



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 10:18 AM UTC

PDB ID : 8PC1 / pdb_00008pc1
EMDB ID : EMD-17593
Title : Sub-tomogram average of the closed conformation of the Nap adhesion complex from the human pathogen Mycoplasma genitalium.
Authors : Sprankel, L.; Scheffer, M.P.; Frangakis, A.S.
Deposited on : 2023-06-09
Resolution : 18.00 Å(reported)
Based on initial models : 6RUT, 6R3T

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

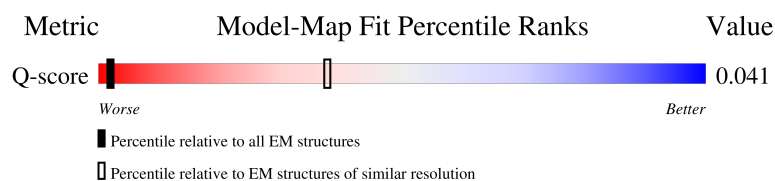
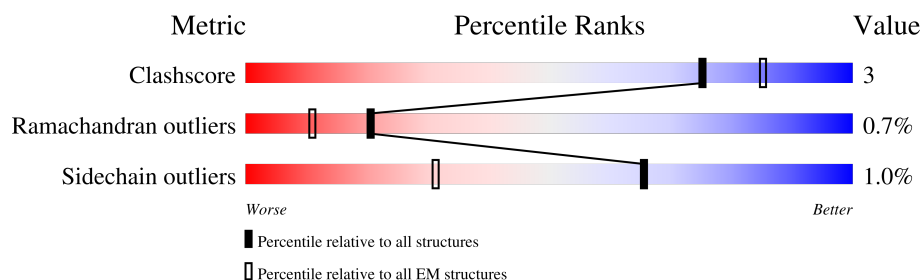
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 18.00 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	24 (17.50 - 18.30)

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

Mol	Chain	Length	Quality of chain
1	B	1444	12% 86% 11%
2	A	1053	9% 56% 26% 14%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 33447 atoms, of which 16454 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 Adhesin P1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	B	1285	Total	C	H	N	O	S	0	0
			19786	6365	9737	1699	1971	14		

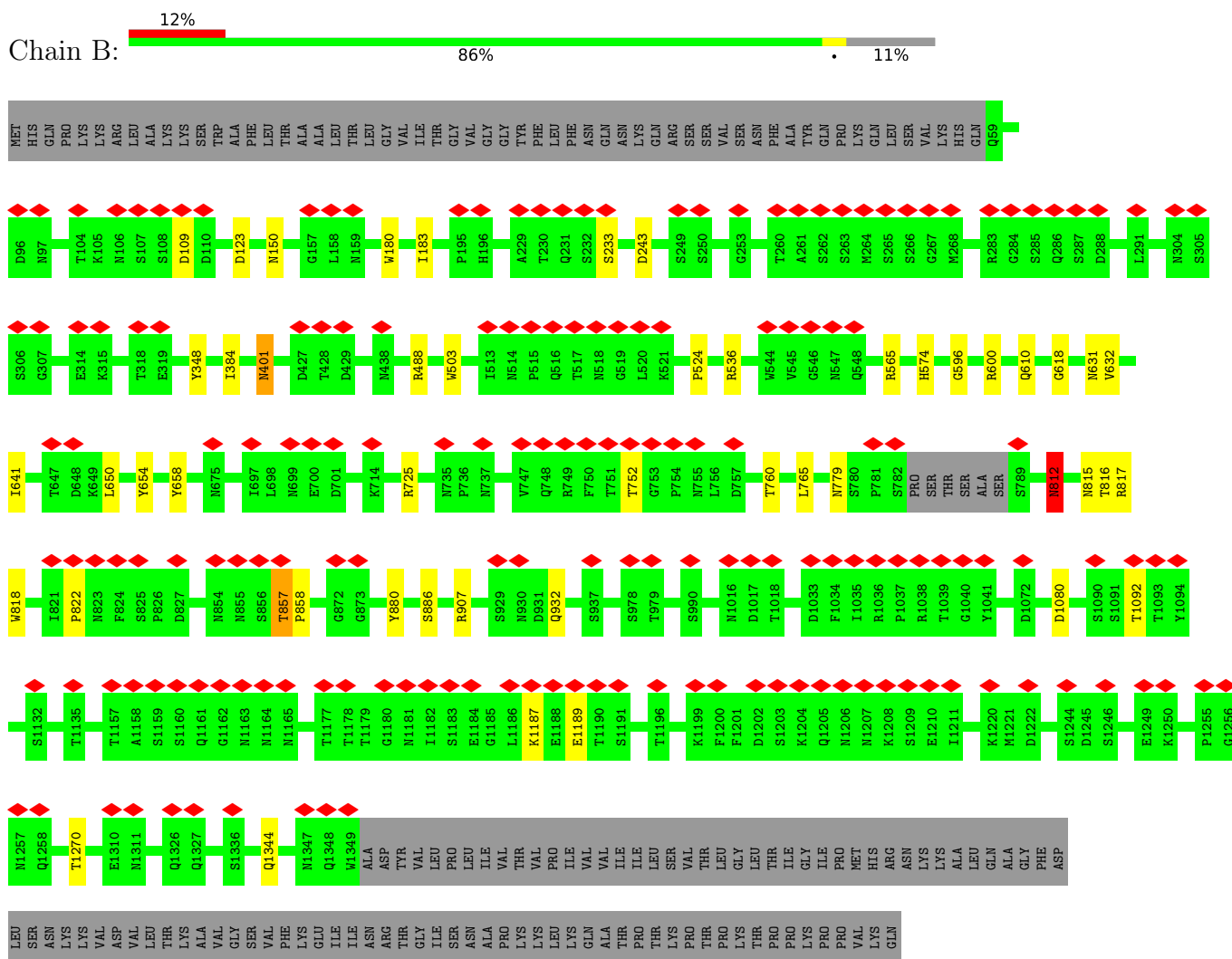
- Molecule 2 is a protein called Mgp-operon protein 3.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	A	902	Total	C	H	N	O	S	0	0
			13661	4350	6717	1165	1423	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: Adhesin P1



• Molecule 2: Mgp-operon protein 3





4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	13870	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 ($e^-/\text{\AA}^2$)	120	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.001	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.000145	Depositor
Map size (Å)	332.8, 332.8, 332.8	wwPDB
Map dimensions	64, 64, 64	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	5.2, 5.2, 5.2	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	B	0.88	0/10303	1.37	18/14029 (0.1%)
2	A	3.21	75/7088 (1.1%)	1.88	281/9641 (2.9%)
All	All	2.16	75/17391 (0.4%)	1.59	299/23670 (1.3%)

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	B	0	2
2	A	0	1
All	All	0	3

All (75) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	936	LEU	CB-CG	152.60	4.58	1.53
2	A	936	LEU	CA-CB	113.33	3.80	1.53
2	A	936	LEU	CG-CD2	77.32	4.07	1.52
2	A	936	LEU	CG-CD1	73.67	3.95	1.52
2	A	936	LEU	N-CA	53.25	2.47	1.46
2	A	935	ALA	C-N	39.70	1.89	1.33
2	A	936	LEU	CA-C	27.67	2.11	1.52
2	A	175	HIS	CE1-NE2	-8.85	1.23	1.32
2	A	191	HIS	CE1-NE2	-8.77	1.23	1.32
2	A	722	HIS	CE1-NE2	-8.77	1.23	1.32
2	A	722	HIS	CD2-NE2	-8.19	1.28	1.37
2	A	175	HIS	CD2-NE2	-8.11	1.28	1.37
2	A	623	ALA	CA-CB	-8.11	1.42	1.53
2	A	191	HIS	CD2-NE2	-8.10	1.28	1.37
2	A	653	ARG	CZ-NH2	-7.87	1.23	1.33
2	A	834	ARG	CZ-NH2	-7.86	1.23	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	576	ARG	CZ-NH2	-7.81	1.23	1.33
2	A	537	ARG	CZ-NH2	-7.77	1.23	1.33
2	A	658	ARG	CZ-NH2	-7.75	1.23	1.33
2	A	188	ARG	CZ-NH2	-7.75	1.23	1.33
2	A	742	ARG	CZ-NH2	-7.70	1.23	1.33
2	A	935	ALA	CA-CB	-7.47	1.43	1.53
2	A	677	ALA	CA-CB	-7.42	1.42	1.53
2	A	762	ALA	CA-CB	-7.23	1.42	1.53
2	A	934	ALA	CA-CB	-7.16	1.42	1.53
2	A	520	ALA	CA-CB	-6.68	1.43	1.53
2	A	201	ALA	CA-CB	-6.67	1.42	1.53
2	A	851	ALA	CA-CB	-6.57	1.43	1.53
2	A	537	ARG	CZ-NH1	-6.45	1.23	1.32
2	A	742	ARG	CZ-NH1	-6.33	1.23	1.32
2	A	514	GLY	N-CA	-6.32	1.38	1.45
2	A	516	GLY	N-CA	-6.30	1.38	1.45
2	A	653	ARG	CZ-NH1	-6.29	1.24	1.32
2	A	188	ARG	CZ-NH1	-6.28	1.24	1.32
2	A	424	ALA	CA-CB	-6.26	1.42	1.53
2	A	837	ALA	CA-CB	-6.25	1.43	1.53
2	A	164	ALA	CA-CB	-6.23	1.42	1.53
2	A	658	ARG	CZ-NH1	-6.23	1.24	1.32
2	A	844	ALA	CA-CB	-6.21	1.43	1.53
2	A	576	ARG	CZ-NH1	-6.21	1.24	1.32
2	A	834	ARG	CZ-NH1	-6.20	1.24	1.32
2	A	759	ALA	CA-CB	-5.92	1.42	1.53
2	A	752	ALA	CA-CB	-5.86	1.43	1.53
2	A	878	ALA	CA-CB	-5.84	1.43	1.53
2	A	619	ALA	CA-CB	-5.77	1.43	1.53
2	A	168	GLY	N-CA	-5.70	1.37	1.45
2	A	834	ARG	N-CA	-5.55	1.39	1.46
2	A	177	GLY	N-CA	-5.50	1.37	1.45
2	A	884	ALA	CA-CB	-5.46	1.43	1.53
2	A	742	ARG	CD-NE	-5.44	1.38	1.46
2	A	578	LEU	CA-CB	-5.42	1.47	1.53
2	A	864	ASN	C-N	-5.39	1.29	1.33
2	A	471	GLY	N-CA	-5.36	1.37	1.45
2	A	834	ARG	CD-NE	-5.36	1.38	1.46
2	A	537	ARG	CD-NE	-5.35	1.38	1.46
2	A	576	ARG	CD-NE	-5.35	1.38	1.46
2	A	835	VAL	N-CA	-5.32	1.39	1.46
2	A	453	ILE	N-CA	-5.29	1.42	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	881	ASP	CA-CB	-5.29	1.48	1.54
2	A	179	GLY	N-CA	-5.26	1.38	1.45
2	A	734	GLY	N-CA	-5.25	1.38	1.45
2	A	807	GLY	N-CA	-5.24	1.37	1.45
2	A	480	GLY	N-CA	-5.24	1.37	1.44
2	A	622	ILE	N-CA	-5.24	1.41	1.46
2	A	210	GLY	N-CA	-5.18	1.37	1.45
2	A	744	GLY	N-CA	-5.16	1.37	1.45
2	A	511	GLY	N-CA	-5.16	1.37	1.45
2	A	708	GLY	N-CA	-5.15	1.38	1.45
2	A	653	ARG	CD-NE	-5.10	1.39	1.46
2	A	791	ALA	CA-CB	-5.08	1.43	1.54
2	A	658	ARG	CD-NE	-5.08	1.39	1.46
2	A	522	GLY	N-CA	-5.08	1.38	1.45
2	A	188	ARG	CD-NE	-5.07	1.39	1.46
2	A	438	GLY	N-CA	-5.06	1.38	1.45
2	A	485	ALA	CA-CB	-5.02	1.43	1.54

