Full wwPDB EM Validation Report (i)

Nov 12, 2022 – 05:33 PM EST

PDB ID	:	6PX3
EMDB ID	:	EMD-20517
Title	:	Set2 bound to nucleosome
Authors	:	Halic, M.; Bilokapic, S.
Deposited on	:	2019-07-24
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 (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:

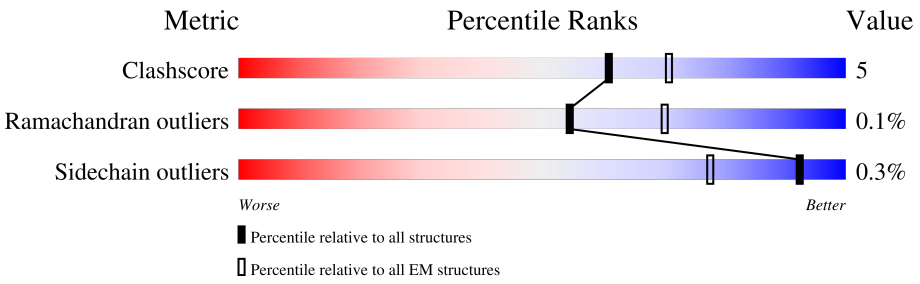
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	136	65% 6% 29%
1	E	136	64% 11% 25%
2	B	103	72% • 24%
2	F	103	70% 6% 24%
3	C	221	24% 69% 12% 19%
3	G	221	43% • 53%
4	D	123	69% 9% 22%
4	H	123	72% 5% 24%

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Mol	Chain	Length	Quality of chain
5	I	149	81% 17%
6	J	149	87% 10%
7	S	939	19% 6% 75%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 14323 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	96	791	500	151	137	3	0	0
1	E	102	834	526	161	143	4	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	36	MET	LYS	engineered mutation	UNP A0A310TTQ1
E	36	MET	LYS	engineered mutation	UNP A0A310TTQ1

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	78	629	397	123	108	1	0	0
2	F	78	622	393	120	108	1	0	0

- Molecule 3 is a protein called Ubiquitin-60S ribosomal protein L40,Histone H2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	179	1393	875	260	257	1	0	0
3	G	103	792	499	155	138		0	0

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-91	MET	-	initiating methionine	UNP P0CH09
C	-90	ASP	-	expression tag	UNP P0CH09
C	-89	SER	-	expression tag	UNP P0CH09

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-88	PRO	-	expression tag	UNP P0CH09
C	-87	ASP	-	expression tag	UNP P0CH09
C	-86	LEU	-	expression tag	UNP P0CH09
C	-85	HIS	-	expression tag	UNP P0CH09
C	-84	HIS	-	expression tag	UNP P0CH09
C	-83	HIS	-	expression tag	UNP P0CH09
C	-82	HIS	-	expression tag	UNP P0CH09
C	-81	HIS	-	expression tag	UNP P0CH09
C	-80	HIS	-	expression tag	UNP P0CH09
C	-79	GLY	-	expression tag	UNP P0CH09
C	-78	THR	-	expression tag	UNP P0CH09
C	-77	LEU	-	expression tag	UNP P0CH09
C	-76	VAL	-	expression tag	UNP P0CH09
C	-75	PRO	-	expression tag	UNP P0CH09
C	-74	ARG	-	expression tag	UNP P0CH09
C	-73	GLY	-	expression tag	UNP P0CH09
C	-72	SER	-	expression tag	UNP P0CH09
C	4	THR	-	linker	UNP P0CH09
C	5	SER	-	linker	UNP P0CH09
C	6	SER	-	linker	UNP P0CH09
C	7	GLY	-	linker	UNP P0CH09
C	8	GLY	-	linker	UNP P0CH09
C	9	SER	-	linker	UNP P0CH09
C	10	GLY	-	linker	UNP P0CH09
C	11	GLY	-	linker	UNP P0CH09
C	12	SER	-	linker	UNP P0CH09
C	13	GLY	-	linker	UNP P0CH09
C	14	GLY	-	linker	UNP P0CH09
C	15	SER	-	linker	UNP P0CH09
C	16	GLY	-	linker	UNP P0CH09
G	-91	MET	-	initiating methionine	UNP P0CH09
G	-90	ASP	-	expression tag	UNP P0CH09
G	-89	SER	-	expression tag	UNP P0CH09
G	-88	PRO	-	expression tag	UNP P0CH09
G	-87	ASP	-	expression tag	UNP P0CH09
G	-86	LEU	-	expression tag	UNP P0CH09
G	-85	HIS	-	expression tag	UNP P0CH09
G	-84	HIS	-	expression tag	UNP P0CH09
G	-83	HIS	-	expression tag	UNP P0CH09
G	-82	HIS	-	expression tag	UNP P0CH09
G	-81	HIS	-	expression tag	UNP P0CH09
G	-80	HIS	-	expression tag	UNP P0CH09

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-79	GLY	-	expression tag	UNP P0CH09
G	-78	THR	-	expression tag	UNP P0CH09
G	-77	LEU	-	expression tag	UNP P0CH09
G	-76	VAL	-	expression tag	UNP P0CH09
G	-75	PRO	-	expression tag	UNP P0CH09
G	-74	ARG	-	expression tag	UNP P0CH09
G	-73	GLY	-	expression tag	UNP P0CH09
G	-72	SER	-	expression tag	UNP P0CH09
G	4	THR	-	linker	UNP P0CH09
G	5	SER	-	linker	UNP P0CH09
G	6	SER	-	linker	UNP P0CH09
G	7	GLY	-	linker	UNP P0CH09
G	8	GLY	-	linker	UNP P0CH09
G	9	SER	-	linker	UNP P0CH09
G	10	GLY	-	linker	UNP P0CH09
G	11	GLY	-	linker	UNP P0CH09
G	12	SER	-	linker	UNP P0CH09
G	13	GLY	-	linker	UNP P0CH09
G	14	GLY	-	linker	UNP P0CH09
G	15	SER	-	linker	UNP P0CH09
G	16	GLY	-	linker	UNP P0CH09

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	96	757	475	140	140	2	0	0
			Total	C	N	O	S		
4	H	94	741	466	135	138	2	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	0	MET	-	initiating methionine	UNP P02281
D	29	THR	SER	engineered mutation	UNP P02281
H	0	MET	-	initiating methionine	UNP P02281
H	29	THR	SER	engineered mutation	UNP P02281

- Molecule 5 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	I	145	2957	1404	537	871	145	0	0

- Molecule 6 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	J	145	2988	1414	560	869	145	0	0

- Molecule 7 is a protein called Histone-lysine N-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	S	233	1816	1125	321	351	19	0	0

- Molecule 8 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
8	S	3	3	3	0

3 Residue-property plots (i)

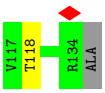
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

Chain A:

- Molecule 1: Histone H3

Chain E:



- Molecule 2: Histone H4

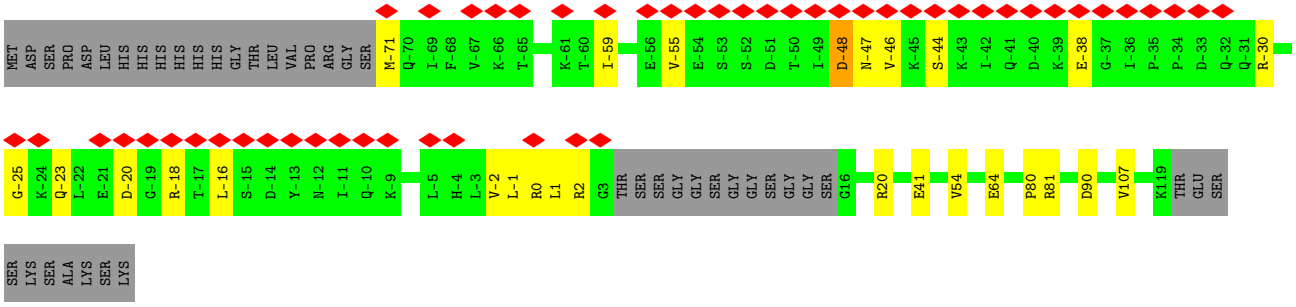
Chain B:

- Molecule 2: Histone H4

Chain F:

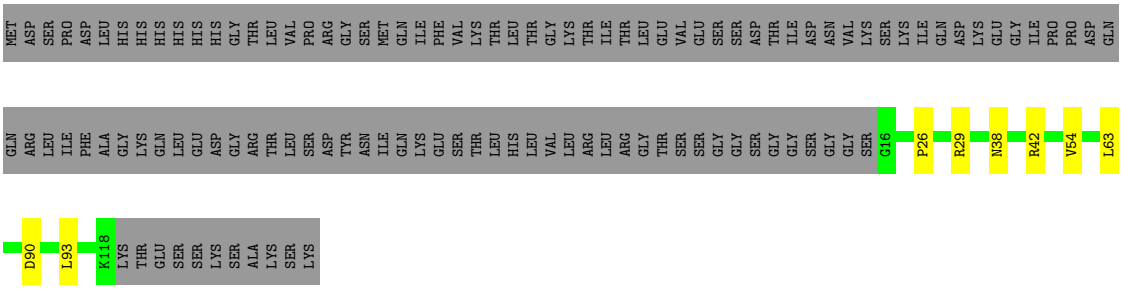
- Molecule 3: Ubiquitin-60S ribosomal protein L40,Histone H2A

Chain C:



• Molecule 3: Ubiquitin-60S ribosomal protein L40,Histone H2A

Chain G:

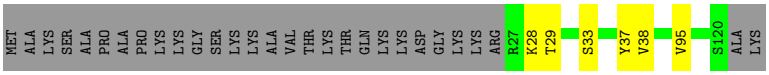


• Molecule 4: Histone H2B 1.1

Chain D:

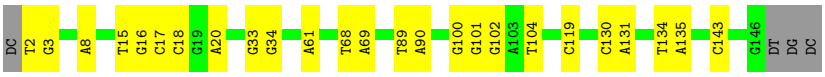
• Molecule 4: Histone H2B 1.1

Chain H:



• Molecule 5: DNA (145-MER)

Chain I:

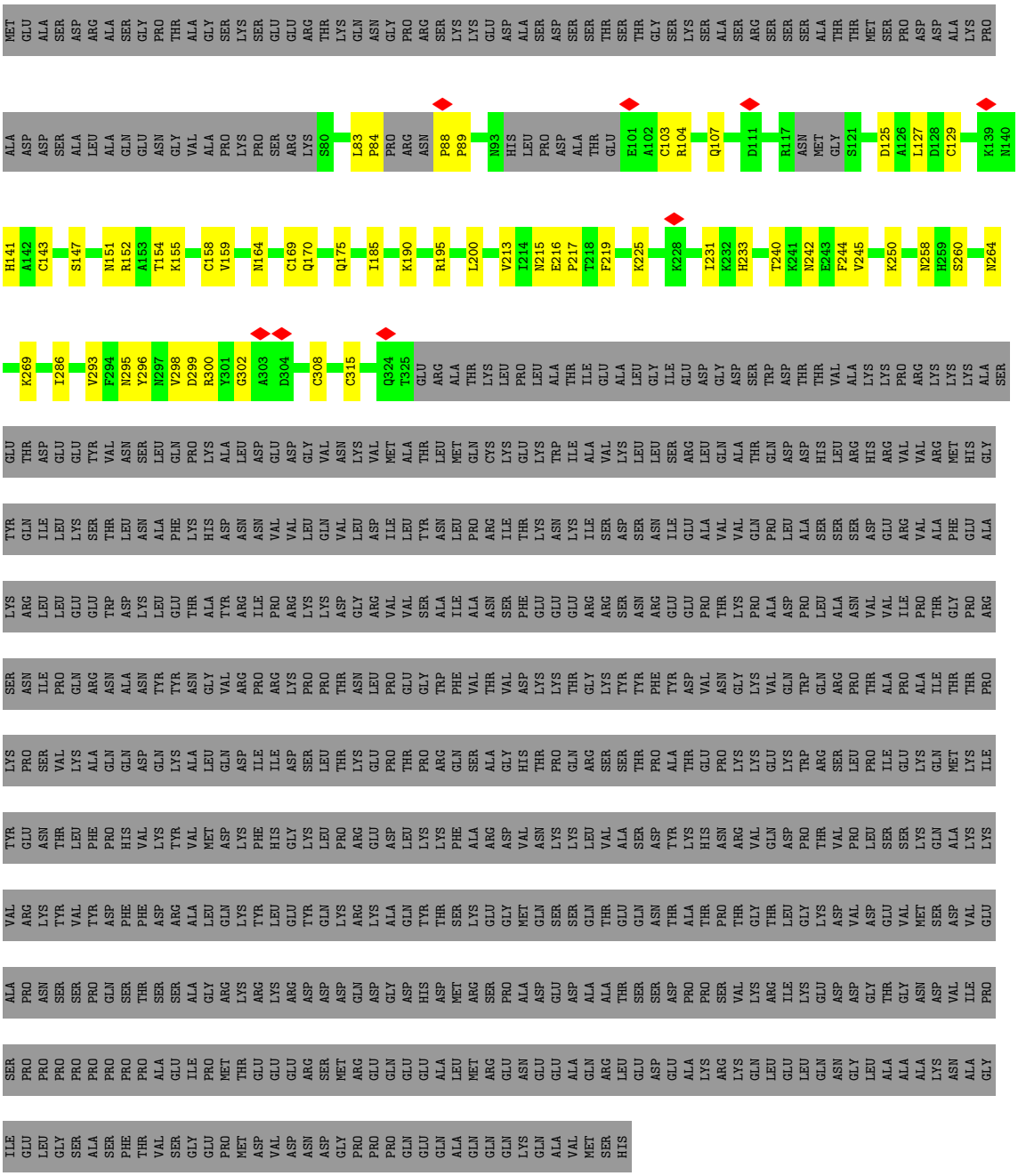


• Molecule 6: DNA (145-MER)

