



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 04:23 PM UTC

PDB ID : 7SPJ / pdb_00007spj
EMDB ID : EMD-24772
Title : Models for C17 reconstruction of Outer Membrane Core Complex (OMCC) of Type IV Secretion System (T4SS) encoded by a plasmid overproducing TraV, TraK and TraB of pED208
Authors : Liu, X.; Khara, P.; Baker, M.L.; Christie, P.J.; Hu, B.
Deposited on : 2021-11-02
Resolution : 3.56 Å(reported)

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

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

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

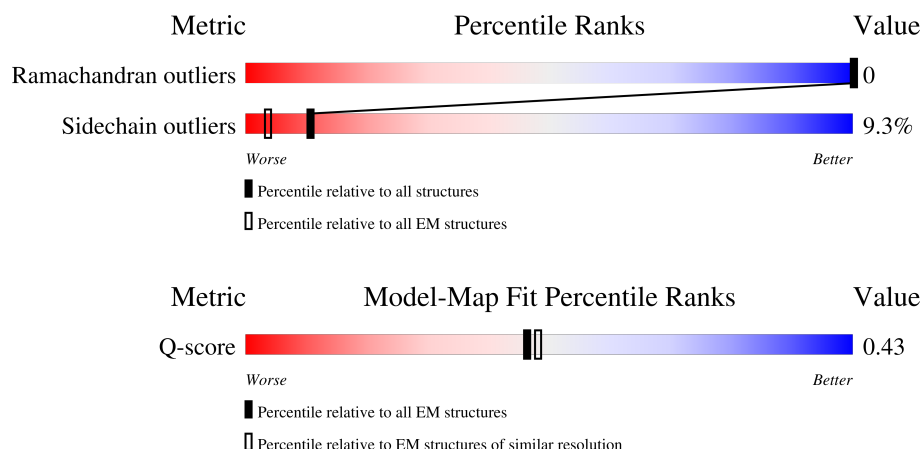
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.56 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.



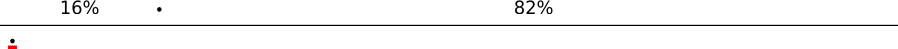
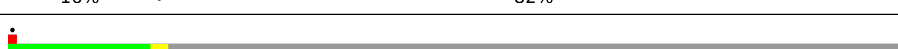
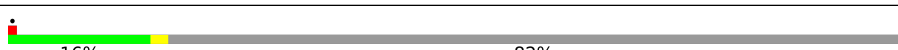
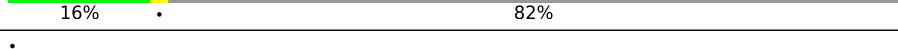
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12891 (3.04 - 4.04)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	AB1	204	16% 82%
1	AB10	204	16% 82%
1	AB11	204	16% 82%
1	AB12	204	16% 82%
1	AB13	204	16% 82%

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Mol	Chain	Length	Quality of chain
1	AB14	204	
1	AB15	204	
1	AB16	204	
1	AB17	204	
1	AB2	204	
1	AB3	204	
1	AB4	204	
1	AB5	204	
1	AB6	204	
1	AB7	204	
1	AB8	204	
1	AB9	204	
2	EF1	453	
2	EF10	453	
2	EF11	453	
2	EF12	453	
2	EF13	453	
2	EF14	453	
2	EF15	453	
2	EF16	453	
2	EF17	453	
2	EF2	453	
2	EF3	453	
2	EF4	453	
2	EF5	453	

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Mol	Chain	Length	Quality of chain
2	EF6	453	39% 57%
2	EF7	453	39% 57%
2	EF8	453	39% 57%
2	EF9	453	39% 57%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 29597 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 TraV.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AB1	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB2	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB3	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB4	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB5	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB6	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB7	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB8	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB9	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB10	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB11	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB12	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB13	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB14	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB15	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB16	37	Total	C	N	O	S	0	0
			261	153	47	56	5		
1	AB17	37	Total	C	N	O	S	0	0
			261	153	47	56	5		

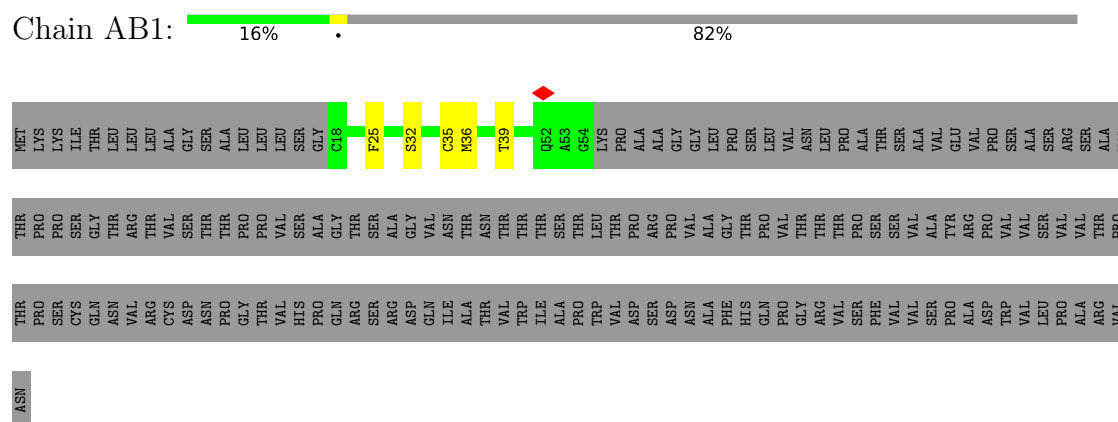
- Molecule 2 is a protein called TraB.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	EF1	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF2	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF3	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF4	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF5	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF6	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF7	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF8	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF9	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF10	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF11	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF12	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF13	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF14	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF15	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF16	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		
2	EF17	196	Total	C	N	O	S	0	0
			1480	925	259	290	6		

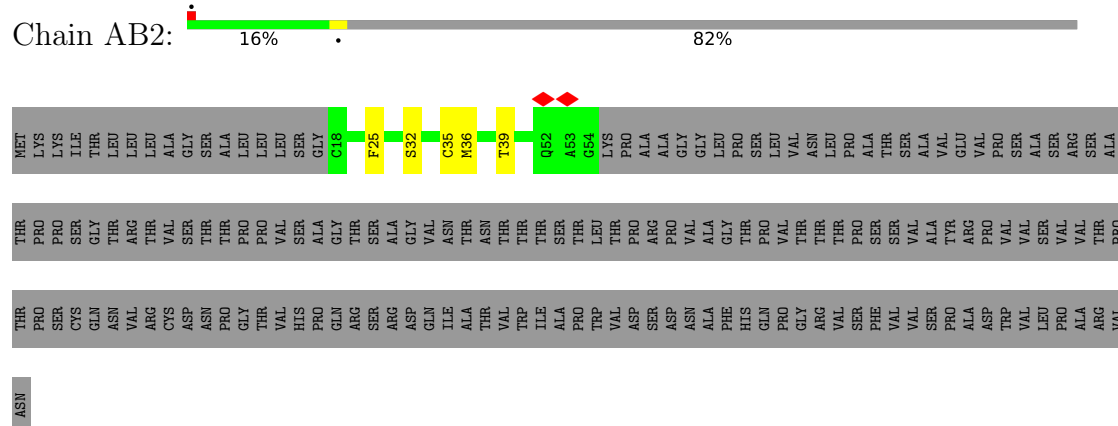
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

