



Full wwPDB EM Validation Report ⓘ

Jun 17, 2025 – 04:32 AM JST

PDB ID : 8ZAR / pdb_00008zar
EMDB ID : EMD-39885
Title : EmrAB-TolC MFS-type tripartite multidrug efflux pump FA
Authors : Du, D.; Zhong, Z.; Tuerxunjiang, M.
Deposited on : 2024-04-25
Resolution : 3.59 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

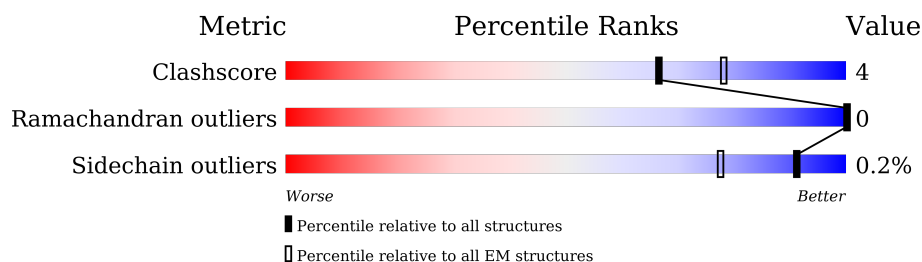
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.59 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	401	
1	B	401	
1	C	401	
1	D	401	
1	E	401	
1	F	401	
2	J	614	
3	G	501	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	H	501	
3	I	501	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 29869 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 Multidrug export protein EmrA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	344	Total	C	N	O	S	0	0
			2638	1641	476	513	8		
1	B	348	Total	C	N	O	S	0	0
			2672	1667	480	517	8		
1	C	349	Total	C	N	O	S	0	0
			2686	1678	482	518	8		
1	D	373	Total	C	N	O	S	0	0
			2877	1811	514	544	8		
1	E	344	Total	C	N	O	S	0	0
			2638	1641	476	513	8		
1	F	344	Total	C	N	O	S	0	0
			2638	1641	476	513	8		

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	391	GLY	-	expression tag	UNP P27303
A	392	GLY	-	expression tag	UNP P27303
A	393	SER	-	expression tag	UNP P27303
A	394	ASP	-	expression tag	UNP P27303
A	395	TYR	-	expression tag	UNP P27303
A	396	LYS	-	expression tag	UNP P27303
A	397	ASP	-	expression tag	UNP P27303
A	398	ASP	-	expression tag	UNP P27303
A	399	ASP	-	expression tag	UNP P27303
A	400	ASP	-	expression tag	UNP P27303
A	401	LYS	-	expression tag	UNP P27303
B	391	GLY	-	expression tag	UNP P27303
B	392	GLY	-	expression tag	UNP P27303
B	393	SER	-	expression tag	UNP P27303
B	394	ASP	-	expression tag	UNP P27303
B	395	TYR	-	expression tag	UNP P27303
B	396	LYS	-	expression tag	UNP P27303
B	397	ASP	-	expression tag	UNP P27303

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	398	ASP	-	expression tag	UNP P27303
B	399	ASP	-	expression tag	UNP P27303
B	400	ASP	-	expression tag	UNP P27303
B	401	LYS	-	expression tag	UNP P27303
C	391	GLY	-	expression tag	UNP P27303
C	392	GLY	-	expression tag	UNP P27303
C	393	SER	-	expression tag	UNP P27303
C	394	ASP	-	expression tag	UNP P27303
C	395	TYR	-	expression tag	UNP P27303
C	396	LYS	-	expression tag	UNP P27303
C	397	ASP	-	expression tag	UNP P27303
C	398	ASP	-	expression tag	UNP P27303
C	399	ASP	-	expression tag	UNP P27303
C	400	ASP	-	expression tag	UNP P27303
C	401	LYS	-	expression tag	UNP P27303
D	391	GLY	-	expression tag	UNP P27303
D	392	GLY	-	expression tag	UNP P27303
D	393	SER	-	expression tag	UNP P27303
D	394	ASP	-	expression tag	UNP P27303
D	395	TYR	-	expression tag	UNP P27303
D	396	LYS	-	expression tag	UNP P27303
D	397	ASP	-	expression tag	UNP P27303
D	398	ASP	-	expression tag	UNP P27303
D	399	ASP	-	expression tag	UNP P27303
D	400	ASP	-	expression tag	UNP P27303
D	401	LYS	-	expression tag	UNP P27303
E	391	GLY	-	expression tag	UNP P27303
E	392	GLY	-	expression tag	UNP P27303
E	393	SER	-	expression tag	UNP P27303
E	394	ASP	-	expression tag	UNP P27303
E	395	TYR	-	expression tag	UNP P27303
E	396	LYS	-	expression tag	UNP P27303
E	397	ASP	-	expression tag	UNP P27303
E	398	ASP	-	expression tag	UNP P27303
E	399	ASP	-	expression tag	UNP P27303
E	400	ASP	-	expression tag	UNP P27303
E	401	LYS	-	expression tag	UNP P27303
F	391	GLY	-	expression tag	UNP P27303
F	392	GLY	-	expression tag	UNP P27303
F	393	SER	-	expression tag	UNP P27303
F	394	ASP	-	expression tag	UNP P27303
F	395	TYR	-	expression tag	UNP P27303

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	396	LYS	-	expression tag	UNP P27303
F	397	ASP	-	expression tag	UNP P27303
F	398	ASP	-	expression tag	UNP P27303
F	399	ASP	-	expression tag	UNP P27303
F	400	ASP	-	expression tag	UNP P27303
F	401	LYS	-	expression tag	UNP P27303

- Molecule 2 is a protein called Multidrug export protein EmrB.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	494	Total	C	N	O	S	0	0
			3805	2503	617	662	23		

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	-110	MET	-	initiating methionine	UNP P0AEJ0
J	-109	GLY	-	expression tag	UNP P0AEJ0
J	-108	MET	-	expression tag	UNP P0AEJ0
J	-107	THR	-	expression tag	UNP P0AEJ0
J	-106	PRO	-	expression tag	UNP P0AEJ0
J	-105	LEU	-	expression tag	UNP P0AEJ0
J	-104	ALA	-	expression tag	UNP P0AEJ0
J	-103	ASP	-	expression tag	UNP P0AEJ0
J	-102	LEU	-	expression tag	UNP P0AEJ0
J	-101	GLU	-	expression tag	UNP P0AEJ0
J	-100	ASP	-	expression tag	UNP P0AEJ0
J	-99	ASN	-	expression tag	UNP P0AEJ0
J	-98	TRP	-	expression tag	UNP P0AEJ0
J	-97	GLU	-	expression tag	UNP P0AEJ0
J	-96	THR	-	expression tag	UNP P0AEJ0
J	-95	LEU	-	expression tag	UNP P0AEJ0
J	-94	ASN	-	expression tag	UNP P0AEJ0
J	-93	ASP	-	expression tag	UNP P0AEJ0
J	-92	ASN	-	expression tag	UNP P0AEJ0
J	-91	LEU	-	expression tag	UNP P0AEJ0
J	-90	LYS	-	expression tag	UNP P0AEJ0
J	-89	VAL	-	expression tag	UNP P0AEJ0
J	-88	ILE	-	expression tag	UNP P0AEJ0
J	-87	GLU	-	expression tag	UNP P0AEJ0
J	-86	LYS	-	expression tag	UNP P0AEJ0
J	-85	ALA	-	expression tag	UNP P0AEJ0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
J	-84	ASP	-	expression tag	UNP P0AEJ0
J	-83	ASN	-	expression tag	UNP P0AEJ0
J	-82	ALA	-	expression tag	UNP P0AEJ0
J	-81	ALA	-	expression tag	UNP P0AEJ0
J	-80	GLN	-	expression tag	UNP P0AEJ0
J	-79	VAL	-	expression tag	UNP P0AEJ0
J	-78	LYS	-	expression tag	UNP P0AEJ0
J	-77	ASP	-	expression tag	UNP P0AEJ0
J	-76	ALA	-	expression tag	UNP P0AEJ0
J	-75	LEU	-	expression tag	UNP P0AEJ0
J	-74	THR	-	expression tag	UNP P0AEJ0
J	-73	LYS	-	expression tag	UNP P0AEJ0
J	-72	MET	-	expression tag	UNP P0AEJ0
J	-71	ARG	-	expression tag	UNP P0AEJ0
J	-70	ALA	-	expression tag	UNP P0AEJ0
J	-69	ALA	-	expression tag	UNP P0AEJ0
J	-68	ALA	-	expression tag	UNP P0AEJ0
J	-67	LEU	-	expression tag	UNP P0AEJ0
J	-66	ASP	-	expression tag	UNP P0AEJ0
J	-65	ALA	-	expression tag	UNP P0AEJ0
J	-64	GLN	-	expression tag	UNP P0AEJ0
J	-63	LYS	-	expression tag	UNP P0AEJ0
J	-62	ALA	-	expression tag	UNP P0AEJ0
J	-61	THR	-	expression tag	UNP P0AEJ0
J	-60	PRO	-	expression tag	UNP P0AEJ0
J	-59	PRO	-	expression tag	UNP P0AEJ0
J	-58	LYS	-	expression tag	UNP P0AEJ0
J	-57	LEU	-	expression tag	UNP P0AEJ0
J	-56	GLU	-	expression tag	UNP P0AEJ0
J	-55	ASP	-	expression tag	UNP P0AEJ0
J	-54	LYS	-	expression tag	UNP P0AEJ0
J	-53	SER	-	expression tag	UNP P0AEJ0
J	-52	PRO	-	expression tag	UNP P0AEJ0
J	-51	ASP	-	expression tag	UNP P0AEJ0
J	-50	SER	-	expression tag	UNP P0AEJ0
J	-49	PRO	-	expression tag	UNP P0AEJ0
J	-48	GLU	-	expression tag	UNP P0AEJ0
J	-47	MET	-	expression tag	UNP P0AEJ0
J	-46	LYS	-	expression tag	UNP P0AEJ0
J	-45	ASP	-	expression tag	UNP P0AEJ0
J	-44	PHE	-	expression tag	UNP P0AEJ0
J	-43	ARG	-	expression tag	UNP P0AEJ0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
J	-42	HIS	-	expression tag	UNP P0AEJ0
J	-41	GLY	-	expression tag	UNP P0AEJ0
J	-40	PHE	-	expression tag	UNP P0AEJ0
J	-39	ASP	-	expression tag	UNP P0AEJ0
J	-38	ILE	-	expression tag	UNP P0AEJ0
J	-37	LEU	-	expression tag	UNP P0AEJ0
J	-36	VAL	-	expression tag	UNP P0AEJ0
J	-35	GLY	-	expression tag	UNP P0AEJ0
J	-34	GLN	-	expression tag	UNP P0AEJ0
J	-33	ILE	-	expression tag	UNP P0AEJ0
J	-32	ASP	-	expression tag	UNP P0AEJ0
J	-31	ASP	-	expression tag	UNP P0AEJ0
J	-30	ALA	-	expression tag	UNP P0AEJ0
J	-29	LEU	-	expression tag	UNP P0AEJ0
J	-28	LYS	-	expression tag	UNP P0AEJ0
J	-27	LEU	-	expression tag	UNP P0AEJ0
J	-26	ALA	-	expression tag	UNP P0AEJ0
J	-25	ASN	-	expression tag	UNP P0AEJ0
J	-24	GLU	-	expression tag	UNP P0AEJ0
J	-23	GLY	-	expression tag	UNP P0AEJ0
J	-22	LYS	-	expression tag	UNP P0AEJ0
J	-21	VAL	-	expression tag	UNP P0AEJ0
J	-20	LYS	-	expression tag	UNP P0AEJ0
J	-19	GLU	-	expression tag	UNP P0AEJ0
J	-18	ALA	-	expression tag	UNP P0AEJ0
J	-17	GLN	-	expression tag	UNP P0AEJ0
J	-16	ALA	-	expression tag	UNP P0AEJ0
J	-15	ALA	-	expression tag	UNP P0AEJ0
J	-14	ALA	-	expression tag	UNP P0AEJ0
J	-13	GLU	-	expression tag	UNP P0AEJ0
J	-12	GLN	-	expression tag	UNP P0AEJ0
J	-11	LEU	-	expression tag	UNP P0AEJ0
J	-10	LYS	-	expression tag	UNP P0AEJ0
J	-9	THR	-	expression tag	UNP P0AEJ0
J	-8	THR	-	expression tag	UNP P0AEJ0
J	-7	ARG	-	expression tag	UNP P0AEJ0
J	-6	ASN	-	expression tag	UNP P0AEJ0
J	-5	ALA	-	expression tag	UNP P0AEJ0
J	-4	TYR	-	expression tag	UNP P0AEJ0
J	-3	ILE	-	expression tag	UNP P0AEJ0
J	-2	GLN	-	expression tag	UNP P0AEJ0
J	-1	LYS	-	expression tag	UNP P0AEJ0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
J	0	TYR	-	expression tag	UNP P0AEJ0
J	1	LEU	-	expression tag	UNP P0AEJ0
J	2	GLU	-	expression tag	UNP P0AEJ0
J	3	ARG	-	expression tag	UNP P0AEJ0
J	4	ALA	-	expression tag	UNP P0AEJ0
J	5	ARG	-	expression tag	UNP P0AEJ0
J	6	SER	-	expression tag	UNP P0AEJ0
J	7	THR	-	expression tag	UNP P0AEJ0
J	8	LEU	-	expression tag	UNP P0AEJ0
J	9	MET	-	expression tag	UNP P0AEJ0

