Full wwPDB EM Validation Report

May 4, 2025 – 08:19 PM EDT

PDB ID	:	9DWM / pdb_00009dwm
EMDB ID	:	EMD-47255
Title	:	DNA polymerase Beta bound to a nucleosome containing a 1-nt gap at SHL-5.5
Authors	:	Weaver, T.M.; Ryan, B.J.; Freudenthal, B.D.
Deposited on	:	2024-10-09
Resolution	:	4.20 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

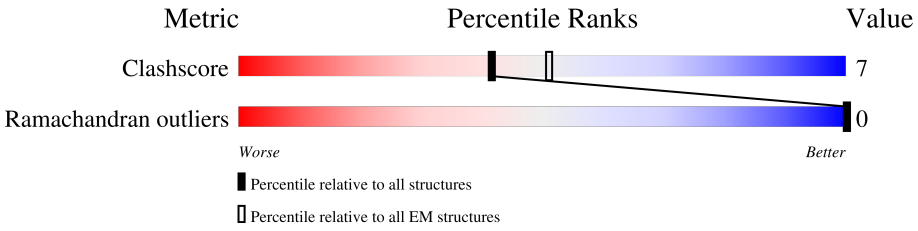
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

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 4.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835

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	135	72% 28%
1	E	135	72% 28%
2	B	102	76% 24%
2	F	102	75% 24%
3	C	129	83% 16%
3	G	129	77% 21%
4	D	125	72% 26%
4	H	125	72% 27%
5	I	127	55% 44%

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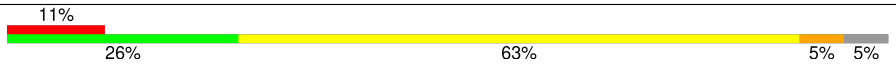
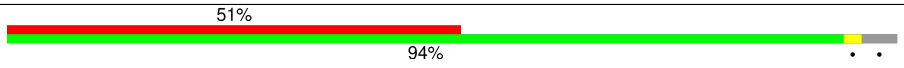
Mol	Chain	Length	Quality of chain
6	J	147	
7	K	19	
8	L	335	

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 11175 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 Histone H3.2.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	97	Total 482	C 288	N 97	O 97	0	0
1	E	97	Total 482	C 288	N 97	O 97	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	110	ALA	CYS	engineered mutation	UNP Q71DI3
E	110	ALA	CYS	engineered mutation	UNP Q71DI3

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	78	Total 382	C 226	N 78	O 78	0	0
2	F	78	Total 382	C 226	N 78	O 78	0	0

- Molecule 3 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	108	Total 531	C 315	N 108	O 108	0	0
3	G	102	Total 501	C 297	N 102	O 102	0	0

- Molecule 4 is a protein called Histone H2B type 1-C/E/F/G/I.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	93	Total 460	C 274	N 93	O 93	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	H	91	Total 450	C 268	N 91	O 91	0	0

- Molecule 5 is a DNA chain called 601 I strand (damaged strand 1).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	126	Total 2566	C 1217	N 466	O 757	P 126	0	0

- Molecule 6 is a DNA chain called 601 J strand (non-damaged strand).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	145	Total 2990	C 1415	N 559	O 871	P 145	0	0

- Molecule 7 is a DNA chain called 601 K strand (damaged strand 2).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	18	Total 366	C 175	N 65	O 108	P 18	0	0

- Molecule 8 is a protein called DNA polymerase beta.

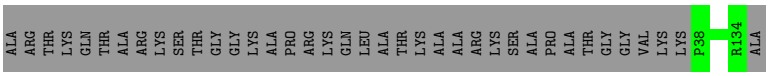
Mol	Chain	Residues	Atoms				AltConf	Trace
8	L	321	Total 1583	C 941	N 321	O 321	0	0

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.

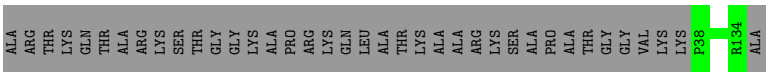
- Molecule 1: Histone H3.2

Chain A:



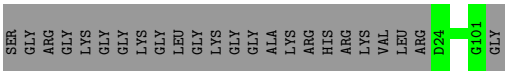
- Molecule 1: Histone H3.2

Chain E:



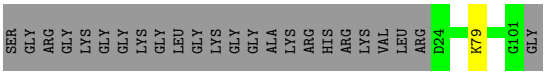
- Molecule 2: Histone H4

Chain B:



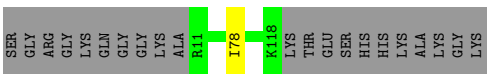
- Molecule 2: Histone H4

Chain F:



- Molecule 3: Histone H2A type 1

Chain C:

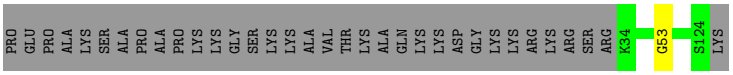


- Molecule 3: Histone H2A type 1

Chain G:

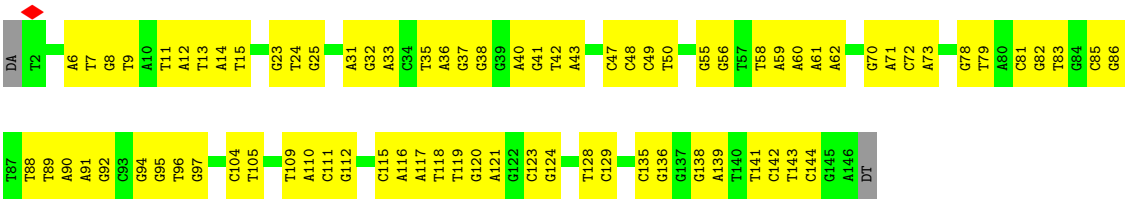
• Molecule 4: Histone H2B type 1-C/E/F/G/I

• Molecule 4: Histone H2B type 1-C/E/F/G/I

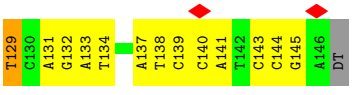


• Molecule 5: 601 I strand (damaged strand 1)

