



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 02:25 AM UTC

PDB ID : 6UVS / pdb_00006uvs
EMDB ID : EMD-20915
Title : Human Connexin-26 (Low pH open conformation)
Authors : Khan, A.K.; Jagielnicki, M.; Purdy, M.D.; Yeager, M.
Deposited on : 2019-11-04
Resolution : 4.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

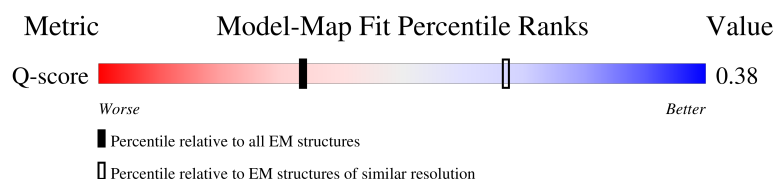
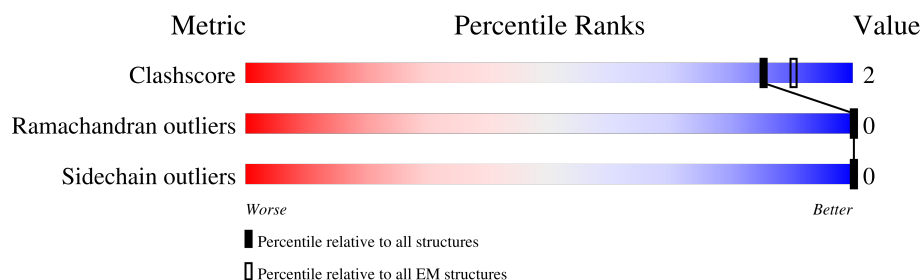
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.20 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.



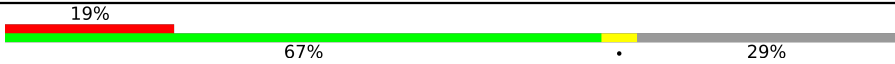
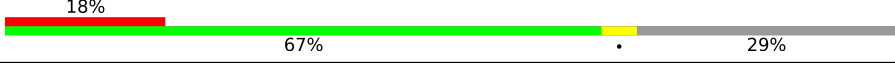
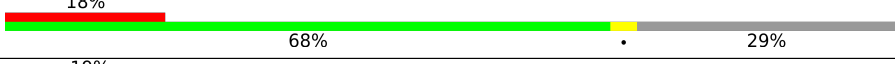
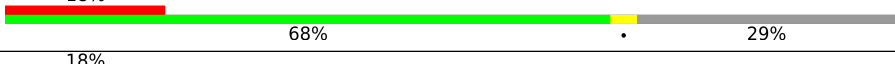
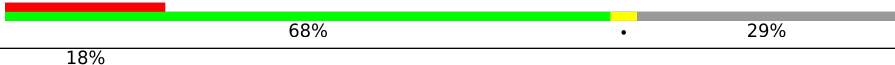
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	226	19% 67% 29%
1	B	226	18% 68% 29%
1	C	226	18% 67% 29%
1	D	226	18% 68% 29%

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Mol	Chain	Length	Quality of chain
1	E	226	
1	F	226	
1	G	226	
1	H	226	
1	I	226	
1	J	226	
1	K	226	
1	L	226	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 17040 atoms, of which 5976 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 Gap junction beta-2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		
1	K	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		
1	L	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		
1	B	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		
1	H	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		
1	C	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		
1	I	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		
1	D	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		
1	J	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		
1	E	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		
1	F	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		
1	G	160	Total	C	H	N	O	0	0
			1420	580	498	178	164		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	211	SER	CYS	engineered mutation	UNP P29033
A	218	SER	CYS	engineered mutation	UNP P29033
K	211	SER	CYS	engineered mutation	UNP P29033
K	218	SER	CYS	engineered mutation	UNP P29033
L	211	SER	CYS	engineered mutation	UNP P29033
L	218	SER	CYS	engineered mutation	UNP P29033

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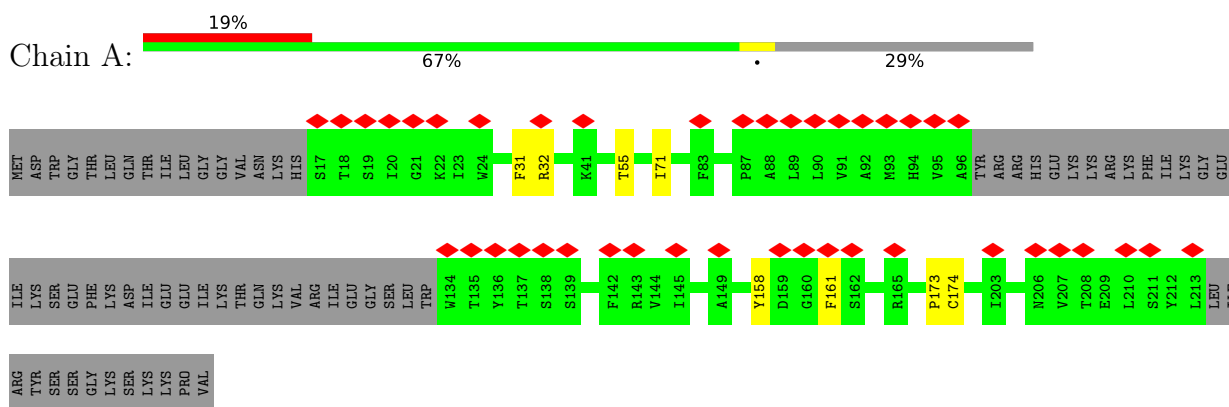
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Chain	Residue	Modelled	Actual	Comment	Reference
B	211	SER	CYS	engineered mutation	UNP P29033
B	218	SER	CYS	engineered mutation	UNP P29033
H	211	SER	CYS	engineered mutation	UNP P29033
H	218	SER	CYS	engineered mutation	UNP P29033
C	211	SER	CYS	engineered mutation	UNP P29033
C	218	SER	CYS	engineered mutation	UNP P29033
I	211	SER	CYS	engineered mutation	UNP P29033
I	218	SER	CYS	engineered mutation	UNP P29033
D	211	SER	CYS	engineered mutation	UNP P29033
D	218	SER	CYS	engineered mutation	UNP P29033
J	211	SER	CYS	engineered mutation	UNP P29033
J	218	SER	CYS	engineered mutation	UNP P29033
E	211	SER	CYS	engineered mutation	UNP P29033
E	218	SER	CYS	engineered mutation	UNP P29033
F	211	SER	CYS	engineered mutation	UNP P29033
F	218	SER	CYS	engineered mutation	UNP P29033
G	211	SER	CYS	engineered mutation	UNP P29033
G	218	SER	CYS	engineered mutation	UNP P29033

