



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 02:53 PM UTC

PDB ID : 8K3I / pdb_00008k3i
EMDB ID : EMD-36852
Title : Cryo-EM structure of PseP apo
Authors : Mori, T.; Awakawa, T.; Adachi, N.; Abe, I.
Deposited on : 2023-07-15
Resolution : 2.83 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

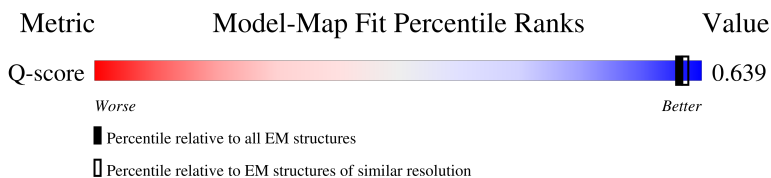
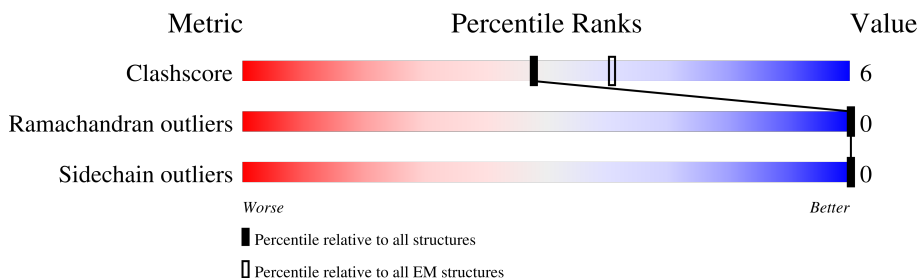
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.83 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	11847 (2.33 - 3.33)

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	815	 50% 9% 41%
1	B	815	 50% 9% 41%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7372 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.

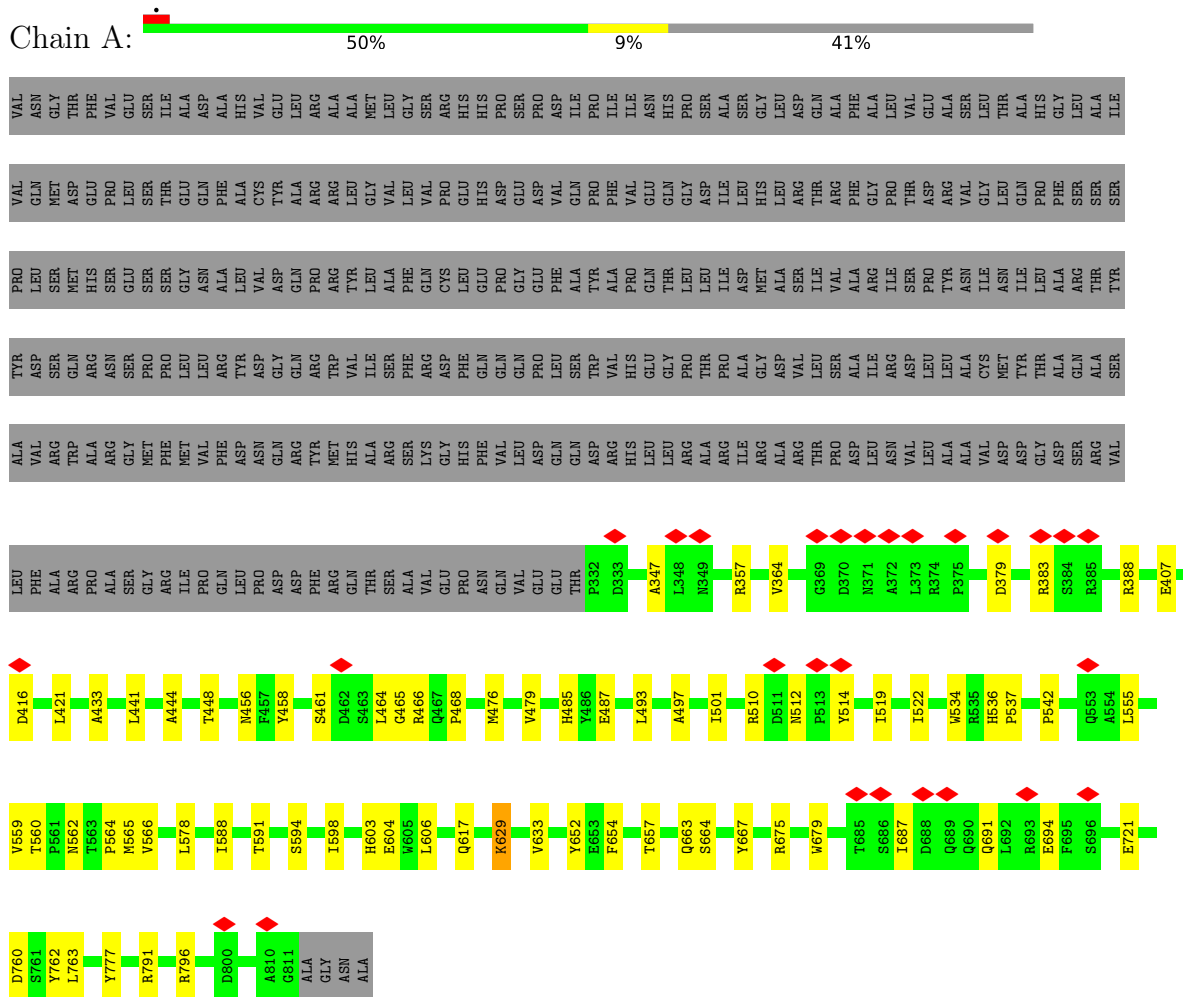
- Molecule 1 is a protein called PseP.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	480	Total	C	N	O	P	S	0	0
			3686	2341	650	682	1	12		
1	B	480	Total	C	N	O	P	S	0	0
			3686	2341	650	682	1	12		

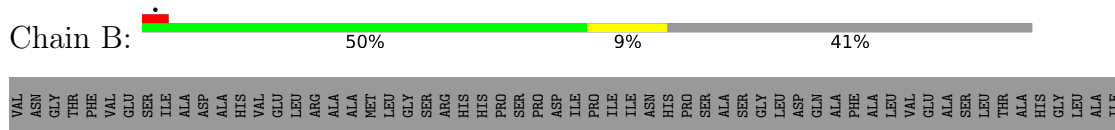
3 Residue-property plots

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

• Molecule 1: PseP



• Molecule 1: PseP



S696	Q553	E407	LEU	ALA	TYR	PRO	VAL
E721	A554	D416	PHE	VAL	ASP	LEU	GLN
Q722	L555		ALA	ARG	SER	SER	GLN
V723			ARG	TRP	GLN	MET	GLU
L727	V559	L421	PRO	ALA	ARG	HIS	ASP
D760	P561	A433	ALA	ARG	ASN	SER	PRO
S761	P562		SER	GLY	SER	GLU	LEU
S762	T563	Y439	ARG	PHE	PRO	SER	THR
L763	P564	C440	ILE	MET	PRO	GLY	GLU
Y777	M565	L441	PRO	VAL	LEU	ASN	GLN
R791	V566	A444	GLN	PHE	ARG	ALA	PHE
R796	L578	T448	LEU	ASP	TYR	LEU	ALA
D800	I588	M456	PRO	ASN	GLN	VAL	ALA
A810	T591	F457	ASP	ASP	GLY	ASP	CYS
G811	S594	Y458	PHE	ARG	TRP	ARG	ARG
ALA		S461	ALA	SER	PHE	PHE	LEU
GLY	I598	D462	VAL	LYS	ARG	GLN	VAL
ASN	H603	S463	GLU	GLY	ASP	CYS	PRO
ALA	E604	L464	PRO	HIS	PHE	LEU	GLU
	W605	G465	ASN	PHE	GLU	GLU	HIS
	L606	R466	GLN	VAL	GLN	GLU	ASP
		Q467	VAL	LEU	GLN	GLY	GLU
	Q617	P468	GLU	ASP	PRO	GLU	ASP
		M476	GLU	GLN	LEU	PHE	VAL
	K629	V479	THR	GLN	SER	ALA	GLN
	V633		P332	ASP	TRP	TYR	PRO
			D333	ARG	VAL	ALA	PHE
	Y652	H486		HIS	HIS	PRO	VAL
	E653	Y486	A347	LEU	GLU	GLN	GLU
F654	E487		L348	LEU	GLY	THR	GLN
			R349	ARG	PRO	LEU	GLY
	L493			ALA	THR	LEU	ASP
			M354	ILE	ALA	ILE	ILE
	A497			ARG	GLY	ASP	HIS
Q663		I501	R357	ALA	ASP	ALA	LEU
S664				ARG	VAL	SER	ARG
Y667	R510		V364	THR	LEU	ILE	THR
	D511			PRO	SER	VAL	THR
R675	N512		G369	ASP	ALA	ALA	PHE
			D370	LEU	ILE	ARG	GLY
W679	P513		N371	ASN	ARG	ILE	PRO
	Y514		A372	VAL	ASP	SER	THR
	I519		L373	LEU	LEU	PRO	ASP
			R374	ALA	ALA	ASN	ARG
	I522		P375	VAL	CYS	ILE	GLY
	W534			ASP	MET	ASN	LEU
	R535		D379	GLY	TYR	ILE	GLN
	H536			ASP	THR	LEU	PRO
	P537		R383	SER	GLN	ALA	PHE
			S384	ARG	ALA	THR	SER
	P542		R385	VAL	SER	TYR	SER
			R388				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	207402	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.173	Depositor
Minimum map value	-0.103	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	249.0, 249.0, 249.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LLP