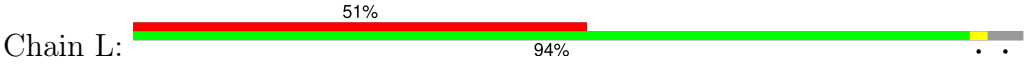
• Molecule 6: 601 J strand (non-damaged strand)

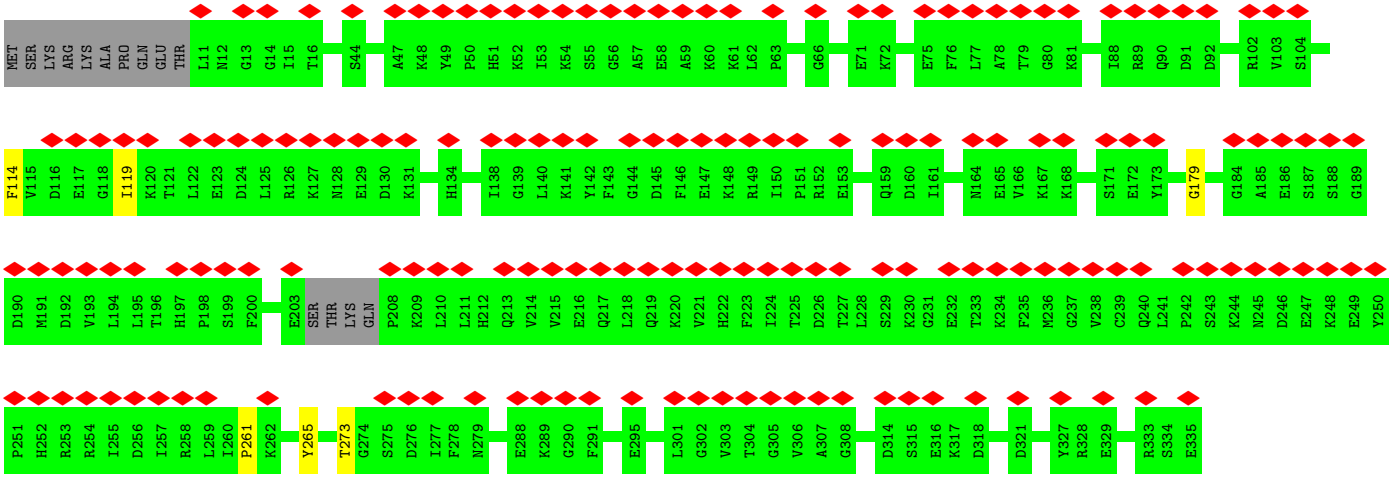


• Molecule 7: 601 K strand (damaged strand 2)



• Molecule 8: DNA polymerase beta




MET SER LYS ARG LYS ALA PRO GLN GLU THR L11 N12 G13 G14 I15 T16 S44 A47 K48 Y49 P50 H51 K52 I53 K54 S55 G56 A57 E58 A59 K60 K61 L62 P63 G66 E71 K72 E75 F76 L77 A78 T79 G80 K81 I88 R89 Q90 D91 D92 R102 V103 S104
F114 V115 D116 E117 G118 I119 K120 T121 L122 E123 D124 L125 R126 K127 N128 E129 D130 K131 H134 I138 G139 L140 K141 Y142 F143 G144 D145 F146 E147 K148 R149 I150 P151 R152 E153 Q159 D160 I161 N164 E165 V166 K167 K168 S171 E172 Y173 G179 G184 A185 E186 S187 S188 G189
D190 M191 D192 V193 L194 L195 T196 H197 P198 S199 F200 E203 SER THR LYS GLN P208 K209 L210 L211 H212 Q213 V214 V215 E216 Q217 L218 Q219 K220 V221 H222 F223 I224 T225 D226 T227 L228 S229 K230 G231 E232 T233 K234 F235 M236 G237 V238 C239 Q240 L241 P242 S243 K244 N245 D246 E247 K248 E249 Y250
P251 H252 R253 R254 I255 D256 I257 R258 L259 I260 P261 K262 Y265 T273 G274 S275 D276 I277 F278 N279 E288 K289 G290 F291 E295 L301 G302 V303 T304 G305 V306 A307 G308 D314 S315 E316 K317 D318 D321 Y327 R328 E329 R333 S334 E335

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7167	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	27.173	Depositor
Minimum map value	-12.772	Depositor
Average map value	0.001	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	5.4	Depositor
Map size (Å)	310.40002, 310.40002, 310.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9700001, 0.9700001, 0.9700001	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	0.15	0/481	0.30	0/670
1	E	0.15	0/481	0.27	0/670
2	B	0.16	0/381	0.26	0/527
2	F	0.16	0/381	0.27	0/527
3	C	0.14	0/530	0.25	0/735
3	G	0.15	0/500	0.26	0/693
4	D	0.16	0/459	0.31	0/638
4	H	0.16	0/449	0.29	0/624
5	I	0.29	0/2874	0.45	0/4429
6	J	0.28	0/3357	0.43	0/5184
7	K	0.38	1/409 (0.2%)	0.45	0/626
8	L	0.10	0/1581	0.24	0/2197
All	All	0.23	1/11883 (0.0%)	0.38	0/17520

