



wwPDB EM Validation Summary Report ⓘ

Sep 23, 2026 – 07:24 am BST

PDB ID : 9TUC / pdb_00009tuc
EMDB ID : EMD-56256
Title : CryoEM structure of DruE:ATPgammaS:DNA from Druantia type III - dimer 5
Authors : Grass, L.M.; Himpich, S.; Hilal, T.; Loll, B.; Wahl, M.C.
Deposited on : 2026-01-08
Resolution : 4.10 Å(reported)

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:

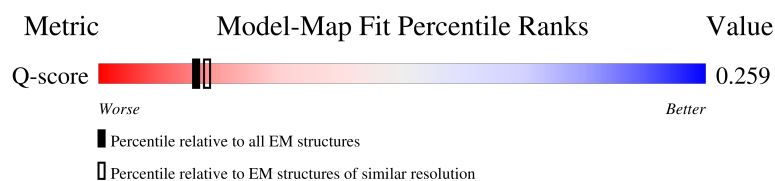
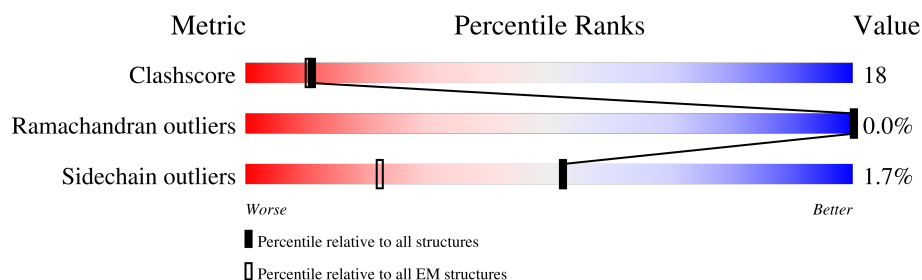
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

1 Overall quality at a glance

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

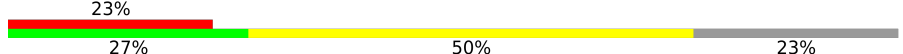
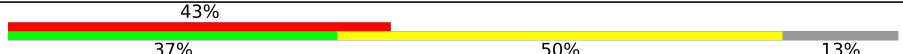
The reported resolution of this entry is 4.10 Å.

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	-
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 $\leq 5\%$. 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	Y	2108	
1	y	2108	
2	I	30	
2	i	30	

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Mol	Chain	Length	Quality of chain
3	G	30	17% 20% 23% 57%
3	g	30	23% 20% 23% 57%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 32402 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 DEAD/DEAH box helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Y	2049	Total	C	N	O	S	0	0
			16281	10268	2916	3025	72		
1	y	1833	Total	C	N	O	S	0	0
			14541	9165	2607	2702	67		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	-3	GLY	-	expression tag	UNP A0A4P8BDA5
Y	-2	ALA	-	expression tag	UNP A0A4P8BDA5
Y	-1	GLU	-	expression tag	UNP A0A4P8BDA5
Y	0	PHE	-	expression tag	UNP A0A4P8BDA5
y	-3	GLY	-	expression tag	UNP A0A4P8BDA5
y	-2	ALA	-	expression tag	UNP A0A4P8BDA5
y	-1	GLU	-	expression tag	UNP A0A4P8BDA5
y	0	PHE	-	expression tag	UNP A0A4P8BDA5

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	i	26	Total	C	N	O	P	0	0
			530	252	96	156	26		
2	I	23	Total	C	N	O	P	0	0
			471	224	85	139	23		

- Molecule 3 is a DNA chain called DNA (5'-D(P*AP*GP*AP*GP*AP*CP*TP*AP*TP*CP*GP*AP*T)-3').

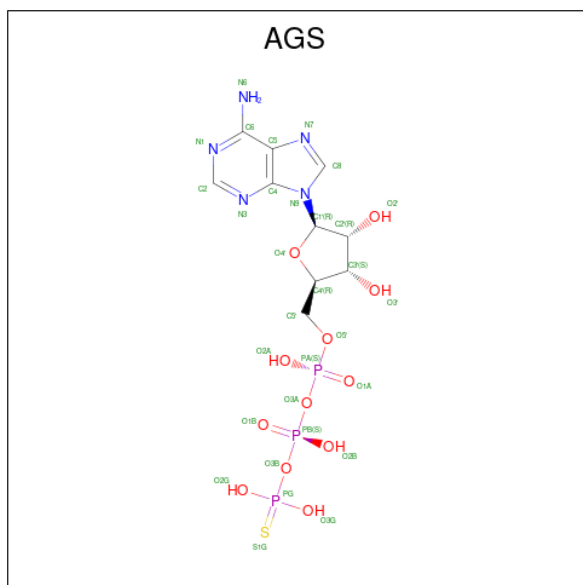
Mol	Chain	Residues	Atoms					AltConf	Trace
3	g	13	Total	C	N	O	P	0	0
			269	128	52	76	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	13	Total	C	N	O	P	0	0
			269	128	52	76	13		

- Molecule 4 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).



Mol	Chain	Residues	Atoms						AltConf
4	Y	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

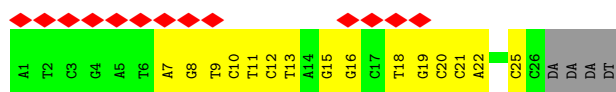
Mol	Chain	Residues	Atoms		AltConf
5	Y	5	Total	Zn	0
			5	5	
5	y	5	Total	Zn	0
			5	5	

