Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:01 PM UTC

PDB ID	:	5A7A / pdb_00005a7a
EMDB ID	:	EMD-3074
Title	:	Novel inter-subunit contacts in Barley Stripe Mosaic Virus revealed by cryo-EM
Authors	:	Clare, D.K.; Pechnikova, E.; Skurat, E.; Makarov, V.; Sokolova, O.S.; Solovyev, A.G.; V Orlova, E.
Deposited on	:	2015-07-03
Resolution	:	4.10 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:

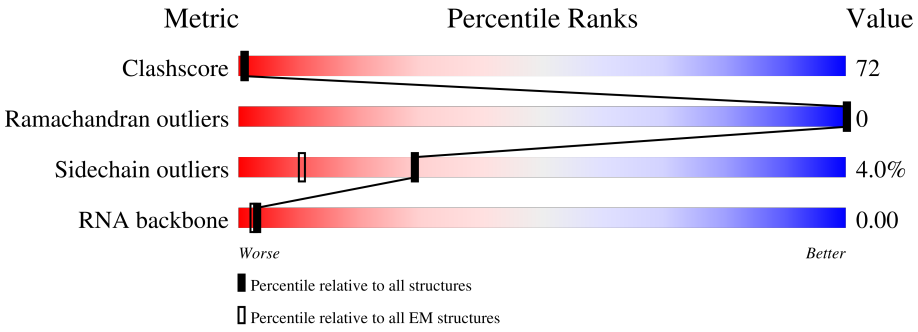
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

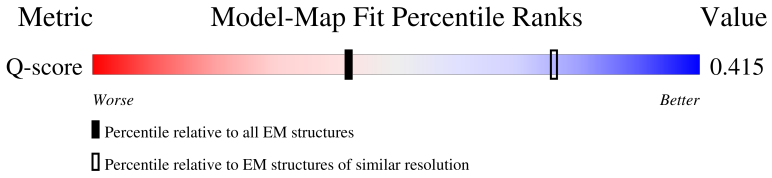
1 Overall quality at a glance

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

The reported resolution of this entry is 4.10 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	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	6458 (3.60 - 4.60)

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	198	27% 50% 11% 12%
2	R	3	33% 67%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1499 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 BARLEY STRIPE MOSAIC VIRUS NARROW.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	175	1432	908	262	262	0	0

- Molecule 2 is a RNA chain called RNA.

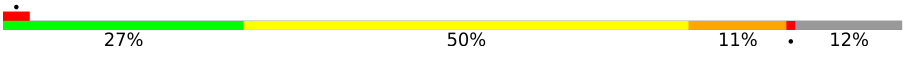
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	R	3	67	30	15	19	3	0	0

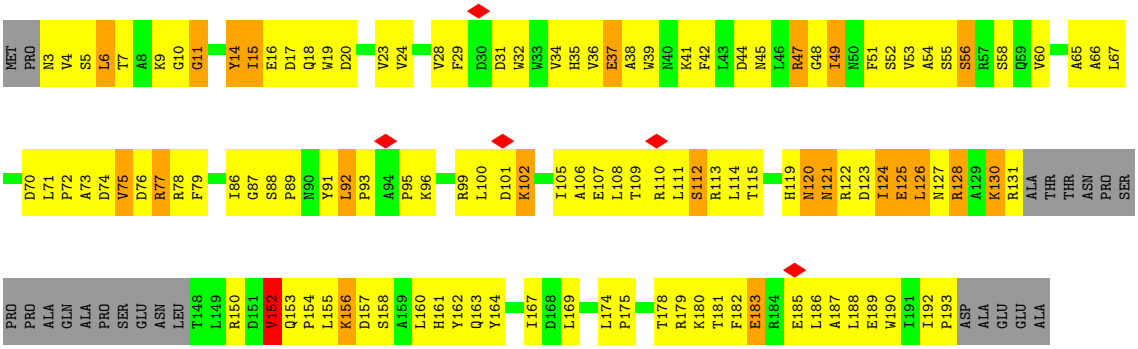
3 Residue-property plots (i)

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

• Molecule 1: BARLEY STRIPE MOSAIC VIRUS NARROW

Chain A:





• Molecule 2: RNA

Chain R:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of particles used	3007	Depositor
Resolution determination method	Not provided	
CTF correction method	PHASE FLIPPED EACH PARTICLE	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	150000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	169.579	Depositor
Minimum map value	-111.187	Depositor
Average map value	0.241	Depositor
Map value standard deviation	19.142	Depositor
Recommended contour level	20	Depositor
Map size (Å)	300.0, 300.0, 300.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

5 Model quality

5.1 Standard geometry

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	0.61	3/1465 (0.2%)	1.34	26/1989 (1.3%)
2	R	0.33	0/75	0.59	0/115
All	All	0.60	3/1540 (0.2%)	1.31	26/2104 (1.2%)

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	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	130	LYS	N-CA	5.89	1.53	1.45
1	A	130	LYS	CA-C	5.59	1.59	1.52
1	A	126	LEU	CA-C	5.22	1.59	1.52

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	126	LEU	N-CA-C	13.80	126.04	111.14
1	A	128	ARG	N-CA-C	10.09	122.27	111.28
1	A	37	GLU	N-CA-C	-8.89	100.20	113.72
1	A	75	VAL	N-CA-C	-8.81	97.48	109.37
1	A	152	VAL	N-CA-C	8.71	121.55	113.10
1	A	58	SER	N-CA-C	-7.83	103.45	113.16
1	A	102	LYS	N-CA-C	-7.76	102.78	111.71
1	A	17	ASP	N-CA-C	-7.68	101.78	112.45
1	A	180	LYS	N-CA-C	-7.23	103.40	111.28
1	A	130	LYS	N-CA-C	7.21	120.03	109.07
1	A	112	SER	N-CA-C	-7.18	103.45	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	121	ASN	N-CA-C	-7.17	103.63	112.38
1	A	77	ARG	N-CA-C	6.33	118.95	110.35
1	A	15	ILE	CA-C-N	-6.07	114.43	125.66
1	A	15	ILE	C-N-CA	-6.07	114.43	125.66
1	A	14	TYR	N-CA-C	-5.95	101.84	110.24
1	A	47	ARG	N-CA-C	5.88	117.38	110.97
1	A	181	THR	N-CA-C	5.80	120.40	112.04
1	A	6	LEU	CB-CA-C	-5.79	109.91	116.63
1	A	112	SER	CA-C-N	-5.75	112.05	122.50
1	A	112	SER	C-N-CA	-5.75	112.05	122.50
1	A	125	GLU	N-CA-C	5.65	117.52	111.36
1	A	183	GLU	N-CA-C	5.64	117.23	111.14
1	A	56	SER	N-CA-C	-5.25	106.26	113.30
1	A	11	GLY	N-CA-C	-5.21	100.82	113.18
1	A	124	ILE	N-CA-C	-5.19	105.48	110.72

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	113	ARG	Peptide
1	A	120	ASN	Peptide

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	1432	0	1408	208	0
2	R	67	0	34	19	0
All	All	1499	0	1442	212	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 72.

