



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 12:59 AM UTC

PDB ID : 8ZPV / pdb_00008zpv
EMDB ID : EMD-60355
Title : Nipah virus polymerase complex
Authors : Wang, Y.R.; Zhang, H.Q.
Deposited on : 2024-05-31
Resolution : 2.90 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
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

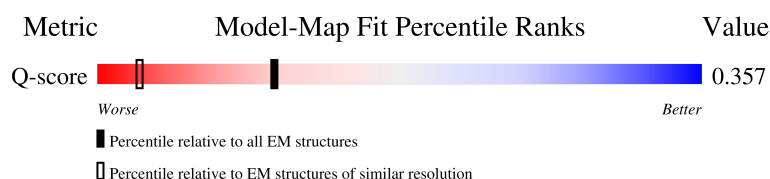
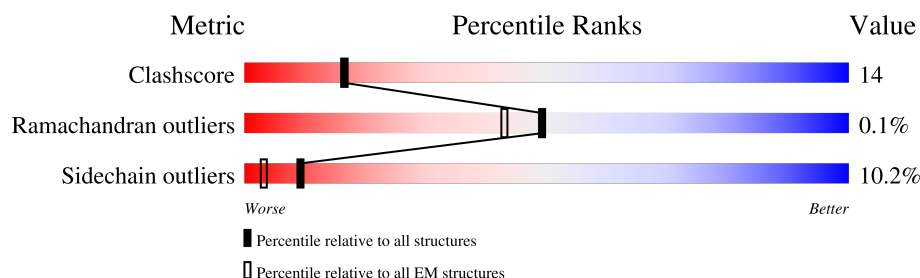
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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	13054 (2.40 - 3.40)

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	2244	
2	B	709	
2	C	709	
2	D	709	

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Mol	Chain	Length	Quality of chain
2	E	709	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12440 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1275	Total	C	N	O	S	0	0
			10260	6533	1758	1903	66		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	581	THR	GLU	conflict	UNP Q997F0

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	51	Total	C	N	O	S	0	0
			400	252	70	77	1		
2	C	54	Total	C	N	O	S	0	0
			425	269	75	80	1		
2	D	117	Total	C	N	O	S	0	0
			922	573	161	183	5		
2	E	55	Total	C	N	O	S	0	0
			431	272	76	82	1		

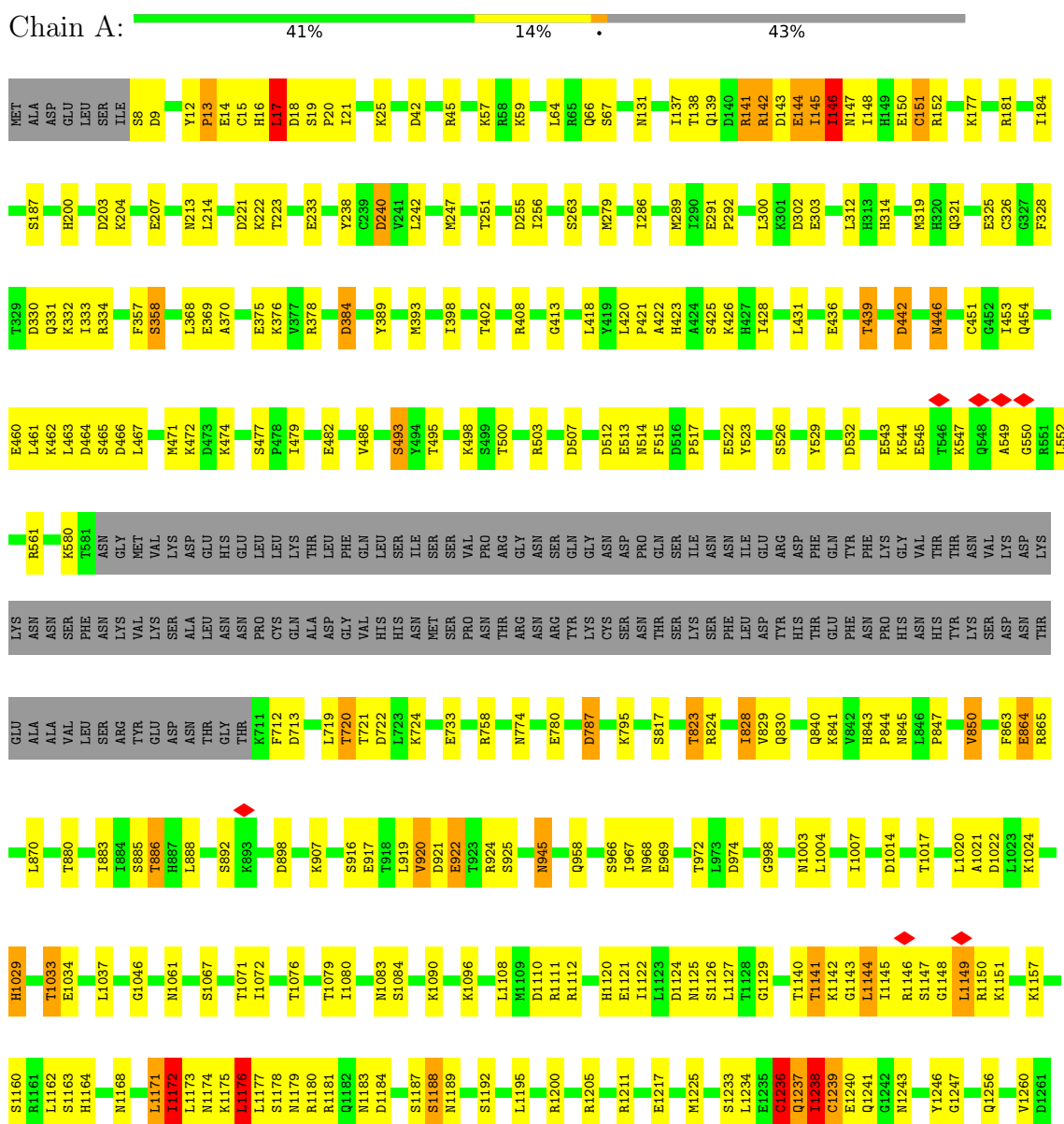
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	

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: RNA-directed RNA polymerase L





- Molecule 2: Phosphoprotein

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	523611	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.364	Depositor
Minimum map value	-0.523	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.042	Depositor
Recommended contour level	0.178	Depositor
Map size (Å)	270.004, 270.004, 270.004	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9643, 0.9643, 0.9643	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: ZN

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	0.50	14/10470 (0.1%)	0.54	19/14152 (0.1%)
2	B	0.21	0/401	0.59	0/539
2	C	0.21	0/427	0.60	0/575
2	D	0.18	0/926	0.47	0/1245
2	E	0.19	0/433	0.56	0/583
All	All	0.46	14/12657 (0.1%)	0.54	19/17094 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
2	B	0	1
All	All	0	6

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	13	PRO	N-CA	18.33	1.68	1.47
1	A	1175	LYS	C-O	-16.00	1.05	1.24
1	A	1176	LEU	C-O	-15.49	1.05	1.24
1	A	1172	ILE	C-O	-12.08	1.10	1.24
1	A	1171	LEU	C-O	-10.27	1.12	1.24
1	A	1173	LEU	C-O	-10.14	1.12	1.24
1	A	1174	ASN	C-O	-9.98	1.12	1.24
1	A	12	TYR	C-N	9.92	1.45	1.33
1	A	1178	SER	C-O	-8.12	1.12	1.24
1	A	1179	ASN	C-O	-7.42	1.14	1.23
1	A	1177	LEU	C-O	-7.16	1.14	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1178	SER	CA-CB	-7.11	1.42	1.53
1	A	1181	ARG	C-O	-6.61	1.15	1.23
1	A	1180	ARG	C-O	-5.79	1.16	1.24

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	12	TYR	CA-C-N	17.56	138.72	119.93
1	A	12	TYR	C-N-CA	17.56	138.72	119.93
1	A	13	PRO	N-CA-C	-9.50	95.78	111.26
1	A	1175	LYS	CA-C-O	-8.32	111.73	120.55
1	A	13	PRO	CA-N-CD	-7.46	101.55	112.00
1	A	1174	ASN	CB-CA-C	-7.41	98.25	110.85
1	A	1176	LEU	CA-C-O	-7.14	112.98	120.55
1	A	1172	ILE	CA-C-O	-6.97	113.70	120.95
1	A	1180	ARG	CB-CA-C	-6.21	99.19	109.99
1	A	1181	ARG	CA-C-O	-6.12	115.07	121.55
1	A	1180	ARG	CB-CG-CD	-5.91	97.70	111.30
1	A	1181	ARG	CB-CG-CD	5.86	124.77	111.30
1	A	1236	CYS	CA-C-N	5.85	132.72	121.54
1	A	1236	CYS	C-N-CA	5.85	132.72	121.54
1	A	1178	SER	CA-C-N	5.75	129.96	120.94
1	A	1178	SER	C-N-CA	5.75	129.96	120.94
1	A	17	LEU	CA-C-N	-5.66	115.39	123.20
1	A	17	LEU	C-N-CA	-5.66	115.39	123.20
1	A	1324	GLN	N-CA-C	-5.44	107.65	114.56

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1172	ILE	Mainchain
1	A	1237	GLN	Peptide
1	A	1238	ILE	Peptide
1	A	145	ILE	Peptide
1	A	828	ILE	Peptide
2	B	536	ILE	Peptide

