



wwPDB EM Validation Summary Report ⓘ

Nov 26, 2022 – 07:28 PM EST

PDB ID : 7T02
EMDB ID : EMD-25577
Title : Cryo-EM structure of DNMT5 pseudo-ternary complex solved by incubation with hemimethylated DNA and SAM
Authors : Wang, J.; Patel, D.J.
Deposited on : 2021-11-29
Resolution : 3.80 Å(reported)
Based on initial model : 7R77

This is a wwPDB EM Validation Summary 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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

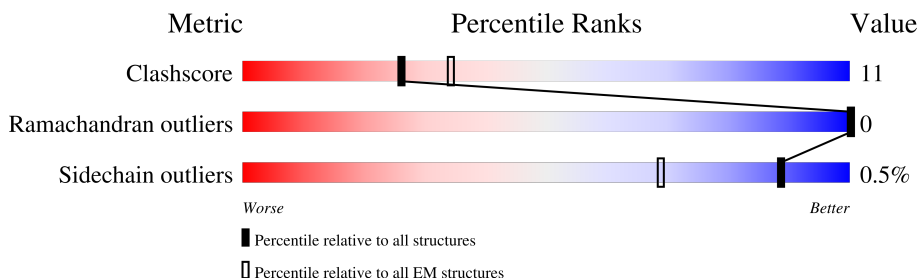
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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)
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 $\leq 5\%$. 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	2348	
2	B	36	
3	D	36	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14359 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 DNA repair protein Rad8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1752	Total	C	N	O	S	0	0
			13843	8712	2500	2562	69		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	MET	-	expression tag	UNP J9VI03
A	31	SER	-	expression tag	UNP J9VI03
A	32	TYR	-	expression tag	UNP J9VI03
A	33	TYR	-	expression tag	UNP J9VI03
A	34	HIS	-	expression tag	UNP J9VI03
A	35	HIS	-	expression tag	UNP J9VI03
A	36	HIS	-	expression tag	UNP J9VI03
A	37	HIS	-	expression tag	UNP J9VI03
A	38	HIS	-	expression tag	UNP J9VI03
A	39	HIS	-	expression tag	UNP J9VI03
A	40	ASP	-	expression tag	UNP J9VI03
A	41	TYR	-	expression tag	UNP J9VI03
A	42	ASP	-	expression tag	UNP J9VI03
A	43	ILE	-	expression tag	UNP J9VI03
A	44	PRO	-	expression tag	UNP J9VI03
A	45	THR	-	expression tag	UNP J9VI03
A	46	THR	-	expression tag	UNP J9VI03
A	47	GLU	-	expression tag	UNP J9VI03
A	48	ASN	-	expression tag	UNP J9VI03
A	49	LEU	-	expression tag	UNP J9VI03
A	50	TYR	-	expression tag	UNP J9VI03
A	51	PHE	-	expression tag	UNP J9VI03
A	52	GLN	-	expression tag	UNP J9VI03
A	53	GLY	-	expression tag	UNP J9VI03
A	54	ALA	-	expression tag	UNP J9VI03
A	55	MET	-	expression tag	UNP J9VI03
A	56	GLY	-	expression tag	UNP J9VI03
A	57	SER	-	expression tag	UNP J9VI03

- Molecule 2 is a DNA chain called DNA (5'-D(P*GP*TP*CP*AP*GP*(5CM)P*GP*CP*AP*TP*GP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	12	Total	C	N	O	P	0	0
			250	118	48	72	12		

- Molecule 3 is a DNA chain called DNA (5'-D(*CP*CP*AP*TP*GP*CP*GP*CP*TP*GP*AP*CP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	13	Total	C	N	O	P	0	0
			261	125	49	75	12		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	A	5	Total	Zn	0
			5	5	

