



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 01:29 PM UTC

PDB ID : 7W6S / pdb_00007w6s
EMDB ID : EMD-32334
Title : CryoEM structure of human KChIP2-Kv4.3 complex
Authors : Ma, D.M.; Guo, J.T.
Deposited on : 2021-12-02
Resolution : 2.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

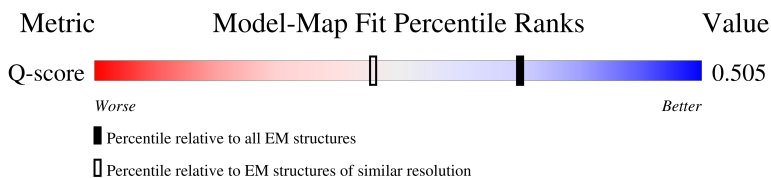
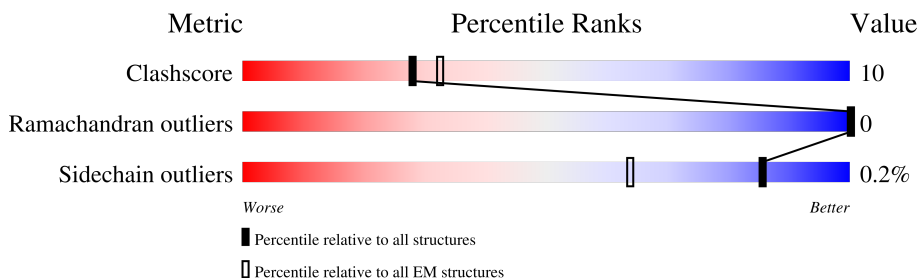
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.



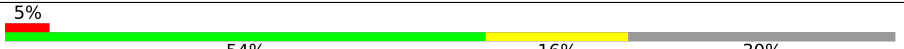
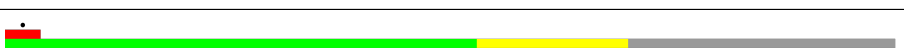
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11806 (2.30 - 3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	286	 5% 44% 18% 37%
1	C	286	 5% 44% 19% 37%
1	E	286	 5% 46% 16% 37%
1	G	286	 5% 46% 16% 37%

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Mol	Chain	Length	Quality of chain
2	B	636	 55% 16% 30%
2	D	636	 55% 16% 30%
2	F	636	 54% 16% 30%
2	H	636	 53% 17% 30%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 20268 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 Kv channel-interacting protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	179	Total	C	N	O	S	0	0
			1465	926	240	289	10		
1	C	179	Total	C	N	O	S	0	0
			1465	926	240	289	10		
1	E	179	Total	C	N	O	S	0	0
			1465	926	240	289	10		
1	G	179	Total	C	N	O	S	0	0
			1465	926	240	289	10		

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	271	LEU	-	expression tag	UNP Q9NS61
A	272	GLU	-	expression tag	UNP Q9NS61
A	273	GLY	-	expression tag	UNP Q9NS61
A	274	GLY	-	expression tag	UNP Q9NS61
A	275	SER	-	expression tag	UNP Q9NS61
A	276	SER	-	expression tag	UNP Q9NS61
A	277	GLY	-	expression tag	UNP Q9NS61
A	278	GLY	-	expression tag	UNP Q9NS61
A	279	HIS	-	expression tag	UNP Q9NS61
A	280	HIS	-	expression tag	UNP Q9NS61
A	281	HIS	-	expression tag	UNP Q9NS61
A	282	HIS	-	expression tag	UNP Q9NS61
A	283	HIS	-	expression tag	UNP Q9NS61
A	284	HIS	-	expression tag	UNP Q9NS61
A	285	HIS	-	expression tag	UNP Q9NS61
A	286	HIS	-	expression tag	UNP Q9NS61
C	271	LEU	-	expression tag	UNP Q9NS61
C	272	GLU	-	expression tag	UNP Q9NS61
C	273	GLY	-	expression tag	UNP Q9NS61
C	274	GLY	-	expression tag	UNP Q9NS61
C	275	SER	-	expression tag	UNP Q9NS61
C	276	SER	-	expression tag	UNP Q9NS61

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Chain	Residue	Modelled	Actual	Comment	Reference
C	277	GLY	-	expression tag	UNP Q9NS61
C	278	GLY	-	expression tag	UNP Q9NS61
C	279	HIS	-	expression tag	UNP Q9NS61
C	280	HIS	-	expression tag	UNP Q9NS61
C	281	HIS	-	expression tag	UNP Q9NS61
C	282	HIS	-	expression tag	UNP Q9NS61
C	283	HIS	-	expression tag	UNP Q9NS61
C	284	HIS	-	expression tag	UNP Q9NS61
C	285	HIS	-	expression tag	UNP Q9NS61
C	286	HIS	-	expression tag	UNP Q9NS61
E	271	LEU	-	expression tag	UNP Q9NS61
E	272	GLU	-	expression tag	UNP Q9NS61
E	273	GLY	-	expression tag	UNP Q9NS61
E	274	GLY	-	expression tag	UNP Q9NS61
E	275	SER	-	expression tag	UNP Q9NS61
E	276	SER	-	expression tag	UNP Q9NS61
E	277	GLY	-	expression tag	UNP Q9NS61
E	278	GLY	-	expression tag	UNP Q9NS61
E	279	HIS	-	expression tag	UNP Q9NS61
E	280	HIS	-	expression tag	UNP Q9NS61
E	281	HIS	-	expression tag	UNP Q9NS61
E	282	HIS	-	expression tag	UNP Q9NS61
E	283	HIS	-	expression tag	UNP Q9NS61
E	284	HIS	-	expression tag	UNP Q9NS61
E	285	HIS	-	expression tag	UNP Q9NS61
E	286	HIS	-	expression tag	UNP Q9NS61
G	271	LEU	-	expression tag	UNP Q9NS61
G	272	GLU	-	expression tag	UNP Q9NS61
G	273	GLY	-	expression tag	UNP Q9NS61
G	274	GLY	-	expression tag	UNP Q9NS61
G	275	SER	-	expression tag	UNP Q9NS61
G	276	SER	-	expression tag	UNP Q9NS61
G	277	GLY	-	expression tag	UNP Q9NS61
G	278	GLY	-	expression tag	UNP Q9NS61
G	279	HIS	-	expression tag	UNP Q9NS61
G	280	HIS	-	expression tag	UNP Q9NS61
G	281	HIS	-	expression tag	UNP Q9NS61
G	282	HIS	-	expression tag	UNP Q9NS61
G	283	HIS	-	expression tag	UNP Q9NS61
G	284	HIS	-	expression tag	UNP Q9NS61
G	285	HIS	-	expression tag	UNP Q9NS61
G	286	HIS	-	expression tag	UNP Q9NS61