All (212) 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:91:TYR:CE2	1:A:93:PRO:HG3	1.46	1.50
1:A:156:LYS:CG	2:R:1:G:H21	1.57	1.16
1:A:91:TYR:CE2	1:A:93:PRO:CG	2.31	1.13
1:A:9:LYS:HE2	1:A:76:ASP:OD1	1.46	1.13
1:A:156:LYS:HG3	2:R:1:G:H21	1.09	1.13
1:A:91:TYR:CD2	1:A:93:PRO:HG3	1.84	1.11
1:A:130:LYS:O	1:A:131:ARG:CG	2.00	1.10
1:A:156:LYS:HG3	2:R:1:G:N2	1.65	1.09
1:A:192:ILE:HB	1:A:193:PRO:HD3	1.34	1.06
1:A:124:ILE:HB	1:A:128:ARG:HH21	1.13	1.06
1:A:156:LYS:CD	2:R:1:G:H21	1.70	1.02
1:A:130:LYS:C	1:A:131:ARG:HG3	1.87	0.99
1:A:124:ILE:HB	1:A:128:ARG:NH2	1.79	0.98
1:A:130:LYS:O	1:A:131:ARG:HG3	1.60	0.97
1:A:108:LEU:CD2	1:A:169:LEU:HD21	1.96	0.95
1:A:93:PRO:O	1:A:95:PRO:HD3	1.67	0.94
1:A:160:LEU:HD22	2:R:1:G:C5	2.03	0.94
1:A:108:LEU:HD21	1:A:169:LEU:HD21	1.47	0.93
1:A:192:ILE:HB	1:A:193:PRO:CD	1.98	0.93
1:A:91:TYR:CD2	1:A:93:PRO:CG	2.50	0.92
1:A:91:TYR:HE2	1:A:93:PRO:HG3	1.26	0.92
1:A:152:VAL:HG13	1:A:155:LEU:HD12	1.51	0.92
1:A:91:TYR:CD2	1:A:93:PRO:HD3	2.04	0.92
1:A:126:LEU:HD12	1:A:127:ASN:N	1.89	0.87
1:A:3:ASN:HA	1:A:5:SER:N	1.88	0.87
1:A:42:PHE:HB2	1:A:67:LEU:HD12	1.57	0.85
1:A:156:LYS:HD3	2:R:1:G:H21	1.40	0.85
1:A:23:VAL:O	1:A:28:VAL:HB	1.76	0.85
1:A:130:LYS:O	1:A:131:ARG:HG2	1.76	0.84
1:A:42:PHE:HB2	1:A:67:LEU:CD1	2.08	0.84
1:A:127:ASN:HA	1:A:130:LYS:O	1.79	0.83
1:A:14:TYR:CD2	1:A:19:TRP:CZ3	2.67	0.83
1:A:74:ASP:O	1:A:77:ARG:N	2.12	0.83
1:A:91:TYR:CD2	1:A:93:PRO:CD	2.62	0.82
1:A:3:ASN:HB2	1:A:4:VAL:HA	1.62	0.81
1:A:99:ARG:HB3	1:A:175:PRO:HG2	1.63	0.80
1:A:124:ILE:O	1:A:128:ARG:HB3	1.82	0.80
1:A:51:PHE:HZ	1:A:115:THR:HG22	1.45	0.80
1:A:156:LYS:HD3	2:R:1:G:N2	1.96	0.80
1:A:9:LYS:CE	1:A:76:ASP:OD1	2.28	0.79
1:A:107:GLU:O	1:A:110:ARG:HB2	1.82	0.79
2:R:2:A:O2'	2:R:3:A:OP1	2.01	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:ASN:O	1:A:122:ARG:N	2.17	0.77
1:A:156:LYS:CD	2:R:1:G:N2	2.48	0.77
1:A:18:GLN:NE2	1:A:187:ALA:O	2.17	0.76
1:A:88:SER:OG	1:A:89:PRO:HD2	1.83	0.76
1:A:152:VAL:CG1	1:A:155:LEU:HB2	2.18	0.74
1:A:4:VAL:O	1:A:6:LEU:HD23	1.88	0.73
1:A:152:VAL:HG12	1:A:155:LEU:HB2	1.69	0.73
1:A:9:LYS:HG3	1:A:77:ARG:HE	1.54	0.73
1:A:79:PHE:O	1:A:179:ARG:HD2	1.88	0.73
1:A:34:VAL:HG11	1:A:39:TRP:HE3	1.54	0.72
1:A:188:LEU:O	1:A:188:LEU:HD12	1.90	0.72
1:A:126:LEU:HD12	1:A:127:ASN:H	1.53	0.72
1:A:15:ILE:O	1:A:16:GLU:HB3	1.88	0.72
1:A:124:ILE:HG13	1:A:125:GLU:N	2.03	0.71
1:A:36:VAL:C	1:A:38:ALA:H	1.96	0.71
1:A:114:LEU:HD23	1:A:162:TYR:HD1	1.56	0.71
1:A:16:GLU:HA	1:A:19:TRP:HB2	1.72	0.70
1:A:3:ASN:HA	1:A:4:VAL:C	2.17	0.70
1:A:93:PRO:O	1:A:95:PRO:CD	2.39	0.69
2:R:2:A:H4'	2:R:3:A:OP2	1.93	0.68
1:A:42:PHE:O	1:A:45:ASN:HB2	1.92	0.68
1:A:34:VAL:HG21	1:A:100:LEU:HD11	1.76	0.68
1:A:109:THR:O	1:A:112:SER:HB3	1.92	0.68
1:A:71:LEU:HD23	1:A:72:PRO:N	2.08	0.68
1:A:91:TYR:CE2	1:A:93:PRO:CB	2.76	0.68
1:A:178:THR:O	1:A:182:PHE:N	2.24	0.68
1:A:106:ALA:O	1:A:109:THR:HG22	1.93	0.67
1:A:5:SER:OG	1:A:6:LEU:N	2.25	0.67
1:A:51:PHE:CZ	1:A:115:THR:HG22	2.28	0.67
1:A:128:ARG:HH11	1:A:128:ARG:HG2	1.58	0.67
1:A:152:VAL:HG13	1:A:155:LEU:CD1	2.22	0.67
1:A:102:LYS:O	1:A:105:ILE:HG13	1.96	0.66
1:A:3:ASN:HA	1:A:5:SER:CB	2.25	0.66
1:A:19:TRP:O	1:A:23:VAL:HB	1.96	0.66
1:A:92:LEU:N	1:A:93:PRO:HD3	2.11	0.66
1:A:3:ASN:HA	1:A:5:SER:HB3	1.78	0.65
1:A:130:LYS:C	1:A:131:ARG:CG	2.56	0.65
1:A:42:PHE:CB	1:A:67:LEU:CD1	2.75	0.65
1:A:105:ILE:HD12	1:A:106:ALA:N	2.11	0.65
1:A:71:LEU:HD23	1:A:72:PRO:HD2	1.80	0.64
1:A:108:LEU:HD23	1:A:169:LEU:HD21	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:SER:OG	2:R:3:A:N6	2.31	0.64
1:A:9:LYS:NZ	1:A:76:ASP:OD2	2.30	0.64
1:A:54:ALA:O	1:A:55:SER:HB3	1.98	0.64
1:A:71:LEU:HD23	1:A:72:PRO:CD	2.28	0.63
1:A:92:LEU:N	1:A:93:PRO:CD	2.61	0.63
1:A:34:VAL:HG11	1:A:39:TRP:CE3	2.34	0.63
1:A:71:LEU:HD22	1:A:73:ALA:H	1.64	0.63
1:A:36:VAL:C	1:A:38:ALA:N	2.55	0.62
1:A:91:TYR:CZ	1:A:93:PRO:HB3	2.35	0.62
1:A:179:ARG:O	1:A:183:GLU:HB2	2.00	0.62
1:A:47:ARG:N	1:A:48:GLY:HA3	2.15	0.61
1:A:88:SER:OG	1:A:89:PRO:CD	2.49	0.61
1:A:9:LYS:HG2	1:A:77:ARG:HG2	1.83	0.61
1:A:157:ASP:O	2:R:3:A:C2	2.55	0.60
1:A:152:VAL:HG12	1:A:152:VAL:O	2.00	0.60
1:A:60:VAL:HG21	1:A:115:THR:HG21	1.84	0.60
1:A:164:TYR:CE1	2:R:2:A:C6	2.89	0.59
1:A:31:ASP:OD1	1:A:32:TRP:N	2.36	0.59
1:A:20:ASP:HA	1:A:24:VAL:HG22	1.85	0.59
1:A:119:HIS:HD2	1:A:121:ASN:HB2	1.68	0.58
1:A:19:TRP:CZ2	1:A:23:VAL:HG11	2.37	0.58
1:A:120:ASN:C	1:A:122:ARG:H	2.10	0.58
1:A:114:LEU:CD2	1:A:162:TYR:HA	2.34	0.58
1:A:36:VAL:O	1:A:37:GLU:HB2	2.04	0.57
1:A:65:ALA:O	1:A:66:ALA:HB3	2.04	0.57