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	10260	0	10301	226	0
2	B	400	0	433	40	0
2	C	425	0	460	34	0
2	D	922	0	959	55	0
2	E	431	0	465	38	0
3	A	2	0	0	0	0
All	All	12440	0	12618	354	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 (354) 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:13:PRO:N	1:A:13:PRO:CA	1.68	1.47
1:A:1236:CYS:HB3	1:A:1239:CYS:HA	1.49	0.93
1:A:426:LYS:H	1:A:426:LYS:CE	1.90	0.85
2:C:532:ARG:HG3	2:D:533:LEU:HD23	1.57	0.85
2:C:543:ILE:HG13	2:C:544:PRO:HD3	1.58	0.85
1:A:145:ILE:O	1:A:147:ASN:N	2.09	0.85
1:A:291:GLU:HG2	1:A:292:PRO:HD3	1.62	0.81
1:A:13:PRO:N	1:A:13:PRO:C	2.38	0.80
1:A:14:GLU:N	1:A:14:GLU:OE2	2.16	0.78
2:B:527:ILE:HG13	2:E:525:LYS:HE3	1.67	0.77
2:B:557:LEU:O	2:B:561:ASN:HB2	1.83	0.77
2:B:556:VAL:O	2:B:560:THR:OG1	2.03	0.76
1:A:421:PRO:HB3	2:B:559:LYS:HE3	1.68	0.76
1:A:426:LYS:H	1:A:426:LYS:HE2	1.52	0.75
1:A:1378:ASP:H	1:A:1380:ARG:HG3	1.51	0.75
2:B:530:ASP:O	2:E:532:ARG:NH2	2.20	0.74
1:A:1238:ILE:H	1:A:1240:GLU:H	1.34	0.74
2:D:532:ARG:NH2	2:E:537:GLU:OE2	2.21	0.73
1:A:545:GLU:HG3	1:A:550:GLY:HA2	1.69	0.73
1:A:16:HIS:CE1	1:A:916:SER:HB3	2.25	0.72
1:A:17:LEU:C	1:A:17:LEU:HD22	2.14	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:691:ASP:OD1	2:D:691:ASP:N	2.20	0.72
2:C:553:ILE:HA	2:C:556:VAL:HG12	1.72	0.72
2:E:547:ILE:HA	2:E:550:LEU:HD12	1.70	0.71
2:D:532:ARG:NH1	2:E:533:LEU:O	2.20	0.71
1:A:141:ARG:NH1	1:A:144:GLU:O	2.24	0.71
2:D:701:VAL:O	2:D:705:ILE:HG12	1.91	0.71
1:A:255:ASP:OD1	1:A:256:ILE:N	2.25	0.70
1:A:463:LEU:HD13	1:A:517:PRO:HB2	1.73	0.69
1:A:1176:LEU:HD23	1:A:1176:LEU:O	1.92	0.69
1:A:145:ILE:HD12	1:A:145:ILE:H	1.60	0.67
1:A:422:ALA:H	2:B:559:LYS:HZ1	1.41	0.66
2:D:547:ILE:HD13	2:D:550:LEU:HD21	1.76	0.66
2:B:551:GLU:O	2:B:555:ARG:CB	2.43	0.66
1:A:375:GLU:OE2	1:A:378:ARG:NH1	2.29	0.66
1:A:924:ARG:NH2	1:A:998:GLY:O	2.29	0.66
1:A:312:LEU:HD23	2:D:663:VAL:HG23	1.79	0.65
1:A:1238:ILE:HB	1:A:1241:GLN:H	1.60	0.65
2:B:551:GLU:O	2:B:555:ARG:HB2	1.96	0.65
2:D:672:ILE:O	2:D:678:ARG:NH1	2.30	0.65
2:D:548:ASN:HA	2:D:551:GLU:HG3	1.79	0.65
2:C:547:ILE:HA	2:C:550:LEU:HD12	1.78	0.65
1:A:17:LEU:HD13	1:A:17:LEU:O	1.97	0.64
2:D:655:MET:SD	2:D:655:MET:N	2.71	0.64
1:A:921:ASP:OD2	1:A:968:ASN:ND2	2.31	0.64
1:A:1112:ARG:HH22	1:A:1437:GLY:HA3	1.62	0.64
1:A:442:ASP:O	1:A:446:ASN:ND2	2.31	0.64
2:D:532:ARG:HE	2:D:535:HIS:HE1	1.44	0.64
1:A:1291:THR:HA	1:A:1295:ARG:HE	1.63	0.63
1:A:1334:LYS:NZ	1:A:1336:ILE:O	2.24	0.63
1:A:8:SER:HB2	1:A:1150:ARG:HH11	1.63	0.63
1:A:795:LYS:NZ	2:C:570:HIS:O	2.24	0.62
2:D:566:THR:HG23	2:D:567:ILE:HG12	1.81	0.62
1:A:1410:ARG:NH1	1:A:1414:ASP:OD1	2.33	0.62
1:A:462:LYS:H	1:A:462:LYS:HD2	1.64	0.61
2:C:555:ARG:NE	2:C:555:ARG:HA	2.15	0.61
1:A:474:LYS:HZ1	1:A:561:ARG:HD2	1.66	0.61
1:A:1126:SER:OG	1:A:1127:LEU:N	2.32	0.61
1:A:1168:ASN:O	1:A:1172:ILE:HG13	2.00	0.60
2:B:536:ILE:HG23	2:C:540:VAL:HG21	1.82	0.60
1:A:8:SER:HB3	1:A:1149:LEU:HD21	1.84	0.60
1:A:240:ASP:OD1	1:A:240:ASP:N	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1046:GLY:O	1:A:1061:ASN:ND2	2.35	0.60
1:A:137:ILE:HG21	1:A:1402:VAL:HG21	1.83	0.59
2:C:522:ASN:O	2:C:526:LEU:HG	2.02	0.59
1:A:522:GLU:O	1:A:526:SER:OG	2.18	0.59
2:E:544:PRO:HA	2:E:547:ILE:HD11	1.85	0.59
1:A:823:THR:OG1	1:A:824:ARG:N	2.36	0.59
1:A:42:ASP:OD1	1:A:42:ASP:N	2.35	0.58
2:D:544:PRO:HA	2:D:547:ILE:HB	1.86	0.58
1:A:358:SER:HB3	1:A:907:LYS:HB2	1.86	0.58
1:A:1084:SER:O	1:A:1090:LYS:NZ	2.37	0.57
1:A:19:SER:HB2	1:A:20:PRO:HD2	1.87	0.57
1:A:828:ILE:HG22	1:A:829:VAL:H	1.70	0.56
1:A:145:ILE:HG22	1:A:146:ILE:H	1.69	0.56
1:A:376:LYS:HD3	1:A:549:ALA:HB1	1.86	0.56
2:D:539:GLN:NE2	2:E:540:VAL:O	2.36	0.56
1:A:147:ASN:O	1:A:150:GLU:N	2.39	0.56
1:A:898:ASP:O	1:A:1368:ARG:NH1	2.38	0.56
2:D:546:ILE:HG12	2:E:547:ILE:HD13	1.88	0.56
1:A:1111:ARG:HD3	1:A:1440:ASP:O	2.05	0.56
2:B:525:LYS:HZ1	2:C:526:LEU:HD13	1.71	0.55
1:A:330:ASP:OD2	1:A:333:ILE:N	2.33	0.55
1:A:1037:LEU:HD22	1:A:1187:SER:HB3	1.88	0.55
1:A:1364:ASN:N	1:A:1364:ASN:OD1	2.39	0.55
2:D:678:ARG:O	2:D:682:ILE:HD12	2.06	0.55
1:A:16:HIS:HE1	1:A:916:SER:HB3	1.72	0.55
1:A:302:ASP:OD1	1:A:303:GLU:N	2.36	0.55
2:D:660:SER:HA	2:D:663:VAL:HG12	1.89	0.55
1:A:16:HIS:ND1	1:A:916:SER:HA	2.22	0.55
2:C:546:ILE:O	2:C:549:LYS:HG3	2.06	0.55
2:C:544:PRO:HA	2:C:547:ILE:HG13	1.89	0.55
2:C:519:GLY:O	2:C:523:SER:OG	2.25	0.55
2:B:525:LYS:O	2:B:529:LEU:HG	2.07	0.55
1:A:184:ILE:O	1:A:187:SER:OG	2.25	0.54
1:A:439:THR:OG1	1:A:442:ASP:OD1	2.21	0.54
2:C:533:LEU:HD23	2:C:533:LEU:H	1.71	0.54
2:E:528:ASN:O	2:E:532:ARG:HD3	2.07	0.54
1:A:131:ASN:HD22	1:A:1029:HIS:HE1	1.56	0.54
1:A:513:GLU:N	1:A:513:GLU:OE1	2.40	0.54
2:D:543:ILE:O	2:D:546:ILE:HG13	2.08	0.54
2:B:546:ILE:HG12	2:C:547:ILE:HD13	1.89	0.54
1:A:442:ASP:OD1	1:A:442:ASP:N	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:378:ARG:NH2	1:A:787:ASP:O	2.40	0.54
1:A:460:GLU:OE1	1:A:462:LYS:NZ	2.35	0.54
1:A:431:LEU:HD11	1:A:436:GLU:HB2	1.89	0.53
1:A:1148:GLY:HA2	1:A:1151:LYS:HG2	1.91	0.53
2:D:559:LYS:HA	2:D:562:THR:HG22	1.90	0.53
1:A:1121:GLU:OE1	1:A:1299:ARG:NH1	2.36	0.53
1:A:369:GLU:OE1	1:A:370:ALA:N	2.41	0.53
2:E:551:GLU:N	2:E:551:GLU:OE1	2.39	0.53
1:A:8:SER:HB2	1:A:1150:ARG:NH1	2.24	0.53
1:A:780:GLU:OE1	1:A:780:GLU:N	2.39	0.53
2:B:539:GLN:HG3	2:C:541:LYS:NZ	2.23	0.53
2:E:526:LEU:HA	2:E:529:LEU:HG	1.90	0.53
2:B:536:ILE:HD11	2:C:537:GLU:HA	1.91	0.52
2:B:546:ILE:HD12	2:B:549:LYS:HG2	1.91	0.52
1:A:1176:LEU:HD23	1:A:1176:LEU:C	2.33	0.52
1:A:150:GLU:OE2	1:A:945:ASN:ND2	2.43	0.52
1:A:503:ARG:NH1	1:A:507:ASP:OD1	2.41	0.52
1:A:580:LYS:HA	1:A:830:GLN:HG2	1.90	0.52
1:A:1110:ASP:OD1	1:A:1211:ARG:NH1	2.34	0.52
1:A:1176:LEU:C	1:A:1176:LEU:CD2	2.83	0.52
1:A:840:GLN:NE2	1:A:841:LYS:O	2.43	0.52
1:A:1387:ASP:N	1:A:1387:ASP:OD1	2.43	0.52
2:B:523:SER:O	2:B:527:ILE:HD12	2.10	0.52
1:A:423:HIS:CE1	2:B:555:ARG:HA	2.45	0.52
2:D:695:GLN:O	2:D:699:ASN:ND2	2.43	0.52
1:A:247:MET:O	1:A:251:THR:HG22	2.10	0.51
1:A:919:LEU:O	1:A:921:ASP:N	2.43	0.51
1:A:1188:SER:OG	1:A:1189:ASN:N	2.43	0.51
2:C:550:LEU:HD21	2:D:550:LEU:HD13	1.91	0.51
1:A:203:ASP:OD1	1:A:204:LYS:N	2.41	0.51
1:A:465:SER:O	1:A:465:SER:OG	2.26	0.51
2:C:546:ILE:HD12	2:C:547:ILE:N	2.26	0.51
1:A:466:ASP:OD1	1:A:467:LEU:N	2.43	0.51
1:A:1341:THR:OG1	1:A:1342:SER:N	2.40	0.51
1:A:1380:ARG:HA	1:A:1385:LYS:HA	1.92	0.51
1:A:885:SER:OG	1:A:886:THR:N	2.44	0.51
2:E:552:SER:HA	2:E:555:ARG:NH2	2.26	0.51
1:A:512:ASP:OD1	1:A:515:PHE:N	2.44	0.51
2:B:553:ILE:HD12	2:E:553:ILE:HD11	1.93	0.51
2:C:553:ILE:HD12	2:D:553:ILE:HB	1.93	0.51
2:D:546:ILE:HD13	2:E:547:ILE:HB	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1144:LEU:O	1:A:1147:SER:OG	2.29	0.50
1:A:1243:ASN:CG	1:A:1425:LYS:HB3	2.36	0.50
2:B:557:LEU:HD21	2:C:557:LEU:HD13	1.93	0.50
1:A:1323:SER:O	1:A:1448:TYR:OH	2.29	0.50
2:D:555:ARG:O	2:D:559:LYS:NZ	2.41	0.50
1:A:529:TYR:O	1:A:758:ARG:NH1	2.43	0.50
1:A:733:GLU:OE2	1:A:733:GLU:N	2.44	0.50
1:A:479:ILE:HG12	1:A:482:GLU:HG2	1.94	0.50
1:A:1436:VAL:O	1:A:1438:GLN:HG2	2.10	0.50
1:A:1376:ASN:OD1	1:A:1377:LEU:N	2.44	0.49
1:A:1436:VAL:HG22	1:A:1437:GLY:H	1.77	0.49
1:A:142:ARG:H	1:A:142:ARG:HD3	1.78	0.49
1:A:787:ASP:OD1	1:A:787:ASP:N	2.38	0.49
1:A:1311:ASN:OD1	1:A:1312:GLU:N	2.45	0.49
1:A:57:LYS:O	1:A:59:LYS:NZ	2.33	0.49
1:A:493:SER:O	1:A:493:SER:OG	2.28	0.49
2:D:697:ILE:HA	2:D:700:THR:HG22	1.94	0.49
1:A:15:CYS:HB2	1:A:177:LYS:HE3	1.95	0.49
1:A:1096:LYS:H	1:A:1096:LYS:HD3	1.77	0.49
2:E:542:GLU:HA	2:E:545:LYS:NZ	2.28	0.49
1:A:1238:ILE:O	1:A:1239:CYS:HB2	2.13	0.48
2:B:543:ILE:O	2:B:547:ILE:HG12	2.13	0.48
1:A:286:ILE:HD12	1:A:319:MET:HE3	1.95	0.48
2:D:668:ILE:O	2:D:672:ILE:HG13	2.13	0.48
1:A:1124:ASP:O	1:A:1129:GLY:HA3	2.13	0.48
2:B:539:GLN:HE21	2:C:541:LYS:HD2	1.78	0.48
1:A:1238:ILE:HD12	1:A:1241:GLN:HA	1.95	0.48
2:B:548:ASN:C	2:B:550:LEU:H	2.22	0.48
1:A:200:HIS:NE2	1:A:207:GLU:OE2	2.41	0.48
1:A:1033:THR:OG1	1:A:1034:GLU:N	2.46	0.48
2:D:542:GLU:OE1	2:D:545:LYS:NZ	2.36	0.48
1:A:421:PRO:HA	2:B:559:LYS:HZ2	1.78	0.48
2:C:549:LYS:O	2:C:553:ILE:HG12	2.14	0.48
2:E:528:ASN:O	2:E:531:MET:HG3	2.13	0.48
1:A:408:ARG:HG2	1:A:413:GLY:HA2	1.96	0.48
1:A:25:LYS:NZ	1:A:233:GLU:OE1	2.47	0.48
