



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 04:13 AM UTC

PDB ID : 8W1O / pdb_00008w1o
EMDB ID : EMD-43727
Title : Cryo-EM structure of BTV virion
Authors : Xia, X.; Sung, P.Y.; Martynowycz, M.W.; Gonen, T.; Roy, P.; Zhou, Z.H.
Deposited on : 2024-02-16
Resolution : 2.80 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:

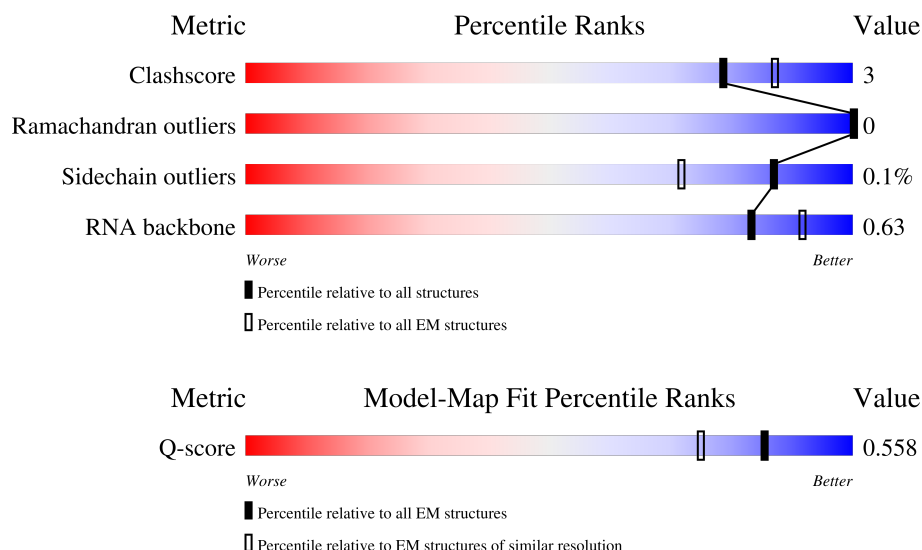
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.80 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.



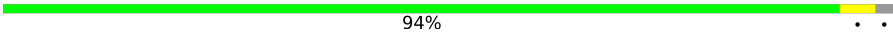
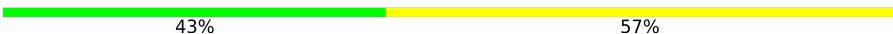
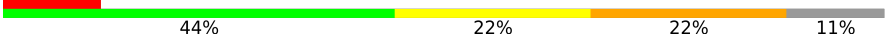
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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

Mol	Chain	Length	Quality of chain
1	A	901	 91% 5%
1	B	901	 91% 8%
1	C	901	 93%

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Mol	Chain	Length	Quality of chain
1	D	901	 94% 6% 5%
1	E	901	 89% 6% 5%
1	F	901	 92% 6% 5%
1	G	901	 91% 5% 5%
1	H	901	 92% 6% 5%
1	I	901	 90% 7% 5%
1	J	901	 90% 8% 5%
2	K	1302	 89% 10% 5%
3	L	7	 43% 57%
4	M	9	 11% 44% 22% 22% 11%
5	N	961	 80% 19%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 89437 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 Core protein VP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	871	Total	C	N	O	S	0	0
			7037	4490	1221	1285	41		
1	B	885	Total	C	N	O	S	0	0
			7150	4561	1239	1309	41		
1	C	875	Total	C	N	O	S	0	0
			7062	4506	1225	1290	41		
1	D	885	Total	C	N	O	S	0	0
			7150	4561	1239	1309	41		
1	E	858	Total	C	N	O	S	0	0
			6926	4425	1200	1261	40		
1	F	885	Total	C	N	O	S	0	0
			7150	4561	1239	1309	41		
1	G	864	Total	C	N	O	S	0	0
			6971	4451	1206	1274	40		
1	H	885	Total	C	N	O	S	0	0
			7150	4561	1239	1309	41		
1	I	875	Total	C	N	O	S	0	0
			7062	4506	1225	1290	41		
1	J	885	Total	C	N	O	S	0	0
			7150	4561	1239	1309	41		

- Molecule 2 is a protein called RNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	1290	Total	C	N	O	S	0	0
			10427	6652	1786	1928	61		

- Molecule 3 is a RNA chain called RNA-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	7	Total	C	N	O	P	0	0
			146	66	23	50	7		

- Molecule 4 is a RNA chain called RNA-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	8	Total	C	N	O	P	0	0
			170	77	31	54	8		

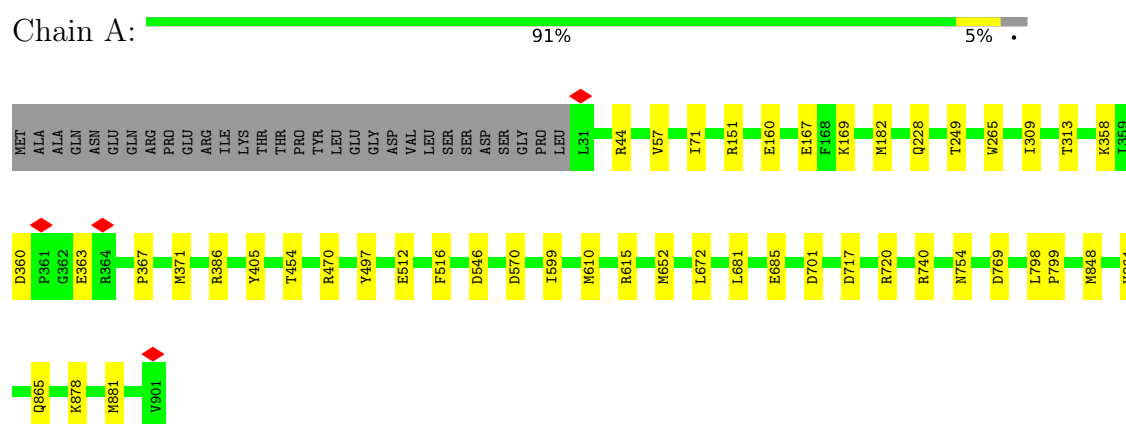
- Molecule 5 is a protein called Outer capsid protein VP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	N	961	Total	C	N	O	S	0	0
			7886	5019	1386	1441	40		

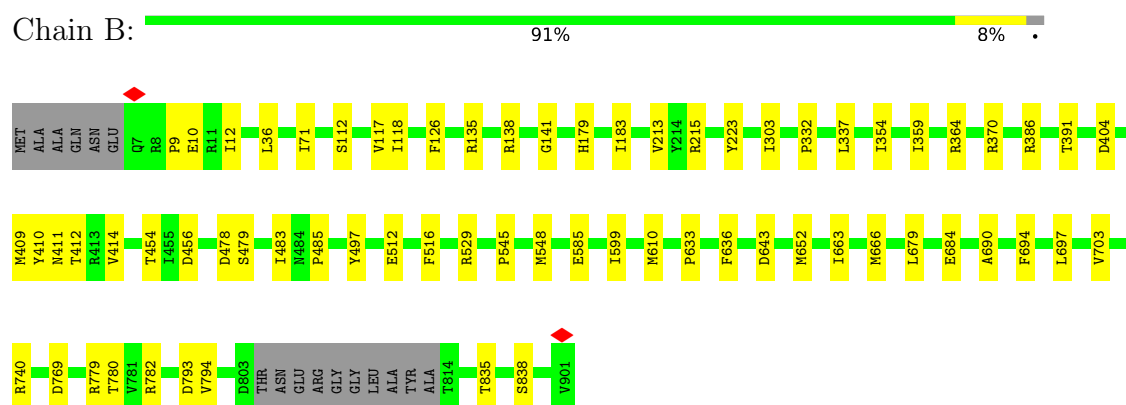
3 Residue-property plots

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.

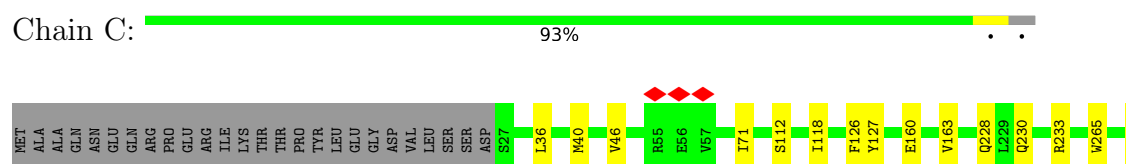
• Molecule 1: Core protein VP3



• Molecule 1: Core protein VP3



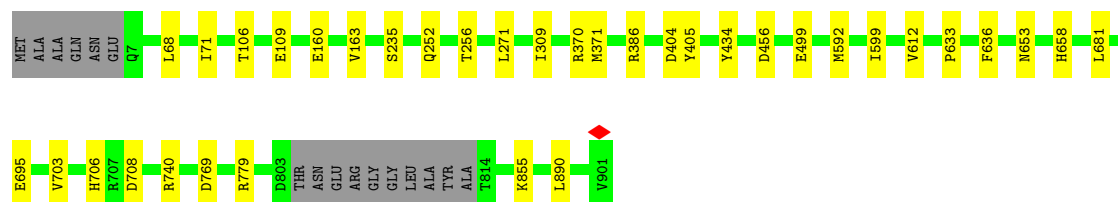
• Molecule 1: Core protein VP3





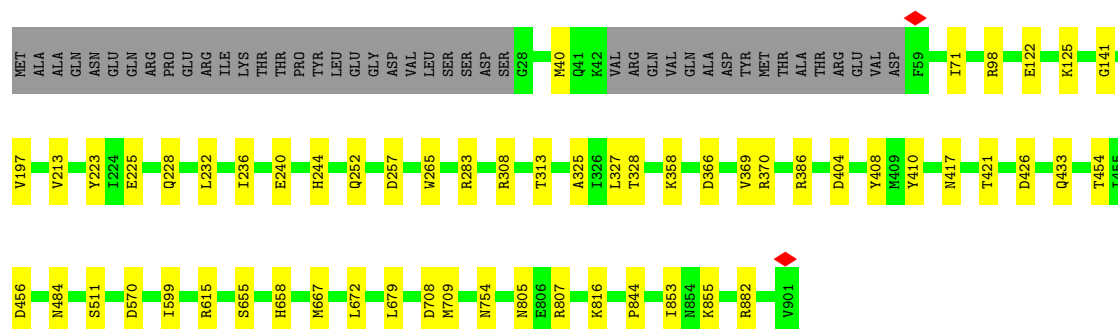
- Molecule 1: Core protein VP3

Chain D: 94%



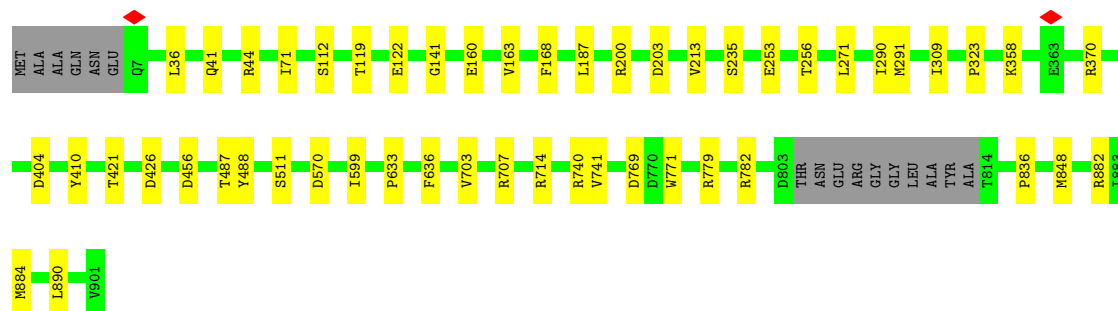
- Molecule 1: Core protein VP3

Chain E: 89% 6% 5%



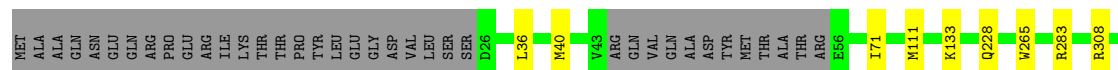
- Molecule 1: Core protein VP3

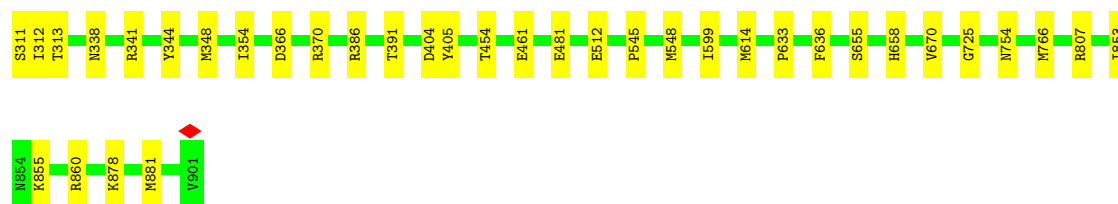
Chain F: 92% 6%



- Molecule 1: Core protein VP3

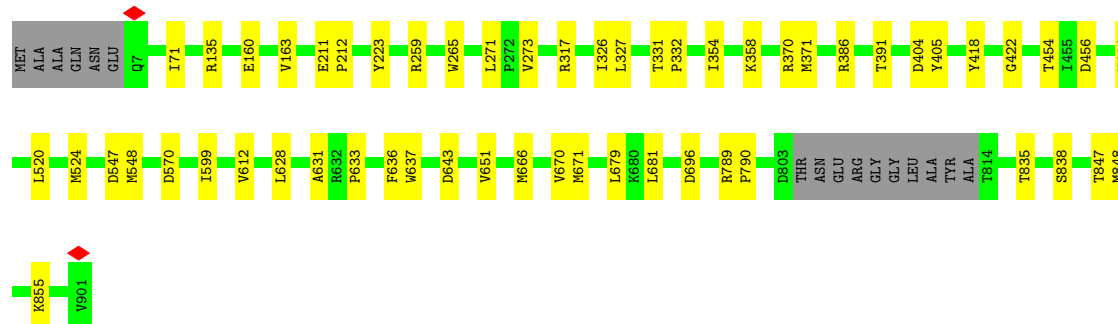
Chain G: 91% 5%





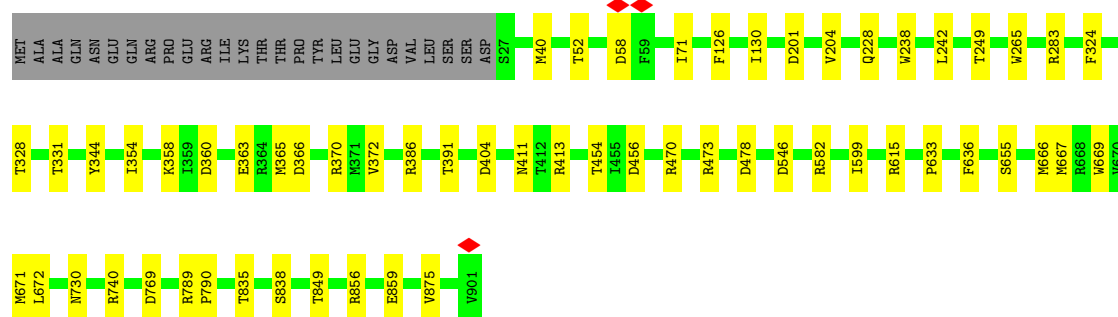
- Molecule 1: Core protein VP3

Chain H: 92% 6% .