SER	L2095	L1855	R1746	GLU	ALA	T1519	S1435	P1355	G1255	R1053
THR	C2098	E1856	W1747	ASP	MET	G1520	L1439	THR	L1256	K1054
ASN	C2099	H1859	I1748	ASP	GLU	S1521	P1440	THR	W1259	L1055
ASP	S2217	E1865	G1751	GLU	LYS	F1523	G1443	SER	A1260	Q1060
	A2218	F1869	T1752	ASN	LYS	K1524	W1444	GLU	H1261	L1061
R2219	A2103	K1870	P1754	LYS	SER	G1530	R1445	HIS	I1262	L1062
L2223	C2104	F1874	V1755	LEU	LEU	M1531	G1458	GLY	A1263	F1063
C2107	M2108	S1756	V1756	VAL	VAL	D1533	G1459	L1365	R1264	R1064
N2226	M2108	D1757	D1757	ASP	ASN	L1534	V1460	ASP	S1267	Q1067
ASP	C2117	D1881	D1757	PRO	VAL	L1534	I1461	ASP	E1268	A1068
ALA	D2016	R1882	A1760	PRO	SER	L1534	A1462	VAL	R1273	S1071
	P2020	R1885	I1761	LYS	LYS	A1540	D1463	VAL	R1277	L1072
Q2123	Q2124	L1886	F1767	PHE	GLU	E1541	GLN	ALA	ASN	H1073
Q2124	A2125	L1886	F1767	SER	GLU	K1544	VAL	ASP	P1278	R1076
A2126	A2126	L1890	H1771	THR	VAL	A1545	TYR	ALA	P1279	F1077
R2127	R2127	S1891	V1774	GLY	HIS	A1545	GLY	ALA	ASN	ASP
R2128	R2128	D1892	E1775	THR	THR	M1550	LYS	GLU	I1284	LEU
L2138	L2138	S1893	E1775	GLY	ALA	A1551	T1470	PRO	ARG	SER
A2236	A2236	K1894	E1775	VAL	ALA	A1551	V1471	GLY	GLY	D1081
N2239	N2239	T1895	E1779	ASN	ASN	A1551	I1472	GLY	GLY	D1082
H2240	H2240	A1896	G1780	PHE	PHE	A1551	I1474	LYS	ARG	G1083
A2241	V2031	PHE	G1780	GLY	GLY	A1551	I1474	ALA	ASP	L1084
	K2032	SER	Q1785	LYS	LYS	A1551	I1474	ALA	ASN	
	Q2038	ALA	Q1785	ALA	ARG	A1551	I1474	ALA	LYS	
L2156	L2156	SER	R1788	VAL	MET	L1567	S1482	LYS	ASN	
T2160	T2160	LYS	D1791	LYS	GLY	A1569	LEU	LYS	A1180	F1089
K2165	K2165	LYS	D1791	GLM	GLY	Q1570	PRO	LYS	T1181	F1090
E2259	E2259	ASP	F1798	ALA	ALA	P1571	ALA	GLY	F1182	L1091
V2266	V2266	TYR	F1798	GLU	GLY	ARG	GLU	ASN	A1183	
R2168	R2168	LYS	R1802	GLU	ASP	GLU	GLU	LYS	S1187	R1095
V2169	V2169	LEU	E1803	LEU	ASP	TRP	PRO	LYS	A1188	
F2172	F2172	PRO	R1812	PRO	HIS	L1575	ALA	SER	I1191	
V2182	V2182	ASN	R1813	ASN	LYS	H1576	THR	GLN	F1300	
L2186	L2186	LYS	D1814	PRO	ASP	D1577	GLY	PRO	F1304	
T2191	T2191	LYS	E1815	PRO	SER	GLY	LEU	ALA	E1305	L1113
L2196	L2196	LYS	L1816	GLY	ASP	GLY	ILE	PHE	D1306	D1114
SER	SER	GLY	A1817	LYS	SER	GLY	D1495	LYS	E1309	E1118
T2285	T2285	LYS	Q1818	ALA	ALA	R1582	K1497	LEU	H1217	
D2287	D2287	LYS	Q1818	LYS	LYS	E1593	A1498	ARG	R1223	
N2288	N2288	PRO	F1717	PRO	ILE	S1594	I1501	LEU	ARG	A1123
T2289	T2289	THR	R1719	THR	THR	L1595	P1504	ARG	GLY	R1124
L2290	L2290	LYS	R1720	LYS	LYS	V1596	G1505	GLY	W1227	L1125
R2294	R2294	GLU	Y1729	GLU	GLU	S1597	P1504	GLY	W1227	
E2297	E2297	GLU	Q1826	GLU	GLU	Q1598	G1505	GLY	R1230	W1129
L2298	L2298	LEU	N1828	LEU	LEU	T1599	K1509	PRO	R1338	R1330
K2301	K2301	GLU	Q1731	GLU	GLU	Q1598	Q1510	GLY	F1240	E1134
T2302	T2302	THR	A1830	THR	THR	I1601	W1511	GLY	W1245	R1137
D2303	D2303	GLU	E1831	GLU	GLU	L1602	P1512	GLY	A1347	R1138
		ALA	I1835	ALA	ALA	L1602	N1513	GLY	R1249	V1139
		ASP	I1835	SER	SER	L1602	E1514	LYS	R1349	
		ASP	I1835	ASP	ASP	L1602	I1515	GLY	L1253	S1144
		GLY	I1835	GLY	GLY	L1602	R1517	SER	D1254	G1145
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
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		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
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		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY	I1835	GLY	GLY	L1602	F1518	GLY		
		GLY								

Y2312
LYS
GLY
ARG
GLY
SER
SER
ILE
SER
SER
MET
THR
ASN
GLU
LYS
ARG
THR
PRO
THR
LEU
THR
VAL
LYS
SER
ASN
PRO
PHE
LYS
ARG
SER
SER
SER
TRP
ALA
LEU
ALA
SER
SER
PHE
ARG
SER
LYS
ARG
SER
MET
GLU
ALA
ARG
ASP
ALA
GLU
GLY
VAL
SER
ASP
ASP
GLU
ASN
SER

GLU
LEU
SER
ASP
ILE
ILE

- Molecule 2: DNA (5'-D(P*GP*TP*CP*AP*GP*(5CM)P*GP*CP*AP*TP*GP*G)-3')



