754:GLY:N	2.28	0.67
1:A:563:LEU:O	1:A:566:THR:OG1	2.09	0.67
1:B:579:ILE:HA	1:B:583:ILE:HD12	1.78	0.66
1:D:568:GLY:O	1:D:696:ARG:NH1	2.29	0.66
1:B:754:GLY:N	1:C:213:TYR:OH	2.28	0.66
1:B:568:GLY:O	1:B:696:ARG:NH1	2.29	0.65
1:B:583:ILE:HG21	1:C:667:VAL:HG11	1.78	0.65
1:B:593:VAL:HG22	1:B:597:PHE:CE2	2.32	0.65
1:D:593:VAL:HG22	1:D:597:PHE:CE2	2.32	0.65
1:D:579:ILE:HA	1:D:583:ILE:HD12	1.80	0.64
1:B:634:LYS:NZ	1:C:642:LEU:O	2.30	0.64
1:A:374:SER:OG	1:A:377:PHE:CE1	2.51	0.64
1:A:667:VAL:HG13	1:D:583:ILE:CG2	2.24	0.63
1:C:374:SER:OG	1:C:377:PHE:CE1	2.51	0.63
1:C:302:ALA:O	1:C:305:THR:OG1	2.16	0.63
1:A:642:LEU:O	1:D:634:LYS:NZ	2.32	0.63
1:A:417:HIS:CG	1:A:690:ARG:HG2	2.35	0.62
1:C:417:HIS:CG	1:C:690:ARG:HG2	2.35	0.61
1:A:593:VAL:HG13	1:A:668:LEU:HD21	1.83	0.61
1:C:593:VAL:HG13	1:C:668:LEU:HD21	1.83	0.61
1:C:374:SER:OG	1:C:377:PHE:CZ	2.54	0.61
1:C:634:LYS:O	1:C:638:GLY:N	2.34	0.60
1:A:569:PHE:O	1:A:573:GLY:N	2.34	0.60
1:D:338:ASN:OD1	1:D:341:GLY:N	2.34	0.60
1:C:569:PHE:O	1:C:573:GLY:N	2.34	0.60
1:A:374:SER:OG	1:A:377:PHE:CZ	2.54	0.60
1:B:609:ILE:HG22	1:B:609:ILE:O	2.02	0.60
1:C:338:ASN:OD1	1:C:341:GLY:N	2.35	0.60
1:D:159:MET:O	1:D:163:THR:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:159:MET:O	1:B:163:THR:N	2.34	0.60
1:B:338:ASN:OD1	1:B:341:GLY:N	2.34	0.59
1:C:293:ASP:OD1	1:C:297:ASN:N	2.35	0.59
1:A:338:ASN:OD1	1:A:341:GLY:N	2.34	0.59
1:A:634:LYS:O	1:A:638:GLY:N	2.34	0.59
1:A:293:ASP:OD1	1:A:297:ASN:N	2.35	0.58
1:D:609:ILE:HG22	1:D:609:ILE:O	2.02	0.58
1:A:293:ASP:OD1	1:A:296:GLY:N	2.37	0.58
1:A:667:VAL:HG11	1:D:583:ILE:HG21	1.83	0.57
1:B:377:PHE:O	1:B:389:LEU:N	2.34	0.57
1:C:293:ASP:OD1	1:C:296:GLY:N	2.38	0.57
1:C:555:MET:SD	1:C:559:TRP:NE1	2.78	0.57
1:C:281:LEU:O	1:C:287:THR:OG1	2.07	0.56
1:C:379:ASP:OD2	1:C:733:ARG:NH2	2.34	0.56
1:A:417:HIS:ND1	1:A:690:ARG:HG2	2.21	0.56
1:C:754:GLY:N	1:D:213:TYR:OH	2.39	0.56
1:D:605:LEU:HD22	1:D:654:PHE:CE1	2.41	0.56
1:B:605:LEU:HD22	1:B:654:PHE:CE1	2.41	0.56
1:B:634:LYS:O	1:B:638:GLY:N	2.36	0.56
1:A:754:GLY:N	1:B:213:TYR:OH	2.39	0.55
1:A:379:ASP:OD2	1:A:733:ARG:NH2	2.34	0.55
1:A:555:MET:SD	1:A:559:TRP:NE1	2.78	0.55
1:C:417:HIS:ND1	1:C:690:ARG:HG2	2.20	0.55
1:A:302:ALA:O	1:A:305:THR:OG1	2.17	0.55
1:D:293:ASP:OD1	1:D:296:GLY:N	2.40	0.55
1:B:293:ASP:OD1	1:B:296:GLY:N	2.40	0.55
1:D:266:LEU:HD23	1:D:299:ILE:HD11	1.89	0.55
1:D:377:PHE:O	1:D:389:LEU:N	2.34	0.55
1:C:363:ARG:O	1:C:374:SER:HB2	2.07	0.55
1:D:634:LYS:O	1:D:638:GLY:N	2.36	0.55
1:A:281:LEU:O	1:A:287:THR:OG1	2.07	0.54
1:B:246:LYS:O	1:B:246:LYS:HG3	2.07	0.54
1:C:123:ILE:HG12	1:C:139:LEU:HD21	1.90	0.54
1:B:643:ASN:OD1	1:B:644:ILE:N	2.41	0.54
1:B:126:ALA:O	1:B:130:GLY:N	2.40	0.54
1:A:363:ARG:O	1:A:374:SER:HB2	2.08	0.53
1:D:126:ALA:O	1:D:130:GLY:N	2.40	0.53
1:D:298:ASN:OD1	1:D:336:THR:OG1	2.23	0.53
1:A:306:VAL:O	1:A:313:GLN:NE2	2.41	0.53
1:D:246:LYS:HG3	1:D:246:LYS:O	2.07	0.53
1:D:391:ASP:OD1	1:D:392:LEU:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:266:LEU:HD23	1:B:299:ILE:HD11	1.89	0.53
1:C:306:VAL:O	1:C:313:GLN:NE2	2.41	0.53
1:D:416:ARG:CZ	1:D:694:LEU:HD21	2.39	0.53
1:A:377:PHE:N	1:A:389:LEU:O	2.42	0.53
1:D:449:PHE:CE2	1:D:453:ILE:HD11	2.44	0.52
1:B:391:ASP:OD1	1:B:392:LEU:N	2.42	0.52
1:B:416:ARG:CZ	1:B:694:LEU:HD21	2.39	0.52
1:C:408:VAL:O	1:C:416:ARG:NH1	2.43	0.52
1:A:123:ILE:HG12	1:A:139:LEU:HD21	1.90	0.52
1:B:416:ARG:NH2	1:B:694:LEU:HD21	2.25	0.52
1:D:643:ASN:OD1	1:D:644:ILE:N	2.41	0.52
1:A:593:VAL:HG22	1:A:597:PHE:CE2	2.45	0.52
1:B:449:PHE:CE2	1:B:453:ILE:HD11	2.44	0.51
1:B:298:ASN:OD1	1:B:336:THR:OG1	2.23	0.51
1:D:416:ARG:NH2	1:D:694:LEU:HD21	2.25	0.51
1:D:306:VAL:O	1:D:313:GLN:NE2	2.44	0.51
1:D:727:ASP:OD1	1:D:728:PHE:N	2.44	0.51
1:B:727:ASP:OD1	1:B:728:PHE:N	2.44	0.51
1:C:593:VAL:HG22	1:C:597:PHE:CE2	2.46	0.50
1:C:377:PHE:N	1:C:389:LEU:O	2.42	0.50
1:A:408:VAL:O	1:A:416:ARG:NH1	2.43	0.50
1:A:417:HIS:O	1:A:421:THR:HG23	2.11	0.50
1:C:417:HIS:O	1:C:421:THR:HG23	2.11	0.50
1:B:306:VAL:O	1:B:313:GLN:NE2	2.44	0.49
1:A:549:ALA:O	1:A:552:VAL:HG22	2.13	0.49
1:B:569:PHE:O	1:B:573:GLY:N	2.45	0.49
1:B:583:ILE:CD1	1:C:671:ASN:HB2	2.41	0.49
1:C:123:ILE:CG1	1:C:139:LEU:HD21	2.43	0.49
1:B:403:VAL:O	1:B:407:THR:HG23	2.12	0.49
1:A:123:ILE:CG1	1:A:139:LEU:HD21	2.43	0.49
1:B:525:VAL:HG13	1:B:557:LEU:HD11	1.95	0.49
1:C:527:PHE:O	1:C:531:VAL:HG23	2.13	0.49
1:C:300:LEU:HD12	1:C:333:LEU:HB3	1.95	0.48
1:D:403:VAL:O	1:D:407:THR:HG23	2.12	0.48
1:C:549:ALA:O	1:C:552:VAL:HG22	2.13	0.48
1:D:300:LEU:HD22	1:D:321:TYR:CD1	2.48	0.48
1:A:671:ASN:HB2	1:D:583:ILE:CD1	2.41	0.48