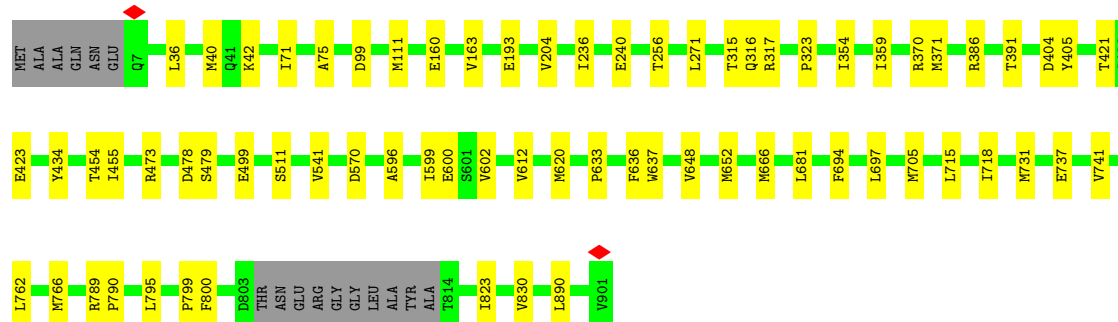
- Molecule 1: Core protein VP3

Chain I: 90% 7% .

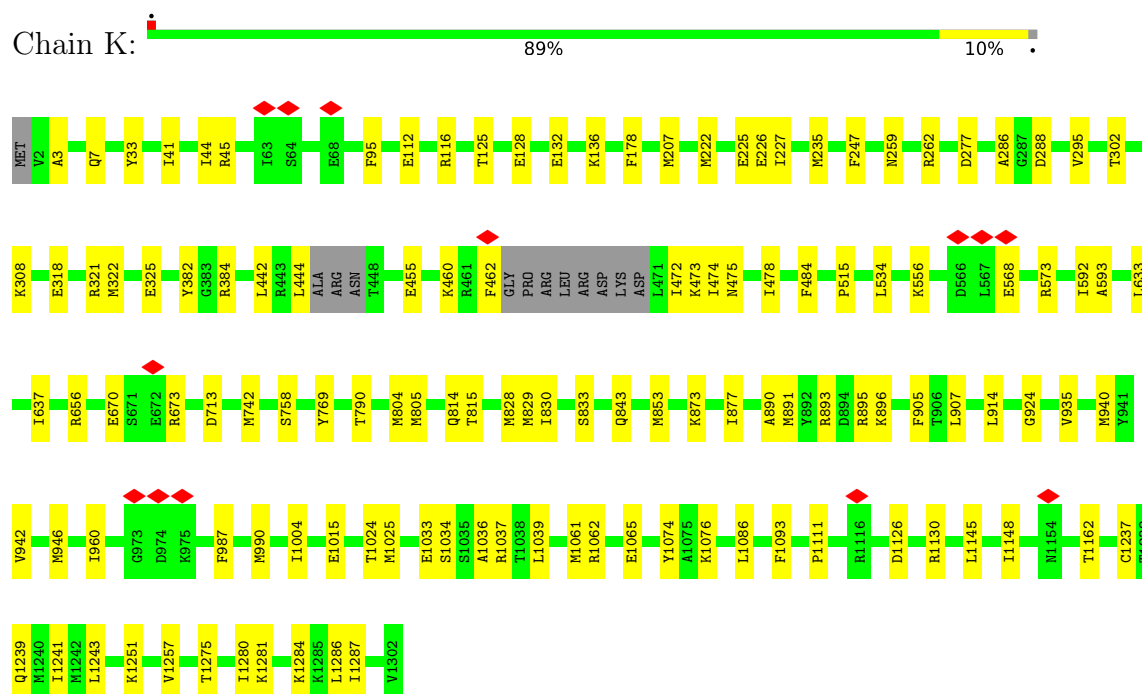


- Molecule 1: Core protein VP3

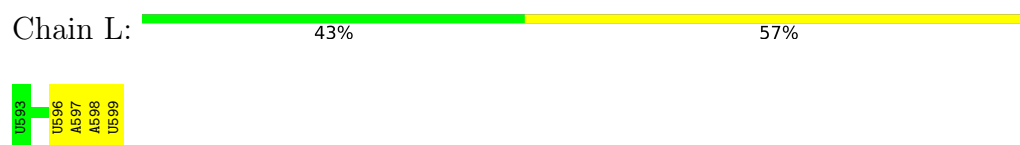
Chain J: 90% 8% .



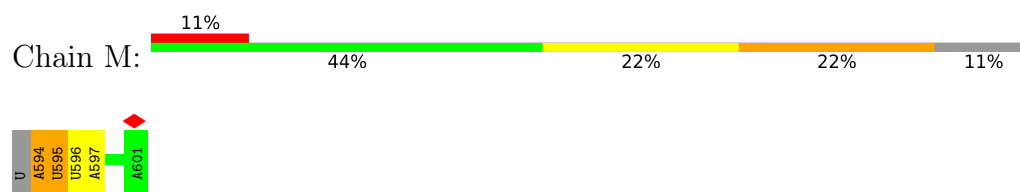
- Molecule 2: RNA-directed RNA polymerase



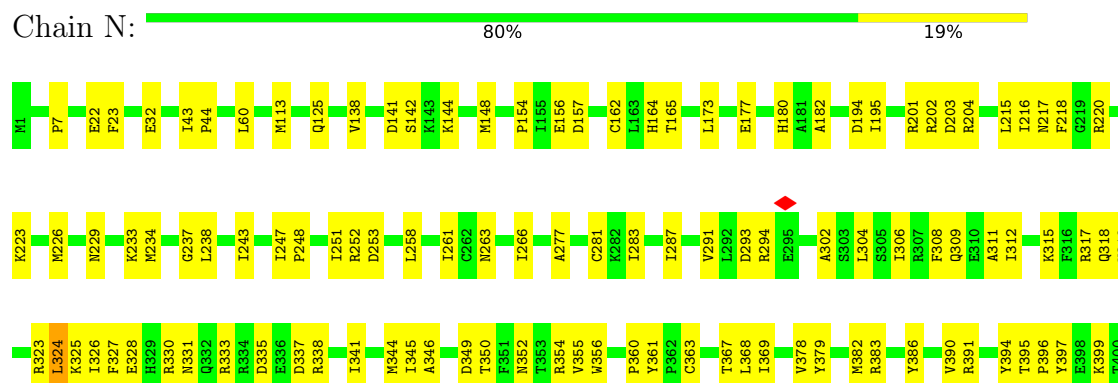
- Molecule 3: RNA-1



- Molecule 4: RNA-2



- Molecule 5: Outer capsid protein VP2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	498646	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.051	Depositor
Minimum map value	-0.003	Depositor
Average map value	0.045	Depositor
Map value standard deviation	0.171	Depositor
Recommended contour level	0.25	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.16	0/7194	0.36	0/9771
1	B	0.16	0/7309	0.35	0/9927
1	C	0.14	0/7220	0.34	0/9807
1	D	0.14	0/7309	0.34	0/9927
1	E	0.14	0/7082	0.34	0/9618
1	F	0.16	0/7309	0.35	0/9927
1	G	0.14	0/7127	0.32	0/9680
1	H	0.15	0/7309	0.34	0/9927
1	I	0.15	0/7220	0.34	0/9807
1	J	0.16	0/7309	0.35	0/9927
2	K	0.13	0/10638	0.33	0/14354
3	L	0.07	0/162	0.12	0/249
4	M	0.12	0/190	0.35	0/293
5	N	0.23	0/8066	0.44	1/10916 (0.0%)
All	All	0.16	0/91444	0.35	1/124130 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	N	324	LEU	N-CA-C	-5.39	105.49	111.36