All (299) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	935	ALA	CA-C-N	-32.84	62.59	121.70
2	A	935	ALA	C-N-CA	-32.84	62.59	121.70
2	A	936	LEU	N-CA-CB	-25.44	67.26	110.50
2	A	936	LEU	CB-CA-C	-24.88	62.82	110.10
2	A	936	LEU	CB-CG-CD1	-23.39	40.54	110.70
2	A	936	LEU	CA-CB-CG	-21.14	42.30	116.30
2	A	936	LEU	CD1-CG-CD2	-19.34	68.25	110.80
2	A	936	LEU	CB-CG-CD2	-16.83	60.21	110.70
2	A	935	ALA	O-C-N	15.10	142.34	121.95
2	A	936	LEU	N-CA-C	-11.89	77.72	111.00
1	B	401	ASN	CA-CB-CG	8.27	120.87	112.60
1	B	812	ASN	CA-CB-CG	7.77	120.37	112.60
2	A	355	PHE	CA-CB-CG	7.66	121.46	113.80
2	A	618	PHE	CA-CB-CG	7.41	121.21	113.80
2	A	681	PHE	CA-CB-CG	7.37	121.17	113.80
2	A	800	ASP	CA-CB-CG	7.36	119.96	112.60
2	A	607	PHE	CA-CB-CG	7.31	121.11	113.80
2	A	519	ASP	CA-CB-CG	7.30	119.91	112.60
2	A	757	ASP	CA-CB-CG	7.24	119.84	112.60
2	A	400	PHE	CA-CB-CG	7.16	120.96	113.80
2	A	748	ASN	CA-CB-CG	7.08	119.69	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	518	PHE	CA-CB-CG	7.07	120.87	113.80
2	A	636	ASN	CA-CB-CG	7.05	119.65	112.60
2	A	211	ASN	CA-CB-CG	7.03	119.63	112.60
2	A	621	SER	CA-C-N	7.03	130.61	123.16
2	A	621	SER	C-N-CA	7.03	130.61	123.16
2	A	477	GLY	CA-C-N	7.01	132.10	122.77
2	A	477	GLY	C-N-CA	7.01	132.10	122.77
2	A	864	ASN	CA-C-N	6.94	130.57	122.52
2	A	864	ASN	C-N-CA	6.94	130.57	122.52
2	A	846	ASN	CA-CB-CG	6.91	119.51	112.60
2	A	723	ASP	CA-CB-CG	6.90	119.50	112.60
2	A	768	GLY	CA-C-N	6.90	128.14	121.65
2	A	768	GLY	C-N-CA	6.90	128.14	121.65
2	A	191	HIS	CA-CB-CG	6.90	120.70	113.80
2	A	843	PHE	CA-CB-CG	6.88	120.68	113.80
2	A	175	HIS	CA-CB-CG	6.86	120.66	113.80
2	A	833	ASN	CA-C-N	6.83	133.79	122.73
2	A	833	ASN	C-N-CA	6.83	133.79	122.73
2	A	542	PHE	CA-CB-CG	6.82	120.62	113.80
2	A	715	ASP	CA-CB-CG	6.80	119.40	112.60
2	A	786	PHE	CA-CB-CG	6.80	120.60	113.80
2	A	422	ASP	CA-CB-CG	6.79	119.39	112.60
2	A	624	ASN	CA-CB-CG	6.75	119.35	112.60
2	A	856	ASP	CA-CB-CG	6.72	119.32	112.60
2	A	734	GLY	N-CA-C	6.69	119.32	111.63
2	A	446	ASP	CA-CB-CG	6.67	119.27	112.60
2	A	845	ASP	CA-CB-CG	6.67	119.27	112.60
2	A	875	PHE	CA-CB-CG	6.65	120.45	113.80
2	A	870	ASN	CA-CB-CG	6.64	119.24	112.60
2	A	675	ASN	CA-CB-CG	6.59	119.19	112.60
2	A	694	ASP	CA-CB-CG	6.53	119.13	112.60
2	A	904	PHE	CA-CB-CG	6.51	120.31	113.80
2	A	933	PHE	CA-CB-CG	6.51	120.31	113.80
2	A	445	ASN	CA-CB-CG	6.50	119.10	112.60
2	A	634	ASP	CA-CB-CG	6.49	119.09	112.60
2	A	577	TYR	CA-C-N	6.48	130.99	123.15
2	A	577	TYR	C-N-CA	6.48	130.99	123.15
2	A	722	HIS	CA-CB-CG	6.43	120.23	113.80
2	A	853	ASN	CA-CB-CG	6.37	118.97	112.60
2	A	196	ASN	CA-CB-CG	6.35	118.95	112.60
2	A	881	ASP	CA-CB-CG	6.33	118.93	112.60
2	A	714	PHE	CA-CB-CG	6.33	120.13	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	384	ILE	N-CA-C	6.32	117.00	110.36
2	A	524	ASN	CA-CB-CG	6.32	118.92	112.60
2	A	541	ILE	CA-C-N	6.28	131.13	122.77
2	A	541	ILE	C-N-CA	6.28	131.13	122.77
2	A	809	PHE	CA-CB-CG	6.28	120.08	113.80
2	A	160	ASN	CA-CB-CG	6.26	118.86	112.60
2	A	194	ASN	CA-CB-CG	6.25	118.85	112.60
2	A	227	ASP	CA-CB-CG	6.21	118.81	112.60
2	A	774	GLN	CA-C-N	6.21	130.92	122.84
2	A	774	GLN	C-N-CA	6.21	130.92	122.84
2	A	834	ARG	CA-C-N	6.21	133.15	121.97
2	A	834	ARG	C-N-CA	6.21	133.15	121.97
2	A	648	ALA	CA-C-N	6.20	130.88	123.19
2	A	648	ALA	C-N-CA	6.20	130.88	123.19
2	A	864	ASN	CA-CB-CG	6.19	118.79	112.60
2	A	204	GLY	N-CA-C	6.16	118.18	110.29
2	A	860	ASP	CA-CB-CG	6.15	118.75	112.60
2	A	788	ALA	CA-C-N	6.11	131.22	123.10
2	A	788	ALA	C-N-CA	6.11	131.22	123.10
2	A	316	PHE	CA-CB-CG	6.11	119.91	113.80
2	A	737	VAL	CA-C-N	6.10	131.13	123.14
2	A	737	VAL	C-N-CA	6.10	131.13	123.14
2	A	658	ARG	CD-NE-CZ	6.10	132.93	124.40
2	A	872	PHE	CA-CB-CG	6.09	119.89	113.80
2	A	450	ASN	CA-CB-CG	6.05	118.65	112.60
2	A	461	ASP	CA-CB-CG	6.05	118.65	112.60
2	A	840	LYS	CA-C-N	6.05	130.98	123.12
2	A	840	LYS	C-N-CA	6.05	130.98	123.12
2	A	188	ARG	CD-NE-CZ	6.02	132.83	124.40
2	A	757	ASP	CA-C-N	6.02	130.95	123.12
2	A	757	ASP	C-N-CA	6.02	130.95	123.12
2	A	662	ASN	CA-CB-CG	6.00	118.60	112.60
2	A	537	ARG	CD-NE-CZ	5.97	132.76	124.40
2	A	739	THR	CA-C-N	5.96	130.73	122.93
2	A	739	THR	C-N-CA	5.96	130.73	122.93
2	A	641	GLY	CA-C-N	5.95	131.21	123.00
2	A	641	GLY	C-N-CA	5.95	131.21	123.00
2	A	474	THR	N-CA-C	5.93	117.79	108.96
2	A	674	ASN	CA-CB-CG	5.90	118.50	112.60
2	A	645	ASN	CA-CB-CG	5.89	118.49	112.60
2	A	660	ASN	CA-CB-CG	5.89	118.49	112.60
2	A	714	PHE	CA-C-N	5.89	131.04	122.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	714	PHE	C-N-CA	5.89	131.04	122.85
2	A	441	ASP	CA-CB-CG	5.87	118.47	112.60
2	A	649	VAL	CA-C-N	5.87	131.14	122.99
2	A	649	VAL	C-N-CA	5.87	131.14	122.99
2	A	655	GLY	N-CA-C	5.87	119.06	110.38
2	A	658	ARG	CA-C-N	5.85	130.45	122.84
2	A	658	ARG	C-N-CA	5.85	130.45	122.84
2	A	653	ARG	CD-NE-CZ	5.83	132.56	124.40
2	A	399	GLY	CA-C-N	5.78	129.07	120.87
2	A	399	GLY	C-N-CA	5.78	129.07	120.87
2	A	791	ALA	CA-C-N	5.76	131.11	122.99
2	A	791	ALA	C-N-CA	5.76	131.11	122.99
2	A	738	ILE	CA-C-N	5.75	130.06	122.30
2	A	738	ILE	C-N-CA	5.75	130.06	122.30
2	A	740	VAL	CA-C-N	5.75	130.93	123.00
2	A	740	VAL	C-N-CA	5.75	130.93	123.00
2	A	804	ASN	CA-CB-CG	5.75	118.34	112.60
2	A	625	PHE	CA-CB-CG	5.71	119.51	113.80
2	A	226	ILE	CA-C-N	5.68	131.01	123.05
2	A	226	ILE	C-N-CA	5.68	131.01	123.05
1	B	488	ARG	NE-CZ-NH2	5.67	124.30	119.20
2	A	729	VAL	N-CA-CB	5.67	117.11	110.82
2	A	157	TYR	CA-C-N	5.66	130.47	122.09
2	A	157	TYR	C-N-CA	5.66	130.47	122.09
2	A	801	ILE	CA-C-N	5.66	130.97	122.99
2	A	801	ILE	C-N-CA	5.66	130.97	122.99
1	B	600	ARG	CA-C-N	5.65	125.76	119.32
1	B	600	ARG	C-N-CA	5.65	125.76	119.32
2	A	656	VAL	CA-C-N	5.64	131.00	122.98
2	A	656	VAL	C-N-CA	5.64	131.00	122.98
2	A	754	THR	CA-C-N	5.63	130.94	122.99
2	A	754	THR	C-N-CA	5.63	130.94	122.99
2	A	659	LEU	CA-C-N	5.61	130.11	122.19
2	A	659	LEU	C-N-CA	5.61	130.11	122.19
2	A	803	LYS	CA-C-N	5.61	129.51	121.50
2	A	803	LYS	C-N-CA	5.61	129.51	121.50
1	B	524	PRO	N-CA-CB	5.60	106.17	102.25
2	A	708	GLY	CA-C-N	5.59	130.87	122.99
2	A	708	GLY	C-N-CA	5.59	130.87	122.99
1	B	150	ASN	CB-CA-C	5.57	115.15	111.20
2	A	732	ASN	CA-C-N	5.56	130.68	123.00
2	A	732	ASN	C-N-CA	5.56	130.68	123.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	680	SER	CA-C-N	5.56	130.99	122.93
