



## wwPDB EM Validation Summary Report ⓘ

May 13, 2025 – 07:31 AM EDT

PDB ID : 6D7T / pdb\_00006d7t  
EMDB ID : EMD-7825  
Title : Cryo-EM structure of human TRPV6-Y467A in complex with 2-Aminoethoxy  
ydiphenyl borate (2-APB)  
Authors : Singh, A.K.; Saotome, K.; McGoldrick, L.L.; Sobolevsky, A.I.  
Deposited on : 2018-04-25  
Resolution : 4.44 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev118  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

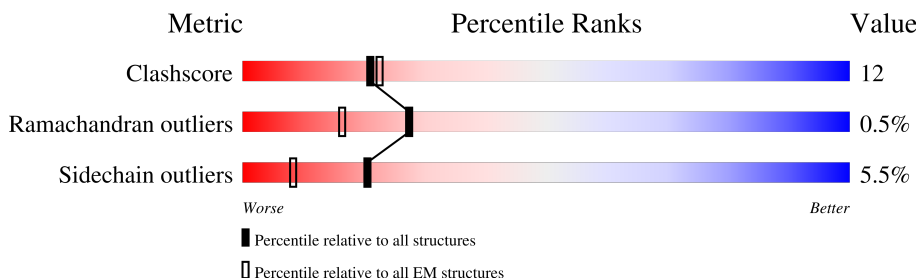
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.44 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	742	<div> <div>33%</div> <div>56%</div> <div>24%</div> <div>18%</div> </div>
1	B	742	<div> <div>33%</div> <div>56%</div> <div>24%</div> <div>18%</div> </div>
1	C	742	<div> <div>33%</div> <div>55%</div> <div>25%</div> <div>18%</div> </div>
1	D	742	<div> <div>32%</div> <div>56%</div> <div>24%</div> <div>18%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19654 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 Transient receptor potential cation channel subfamily V member 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	611	Total	C	N	O	S	0	0
			4896	3162	830	864	40		
1	B	611	Total	C	N	O	S	0	0
			4896	3162	830	864	40		
1	C	611	Total	C	N	O	S	0	0
			4896	3162	830	864	40		
1	D	611	Total	C	N	O	S	0	0
			4896	3162	830	864	40		

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	467	ALA	TYR	engineered mutation	UNP Q9H1D0
A	726	LEU	-	expression tag	UNP Q9H1D0
A	727	VAL	-	expression tag	UNP Q9H1D0
A	728	PRO	-	expression tag	UNP Q9H1D0
A	729	ARG	-	expression tag	UNP Q9H1D0
A	730	GLY	-	expression tag	UNP Q9H1D0
A	731	SER	-	expression tag	UNP Q9H1D0
A	732	ALA	-	expression tag	UNP Q9H1D0
A	733	ALA	-	expression tag	UNP Q9H1D0
A	734	ALA	-	expression tag	UNP Q9H1D0
A	735	TRP	-	expression tag	UNP Q9H1D0
A	736	SER	-	expression tag	UNP Q9H1D0
A	737	HIS	-	expression tag	UNP Q9H1D0
A	738	PRO	-	expression tag	UNP Q9H1D0
A	739	GLN	-	expression tag	UNP Q9H1D0
A	740	PHE	-	expression tag	UNP Q9H1D0
A	741	GLU	-	expression tag	UNP Q9H1D0
A	742	LYS	-	expression tag	UNP Q9H1D0
B	467	ALA	TYR	engineered mutation	UNP Q9H1D0
B	726	LEU	-	expression tag	UNP Q9H1D0
B	727	VAL	-	expression tag	UNP Q9H1D0

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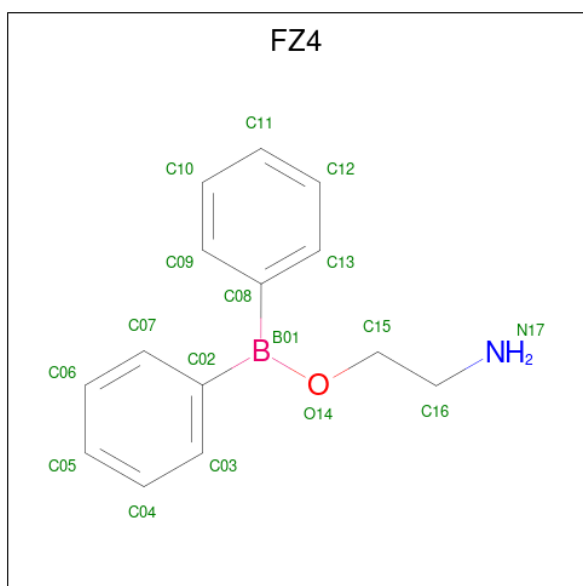
Chain	Residue	Modelled	Actual	Comment	Reference
B	728	PRO	-	expression tag	UNP Q9H1D0
B	729	ARG	-	expression tag	UNP Q9H1D0
B	730	GLY	-	expression tag	UNP Q9H1D0
B	731	SER	-	expression tag	UNP Q9H1D0
B	732	ALA	-	expression tag	UNP Q9H1D0
B	733	ALA	-	expression tag	UNP Q9H1D0
B	734	ALA	-	expression tag	UNP Q9H1D0
B	735	TRP	-	expression tag	UNP Q9H1D0
B	736	SER	-	expression tag	UNP Q9H1D0
B	737	HIS	-	expression tag	UNP Q9H1D0
B	738	PRO	-	expression tag	UNP Q9H1D0
B	739	GLN	-	expression tag	UNP Q9H1D0
B	740	PHE	-	expression tag	UNP Q9H1D0
B	741	GLU	-	expression tag	UNP Q9H1D0
B	742	LYS	-	expression tag	UNP Q9H1D0
C	467	ALA	TYR	engineered mutation	UNP Q9H1D0
C	726	LEU	-	expression tag	UNP Q9H1D0
C	727	VAL	-	expression tag	UNP Q9H1D0
C	728	PRO	-	expression tag	UNP Q9H1D0
C	729	ARG	-	expression tag	UNP Q9H1D0
C	730	GLY	-	expression tag	UNP Q9H1D0
C	731	SER	-	expression tag	UNP Q9H1D0
C	732	ALA	-	expression tag	UNP Q9H1D0
C	733	ALA	-	expression tag	UNP Q9H1D0
C	734	ALA	-	expression tag	UNP Q9H1D0
C	735	TRP	-	expression tag	UNP Q9H1D0
C	736	SER	-	expression tag	UNP Q9H1D0
C	737	HIS	-	expression tag	UNP Q9H1D0
C	738	PRO	-	expression tag	UNP Q9H1D0
C	739	GLN	-	expression tag	UNP Q9H1D0
C	740	PHE	-	expression tag	UNP Q9H1D0
C	741	GLU	-	expression tag	UNP Q9H1D0
C	742	LYS	-	expression tag	UNP Q9H1D0
D	467	ALA	TYR	engineered mutation	UNP Q9H1D0
D	726	LEU	-	expression tag	UNP Q9H1D0
D	727	VAL	-	expression tag	UNP Q9H1D0
D	728	PRO	-	expression tag	UNP Q9H1D0
D	729	ARG	-	expression tag	UNP Q9H1D0
D	730	GLY	-	expression tag	UNP Q9H1D0
D	731	SER	-	expression tag	UNP Q9H1D0
D	732	ALA	-	expression tag	UNP Q9H1D0
D	733	ALA	-	expression tag	UNP Q9H1D0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	734	ALA	-	expression tag	UNP Q9H1D0
D	735	TRP	-	expression tag	UNP Q9H1D0
D	736	SER	-	expression tag	UNP Q9H1D0
D	737	HIS	-	expression tag	UNP Q9H1D0
D	738	PRO	-	expression tag	UNP Q9H1D0
D	739	GLN	-	expression tag	UNP Q9H1D0
D	740	PHE	-	expression tag	UNP Q9H1D0
D	741	GLU	-	expression tag	UNP Q9H1D0
D	742	LYS	-	expression tag	UNP Q9H1D0