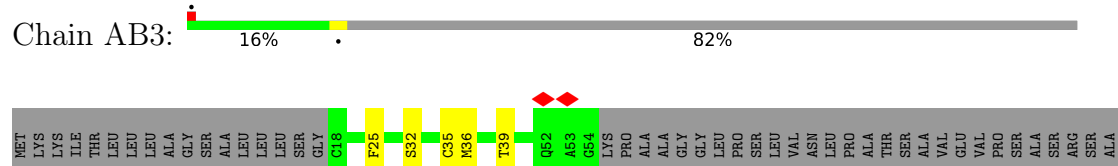
• Molecule 1: TraV



• Molecule 1: TraV



• Molecule 1: TraV



ASN



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

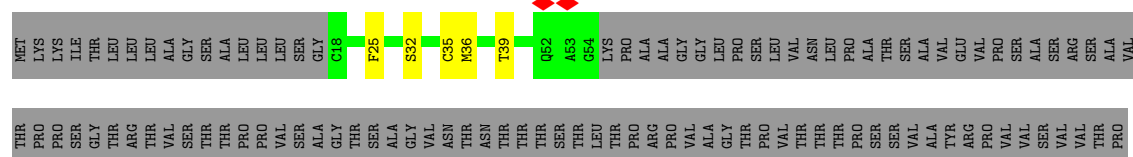


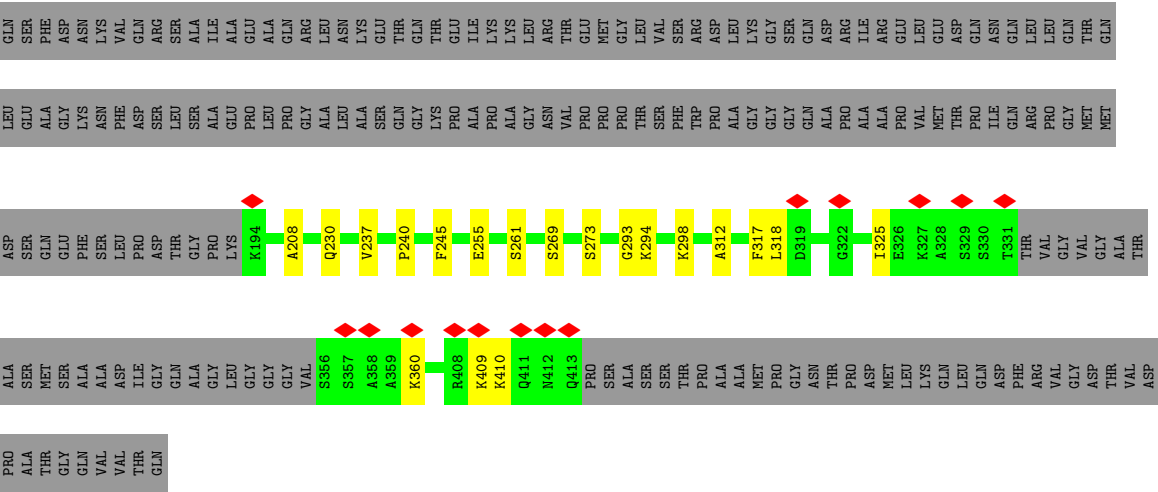
PRO	THR	PRO	PRO	SER	CYS	GLN	ASN	VAL	ARG	CYS	ASP	ASN	PRO	THR	THR	HIS	PRO	GLN	ARG	SER	ARG	ASP	GLN	ILE	ALA	ALA	THR	TRP	TRP	ILE	ALA	PRO	PRO	TRP	TRP	VAL	VAL	ASP	SER	ASP	ASN	ALA	ALA	PHE	HIS	GLN	PRO	GLY	ARG	VAL	SER	SER	ALA	ALA	ASP	TRP	VAL	LEU	PRO	ALA
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ASN

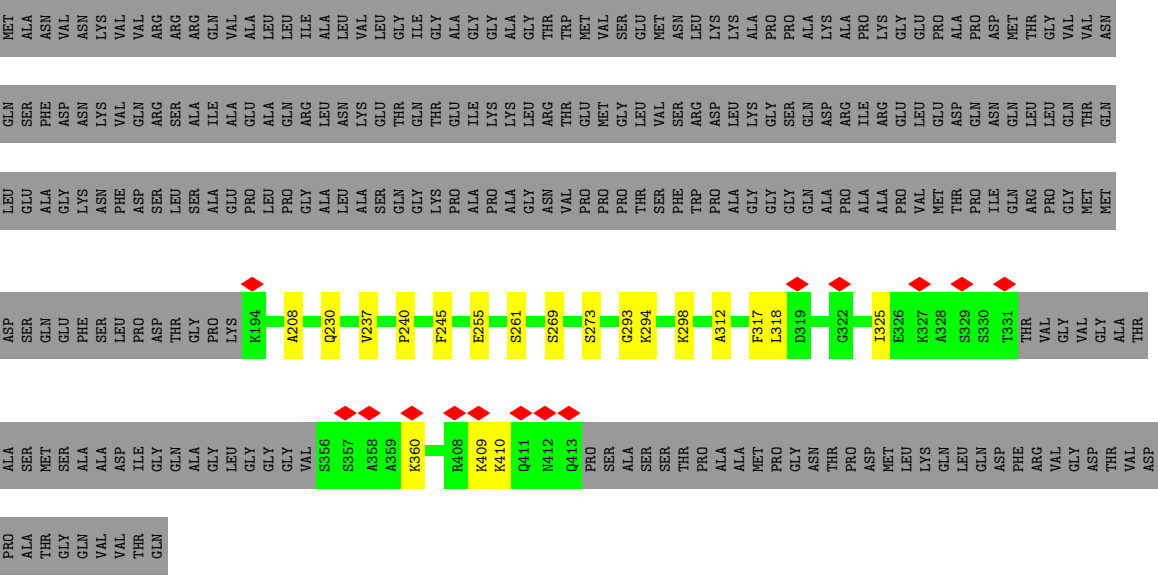
ASN

VAL	ASN
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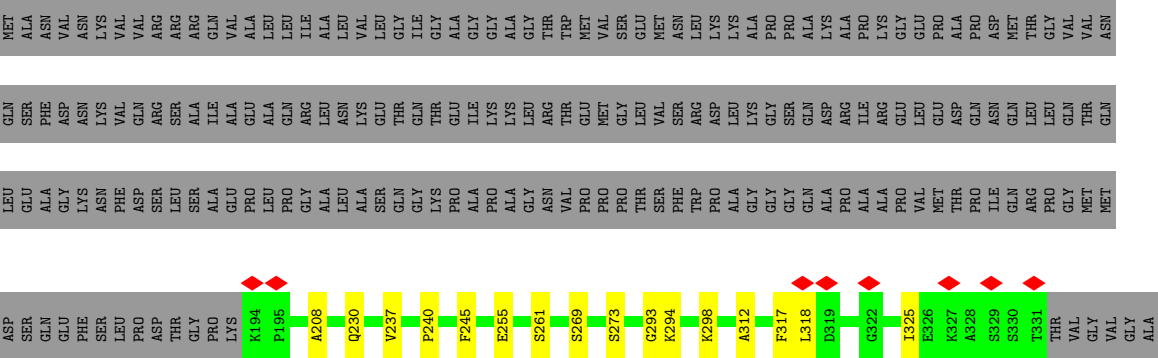