- Molecule 3 is a protein called Outer membrane protein TolC.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	428	Total	C	N	O	S	0	0
			3305	2038	586	676	5		
3	H	428	Total	C	N	O	S	0	0
			3305	2038	586	676	5		
3	I	428	Total	C	N	O	S	0	0
			3305	2038	586	676	5		

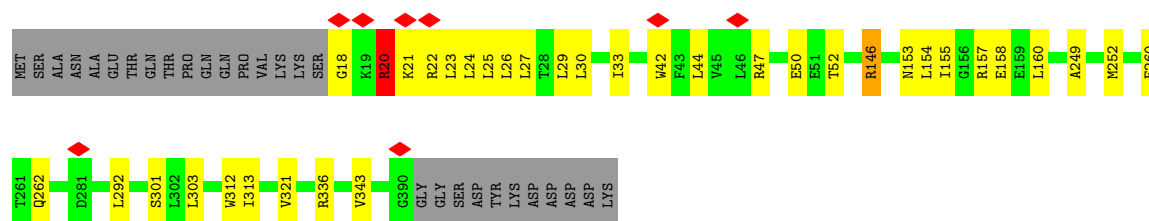
There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	169	LEU	VAL	engineered mutation	UNP P02930
G	472	ASP	-	expression tag	UNP P02930
G	473	TYR	-	expression tag	UNP P02930
G	474	LYS	-	expression tag	UNP P02930
G	475	ASP	-	expression tag	UNP P02930
G	476	ASP	-	expression tag	UNP P02930
G	477	ASP	-	expression tag	UNP P02930
G	478	ASP	-	expression tag	UNP P02930
G	479	LYS	-	expression tag	UNP P02930
H	169	LEU	VAL	engineered mutation	UNP P02930
H	472	ASP	-	expression tag	UNP P02930
H	473	TYR	-	expression tag	UNP P02930
H	474	LYS	-	expression tag	UNP P02930
H	475	ASP	-	expression tag	UNP P02930
H	476	ASP	-	expression tag	UNP P02930
H	477	ASP	-	expression tag	UNP P02930
H	478	ASP	-	expression tag	UNP P02930
H	479	LYS	-	expression tag	UNP P02930

Continued on next page...

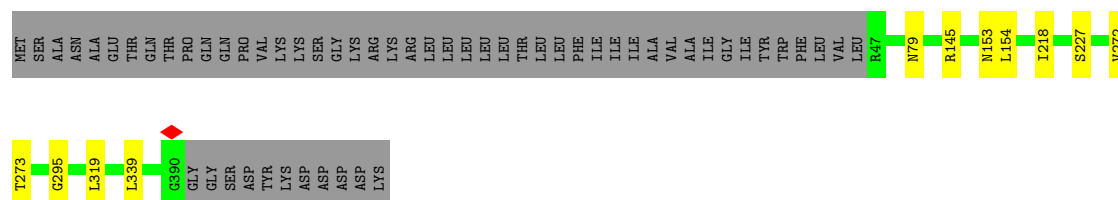
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	169	LEU	VAL	engineered mutation	UNP P02930
I	472	ASP	-	expression tag	UNP P02930
I	473	TYR	-	expression tag	UNP P02930
I	474	LYS	-	expression tag	UNP P02930
I	475	ASP	-	expression tag	UNP P02930
I	476	ASP	-	expression tag	UNP P02930
I	477	ASP	-	expression tag	UNP P02930
I	478	ASP	-	expression tag	UNP P02930
I	479	LYS	-	expression tag	UNP P02930



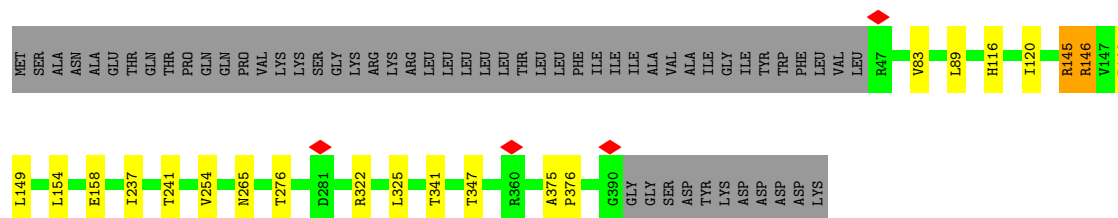
- Molecule 1: Multidrug export protein EmrA

Chain E: 83% 14%



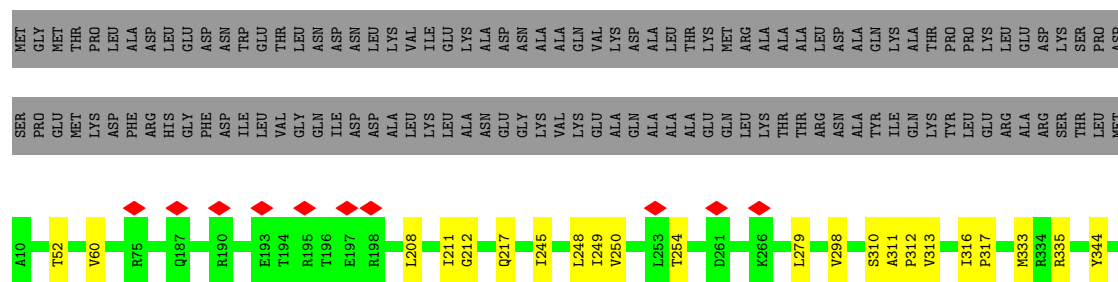
- Molecule 1: Multidrug export protein EmrA

Chain F: 81% 5% 14%



- Molecule 2: Multidrug export protein EmrB

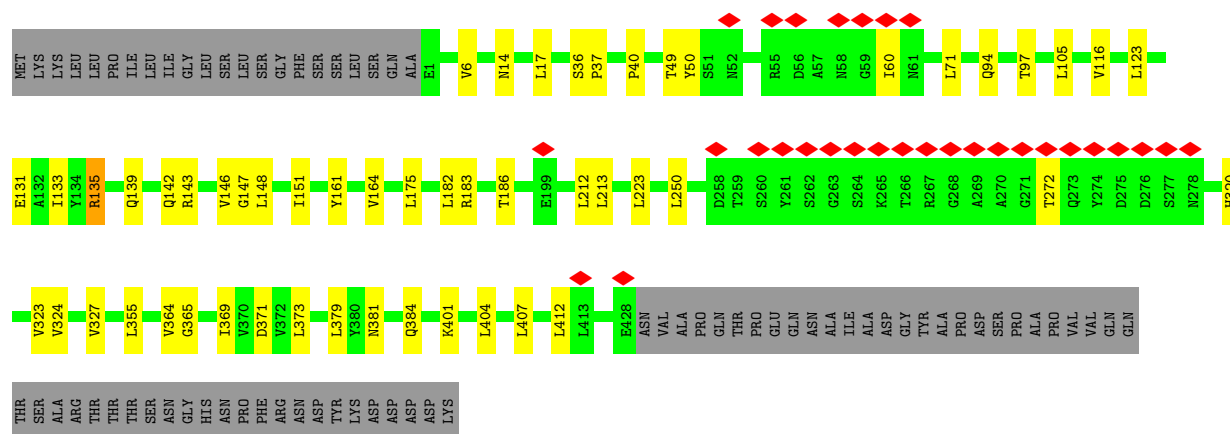
Chain J: 75% 5% 20%



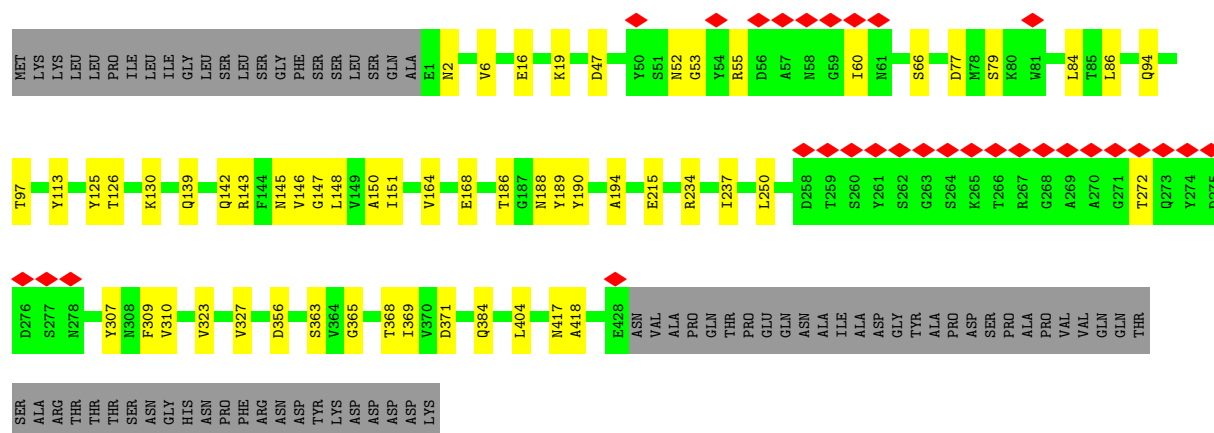
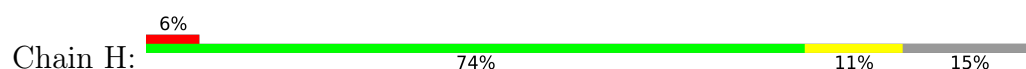
- Molecule 3: Outer membrane protein TolC