- Molecule 2 is 2-aminoethyl diphenylborinate (CCD ID: FZ4) (formula: C<sub>14</sub>H<sub>16</sub>BNO).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	B	C	N	O	0
			17	1	14	1	1	
2	B	1	Total	B	C	N	O	0
			17	1	14	1	1	
2	C	1	Total	B	C	N	O	0
			17	1	14	1	1	
2	D	1	Total	B	C	N	O	0
			17	1	14	1	1	

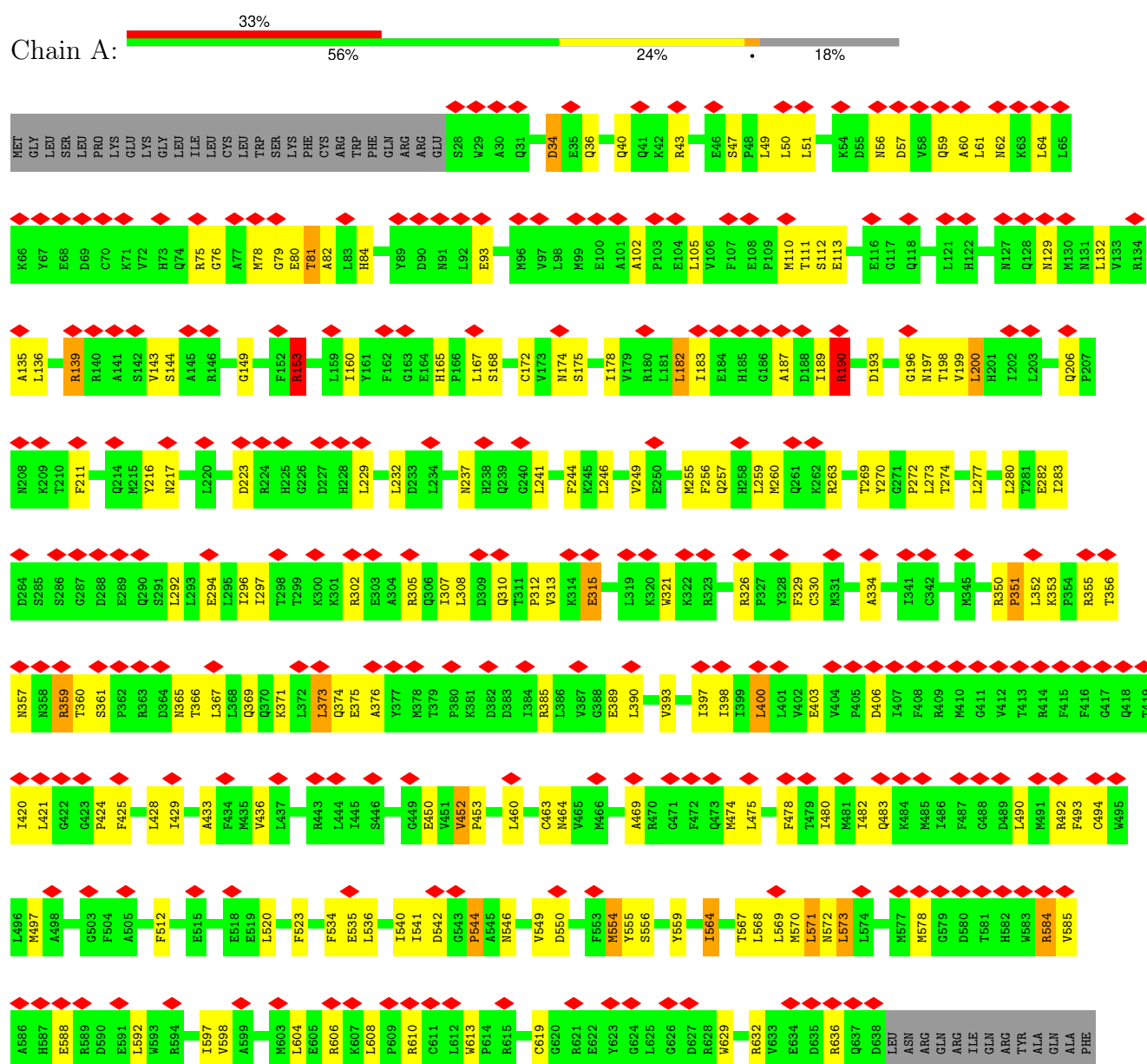
- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