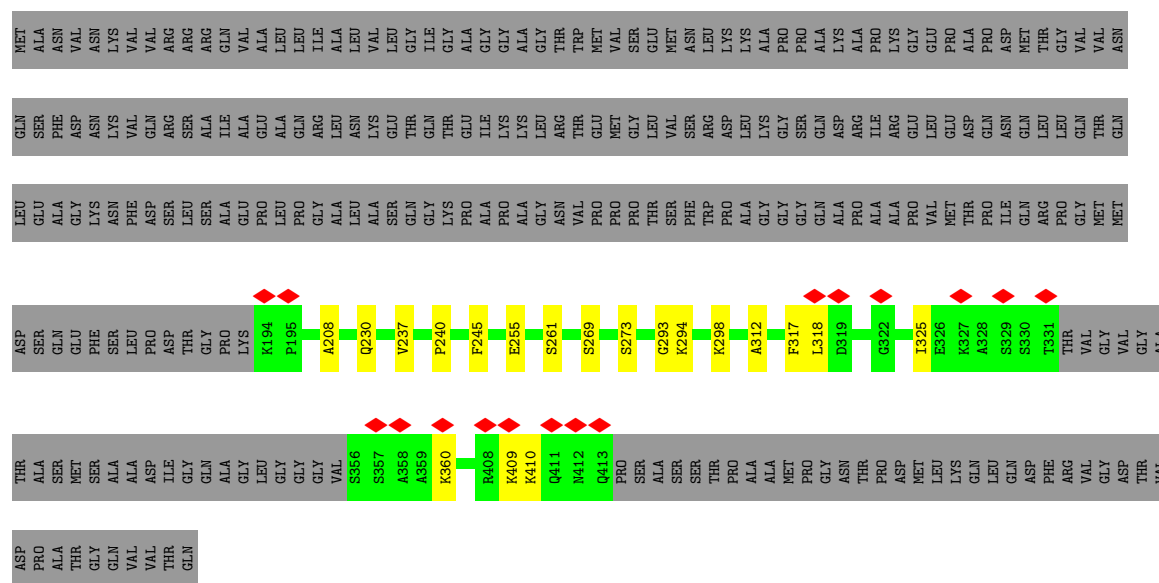
• Molecule 2: TraB



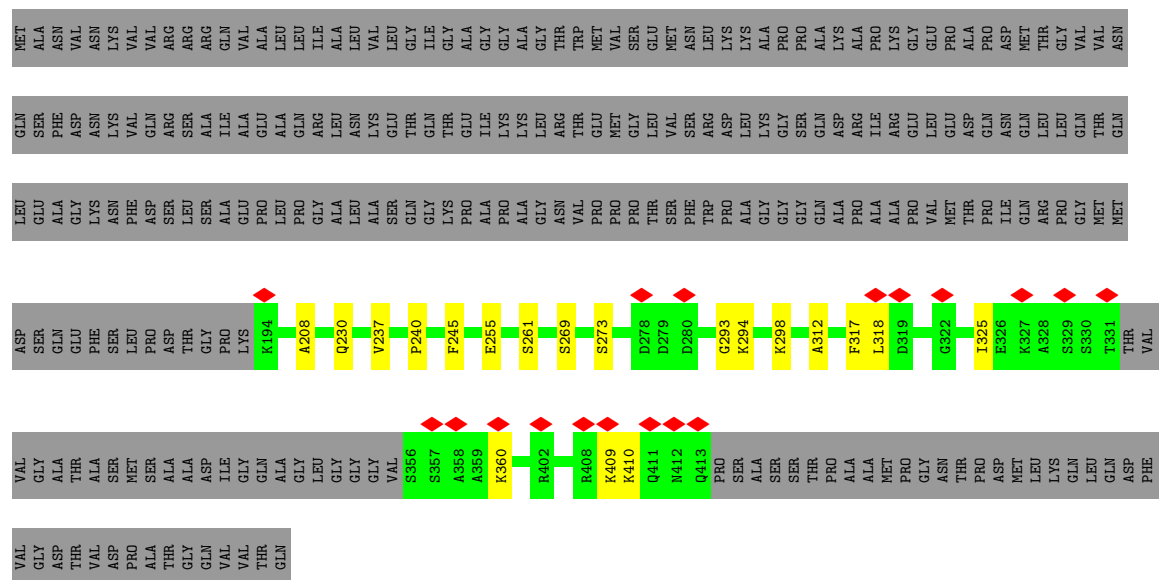
• Molecule 2: TraB



- Molecule 2: TraB



- Molecule 2: TraB



- Molecule 2: TraB

Frequency	Percentage
Never	3%
Sometimes	39%
Often	57%

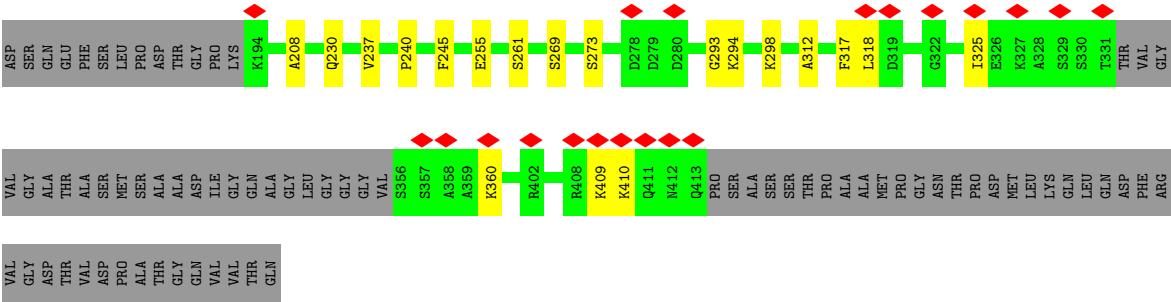


39%

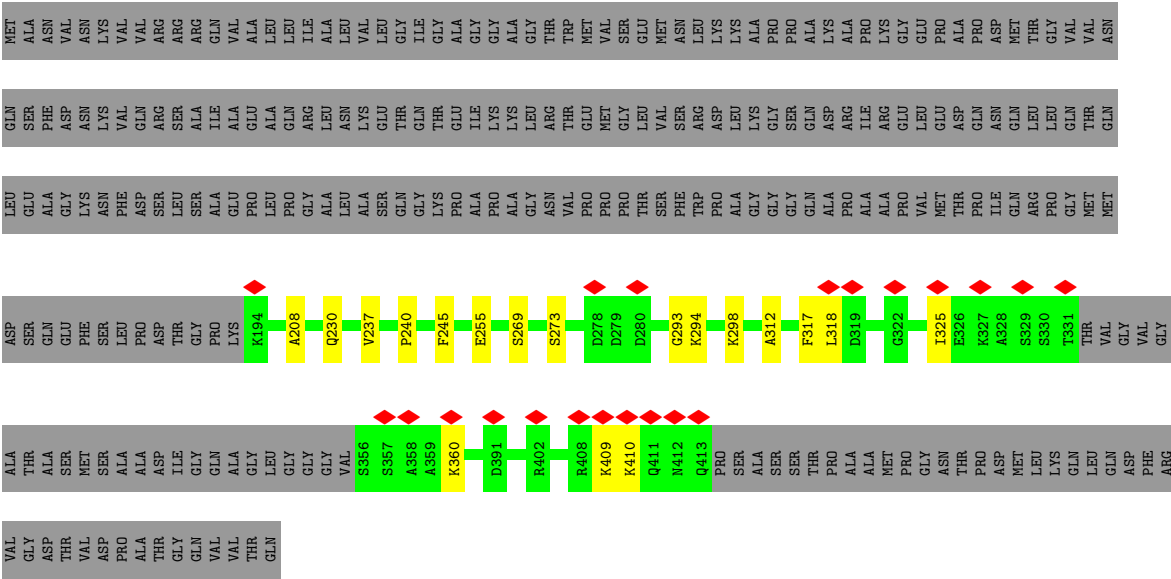


Response	Percentage
Yes	39%
No	57%

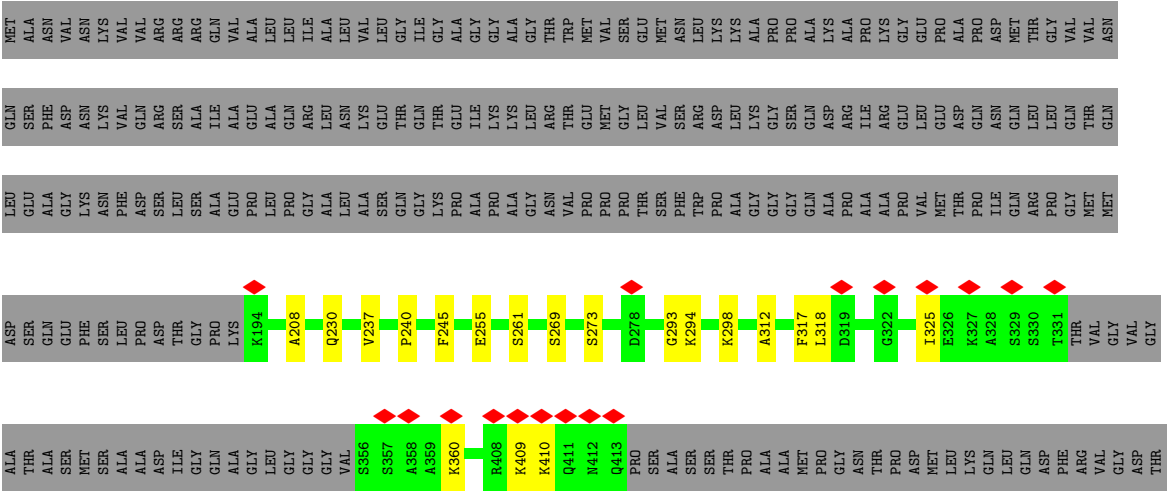




• Molecule 2: TraB



• Molecule 2: TraB



VAL
ASP
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THR
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● Molecule 2: TraB

Chain EF15:  39% 57%

MET
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● Molecule 2: TraB

Chain EF16:  39% 57%

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Q230
V237
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S273
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● Molecule 2: TraB

Chain EF17:  39% 57%

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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C17	Depositor
Number of particles used	26000	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 ($e^-/\text{\AA}^2$)	40	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	1.908	Depositor
Minimum map value	-0.933	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.38	Depositor
Map size (Å)	426.08, 426.08, 426.08	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0652, 1.0652, 1.0652	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	AB1	0.76	0/261	0.92	1/348 (0.3%)
1	AB10	0.76	0/261	0.92	1/348 (0.3%)
1	AB11	0.76	0/261	0.92	1/348 (0.3%)
1	AB12	0.76	0/261	0.92	1/348 (0.3%)
1	AB13	0.76	0/261	0.92	1/348 (0.3%)
1	AB14	0.76	0/261	0.92	1/348 (0.3%)
1	AB15	0.76	0/261	0.92	1/348 (0.3%)
1	AB16	0.76	0/261	0.92	1/348 (0.3%)
1	AB17	0.76	0/261	0.92	1/348 (0.3%)
1	AB2	0.76	0/261	0.92	1/348 (0.3%)
1	AB3	0.76	0/261	0.92	1/348 (0.3%)
1	AB4	0.76	0/261	0.92	1/348 (0.3%)
1	AB5	0.76	0/261	0.92	1/348 (0.3%)
1	AB6	0.76	0/261	0.92	1/348 (0.3%)
1	AB7	0.76	0/261	0.92	1/348 (0.3%)
1	AB8	0.76	0/261	0.92	1/348 (0.3%)
1	AB9	0.76	0/261	0.92	1/348 (0.3%)
2	EF1	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF10	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF11	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF12	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF13	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF14	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF15	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF16	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF17	0.73	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF2	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF3	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF4	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF5	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF6	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF7	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF8	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)
2	EF9	0.72	1/1502 (0.1%)	0.97	5/2021 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.73	17/29971 (0.1%)	0.96	102/40273 (0.3%)

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	EF7	312	ALA	C-O	6.46	1.31	1.24
2	EF17	312	ALA	C-O	6.44	1.31	1.24
2	EF11	312	ALA	C-O	6.44	1.31	1.24
2	EF4	312	ALA	C-O	6.43	1.31	1.24
2	EF15	312	ALA	C-O	6.42	1.31	1.24

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	EF12	317	PHE	N-CA-C	-9.96	100.25	111.71
2	EF5	317	PHE	N-CA-C	-9.95	100.27	111.71
2	EF16	317	PHE	N-CA-C	-9.95	100.27	111.71
2	EF6	317	PHE	N-CA-C	-9.95	100.27	111.71
2	EF10	317	PHE	N-CA-C	-9.95	100.27	111.71

