Full wwPDB EM Validation Report ⓘ

Sep 5, 2026 – 12:25 PM EDT

PDB ID	:	9EEF / pdb_00009eef
EMDB ID	:	EMD-47955
Title	:	Human Kv1.3 mutant - G427H
Authors	:	Selvakumar, P.; Swartz, K.J.
Deposited on	:	2024-11-19
Resolution	:	3.54 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:

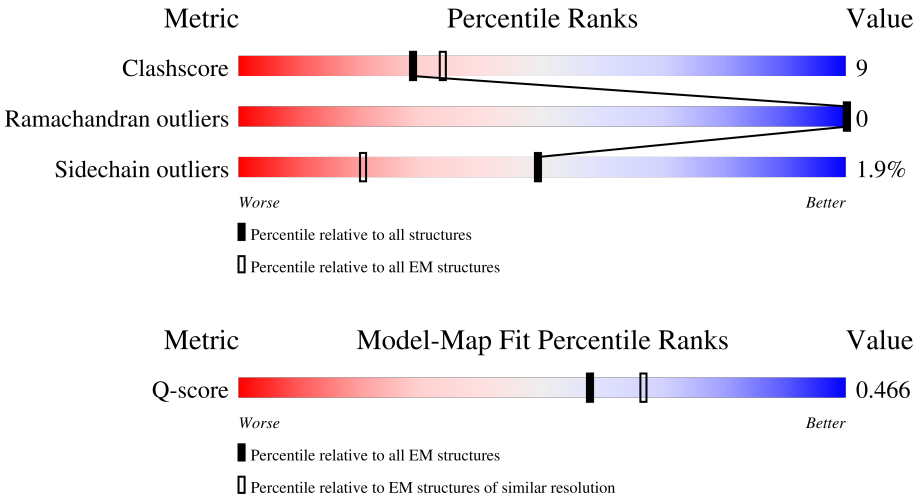
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 3.54 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	12891 (3.04 - 4.04)

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	856	5% 31% 9% 59%
1	B	856	5% 32% 9% 59%
1	C	856	5% 32% 9% 59%
1	D	856	5% 32% 9% 59%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 11400 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	349	Total	C	N	O	S	0	0
			2849	1876	472	490	11		
1	B	349	Total	C	N	O	S	0	0
			2849	1876	472	490	11		
1	C	349	Total	C	N	O	S	0	0
			2849	1876	472	490	11		
1	D	349	Total	C	N	O	S	0	0
			2849	1876	472	490	11		

There are 224 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	427	HIS	GLY	engineered mutation	UNP P22001
A	576	SER	-	linker	UNP P22001
A	577	LEU	-	linker	UNP P22001
A	578	GLU	-	linker	UNP P22001
A	579	VAL	-	linker	UNP P22001
A	580	LEU	-	linker	UNP P22001
A	581	PHE	-	linker	UNP P22001
A	582	GLN	-	linker	UNP P22001
A	583	GLY	-	linker	UNP P22001
A	584	PRO	-	linker	UNP P22001
A	585	ALA	-	linker	UNP P22001
A	586	ALA	-	linker	UNP P22001
A	587	ALA	-	linker	UNP P22001
A	588	MET	-	linker	UNP P22001
A	589	VAL	-	linker	UNP P22001
A	634	LEU	PHE	engineered mutation	UNP P42212
A	652	LEU	PHE	engineered mutation	UNP P42212
A	653	GLY	SER	engineered mutation	UNP P42212
A	656	LEU	VAL	engineered mutation	UNP P42212
A	660	ALA	SER	engineered mutation	UNP P42212
A	741	THR	MET	engineered mutation	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	751	ALA	VAL	engineered mutation	UNP P42212
A	763	GLY	SER	engineered mutation	UNP P42212
A	791	TYR	THR	engineered mutation	UNP P42212
A	794	LYS	ALA	engineered mutation	UNP P42212
A	819	LEU	HIS	engineered mutation	UNP P42212
A	827	SER	-	expression tag	UNP P42212
A	828	ALA	-	expression tag	UNP P42212
A	829	TRP	-	expression tag	UNP P42212
A	830	SER	-	expression tag	UNP P42212
A	831	HIS	-	expression tag	UNP P42212
A	832	PRO	-	expression tag	UNP P42212
A	833	GLN	-	expression tag	UNP P42212
A	834	PHE	-	expression tag	UNP P42212
A	835	GLU	-	expression tag	UNP P42212
A	836	LYS	-	expression tag	UNP P42212
A	837	GLY	-	expression tag	UNP P42212
A	838	GLY	-	expression tag	UNP P42212
A	839	GLY	-	expression tag	UNP P42212
A	840	SER	-	expression tag	UNP P42212
A	841	GLY	-	expression tag	UNP P42212
A	842	GLY	-	expression tag	UNP P42212
A	843	GLY	-	expression tag	UNP P42212
A	844	SER	-	expression tag	UNP P42212
A	845	GLY	-	expression tag	UNP P42212
A	846	GLY	-	expression tag	UNP P42212
A	847	GLY	-	expression tag	UNP P42212
A	848	SER	-	expression tag	UNP P42212
A	849	TRP	-	expression tag	UNP P42212
A	850	SER	-	expression tag	UNP P42212
A	851	HIS	-	expression tag	UNP P42212
A	852	PRO	-	expression tag	UNP P42212
A	853	GLN	-	expression tag	UNP P42212
A	854	PHE	-	expression tag	UNP P42212
A	855	GLU	-	expression tag	UNP P42212
A	856	LYS	-	expression tag	UNP P42212
B	427	HIS	GLY	engineered mutation	UNP P22001
B	576	SER	-	linker	UNP P22001
B	577	LEU	-	linker	UNP P22001
B	578	GLU	-	linker	UNP P22001
B	579	VAL	-	linker	UNP P22001
B	580	LEU	-	linker	UNP P22001
B	581	PHE	-	linker	UNP P22001

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

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Chain	Residue	Modelled	Actual	Comment	Reference
B	850	SER	-	expression tag	UNP P42212
B	851	HIS	-	expression tag	UNP P42212
B	852	PRO	-	expression tag	UNP P42212
B	853	GLN	-	expression tag	UNP P42212
B	854	PHE	-	expression tag	UNP P42212
B	855	GLU	-	expression tag	UNP P42212
B	856	LYS	-	expression tag	UNP P42212
C	427	HIS	GLY	engineered mutation	UNP P22001
C	576	SER	-	linker	UNP P22001
C	577	LEU	-	linker	UNP P22001
C	578	GLU	-	linker	UNP P22001
C	579	VAL	-	linker	UNP P22001
C	580	LEU	-	linker	UNP P22001
C	581	PHE	-	linker	UNP P22001
C	582	GLN	-	linker	UNP P22001
C	583	GLY	-	linker	UNP P22001
C	584	PRO	-	linker	UNP P22001
C	585	ALA	-	linker	UNP P22001
C	586	ALA	-	linker	UNP P22001
C	587	ALA	-	linker	UNP P22001
C	588	MET	-	linker	UNP P22001
C	589	VAL	-	linker	UNP P22001
C	634	LEU	PHE	engineered mutation	UNP P42212
C	652	LEU	PHE	engineered mutation	UNP P42212
C	653	GLY	SER	engineered mutation	UNP P42212
C	656	LEU	VAL	engineered mutation	UNP P42212
C	660	ALA	SER	engineered mutation	UNP P42212
C	741	THR	MET	engineered mutation	UNP P42212
C	751	ALA	VAL	engineered mutation	UNP P42212
C	763	GLY	SER	engineered mutation	UNP P42212
C	791	TYR	THR	engineered mutation	UNP P42212
C	794	LYS	ALA	engineered mutation	UNP P42212
C	819	LEU	HIS	engineered mutation	UNP P42212
C	827	SER	-	expression tag	UNP P42212
C	828	ALA	-	expression tag	UNP P42212
C	829	TRP	-	expression tag	UNP P42212
C	830	SER	-	expression tag	UNP P42212
C	831	HIS	-	expression tag	UNP P42212
C	832	PRO	-	expression tag	UNP P42212
C	833	GLN	-	expression tag	UNP P42212
C	834	PHE	-	expression tag	UNP P42212
C	835	GLU	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
C	836	LYS	-	expression tag	UNP P42212
C	837	GLY	-	expression tag	UNP P42212
C	838	GLY	-	expression tag	UNP P42212
C	839	GLY	-	expression tag	UNP P42212
C	840	SER	-	expression tag	UNP P42212
C	841	GLY	-	expression tag	UNP P42212
C	842	GLY	-	expression tag	UNP P42212
C	843	GLY	-	expression tag	UNP P42212
C	844	SER	-	expression tag	UNP P42212
C	845	GLY	-	expression tag	UNP P42212
C	846	GLY	-	expression tag	UNP P42212
C	847	GLY	-	expression tag	UNP P42212
C	848	SER	-	expression tag	UNP P42212
C	849	TRP	-	expression tag	UNP P42212
C	850	SER	-	expression tag	UNP P42212
C	851	HIS	-	expression tag	UNP P42212
C	852	PRO	-	expression tag	UNP P42212
C	853	GLN	-	expression tag	UNP P42212
C	854	PHE	-	expression tag	UNP P42212
C	855	GLU	-	expression tag	UNP P42212
C	856	LYS	-	expression tag	UNP P42212
D	427	HIS	GLY	engineered mutation	UNP P22001
D	576	SER	-	linker	UNP P22001
D	577	LEU	-	linker	UNP P22001
D	578	GLU	-	linker	UNP P22001
D	579	VAL	-	linker	UNP P22001
D	580	LEU	-	linker	UNP P22001
D	581	PHE	-	linker	UNP P22001
D	582	GLN	-	linker	UNP P22001
D	583	GLY	-	linker	UNP P22001
D	584	PRO	-	linker	UNP P22001
D	585	ALA	-	linker	UNP P22001
D	586	ALA	-	linker	UNP P22001
D	587	ALA	-	linker	UNP P22001
D	588	MET	-	linker	UNP P22001
D	589	VAL	-	linker	UNP P22001
D	634	LEU	PHE	engineered mutation	UNP P42212
D	652	LEU	PHE	engineered mutation	UNP P42212
D	653	GLY	SER	engineered mutation	UNP P42212
D	656	LEU	VAL	engineered mutation	UNP P42212
D	660	ALA	SER	engineered mutation	UNP P42212
D	741	THR	MET	engineered mutation	UNP P42212