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	K	129	DT	OP3-P	6.06	1.60	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	482	0	223	0	0
1	E	482	0	223	0	0
2	B	382	0	180	0	0
2	F	382	0	180	1	0
3	C	531	0	264	1	0
3	G	501	0	246	2	0
4	D	460	0	212	2	0
4	H	450	0	208	1	0
5	I	2566	0	1413	39	0
6	J	2990	0	1628	56	0
7	K	366	0	204	10	0
8	L	1583	0	701	3	0
All	All	11175	0	5682	112	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (112) 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)
8:L:179:GLY:H	8:L:273:THR:HA	1.62	0.65
6:J:31:DA:H2”	6:J:32:DG:H5”	1.79	0.64
6:J:7:DT:H2”	6:J:8:DG:H5”	1.80	0.63
5:I:123:DC:H2”	5:I:124:DA:H5”	1.86	0.58
6:J:120:DG:H1’	6:J:121:DA:C5	2.39	0.58
6:J:24:DT:H2”	6:J:25:DG:H5”	1.87	0.57
6:J:138:DG:H2’	6:J:139:DA:C8	2.39	0.57
5:I:47:DC:H2”	5:I:48:DT:H72	1.87	0.56
6:J:94:DG:H2’	6:J:95:DG:C8	2.41	0.56
6:J:72:DC:H2”	6:J:73:DA:H8	1.71	0.55
4:D:119:THR:O	4:D:123:SER:N	2.40	0.55
6:J:119:DT:H2”	6:J:120:DG:N7	2.22	0.55
6:J:96:DT:H2’	6:J:97:DG:C8	2.42	0.54
6:J:49:DC:H2”	6:J:50:DT:H71	1.89	0.54
5:I:22:DG:H2’	5:I:23:DC:C6	2.43	0.54
6:J:13:DT:H2”	6:J:14:DA:C8	2.42	0.53
5:I:109:DC:H2”	5:I:110:DC:C6	2.44	0.53
5:I:78:DC:H2”	5:I:79:DC:C5	2.44	0.53
6:J:31:DA:H2”	6:J:32:DG:H8	1.73	0.53
7:K:132:DG:H2”	7:K:133:DA:H5”	1.91	0.53
7:K:131:DA:H2”	7:K:132:DG:C8	2.44	0.52
5:I:102:DG:H2”	5:I:103:DA:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:94:DG:H2'	5:I:95:DC:C6	2.45	0.52
3:G:78:ILE:N	4:H:53:GLY:O	2.42	0.51
5:I:96:DC:H2'	5:I:97:DA:C8	2.46	0.50
8:L:261:PRO:O	8:L:265:TYR:N	2.45	0.50
5:I:29:DA:H2"	5:I:30:DA:C8	2.46	0.50
6:J:91:DA:H2"	6:J:92:DG:H5"	1.92	0.49
6:J:89:DT:H2"	6:J:90:DA:C8	2.47	0.49
6:J:88:DT:H2"	6:J:89:DT:C5	2.48	0.49
6:J:81:DC:H2"	6:J:82:DG:C8	2.48	0.49
6:J:61:DA:H2"	6:J:62:DA:C8	2.48	0.49
5:I:19:DG:H1'	5:I:20:DA:C5	2.47	0.49
5:I:74:DC:H2'	5:I:75:DT:C6	2.48	0.49
3:C:78:ILE:N	4:D:53:GLY:O	2.39	0.48
6:J:143:DT:H2"	6:J:144:DC:C5	2.48	0.48
6:J:23:DG:H2'	6:J:24:DT:H71	1.95	0.48
5:I:89:DT:H2"	5:I:90:DA:N7	2.29	0.48
5:I:23:DC:H2'	5:I:24:DC:C6	2.48	0.47
6:J:82:DG:H2'	6:J:83:DT:C6	2.49	0.47
6:J:82:DG:H2'	6:J:83:DT:H71	1.95	0.47
6:J:35:DT:H2"	6:J:36:DA:H5'	1.96	0.47
7:K:133:DA:H2'	7:K:134:DT:H71	1.97	0.47
6:J:37:DG:H4'	6:J:38:DG:H5'	1.97	0.46
5:I:72:DC:H2"	5:I:73:DG:C8	2.51	0.46
6:J:47:DC:H4'	6:J:48:DC:H5'	1.96	0.46
6:J:94:DG:H2'	6:J:95:DG:H8	1.80	0.46
6:J:135:DC:H2"	6:J:136:DG:C8	2.51	0.46
2:F:79:LYS:N	5:I:102:DG:OP1	2.49	0.46
6:J:111:DC:H2"	6:J:112:DG:C8	2.51	0.46
6:J:32:DG:H2"	6:J:33:DA:H8	1.79	0.46
7:K:137:DA:H2'	7:K:138:DT:C6	2.51	0.46
6:J:60:DA:H2"	6:J:61:DA:H8	1.81	0.46
5:I:64:DC:H2"	5:I:65:DA:C8	2.52	0.45
5:I:69:DA:H2"	5:I:70:DC:C5	2.52	0.45
6:J:85:DC:H2"	6:J:86:DG:C8	2.52	0.45
8:L:114:PHE:O	8:L:119:ILE:N	2.50	0.45
6:J:115:DC:H2"	6:J:116:DA:C8	2.52	0.44
5:I:17:DC:H2"	5:I:18:DC:C5	2.52	0.44
5:I:66:DC:H2"	5:I:67:DG:C8	2.51	0.44
5:I:70:DC:H1'	5:I:71:DG:C8	2.53	0.44
6:J:42:DT:H2"	6:J:43:DA:C8	2.53	0.44
5:I:102:DG:H2"	5:I:103:DA:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:73:DG:H2'	5:I:74:DC:C6	2.53	0.43
5:I:34:DG:H2'	5:I:35:DT:C6	2.53	0.43
5:I:109:DC:H2"	5:I:110:DC:C5	2.53	0.43
7:K:140:DC:H1'	7:K:141:DA:C8	2.53	0.43
6:J:6:DA:H1'	6:J:7:DT:OP2	2.18	0.43
3:G:16:THR:O	3:G:20:ARG:N	2.41	0.43
5:I:93:DC:H2"	5:I:94:DG:H8	1.84	0.43
6:J:109:DT:H2"	6:J:110:DA:N7	2.34	0.43
5:I:7:DA:H2"	5:I:8:DA:C8	2.54	0.43
6:J:78:DG:H2"	6:J:79:DT:C5	2.54	0.43
7:K:140:DC:H1'	7:K:141:DA:N7	2.34	0.43
6:J:70:DG:H2"	6:J:71:DA:C8	2.53	0.42
6:J:95:DG:C8	6:J:96:DT:H72	2.54	0.42
5:I:99:DG:H2"	5:I:100:DG:N7	2.35	0.42
6:J:135:DC:H2"	6:J:136:DG:H8	1.84	0.42
7:K:139:DC:H2"	7:K:140:DC:C6	2.54	0.42
5:I:45:DC:H2'	5:I:46:DT:C6	2.54	0.42
5:I:74:DC:C6	5:I:75:DT:H72	2.55	0.42
6:J:9:DT:H6	6:J:9:DT:H2'	1.63	0.42
7:K:129:DT:H6	7:K:129:DT:H2'	1.69	0.42
6:J:31:DA:H2"	6:J:32:DG:C8	2.53	0.42
6:J:14:DA:H1'	6:J:15:DT:H5"	2.00	0.42
6:J:117:DA:C8	6:J:118:DT:H72	2.55	0.42
5:I:36:DC:H2"	5:I:37:DG:C8	2.55	0.42
6:J:32:DG:H2"	6:J:33:DA:H5'	2.02	0.41
7:K:144:DC:H2"	7:K:145:DG:O4'	2.20	0.41
5:I:117:DT:H2"	5:I:118:DC:H5'	2.03	0.41
6:J:58:DT:H2"	6:J:59:DA:N7	2.35	0.41
5:I:46:DT:H2"	5:I:47:DC:C6	2.55	0.41
5:I:48:DT:H1'	5:I:49:DA:C4	2.55	0.41
6:J:55:DG:H2"	6:J:56:DG:C8	2.55	0.41
6:J:104:DC:C6	6:J:105:DT:H72	2.55	0.41
5:I:79:DC:H2"	5:I:80:DC:C5	2.55	0.41
6:J:40:DA:H2"	6:J:41:DG:C8	2.56	0.41
6:J:123:DC:H2"	6:J:124:DG:C8	2.56	0.41
7:K:143:DC:H6	7:K:143:DC:H2'	1.71	0.41
6:J:141:DT:H2"	6:J:142:DC:C5	2.56	0.41
5:I:24:DC:H2"	5:I:25:DG:C8	2.56	0.41
5:I:71:DG:C8	5:I:71:DG:H5'	2.55	0.41
5:I:4:DG:H2"	5:I:5:DA:N7	2.36	0.41
5:I:77:DT:H2"	5:I:78:DC:C6	2.56	0.41