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	AB1	35/204 (17%)	32 (91%)	3 (9%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AB10	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB11	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB12	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB13	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB14	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB15	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB16	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB17	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB2	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB3	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB4	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB5	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB6	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB7	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB8	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
1	AB9	35/204 (17%)	32 (91%)	3 (9%)	0	100	100
2	EF1	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF10	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF11	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF12	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF13	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF14	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF15	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF16	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF17	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF2	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF3	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF4	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF5	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF6	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF7	192/453 (42%)	186 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	EF8	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
2	EF9	192/453 (42%)	186 (97%)	6 (3%)	0	100	100
All	All	3859/11169 (35%)	3706 (96%)	153 (4%)	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	AB1	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB10	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB11	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB12	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB13	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB14	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB15	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB16	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB17	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB2	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB3	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB4	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB5	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB6	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB7	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB8	28/168 (17%)	24 (86%)	4 (14%)	3	18
1	AB9	28/168 (17%)	24 (86%)	4 (14%)	3	18
2	EF1	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF10	155/353 (44%)	142 (92%)	13 (8%)	10	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	EF11	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF12	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF13	155/353 (44%)	143 (92%)	12 (8%)	12	37
2	EF14	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF15	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF16	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF17	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF2	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF3	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF4	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF5	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF6	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF7	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF8	155/353 (44%)	142 (92%)	13 (8%)	10	35
2	EF9	155/353 (44%)	142 (92%)	13 (8%)	10	35
All	All	3111/8857 (35%)	2823 (91%)	288 (9%)	11	32

5 of 288 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	EF13	298	LYS
2	EF17	409	LYS
2	EF14	245	PHE
2	EF15	409	LYS
2	EF3	255	GLU

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [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.

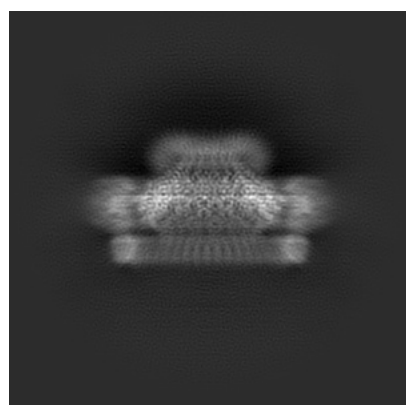
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24772. These allow visual inspection of the internal detail of the map and identification of artifacts.