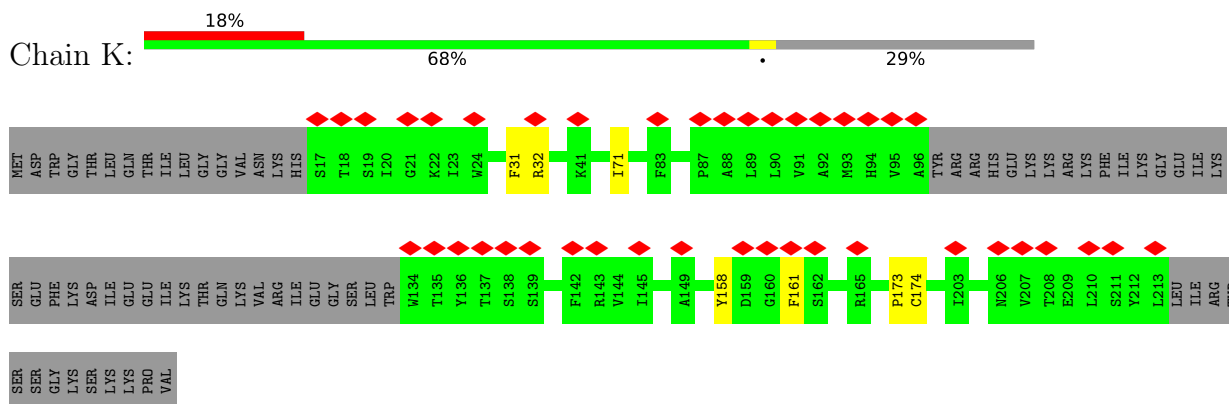
3 Residue-property plots

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.

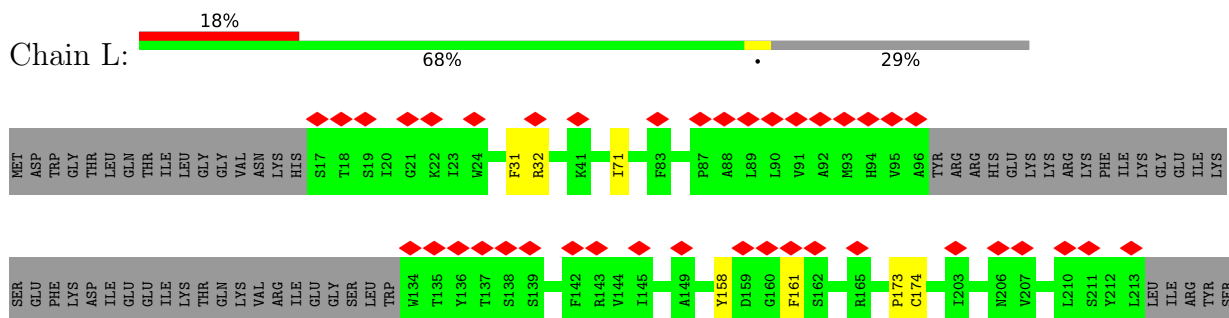
- Molecule 1: Gap junction beta-2 protein



- Molecule 1: Gap junction beta-2 protein



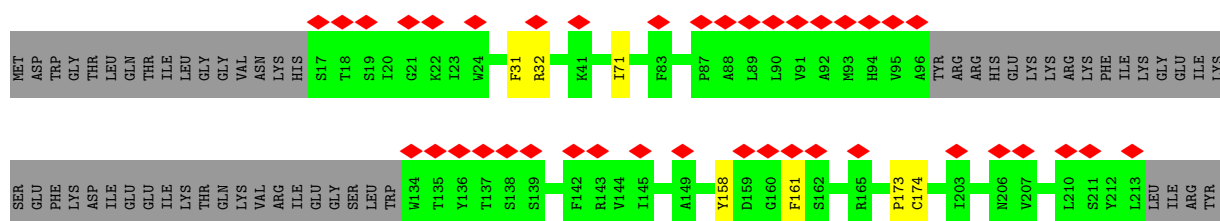
- Molecule 1: Gap junction beta-2 protein



SER
GLY
LYS
SER
LYS
LYS
PRO
VAL

- Molecule 1: Gap junction beta-2 protein

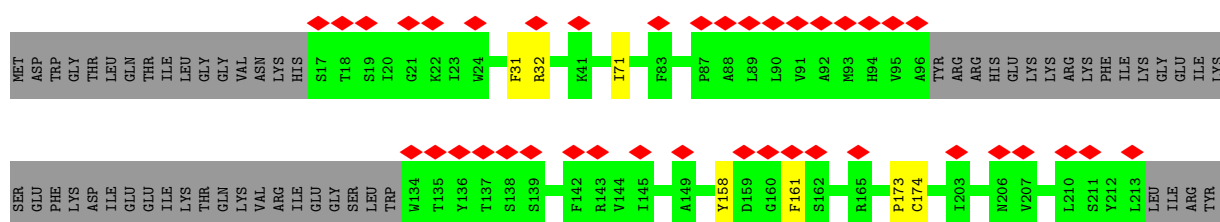
Chain B: 



SER
GLY
LYS
SER
LYS
LYS
PRO
VAL

- Molecule 1: Gap junction beta-2 protein

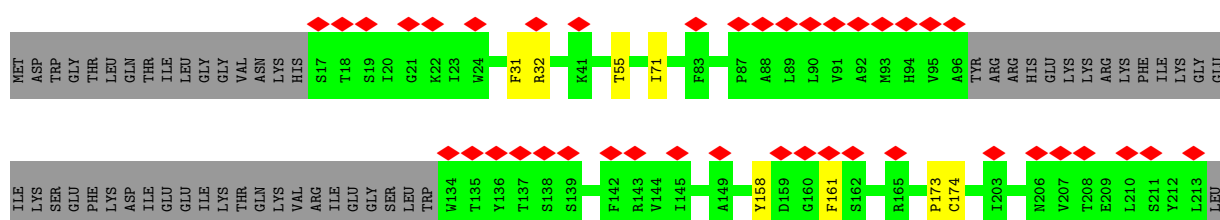
Chain H: 



SER
GLY
LYS
SER
LYS
LYS
PRO
VAL

- Molecule 1: Gap junction beta-2 protein

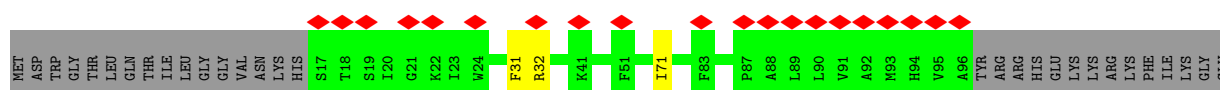
Chain C: 