1:B:583:ILE:HD11	1:C:671:ASN:CB	2.42	0.48
1:A:433:TRP:HA	1:A:437:ALA:HB3	1.96	0.48
1:C:676:LEU:CD2	1:D:670:LEU:HD11	2.44	0.48
1:B:379:ASP:OD1	1:B:750:ASN:ND2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:552:VAL:HG21	1:D:608:LEU:HD11	1.95	0.48
1:B:300:LEU:HD22	1:B:321:TYR:CD1	2.48	0.47
1:D:379:ASP:OD1	1:D:750:ASN:ND2	2.47	0.47
1:A:527:PHE:O	1:A:531:VAL:HG23	2.13	0.47
1:D:593:VAL:O	1:D:596:VAL:HG12	2.15	0.47
1:A:300:LEU:HD12	1:A:333:LEU:HB3	1.96	0.47
1:D:525:VAL:HG13	1:D:557:LEU:HD11	1.95	0.47
1:B:593:VAL:O	1:B:596:VAL:HG12	2.14	0.47
1:B:567:ARG:NH1	1:B:699:THR:HG21	2.30	0.47
1:D:569:PHE:O	1:D:573:GLY:N	2.45	0.47
1:A:329:GLY:HA2	1:A:373:LEU:HD11	1.96	0.47
1:A:671:ASN:CB	1:D:583:ILE:HD11	2.43	0.47
1:C:433:TRP:HA	1:C:437:ALA:HB3	1.96	0.47
1:A:246:LYS:O	1:A:246:LYS:HG3	2.14	0.47
1:C:579:ILE:HG13	1:D:671:ASN:ND2	2.30	0.47
1:C:246:LYS:O	1:C:246:LYS:HG3	2.15	0.47
1:B:656:PHE:O	1:B:660:THR:HG23	2.16	0.46
1:A:579:ILE:HG13	1:B:671:ASN:ND2	2.30	0.46
1:C:329:GLY:HA2	1:C:373:LEU:HD11	1.96	0.46
1:A:552:VAL:HG21	1:B:608:LEU:HD11	1.97	0.46
1:C:315:ASP:O	1:C:319:ARG:NH2	2.48	0.46
1:A:676:LEU:CD2	1:B:670:LEU:HD11	2.46	0.46
1:D:656:PHE:O	1:D:660:THR:HG23	2.16	0.46
1:D:567:ARG:NH1	1:D:699:THR:HG21	2.30	0.46
1:A:315:ASP:O	1:A:319:ARG:NH2	2.48	0.46
1:D:129:GLU:O	1:D:180:ASN:ND2	2.49	0.46
1:B:129:GLU:O	1:B:180:ASN:ND2	2.49	0.45
1:D:378:THR:OG1	1:D:747:SER:O	2.35	0.45
1:A:297:ASN:HB3	1:A:301:HIS:HB2	1.99	0.45
1:C:297:ASN:HB3	1:C:301:HIS:HB2	1.99	0.45
1:C:680:THR:HA	1:C:684:VAL:HG21	1.98	0.45
1:D:127:VAL:HG13	1:D:175:ALA:HB2	1.99	0.45
1:A:680:THR:HA	1:A:684:VAL:HG21	1.99	0.45
1:B:343:THR:HB	1:B:344:PRO:HD2	1.99	0.45
1:C:416:ARG:NH2	1:C:694:LEU:HD21	2.32	0.44
1:B:293:ASP:OD1	1:B:297:ASN:N	2.50	0.44
1:B:127:VAL:HG13	1:B:175:ALA:HB2	1.99	0.44
1:B:527:PHE:O	1:B:531:VAL:HG23	2.17	0.44
1:B:378:THR:OG1	1:B:747:SER:O	2.35	0.44
1:D:452:ASN:O	1:D:456:THR:HG23	2.18	0.44
1:A:416:ARG:NH2	1:A:694:LEU:HD21	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:527:PHE:O	1:D:531:VAL:HG23	2.17	0.44
1:D:459:SER:HB3	1:D:555:MET:HE1	2.00	0.43
1:B:609:ILE:O	1:B:609:ILE:CG2	2.66	0.43
1:B:452:ASN:O	1:B:456:THR:HG23	2.18	0.43
1:D:343:THR:HB	1:D:344:PRO:HD2	1.99	0.43
1:A:635:LEU:CD1	1:D:639:LEU:HD11	2.49	0.43
1:B:639:LEU:HD11	1:C:635:LEU:CD1	2.48	0.43
1:A:525:VAL:HG13	1:A:557:LEU:HD11	2.01	0.43
1:A:247:GLY:O	1:A:251:ASN:N	2.52	0.43
1:B:603:VAL:HG23	1:B:604:ALA:N	2.34	0.43
1:B:593:VAL:HG22	1:B:597:PHE:HE2	1.81	0.43
1:B:127:VAL:CG1	1:B:175:ALA:HB2	2.49	0.43
1:D:127:VAL:CG1	1:D:175:ALA:HB2	2.49	0.43
1:D:293:ASP:OD1	1:D:297:ASN:N	2.50	0.43
1:D:603:VAL:HG23	1:D:604:ALA:N	2.34	0.42
1:B:456:THR:HA	1:B:555:MET:HE1	2.00	0.42
1:C:300:LEU:HD22	1:C:321:TYR:CE1	2.54	0.42
1:D:385:VAL:HG22	1:D:737:VAL:HG22	2.02	0.42
1:C:593:VAL:CG1	1:C:668:LEU:HD21	2.49	0.42
1:D:194:ALA:O	1:D:198:ASP:N	2.52	0.42
1:C:247:GLY:O	1:C:251:ASN:N	2.52	0.42
1:B:385:VAL:HG22	1:B:737:VAL:HG22	2.02	0.42
1:B:669:LEU:O	1:B:672:MET:HG2	2.20	0.42
1:A:123:ILE:HG12	1:A:139:LEU:CD2	2.50	0.42
1:A:300:LEU:HD22	1:A:321:TYR:CE1	2.54	0.42
1:B:194:ALA:O	1:B:198:ASP:N	2.52	0.42
1:D:669:LEU:O	1:D:672:MET:HG2	2.20	0.42
1:A:593:VAL:CG1	1:A:668:LEU:HD21	2.49	0.41
1:A:456:THR:HG22	1:A:555:MET:SD	2.61	0.41
1:B:300:LEU:HD22	1:B:321:TYR:CE1	2.56	0.41
1:A:410:ASN:OD1	1:A:410:ASN:O	2.39	0.41
1:B:410:ASN:O	1:B:410:ASN:OD1	2.39	0.41
1:B:751:GLU:OE2	1:C:178:ASN:ND2	2.39	0.41
1:C:525:VAL:HG13	1:C:557:LEU:HD11	2.01	0.41
1:C:123:ILE:HG12	1:C:139:LEU:CD2	2.50	0.41
1:B:676:LEU:HD11	1:C:670:LEU:HD21	2.02	0.41
1:C:695:GLN:O	1:C:699:THR:HG23	2.21	0.41
1:D:401:ASN:OD1	1:D:401:ASN:O	2.38	0.41
1:D:609:ILE:O	1:D:609:ILE:CG2	2.66	0.41
1:A:594:TYR:OH	1:A:636:THR:HG21	2.21	0.41
1:A:686:LYS:O	1:A:690:ARG:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:695:GLN:O	1:A:699:THR:HG23	2.21	0.41
1:A:403:VAL:O	1:A:407:THR:HG23	2.21	0.40
1:B:401:ASN:OD1	1:B:401:ASN:O	2.38	0.40
1:D:410:ASN:OD1	1:D:410:ASN:O	2.39	0.40
1:A:178:ASN:ND2	1:D:751:GLU:OE2	2.39	0.40
1:C:321:TYR:OH	1:C:334:GLU:OE2	2.36	0.40
1:A:554:ALA:O	1:A:558:GLY:N	2.39	0.40
1:C:403:VAL:O	1:C:407:THR:HG23	2.21	0.40
1:A:670:LEU:HD21	1:D:676:LEU:HD11	2.02	0.40
1:B:379:ASP:OD2	1:B:733:ARG:NH2	2.52	0.40
1:C:214:GLU:HB3	1:C:246:LYS:O	2.21	0.40
1:C:456:THR:HG22	1:C:555:MET:SD	2.61	0.40
1:C:594:TYR:OH	1:C:636:THR:HG21	2.21	0.40
1:C:754:GLY:H	1:D:213:TYR:HH	1.69	0.40
1:B:379:ASP:OD2	1:B:733:ARG:NH1	2.52	0.40
1:C:226:ARG:NH1	1:C:272:THR:O	2.55	0.40
1:C:410:ASN:OD1	1:C:410:ASN:O	2.39	0.40