DT	DG	DT	DA	DT	DG	DG	DT	DC	DT	DT	DA	DG	DG	DC	DA	DA	DT	DT	DC	DT	DA	DG	DT	G25	A28	G29	C30	G31	C32	G36
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- Molecule 3: DNA (5'-D(*CP*CP*AP*TP*GP*CP*GP*CP*TP*GP*AP*CP*A)-3')



G1	C2	A3	T4	G5	G6	G7	G8	T9	G10	A13	DC	DA	DA	DG	DA	DA	DT	DT	DT	DC	DC	DT	DA	DA	DG	DA	DC	DC	DA	DA	DA
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	50146	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 ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	22500	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.172	Depositor
Minimum map value	-0.091	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	272.384, 272.384, 272.384	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.064, 1.064, 1.064	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: 5CM, 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	0.48	0/14113	0.58	0/19089
2	B	1.19	0/257	0.96	0/393
3	D	1.22	0/292	0.91	0/448
All	All	0.52	0/14662	0.60	0/19930

There are no bond length outliers.

There are no bond angle outliers.

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	13843	0	13810	310	0
2	B	250	0	137	4	0
3	D	261	0	147	7	0
4	A	5	0	0	0	0
All	All	14359	0	14094	316	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 11.

The worst 5 of 316 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:512:PHE:HE1	1:A:547:ARG:HG2	1.45	0.80
1:A:1259:TRP:HB2	1:A:1366:SER:HB3	1.66	0.77
1:A:789:GLU:HG2	1:A:791:HIS:HB3	1.68	0.76
1:A:1261:HIS:HD2	1:A:1262:ILE:HG12	1.52	0.74
1:A:2010:ILE:HG13	1:A:2012:PRO:HD2	1.68	0.74

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	1708/2348 (73%)	1567 (92%)	141 (8%)	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	1496/2015 (74%)	1489 (100%)	7 (0%)	88	94

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1125	LEU
1	A	1253	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1732	LYS
1	A	1256	LEU
1	A	696	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1261	HIS
1	A	1828	ASN
1	A	2278	HIS
1	A	816	HIS
1	A	473	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	5CM	B	30	2,3	17,21,22	5.03	13 (76%)	24,30,33	1.59	5 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	5CM	B	30	2,3	-	0/7/21/22	0/2/2/2

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	30	5CM	O4'-C1'	8.98	1.62	1.42
2	B	30	5CM	C6-C5	8.29	1.48	1.34
2	B	30	5CM	C2'-C1'	-7.61	1.31	1.52
2	B	30	5CM	O4'-C4'	-7.50	1.28	1.45
2	B	30	5CM	C4-N3	6.09	1.44	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	30	5CM	C5-C6-N1	-3.68	119.56	123.34
2	B	30	5CM	O4'-C1'-C2'	-3.54	99.56	106.25
2	B	30	5CM	C4'-O4'-C1'	-3.01	102.17	109.45
2	B	30	5CM	O4'-C1'-N1	2.89	113.03	107.86
2	B	30	5CM	C5-C4-N4	-2.14	118.28	121.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 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.

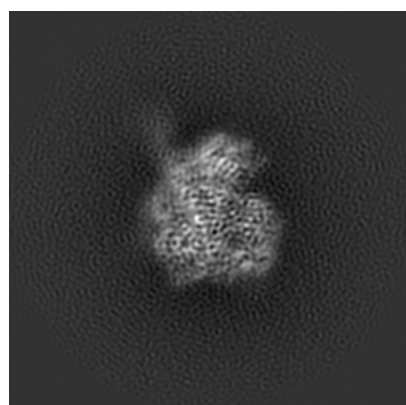
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25577. These allow visual inspection of the internal detail of the map and identification of artifacts.

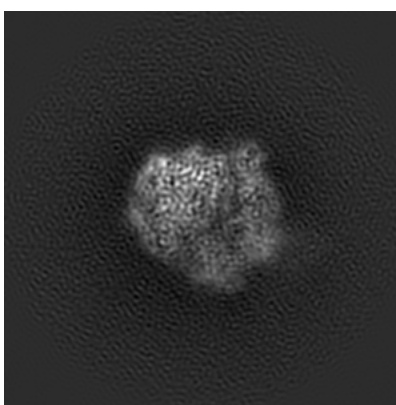
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

