Full wwPDB EM Validation Report ⓘ

Sep 1, 2026 – 04:16 PM JST

PDB ID	:	9JSM / pdb_00009jsm
EMDB ID	:	EMD-61777
Title	:	Clostridium perfringens iota toxin pore Ib in prepore VI state
Authors	:	Yamada, T.; Sugita, Y.; Yoshida, T.; Noda, T.; Tsuge, H.
Deposited on	:	2024-09-30
Resolution	:	3.73 Å(reported)
Based on initial models	:	., 6klx

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:

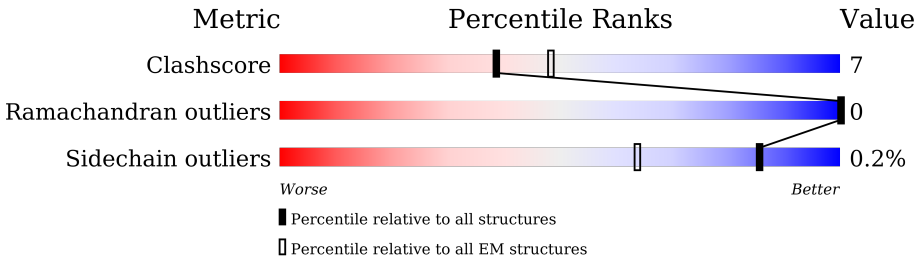
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

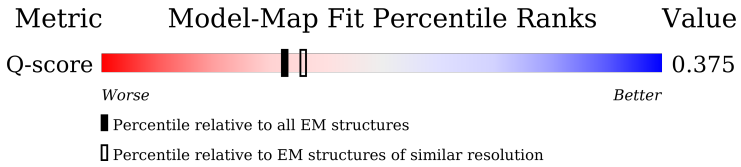
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.73 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	10415 (3.23 - 4.23)

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	531	68% 16% 16%
1	B	531	66% 17% 16%
1	C	531	7% 73% 11% 16%
1	D	531	67% 17% 16%

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Mol	Chain	Length	Quality of chain
1	E	531	
1	F	531	
1	G	531	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 24760 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 Iota toxin component Ib.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	444	Total	C	N	O	S	0	0
			3446	2200	547	694	5		
1	B	445	Total	C	N	O	S	0	0
			3450	2200	547	697	6		
1	C	448	Total	C	N	O	S	0	0
			3472	2215	551	700	6		
1	D	447	Total	C	N	O	S	0	0
			3464	2207	549	702	6		
1	E	442	Total	C	N	O	S	0	0
			3425	2181	544	695	5		
1	F	478	Total	C	N	O	S	0	0
			3684	2338	588	753	5		
1	G	494	Total	C	N	O	S	0	0
			3798	2401	610	782	5		

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
2	A	3	Total	Ca	0
			3	3	
2	B	3	Total	Ca	0
			3	3	
2	C	3	Total	Ca	0
			3	3	
2	D	3	Total	Ca	0
			3	3	
2	E	3	Total	Ca	0
			3	3	
2	F	3	Total	Ca	0
			3	3	
2	G	3	Total	Ca	0
			3	3	

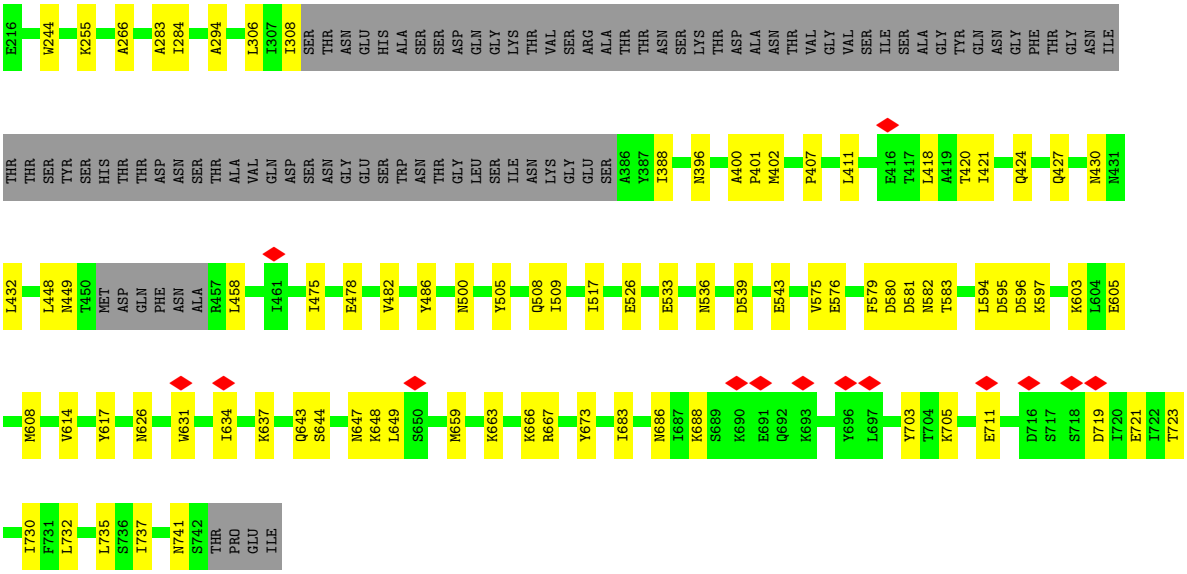
3 Residue-property plots (i)

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: Iota toxin component Ib

Chain A:

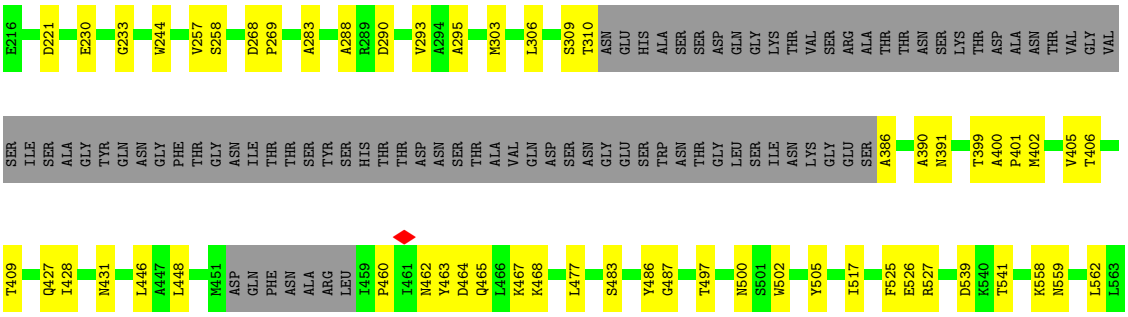


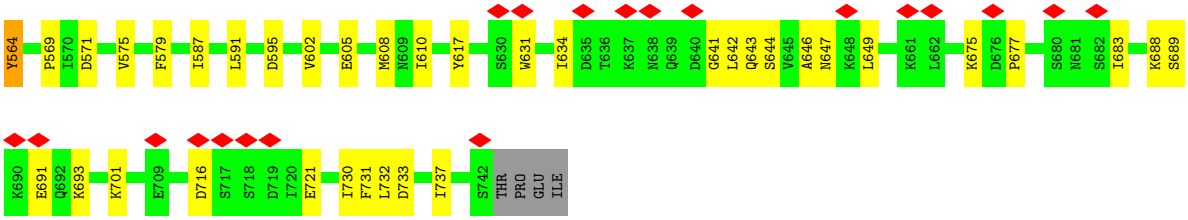


• Molecule 1: Iota toxin component Ib

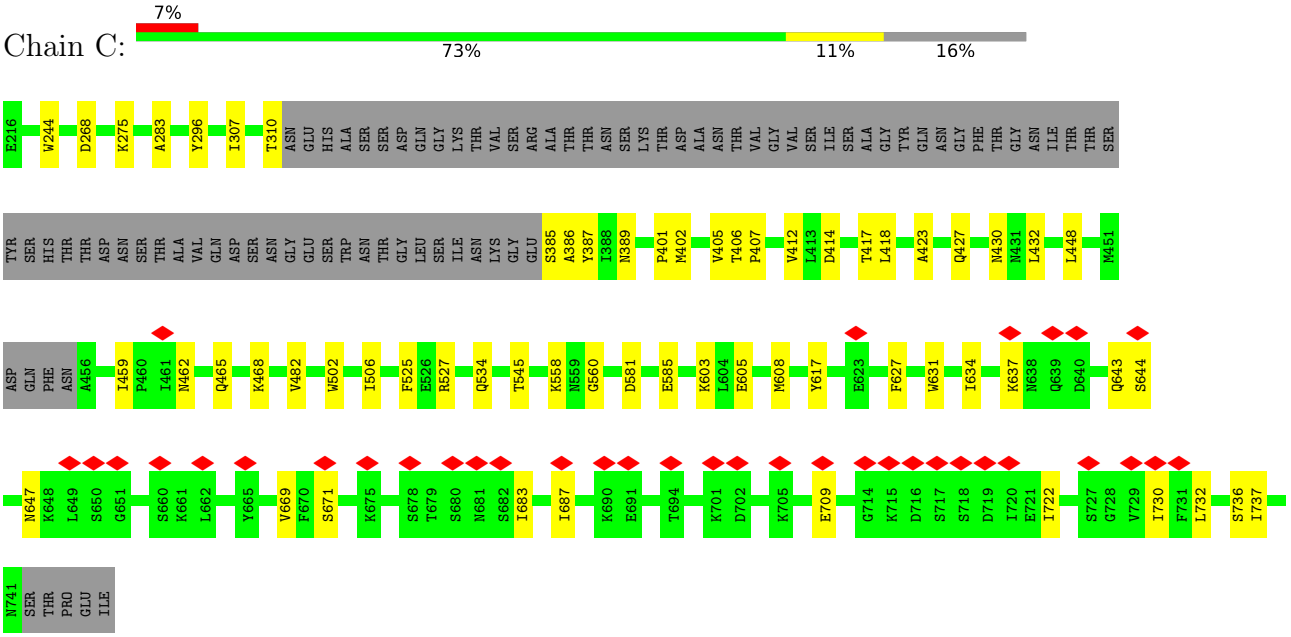
Chain B:



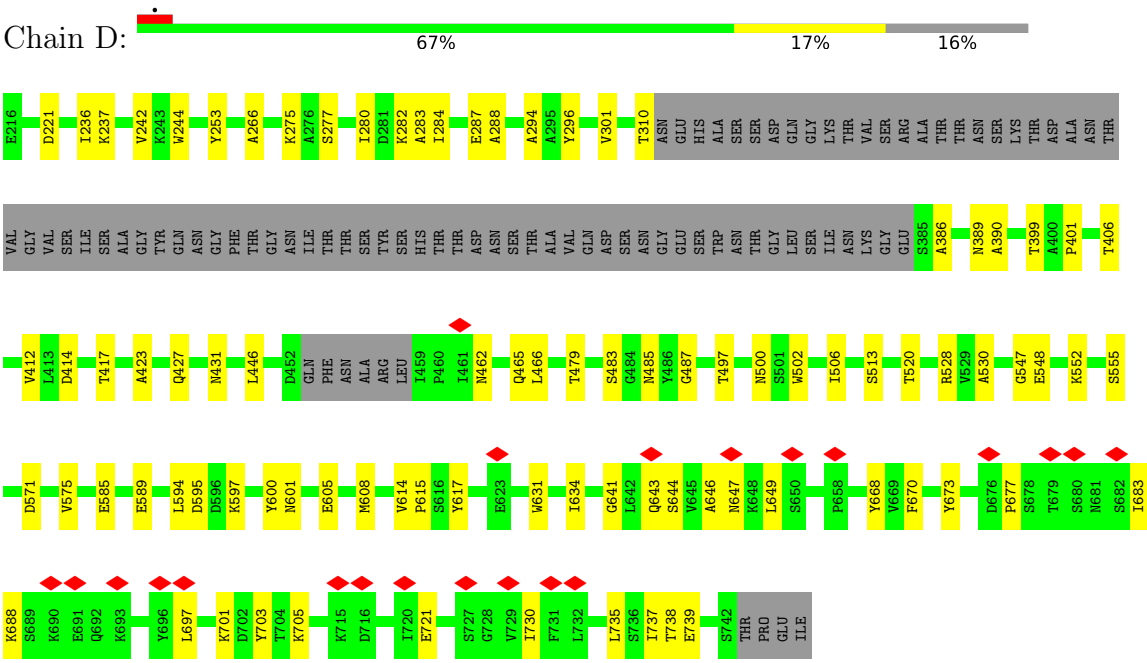




• Molecule 1: Iota toxin component Ib

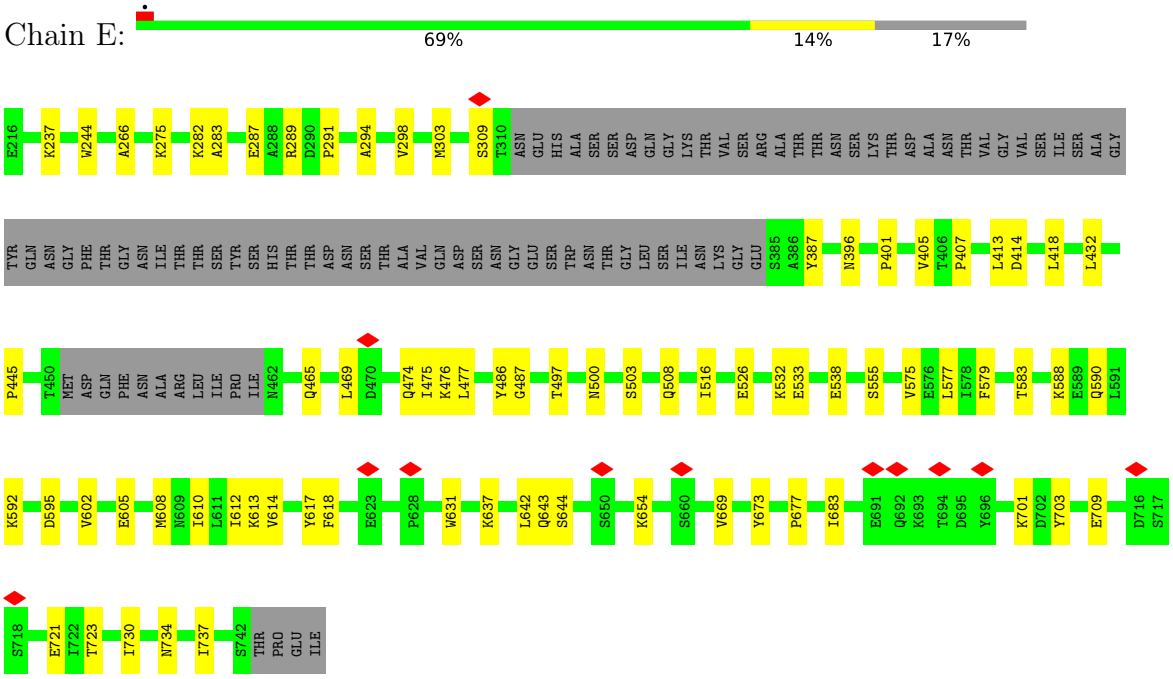


• Molecule 1: Iota toxin component Ib



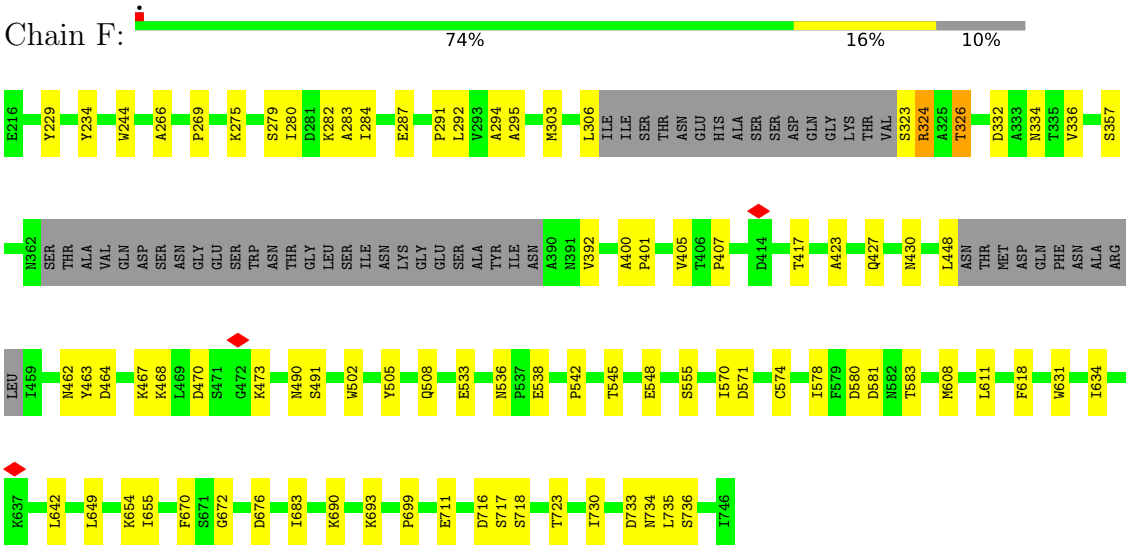
• Molecule 1: Iota toxin component Ib

Chain E:



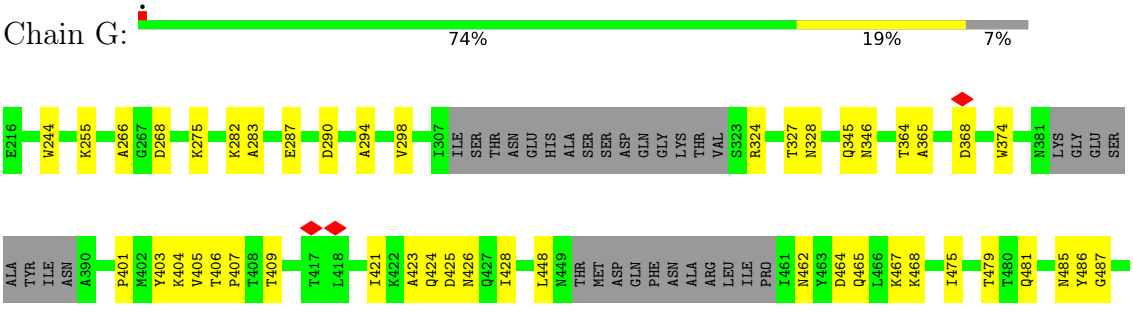
• Molecule 1: Iota toxin component Ib

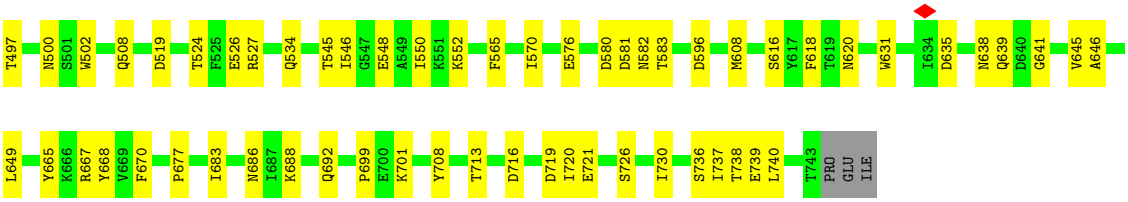
Chain F:



• Molecule 1: Iota toxin component Ib

Chain G:




T497
N500
S501
W502
Q508
D519
T524
F525
E526
R527
Q534
T545
I546
G547
E548
A549
I550
K551
K552
F565
I570
E576
D580
D581
N582
T583
D596
M608
S616
Y617
F618
T619
N620
W631
I634
D635
N638
Q639
D640
G641
V645
A646
L649
Y665
K666
R667
Y668
V669
F670
P677
I683
N686
I687
K688
Q692
P699
E700
K701
Y708
T713
D716
D719
I720
E721
S726
I730
S736
I737
T738
E739
L740
T743
PRO
GLU
ILE

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	7672	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 ($e^-/Å^2$)	50.0	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.838	Depositor
Minimum map value	-0.362	Depositor
Average map value	0.013	Depositor
Map value standard deviation	0.084	Depositor
Recommended contour level	0.182	Depositor
Map size (Å)	191.84, 191.84, 191.84	wwPDB
Map dimensions	218, 218, 218	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.88, 0.88, 0.88	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.12	0/3504	0.28	0/4727
1	B	0.12	0/3508	0.29	0/4733
1	C	0.12	0/3530	0.28	0/4762
1	D	0.11	0/3522	0.27	0/4752
1	E	0.11	0/3482	0.28	0/4697
1	F	0.16	0/3746	0.37	1/5058 (0.0%)
1	G	0.13	0/3859	0.32	0/5211
All	All	0.13	0/25151	0.30	1/33940 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	326	THR	CB-CA-C	-5.39	98.68	109.35

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	3446	0	3372	52	0
1	B	3450	0	3373	59	0
1	C	3472	0	3398	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3464	0	3382	55	0
1	E	3425	0	3340	46	0
1	F	3684	0	3581	57	0
1	G	3798	0	3674	64	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
2	E	3	0	0	0	0
2	F	3	0	0	0	0
2	G	3	0	0	0	0
All	All	24760	0	24120	357	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 7.