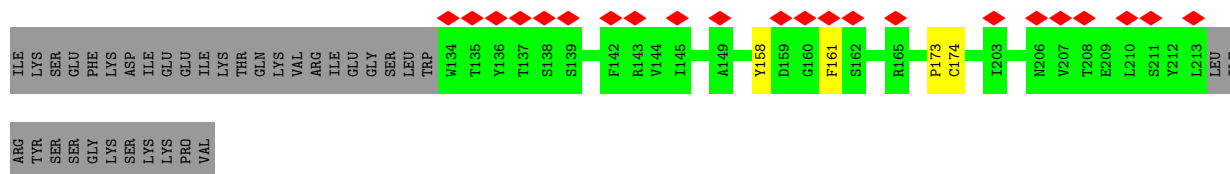


ARG
THR
SER
SER
GLY
GLY
LYS
LYS
PRO
VAL

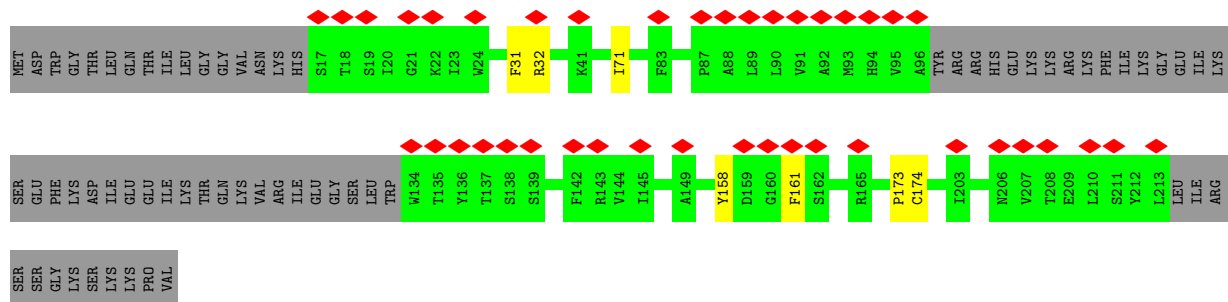
- Molecule 1: Gap junction beta-2 protein

Chain I: 

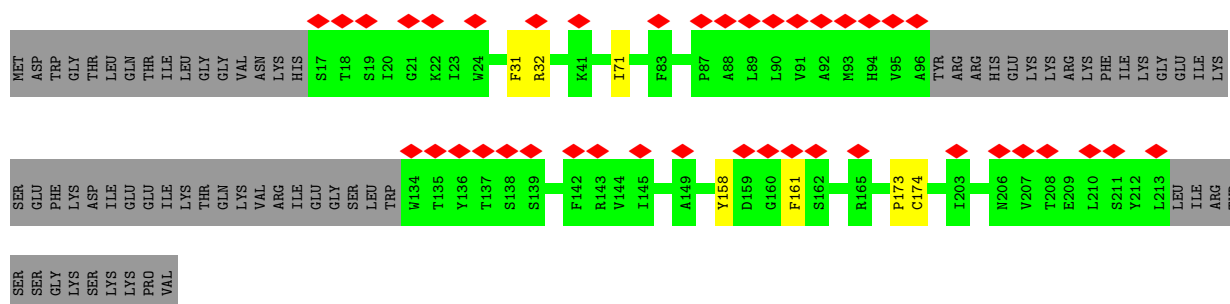




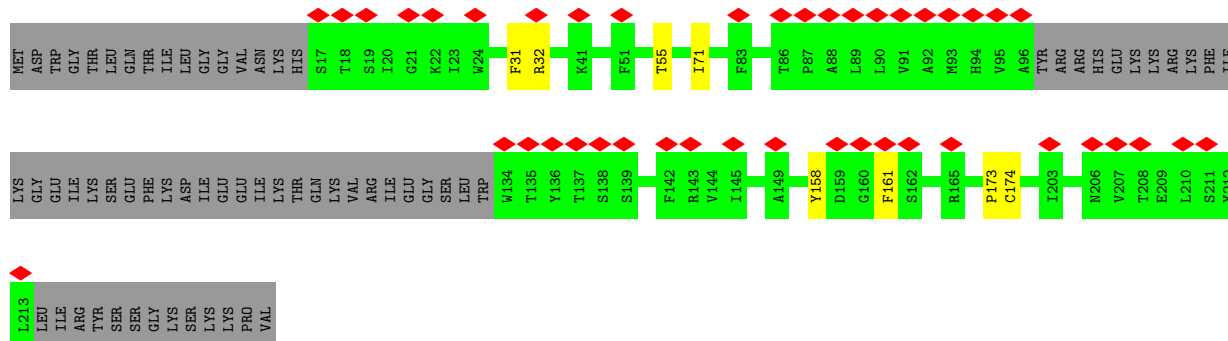
- Molecule 1: Gap junction beta-2 protein



- Molecule 1: Gap junction beta-2 protein

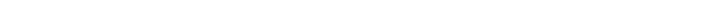


- Molecule 1: Gap junction beta-2 protein



- Molecule 1: Gap junction beta-2 protein

SER	LYS	LYS	LYS	PRO	VAL	LYS	SER	ASP	GLU	PHE	LYS	ASP	ILE	GLU	ILE	LYS	THR	GLN	THR	GLY	ASN	VAL	ARG	ILE	GLU	GLY	TRP	W134	T135	Y136	T137	S138	S139	F142	R143	V144	I145	Y158	D159	G160	F161	S162	R165	P173	C174	V207	T208	E209	L210	S211	Y212	L213	ILE	ILE	TYR	SER	SER	LYS
MET	ASP	TRP	GLY	THR	LEU	GLN	THR	ILE	LEU	GLY	GLY	VAL	ASN	LYS	HIS	S17	T18	S19	I20	G21	W24	F31	R32	K41	F51	I71	F83	P87	A88	L89	L90	V91	A92	M93	H94	V95	A96	TYR	ARG	ARG	HIS	GLU	LYS	LYS	ARG	LYS	PHE	ILE	LYS	GLY	GLU	TYR						

- Chain G:  18% 67% 15%

TYR	GLY	MET
SER	ILE	ASP
SER	ILE	TRP
GLY	LYS	GLY
LYS	SER	THR
SER	GLU	LEU
LYS	PHE	GLN
LYS	THR	THR
PRO	ASP	ILE
VAL	ILE	LEU
	GLU	GLY
	GLU	GLY
	ILE	VAL
	LYS	ASN
	THR	LYS
	GLN	HIS
	LYS	S17
	VAL	T18
	ARG	S19
	ILE	I20
	GLU	G21
	GLY	K22
	SER	I23
	LEU	V24
	TRP	
	W134	
	T135	F31
	Y136	R32
	T137	
	S138	K41
	S139	
		F51
	F142	
	R143	T55
	V144	
	I145	I71
	A149	F83
	Y158	F87
	D159	A88
	G160	L89
	F161	L90
	S162	V91
		A92
	R165	H93
		H94
	P173	V95
	C174	A96
	V207	T97
	T208	ARG
	E209	ARG
	L210	GLU
	S211	LYS
	Y212	LYS
	L213	ARG
	LEU	LYS
		PHE
		ILE

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D6	Depositor
Number of particles used	25236	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.101	Depositor
Minimum map value	-0.045	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	250.15999, 250.15999, 250.15999	wwPDB
Map dimensions	236, 236, 236	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.67	1/943 (0.1%)	0.76	0/1312
1	B	0.67	1/943 (0.1%)	0.76	0/1312
1	C	0.67	1/943 (0.1%)	0.76	0/1312
1	D	0.67	1/943 (0.1%)	0.76	0/1312
1	E	0.67	1/943 (0.1%)	0.76	0/1312
1	F	0.67	1/943 (0.1%)	0.76	0/1312
1	G	0.67	1/943 (0.1%)	0.76	0/1312
1	H	0.67	1/943 (0.1%)	0.76	0/1312
1	I	0.67	1/943 (0.1%)	0.76	0/1312
1	J	0.67	1/943 (0.1%)	0.76	0/1312
1	K	0.67	1/943 (0.1%)	0.76	0/1312
1	L	0.67	1/943 (0.1%)	0.76	0/1312
All	All	0.67	12/11316 (0.1%)	0.76	0/15744