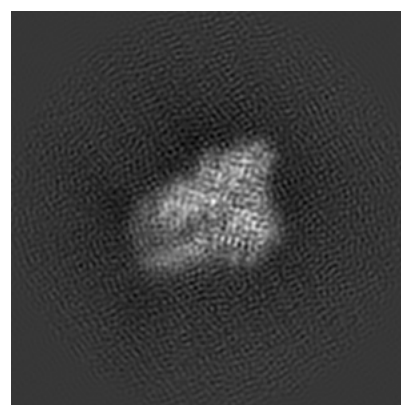
6.1.1 Primary map



X



Y

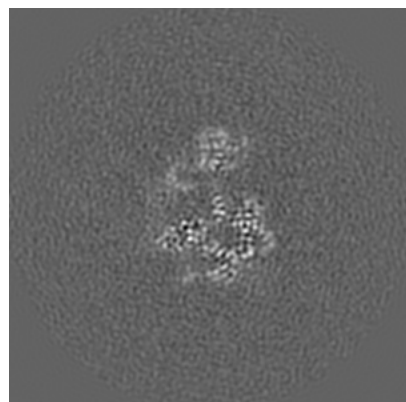


Z

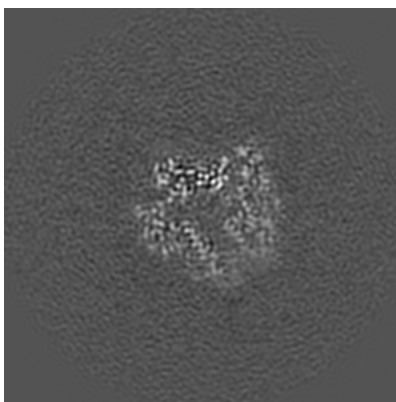
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

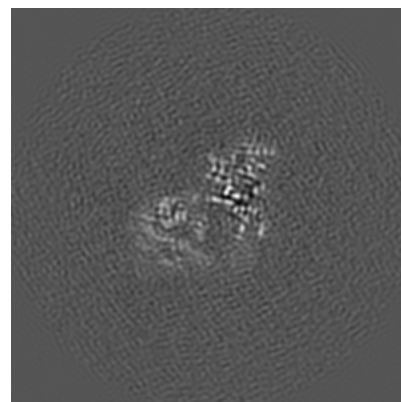
6.2.1 Primary map



X Index: 128



Y Index: 128

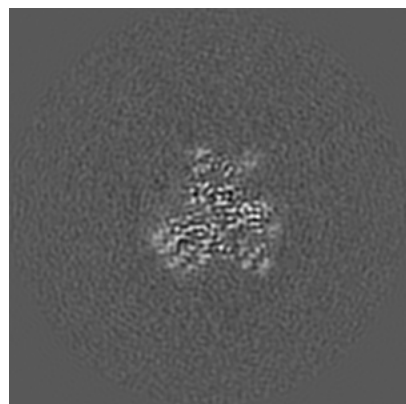


Z Index: 128

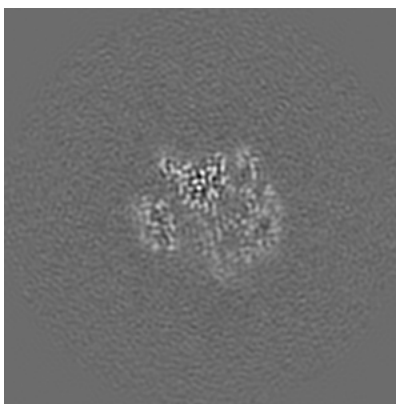
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

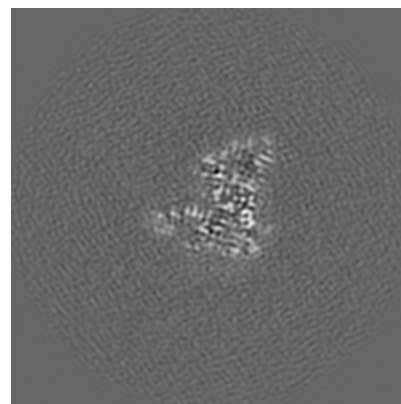
6.3.1 Primary map



X Index: 152



Y Index: 134

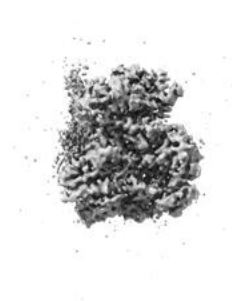


Z Index: 115

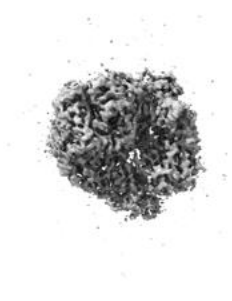
The images above show the largest variance slices of the map in three orthogonal directions.