1:A:328:PHE:O	1:A:334:ARG:NH1	2.45	0.48
2:B:552:SER:OG	2:C:554:ASP:OD2	2.30	0.48
1:A:151:CYS:SG	1:A:152:ARG:N	2.87	0.47
1:A:426:LYS:HE2	1:A:426:LYS:N	2.24	0.47
1:A:16:HIS:CE1	1:A:916:SER:CB	2.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:843:HIS:ND1	1:A:845:ASN:OD1	2.47	0.47
1:A:389:TYR:CZ	1:A:393:MET:HG3	2.49	0.47
1:A:886:THR:O	1:A:886:THR:OG1	2.29	0.47
1:A:1112:ARG:NH2	1:A:1437:GLY:HA3	2.28	0.47
2:D:521:ILE:HG13	2:D:522:ASN:H	1.79	0.47
2:D:548:ASN:O	2:D:551:GLU:HG3	2.14	0.47
2:E:543:ILE:HG13	2:E:544:PRO:HD3	1.97	0.47
1:A:1014:ASP:OD2	1:A:1017:THR:OG1	2.28	0.47
1:A:1237:GLN:O	1:A:1238:ILE:HG12	2.14	0.47
2:D:695:GLN:HG3	2:D:699:ASN:HD21	1.79	0.47
1:A:423:HIS:CG	2:B:555:ARG:HA	2.50	0.47
2:B:551:GLU:O	2:B:555:ARG:HB3	2.13	0.47
1:A:972:THR:OG1	1:A:974:ASP:OD1	2.29	0.47
2:D:534:ASN:O	2:D:537:GLU:HG3	2.14	0.47
1:A:829:VAL:HG23	1:A:830:GLN:H	1.79	0.47
2:C:555:ARG:HA	2:C:555:ARG:HE	1.78	0.47
1:A:1323:SER:O	1:A:1323:SER:OG	2.28	0.46
2:C:521:ILE:O	2:C:524:ILE:HG13	2.15	0.46
1:A:1183:ASN:OD1	1:A:1184:ASP:N	2.41	0.46
2:D:532:ARG:HA	2:D:535:HIS:ND1	2.29	0.46
2:D:676:GLU:OE1	2:D:677:LEU:N	2.34	0.46
1:A:142:ARG:HE	1:A:143:ASP:H	1.62	0.46
1:A:1021:ALA:O	1:A:1024:LYS:HG2	2.15	0.46
1:A:1200:ARG:NH1	1:A:1217:GLU:OE2	2.49	0.46
2:D:520:VAL:HA	2:D:523:SER:HB2	1.97	0.46
1:A:291:GLU:H	1:A:291:GLU:CD	2.24	0.46
1:A:319:MET:HE2	1:A:319:MET:HB3	1.78	0.46
2:B:525:LYS:HA	2:B:528:ASN:ND2	2.30	0.46
2:C:525:LYS:NZ	2:D:523:SER:HA	2.31	0.46
1:A:974:ASP:OD1	1:A:974:ASP:N	2.47	0.46
2:B:559:LYS:HA	2:B:562:THR:HG22	1.98	0.46
1:A:59:LYS:HB2	1:A:59:LYS:HE2	1.70	0.46
1:A:1374:ASN:HB3	1:A:1396:MET:HE2	1.97	0.46
2:D:547:ILE:HA	2:D:550:LEU:HG	1.98	0.46
2:E:523:SER:O	2:E:527:ILE:HG13	2.16	0.46
1:A:712:PHE:HD1	1:A:844:PRO:HD3	1.81	0.46
1:A:722:ASP:OD1	1:A:724:LYS:HG2	2.15	0.46
1:A:1067:SER:O	1:A:1071:THR:HG23	2.15	0.46
1:A:945:ASN:OD1	1:A:945:ASN:N	2.47	0.46
1:A:426:LYS:H	1:A:426:LYS:CD	2.28	0.45
2:D:537:GLU:HA	2:D:540:VAL:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:545:LYS:HA	2:B:548:ASN:OD1	2.16	0.45
1:A:181:ARG:HH12	1:A:920:VAL:HG21	1.81	0.45
1:A:1439:VAL:HG23	1:A:1440:ASP:H	1.82	0.45
2:B:525:LYS:HA	2:B:528:ASN:HD22	1.81	0.45
2:B:555:ARG:HG2	2:B:556:VAL:HG22	1.98	0.45
1:A:864:GLU:OE2	1:A:865:ARG:N	2.50	0.45
2:D:523:SER:O	2:D:527:ILE:HG12	2.17	0.45
1:A:712:PHE:CD1	1:A:844:PRO:HD3	2.51	0.45
1:A:1443:LEU:HD13	1:A:1444:PRO:HD2	1.98	0.45
1:A:1020:LEU:HD13	1:A:1195:LEU:HB3	1.99	0.45
2:C:541:LYS:O	2:C:544:PRO:HD2	2.16	0.45
1:A:1072:ILE:O	1:A:1076:THR:HG23	2.16	0.45
2:D:674:ASP:HB2	2:D:676:GLU:OE1	2.17	0.45
1:A:922:GLU:HB3	1:A:925:SER:OG	2.17	0.45
1:A:1096:LYS:HE2	1:A:1449:THR:HG21	1.99	0.45
1:A:1319:TRP:HA	1:A:1322:ALA:HB3	1.99	0.45
1:A:398:ILE:O	1:A:402:THR:HG22	2.17	0.45
1:A:1148:GLY:O	1:A:1151:LYS:HG2	2.17	0.45
1:A:1243:ASN:ND2	1:A:1425:LYS:HB3	2.32	0.45
2:B:524:ILE:HD12	2:B:525:LYS:H	1.81	0.44
2:D:662:ASP:O	2:D:666:THR:HG23	2.16	0.44
1:A:1435:ASP:OD1	1:A:1436:VAL:N	2.48	0.44
1:A:1120:HIS:C	1:A:1122:ILE:H	2.25	0.44
1:A:1327:ASN:ND2	1:A:1331:ASP:OD2	2.51	0.44
2:D:532:ARG:NH1	2:E:533:LEU:HD13	2.32	0.44
1:A:279:MET:HE3	1:A:326:CYS:SG	2.58	0.44
2:D:673:LYS:O	2:D:678:ARG:NH2	2.51	0.44
2:E:535:HIS:CD2	2:E:539:GLN:HE22	2.35	0.44
1:A:1157:LYS:HE3	1:A:1157:LYS:HB3	1.84	0.44
2:E:544:PRO:HA	2:E:547:ILE:CD1	2.47	0.44
1:A:18:ASP:HA	1:A:544:LYS:NZ	2.32	0.44
2:D:680:GLU:OE1	2:D:681:LEU:HG	2.17	0.44
1:A:331:GLN:HE21	1:A:332:LYS:HG2	1.83	0.44
1:A:20:PRO:HB2	1:A:368:LEU:HD12	2.00	0.43
1:A:384:ASP:OD1	1:A:384:ASP:N	2.49	0.43
1:A:547:LYS:HG3	1:A:550:GLY:H	1.83	0.43
2:E:537:GLU:HA	2:E:540:VAL:HG12	2.01	0.43
1:A:1142:LYS:HG2	1:A:1146:ARG:HH21	1.83	0.43
2:C:546:ILE:HD12	2:C:547:ILE:HG23	2.00	0.43
2:E:558:ALA:O	2:E:562:THR:HG22	2.18	0.43
2:E:568:GLU:HG2	2:E:570:HIS:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:HIS:ND1	1:A:880:THR:O	2.51	0.43
1:A:1312:GLU:HA	1:A:1315:TRP:HB2	2.01	0.43
1:A:1378:ASP:HB2	1:A:1385:LYS:HE3	2.00	0.43
2:D:697:ILE:O	2:D:701:VAL:HG12	2.19	0.43
1:A:17:LEU:HD22	1:A:17:LEU:O	2.18	0.43
1:A:958:GLN:O	1:A:958:GLN:NE2	2.49	0.43
2:B:526:LEU:HA	2:B:529:LEU:HD12	2.00	0.43
1:A:1188:SER:OG	1:A:1189:ASN:ND2	2.52	0.43
1:A:45:ARG:HG3	1:A:774:ASN:HA	1.99	0.43
1:A:523:TYR:OH	1:A:532:ASP:OD2	2.22	0.43
2:C:564:LEU:HD12	2:C:564:LEU:H	1.84	0.43
1:A:375:GLU:HA	1:A:378:ARG:NH1	2.33	0.43
1:A:425:SER:O	1:A:428:ILE:N	2.51	0.43
1:A:1076:THR:HA	1:A:1079:THR:HG22	2.01	0.42
2:B:539:GLN:HG3	2:C:541:LYS:HZ2	1.82	0.42
2:E:546:ILE:HA	2:E:549:LYS:HE3	2.00	0.42
1:A:16:HIS:CE1	1:A:916:SER:CA	3.02	0.42
1:A:233:GLU:OE2	1:A:233:GLU:N	2.50	0.42
1:A:289:MET:HB3	1:A:289:MET:HE3	1.76	0.42
1:A:1378:ASP:N	1:A:1380:ARG:HG3	2.28	0.42
2:E:520:VAL:HG23	2:E:521:ILE:H	1.84	0.42
1:A:131:ASN:HD22	1:A:1029:HIS:CE1	2.37	0.42
1:A:719:LEU:HD11	1:A:863:PHE:HB2	2.01	0.42
1:A:1090:LYS:HD3	1:A:1090:LYS:HA	1.79	0.42
2:D:693:GLU:O	2:D:697:ILE:HG22	2.20	0.42
1:A:1143:GLY:HA2	1:A:1146:ARG:HD2	2.01	0.42
1:A:1233:SER:O	1:A:1234:LEU:HD23	2.19	0.42
2:D:539:GLN:NE2	2:E:540:VAL:HG22	2.35	0.42
1:A:423:HIS:HB3	2:B:554:ASP:OD1	2.20	0.42
1:A:847:PRO:O	1:A:850:VAL:HG22	2.19	0.42
1:A:1172:ILE:O	1:A:1172:ILE:HG22	2.20	0.42
1:A:1225:MET:SD	1:A:1424:VAL:HG23	2.60	0.42
2:E:543:ILE:O	2:E:547:ILE:HG13	2.19	0.42
1:A:1325:ARG:HA	1:A:1325:ARG:HD2	1.79	0.42
1:A:1004:LEU:O	1:A:1007:ILE:HG12	2.19	0.42
1:A:1331:ASP:HB3	1:A:1333:LEU:HD13	2.00	0.42
1:A:66:GLN:HE21	1:A:213:ASN:HD22	1.67	0.42
1:A:426:LYS:H	1:A:426:LYS:NZ	2.15	0.42
1:A:467:LEU:O	1:A:471:MET:HG2	2.20	0.42
1:A:547:LYS:HE2	1:A:550:GLY:N	2.35	0.42
2:C:544:PRO:HA	2:C:547:ILE:CG1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:533:LEU:HD11	2:E:533:LEU:HD21	2.02	0.42
1:A:720:THR:HG23	1:A:883:ILE:HB	2.02	0.41
1:A:1332:VAL:HG23	1:A:1332:VAL:O	2.20	0.41
2:D:557:LEU:HA	2:D:560:THR:HG22	2.02	0.41
2:B:533:LEU:HB2	2:E:532:ARG:NH2	2.35	0.41
2:D:539:GLN:HE22	2:E:540:VAL:HG22	1.85	0.41
1:A:141:ARG:HE	1:A:141:ARG:H	1.67	0.41
1:A:1292:LYS:HG2	1:A:1294:LEU:H	1.83	0.41
2:D:682:ILE:O	2:D:686:ASN:ND2	2.44	0.41
2:E:541:LYS:HA	2:E:541:LYS:HD2	1.84	0.41
1:A:66:GLN:NE2	1:A:213:ASN:HD22	2.18	0.41
1:A:1163:SER:OG	1:A:1164:HIS:ND1	2.51	0.41
2:B:524:ILE:HD12	2:B:525:LYS:N	2.35	0.41
2:B:539:GLN:NE2	2:C:541:LYS:HD2	2.35	0.41
2:D:535:HIS:HA	2:D:538:GLU:HG3	2.03	0.41
1:A:17:LEU:O	1:A:17:LEU:CD1	2.68	0.41
1:A:1443:LEU:HD22	1:A:1444:PRO:HD2	2.03	0.41
2:D:532:ARG:HH11	2:E:533:LEU:HD13	1.85	0.41
2:D:677:LEU:HA	2:D:680:GLU:HG3	2.03	0.41
1:A:238:TYR:O	1:A:242:LEU:HD12	2.19	0.41
1:A:733:GLU:HB2	2:C:567:ILE:HD11	2.03	0.41
1:A:1262:ARG:HA	1:A:1264:HIS:CE1	2.56	0.41
2:D:571:LEU:HD12	2:D:571:LEU:HA	1.85	0.41
2:D:705:ILE:HG12	2:D:705:ILE:H	1.65	0.41
1:A:17:LEU:O	1:A:544:LYS:NZ	2.53	0.41
1:A:1246:TYR:HD2	1:A:1247:GLY:O	2.04	0.41
2:E:547:ILE:HG13	2:E:547:ILE:H	1.76	0.41
1:A:423:HIS:ND1	2:B:555:ARG:HA	2.35	0.41
1:A:425:SER:HA	1:A:426:LYS:NZ	2.36	0.41
1:A:870:LEU:HD23	1:A:870:LEU:HA	1.89	0.41
1:A:1319:TRP:HZ3	1:A:1333:LEU:HG	1.85	0.41
2:E:527:ILE:HD12	2:E:528:ASN:N	2.36	0.41
1:A:453:ILE:HG12	1:A:454:GLN:N	2.36	0.41
1:A:1141:THR:HG23	1:A:1144:LEU:HD23	2.03	0.41
1:A:321:GLN:NE2	1:A:325:GLU:OE1	2.38	0.40
1:A:1125:ASN:O	1:A:1325:ARG:NH2	2.54	0.40
2:E:554:ASP:OD1	2:E:555:ARG:N	2.55	0.40
1:A:1295:ARG:O	1:A:1298:ILE:HG13	2.21	0.40
2:B:534:ASN:H	2:E:532:ARG:HH22	1.69	0.40
1:A:1120:HIS:O	1:A:1121:GLU:HB3	2.20	0.40
2:C:538:GLU:OE1	2:C:539:GLN:HG2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:ASP:OD1	1:A:222:LYS:N	2.54	0.40
1:A:1384:GLU:H	1:A:1384:GLU:HG3	1.70	0.40
2:E:545:LYS:H	2:E:545:LYS:HD3	1.87	0.40
1:A:300:LEU:HA	1:A:300:LEU:HD23	1.81	0.40
1:A:420:LEU:HD23	1:A:420:LEU:HA	1.92	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	1267/2244 (56%)	1166 (92%)	99 (8%)	2 (0%)	43	72
2	B	49/709 (7%)	40 (82%)	9 (18%)	0	100	100
2	C	52/709 (7%)	45 (86%)	7 (14%)	0	100	100
2	D	113/709 (16%)	105 (93%)	8 (7%)	0	100	100
2	E	53/709 (8%)	50 (94%)	3 (6%)	0	100	100
All	All	1534/5080 (30%)	1406 (92%)	126 (8%)	2 (0%)	49	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	146	ILE
1	A	922	GLU

