Full wwPDB EM Validation Report (i)

Feb 22, 2024 – 04:05 PM EST

PDB ID	:	7T55
EMDB ID	:	EMD-25695
Title	:	Cryo-EM structure of PCAT1 in the inward-facing wide conformation under ATP turnover condition
Authors	:	Kieuvongngam, V.; Chen, J.
Deposited on	:	2021-12-11
Resolution	:	4.10 Å(reported)
Based on initial model	:	4RY2

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 (i) 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 (1)) were used in the production of this report:

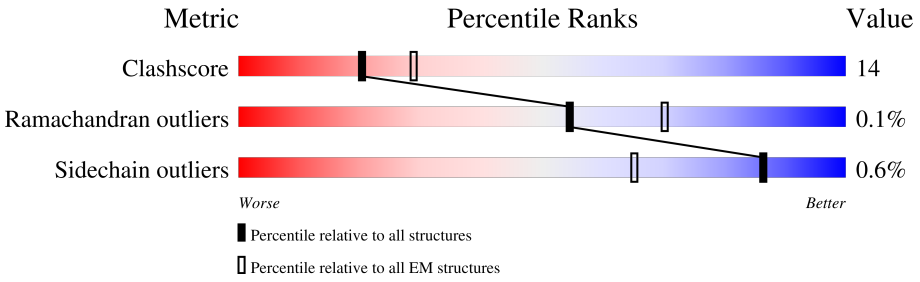
EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	730	6% 73% 25% •
1	B	730	6% 74% 24% •
2	C	93	• 14% • 82%
2	D	93	• 11% 8% 82%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ATP	A	801	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11460 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 ABC-type bacteriocin transporter.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	715	5581	3612	913	1028	28	0	0
1	B	715	5581	3612	913	1028	28	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP A3DCU1
A	-1	ASN	-	expression tag	UNP A3DCU1
A	0	ALA	-	expression tag	UNP A3DCU1
B	-2	SER	-	expression tag	UNP A3DCU1
B	-1	ASN	-	expression tag	UNP A3DCU1
B	0	ALA	-	expression tag	UNP A3DCU1

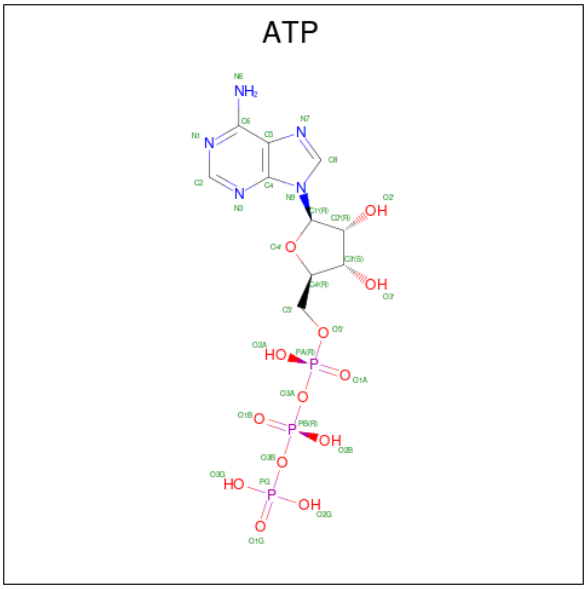
- Molecule 2 is a protein called PCAT1 peptide substrate.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	17	117	69	17	29	2	0	0
2	D	17	117	69	17	29	2	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	SER	-	expression tag	UNP A3DCU2
C	-1	ASN	-	expression tag	UNP A3DCU2
C	0	ALA	-	expression tag	UNP A3DCU2
D	-2	SER	-	expression tag	UNP A3DCU2
D	-1	ASN	-	expression tag	UNP A3DCU2
D	0	ALA	-	expression tag	UNP A3DCU2

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
3	A	1	31	10	5	13	3	0
			Total	C	N	O	P	
3	B	1	31	10	5	13	3	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

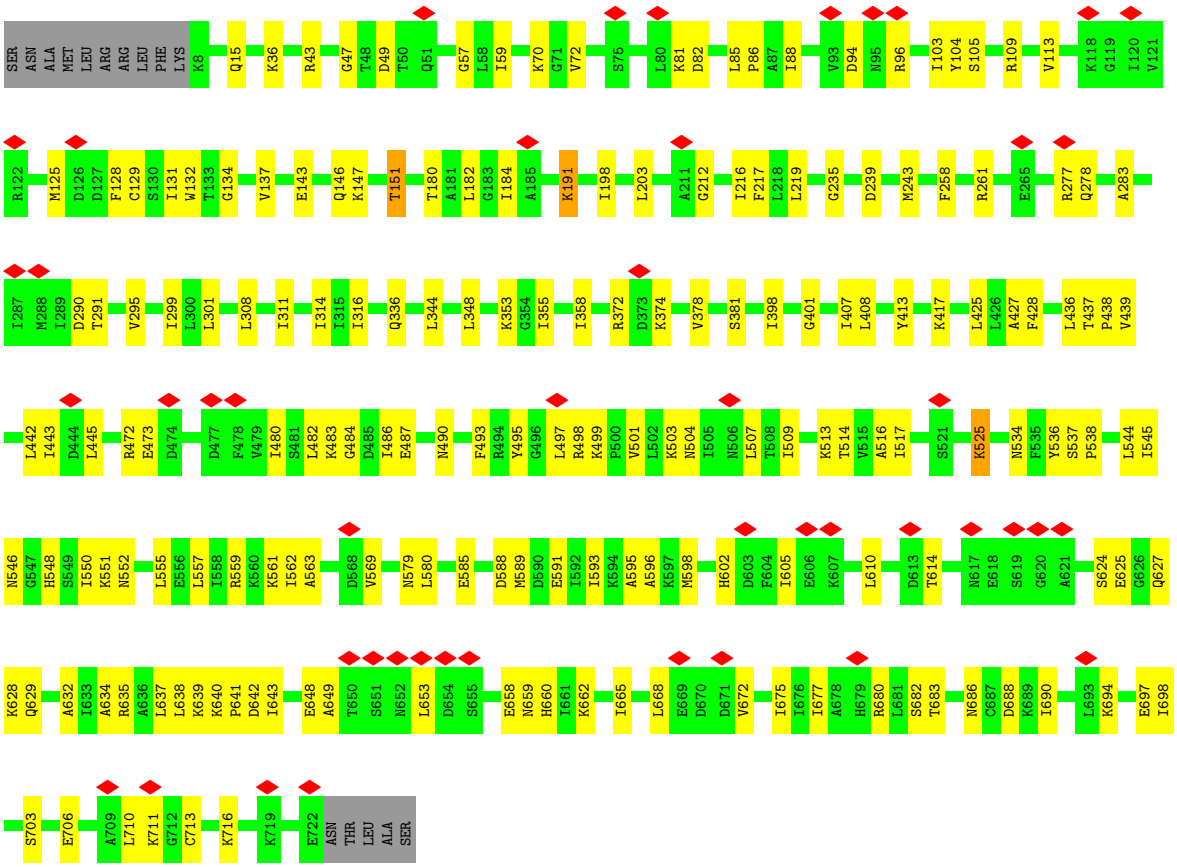
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
4	A	1	1	1	0
			Total	Mg	
4	B	1	1	1	0

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.

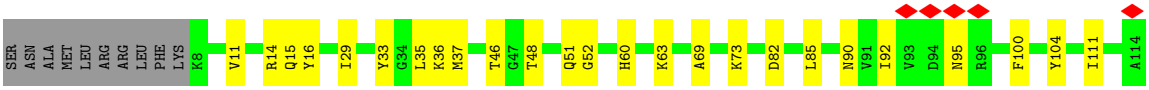
• Molecule 1: ABC-type bacteriocin transporter

Chain A:



• Molecule 1: ABC-type bacteriocin transporter

Chain B:



D115 P116 G117 I120 V121 R122 M125 D126 D127 F128 I131 L138 L139 E140 P141 A144 G148 D149 Y150 T151 Q152 N153 M154 L182 K191 F192 L193 D196 L197 I198 K199 D205 I209 G212 I216 F217 I221 I238 D239 I242 M243 M244 M255

V263 F270 M271 D272 I276 R277 I280 T284 L285 T286 I287 M288 I289 D290 T291 I292 M293 I296 L301 L308 I311 I314 L318 I322 P329 K343 I355 Q366 K374 L388 S394 L395 I398 G401 I407 I416

M420 Q424 A427 F428 L431 L432 T437 P438 S456 N457 R458 E461 E464 E468 R472 E473 D477 F478 L482 K483 G484 D485 I486 N490 V491 D492 F493 R494 L497 R498 K499 P500 K503 N504 I505 N506 L507 T508 I509 P510 K511 G512 K513 A516

S521 N534 F535 G541 I545 S549 N552 I553 L557 I558 R559 K560 K561 I562 A563 D568 I571 N579 L580 D588 A595 M598 A601 F604 I605 E606 K607 L608 Y612 D613 T614 N617 E618 S619 G620 A621 N622 L623 S624 E625 K628 L631

R635 P641 D642 I643 L644 D647 T650 S651 N652 L653 D654 S655 Y666 G667 L668 E669 V674 I677 R680 T683 I684 V685 I690 Y691 L692 D695 G696 E697 I698 V699 S703 H704 T705 E706 A709 L710 K711 G712 C713 K716 K719 E722 ASN THR

LEU ALA SER

- Molecule 2: PCAT1 peptide substrate

Chain C:

SER ASN ALA MET SER GLU ALA LYS LYS LEU N8 T14 E17 L18 G24 SER THR PHE SER ILE GLN CYS GLN LYS ASP TYR THR TYR LYS PRO SER LEU PRO VAL VAL LYS TYR GLY VAL VAL ILE ASP GLU PRO GLU VAL VAL ILE LYS TYR GLY VAL GLY PRO ILE VAL GLY

ILE LYS TYR GLY VAL GLU PRO ILE GLY PRO ILE GLN PRO MET TYR GLY ILE LYS PRO VAL GLU THR LEU LYS

- Molecule 2: PCAT1 peptide substrate

Chain D:

SER ASN ALA MET SER GLU ALA LYS LYS LEU N8 R11 E12 L13 T14 D15 L18 M19 E20 M21 T22 G23 G24 SER THR PHE SER ILE GLN CYS GLN LYS ASP TYR THR TYR LYS PRO SER LEU PRO VAL VAL LYS TYR GLY VAL VAL ILE ASP GLU PRO GLU VAL VAL ILE LYS TYR

GLY VAL GLY PRO ILE VAL GLY ILE LYS TYR GLY VAL GLU PRO ILE GLY PRO ILE GLN PRO MET TYR GLY ILE LYS PRO VAL GLU THR LEU LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	134000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	1.5	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.011	Depositor
Minimum map value	-0.353	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.034	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	309.0, 309.0, 309.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.03, 1.03, 1.03	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.27	0/5669	0.47	0/7642
1	B	0.27	0/5669	0.48	0/7642
2	C	0.23	0/116	0.42	0/154
2	D	0.24	0/116	0.54	0/154
All	All	0.27	0/11570	0.47	0/15592

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 (i)

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	5581	0	5808	191	0
1	B	5581	0	5808	134	0
2	C	117	0	96	3	0
2	D	117	0	96	7	0
3	A	31	0	12	11	0
3	B	31	0	12	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
All	All	11460	0	11832	316	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 14.