1:A:15:ILE:HD12	1:A:189:GLU:O	2.04	0.57
1:A:101:ASP:OD1	1:A:102:LYS:N	2.37	0.57
1:A:114:LEU:HD21	1:A:162:TYR:HA	1.87	0.57
1:A:120:ASN:C	1:A:122:ARG:N	2.57	0.57
1:A:44:ASP:HA	1:A:47:ARG:HB2	1.87	0.57
1:A:182:PHE:CZ	1:A:188:LEU:HD21	2.40	0.57
1:A:192:ILE:CB	1:A:193:PRO:HD3	2.22	0.56
1:A:127:ASN:O	1:A:131:ARG:HD3	2.05	0.56
1:A:111:LEU:HD23	1:A:162:TYR:CE1	2.41	0.55
1:A:5:SER:HG	1:A:6:LEU:H	1.55	0.55
1:A:44:ASP:OD1	1:A:47:ARG:NH2	2.40	0.55
1:A:182:PHE:CE2	1:A:188:LEU:HD21	2.42	0.55
1:A:19:TRP:CE3	1:A:23:VAL:HG21	2.42	0.54
1:A:75:VAL:HA	1:A:76:ASP:C	2.31	0.54
1:A:108:LEU:HD21	1:A:169:LEU:CD2	2.29	0.54
1:A:121:ASN:HA	1:A:150:ARG:NH1	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:ASP:OD1	1:A:75:VAL:O	2.25	0.54
1:A:9:LYS:CE	1:A:76:ASP:CG	2.81	0.54
1:A:3:ASN:CB	1:A:4:VAL:HA	2.36	0.54
1:A:91:TYR:CG	1:A:93:PRO:HD3	2.43	0.53
1:A:91:TYR:CE2	1:A:93:PRO:HB3	2.43	0.53
1:A:127:ASN:O	1:A:131:ARG:CG	2.57	0.53
1:A:78:ARG:HH12	1:A:190:TRP:HB3	1.72	0.52
1:A:120:ASN:O	1:A:121:ASN:C	2.52	0.52
1:A:156:LYS:CG	2:R:1:G:N2	2.37	0.52
1:A:121:ASN:C	1:A:123:ASP:H	2.17	0.52
1:A:185:GLU:HA	1:A:185:GLU:OE1	2.08	0.52
1:A:189:GLU:HG3	1:A:190:TRP:H	1.74	0.52
1:A:124:ILE:O	1:A:128:ARG:CB	2.56	0.52
2:R:3:A:H5”	2:R:3:A:N3	2.25	0.52
1:A:188:LEU:HD12	1:A:188:LEU:C	2.34	0.52
1:A:121:ASN:O	1:A:124:ILE:HG23	2.10	0.51
1:A:9:LYS:HE2	1:A:76:ASP:CG	2.29	0.51
1:A:23:VAL:HG12	1:A:28:VAL:HG11	1.91	0.51
1:A:48:GLY:O	1:A:49:ILE:HG13	2.11	0.50
1:A:152:VAL:HG13	1:A:155:LEU:HB2	1.92	0.50
1:A:15:ILE:O	1:A:16:GLU:CB	2.51	0.50
1:A:42:PHE:CG	1:A:67:LEU:CD1	2.95	0.50
1:A:34:VAL:CG2	1:A:100:LEU:HD11	2.42	0.49
1:A:78:ARG:HE	1:A:179:ARG:HE	1.59	0.49
1:A:100:LEU:CD2	1:A:174:LEU:HD13	2.43	0.49
1:A:126:LEU:O	1:A:130:LYS:HB3	2.12	0.49
1:A:186:LEU:O	1:A:188:LEU:N	2.46	0.49
1:A:35:HIS:ND1	1:A:96:LYS:O	2.46	0.49
1:A:164:TYR:CE2	2:R:2:A:N7	2.82	0.48
1:A:51:PHE:HA	1:A:52:SER:HB3	1.96	0.48
1:A:73:ALA:HB2	1:A:79:PHE:HA	1.95	0.48
1:A:127:ASN:HA	1:A:131:ARG:HG2	1.94	0.48
1:A:79:PHE:HD2	1:A:179:ARG:HG3	1.79	0.47
1:A:35:HIS:HB3	1:A:38:ALA:HB3	1.96	0.47
1:A:128:ARG:HG2	1:A:128:ARG:NH1	2.27	0.47
1:A:19:TRP:O	1:A:23:VAL:CB	2.62	0.47
1:A:121:ASN:HA	1:A:150:ARG:HH12	1.80	0.47
1:A:16:GLU:HA	1:A:19:TRP:CB	2.43	0.46
1:A:32:TRP:HE3	1:A:100:LEU:HD12	1.81	0.46
1:A:14:TYR:HD2	1:A:19:TRP:CZ3	2.27	0.46
1:A:153:GLN:N	1:A:154:PRO:CD	2.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:ARG:NH1	1:A:190:TRP:CG	2.84	0.46
1:A:24:VAL:HG12	1:A:29:PHE:CE2	2.51	0.45
1:A:35:HIS:O	1:A:38:ALA:HB3	2.17	0.45
1:A:4:VAL:HG22	1:A:70:ASP:O	2.16	0.45
1:A:9:LYS:NZ	1:A:76:ASP:CG	2.74	0.45
1:A:86:ILE:HG22	1:A:87:GLY:N	2.31	0.45
1:A:114:LEU:HD11	1:A:161:HIS:ND1	2.31	0.45
1:A:163:GLN:O	1:A:167:ILE:HG12	2.17	0.45
1:A:78:ARG:HE	1:A:179:ARG:NE	2.14	0.45
1:A:51:PHE:HA	1:A:52:SER:CB	2.45	0.45
1:A:78:ARG:HH12	1:A:190:TRP:CB	2.30	0.44
1:A:102:LYS:HD2	1:A:102:LYS:HA	1.61	0.44
1:A:49:ILE:HG23	1:A:56:SER:O	2.17	0.44
1:A:86:ILE:CG2	1:A:87:GLY:N	2.81	0.44
1:A:76:ASP:OD1	1:A:76:ASP:N	2.47	0.44
1:A:34:VAL:HG13	1:A:67:LEU:HD21	1.99	0.44
1:A:124:ILE:CG1	1:A:125:GLU:N	2.79	0.44
1:A:128:ARG:HH11	1:A:128:ARG:CG	2.29	0.43
1:A:3:ASN:CA	1:A:4:VAL:C	2.90	0.43
1:A:54:ALA:O	1:A:55:SER:CB	2.62	0.43
1:A:114:LEU:HD21	1:A:162:TYR:CA	2.48	0.43
1:A:14:TYR:O	1:A:15:ILE:C	2.60	0.43
1:A:111:LEU:HD23	1:A:162:TYR:HE1	1.82	0.43
1:A:32:TRP:CE3	1:A:105:ILE:HG22	2.53	0.43
1:A:6:LEU:O	1:A:7:THR:C	2.62	0.43
1:A:160:LEU:HD22	2:R:1:G:N7	2.33	0.42
1:A:75:VAL:O	1:A:75:VAL:HG13	2.17	0.42
1:A:182:PHE:O	1:A:182:PHE:CG	2.73	0.42
1:A:124:ILE:CB	1:A:128:ARG:HH21	2.04	0.42
1:A:4:VAL:O	1:A:5:SER:C	2.62	0.42
1:A:34:VAL:HG12	1:A:39:TRP:HB2	2.01	0.42
1:A:164:TYR:CZ	2:R:2:A:C5	3.08	0.42
1:A:9:LYS:CE	1:A:76:ASP:OD2	2.68	0.41
1:A:42:PHE:CG	1:A:67:LEU:HD13	2.55	0.41
1:A:127:ASN:O	1:A:131:ARG:CD	2.69	0.41
1:A:79:PHE:HB3	1:A:179:ARG:CG	2.50	0.41
1:A:10:GLY:O	1:A:11:GLY:C	2.63	0.41
1:A:14:TYR:CD2	1:A:19:TRP:HZ3	2.32	0.41
1:A:35:HIS:HE1	1:A:96:LYS:H	1.66	0.41
2:R:2:A:HO2'	2:R:3:A:P	2.41	0.41
1:A:3:ASN:HA	1:A:5:SER:CA	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:THR:HA	1:A:112:SER:HB2	2.02	0.41
1:A:160:LEU:HA	1:A:160:LEU:HD12	1.76	0.41
1:A:54:ALA:C	1:A:56:SER:H	2.28	0.40
1:A:65:ALA:O	1:A:66:ALA:CB	2.69	0.40
1:A:121:ASN:CA	1:A:150:ARG:HH12	2.34	0.40
1:A:128:ARG:NH1	1:A:128:ARG:CG	2.85	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	171/198 (86%)	159 (93%)	12 (7%)	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	151/169 (89%)	145 (96%)	6 (4%)	28 50