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	607/826 (74%)	590 (97%)	17 (3%)	0	100	100
1	B	607/826 (74%)	583 (96%)	24 (4%)	0	100	100
1	C	607/826 (74%)	590 (97%)	17 (3%)	0	100	100
1	D	607/826 (74%)	582 (96%)	25 (4%)	0	100	100
All	All	2428/3304 (74%)	2345 (97%)	83 (3%)	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	403/732 (55%)	403 (100%)	0	100	100
1	B	396/732 (54%)	395 (100%)	1 (0%)	92	95
1	C	403/732 (55%)	403 (100%)	0	100	100
1	D	396/732 (54%)	395 (100%)	1 (0%)	92	95
All	All	1598/2928 (55%)	1596 (100%)	2 (0%)	93	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	677	MET
1	D	677	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	301	HIS
1	A	339	ASN
1	A	452	ASN
1	A	645	GLN
1	A	671	ASN
1	B	339	ASN
1	B	426	HIS
1	B	585	HIS
1	B	671	ASN
1	C	301	HIS
1	C	339	ASN
1	C	452	ASN
1	C	645	GLN
1	C	671	ASN
1	D	339	ASN
1	D	426	HIS
1	D	585	HIS

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Mol	Chain	Res	Type
1	D	671	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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)

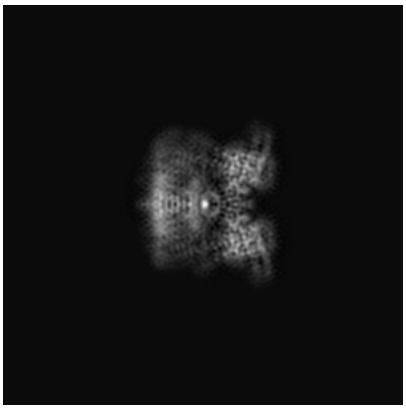
This section contains visualisations of the EMDB entry EMD-9120. These allow visual inspection of the internal detail of the map and identification of artifacts.

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.

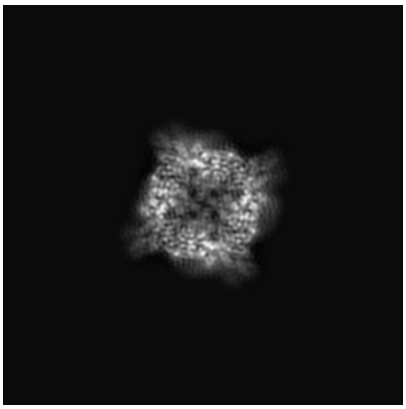
6.1 Orthogonal projections (i)