All (357) 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:462:ASN:H	1:B:465:GLN:HE22	1.33	0.77
1:B:688:LYS:HB3	1:B:721:GLU:H	1.52	0.74
1:F:282:LYS:HB2	1:G:508:GLN:HG3	1.69	0.74
1:E:303:MET:HE3	1:E:477:LEU:HD22	1.69	0.73
1:B:631:TRP:CZ2	1:B:631:TRP:CZ3	2.77	0.71
1:C:631:TRP:CZ2	1:C:631:TRP:CZ3	2.77	0.71
1:A:244:TRP:CZ2	1:A:244:TRP:CZ3	2.77	0.71
1:E:282:LYS:HB2	1:F:508:GLN:HG3	1.72	0.71
1:B:409:THR:HB	1:B:477:LEU:HD11	1.71	0.71
1:B:244:TRP:CZ2	1:B:244:TRP:CZ3	2.77	0.71
1:E:244:TRP:CZ2	1:E:244:TRP:CZ3	2.77	0.71
1:F:244:TRP:CZ3	1:F:244:TRP:CZ2	2.77	0.71
1:F:583:THR:HG23	1:F:608:MET:HG2	1.70	0.71
1:G:244:TRP:CZ2	1:G:244:TRP:CZ3	2.77	0.71
1:G:631:TRP:CZ2	1:G:631:TRP:CZ3	2.77	0.70
1:E:631:TRP:CZ2	1:E:631:TRP:CZ3	2.77	0.70
1:C:244:TRP:CZ2	1:C:244:TRP:CZ3	2.77	0.70
1:G:374:TRP:CZ2	1:G:374:TRP:CZ3	2.77	0.69
1:F:502:TRP:CZ2	1:F:502:TRP:CZ3	2.77	0.69
1:B:309:SER:OG	1:C:462:ASN:ND2	2.25	0.69
1:G:324:ARG:HG3	1:G:368:ASP:HB3	1.75	0.69
1:A:631:TRP:CZ2	1:A:631:TRP:CZ3	2.77	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:462:ASN:OD1	1:F:463:TYR:N	2.26	0.68
1:A:688:LYS:HB3	1:A:721:GLU:H	1.57	0.68
1:D:244:TRP:CZ3	1:D:244:TRP:CZ2	2.77	0.68
1:D:485:ASN:ND2	1:D:500:ASN:O	2.25	0.68
1:D:631:TRP:CZ3	1:D:631:TRP:CZ2	2.77	0.68
1:D:548:GLU:HG3	1:D:552:LYS:HE2	1.76	0.68
1:D:688:LYS:HB3	1:D:721:GLU:H	1.59	0.67
1:D:280:ILE:HD12	1:D:284:ILE:HD12	1.78	0.65
1:A:449:ASN:HA	1:A:458:LEU:HD23	1.77	0.65
1:E:418:LEU:HD11	1:E:465:GLN:HG2	1.78	0.64
1:D:282:LYS:HB2	1:E:508:GLN:HG3	1.79	0.64
1:A:508:GLN:HG3	1:G:282:LYS:HB2	1.78	0.64
1:F:405:VAL:HG12	1:F:407:PRO:HD3	1.80	0.63
1:A:430:ASN:OD1	1:B:483:SER:OG	2.16	0.63
1:C:617:TYR:HB3	1:C:627:PHE:HE1	1.63	0.63
1:F:683:ILE:HD11	1:F:730:ILE:HG21	1.80	0.62
1:G:576:GLU:HG3	1:G:738:THR:HG21	1.80	0.62
1:D:585:GLU:O	1:D:589:GLU:HG2	1.99	0.61
1:F:292:LEU:HD21	1:F:542:PRO:HD2	1.82	0.61
1:F:690:LYS:NZ	1:F:711:GLU:OE2	2.30	0.61
1:G:683:ILE:HD11	1:G:730:ILE:HG13	1.83	0.61
1:G:667:ARG:HG3	1:G:740:LEU:HB2	1.82	0.61
1:D:631:TRP:HB2	1:D:634:ILE:HD13	1.83	0.60
1:A:581:ASP:OD1	1:A:582:ASN:N	2.34	0.60
1:D:310:THR:HA	1:D:386:ALA:HA	1.82	0.60
1:B:605:GLU:H	1:B:608:MET:HE2	1.67	0.60
1:A:424:GLN:H	1:A:427:GLN:HE21	1.49	0.60
1:C:671:SER:HB2	1:C:736:SER:HB2	1.84	0.60
1:C:683:ILE:HD11	1:C:730:ILE:HG21	1.83	0.59
1:G:583:THR:HG23	1:G:608:MET:HG2	1.84	0.59
1:F:654:LYS:HE3	1:F:723:THR:HG22	1.85	0.59
1:F:642:LEU:HD23	1:F:733:ASP:HB3	1.84	0.59
1:F:287:GLU:HB3	1:F:555:SER:HB3	1.83	0.59
1:F:303:MET:HE2	1:F:326:THR:CG2	2.33	0.58
1:B:431:ASN:HD21	1:C:506:ILE:HB	1.68	0.58
1:E:618:PHE:HZ	1:E:734:ASN:HD22	1.51	0.58
1:G:665:TYR:H	1:G:713:THR:HA	1.69	0.58
1:B:683:ILE:HD11	1:B:730:ILE:HG21	1.84	0.58
1:A:579:PHE:HB3	1:A:583:THR:HB	1.86	0.58
1:A:421:ILE:HG21	1:A:448:LEU:HD11	1.85	0.58
1:D:670:PHE:HZ	1:D:735:LEU:HD23	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:406:THR:HG23	1:C:423:ALA:HB3	1.86	0.57
1:G:364:THR:OG1	1:G:475:ILE:O	2.20	0.57
1:D:406:THR:HG23	1:D:423:ALA:HB3	1.87	0.57
1:G:327:THR:O	1:G:365:ALA:N	2.37	0.57
1:D:275:LYS:NZ	1:D:288:ALA:O	2.33	0.57
1:C:283:ALA:HB3	1:C:401:PRO:HG3	1.86	0.57
1:E:487:GLY:HA2	1:E:497:THR:HG22	1.87	0.57
1:B:390:ALA:O	1:B:448:LEU:N	2.38	0.57
1:C:310:THR:HA	1:C:386:ALA:HA	1.87	0.56
1:E:474:GLN:HE22	1:E:476:LYS:HE2	1.70	0.56
1:D:605:GLU:H	1:D:608:MET:HE2	1.71	0.56
1:E:654:LYS:NZ	1:E:721:GLU:OE2	2.39	0.56
1:F:618:PHE:HD1	1:F:736:SER:HB3	1.71	0.56
1:G:677:PRO:O	1:G:701:LYS:NZ	2.34	0.56
1:A:605:GLU:HB2	1:A:608:MET:HE1	1.87	0.56
1:A:686:ASN:HB2	1:A:723:THR:HB	1.87	0.56
1:B:647:ASN:HB3	1:B:732:LEU:HB2	1.88	0.55
1:F:303:MET:HE2	1:F:326:THR:HG22	1.88	0.55
1:G:464:ASP:HA	1:G:467:LYS:HE2	1.89	0.55
1:G:649:LEU:HG	1:G:726:SER:HB3	1.87	0.55
1:A:732:LEU:HD12	1:A:735:LEU:HD21	1.89	0.55
1:B:460:PRO:HB3	1:B:465:GLN:HE21	1.70	0.55
1:F:303:MET:HA	1:F:392:VAL:HA	1.88	0.55
1:E:721:GLU:OE2	1:E:723:THR:OG1	2.23	0.55
1:D:301:VAL:H	1:D:479:THR:HG21	1.71	0.55
1:F:275:LYS:HE3	1:F:291:PRO:HA	1.89	0.55
1:B:269:PRO:HG3	1:B:505:TYR:CD2	2.42	0.54
1:A:576:GLU:OE1	1:A:705:LYS:NZ	2.33	0.54
1:G:546:ILE:O	1:G:550:ILE:HG12	2.08	0.54
1:G:719:ASP:OD2	1:G:720:ILE:N	2.40	0.54
1:G:465:GLN:HA	1:G:468:LYS:HE2	1.89	0.54
1:C:387:TYR:HE1	1:C:459:ILE:HD12	1.73	0.54
1:G:266:ALA:HB1	1:G:294:ALA:HB2	1.89	0.54
1:A:659:MET:HE1	1:A:719:ASP:HA	1.90	0.54
1:C:617:TYR:HB2	1:C:737:ILE:HB	1.90	0.54
1:F:631:TRP:HB2	1:F:634:ILE:HD11	1.90	0.53
1:A:306:LEU:HD21	1:A:475:ILE:HD12	1.90	0.53
1:E:590:GLN:HG2	1:E:602:VAL:HG13	1.89	0.53
1:E:605:GLU:H	1:E:608:MET:HE3	1.74	0.53
1:D:649:LEU:HD23	1:D:730:ILE:HD11	1.91	0.53
1:C:418:LEU:HD11	1:C:465:GLN:HG2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:683:ILE:HD11	1:E:730:ILE:HG21	1.89	0.53
1:G:486:TYR:HB3	1:G:502:TRP:NE1	2.24	0.53
1:E:643:GLN:HG2	1:E:644:SER:H	1.74	0.52
1:F:649:LEU:N	1:F:730:ILE:O	2.42	0.52
1:G:298:VAL:HG21	1:G:526:GLU:HB3	1.91	0.52
1:C:405:VAL:HG21	1:C:432:LEU:HD22	1.90	0.52
1:D:643:GLN:HG2	1:D:644:SER:H	1.73	0.52
1:F:295:ALA:HB1	1:F:400:ALA:HB2	1.92	0.52
1:G:424:GLN:HG2	1:G:425:ASP:N	2.25	0.52
1:D:547:GLY:HA2	1:D:600:TYR:HD2	1.75	0.52
1:D:594:LEU:O	1:D:597:LYS:NZ	2.43	0.52
1:E:445:PRO:O	1:F:417:THR:OG1	2.27	0.52
1:A:283:ALA:HB3	1:A:401:PRO:HG3	1.92	0.52
1:D:389:ASN:OD1	1:D:390:ALA:N	2.42	0.51
1:F:334:ASN:OD1	1:F:357:SER:N	2.38	0.51
1:A:266:ALA:HB1	1:A:294:ALA:HB2	1.92	0.51
1:D:673:TYR:CZ	1:D:705:LYS:HD3	2.45	0.51
1:D:673:TYR:HB3	1:D:703:TYR:CD1	2.44	0.51
1:A:427:GLN:OE1	1:A:448:LEU:HA	2.10	0.51
1:F:430:ASN:HD22	1:G:481:GLN:CD	2.18	0.51
1:B:295:ALA:HB1	1:B:400:ALA:HB2	1.92	0.51
1:C:430:ASN:OD1	1:D:483:SER:OG	2.29	0.51
1:E:405:VAL:HG12	1:E:407:PRO:HD3	1.93	0.51
1:F:266:ALA:HB1	1:F:294:ALA:HB2	1.91	0.51
1:F:545:THR:HG22	1:F:548:GLU:HG2	1.92	0.51
1:B:402:MET:HG2	1:B:405:VAL:HG12	1.93	0.51
1:D:288:ALA:HB2	1:D:399:THR:HB	1.91	0.51
1:D:431:ASN:ND2	1:E:503:SER:O	2.35	0.51
1:E:516:ILE:HG12	1:E:610:ILE:HD12	1.93	0.51
1:F:280:ILE:HD12	1:F:284:ILE:HD12	1.93	0.51
1:F:717:SER:OG	1:F:718:SER:N	2.44	0.51
1:B:677:PRO:HA	1:B:701:LYS:HG2	1.92	0.50
1:E:287:GLU:HB3	1:E:555:SER:HB3	1.93	0.50
1:C:647:ASN:HB3	1:C:732:LEU:HB2	1.92	0.50
1:D:462:ASN:OD1	1:D:465:GLN:NE2	2.43	0.50
1:B:517:ILE:HG12	1:B:526:GLU:HG3	1.92	0.50
1:B:587:ILE:O	1:B:591:LEU:HG	2.12	0.50
1:F:427:GLN:HE21	1:F:448:LEU:HB2	1.76	0.50
1:B:283:ALA:HB3	1:B:401:PRO:HG3	1.93	0.50
1:G:345:GLN:NE2	1:G:346:ASN:OD1	2.44	0.50
1:G:580:ASP:OD1	1:G:581:ASP:N	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:649:LEU:HD23	1:B:730:ILE:HD11	1.93	0.50
1:F:578:ILE:HD12	1:F:611:LEU:HD22	1.94	0.50
1:A:306:LEU:HD11	1:A:388:ILE:HD11	1.94	0.49
1:A:411:LEU:O	1:A:418:LEU:N	2.43	0.49
1:E:669:VAL:HG22	1:E:709:GLU:HA	1.94	0.49
1:C:605:GLU:O	1:C:608:MET:HE3	2.12	0.49
1:E:677:PRO:HA	1:E:701:LYS:HD3	1.94	0.49
1:A:580:ASP:OD1	1:A:583:THR:OG1	2.28	0.49
1:E:396:ASN:HB2	1:E:432:LEU:HG	1.95	0.49
1:G:287:GLU:OE1	1:G:527:ARG:NE	2.46	0.49
1:C:634:ILE:HG22	1:C:647:ASN:HD21	1.78	0.49
1:B:486:TYR:HB3	1:B:502:TRP:CE2	2.48	0.49
1:D:487:GLY:HA2	1:D:497:THR:HG22	1.95	0.48
1:A:667:ARG:HG3	1:A:711:GLU:HG3	1.95	0.48
1:D:634:ILE:HG22	1:D:647:ASN:HD21	1.77	0.48
1:A:420:THR:O	1:G:426:ASN:ND2	2.44	0.48
1:A:643:GLN:HG2	1:A:644:SER:H	1.78	0.48
1:B:564:TYR:HE1	1:B:569:PRO:HG3	1.77	0.48
1:C:268:ASP:OD2	1:C:275:LYS:NZ	2.43	0.48
1:C:643:GLN:HG2	1:C:644:SER:H	1.79	0.48
1:D:236:ILE:HG21	1:D:277:SER:HA	1.96	0.48
1:G:618:PHE:CZ	1:G:620:ASN:HB3	2.48	0.48
1:F:464:ASP:O	1:F:468:LYS:HG3	2.13	0.48
1:A:308:ILE:HD12	1:A:388:ILE:HD12	1.94	0.48
1:B:487:GLY:HA2	1:B:497:THR:HG22	1.95	0.48
1:F:533:GLU:OE2	1:F:536:ASN:ND2	2.39	0.48
1:B:643:GLN:HG2	1:B:644:SER:H	1.77	0.48
1:C:412:VAL:HG12	1:C:417:THR:HA	1.96	0.48
1:D:643:GLN:HG2	1:D:644:SER:N	2.29	0.48
1:E:595:ASP:N	1:E:595:ASP:OD1	2.47	0.48
1:D:683:ILE:O	1:D:697:LEU:N	2.41	0.47
1:G:699:PRO:HG2	1:G:730:ILE:HD12	1.96	0.47
1:B:571:ASP:O	1:B:575:VAL:HG12	2.14	0.47
1:E:275:LYS:HE3	1:E:291:PRO:HA	1.95	0.47
1:B:303:MET:HE1	1:B:306:LEU:HD21	1.97	0.47
1:B:634:ILE:HG22	1:B:647:ASN:HD21	1.79	0.47
1:F:423:ALA:HB1	1:F:427:GLN:HB2	1.96	0.47
1:A:617:TYR:HB2	1:A:737:ILE:HG22	1.95	0.47
1:C:617:TYR:HB3	1:C:627:PHE:CE1	2.48	0.47
1:E:532:LYS:NZ	1:E:533:GLU:O	2.33	0.47
1:B:464:ASP:O	1:B:468:LYS:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:487:GLY:HA2	1:G:497:THR:HG22	1.97	0.47