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	LYS
1	A	49	ILE
1	A	53	VAL
1	A	92	LEU
1	A	152	VAL
1	A	156	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	R	2/3 (66%)	2 (100%)	1 (50%)

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	R	2	A
2	R	3	A

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	R	2	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

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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.

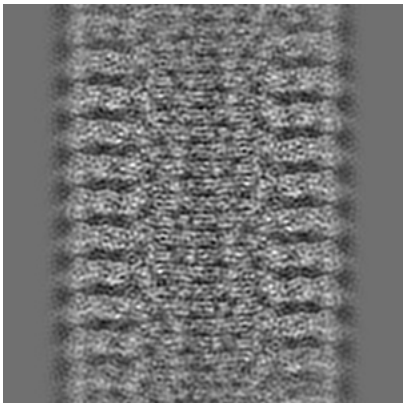
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-3074. These allow visual inspection of the internal detail of the map and identification of artifacts.

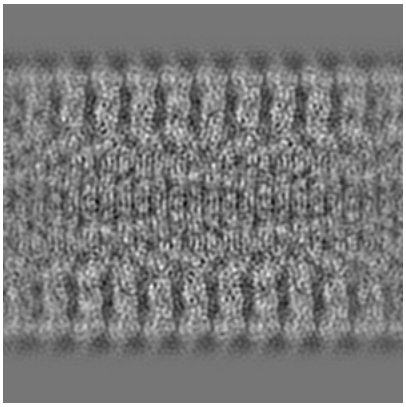
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

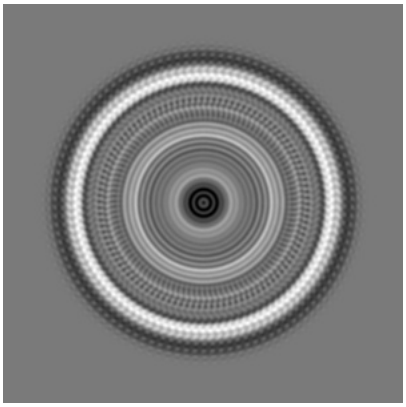
6.1.1 Primary map



X



Y

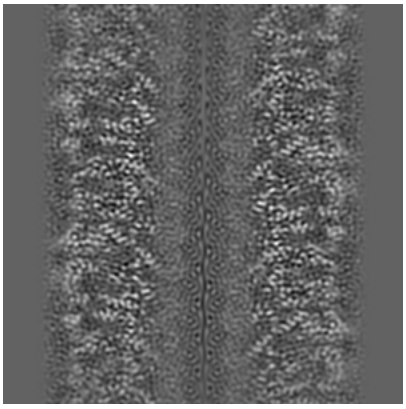


Z

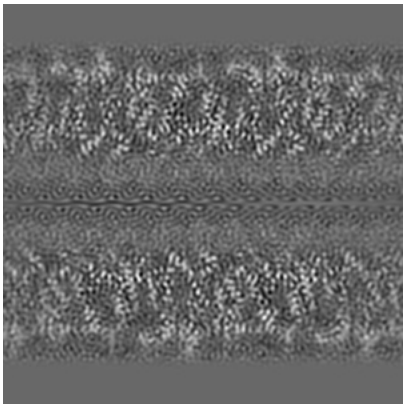
The images above show the map projected in three orthogonal directions.

6.2 Central slices

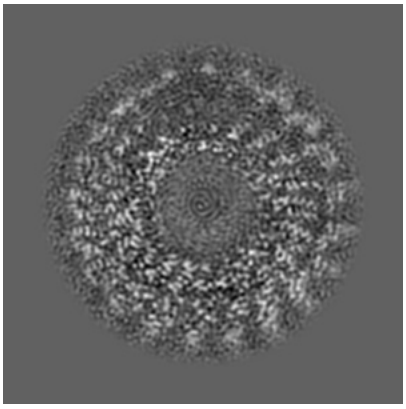
6.2.1 Primary map



X Index: 150



Y Index: 150

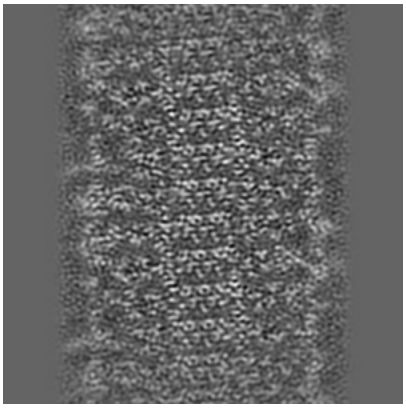


Z Index: 150

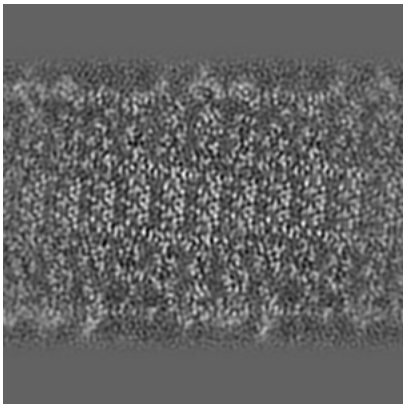
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