6.1.1 Primary map

X

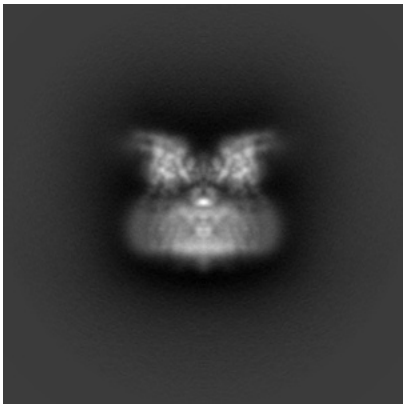


Y

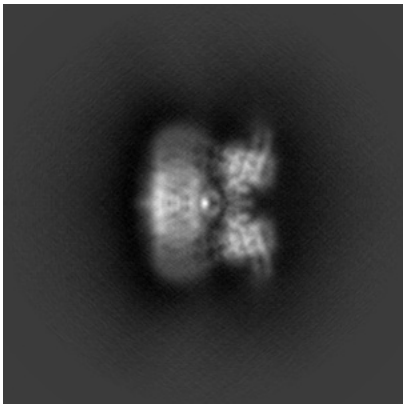


Z

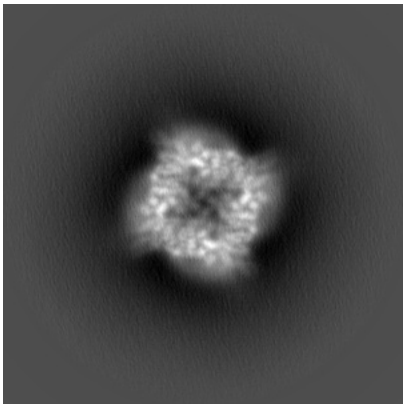
6.1.2 Raw map



X



Y



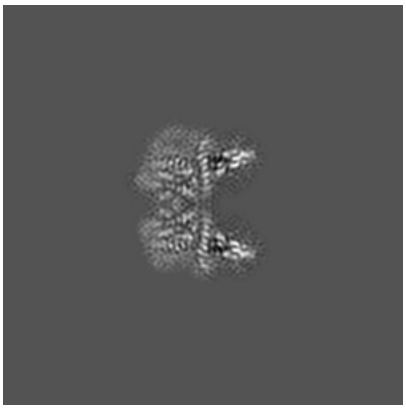
Z

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

6.2 Central slices (i)

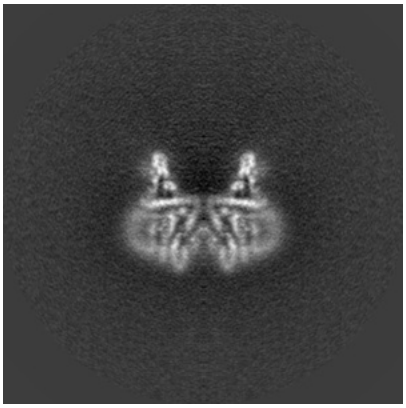
6.2.1 Primary map

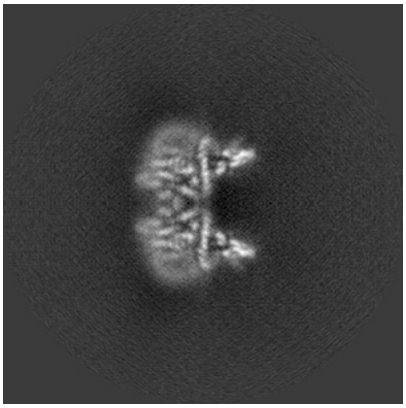
X Index: 144

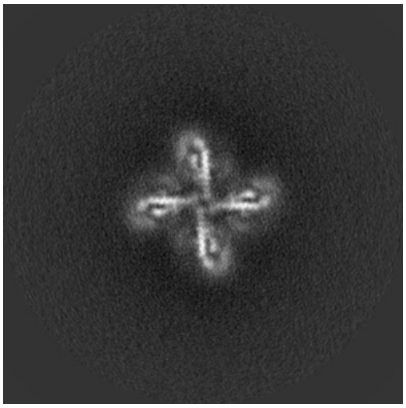

Y Index: 144

Z Index: 144

6.2.2 Raw map


X Index: 144

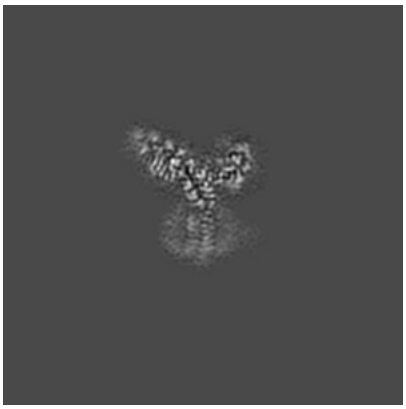

Y Index: 144


Z Index: 144

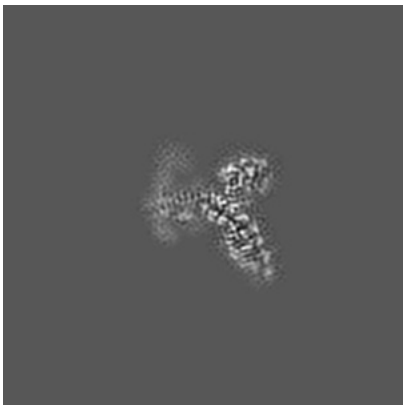
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

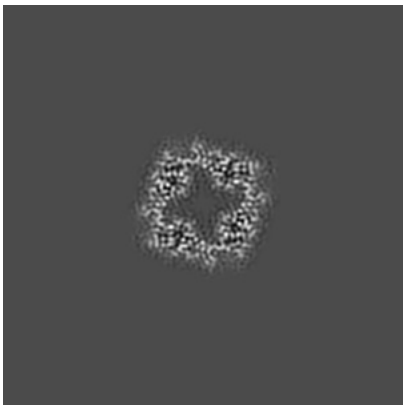
6.3.1 Primary map



X Index: 172

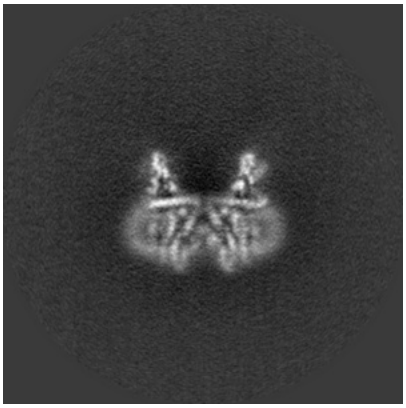


Y Index: 117

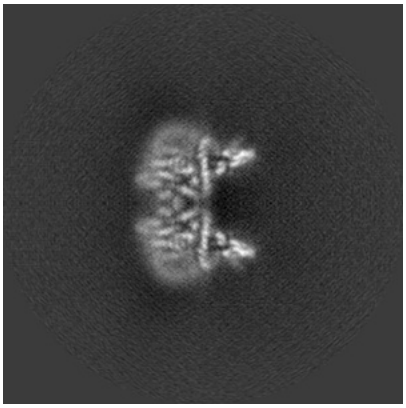


Z Index: 168

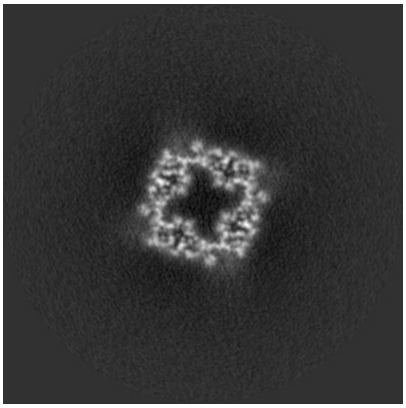
6.3.2 Raw map



X Index: 143



Y Index: 144

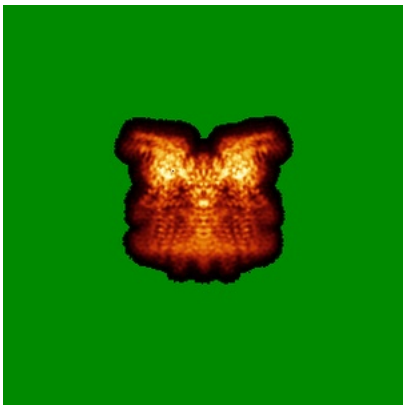


Z Index: 168

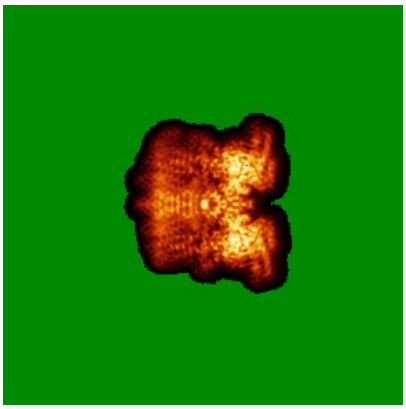
The images above show the largest variance slices of the map in three orthogonal directions.