1:F:283:ALA:HB3	1:F:401:PRO:HG3	1.96	0.47
1:E:673:TYR:HB3	1:E:703:TYR:CD1	2.49	0.47
1:G:670:PHE:HB3	1:G:708:TYR:HB2	1.97	0.47
1:B:579:PHE:HE1	1:B:610:ILE:HG23	1.79	0.47
1:G:465:GLN:HA	1:G:468:LYS:HG2	1.97	0.46
1:F:654:LYS:HE2	1:F:654:LYS:HA	1.98	0.46
1:G:328:ASN:HA	1:G:364:THR:HA	1.97	0.46
1:G:406:THR:OG1	1:G:423:ALA:O	2.32	0.46
1:G:686:ASN:HD21	1:G:692:GLN:HE21	1.62	0.46
1:A:517:ILE:HG12	1:A:526:GLU:HG3	1.97	0.46
1:B:406:THR:HG22	1:B:428:ILE:HG12	1.97	0.46
1:B:643:GLN:HG2	1:B:644:SER:N	2.31	0.46
1:G:519:ASP:OD1	1:G:524:THR:OG1	2.28	0.46
1:C:427:GLN:HE21	1:C:448:LEU:HA	1.81	0.46
1:F:570:ILE:HG22	1:F:570:ILE:O	2.14	0.46
1:G:268:ASP:OD2	1:G:275:LYS:NZ	2.35	0.46
1:G:290:ASP:OD2	1:G:552:LYS:HE3	2.15	0.46
1:C:307:ILE:HB	1:C:389:ASN:HB3	1.97	0.46
1:G:596:ASP:OD1	1:G:596:ASP:N	2.49	0.46
1:B:221:ASP:OD1	1:B:221:ASP:N	2.46	0.46
1:D:513:SER:HA	1:D:530:ALA:HA	1.96	0.46
1:D:237:LYS:HD3	1:D:242:VAL:HG21	1.97	0.46
1:F:229:TYR:HB3	1:F:234:TYR:HB3	1.98	0.46
1:F:670:PHE:CZ	1:F:735:LEU:HD22	2.51	0.46
1:B:642:LEU:HD23	1:B:733:ASP:HB3	1.98	0.45
1:F:676:ASP:HB2	1:F:699:PRO:HB2	1.99	0.45
1:G:565:PHE:HB3	1:G:570:ILE:HG13	1.97	0.45
1:C:687:ILE:HG12	1:C:722:ILE:HG23	1.98	0.45
1:E:283:ALA:HB3	1:E:401:PRO:HG3	1.97	0.45
1:A:643:GLN:HG2	1:A:644:SER:N	2.31	0.45
1:C:414:ASP:OD2	1:C:468:LYS:NZ	2.36	0.45
1:G:486:TYR:CE1	1:G:500:ASN:HB3	2.51	0.45
1:C:525:PHE:HB3	1:C:527:ARG:CZ	2.47	0.45
1:F:306:LEU:O	1:F:324:ARG:N	2.50	0.45
1:E:486:TYR:CE2	1:E:500:ASN:HB3	2.51	0.45
1:D:668:TYR:CZ	1:D:739:GLU:HG3	2.52	0.45
1:E:266:ALA:HB1	1:E:294:ALA:HB2	1.98	0.45
1:F:303:MET:HE2	1:F:326:THR:HG21	1.99	0.45
1:G:638:ASN:HB3	1:G:645:VAL:HG23	1.98	0.45
1:A:244:TRP:CD1	1:A:255:LYS:HD2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:587:ILE:HD11	1:B:602:VAL:HG21	1.98	0.45
1:B:539:ASP:OD1	1:B:541:THR:OG1	2.28	0.45
1:D:520:THR:HG22	1:D:614:VAL:HG21	1.99	0.45
1:C:268:ASP:N	1:C:268:ASP:OD1	2.50	0.45
1:C:502:TRP:O	1:C:506:ILE:HG12	2.16	0.45
1:D:595:ASP:OD1	1:D:595:ASP:N	2.43	0.45
1:A:575:VAL:HG23	1:A:614:VAL:HA	1.98	0.44
1:E:289:ARG:CZ	1:F:536:ASN:HD21	2.30	0.44
1:F:303:MET:HE1	1:F:306:LEU:HB2	1.98	0.44
1:A:595:ASP:OD1	1:A:596:ASP:N	2.50	0.44
1:E:309:SER:O	1:E:387:TYR:N	2.47	0.44
1:E:588:LYS:O	1:E:592:LYS:HG2	2.17	0.44
1:B:617:TYR:HB2	1:B:737:ILE:HB	2.00	0.44
1:E:637:LYS:HD2	1:E:637:LYS:HA	1.77	0.44
1:B:486:TYR:CE1	1:B:500:ASN:HB3	2.52	0.44
1:D:287:GLU:HB3	1:D:555:SER:HB2	1.98	0.44
1:D:386:ALA:HB2	1:D:466:LEU:HD21	1.98	0.44
1:G:649:LEU:N	1:G:730:ILE:O	2.47	0.44
1:G:668:TYR:CE1	1:G:739:GLU:HG2	2.53	0.44
1:C:581:ASP:O	1:C:585:GLU:HG2	2.17	0.44
1:D:615:PRO:HA	1:D:738:THR:HG22	1.98	0.44
1:D:673:TYR:HD2	1:D:703:TYR:HB3	1.83	0.44
1:F:334:ASN:HD22	1:F:611:LEU:HD12	1.83	0.44
1:B:390:ALA:HB3	1:B:448:LEU:HB3	1.99	0.44
1:D:547:GLY:N	1:D:600:TYR:O	2.49	0.44
1:A:637:LYS:O	1:A:648:LYS:NZ	2.38	0.44
1:D:414:ASP:N	1:D:414:ASP:OD1	2.48	0.44
1:D:571:ASP:O	1:D:575:VAL:HG12	2.18	0.44
1:E:613:LYS:HB3	1:E:613:LYS:HE3	1.87	0.44
1:B:233:GLY:HA2	1:B:257:VAL:HG22	1.98	0.44
1:E:575:VAL:HG23	1:E:614:VAL:HA	2.00	0.44
1:G:638:ASN:OD1	1:G:639:GLN:N	2.50	0.44
1:B:290:ASP:HB3	1:B:293:VAL:HG12	1.99	0.44
1:D:221:ASP:OD1	1:D:221:ASP:N	2.46	0.44
1:A:536:ASN:HB3	1:A:539:ASP:HB2	1.99	0.43
1:A:634:ILE:HG22	1:A:647:ASN:HD21	1.83	0.43
1:B:558:LYS:HB3	1:B:558:LYS:HE2	1.74	0.43
1:B:310:THR:HA	1:B:386:ALA:HA	2.00	0.43
1:A:478:GLU:OE2	1:A:478:GLU:N	2.51	0.43
1:B:268:ASP:OD1	1:B:268:ASP:N	2.43	0.43
1:B:716:ASP:OD1	1:B:716:ASP:N	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:244:TRP:CD1	1:G:255:LYS:HD2	2.54	0.43
1:G:283:ALA:HB3	1:G:401:PRO:HG3	1.99	0.43
1:A:533:GLU:HB3	1:A:536:ASN:HB2	2.00	0.43
1:A:683:ILE:HD11	1:A:730:ILE:HG21	1.99	0.43
1:E:577:LEU:HD22	1:E:612:ILE:HG12	1.99	0.43
1:G:421:ILE:HD12	1:G:448:LEU:HD22	2.00	0.43
1:G:618:PHE:HD1	1:G:736:SER:HB3	1.83	0.43
1:A:663:LYS:HB2	1:A:666:LYS:HG3	2.00	0.43
1:B:605:GLU:H	1:B:608:MET:CE	2.30	0.43
1:F:467:LYS:HA	1:F:470:ASP:HB2	2.00	0.43
1:C:637:LYS:HD2	1:C:637:LYS:HA	1.78	0.43
1:E:237:LYS:HA	1:F:538:GLU:OE2	2.19	0.43
1:G:405:VAL:HG12	1:G:407:PRO:HD3	2.00	0.43
1:G:641:GLY:HA2	1:G:646:ALA:HB2	2.01	0.43
1:A:637:LYS:HA	1:A:637:LYS:HD2	1.81	0.43
1:D:283:ALA:HB3	1:D:401:PRO:HG3	2.01	0.43
1:G:688:LYS:HB2	1:G:721:GLU:HB3	2.00	0.43
1:A:284:ILE:HD13	1:A:400:ALA:HA	2.00	0.43
1:G:404:LYS:HD3	1:G:428:ILE:HG21	2.01	0.43
1:B:391:ASN:HD21	1:C:417:THR:H	1.67	0.42
1:D:253:TYR:HE1	1:E:538:GLU:HG2	1.84	0.42
1:D:677:PRO:HA	1:D:701:LYS:HG2	2.00	0.42
1:C:558:LYS:HE2	1:C:560:GLY:O	2.19	0.42
1:D:641:GLY:HA2	1:D:646:ALA:HB2	2.01	0.42
1:A:594:LEU:O	1:A:597:LYS:NZ	2.50	0.42
1:B:463:TYR:O	1:B:467:LYS:N	2.49	0.42
1:C:534:GLN:NE2	1:C:605:GLU:HG3	2.34	0.42
1:G:462:ASN:ND2	1:G:465:GLN:OE1	2.52	0.42
1:B:641:GLY:HA2	1:B:646:ALA:HB2	2.00	0.42
1:D:617:TYR:HB2	1:D:737:ILE:HB	2.02	0.42
1:G:409:THR:HG22	1:G:479:THR:HA	2.02	0.42
1:G:582:ASN:OD1	1:G:583:THR:N	2.52	0.42
1:A:649:LEU:HD23	1:A:730:ILE:HD11	2.02	0.42
1:E:469:LEU:HD21	1:E:475:ILE:HG13	2.02	0.42
1:A:543:GLU:OE1	1:A:603:LYS:NZ	2.49	0.42
1:D:266:ALA:HB1	1:D:294:ALA:HB2	2.01	0.42
1:E:643:GLN:HG2	1:E:644:SER:N	2.34	0.42
1:F:580:ASP:OD1	1:F:581:ASP:N	2.51	0.42
1:B:689:SER:OG	1:B:691:GLU:O	2.38	0.42
1:C:669:VAL:HG22	1:C:709:GLU:HA	2.02	0.42
1:D:427:GLN:HA	1:D:446:LEU:HD21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:PRO:HB3	1:A:482:VAL:HG12	2.02	0.41
1:B:675:LYS:HB3	1:B:731:PHE:HB2	2.02	0.41
1:D:670:PHE:CZ	1:D:735:LEU:HD23	2.53	0.41
1:C:405:VAL:HG12	1:C:407:PRO:HD3	2.02	0.41
1:C:432:LEU:HD12	1:C:432:LEU:HA	1.88	0.41
1:E:579:PHE:HB3	1:E:583:THR:HB	2.02	0.41
1:E:642:LEU:HD23	1:E:642:LEU:HA	1.93	0.41
1:A:486:TYR:CE1	1:A:500:ASN:HB3	2.56	0.41
1:A:673:TYR:HB3	1:A:703:TYR:CD1	2.55	0.41
1:B:595:ASP:OD1	1:B:595:ASP:N	2.52	0.41
1:E:617:TYR:HB2	1:E:737:ILE:HB	2.02	0.41
1:F:468:LYS:O	1:F:473:LYS:HB2	2.20	0.41
1:F:631:TRP:NE1	1:F:655:ILE:HD12	2.35	0.41
1:A:505:TYR:O	1:A:509:ILE:HG12	2.20	0.41
1:F:279:SER:O	1:F:279:SER:OG	2.36	0.41
1:B:288:ALA:HB2	1:B:399:THR:HB	2.02	0.41
1:F:571:ASP:HB3	1:F:574:CYS:SG	2.61	0.41
1:G:403:TYR:O	1:G:485:ASN:N	2.54	0.41
1:G:545:THR:OG1	1:G:548:GLU:HG3	2.21	0.41
1:G:635:ASP:N	1:G:635:ASP:OD1	2.54	0.41
1:F:332:ASP:O	1:F:336:VAL:HG23	2.20	0.41
1:F:490:ASN:OD1	1:F:491:SER:N	2.53	0.41
1:A:396:ASN:HB2	1:A:432:LEU:HG	2.03	0.41
1:A:402:MET:HE1	1:A:482:VAL:HG23	2.02	0.41
1:B:230:GLU:OE2	1:B:258:SER:OG	2.38	0.41
1:B:431:ASN:ND2	1:C:506:ILE:HB	2.34	0.41
1:C:402:MET:HE1	1:C:482:VAL:HG13	2.03	0.41
1:D:296:TYR:HD2	1:D:528:ARG:HG3	1.86	0.41
1:E:413:LEU:HG	1:E:414:ASP:OD1	2.21	0.41
1:G:616:SER:N	1:G:737:ILE:O	2.54	0.41
1:A:741:ASN:OD1	1:A:741:ASN:N	2.54	0.41
1:B:559:ASN:OD1	1:B:562:LEU:HB3	2.21	0.41
1:C:385:SER:OG	1:C:386:ALA:N	2.54	0.41
1:G:406:THR:HG23	1:G:406:THR:O	2.21	0.41
1:F:672:GLY:HA2	1:F:734:ASN:O	2.20	0.40
1:A:617:TYR:HA	1:A:626:ASN:HD21	1.87	0.40
1:E:298:VAL:HG21	1:E:526:GLU:HB3	2.02	0.40
1:B:693:LYS:HA	1:B:693:LYS:HD3	1.89	0.40
1:D:412:VAL:HA	1:D:417:THR:HA	2.02	0.40
1:F:693:LYS:HE3	1:F:693:LYS:HB3	1.83	0.40
1:F:716:ASP:OD1	1:F:716:ASP:N	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:534:GLN:OE1	1:G:534:GLN:N	2.48	0.40
1:B:525:PHE:HB3	1:B:527:ARG:CZ	2.52	0.40
1:D:502:TRP:O	1:D:506:ILE:HG12	2.21	0.40
1:F:269:PRO:HG3	1:F:505:TYR:CD2	2.56	0.40
1:B:427:GLN:HG2	1:B:446:LEU:HD13	2.04	0.40
1:C:545:THR:HA	1:C:603:LYS:HA	2.04	0.40
1:G:716:ASP:OD1	1:G:716:ASP:N	2.49	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	438/531 (82%)	424 (97%)	14 (3%)	0	100	100
1	B	439/531 (83%)	424 (97%)	15 (3%)	0	100	100
1	C	442/531 (83%)	428 (97%)	14 (3%)	0	100	100
1	D	441/531 (83%)	426 (97%)	15 (3%)	0	100	100
1	E	436/531 (82%)	424 (97%)	12 (3%)	0	100	100
1	F	470/531 (88%)	455 (97%)	15 (3%)	0	100	100
1	G	486/531 (92%)	469 (96%)	17 (4%)	0	100	100
All	All	3152/3717 (85%)	3050 (97%)	102 (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	395/468 (84%)	395 (100%)	0	100 100
1	B	396/468 (85%)	395 (100%)	1 (0%)	86 83
1	C	398/468 (85%)	397 (100%)	1 (0%)	86 83
1	D	398/468 (85%)	397 (100%)	1 (0%)	86 83
1	E	393/468 (84%)	393 (100%)	0	100 100
1	F	423/468 (90%)	421 (100%)	2 (0%)	81 80
1	G	436/468 (93%)	436 (100%)	0	100 100
All	All	2839/3276 (87%)	2834 (100%)	5 (0%)	85 86