Chain J:

- Molecule 7: Histone-lysine N-methyltransferase

Chain S:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	67000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	75, 75, 75, 75	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K2 BASE (4k x 4k), GATAN K2 BASE (4k x 4k), GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	0.082	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	249.59999, 249.59999, 249.59999	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	A	0.32	0/803	0.51	0/1078
1	E	0.32	0/846	0.52	0/1134
2	B	0.32	0/636	0.52	0/852
2	F	0.33	0/629	0.54	0/843
3	C	0.34	0/1408	0.56	1/1897 (0.1%)
3	G	0.35	0/802	0.55	0/1083
4	D	0.31	0/768	0.47	0/1032
4	H	0.33	0/752	0.49	0/1011
5	I	1.01	1/3313 (0.0%)	1.03	3/5107 (0.1%)
6	J	1.00	0/3355	1.00	2/5180 (0.0%)
7	S	0.29	0/1849	0.58	3/2485 (0.1%)
All	All	0.71	1/15161 (0.0%)	0.80	9/21702 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	143	DC	C3'-O3'	5.04	1.50	1.44

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	S	88	PRO	N-CA-CB	5.97	110.46	103.30
7	S	89	PRO	N-CA-CB	5.92	110.41	103.30
7	S	84	PRO	N-CA-CB	5.79	110.25	103.30
5	I	102	DG	O4'-C1'-N9	-5.30	104.29	108.00
5	I	20	DA	O4'-C1'-N9	-5.24	104.33	108.00
6	J	126	DC	P-O3'-C3'	5.24	125.98	119.70
3	C	-48	ASP	CB-CG-OD2	5.20	122.98	118.30
5	I	143	DC	P-O3'-C3'	5.06	125.78	119.70
6	J	102	DA	O4'-C1'-N9	-5.00	104.50	108.00

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	791	0	828	7	0
1	E	834	0	877	15	0
2	B	629	0	670	5	0
2	F	622	0	660	5	0
3	C	1393	0	1466	43	0
3	G	792	0	842	7	0
4	D	757	0	786	27	0
4	H	741	0	768	8	0
5	I	2957	0	1628	15	0
6	J	2988	0	1627	9	0
7	S	1816	0	1672	33	0
8	S	3	0	0	0	0
All	All	14323	0	11824	120	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 5.