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

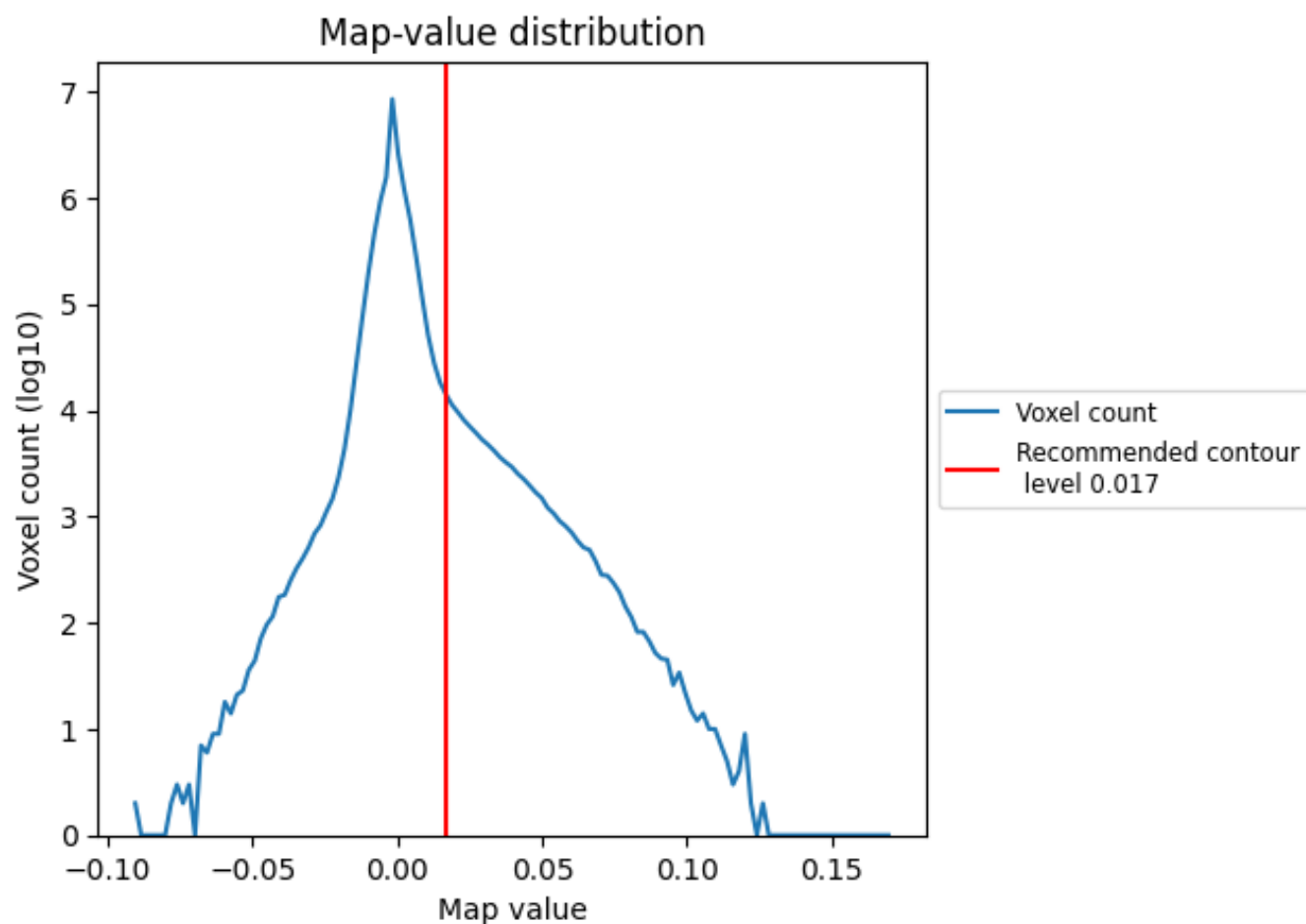
6.5 Mask visualisation

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

7 Map analysis [i](#)

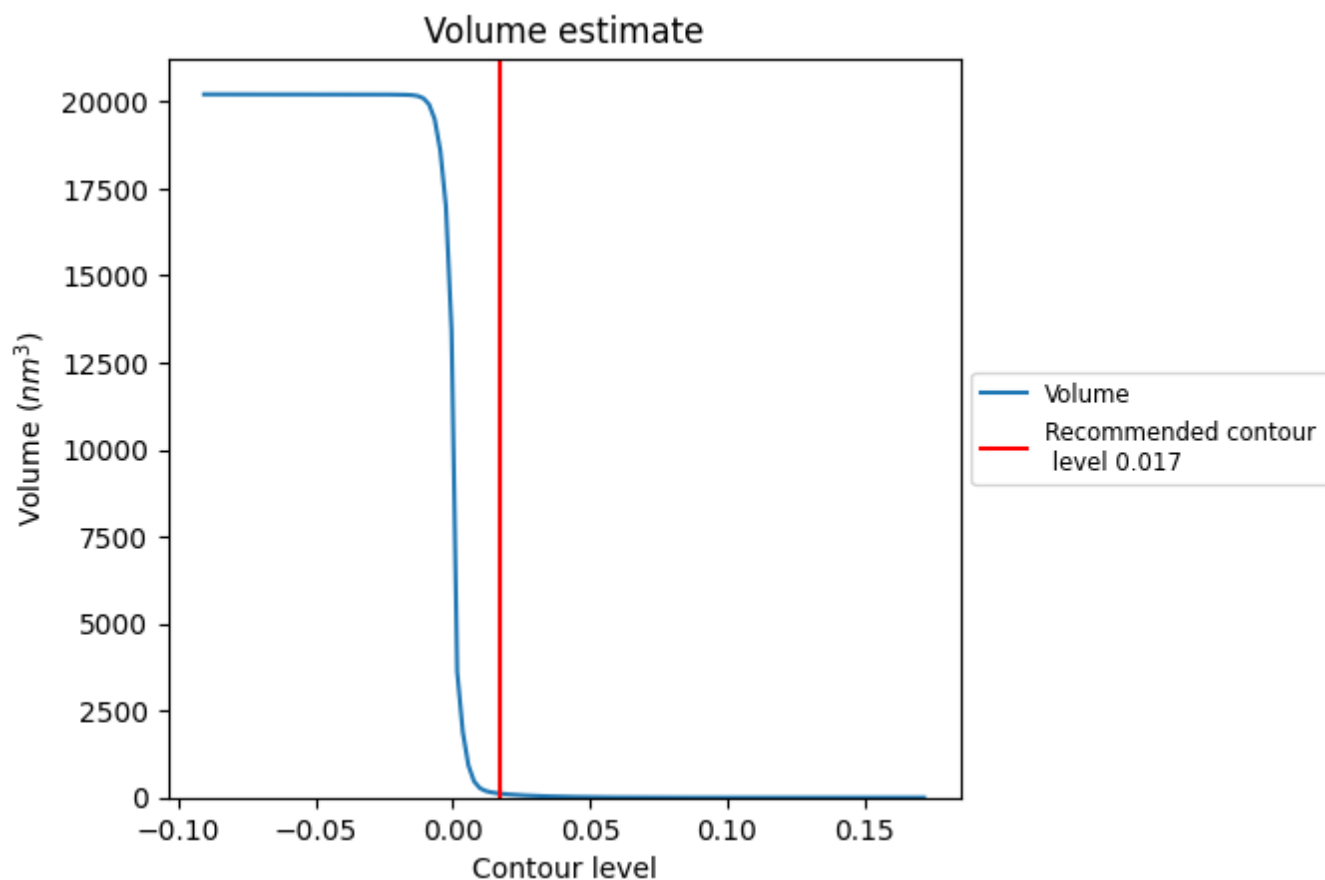
This section contains the results of statistical analysis of the map.