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

Mol	Chain	Res	Type
1	B	564	TYR
1	C	296	TYR
1	D	601	ASN
1	F	323	SER
1	F	324	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	274	GLN
1	A	465	GLN
1	A	474	GLN
1	A	508	GLN
1	A	601	ASN
1	A	686	ASN
1	B	485	ASN
1	B	625	ASN
1	B	633	ASN
1	B	639	GLN
1	B	734	ASN
1	C	462	ASN
1	C	465	GLN
1	C	492	GLN
1	C	500	ASN
1	C	601	ASN

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Mol	Chain	Res	Type
1	C	625	ASN
1	C	639	GLN
1	D	264	ASN
1	D	424	GLN
1	D	427	GLN
1	D	633	ASN
1	E	424	GLN
1	E	449	ASN
1	E	582	ASN
1	E	633	ASN
1	E	734	ASN
1	F	264	ASN
1	F	430	ASN
1	F	500	ASN
1	F	625	ASN
1	G	345	GLN
1	G	370	ASN
1	G	435	ASN
1	G	639	GLN
1	G	692	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 21 ligands modelled in this entry, 21 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

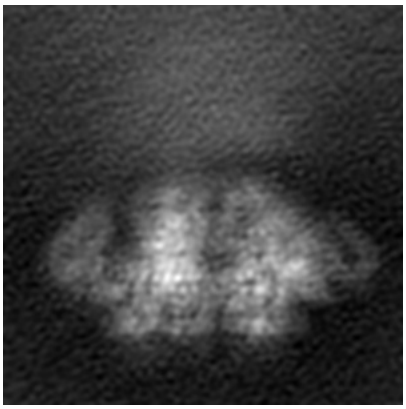
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-61777. These allow visual inspection of the internal detail of the map and identification of artifacts.

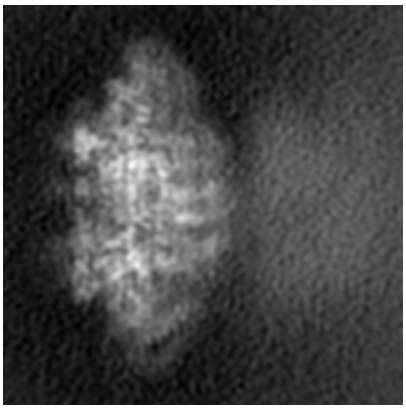
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

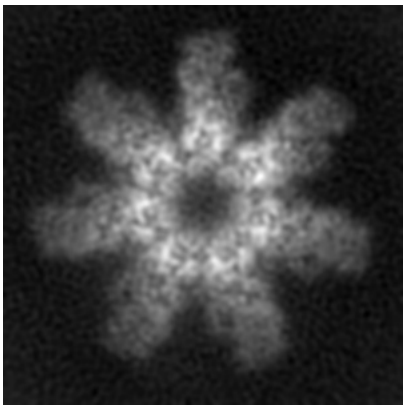
6.1.1 Primary map



X

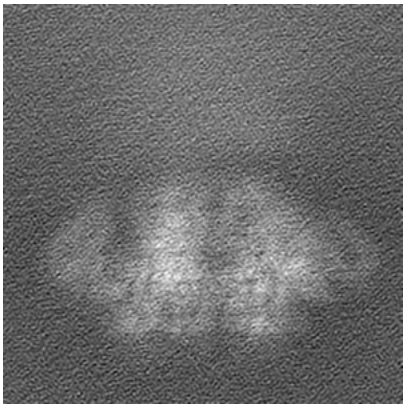


Y

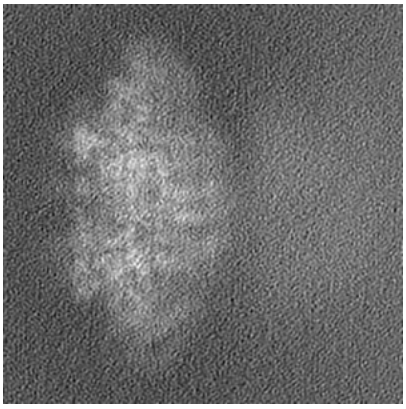


Z

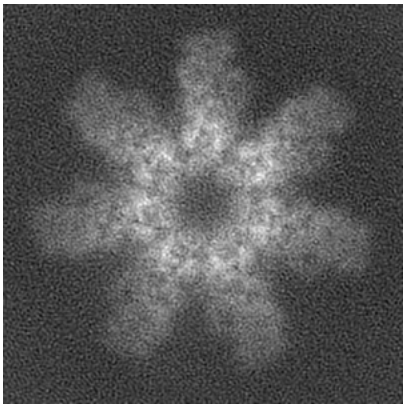
6.1.2 Raw map



X



Y

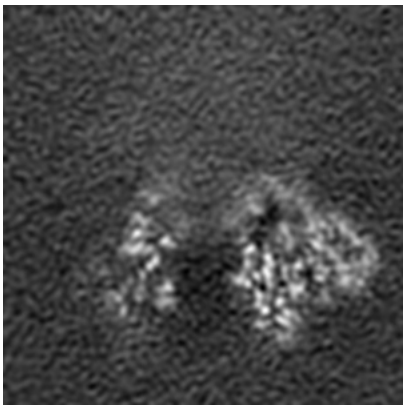


Z

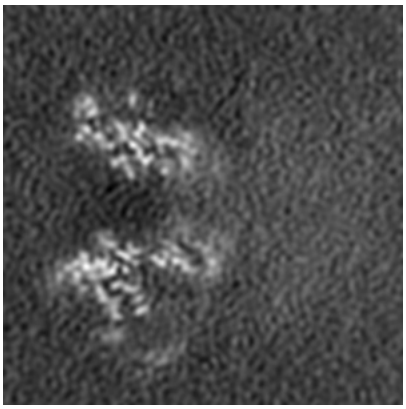
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