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	1144/2046 (56%)	1047 (92%)	97 (8%)	10	31
2	B	47/625 (8%)	35 (74%)	12 (26%)	0	2
2	C	50/625 (8%)	43 (86%)	7 (14%)	3	11
2	D	107/625 (17%)	86 (80%)	21 (20%)	1	5
2	E	51/625 (8%)	45 (88%)	6 (12%)	5	17
All	All	1399/4546 (31%)	1256 (90%)	143 (10%)	9	23

All (143) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ASP
1	A	17	LEU
1	A	21	ILE
1	A	64	LEU
1	A	67	SER
1	A	138	THR
1	A	139	GLN
1	A	141	ARG
1	A	142	ARG
1	A	144	GLU
1	A	146	ILE
1	A	148	ILE
1	A	151	CYS
1	A	214	LEU
1	A	223	THR
1	A	240	ASP
1	A	263	SER
1	A	357	PHE
1	A	358	SER
1	A	384	ASP
1	A	418	LEU
1	A	439	THR
1	A	442	ASP
1	A	446	ASN
1	A	451	CYS
1	A	461	LEU
1	A	464	ASP
1	A	472	LYS

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Mol	Chain	Res	Type
1	A	477	SER
1	A	486	VAL
1	A	493	SER
1	A	495	THR
1	A	498	LYS
1	A	500	THR
1	A	514	ASN
1	A	543	GLU
1	A	552	LEU
1	A	713	ASP
1	A	720	THR
1	A	721	THR
1	A	787	ASP
1	A	817	SER
1	A	823	THR
1	A	850	VAL
1	A	864	GLU
1	A	886	THR
1	A	888	LEU
1	A	892	SER
1	A	917	GLU
1	A	920	VAL
1	A	945	ASN
1	A	966	SER
1	A	967	ILE
1	A	969	GLU
1	A	1003	ASN
1	A	1022	ASP
1	A	1029	HIS
1	A	1033	THR
1	A	1080	ILE
1	A	1083	ASN
1	A	1108	LEU
1	A	1140	THR
1	A	1141	THR
1	A	1144	LEU
1	A	1145	ILE
1	A	1149	LEU
1	A	1160	SER
1	A	1162	LEU
1	A	1171	LEU
1	A	1176	LEU

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Continued from previous page...