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

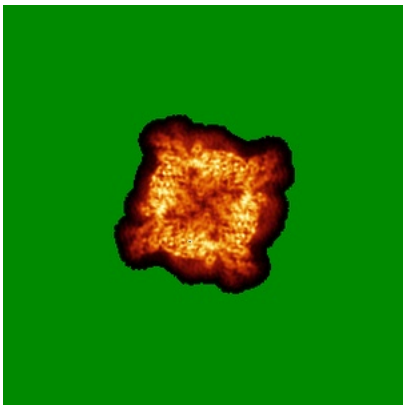
6.4.1 Primary map



X

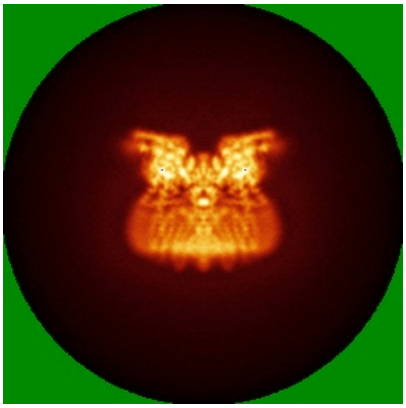


Y

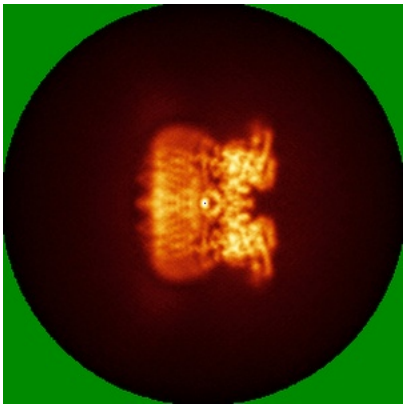


Z

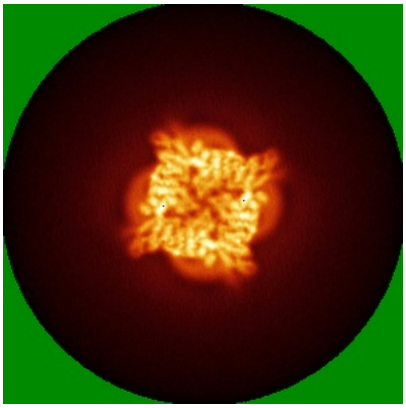
6.4.2 Raw map



X



Y

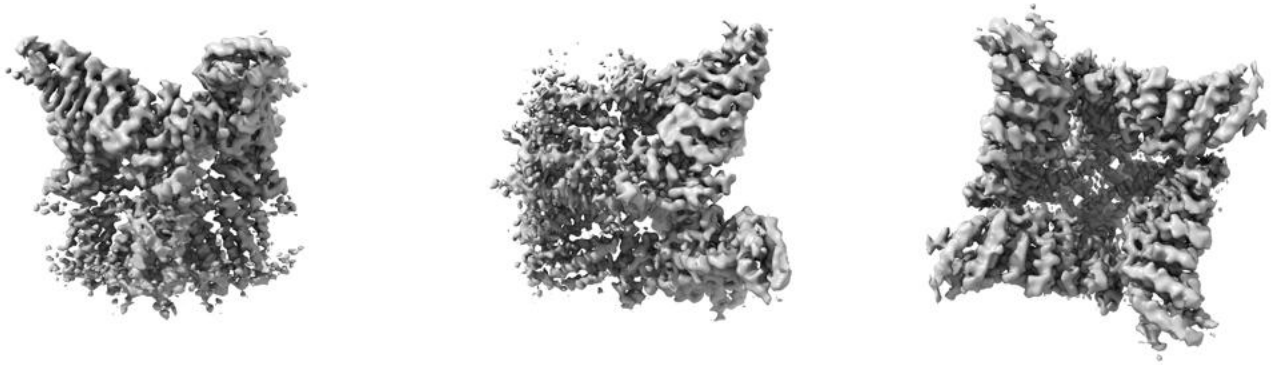


Z

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)

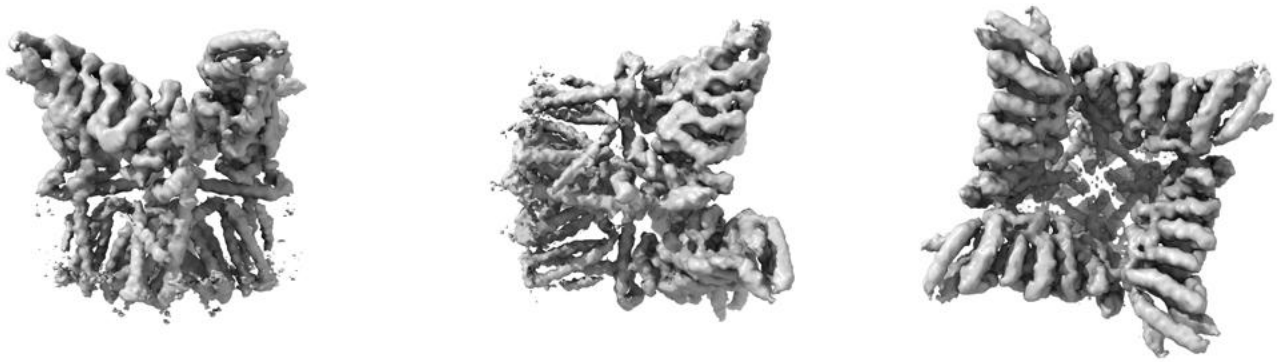
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.065. 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.

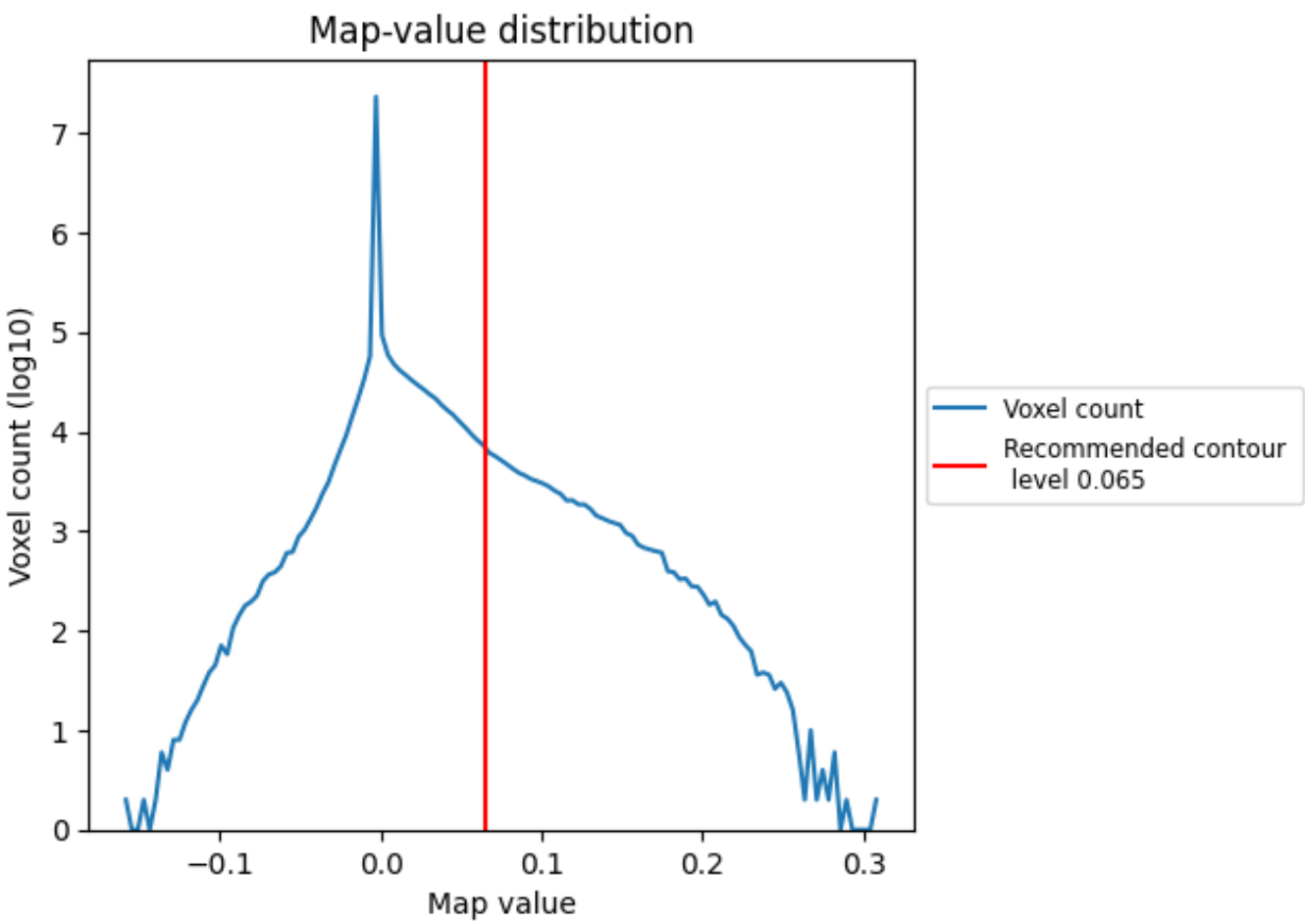
6.6 Mask visualisation (i)