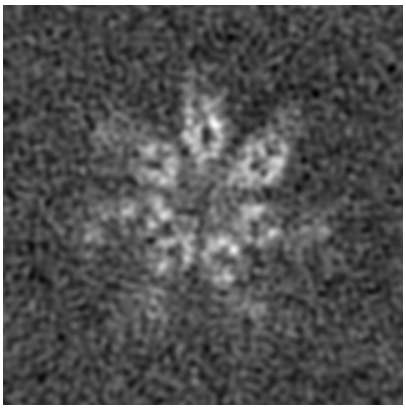
6.2.1 Primary map



X Index: 109



Y Index: 109

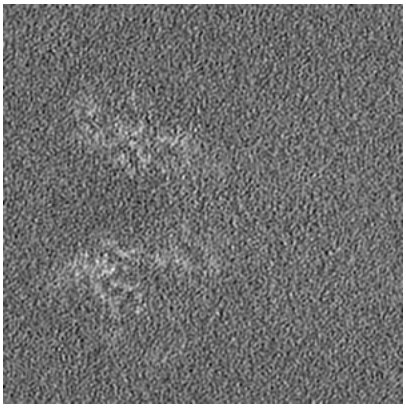


Z Index: 109

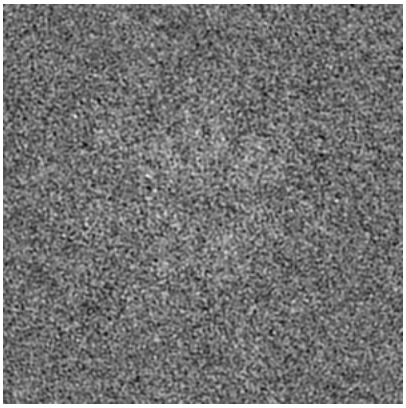
6.2.2 Raw map



X Index: 109



Y Index: 109

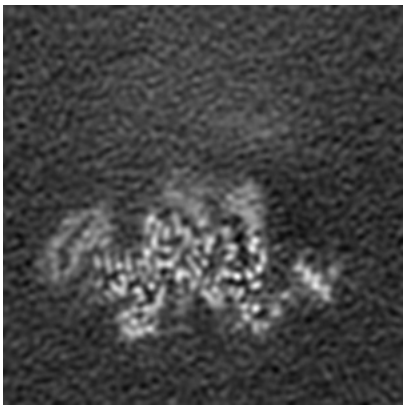


Z Index: 109

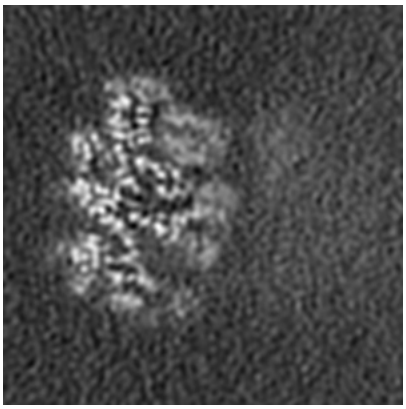
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

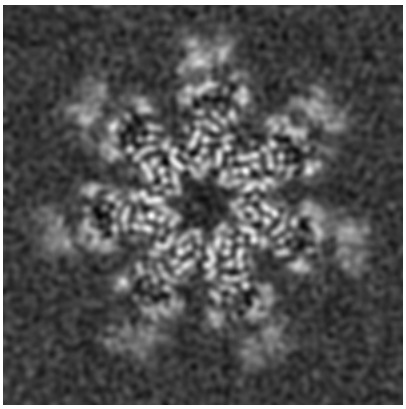
6.3.1 Primary map



X Index: 131



Y Index: 140

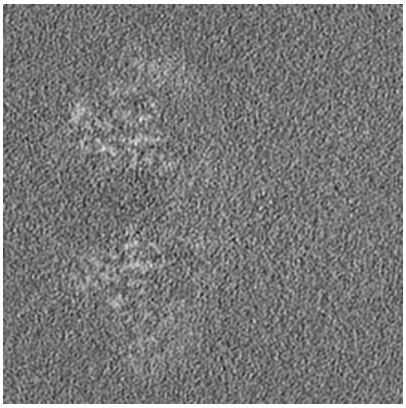


Z Index: 69

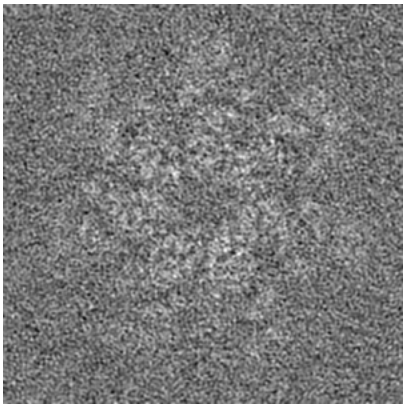
6.3.2 Raw map



X Index: 116



Y Index: 101

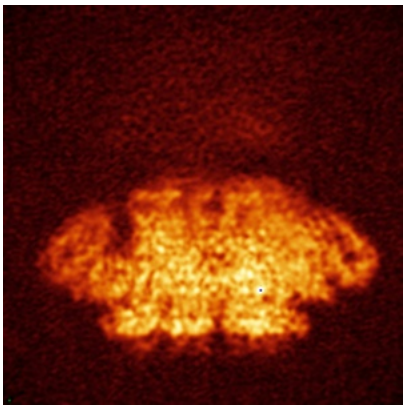


Z Index: 70

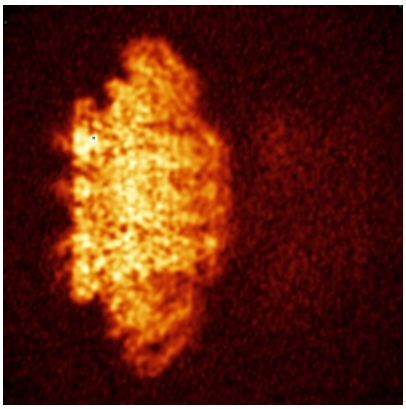
The images above show the largest variance slices of the map in three orthogonal directions.

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

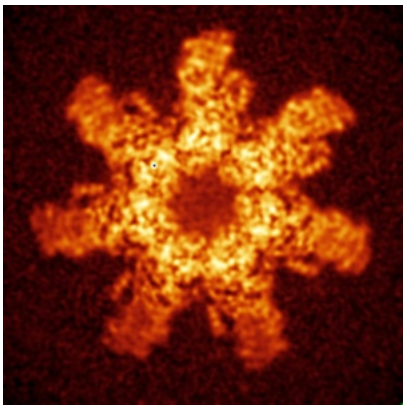
6.4.1 Primary map



X

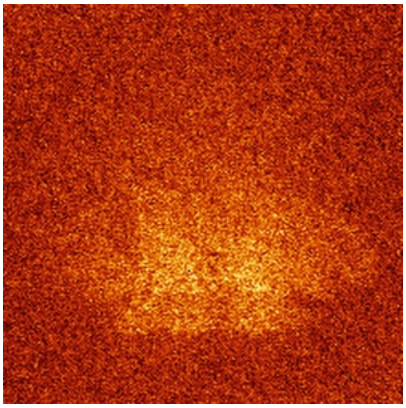


Y

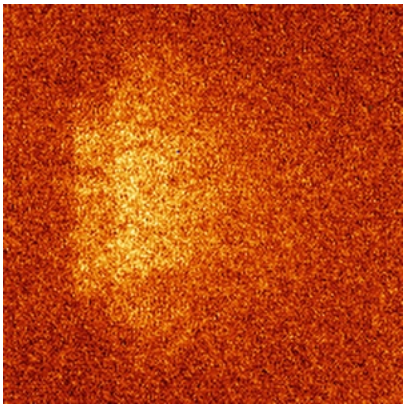


Z

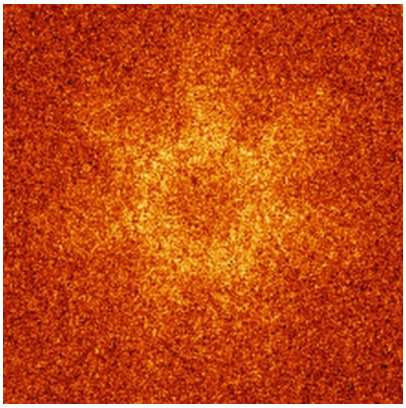
6.4.2 Raw map



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 0.182. 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.