### 3 Residue-property plots

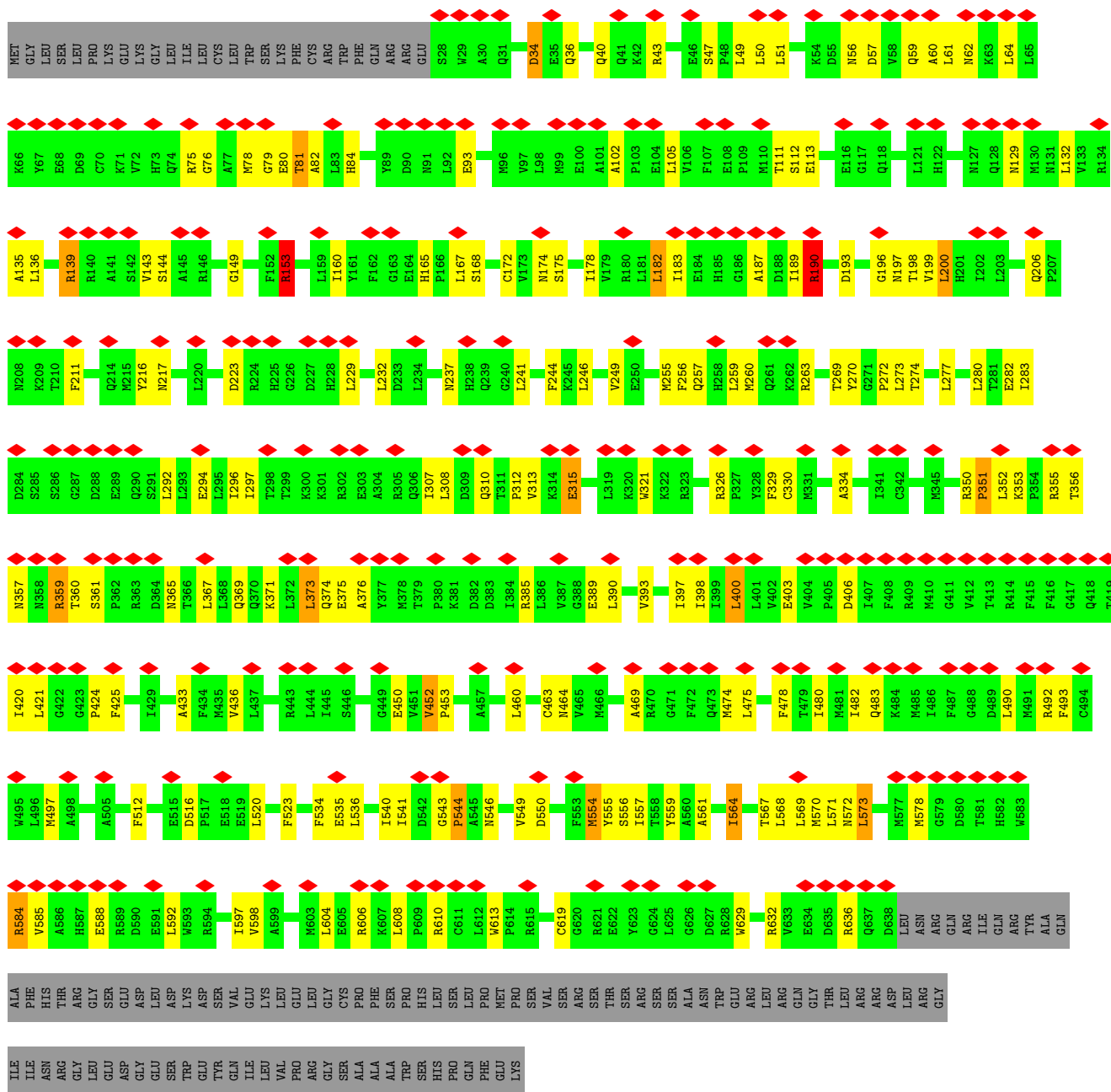
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 6



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

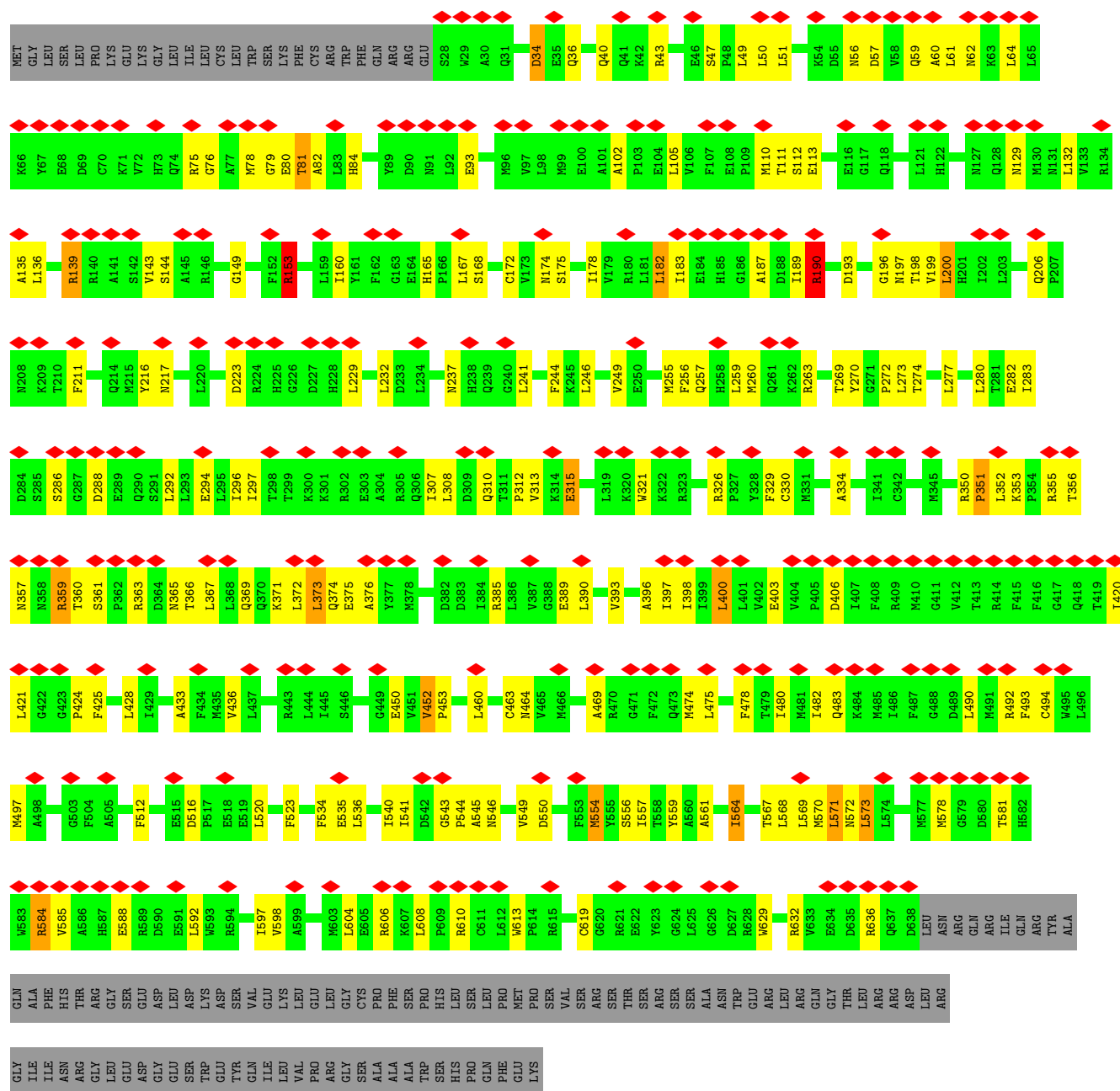
• Molecule 1: Transient receptor potential cation channel subfamily V member 6



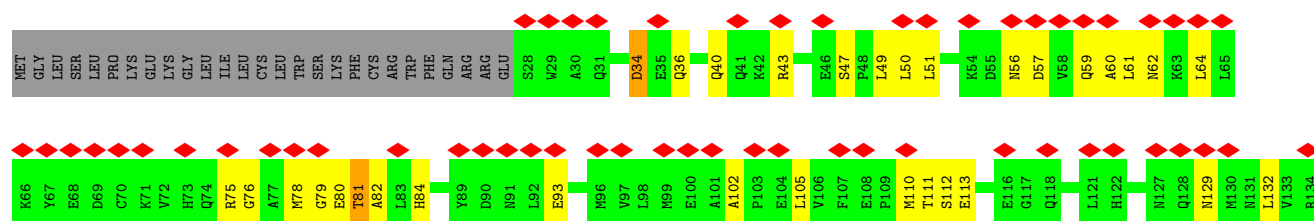
• Molecule 1: Transient receptor potential cation channel subfamily V member 6