All (120) 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)
3:C:-23:GLN:NE2	4:D:106:HIS:CE1	2.01	1.27
3:C:-48:ASP:OD1	3:C:-20:ASP:HB3	1.40	1.21
3:C:-25:GLY:O	3:C:90:ASP:OD1	1.74	1.05
3:C:-23:GLN:CD	4:D:106:HIS:CE1	2.30	1.04
3:C:-23:GLN:NE2	4:D:106:HIS:ND1	2.11	0.99
3:C:2:ARG:HH11	4:D:113:LYS:HE3	1.27	0.99
4:H:29:THR:HB	5:I:104:DT:OP1	1.63	0.98
3:C:-48:ASP:OD1	3:C:-20:ASP:CB	2.17	0.93
7:S:143:CYS:HB2	7:S:169:CYS:SG	2.18	0.84
3:C:-2:VAL:HG21	3:C:64:GLU:OE2	1.83	0.79
4:H:29:THR:CB	5:I:104:DT:OP1	2.33	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:69:ARG:HE	2:F:25:ASN:HD21	1.36	0.73
3:C:-30:ARG:HG3	3:C:-23:GLN:NE2	2.07	0.70
3:C:2:ARG:NH1	4:D:113:LYS:HE3	2.05	0.66
3:C:-47:ASN:O	3:C:-44:SER:OG	2.11	0.65
3:C:-2:VAL:CG2	3:C:64:GLU:OE2	2.45	0.64
3:C:-23:GLN:CD	4:D:106:HIS:ND1	2.46	0.64
3:C:-23:GLN:HE21	4:D:106:HIS:CE1	2.11	0.63
7:S:296:TYR:HB3	7:S:298:VAL:HG13	1.81	0.62
3:C:-23:GLN:OE1	4:D:106:HIS:CG	2.52	0.62
7:S:213:VAL:HG22	7:S:245:VAL:HG12	1.81	0.62
7:S:308:CYS:HB3	7:S:315:CYS:SG	2.40	0.61
7:S:260:SER:O	7:S:295:ASN:ND2	2.33	0.61
1:A:122:LYS:HG3	1:E:113:HIS:HE1	1.65	0.60
7:S:190:LYS:O	7:S:258:ASN:ND2	2.35	0.60
3:C:-23:GLN:CD	4:D:106:HIS:NE2	2.54	0.60
7:S:143:CYS:CB	7:S:169:CYS:SG	2.86	0.60
4:D:92:GLN:HG2	4:D:96:ARG:HH11	1.68	0.59
7:S:141:HIS:HB3	7:S:170:GLN:HB2	1.84	0.59
3:C:-23:GLN:CG	4:D:106:HIS:NE2	2.65	0.59
1:A:123:ASP:OD1	1:E:113:HIS:NE2	2.36	0.58
3:C:-23:GLN:HG2	4:D:106:HIS:NE2	2.17	0.58
3:C:-25:GLY:C	3:C:90:ASP:OD1	2.41	0.58
3:C:-30:ARG:HG3	3:C:-23:GLN:HE21	1.68	0.58
3:C:-23:GLN:CG	4:D:106:HIS:CE1	2.86	0.57
7:S:129:CYS:O	7:S:164:ASN:ND2	2.31	0.57
7:S:103:CYS:SG	7:S:104:ARG:N	2.77	0.57
1:E:39:HIS:O	7:S:269:LYS:NZ	2.35	0.56
3:G:54:VAL:HG21	4:H:95:VAL:HG21	1.88	0.56
1:E:49:ARG:NH2	7:S:154:THR:O	2.40	0.54
1:E:118:THR:OG1	2:F:45:ARG:NH1	2.42	0.53
7:S:141:HIS:ND1	7:S:170:GLN:OE1	2.42	0.53
3:C:2:ARG:NH1	4:D:113:LYS:HG2	2.23	0.53
7:S:147:SER:O	7:S:152:ARG:NH2	2.42	0.52
7:S:300:ARG:NH1	7:S:302:GLY:O	2.40	0.52
3:C:-25:GLY:CA	3:C:90:ASP:OD1	2.58	0.52
3:C:-23:GLN:CD	4:D:106:HIS:CG	2.82	0.52
7:S:151:ASN:ND2	7:S:158:CYS:SG	2.81	0.52
7:S:185:ILE:HB	7:S:195:ARG:HD2	1.90	0.52
7:S:216:GLU:HG2	7:S:217:PRO:HD3	1.92	0.52
3:C:-23:GLN:HG2	4:D:106:HIS:CE1	2.46	0.51
7:S:200:LEU:HB2	7:S:286:ILE:HB	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:20:ARG:NH2	4:D:121:ALA:O	2.43	0.51
3:C:-23:GLN:CD	4:D:106:HIS:CD2	2.85	0.51
3:C:54:VAL:HG21	4:D:95:VAL:HG21	1.93	0.50
7:S:159:VAL:HA	7:S:175:GLN:HE22	1.75	0.50
1:E:45:THR:HG21	7:S:155:LYS:HD2	1.93	0.50
3:G:26:PRO:HG3	4:H:37:TYR:CZ	2.46	0.50
3:C:2:ARG:HH12	4:D:113:LYS:HG2	1.77	0.49
3:C:-25:GLY:HA3	3:C:90:ASP:OD1	2.11	0.49
3:G:42:ARG:HG2	6:J:113:DA:H5"	1.95	0.49
1:E:66:PRO:HG3	6:J:91:DA:OP1	2.13	0.48
4:H:29:THR:CG2	5:I:104:DT:OP1	2.61	0.48
3:C:2:ARG:HH11	4:D:113:LYS:CE	2.11	0.48
7:S:215:ASN:O	7:S:219:PHE:CB	2.61	0.48
1:A:46:VAL:HG13	1:A:49:ARG:HH21	1.77	0.48
3:C:1:LEU:HD22	4:D:44:GLN:NE2	2.29	0.48
1:E:116:ARG:NH1	1:E:118:THR:O	2.47	0.47
2:F:30:THR:HG21	5:I:61:DA:H5"	1.97	0.47
2:B:75:HIS:CE1	4:D:90:GLU:HG2	2.49	0.47
3:C:-48:ASP:CG	3:C:-20:ASP:HB3	2.24	0.47
1:E:56:LYS:HE3	7:S:127:LEU:HD23	1.97	0.47
1:E:97:GLU:OE1	2:F:40:ARG:NH1	2.43	0.47
1:A:61:LEU:HD12	2:B:37:LEU:HD23	1.97	0.46
3:G:29:ARG:NH1	4:H:33:SER:O	2.49	0.46
3:C:0:ARG:HD2	4:D:113:LYS:NZ	2.31	0.45
1:A:100:LEU:HD11	2:B:58:LEU:HD22	1.97	0.45
5:I:134:DT:H2"	5:I:135:DA:C8	2.51	0.45
1:E:34:GLY:HA3	7:S:300:ARG:HA	1.99	0.45
3:C:41:GLU:HG3	3:G:38:ASN:HD21	1.81	0.45
3:G:63:LEU:HD11	4:H:38:VAL:HG13	1.98	0.45
6:J:17:DT:H2"	6:J:18:DG:C8	2.51	0.45
5:I:2:DT:H2"	5:I:3:DG:C8	2.52	0.45
5:I:68:DT:H2"	5:I:69:DA:C8	2.53	0.44
3:C:81:ARG:NH1	3:C:107:VAL:O	2.41	0.44
5:I:119:DC:N4	6:J:28:DT:O4	2.51	0.44
1:E:35:VAL:HG23	7:S:244:PHE:HE1	1.83	0.44
7:S:107:GLN:HB3	7:S:250:LYS:HG3	2.00	0.44
2:B:58:LEU:HD12	2:B:58:LEU:HA	1.73	0.44
5:I:15:DT:H2"	5:I:16:DG:C8	2.53	0.43
3:C:-30:ARG:CG	3:C:-23:GLN:NE2	2.79	0.43
7:S:213:VAL:HA	7:S:244:PHE:O	2.19	0.43
3:C:-48:ASP:OD1	3:C:-20:ASP:CG	2.56	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:78:ARG:NH1	2:F:82:THR:OG1	2.51	0.42
3:G:90:ASP:HB3	3:G:93:LEU:HB2	2.01	0.42
1:E:60:LEU:HD12	1:E:64:LYS:HE3	2.01	0.42
7:S:240:THR:HG23	7:S:242:ASN:H	1.84	0.42
1:A:49:ARG:NH1	5:I:8:DA:H4'	2.35	0.42
3:C:-46:VAL:HG21	3:C:-16:LEU:HD21	2.02	0.42
3:C:-71:MET:HB3	3:C:-55:VAL:O	2.19	0.42
5:I:89:DT:H2"	5:I:90:DA:C8	2.55	0.42
7:S:264:ASN:HD21	7:S:293:VAL:H	1.66	0.42
1:A:102:ALA:HB1	1:A:131:ARG:HH22	1.85	0.41
6:J:145:DC:H2"	6:J:146:DA:C8	2.55	0.41
3:C:80:PRO:HD3	4:D:55:ALA:HB2	2.02	0.41
7:S:231:ILE:HG12	7:S:233:HIS:H	1.84	0.41
4:D:31:LYS:NZ	4:D:32:GLU:O	2.44	0.41
5:I:100:DG:H2"	5:I:101:DG:C8	2.56	0.41
3:C:-23:GLN:OE1	4:D:106:HIS:CD2	2.73	0.41
5:I:33:DG:H2"	5:I:34:DG:H5"	2.03	0.41
6:J:32:DG:H1'	6:J:33:DA:H5'	2.03	0.41
7:S:225:LYS:HE2	7:S:225:LYS:HB2	1.81	0.41
1:E:35:VAL:HG13	7:S:299:ASP:HB2	2.03	0.41
7:S:125:ASP:OD1	7:S:125:ASP:N	2.54	0.41
5:I:17:DC:H2"	5:I:18:DC:C5	2.57	0.40
3:C:-59:ILE:HG21	3:C:-38:GLU:HG2	2.03	0.40
6:J:89:DT:H2"	6:J:90:DA:C8	2.57	0.40
4:H:28:LYS:HD3	6:J:124:DG:H3'	2.02	0.40
2:B:36:ARG:HH12	6:J:61:DA:P	2.43	0.40
5:I:130:DC:H2"	5:I:131:DA:N7	2.36	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	94/136 (69%)	91 (97%)	3 (3%)	0	100	100
1	E	100/136 (74%)	98 (98%)	2 (2%)	0	100	100
2	B	76/103 (74%)	74 (97%)	2 (3%)	0	100	100
2	F	76/103 (74%)	73 (96%)	3 (4%)	0	100	100
3	C	175/221 (79%)	174 (99%)	1 (1%)	0	100	100
3	G	101/221 (46%)	99 (98%)	2 (2%)	0	100	100
4	D	94/123 (76%)	92 (98%)	2 (2%)	0	100	100
4	H	92/123 (75%)	90 (98%)	2 (2%)	0	100	100
7	S	225/939 (24%)	195 (87%)	29 (13%)	1 (0%)	34	71
All	All	1033/2105 (49%)	986 (96%)	46 (4%)	1 (0%)	54	84