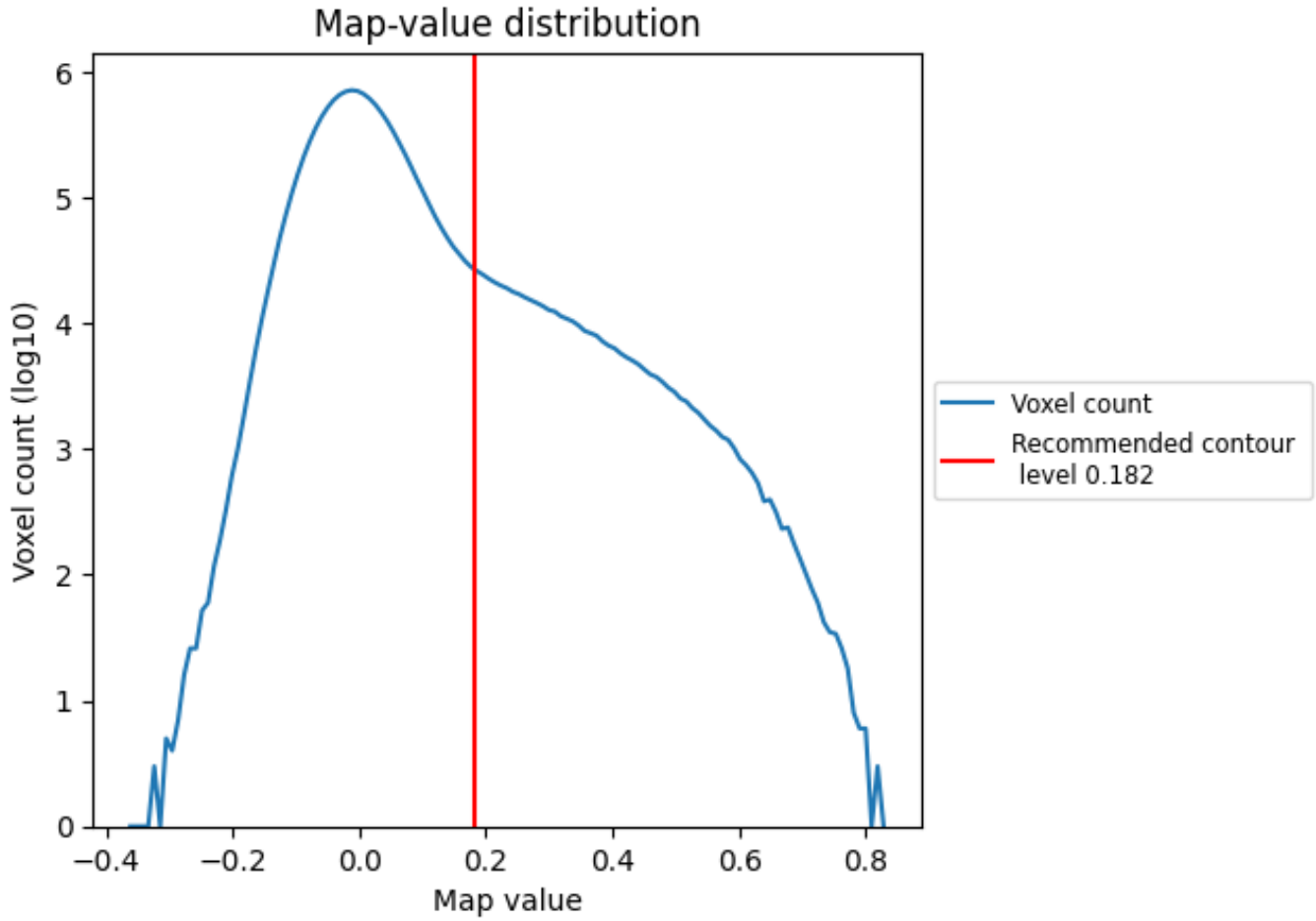
6.6 Mask visualisation (i)

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

7 Map analysis

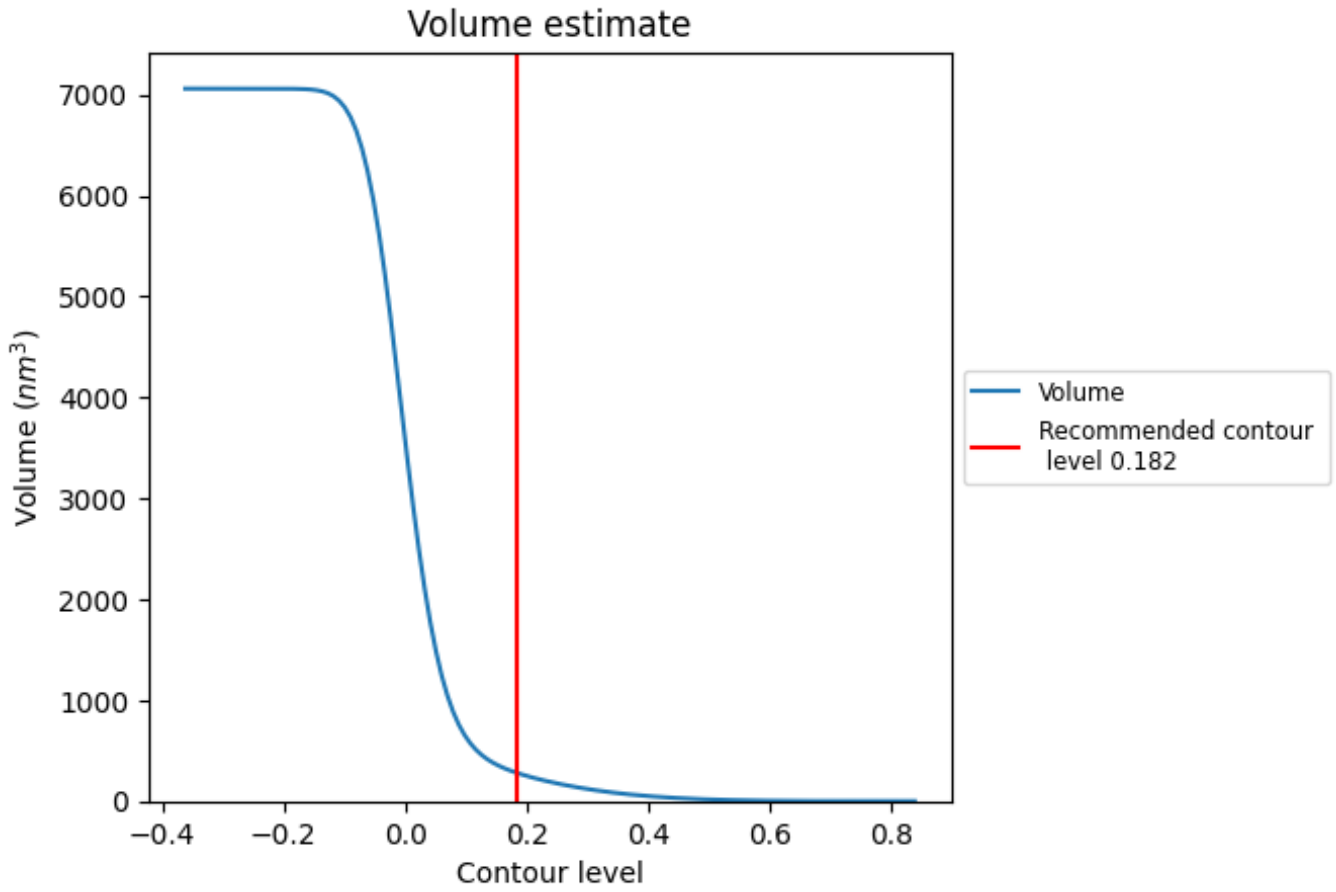
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

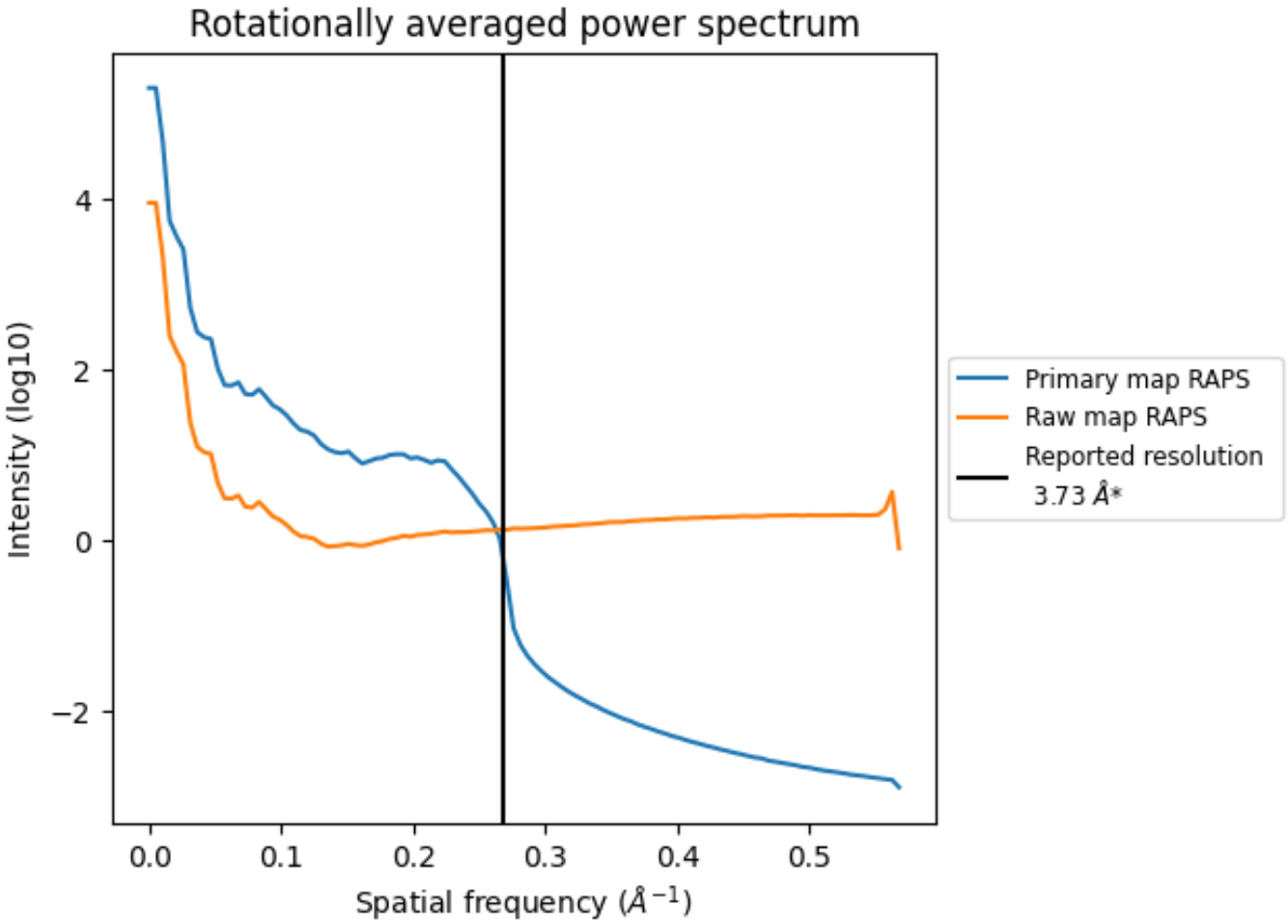
7.2 Volume estimate



The volume at the recommended contour level is 283 nm^3; this corresponds to an approximate mass of 256 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)