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	161	PHE	CA-C	5.99	1.60	1.52
1	H	161	PHE	CA-C	5.98	1.60	1.52
1	C	161	PHE	CA-C	5.98	1.60	1.52
1	G	161	PHE	CA-C	5.98	1.60	1.52
1	E	161	PHE	CA-C	5.98	1.60	1.52
1	K	161	PHE	CA-C	5.98	1.60	1.52
1	J	161	PHE	CA-C	5.97	1.60	1.52
1	I	161	PHE	CA-C	5.97	1.60	1.52
1	A	161	PHE	CA-C	5.96	1.60	1.52
1	D	161	PHE	CA-C	5.96	1.60	1.52
1	L	161	PHE	CA-C	5.96	1.60	1.52
1	B	161	PHE	CA-C	5.92	1.60	1.52

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	922	498	523	4	0
1	B	922	498	523	3	0
1	C	922	498	523	4	0
1	D	922	498	523	3	0
1	E	922	498	523	4	0
1	F	922	498	523	3	0
1	G	922	498	523	4	0
1	H	922	498	523	3	0
1	I	922	498	523	3	0
1	J	922	498	523	3	0
1	K	922	498	523	3	0
1	L	922	498	523	3	0
All	All	11064	5976	6276	38	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 2.

All (38) 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:J:71:ILE:O	1:J:158:TYR:OH	2.15	0.65
1:I:71:ILE:O	1:I:158:TYR:OH	2.15	0.65
1:C:71:ILE:O	1:C:158:TYR:OH	2.15	0.65
1:E:71:ILE:O	1:E:158:TYR:OH	2.15	0.65
1:G:71:ILE:O	1:G:158:TYR:OH	2.15	0.65
1:D:71:ILE:O	1:D:158:TYR:OH	2.15	0.64
1:B:71:ILE:O	1:B:158:TYR:OH	2.15	0.64
1:K:71:ILE:O	1:K:158:TYR:OH	2.15	0.64
1:F:71:ILE:O	1:F:158:TYR:OH	2.15	0.63
1:A:71:ILE:O	1:A:158:TYR:OH	2.15	0.63
1:H:71:ILE:O	1:H:158:TYR:OH	2.15	0.62
1:L:71:ILE:O	1:L:158:TYR:OH	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:THR:HA	1:E:55:THR:HA	1.95	0.47
1:I:173:PRO:CD	1:I:174:CYS:H	2.30	0.45
1:J:173:PRO:CD	1:J:174:CYS:H	2.30	0.44
1:F:173:PRO:CD	1:F:174:CYS:H	2.30	0.44
1:A:173:PRO:CD	1:A:174:CYS:H	2.30	0.44
1:C:173:PRO:CD	1:C:174:CYS:H	2.30	0.44
1:D:173:PRO:CD	1:D:174:CYS:H	2.31	0.44
1:E:173:PRO:CD	1:E:174:CYS:H	2.31	0.44
1:G:173:PRO:CD	1:G:174:CYS:H	2.30	0.44
1:B:173:PRO:CD	1:B:174:CYS:H	2.30	0.43
1:K:173:PRO:CD	1:K:174:CYS:H	2.31	0.43
1:C:55:THR:HA	1:G:55:THR:HA	2.00	0.43
1:H:173:PRO:CD	1:H:174:CYS:H	2.30	0.43
1:L:173:PRO:CD	1:L:174:CYS:H	2.31	0.43
1:A:31:PHE:O	1:A:32:ARG:C	2.62	0.43
1:F:31:PHE:O	1:F:32:ARG:C	2.62	0.43
1:D:31:PHE:O	1:D:32:ARG:C	2.62	0.42
1:J:31:PHE:O	1:J:32:ARG:C	2.62	0.42
1:E:31:PHE:O	1:E:32:ARG:C	2.62	0.42
1:I:31:PHE:O	1:I:32:ARG:C	2.62	0.42
1:G:31:PHE:O	1:G:32:ARG:C	2.62	0.42
1:K:31:PHE:O	1:K:32:ARG:C	2.62	0.41
1:C:31:PHE:O	1:C:32:ARG:C	2.62	0.41
1:L:31:PHE:O	1:L:32:ARG:C	2.62	0.41
1:H:31:PHE:O	1:H:32:ARG:C	2.62	0.41
1:B:31:PHE:O	1:B:32:ARG:C	2.62	0.41

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	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
1	B	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
1	C	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
1	D	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
1	E	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
1	F	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
1	G	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
1	H	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
1	I	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
1	J	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
1	K	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
1	L	156/226 (69%)	131 (84%)	25 (16%)	0	100	100
All	All	1872/2712 (69%)	1572 (84%)	300 (16%)	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	24/204 (12%)	24 (100%)	0	100	100
1	B	24/204 (12%)	24 (100%)	0	100	100
1	C	24/204 (12%)	24 (100%)	0	100	100
1	D	24/204 (12%)	24 (100%)	0	100	100
1	E	24/204 (12%)	24 (100%)	0	100	100
1	F	24/204 (12%)	24 (100%)	0	100	100
1	G	24/204 (12%)	24 (100%)	0	100	100
1	H	24/204 (12%)	24 (100%)	0	100	100
1	I	24/204 (12%)	24 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	24/204 (12%)	24 (100%)	0	100	100
1	K	24/204 (12%)	24 (100%)	0	100	100
1	L	24/204 (12%)	24 (100%)	0	100	100
All	All	288/2448 (12%)	288 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	K	48	GLN
1	L	48	GLN
1	B	48	GLN
1	H	48	GLN
1	C	48	GLN
1	I	48	GLN
1	D	48	GLN
1	J	48	GLN
1	E	48	GLN
1	F	48	GLN
1	G	48	GLN

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

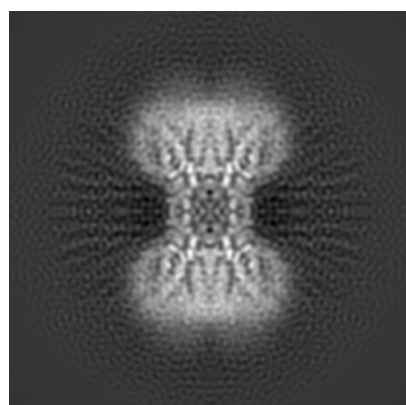
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20915. These allow visual inspection of the internal detail of the map and identification of artifacts.