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	7037	0	7021	28	0
1	B	7150	0	7137	40	0
1	C	7062	0	7047	23	0
1	D	7150	0	7137	21	0
1	E	6926	0	6916	36	0
1	F	7150	0	7137	30	0
1	G	6971	0	6953	27	0
1	H	7150	0	7137	32	0
1	I	7062	0	7047	36	0
1	J	7150	0	7137	40	0
2	K	10427	0	10506	78	0
3	L	146	0	74	4	0
4	M	170	0	86	4	0
5	N	7886	0	7852	130	0
All	All	89437	0	89187	495	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (495) 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)
5:N:156:GLU:HB3	5:N:162:CYS:SG	2.22	0.79
5:N:643:ARG:NH1	5:N:645:CYS:SG	2.56	0.78
5:N:233:LYS:HE2	5:N:238:LEU:HD11	1.67	0.77
1:F:386:ARG:HH21	1:F:456:ASP:H	1.34	0.75
5:N:416:PHE:O	5:N:549:ARG:NH2	2.20	0.75
1:I:365:MET:HE3	1:I:366:ASP:H	1.51	0.75
5:N:355:VAL:HG13	5:N:368:LEU:HD12	1.70	0.74
5:N:397:TYR:CE1	5:N:399:LYS:HD3	2.24	0.73
5:N:910:ASP:OD1	5:N:911:GLU:N	2.22	0.72
5:N:539:GLN:O	5:N:549:ARG:NH1	2.24	0.71
2:K:935:VAL:O	2:K:1239:GLN:NE2	2.24	0.70
5:N:294:ARG:HD2	5:N:360:PRO:HB3	1.73	0.70
1:F:882:ARG:NH1	1:F:884:MET:SD	2.65	0.70
5:N:330:ARG:HB3	5:N:333:ARG:HD3	1.74	0.70
5:N:251:ILE:HD11	5:N:287:ILE:HG13	1.74	0.69
1:J:789:ARG:NH1	1:J:790:PRO:O	2.24	0.69
5:N:456:ILE:HD11	5:N:519:LYS:HE3	1.74	0.69
5:N:328:GLU:OE2	5:N:330:ARG:NH2	2.26	0.69
5:N:344:MET:HG3	5:N:378:VAL:HG11	1.75	0.68
2:K:460:LYS:HE2	2:K:462:PHE:CZ	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:253:GLU:OE1	1:G:807:ARG:NH2	2.28	0.67
1:C:228:GLN:NE2	1:C:265:TRP:O	2.28	0.66
1:G:228:GLN:NE2	1:G:265:TRP:O	2.26	0.66
1:D:653:ASN:OD1	1:D:658:HIS:ND1	2.26	0.66
2:K:914:LEU:HB2	2:K:960:ILE:HD11	1.78	0.65
1:B:386:ARG:HH21	1:B:456:ASP:H	1.42	0.65
2:K:942:VAL:HG12	2:K:946:MET:HE2	1.77	0.65
2:K:592:ILE:HG12	2:K:805:MET:HG2	1.78	0.65
1:I:228:GLN:NE2	1:I:265:TRP:O	2.29	0.64
1:A:44:ARG:NH1	2:K:226:GLU:OE1	2.30	0.64
5:N:318:GLN:O	5:N:323:ARG:NH2	2.29	0.63
1:A:228:GLN:NE2	1:A:265:TRP:O	2.32	0.62
1:H:520:LEU:HD11	1:H:524:MET:HE3	1.81	0.62
5:N:157:ASP:N	5:N:162:CYS:SG	2.72	0.62
5:N:395:THR:HB	5:N:396:PRO:HD3	1.80	0.62
5:N:538:ALA:HB2	5:N:551:LEU:HD12	1.81	0.62
1:D:68:LEU:HB3	1:D:592:MET:HE1	1.82	0.62
1:C:486:THR:HG23	1:C:487:THR:HG23	1.82	0.62
1:H:386:ARG:NH2	1:H:454:THR:O	2.31	0.62
1:B:112:SER:O	1:B:782:ARG:NH1	2.33	0.61
5:N:690:ASP:OD1	5:N:691:VAL:N	2.29	0.61
1:H:135:ARG:NH1	1:H:643:ASP:OD2	2.34	0.61
1:J:386:ARG:NH2	1:J:454:THR:O	2.32	0.61
1:B:835:THR:HB	1:B:838:SER:HB3	1.83	0.60
1:B:610:MET:HE1	1:B:652:MET:HE1	1.82	0.60
1:C:430:GLY:O	1:C:433:GLN:NE2	2.33	0.60
1:D:370:ARG:NH2	1:D:404:ASP:OD2	2.35	0.60
1:E:308:ARG:NH1	1:G:366:ASP:OD2	2.35	0.60
1:H:370:ARG:NH2	1:H:404:ASP:OD2	2.33	0.60
5:N:418:ALA:HB1	5:N:422:ILE:HD12	1.82	0.60
5:N:702:ARG:O	5:N:827:TYR:OH	2.20	0.60
1:C:386:ARG:NH2	1:C:454:THR:O	2.35	0.60
1:G:338:ASN:OD1	1:G:341:ARG:NH2	2.33	0.60
1:J:705:MET:HE2	1:J:799:PRO:HD2	1.84	0.60
5:N:378:VAL:HG12	5:N:382:MET:HE2	1.83	0.59
1:B:370:ARG:NH2	1:B:404:ASP:OD2	2.32	0.59
5:N:277:ALA:HB3	5:N:309:GLN:HG3	1.83	0.59
5:N:283:ILE:O	5:N:287:ILE:HD12	2.02	0.59
1:J:317:ARG:NH2	2:K:288:ASP:OD1	2.34	0.59
1:I:386:ARG:NH2	1:I:454:THR:O	2.34	0.59
1:D:703:VAL:HG21	1:D:779:ARG:HD2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:308:ARG:NH1	1:E:366:ASP:OD2	2.35	0.59
5:N:525:MET:SD	5:N:525:MET:N	2.74	0.59
1:J:193:GLU:HB2	1:J:204:VAL:HB	1.85	0.58
1:I:856:ARG:NH2	1:I:859:GLU:OE1	2.36	0.58
1:G:308:ARG:NH1	1:I:366:ASP:OD2	2.36	0.58
1:A:610:MET:HE1	1:A:652:MET:HE1	1.86	0.58
5:N:113:MET:HE1	5:N:836:VAL:HG12	1.86	0.58
2:K:3:ALA:O	2:K:7:GLN:NE2	2.37	0.57
5:N:397:TYR:CZ	5:N:399:LYS:HD3	2.38	0.57
1:F:370:ARG:NH2	1:F:404:ASP:OD2	2.34	0.57
2:K:670:GLU:HA	2:K:673:ARG:HE	1.69	0.57
1:B:364:ARG:HH22	2:K:556:LYS:HA	1.69	0.57
1:E:228:GLN:NE2	1:E:265:TRP:O	2.37	0.57
2:K:125:THR:OG1	2:K:128:GLU:OE1	2.22	0.57
5:N:141:ASP:OD1	5:N:142:SER:N	2.37	0.57
5:N:404:GLU:HG3	5:N:504:LYS:HG2	1.85	0.57
1:A:740:ARG:NH2	1:A:769:ASP:O	2.35	0.57
2:K:1062:ARG:NH2	2:K:1065:GLU:O	2.38	0.57
5:N:432:ASN:OD1	5:N:433:HIS:ND1	2.38	0.57
1:B:9:PRO:HA	1:B:12:ILE:HD12	1.86	0.57
1:G:71:ILE:HG21	1:G:599:ILE:HG23	1.87	0.57
1:G:725:GLY:O	1:G:860:ARG:NH1	2.37	0.57
5:N:669:ASP:OD1	5:N:670:ILE:N	2.36	0.57
1:F:358:LYS:HB2	1:F:570:ASP:HB3	1.85	0.56
1:C:283:ARG:O	1:C:655:SER:OG	2.20	0.56
5:N:194:ASP:OD1	5:N:223:LYS:NZ	2.38	0.56
1:E:257:ASP:OD2	1:E:882:ARG:NH2	2.38	0.56
5:N:587:GLN:NE2	5:N:591:ASP:OD2	2.39	0.56
1:D:386:ARG:HH21	1:D:456:ASP:H	1.54	0.56
5:N:148:MET:HE2	5:N:858:ILE:HD12	1.85	0.56
5:N:363:CYS:O	5:N:367:THR:HG23	2.06	0.56
2:K:1281:LYS:HG2	2:K:1286:LEU:HD23	1.86	0.56
1:F:740:ARG:NH2	1:F:769:ASP:O	2.38	0.56
2:K:1280:ILE:HG13	2:K:1284:LYS:HE2	1.87	0.56
5:N:473:ILE:HD11	5:N:813:ILE:HG13	1.87	0.56
1:J:715:LEU:HD12	1:J:718:ILE:HD13	1.88	0.56
5:N:234:MET:SD	5:N:511:VAL:HG21	2.45	0.56
1:C:40:MET:HE1	2:K:1162:THR:HB	1.87	0.55
1:D:235:SER:HB3	1:D:271:LEU:HD23	1.88	0.55
1:D:256:THR:HG23	1:E:754:ASN:HA	1.88	0.55
1:B:10:GLU:HG3	1:B:483:ILE:HD11	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:41:GLN:OE1	1:F:44:ARG:NH2	2.39	0.55
2:K:828:MET:HE3	3:L:597:A:H5'	1.89	0.55
2:K:1145:LEU:HD23	2:K:1148:ILE:HD11	1.87	0.55
2:K:455:GLU:HB3	2:K:473:LYS:HE3	1.88	0.55
1:G:308:ARG:HA	1:G:311:SER:HB2	1.90	0.54
1:J:315:THR:HG22	1:J:316:GLN:H	1.73	0.54
5:N:281:CYS:SG	5:N:309:GLN:NE2	2.77	0.54
1:B:117:VAL:HA	1:B:780:THR:HG21	1.90	0.54
1:I:835:THR:HB	1:I:838:SER:HB3	1.89	0.54
5:N:341:ILE:O	5:N:345:ILE:HD12	2.08	0.54
1:A:754:ASN:HA	1:J:256:THR:HG23	1.89	0.54
1:G:386:ARG:NH2	1:G:454:THR:O	2.40	0.54
1:J:596:ALA:O	1:J:600:GLU:HG3	2.08	0.54
1:H:696:ASP:OD1	1:H:855:LYS:NZ	2.41	0.54
5:N:352:ASN:C	5:N:394:TYR:CD1	2.85	0.54
5:N:889:ARG:HG3	5:N:892:LEU:HD12	1.90	0.54
1:E:358:LYS:HB3	1:E:570:ASP:HB3	1.90	0.54
1:F:200:ARG:NH1	1:F:203:ASP:OD1	2.38	0.54
1:F:235:SER:HB3	1:F:271:LEU:HD12	1.88	0.54
1:I:324:PHE:O	1:I:328:THR:HG23	2.07	0.54
1:F:112:SER:O	1:F:782:ARG:NH1	2.41	0.54
5:N:173:LEU:HD21	5:N:626:LEU:HD13	1.90	0.54
1:B:411:ASN:OD1	1:B:412:THR:N	2.40	0.53
5:N:535:GLU:OE2	5:N:551:LEU:HB2	2.08	0.53
1:F:71:ILE:HG21	1:F:599:ILE:HG23	1.89	0.53
5:N:472:MET:HE1	5:N:813:ILE:HG23	1.90	0.53
2:K:1034:SER:HA	2:K:1037:ARG:HE	1.73	0.53
1:B:545:PRO:HG2	1:B:548:MET:HE3	1.91	0.53
5:N:154:PRO:HG2	5:N:164:HIS:ND1	2.23	0.53
5:N:324:LEU:HD23	5:N:325:LYS:HZ1	1.74	0.53
1:F:256:THR:HG23	1:G:754:ASN:HA	1.91	0.53
1:D:740:ARG:NH2	1:D:769:ASP:O	2.36	0.52
1:F:707:ARG:HG3	1:F:848:MET:HE1	1.91	0.52
1:J:71:ILE:HG21	1:J:599:ILE:HG23	1.90	0.52
1:C:853:ILE:HG22	1:C:855:LYS:H	1.74	0.52
2:K:568:GLU:O	4:M:597:A:O2'	2.27	0.52
1:A:44:ARG:NH2	2:K:225:GLU:OE1	2.42	0.52
5:N:201:ARG:NH1	5:N:203:ASP:O	2.42	0.52
1:E:853:ILE:HG22	1:E:855:LYS:H	1.75	0.52
2:K:33:TYR:HB3	2:K:907:LEU:HD11	1.92	0.52
1:E:327:LEU:HD11	1:E:369:VAL:HG22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:N:277:ALA:HB2	5:N:312:ILE:HG13	1.91	0.51
1:B:332:PRO:HB2	1:B:337:LEU:HD12	1.92	0.51
5:N:337:ASP:O	5:N:341:ILE:HG12	2.10	0.51
5:N:758:GLN:HA	5:N:776:GLU:OE2	2.11	0.51
5:N:156:GLU:CB	5:N:162:CYS:SG	2.96	0.51
1:F:386:ARG:NH2	1:F:456:ASP:H	2.05	0.51
1:J:715:LEU:HD11	1:J:830:VAL:HG11	1.92	0.51
5:N:354:ARG:HG3	5:N:379:TYR:CE2	2.45	0.51
1:J:455:ILE:HB	1:J:473:ARG:HH21	1.76	0.51
2:K:384:ARG:NH2	2:K:833:SER:O	2.43	0.51
5:N:177:GLU:HA	5:N:180:HIS:CE1	2.46	0.51
5:N:435:THR:HA	5:N:654:PRO:HD2	1.91	0.51
1:B:386:ARG:NH2	1:B:454:THR:O	2.38	0.50
1:E:386:ARG:HH21	1:E:456:ASP:H	1.57	0.50
1:J:541:VAL:HG12	1:J:600:GLU:OE2	2.10	0.50
1:B:141:GLY:HA2	1:B:213:VAL:HG13	1.94	0.50
2:K:1033:GLU:OE2	2:K:1036:ALA:N	2.31	0.50
2:K:472:ILE:HG22	2:K:473:LYS:N	2.26	0.50
1:B:215:ARG:HD3	1:B:690:ALA:HB2	1.94	0.50
1:J:789:ARG:HH12	1:J:795:LEU:HD12	1.75	0.50
5:N:401:ARG:HA	5:N:404:GLU:CD	2.37	0.50
2:K:843:GLN:NE2	2:K:924:GLY:O	2.38	0.50
1:C:230:GLN:OE1	1:C:233:ARG:NH2	2.44	0.50
1:D:252:GLN:OE1	1:E:816:LYS:NZ	2.34	0.49
1:E:325:ALA:O	1:E:328:THR:OG1	2.29	0.49
1:J:370:ARG:NH2	1:J:404:ASP:OD2	2.37	0.49
1:H:547:ASP:OD1	1:H:548:MET:N	2.46	0.49
1:A:470:ARG:NH1	1:A:546:ASP:OD1	2.38	0.49
1:A:701:ASP:N	1:A:701:ASP:OD1	2.44	0.49
1:G:878:LYS:HB2	1:G:881:MET:HG3	1.94	0.49
2:K:277:ASP:HB2	2:K:308:LYS:HD2	1.93	0.49
2:K:1015:GLU:OE2	2:K:1024:THR:OG1	2.30	0.49
1:D:309:ILE:HA	1:E:658:HIS:HB2	1.93	0.49
1:J:111:MET:HE2	1:J:697:LEU:HA	1.93	0.49
3:L:599:U:H3	4:M:594:A:H61	1.61	0.49
1:B:71:ILE:HG21	1:B:599:ILE:HG23	1.94	0.49
1:B:740:ARG:NH1	1:B:769:ASP:O	2.46	0.49
1:I:71:ILE:HG21	1:I:599:ILE:HG23	1.95	0.49
1:J:323:PRO:HG3	1:J:511:SER:HB3	1.95	0.49
2:K:318:GLU:HB3	2:K:322:MET:HE3	1.94	0.49
5:N:326:ILE:O	5:N:333:ARG:NH2	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:410:TYR:OH	1:B:512:GLU:OE2	2.31	0.49
5:N:318:GLN:O	5:N:323:ARG:NE	2.46	0.49
5:N:352:ASN:C	5:N:394:TYR:HD1	2.21	0.49
5:N:426:HIS:ND1	5:N:427:TRP:O	2.42	0.49
1:E:313:THR:O	1:E:511:SER:OG	2.31	0.49
1:J:637:TRP:CE3	1:J:666:MET:HG2	2.47	0.49
5:N:215:LEU:HD21	5:N:220:ARG:HD2	1.94	0.49
5:N:439:THR:HG22	5:N:650:VAL:HG12	1.94	0.48
1:E:283:ARG:O	1:E:655:SER:OG	2.24	0.48
5:N:465:TYR:CE2	5:N:469:ILE:HD11	2.48	0.48
5:N:465:TYR:CZ	5:N:469:ILE:HD11	2.48	0.48
1:D:371:MET:HB3	1:D:405:TYR:HD1	1.79	0.48
1:G:853:ILE:HG22	1:G:855:LYS:H	1.78	0.48
2:K:1126:ASP:O	2:K:1130:ARG:HG3	2.13	0.48
1:E:667:MET:HA	1:E:667:MET:HE2	1.96	0.48
1:G:312:ILE:HG13	1:G:313:THR:HG23	1.96	0.48
5:N:291:VAL:HG21	5:N:369:ILE:HD13	1.95	0.48
1:I:40:MET:HE1	2:K:946:MET:HG2	1.95	0.48
5:N:201:ARG:HH12	5:N:204:ARG:HA	1.78	0.48
2:K:1093:PHE:HB3	2:K:1111:PRO:HG3	1.95	0.48
5:N:383:ARG:HD3	5:N:402:GLU:OE1	2.14	0.48
1:B:364:ARG:NH2	2:K:556:LYS:HA	2.29	0.48
1:J:42:LYS:NZ	1:J:570:ASP:OD1	2.44	0.48
2:K:893:ARG:HH12	2:K:896:LYS:HE3	1.78	0.48
1:A:717:ASP:OD2	1:A:720:ARG:NH1	2.47	0.48
1:D:271:LEU:HD21	1:D:890:LEU:HB3	1.94	0.48
1:G:283:ARG:O	1:G:655:SER:OG	2.25	0.48
1:G:614:MET:HG2	1:G:670:VAL:HG21	1.95	0.48
1:I:740:ARG:NH2	1:I:769:ASP:O	2.46	0.48
1:B:529:ARG:NE	1:B:585:GLU:OE1	2.46	0.47
1:C:118:ILE:HD12	1:C:126:PHE:HD1	1.79	0.47
1:E:386:ARG:NH2	1:E:454:THR:O	2.46	0.47
2:K:633:LEU:O	2:K:637:ILE:HD12	2.14	0.47
5:N:537:ILE:HA	5:N:550:THR:HG22	1.96	0.47
1:A:681:LEU:O	1:A:685:GLU:HG3	2.14	0.47
1:J:36:LEU:O	1:J:40:MET:HG2	2.13	0.47
1:J:620:MET:HE1	1:J:694:PHE:CZ	2.49	0.47
5:N:317:ARG:HG2	5:N:319:HIS:H	1.79	0.47
1:H:259:ARG:HG3	1:H:265:TRP:CZ2	2.49	0.47
5:N:182:ALA:HB2	5:N:572:ILE:HG22	1.97	0.47
5:N:346:ALA:O	5:N:350:THR:HG23	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:612:VAL:HG21	1:D:681:LEU:HD11	1.97	0.47
5:N:252:ARG:HG3	5:N:253:ASP:N	2.30	0.47
5:N:349:ASP:OD1	5:N:391:ARG:NH1	2.47	0.47
1:E:709:MET:HG2	1:E:844:PRO:HB2	1.97	0.47
1:G:405:TYR:OH	1:G:512:GLU:OE2	2.32	0.47
5:N:164:HIS:O	5:N:165:THR:C	2.58	0.47
5:N:226:MET:HE2	5:N:423:LYS:HG2	1.97	0.47
1:A:167:GLU:OE1	1:A:169:LYS:NZ	2.48	0.47
1:A:405:TYR:OH	1:A:512:GLU:OE2	2.33	0.47
1:B:135:ARG:NH1	1:B:643:ASP:OD2	2.48	0.47
1:J:478:ASP:OD1	1:J:479:SER:N	2.48	0.47
2:K:132:GLU:O	2:K:136:LYS:HG2	2.15	0.47
1:H:317:ARG:NH2	1:I:52:THR:O	2.46	0.47
1:I:331:THR:HG21	2:K:1257:VAL:HG12	1.96	0.47
1:I:360:ASP:HB3	1:I:363:GLU:HB2	1.97	0.47
3:L:596:U:H2'	3:L:597:A:C8	2.50	0.47
2:K:472:ILE:CG2	2:K:473:LYS:N	2.77	0.47
2:K:1061:MET:HE1	2:K:1076:LYS:HG3	1.97	0.46
1:J:731:MET:HE2	1:J:823:ILE:HG21	1.98	0.46
2:K:593:ALA:HB3	2:K:804:MET:HB2	1.96	0.46
1:A:367:PRO:O	1:A:371:MET:HG3	2.15	0.46
2:K:895:ARG:NH2	2:K:905:PHE:O	2.48	0.46
1:G:461:GLU:OE1	1:H:422:GLY:HA3	2.15	0.46
1:I:473:ARG:HH21	1:I:478:ASP:HB2	1.80	0.46
1:A:861:VAL:HB	1:A:865:GLN:HG2	1.97	0.46
1:E:240:GLU:OE2	1:E:252:GLN:NE2	2.45	0.46
5:N:195:ILE:HG12	5:N:243:ILE:CD1	2.45	0.46
5:N:352:ASN:OD1	5:N:394:TYR:HA	2.15	0.46
1:H:358:LYS:HB2	1:H:570:ASP:HB3	1.98	0.46
2:K:259:ASN:OD1	2:K:262:ARG:NH1	2.49	0.46
1:B:694:PHE:HD1	1:B:697:LEU:HD12	1.81	0.46
5:N:546:MET:HG2	5:N:590:TYR:HA	1.98	0.46
1:B:138:ARG:NE	1:B:684:GLU:OE1	2.48	0.46