2	A	680	SER	C-N-CA	5.56	130.99	122.93
2	A	783	SER	CA-C-N	5.54	127.64	120.44
2	A	783	SER	C-N-CA	5.54	127.64	120.44
2	A	881	ASP	CA-C-N	5.53	128.69	120.95
2	A	881	ASP	C-N-CA	5.53	128.69	120.95
2	A	839	GLY	CA-C-N	5.53	130.79	123.05
2	A	839	GLY	C-N-CA	5.53	130.79	123.05
2	A	713	ILE	CA-C-N	5.49	130.91	123.11
2	A	713	ILE	C-N-CA	5.49	130.91	123.11
2	A	195	ASN	CA-CB-CG	5.48	118.08	112.60
2	A	760	PRO	CA-C-N	5.47	130.55	123.00
2	A	760	PRO	C-N-CA	5.47	130.55	123.00
2	A	164	ALA	CA-C-N	5.46	131.14	122.94
2	A	164	ALA	C-N-CA	5.46	131.14	122.94
2	A	812	ASP	CA-C-N	5.45	127.52	120.44
2	A	812	ASP	C-N-CA	5.45	127.52	120.44
2	A	452	PRO	CA-C-N	5.43	129.14	121.53
2	A	452	PRO	C-N-CA	5.43	129.14	121.53
2	A	154	LEU	N-CA-CB	5.43	118.33	109.69
2	A	904	PHE	CA-C-N	5.42	127.81	120.38
2	A	904	PHE	C-N-CA	5.42	127.81	120.38
1	B	907	ARG	NE-CZ-NH2	5.41	124.07	119.20
1	B	109	ASP	CA-CB-CG	5.41	118.00	112.60
2	A	849	LEU	CA-C-N	5.40	127.95	120.29
2	A	849	LEU	C-N-CA	5.40	127.95	120.29
2	A	811	ILE	CA-C-N	5.39	131.55	123.24
2	A	811	ILE	C-N-CA	5.39	131.55	123.24
2	A	841	VAL	CA-C-N	5.38	131.10	123.14
2	A	841	VAL	C-N-CA	5.38	131.10	123.14
2	A	830	TYR	N-CA-CB	5.38	118.18	110.06
2	A	440	LYS	N-CA-CB	5.36	117.78	110.01
2	A	673	ASP	CA-C-N	5.35	127.40	120.44
2	A	673	ASP	C-N-CA	5.35	127.40	120.44
2	A	650	VAL	CA-C-N	5.34	129.06	121.42
2	A	650	VAL	C-N-CA	5.34	129.06	121.42
2	A	901	ARG	CA-C-N	5.33	130.35	122.94
2	A	901	ARG	C-N-CA	5.33	130.35	122.94
2	A	657	VAL	CA-C-N	5.33	130.07	122.72
2	A	657	VAL	C-N-CA	5.33	130.07	122.72
2	A	882	GLN	N-CA-CB	5.33	117.79	109.85
2	A	863	ILE	N-CA-CB	5.32	116.77	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	156	LYS	CA-C-N	5.31	131.00	122.83
2	A	156	LYS	C-N-CA	5.31	131.00	122.83
1	B	1080	ASP	CA-C-N	5.30	125.02	119.82
1	B	1080	ASP	C-N-CA	5.30	125.02	119.82
2	A	427	TRP	CA-C-N	5.28	128.21	120.71
2	A	427	TRP	C-N-CA	5.28	128.21	120.71
2	A	850	GLN	CA-C-N	5.27	127.61	120.65
2	A	850	GLN	C-N-CA	5.27	127.61	120.65
2	A	517	VAL	N-CA-CB	5.26	116.70	110.55
2	A	859	VAL	N-CA-CB	5.26	116.34	110.51
2	A	428	SER	N-CA-CB	5.25	117.76	109.83
2	A	644	ALA	CA-C-N	5.25	128.17	120.71
2	A	644	ALA	C-N-CA	5.25	128.17	120.71
2	A	756	LEU	CA-C-N	5.24	130.46	122.24
2	A	756	LEU	C-N-CA	5.24	130.46	122.24
2	A	776	LEU	N-CA-CB	5.23	117.73	109.83
2	A	686	PHE	CA-CB-CG	5.22	119.03	113.80
2	A	807	GLY	N-CA-C	5.22	120.95	114.37
2	A	622	ILE	CA-C-N	5.22	129.76	121.99
2	A	622	ILE	C-N-CA	5.22	129.76	121.99
2	A	651	LEU	CA-C-N	5.22	130.93	122.53
2	A	651	LEU	C-N-CA	5.22	130.93	122.53
2	A	625	PHE	CA-C-N	5.21	130.76	122.94
2	A	625	PHE	C-N-CA	5.21	130.76	122.94
2	A	423	GLN	CA-C-N	5.20	128.26	120.87
2	A	423	GLN	C-N-CA	5.20	128.26	120.87
2	A	669	LEU	N-CA-CB	5.20	117.65	109.69
2	A	720	PRO	CA-C-N	5.20	127.20	120.44
2	A	720	PRO	C-N-CA	5.20	127.20	120.44
2	A	845	ASP	N-CA-CB	5.20	117.69	110.26
2	A	438	GLY	CA-C-N	5.20	127.19	120.44
2	A	438	GLY	C-N-CA	5.20	127.19	120.44
2	A	171	GLN	CB-CG-CD	5.19	121.43	112.60
2	A	902	ILE	CA-C-N	5.19	128.85	121.42
2	A	902	ILE	C-N-CA	5.19	128.85	121.42
2	A	185	THR	CA-C-N	5.19	127.50	120.44
2	A	185	THR	C-N-CA	5.19	127.50	120.44
2	A	508	ASN	CA-C-N	5.19	130.48	123.11
2	A	508	ASN	C-N-CA	5.19	130.48	123.11
2	A	208	THR	CA-C-N	5.18	130.34	122.11
2	A	208	THR	C-N-CA	5.18	130.34	122.11
2	A	696	THR	CA-C-N	5.17	130.67	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	696	THR	C-N-CA	5.17	130.67	122.60
2	A	637	PRO	CA-C-N	5.17	130.85	122.68
2	A	637	PRO	C-N-CA	5.17	130.85	122.68
2	A	491	ASP	CA-C-N	5.17	130.78	122.83
2	A	491	ASP	C-N-CA	5.17	130.78	122.83
2	A	163	LEU	CA-C-N	5.16	128.04	120.71
2	A	163	LEU	C-N-CA	5.16	128.04	120.71
1	B	932	GLN	N-CA-C	5.15	117.35	110.35
2	A	655	GLY	CA-C-N	5.15	129.52	121.85
2	A	655	GLY	C-N-CA	5.15	129.52	121.85
2	A	846	ASN	CA-C-N	5.14	127.17	120.28
2	A	846	ASN	C-N-CA	5.14	127.17	120.28
2	A	862	ILE	CA-C-N	5.14	127.04	120.56
2	A	862	ILE	C-N-CA	5.14	127.04	120.56
1	B	886	SER	CA-C-N	5.14	127.85	122.14
1	B	886	SER	C-N-CA	5.14	127.85	122.14
2	A	843	PHE	CA-C-N	5.14	128.16	120.87
2	A	843	PHE	C-N-CA	5.14	128.16	120.87
2	A	797	ASN	CA-C-N	5.13	130.87	122.81
2	A	797	ASN	C-N-CA	5.13	130.87	122.81
2	A	192	ASP	CA-C-N	5.12	131.82	122.50
2	A	192	ASP	C-N-CA	5.12	131.82	122.50
2	A	515	ILE	N-CA-CB	5.12	116.54	110.55
2	A	748	ASN	CA-C-N	5.11	127.39	120.44
2	A	748	ASN	C-N-CA	5.11	127.39	120.44
2	A	179	GLY	CA-C-N	5.11	130.51	122.49
2	A	179	GLY	C-N-CA	5.11	130.51	122.49
2	A	728	PRO	CA-C-N	5.11	128.84	121.18
2	A	728	PRO	C-N-CA	5.11	128.84	121.18
2	A	723	ASP	N-CA-CB	5.09	117.22	110.29
2	A	769	ILE	N-CA-CB	5.09	117.37	112.28
2	A	440	LYS	CA-C-N	5.09	127.06	120.44
2	A	440	LYS	C-N-CA	5.09	127.06	120.44
2	A	226	ILE	N-CA-CB	5.09	116.50	110.55
1	B	654	TYR	CA-C-N	5.08	126.20	119.84
1	B	654	TYR	C-N-CA	5.08	126.20	119.84
2	A	445	ASN	N-CA-CB	5.08	117.46	109.69
2	A	861	GLU	N-CA-CB	5.08	117.38	110.01
2	A	860	ASP	CA-C-N	5.08	127.04	120.44
2	A	860	ASP	C-N-CA	5.08	127.04	120.44
2	A	713	ILE	N-CA-CB	5.07	116.45	110.82
2	A	804	ASN	N-CA-CB	5.07	117.81	109.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	707	SER	N-CA-CB	5.07	117.66	110.16
2	A	842	GLU	CA-C-N	5.06	127.96	120.82
2	A	842	GLU	C-N-CA	5.06	127.96	120.82
2	A	154	LEU	CA-C-N	5.06	130.53	122.94
2	A	154	LEU	C-N-CA	5.06	130.53	122.94
2	A	877	PRO	CA-C-N	5.06	129.17	120.72
2	A	877	PRO	C-N-CA	5.06	129.17	120.72
2	A	478	THR	CA-C-N	5.05	130.18	122.29
2	A	478	THR	C-N-CA	5.05	130.18	122.29
2	A	712	TYR	CA-C-N	5.05	128.76	121.18
2	A	712	TYR	C-N-CA	5.05	128.76	121.18
2	A	315	SER	CA-C-N	5.05	127.46	120.29
2	A	315	SER	C-N-CA	5.05	127.46	120.29
2	A	836	ASP	CA-C-N	5.04	127.54	120.28
2	A	836	ASP	C-N-CA	5.04	127.54	120.28
2	A	859	VAL	CA-C-N	5.04	126.99	120.44
2	A	859	VAL	C-N-CA	5.04	126.99	120.44
2	A	694	ASP	N-CA-CB	5.04	117.29	109.48
2	A	847	SER	CA-C-N	5.03	127.36	120.46
2	A	847	SER	C-N-CA	5.03	127.36	120.46
2	A	742	ARG	CA-CB-CG	5.02	124.14	114.10
2	A	532	GLU	CA-CB-CG	5.01	124.13	114.10
2	A	517	VAL	CA-C-N	5.01	126.95	120.44
2	A	517	VAL	C-N-CA	5.01	126.95	120.44
1	B	565	ARG	NE-CZ-NH2	5.00	123.70	119.20
2	A	814	GLN	N-CA-CB	5.00	117.39	109.94