Chain G: 6% 75% 10% 15%

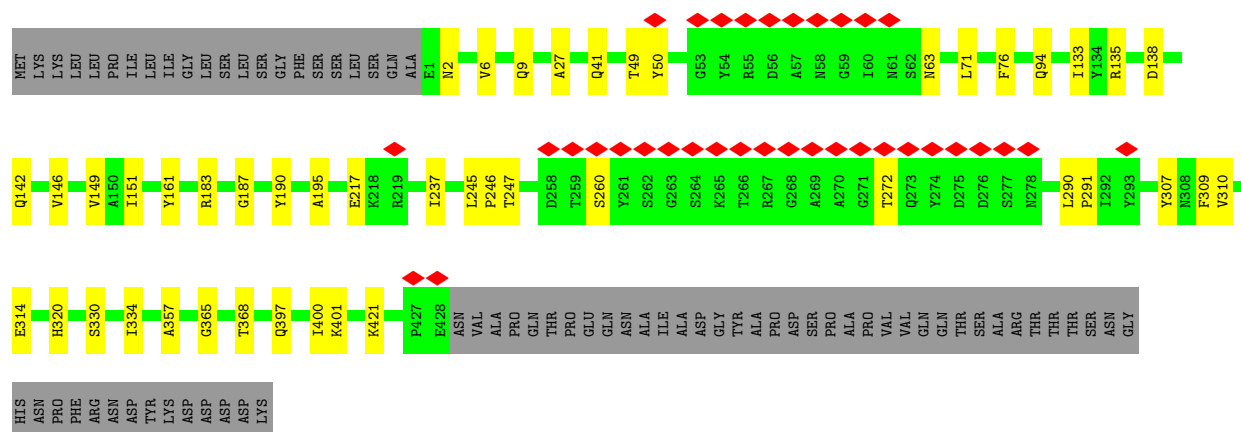
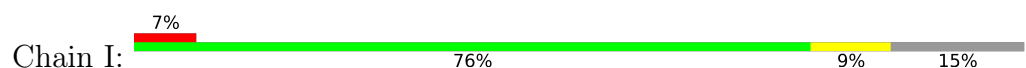




- Molecule 3: Outer membrane protein TolC



- Molecule 3: Outer membrane protein TolC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18440	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI/PHILIPS CM300FEG/HE	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.6	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.965	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	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	0.23	0/2674	0.39	0/3638
1	B	0.32	0/2709	0.48	1/3686 (0.0%)
1	C	0.28	0/2725	0.45	0/3709
1	D	0.40	0/2918	0.64	2/3969 (0.1%)
1	E	0.21	0/2674	0.34	0/3638
1	F	0.25	0/2674	0.38	0/3638
2	J	0.24	0/3903	0.40	0/5331
3	G	0.28	0/3346	0.48	0/4545
3	H	0.27	0/3346	0.41	0/4545
3	I	0.29	0/3346	0.48	1/4545 (0.0%)
All	All	0.28	0/30315	0.45	4/41244 (0.0%)

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	B	0	5
1	C	0	2
1	D	0	5
1	E	0	1
1	F	0	2
2	J	0	1
3	G	0	2
3	H	0	1
3	I	0	1
All	All	0	21

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	20	ARG	N-CA-C	-6.70	103.07	111.11
1	D	20	ARG	CA-C-O	-5.43	115.09	120.90
3	I	151	ILE	CA-C-O	-5.10	115.11	120.57
1	B	144	ASN	N-CA-C	-5.02	105.33	111.75

There are no chirality outliers.

All (21) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	145	ARG	Sidechain
1	B	145	ARG	Sidechain
1	B	146	ARG	Sidechain
1	B	228	ARG	Sidechain
1	B	229	ARG	Sidechain
1	B	47	ARG	Sidechain
1	C	145	ARG	Sidechain
1	C	47	ARG	Sidechain
1	D	146	ARG	Sidechain
1	D	20	ARG	Sidechain
1	D	22	ARG	Sidechain
1	D	336	ARG	Sidechain
1	D	47	ARG	Sidechain
1	E	145	ARG	Sidechain
1	F	145	ARG	Sidechain
1	F	146	ARG	Sidechain
3	G	135	ARG	Sidechain
3	G	183	ARG	Sidechain
3	H	55	ARG	Sidechain
3	I	135	ARG	Sidechain
2	J	335	ARG	Sidechain

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	2638	0	2676	16	0
1	B	2672	0	2716	30	0
1	C	2686	0	2726	17	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2877	0	2960	33	0
1	E	2638	0	2676	8	0
1	F	2638	0	2676	16	0
2	J	3805	0	3896	25	0
3	G	3305	0	3256	44	0
3	H	3305	0	3256	50	0
3	I	3305	0	3256	38	0
All	All	29869	0	30094	224	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 4.