L2083	A2092	L2097	R2098	G2104	A1997	E2002	D2003	R2004	Q2005	Q2006	S1917	R1918	F1919	W1920	S1921	L1922	Q1925	L2010	L2011	L2012	E2013	E2014	G2015	L2016	L2017	G2018	P2019	A2020	W2021	I2025	T2029	GLY	ASP	ASN	GLN	SER	THR	GLU	HIS	G2038	R2039	E2040	L2041	T2042	V2043	T2044	Q2050	H2051	Y2052	V2053	L2054	L2055	D2056	M2057	E2066	D2067	V2076	Q2077	Q2078	Q2079	V2080	E2081	R2082
G1786	R1804	R1807	L1810	M1813	P1814	R1817	V1820	A1824	Q1827	G1828	M1829	R1834	N1951	S1952	T1955	A1956	R1957	E1961	L1962	L1963	T1964	E1965	L1966	V1967	S1867	T1872	L1873	Q1884	T1885	L1891	L1892	R1901	I1902	N1903	L1904	C1905	E1906	Q1990	M1996																								
H1688	H1689	C1690	L1691	L1692	S1693	T1694	Y1699	W1700	R1701	R1702	L1703	H1707	L1712	T1713	N1714	D1731	G1732	S1733	R1734	V1735	E1736	T1737	R1841	Q1844	S1845	Q1846	Q1847	D1851	D1852	G1859	S1867	T1872	L1873	Q1884	T1885	L1891	L1892	R1901	I1902	N1903	L1904	C1905	E1906	Q1990	M1996																		
H1580	L1581	D1588	M1589	V1590	E1591	L1601	R1603	A1607	A1608	R1609	S1610	A1611	A1614	L1615	L1619	T1625	E1626	N1627	L1628	V1629	L1632	Q1635	L1638	D1639	Q1746	Y1753	D1754	G1642	Y1643	T1644	G1645	F1649	I1650	A1655	G1659	L1664	D1670	A1675	R1676	L1679	D1680	C1681	D1684																				
H1513	G1517	E1518	H1521	G1522	V1523	A1524	C1526	L1527	S1528	C1529	R1530	E1531	S1534	Q1535	T1536	Q1537	P1538	Q1539	R1540	N1544	L1545	L1546	N1547	P1548	E1549	R1550	E1551	N1552	T1553	H1554	V1555	L1556	L1557	R1558	G1559	G1560	S1561	N1562	D1563	R1564	Q1565	N1568	K1569	C1570	C1571	H1572	G1573	H1574	V1575	H1576	L1579												
V1404	S1407	G1408	Q1409	E1410	L1411	S1412	G1413	W1419	F1420	W1421	R1424	K1425	C1426	T1433	T1434	H1435	P1436	C1439	C1442	K1443	A1444	D1445	L1446	Q1447	Q1448	R1453	P1457	V1458	G1459	F1460	A1461	T1462	D1463	I1464	R1465	Y1466	Q1467	A1468	H1469	A1476	Q1477	L1478	P1479	D1482	P1483	R1484	H1507																
V1329	N1332	L1333	F1334	N1335	Y1336	L1337	T1338	A1339	D1340	E1341	L1342	E1343	R1346	A1347	T1348	LYS	THR	GLN	ALA	ASP	PRO	ASN	GLY	GLY	GLU	SER	PHE	R1364	R1365	K1368	L1374	A1377	L1378	R1379	E1380	Y1381	A1385	D1386	V1387	V1388	L1389	G1390	G1391	K1392	V1393	S1396	T1399																
L1238	K1239	R1240	L1241	T1242	Q1243	G1244	T1245	L1246	L1247	M1248	L1255	L1256	Q1260	A1261	M1262	M1263	W1270	I1276	L1277	L1278	E1279	N1280	L1281	E1282	A1283	L1284	S1288	A1290	W1291	E1292	E1293	T1294	G1297	K1298	L1304	Y1307	R1308	A1310	K1315	L1316	S1318	E1319	A1320	F1321	L1322	H1325																	
R1132	A1133	G1134	R1135	C1150	H1155	G1156	M1157	E1158	W1165	R1175	V1176	R1177	Q1185	R1186	R1187	V1188	N1189	A1190	L1191	V1192	L1193	G1194	L1195	E1196	L1197	V1201	L1207	S1208	C1209	K1210	W1211	F1212	F1213	E1217	S1218	Q1219	C1220	R1221	F1223	L1224	L1227	Q1230	A1231	D1232	Q1233	L1234	A1235																
N1044	A1045	L1046	I1047	H1048	E1052	E1053	G1054	L1055	W1056	S1057	T1058	R1059	D1061	A1064	R1071	L1072	E1073	E1074	R1079	T1080	Q1083	L1084	Q1085	F1086	M1087	E1088	K1089	K1092	S1093	G1094	K1095	N1097	V1098	C1101	M1105	E1106	I1111	M1114	V1122	A1126	P1126	E1127	A1128																				
N876	E877	Q878	Y879	P880	M883	R886	F887	P888	M891	L892	Q893	P895	D896	K897	K898	N899	K900	K903	R904	D905	Q906	L907	W908	P909	R914	H915	Y916	N917	P918	V919	I920	K921	L922	V926	I930	Q931	Q934	A935	H936	W937	S939	L940	H943	L944	M945	I946	E947	V948															

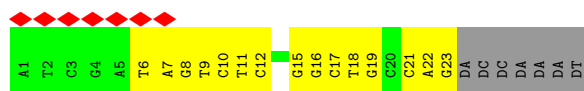
• Molecule 1: DEAD/DEAH box helicase



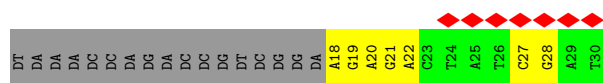




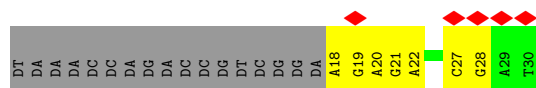
- Molecule 2: DNA (5'-D(P*AP*TP*CP*GP*AP*TP*AP*GP*TP*CP*TP*CP*TP*AP*GP*GP*CP*TP*GP*CP*CP*AP*G)-3')



- Molecule 3: DNA (5'-D(P*AP*GP*AP*GP*AP*CP*TP*AP*TP*CP*GP*AP*T)-3')