Mol	Chain	Res	Type
1	A	1188	SER
1	A	1192	SER
1	A	1205	ARG
1	A	1236	CYS
1	A	1238	ILE
1	A	1239	CYS
1	A	1256	GLN
1	A	1260	VAL
1	A	1263	GLU
1	A	1265	SER
1	A	1294	LEU
1	A	1302	THR
1	A	1312	GLU
1	A	1314	CYS
1	A	1330	LEU
1	A	1336	ILE
1	A	1341	THR
1	A	1367	SER
1	A	1411	LEU
1	A	1413	THR
1	A	1425	LYS
1	A	1433	VAL
1	A	1439	VAL
1	A	1440	ASP
1	A	1443	LEU
1	A	1449	THR
1	A	1451	VAL
2	B	522	ASN
2	B	524	ILE
2	B	527	ILE
2	B	528	ASN
2	B	536	ILE
2	B	538	GLU
2	B	548	ASN
2	B	549	LYS
2	B	550	LEU
2	B	553	ILE
2	B	556	VAL
2	B	565	SER
2	C	520	VAL
2	C	521	ILE
2	C	533	LEU

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Mol	Chain	Res	Type
2	C	542	GLU
2	C	554	ASP
2	C	565	SER
2	C	570	HIS
2	D	533	LEU
2	D	551	GLU
2	D	555	ARG
2	D	560	THR
2	D	561	ASN
2	D	564	LEU
2	D	568	GLU
2	D	573	SER
2	D	576	ILE
2	D	578	ILE
2	D	655	MET
2	D	657	ASP
2	D	674	ASP
2	D	676	GLU
2	D	680	GLU
2	D	682	ILE
2	D	690	ASN
2	D	691	ASP
2	D	696	GLU
2	D	703	ASP
2	D	705	ILE
2	E	530	ASP
2	E	533	LEU
2	E	535	HIS
2	E	542	GLU
2	E	545	LYS
2	E	567	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	66	GLN
1	A	131	ASN
1	A	135	ASN
1	A	299	GLN
1	A	331	GLN
1	A	411	HIS

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Mol	Chain	Res	Type
1	A	446	ASN
1	A	536	ASN
1	A	929	ASN
1	A	951	ASN
1	A	1029	HIS
1	A	1038	GLN
1	A	1120	HIS
1	A	1169	GLN
1	A	1189	ASN
1	A	1256	GLN
1	A	1327	ASN
1	A	1394	GLN
1	A	1417	ASN
2	B	539	GLN
2	D	690	ASN
2	D	695	GLN
2	D	699	ASN
2	E	522	ASN
2	E	534	ASN

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 2 ligands modelled in this entry, 2 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

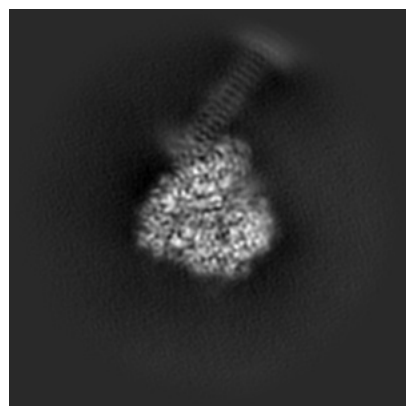
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60355. These allow visual inspection of the internal detail of the map and identification of artifacts.

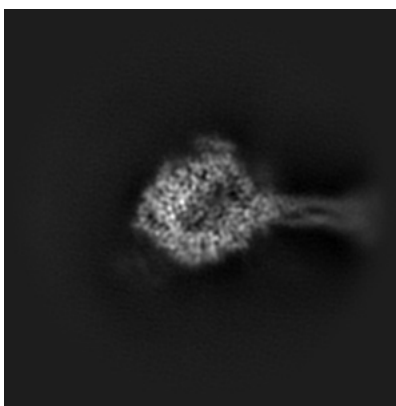
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

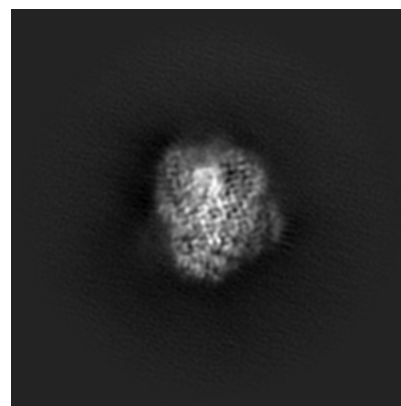
6.1.1 Primary map



X

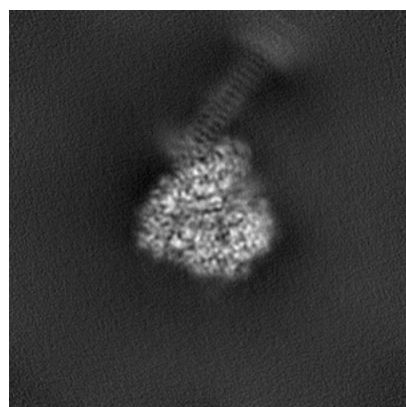


Y

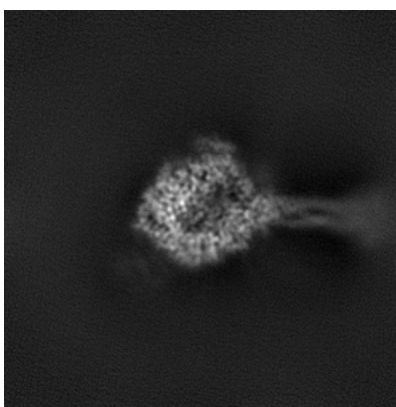


Z

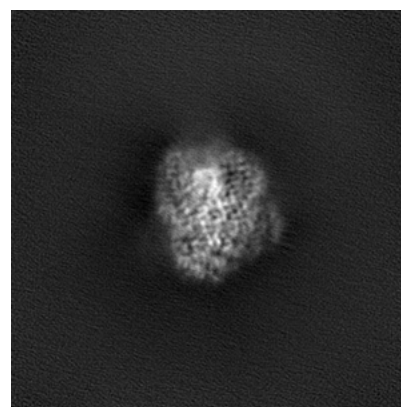
6.1.2 Raw map



X



Y

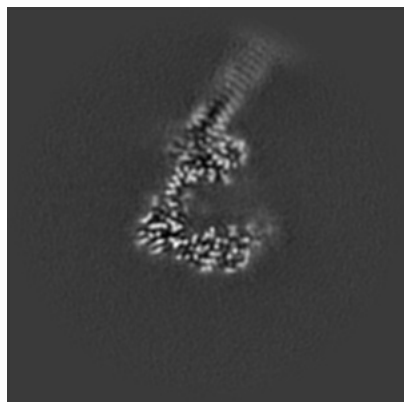


Z

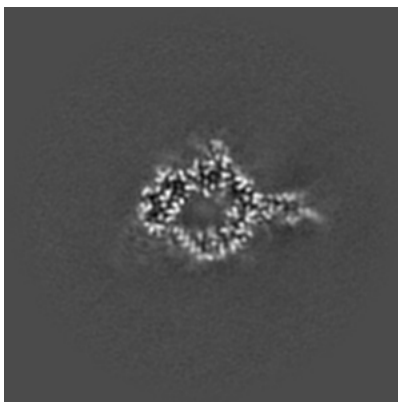
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

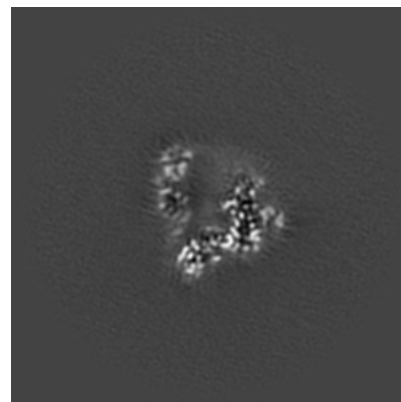
6.2.1 Primary map



X Index: 140

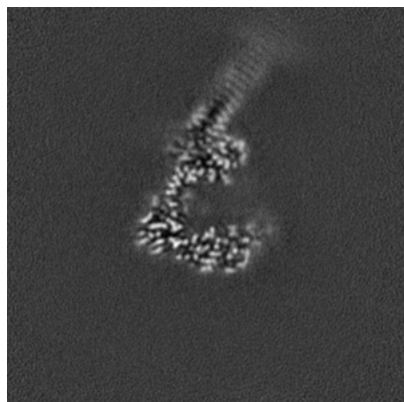


Y Index: 140

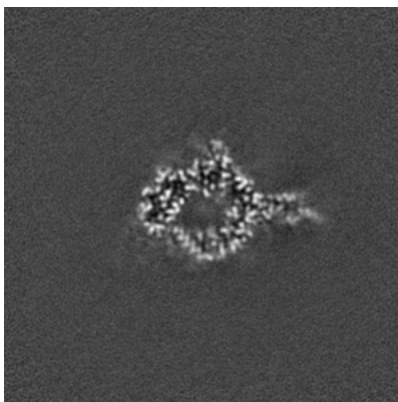


Z Index: 140

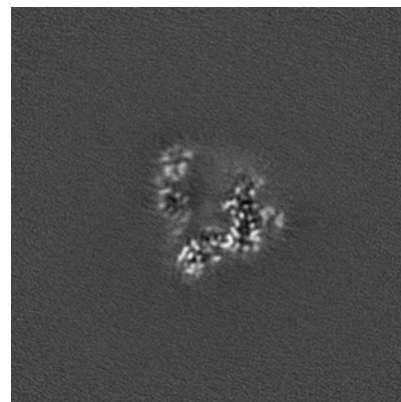
6.2.2 Raw map



X Index: 140



Y Index: 140

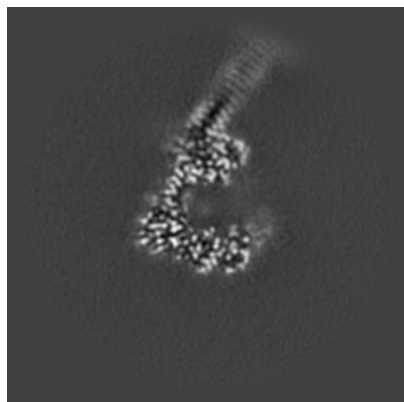


Z Index: 140

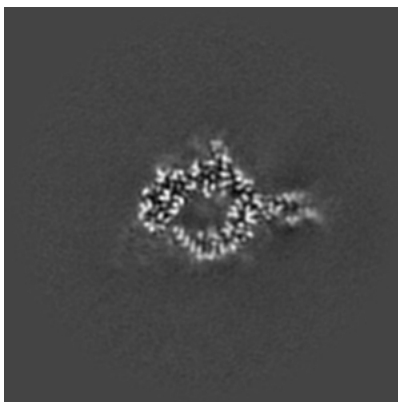
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