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.

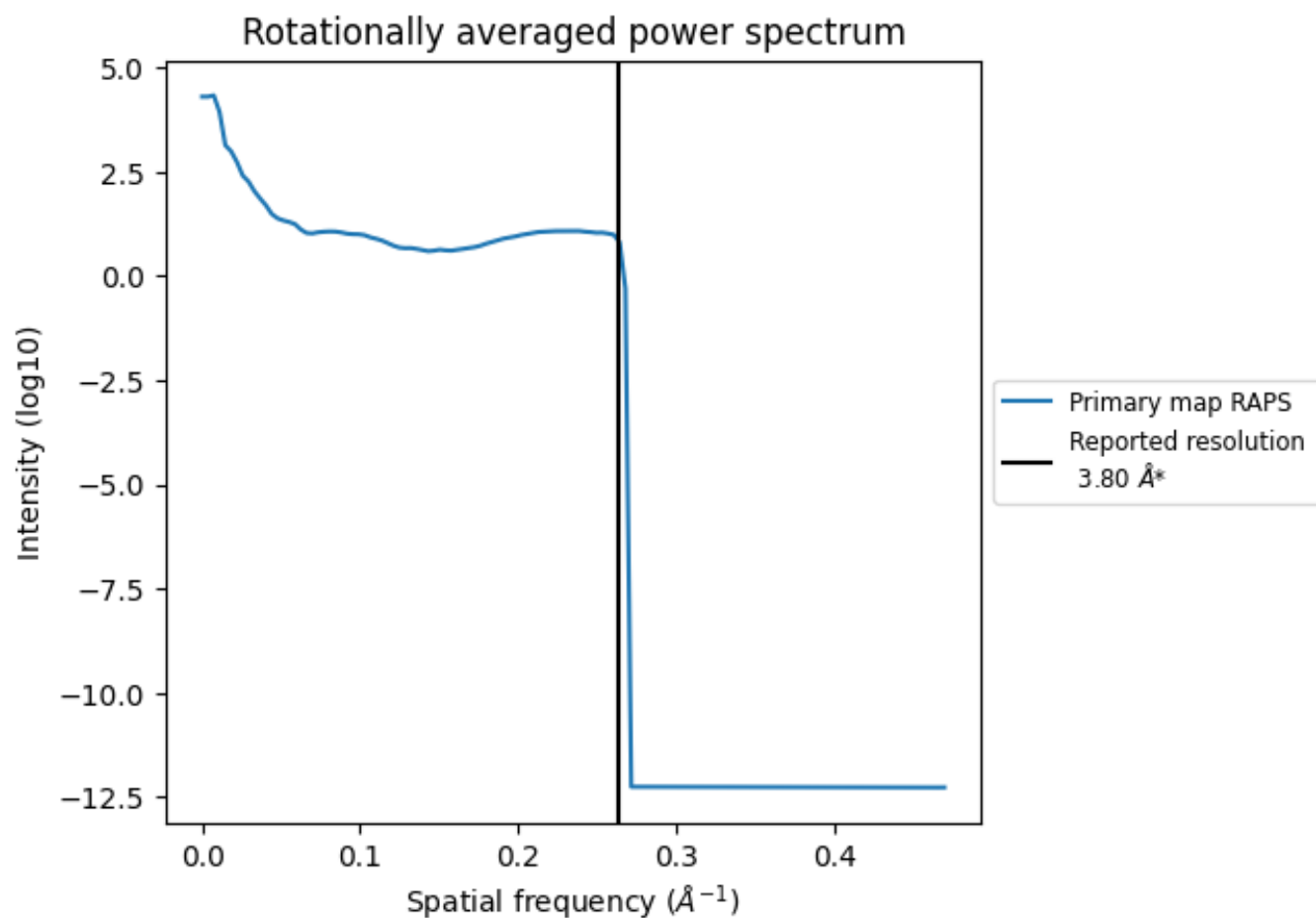
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 118 nm³; this corresponds to an approximate mass of 106 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 0.263 \AA^{-1}