All (316) 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:A:36:LYS:HE3	1:A:151:THR:CG2	1.50	1.38
1:A:493:PHE:CZ	1:A:536:TYR:HB3	1.80	1.15
1:A:629:GLN:HE22	1:A:649:ALA:HB2	1.09	1.14
1:A:495:TYR:CE2	3:A:801:ATP:C6	2.37	1.12
1:A:36:LYS:HE3	1:A:151:THR:HG22	1.18	1.08
1:A:36:LYS:HE3	1:A:151:THR:HG21	1.28	1.07
1:A:495:TYR:CE2	3:A:801:ATP:N1	2.24	1.06
1:A:625:GLU:HA	1:A:628:LYS:CD	1.85	1.06
1:A:493:PHE:CZ	1:A:536:TYR:CB	2.42	1.03
1:B:482:LEU:H	1:B:482:LEU:HD23	1.22	1.03
1:A:493:PHE:HZ	1:A:536:TYR:HB3	1.16	0.97
1:A:625:GLU:HA	1:A:628:LYS:CG	1.98	0.94
1:A:482:LEU:HD23	1:A:642:ASP:HB2	1.47	0.94
1:A:495:TYR:HE2	3:A:801:ATP:N1	1.63	0.93
1:A:629:GLN:NE2	1:A:649:ALA:HB2	1.84	0.93
1:A:525:LYS:O	1:A:677:ILE:HD13	1.71	0.91
1:A:495:TYR:CD2	3:A:801:ATP:C6	2.60	0.89
1:B:69:ALA:HA	1:B:138:LEU:O	1.73	0.89
1:A:625:GLU:HA	1:A:628:LYS:HG2	1.55	0.88
1:A:36:LYS:CE	1:A:151:THR:CG2	2.46	0.87
1:B:557:LEU:HD11	1:B:561:LYS:CE	2.04	0.87
1:A:36:LYS:CE	1:A:151:THR:HG21	2.06	0.86
1:A:625:GLU:HA	1:A:628:LYS:HD2	1.58	0.86
1:A:525:LYS:HE2	3:A:801:ATP:O1G	1.76	0.85
1:A:36:LYS:CE	1:A:151:THR:HG22	2.06	0.83
1:A:629:GLN:HE22	1:A:649:ALA:CB	1.93	0.80
1:A:482:LEU:HD21	1:A:643:ILE:HG13	1.63	0.80
1:A:548:HIS:HE1	1:A:552:ASN:HB2	1.48	0.79
1:B:308:LEU:HD22	1:B:428:PHE:CE2	2.19	0.78
1:A:625:GLU:CA	1:A:628:LYS:HG2	2.13	0.78
1:A:486:ILE:HB	1:A:509:ILE:HB	1.66	0.77
1:B:308:LEU:HD21	1:B:407:ILE:HG12	1.67	0.76
1:B:482:LEU:H	1:B:482:LEU:CD2	1.97	0.76
1:B:557:LEU:HD11	1:B:561:LYS:NZ	2.00	0.75
1:A:625:GLU:O	1:A:628:LYS:CG	2.35	0.75
1:A:495:TYR:HE1	1:A:501:VAL:HG11	1.52	0.74
1:A:493:PHE:CE1	1:A:537:SER:O	2.41	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:482:LEU:HD22	1:A:561:LYS:HG3	1.71	0.73
1:A:493:PHE:HE1	1:A:537:SER:O	1.70	0.73
1:A:625:GLU:O	1:A:628:LYS:HG2	1.89	0.73
1:B:37:MET:SD	1:B:150:TYR:CD1	2.82	0.72
1:B:16:TYR:HB3	1:B:458:ARG:HD3	1.70	0.72
1:B:486:ILE:HB	1:B:509:ILE:HB	1.69	0.72
1:B:482:LEU:HD23	1:B:482:LEU:N	2.02	0.72
1:A:493:PHE:CZ	1:A:536:TYR:HB2	2.23	0.72
1:A:495:TYR:CE2	3:A:801:ATP:C2	2.78	0.72
1:B:557:LEU:HD11	1:B:561:LYS:HE3	1.71	0.72
1:A:625:GLU:C	1:A:628:LYS:HG2	2.11	0.71
1:A:482:LEU:CD2	1:A:643:ILE:HG13	2.20	0.70
1:A:639:LYS:HD2	1:A:641:PRO:HB3	1.73	0.70
1:A:482:LEU:CD2	1:A:561:LYS:HG3	2.21	0.70
1:A:109:ARG:HD3	1:A:125:MET:HG2	1.74	0.70
1:A:482:LEU:HD21	1:A:643:ILE:CD1	2.22	0.70
1:A:291:THR:HG22	1:A:442:LEU:HD11	1.73	0.70
1:B:239:ASP:HB2	1:B:277:ARG:HG3	1.73	0.70
1:A:191:LYS:HB2	1:A:427:ALA:HB2	1.74	0.69
1:A:640:LYS:N	1:A:641:PRO:HD3	2.05	0.69
1:B:308:LEU:HD22	1:B:428:PHE:HE2	1.54	0.69
1:A:495:TYR:CD2	3:A:801:ATP:N6	2.61	0.69
1:B:713:CYS:HA	1:B:716:LYS:HE2	1.73	0.69
1:A:372:ARG:HA	1:B:244:MET:HE1	1.75	0.69
1:A:648:GLU:HB3	1:A:653:LEU:HD11	1.73	0.69
1:A:482:LEU:HD21	1:A:643:ILE:CG1	2.23	0.68
1:A:480:ILE:HD12	1:A:557:LEU:HD22	1.76	0.67
1:B:557:LEU:CD1	1:B:561:LYS:HE3	2.24	0.67
1:A:493:PHE:HD1	1:A:538:PRO:HA	1.59	0.67
1:B:182:LEU:HD12	1:B:216:ILE:HG23	1.75	0.67
1:A:665:ILE:HA	1:A:668:LEU:HD23	1.76	0.66
1:A:49:ASP:OD2	1:A:498:ARG:NH2	2.28	0.66
1:A:649:ALA:HB3	1:A:653:LEU:HG	1.78	0.65
1:A:561:LYS:CD	1:A:642:ASP:H	2.10	0.65
1:B:484:GLY:HA2	1:B:511:LYS:HE3	1.78	0.65
1:A:483:LYS:NZ	1:A:672:VAL:HA	2.12	0.65
1:A:495:TYR:CE1	1:A:501:VAL:HG11	2.32	0.65
1:A:525:LYS:HB2	1:A:677:ILE:HG21	1.77	0.64
1:B:301:LEU:HD21	1:B:431:LEU:HD22	1.79	0.63
1:A:484:GLY:HA3	1:A:546:ASN:HB3	1.80	0.63
1:A:625:GLU:HA	1:A:628:LYS:CE	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:625:GLU:O	1:A:628:LYS:HG3	1.98	0.63
1:B:516:ALA:HB3	1:B:690:ILE:HG22	1.80	0.62
1:A:490:ASN:HA	1:A:504:ASN:HB2	1.82	0.62
1:B:73:LYS:HD3	2:D:13:LEU:HD13	1.81	0.62
1:B:285:LEU:O	1:B:289:ILE:HG12	1.99	0.62
1:A:639:LYS:HB3	1:A:641:PRO:HG3	1.80	0.62
1:B:580:LEU:HD12	1:B:635:ARG:HG2	1.80	0.62
1:A:82:ASP:OD2	2:C:8:ASN:N	2.32	0.62
1:A:308:LEU:HD11	1:A:407:ILE:HG23	1.81	0.62
1:B:483:LYS:H	1:B:483:LYS:HD2	1.65	0.61
1:B:625:GLU:OE1	1:B:652:ASN:ND2	2.33	0.61
1:B:90:ASN:ND2	2:D:21:MET:SD	2.74	0.61
1:B:14:ARG:NH2	1:B:117:GLY:O	2.32	0.61
1:B:29:ILE:HG21	1:B:139:LEU:HD12	1.81	0.60
1:B:276:ILE:HD11	1:B:456:SER:HA	1.82	0.60
1:A:648:GLU:OE1	1:A:680:ARG:NH2	2.34	0.60
1:A:516:ALA:HB3	1:A:690:ILE:HG22	1.82	0.60
1:A:563:ALA:HB2	1:A:641:PRO:CG	2.32	0.60
1:B:199:LYS:HE3	1:B:199:LYS:HA	1.83	0.59
1:B:491:VAL:HA	1:B:541:GLY:HA3	1.83	0.59
1:A:43:ARG:HH12	1:A:261:ARG:HG2	1.67	0.59
1:A:103:ILE:HG22	1:A:113:VAL:HG22	1.85	0.58
1:A:94:ASP:OD2	1:A:96:ARG:NH1	2.35	0.58
1:B:604:PHE:HB2	1:B:607:LYS:HE3	1.85	0.58
1:A:495:TYR:CZ	3:A:801:ATP:C2	2.92	0.58
1:B:33:TYR:CD2	1:B:141:PRO:HG3	2.39	0.58
1:A:498:ARG:HG3	1:A:499:LYS:H	1.69	0.58
1:A:680:ARG:HH11	1:A:682:SER:HB2	1.69	0.57
1:A:480:ILE:O	1:A:480:ILE:HG13	2.04	0.57
1:A:563:ALA:HB2	1:A:641:PRO:HG2	1.85	0.57
1:B:472:ARG:NH2	1:B:553:ILE:O	2.38	0.57
1:B:571:ILE:HD11	1:B:623:LEU:HD13	1.85	0.57
1:B:212:GLY:O	1:B:216:ILE:HG12	2.05	0.57
1:B:35:LEU:HD12	1:B:148:GLY:O	2.05	0.56
1:B:322:ILE:HD12	1:B:395:LEU:HD23	1.86	0.56
1:B:472:ARG:NH1	1:B:534:ASN:HD21	2.02	0.56
1:B:513:LYS:HE3	1:B:513:LYS:HA	1.87	0.56
1:A:625:GLU:CA	1:A:628:LYS:HD2	2.32	0.56
1:B:36:LYS:CD	1:B:151:THR:CG2	2.83	0.56
1:B:60:HIS:HA	1:B:63:LYS:NZ	2.21	0.56
1:A:85:LEU:HD13	1:A:105:SER:HA	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:608:LEU:HD13	1:B:614:THR:HG21	1.88	0.56
1:A:588:ASP:OD1	1:A:589:MET:N	2.39	0.55
1:A:598:MET:HG3	1:A:637:LEU:HD13	1.89	0.55
1:A:295:VAL:O	1:A:299:ILE:HD12	2.06	0.55
1:A:625:GLU:CA	1:A:628:LYS:CG	2.76	0.55
1:A:217:PHE:CZ	1:B:401:GLY:HA3	2.41	0.55
1:A:439:VAL:O	1:A:443:ILE:HG12	2.06	0.55
1:A:561:LYS:HD3	1:A:642:ASP:H	1.72	0.55
1:A:513:LYS:HE3	1:A:688:ASP:HB3	1.89	0.55
1:A:561:LYS:HD2	1:A:642:ASP:H	1.70	0.55
1:A:353:LYS:HD2	1:B:263:VAL:HG11	1.87	0.54
1:B:486:ILE:HG13	1:B:545:ILE:HD13	1.88	0.54
1:A:355:ILE:HA	1:A:358:ILE:HG22	1.90	0.54
1:A:239:ASP:O	1:A:243:MET:HG3	2.08	0.54
1:A:624:SER:OG	1:A:627:GLN:HG3	2.06	0.54
1:B:563:ALA:HB3	1:B:644:LEU:HA	1.89	0.54
1:A:545:ILE:O	1:A:548:HIS:N	2.39	0.53
1:A:585:GLU:OE2	1:B:366:GLN:NE2	2.41	0.53
1:B:557:LEU:CD1	1:B:561:LYS:CE	2.81	0.53
1:B:483:LYS:H	1:B:483:LYS:CD	2.21	0.53
1:A:86:PRO:HB3	1:A:104:TYR:HA	1.91	0.53
1:A:235:GLY:HA3	1:A:277:ARG:HH21	1.75	0.52
1:B:11:VAL:O	1:B:104:TYR:OH	2.20	0.52
1:B:482:LEU:CD1	1:B:642:ASP:OD1	2.57	0.52
1:A:625:GLU:HA	1:A:628:LYS:HE3	1.92	0.51
1:A:47:GLY:HA3	1:A:497:LEU:HD13	1.92	0.51
1:A:595:ALA:HA	1:A:598:MET:HG2	1.92	0.51
1:B:311:ILE:O	1:B:314:ILE:HG22	2.11	0.51
1:B:483:LYS:HD2	1:B:483:LYS:N	2.26	0.51
1:A:401:GLY:HA3	1:B:217:PHE:CZ	2.46	0.51
1:B:289:ILE:O	1:B:293:MET:HG2	2.09	0.51
1:B:301:LEU:HD22	1:B:428:PHE:CE1	2.45	0.51
1:A:534:ASN:HD21	1:A:550:ILE:HG22	1.76	0.51
1:B:549:SER:OG	1:B:552:ASN:OD1	2.28	0.51
1:A:561:LYS:HD2	1:A:642:ASP:CG	2.31	0.50
1:B:308:LEU:HD22	1:B:428:PHE:CZ	2.47	0.50
1:B:308:LEU:HD23	1:B:308:LEU:O	2.11	0.50
1:A:525:LYS:HB2	1:A:677:ILE:CG2	2.42	0.50
1:A:569:VAL:CG2	1:A:628:LYS:HD3	2.41	0.50
1:A:132:TRP:HZ3	1:A:134:GLY:HA2	1.77	0.50
1:A:401:GLY:HA3	1:B:217:PHE:CE2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:394:SER:O	1:B:398:ILE:HG12	2.12	0.49