- Molecule 3: DNA (5'-D(P*AP*GP*AP*GP*AP*CP*TP*AP*TP*CP*GP*AP*T)-3')



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21364	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.293	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	319.488, 319.488, 319.488	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1093334, 1.1093334, 1.1093334	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, AGS

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	Y	0.13	0/16646	0.32	0/22561
1	y	0.11	0/14866	0.31	0/20143
2	I	0.17	0/527	0.36	0/811
2	i	0.19	0/593	0.36	0/912
3	G	0.15	0/302	0.34	0/464
3	g	0.13	0/302	0.29	0/464
All	All	0.12	0/33236	0.31	0/45355

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	Y	16281	0	16091	633	0
1	y	14541	0	14388	516	0
2	I	471	0	260	24	0
2	i	530	0	293	19	0
3	G	269	0	147	9	0
3	g	269	0	147	8	0
4	Y	31	0	12	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	Y	5	0	0	0	0
5	y	5	0	0	0	0
All	All	32402	0	31338	1172	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 18.

The worst 5 of 1172 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:Y:1426:CYS:HB3	1:Y:1442:CYS:SG	1.98	1.03
1:y:942:ASN:HA	1:y:945:MET:HE2	1.47	0.96
3:G:21:DG:N2	2:I:10:DC:O2	2.02	0.92
1:Y:1526:CYS:SG	1:Y:1554:HIS:CE1	2.62	0.92
2:i:10:DC:O2	3:g:21:DG:N2	2.04	0.90

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	Y	2041/2108 (97%)	1932 (95%)	108 (5%)	1 (0%)	100	100
1	y	1827/2108 (87%)	1766 (97%)	61 (3%)	0	100	100
All	All	3868/4216 (92%)	3698 (96%)	169 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Y	343	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Y	1747/1795 (97%)	1719 (98%)	28 (2%)	55	69
1	y	1564/1795 (87%)	1537 (98%)	27 (2%)	53	68
All	All	3311/3590 (92%)	3256 (98%)	55 (2%)	52	68

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	y	52	LEU
1	y	632	LEU
1	y	1735	VAL
1	y	1148	THR
1	y	224	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	y	136	GLN
1	y	751	GLN
1	y	148	GLN
1	y	439	ASN
1	y	813	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 10 are monoatomic - leaving 1 for Mogul analysis.

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$
4	AGS	Y	2201	-	29,33,33	0.47	1 (3%)	39,52,52	0.68	1 (2%)

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
4	AGS	Y	2201	-	-	10/21/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Y	2201	AGS	PG-S1G	2.15	1.95	1.90

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Y	2201	AGS	PA-O3A-PB	-3.52	120.74	132.83

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	Y	2201	AGS	C5'-O5'-PA-O1A

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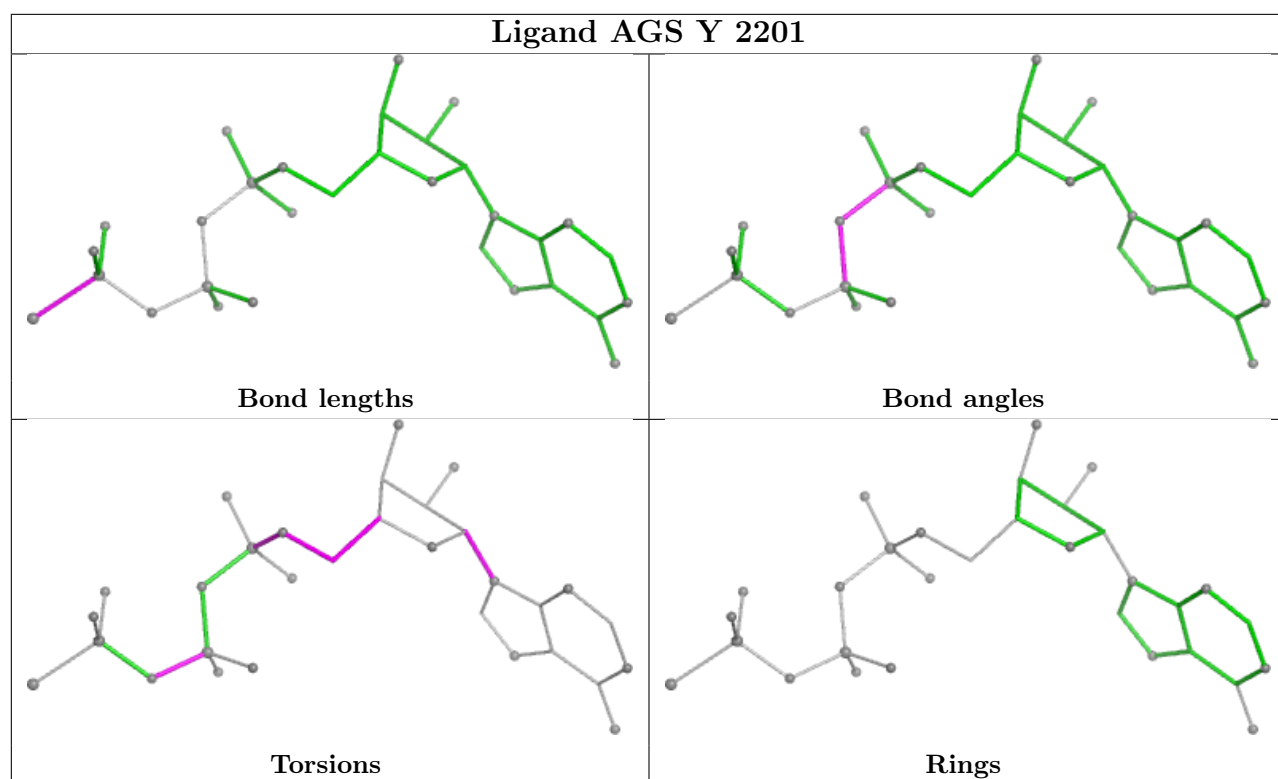
Mol	Chain	Res	Type	Atoms
4	Y	2201	AGS	C2'-C1'-N9-C8
4	Y	2201	AGS	C5'-O5'-PA-O3A
4	Y	2201	AGS	C5'-O5'-PA-O2A
4	Y	2201	AGS	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	Y	2201	AGS	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

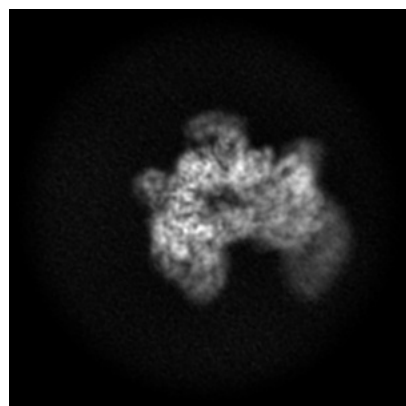
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-56256. These allow visual inspection of the internal detail of the map and identification of artifacts.