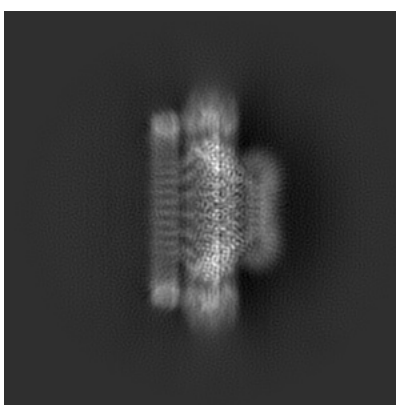
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

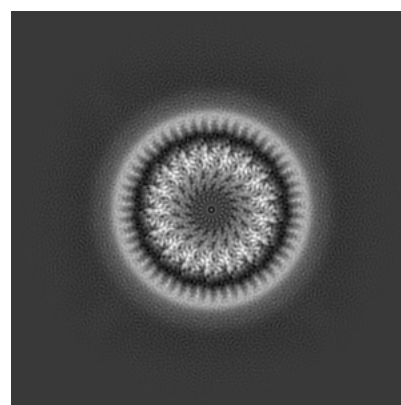
6.1.1 Primary map



X



Y

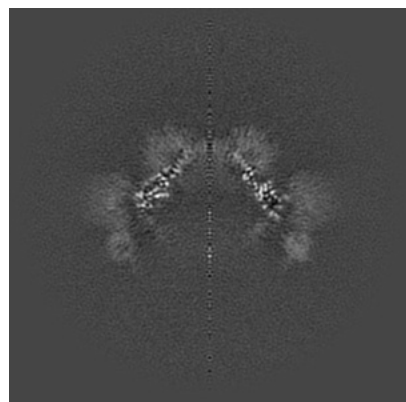


Z

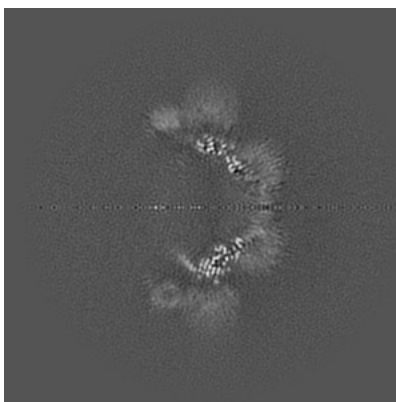
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

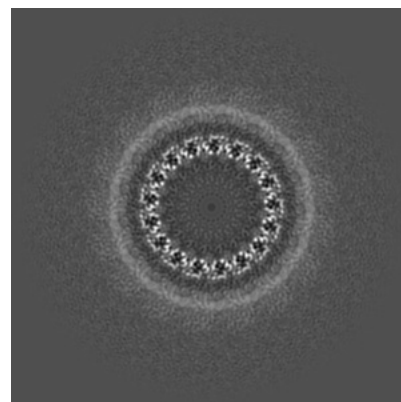
6.2.1 Primary map



X Index: 200



Y Index: 200

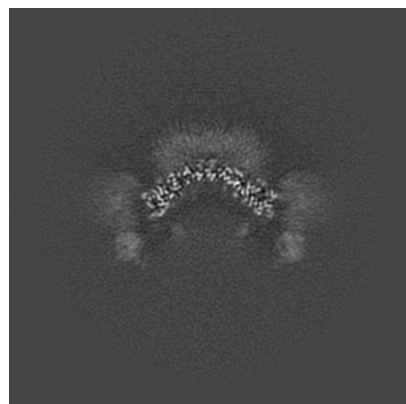


Z Index: 200

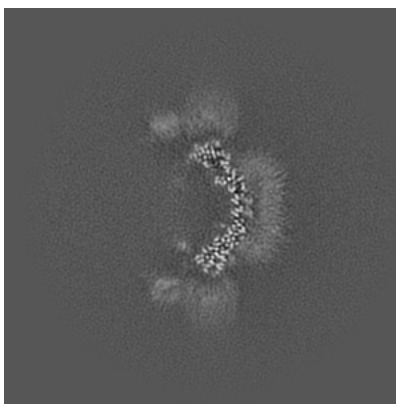
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

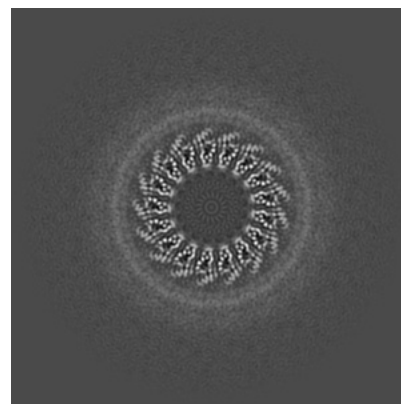
6.3.1 Primary map



X Index: 166



Y Index: 167

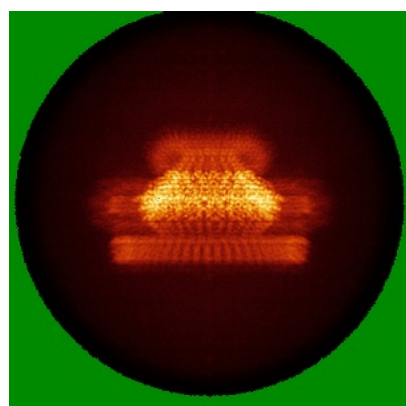


Z Index: 212

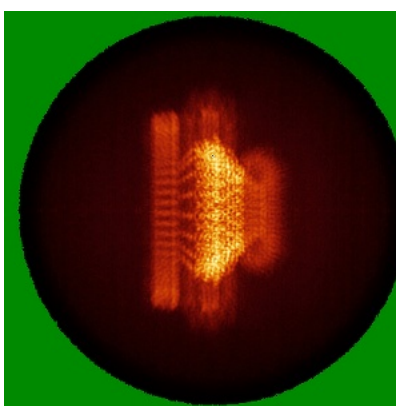
The images above show the largest variance slices of the map in three orthogonal directions.