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

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

Mol	Chain	Residues	Atoms	AltConf
2	A	4	Total K 4 4	0

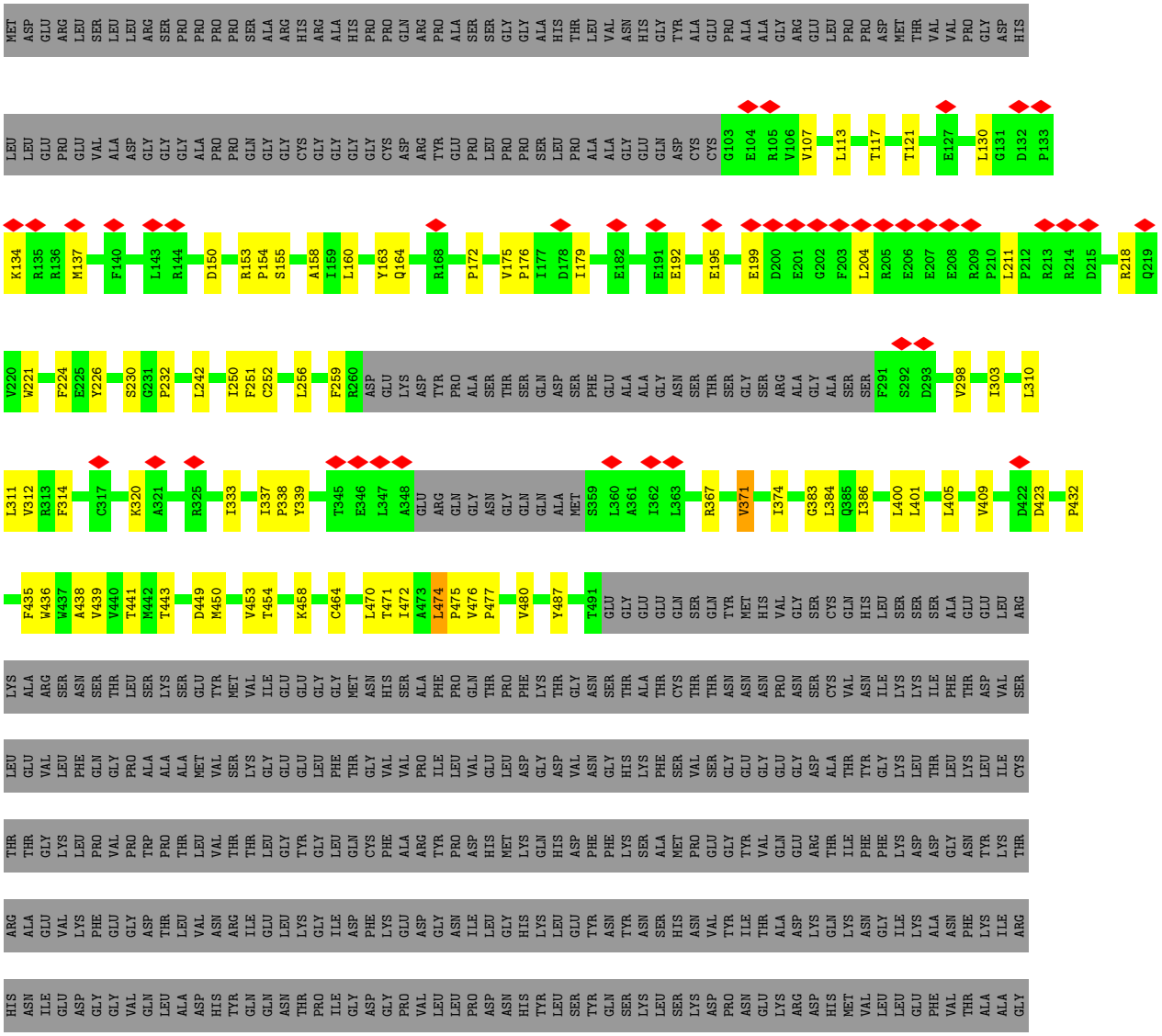
3 Residue-property plots (i)

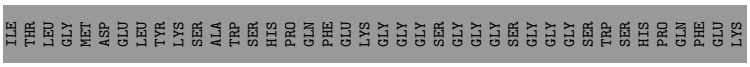
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Potassium voltage-gated channel subfamily A member 3,Green fluorescent protein

Chain A:



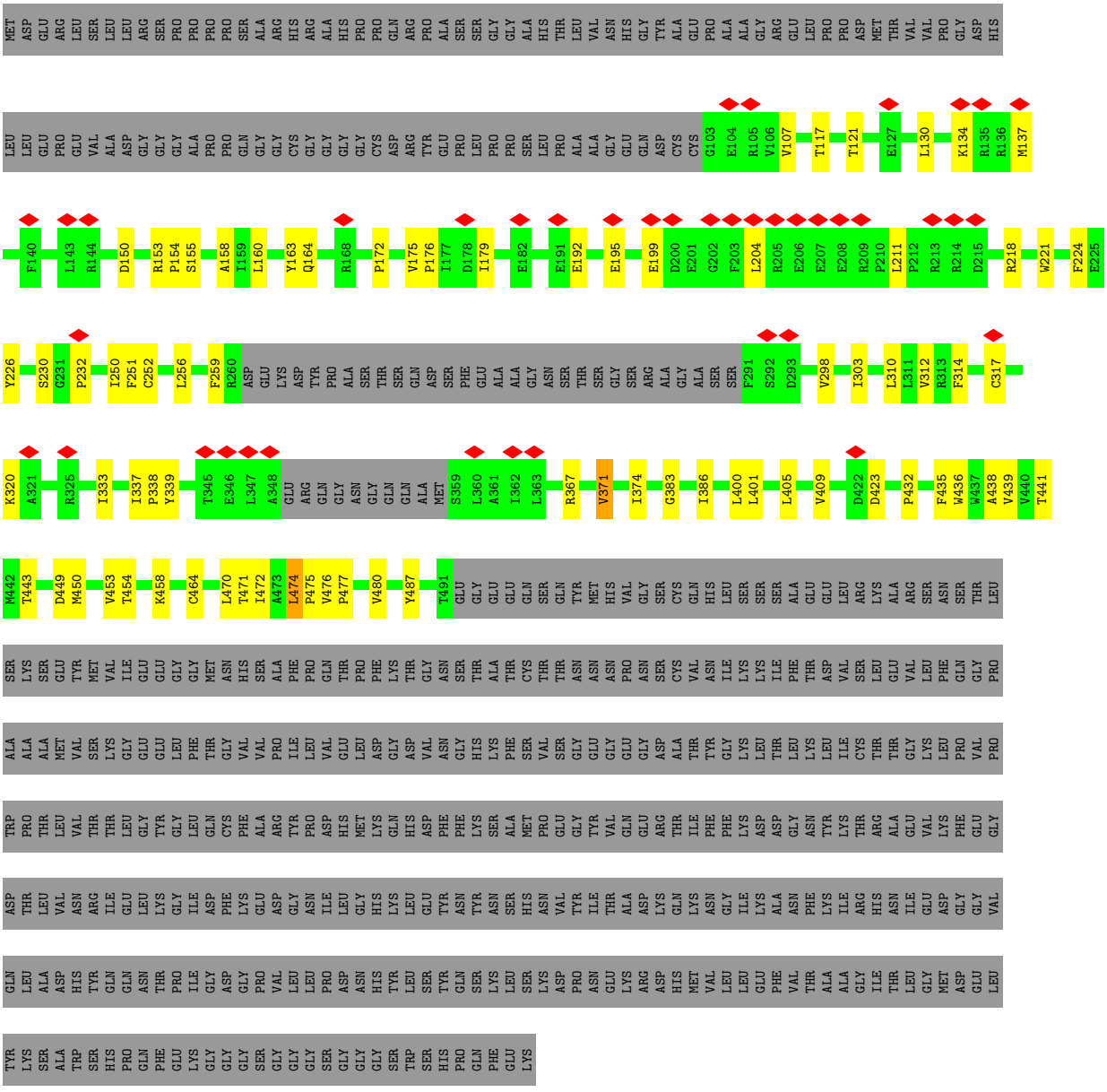




• Molecule 1: Potassium voltage-gated channel subfamily A member 3,Green fluorescent protein

Chain B:



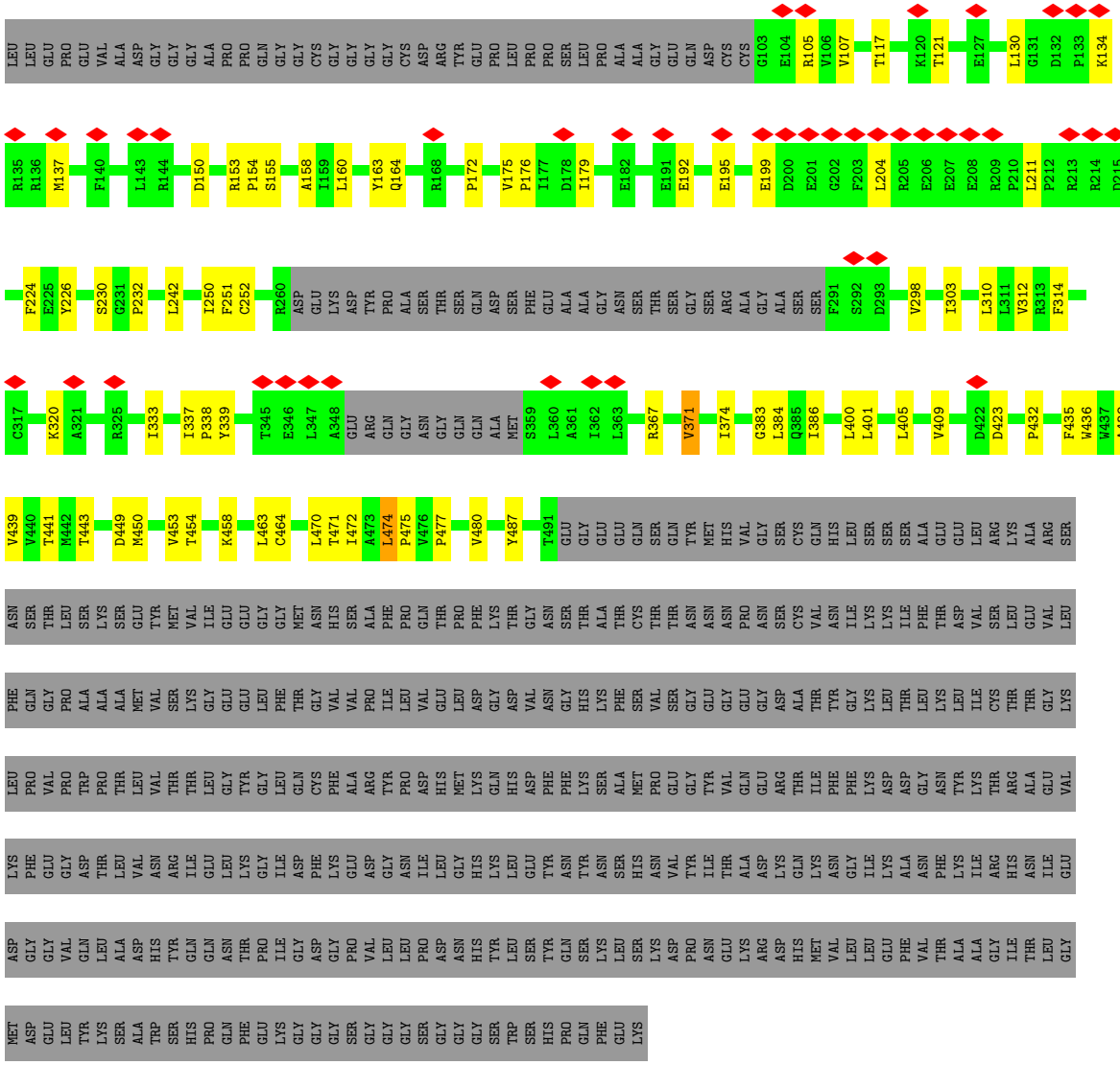


• Molecule 1: Potassium voltage-gated channel subfamily A member 3,Green fluorescent protein

Chain C:



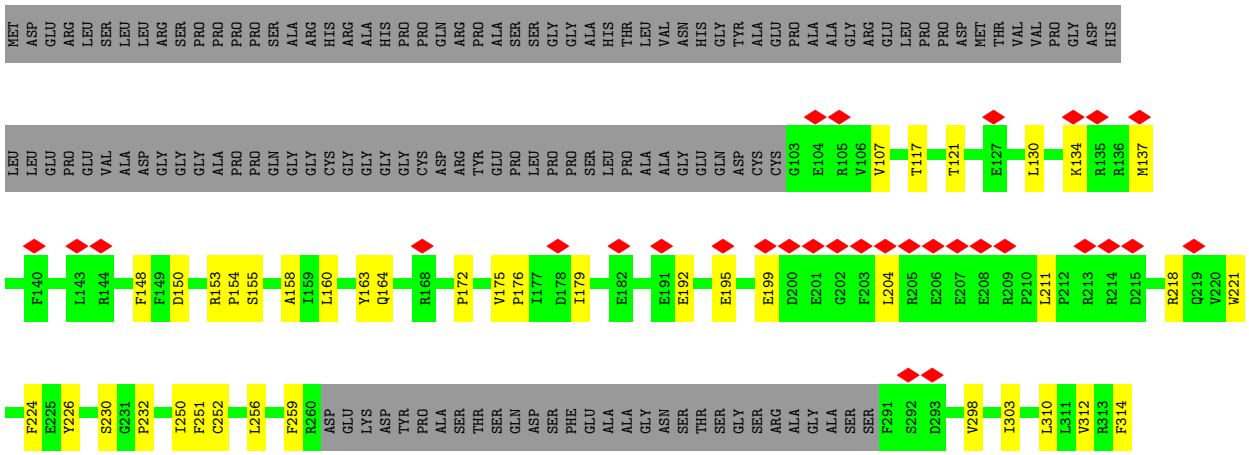


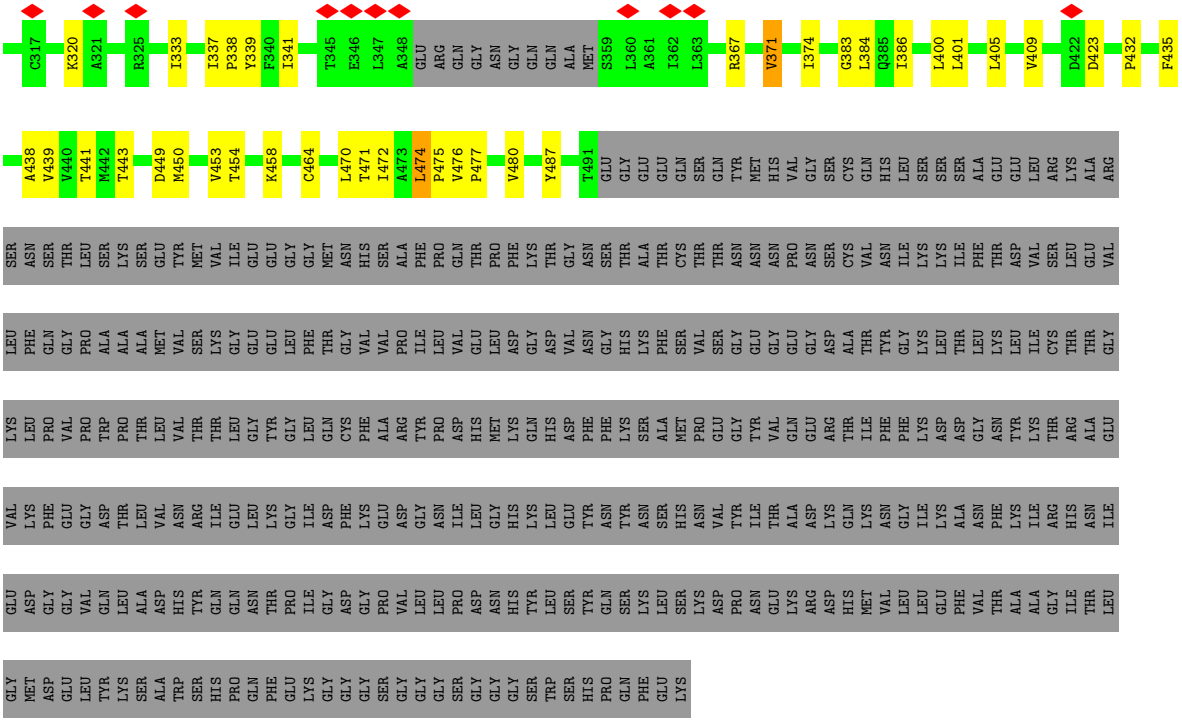


• Molecule 1: Potassium voltage-gated channel subfamily A member 3,Green fluorescent protein

Chain D:






C317 K320 A321 R325 I333 I337 P338 Y339 F340 I341 T345 E346 L347 A348 GLU ARG GLN GLY ASN GLY GLN GLN ALA MET S359 L360 A361 I362 L363 R367 V371 I374 G383 L384 Q385 I386 L400 L401 L405 V409 D422 D423 P432 F435
A438 V439 V440 T441 M442 T443 D449 M450 V453 T454 K458 C464 L470 T471 I472 A473 L474 P475 V476 P477 V480 Y487 T491 GLU GLY GLU GLU GLN SER GLN TYR MET HIS VAL GLY SER CYS GLN HIS LEU SER SER SER ALA GLU GLU LEU ARG LYS ALA ARG
SER ASN SER THR LEU SER LYS SER GLU TYR MET VAL ILE GLU GLU GLY GLY MET ASN HIS SER ALA PHE PRO GLN THR PRO PHE LYS THR GLY ASN SER THR ALA THR CYS THR THR ASN ASN ASN PRO ASN SER CYS VAL ASN ILE LYS LYS ILE PHE THR ASP VAL SER LEU GLU VAL
LEU PHE GLN GLY PRO ALA ALA ALA MET VAL SER LYS GLY GLU GLU LEU PHE THR GLY VAL VAL PRO ILE LEU VAL GLU LEU ASP GLY ASP VAL ASN GLY HIS LYS PHE SER VAL SER GLY GLU GLY GLU GLY ASP ALA THR TYR GLY LYS LEU THR LEU LYS LEU ILE CYS THR THR GLY
LYS LEU PRO VAL PRO TRP PRO THR LEU VAL THR THR LEU GLY TYR GLY LEU GLN CYS PHE ALA ARG TYR PRO ASP HIS MET LYS GLN HIS ASP PHE PHE LYS SER ALA MET PRO GLU GLY TYR VAL GLN GLU ARG THR ILE PHE PHE LYS ASP ASP GLY ASN TYR LYS THR ARG ALA GLU
VAL LYS PHE GLU GLY ASP THR LEU VAL ASN ARG ILE GLU LEU LYS GLY ILE ASP PHE LYS GLU ASP GLY ASN ILE LEU LEU GLY HIS LYS LEU GLU TYR ASN TYR ASN SER HIS ASN VAL TYR ILE THR ALA ASP LYS GLN LYS ASN GLY ILE LYS ALA ASN PHE LYS ILE ARG HIS ASN ILE
GLU ASP GLY GLY VAL GLN LEU ALA ASP HIS TYR GLN GLN ASN THR PRO ILE GLY ASP GLY PRO VAL LEU LEU PRO ASP ASN HIS TYR LEU SER TYR GLN SER LYS LEU SER LYS ASP PRO ASN GLU LYS ARG ASP HIS MET VAL LEU LEU GLU PHE VAL THR ALA ALA GLY ILE THR LEU
GLY MET ASP GLU LEU TYR LYS SER ALA TRP SER HIS PRO GLN PHE GLU LYS GLY GLY GLY SER GLY GLY GLY SER GLY GLY GLY SER TRP SER HIS PRO GLN PHE GLU LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	139210	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.038	Depositor
Minimum map value	-1.379	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	265.6, 265.6, 265.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83000004, 0.83000004, 0.83000004	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	0.63	0/2923	0.72	0/3961
1	B	0.63	0/2923	0.72	0/3961
1	C	0.63	0/2923	0.72	0/3961
1	D	0.63	0/2923	0.72	0/3961
All	All	0.63	0/11692	0.72	0/15844

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2849	0	2881	63	0
1	B	2849	0	2881	60	0
1	C	2849	0	2881	57	0
1	D	2849	0	2881	60	0
2	A	4	0	0	0	0
All	All	11400	0	11524	216	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 9.