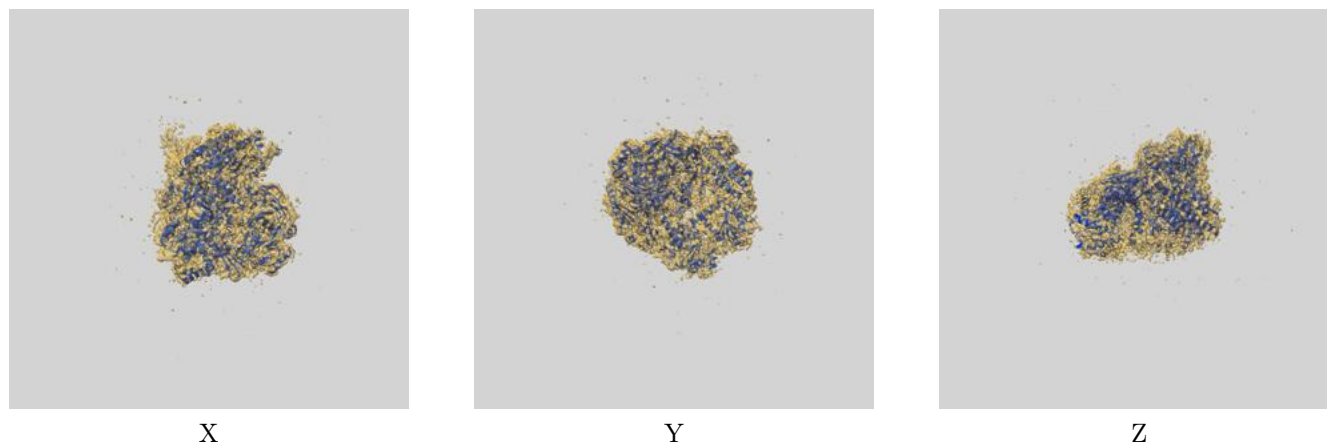
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

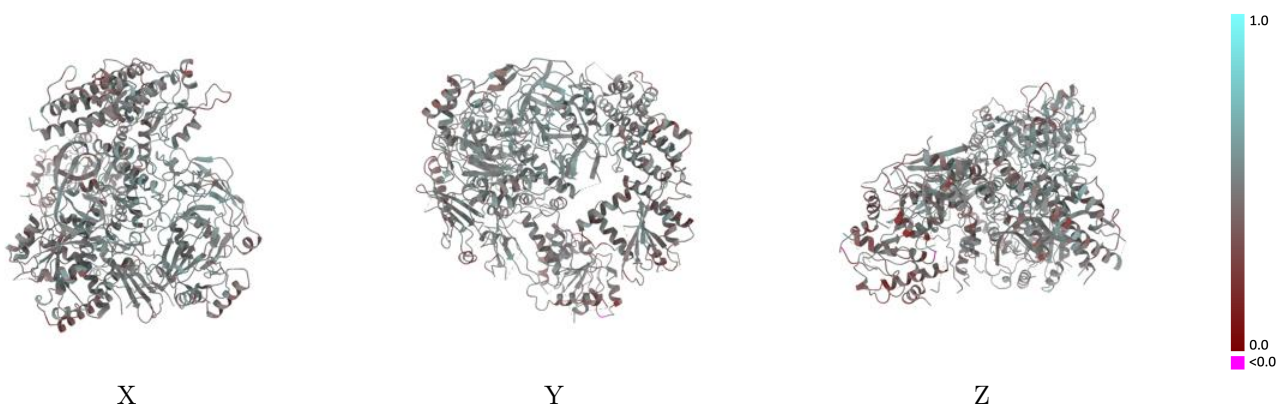
This section contains information regarding the fit between EMDB map EMD-25577 and PDB model 7T02. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