1:B:497:TYR:OH	1:B:516:PHE:O	2.28	0.46
1:I:344:TYR:OH	1:I:582:ARG:O	2.25	0.46
1:J:271:LEU:HD12	1:J:890:LEU:HB3	1.98	0.46
1:F:119:THR:OG1	1:F:122:GLU:OE1	2.33	0.46
1:I:667:MET:HB3	1:I:671:MET:HE1	1.98	0.46
1:B:633:PRO:HA	1:B:636:PHE:CE2	2.51	0.46
1:C:777:VAL:O	1:C:779:ARG:NH1	2.46	0.46
1:E:71:ILE:HG21	1:E:599:ILE:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:N:686:ARG:HG3	5:N:686:ARG:HH11	1.81	0.46
1:E:417:ASN:ND2	1:E:433:GLN:OE1	2.49	0.45
1:H:637:TRP:CE3	1:H:666:MET:HG2	2.51	0.45
1:J:371:MET:HB3	1:J:405:TYR:HD1	1.80	0.45
1:C:46:VAL:HG11	2:K:1004:ILE:HG13	1.98	0.45
1:F:309:ILE:HA	1:G:658:HIS:HB2	1.98	0.45
1:C:629:ILE:HG23	1:C:630:GLN:HG3	1.99	0.45
1:E:232:LEU:O	1:E:236:ILE:HG12	2.17	0.45
1:C:71:ILE:HG21	1:C:599:ILE:HG23	1.99	0.45
2:K:318:GLU:O	2:K:322:MET:HG3	2.16	0.45
5:N:248:PRO:HG2	5:N:251:ILE:HG22	1.98	0.45
5:N:304:LEU:HD13	5:N:361:TYR:CE2	2.52	0.45
1:I:615:ARG:NH2	1:I:672:LEU:O	2.50	0.45
1:I:730:ASN:HD22	1:I:849:THR:HG23	1.81	0.45
4:M:595:U:H2'	4:M:596:U:C6	2.52	0.45
1:E:615:ARG:NH2	1:E:672:LEU:O	2.49	0.45
1:E:708:ASP:OD1	1:E:709:MET:N	2.41	0.45
1:H:494:TYR:HD1	1:H:524:MET:HE2	1.82	0.45
5:N:195:ILE:HG12	5:N:243:ILE:HD12	1.99	0.45
5:N:237:GLY:HA2	5:N:511:VAL:HG23	1.99	0.45
5:N:437:GLU:O	5:N:438:ILE:HD13	2.16	0.45
5:N:460:PHE:CD2	5:N:771:MET:HE1	2.52	0.45
1:F:703:VAL:HG21	1:F:779:ARG:HD2	1.98	0.45
1:G:481:GLU:OE2	1:H:418:TYR:OH	2.26	0.45
1:H:211:GLU:HG3	1:H:212:PRO:HD3	1.97	0.45
1:I:669:TRP:HA	1:I:672:LEU:HD12	1.99	0.45
5:N:263:ASN:HA	5:N:266:ILE:HG22	1.99	0.45
1:I:666:MET:HE3	1:I:666:MET:HB3	1.88	0.45
5:N:22:GLU:OE1	5:N:144:LYS:NZ	2.36	0.45
1:D:386:ARG:HH21	1:D:456:ASP:N	2.15	0.45
1:I:358:LYS:HE2	1:I:358:LYS:HB3	1.73	0.45
2:K:112:GLU:OE2	2:K:116:ARG:NE	2.47	0.45
1:G:766:MET:HA	1:G:766:MET:HE2	1.99	0.45
1:J:633:PRO:HA	1:J:636:PHE:CE2	2.52	0.45
2:K:1086:LEU:HD12	2:K:1251:LYS:HG2	1.98	0.45
5:N:323:ARG:HB2	5:N:327:PHE:CD2	2.52	0.45
2:K:41:ILE:HD12	2:K:44:ILE:HD11	2.00	0.44
5:N:311:ALA:O	5:N:315:LYS:N	2.48	0.44
1:D:71:ILE:HG21	1:D:599:ILE:HG23	1.99	0.44
5:N:215:LEU:HD13	5:N:218:PHE:O	2.17	0.44
5:N:324:LEU:HD23	5:N:325:LYS:NZ	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:741:VAL:HG22	1:F:771:TRP:HB2	1.99	0.44
2:K:222:MET:HG3	2:K:227:ILE:HG13	1.98	0.44
5:N:328:GLU:O	5:N:333:ARG:NH2	2.50	0.44
1:C:312:ILE:O	1:E:408:TYR:OH	2.31	0.44
1:F:36:LEU:HD21	1:F:290:ILE:HG13	1.99	0.44
1:I:249:THR:HG22	1:J:359:ILE:HD11	1.99	0.44
5:N:341:ILE:HG13	5:N:386:TYR:HE2	1.82	0.44
2:K:95:PHE:HZ	2:K:178:PHE:HE2	1.66	0.44
5:N:261:ILE:HD12	5:N:261:ILE:H	1.82	0.44
5:N:390:VAL:HA	5:N:394:TYR:HE2	1.82	0.44
1:E:40:MET:HE1	2:K:1287:ILE:H	1.83	0.44
1:G:354:ILE:HD12	1:G:391:THR:HG22	1.99	0.44
1:G:545:PRO:HG2	1:G:548:MET:HE3	1.99	0.44
1:I:327:LEU:HD23	1:I:327:LEU:HA	1.89	0.44
1:I:411:ASN:OD1	1:I:413:ARG:HG2	2.17	0.44
1:G:344:TYR:O	1:G:348:MET:HG3	2.18	0.44
1:F:487:THR:OG1	1:F:488:TYR:N	2.51	0.44
1:E:141:GLY:HA2	1:E:213:VAL:HG13	1.98	0.44
1:G:633:PRO:HA	1:G:636:PHE:CE2	2.53	0.44
2:K:474:ILE:HD11	2:K:1039:LEU:HD13	2.00	0.44
5:N:293:ASP:OD1	5:N:293:ASP:N	2.50	0.44
1:A:57:VAL:HA	2:K:302:THR:HG23	2.00	0.43
1:E:197:VAL:HG13	1:E:225:GLU:OE1	2.17	0.43
2:K:442:LEU:HD11	2:K:484:PHE:HE1	1.83	0.43
5:N:324:LEU:O	5:N:328:GLU:HB2	2.18	0.43
5:N:516:TYR:O	5:N:517:PHE:C	2.61	0.43
1:F:141:GLY:HA2	1:F:213:VAL:HG13	1.99	0.43
1:H:386:ARG:NH2	1:H:456:ASP:OD1	2.44	0.43
1:J:648:VAL:HG12	1:J:652:MET:HE2	1.99	0.43
2:K:830:ILE:HG21	2:K:853:MET:HE1	1.99	0.43
1:B:36:LEU:HD23	1:B:36:LEU:HA	1.87	0.43
1:E:421:THR:OG1	1:E:426:ASP:OD2	2.29	0.43
1:G:370:ARG:NH2	1:G:404:ASP:OD2	2.35	0.43
2:K:987:PHE:HA	2:K:990:MET:HG2	1.99	0.43
5:N:740:ASN:HD21	5:N:764:LEU:HB2	1.83	0.43
1:D:633:PRO:HA	1:D:636:PHE:CE2	2.53	0.43
1:J:421:THR:HG22	1:J:423:GLU:H	1.83	0.43
1:F:714:ARG:HE	1:F:836:PRO:HB3	1.84	0.43
1:G:36:LEU:O	1:G:40:MET:HG3	2.18	0.43
1:H:670:VAL:HG12	1:H:671:MET:HE2	1.99	0.43
1:J:705:MET:HE1	1:J:800:PHE:HE2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:N:7:PRO:HD2	5:N:23:PHE:O	2.19	0.43
5:N:291:VAL:HG21	5:N:369:ILE:HG21	2.00	0.43
2:K:1025:MET:HE2	2:K:1025:MET:HB3	1.91	0.43
1:C:36:LEU:O	1:C:40:MET:HG2	2.19	0.43
1:F:633:PRO:HA	1:F:636:PHE:CE2	2.54	0.43
1:H:71:ILE:HG21	1:H:599:ILE:HG23	2.01	0.43
1:I:386:ARG:HH21	1:I:456:ASP:H	1.67	0.43
2:K:656:ARG:NH1	2:K:713:ASP:OD1	2.51	0.43
5:N:138:VAL:HG21	5:N:858:ILE:HD11	2.00	0.43
1:E:98:ARG:HG3	1:E:98:ARG:HH11	1.84	0.43
2:K:235:MET:HE3	2:K:235:MET:HB3	1.85	0.43
2:K:573:ARG:NH1	2:K:815:THR:OG1	2.49	0.43
5:N:32:GLU:CD	5:N:32:GLU:H	2.27	0.43
5:N:216:ILE:HG13	5:N:217:ASN:N	2.34	0.43
5:N:864:ILE:HB	5:N:870:CYS:SG	2.58	0.43
1:F:421:THR:OG1	1:F:426:ASP:OD2	2.29	0.43
1:J:99:ASP:N	1:J:99:ASP:OD1	2.51	0.43
1:B:793:ASP:OD1	1:B:794:VAL:N	2.51	0.43
1:E:805:ASN:OD1	1:E:807:ARG:NH2	2.52	0.43
1:H:371:MET:HB3	1:H:405:TYR:HD1	1.84	0.43
2:K:321:ARG:NH1	2:K:325:GLU:OE2	2.51	0.43
2:K:940:MET:HE1	2:K:1243:LEU:HD22	2.01	0.43
5:N:60:LEU:HD23	5:N:60:LEU:HA	1.83	0.43
1:C:160:GLU:O	1:C:163:VAL:HG12	2.19	0.42
1:C:470:ARG:NH1	1:C:546:ASP:OD1	2.41	0.42
2:K:758:SER:HB3	2:K:769:TYR:HB2	2.01	0.42
5:N:390:VAL:HB	5:N:394:TYR:HD2	1.83	0.42
5:N:637:LEU:HD12	5:N:741:PHE:CE2	2.54	0.42
1:E:484:ASN:HD22	1:F:410:TYR:HB2	1.85	0.42
1:H:633:PRO:HA	1:H:636:PHE:CE2	2.54	0.42
1:D:695:GLU:OE2	1:D:855:LYS:HG2	2.18	0.42
5:N:330:ARG:HG3	5:N:331:ASN:H	1.84	0.42
1:A:249:THR:HG22	1:B:359:ILE:HD11	2.01	0.42
1:I:633:PRO:HA	1:I:636:PHE:CE2	2.54	0.42
2:K:1237:CYS:O	2:K:1241:ILE:HG12	2.19	0.42
2:K:1281:LYS:HB3	2:K:1287:ILE:HG12	2.01	0.42
5:N:360:PRO:HD2	5:N:361:TYR:HD1	1.83	0.42
1:H:160:GLU:O	1:H:163:VAL:HG12	2.20	0.42
2:K:474:ILE:HG22	2:K:475:ASN:N	2.34	0.42
5:N:43:ILE:N	5:N:44:PRO:HD2	2.35	0.42
1:I:283:ARG:O	1:I:655:SER:OG	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:612:VAL:HG21	1:J:681:LEU:HD11	2.01	0.42
5:N:354:ARG:HD3	5:N:356:TRP:CZ2	2.55	0.42
5:N:383:ARG:NH1	5:N:383:ARG:O	2.53	0.42
5:N:390:VAL:HG23	5:N:399:LYS:HD2	2.01	0.42
1:B:179:HIS:O	1:B:183:ILE:HG12	2.20	0.42
1:J:354:ILE:HD12	1:J:391:THR:HG22	2.02	0.42
2:K:515:PRO:HB3	2:K:829:MET:HE3	2.00	0.42
4:M:594:A:O2'	4:M:595:U:OP1	2.36	0.42
5:N:437:GLU:C	5:N:438:ILE:HD13	2.43	0.42
1:A:309:ILE:O	1:A:313:THR:OG1	2.21	0.42
1:H:271:LEU:O	1:H:273:VAL:HG23	2.20	0.42
1:H:847:THR:C	1:H:848:MET:HE2	2.45	0.42
1:I:354:ILE:HD12	1:I:391:THR:HG22	2.01	0.42
5:N:229:ASN:OD1	5:N:229:ASN:N	2.52	0.42
1:C:127:TYR:HD1	1:C:617:LEU:HD22	1.84	0.42
1:E:122:GLU:CD	1:E:125:LYS:HD3	2.45	0.42
2:K:259:ASN:HA	2:K:262:ARG:HG3	2.02	0.42
1:A:878:LYS:HB2	1:A:881:MET:HG2	2.02	0.42
1:B:703:VAL:HG21	1:B:779:ARG:HD2	2.02	0.42
1:H:71:ILE:HD11	1:H:651:VAL:HG21	2.01	0.42
5:N:451:GLU:OE1	5:N:451:GLU:HA	2.20	0.42
1:D:106:THR:HA	1:D:109:GLU:HG2	2.02	0.41
1:H:628:LEU:HD12	1:H:631:ALA:HB2	2.02	0.41
1:I:204:VAL:HG12	1:I:875:VAL:HG22	2.02	0.41
1:J:434:TYR:OH	1:J:499:GLU:OE1	2.33	0.41
1:J:762:LEU:O	1:J:766:MET:HG2	2.20	0.41
5:N:308:PHE:CZ	5:N:312:ILE:HD11	2.56	0.41
1:A:360:ASP:HB3	1:A:363:GLU:HG2	2.02	0.41
5:N:302:ALA:O	5:N:306:ILE:HG12	2.20	0.41
1:C:327:LEU:HD12	1:C:327:LEU:HA	1.92	0.41
1:I:327:LEU:HD12	1:I:372:VAL:HG21	2.02	0.41
2:K:873:LYS:O	2:K:877:ILE:HG12	2.21	0.41
1:A:151:ARG:HB3	1:A:160:GLU:OE2	2.19	0.41
1:A:497:TYR:OH	1:A:516:PHE:O	2.38	0.41
1:D:706:HIS:ND1	1:D:708:ASP:OD1	2.41	0.41
1:F:291:MET:HE3	1:F:291:MET:HB3	1.89	0.41
1:J:236:ILE:O	1:J:240:GLU:HG3	2.21	0.41
1:J:737:GLU:O	1:J:741:VAL:HG23	2.21	0.41
2:K:382:TYR:HA	2:K:515:PRO:O	2.20	0.41
2:K:444:LEU:HG	2:K:534:LEU:HD22	2.01	0.41
5:N:247:ILE:HG22	5:N:248:PRO:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:N:335:ASP:O	5:N:338:ARG:HB2	2.21	0.41
5:N:807:ASN:OD1	5:N:808:GLU:N	2.46	0.41
1:A:358:LYS:HB3	1:A:570:ASP:HB2	2.01	0.41
1:B:478:ASP:OD1	1:B:479:SER:N	2.54	0.41
1:E:386:ARG:NH2	1:E:456:ASP:OD2	2.53	0.41
1:H:354:ILE:HD12	1:H:391:THR:HG22	2.03	0.41
1:J:160:GLU:O	1:J:163:VAL:HG12	2.21	0.41
2:K:478:ILE:HD12	2:K:478:ILE:H	1.86	0.41
2:K:890:ALA:O	2:K:891:MET:HE2	2.21	0.41
5:N:315:LYS:HE3	5:N:349:ASP:OD2	2.20	0.41
1:E:223:TYR:CD2	1:E:679:LEU:HD13	2.55	0.41
1:F:160:GLU:O	1:F:163:VAL:HG12	2.21	0.41
1:H:835:THR:HB	1:H:838:SER:HB3	2.02	0.41
1:J:75:ALA:HB2	1:J:602:VAL:HG21	2.03	0.41
1:A:182:MET:HE2	1:A:182:MET:HB3	1.94	0.41
1:E:370:ARG:NH2	1:E:404:ASP:OD2	2.39	0.41
1:I:789:ARG:HA	1:I:790:PRO:HD3	1.94	0.41
2:K:45:ARG:HD2	2:K:45:ARG:HA	1.73	0.41
2:K:1074:TYR:HE1	2:K:1275:THR:HG21	1.85	0.41
5:N:125:GLN:HA	5:N:125:GLN:OE1	2.21	0.41
1:A:615:ARG:NH2	1:A:672:LEU:O	2.54	0.41
1:A:798:LEU:HA	1:A:799:PRO:HD3	1.92	0.41
1:B:118:ILE:HG12	1:B:780:THR:HG23	2.01	0.41
1:B:409:MET:HE2	1:B:414:VAL:HG22	2.03	0.41
1:F:271:LEU:HD11	1:F:890:LEU:HB3	2.03	0.41
1:F:323:PRO:HG3	1:F:511:SER:HB3	2.02	0.41
1:H:612:VAL:HG21	1:H:681:LEU:HD11	2.03	0.41
1:I:126:PHE:O	1:I:130:ILE:HG12	2.21	0.41
1:I:238:TRP:CH2	1:I:242:LEU:HD22	2.55	0.41
5:N:202:ARG:HA	5:N:202:ARG:HH11	1.85	0.41
5:N:258:LEU:HD21	5:N:283:ILE:HG21	2.03	0.41
5:N:323:ARG:HB2	5:N:327:PHE:CE2	2.56	0.41
5:N:632:PHE:O	5:N:636:ILE:HG12	2.20	0.41
5:N:805:LYS:HE2	5:N:805:LYS:HB2	1.94	0.41
1:B:485:PRO:HD2	1:C:663:ILE:HD11	2.03	0.41
1:C:517:ARG:NH2	1:E:410:TYR:OH	2.54	0.41
1:H:223:TYR:CD1	1:H:679:LEU:HD13	2.56	0.41
1:H:789:ARG:HA	1:H:790:PRO:HD3	1.95	0.41
1:I:370:ARG:NH2	1:I:404:ASP:OD2	2.40	0.41
1:I:470:ARG:NH1	1:I:546:ASP:OD1	2.47	0.41
2:K:207:MET:HG2	2:K:247:PHE:HE1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:N:500:GLU:HG3	5:N:501:LYS:N	2.36	0.41
1:A:848:MET:HE3	1:A:848:MET:HB3	1.97	0.40
1:B:303:ILE:HG13	1:B:585:GLU:HG3	2.03	0.40
1:D:434:TYR:OH	1:D:499:GLU:OE1	2.36	0.40
1:J:620:MET:HE1	1:J:694:PHE:HZ	1.84	0.40
1:B:223:TYR:CD1	1:B:679:LEU:HD13	2.57	0.40
1:B:354:ILE:HD12	1:B:391:THR:HG22	2.04	0.40
1:B:663:ILE:HA	1:B:666:MET:HE2	2.03	0.40
1:G:111:MET:HE1	1:G:133:LYS:HB3	2.04	0.40
2:K:742:MET:HA	2:K:790:THR:HG21	2.03	0.40
2:K:814:GLN:HG3	3:L:598:A:H5'	2.04	0.40
1:A:71:ILE:HG21	1:A:599:ILE:HG23	2.03	0.40
1:C:112:SER:O	1:C:782:ARG:NH1	2.54	0.40
1:H:331:THR:HA	1:H:332:PRO:HD3	1.94	0.40
1:B:118:ILE:HD12	1:B:126:PHE:HD2	1.86	0.40
1:B:386:ARG:HH21	1:B:456:ASP:N	2.14	0.40
1:F:168:PHE:CZ	1:F:187:LEU:HD11	2.56	0.40
1:I:201:ASP:N	1:I:201:ASP:OD1	2.53	0.40
2:K:286:ALA:HB2	2:K:295:VAL:HG22	2.03	0.40
5:N:555:THR:HG23	5:N:561:LEU:HD22	2.04	0.40
1:A:386:ARG:NH2	1:A:454:THR:O	2.55	0.40
1:D:160:GLU:O	1:D:163:VAL:HG12	2.21	0.40
1:H:326:ILE:HG13	1:H:327:LEU:N	2.35	0.40
1:H:456:ASP:OD1	1:H:456:ASP:N	2.55	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	869/901 (96%)	855 (98%)	14 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	881/901 (98%)	863 (98%)	18 (2%)	0	100	100
1	C	873/901 (97%)	859 (98%)	14 (2%)	0	100	100
1	D	881/901 (98%)	862 (98%)	19 (2%)	0	100	100
1	E	854/901 (95%)	841 (98%)	13 (2%)	0	100	100
1	F	881/901 (98%)	854 (97%)	27 (3%)	0	100	100
1	G	860/901 (95%)	845 (98%)	15 (2%)	0	100	100
1	H	881/901 (98%)	861 (98%)	20 (2%)	0	100	100
1	I	873/901 (97%)	857 (98%)	16 (2%)	0	100	100
1	J	881/901 (98%)	858 (97%)	23 (3%)	0	100	100
2	K	1284/1302 (99%)	1255 (98%)	29 (2%)	0	100	100
5	N	959/961 (100%)	924 (96%)	35 (4%)	0	100	100
All	All	10977/11273 (97%)	10734 (98%)	243 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	766/792 (97%)	766 (100%)	0	100	100
1	B	782/792 (99%)	782 (100%)	0	100	100
1	C	769/792 (97%)	769 (100%)	0	100	100
1	D	782/792 (99%)	782 (100%)	0	100	100
1	E	754/792 (95%)	753 (100%)	1 (0%)	88	97
1	F	782/792 (99%)	782 (100%)	0	100	100
1	G	760/792 (96%)	760 (100%)	0	100	100
1	H	782/792 (99%)	782 (100%)	0	100	100
1	I	769/792 (97%)	768 (100%)	1 (0%)	88	97
1	J	782/792 (99%)	782 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	K	1151/1161 (99%)	1151 (100%)	0	100	100
5	N	863/863 (100%)	858 (99%)	5 (1%)	78	92
All	All	9742/9944 (98%)	9735 (100%)	7 (0%)	87	97