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	S	83	LEU

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	84/111 (76%)	84 (100%)	0	100	100
1	E	88/111 (79%)	87 (99%)	1 (1%)	73	84
2	B	65/79 (82%)	65 (100%)	0	100	100
2	F	64/79 (81%)	64 (100%)	0	100	100
3	C	150/184 (82%)	148 (99%)	2 (1%)	69	81
3	G	81/184 (44%)	81 (100%)	0	100	100
4	D	82/103 (80%)	82 (100%)	0	100	100
4	H	81/103 (79%)	81 (100%)	0	100	100
7	S	190/817 (23%)	190 (100%)	0	100	100
All	All	885/1771 (50%)	882 (100%)	3 (0%)	92	95

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	-18	ARG
3	C	-1	LEU
1	E	110	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	GLN
3	C	-32	GLN
3	C	104	GLN
4	D	44	GLN
4	D	46	HIS
1	E	68	GLN
2	F	25	ASN
3	G	24	GLN
3	G	38	ASN
7	S	215	ASN
7	S	242	ASN
7	S	295	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

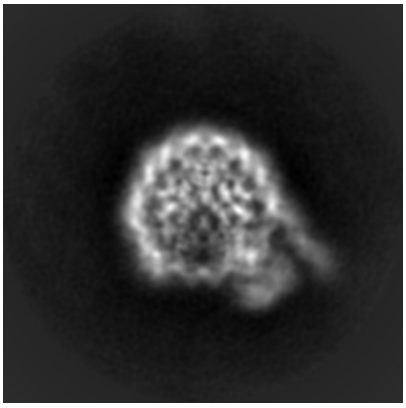
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-20517. These allow visual inspection of the internal detail of the map and identification of artifacts.

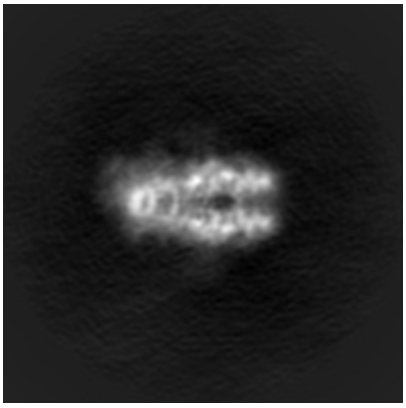
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

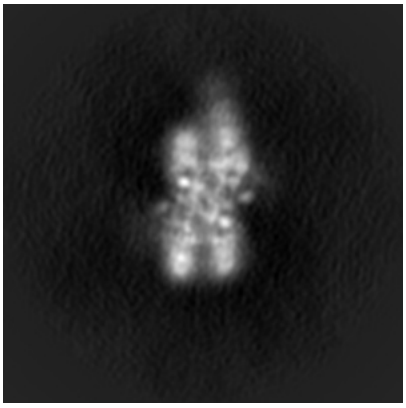
6.1.1 Primary map



X



Y

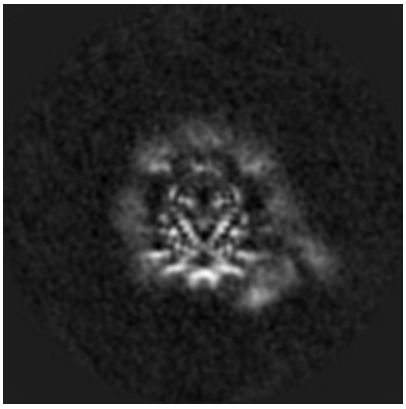


Z

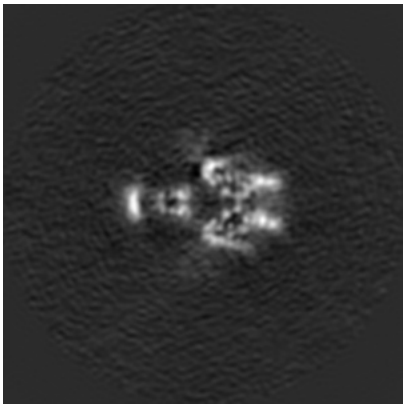
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

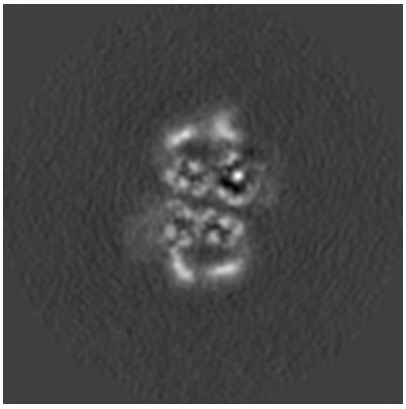
6.2.1 Primary map



X Index: 120



Y Index: 120

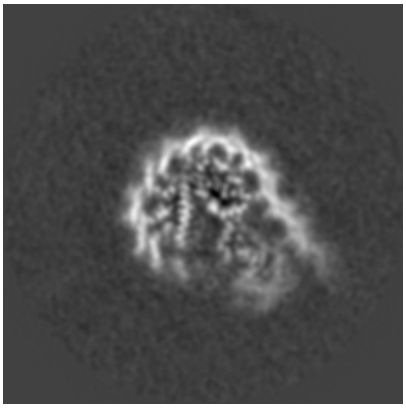


Z Index: 120

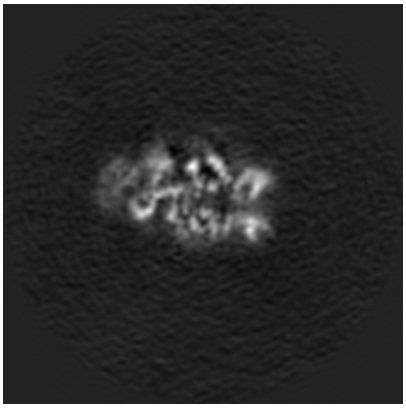
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

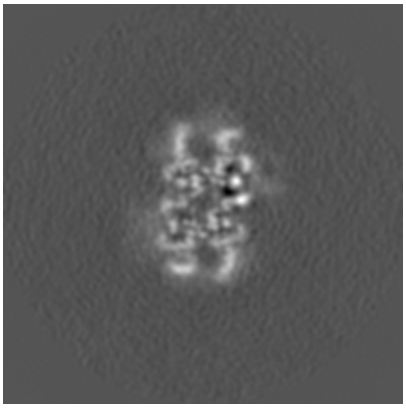
6.3.1 Primary map



X Index: 132



Y Index: 143

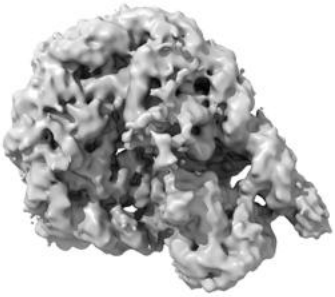


Z Index: 125

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

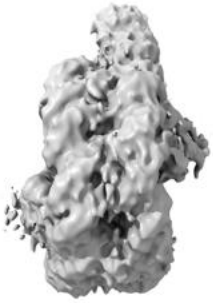
6.4 Orthogonal surface views (i)