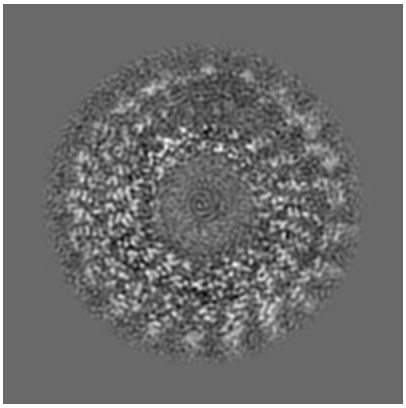
6.3.1 Primary map



X Index: 199



Y Index: 100

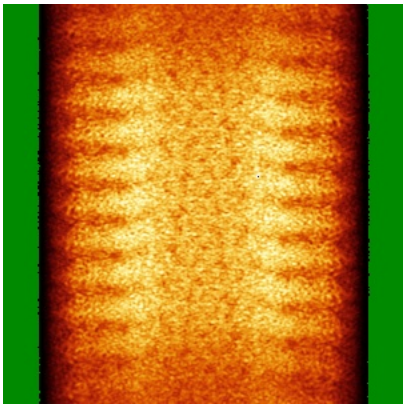


Z Index: 149

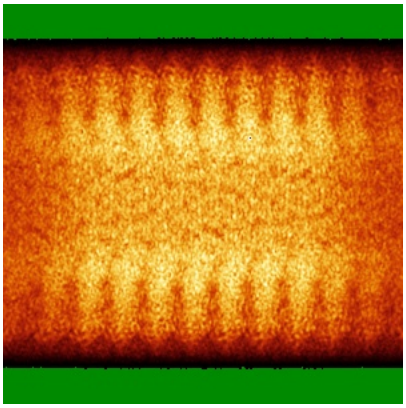
The images above show the largest variance slices of the map in three orthogonal directions.

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

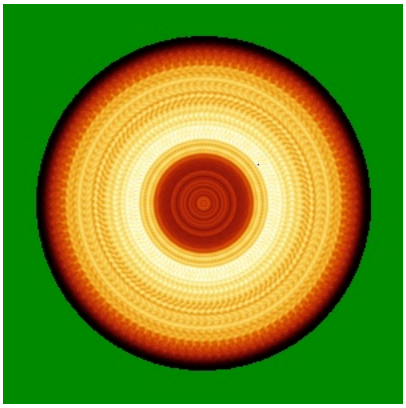
6.4.1 Primary map



X



Y

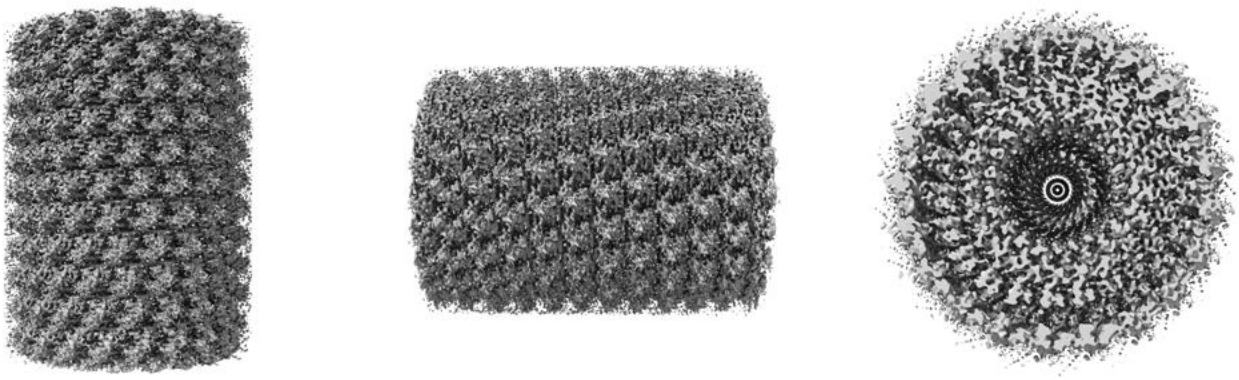


Z

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 20.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

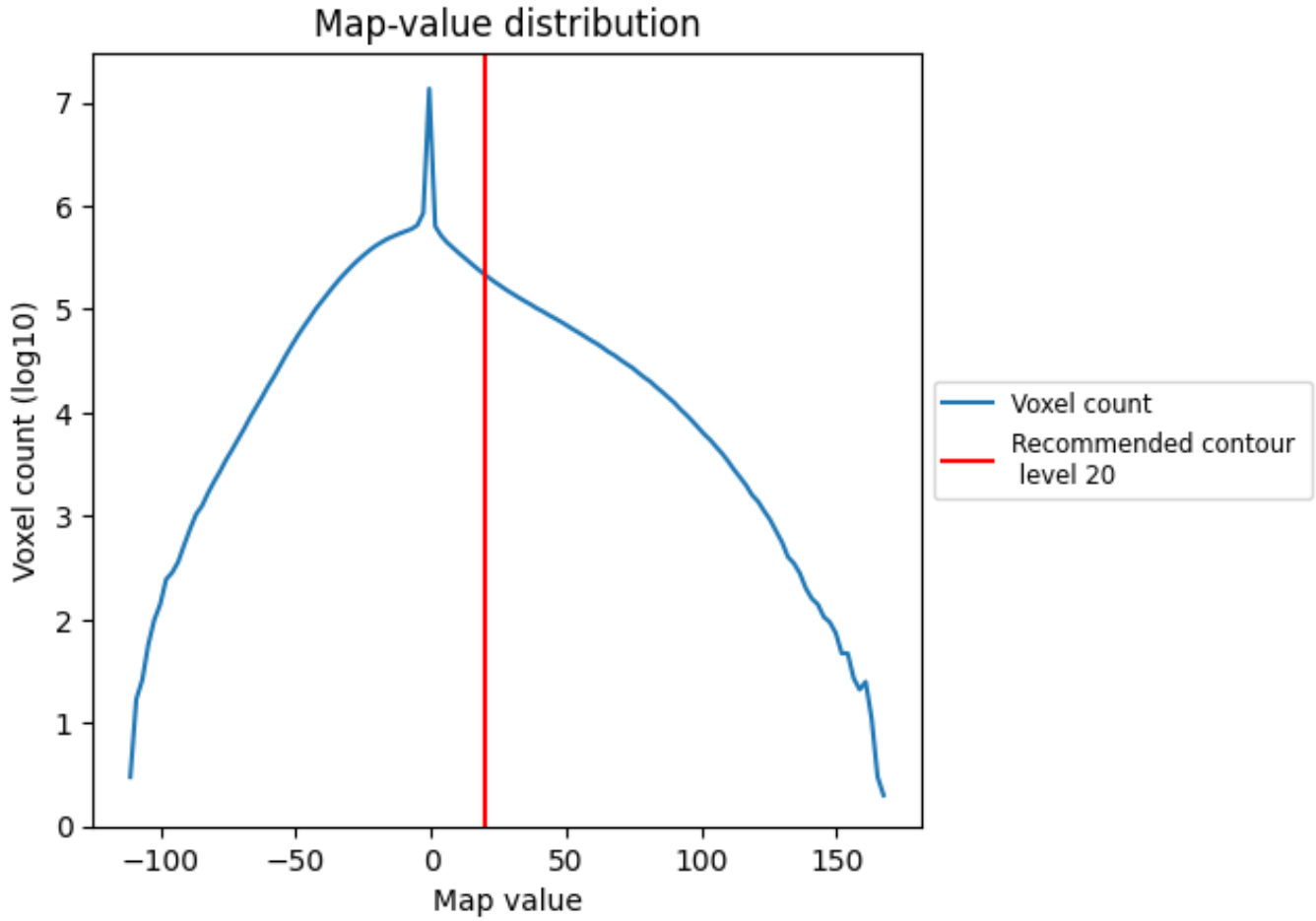
6.6 Mask visualisation (i)