Continued on next page...

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:37:DG:H1'	6:J:38:DG:C8	2.56	0.41
6:J:128:DT:H1'	6:J:129:DC:C2	2.55	0.41
6:J:13:DT:H2"	6:J:14:DA:H8	1.86	0.40
6:J:72:DC:H2"	6:J:73:DA:C8	2.53	0.40
6:J:82:DG:H2"	6:J:83:DT:O5'	2.21	0.40
5:I:80:DC:H2"	5:I:81:DC:C5	2.57	0.40
6:J:11:DT:H2"	6:J:12:DA:C8	2.57	0.40
6:J:42:DT:H2"	6:J:43:DA:H8	1.87	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	95/135 (70%)	93 (98%)	2 (2%)	0	100	100
1	E	95/135 (70%)	92 (97%)	3 (3%)	0	100	100
2	B	76/102 (74%)	69 (91%)	7 (9%)	0	100	100
2	F	76/102 (74%)	74 (97%)	2 (3%)	0	100	100
3	C	106/129 (82%)	101 (95%)	5 (5%)	0	100	100
3	G	100/129 (78%)	96 (96%)	4 (4%)	0	100	100
4	D	91/125 (73%)	90 (99%)	1 (1%)	0	100	100
4	H	89/125 (71%)	87 (98%)	2 (2%)	0	100	100
8	L	317/335 (95%)	312 (98%)	5 (2%)	0	100	100
All	All	1045/1317 (79%)	1014 (97%)	31 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

There are no protein residues with a non-rotameric sidechain to report in this entry.

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

There are no ligands in this entry.

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.

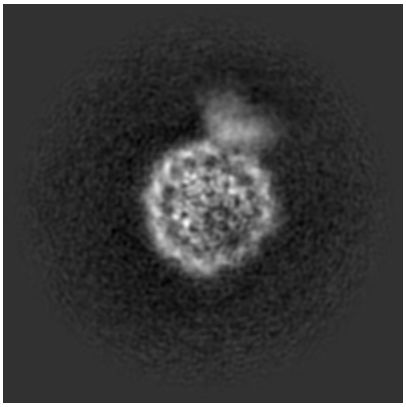
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-47255. These allow visual inspection of the internal detail of the map and identification of artifacts.

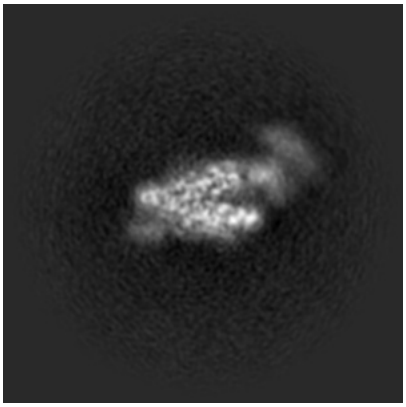
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

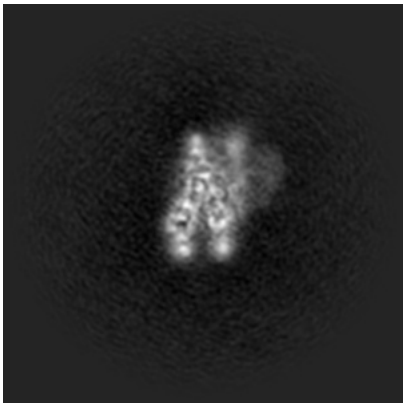
6.1.1 Primary map



X



Y

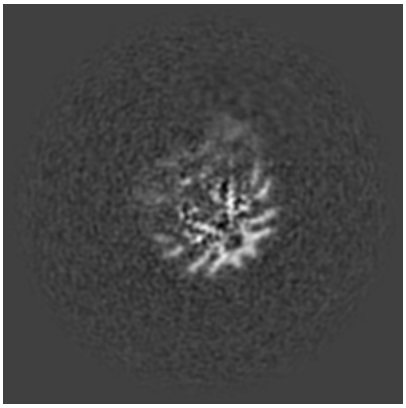


Z

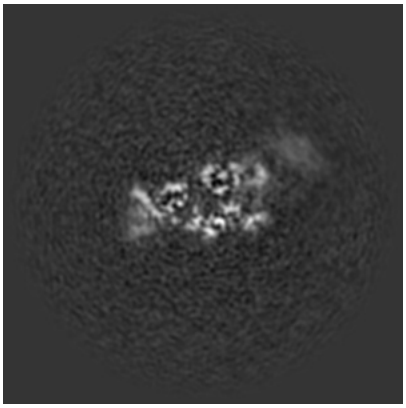
The images above show the map projected in three orthogonal directions.