All (224) 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)
3:H:368:THR:HG22	3:H:371:ASP:OD1	1.51	1.10
1:D:154:LEU:O	3:H:368:THR:OG1	1.78	1.01
1:B:154:LEU:CD1	3:I:142:GLN:HG3	1.93	0.99
3:I:142:GLN:O	3:I:146:VAL:HG23	1.75	0.86
3:H:237:ILE:HD11	3:H:309:PHE:HB2	1.63	0.79
1:B:154:LEU:HD13	3:I:142:GLN:HG3	1.65	0.78
3:H:368:THR:CG2	3:H:371:ASP:OD1	2.32	0.74
1:B:149:LEU:HD21	3:I:146:VAL:HG21	1.70	0.72
1:D:24:LEU:HD13	2:J:250:VAL:HG12	1.75	0.68
1:B:145:ARG:O	3:I:146:VAL:HG11	1.94	0.67
1:C:153:ASN:O	3:H:151:ILE:HG22	1.94	0.67
1:C:158:GLU:HB2	3:H:147:GLY:O	1.96	0.66
3:G:116:VAL:HG21	3:G:182:LEU:HD22	1.78	0.64
1:A:129:ILE:HD11	1:A:181:TYR:CB	2.27	0.64
1:B:156:GLY:N	3:I:368:THR:HG22	2.12	0.64
1:B:278:ILE:HG23	1:B:279:TYR:CD1	2.32	0.64
3:H:186:THR:HG21	3:H:190:TYR:HE2	1.63	0.64
2:J:344:TYR:CD2	2:J:374:ALA:HB1	2.33	0.64
1:D:157:ARG:NH2	3:H:363:SER:O	2.31	0.63
1:B:62:ILE:HD13	1:C:232:GLN:HB2	1.79	0.63
1:F:254:VAL:HG23	1:F:325:LEU:HD11	1.81	0.63
1:C:153:ASN:O	3:H:151:ILE:CG2	2.47	0.62
3:G:17:LEU:HD12	3:G:105:LEU:CD2	2.29	0.62
3:H:234:ARG:HA	3:H:237:ILE:HD12	1.81	0.62
1:D:24:LEU:HD22	2:J:250:VAL:CG1	2.29	0.62
1:D:249:ALA:HA	1:D:252:MET:HE3	1.82	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:LEU:CD2	3:I:146:VAL:HG21	2.30	0.61
1:D:21:LYS:HA	1:D:24:LEU:HG	1.83	0.61
1:D:153:ASN:HD21	3:H:369:ILE:HD12	1.66	0.61
1:F:375:ALA:HB3	1:F:376:PRO:HD3	1.82	0.61
1:A:129:ILE:HD11	1:A:181:TYR:HB3	1.81	0.60
1:B:77:ALA:HB1	1:B:226:VAL:HG21	1.83	0.60
1:D:18:GLY:O	1:D:21:LYS:HB2	2.02	0.59
3:G:133:ILE:HG13	3:G:164:VAL:HG11	1.82	0.59
2:J:208:LEU:CB	2:J:248:LEU:HD13	2.33	0.59
1:B:145:ARG:O	3:I:146:VAL:CG1	2.50	0.59
3:I:237:ILE:HD11	3:I:309:PHE:CB	2.32	0.59
1:F:116:HIS:CE1	1:F:120:ILE:HD11	2.37	0.59
3:I:138:ASP:O	3:I:142:GLN:HG2	2.03	0.58
1:D:21:LYS:O	1:D:25:LEU:HD12	2.03	0.58
3:G:355:LEU:HD23	3:G:379:LEU:HD22	1.86	0.58
3:H:77:ASP:OD2	3:H:79:SER:OG	2.18	0.58
1:F:148:PRO:HG2	3:G:146:VAL:HG21	1.85	0.58
1:F:158:GLU:HB2	3:G:365:GLY:O	2.04	0.58
1:C:157:ARG:NH2	3:H:145:ASN:O	2.37	0.57
1:C:156:GLY:N	3:H:150:ALA:HB2	2.18	0.57
3:G:40:PRO:HB3	3:G:71:LEU:HD11	1.86	0.57
1:B:62:ILE:CG2	1:B:222:MET:HE3	2.35	0.56
1:B:154:LEU:HD12	3:I:142:GLN:HG3	1.83	0.56
3:I:27:ALA:CB	3:I:94:GLN:HG3	2.36	0.56
3:H:52:ASN:OD1	3:H:60:ILE:O	2.24	0.56
1:B:154:LEU:HD13	3:I:142:GLN:CG	2.36	0.55
1:C:154:LEU:HD23	3:I:357:ALA:HA	1.89	0.55
3:I:237:ILE:HD11	3:I:309:PHE:HB2	1.87	0.55
3:H:143:ARG:O	3:H:146:VAL:HG22	2.07	0.54
1:B:62:ILE:HG22	1:B:222:MET:HE3	1.89	0.54
1:B:149:LEU:HD21	3:I:146:VAL:CG2	2.38	0.54
1:D:20:ARG:O	1:D:24:LEU:HG	2.08	0.54
1:D:23:LEU:HA	1:D:26:LEU:HB2	1.91	0.53
2:J:208:LEU:HB3	2:J:248:LEU:HD13	1.90	0.52
3:G:17:LEU:HD12	3:G:105:LEU:HD23	1.89	0.52
3:G:135:ARG:HH12	3:G:369:ILE:HD13	1.74	0.52
1:C:263:ILE:HD12	1:C:292:LEU:HD23	1.91	0.52
1:D:24:LEU:HD22	2:J:250:VAL:HG13	1.89	0.52
1:D:146:ARG:HH22	3:H:148:LEU:HD22	1.74	0.52
3:I:76:PHE:O	3:I:247:THR:OG1	2.12	0.52
1:D:301:SER:OG	1:D:303:LEU:O	2.23	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:17:LEU:HD12	3:G:105:LEU:HD22	1.92	0.51
1:D:153:ASN:HD21	3:H:369:ILE:CD1	2.24	0.51
2:J:208:LEU:HB2	2:J:248:LEU:HD13	1.93	0.51
1:D:50:GLU:CG	1:D:262:GLN:HB3	2.40	0.51
3:G:6:VAL:HG13	3:G:186:THR:HG21	1.93	0.51
1:A:246:VAL:HG13	1:A:246:VAL:O	2.10	0.50
3:G:135:ARG:HG3	3:G:135:ARG:HH11	1.76	0.50
3:H:237:ILE:HD11	3:H:309:PHE:CB	2.38	0.50
1:F:154:LEU:HD13	3:G:139:GLN:HA	1.94	0.50
1:B:146:ARG:HG3	1:B:155:ILE:CD1	2.42	0.50
3:I:397:GLN:O	3:I:401:LYS:HG2	2.11	0.50
3:I:307:TYR:O	3:I:310:VAL:HG22	2.12	0.50
1:C:158:GLU:HB2	3:H:148:LEU:HA	1.95	0.49
3:H:19:LYS:HA	3:I:314:GLU:OE1	2.12	0.49
3:H:142:GLN:O	3:H:146:VAL:HG13	2.13	0.49
3:H:126:THR:HG21	3:H:168:GLU:HA	1.94	0.49
2:J:208:LEU:HB3	2:J:248:LEU:HB2	1.95	0.48
3:H:84:LEU:HD23	3:H:84:LEU:C	2.38	0.48
3:I:2:ASN:O	3:I:6:VAL:HG23	2.12	0.48
3:I:9:GLN:OE1	3:I:190:TYR:OH	2.31	0.48
1:D:21:LYS:HG3	2:J:254:THR:HG21	1.95	0.48
2:J:279:LEU:HB2	2:J:491:LEU:HD11	1.96	0.48
1:E:153:ASN:ND2	1:E:153:ASN:O	2.46	0.48
1:B:157:ARG:NH1	3:I:365:GLY:HA3	2.29	0.48
1:B:80:THR:O	1:B:80:THR:OG1	2.30	0.48
3:H:47:ASP:OD1	3:H:47:ASP:O	2.31	0.48
1:C:294:MET:HE1	1:D:249:ALA:HB2	1.96	0.47
1:D:27:LEU:HA	1:D:30:LEU:HD12	1.95	0.47
1:C:278:ILE:HD13	1:C:339:LEU:HD13	1.96	0.47
1:A:115:THR:HG21	1:A:196:GLN:HG3	1.96	0.47
2:J:310:SER:O	2:J:313:VAL:HG12	2.15	0.47
3:G:131:GLU:OE1	3:G:373:LEU:HD13	2.15	0.47
3:G:94:GLN:O	3:G:97:THR:OG1	2.29	0.47
3:H:215:GLU:HB3	3:H:404:LEU:HD11	1.96	0.47
1:A:78:ASP:O	1:F:322:ARG:NH1	2.47	0.47
1:A:156:GLY:HA2	3:I:149:VAL:O	2.15	0.47
1:C:263:ILE:HG23	1:C:292:LEU:CD2	2.45	0.46
3:H:250:LEU:C	3:H:250:LEU:HD23	2.40	0.46
3:I:217:GLU:OE1	3:I:320:HIS:CE1	2.68	0.46
1:F:148:PRO:CG	3:G:146:VAL:HG21	2.45	0.46
2:J:298:VAL:HG12	2:J:298:VAL:O	2.14	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:276:THR:OG1	1:B:278:ILE:HG22	2.15	0.46
2:J:60:VAL:HG22	2:J:217:GLN:HB3	1.97	0.46
2:J:333:MET:HE1	2:J:384:THR:CG2	2.45	0.46
1:B:74:LYS:HB2	1:B:91:THR:HG22	1.97	0.46
1:D:29:LEU:O	1:D:33:ILE:HD12	2.15	0.46
1:D:312:TRP:C	1:D:313:ILE:HD12	2.40	0.46
3:H:130:LYS:HA	3:H:164:VAL:HG21	1.98	0.46
3:I:183:ARG:O	3:I:187:GLY:N	2.46	0.46
1:D:292:LEU:HD23	1:D:321:VAL:HG22	1.97	0.46
1:A:237:ILE:HD12	1:A:243:LEU:HD21	1.97	0.46
1:C:351:ASP:OD1	1:C:353:GLN:N	2.49	0.46
3:H:47:ASP:OD1	3:H:66:SER:OG	2.33	0.45
1:B:278:ILE:HG23	1:B:279:TYR:HD1	1.80	0.45
1:D:52:THR:HG22	1:D:343:VAL:CG2	2.47	0.45
1:D:153:ASN:ND2	3:H:369:ILE:HD12	2.30	0.45
3:G:123:LEU:C	3:G:123:LEU:HD23	2.41	0.45
2:J:208:LEU:HD13	2:J:248:LEU:HA	1.98	0.45
3:G:143:ARG:O	3:G:147:GLY:O	2.35	0.45
3:G:272:THR:HG22	3:G:272:THR:O	2.17	0.45
3:H:125:TYR:CD2	3:H:384:GLN:HB2	2.52	0.45
3:H:188:ASN:OD1	3:H:189:TYR:N	2.50	0.45
1:A:145:ARG:HG3	3:G:364:VAL:HB	1.97	0.45
3:G:250:LEU:HD23	3:G:250:LEU:C	2.41	0.45
3:H:19:LYS:CA	3:I:314:GLU:OE1	2.64	0.45
3:H:52:ASN:O	3:H:53:GLY:C	2.58	0.45
1:A:366:VAL:O	1:A:366:VAL:HG22	2.17	0.45
1:E:295:GLY:O	1:E:319:LEU:HD12	2.17	0.45
3:H:186:THR:HG21	3:H:190:TYR:CE2	2.49	0.45
1:D:153:ASN:ND2	3:H:369:ILE:CD1	2.80	0.45
1:F:276:THR:HG22	1:F:341:THR:HG22	1.99	0.45
3:H:16:GLU:N	3:H:16:GLU:OE1	2.50	0.44
3:I:133:ILE:HG21	3:I:161:TYR:HA	1.99	0.44
1:C:376:PRO:O	1:C:380:LEU:HD13	2.17	0.44
1:D:313:ILE:HD12	1:D:313:ILE:N	2.32	0.44
3:G:14:ASN:ND2	3:G:105:LEU:HD13	2.32	0.44
3:H:186:THR:HG23	3:H:188:ASN:H	1.82	0.44
3:I:272:THR:HG22	3:I:272:THR:O	2.17	0.44
1:D:158:GLU:N	3:H:365:GLY:O	2.49	0.44
2:J:316:ILE:HB	2:J:317:PRO:HD3	2.00	0.44
2:J:499:LYS:O	2:J:501:PRO:HD2	2.18	0.44
1:E:218:ILE:HD12	1:E:218:ILE:N	2.32	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:36:SER:N	3:G:37:PRO:HD2	2.34	0.43
3:G:135:ARG:HH11	3:G:135:ARG:CG	2.31	0.43
3:H:417:ASN:OD1	3:H:418:ALA:N	2.51	0.43
1:D:153:ASN:ND2	1:D:153:ASN:O	2.51	0.43
2:J:311:ALA:N	2:J:312:PRO:HD2	2.33	0.43
3:G:60:ILE:HG23	3:G:60:ILE:O	2.19	0.43
3:H:323:VAL:O	3:H:327:VAL:HG23	2.19	0.43
1:B:295:GLY:O	1:B:299:ALA:HB3	2.19	0.43
1:E:79:ASN:ND2	1:E:227:SER:O	2.51	0.43
3:G:320:HIS:O	3:G:323:VAL:HG12	2.19	0.43
3:G:324:VAL:O	3:G:327:VAL:HG12	2.19	0.43
3:G:381:ASN:HA	3:G:384:GLN:HG2	2.00	0.43
3:I:195:ALA:N	3:I:421:LYS:O	2.48	0.43
1:F:265:ASN:O	1:F:347:THR:HG23	2.19	0.43
1:C:272:VAL:HG12	1:C:273:THR:N	2.34	0.43
1:F:83:VAL:HG11	1:F:89:LEU:HD21	2.00	0.43
1:D:260:GLU:OE2	1:E:339:LEU:HA	2.19	0.43
2:J:384:THR:O	2:J:388:SER:OG	2.34	0.43
3:G:213:LEU:HD23	3:G:327:VAL:HG11	2.01	0.43
3:G:401:LYS:HB3	3:G:407:LEU:CD1	2.48	0.43
3:H:272:THR:HG22	3:H:272:THR:O	2.19	0.43
3:I:49:THR:HG22	3:I:50:TYR:N	2.33	0.43
3:I:397:GLN:O	3:I:400:ILE:HG22	2.19	0.43
1:A:365:ALA:HB1	1:B:233:PRO:HG2	2.01	0.42
1:F:149:LEU:HD11	3:G:143:ARG:HG2	1.99	0.42
3:G:223:LEU:HD12	3:G:223:LEU:C	2.44	0.42
1:B:143:TYR:O	1:B:147:VAL:HG23	2.19	0.42
2:J:52:THR:O	2:J:52:THR:HG22	2.19	0.42
3:G:49:THR:HG22	3:G:50:TYR:N	2.34	0.42
3:I:290:LEU:HD12	3:I:291:PRO:HD2	2.02	0.42
1:A:291:GLY:C	1:A:292:LEU:HD12	2.44	0.42
3:H:86:LEU:HD12	3:H:86:LEU:C	2.44	0.42
3:I:245:LEU:HD23	3:I:246:PRO:O	2.19	0.42
3:H:307:TYR:O	3:H:310:VAL:HG12	2.19	0.42
3:G:40:PRO:CB	3:G:71:LEU:HD11	2.49	0.42
1:A:77:ALA:HB1	1:A:226:VAL:HG21	2.02	0.42
1:E:153:ASN:HD21	3:G:151:ILE:HB	1.85	0.42
1:F:149:LEU:CD2	3:G:142:GLN:HB3	2.49	0.42
2:J:333:MET:HE1	2:J:384:THR:HG22	2.01	0.42
2:J:404:PHE:CZ	2:J:408:LEU:HD11	2.55	0.42
1:A:72:VAL:HG13	1:A:90:VAL:HG13	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:21:LYS:HA	1:D:24:LEU:CG	2.48	0.42
1:E:154:LEU:HD11	3:H:356:ASP:OD2	2.20	0.42
3:I:330:SER:O	3:I:334:ILE:HG12	2.19	0.42
1:B:157:ARG:NH1	3:I:365:GLY:CA	2.83	0.41
2:J:387:LEU:N	2:J:387:LEU:HD12	2.35	0.41
1:A:303:LEU:HD12	1:A:303:LEU:N	2.35	0.41
3:G:412:LEU:C	3:G:412:LEU:HD23	2.45	0.41
3:H:113:TYR:OH	3:H:194:ALA:O	2.28	0.41
1:E:272:VAL:HG12	1:E:273:THR:N	2.35	0.41
3:G:161:TYR:O	3:G:164:VAL:HG22	2.20	0.41
3:G:371:ASP:N	3:G:371:ASP:OD1	2.53	0.41
1:B:140:GLN:NE2	1:B:144:ASN:HD21	2.18	0.41
2:J:211:ILE:HG23	2:J:212:GLY:N	2.35	0.41
3:H:2:ASN:O	3:H:6:VAL:HG23	2.21	0.41
1:F:149:LEU:CD1	3:G:143:ARG:HG2	2.51	0.41
1:F:237:ILE:CD1	1:F:241:THR:HG21	2.51	0.41
3:G:123:LEU:HD13	3:G:175:LEU:HD22	2.03	0.41
2:J:245:ILE:HG22	2:J:249:ILE:HD12	2.02	0.41
3:H:94:GLN:O	3:H:97:THR:HG22	2.21	0.41
3:I:41:GLN:O	3:I:71:LEU:HD23	2.21	0.41
1:D:154:LEU:HD23	3:H:139:GLN:HA	2.02	0.41
3:G:401:LYS:CG	3:G:407:LEU:HG	2.51	0.41
1:A:79:ASN:ND2	1:A:227:SER:O	2.54	0.41
1:B:75:VAL:HG11	1:B:229:ARG:CZ	2.51	0.41
1:B:258:PHE:HD2	1:B:321:VAL:HG22	1.85	0.41
1:B:144:ASN:N	1:B:144:ASN:HD22	2.19	0.41
1:C:274:ILE:HD12	1:C:325:LEU:HD21	2.02	0.41
1:D:155:ILE:HD11	1:D:160:LEU:HD21	2.03	0.41
1:A:364:VAL:HG11	1:B:78:ASP:OD1	2.22	0.40
1:C:90:VAL:HG12	1:C:91:THR:N	2.36	0.40
1:F:145:ARG:HA	3:G:146:VAL:CG1	2.50	0.40
3:G:212:LEU:HD22	3:G:404:LEU:HD11	2.02	0.40
1:D:146:ARG:HH12	3:H:148:LEU:HD21	1.86	0.40
3:I:63:ASN:OD1	3:I:260:SER:O	2.39	0.40