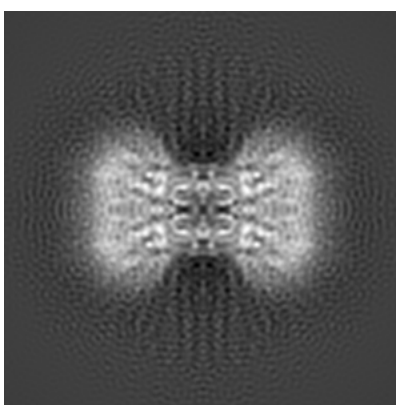
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

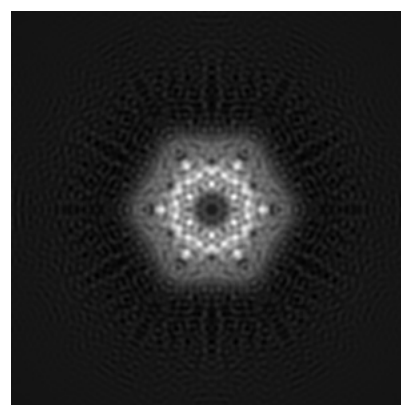
6.1.1 Primary map



X



Y

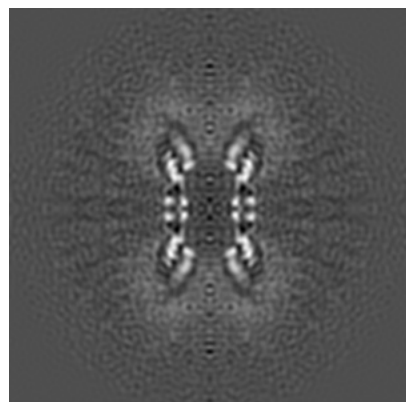


Z

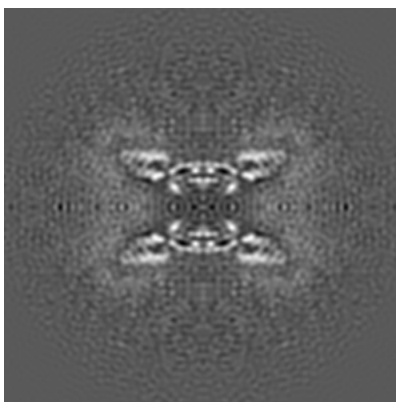
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

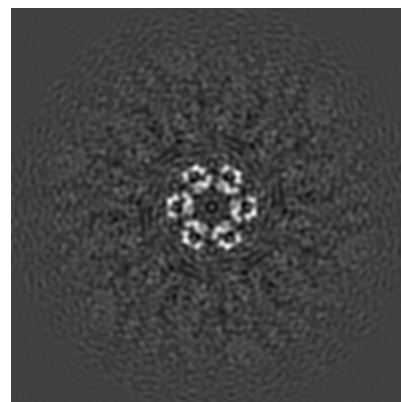
6.2.1 Primary map



X Index: 118



Y Index: 118

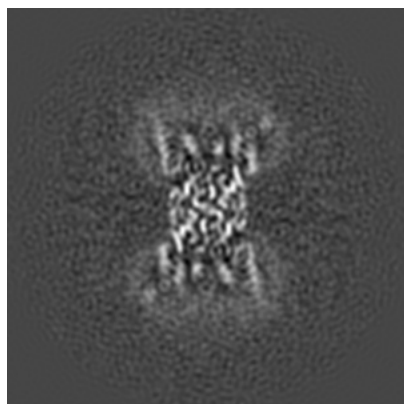


Z Index: 118

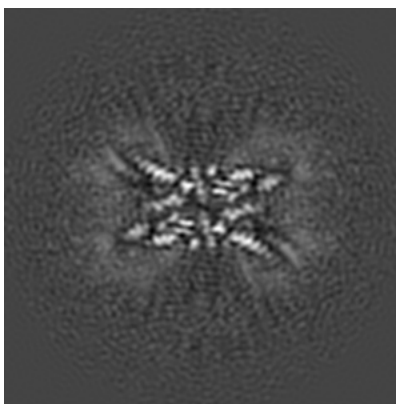
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

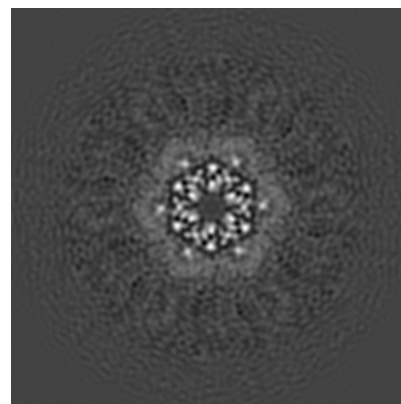
6.3.1 Primary map



X Index: 132



Y Index: 107

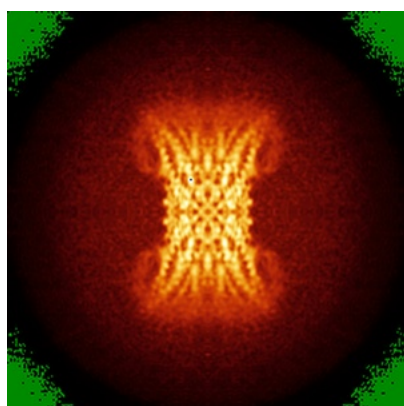


Z Index: 142

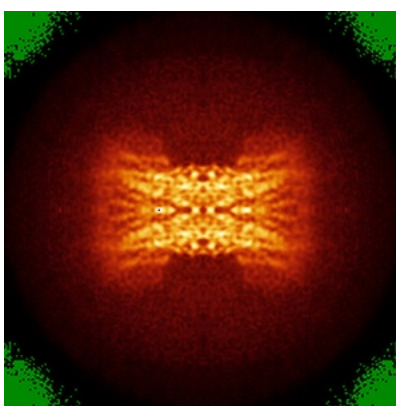
The images above show the largest variance slices of the map in three orthogonal directions.