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	584	TYR	Sidechain
1	B	348	TYR	Sidechain
1	B	880	TYR	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	B	10049	9737	9727	3	0
2	A	6944	6717	6713	100	0
All	All	16993	16454	16440	103	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 3.

All (103) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:935:ALA:C	2:A:936:LEU:N	1.88	1.30
2:A:936:LEU:CA	2:A:936:LEU:C	2.11	1.24
2:A:935:ALA:C	2:A:936:LEU:CA	2.32	1.03
2:A:856:ASP:O	2:A:936:LEU:HD12	1.71	0.91
2:A:429:THR:HG1	2:A:538:THR:HG1	1.24	0.83
2:A:428:SER:OG	2:A:519:ASP:OD2	1.96	0.81
2:A:935:ALA:O	2:A:936:LEU:CA	2.28	0.81
2:A:858:THR:OG1	2:A:936:LEU:HB2	1.84	0.78
2:A:936:LEU:N	2:A:936:LEU:CA	2.47	0.77
2:A:264:THR:OG1	2:A:266:ASN:OD1	2.04	0.71
2:A:130:TYR:OH	2:A:327:ARG:O	2.08	0.70
2:A:856:ASP:O	2:A:936:LEU:CD1	2.40	0.69
2:A:430:THR:OG1	2:A:519:ASP:OD1	2.10	0.69
2:A:935:ALA:CA	2:A:936:LEU:N	2.55	0.69
2:A:889:THR:OG1	2:A:897:SER:OG	2.05	0.68
2:A:148:LEU:HD23	2:A:149:ILE:N	2.09	0.67
2:A:889:THR:O	2:A:897:SER:N	2.31	0.63
2:A:445:ASN:O	2:A:537:ARG:NH2	2.31	0.63
2:A:723:ASP:OD1	2:A:724:GLY:N	2.31	0.62
2:A:270:ASN:O	2:A:726:GLN:NE2	2.33	0.60
2:A:889:THR:OG1	2:A:897:SER:O	2.17	0.59
2:A:784:GLU:O	2:A:804:ASN:ND2	2.35	0.58
2:A:65:GLN:OE1	2:A:83:ARG:NE	2.37	0.58
2:A:169:LYS:NZ	2:A:419:SER:O	2.36	0.58
2:A:280:ILE:HG23	2:A:293:GLN:CD	2.30	0.57
2:A:420:THR:HG22	2:A:420:THR:O	2.04	0.57
2:A:889:THR:N	2:A:897:SER:O	2.33	0.56
2:A:145:LEU:HD23	2:A:216:LEU:HD13	1.89	0.55
2:A:370:SER:OG	2:A:498:ILE:N	2.39	0.55
2:A:163:LEU:HD12	2:A:510:TYR:CE1	2.42	0.55
2:A:87:VAL:O	2:A:289:ASN:ND2	2.37	0.54
2:A:163:LEU:HD12	2:A:510:TYR:HE1	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:908:ASN:OD1	2:A:909:PHE:N	2.40	0.54
2:A:588:ILE:HD11	2:A:604:VAL:HG13	1.89	0.54
2:A:156:LYS:HG3	2:A:696:THR:HG21	1.89	0.53
2:A:431:THR:HB	2:A:534:LEU:HD12	1.91	0.53
2:A:521:LEU:HD12	2:A:582:TYR:HA	1.91	0.53
2:A:109:SER:O	2:A:132:LEU:HD12	2.09	0.52
2:A:878:ALA:N	2:A:882:GLN:OE1	2.40	0.52
2:A:389:ASP:OD2	2:A:631:ALA:N	2.42	0.52
2:A:323:TRP:CD1	2:A:337:PRO:HB3	2.45	0.51
2:A:186:SER:O	2:A:189:ASN:ND2	2.43	0.51
2:A:521:LEU:HD11	2:A:585:SER:OG	2.11	0.51
2:A:935:ALA:N	2:A:936:LEU:N	2.59	0.51
2:A:754:THR:HG23	2:A:755:THR:HG23	1.92	0.50
2:A:401:LYS:NZ	2:A:538:THR:O	2.43	0.50
2:A:148:LEU:HD21	2:A:502:ILE:HG12	1.93	0.50
2:A:295:TYR:O	2:A:298:SER:OG	2.27	0.50
2:A:119:ASN:C	2:A:120:ILE:HD12	2.37	0.50
2:A:141:MET:O	2:A:145:LEU:HD13	2.12	0.50
2:A:395:ILE:HD12	2:A:552:LEU:HD11	1.93	0.49
2:A:254:SER:OG	2:A:270:ASN:ND2	2.38	0.49
2:A:77:PHE:CD2	2:A:304:VAL:HG11	2.48	0.48
2:A:271:THR:O	2:A:275:LEU:HD23	2.14	0.48
2:A:490:LYS:N	2:A:490:LYS:HD3	2.29	0.48
2:A:556:LYS:O	2:A:556:LYS:HD2	2.14	0.47
2:A:656:VAL:HG11	2:A:764:ALA:HB2	1.96	0.47
2:A:471:GLY:O	2:A:482:ILE:N	2.47	0.47
2:A:33:ASP:OD1	2:A:36:ASN:N	2.47	0.46
2:A:48:THR:O	2:A:49:ASP:OD1	2.34	0.46
2:A:305:THR:HG22	2:A:306:ASN:N	2.31	0.46
1:B:180:TRP:HA	1:B:183:ILE:HG22	1.97	0.45
2:A:369:ASN:O	2:A:371:HIS:N	2.48	0.45
2:A:651:LEU:HD23	2:A:656:VAL:HG12	1.98	0.45
2:A:58:ALA:HA	2:A:126:MET:HE3	1.99	0.45
2:A:72:HIS:HB2	2:A:304:VAL:HG21	1.98	0.45
2:A:902:ILE:HD13	2:A:925:PHE:CE2	2.51	0.45
2:A:119:ASN:O	2:A:120:ILE:HB	2.17	0.45
2:A:189:ASN:OD1	2:A:190:GLN:N	2.50	0.44
2:A:242:SER:OG	2:A:243:THR:N	2.50	0.44
2:A:665:ASN:O	2:A:665:ASN:OD1	2.36	0.44
2:A:67:ALA:HB2	2:A:81:LYS:HD2	1.99	0.44
2:A:388:ILE:HD11	2:A:395:ILE:CG2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:902:ILE:HD13	2:A:925:PHE:CZ	2.53	0.43
2:A:395:ILE:HD12	2:A:552:LEU:CD1	2.48	0.43
2:A:713:ILE:HD11	2:A:779:VAL:HG11	2.01	0.43
2:A:342:ASN:O	2:A:568:VAL:N	2.43	0.43
2:A:496:VAL:O	2:A:496:VAL:HG13	2.19	0.43
2:A:132:LEU:HD23	2:A:323:TRP:CB	2.49	0.42
2:A:547:VAL:HG23	2:A:551:GLU:HG3	2.01	0.42
2:A:796:GLN:OE1	2:A:797:ASN:N	2.53	0.42
2:A:911:ASP:OD1	2:A:911:ASP:N	2.53	0.42
1:B:857:THR:HB	1:B:858:PRO:CD	2.50	0.42
2:A:407:TYR:N	2:A:499:ASN:O	2.53	0.42
2:A:103:SER:O	2:A:104:GLN:HG3	2.20	0.41
2:A:368:THR:HG23	2:A:369:ASN:N	2.35	0.41
2:A:845:ASP:O	2:A:848:VAL:HG12	2.19	0.41
2:A:96:ASN:ND2	2:A:142:ASN:OD1	2.53	0.41
2:A:158:THR:O	2:A:619:ALA:HB3	2.19	0.41
2:A:342:ASN:ND2	2:A:565:ASP:OD1	2.54	0.41
2:A:469:TYR:CD1	2:A:469:TYR:N	2.88	0.41
2:A:841:VAL:O	2:A:841:VAL:HG13	2.19	0.41
2:A:275:LEU:HD13	2:A:280:ILE:HD13	2.03	0.41
2:A:161:SER:OG	2:A:226:ILE:O	2.15	0.41
2:A:462:THR:HB	2:A:594:PHE:CE2	2.55	0.41
2:A:912:LEU:HD23	2:A:912:LEU:C	2.45	0.41
2:A:111:VAL:HG13	2:A:132:LEU:HD11	2.03	0.41
2:A:70:THR:HG21	2:A:304:VAL:HG13	2.02	0.40
2:A:299:THR:HA	2:A:323:TRP:HZ3	1.87	0.40
1:B:574:HIS:CE1	1:B:596:GLY:HA3	2.56	0.40
2:A:84:ASP:O	2:A:84:ASP:OD1	2.40	0.40
2:A:44:ALA:HB1	2:A:790:ILE:HD11	2.02	0.40
2:A:351:LYS:HG3	2:A:355:PHE:CE2	2.56	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	B	1281/1444 (89%)	1187 (93%)	81 (6%)	13 (1%)	12	49
2	A	896/1053 (85%)	842 (94%)	52 (6%)	2 (0%)	43	78
All	All	2177/2497 (87%)	2029 (93%)	133 (6%)	15 (1%)	20	56

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1092	THR
1	B	779	ASN
1	B	812	ASN
1	B	233	SER
1	B	815	ASN
1	B	817	ARG
1	B	1187	LYS
2	A	120	ILE
1	B	818	TRP
1	B	822	PRO
1	B	857	THR
1	B	1189	GLU
2	A	284	ASP
1	B	641	ILE
1	B	618	GLY