6.2 Central slices

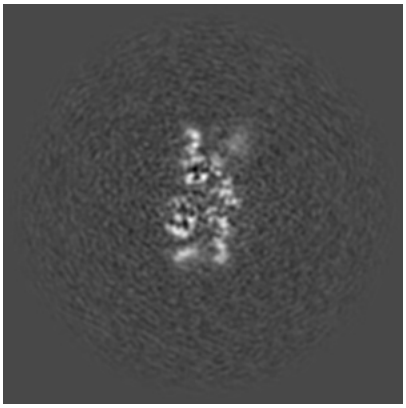
6.2.1 Primary map



X Index: 160



Y Index: 160

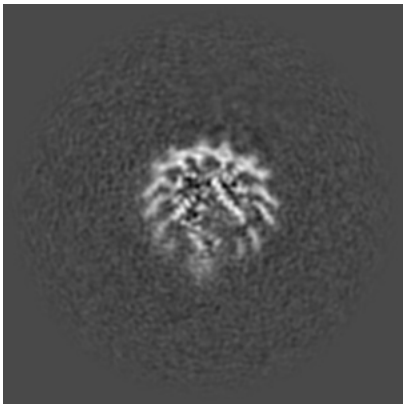


Z Index: 160

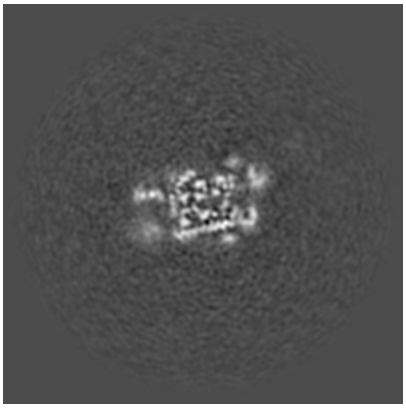
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

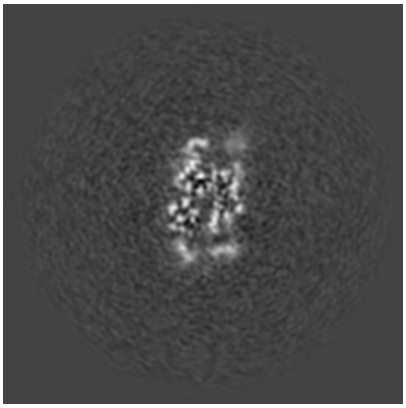
6.3.1 Primary map



X Index: 149



Y Index: 147

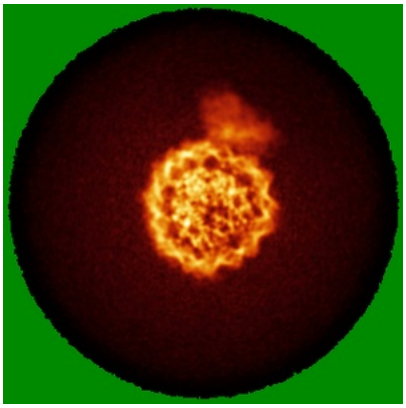


Z Index: 170

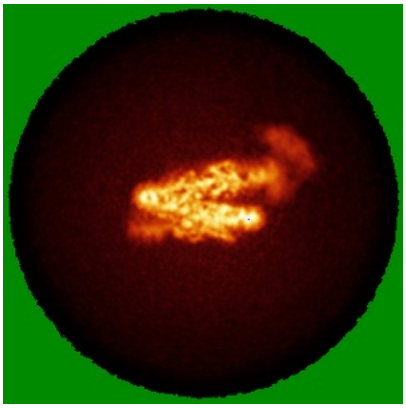
The images above show the largest variance slices of the map in three orthogonal directions.

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

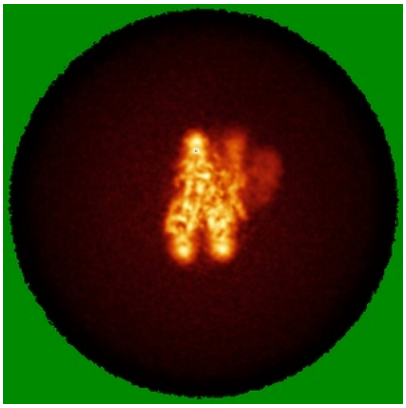
6.4.1 Primary map



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

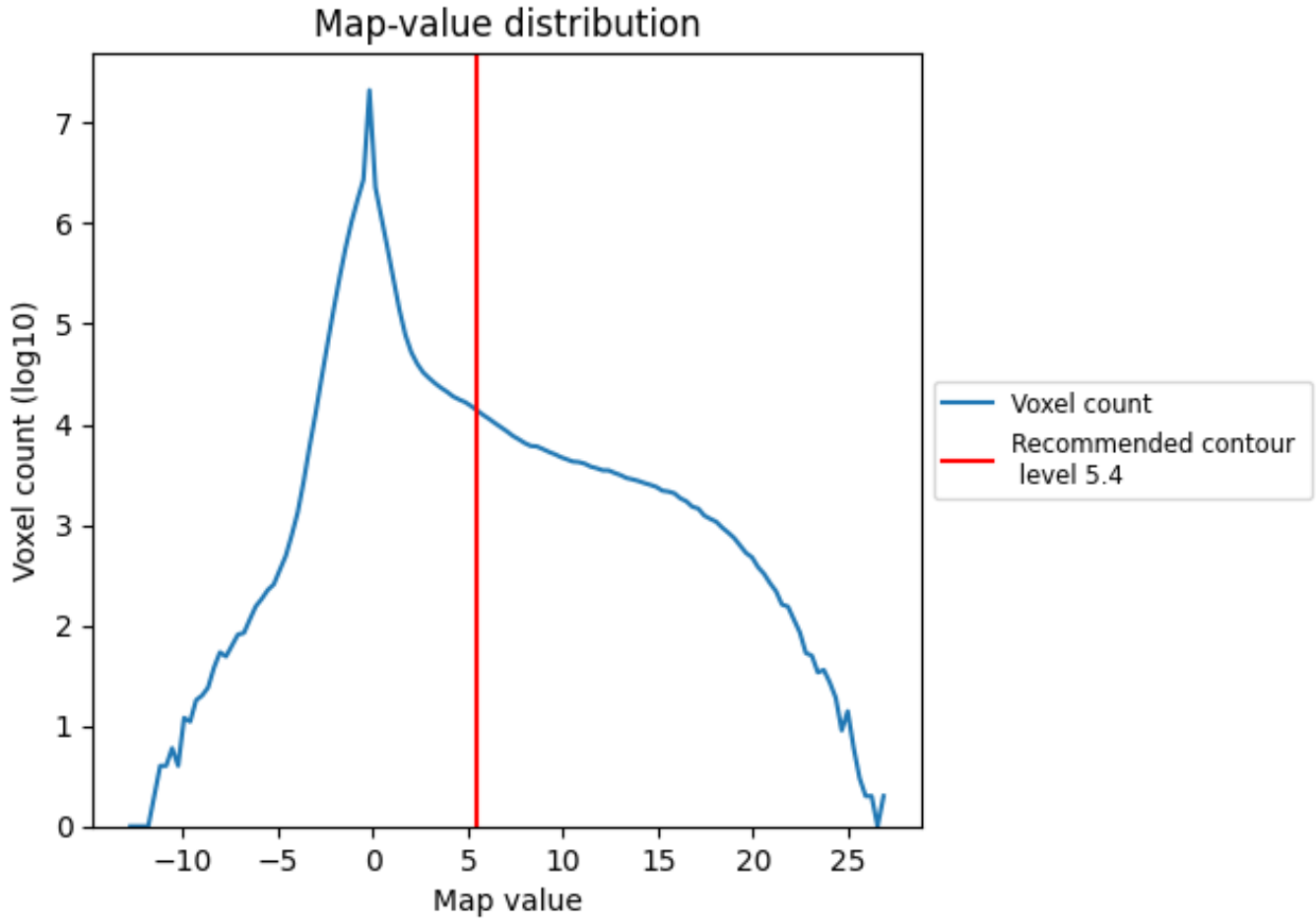
6.6 Mask visualisation (i)