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	0.17	0/3745	0.32	0/5101
1	B	0.18	0/3745	0.33	0/5101
All	All	0.17	0/7490	0.32	0/10202

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3686	0	3598	43	0
1	B	3686	0	3598	46	0
All	All	7372	0	7196	86	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 6.

All (86) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:466:ARG:HG2	1:B:468:PRO:HD2	1.55	0.87
1:A:466:ARG:HG2	1:A:468:PRO:HD2	1.55	0.86
1:B:416:ASP:OD2	1:B:762:TYR:OH	2.06	0.72
1:A:461:SER:HB3	1:A:664:SER:HB3	1.75	0.69
1:A:416:ASP:OD2	1:A:762:TYR:OH	2.06	0.69
1:A:357:ARG:HD3	1:A:407:GLU:HB3	1.75	0.67
1:B:357:ARG:HD3	1:B:407:GLU:HB3	1.75	0.66
1:B:461:SER:HB3	1:B:664:SER:HB3	1.77	0.66
1:A:663:GLN:HE21	1:B:663:GLN:HE21	1.45	0.64
1:A:364:VAL:HG21	1:A:762:TYR:HD2	1.65	0.62
1:A:464:LEU:HD11	1:A:652:TYR:HB2	1.83	0.61
1:B:464:LEU:HD11	1:B:652:TYR:HB2	1.82	0.61
1:B:364:VAL:HG21	1:B:762:TYR:HD2	1.65	0.60
1:A:512:ASN:HD21	1:A:564:PRO:HB3	1.65	0.60
1:B:606:LEU:HD12	1:B:721:GLU:HG3	1.84	0.60
1:A:560:THR:HG22	1:A:562:ASN:H	1.67	0.60
1:A:606:LEU:HD12	1:A:721:GLU:HG3	1.84	0.60
1:B:512:ASN:HD21	1:B:564:PRO:HB3	1.66	0.59
1:B:560:THR:HG22	1:B:562:ASN:H	1.66	0.59
1:A:687:ILE:HG23	1:A:691:GLN:HB2	1.85	0.58
1:B:687:ILE:HG23	1:B:691:GLN:HB2	1.85	0.58
1:A:485:HIS:NE2	1:A:487:GLU:OE2	2.35	0.57
1:B:675:ARG:HD3	1:B:694:GLU:HB3	1.86	0.57
1:A:675:ARG:HD3	1:A:694:GLU:HB3	1.86	0.57
1:B:439:TYR:OH	1:B:723:VAL:HG11	2.05	0.56
1:B:485:HIS:NE2	1:B:487:GLU:OE2	2.36	0.55
1:B:485:HIS:O	1:B:617:GLN:NE2	2.39	0.54
1:A:485:HIS:O	1:A:617:GLN:NE2	2.39	0.53
1:A:760:ASP:HB3	1:A:763:LEU:HB3	1.91	0.52
1:B:416:ASP:O	1:B:421:LEU:HB2	2.08	0.52
1:B:760:ASP:HB3	1:B:763:LEU:HB3	1.91	0.52
1:A:416:ASP:O	1:A:421:LEU:HB2	2.09	0.52
1:B:465:GLY:HA3	1:B:493:LEU:HD12	1.92	0.51
1:A:465:GLY:HA3	1:A:493:LEU:HD12	1.92	0.51
1:B:465:GLY:HA2	1:B:667:TYR:OH	2.11	0.51
1:A:465:GLY:HA2	1:A:667:TYR:OH	2.11	0.50
1:B:347:ALA:O	1:B:388:ARG:NH1	2.36	0.49
1:A:347:ALA:O	1:A:388:ARG:NH1	2.36	0.48
1:A:519:ILE:HB	1:A:566:VAL:HG22	1.96	0.47
1:B:456:ASN:HA	1:B:458:TYR:CE1	2.50	0.47
1:B:519:ILE:HB	1:B:566:VAL:HG22	1.96	0.47
1:A:456:ASN:HA	1:A:458:TYR:CE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:510:ARG:HH21	1:A:654:PHE:HE2	1.62	0.46
1:B:510:ARG:HH21	1:B:654:PHE:HE2	1.62	0.46
1:A:441:LEU:HD13	1:A:633:VAL:HG11	1.98	0.46
1:B:441:LEU:HD13	1:B:633:VAL:HG11	1.97	0.45
1:B:512:ASN:ND2	1:B:564:PRO:HB3	2.29	0.45
1:A:514:TYR:CE2	1:A:594:SER:HB2	2.52	0.45
1:B:514:TYR:CE2	1:B:594:SER:HB2	2.52	0.45
1:A:433:ALA:O	1:A:796:ARG:NH1	2.50	0.45
1:A:687:ILE:HD12	1:A:691:GLN:HG2	1.99	0.45
1:A:512:ASN:ND2	1:A:564:PRO:HB3	2.30	0.44
1:B:679:TRP:CZ2	1:B:691:GLN:HB3	2.53	0.44
1:B:687:ILE:HD12	1:B:691:GLN:HG2	1.99	0.44
1:B:379:ASP:HB3	1:B:383:ARG:CZ	2.47	0.44
1:B:433:ALA:O	1:B:796:ARG:NH1	2.50	0.44
1:B:476:MET:O	1:B:479:VAL:HG12	2.18	0.44
1:B:354:MET:SD	1:B:357:ARG:NH2	2.79	0.44
1:B:578:LEU:HD11	1:B:604:GLU:HG3	1.99	0.44
1:A:522:ILE:HG13	1:A:542:PRO:HA	2.00	0.44
1:B:444:ALA:O	1:B:448:THR:HG23	2.18	0.44
1:A:578:LEU:HD11	1:A:604:GLU:HG3	1.99	0.43
1:A:777:TYR:HB3	1:A:791:ARG:HB3	2.00	0.43
1:A:588:ILE:O	1:A:591:THR:OG1	2.34	0.43
1:A:679:TRP:CZ2	1:A:691:GLN:HB3	2.53	0.43
1:B:497:ALA:O	1:B:501:ILE:HD12	2.18	0.43
1:A:379:ASP:HB3	1:A:383:ARG:CZ	2.48	0.43
1:B:522:ILE:HG13	1:B:542:PRO:HA	2.00	0.43
1:B:536:HIS:CG	1:B:537:PRO:HD2	2.54	0.43
1:A:476:MET:O	1:A:479:VAL:HG12	2.18	0.42
1:A:536:HIS:CG	1:A:537:PRO:HD2	2.54	0.42
1:A:555:LEU:O	1:A:559:VAL:HG23	2.18	0.42
1:B:555:LEU:O	1:B:559:VAL:HG23	2.18	0.42
1:B:777:TYR:HB3	1:B:791:ARG:HB3	2.00	0.42
1:A:444:ALA:O	1:A:448:THR:HG23	2.19	0.42
1:A:534:TRP:CH2	1:B:657:THR:HB	2.55	0.42
1:A:603:HIS:CE1	1:A:629:LLP:HD2	2.55	0.42
1:A:657:THR:HB	1:B:534:TRP:CH2	2.55	0.41
1:B:603:HIS:CE1	1:B:629:LLP:HD2	2.55	0.41
1:A:497:ALA:O	1:A:501:ILE:HD12	2.20	0.41
1:B:476:MET:HE2	1:B:476:MET:HB3	1.83	0.41
1:B:727:LEU:HD23	1:B:727:LEU:HA	1.90	0.41
1:A:364:VAL:HG11	1:A:762:TYR:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:588:ILE:O	1:B:591:THR:OG1	2.34	0.41
1:A:565:MET:HE3	1:A:598:ILE:HD13	2.03	0.40
1:B:565:MET:HE3	1:B:598:ILE:HD13	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	477/815 (58%)	463 (97%)	14 (3%)	0	100	100
1	B	477/815 (58%)	464 (97%)	13 (3%)	0	100	100
All	All	954/1630 (58%)	927 (97%)	27 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	379/682 (56%)	379 (100%)	0	100	100
1	B	379/682 (56%)	379 (100%)	0	100	100
All	All	758/1364 (56%)	758 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	352	ASN
1	A	512	ASN
1	A	562	ASN
1	A	663	GLN
1	B	352	ASN
1	B	512	ASN
1	B	562	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	LLP	B	629	1	23,24,25	2.51	7 (30%)	25,32,34	1.30	4 (16%)
1	LLP	A	629	1	23,24,25	2.52	7 (30%)	25,32,34	1.31	4 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	LLP	B	629	1	-	10/16/17/19	0/1/1/1
1	LLP	A	629	1	-	10/16/17/19	0/1/1/1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	629	LLP	C4-C4'	7.15	1.61	1.46
1	B	629	LLP	C4-C4'	7.10	1.61	1.46
1	B	629	LLP	C4'-NZ	4.88	1.43	1.27
1	A	629	LLP	C4'-NZ	4.84	1.43	1.27
1	A	629	LLP	C4-C5	-4.03	1.36	1.42
1	B	629	LLP	C4-C5	-4.02	1.36	1.42
1	B	629	LLP	C2'-C2	3.68	1.56	1.50
1	A	629	LLP	C2'-C2	3.62	1.56	1.50
1	B	629	LLP	C6-N1	3.09	1.40	1.34
1	A	629	LLP	C6-N1	3.08	1.40	1.34
1	A	629	LLP	C5'-C5	2.11	1.56	1.50
1	A	629	LLP	C4-C3	-2.11	1.37	1.41
1	B	629	LLP	C5'-C5	2.10	1.56	1.50
1	B	629	LLP	C4-C3	-2.08	1.37	1.41