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	B	1122/1267 (89%)	1104 (98%)	18 (2%)	55	70
2	A	787/914 (86%)	785 (100%)	2 (0%)	86	86
All	All	1909/2181 (88%)	1889 (99%)	20 (1%)	65	78

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	123	ASP
1	B	243	ASP
1	B	401	ASN
1	B	503	TRP
1	B	536	ARG
1	B	610	GLN
1	B	631	ASN
1	B	632	VAL
1	B	650	LEU
1	B	658	TYR
1	B	725	ARG
1	B	752	THR
1	B	760	THR
1	B	765	LEU
1	B	812	ASN
1	B	816	THR
1	B	1270	THR
1	B	1344	GLN
2	A	461	ASP
2	A	469	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	74	ASN
1	B	99	ASN
1	B	199	ASN
1	B	304	ASN
1	B	369	ASN
1	B	462	ASN
1	B	574	HIS
1	B	582	GLN
1	B	665	GLN
1	B	716	ASN
1	B	779	ASN
1	B	809	GLN
1	B	862	ASN
1	B	901	ASN
1	B	908	ASN
1	B	1105	GLN
1	B	1165	ASN
1	B	1193	GLN
1	B	1344	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	1348	GLN
2	A	36	ASN
2	A	72	HIS
2	A	96	ASN
2	A	180	GLN
2	A	246	ASN
2	A	308	HIS
2	A	499	ASN
2	A	583	ASN
2	A	645	ASN
2	A	704	ASN
2	A	774	GLN
2	A	853	ASN
2	A	870	ASN
2	A	913	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	935:ALA	C	936:LEU	N	1.88

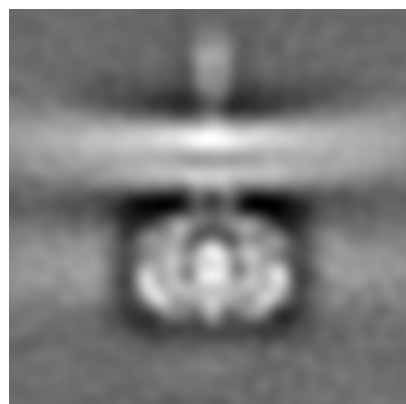
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17593. These allow visual inspection of the internal detail of the map and identification of artifacts.

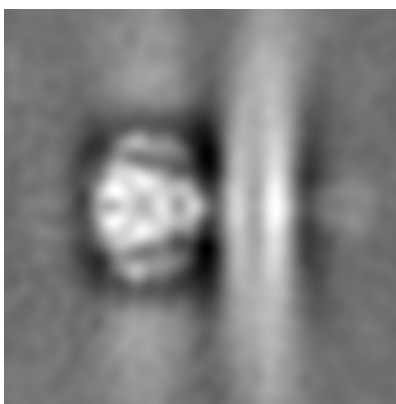
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

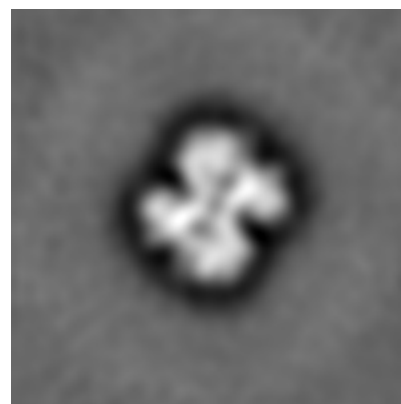
6.1.1 Primary map



X

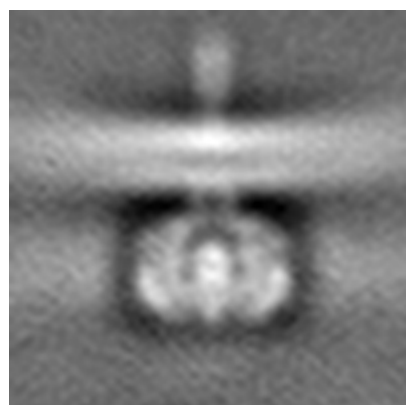


Y

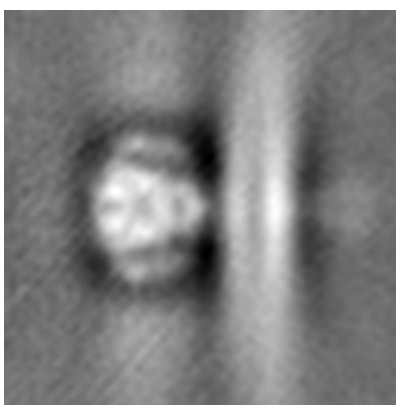


Z

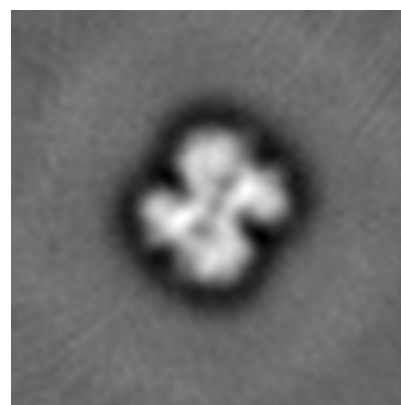
6.1.2 Raw map



X



Y

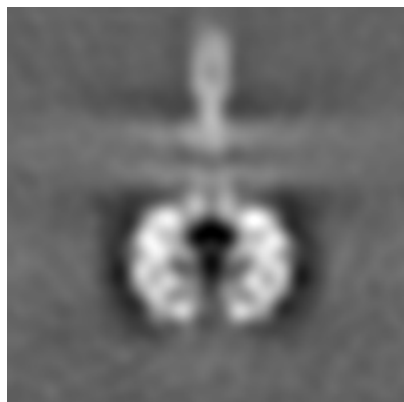


Z

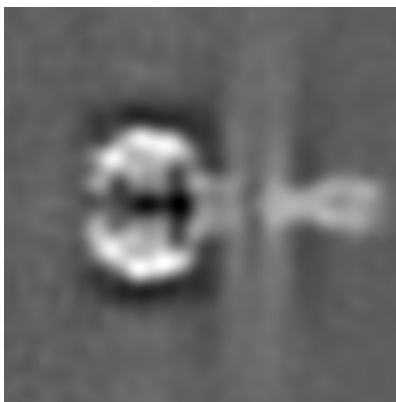
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

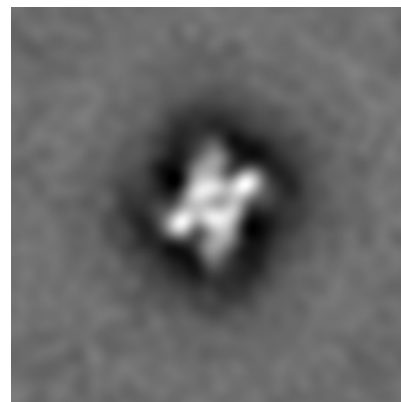
6.2.1 Primary map



X Index: 32



Y Index: 32

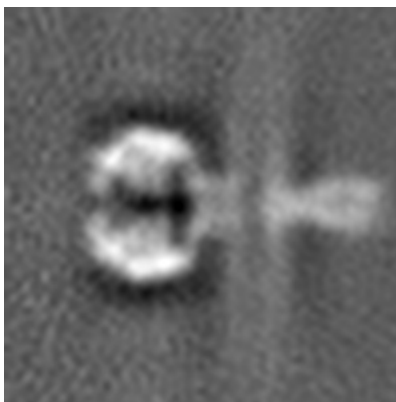


Z Index: 32

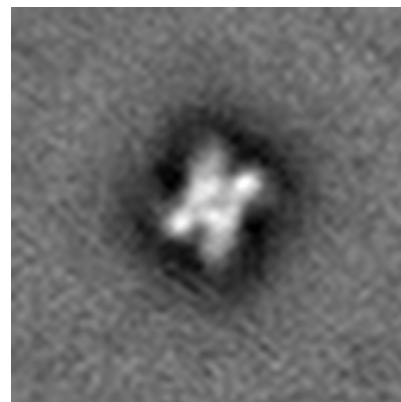
6.2.2 Raw map



X Index: 32



Y Index: 32

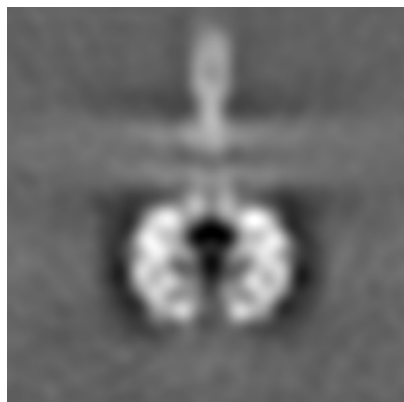


Z Index: 32

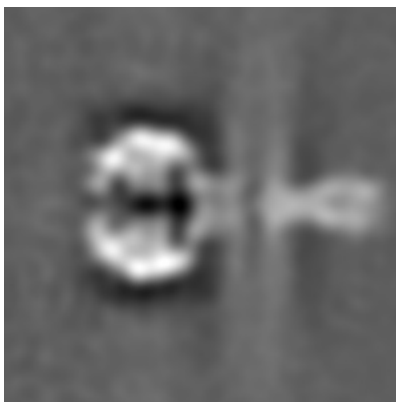
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