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

Mol	Chain	Res	Type
1	E	244	HIS
1	I	58	ASP
5	N	502	ASP
5	N	504	LYS
5	N	511	VAL
5	N	512	THR
5	N	513	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (80) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	393	ASN
1	A	397	GLN
1	A	484	ASN
1	A	539	HIS
1	A	563	ASN
1	A	581	ASN
1	A	630	GLN
1	A	723	GLN
1	B	113	GLN
1	B	185	ASN
1	B	221	GLN
1	B	397	GLN
1	B	417	ASN
1	B	581	ASN
1	B	616	HIS
1	B	658	HIS
1	B	659	ASN
1	B	829	ASN
1	B	854	ASN
1	C	45	GLN
1	C	184	GLN
1	C	397	GLN

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Mol	Chain	Res	Type
1	C	539	HIS
1	C	550	ASN
1	C	581	ASN
1	C	752	GLN
1	D	65	GLN
1	D	113	GLN
1	D	185	ASN
1	D	230	GLN
1	D	411	ASN
1	D	659	ASN
1	E	417	ASN
1	E	581	ASN
1	E	706	HIS
1	E	752	GLN
1	E	754	ASN
1	E	829	ASN
1	F	335	GLN
1	F	397	GLN
1	F	415	GLN
1	F	656	HIS
1	G	415	GLN
1	G	433	GLN
1	G	484	ASN
1	G	752	GLN
1	G	754	ASN
1	H	65	GLN
1	H	184	GLN
1	H	221	GLN
1	H	539	HIS
1	H	581	ASN
1	H	659	ASN
1	H	843	ASN
1	I	221	GLN
1	I	393	ASN
1	I	550	ASN
1	I	563	ASN
1	I	581	ASN
1	I	702	GLN
1	J	234	ASN
1	J	532	GLN
1	J	539	HIS
2	K	55	GLN

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Mol	Chain	Res	Type
2	K	176	ASN
2	K	217	ASN
2	K	814	GLN
2	K	969	ASN
2	K	1212	GLN
2	K	1296	ASN
2	K	1299	ASN
5	N	171	ASN
5	N	172	HIS
5	N	206	GLN
5	N	263	ASN
5	N	481	GLN
5	N	534	HIS
5	N	639	GLN
5	N	740	ASN
5	N	947	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	L	6/7 (85%)	0	0
4	M	8/9 (88%)	1 (12%)	1 (12%)
All	All	14/16 (87%)	1 (7%)	1 (7%)

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	M	595	U

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	M	594	A

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

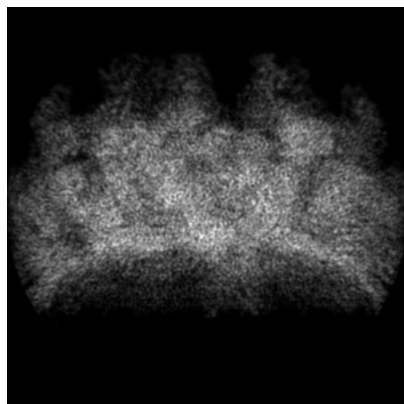
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43727. These allow visual inspection of the internal detail of the map and identification of artifacts.