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	629	LLP	C4-C4'-NZ	-3.23	109.16	124.04
1	A	629	LLP	C4-C4'-NZ	-3.22	109.17	124.04
1	B	629	LLP	CE-NZ-C4'	-2.78	109.80	118.72
1	A	629	LLP	CE-NZ-C4'	-2.77	109.85	118.72
1	A	629	LLP	C5-C6-N1	-2.38	119.97	123.83
1	B	629	LLP	C5-C6-N1	-2.34	120.03	123.83
1	B	629	LLP	C3-C4-C5	2.04	119.91	118.28
1	A	629	LLP	C3-C4-C5	2.01	119.89	118.28

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	629	LLP	C4-C4'-NZ-CE
1	A	629	LLP	C-CA-CB-CG
1	B	629	LLP	C4-C4'-NZ-CE
1	B	629	LLP	C-CA-CB-CG
1	A	629	LLP	CG-CD-CE-NZ
1	B	629	LLP	CG-CD-CE-NZ
1	B	629	LLP	CE-CD-CG-CB
1	A	629	LLP	CE-CD-CG-CB
1	A	629	LLP	CA-CB-CG-CD
1	B	629	LLP	CA-CB-CG-CD
1	A	629	LLP	C3-C4-C4'-NZ

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
1	B	629	LLP	C3-C4-C4'-NZ
1	A	629	LLP	C5-C4-C4'-NZ
1	B	629	LLP	C5-C4-C4'-NZ
1	A	629	LLP	N-CA-CB-CG
1	B	629	LLP	N-CA-CB-CG
1	A	629	LLP	C6-C5-C5'-OP4
1	B	629	LLP	C6-C5-C5'-OP4
1	A	629	LLP	C4-C5-C5'-OP4
1	B	629	LLP	C4-C5-C5'-OP4

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	629	LLP	1	0
1	A	629	LLP	1	0

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.

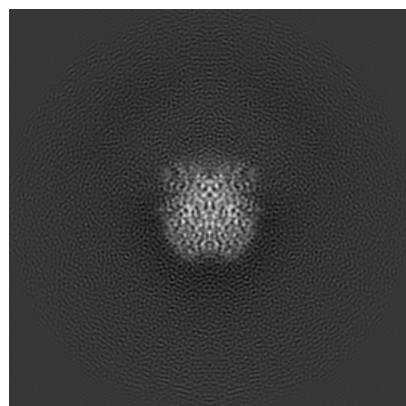
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36852. These allow visual inspection of the internal detail of the map and identification of artifacts.

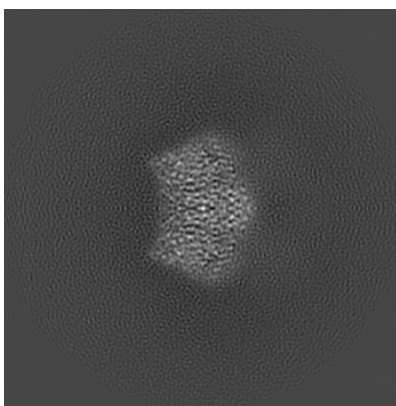
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