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

7 Map analysis

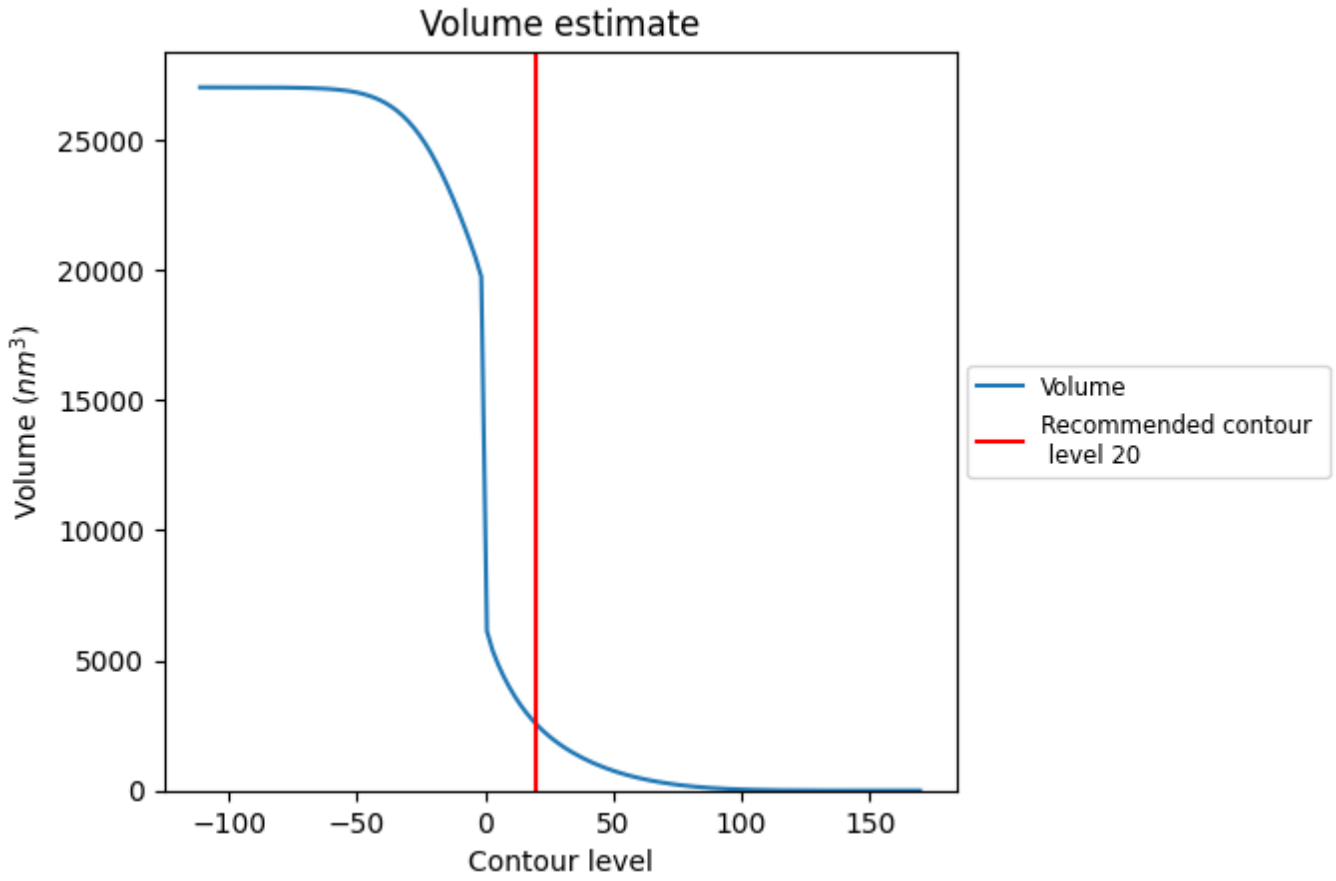
This section contains the results of statistical analysis of the map.

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.