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

7 Map analysis (i)

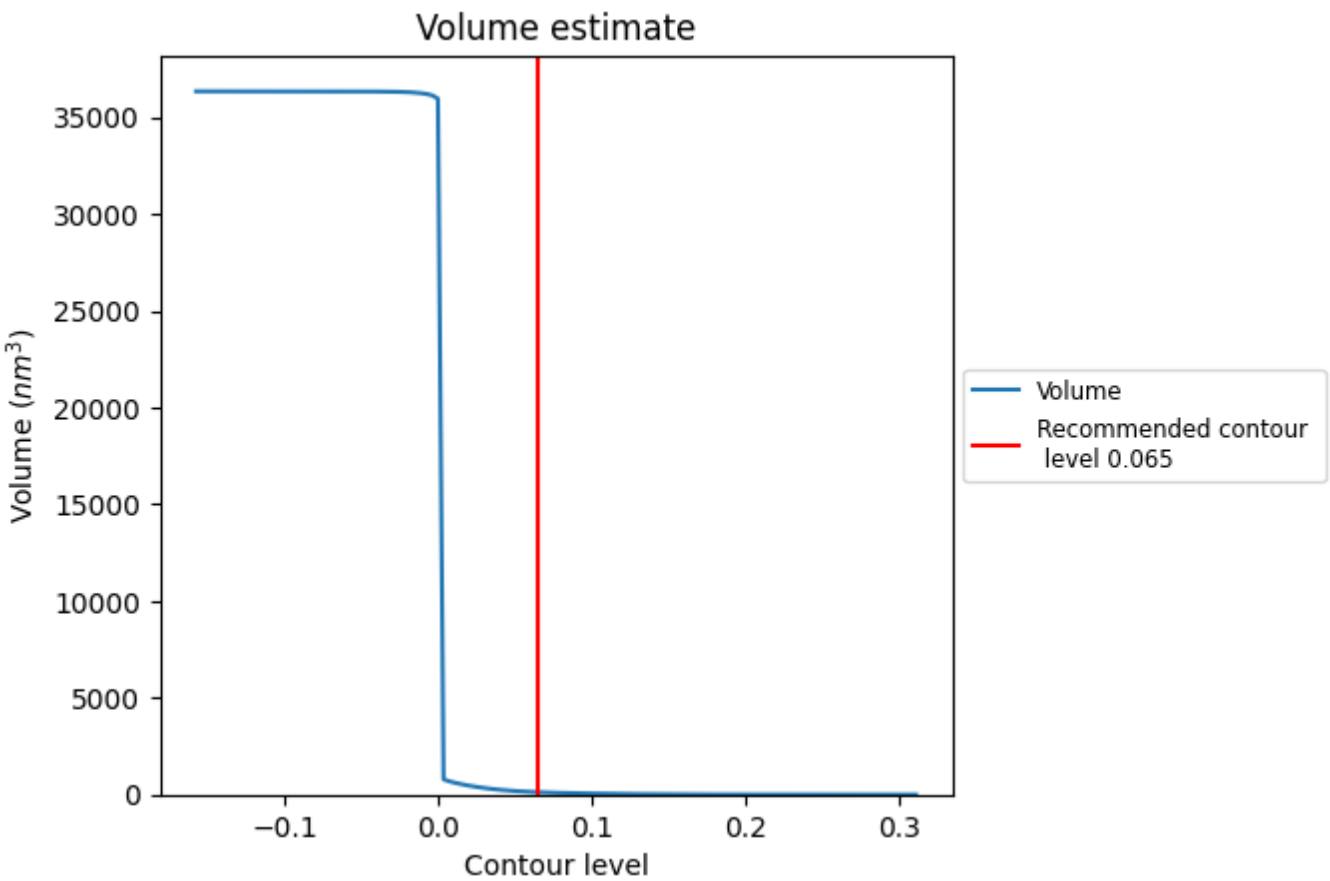
This section contains the results of statistical analysis of the map.

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.

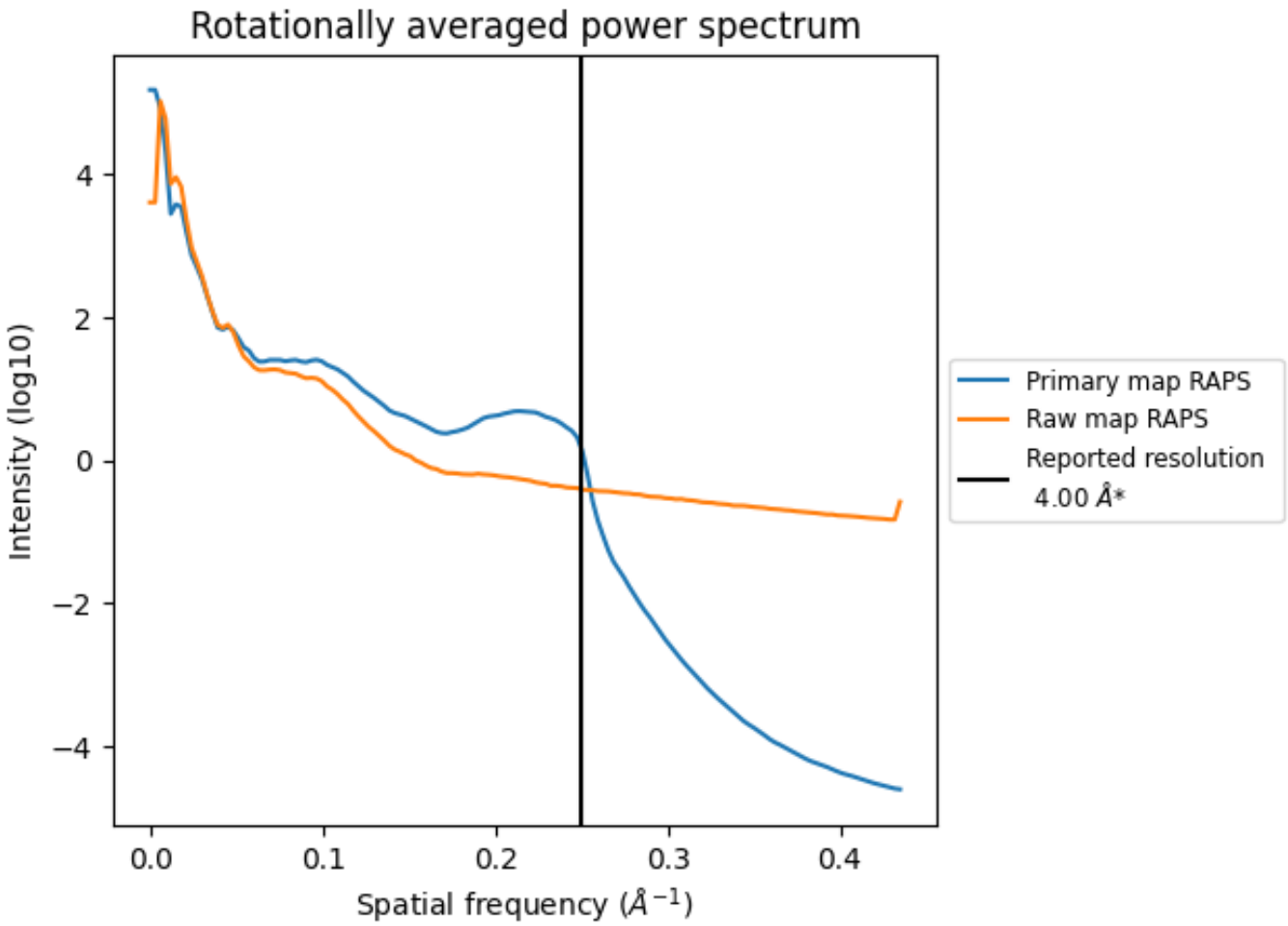
7.2 Volume estimate (i)