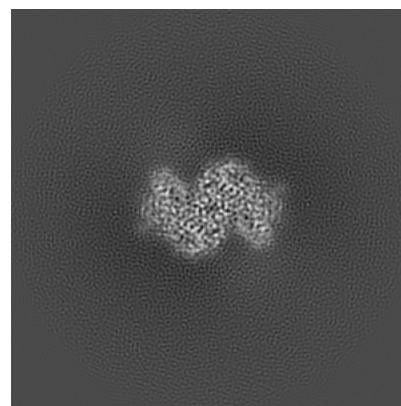
6.1.1 Primary map



X

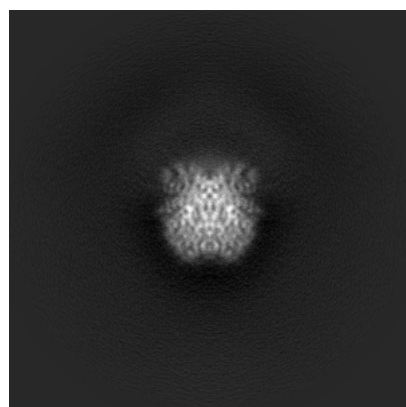


Y

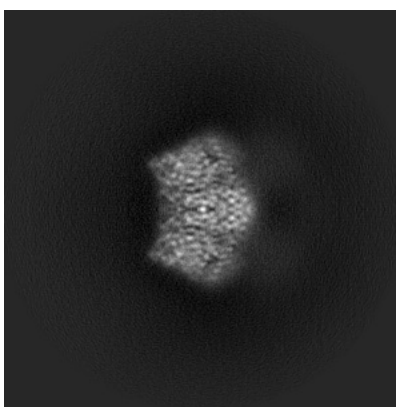


Z

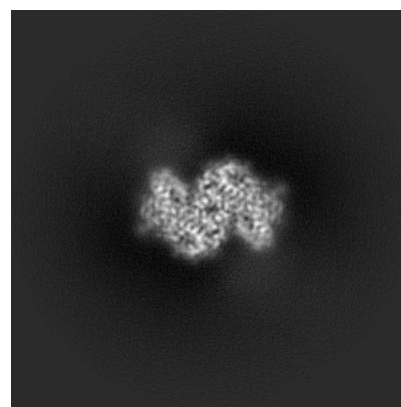
6.1.2 Raw map



X



Y

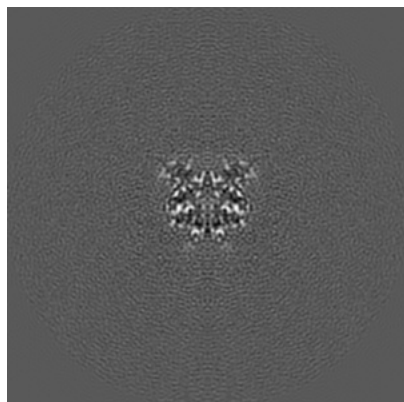


Z

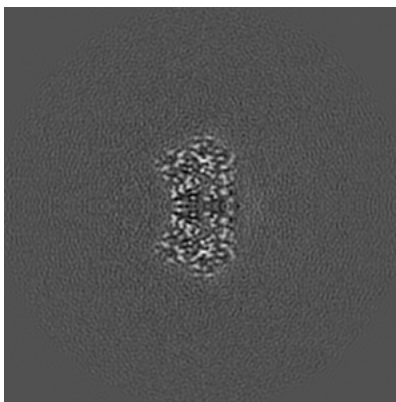
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

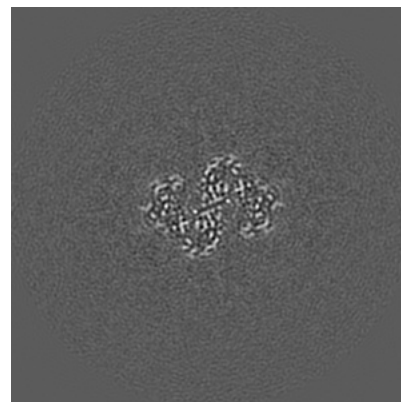
6.2.1 Primary map



X Index: 150

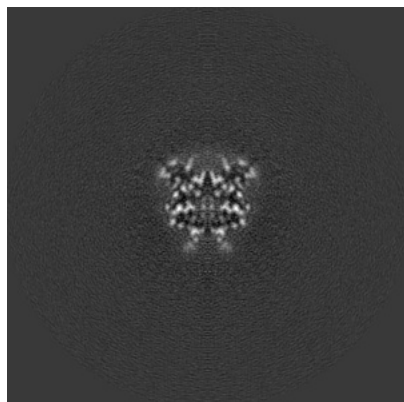


Y Index: 150

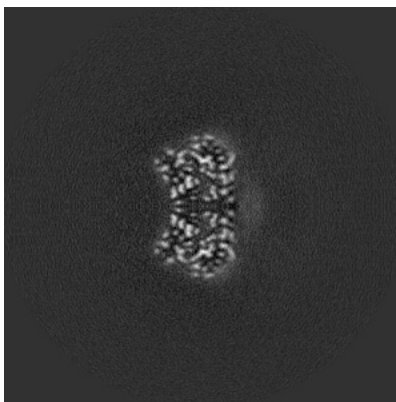


Z Index: 150

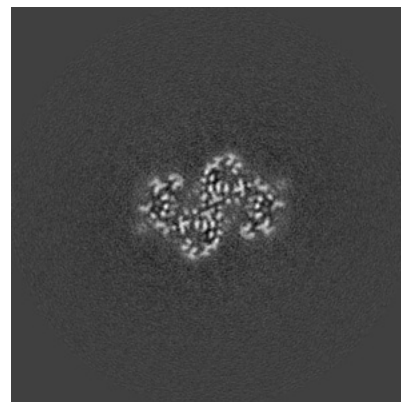
6.2.2 Raw map



X Index: 150



Y Index: 150

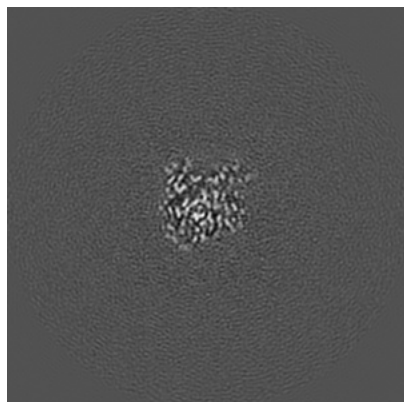


Z Index: 150

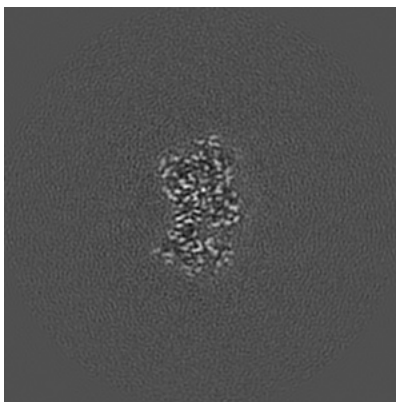
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

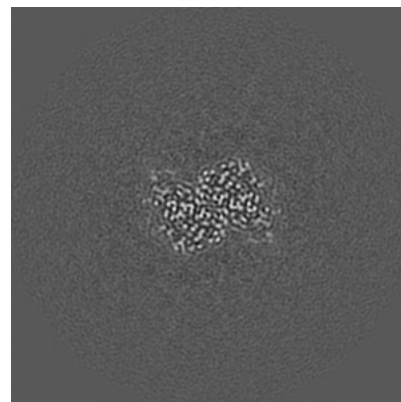
6.3.1 Primary map



X Index: 144

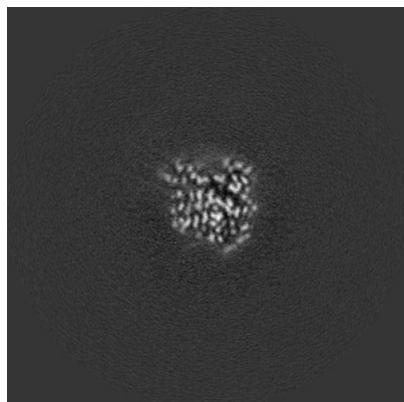


Y Index: 154

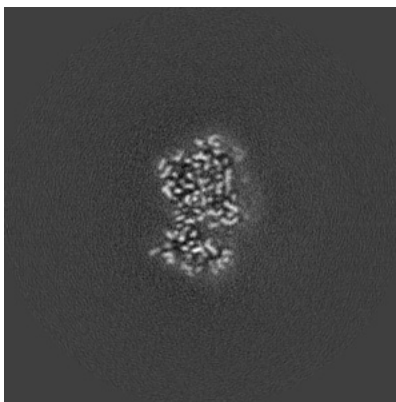


Z Index: 138

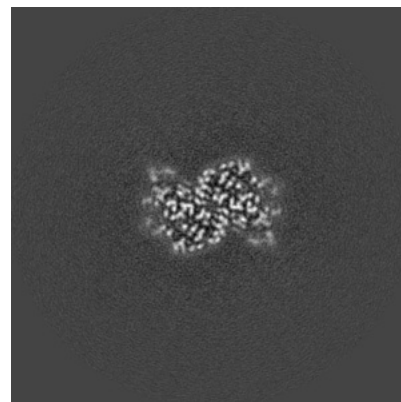
6.3.2 Raw map



X Index: 156



Y Index: 155

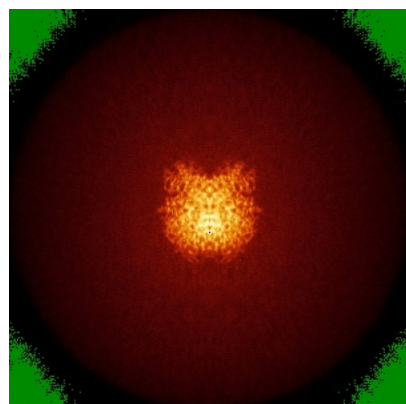


Z Index: 138

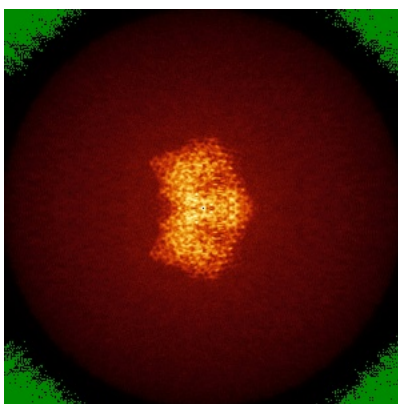
The images above show the largest variance slices of the map in three orthogonal directions.