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

7 Map analysis

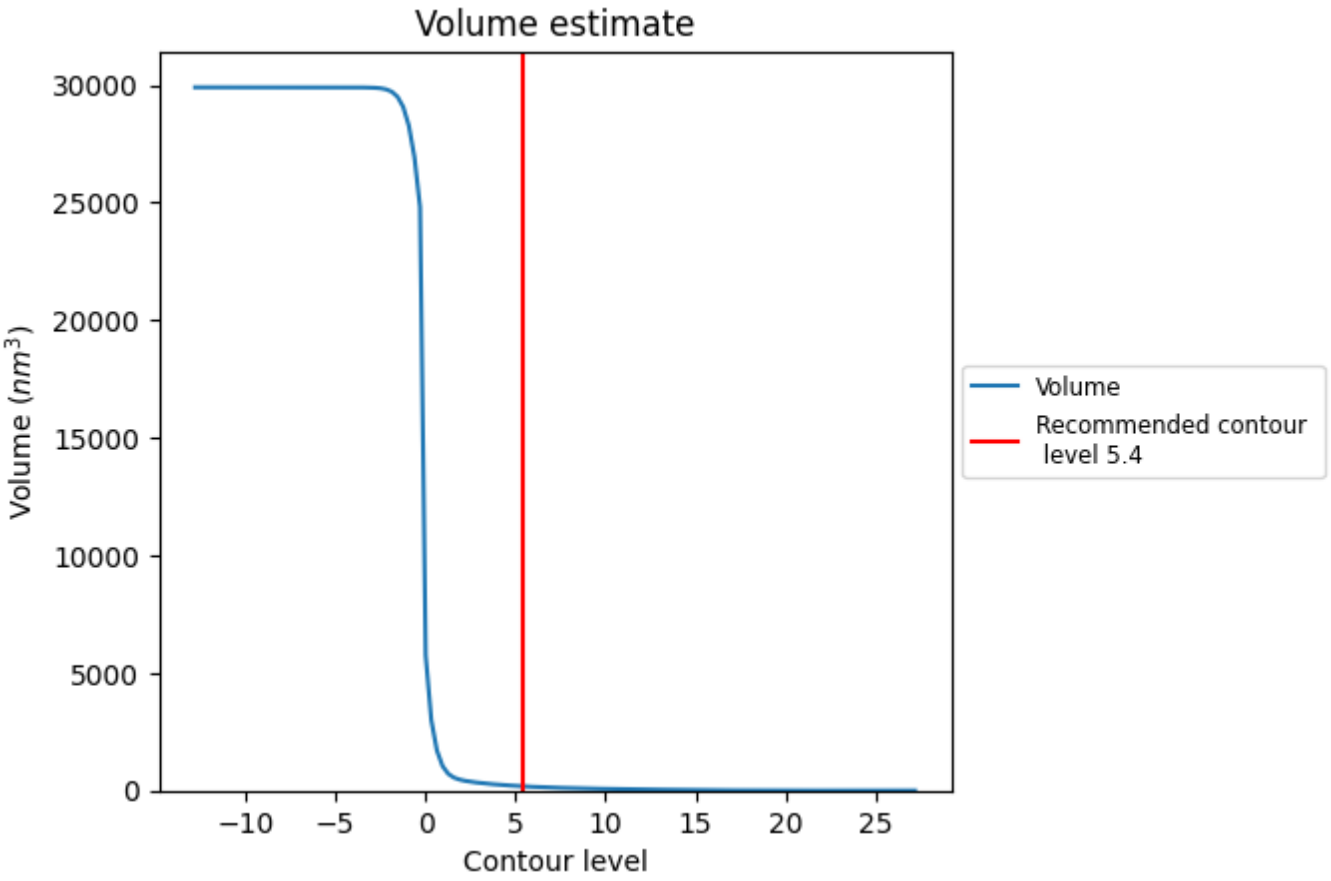
This section contains the results of statistical analysis of the map.

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.