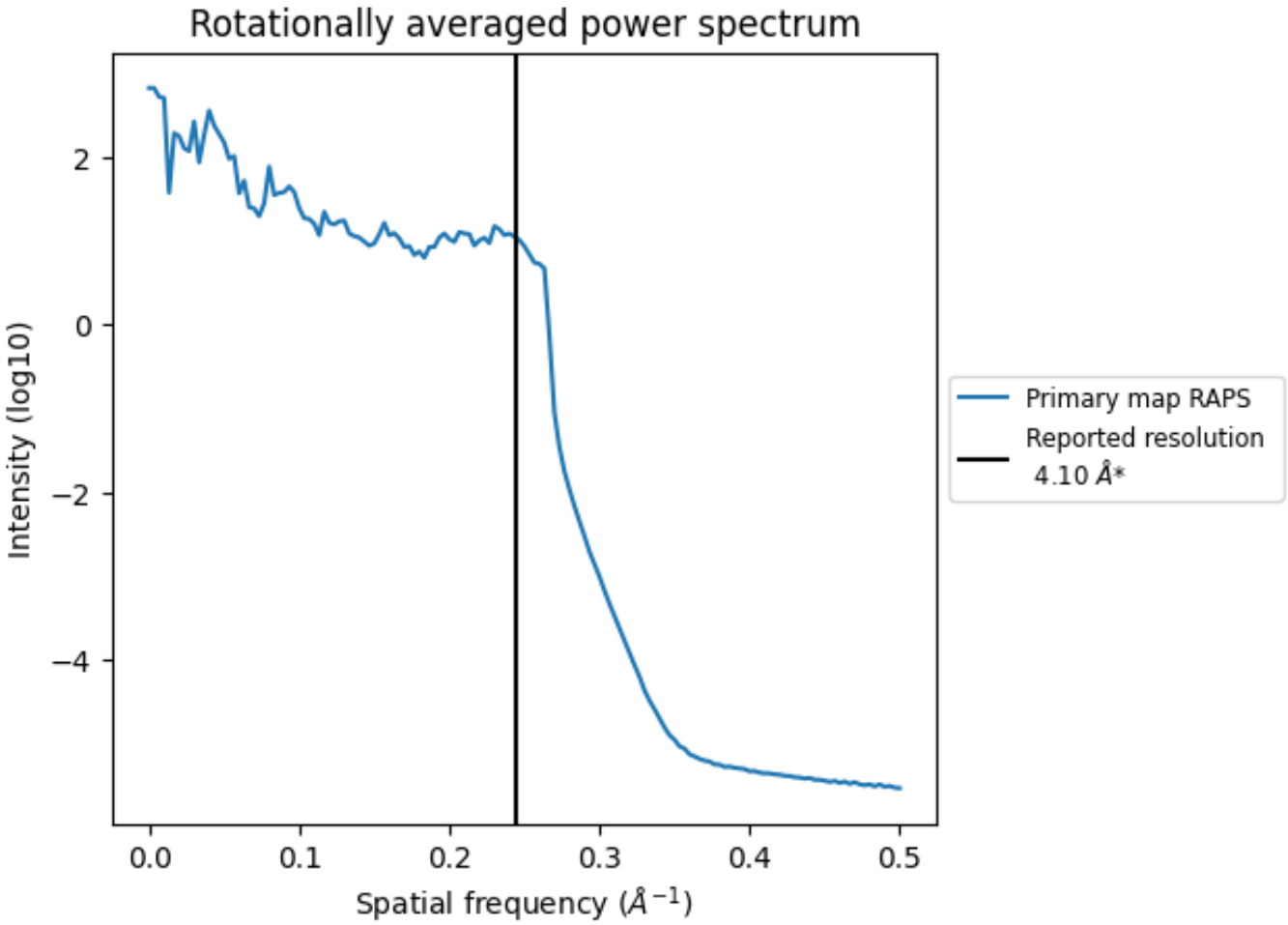
7.2 Volume estimate



The volume at the recommended contour level is 2543 nm^3; this corresponds to an approximate mass of 2297 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

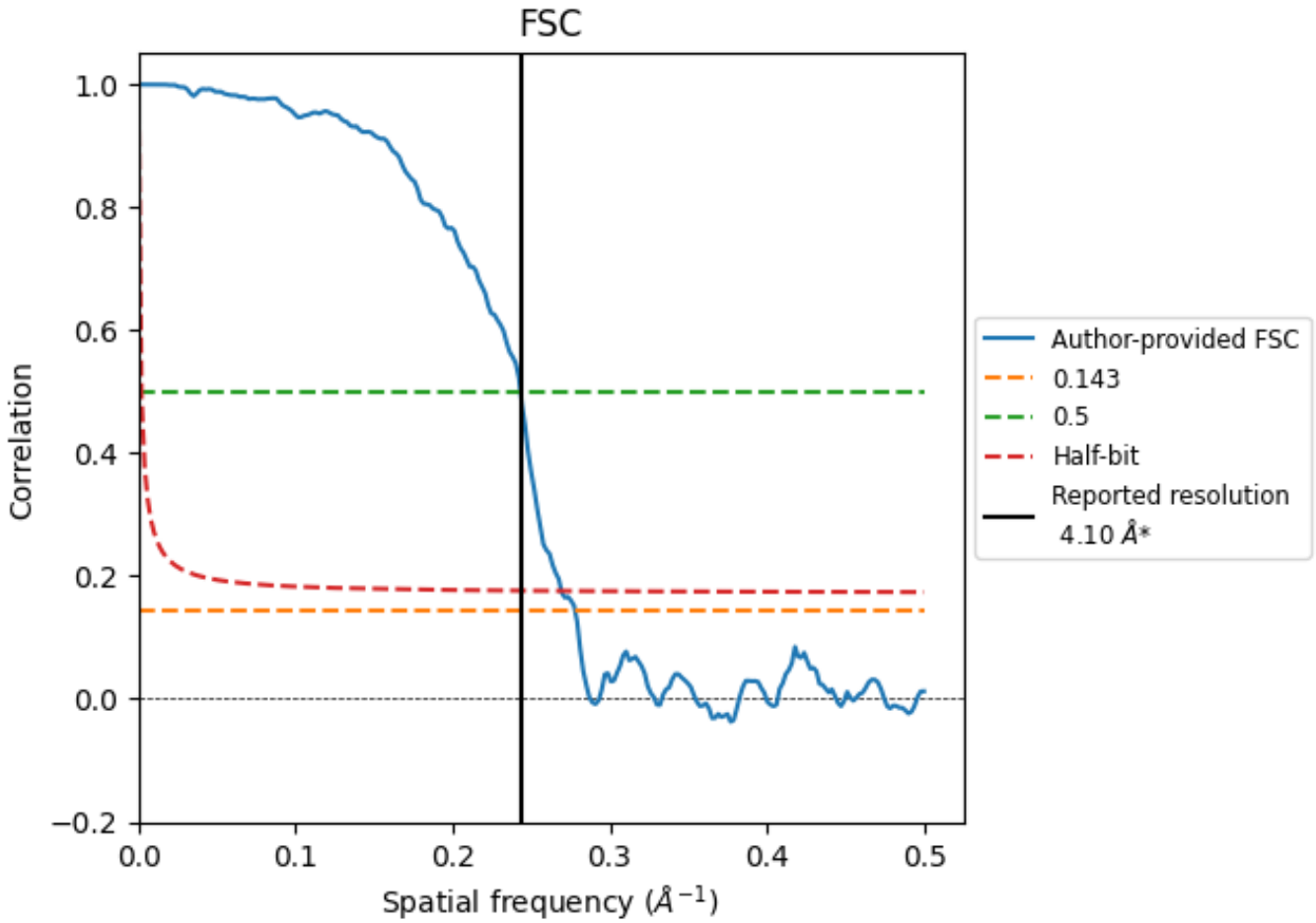


*Reported resolution corresponds to spatial frequency of 0.244 Å^{-1}

8 Fourier-Shell correlation

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 0.244 Å^{-1}

8.2 Resolution estimates (i)

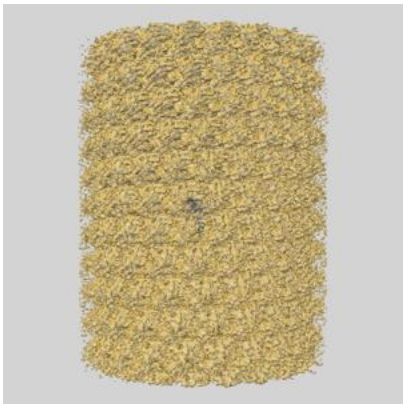
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	3.60	4.11	3.71
Unmasked-calculated*	-	-	-

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

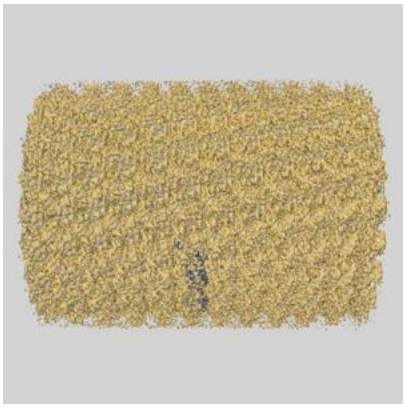
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-3074 and PDB model 5A7A. Per-residue inclusion information can be found in section 3 on page 4.