6.4.1 Primary map



X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

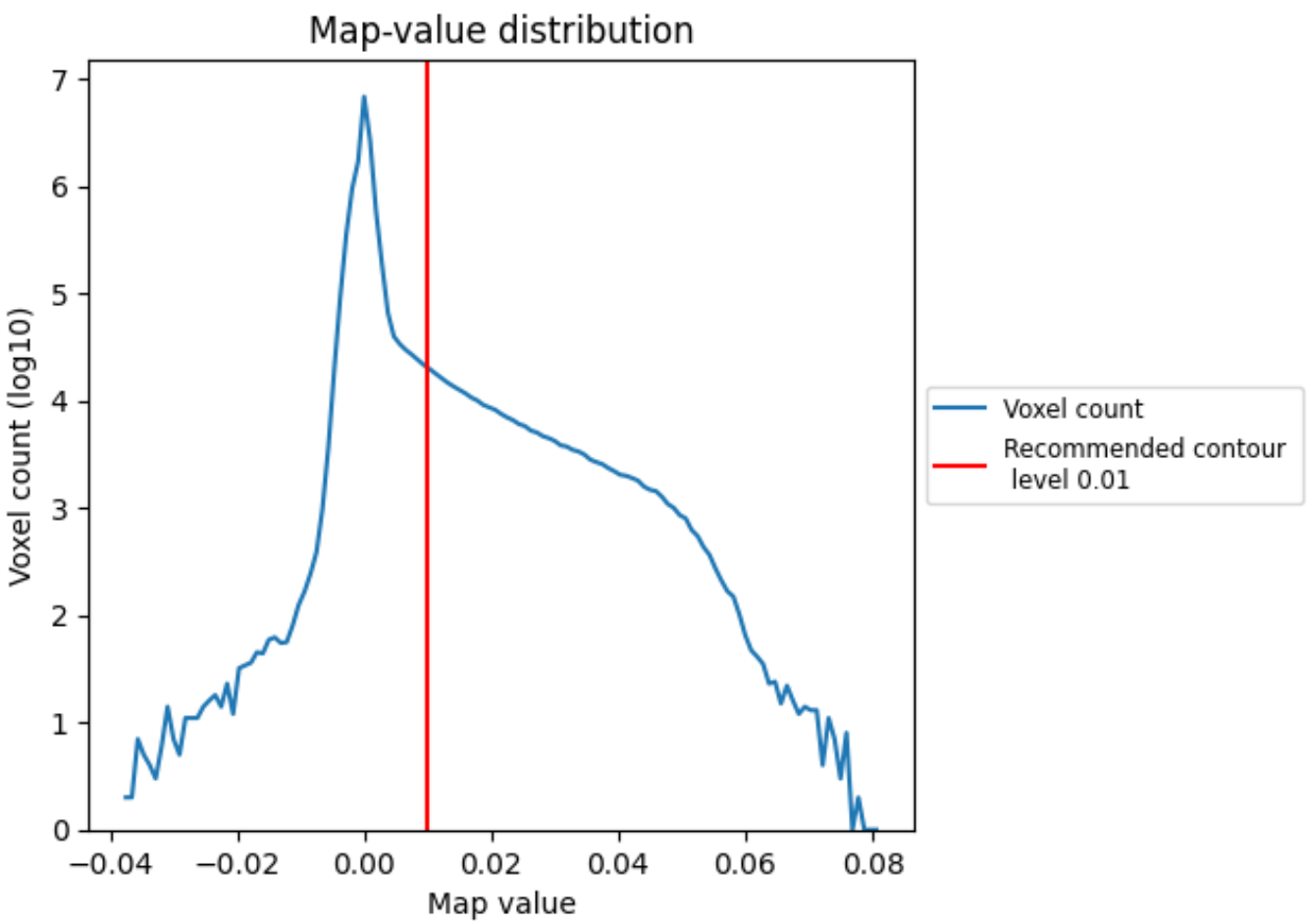
6.5 Mask visualisation (i)

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

7 Map analysis (i)

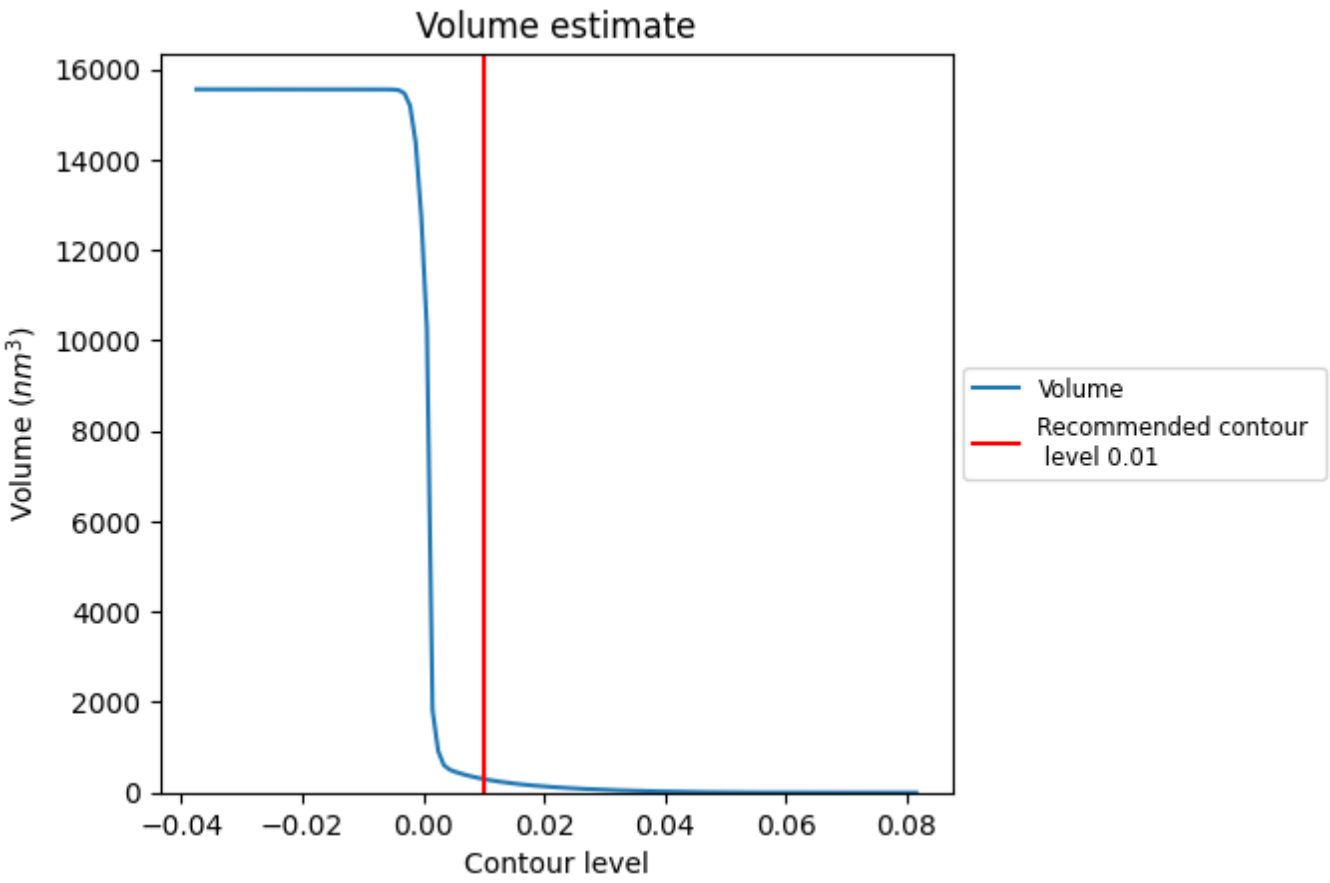
This section contains the results of statistical analysis of the map.