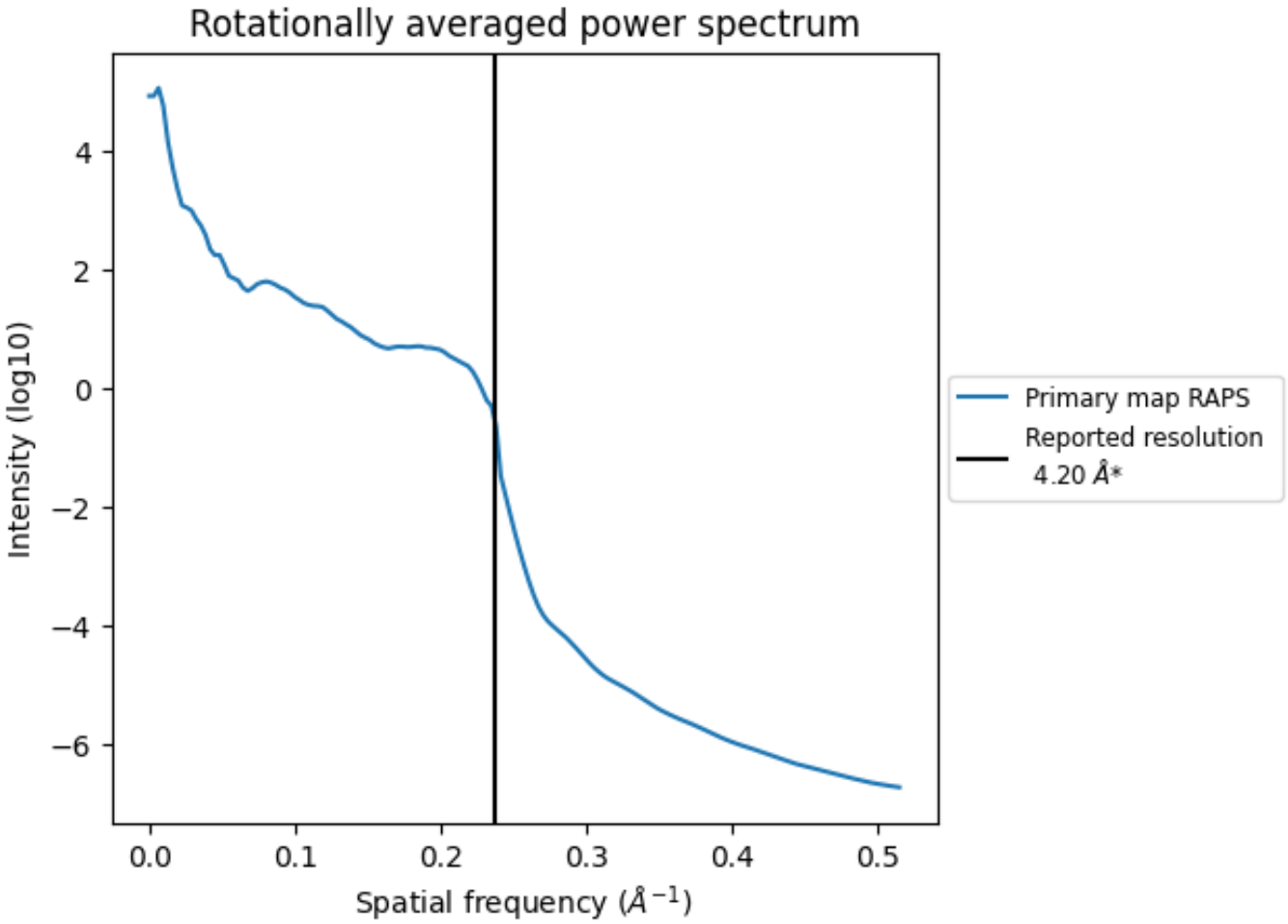
7.2 Volume estimate



The volume at the recommended contour level is 182 nm^3; this corresponds to an approximate mass of 165 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 0.238 Å^{-1}

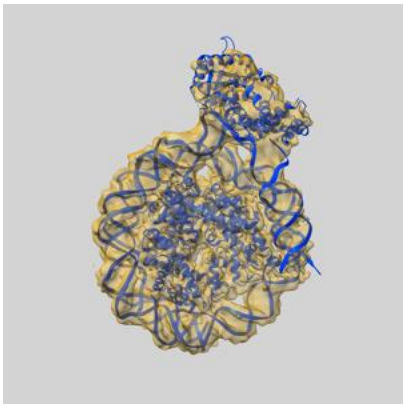
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

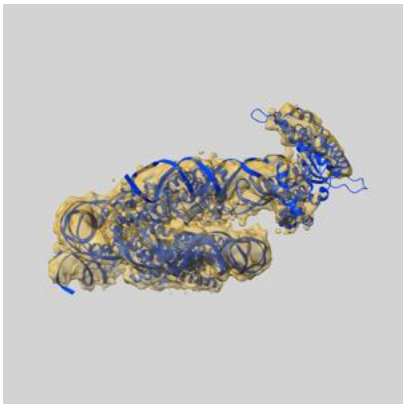
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-47255 and PDB model 9DWM. Per-residue inclusion information can be found in section 3 on page 6.

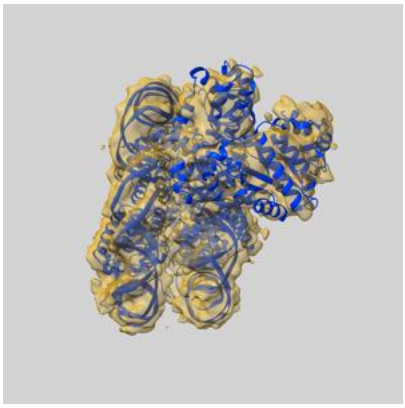
9.1 Map-model overlay



X



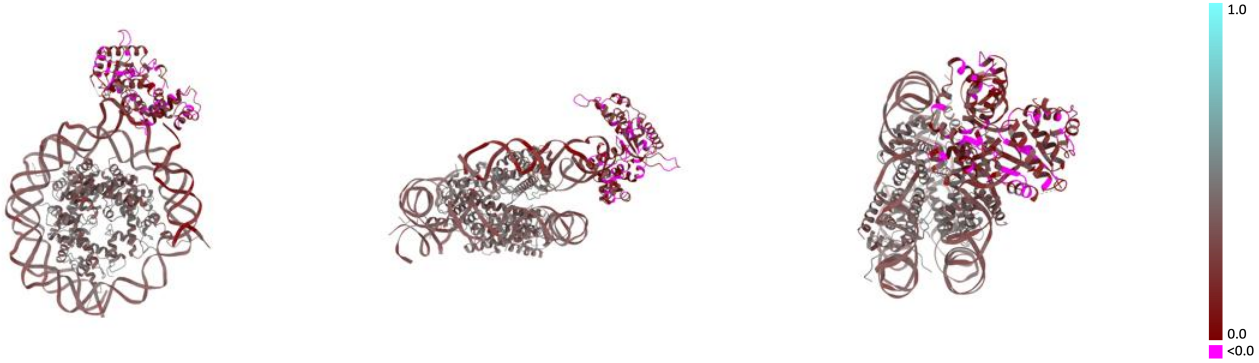
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.4 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.