All (216) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:117:THR:HG21	1:C:160:LEU:HD11	1.79	0.65
1:C:121:THR:HG21	1:C:164:GLN:HG2	1.78	0.65
1:D:121:THR:HG21	1:D:164:GLN:HG2	1.78	0.64
1:A:121:THR:HG21	1:A:164:GLN:HG2	1.78	0.64
1:A:117:THR:HG21	1:A:160:LEU:HD11	1.79	0.64
1:B:121:THR:HG21	1:B:164:GLN:HG2	1.78	0.64
1:B:117:THR:HG21	1:B:160:LEU:HD11	1.79	0.63
1:D:117:THR:HG21	1:D:160:LEU:HD11	1.79	0.63
1:A:474:LEU:HD12	1:B:480:VAL:HG22	1.82	0.61
1:A:443:THR:HG22	1:A:472:ILE:CD1	2.32	0.60
1:C:443:THR:HG22	1:C:472:ILE:CD1	2.32	0.60
1:D:176:PRO:HD2	1:D:179:ILE:HD12	1.84	0.60
1:A:176:PRO:HD2	1:A:179:ILE:HD12	1.84	0.60
1:A:401:LEU:O	1:A:405:LEU:HD13	2.02	0.59
1:B:401:LEU:O	1:B:405:LEU:HD13	2.02	0.59
1:C:401:LEU:O	1:C:405:LEU:HD13	2.02	0.59
1:D:443:THR:HG22	1:D:472:ILE:CD1	2.32	0.59
1:B:443:THR:HG22	1:B:472:ILE:CD1	2.32	0.59
1:A:480:VAL:HG22	1:D:474:LEU:HD12	1.85	0.59
1:D:401:LEU:O	1:D:405:LEU:HD13	2.02	0.59
1:C:176:PRO:HD2	1:C:179:ILE:HD12	1.84	0.58
1:A:480:VAL:HG11	1:D:477:PRO:HG3	1.86	0.58
1:B:176:PRO:HD2	1:B:179:ILE:HD12	1.84	0.57
1:B:474:LEU:HD12	1:C:480:VAL:HG22	1.85	0.57
1:A:477:PRO:HG3	1:B:480:VAL:HG11	1.86	0.57
1:C:477:PRO:HG3	1:D:480:VAL:HG11	1.86	0.57
1:C:474:LEU:HD12	1:D:480:VAL:HG22	1.86	0.56
1:B:386:ILE:HD13	1:B:487:TYR:HD1	1.71	0.55
1:A:386:ILE:HD13	1:A:487:TYR:HD1	1.71	0.55
1:B:251:PHE:CE2	1:B:371:VAL:HG23	2.42	0.55
1:B:401:LEU:HD11	1:B:472:ILE:HG23	1.89	0.55
1:C:386:ILE:HD13	1:C:487:TYR:HD1	1.71	0.55
1:C:401:LEU:HD11	1:C:472:ILE:HG23	1.89	0.55
1:A:251:PHE:CE2	1:A:371:VAL:HG23	2.42	0.55
1:C:251:PHE:CE2	1:C:371:VAL:HG23	2.42	0.54
1:D:386:ILE:HD13	1:D:487:TYR:HD1	1.71	0.54
1:A:401:LEU:HD11	1:A:472:ILE:HG23	1.89	0.54
1:D:401:LEU:HD11	1:D:472:ILE:HG23	1.89	0.54
1:B:477:PRO:HG3	1:C:480:VAL:HG11	1.89	0.54
1:D:251:PHE:CE2	1:D:371:VAL:HG23	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:405:LEU:HD11	1:C:472:ILE:HG12	1.90	0.53
1:D:405:LEU:HD11	1:D:472:ILE:HG12	1.91	0.52
1:D:250:ILE:HG13	1:D:298:VAL:HG11	1.91	0.52
1:A:211:LEU:HD13	1:A:218:ARG:HD2	1.92	0.52
1:B:405:LEU:HD11	1:B:472:ILE:HG12	1.91	0.51
1:B:211:LEU:HD13	1:B:218:ARG:HD2	1.92	0.51
1:B:250:ILE:HG13	1:B:298:VAL:HG11	1.91	0.51
1:A:405:LEU:HD11	1:A:472:ILE:HG12	1.91	0.51
1:C:230:SER:OG	1:C:232:PRO:HD2	2.11	0.51
1:A:230:SER:OG	1:A:232:PRO:HD2	2.11	0.51
1:C:211:LEU:HD13	1:C:218:ARG:HD2	1.92	0.51
1:D:211:LEU:HD13	1:D:218:ARG:HD2	1.92	0.51
1:C:250:ILE:HG13	1:C:298:VAL:HG11	1.92	0.51
1:A:250:ILE:HG13	1:A:298:VAL:HG11	1.91	0.51
1:B:333:ILE:HG22	1:B:337:ILE:HD11	1.93	0.51
1:B:435:PHE:O	1:B:439:VAL:HG22	2.12	0.50
1:D:230:SER:OG	1:D:232:PRO:HD2	2.11	0.50
1:D:333:ILE:HG22	1:D:337:ILE:HD11	1.94	0.50
1:C:164:GLN:OE1	1:D:150:ASP:HB2	2.11	0.50
1:B:230:SER:OG	1:B:232:PRO:HD2	2.11	0.50
1:A:435:PHE:O	1:A:439:VAL:HG22	2.12	0.50
1:C:435:PHE:O	1:C:439:VAL:HG22	2.12	0.50
1:B:164:GLN:OE1	1:C:150:ASP:HB2	2.12	0.49
1:D:192:GLU:O	1:D:195:GLU:HG2	2.13	0.49
1:A:192:GLU:O	1:A:195:GLU:HG2	2.13	0.49
1:C:333:ILE:HG22	1:C:337:ILE:HD11	1.94	0.49
1:D:435:PHE:O	1:D:439:VAL:HG22	2.11	0.49
1:C:192:GLU:O	1:C:195:GLU:HG2	2.13	0.49
1:B:192:GLU:O	1:B:195:GLU:HG2	2.13	0.49
1:C:470:LEU:O	1:C:474:LEU:HD13	2.13	0.49
1:A:150:ASP:HB2	1:D:164:GLN:OE1	2.13	0.49
1:A:333:ILE:O	1:A:337:ILE:HG13	2.13	0.49
1:B:333:ILE:O	1:B:337:ILE:HG13	2.13	0.48
1:D:333:ILE:O	1:D:337:ILE:HG13	2.13	0.48
1:A:333:ILE:HG22	1:A:337:ILE:HD11	1.94	0.48
1:B:470:LEU:O	1:B:474:LEU:HD13	2.13	0.48
1:D:470:LEU:O	1:D:474:LEU:HD13	2.13	0.48
1:D:303:ILE:HG21	1:D:339:TYR:CD2	2.49	0.48
1:C:303:ILE:HG21	1:C:339:TYR:CD2	2.49	0.47
1:C:449:ASP:OD1	1:C:450:MET:N	2.48	0.47
1:A:303:ILE:HG21	1:A:339:TYR:CD2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:LEU:O	1:A:474:LEU:HD13	2.13	0.47
1:D:449:ASP:OD1	1:D:450:MET:N	2.48	0.47
1:A:130:LEU:HD13	1:A:163:TYR:HE2	1.80	0.47
1:B:303:ILE:HG21	1:B:339:TYR:CD2	2.49	0.47
1:C:333:ILE:O	1:C:337:ILE:HG13	2.13	0.47
1:D:130:LEU:HD13	1:D:163:TYR:HE2	1.80	0.47
1:D:251:PHE:HE2	1:D:371:VAL:HG23	1.79	0.47
1:B:449:ASP:OD1	1:B:450:MET:N	2.48	0.47
1:C:130:LEU:HD13	1:C:163:TYR:HE2	1.80	0.47
1:C:441:THR:HG21	1:C:464:CYS:HB3	1.97	0.47
1:A:153:ARG:HB2	1:A:154:PRO:HD3	1.97	0.47
1:A:441:THR:HG21	1:A:464:CYS:HB3	1.97	0.47
1:B:158:ALA:HB2	1:B:172:PRO:HD3	1.97	0.47
1:A:449:ASP:OD1	1:A:450:MET:N	2.48	0.46
1:B:153:ARG:HB2	1:B:154:PRO:HD3	1.97	0.46
1:B:441:THR:HG21	1:B:464:CYS:HB3	1.97	0.46
1:C:251:PHE:HE2	1:C:371:VAL:HG23	1.79	0.46
1:A:251:PHE:HE2	1:A:371:VAL:HG23	1.79	0.46
1:B:130:LEU:HD13	1:B:163:TYR:HE2	1.80	0.46
1:C:310:LEU:HD21	1:C:333:ILE:HG12	1.97	0.46
1:D:441:THR:HG21	1:D:464:CYS:HB3	1.97	0.46
1:A:158:ALA:HB2	1:A:172:PRO:HD3	1.97	0.46
1:A:154:PRO:HB2	1:A:175:VAL:HG23	1.98	0.46
1:B:251:PHE:HE2	1:B:371:VAL:HG23	1.79	0.46
1:C:158:ALA:HB2	1:C:172:PRO:HD3	1.97	0.46
1:D:310:LEU:HD21	1:D:333:ILE:HG12	1.97	0.46
1:B:154:PRO:HB2	1:B:175:VAL:HG23	1.98	0.46
1:A:310:LEU:HD21	1:A:333:ILE:HG12	1.97	0.45
1:B:310:LEU:HD21	1:B:333:ILE:HG12	1.97	0.45
1:C:153:ARG:HB2	1:C:154:PRO:HD3	1.97	0.45
1:B:371:VAL:O	1:B:374:ILE:HG22	2.17	0.45
1:D:153:ARG:HB2	1:D:154:PRO:HD3	1.97	0.45
1:D:158:ALA:HB2	1:D:172:PRO:HD3	1.97	0.45
1:B:130:LEU:HD13	1:B:163:TYR:CE2	2.52	0.45
1:D:154:PRO:HB2	1:D:175:VAL:HG23	1.98	0.45
1:C:371:VAL:O	1:C:374:ILE:HG22	2.17	0.45
1:A:371:VAL:O	1:A:374:ILE:HG22	2.17	0.45
1:C:130:LEU:HD13	1:C:163:TYR:CE2	2.52	0.45
1:C:384:LEU:HA	1:C:384:LEU:HD12	1.81	0.45
1:A:130:LEU:HD13	1:A:163:TYR:CE2	2.52	0.44
1:C:432:PRO:HD3	1:D:252:CYS:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:371:VAL:O	1:D:374:ILE:HG22	2.17	0.44
1:A:432:PRO:HD3	1:B:252:CYS:O	2.17	0.44
1:A:454:THR:O	1:A:458:LYS:HG3	2.18	0.44
1:C:154:PRO:HB2	1:C:175:VAL:HG23	1.98	0.44
1:A:164:GLN:OE1	1:B:150:ASP:HB2	2.17	0.44
1:B:454:THR:O	1:B:458:LYS:HG3	2.18	0.44
1:D:130:LEU:HD13	1:D:163:TYR:CE2	2.52	0.44
1:D:454:THR:O	1:D:458:LYS:HG3	2.18	0.44
1:C:454:THR:O	1:C:458:LYS:HG3	2.18	0.44
1:C:154:PRO:HB2	1:C:175:VAL:CG2	2.48	0.44
1:A:224:PHE:CE1	1:A:312:VAL:HG11	2.53	0.43
1:A:458:LYS:HZ2	1:B:436:TRP:CD1	2.35	0.43
1:B:154:PRO:HB2	1:B:175:VAL:CG2	2.48	0.43
1:C:400:LEU:HD21	1:D:383:GLY:HA3	2.00	0.43
1:B:224:PHE:CE1	1:B:312:VAL:HG11	2.53	0.43
1:B:155:SER:HB2	1:B:175:VAL:HG21	2.00	0.43
1:D:154:PRO:HB2	1:D:175:VAL:CG2	2.48	0.43
1:D:221:TRP:CD1	1:D:226:TYR:HE2	2.37	0.43
1:A:436:TRP:CD1	1:D:458:LYS:HZ2	2.37	0.43
1:B:458:LYS:HZ2	1:C:436:TRP:CD1	2.36	0.43
1:C:155:SER:HB2	1:C:175:VAL:HG21	2.00	0.43
1:A:154:PRO:HB2	1:A:175:VAL:CG2	2.48	0.43
1:A:155:SER:HB2	1:A:175:VAL:HG21	2.01	0.43
1:A:250:ILE:HD13	1:A:250:ILE:HA	1.85	0.43
1:C:224:PHE:CE1	1:C:312:VAL:HG11	2.53	0.43
1:C:401:LEU:CD1	1:C:472:ILE:HA	2.49	0.43
1:D:155:SER:HB2	1:D:175:VAL:HG21	2.00	0.43
1:D:401:LEU:CD1	1:D:472:ILE:HA	2.49	0.43
1:D:224:PHE:CE1	1:D:312:VAL:HG11	2.53	0.43
1:A:221:TRP:CD1	1:A:226:TYR:HE2	2.37	0.42
1:A:471:THR:O	1:A:475:PRO:HD3	2.19	0.42
1:B:221:TRP:CD1	1:B:226:TYR:HE2	2.37	0.42
1:B:401:LEU:HD11	1:B:472:ILE:HA	2.02	0.42
1:A:401:LEU:HD11	1:A:472:ILE:HA	2.02	0.42
1:B:471:THR:O	1:B:475:PRO:CD	2.68	0.42
1:C:221:TRP:CD1	1:C:226:TYR:HE2	2.37	0.42
1:D:199:GLU:HG2	1:D:204:LEU:HD13	2.02	0.42
1:A:443:THR:HG22	1:A:472:ILE:HD12	2.02	0.42
1:B:401:LEU:CD1	1:B:472:ILE:HA	2.49	0.42
1:B:471:THR:O	1:B:475:PRO:HD3	2.20	0.42
1:C:409:VAL:HG13	1:C:438:ALA:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:GLU:HG2	1:A:204:LEU:HD13	2.02	0.42
1:A:401:LEU:CD1	1:A:472:ILE:HA	2.49	0.42
1:C:199:GLU:HG2	1:C:204:LEU:HD13	2.02	0.42
1:D:401:LEU:HD11	1:D:472:ILE:HA	2.02	0.42
1:B:409:VAL:HG13	1:B:438:ALA:HB3	2.02	0.42
1:C:401:LEU:HD11	1:C:472:ILE:HA	2.02	0.42
1:C:471:THR:O	1:C:475:PRO:HD3	2.19	0.42
1:D:384:LEU:HD12	1:D:384:LEU:HA	1.81	0.42
1:A:383:GLY:HA3	1:D:400:LEU:HD21	2.02	0.42
1:A:384:LEU:HD12	1:A:384:LEU:HA	1.81	0.42
1:C:471:THR:O	1:C:475:PRO:CD	2.68	0.42
1:D:409:VAL:HG13	1:D:438:ALA:HB3	2.02	0.42
1:D:471:THR:O	1:D:475:PRO:HD3	2.19	0.41
1:A:134:LYS:O	1:A:137:MET:HG2	2.20	0.41
1:A:471:THR:O	1:A:475:PRO:CD	2.68	0.41
1:B:160:LEU:HD12	1:B:160:LEU:HA	1.84	0.41
1:D:471:THR:O	1:D:475:PRO:CD	2.68	0.41
1:C:242:LEU:HD23	1:C:242:LEU:HA	1.87	0.41
1:B:320:LYS:HE2	1:B:320:LYS:HB3	1.89	0.41
1:C:134:LYS:O	1:C:137:MET:HG2	2.20	0.41
1:A:160:LEU:HD12	1:A:160:LEU:HA	1.84	0.41
1:B:432:PRO:HD3	1:C:252:CYS:O	2.20	0.41
1:D:134:LYS:O	1:D:137:MET:HG2	2.20	0.41
1:B:199:GLU:HG2	1:B:204:LEU:HD13	2.02	0.41
1:B:314:PHE:O	1:B:317:CYS:SG	2.79	0.41
1:A:409:VAL:HG13	1:A:438:ALA:HB3	2.02	0.41
1:C:463:LEU:HD13	1:C:463:LEU:HA	1.97	0.41
1:A:252:CYS:O	1:D:432:PRO:HD3	2.20	0.41
1:A:311:LEU:HD23	1:A:311:LEU:HA	1.90	0.41
1:B:314:PHE:HE1	1:B:320:LYS:HG3	1.86	0.41
1:C:105:ARG:HG2	1:D:148:PHE:HE2	1.86	0.41
1:C:337:ILE:N	1:C:338:PRO:HD2	2.36	0.41
1:D:320:LYS:HE2	1:D:320:LYS:HB3	1.89	0.41
1:D:476:VAL:N	1:D:477:PRO:HD2	2.36	0.41
1:A:242:LEU:HA	1:A:242:LEU:HD23	1.87	0.41
1:A:476:VAL:N	1:A:477:PRO:HD2	2.36	0.41
1:B:337:ILE:N	1:B:338:PRO:HD2	2.36	0.41
1:B:400:LEU:HD21	1:C:383:GLY:HA3	2.03	0.41
1:D:314:PHE:HE1	1:D:320:LYS:HG3	1.86	0.41
1:B:134:LYS:O	1:B:137:MET:HG2	2.20	0.40
1:B:256:LEU:HB2	1:B:259:PHE:HD1	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:LEU:HB2	1:A:153:ARG:NH1	2.37	0.40
1:A:314:PHE:HE1	1:A:320:LYS:HG3	1.86	0.40
1:B:476:VAL:N	1:B:477:PRO:HD2	2.36	0.40
1:D:256:LEU:HB2	1:D:259:PHE:HD1	1.86	0.40
1:A:337:ILE:N	1:A:338:PRO:HD2	2.36	0.40
1:A:400:LEU:HD21	1:B:383:GLY:HA3	2.04	0.40
1:C:314:PHE:HE1	1:C:320:LYS:HG3	1.86	0.40
1:D:250:ILE:HG13	1:D:298:VAL:CG1	2.51	0.40
1:A:256:LEU:HB2	1:A:259:PHE:HD1	1.86	0.40
1:B:250:ILE:HG13	1:B:298:VAL:CG1	2.51	0.40
1:D:338:PRO:HA	1:D:341:ILE:HG12	2.04	0.40
1:D:443:THR:HG22	1:D:472:ILE:HD12	2.02	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	343/856 (40%)	328 (96%)	15 (4%)	0	100	100
1	B	343/856 (40%)	328 (96%)	15 (4%)	0	100	100
1	C	343/856 (40%)	328 (96%)	15 (4%)	0	100	100
1	D	343/856 (40%)	328 (96%)	15 (4%)	0	100	100
All	All	1372/3424 (40%)	1312 (96%)	60 (4%)	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	311/725 (43%)	305 (98%)	6 (2%)	50	67
1	B	311/725 (43%)	305 (98%)	6 (2%)	50	67
1	C	311/725 (43%)	305 (98%)	6 (2%)	50	67
1	D	311/725 (43%)	305 (98%)	6 (2%)	50	67
All	All	1244/2900 (43%)	1220 (98%)	24 (2%)	49	67