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

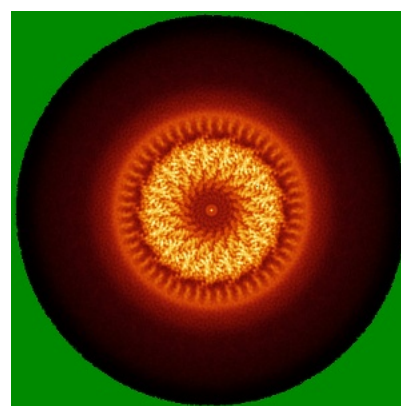
6.4.1 Primary map



X



Y

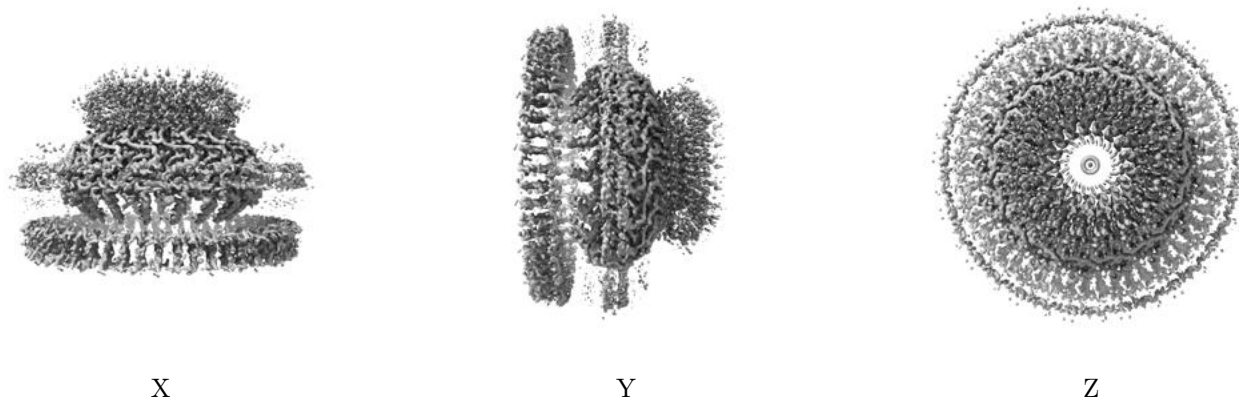


Z

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

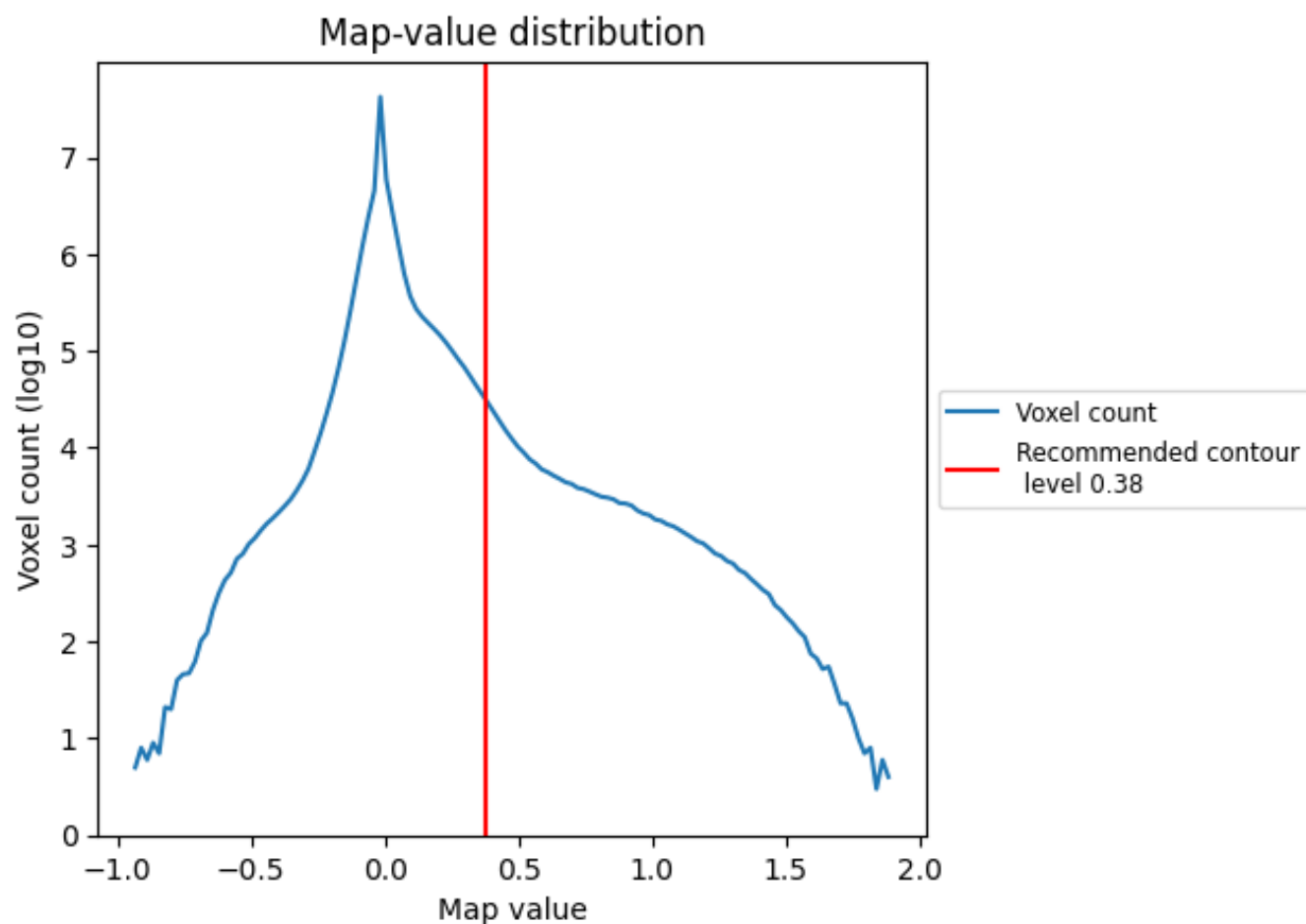
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

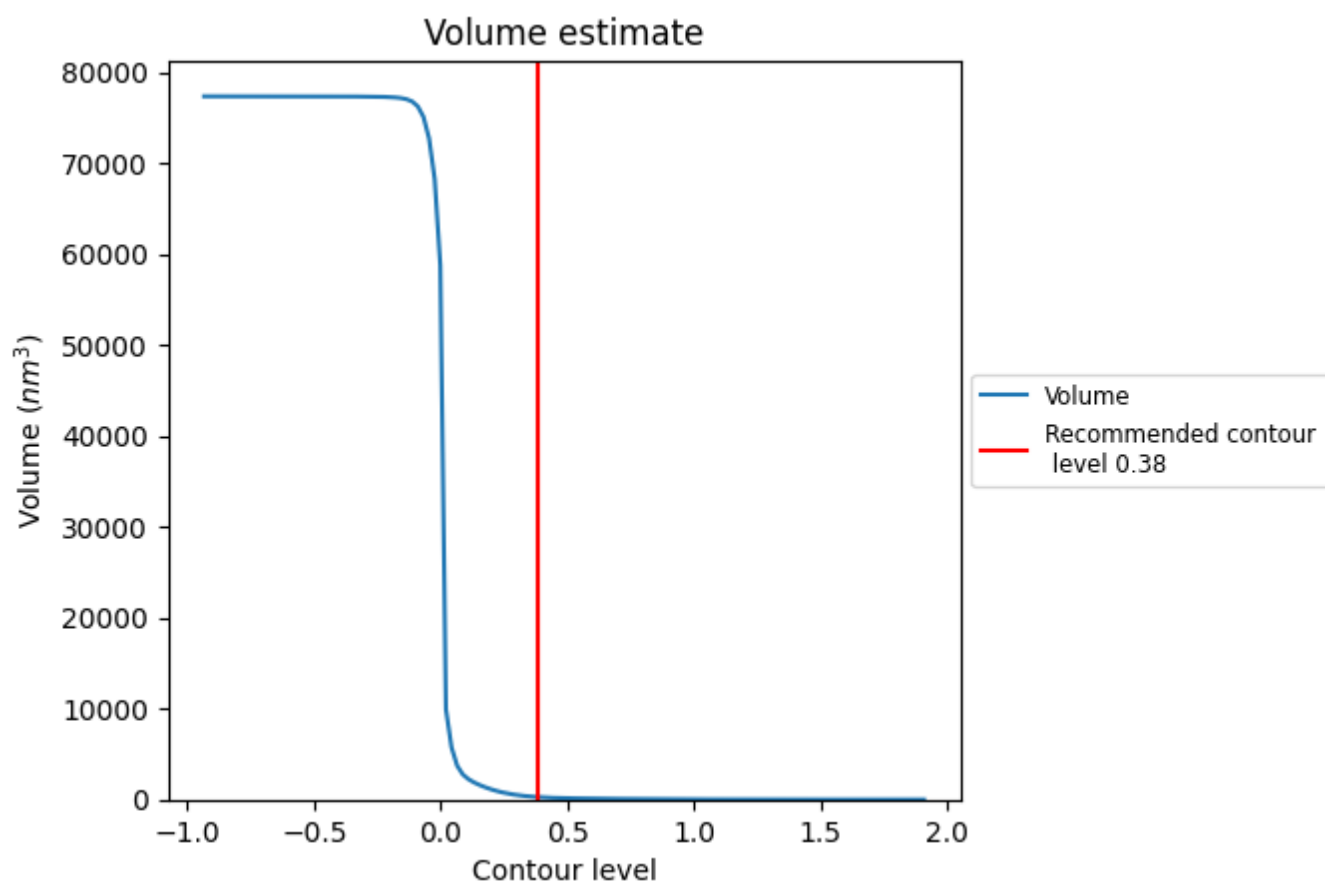
This section contains the results of statistical analysis of the map.