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

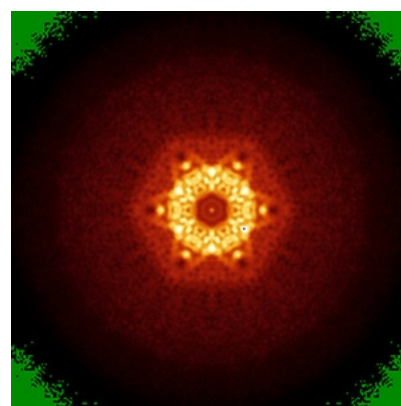
6.4.1 Primary map



X



Y

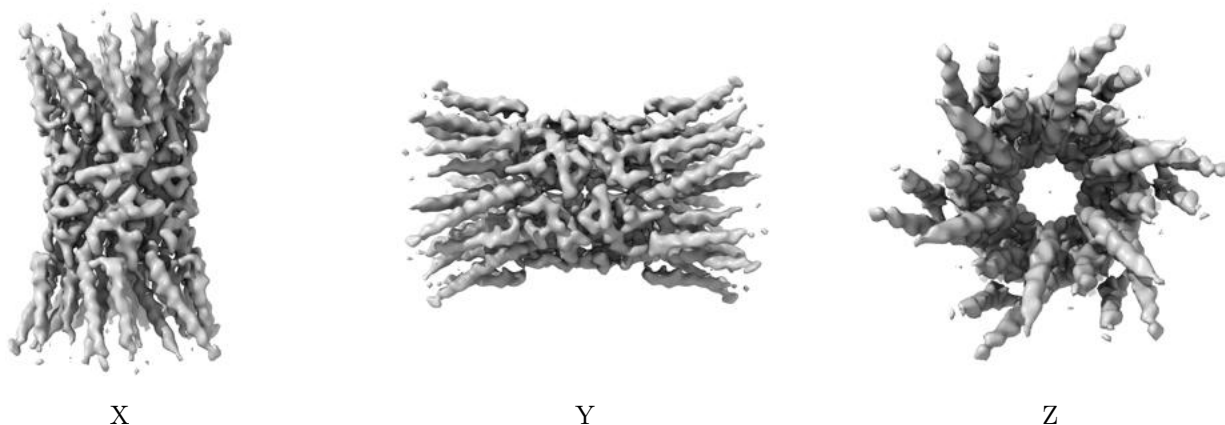


Z

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

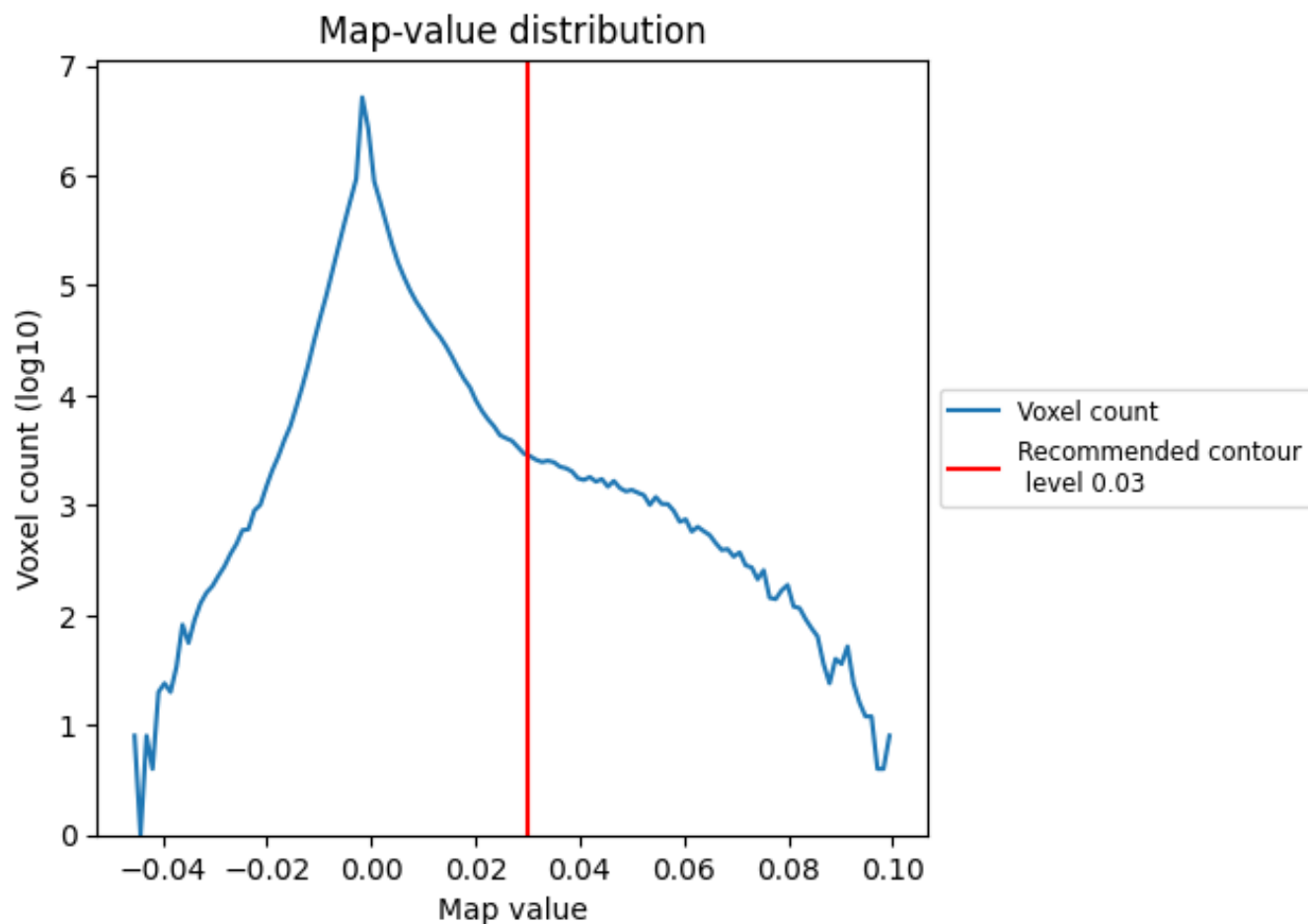
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

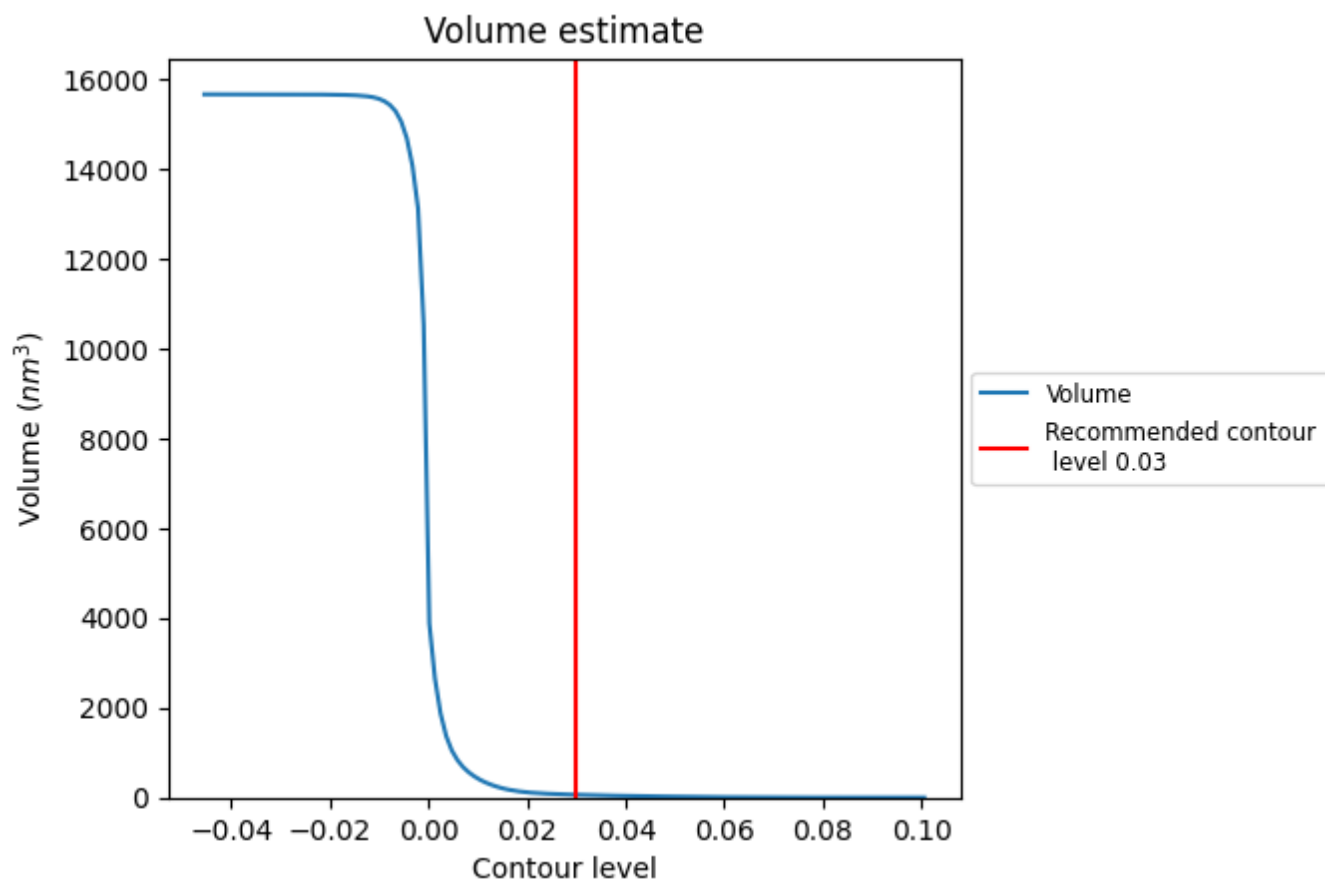
This section contains the results of statistical analysis of the map.