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	107	VAL
1	A	367	ARG
1	A	371	VAL
1	A	423	ASP
1	A	453	VAL
1	A	474	LEU
1	B	107	VAL
1	B	367	ARG
1	B	371	VAL
1	B	423	ASP
1	B	453	VAL
1	B	474	LEU
1	C	107	VAL
1	C	367	ARG
1	C	371	VAL
1	C	423	ASP
1	C	453	VAL
1	C	474	LEU
1	D	107	VAL
1	D	367	ARG
1	D	371	VAL
1	D	423	ASP
1	D	453	VAL
1	D	474	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

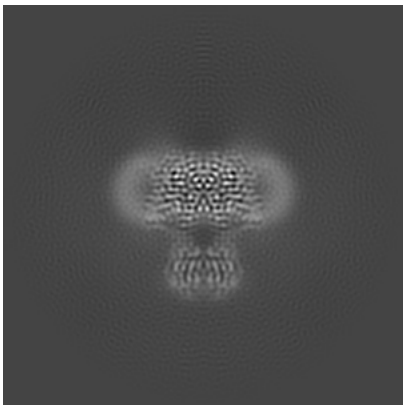
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-47955. These allow visual inspection of the internal detail of the map and identification of artifacts.

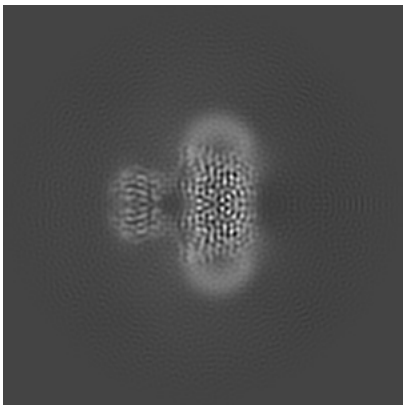
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

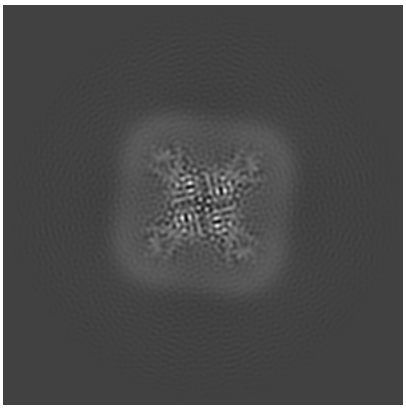
6.1.1 Primary map



X

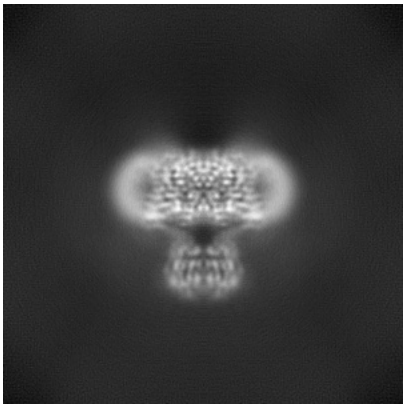


Y

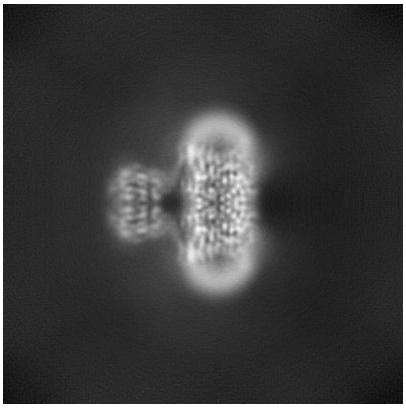


Z

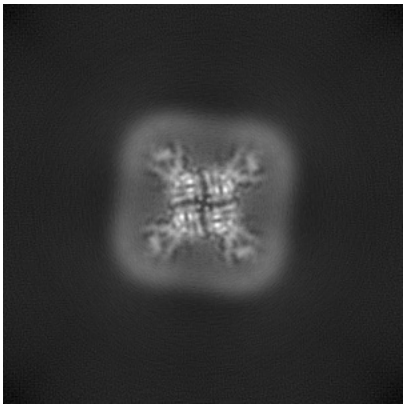
6.1.2 Raw map



X



Y

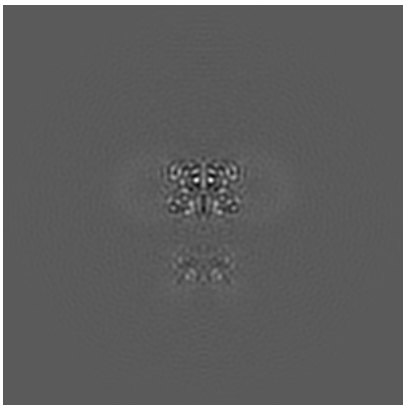


Z

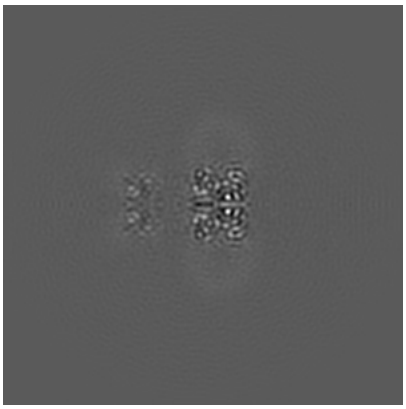
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

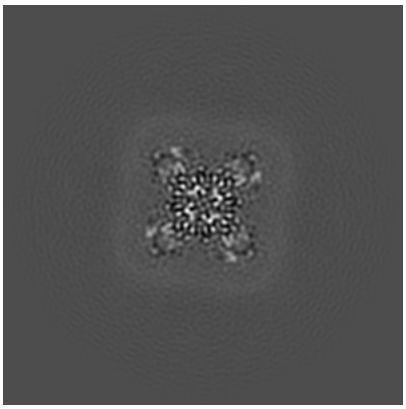
6.2.1 Primary map



X Index: 160

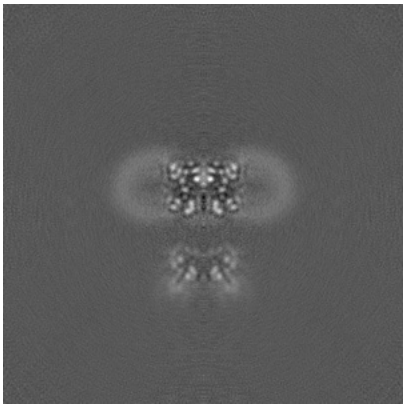


Y Index: 160

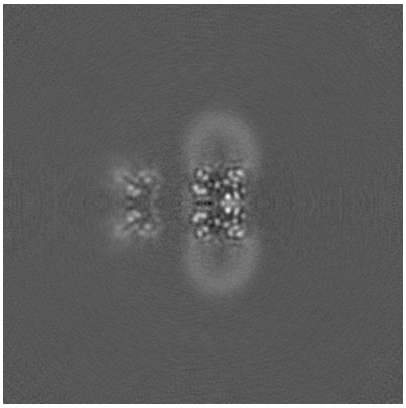


Z Index: 160

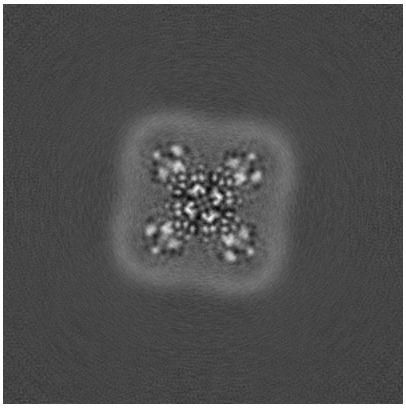
6.2.2 Raw map



X Index: 160



Y Index: 160

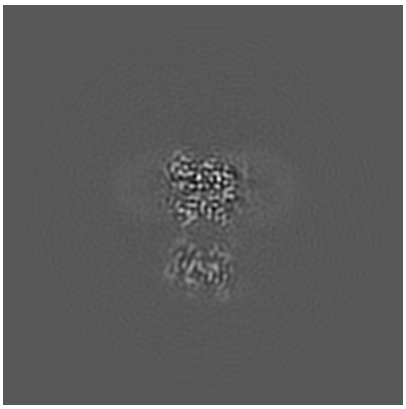


Z Index: 160

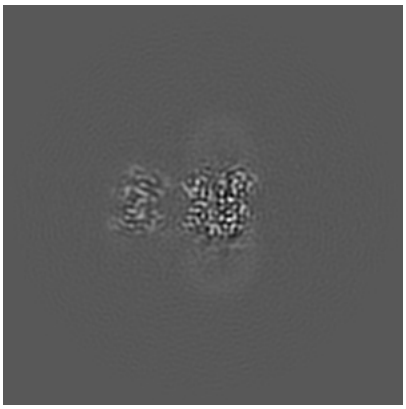
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