- Molecule 1: Transient receptor potential cation channel subfamily V member 6



GLU	ASP	GLY	GLU	GLU	SER	TRP	GLU	TYR	GLN	ILE	GLU	LEU	VAL	PRO	GLY	ARG	GLY	CYS	PRO	ALA	ALA	ALA	ALA	TRP	HIS	SER	PRO	GLN	PHE	PRO	MET	LYS	SER	GLU	ASP	GLY	LEU	ASP	ASP	ASP	LYS	ASP	TYR	GLN	ILE	GLU	ASN	ARG	GLY	ILE	ILE	ASN	ARG	GLY	GLU	LEU	ASN	ARG	GLN	ALA	ALA	PHE	HIS	THR	ARG	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
D590	E591	L592	F593	R594	I597	V598	A599	M603	L604	E605	R606	R607	L608	P609	R610	C611	L612	W613	P614	R615	C619	G620	R621	E622	Y623	G624	SER	ARG	GLN	PHE	PRO	MET	LYS	SER	VAL	SER	ARG	E622	F653	M554	Y555	S556	Y559	I564	T567	L568	L569	M570	L571	N572	L573	L574	Q637	D638	LEU	ARG	ASP	ASN	LEU	ARG	GLN	ARG	GLY	ILE	ILE	ASN	ARG	TYR	ALA	ALA	GLN	ALA	ALA	PHE	HIS	THR	ARG	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
P424	F425	L428	I429	A433	F434	M435	V436	L437	R443	L444	I445	S446	G449	E450	V451	V452	P453	L460	C463	N464	V465	M466	A469	R470	G471	F472	Q473	M474	L475	F478	T479	I480	M481	I482	Q483	K484	M485	I486	F487	G488	D489	L490	M491	R492	F493	C494	W495	L496	M497	A498																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	77460	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI 20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	43.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.200	Depositor
Minimum map value	-0.111	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0669	Depositor
Map size (Å)	248.88, 248.88, 248.88	wwPDB
Map dimensions	204, 204, 204	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.22, 1.22, 1.22	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: CA, FZ4

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	0.47	2/5008 (0.0%)	0.86	13/6795 (0.2%)
1	B	0.47	2/5008 (0.0%)	0.86	13/6795 (0.2%)
1	C	0.49	2/5008 (0.0%)	0.85	11/6795 (0.2%)
1	D	0.68	3/5008 (0.1%)	0.89	17/6795 (0.3%)
All	All	0.54	9/20032 (0.0%)	0.87	54/27180 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	3
1	C	0	4
1	D	0	4
All	All	0	14

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	544	PRO	C-N	32.19	1.73	1.33
1	D	540	ILE	C-N	17.08	1.55	1.34
1	C	540	ILE	C-N	-13.26	1.10	1.33
1	A	540	ILE	C-N	10.28	1.51	1.33
1	B	540	ILE	C-N	10.28	1.51	1.33

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	544	PRO	O-C-N	-11.76	110.57	123.03
1	D	540	ILE	CA-C-N	-11.07	102.63	120.13
1	D	540	ILE	C-N-CA	-11.07	102.63	120.13
1	D	540	ILE	O-C-N	7.95	132.50	122.57
1	A	153	ARG	CG-CD-NE	6.98	127.36	112.00

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	129	ASN	Peptide
1	A	223	ASP	Peptide
1	A	351	PRO	Peptide
1	B	129	ASN	Peptide
1	B	223	ASP	Peptide

## 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	4896	0	4954	122	0
1	B	4896	0	4954	119	0
1	C	4896	0	4953	129	0
1	D	4896	0	4953	134	0
2	A	17	0	0	0	0
2	B	17	0	0	0	0
2	C	17	0	0	0	0
2	D	17	0	0	0	0
3	A	2	0	0	0	0
All	All	19654	0	19814	463	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 12.

The worst 5 of 463 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:D:544:PRO:C	1:D:545:ALA:N	1.73	1.46
1:D:535:GLU:OE1	1:D:541:ILE:HB	1.54	1.06
1:D:535:GLU:CD	1:D:541:ILE:HB	1.93	0.93
1:B:535:GLU:HG3	1:C:559:TYR:HE2	1.58	0.68
1:A:535:GLU:HG3	1:B:559:TYR:HE2	1.58	0.68

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	609/742 (82%)	541 (89%)	65 (11%)	3 (0%)	25	64
1	B	609/742 (82%)	540 (89%)	66 (11%)	3 (0%)	25	64
1	C	609/742 (82%)	541 (89%)	64 (10%)	4 (1%)	19	56
1	D	609/742 (82%)	540 (89%)	66 (11%)	3 (0%)	25	64
All	All	2436/2968 (82%)	2162 (89%)	261 (11%)	13 (0%)	27	64

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	585	VAL
1	B	585	VAL
1	C	585	VAL
1	D	585	VAL
1	C	545	ALA

### 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	529/645 (82%)	500 (94%)	29 (6%)	18	40
1	B	529/645 (82%)	500 (94%)	29 (6%)	18	40
1	C	529/645 (82%)	500 (94%)	29 (6%)	18	40
1	D	529/645 (82%)	500 (94%)	29 (6%)	18	40
All	All	2116/2580 (82%)	2000 (94%)	116 (6%)	20	40

5 of 116 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	608	LEU
1	D	564	ILE
1	C	352	LEU
1	D	556	SER
1	D	315	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	464	ASN
1	D	208	ASN
1	C	522	HIS
1	D	127	ASN
1	D	370	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 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FZ4	C	801	-	17,18,18	0.76	0	18,22,22	1.52	2 (11%)
2	FZ4	B	801	-	17,18,18	0.75	0	18,22,22	1.50	2 (11%)
2	FZ4	A	801	-	17,18,18	0.76	0	18,22,22	1.51	2 (11%)
2	FZ4	D	801	-	17,18,18	0.77	0	18,22,22	1.51	2 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FZ4	C	801	-	-	7/12/12/12	0/2/2/2
2	FZ4	B	801	-	-	7/12/12/12	0/2/2/2
2	FZ4	A	801	-	-	7/12/12/12	0/2/2/2
2	FZ4	D	801	-	-	7/12/12/12	0/2/2/2

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	801	FZ4	C13-C08-C09	3.18	120.51	116.86
2	D	801	FZ4	C13-C08-C09	3.16	120.49	116.86
2	A	801	FZ4	C13-C08-C09	3.16	120.48	116.86
2	B	801	FZ4	C13-C08-C09	3.15	120.48	116.86
2	D	801	FZ4	C07-C02-C03	3.13	120.46	116.86

There are no chirality outliers.