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

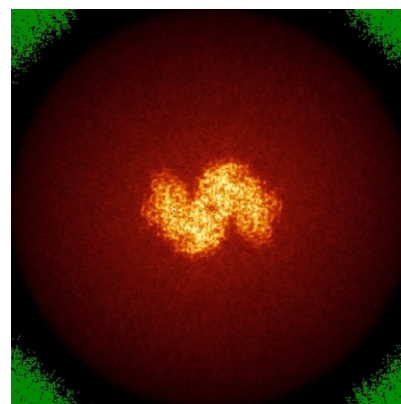
6.4.1 Primary map



X

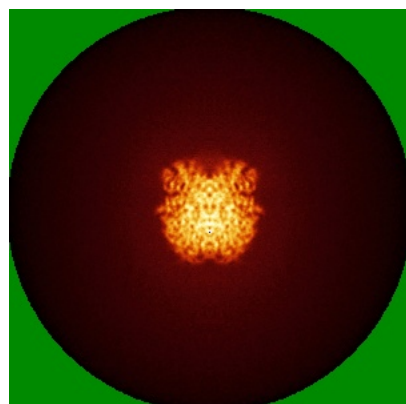


Y

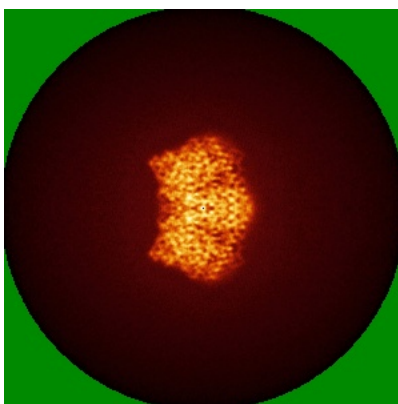


Z

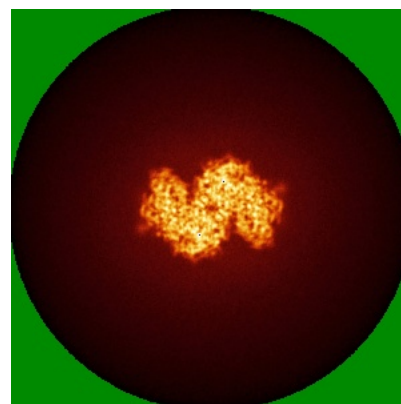
6.4.2 Raw map



X



Y

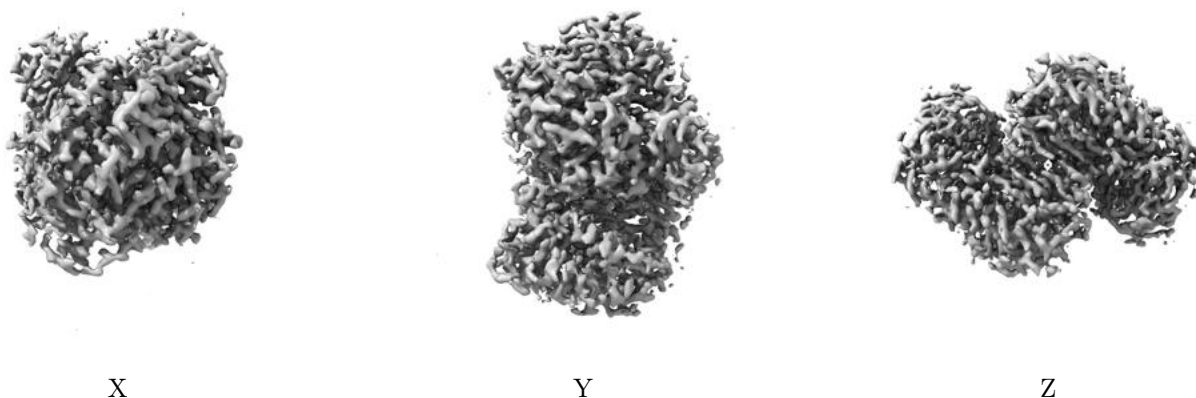


Z

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.

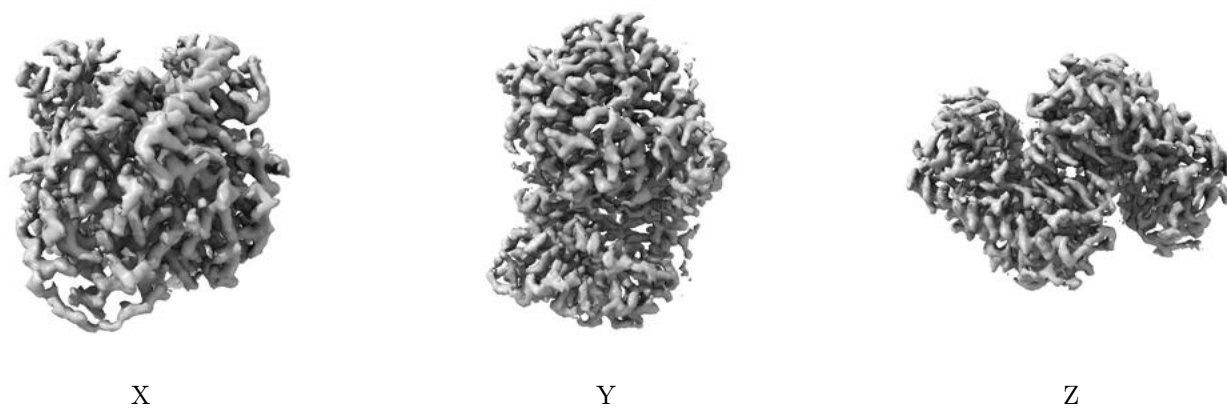
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.035. 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.

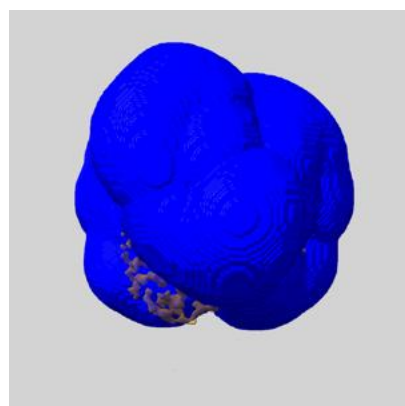
6.6 Mask visualisation [i](#)

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

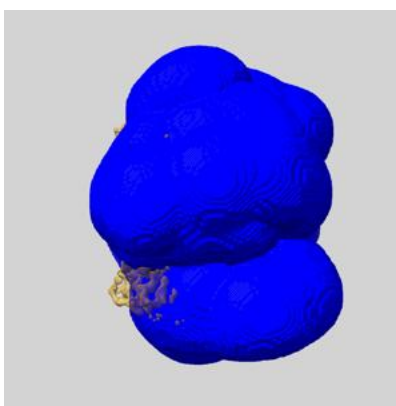
A mask typically either:

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

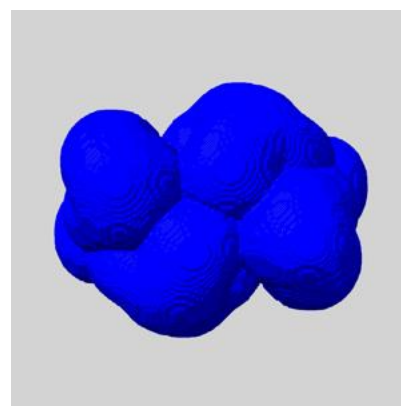
6.6.1 emd_36852_msk_1.map [i](#)