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.

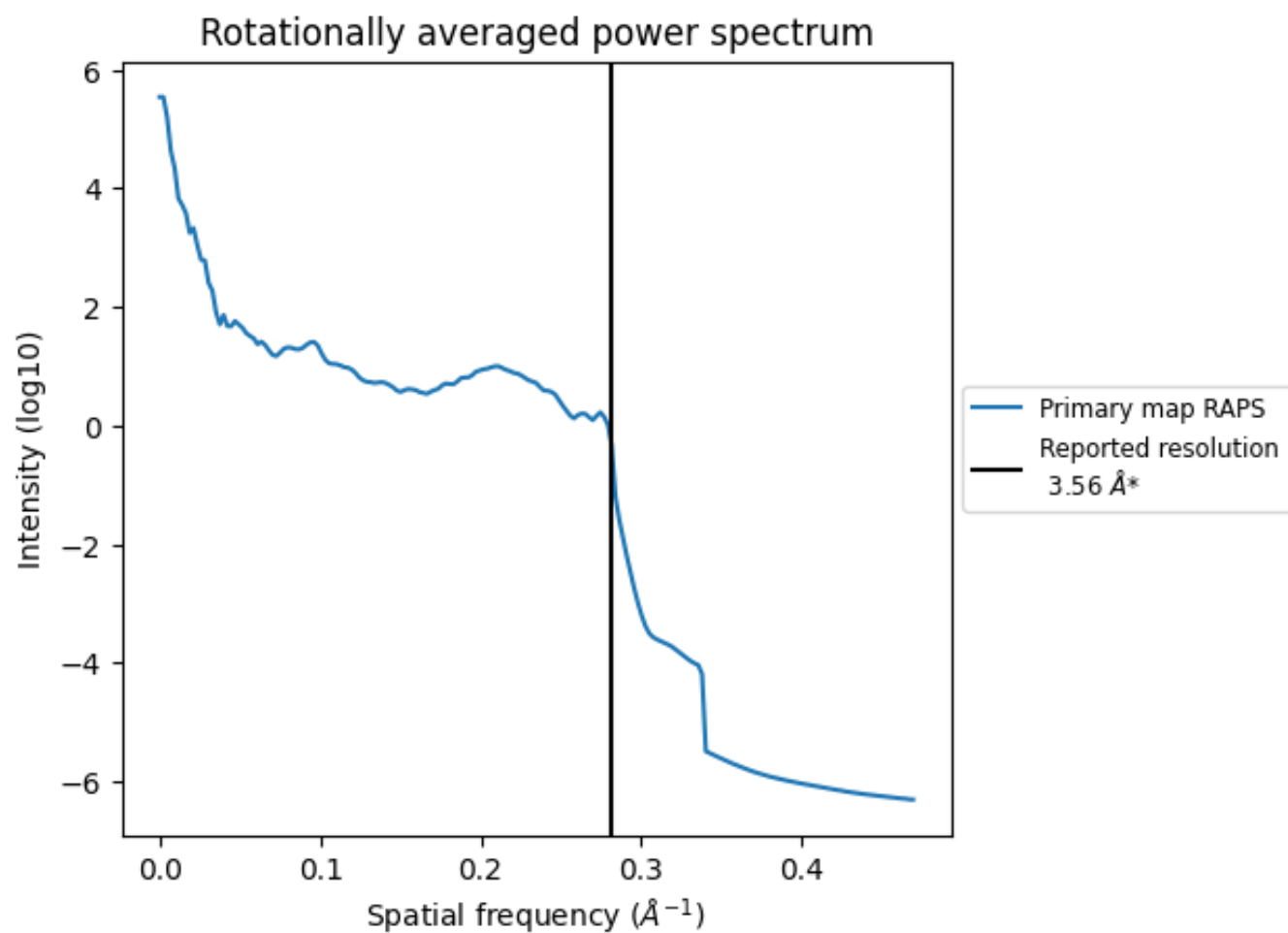
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 279 nm³; this corresponds to an approximate mass of 252 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 0.281 Å⁻¹

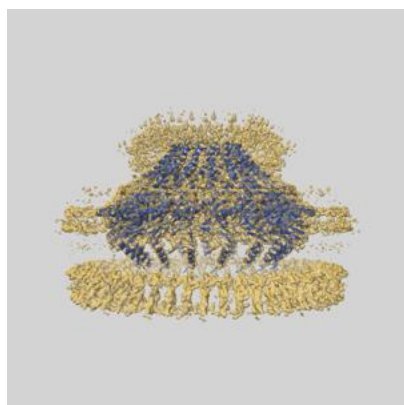
8 Fourier-Shell correlation

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

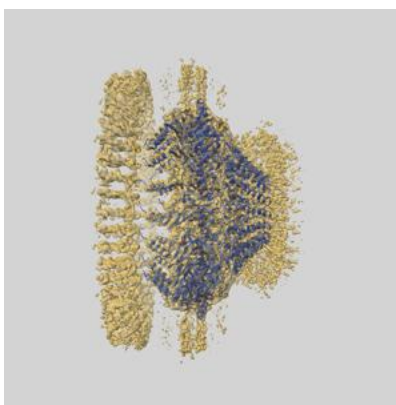
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24772 and PDB model 7SPJ. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