1:B:82:ASP:OD2	2:D:8:ASN:N	2.45	0.49
1:B:152:GLN:CD	1:B:152:GLN:H	2.16	0.49
1:B:318:LEU:O	1:B:322:ILE:HG12	2.12	0.49
1:A:198:ILE:HA	1:B:416:ILE:HD11	1.95	0.49
1:A:659:ASN:OD1	1:A:660:HIS:N	2.46	0.49
1:A:610:LEU:O	1:A:614:THR:OG1	2.29	0.49
1:A:495:TYR:OH	3:A:801:ATP:C2	2.66	0.49
1:A:413:TYR:CE1	1:A:417:LYS:HE3	2.48	0.49
1:B:625:GLU:HA	1:B:628:LYS:HD3	1.94	0.49
1:A:713:CYS:HA	1:A:716:LYS:HE2	1.94	0.49
1:A:473:GLU:H	1:A:551:LYS:HE2	1.78	0.48
1:A:495:TYR:HD2	3:A:801:ATP:N6	2.07	0.48
1:A:658:GLU:OE2	1:A:680:ARG:NH2	2.46	0.48
1:B:15:GLN:OE1	1:B:117:GLY:HA2	2.12	0.48
1:A:180:THR:O	1:A:184:ILE:HG12	2.13	0.48
1:A:258:PHE:CE2	1:B:355:ILE:HD13	2.49	0.48
1:A:408:LEU:HD13	1:A:425:LEU:HD21	1.95	0.48
1:A:706:GLU:O	1:A:710:LEU:HG	2.14	0.48
1:B:468:GLU:OE2	1:B:559:ARG:NH2	2.47	0.48
1:A:482:LEU:HB3	1:A:642:ASP:OD2	2.14	0.48
1:A:316:ILE:HD11	1:A:436:LEU:HD22	1.96	0.48
1:B:437:THR:OG1	1:B:438:PRO:HD3	2.14	0.48
1:B:563:ALA:HB2	1:B:641:PRO:HG3	1.95	0.47
1:B:15:GLN:NE2	1:B:116:PRO:HB2	2.28	0.47
1:A:336:GLN:OE1	1:A:381:SER:OG	2.24	0.47
1:A:487:GLU:HB3	1:A:544:LEU:HB3	1.95	0.47
1:A:301:LEU:HD13	1:A:428:PHE:CZ	2.50	0.47
1:A:569:VAL:HG21	1:A:628:LYS:HG3	1.97	0.47
1:B:428:PHE:O	1:B:432:LEU:HG	2.14	0.47
1:B:482:LEU:HD11	1:B:642:ASP:OD1	2.15	0.47
1:A:132:TRP:CZ3	1:A:134:GLY:HA2	2.50	0.47
1:A:398:ILE:HG12	1:B:221:ILE:HG21	1.97	0.47
1:B:193:LEU:HD12	1:B:197:LEU:HB2	1.96	0.47
1:B:308:LEU:HD11	1:B:407:ILE:HG23	1.96	0.47
1:B:329:PRO:HB2	1:B:388:LEU:HD21	1.97	0.47
1:B:558:ILE:O	1:B:562:ILE:HG12	2.15	0.47
1:B:128:PHE:O	1:B:131:ILE:HG22	2.15	0.47
1:A:562:ILE:HG12	1:A:643:ILE:HD12	1.97	0.47
1:A:680:ARG:HH12	1:A:683:THR:HG23	1.80	0.47
1:B:100:PHE:CE1	2:D:23:GLY:HA3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:GLY:HA2	1:A:497:LEU:CD2	2.45	0.46
1:B:680:ARG:NH1	1:B:683:THR:OG1	2.46	0.46
1:A:239:ASP:CG	1:A:277:ARG:HD2	2.35	0.46
1:A:482:LEU:HD21	1:A:643:ILE:HD12	1.95	0.46
1:B:494:ARG:HB3	1:B:500:PRO:HG3	1.97	0.46
1:A:129:CYS:HA	1:A:132:TRP:NE1	2.30	0.46
1:A:486:ILE:HD13	1:A:545:ILE:HD13	1.97	0.46
1:B:500:PRO:HB2	1:B:503:LYS:NZ	2.31	0.46
1:A:507:LEU:HD21	1:A:698:ILE:HG13	1.96	0.46
1:A:640:LYS:N	1:A:641:PRO:CD	2.74	0.46
1:A:513:LYS:HE3	1:A:688:ASP:CB	2.46	0.46
1:A:348:LEU:HD21	1:B:270:PHE:CE2	2.50	0.46
1:B:154:MET:SD	1:B:464:GLU:OE2	2.74	0.46
1:B:301:LEU:HD22	1:B:428:PHE:CD1	2.51	0.46
1:B:457:ASN:O	1:B:461:GLU:HG3	2.16	0.46
1:A:311:ILE:O	1:A:314:ILE:HG22	2.16	0.46
1:B:60:HIS:HA	1:B:63:LYS:HZ2	1.80	0.46
1:B:193:LEU:O	1:B:198:ILE:HG12	2.15	0.46
1:A:589:MET:O	1:A:593:ILE:HG12	2.15	0.45
1:A:694:LYS:O	1:A:697:GLU:N	2.45	0.45
1:A:283:ALA:HA	1:A:445:LEU:HD11	1.97	0.45
1:A:563:ALA:CB	1:A:641:PRO:HG2	2.46	0.45
1:B:685:VAL:HG22	1:B:704:HIS:CE1	2.52	0.45
1:A:47:GLY:HA3	1:A:497:LEU:CD1	2.46	0.45
1:A:473:GLU:HB3	1:A:551:LYS:HZ3	1.81	0.45
1:B:36:LYS:HD3	1:B:151:THR:CG2	2.45	0.45
1:B:703:SER:N	1:B:706:GLU:OE2	2.33	0.45
1:A:473:GLU:O	1:A:552:ASN:ND2	2.45	0.45
1:A:625:GLU:CB	1:A:628:LYS:HD2	2.47	0.45
1:A:437:THR:OG1	1:A:438:PRO:HD3	2.15	0.45
1:A:507:LEU:HD21	1:A:698:ILE:HG21	1.99	0.45
1:A:632:ALA:HA	1:A:635:ARG:HD3	1.97	0.45
1:A:277:ARG:HG3	1:A:278:GLN:N	2.31	0.45
1:A:36:LYS:CD	1:A:151:THR:HG21	2.46	0.45
1:A:497:LEU:N	1:A:497:LEU:HD12	2.31	0.44
1:B:595:ALA:HA	1:B:598:MET:HG2	1.98	0.44
1:B:51:GLN:HG2	1:B:52:GLY:N	2.32	0.44
1:A:495:TYR:CE2	3:A:801:ATP:C5	3.02	0.44
1:B:191:LYS:HB2	1:B:427:ALA:HB2	1.99	0.44
1:B:473:GLU:OE1	1:B:473:GLU:HA	2.18	0.44
1:A:146:GLN:NE2	1:A:147:LYS:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:LEU:HD21	1:B:416:ILE:HG21	2.00	0.44
1:A:634:ALA:O	1:A:638:LEU:HG	2.17	0.44
1:A:503:LYS:HD2	1:A:697:GLU:OE2	2.18	0.44
1:B:490:ASN:HA	1:B:504:ASN:OD1	2.18	0.44
1:B:562:ILE:HD13	1:B:643:ILE:HG21	2.00	0.44
1:A:88:ILE:HG23	1:A:137:VAL:HB	2.00	0.43
1:B:152:GLN:N	1:B:152:GLN:OE1	2.51	0.43
1:A:472:ARG:HH21	1:A:551:LYS:HA	1.83	0.43
1:A:639:LYS:HD2	1:A:641:PRO:CB	2.46	0.43
1:B:73:LYS:N	2:D:11:ARG:O	2.49	0.43
1:B:255:MET:HG3	1:B:535:PHE:HB3	2.00	0.43
1:A:517:ILE:HD13	1:A:675:ILE:HG23	2.00	0.43
1:B:631:LEU:O	1:B:635:ARG:HG3	2.18	0.43
2:C:14:THR:HG23	2:C:17:GLU:H	1.83	0.43
1:B:100:PHE:HE1	2:D:23:GLY:HA3	1.83	0.43
1:B:644:LEU:HB3	1:B:674:VAL:HG22	2.00	0.43
1:A:483:LYS:HZ3	1:A:672:VAL:HA	1.83	0.43
1:B:508:THR:O	1:B:691:TYR:OH	2.33	0.43
1:B:289:ILE:HG13	1:B:290:ASP:N	2.34	0.43
1:B:617:ASN:OD1	1:B:618:GLU:N	2.51	0.43
1:A:59:ILE:HD13	2:C:18:LEU:HD13	1.99	0.43
1:A:109:ARG:O	1:A:109:ARG:HG2	2.18	0.43
1:B:343:LYS:HD3	1:B:374:LYS:NZ	2.34	0.43
1:B:680:ARG:H	1:B:680:ARG:HD3	1.83	0.43
1:B:507:LEU:HD11	1:B:698:ILE:HG13	2.01	0.43
1:A:507:LEU:HD11	1:A:698:ILE:HG13	2.01	0.42
1:B:482:LEU:HD12	1:B:642:ASP:OD1	2.19	0.42
1:A:57:GLY:HA2	1:A:497:LEU:HD22	1.99	0.42
1:A:596:ALA:HB3	1:A:602:HIS:CE1	2.55	0.42
1:A:680:ARG:NH1	1:A:682:SER:HB2	2.32	0.42
1:B:46:THR:HG23	1:B:48:THR:HG23	2.01	0.42
1:B:205:ASP:O	1:B:209:ILE:HG12	2.19	0.42
1:B:647:ASP:OD1	1:B:677:ILE:HB	2.19	0.42
1:A:639:LYS:HD2	1:A:641:PRO:HG3	2.01	0.42
1:B:492:ASP:OD1	1:B:493:PHE:N	2.53	0.42
1:A:290:ASP:HB3	1:A:438:PRO:HB3	2.02	0.42
1:B:568:ASP:OD1	1:B:568:ASP:N	2.46	0.42
1:A:602:HIS:O	1:A:605:ILE:HG12	2.19	0.42
1:B:111:ILE:HG12	1:B:125:MET:HE1	2.01	0.42
2:D:15:ASP:HA	2:D:18:LEU:HD12	2.01	0.42
1:B:92:ILE:HG22	1:B:95:ASN:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:420:MET:HG3	1:B:424:GLN:HB2	2.00	0.42
1:A:128:PHE:O	1:A:131:ILE:HG22	2.19	0.42
1:A:212:GLY:O	1:A:216:ILE:HG12	2.20	0.42
1:A:563:ALA:HB2	1:A:641:PRO:HG3	2.00	0.42
1:A:182:LEU:HD21	1:A:219:LEU:HD23	2.02	0.42
1:B:292:ILE:O	1:B:296:ILE:HG12	2.19	0.42
1:A:70:LYS:HG3	1:A:72:VAL:HG23	2.02	0.42
1:A:143:GLU:OE1	1:A:143:GLU:HA	2.20	0.42
1:B:431:LEU:HD23	1:B:431:LEU:O	2.20	0.42
1:B:692:LEU:HD23	1:B:699:VAL:HG21	2.01	0.41
1:A:580:LEU:HB3	1:A:638:LEU:HD11	2.01	0.41
1:A:81:LYS:NZ	1:A:81:LYS:HB2	2.35	0.41
1:B:46:THR:O	1:B:497:LEU:HD11	2.20	0.41
1:B:280:ILE:O	1:B:284:THR:OG1	2.30	0.41
1:B:85:LEU:HD23	1:B:104:TYR:O	2.21	0.41
1:A:85:LEU:HB3	1:A:104:TYR:O	2.20	0.41
1:A:495:TYR:CE1	1:A:501:VAL:HG21	2.55	0.41
1:A:588:ASP:HB3	1:A:591:GLU:OE1	2.21	0.41
1:B:238:ILE:O	1:B:242:ILE:HG12	2.21	0.41
1:B:601:ALA:HA	1:B:604:PHE:CE2	2.55	0.41
1:A:344:LEU:HD22	1:A:378:VAL:HG21	2.03	0.41
1:A:555:LEU:HD21	1:A:559:ARG:HE	1.86	0.41
1:B:507:LEU:HD22	1:B:691:TYR:CE2	2.56	0.41
1:A:514:THR:O	1:A:688:ASP:HB2	2.21	0.41
1:A:711:LYS:O	1:A:711:LYS:HG3	2.21	0.41
1:A:128:PHE:O	1:A:132:TRP:HD1	2.04	0.40
1:A:548:HIS:CE1	1:A:552:ASN:HB2	2.40	0.40
1:B:499:LYS:NZ	1:B:500:PRO:HD2	2.36	0.40
1:A:569:VAL:HG23	1:A:628:LYS:HD3	2.02	0.40
1:A:662:LYS:NZ	1:A:686:ASN:HD22	2.19	0.40
1:A:703:SER:HB2	1:A:706:GLU:OE1	2.21	0.40
1:B:697:GLU:OE2	1:B:697:GLU:HA	2.20	0.40
1:A:344:LEU:HA	1:A:374:LYS:NZ	2.37	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	713/730 (98%)	693 (97%)	19 (3%)	1 (0%)	51	84
1	B	713/730 (98%)	691 (97%)	22 (3%)	0	100	100
2	C	15/93 (16%)	14 (93%)	1 (7%)	0	100	100
2	D	15/93 (16%)	15 (100%)	0	0	100	100
All	All	1456/1646 (88%)	1413 (97%)	42 (3%)	1 (0%)	54	84