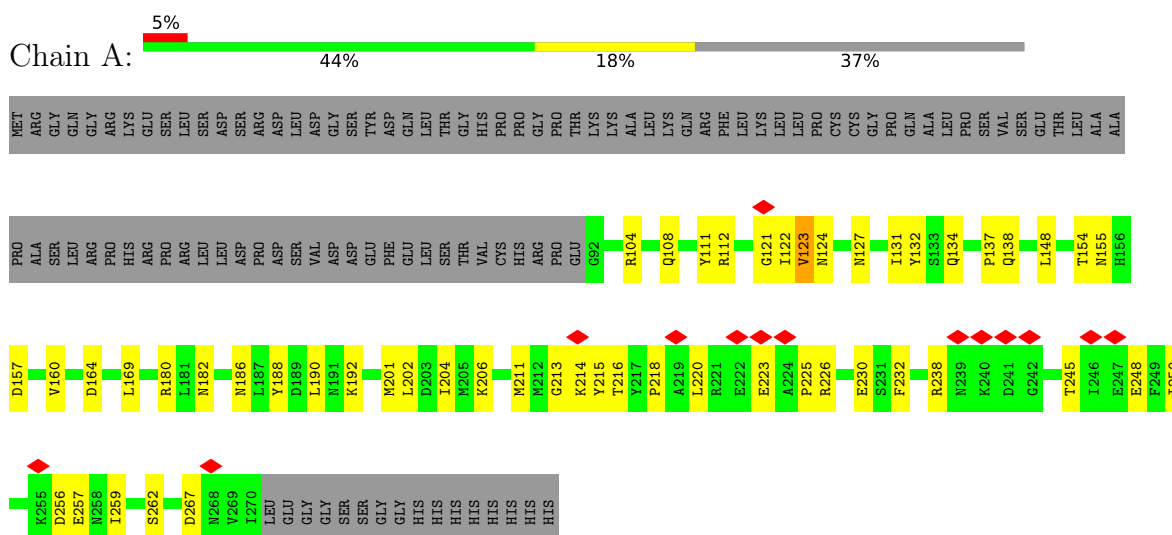
- Molecule 2 is a protein called Isoform 2 of Potassium voltage-gated channel subfamily D member 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	448	Total	C	N	O	S	0	0
			3602	2334	612	632	24		
2	D	448	Total	C	N	O	S	0	0
			3602	2334	612	632	24		
2	F	448	Total	C	N	O	S	0	0
			3602	2334	612	632	24		
2	H	448	Total	C	N	O	S	0	0
			3602	2334	612	632	24		

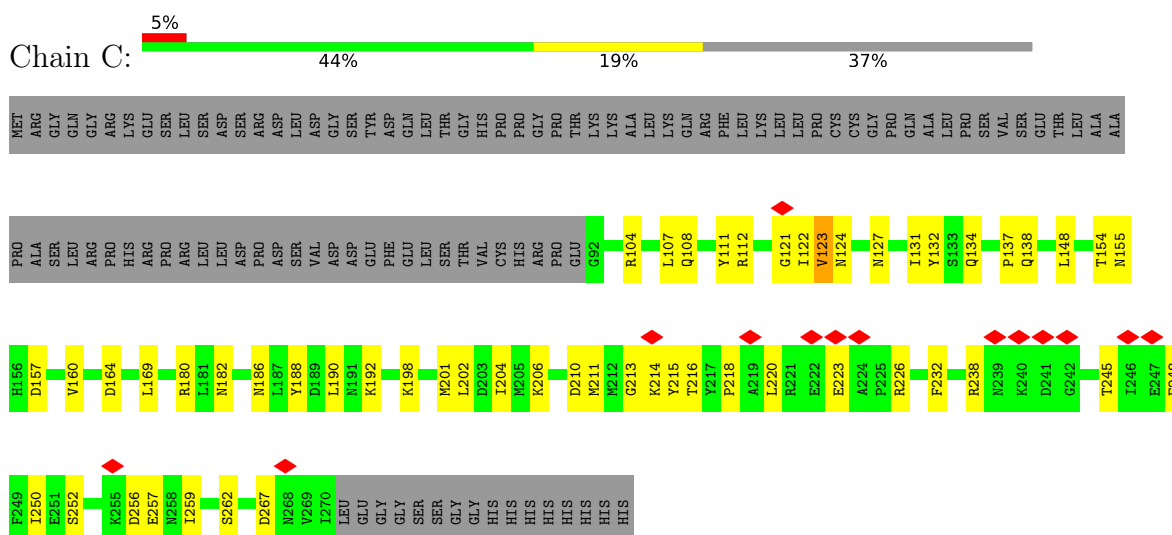
3 Residue-property plots

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: Kv channel-interacting protein 2