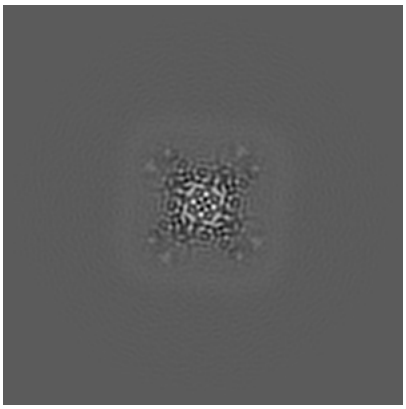
6.3.1 Primary map



X Index: 150

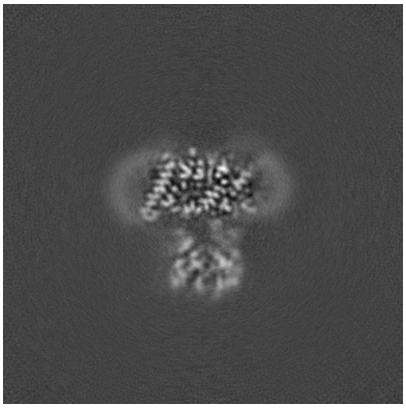


Y Index: 150

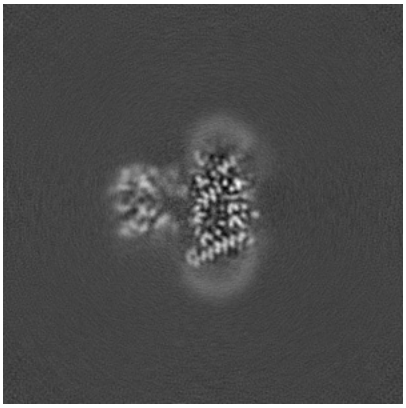


Z Index: 185

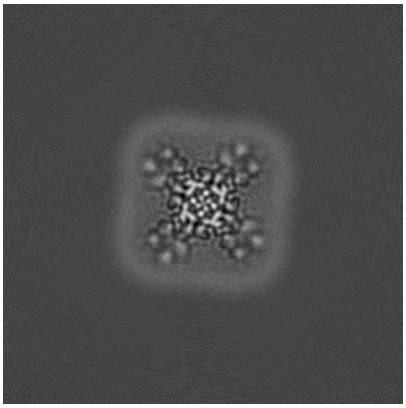
6.3.2 Raw map



X Index: 181



Y Index: 139

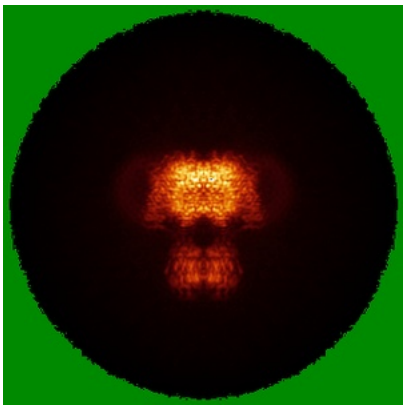


Z Index: 185

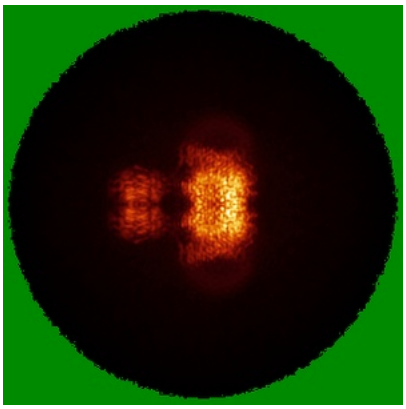
The images above show the largest variance slices of the map in three orthogonal directions.

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

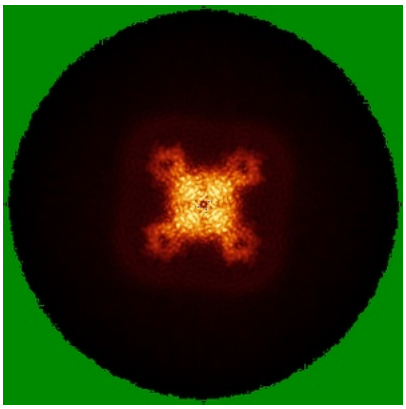
6.4.1 Primary map



X

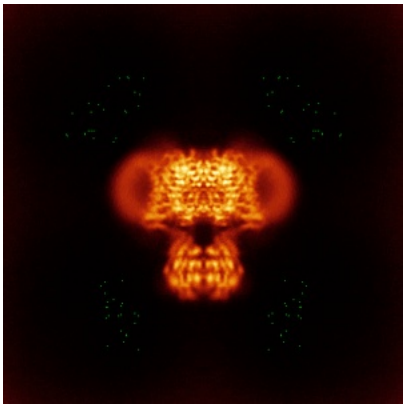


Y

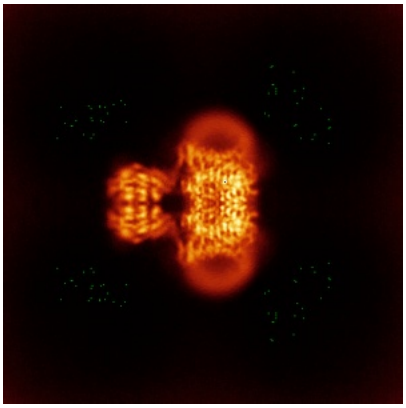


Z

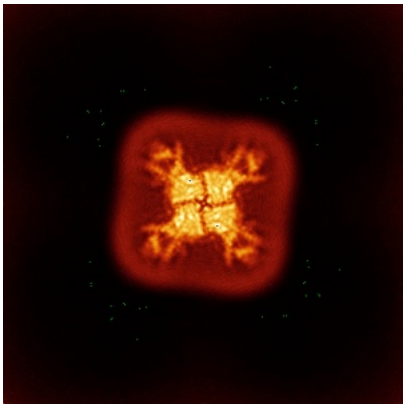
6.4.2 Raw map



X



Y

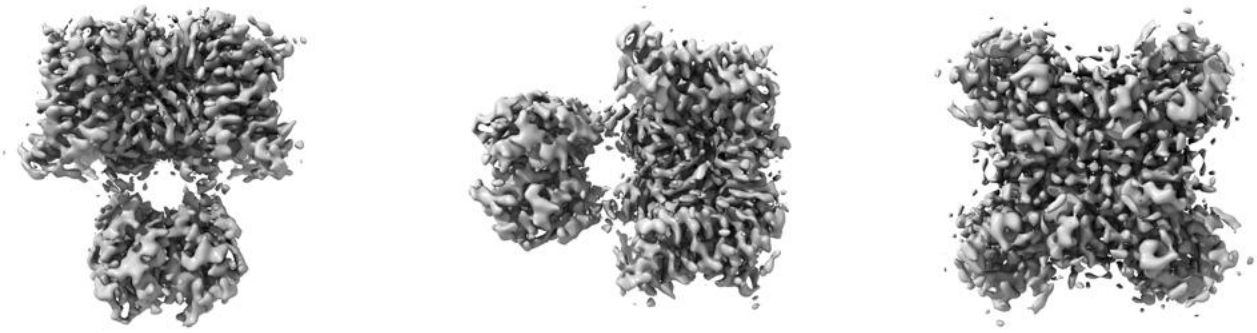


Z

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)

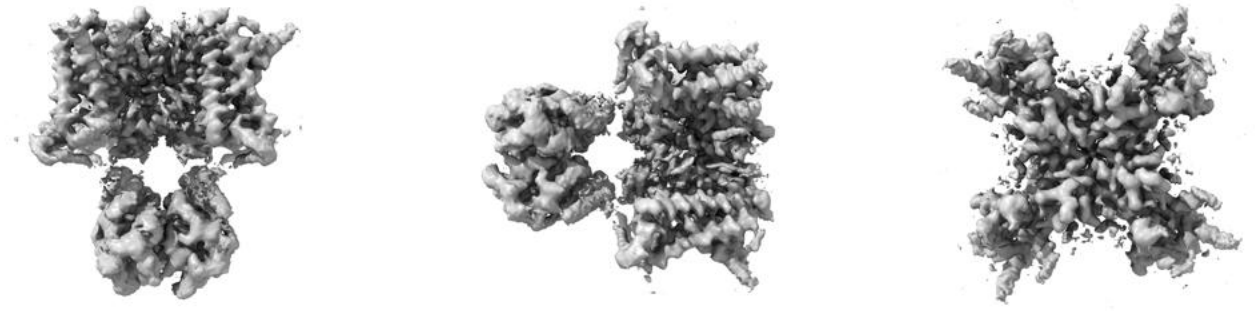
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

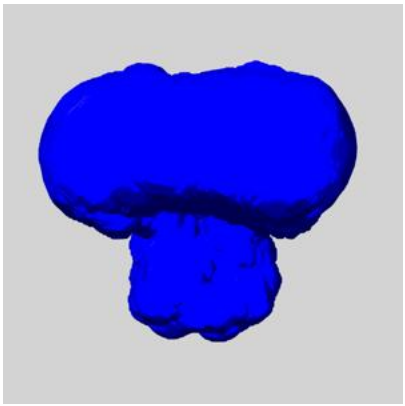
6.6 Mask visualisation (i)

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

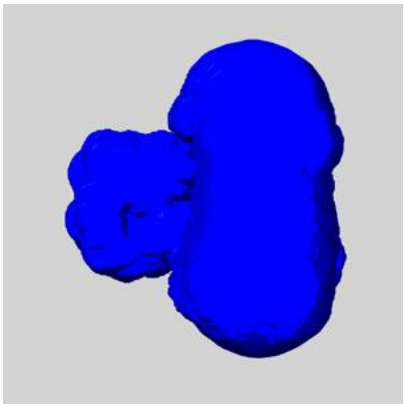
A mask typically either:

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

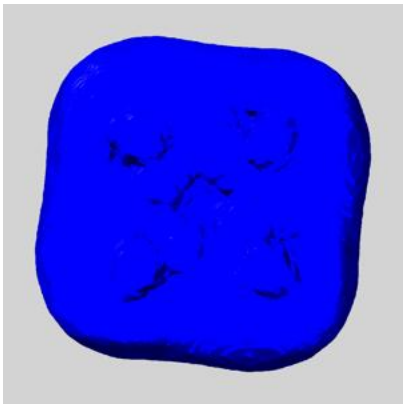
6.6.1 emd_47955_msk_1.map (i)