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.

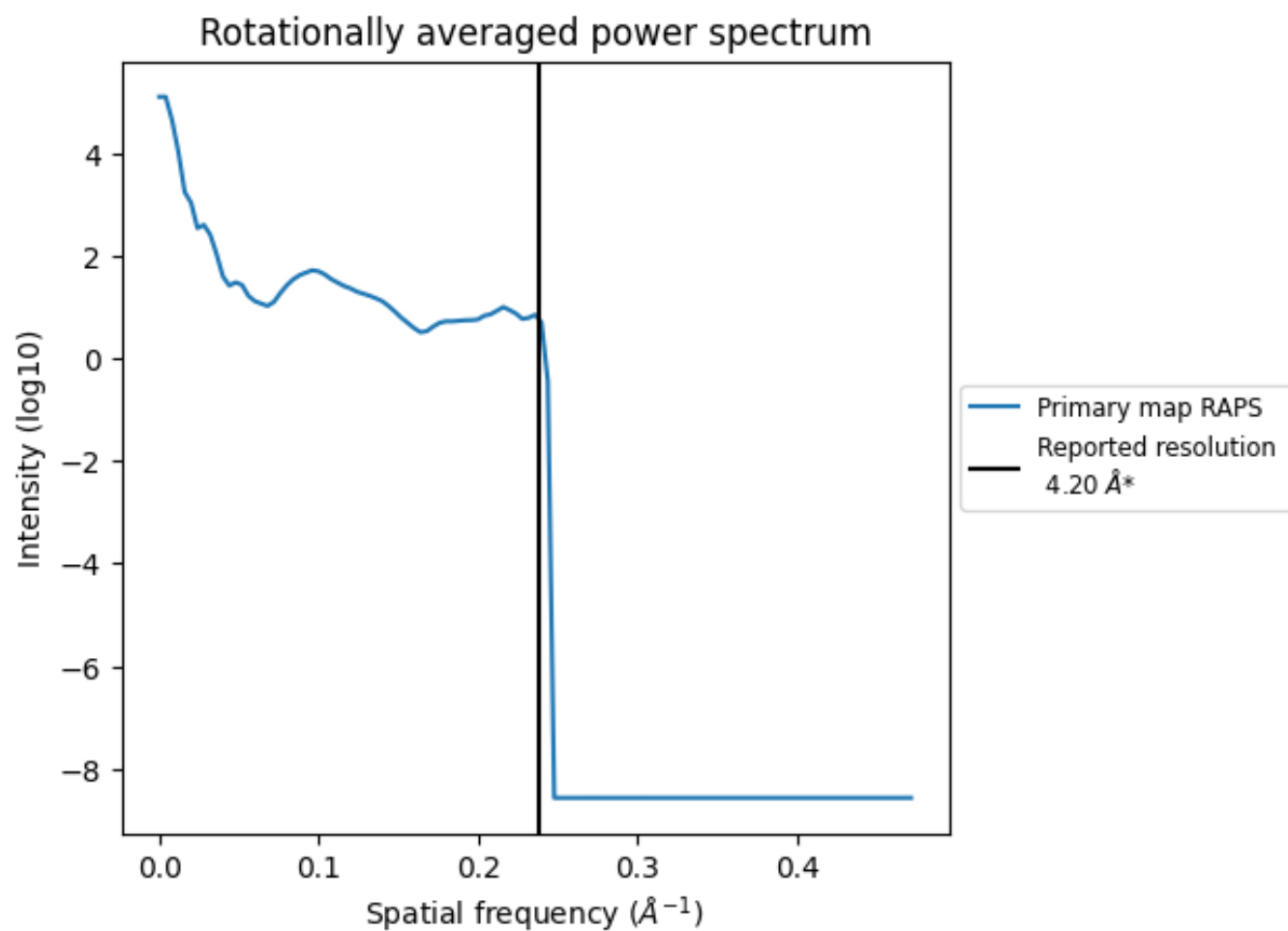
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 62 nm³; this corresponds to an approximate mass of 56 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 0.238 Å⁻¹

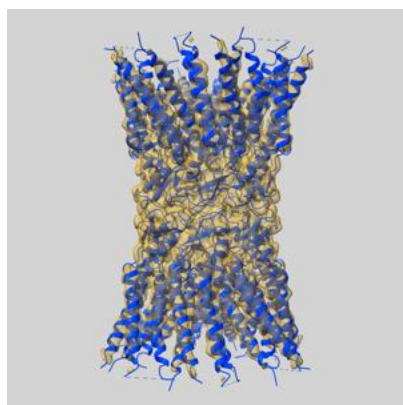
8 Fourier-Shell correlation

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

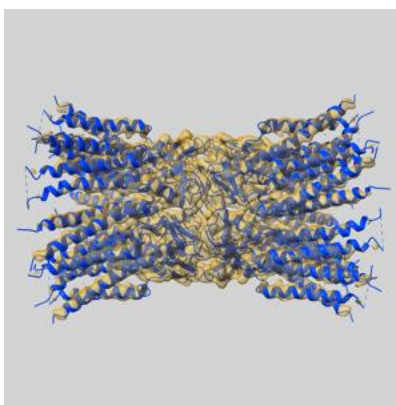
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20915 and PDB model 6UVS. Per-residue inclusion information can be found in section 3 on page 6.