5 of 28 torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
2	A	801	FZ4	O14-B01-C02-C03
2	A	801	FZ4	O14-B01-C02-C07
2	A	801	FZ4	C02-B01-O14-C15
2	A	801	FZ4	C08-B01-O14-C15
2	A	801	FZ4	O14-C15-C16-N17

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	1
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	544:PRO	C	545:ALA	N	1.73
1	C	540:ILE	C	541:ILE	N	1.10

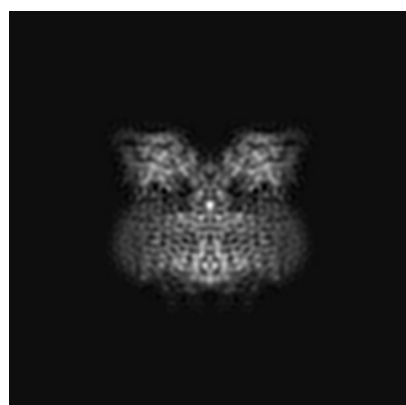
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7825. These allow visual inspection of the internal detail of the map and identification of artifacts.

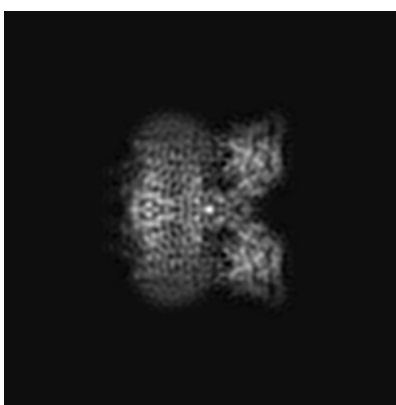
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

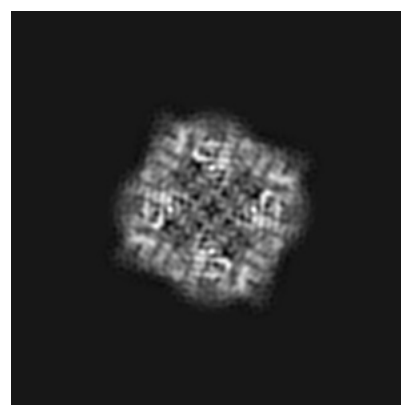
#### 6.1.1 Primary map



X



Y



Z

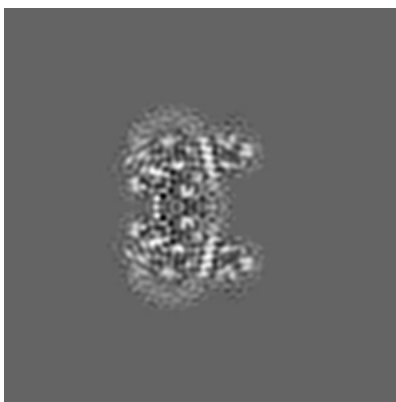
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

#### 6.2.1 Primary map



X Index: 102



Y Index: 102



Z Index: 102

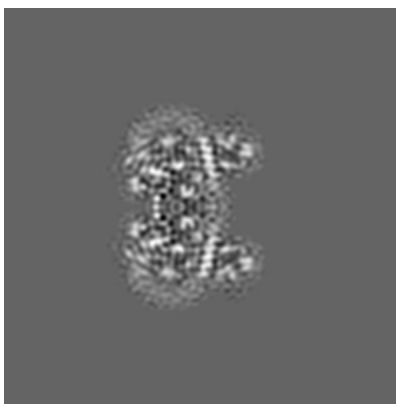
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

### 6.3.1 Primary map



X Index: 102



Y Index: 102

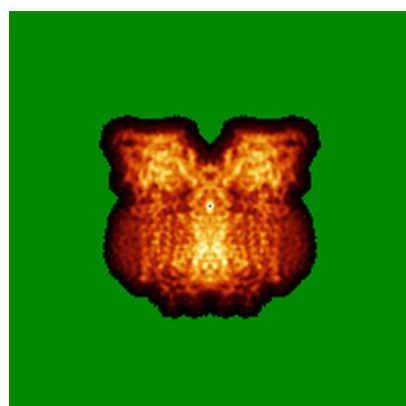


Z Index: 122

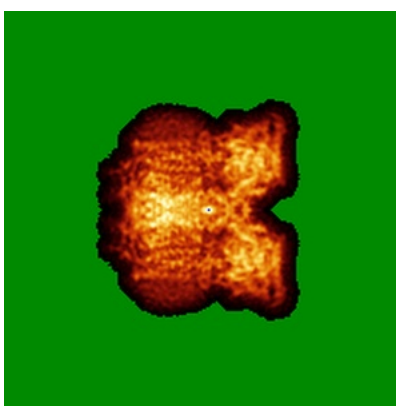
The images above show the largest variance slices of the map in three orthogonal directions.

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

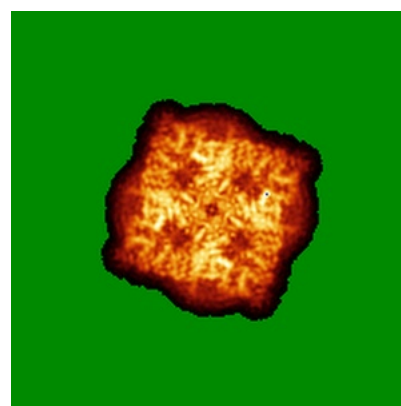
### 6.4.1 Primary map



X



Y

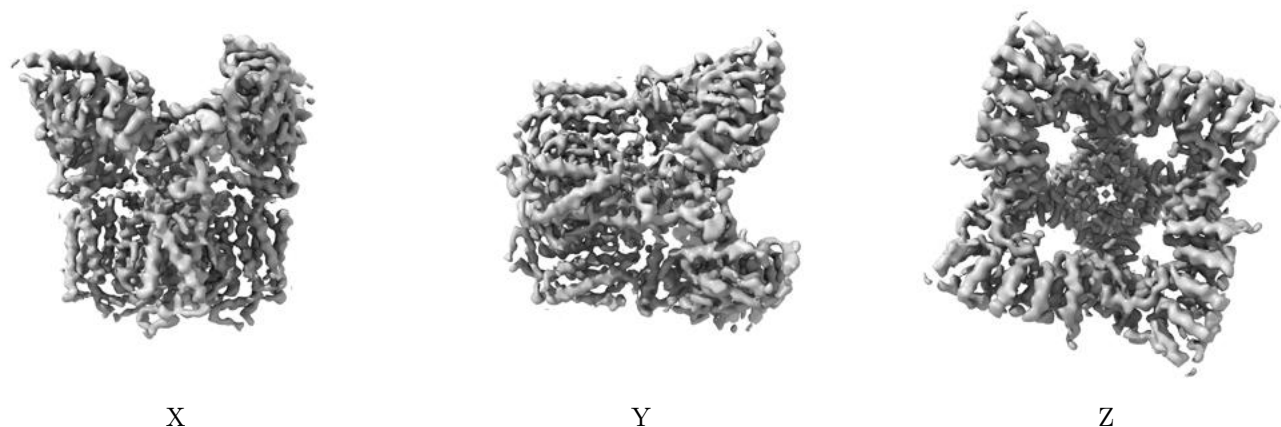


Z

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 0.0669. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