X



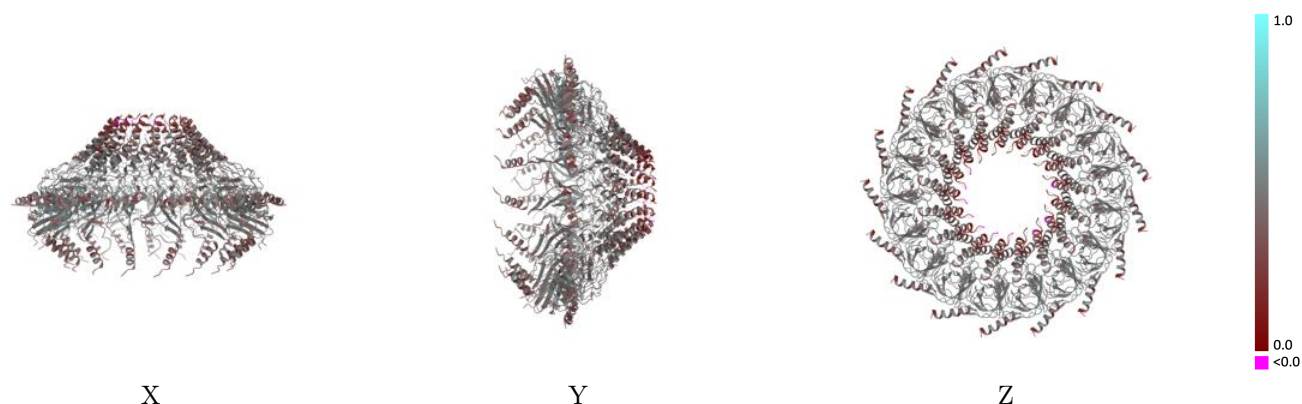
Y



Z

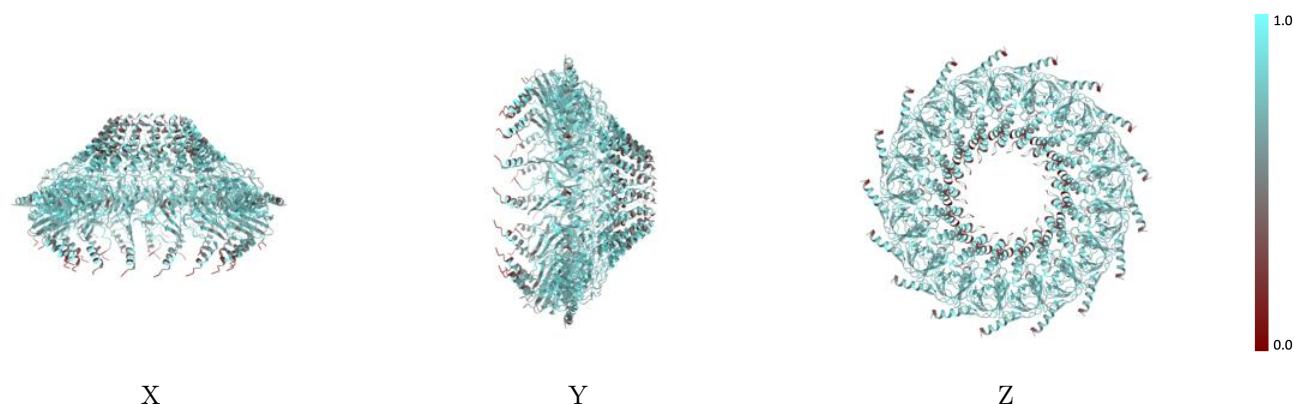
The images above show the 3D surface view of the map at the recommended contour level 0.38 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



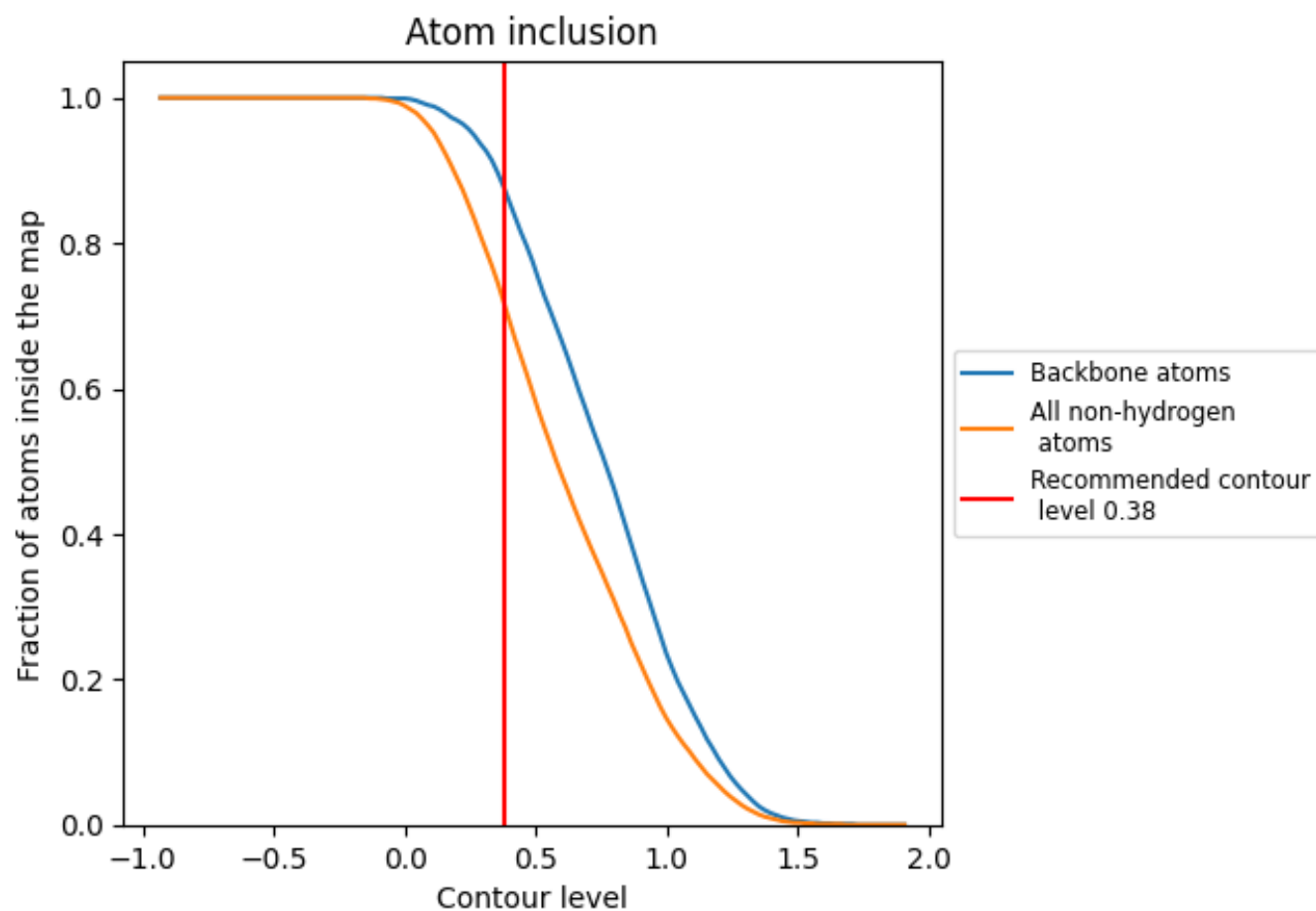
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.38).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 72% 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 (0.38) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7160	 0.4300
AB1	 0.7070	 0.4350
AB10	 0.6990	 0.4060
AB11	 0.7070	 0.4110
AB12	 0.6990	 0.4130
AB13	 0.7030	 0.4210
AB14	 0.7030	 0.4260
AB15	 0.7180	 0.4280
AB16	 0.7180	 0.4330
AB17	 0.7220	 0.4330
AB2	 0.6950	 0.4330
AB3	 0.6870	 0.4290
AB4	 0.6790	 0.4290
AB5	 0.6910	 0.4230
AB6	 0.6790	 0.4170
AB7	 0.6830	 0.4130
AB8	 0.6910	 0.4120
AB9	 0.6910	 0.4080
EF1	 0.7320	 0.4490
EF10	 0.7070	 0.4170
EF11	 0.7040	 0.4170
EF12	 0.7120	 0.4220
EF13	 0.7090	 0.4270
EF14	 0.7160	 0.4330
EF15	 0.7280	 0.4400
EF16	 0.7320	 0.4450
EF17	 0.7350	 0.4500
EF2	 0.7340	 0.4470
EF3	 0.7240	 0.4430
EF4	 0.7220	 0.4360
EF5	 0.7260	 0.4310
EF6	 0.7180	 0.4250
EF7	 0.7170	 0.4220
EF8	 0.7080	 0.4180
EF9	 0.7050	 0.4140