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.

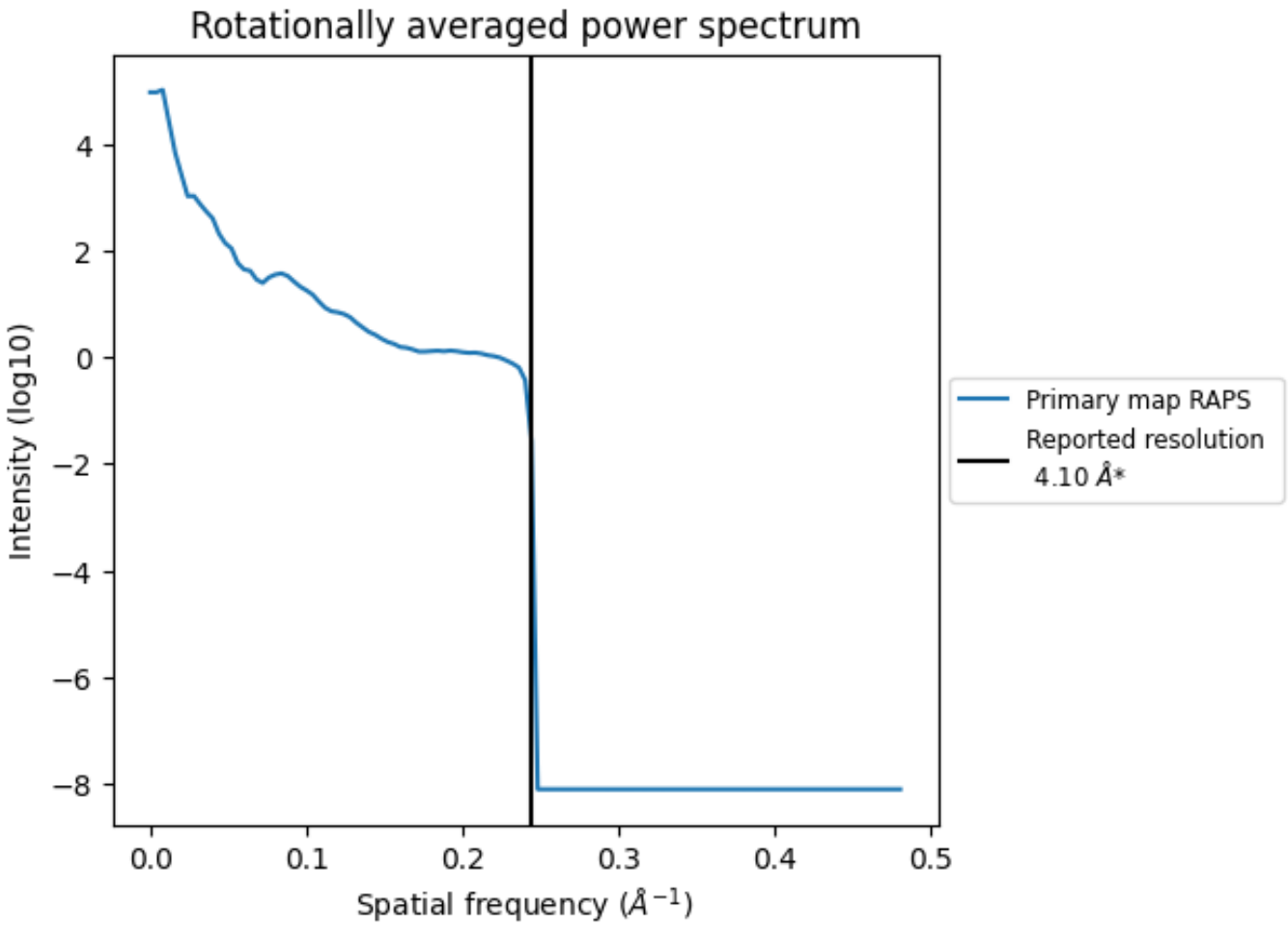
7.2 Volume estimate (i)



The volume at the recommended contour level is 300 nm^3; this corresponds to an approximate mass of 271 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}

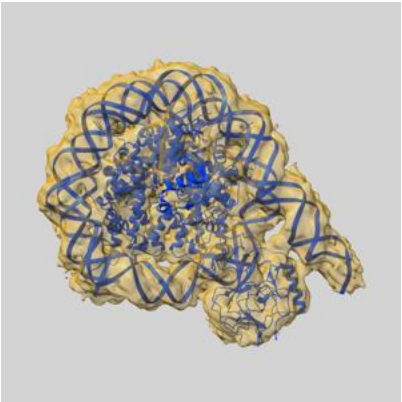
8 Fourier-Shell correlation (i)

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

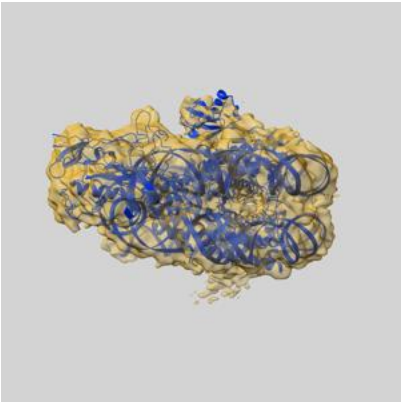
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-20517 and PDB model 6PX3. Per-residue inclusion information can be found in section 3 on page 8.

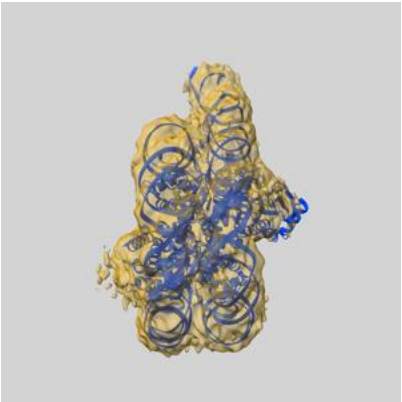
9.1 Map-model overlay (i)