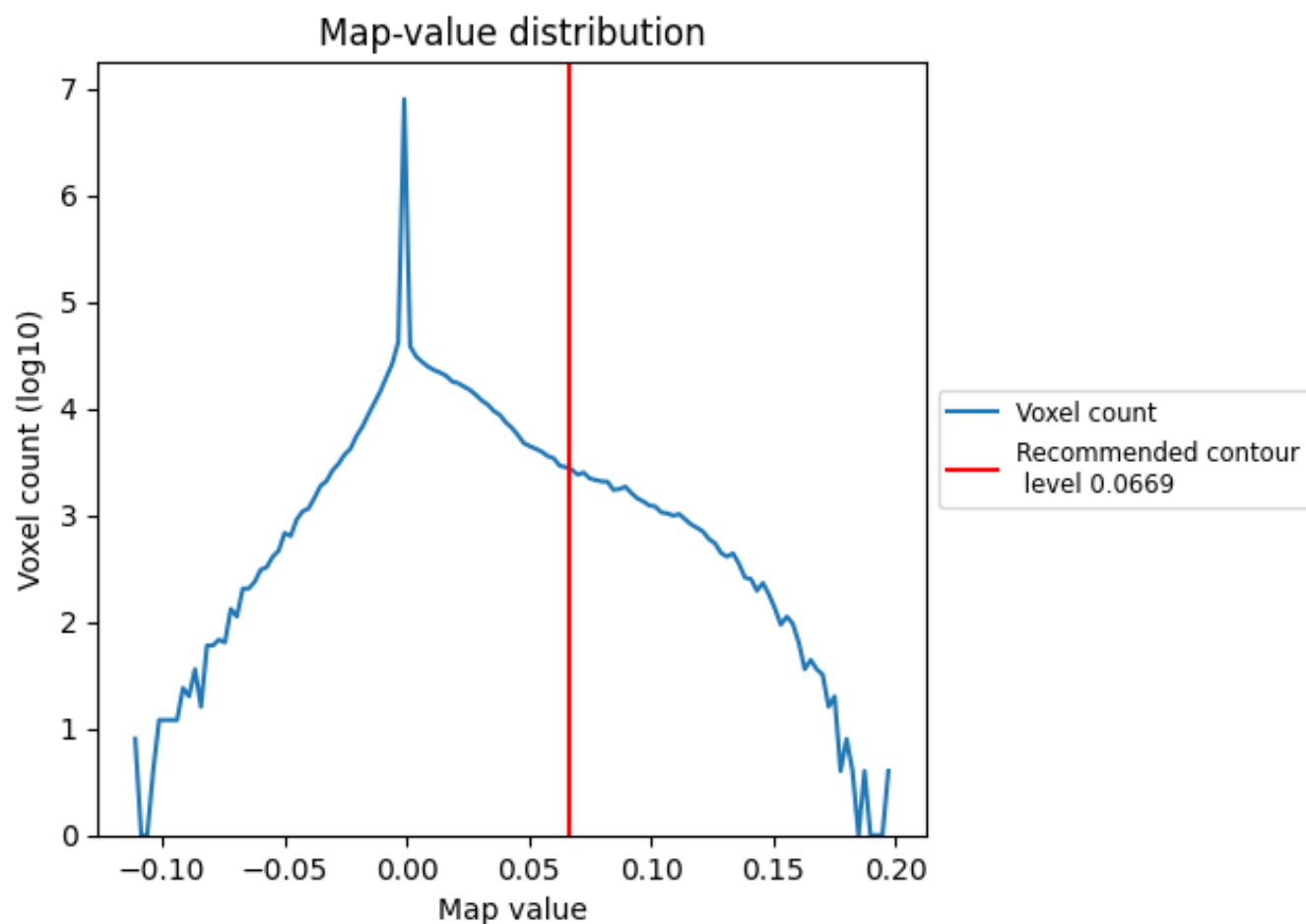
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

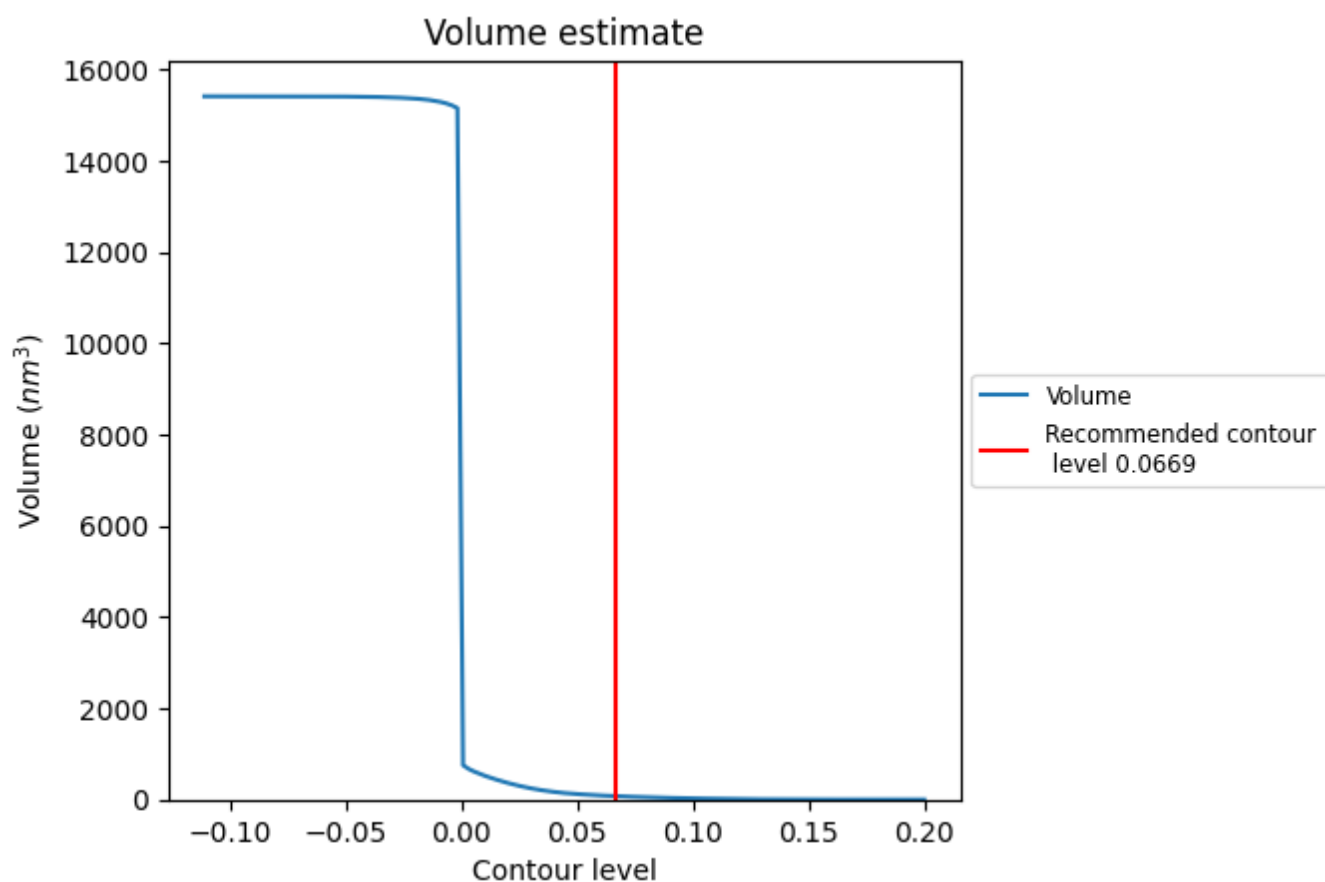
This section contains the results of statistical analysis of the map.