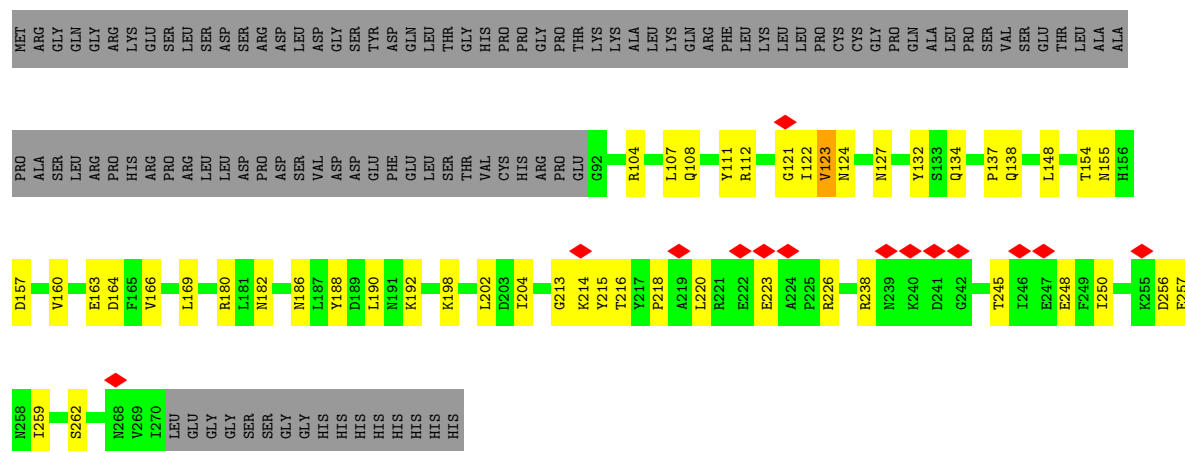


• Molecule 1: Kv channel-interacting protein 2

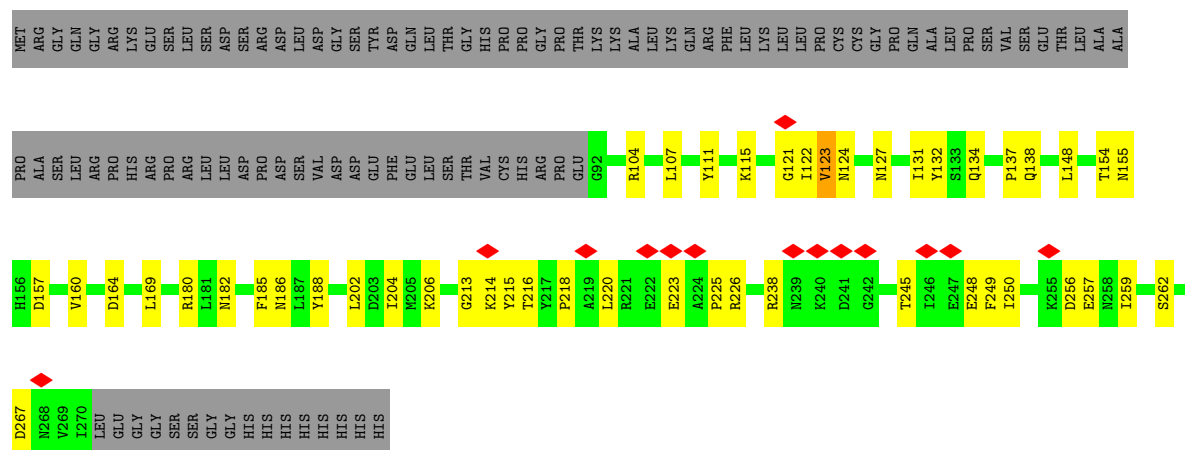


• Molecule 1: Kv channel-interacting protein 2

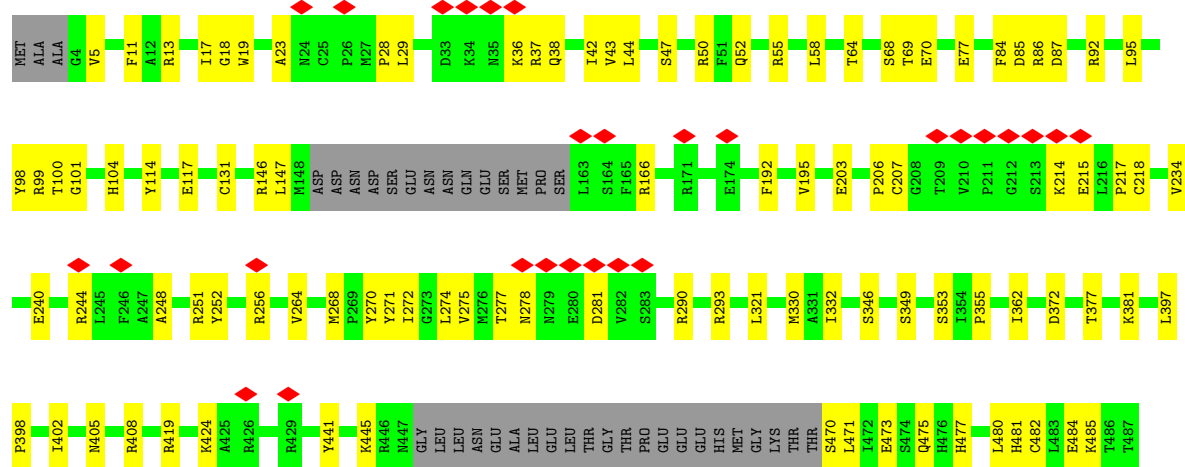




• Molecule 1: Kv channel-interacting protein 2



• Molecule 2: Isoform 2 of Potassium voltage-gated channel subfamily D member 3



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

- Molecule 2: Isoform 2 of Potassium voltage-gated channel subfamily D member 3

Chain D: 

MET	ALA	ALA	G4	V5	F11	A12	R13	I17	G18	W19	A23	N24	C25	P26	M27	L29	D33	K34	N35	K36	R37	Q38	I42	V43	L44	S47	R50	F51	Q52	R55	L58	S68	T69	E70	E77	F84	D85	R86	D87	R92	L95	R99	T100				
G101	K102	L103	E117	I128	C131	R146	L147	M148	ASP	ASP	ASN	ASP	C25	SER	GLU	ASN	GLN	SER	MET	PRO	SER	L163	S164	F165	R166	R171	E174	T180	F192	V195	E203	P206	C207	G208	T209	V210	P211	G212	S213	K214	E215	L216	P217	C218	V234		
F237	E240	R244	L245	F246	R251	Y252	R256	A266	I267	M268	P269	Y270	Y271	I272	G273	L274	V275	M276	T277	N278	N279	E280	F281	V282	S283	R290	R293	R296	I297	F298	S301	L307	T332	S346	S349	S353	I354	P355	I362	D372	T377						
K381	L397	P398	M405	R408	K424	A425	R426	L427	A428	R429	T430	R431	Y441	K445	R446	M447	GLY	LEU	LEU	ASN	GLU	ALA	LEU	LEU	LEU	GLY	THR	PRO	GLU	GLU	HIS	MET	GLY	LYS	THR	S470	L471	T472	S474	Q475	H476	H477	L480	H481	E484	K485	T486
T487	ASN	HIS	GLU	PHE	ILE	ASP	GLU	GLN	MET	THR	GLY	GLN	ASN	CYS	MET	GLU	GLN	SER	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
ARG	LEU	ARG	SER	MET	GLN	GLU	LEU	SER	THR	THR	GLY	GLN	ILE	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
GLY	GLU	SER	ARG	PRO	PRO	ALA	SER	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	

- Molecule 2: Isoform 2 of Potassium voltage-gated channel subfamily D member 3

Chain F: 