X



Y

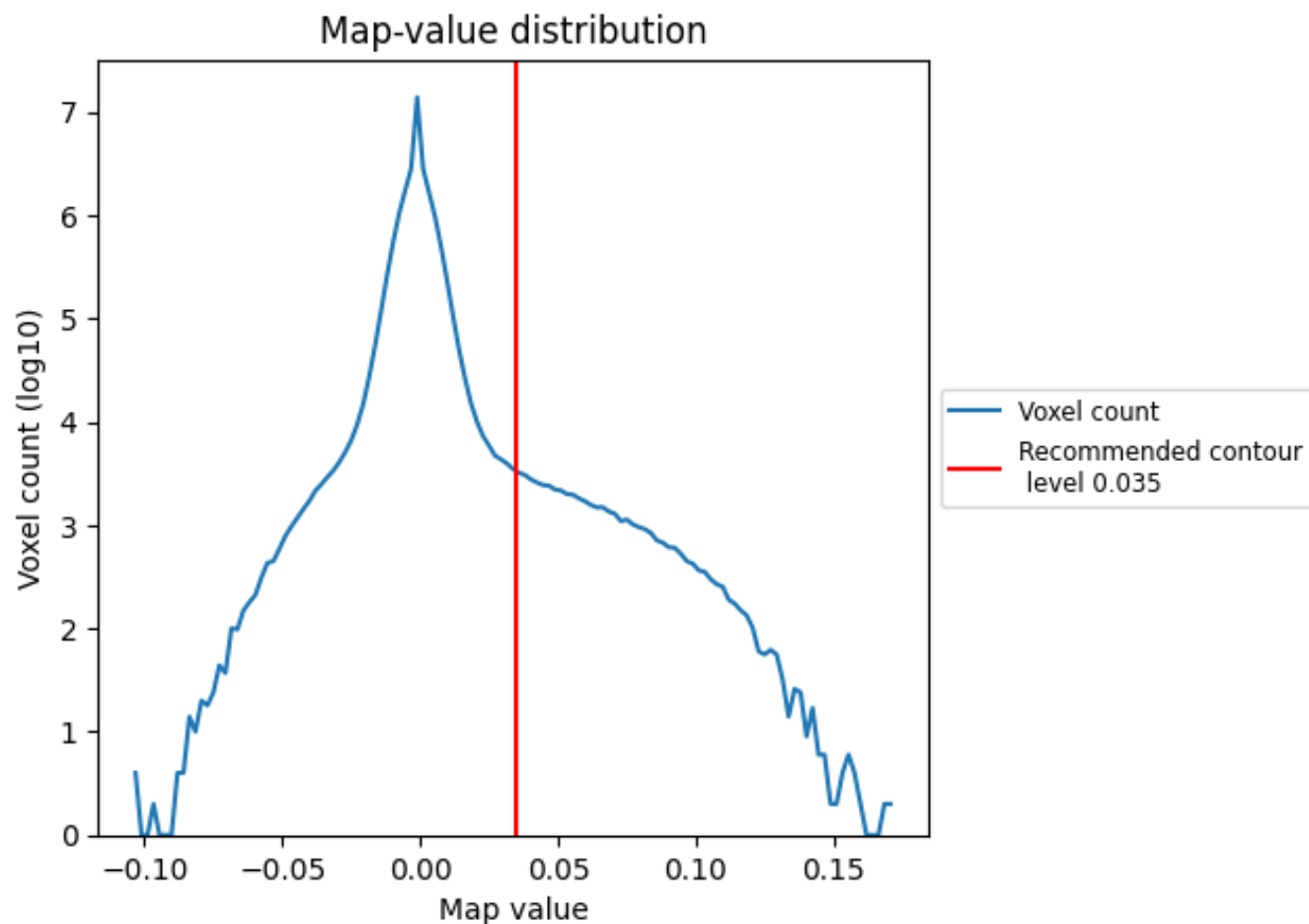


Z

7 Map analysis [i](#)

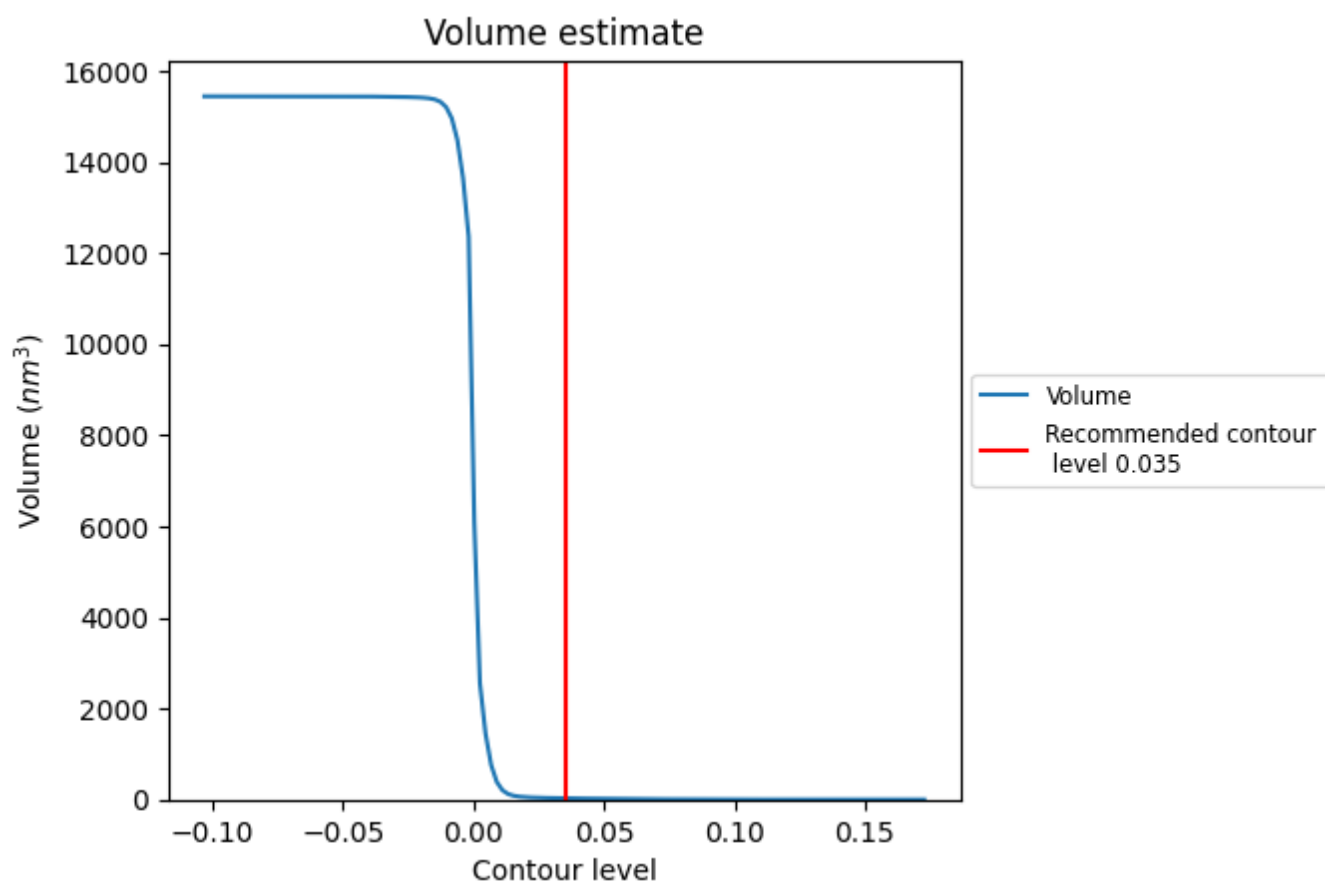
This section contains the results of statistical analysis of the map.

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.