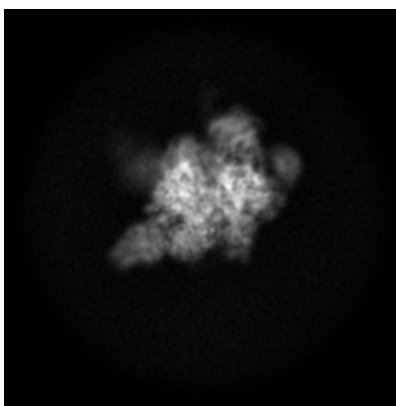
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

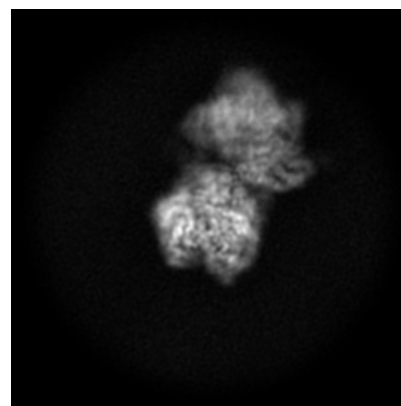
6.1.1 Primary map



X

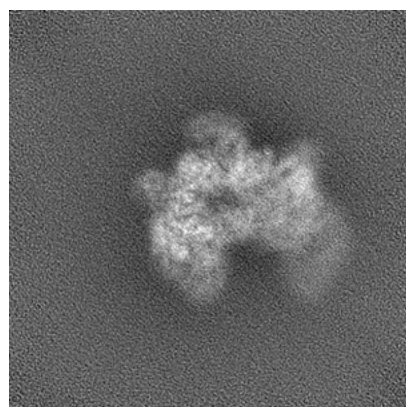


Y

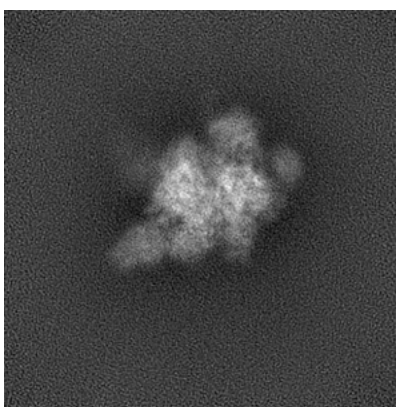


Z

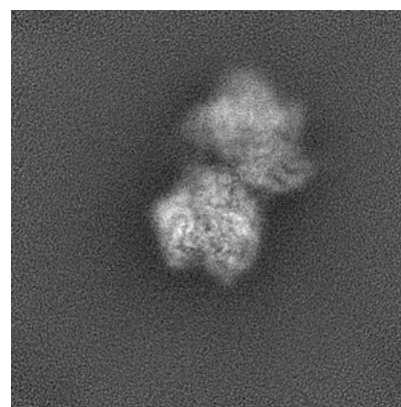
6.1.2 Raw map



X



Y

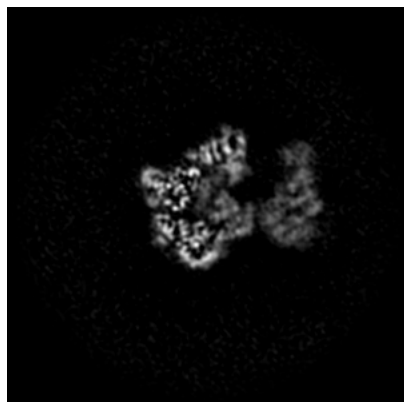


Z

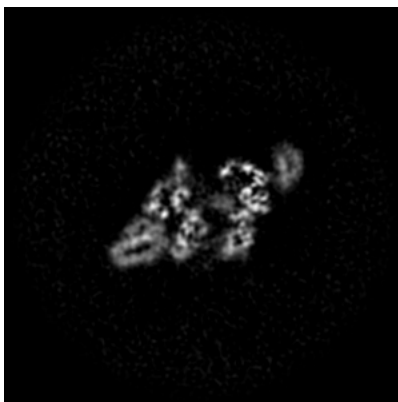
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