The volume at the recommended contour level is 121 nm^3; this corresponds to an approximate mass of 110 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 (i)

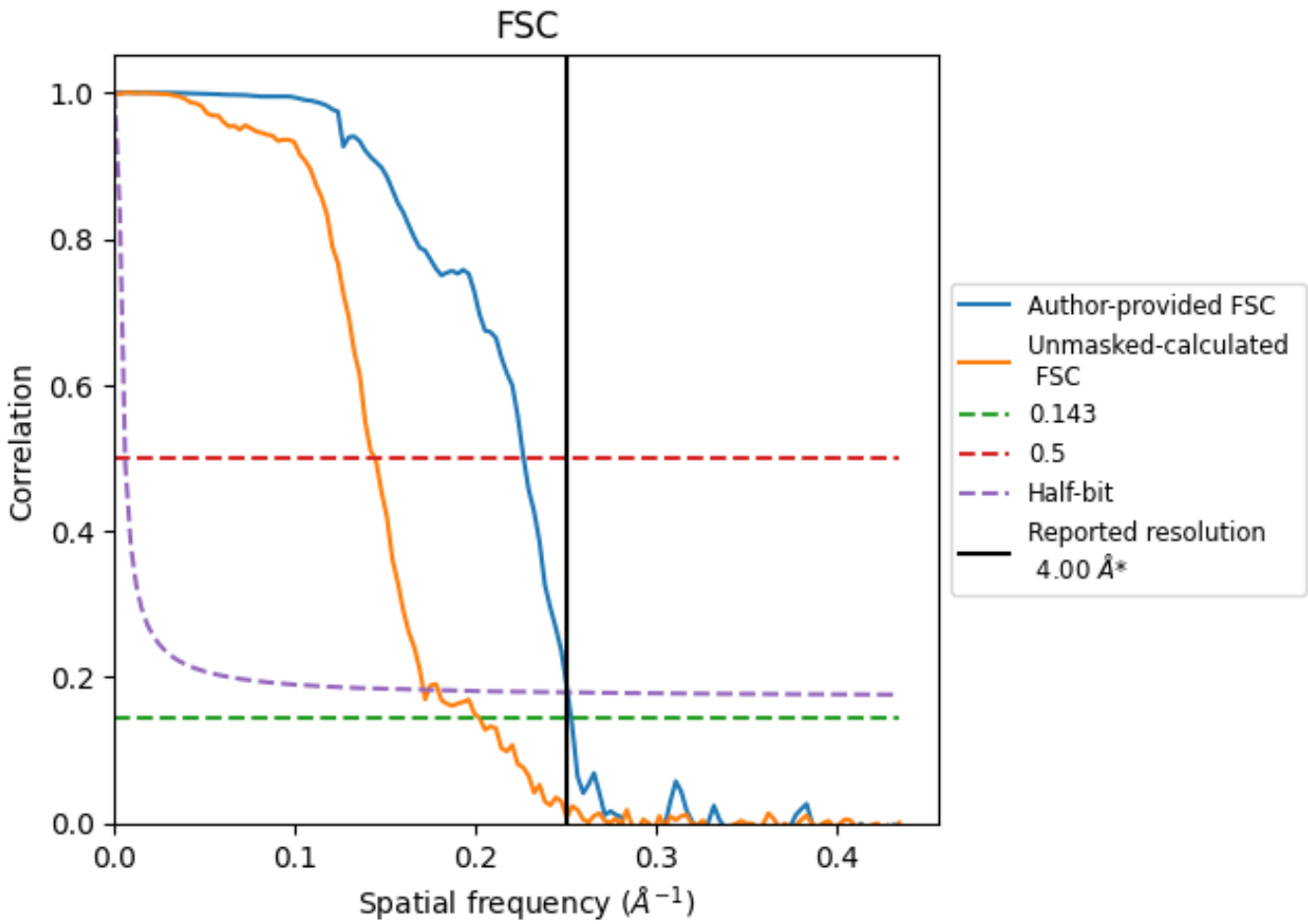


*Reported resolution corresponds to spatial frequency of 0.250 Å^{-1}

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 0.250 Å^{-1}

8.2 Resolution estimates (i)

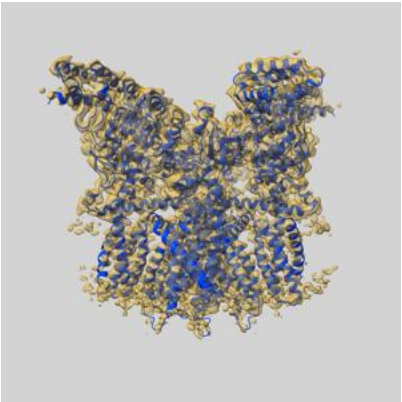
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.95	4.41	3.98
Unmasked-calculated*	4.94	6.94	5.84

*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 4.94 differs from the reported value 4.0 by more than 10 %

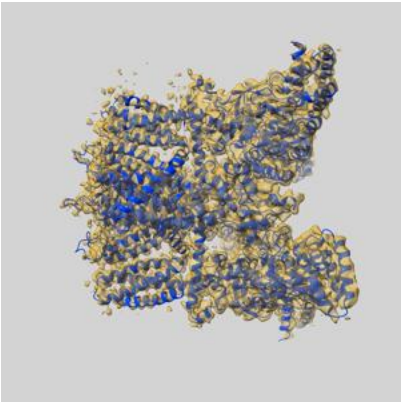
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-9120 and PDB model 6MHW. Per-residue inclusion information can be found in section 3 on page 8.