X



Y

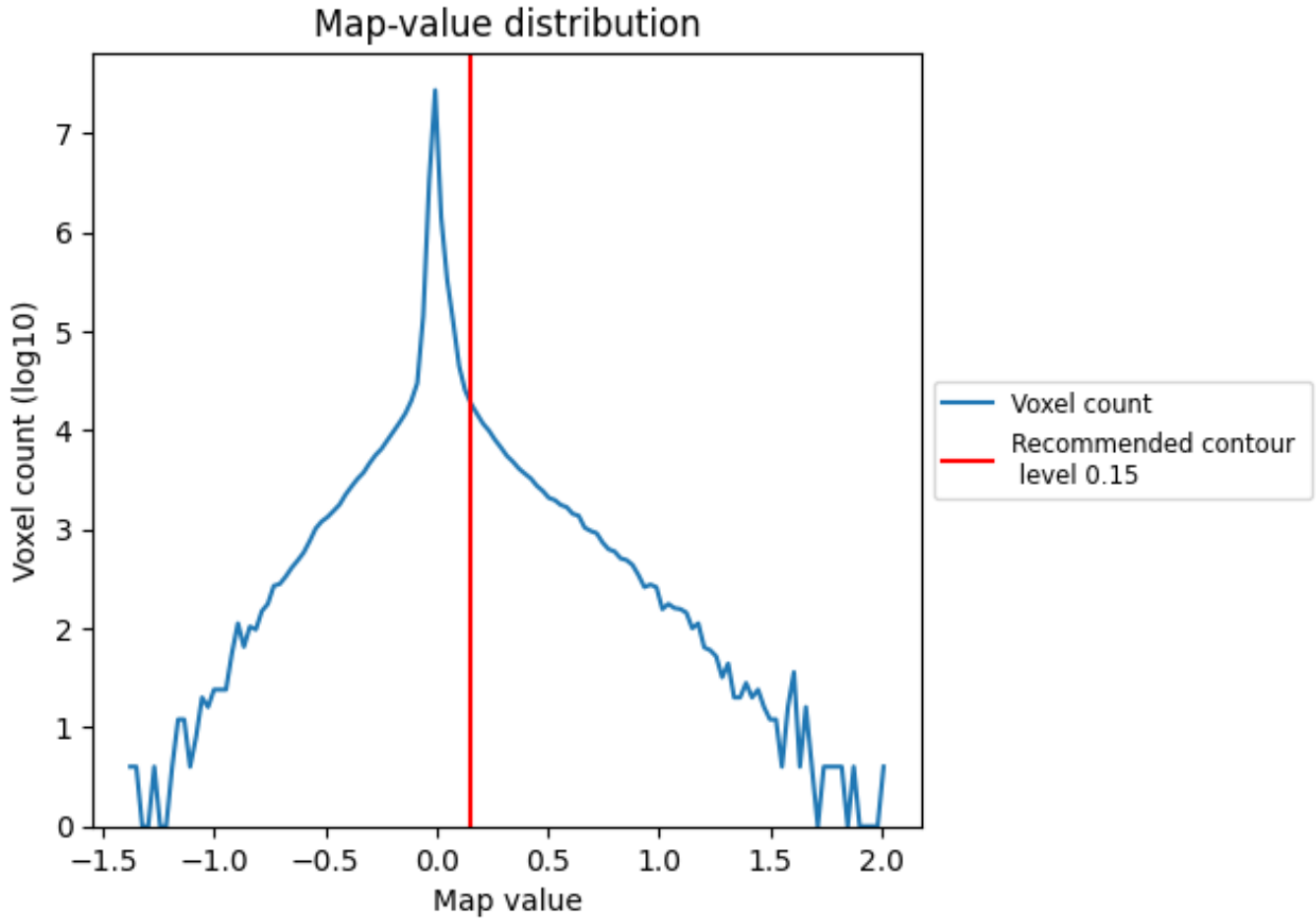


Z

7 Map analysis

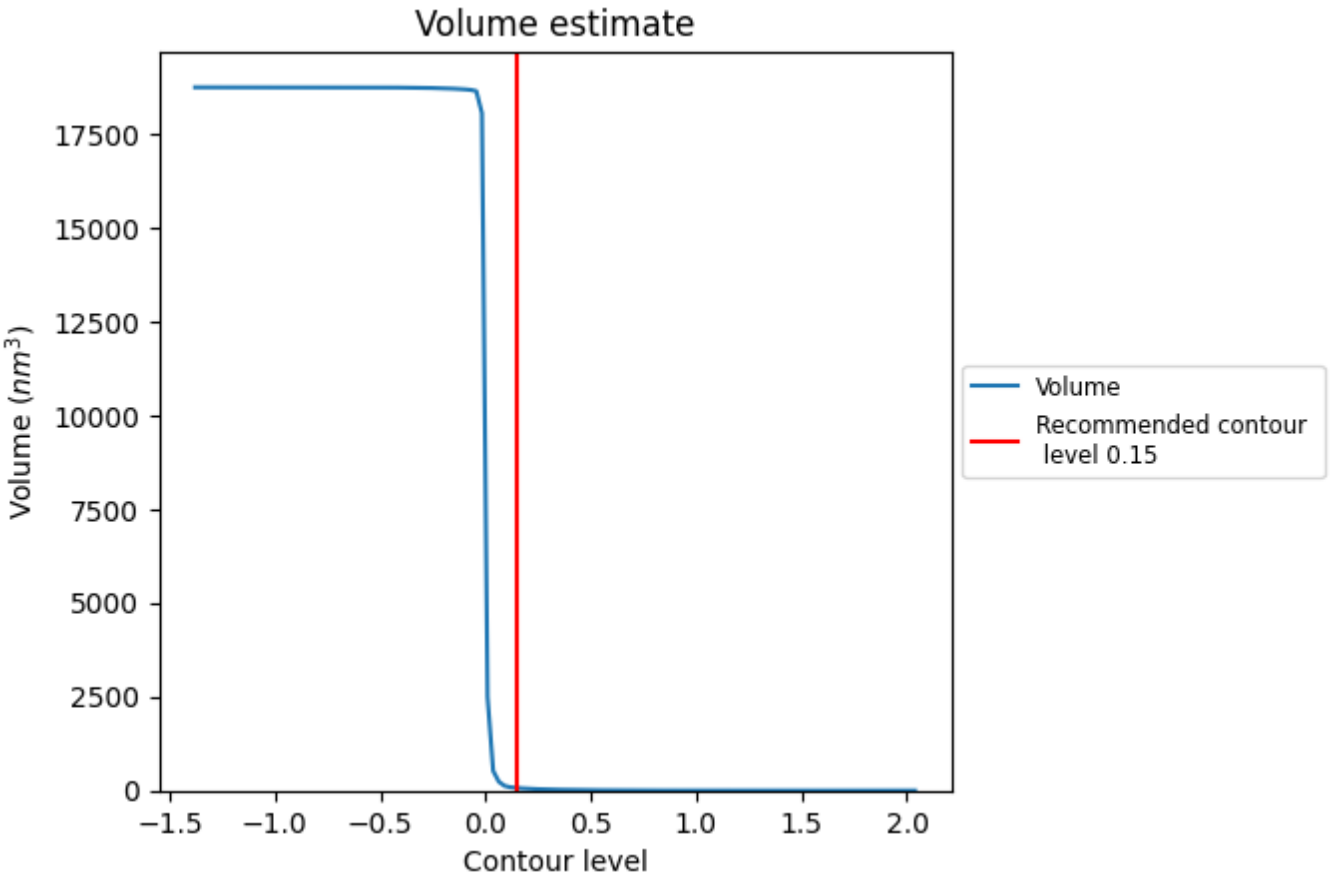
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

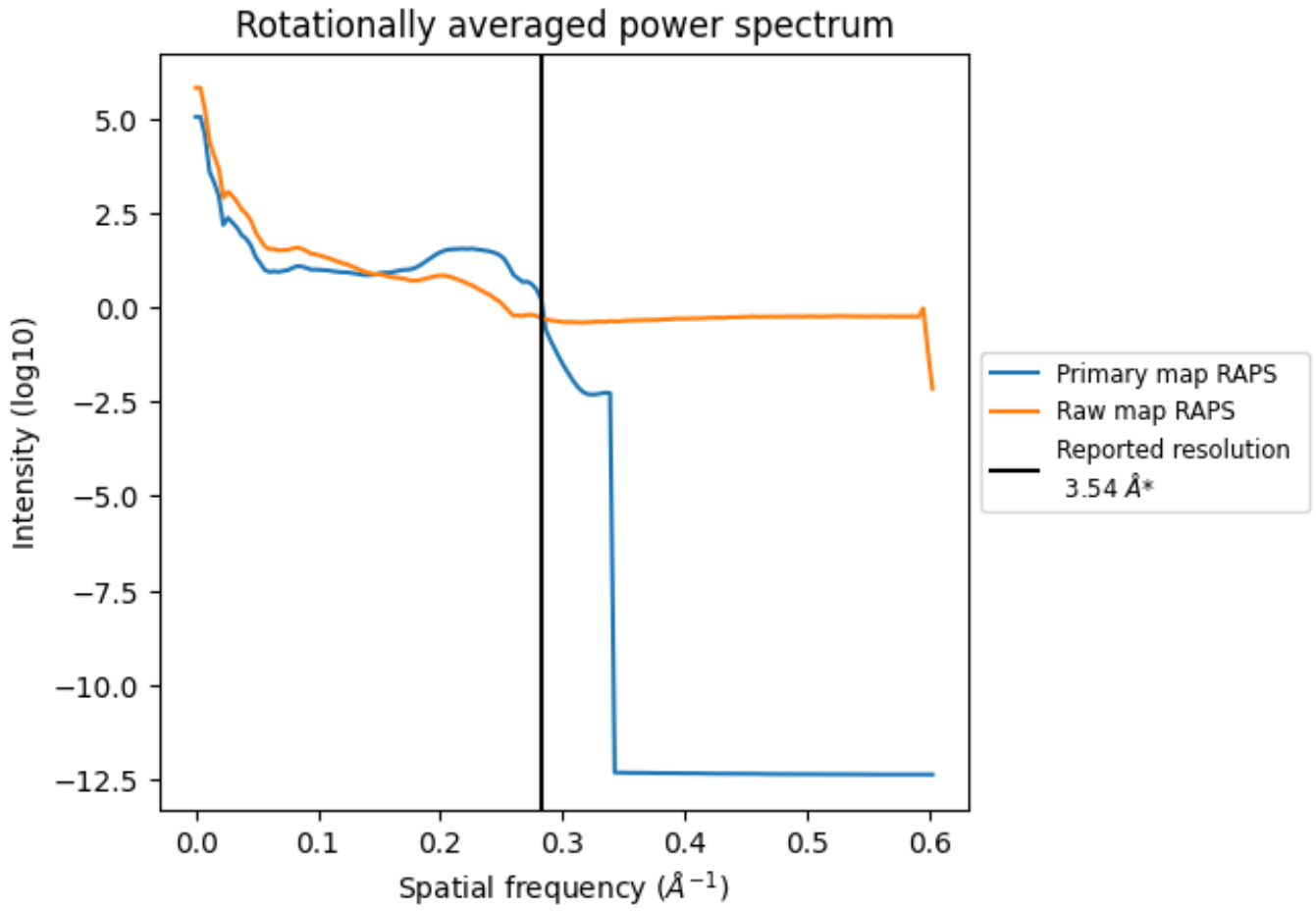
7.2 Volume estimate



The volume at the recommended contour level is 68 nm^3; this corresponds to an approximate mass of 62 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)