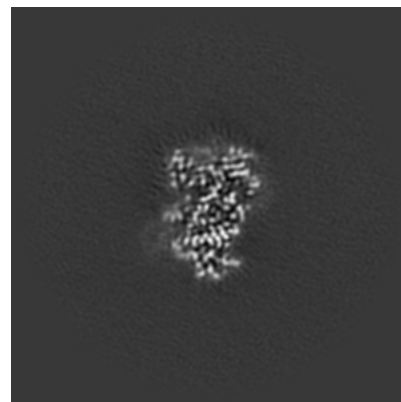
6.3.1 Primary map



X Index: 139

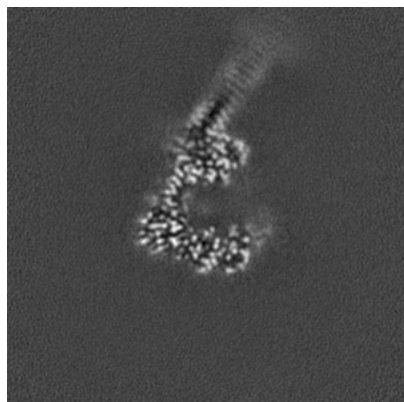


Y Index: 141

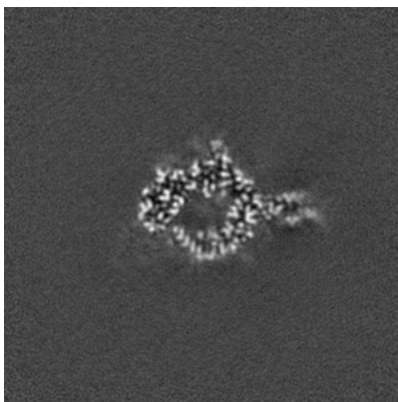


Z Index: 116

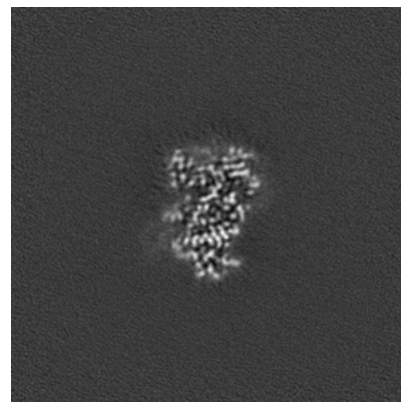
6.3.2 Raw map



X Index: 139



Y Index: 141

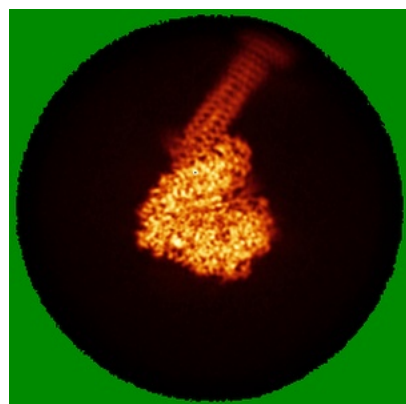


Z Index: 116

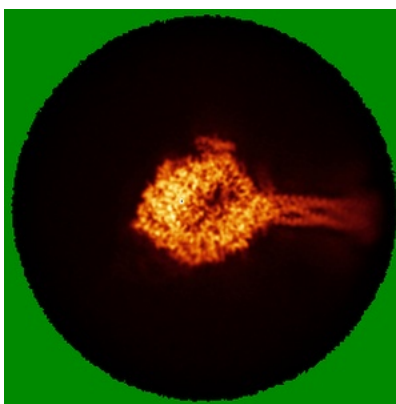
The images above show the largest variance slices of the map in three orthogonal directions.

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

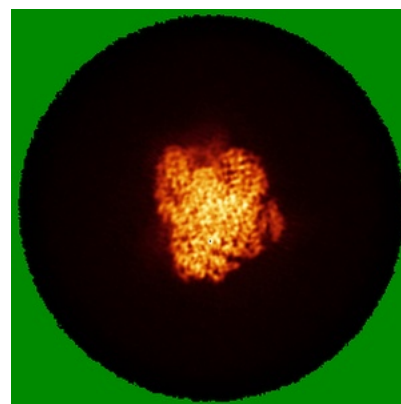
6.4.1 Primary map



X

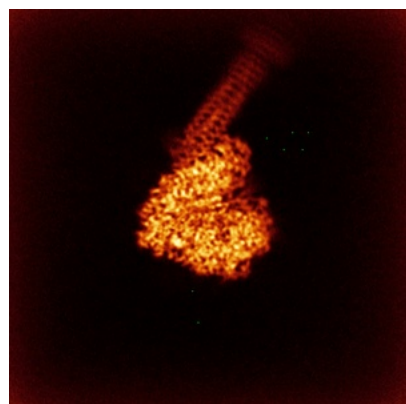


Y

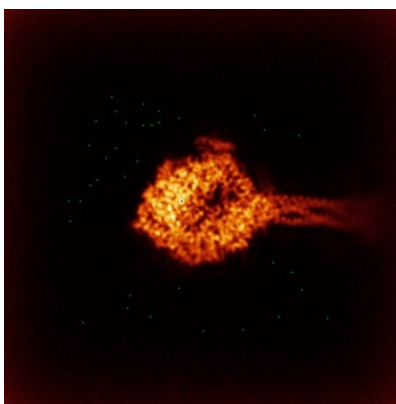


Z

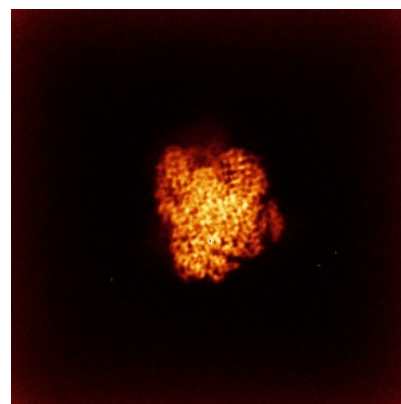
6.4.2 Raw map



X



Y

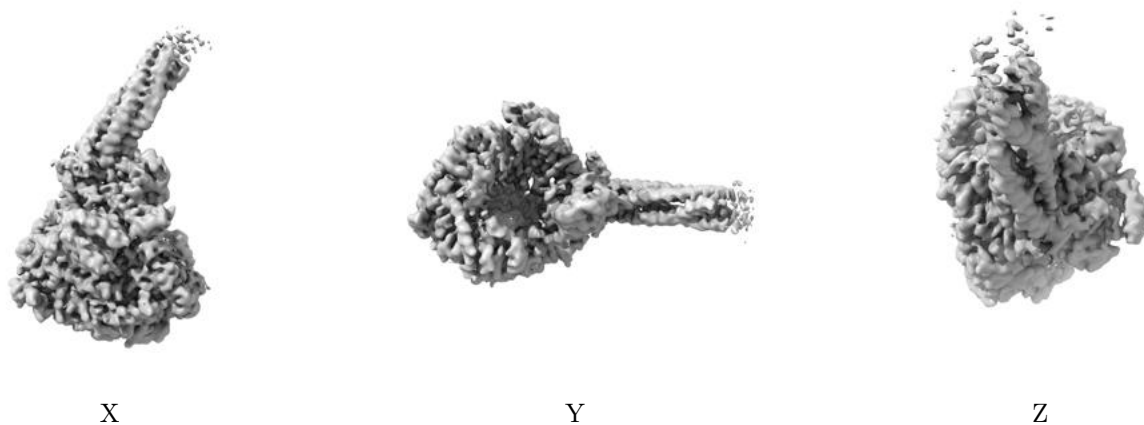


Z

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.

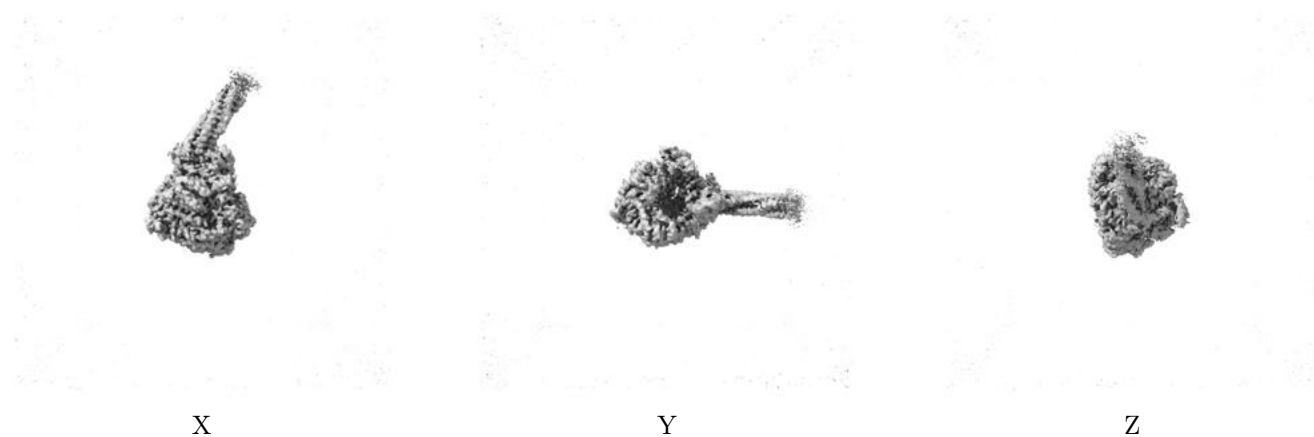
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.178. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

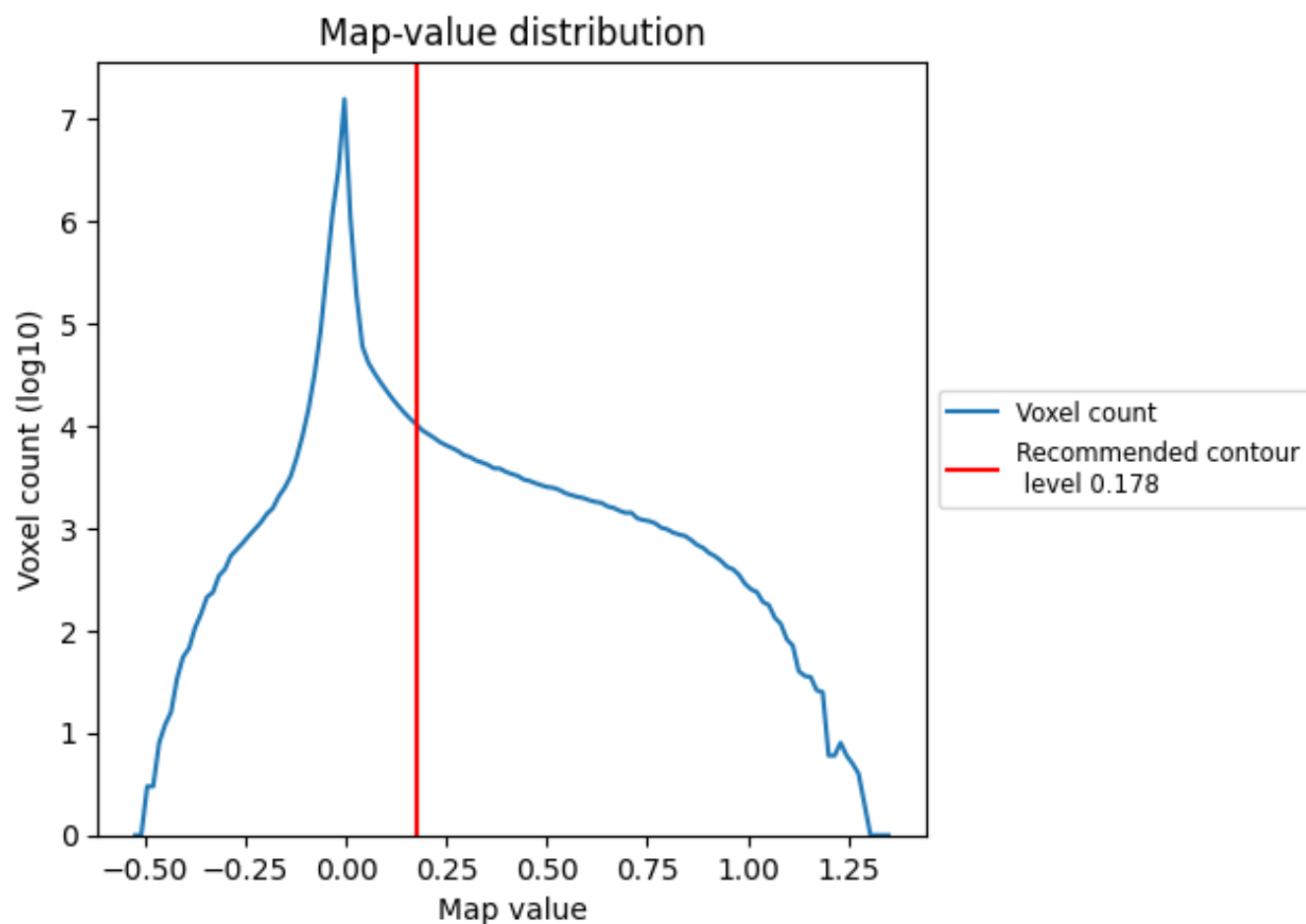
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