MET	ALA	ALA	G4	V5	F11	A12	R13	I17	G18	N24	C25	P26	M27	L29	D33	K34	N35	K36	R37	Q38	I42	V43	L44	R50	F51	Q52	R55	L58	L65	S68	T69	E70	E77	F84	D85	R86	D87	R92	R99	T100	G101	R102	L103	H104		
Y114	E117	G4	I128	C131	R146	L147	M148	ASP	ASP	ASN	ASP	ASN	SER	GLU	ASN	ASN	GLN	GLU	MET	PRO	SER	L163	S164	F165	R166	R171	E174	T180	F192	V195	E203	P206	C207	G208	T209	V210	P211	G212	S213	K214	E215	L216	P217	C218	V234	T237
E240	R244	L245	F246	A247	P249	S250	R251	Y252	R253	R256	D263	A266	I267	Y270	Y271	I272	G273	L274	V275	M276	T277	N278	N279	E280	V282	S283	R290	R293	R296	L307	L321	M330	A331	I332	S346	S349	S353	I354	P355	I362						

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	240437	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64	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	0.092	Depositor
Minimum map value	-0.053	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0109	Depositor
Map size (Å)	273.78003, 273.78003, 273.78003	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.014, 1.014, 1.014	Depositor

5 Model quality

5.1 Standard geometry

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	0.22	0/1494	0.45	0/2009
1	C	0.21	0/1494	0.44	0/2009
1	E	0.21	0/1494	0.44	0/2009
1	G	0.21	0/1494	0.45	0/2009
2	B	0.25	0/3692	0.40	0/4998
2	D	0.24	0/3692	0.40	0/4998
2	F	0.24	0/3692	0.40	0/4998
2	H	0.25	0/3692	0.40	0/4998
All	All	0.24	0/20744	0.41	0/28028

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	1
1	C	0	1
1	E	0	1
1	G	0	1
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	121	GLY	Peptide
1	C	121	GLY	Peptide
1	E	121	GLY	Peptide
1	G	121	GLY	Peptide

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	1465	0	1390	39	0
1	C	1465	0	1390	40	0
1	E	1465	0	1390	34	0
1	G	1465	0	1390	36	0
2	B	3602	0	3615	73	0
2	D	3602	0	3615	73	0
2	F	3602	0	3615	76	0
2	H	3602	0	3615	79	0
All	All	20268	0	20020	387	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 10.

The worst 5 of 387 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)
2:F:166:ARG:HH12	2:F:251:ARG:HH21	1.33	0.76
2:H:166:ARG:HH12	2:H:251:ARG:HH21	1.32	0.76
1:A:104:ARG:NH1	2:H:77:GLU:OE1	2.20	0.75
2:B:166:ARG:HH12	2:B:251:ARG:HH21	1.32	0.75
2:D:166:ARG:HH12	2:D:251:ARG:HH21	1.32	0.75

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	177/286 (62%)	163 (92%)	14 (8%)	0	100	100
1	C	177/286 (62%)	164 (93%)	13 (7%)	0	100	100
1	E	177/286 (62%)	163 (92%)	14 (8%)	0	100	100
1	G	177/286 (62%)	164 (93%)	13 (7%)	0	100	100
2	B	442/636 (70%)	416 (94%)	26 (6%)	0	100	100
2	D	442/636 (70%)	417 (94%)	25 (6%)	0	100	100
2	F	442/636 (70%)	416 (94%)	26 (6%)	0	100	100
2	H	442/636 (70%)	417 (94%)	25 (6%)	0	100	100
All	All	2476/3688 (67%)	2320 (94%)	156 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	162/255 (64%)	161 (99%)	1 (1%)	78	92
1	C	162/255 (64%)	161 (99%)	1 (1%)	78	92
1	E	162/255 (64%)	161 (99%)	1 (1%)	78	92
1	G	162/255 (64%)	161 (99%)	1 (1%)	78	92
2	B	390/560 (70%)	390 (100%)	0	100	100
2	D	390/560 (70%)	390 (100%)	0	100	100
2	F	390/560 (70%)	390 (100%)	0	100	100
2	H	390/560 (70%)	390 (100%)	0	100	100
All	All	2208/3260 (68%)	2204 (100%)	4 (0%)	85	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	123	VAL
1	C	123	VAL

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Mol	Chain	Res	Type
1	E	123	VAL
1	G	123	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	278	ASN
2	H	279	ASN
1	C	254	GLN
1	C	182	ASN
2	H	405	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 oligosaccharides 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.

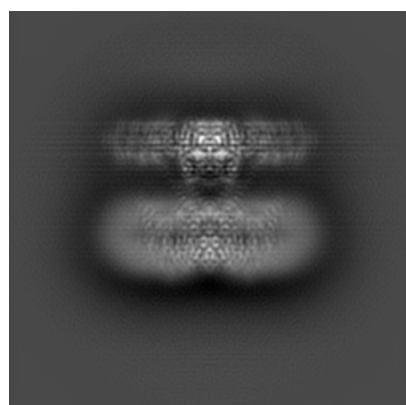
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32334. These allow visual inspection of the internal detail of the map and identification of artifacts.

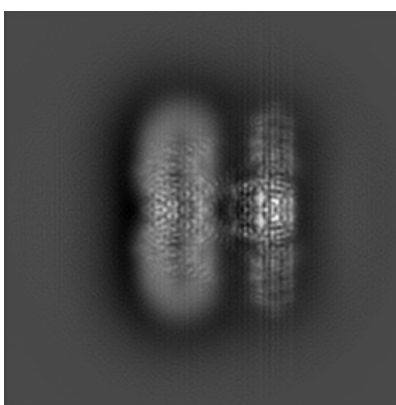
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

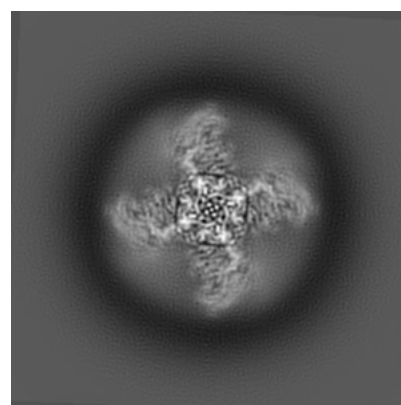
6.1.1 Primary map



X



Y

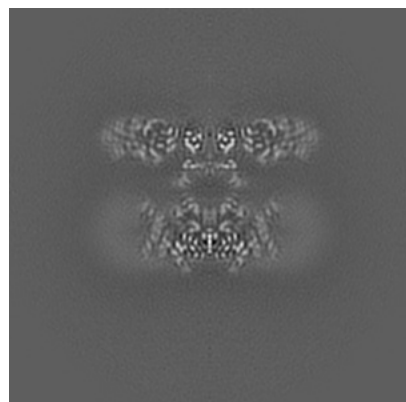


Z

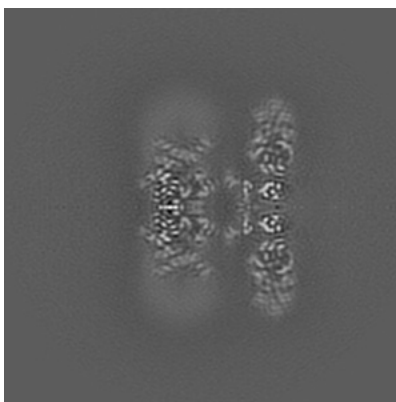
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