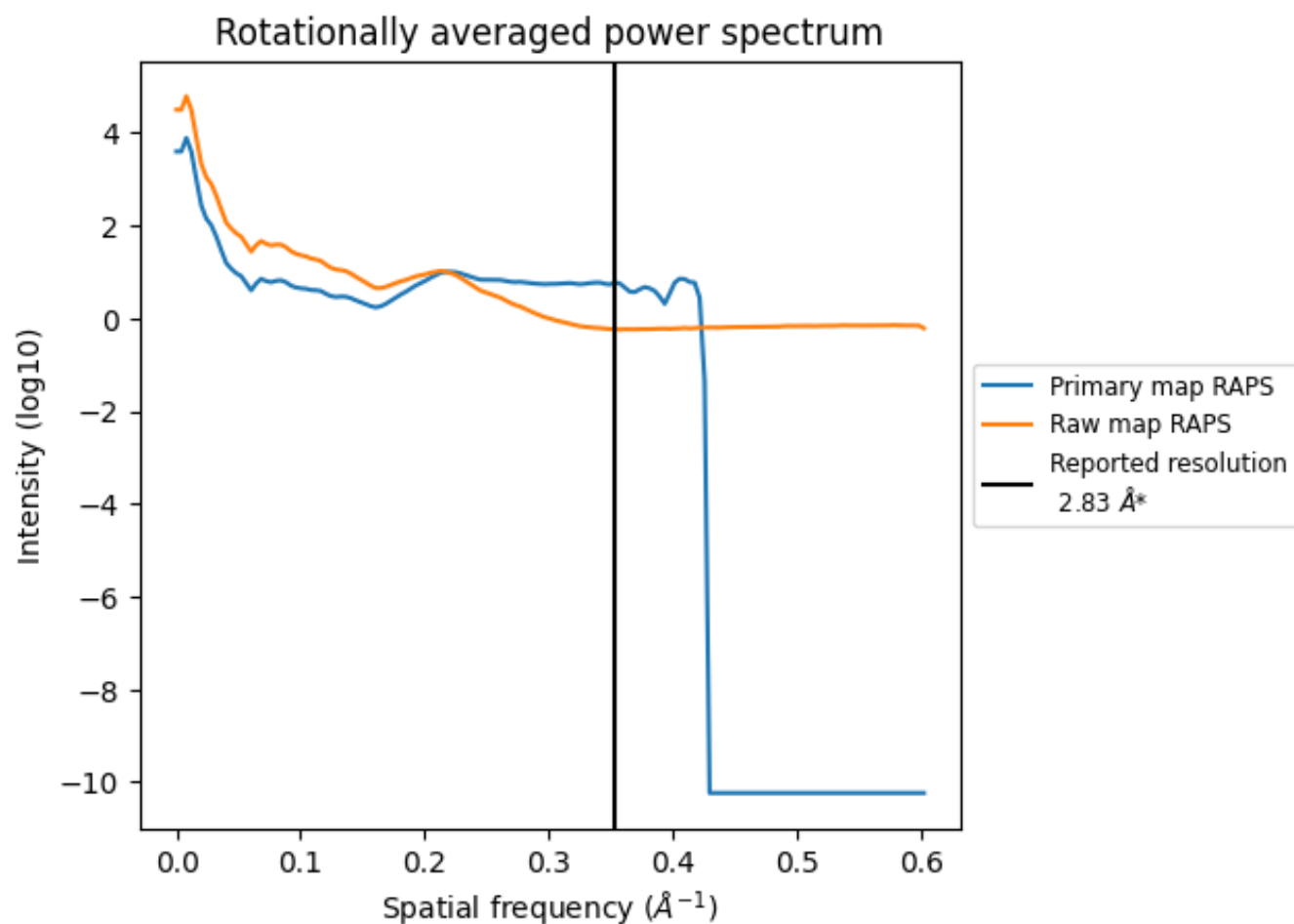
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 28 nm³; this corresponds to an approximate mass of 26 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 ⓘ

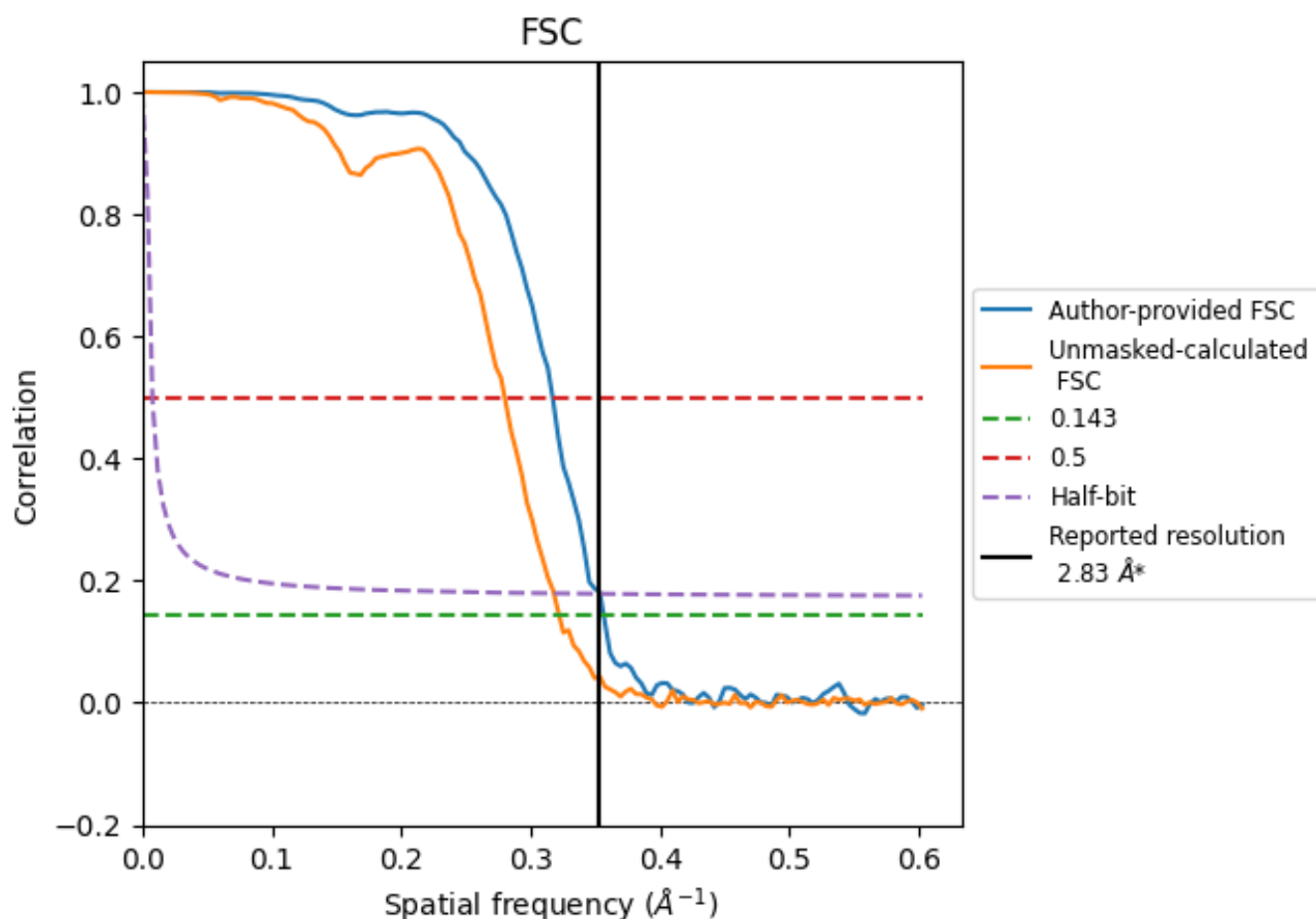


*Reported resolution corresponds to spatial frequency of 0.353 Å⁻¹

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 0.353 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

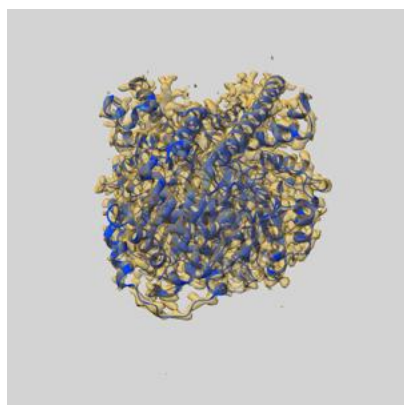
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.83	-	-
Author-provided FSC curve	2.81	3.15	2.83
Unmasked-calculated*	3.10	3.57	3.15

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

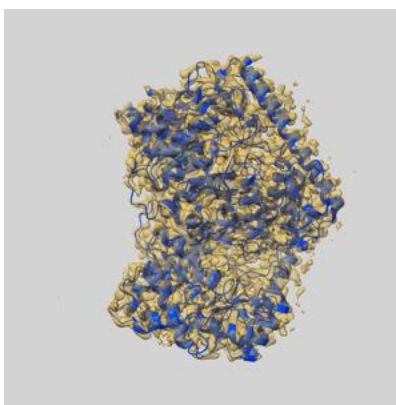
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-36852 and PDB model 8K3I. Per-residue inclusion information can be found in section 3 on page 4.