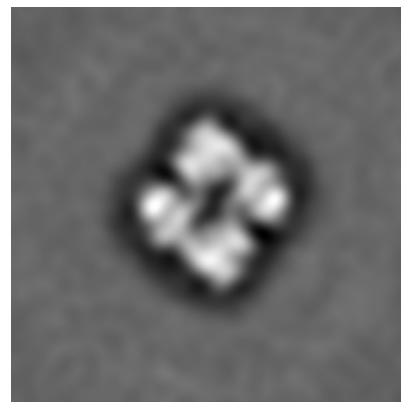
6.3.1 Primary map



X Index: 32



Y Index: 32

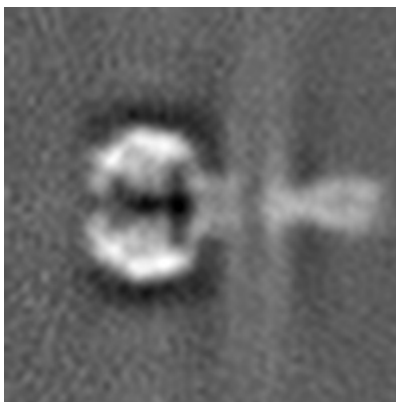


Z Index: 25

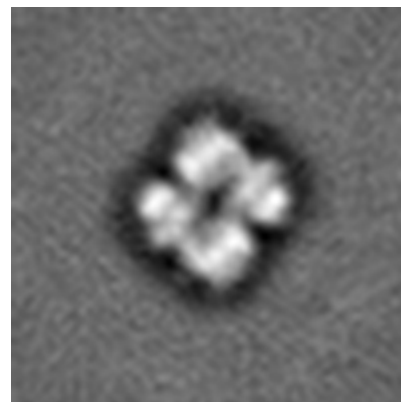
6.3.2 Raw map



X Index: 32



Y Index: 32

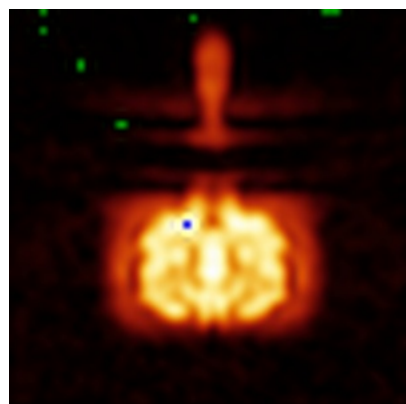


Z Index: 24

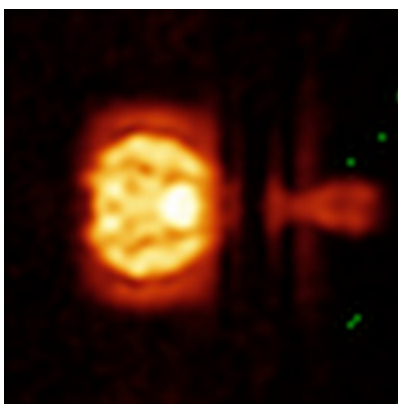
The images above show the largest variance slices of the map in three orthogonal directions.

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

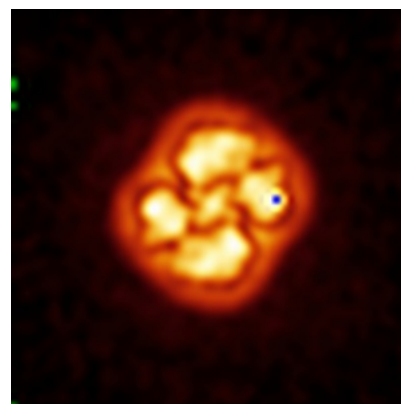
6.4.1 Primary map



X

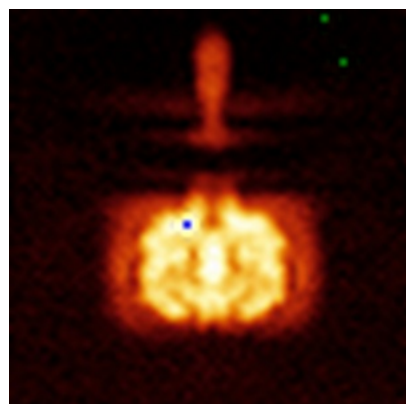


Y

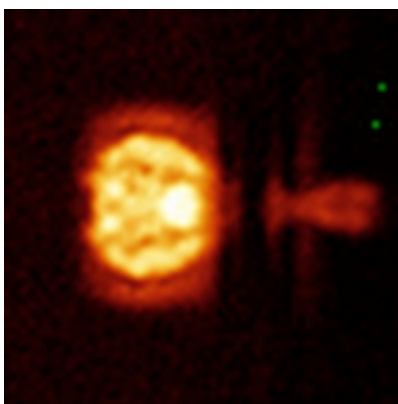


Z

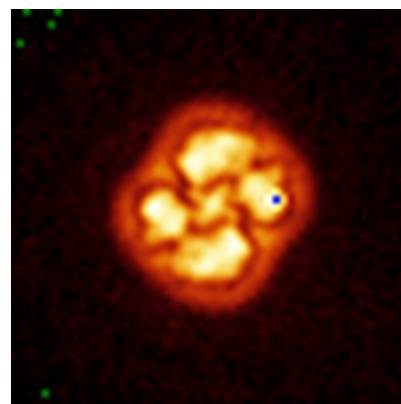
6.4.2 Raw map



X



Y

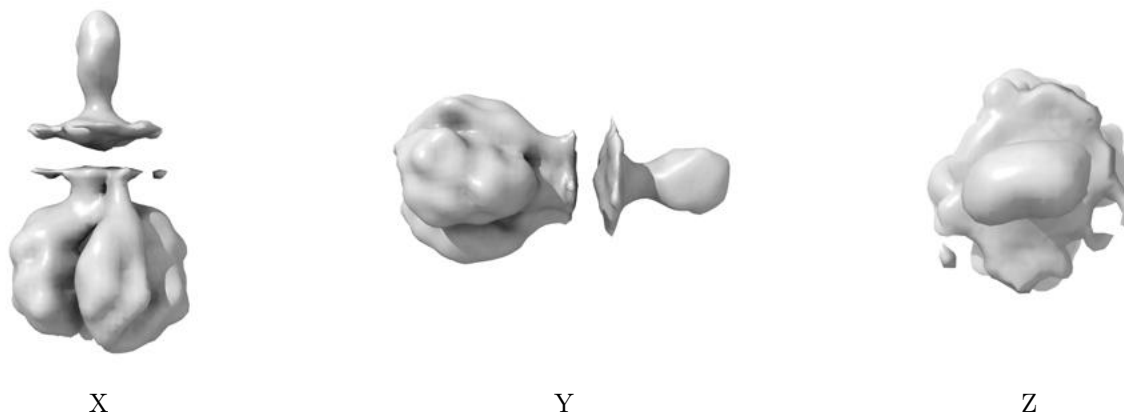


Z

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.

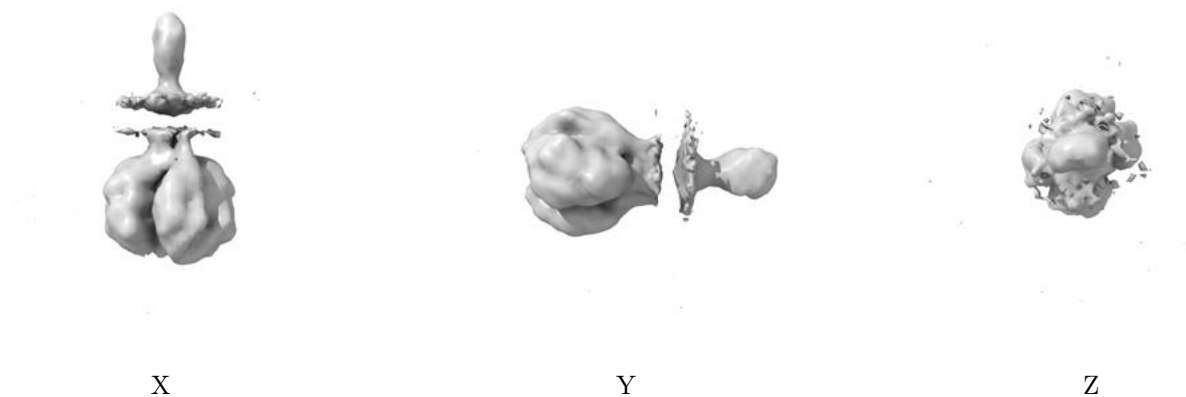
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.000145. 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.

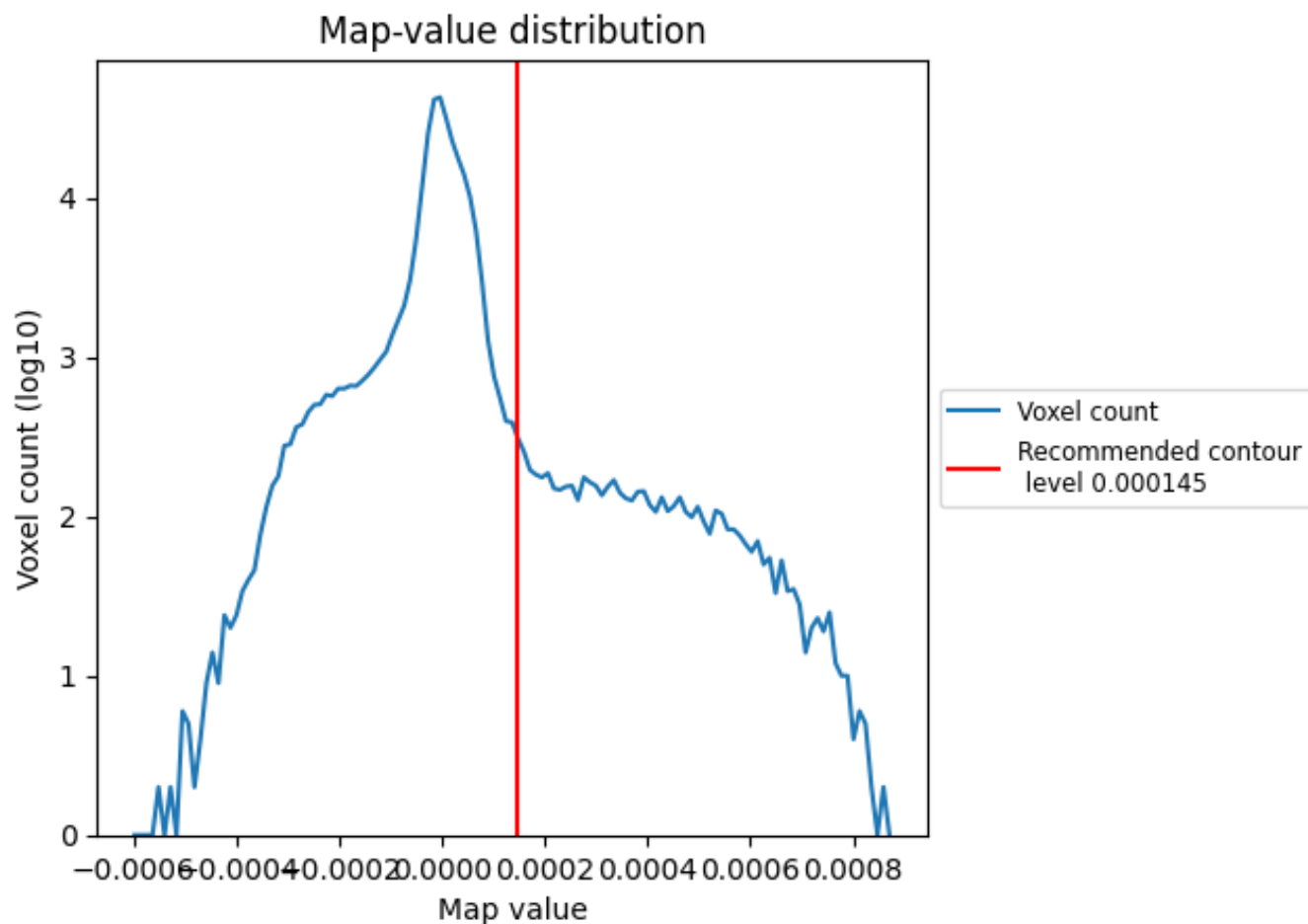
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