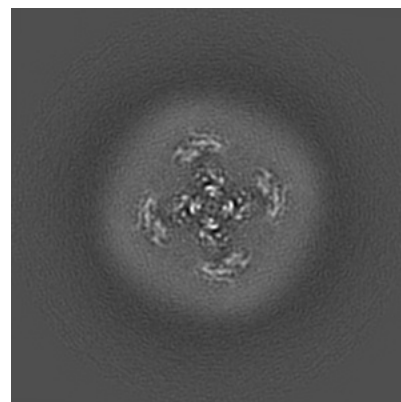
6.2.1 Primary map



X Index: 135



Y Index: 135

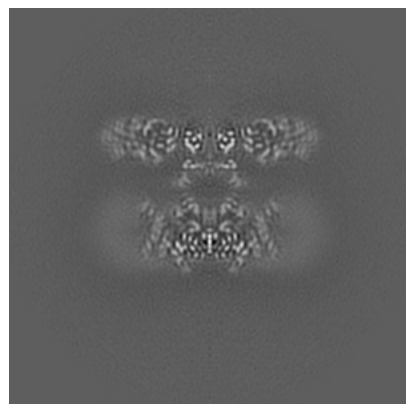


Z Index: 135

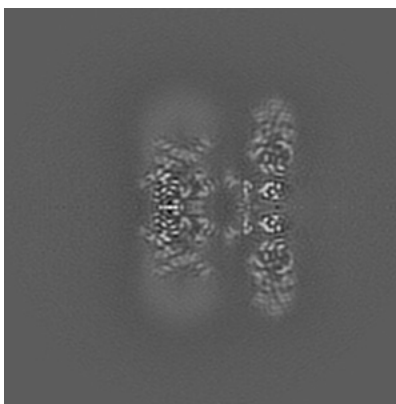
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

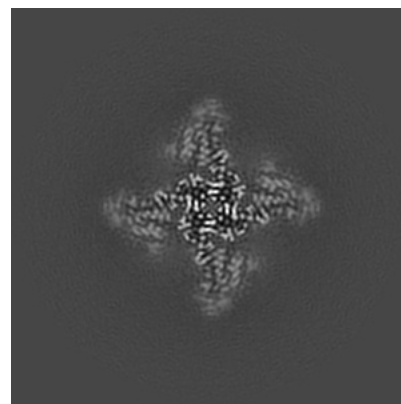
6.3.1 Primary map



X Index: 135



Y Index: 135

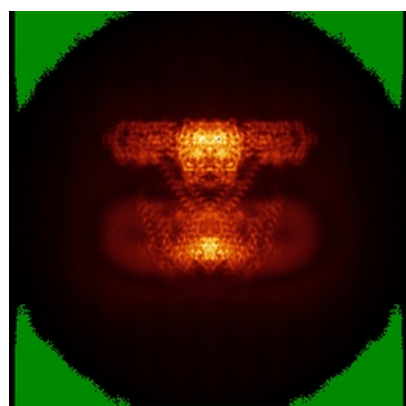


Z Index: 181

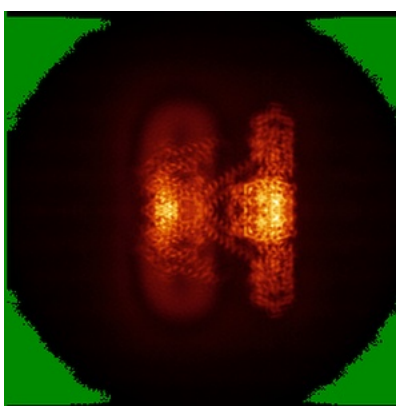
The images above show the largest variance slices of the map in three orthogonal directions.

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

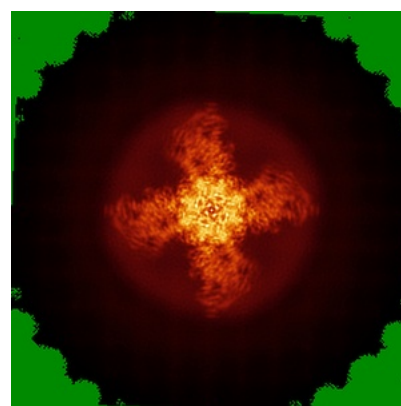
6.4.1 Primary map



X



Y

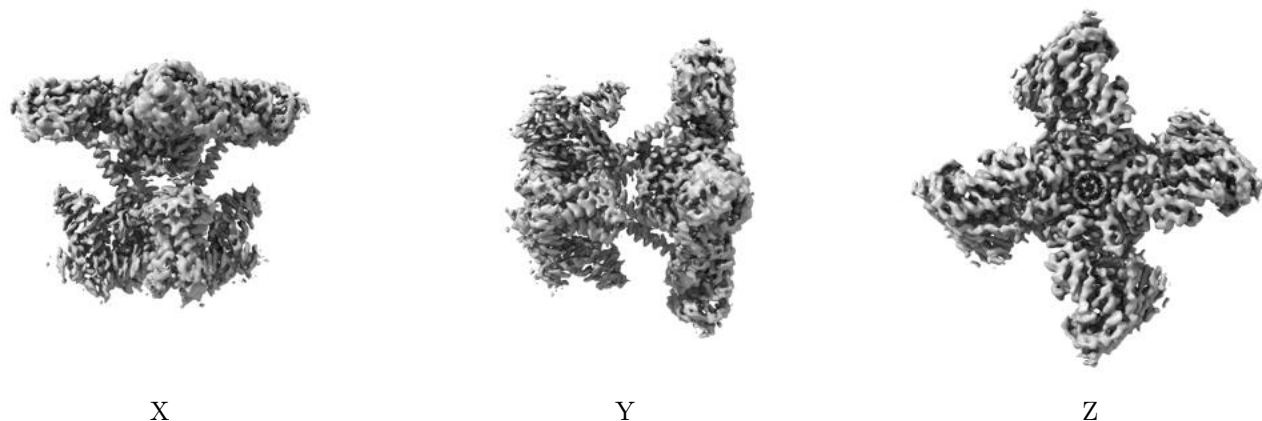


Z

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 0.0109. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