### 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.

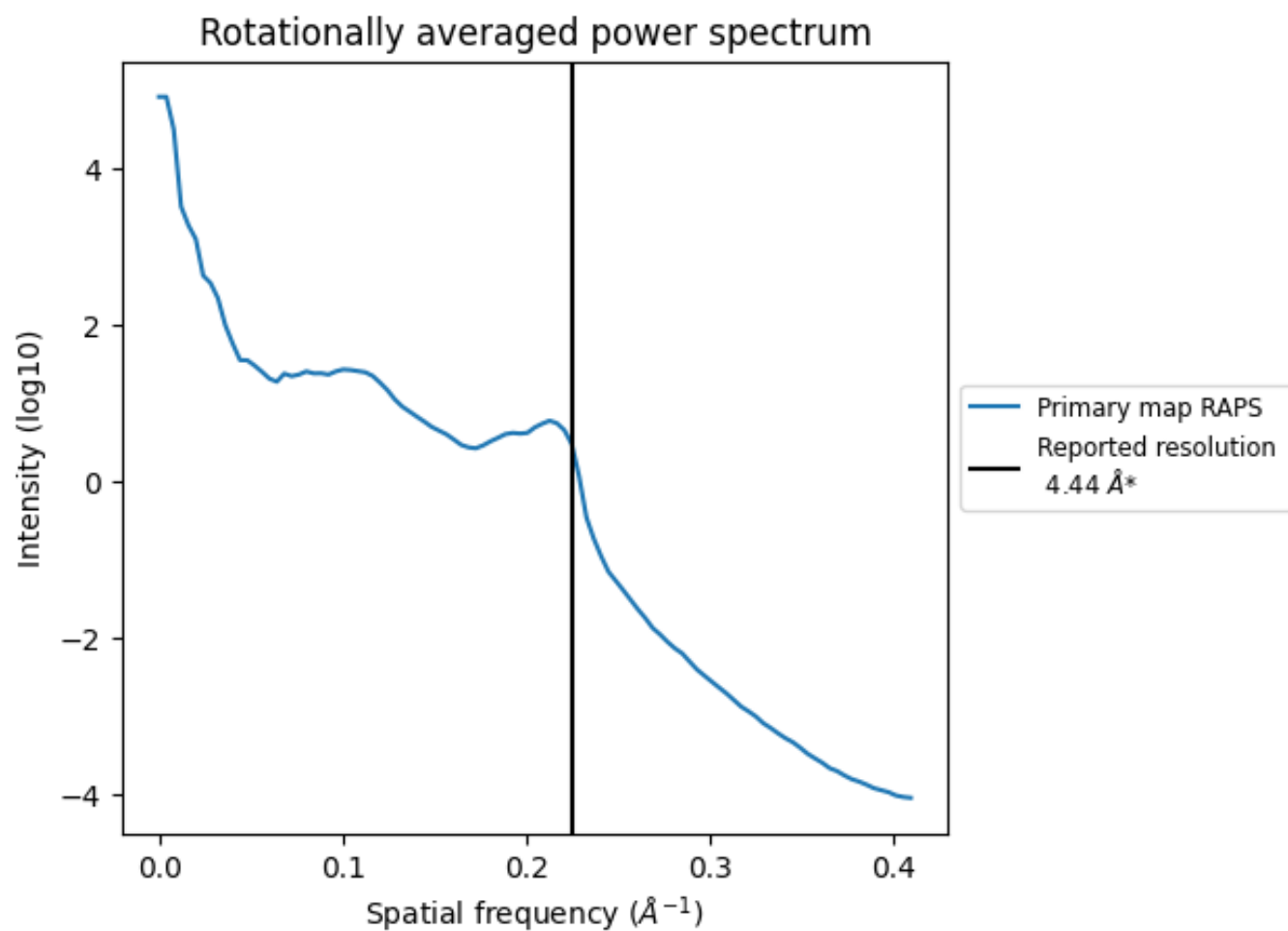
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 74 nm<sup>3</sup>; this corresponds to an approximate mass of 67 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 0.225 Å<sup>-1</sup>

## 8 Fourier-Shell correlation

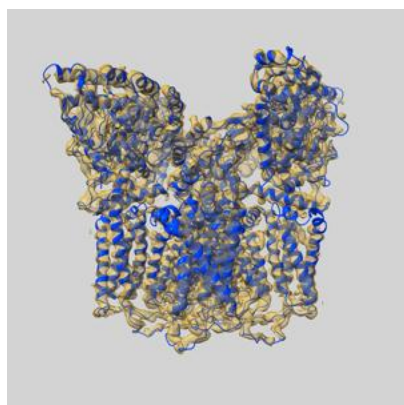
This section was not generated. No FSC curve or half-maps provided.



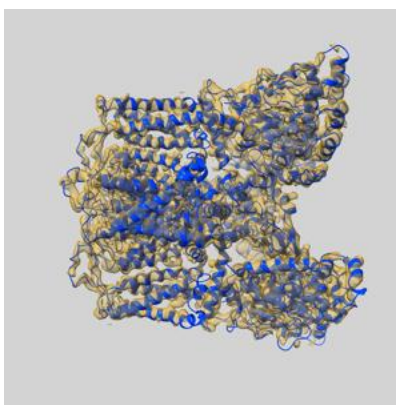
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7825 and PDB model 6D7T. Per-residue inclusion information can be found in section [3](#) on page [7](#).

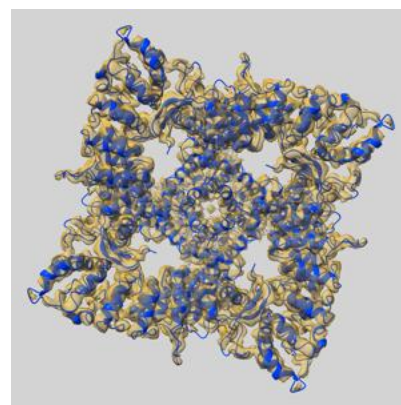
### 9.1 Map-model overlay [i](#)