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	525	LYS

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	612/625 (98%)	608 (99%)	4 (1%)	84	90
1	B	612/625 (98%)	609 (100%)	3 (0%)	88	93
2	C	11/81 (14%)	11 (100%)	0	100	100
2	D	11/81 (14%)	11 (100%)	0	100	100
All	All	1246/1412 (88%)	1239 (99%)	7 (1%)	86	92

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	151	THR
1	A	191	LYS
1	A	579	ASN
1	B	482	LEU
1	B	579	ASN
1	B	680	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	602	HIS
1	A	629	GLN
1	B	64	GLN
1	B	534	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	$\#\|Z\| > 2$
3	ATP	A	801	4	26,33,33	0.66	0	31,52,52	0.77	1 (3%)
3	ATP	B	801	4	26,33,33	0.66	0	31,52,52	0.77	1 (3%)

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
3	ATP	A	801	4	-	2/18/38/38	0/3/3/3
3	ATP	B	801	4	-	2/18/38/38	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	801	ATP	C5-C6-N6	2.25	123.77	120.35
3	A	801	ATP	C5-C6-N6	2.23	123.75	120.35

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	801	ATP	PG-O3B-PB-O1B
3	B	801	ATP	PG-O3B-PB-O1B
3	A	801	ATP	C5'-O5'-PA-O3A
3	B	801	ATP	C5'-O5'-PA-O3A

There are no ring outliers.

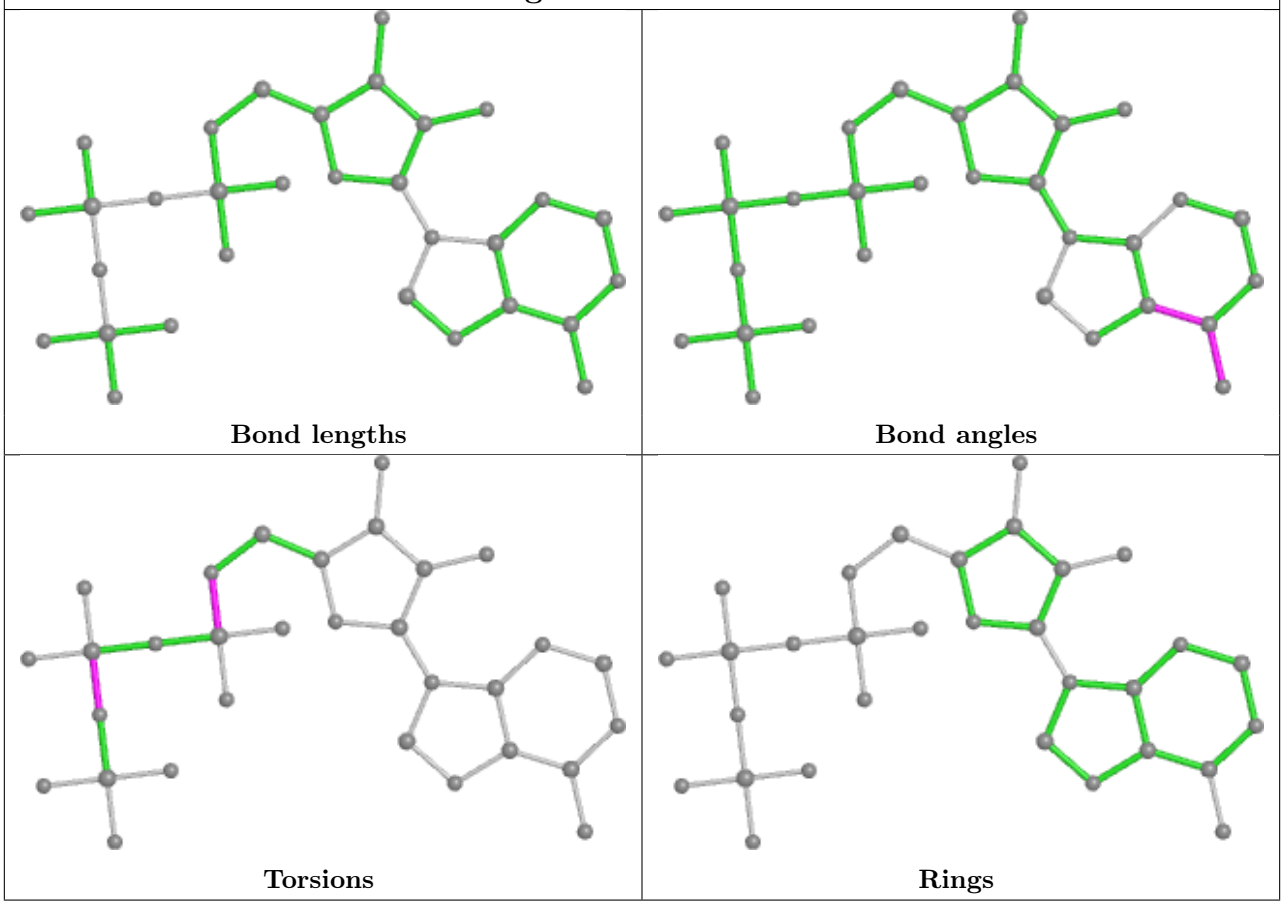
1 monomer is involved in 11 short contacts:

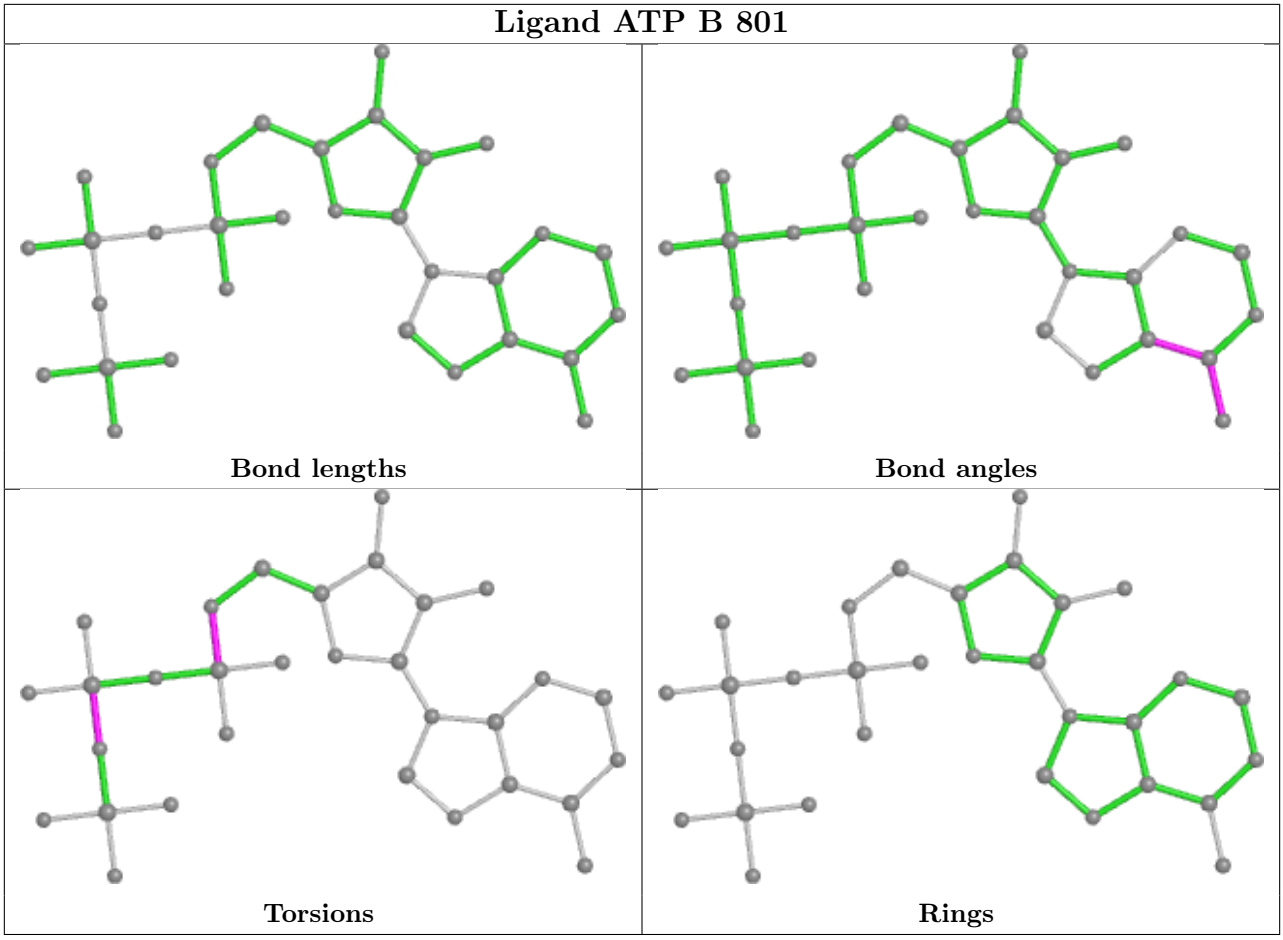
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	801	ATP	11	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand ATP A 801





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.

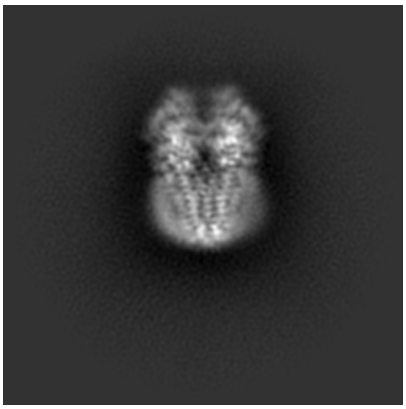
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-25695. These allow visual inspection of the internal detail of the map and identification of artifacts.

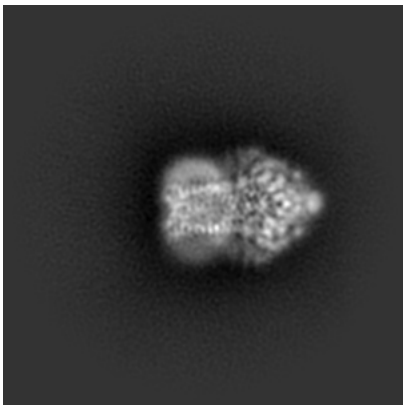
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

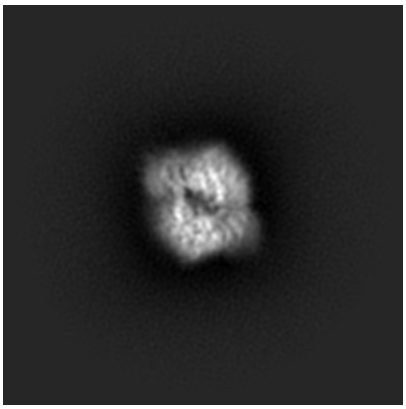
6.1.1 Primary map



X

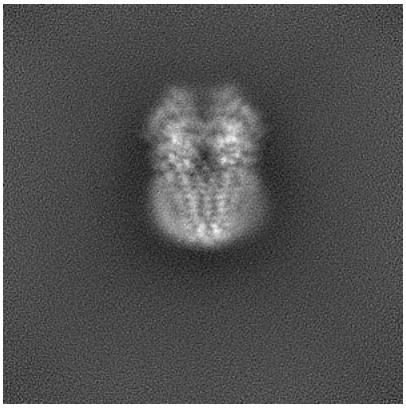


Y

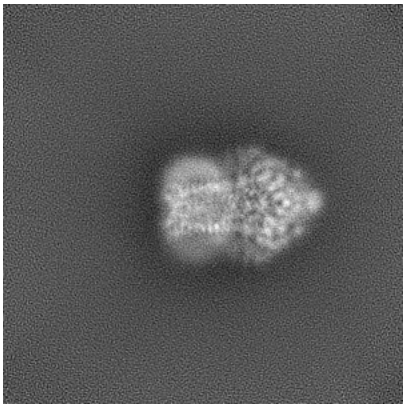


Z

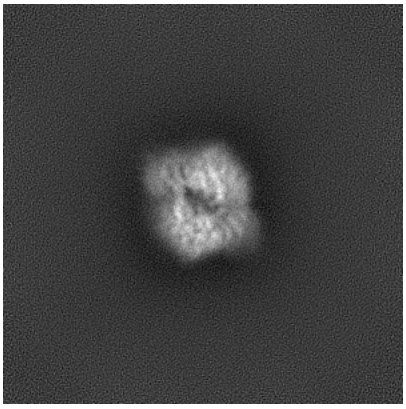
6.1.2 Raw map



X



Y



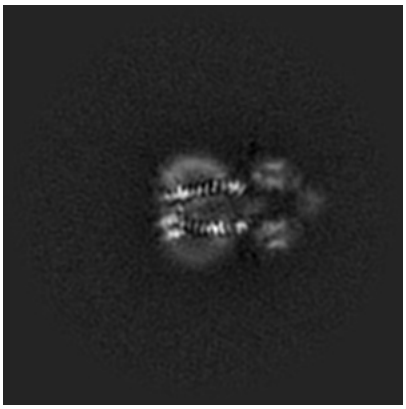
Z

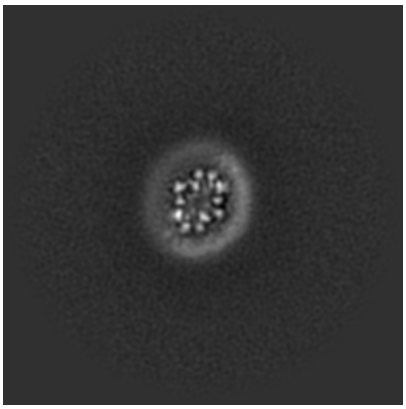
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

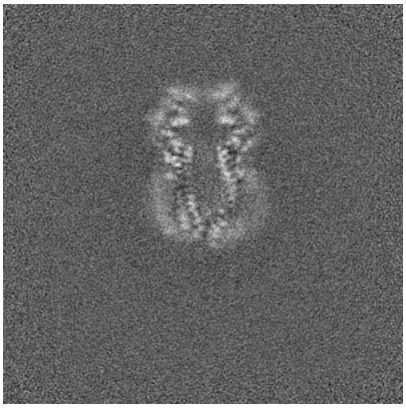
6.2.1 Primary map

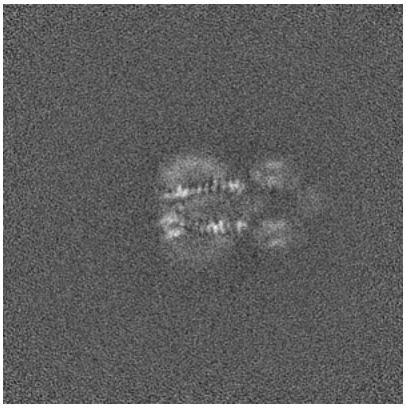
X Index: 150

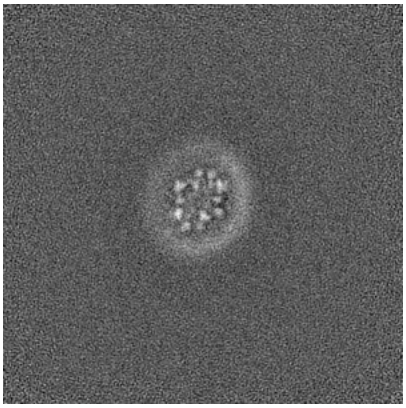

Y Index: 150


Z Index: 150

6.2.2 Raw map


X Index: 150

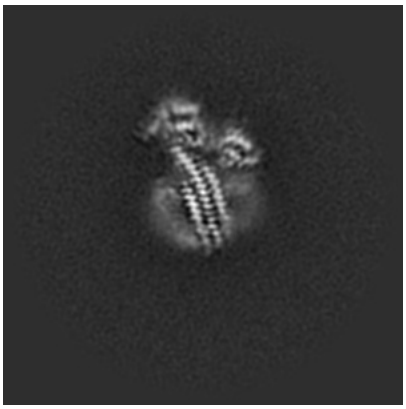

Y Index: 150

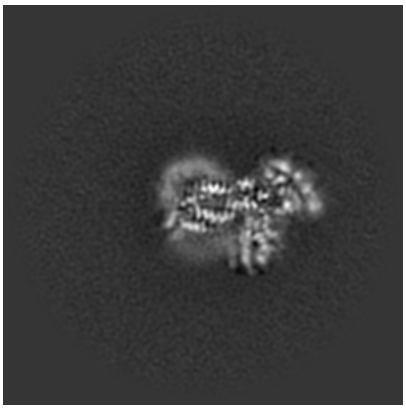

Z Index: 150

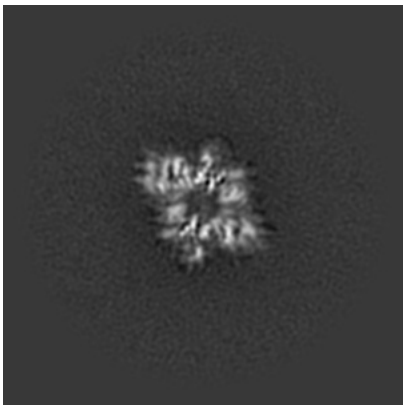
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