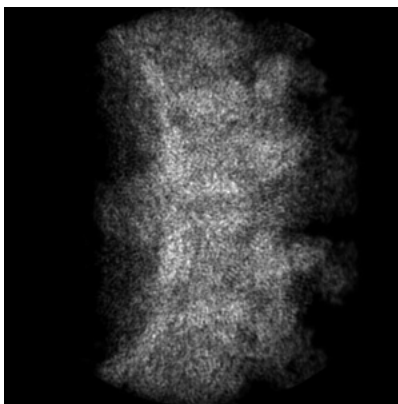
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

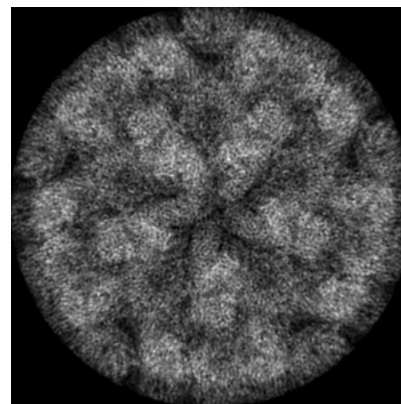
6.1.1 Primary map



X

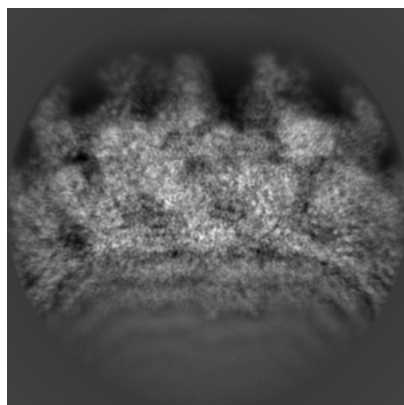


Y

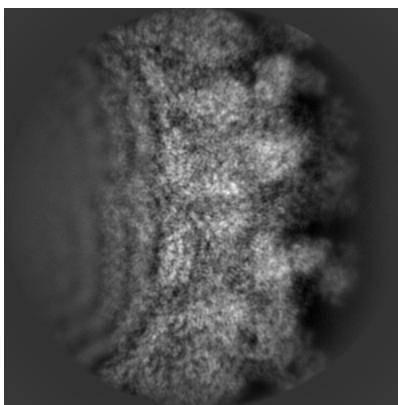


Z

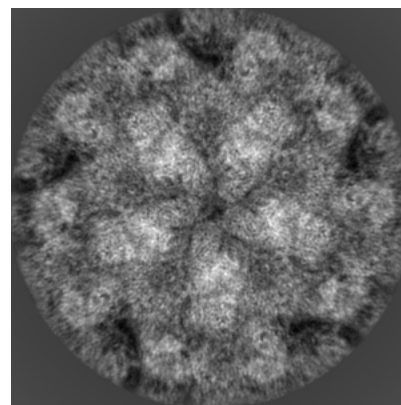
6.1.2 Raw map



X



Y



Z

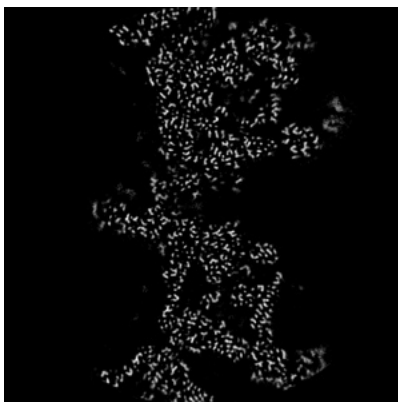
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

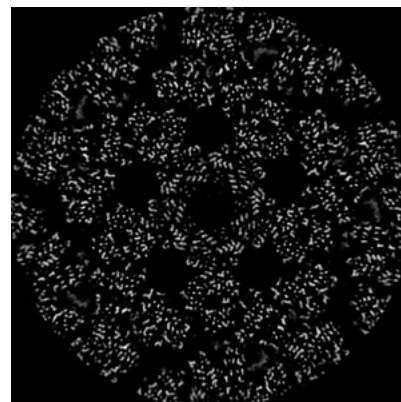
6.2.1 Primary map



X Index: 192

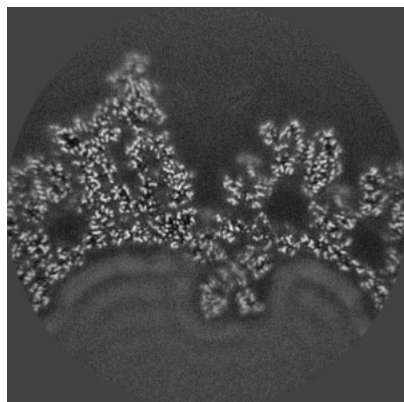


Y Index: 192

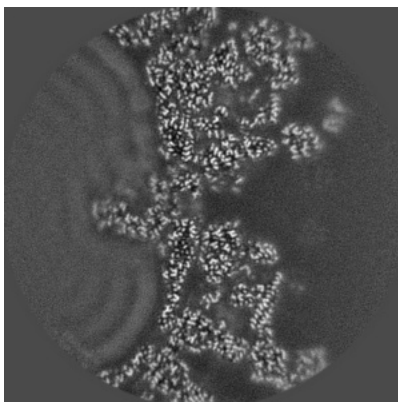


Z Index: 192

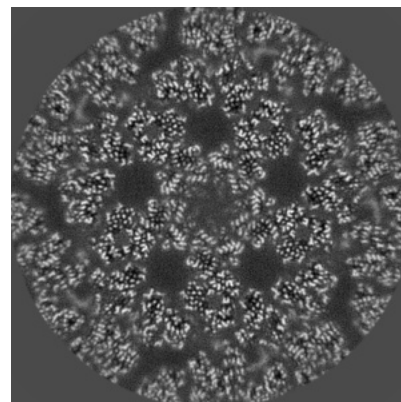
6.2.2 Raw map



X Index: 192



Y Index: 192



Z Index: 192

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

6.3 Largest variance slices [i](#)

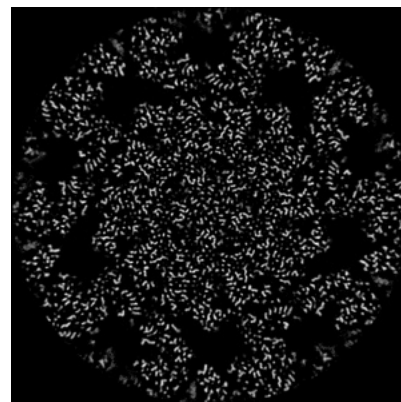
6.3.1 Primary map



X Index: 144

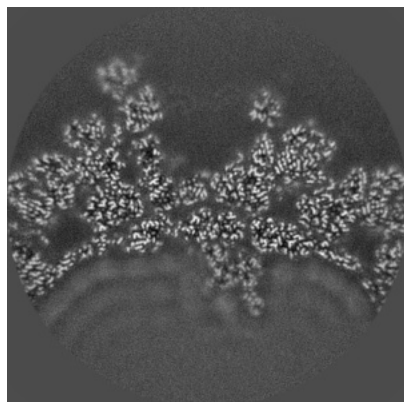


Y Index: 236

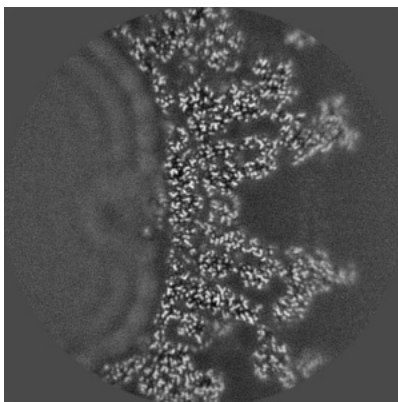


Z Index: 163

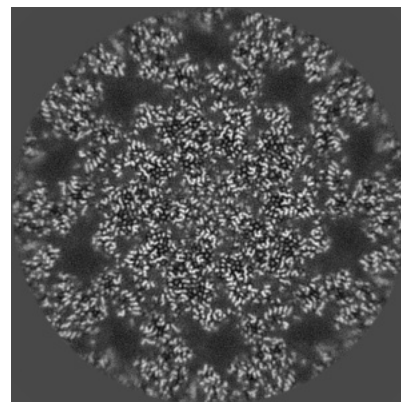
6.3.2 Raw map



X Index: 208



Y Index: 175

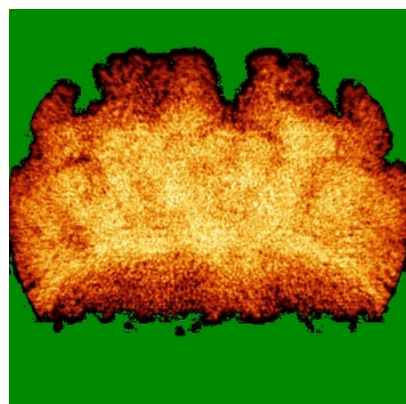


Z Index: 163

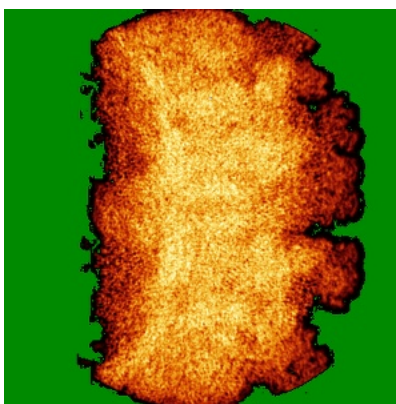
The images above show the largest variance slices of the map in three orthogonal directions.