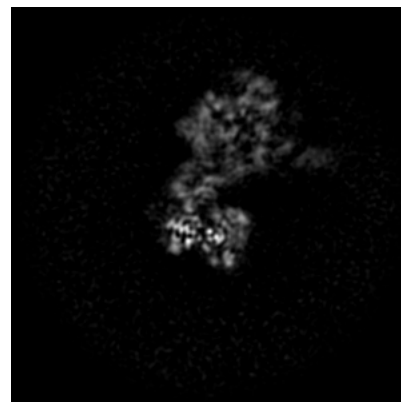
6.2.1 Primary map



X Index: 144

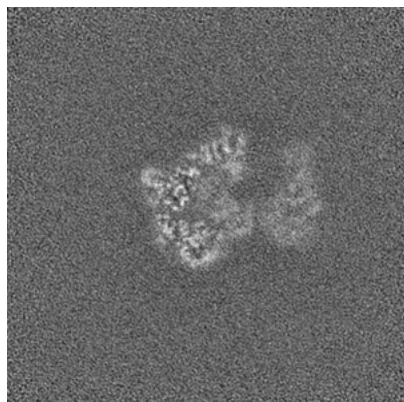


Y Index: 144

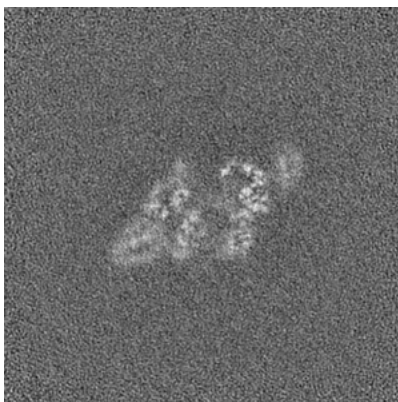


Z Index: 144

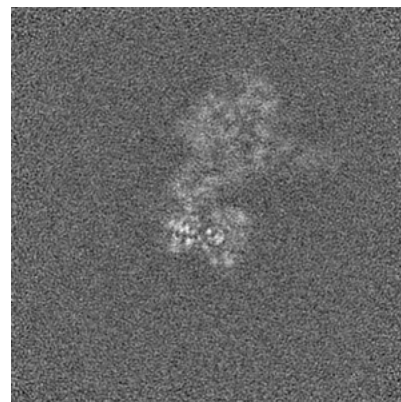
6.2.2 Raw map



X Index: 144



Y Index: 144

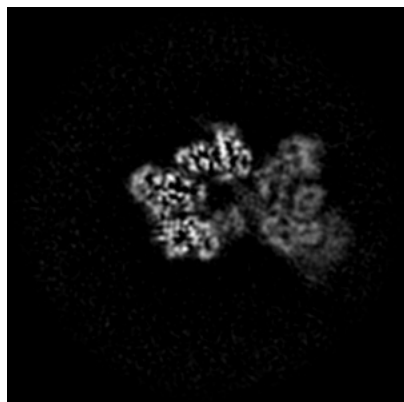


Z Index: 144

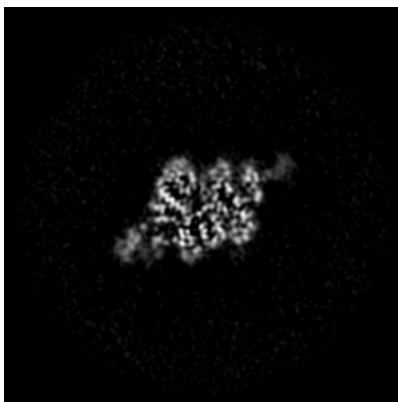
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

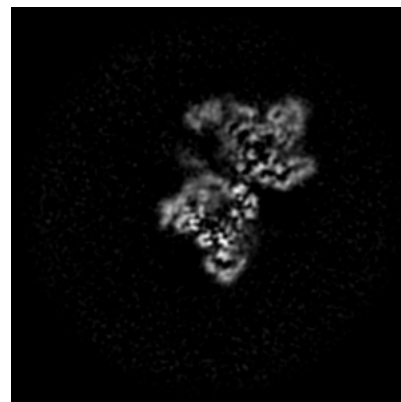
6.3.1 Primary map



X Index: 154

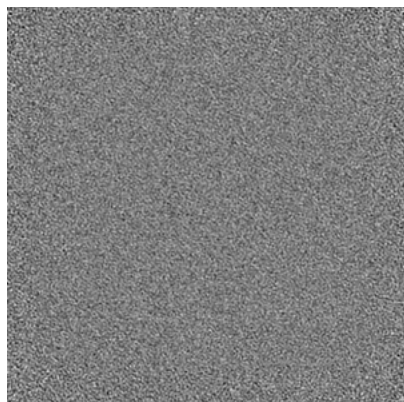


Y Index: 127

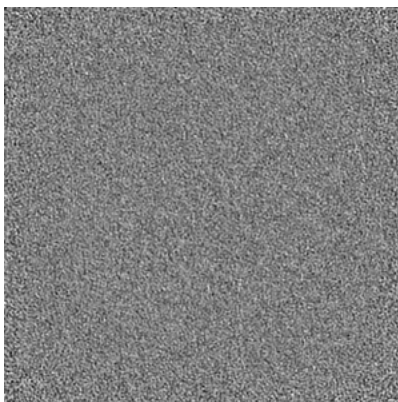


Z Index: 164

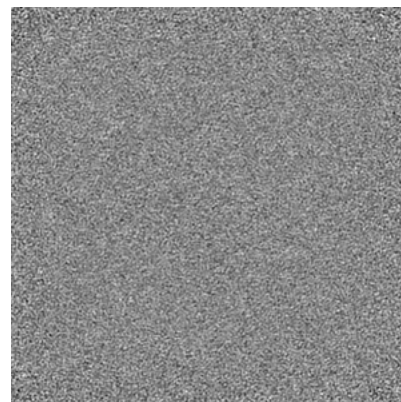
6.3.2 Raw map



X Index: 0



Y Index: 0

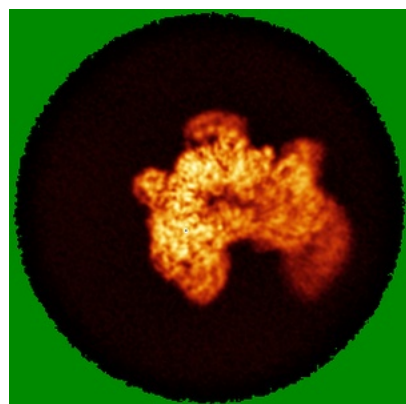


Z Index: 287

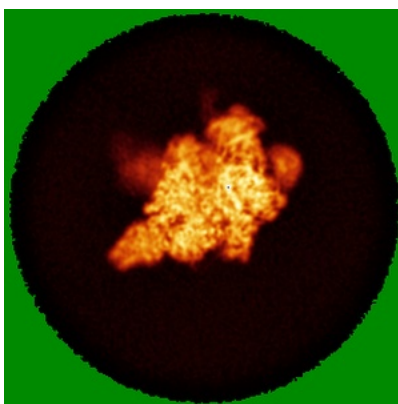
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