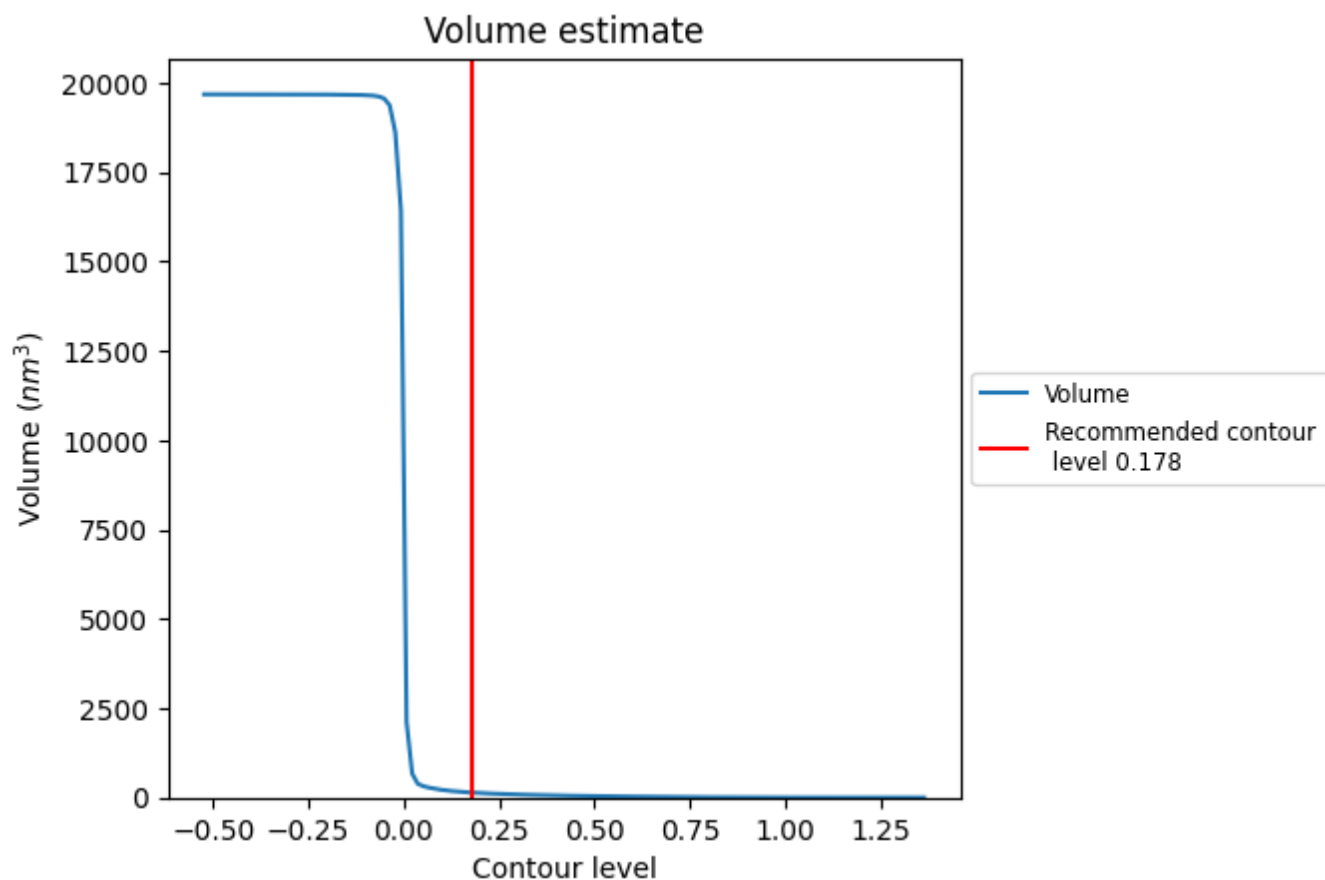
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

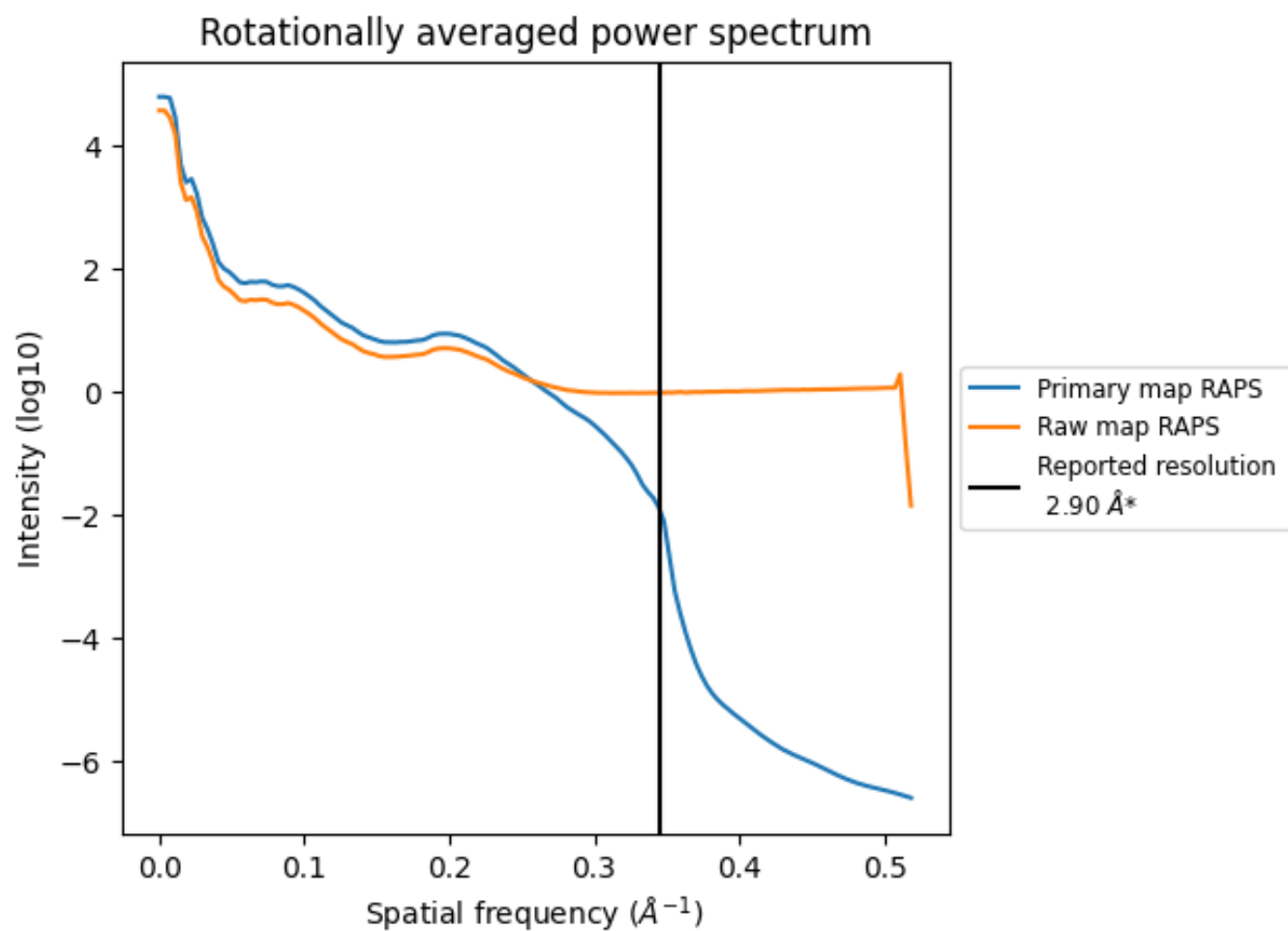
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 139 nm^3 ; this corresponds to an approximate mass of 126 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 ⓘ