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

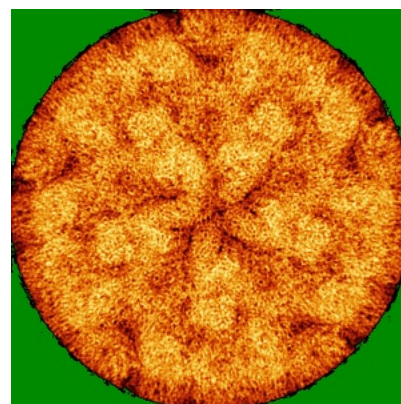
6.4.1 Primary map



X

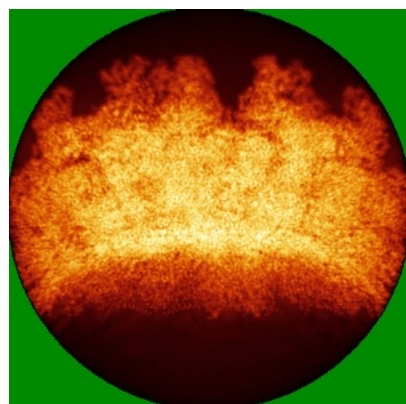


Y

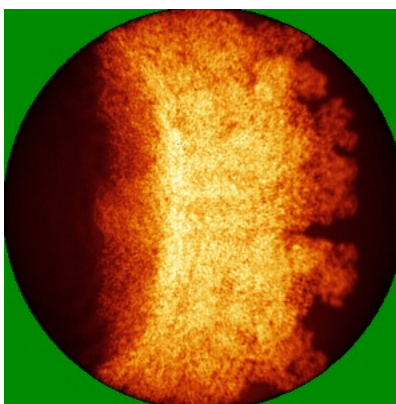


Z

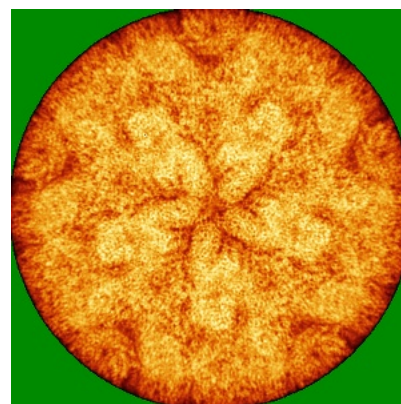
6.4.2 Raw map



X



Y

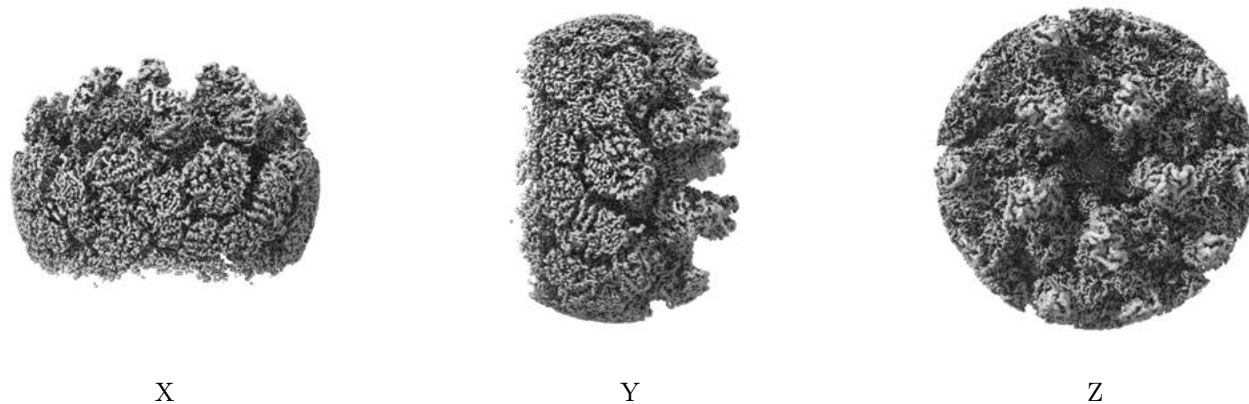


Z

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

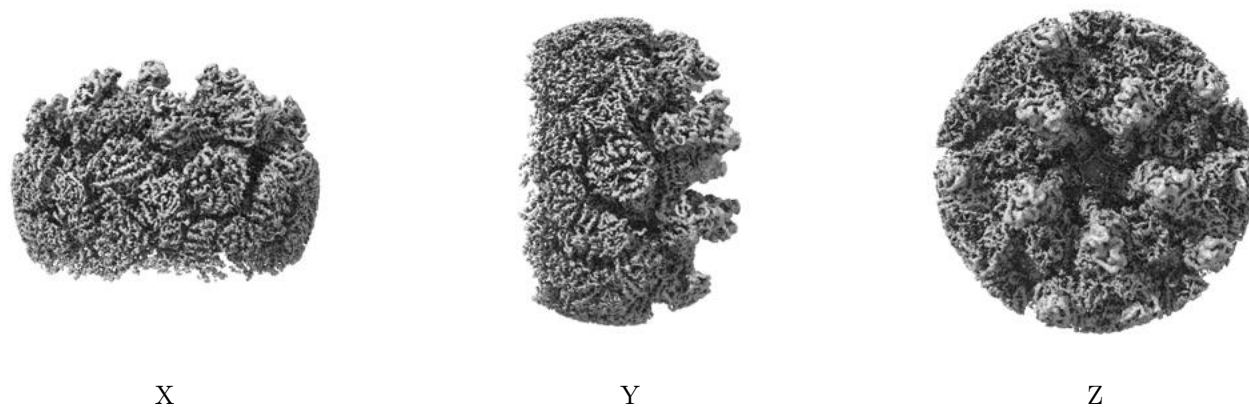
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

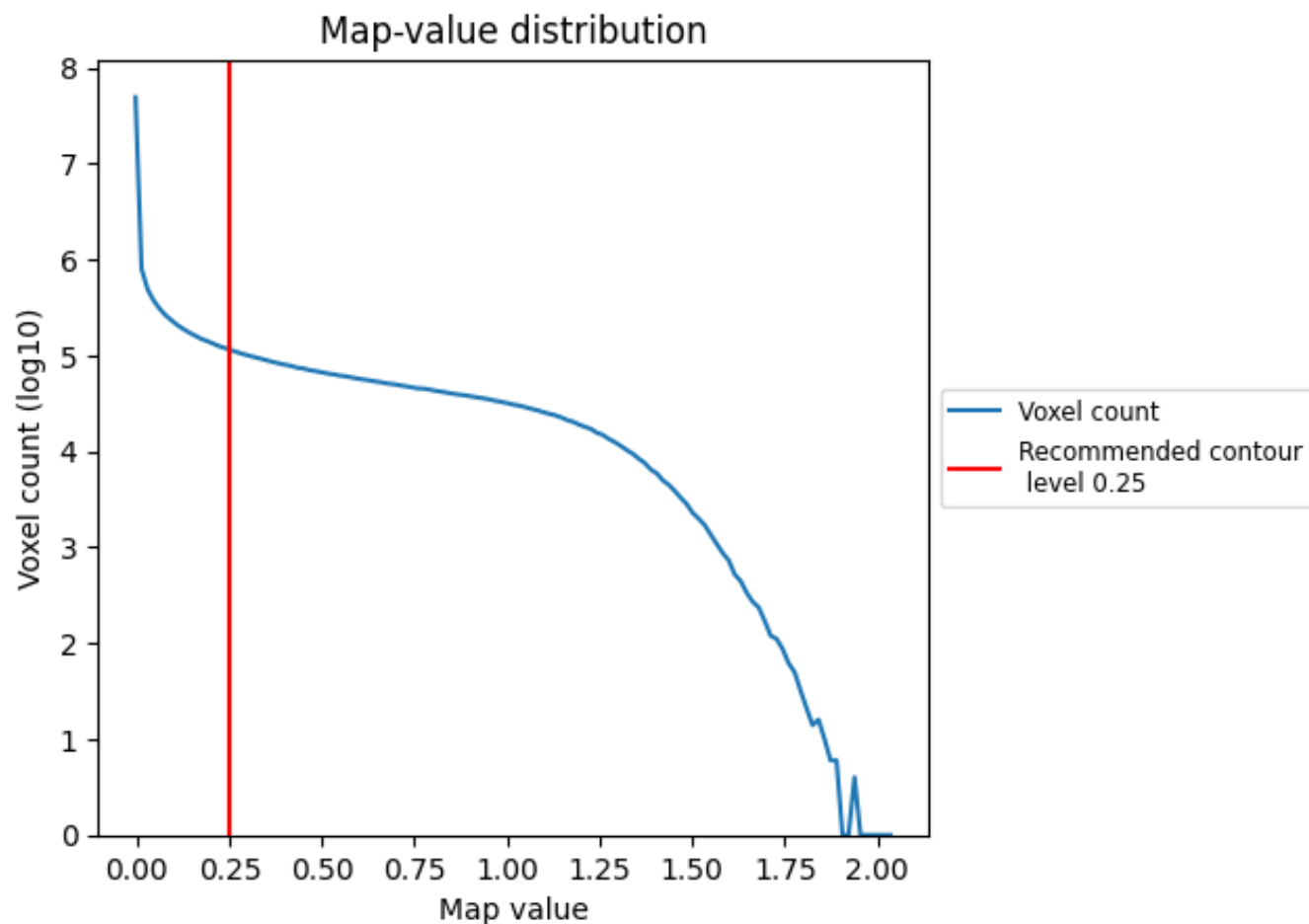
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

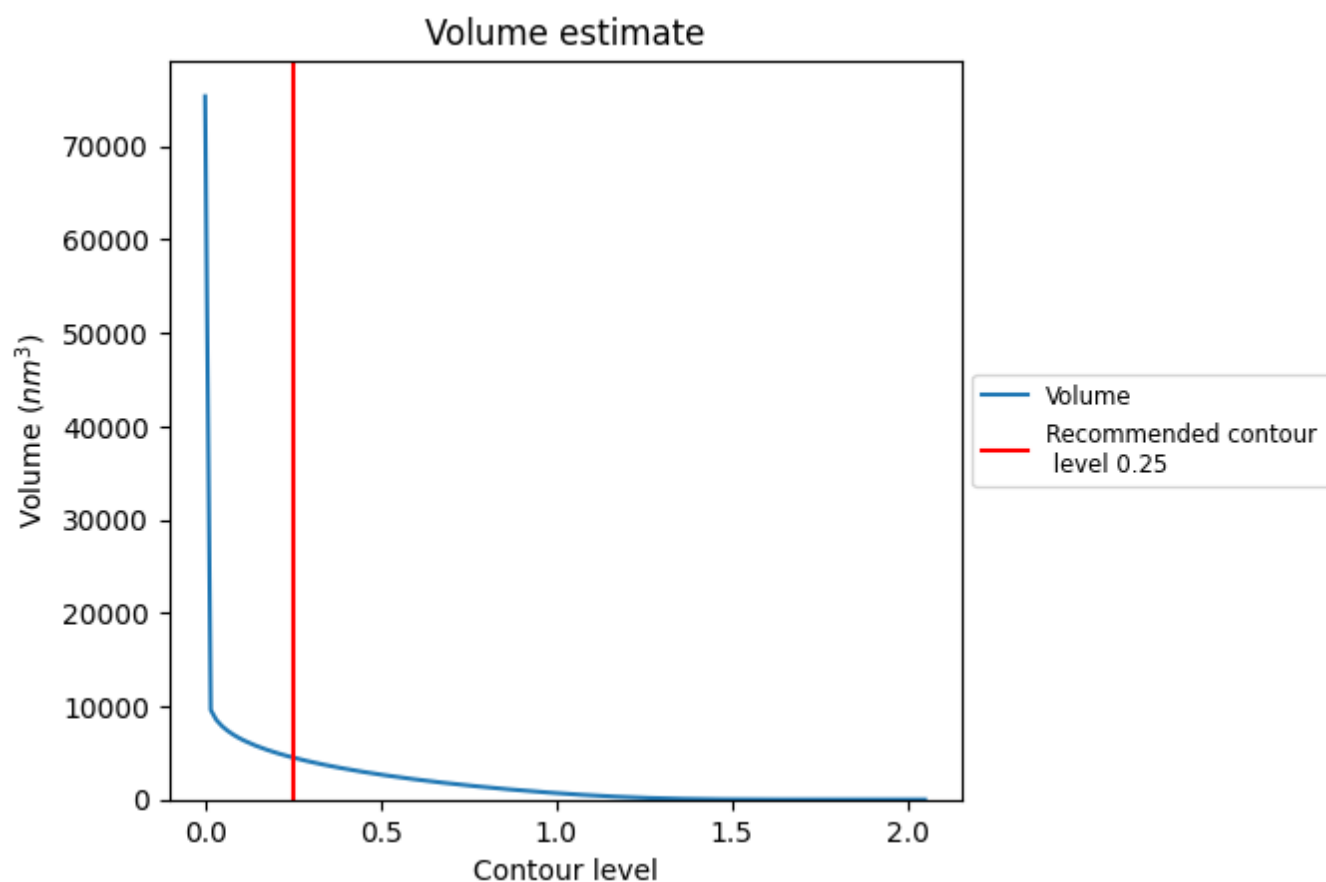
This section contains the results of statistical analysis of the map.

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.

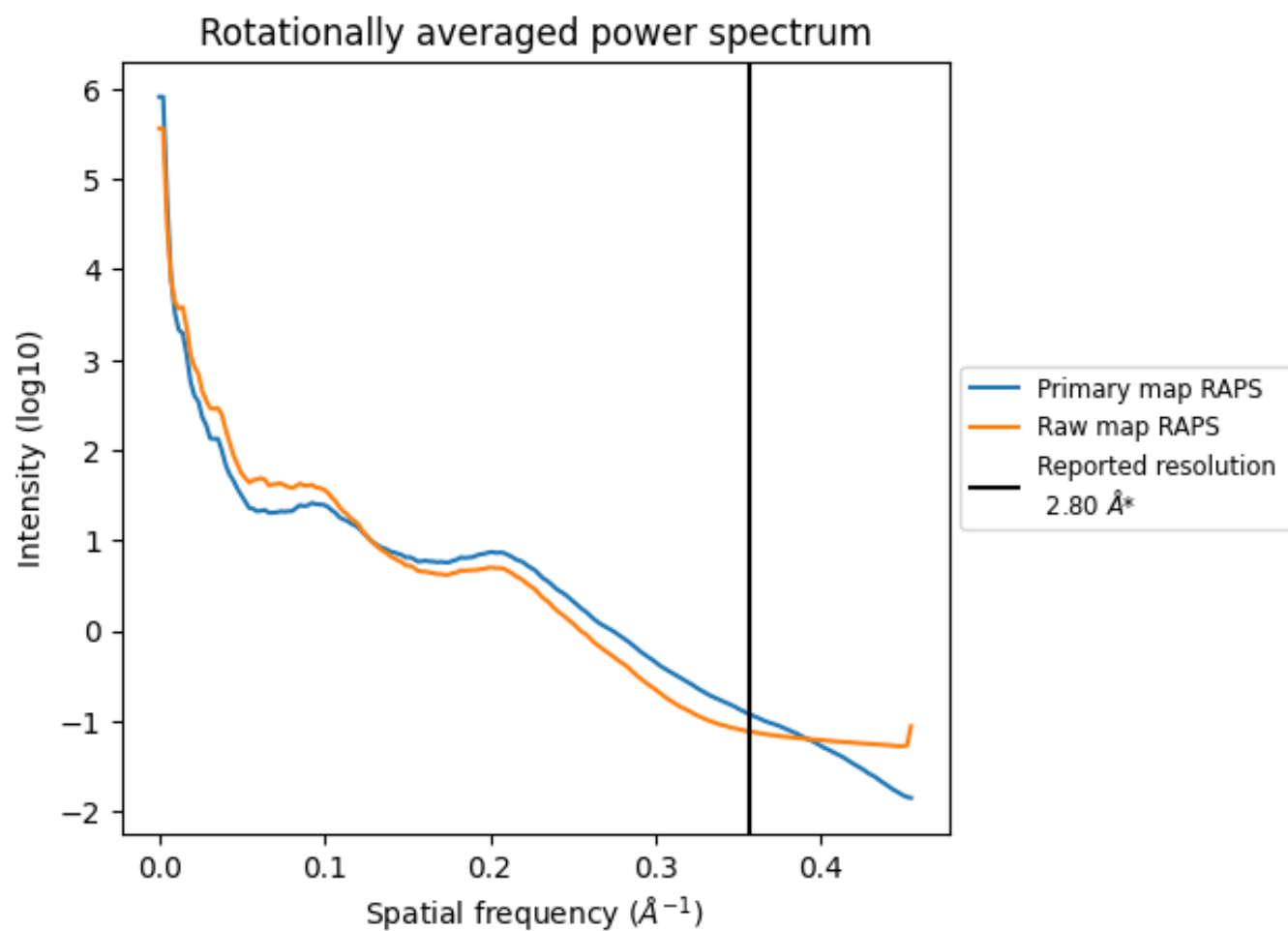
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4484 nm³; this corresponds to an approximate mass of 4050 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 ⓘ