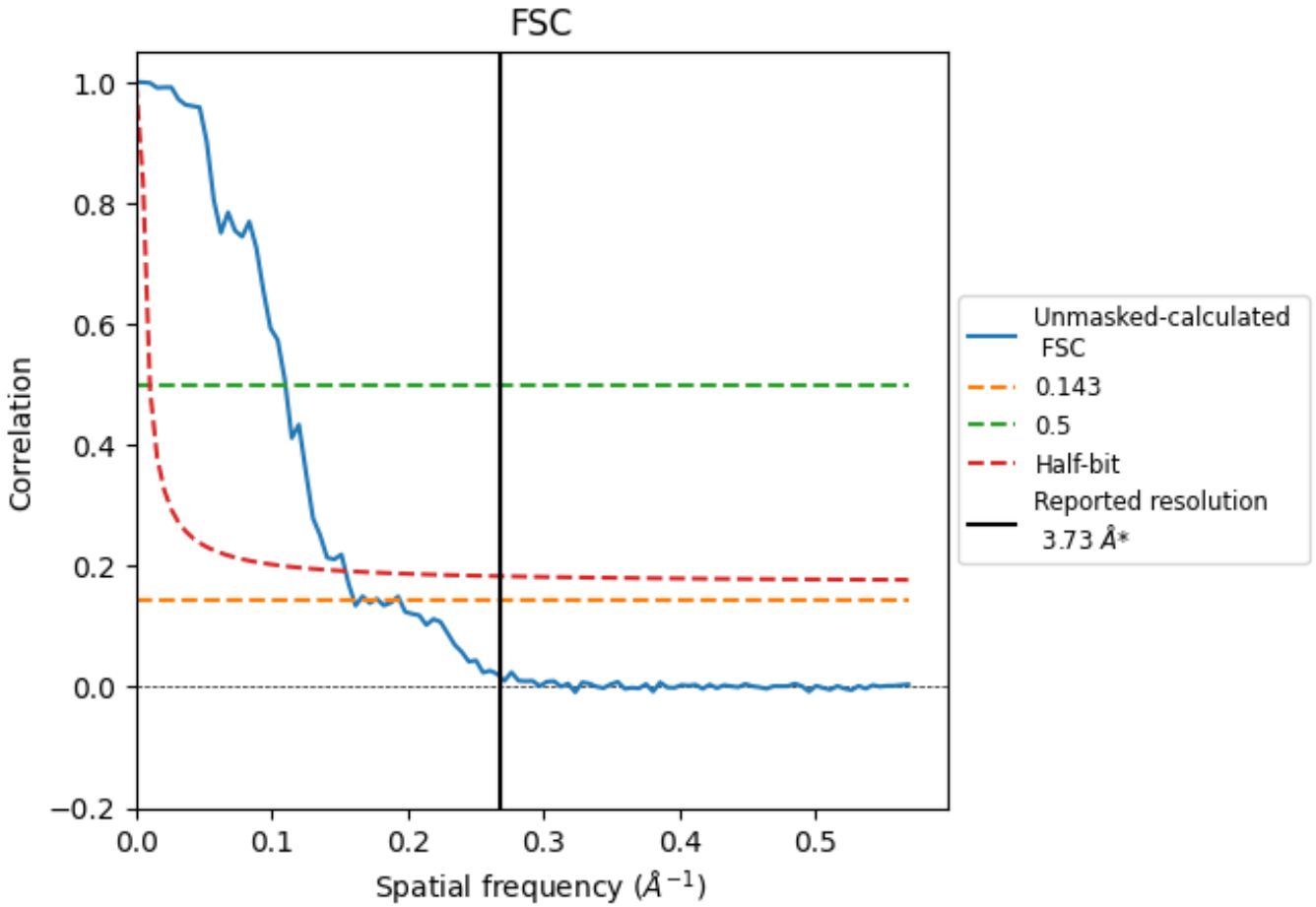


*Reported resolution corresponds to spatial frequency of 0.268 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.268 Å^{-1}

8.2 Resolution estimates (i)

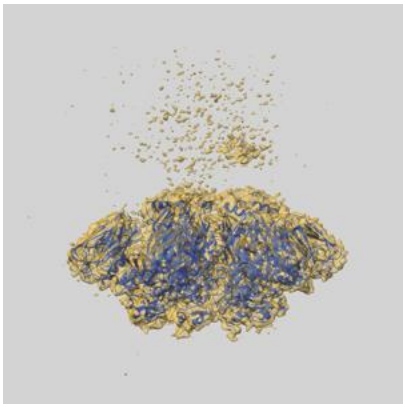
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.73	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.23	9.10	6.49

*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 6.23 differs from the reported value 3.73 by more than 10 %

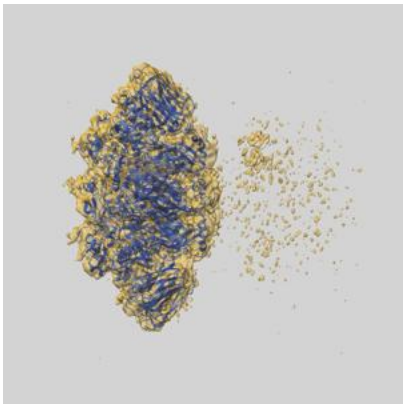
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-61777 and PDB model 9JSM. Per-residue inclusion information can be found in section 3 on page 5.

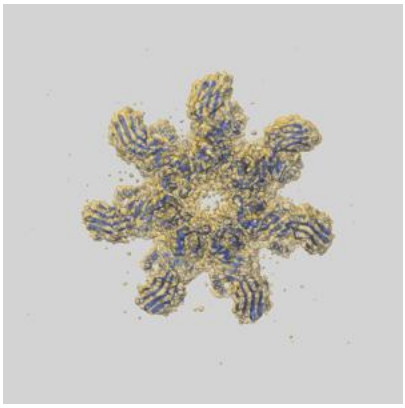
9.1 Map-model overlay



X



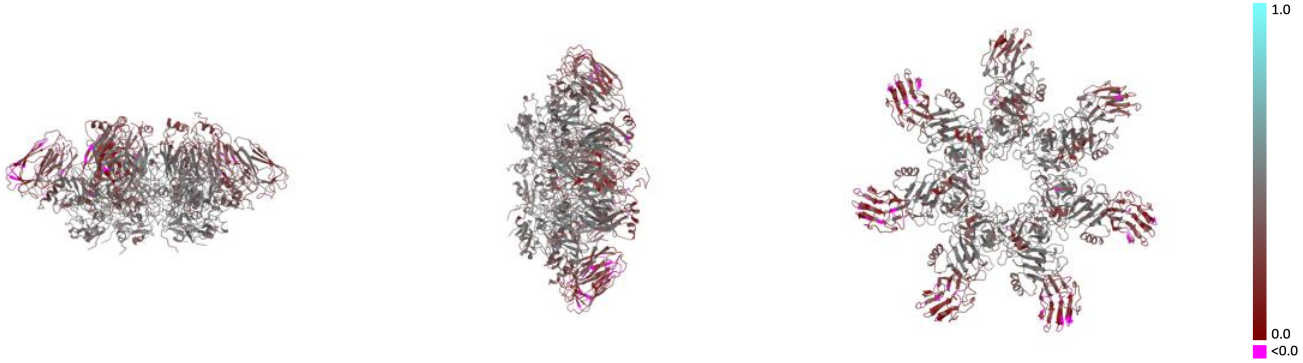
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.182 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.

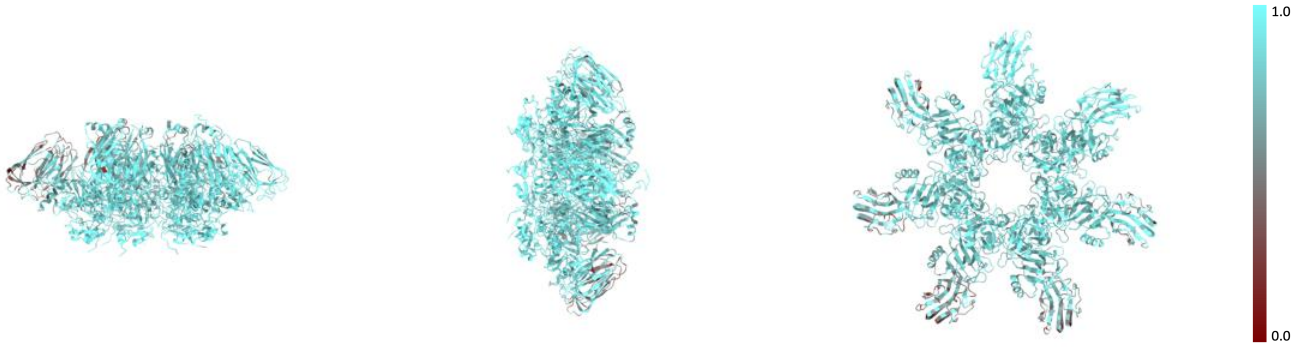
9.2 Q-score mapped to coordinate model



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.

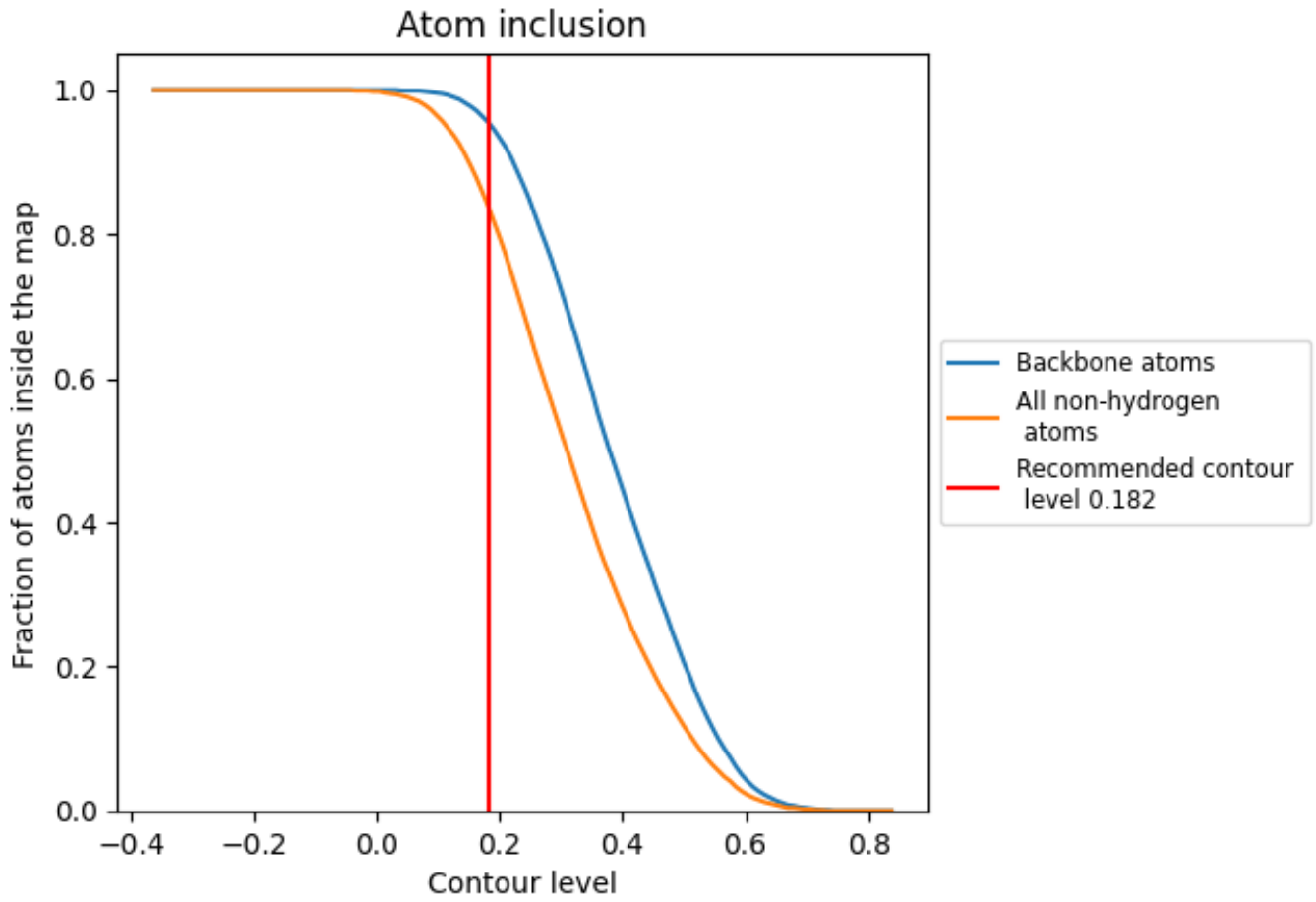
9.3 Atom inclusion mapped to coordinate model



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 (0.182).

9.4 Atom inclusion (i)



At the recommended contour level, 96% of all backbone atoms, 84% 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 (0.182) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8380	0.3750
A	0.8410	0.3670
B	0.8060	0.3550
C	0.7710	0.3680
D	0.8030	0.3670
E	0.8540	0.3690
F	0.8870	0.3980
G	0.8960	0.3990