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	342/401 (85%)	322 (94%)	20 (6%)	0	100	100
1	B	346/401 (86%)	331 (96%)	15 (4%)	0	100	100
1	C	347/401 (86%)	339 (98%)	8 (2%)	0	100	100
1	D	371/401 (92%)	355 (96%)	16 (4%)	0	100	100
1	E	342/401 (85%)	325 (95%)	17 (5%)	0	100	100
1	F	342/401 (85%)	334 (98%)	8 (2%)	0	100	100
2	J	492/614 (80%)	474 (96%)	18 (4%)	0	100	100
3	G	426/501 (85%)	418 (98%)	8 (2%)	0	100	100
3	H	426/501 (85%)	416 (98%)	10 (2%)	0	100	100
3	I	426/501 (85%)	415 (97%)	11 (3%)	0	100	100
All	All	3860/4523 (85%)	3729 (97%)	131 (3%)	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	286/335 (85%)	285 (100%)	1 (0%)	91	96
1	B	290/335 (87%)	290 (100%)	0	100	100
1	C	291/335 (87%)	291 (100%)	0	100	100
1	D	311/335 (93%)	309 (99%)	2 (1%)	84	92

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	286/335 (85%)	286 (100%)	0	100	100
1	F	286/335 (85%)	285 (100%)	1 (0%)	91	96
2	J	408/506 (81%)	408 (100%)	0	100	100
3	G	358/420 (85%)	357 (100%)	1 (0%)	91	96
3	H	358/420 (85%)	358 (100%)	0	100	100
3	I	358/420 (85%)	358 (100%)	0	100	100
All	All	3232/3776 (86%)	3227 (100%)	5 (0%)	91	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	ASN
1	D	42	TRP
1	D	44	LEU
1	F	146	ARG
3	G	148	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	ASN
1	A	124	GLN
1	A	179	GLN
1	A	265	ASN
1	B	114	GLN
1	B	144	ASN
1	C	117	GLN
1	C	200	GLN
1	D	153	ASN
1	D	306	GLN
1	E	124	GLN
1	E	153	ASN
1	E	257	ASN
1	E	265	ASN
1	E	311	ASN
1	F	121	ASN
1	F	140	GLN
1	F	144	ASN
1	F	346	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	J	174	ASN
2	J	257	ASN
2	J	269	ASN
3	G	9	GLN
3	G	14	ASN
3	G	136	GLN
3	G	142	GLN
3	G	200	ASN
3	G	225	GLN
3	G	244	HIS
3	G	410	GLN
3	H	2	ASN
3	H	9	GLN
3	H	102	GLN
3	H	103	GLN
3	H	139	GLN
3	H	320	HIS
3	I	32	ASN
3	I	188	ASN
3	I	220	ASN
3	I	320	HIS
3	I	332	ASN
3	I	335	ASN
3	I	346	GLN
3	I	352	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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.

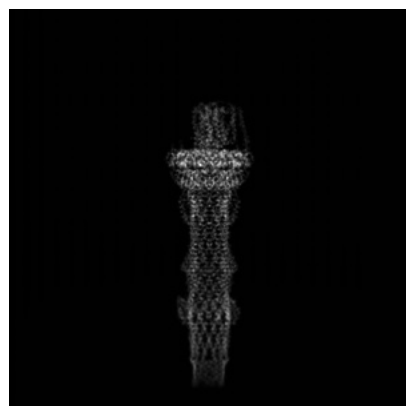
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39885. These allow visual inspection of the internal detail of the map and identification of artifacts.

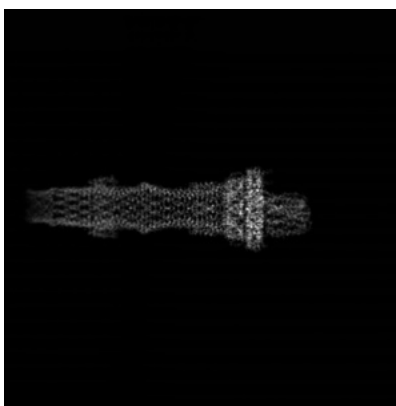
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

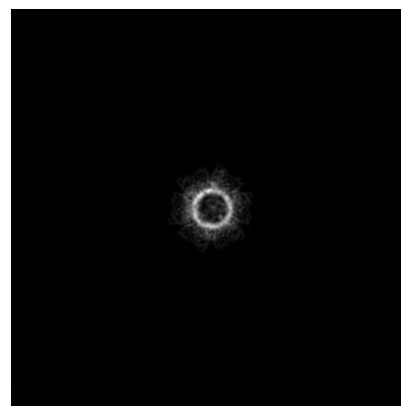
6.1.1 Primary map



X

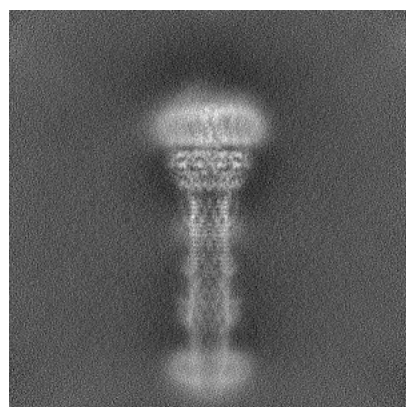


Y

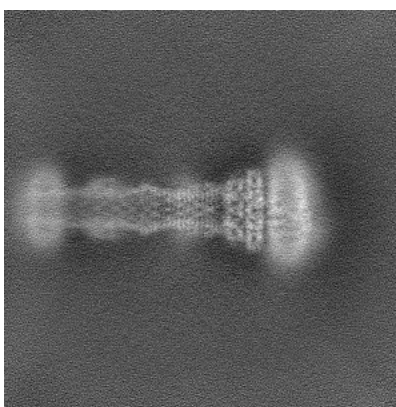


Z

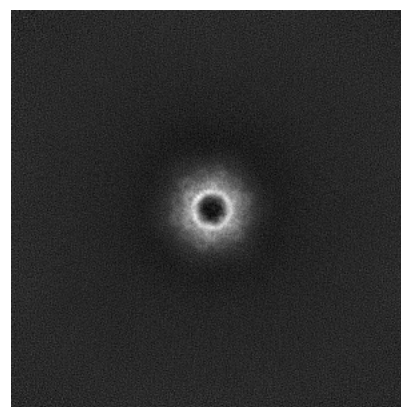
6.1.2 Raw map



X



Y

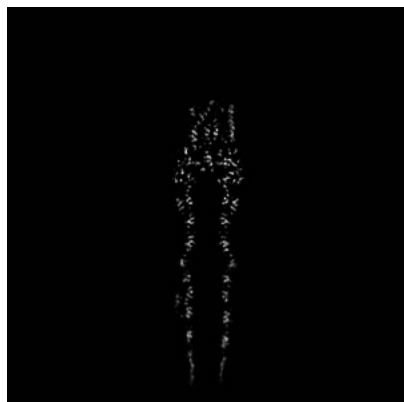


Z

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

6.2 Central slices [i](#)

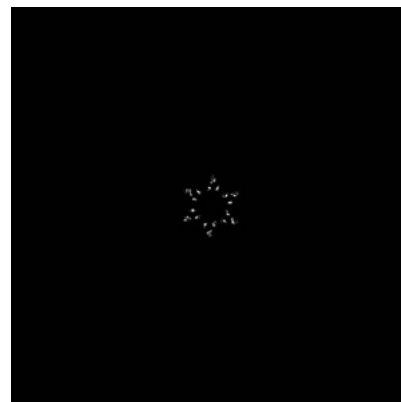
6.2.1 Primary map



X Index: 200

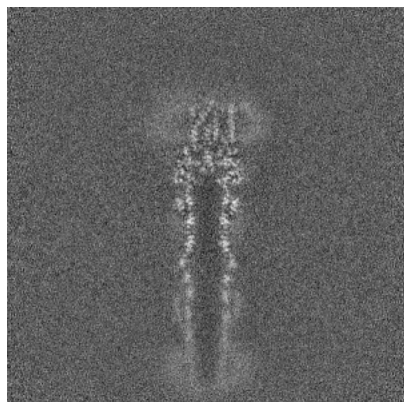


Y Index: 200

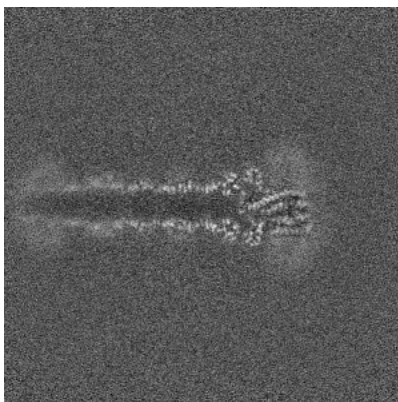


Z Index: 200

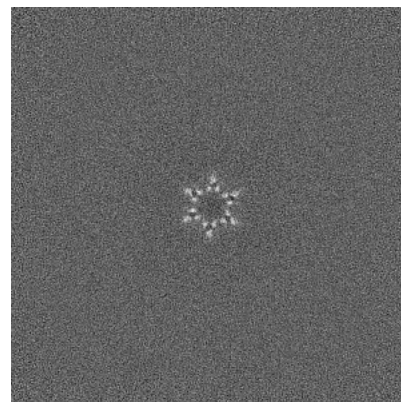
6.2.2 Raw map



X Index: 200



Y Index: 200



Z Index: 200

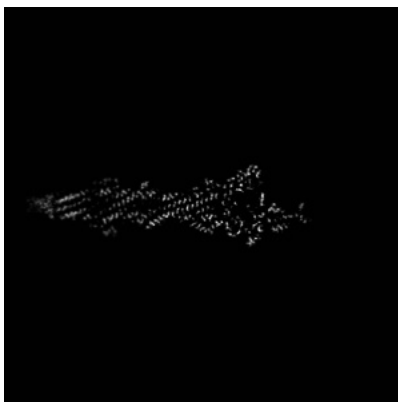
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