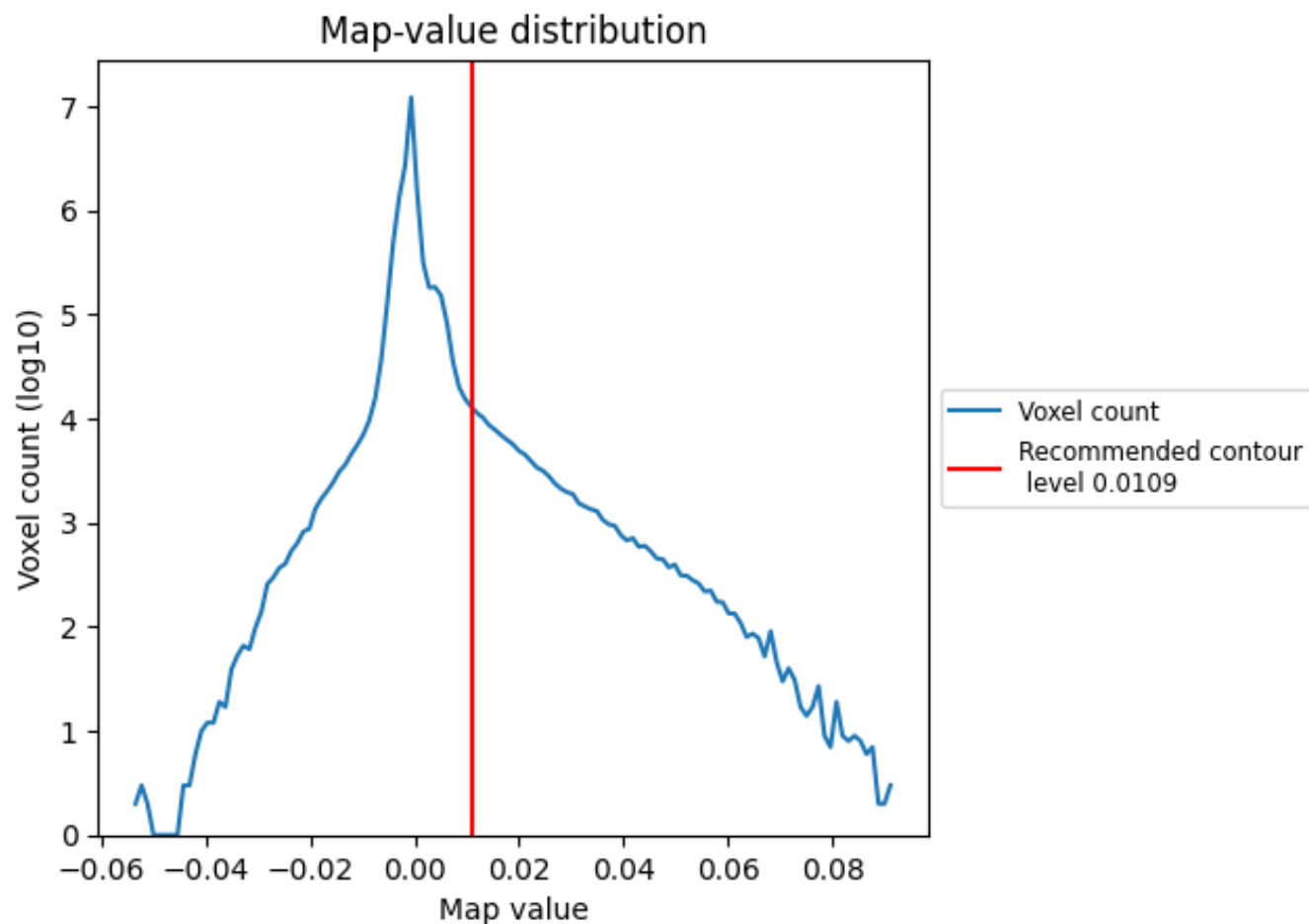
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

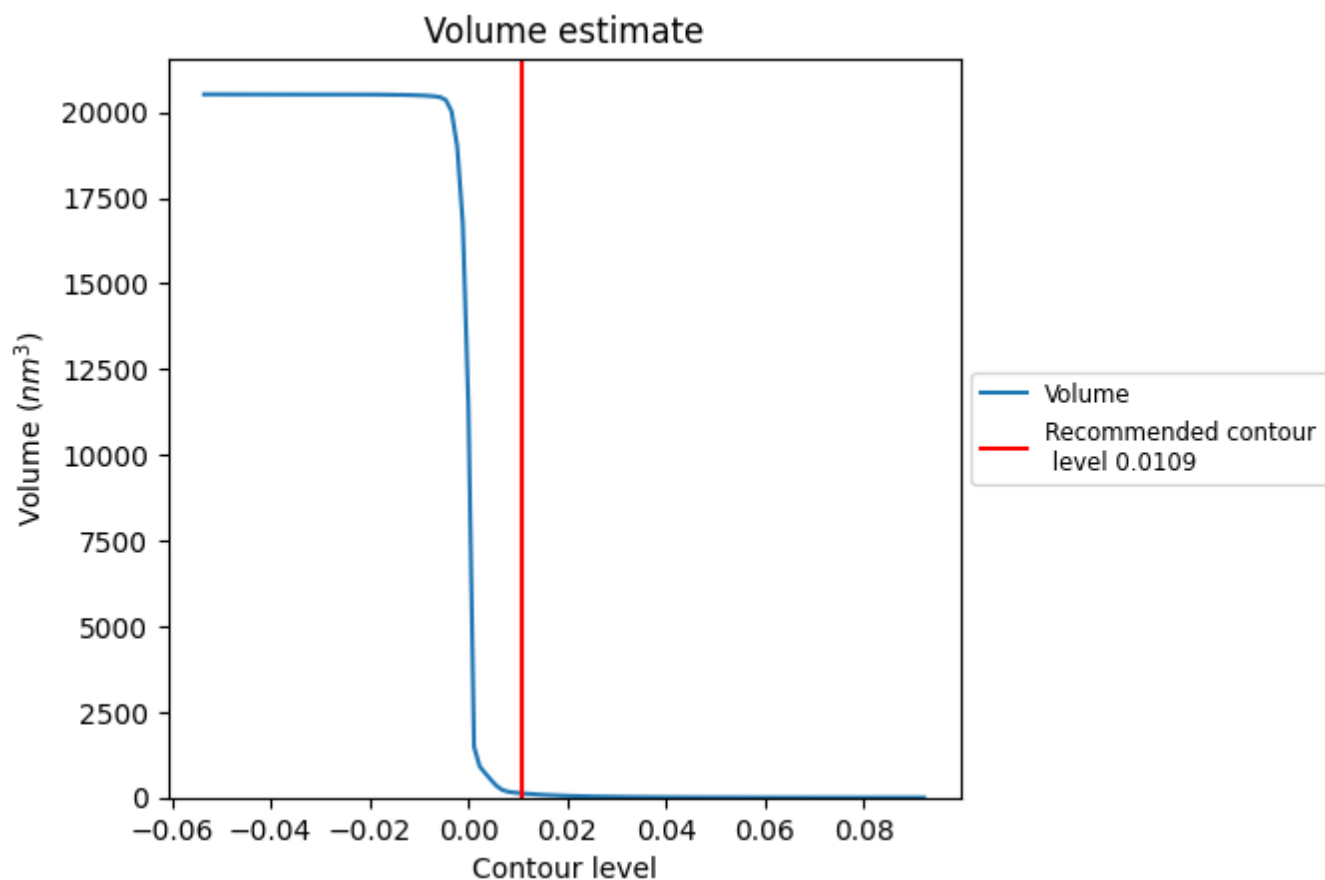
This section contains the results of statistical analysis of the map.