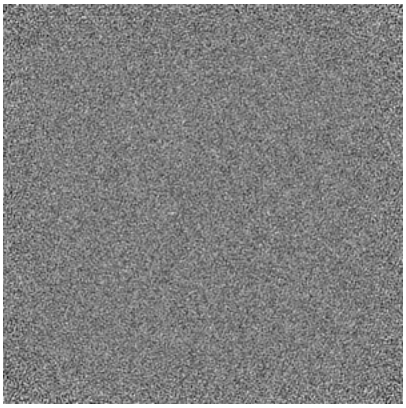
6.3.1 Primary map

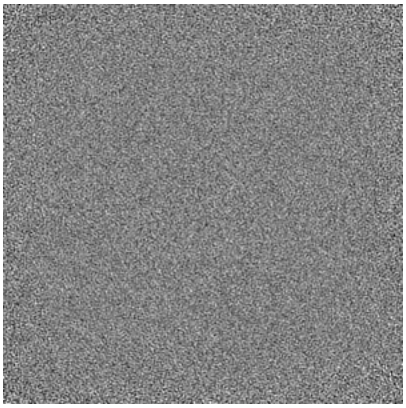

X Index: 131

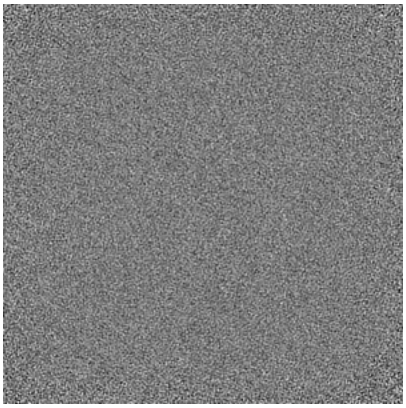

Y Index: 165


Z Index: 196

6.3.2 Raw map


X Index: 0

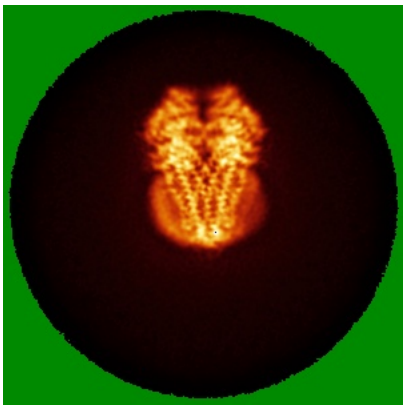

Y Index: 0

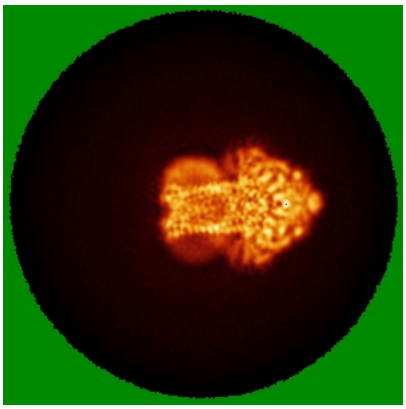

Z Index: 0

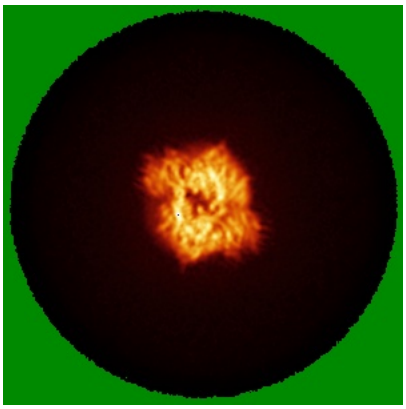
The images above show the largest variance slices of the map in three orthogonal directions.

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

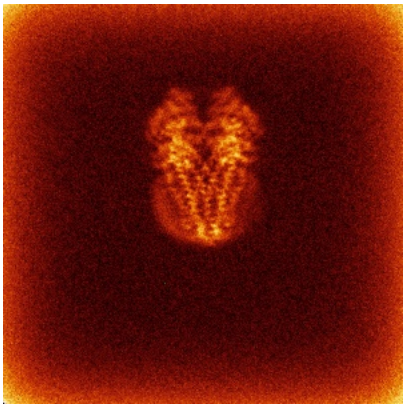
6.4.1 Primary map

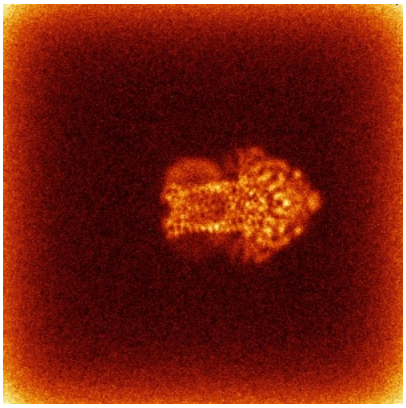

X

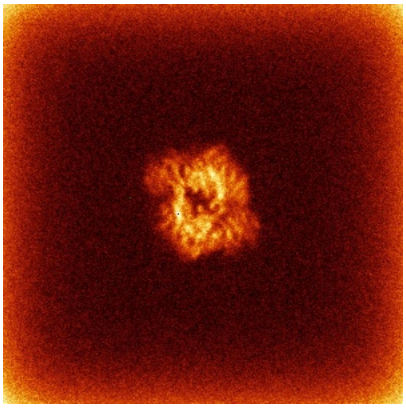

Y


Z

6.4.2 Raw map


X

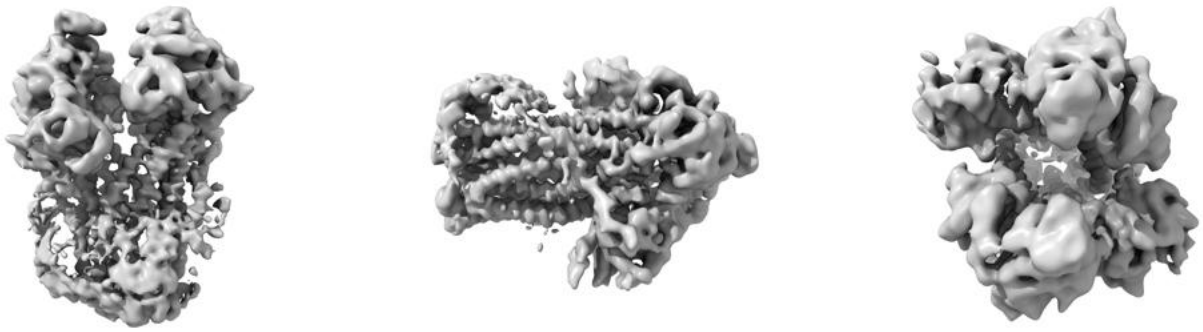

Y


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. 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

X Y Z

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.

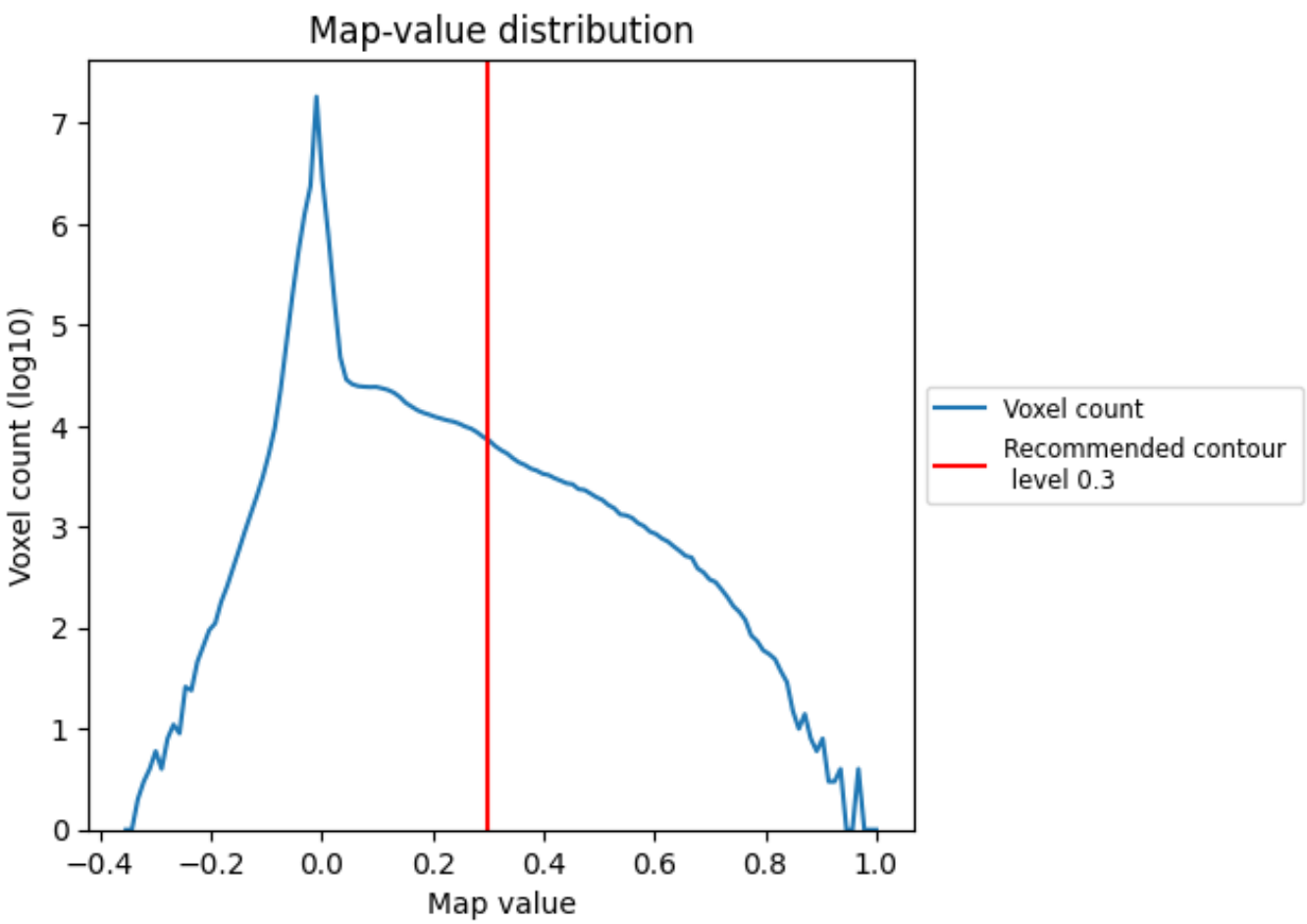
6.6 Mask visualisation (i)