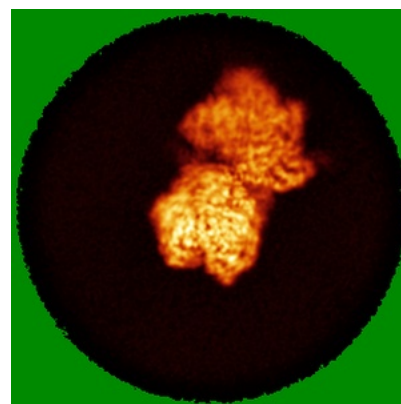
6.4.1 Primary map



X

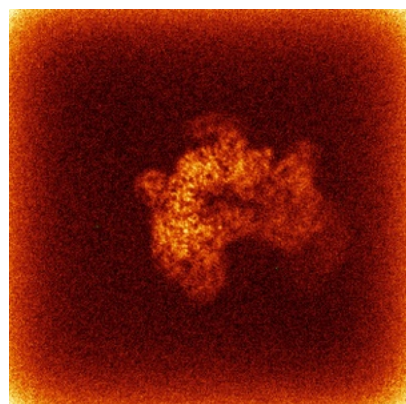


Y

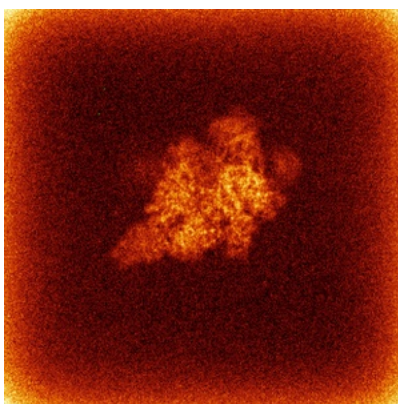


Z

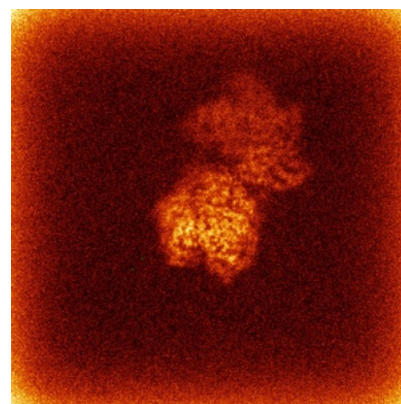
6.4.2 Raw map



X



Y

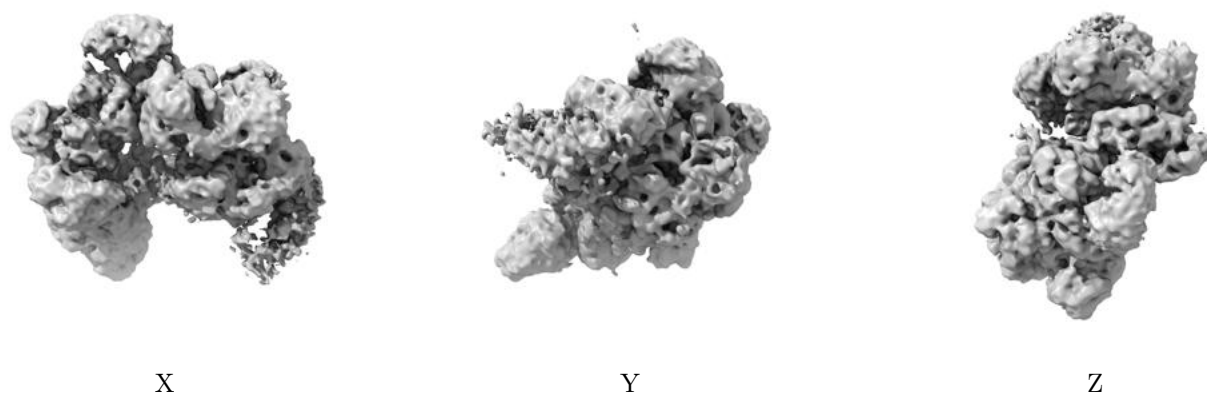


Z

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

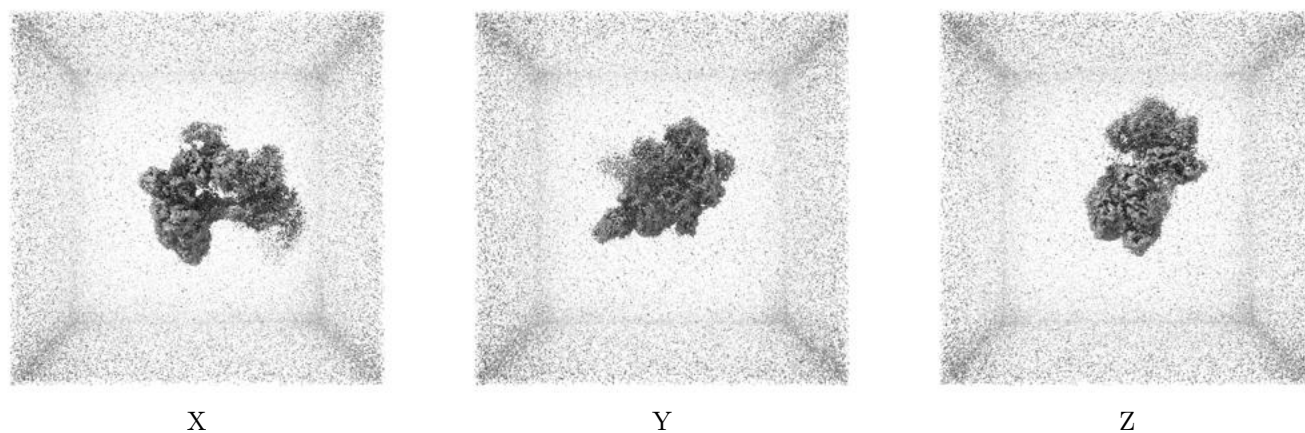
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