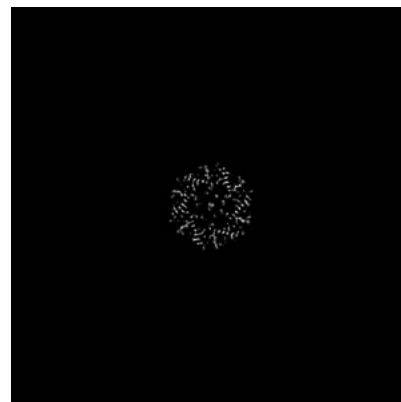
6.3.1 Primary map



X Index: 184

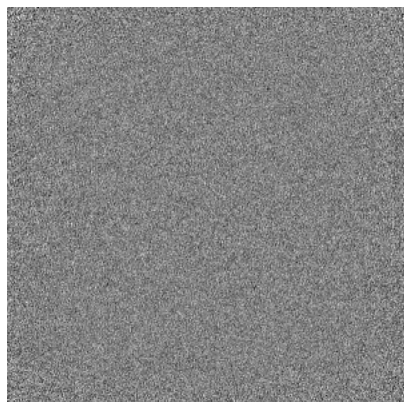


Y Index: 215

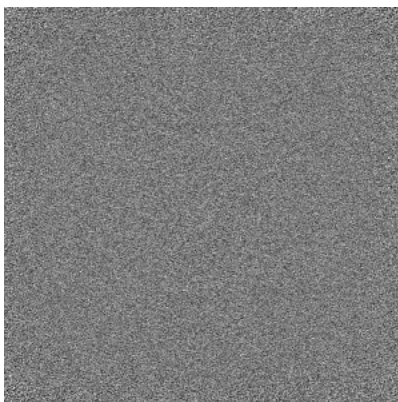


Z Index: 246

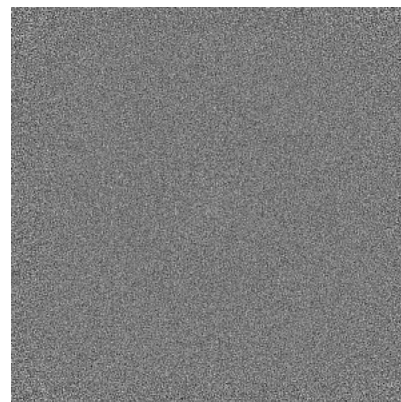
6.3.2 Raw map



X Index: 0



Y Index: 0

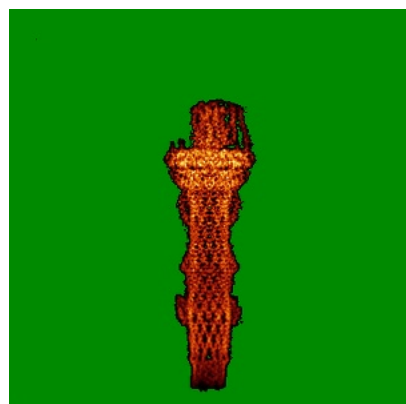


Z Index: 0

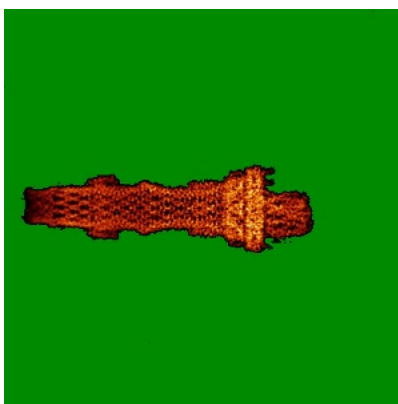
The images above show the largest variance slices of the map in three orthogonal directions.

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

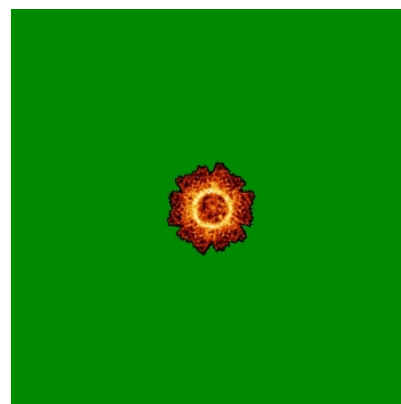
6.4.1 Primary map



X

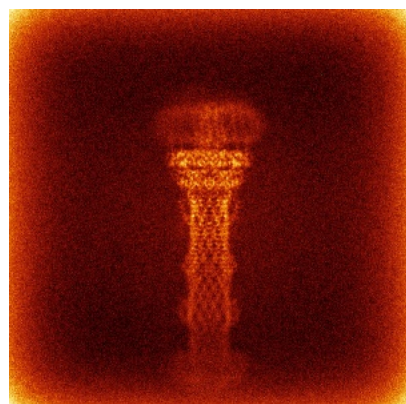


Y

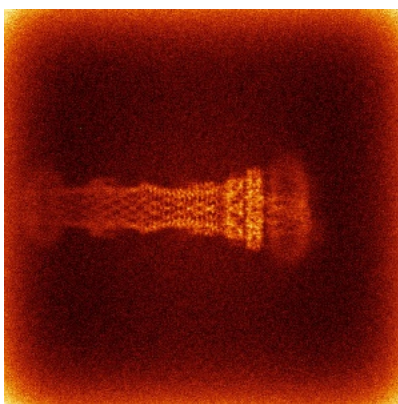


Z

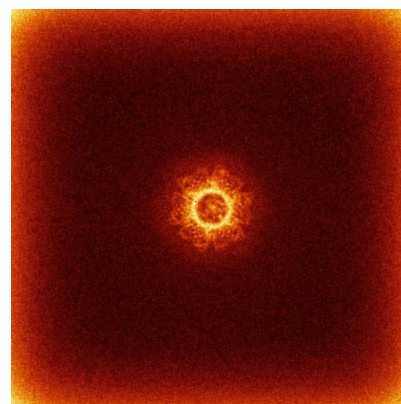
6.4.2 Raw map



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.

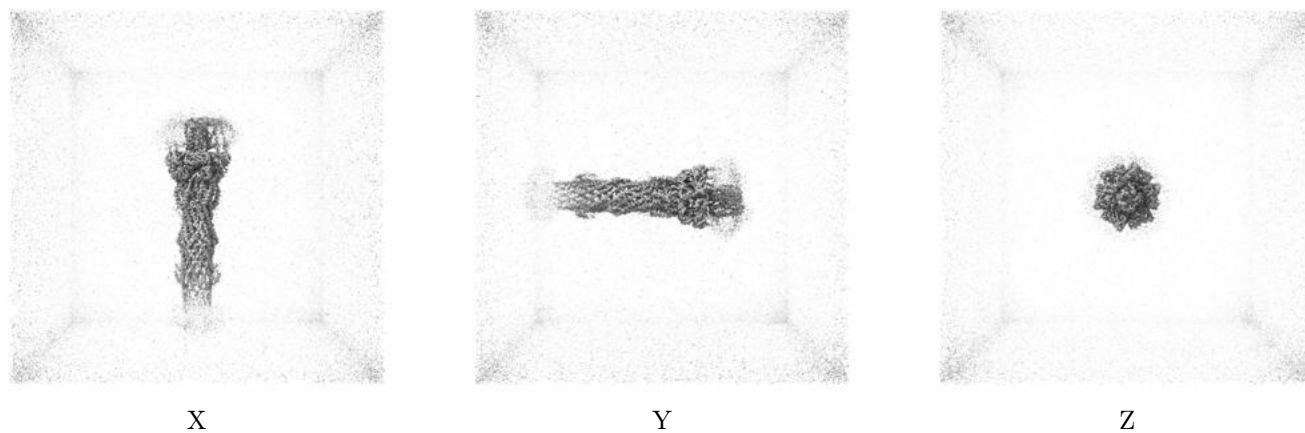
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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



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.

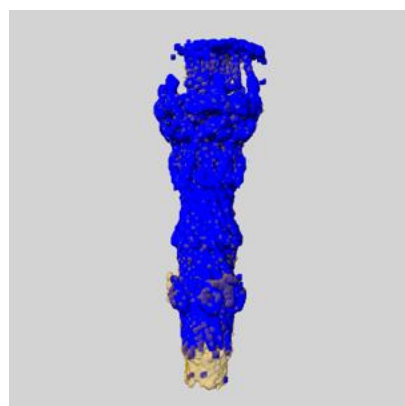
6.6 Mask visualisation [i](#)

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

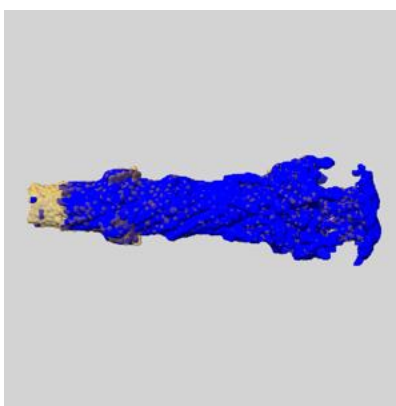
A mask typically either:

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

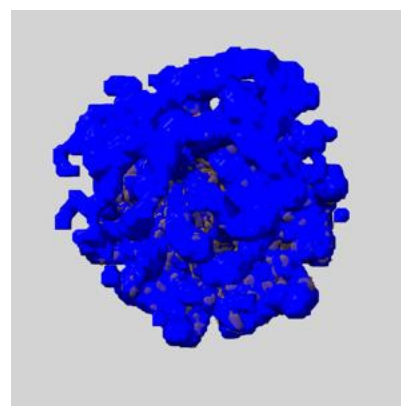
6.6.1 emd_39885_msk_1.map [i](#)