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

7 Map analysis (i)

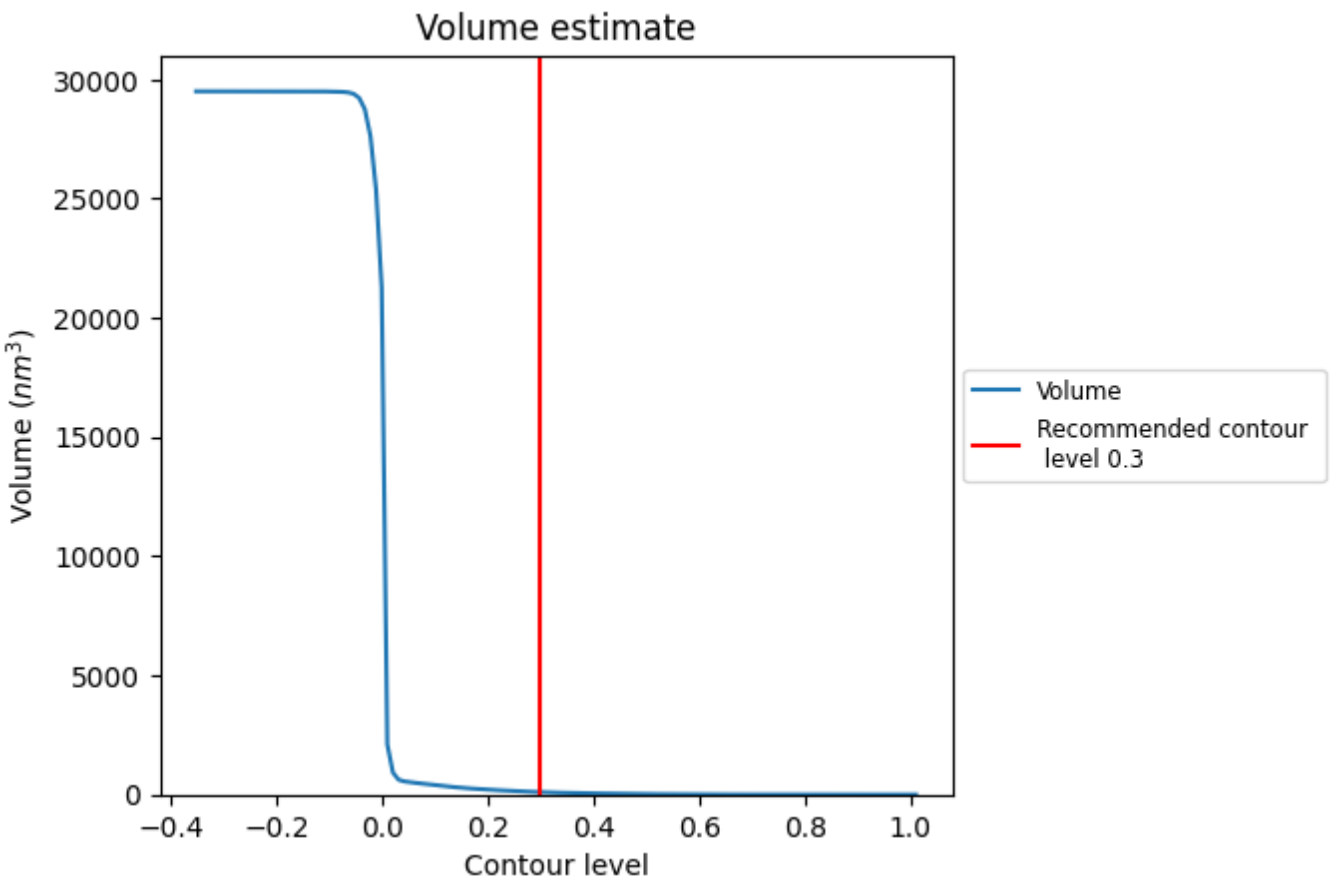
This section contains the results of statistical analysis of the map.

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.

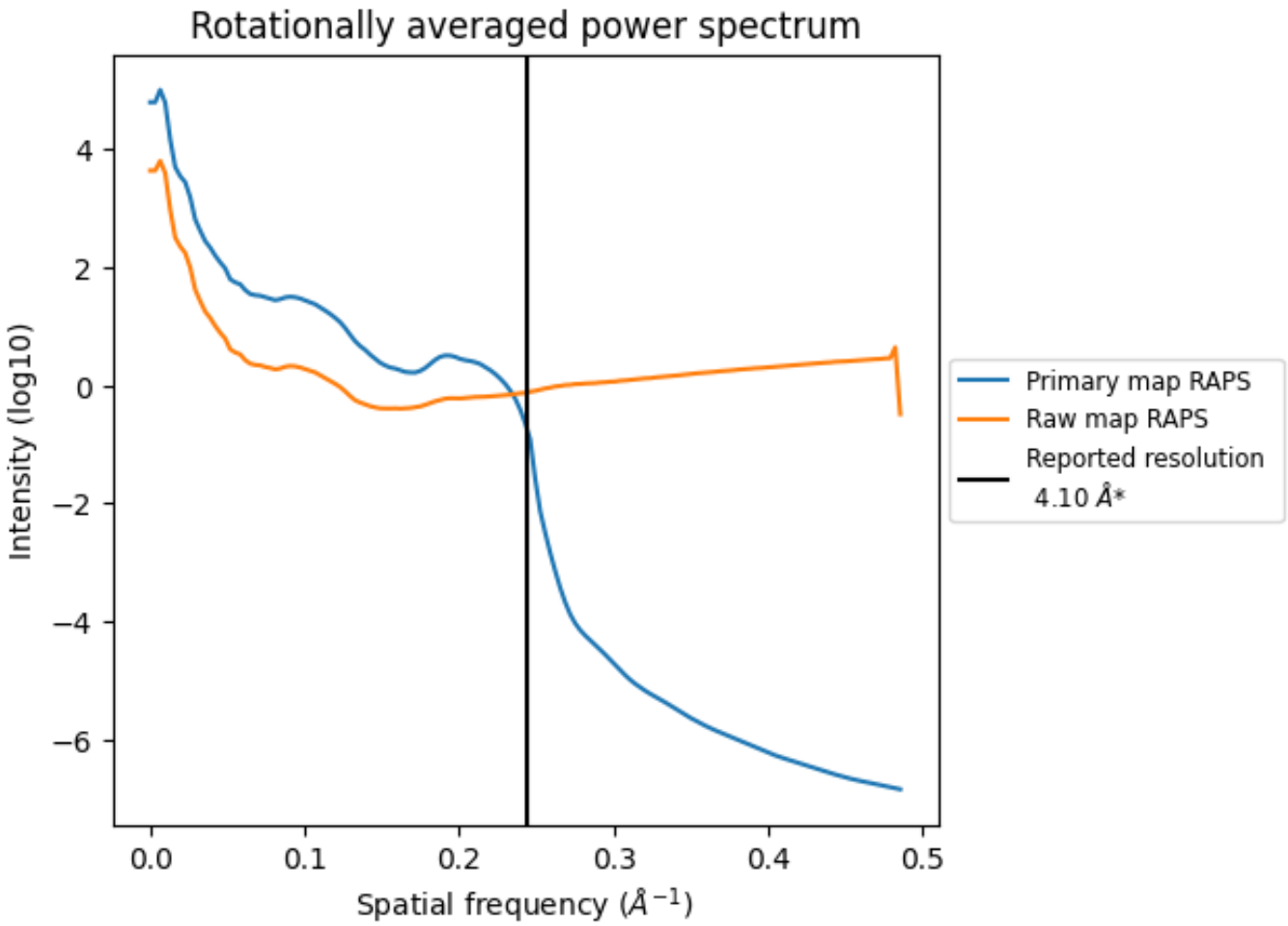
7.2 Volume estimate (i)



The volume at the recommended contour level is 101 nm^3; this corresponds to an approximate mass of 91 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 (i)