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.

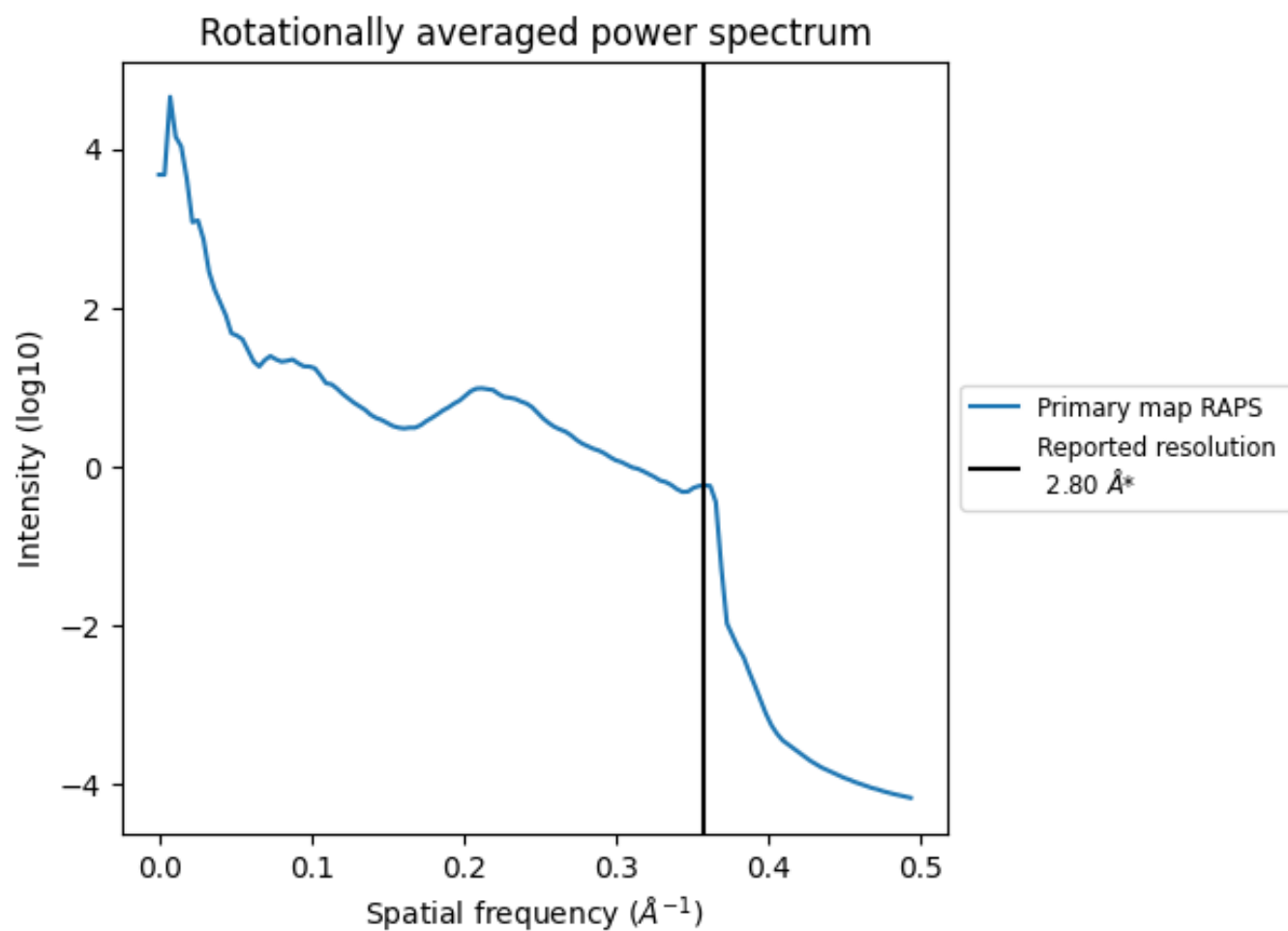
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 123 nm³; this corresponds to an approximate mass of 111 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 0.357 Å⁻¹

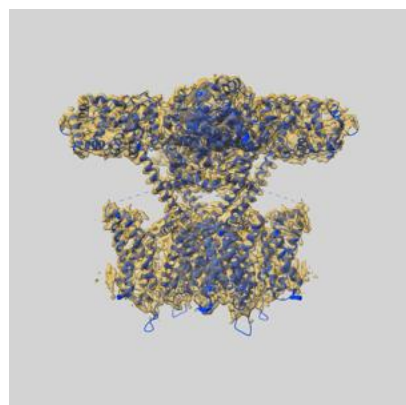
8 Fourier-Shell correlation

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

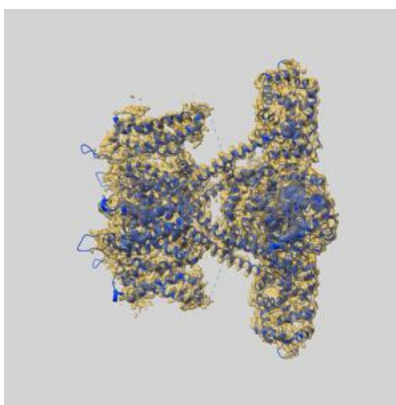
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32334 and PDB model 7W6S. Per-residue inclusion information can be found in section 3 on page 7.