X



Y

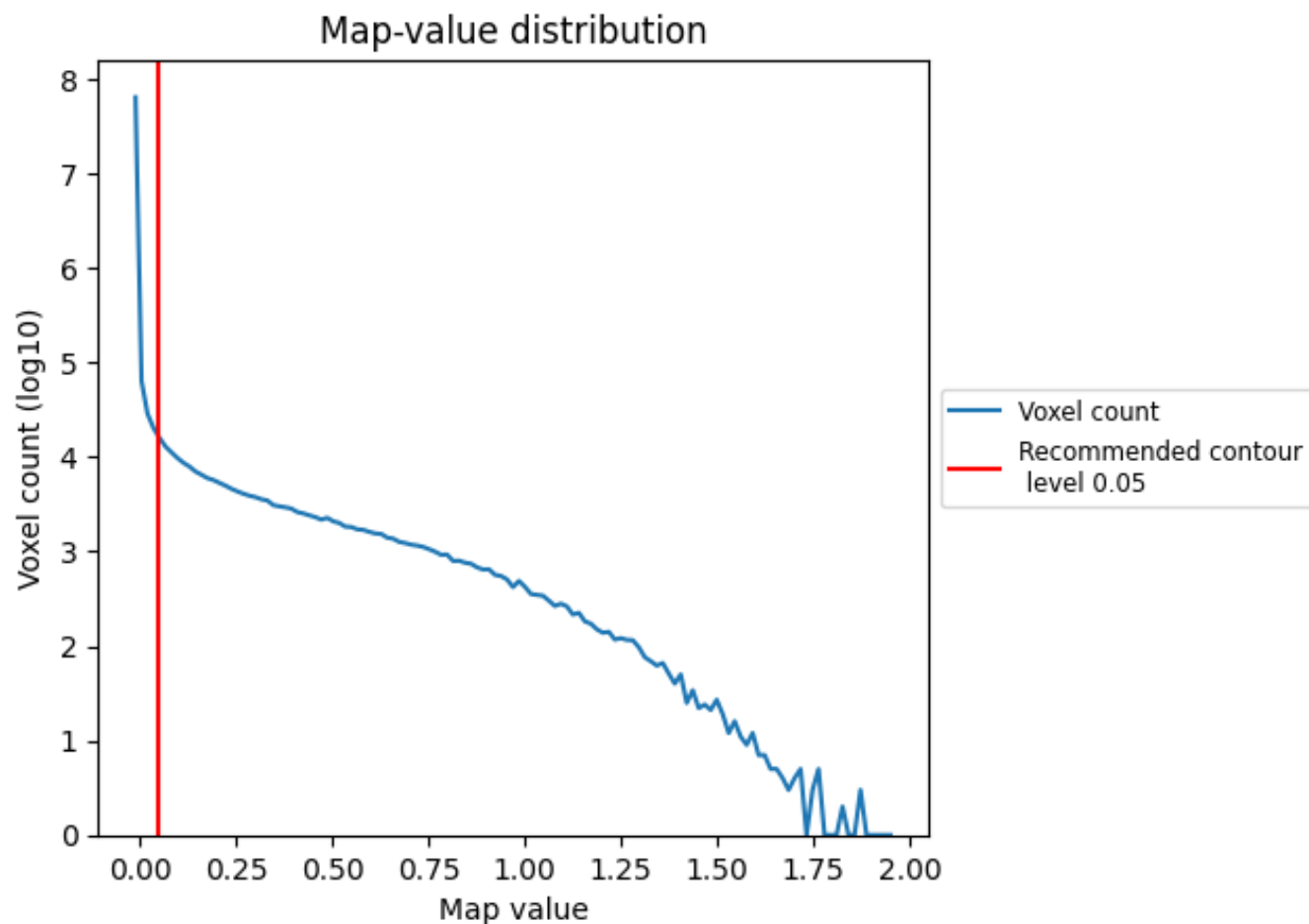


Z

7 Map analysis [i](#)

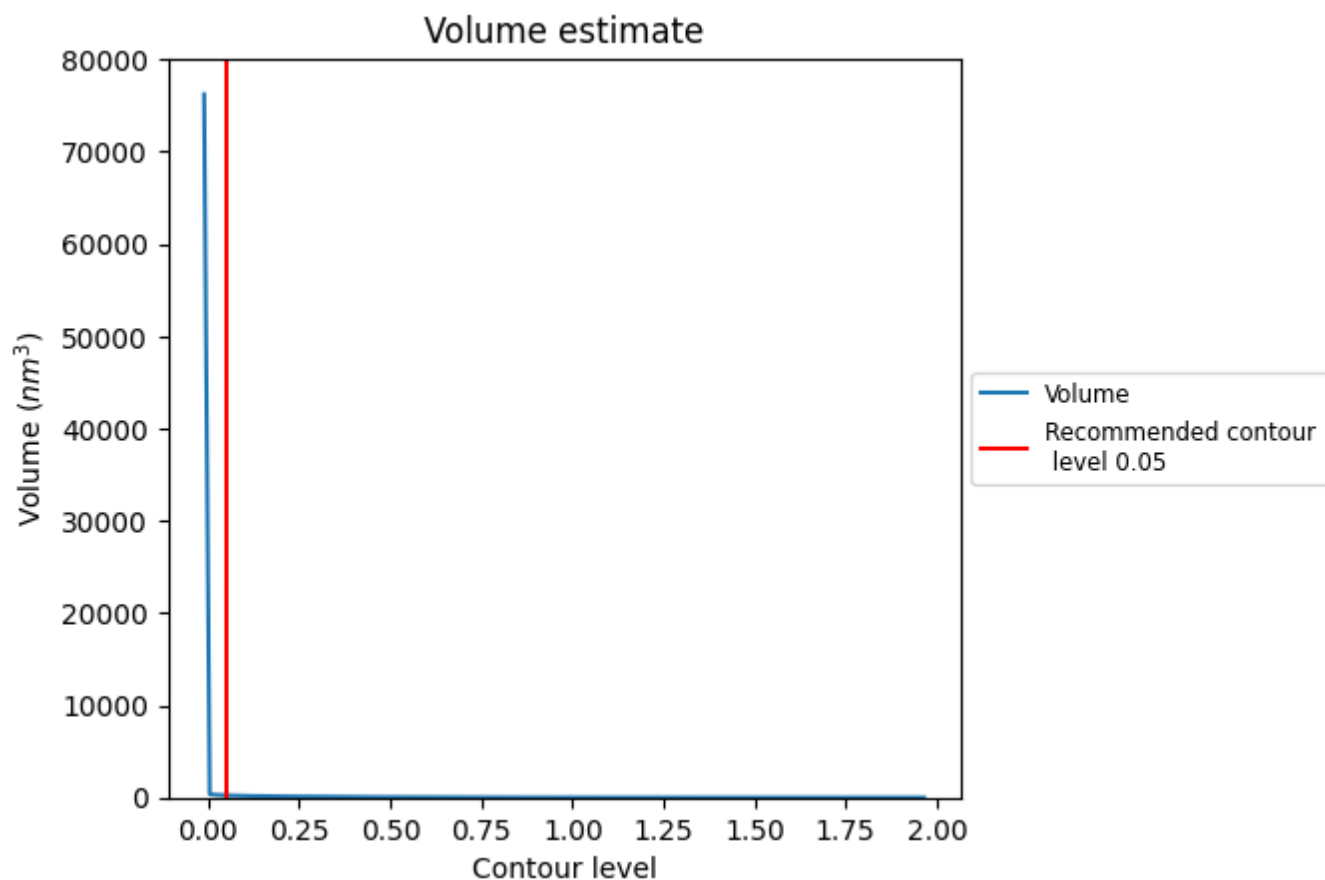
This section contains the results of statistical analysis of the map.

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.

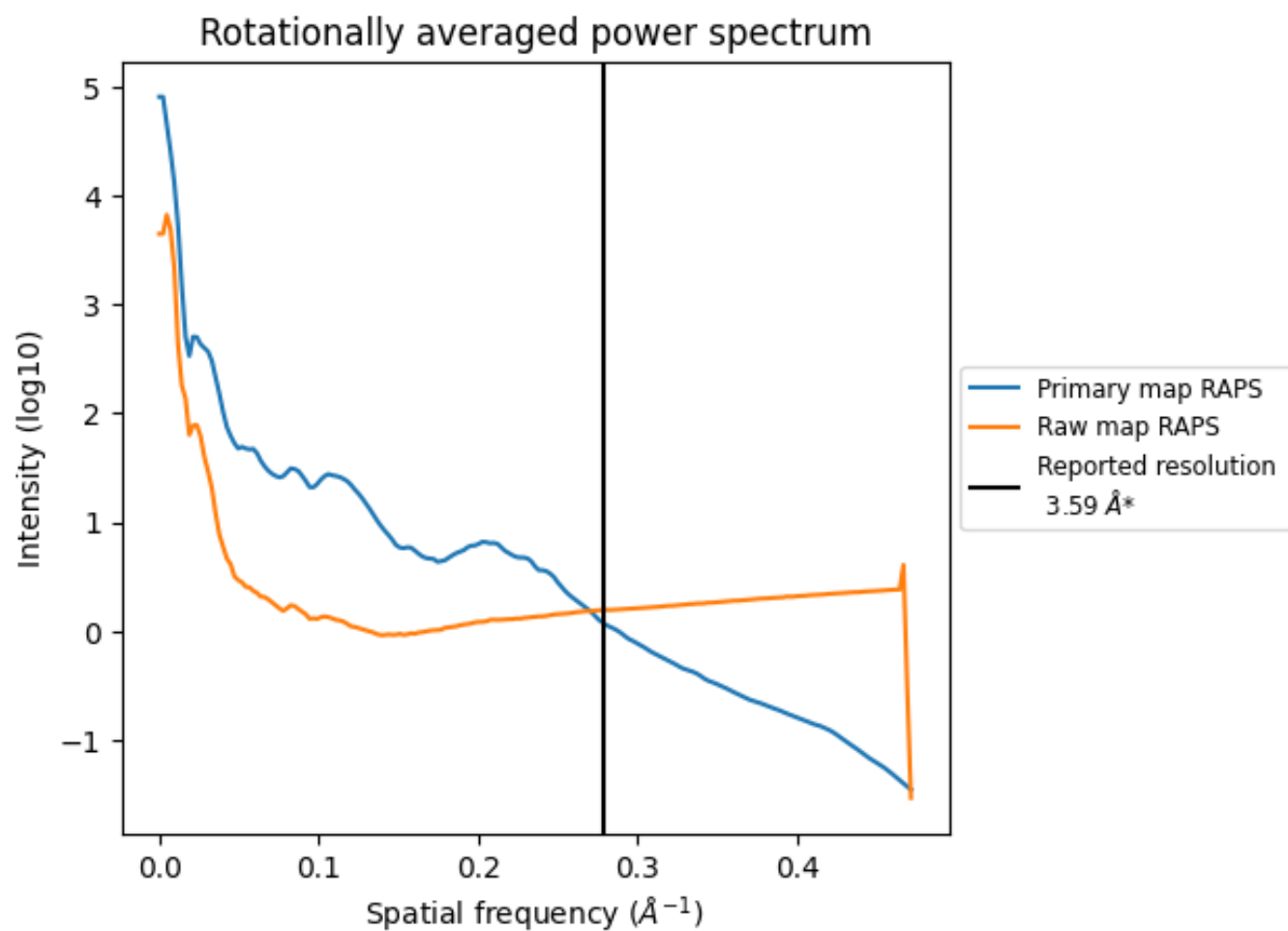
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 237 nm^3 ; this corresponds to an approximate mass of 214 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 ⓘ

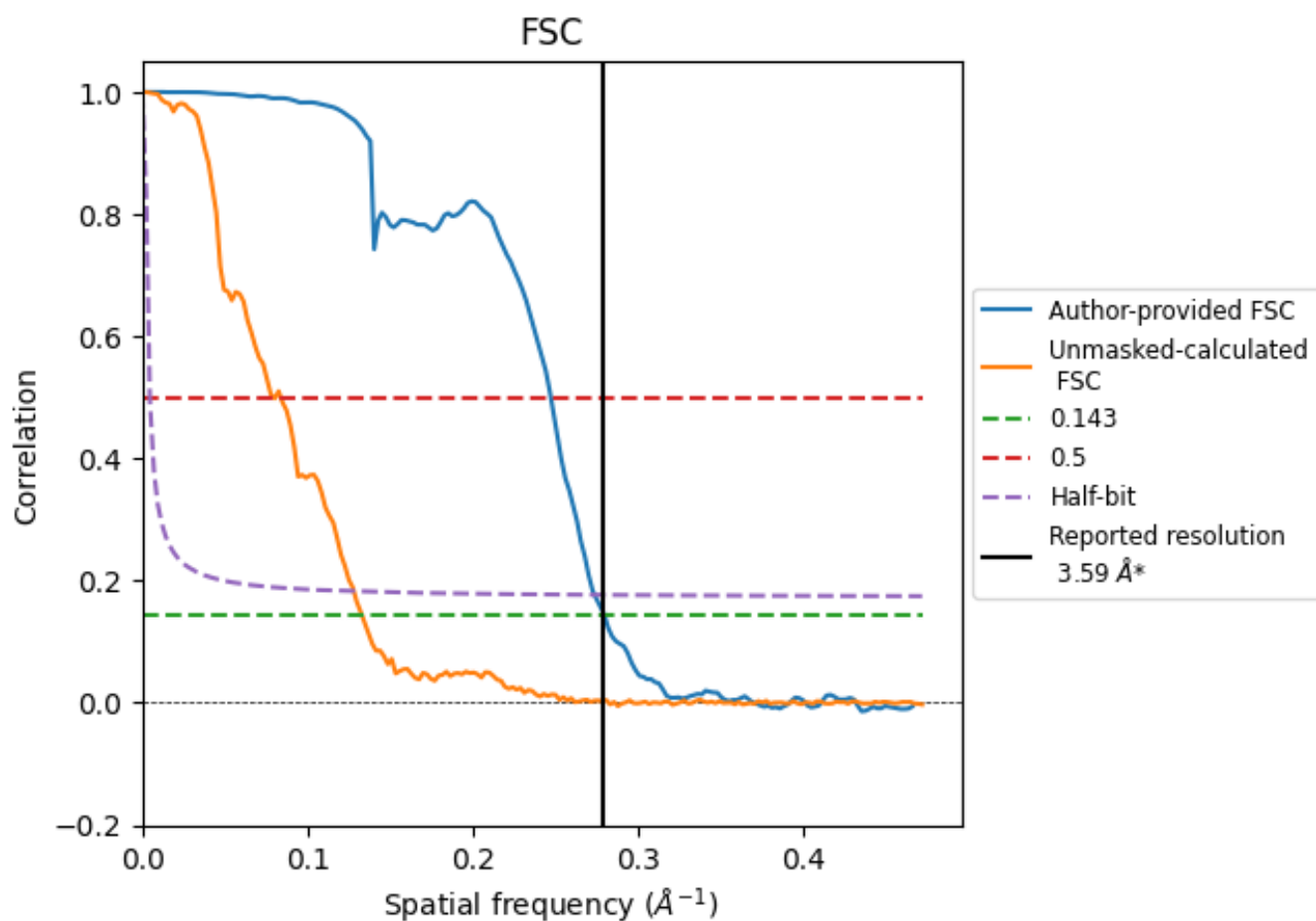


*Reported resolution corresponds to spatial frequency of 0.279 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.279 \AA^{-1}