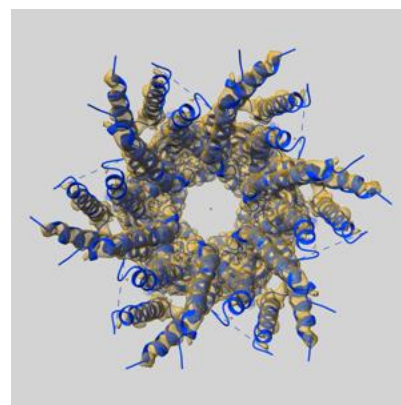
9.1 Map-model overlay [i](#)



X



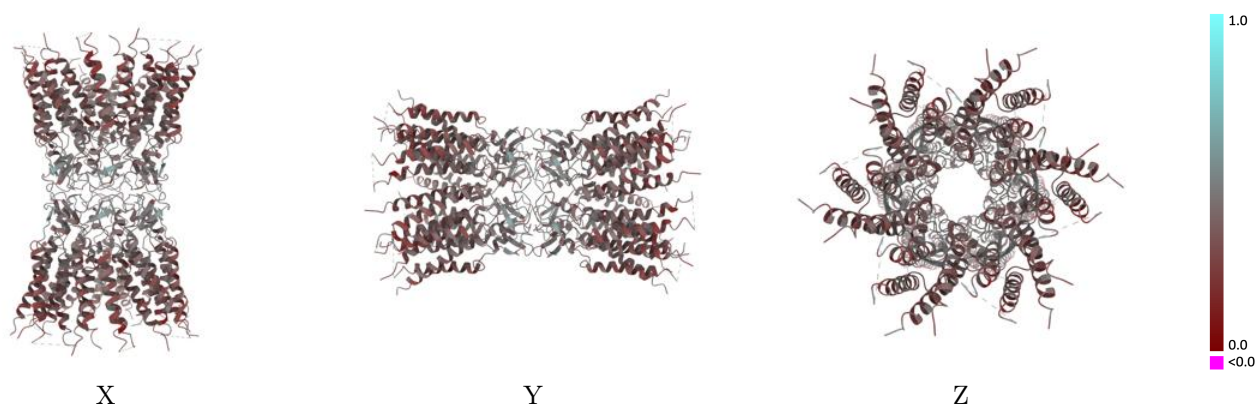
Y



Z

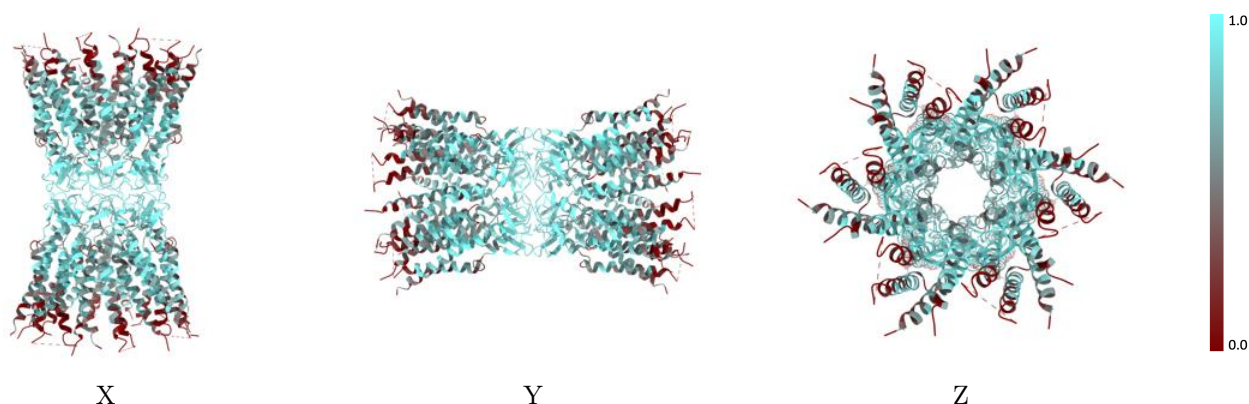
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



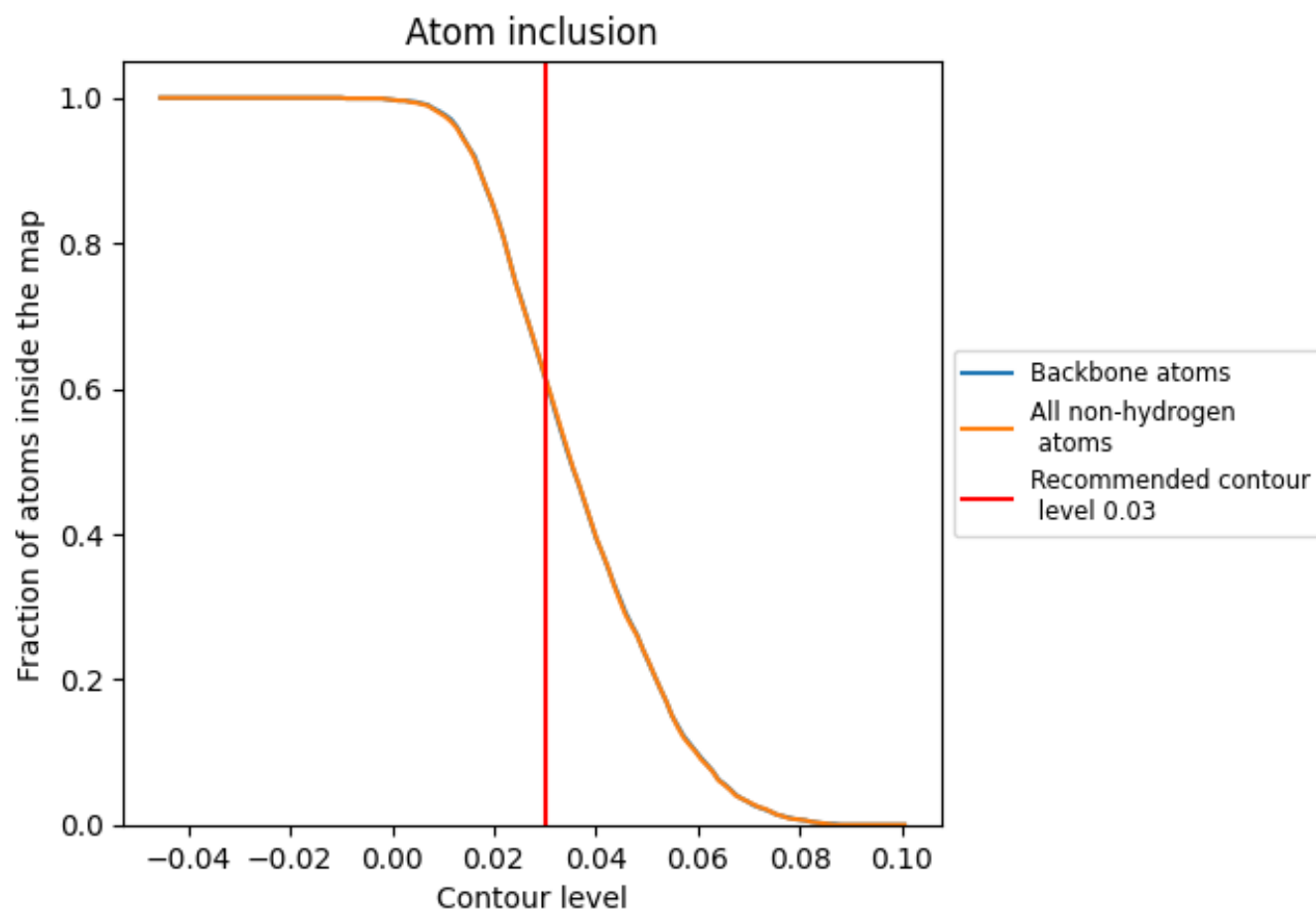
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 62% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6170	0.3800
A	0.6300	0.3800
B	0.6250	0.3810
C	0.6280	0.3850
D	0.6300	0.3820
E	0.6160	0.3770
F	0.6300	0.3810
G	0.6310	0.3840
H	0.6210	0.3780
I	0.6280	0.3790
J	0.6260	0.3760
K	0.6330	0.3830
L	0.6270	0.3790

1.0

0.0

<0.0