X



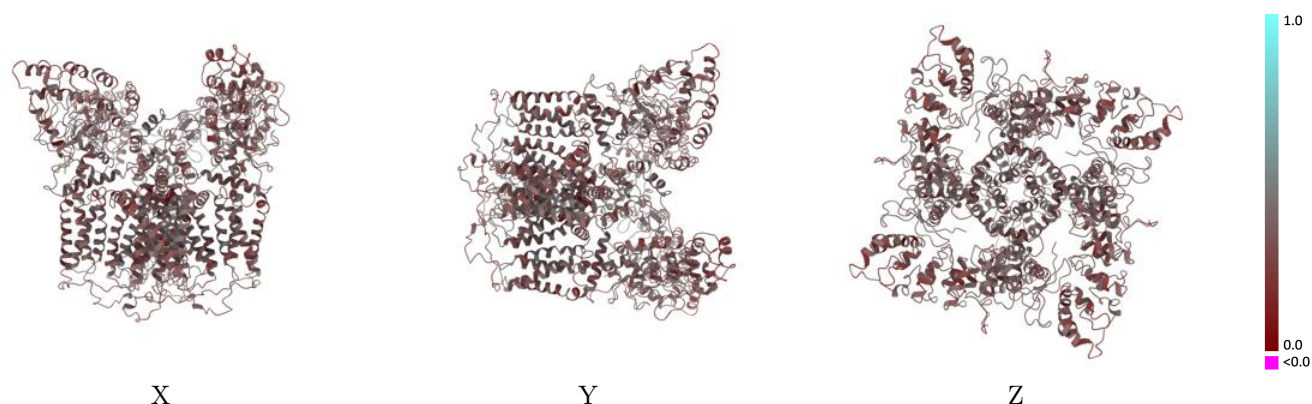
Y



Z

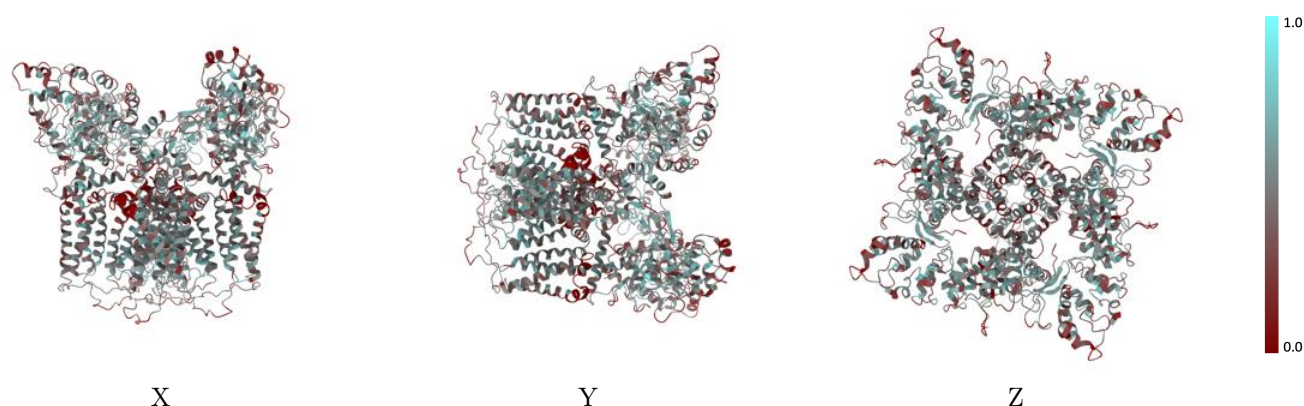
The images above show the 3D surface view of the map at the recommended contour level 0.0669 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



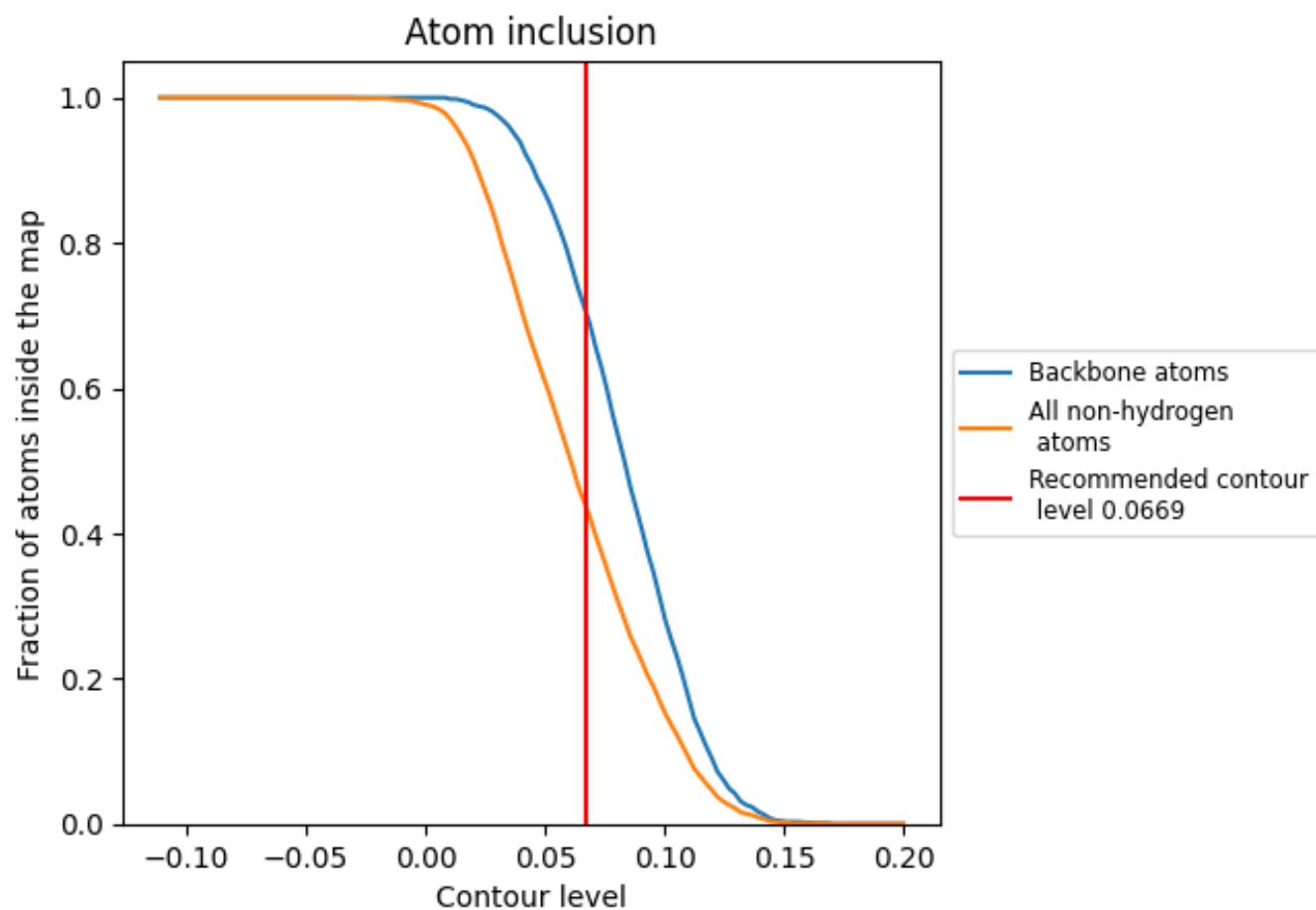
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0669).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 44% 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 (0.0669) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4380	<div></div> 0.3540
A	<div></div> 0.4380	<div></div> 0.3540
B	<div></div> 0.4380	<div></div> 0.3540
C	<div></div> 0.4390	<div></div> 0.3530
D	<div></div> 0.4370	<div></div> 0.3540