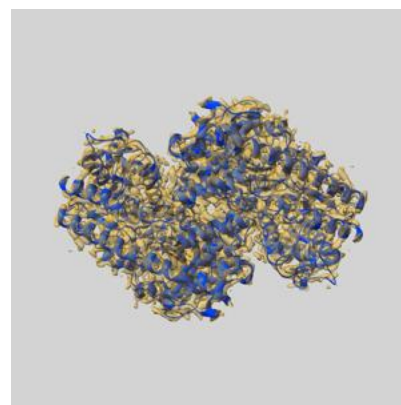
9.1 Map-model overlay [i](#)



X



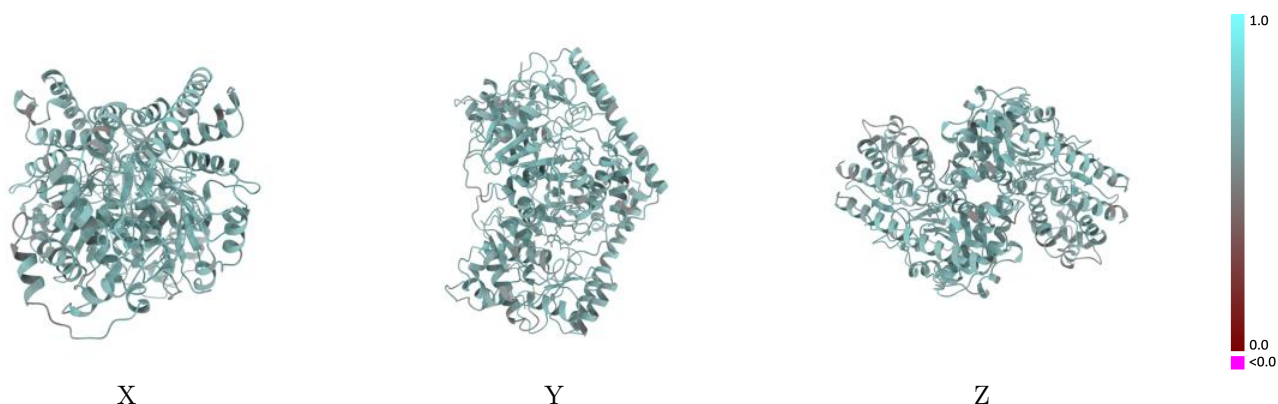
Y



Z

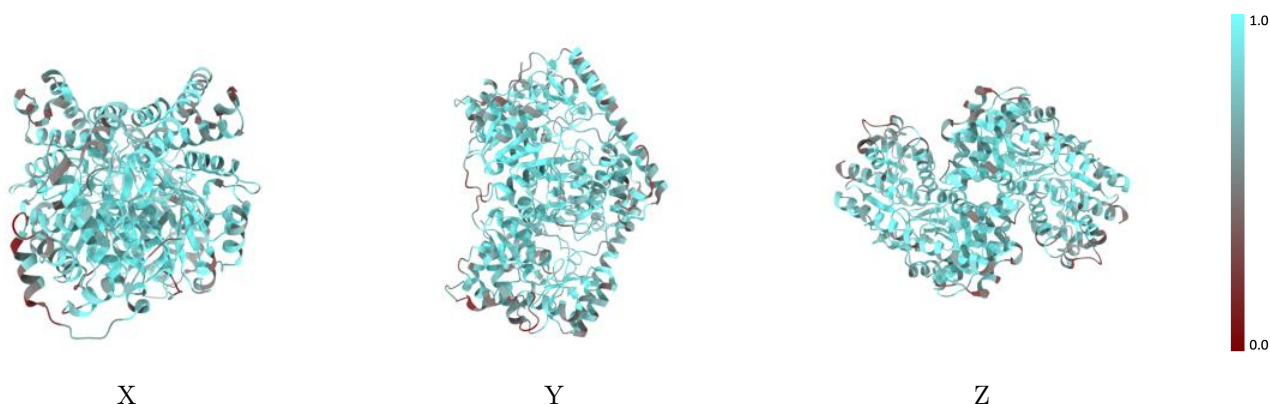
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



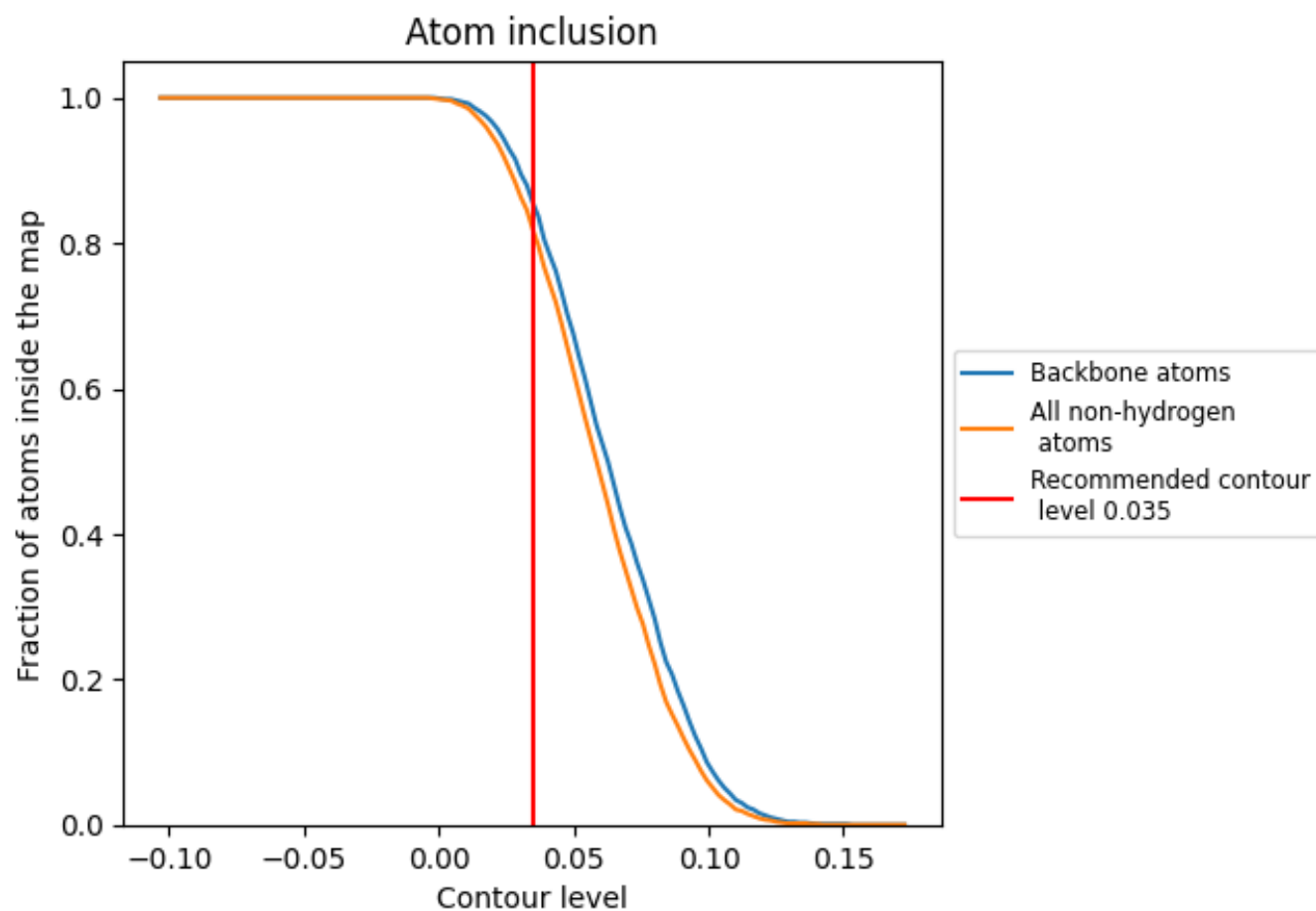
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 82% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8170	0.6390
A	0.8180	0.6400
B	0.8170	0.6380