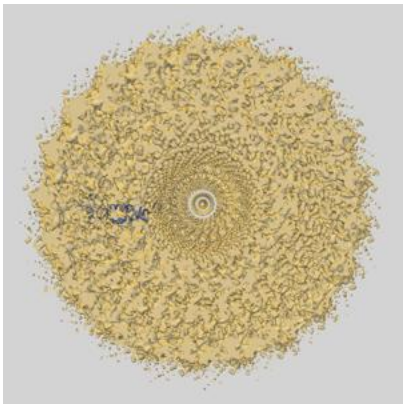
9.1 Map-model overlay



X



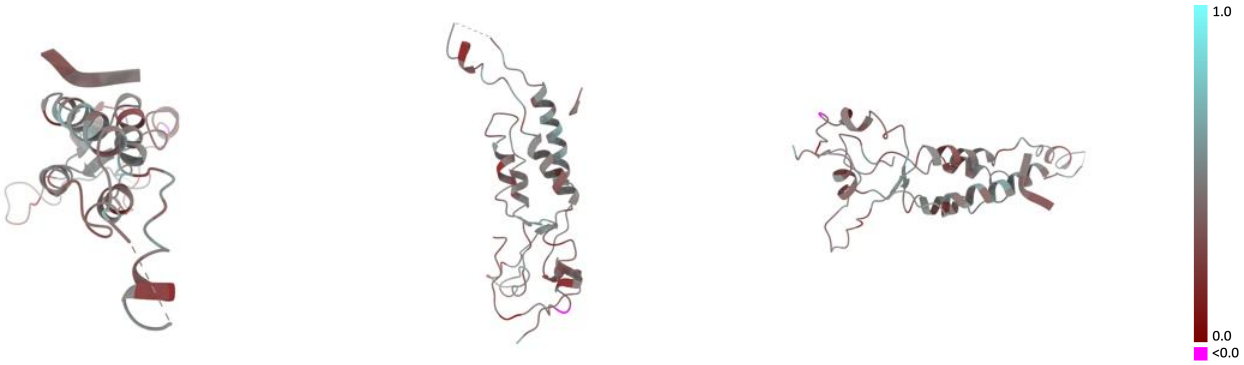
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 20.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

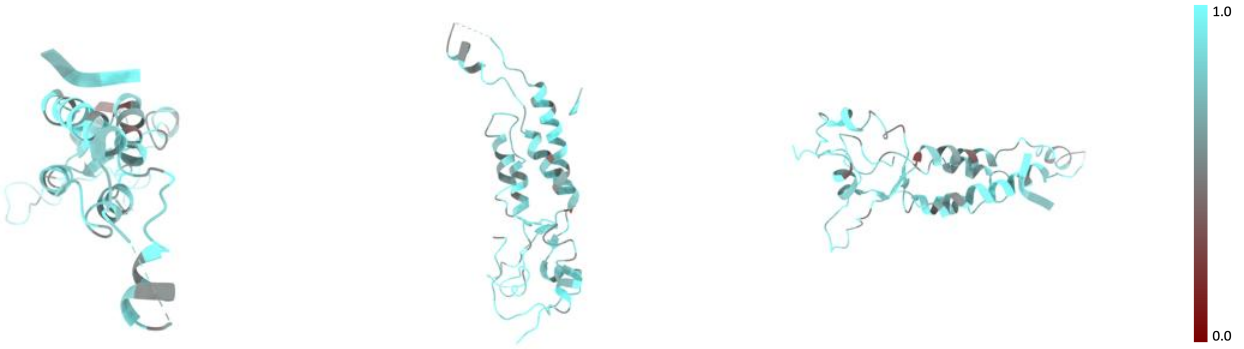
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

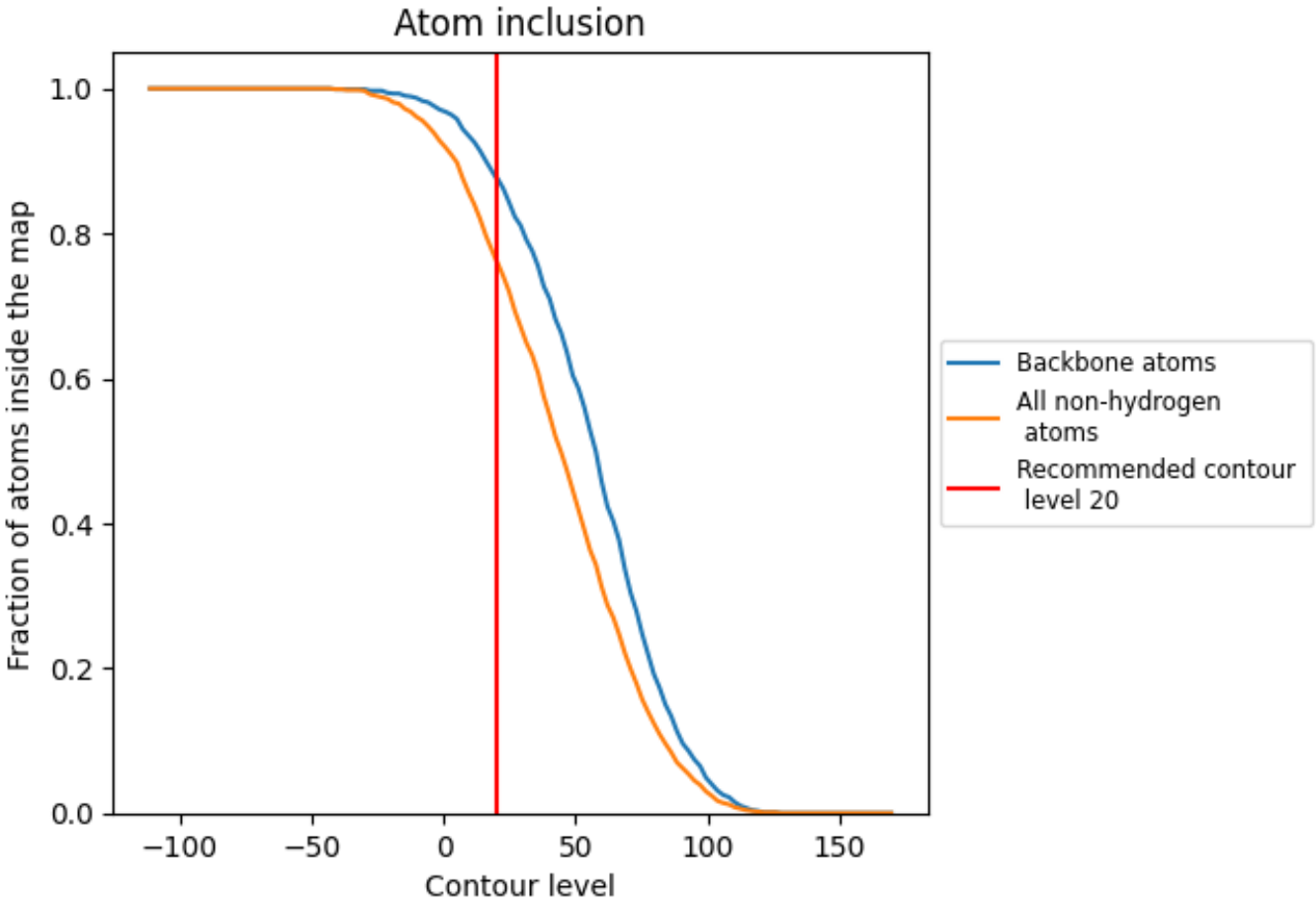
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (20).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 76% 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 (20) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7620	0.4150
A	0.7610	0.4170
R	0.7760	0.3850