8.2 Resolution estimates [i](#)

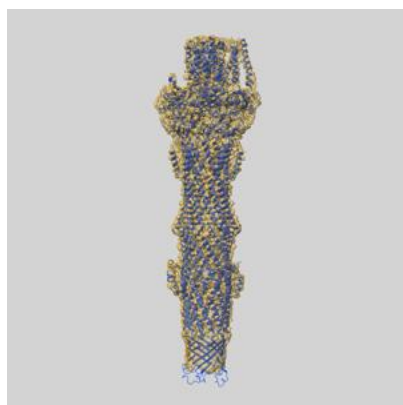
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.59	-	-
Author-provided FSC curve	3.58	4.05	3.65
Unmasked-calculated*	7.52	12.56	7.81

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.52 differs from the reported value 3.59 by more than 10 %

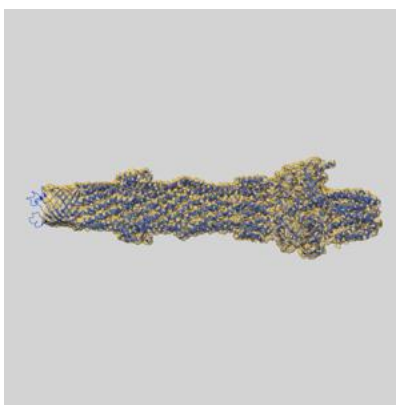
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-39885 and PDB model 8ZAR. Per-residue inclusion information can be found in section 3 on page 11.

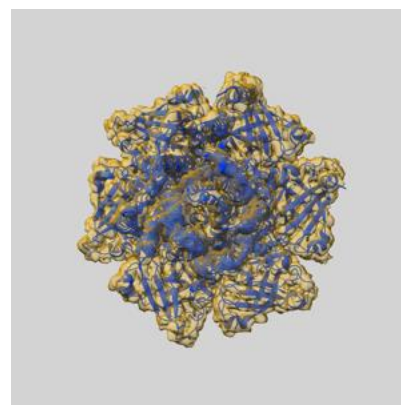
9.1 Map-model overlay [i](#)



X



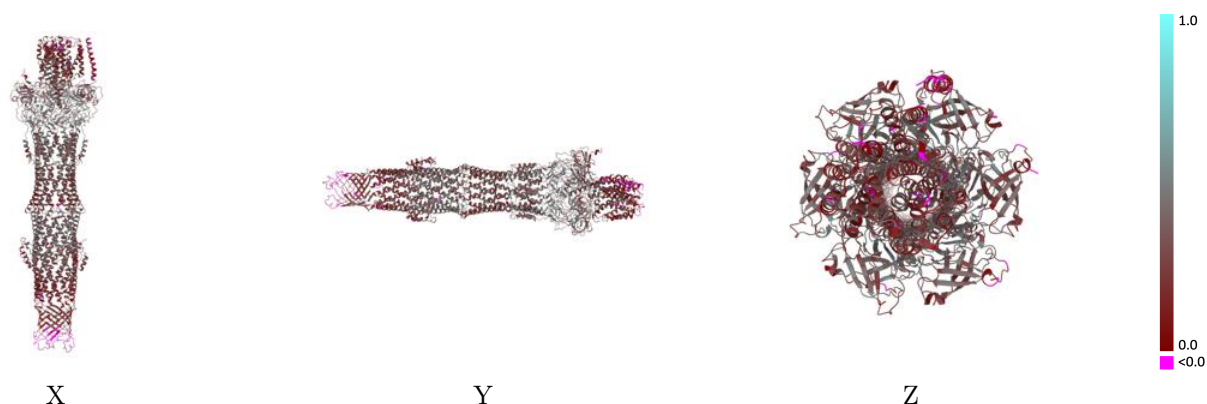
Y



Z

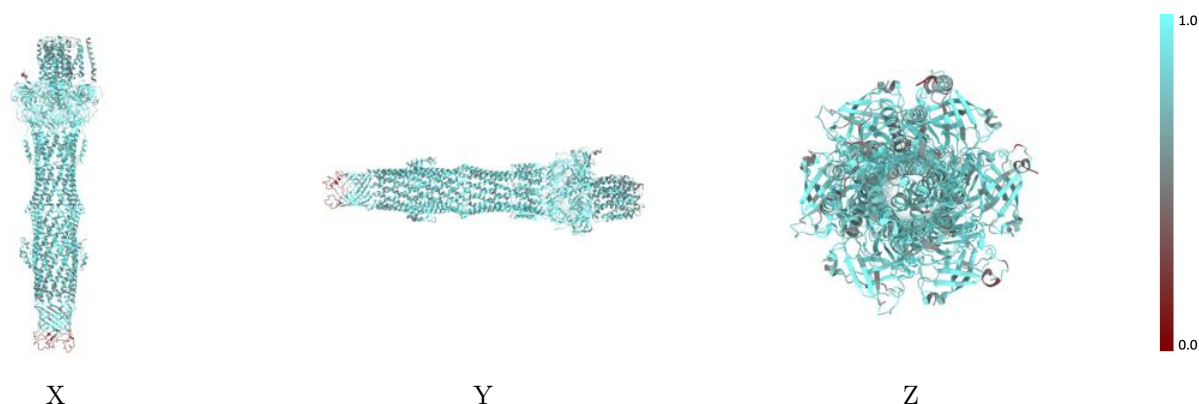
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



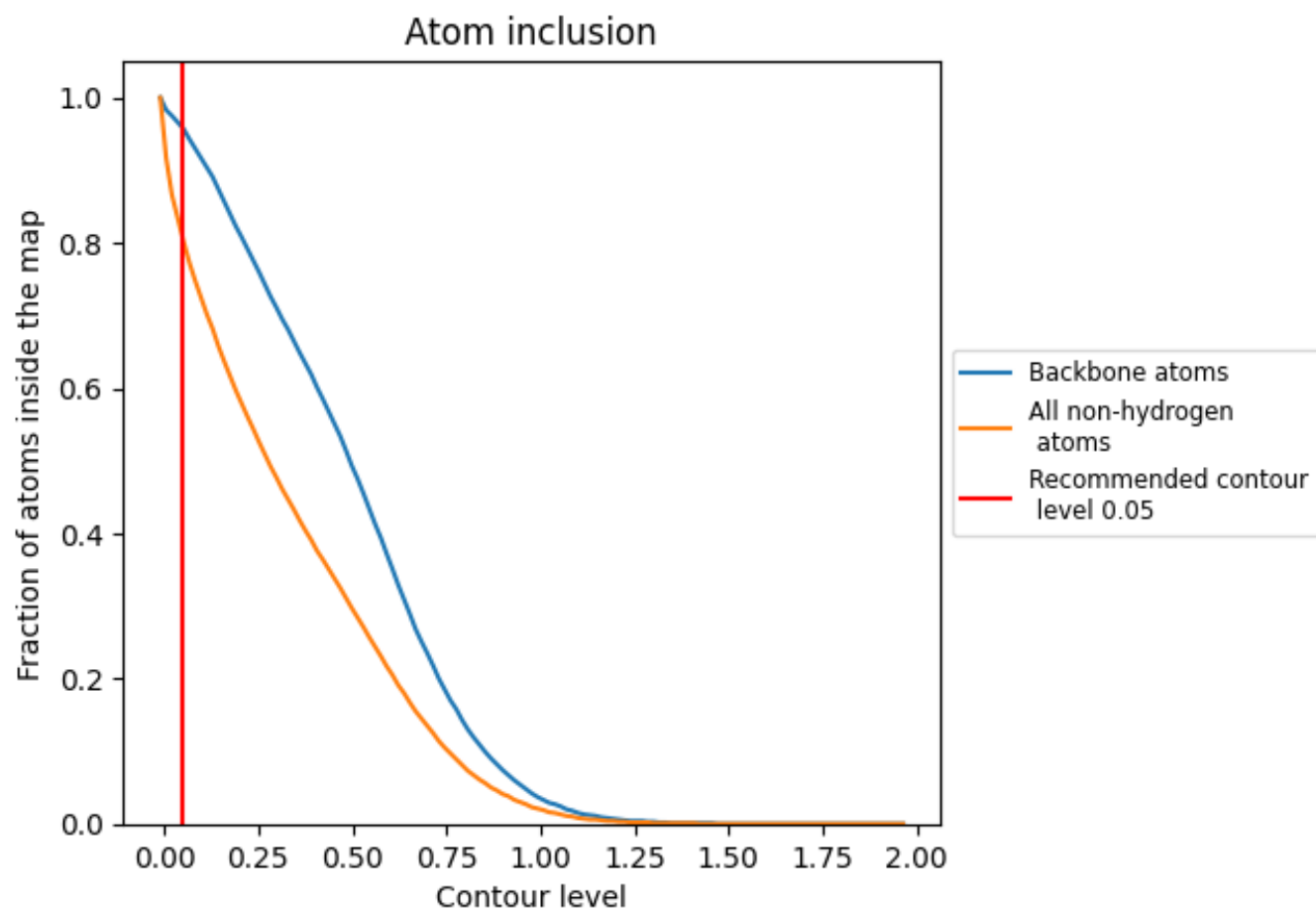
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 80% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8050	<div></div> 0.3190
A	<div></div> 0.8480	<div></div> 0.3670
B	<div></div> 0.8460	<div></div> 0.3600
C	<div></div> 0.8380	<div></div> 0.3650
D	<div></div> 0.8270	<div></div> 0.3400
E	<div></div> 0.8550	<div></div> 0.3620
F	<div></div> 0.8580	<div></div> 0.3760
G	<div></div> 0.7600	<div></div> 0.2770
H	<div></div> 0.7630	<div></div> 0.2830
I	<div></div> 0.7550	<div></div> 0.2740
J	<div></div> 0.7500	<div></div> 0.2440

1.0

0.0

<0.0