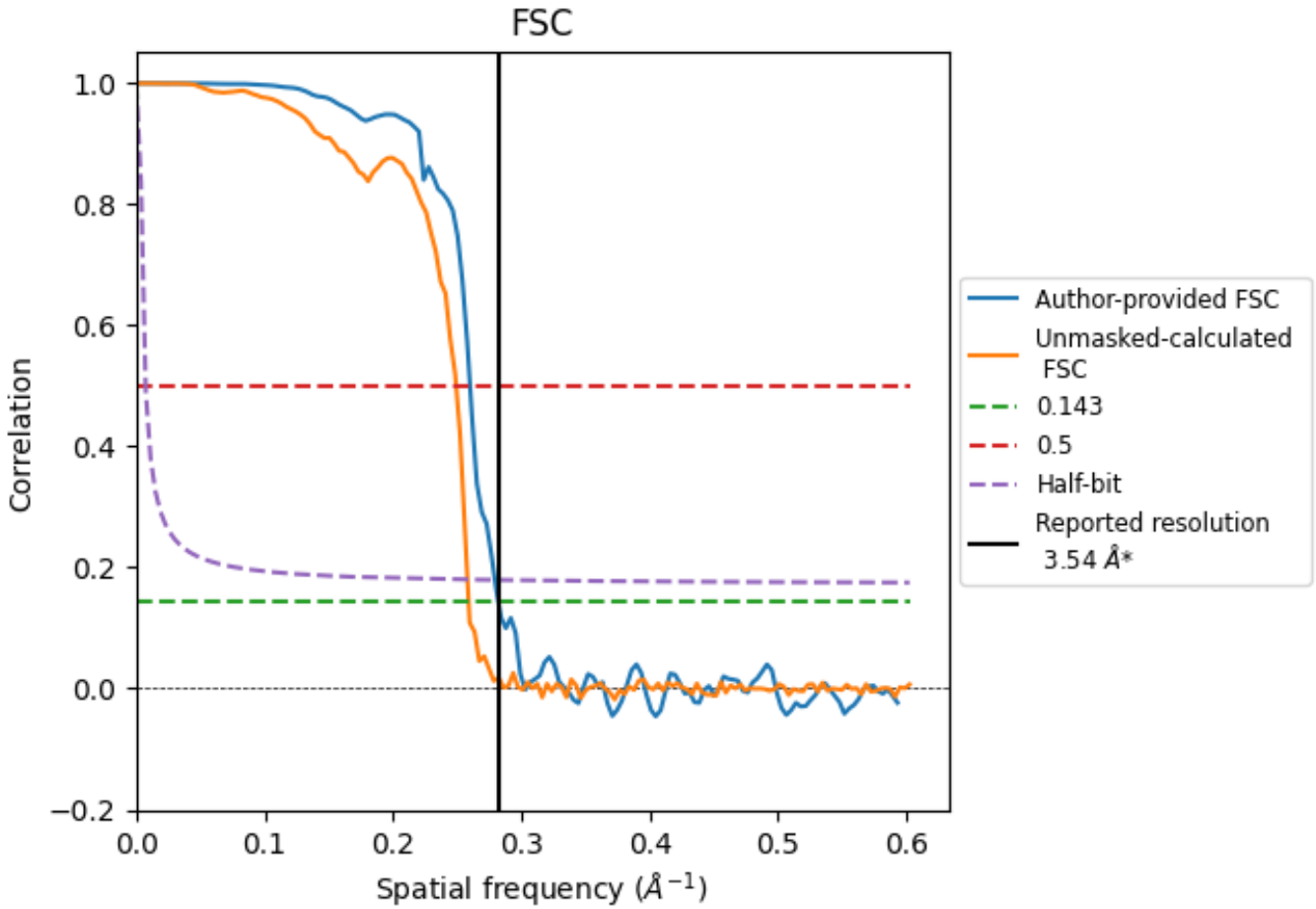


*Reported resolution corresponds to spatial frequency of 0.282 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.282 $Å^{-1}$

8.2 Resolution estimates (i)

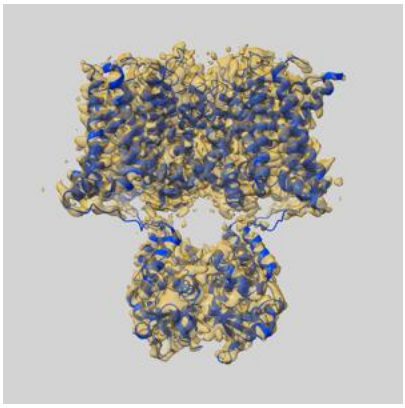
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	3.54	3.84	3.58
Unmasked-calculated*	3.86	4.01	3.87

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

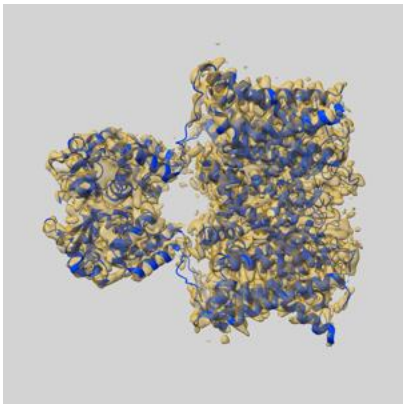
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-47955 and PDB model 9EEF. Per-residue inclusion information can be found in section 3 on page 9.

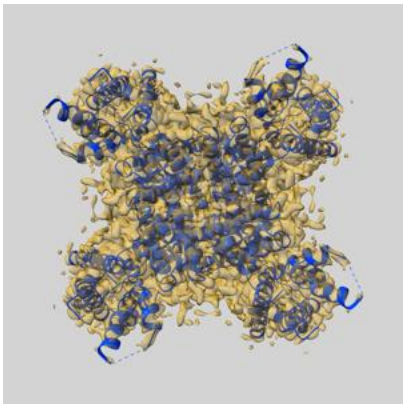
9.1 Map-model overlay



X



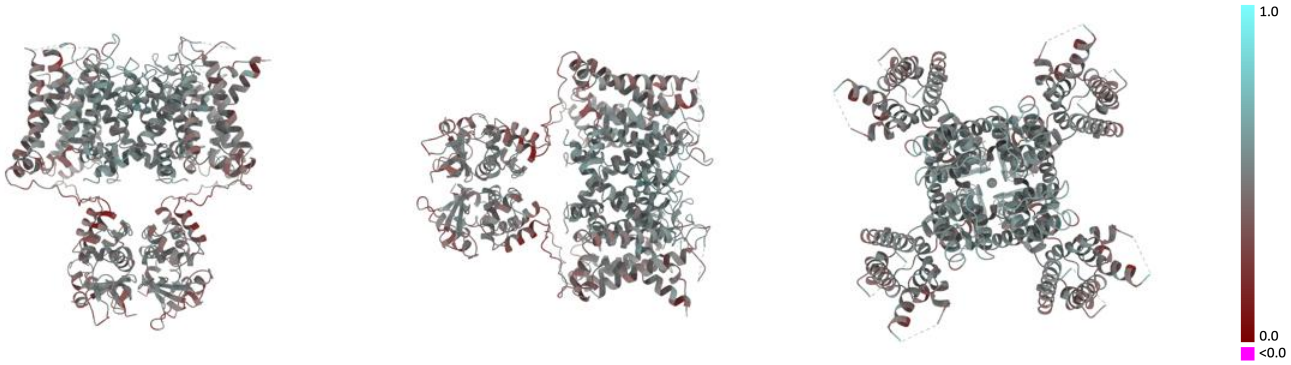
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.15 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.

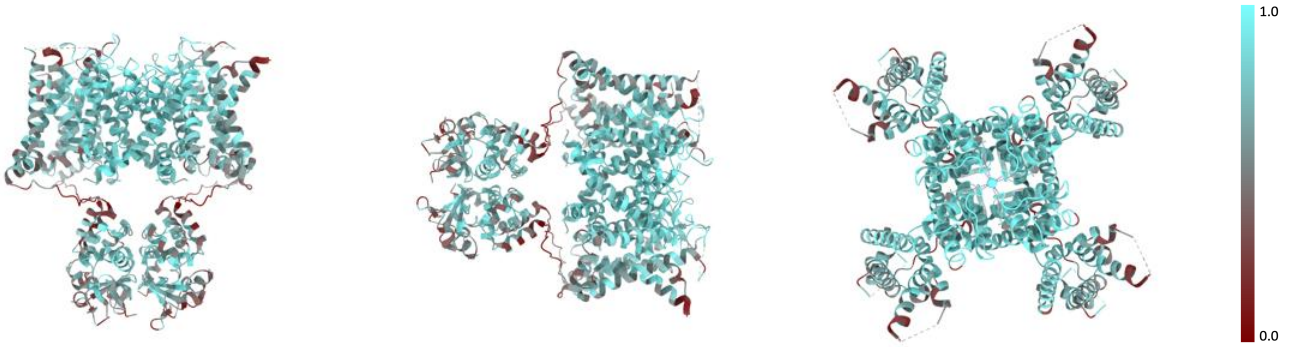
9.2 Q-score mapped to coordinate model (i)



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.

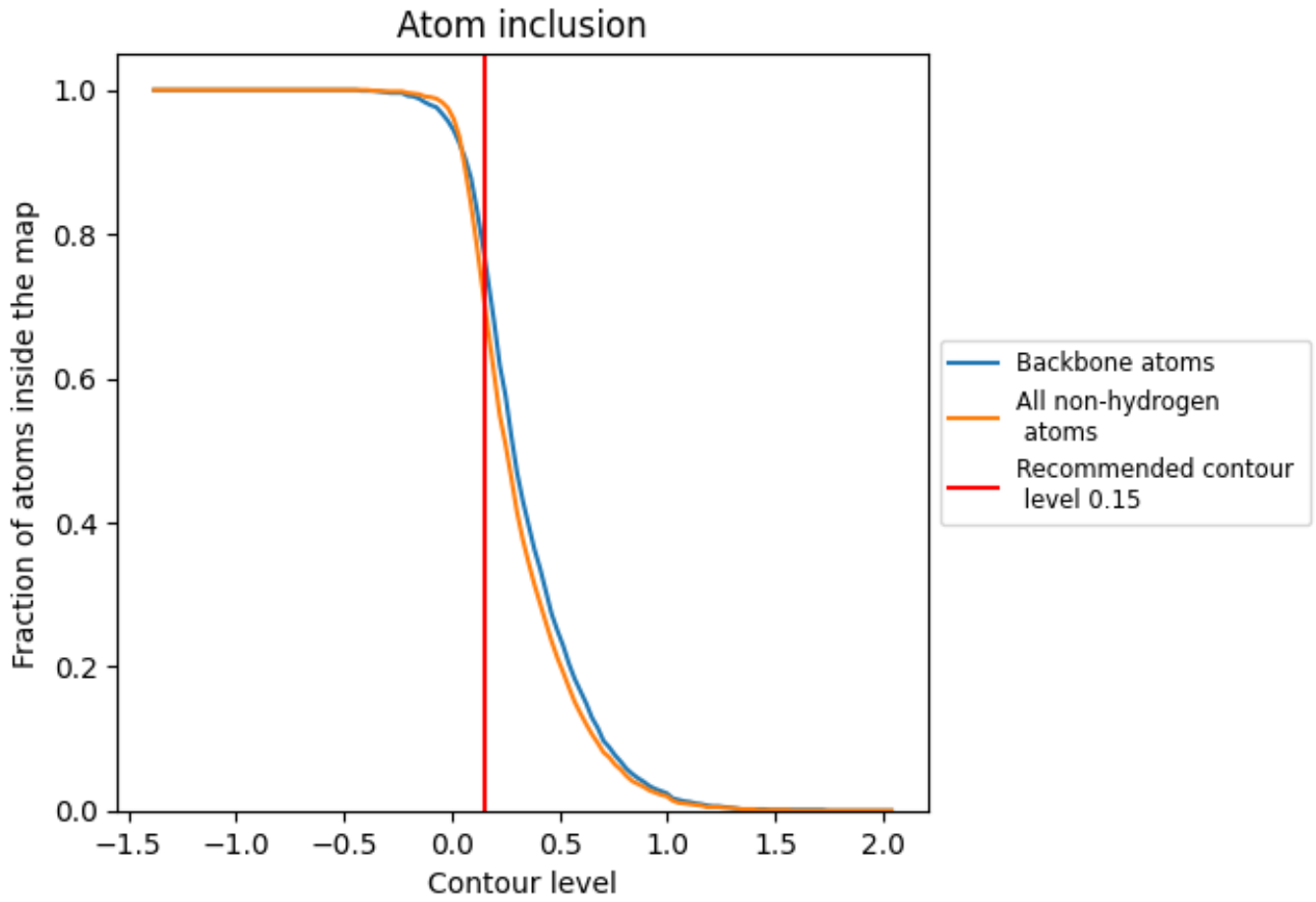
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.15).

9.4 Atom inclusion (i)



At the recommended contour level, 77% of all backbone atoms, 71% 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 (0.15) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.7080	0.4660
A	0.7100	0.4680
B	0.7080	0.4650
C	0.7080	0.4660
D	0.7070	0.4660