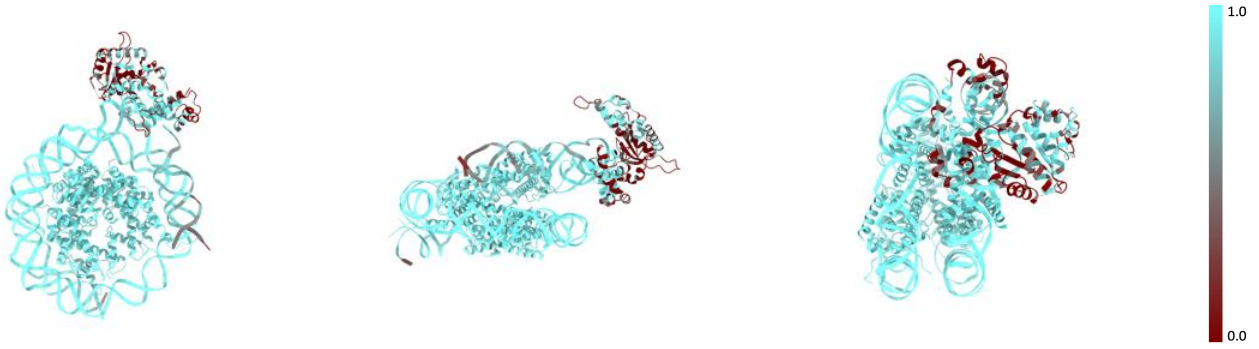
9.2 Q-score mapped to coordinate model (i)



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.

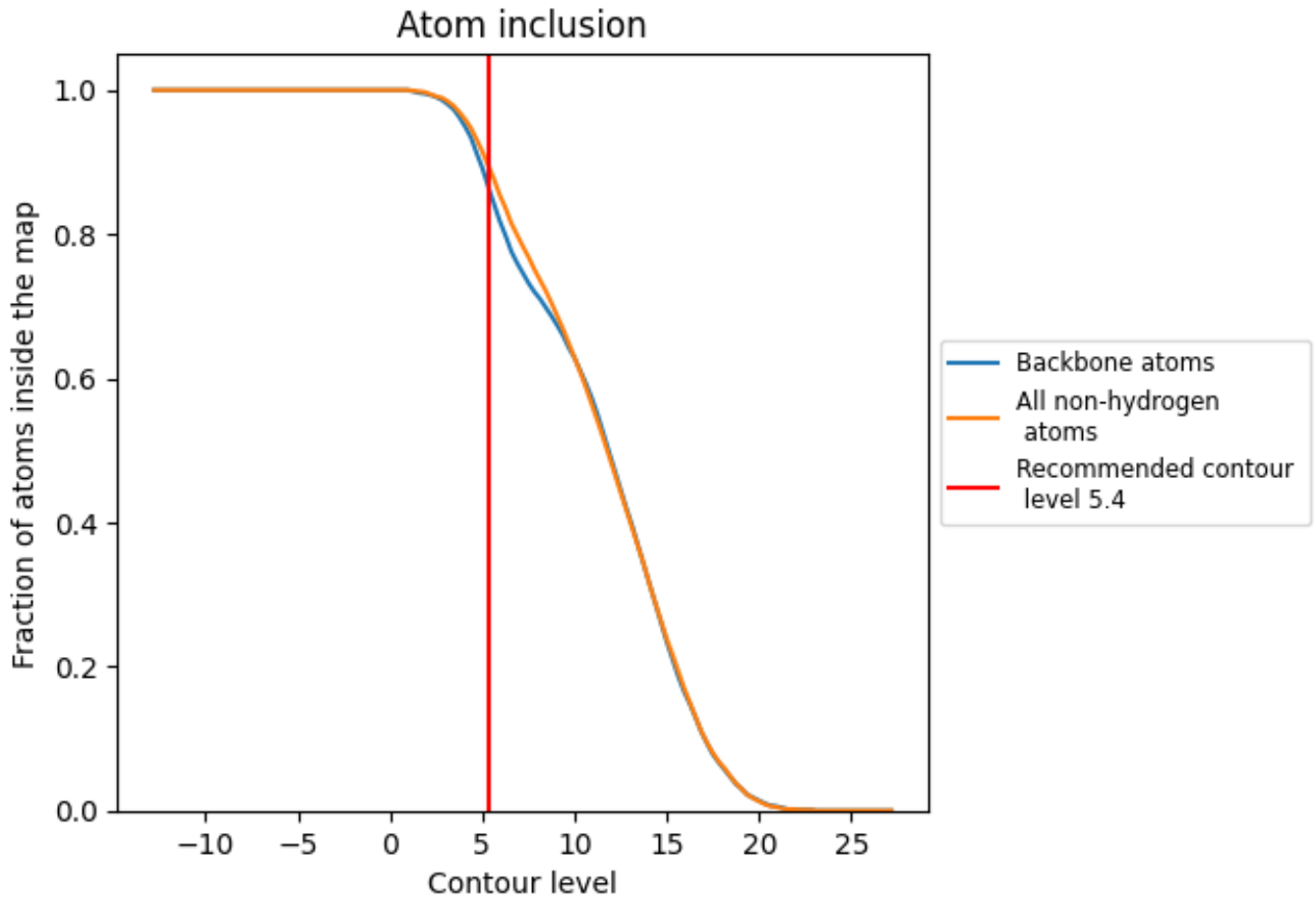
9.3 Atom inclusion mapped to coordinate model (i)



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 (5.4).

9.4 Atom inclusion (i)



At the recommended contour level, 86% 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 (5.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8910	0.3100
A	0.9860	0.4000
B	0.9950	0.4220
C	0.9870	0.4220
D	0.9910	0.3940
E	0.9860	0.4110
F	0.9970	0.4170
G	0.9820	0.4090
H	0.9840	0.3810
I	0.9800	0.3160
J	0.9490	0.3080
K	0.6180	0.1480
L	0.4730	0.1140