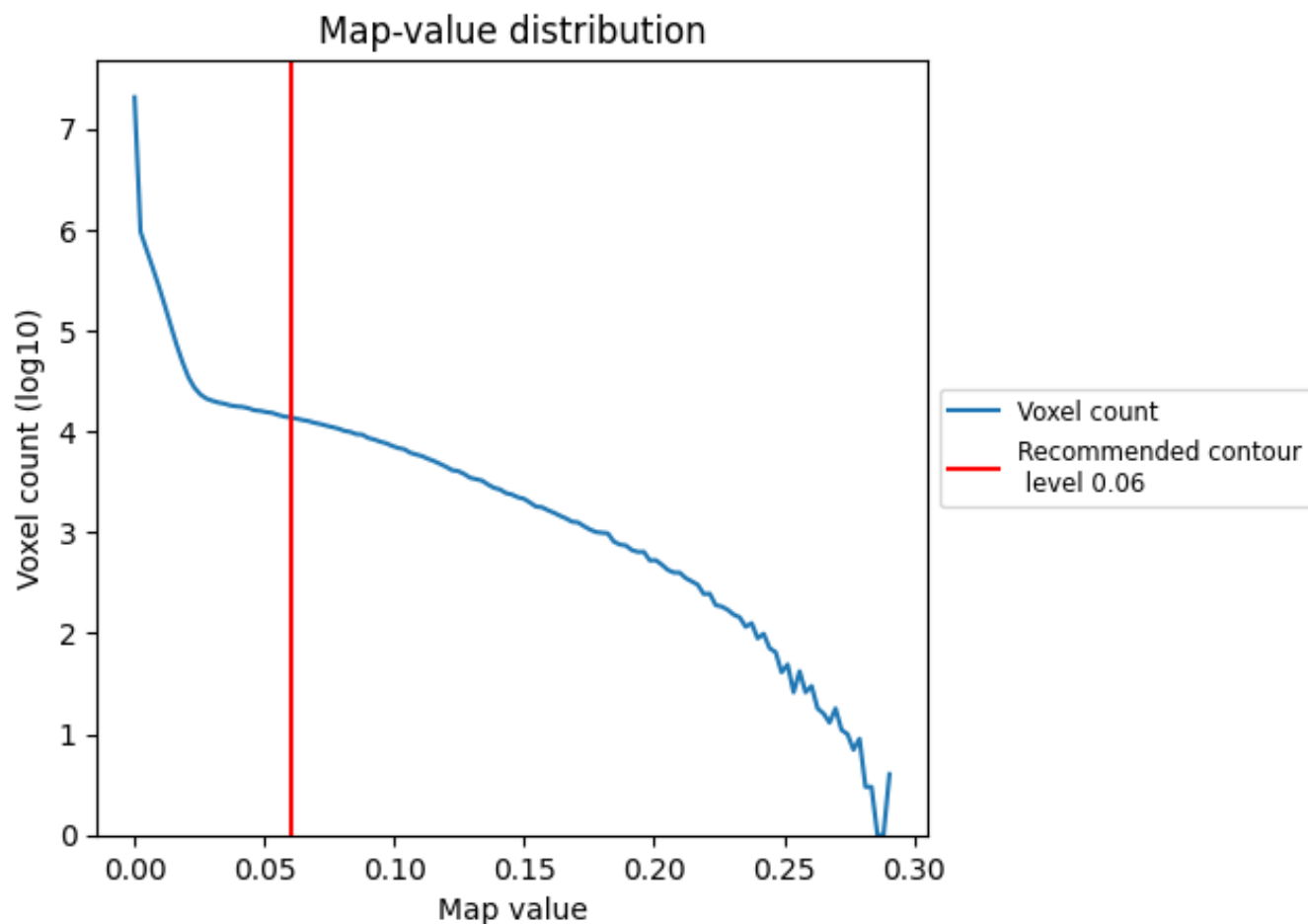
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