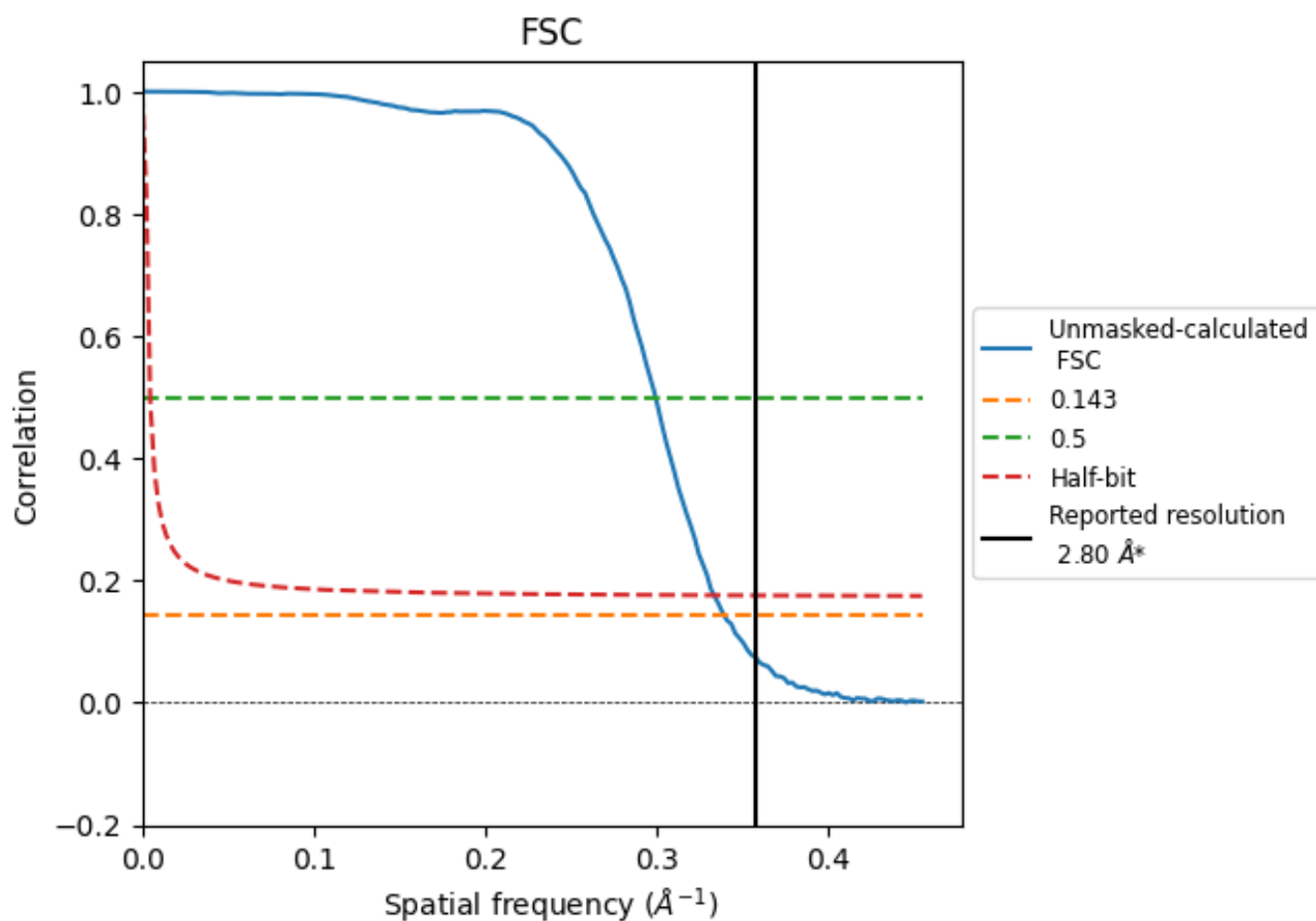


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

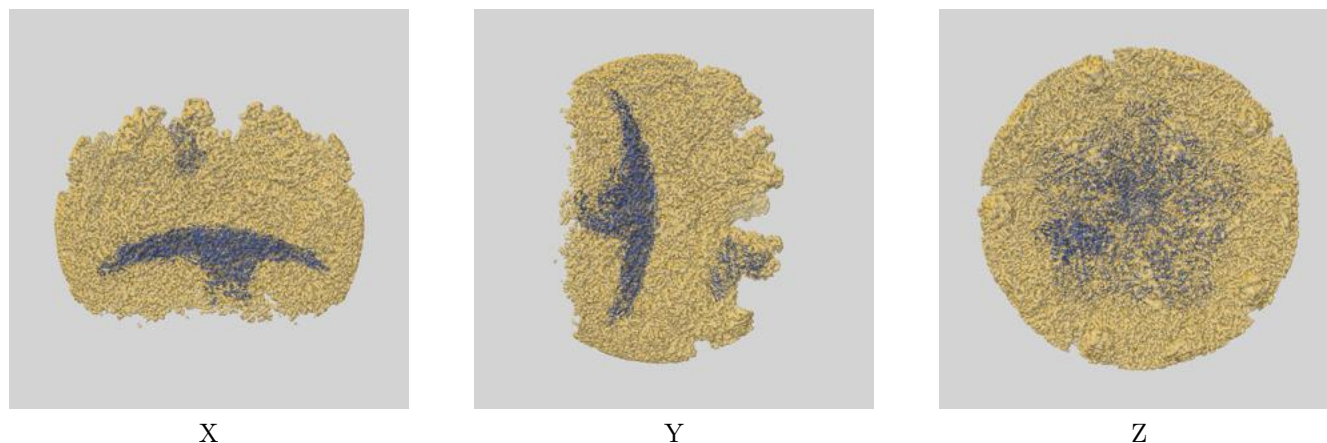
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.95	3.34	3.00

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

9 Map-model fit [i](#)

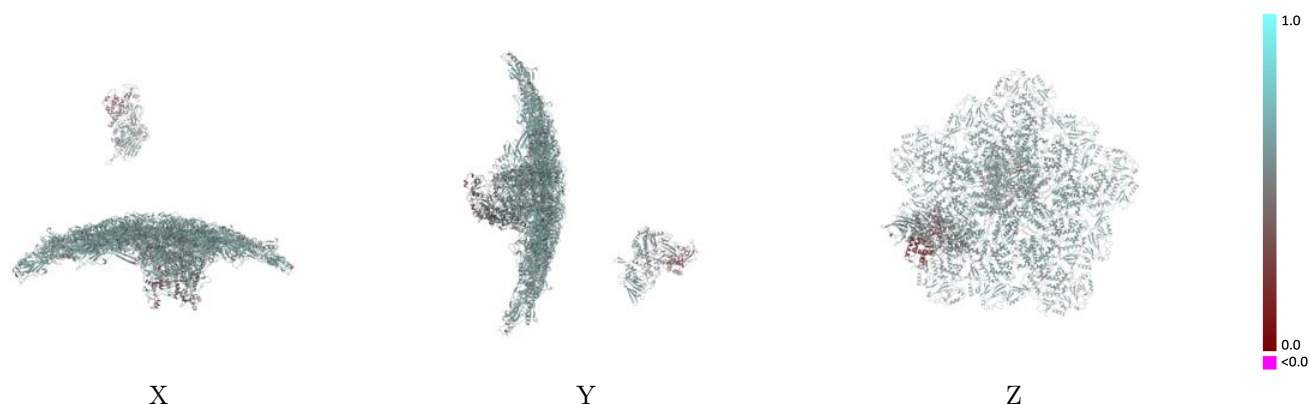
This section contains information regarding the fit between EMDB map EMD-43727 and PDB model 8W1O. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



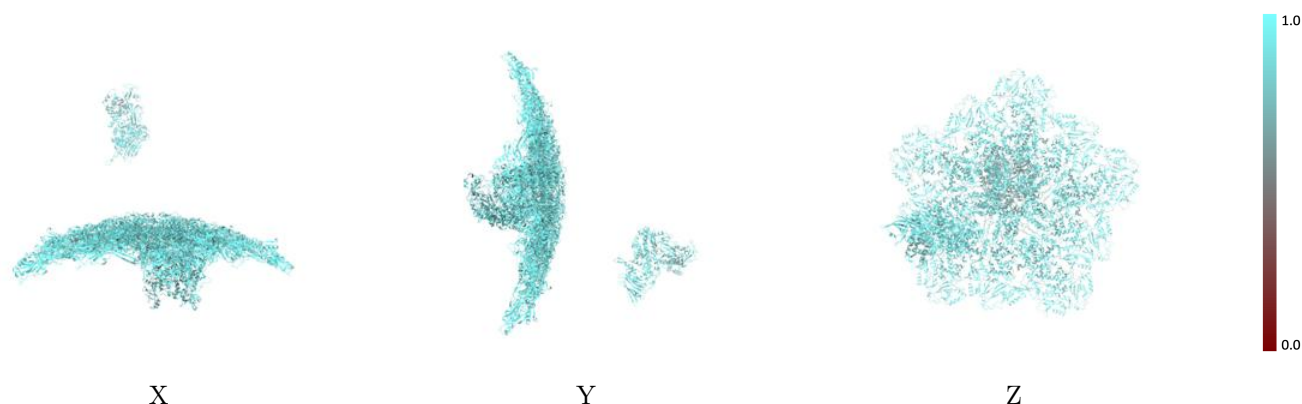
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



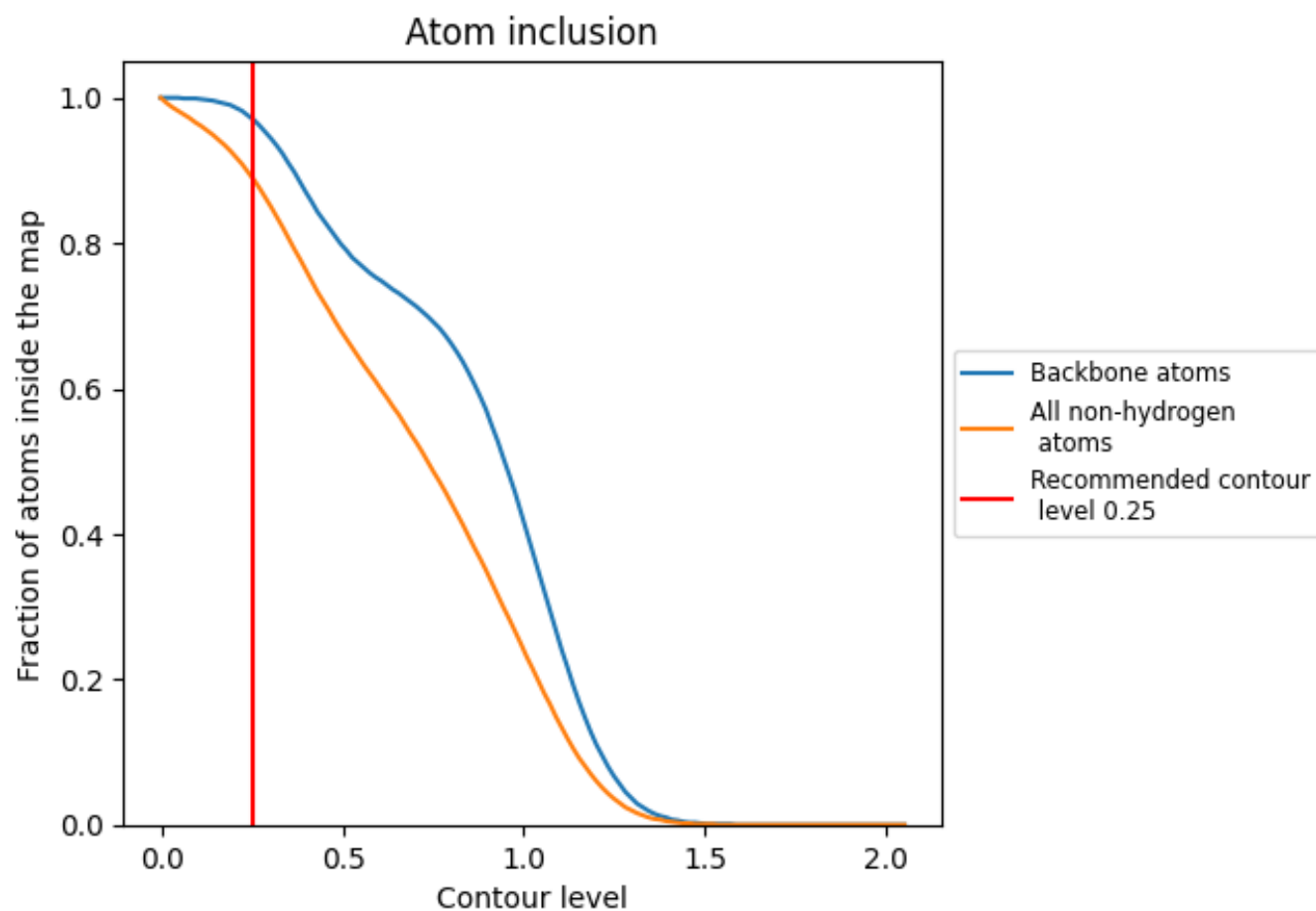
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 89% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8900	0.5580
A	0.9000	0.5780
B	0.9010	0.5710
C	0.8970	0.5750
D	0.9040	0.5700
E	0.9040	0.5790
F	0.9040	0.5700
G	0.9040	0.5780
H	0.9000	0.5670
I	0.9000	0.5770
J	0.8980	0.5680
K	0.8380	0.5120
L	0.8770	0.5260
M	0.7410	0.4910
N	0.8630	0.4880