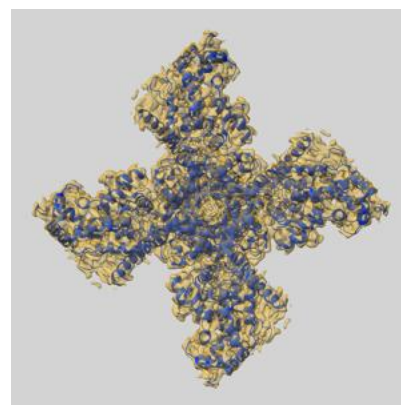
9.1 Map-model overlay [i](#)



X



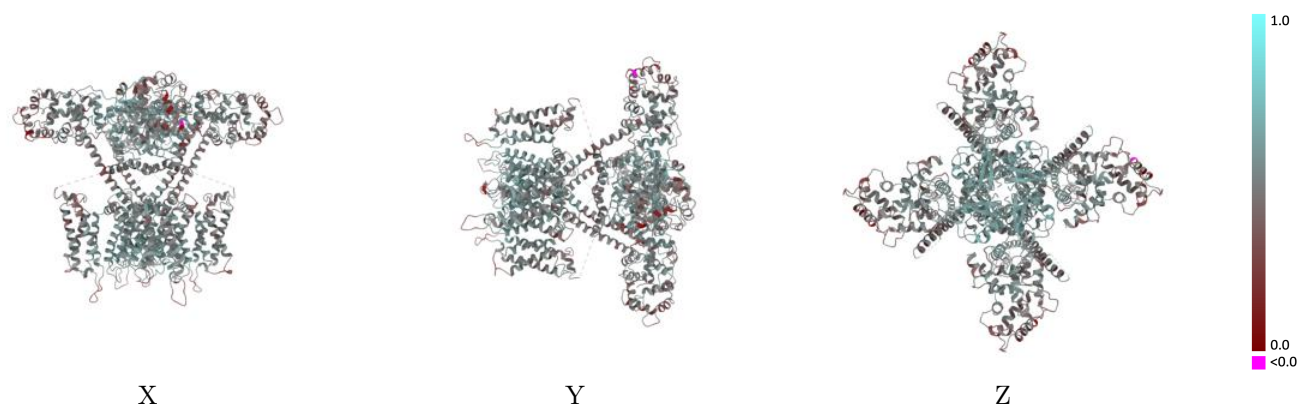
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0109 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

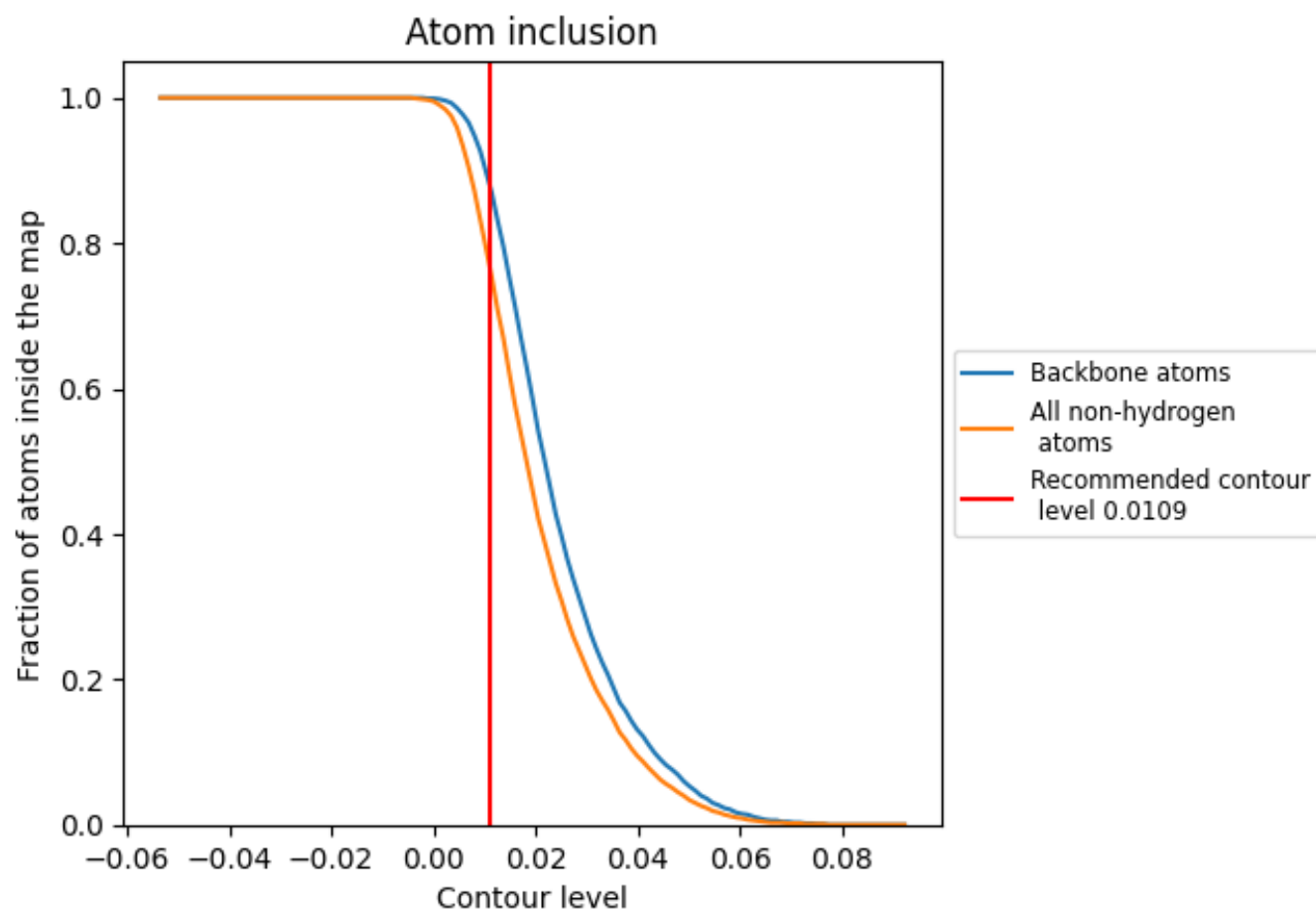


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 77% 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 (0.0109) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7720	0.5050
A	0.7400	0.4580
B	0.7850	0.5230
C	0.7400	0.4600
D	0.7850	0.5230
E	0.7420	0.4620
F	0.7830	0.5230
G	0.7410	0.4610
H	0.7840	0.5250

1.0

0.0

<0.0