X



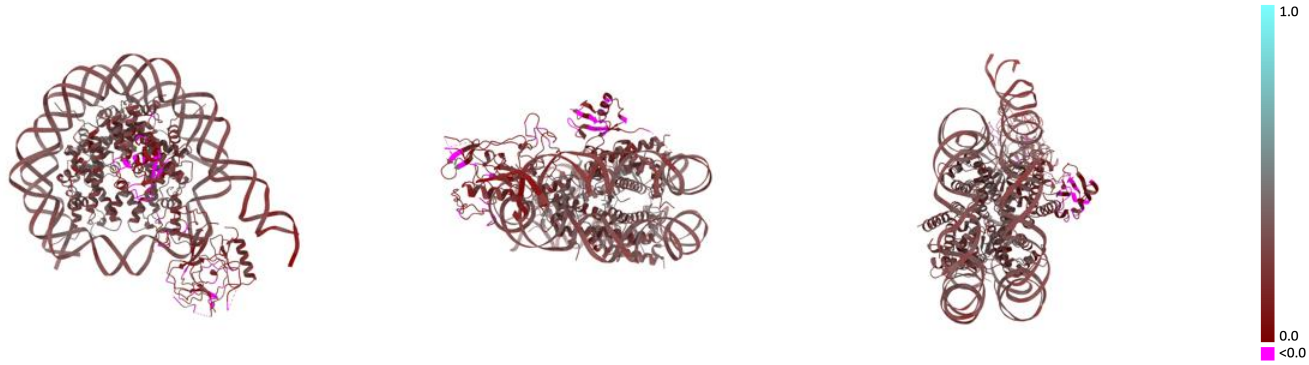
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01 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.

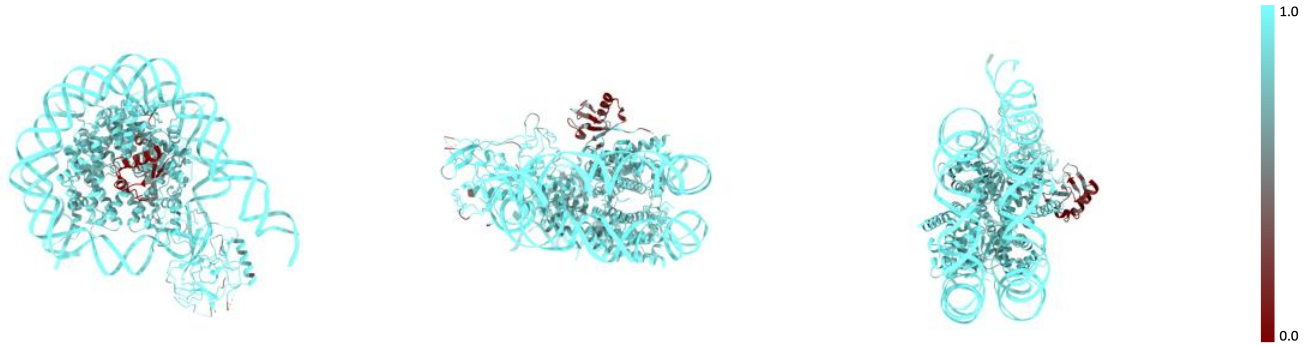
9.2 Q-score mapped to coordinate model (i)



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.

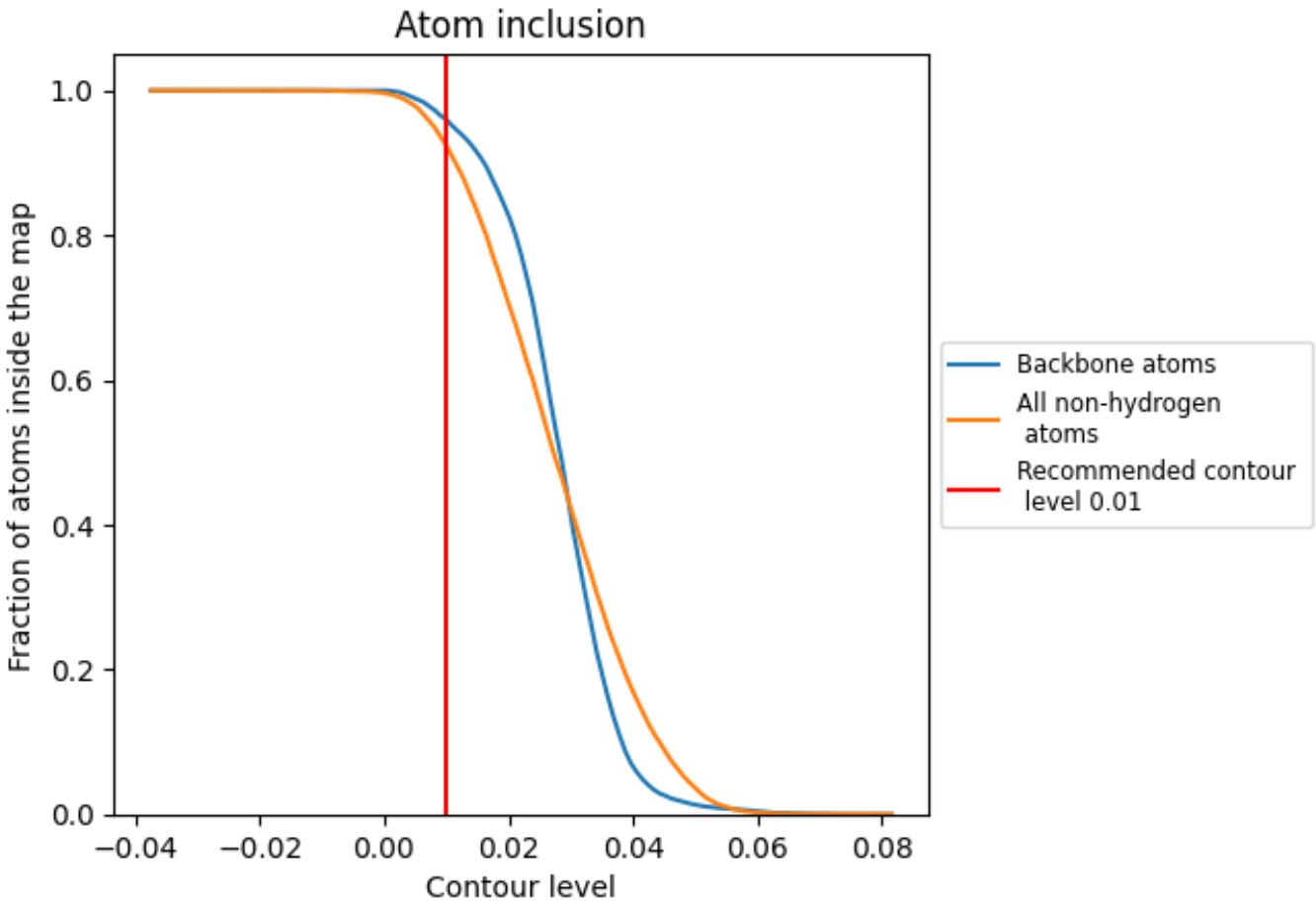
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 96% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9235	0.2610
A	0.9226	0.2860
B	0.9187	0.2940
C	0.6233	0.1830
D	0.9090	0.2740
E	0.9066	0.2840
F	0.9247	0.3050
G	0.9400	0.3030
H	0.9391	0.2830
I	0.9953	0.2850
J	0.9967	0.2860
S	0.9129	0.1600