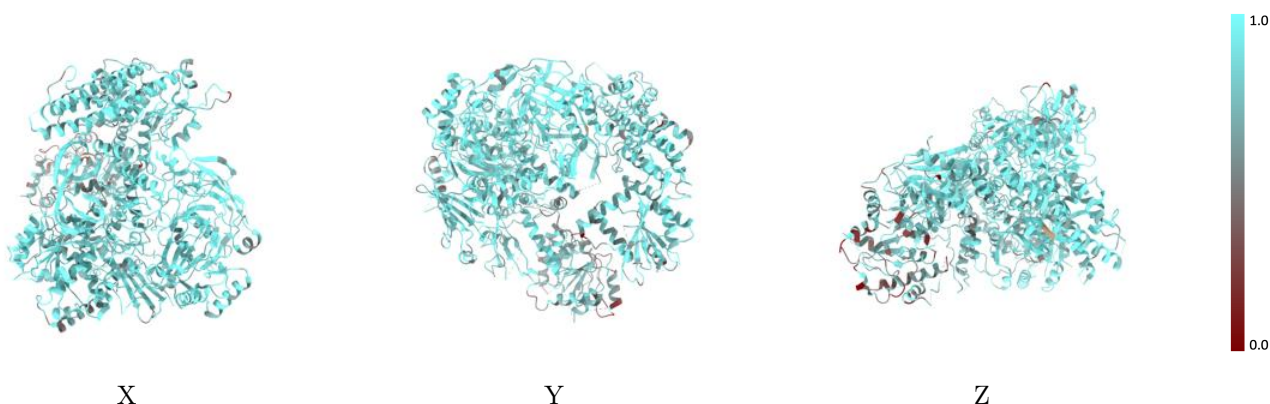
The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



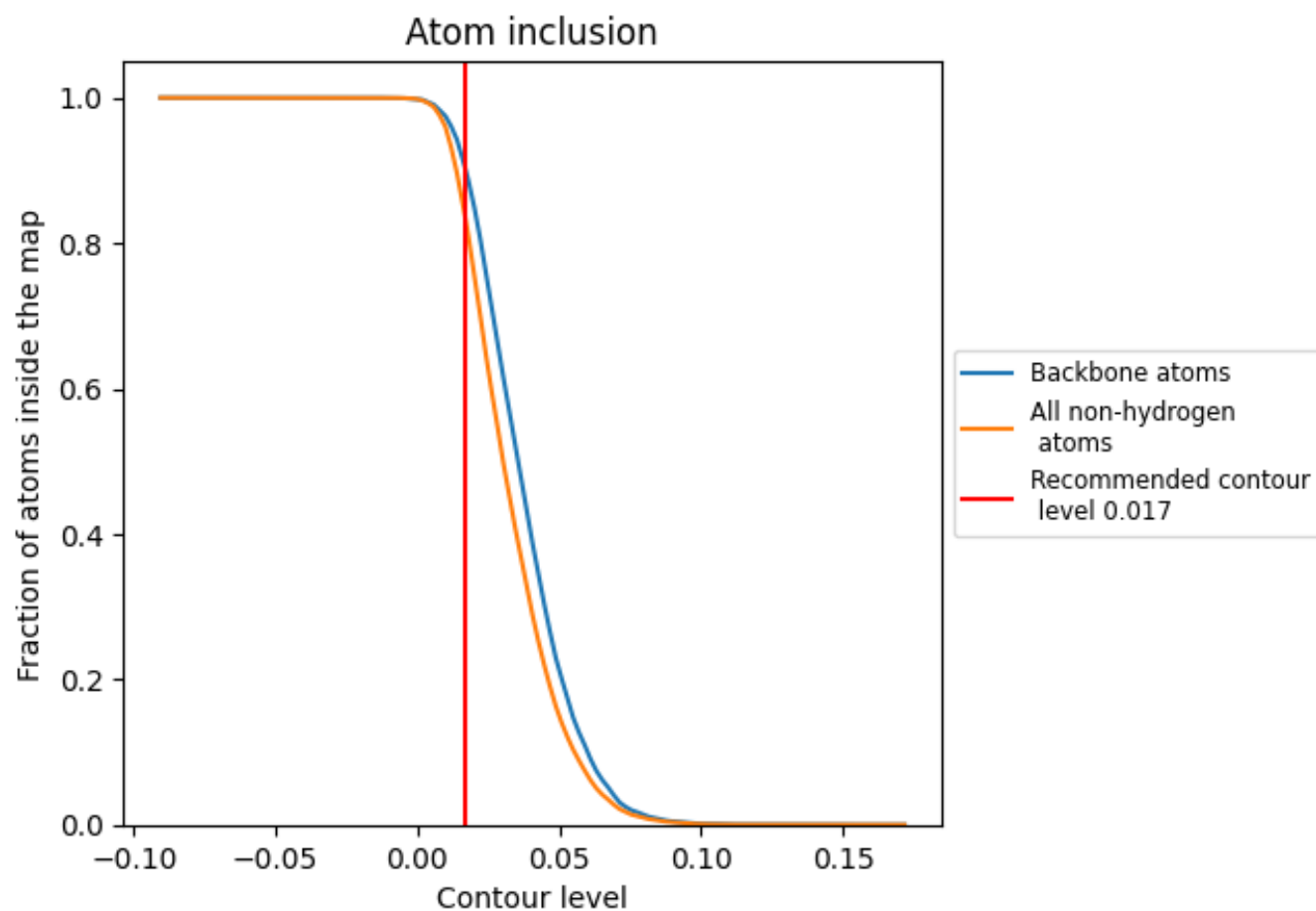
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.017).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 83% 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 (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8324	<div></div> 0.4770
A	<div></div> 0.8283	<div></div> 0.4770
B	<div></div> 0.9400	<div></div> 0.4920
D	<div></div> 0.9425	<div></div> 0.5050