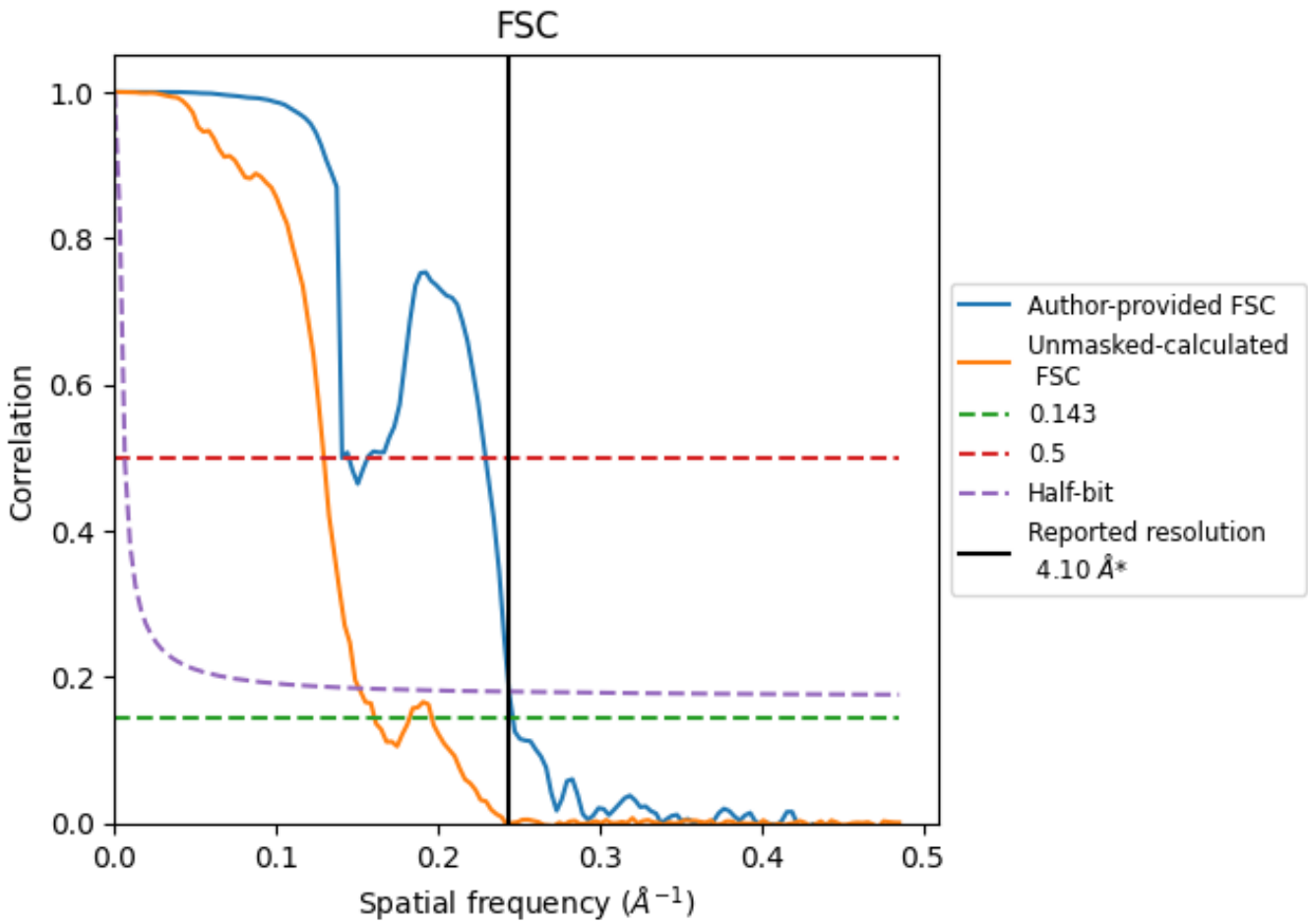


*Reported resolution corresponds to spatial frequency of 0.244 Å^{-1}

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 0.244 Å^{-1}

8.2 Resolution estimates (i)

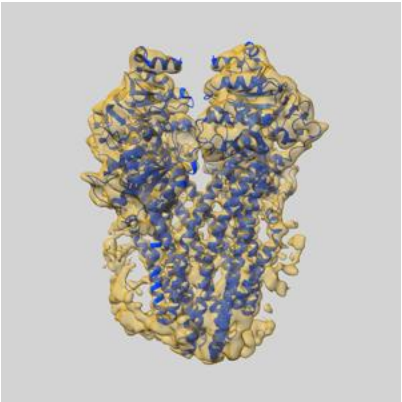
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.06	7.10	4.10
Unmasked-calculated*	6.21	7.72	6.61

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.21 differs from the reported value 4.1 by more than 10 %

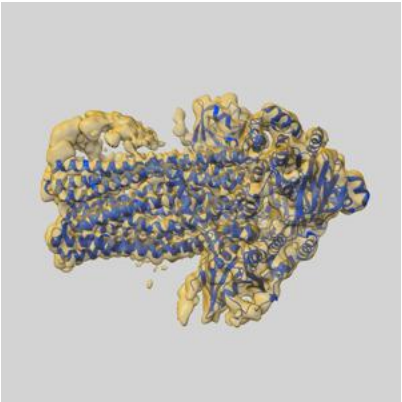
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-25695 and PDB model 7T55. Per-residue inclusion information can be found in section 3 on page 5.

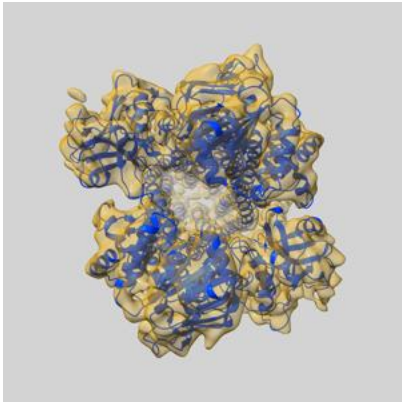
9.1 Map-model overlay (i)



X



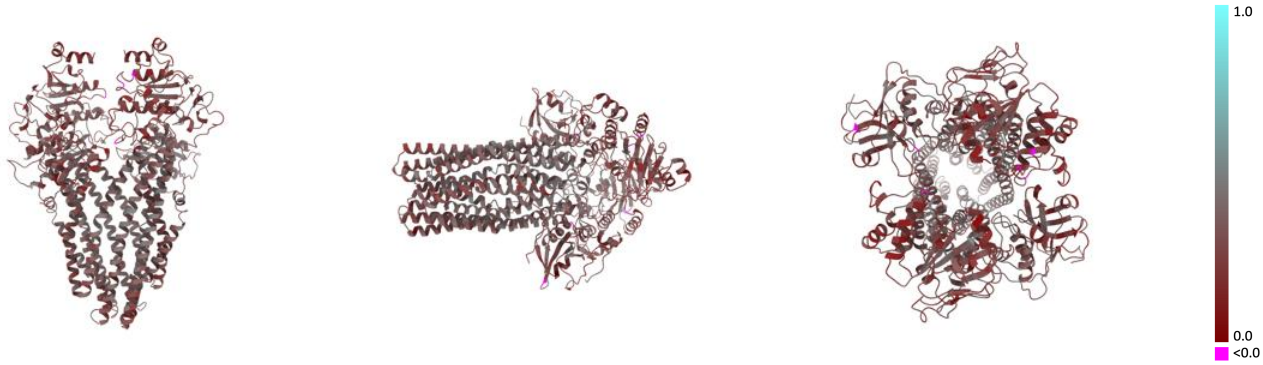
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3 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.

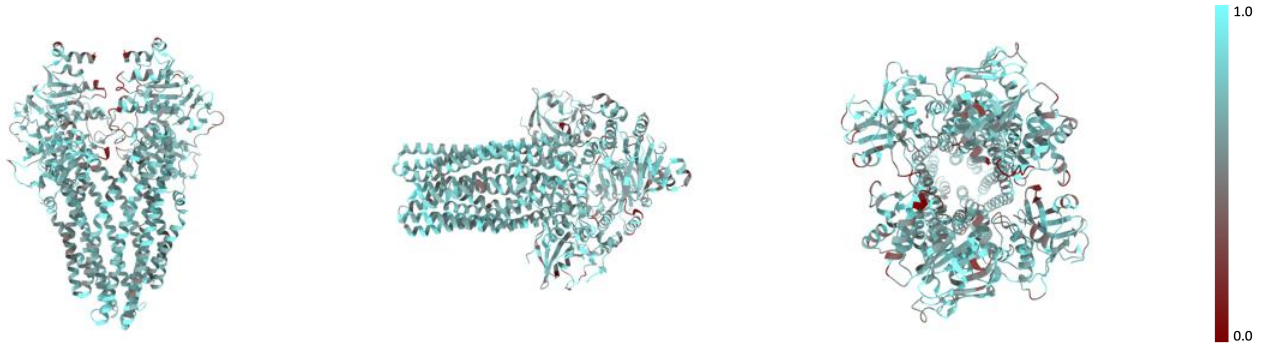
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

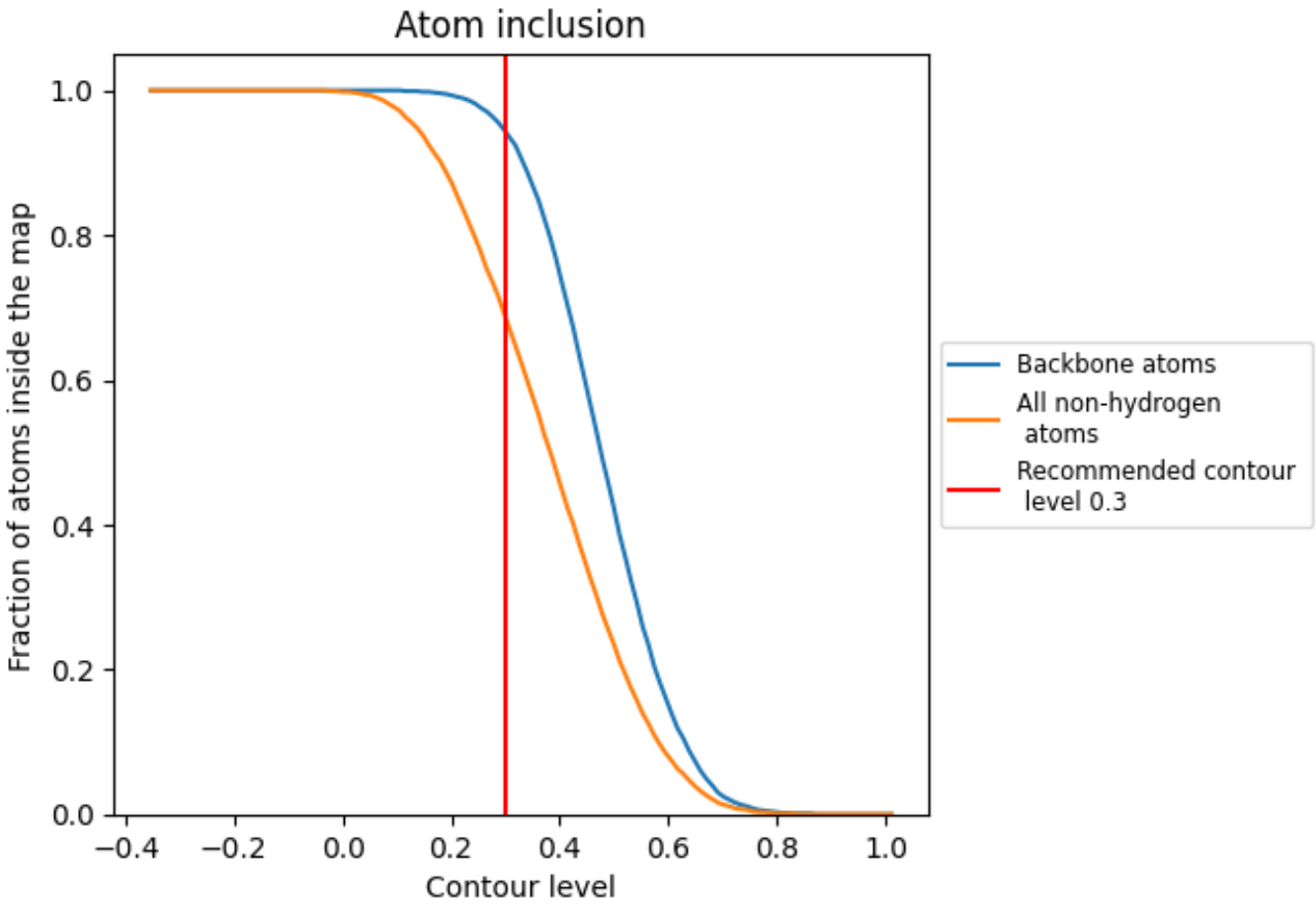
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.3).

9.4 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 69% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6870	0.3190
A	0.6860	0.3190
B	0.6880	0.3200
C	0.7180	0.3040
D	0.6150	0.2660