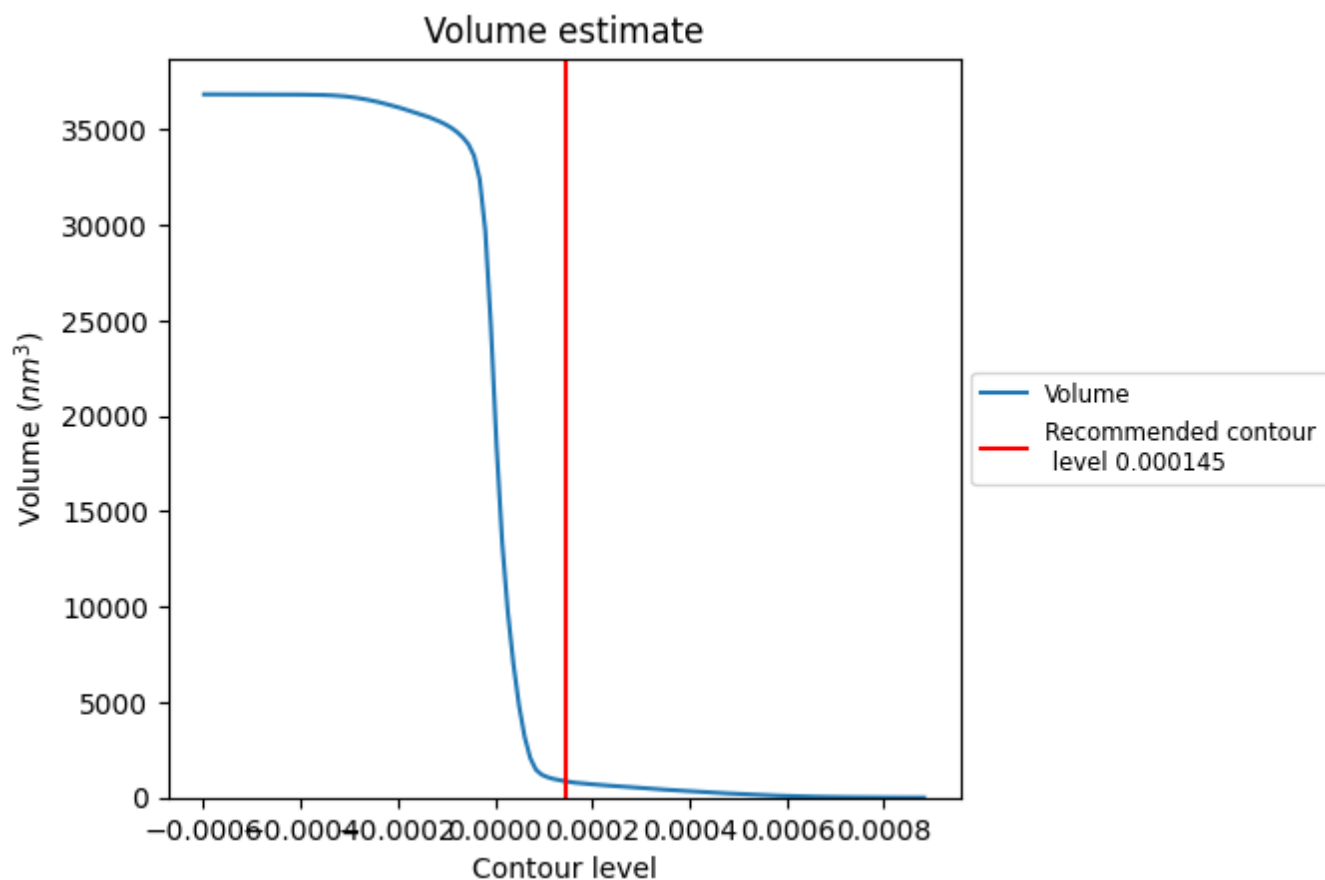
This section contains the results of statistical analysis of the map.

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.

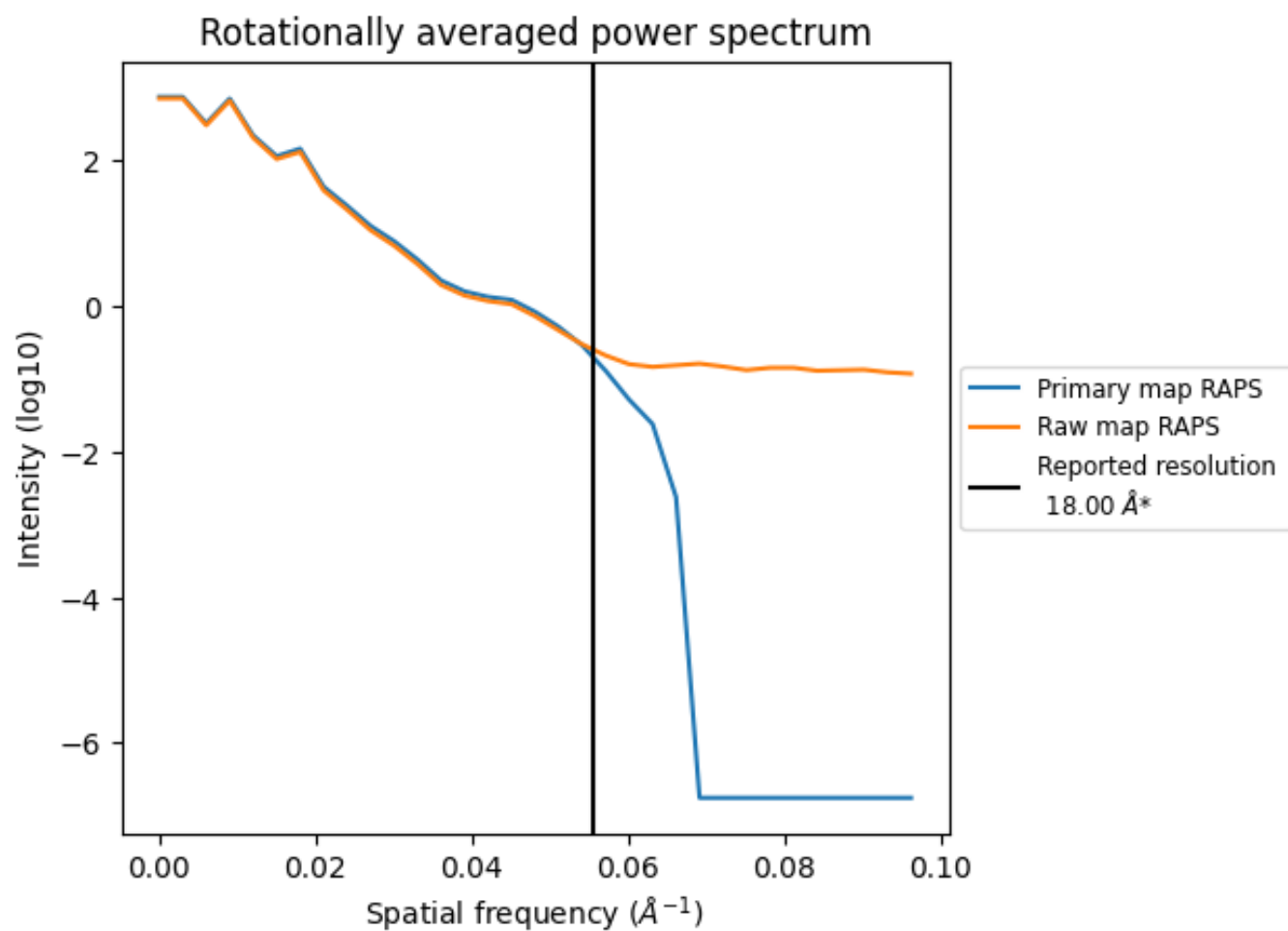
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 852 nm³; this corresponds to an approximate mass of 770 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 ⓘ

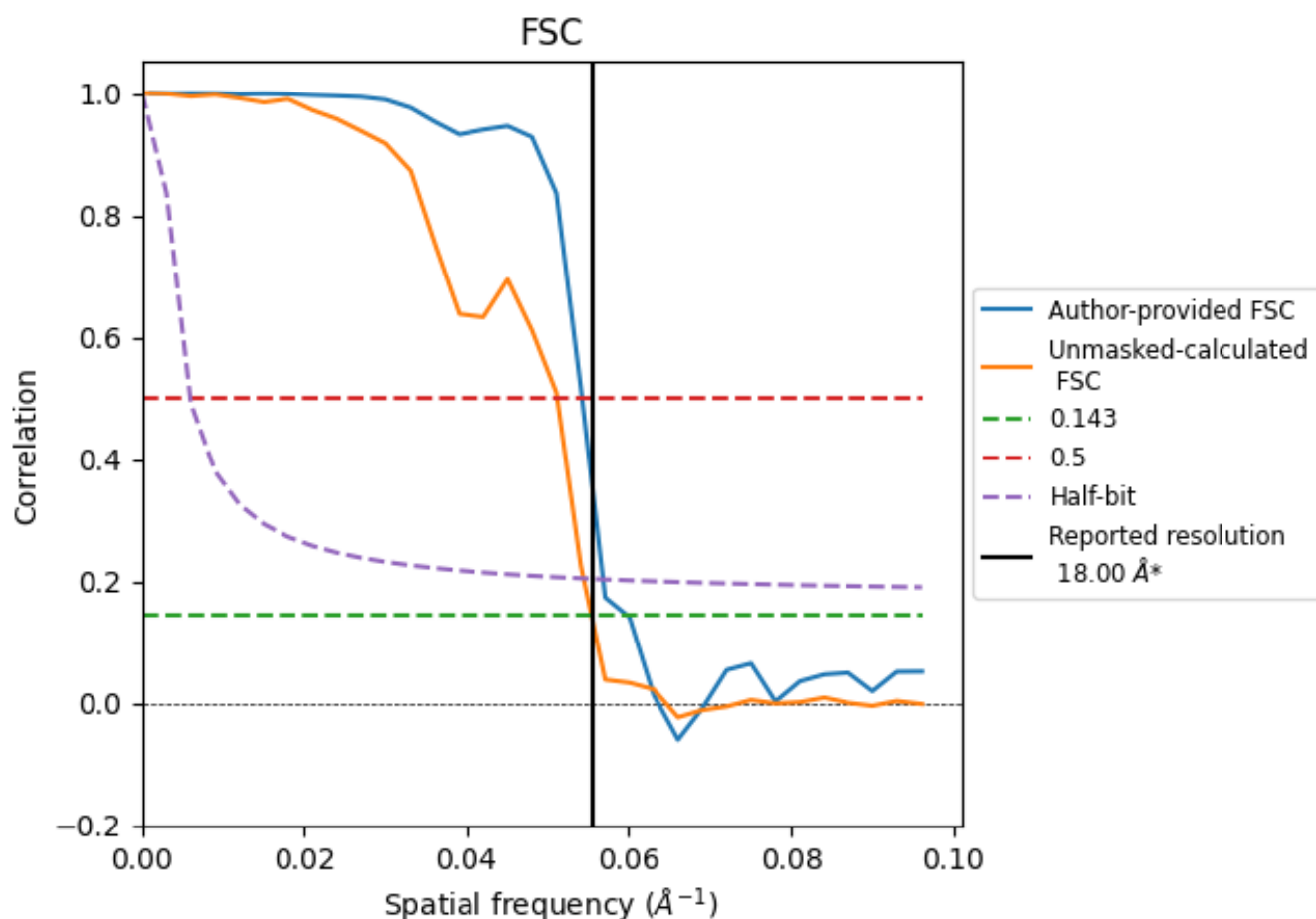


*Reported resolution corresponds to spatial frequency of 0.056 $\text{\AA}^{-1}$

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 $0.056 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