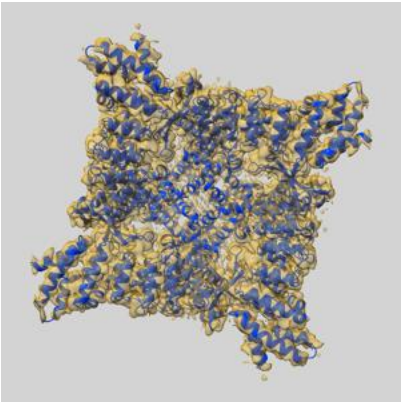
9.1 Map-model overlay (i)



X



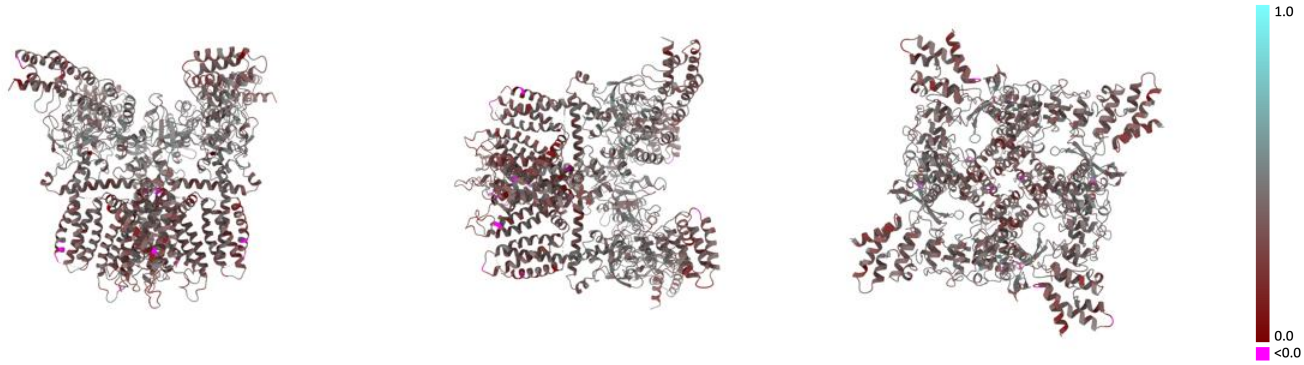
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.065 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.

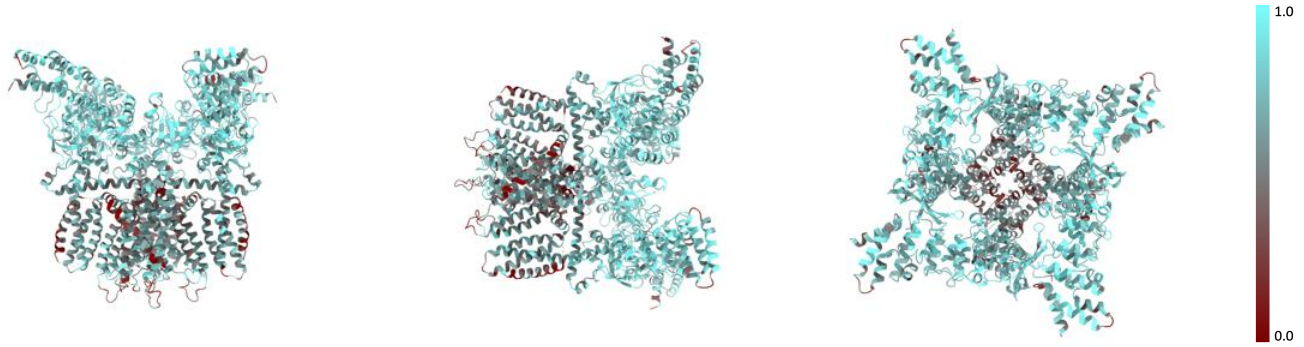
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

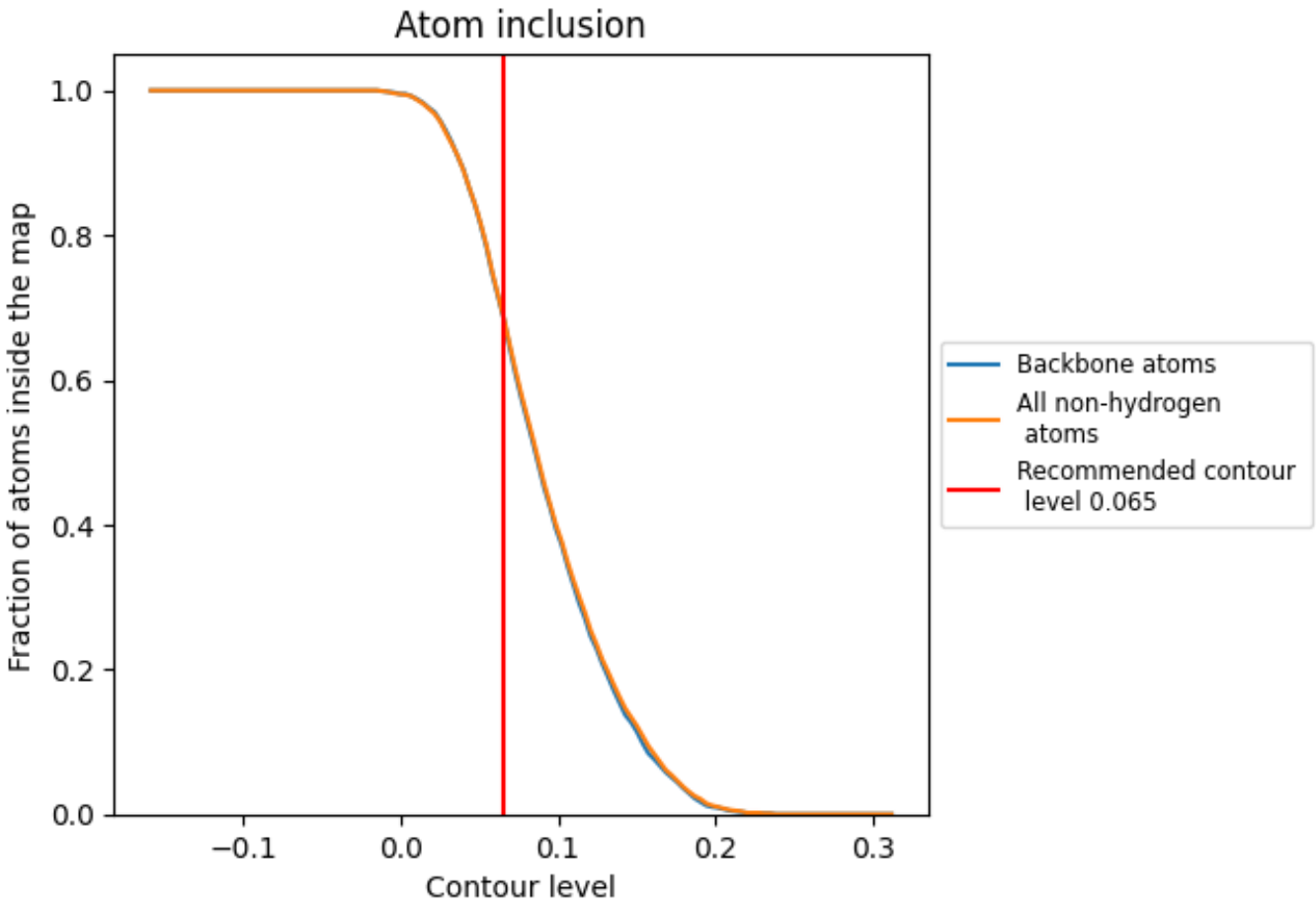
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.065).

9.4 Atom inclusion (i)



At the recommended contour level, 69% of all backbone atoms, 69% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6910	0.3910
A	0.6850	0.3890
B	0.7020	0.3920
C	0.6840	0.3910
D	0.7020	0.3940