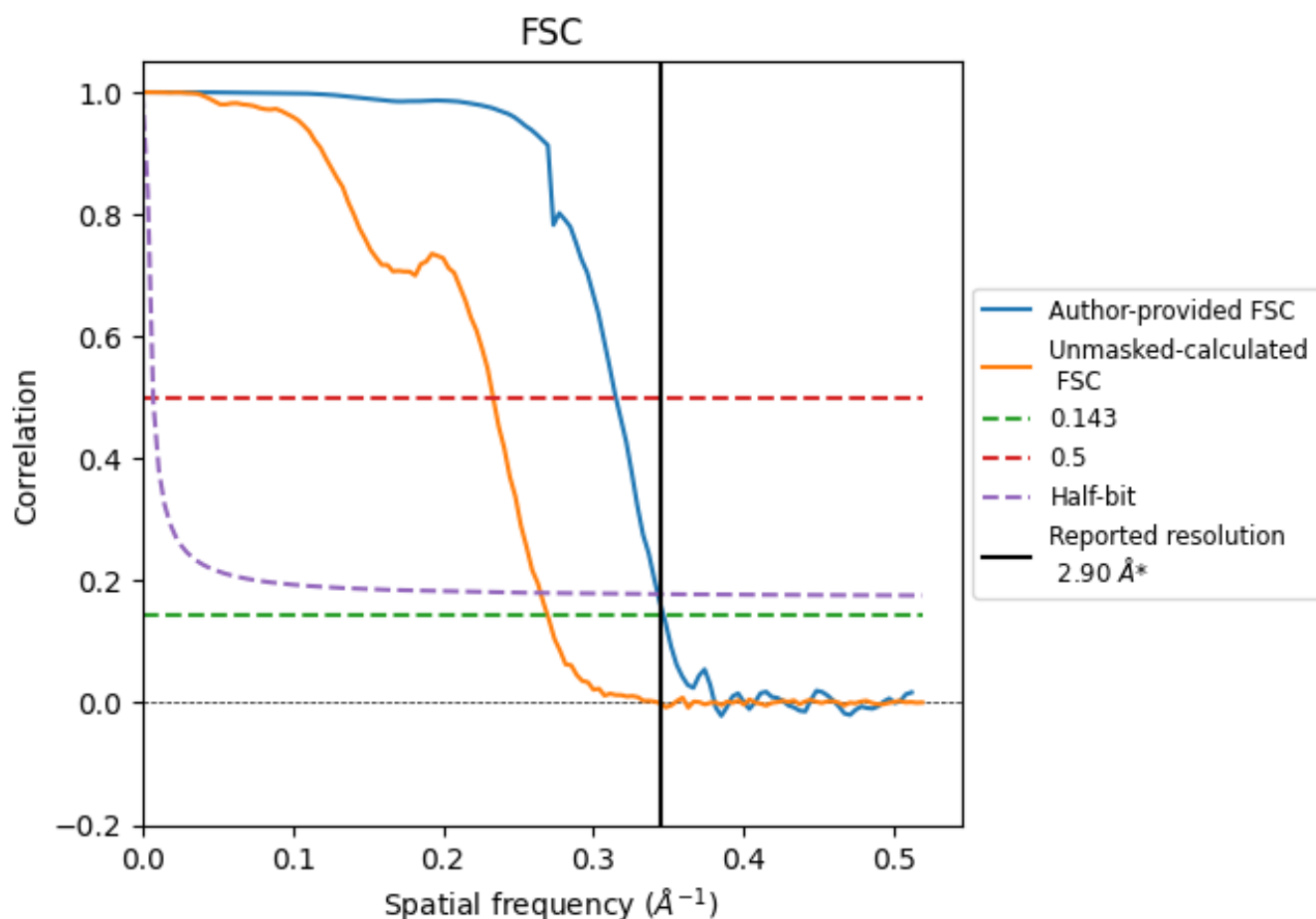


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

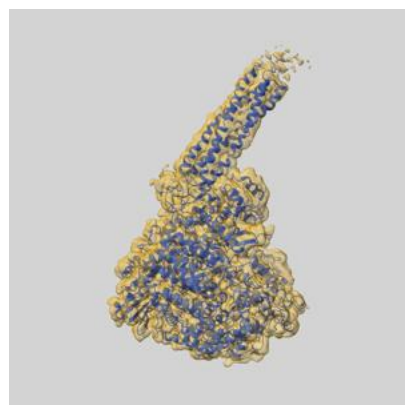
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.89	3.18	2.92
Unmasked-calculated*	3.71	4.28	3.78

*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 3.71 differs from the reported value 2.9 by more than 10 %

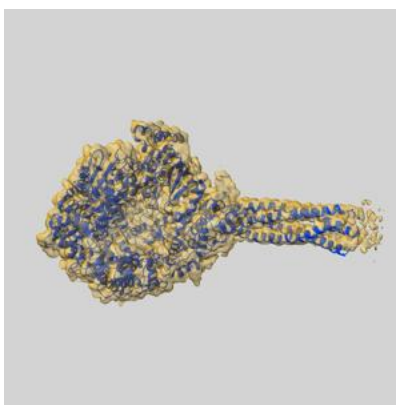
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60355 and PDB model 8ZPV. Per-residue inclusion information can be found in section 3 on page 5.

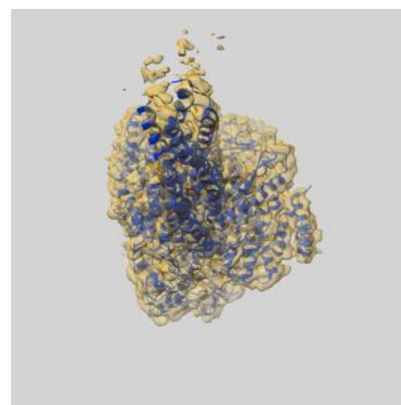
9.1 Map-model overlay [i](#)



X



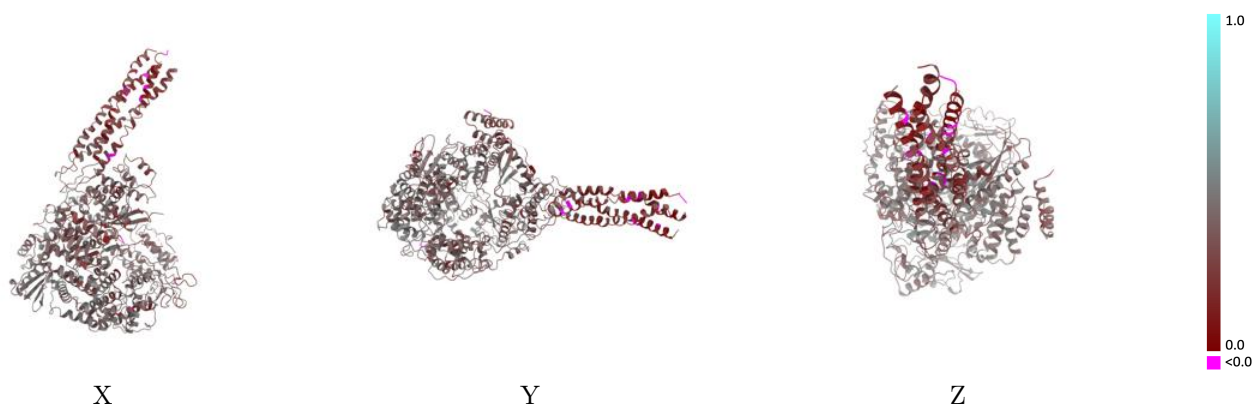
Y



Z

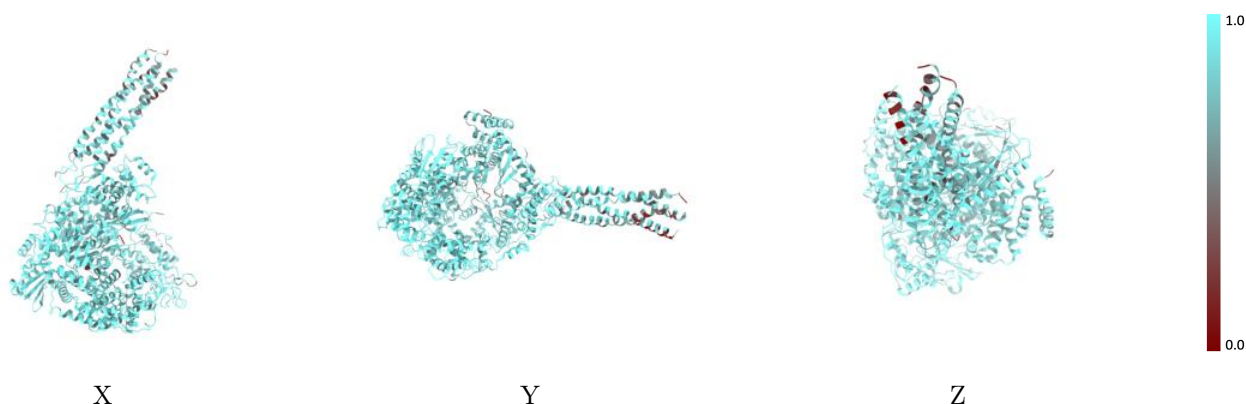
The images above show the 3D surface view of the map at the recommended contour level 0.178 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



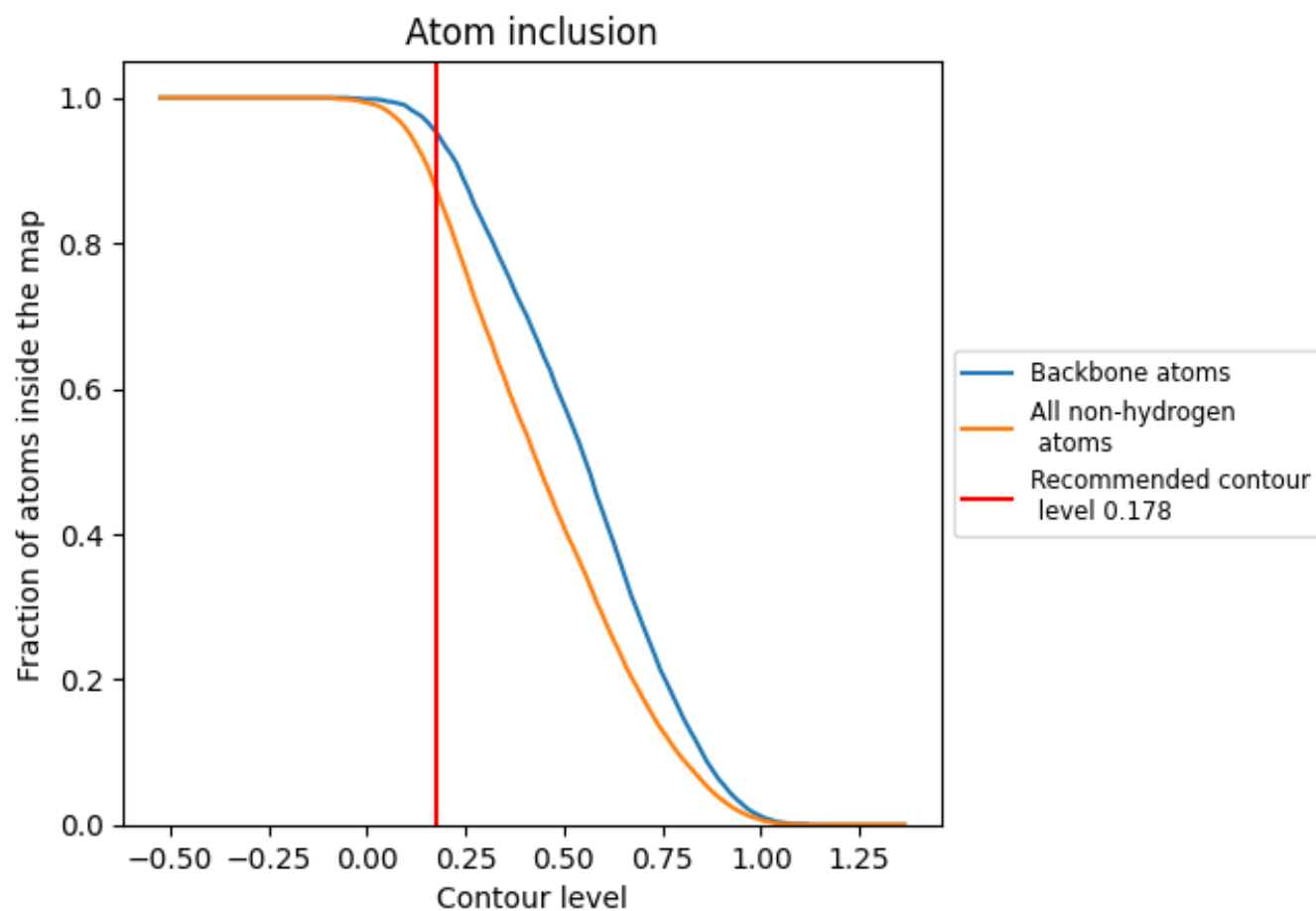
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.178).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 87% 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 (0.178) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8720	0.3570
A	0.9000	0.3840
B	0.7550	0.1610
C	0.7340	0.2180
D	0.7570	0.2520
E	0.6960	0.2470