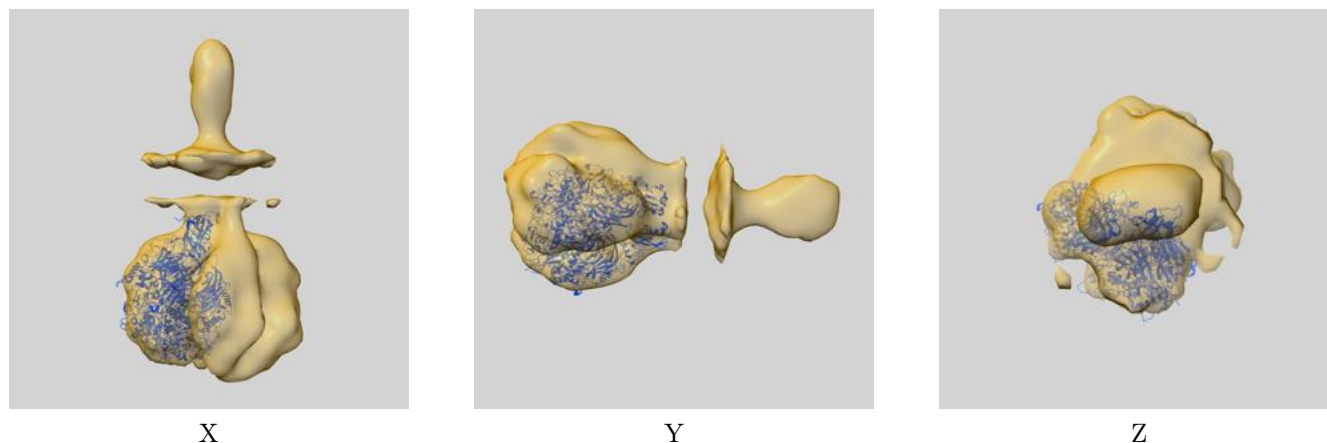
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	18.00	-	-
Author-provided FSC curve	16.69	18.45	17.61
Unmasked-calculated*	18.05	19.53	18.38

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

9 Map-model fit [i](#)

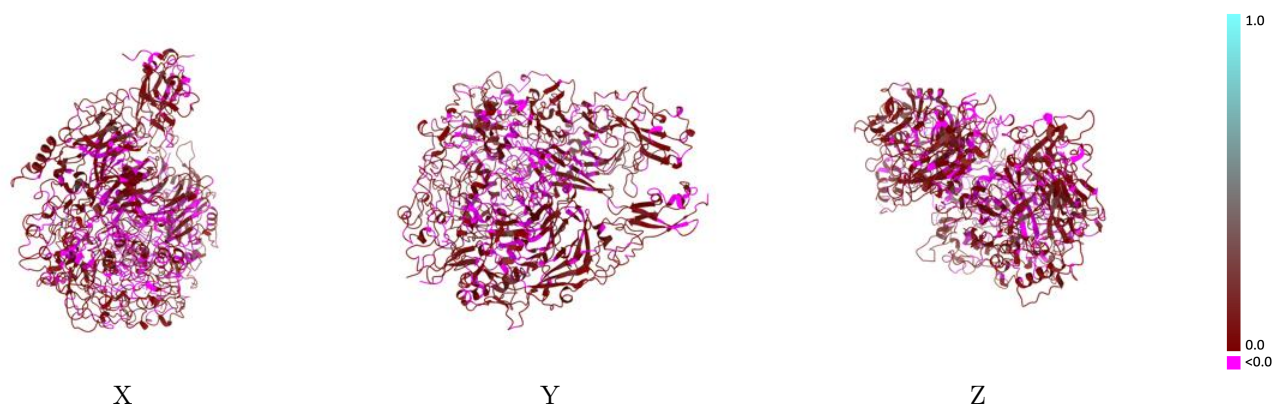
This section contains information regarding the fit between EMDB map EMD-17593 and PDB model 8PC1. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



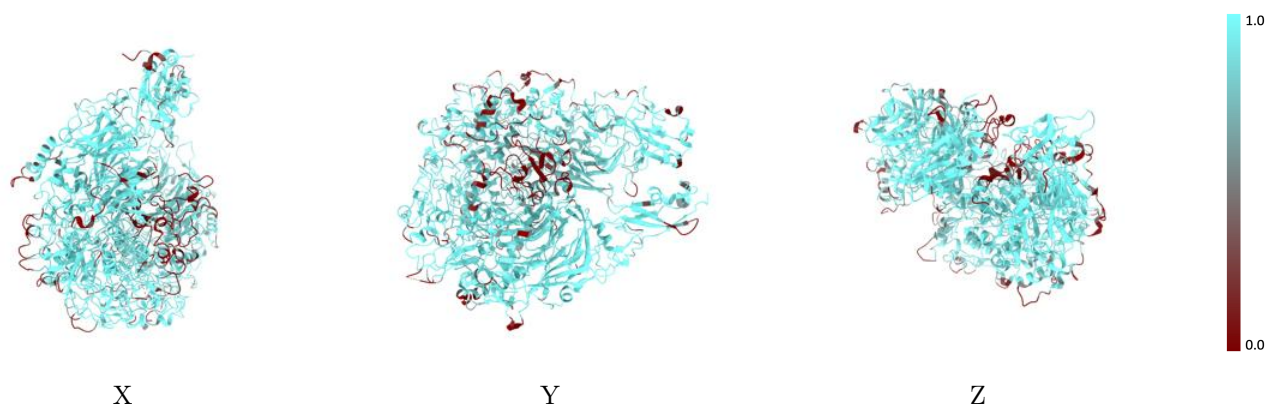
The images above show the 3D surface view of the map at the recommended contour level 0.000145 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



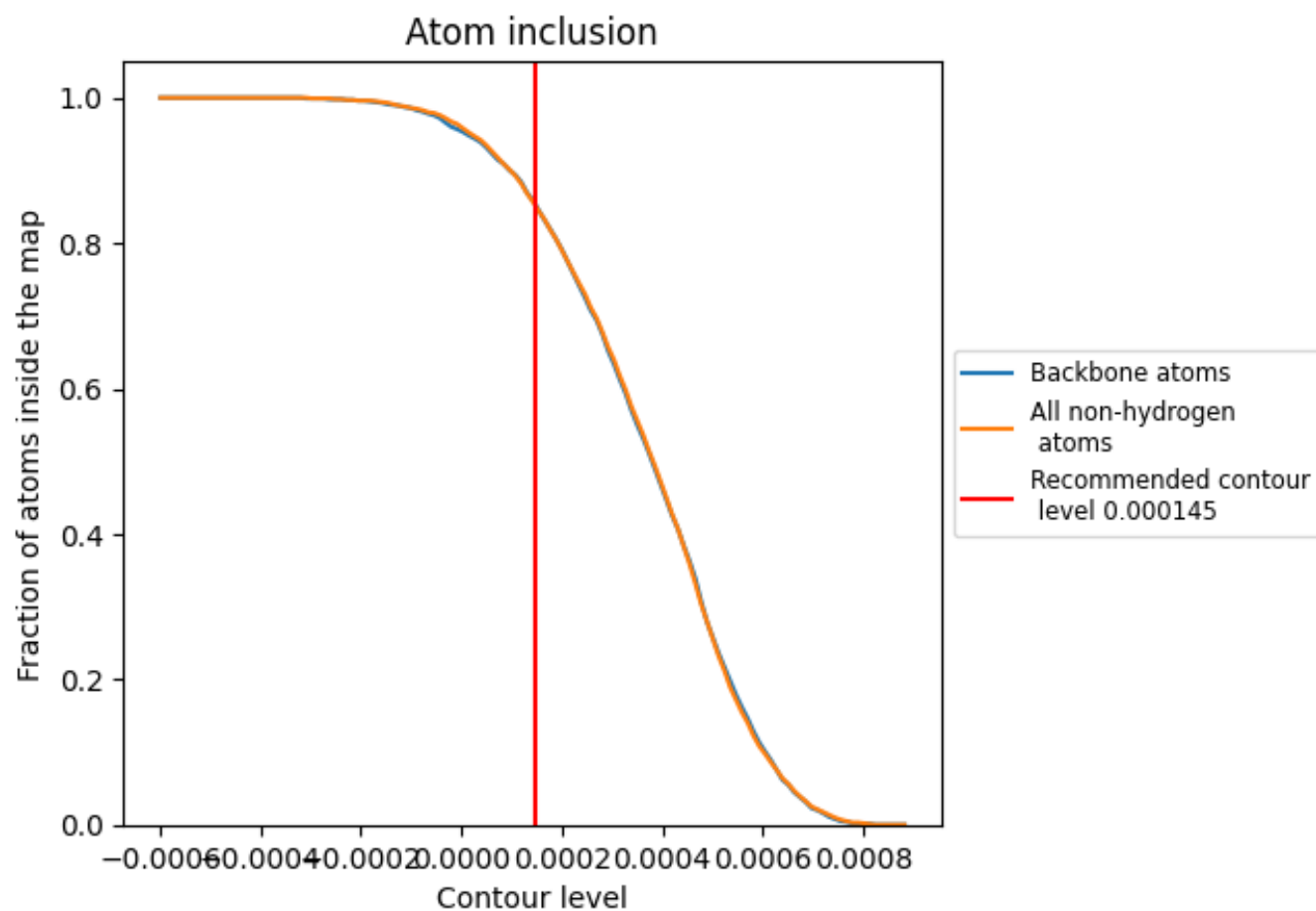
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.000145).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 85% 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 (0.000145) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8540	0.0410
A	0.8720	0.0410
B	0.8450	0.0410