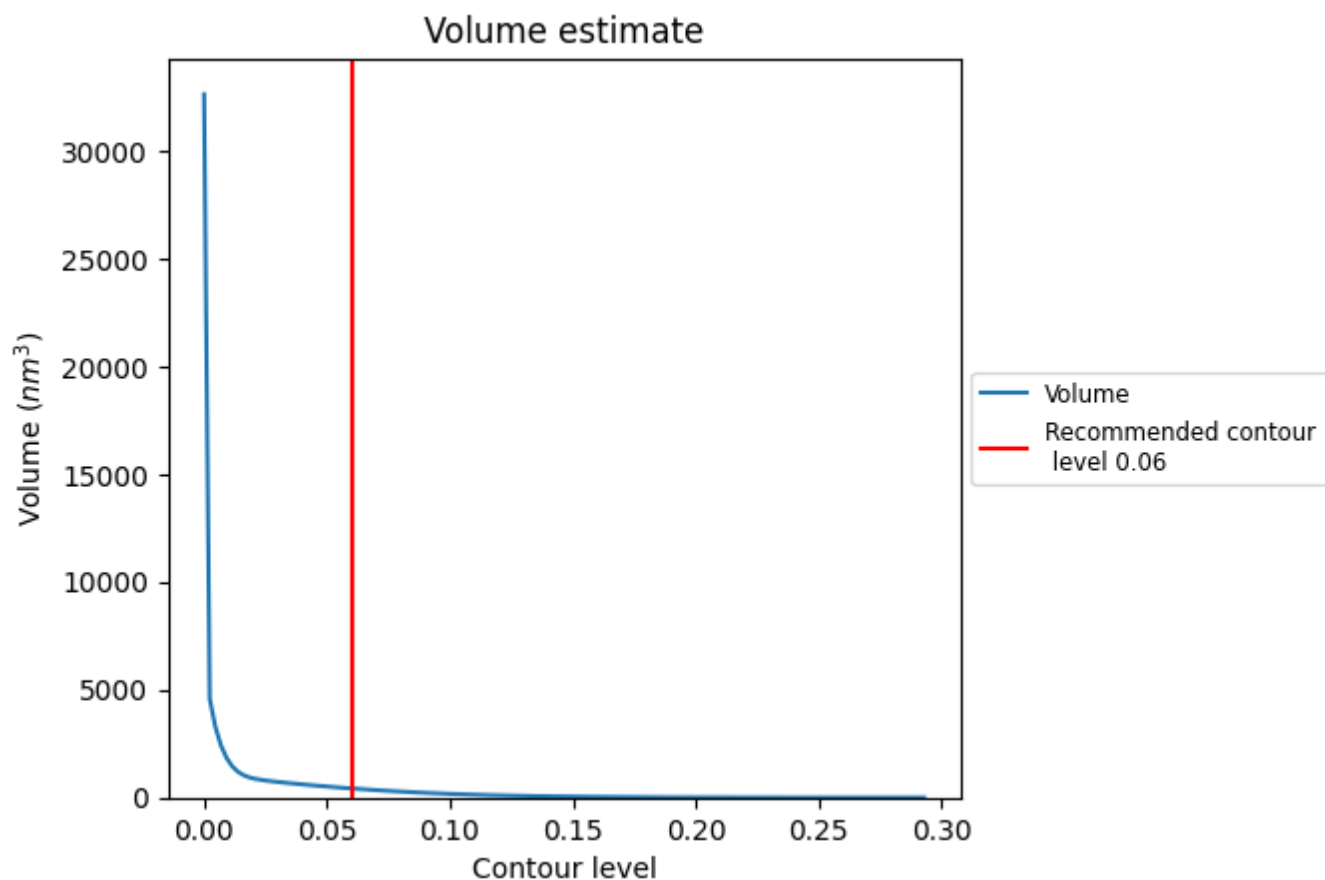
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

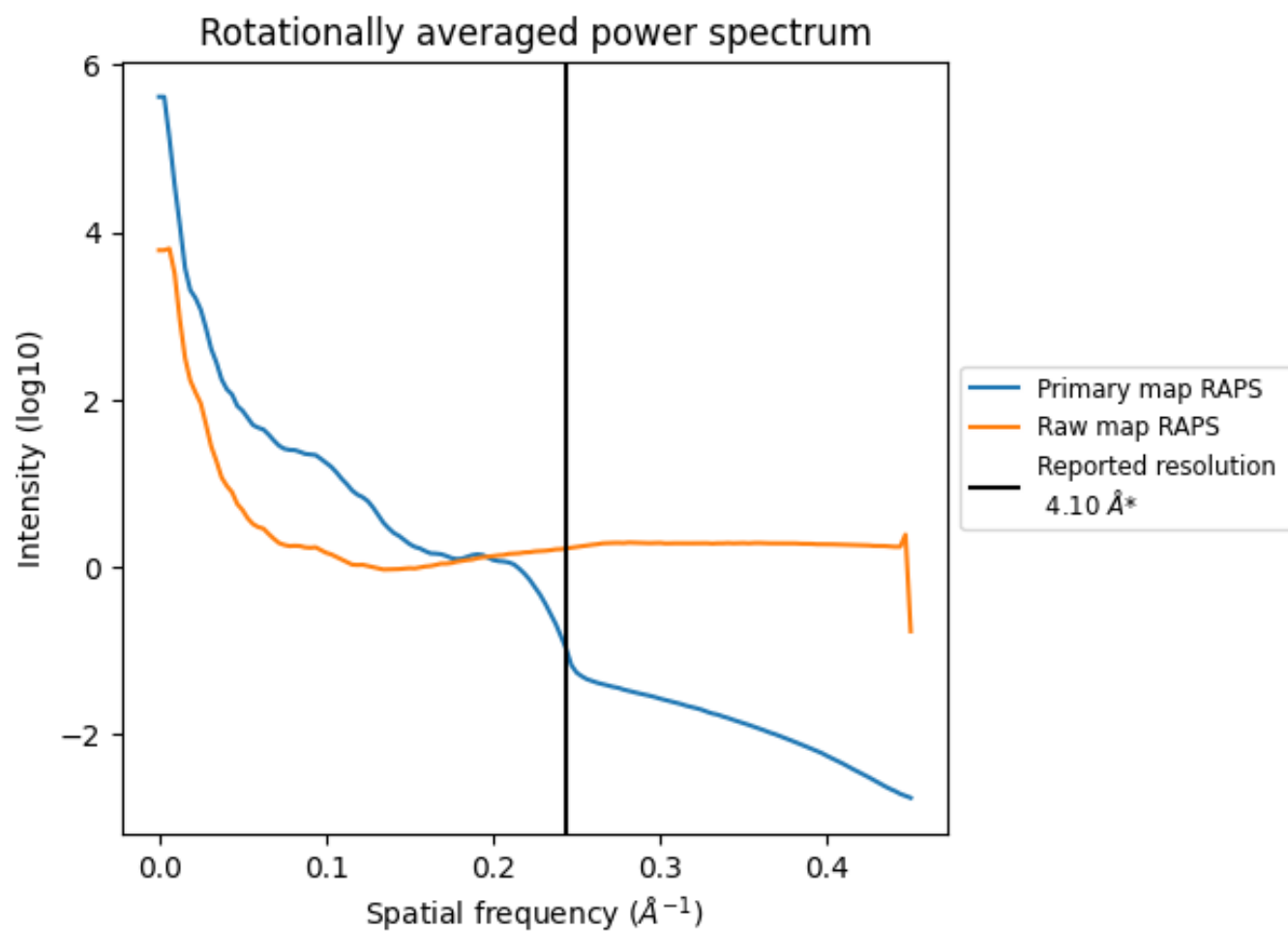
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 421 nm³; this corresponds to an approximate mass of 381 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 ⓘ

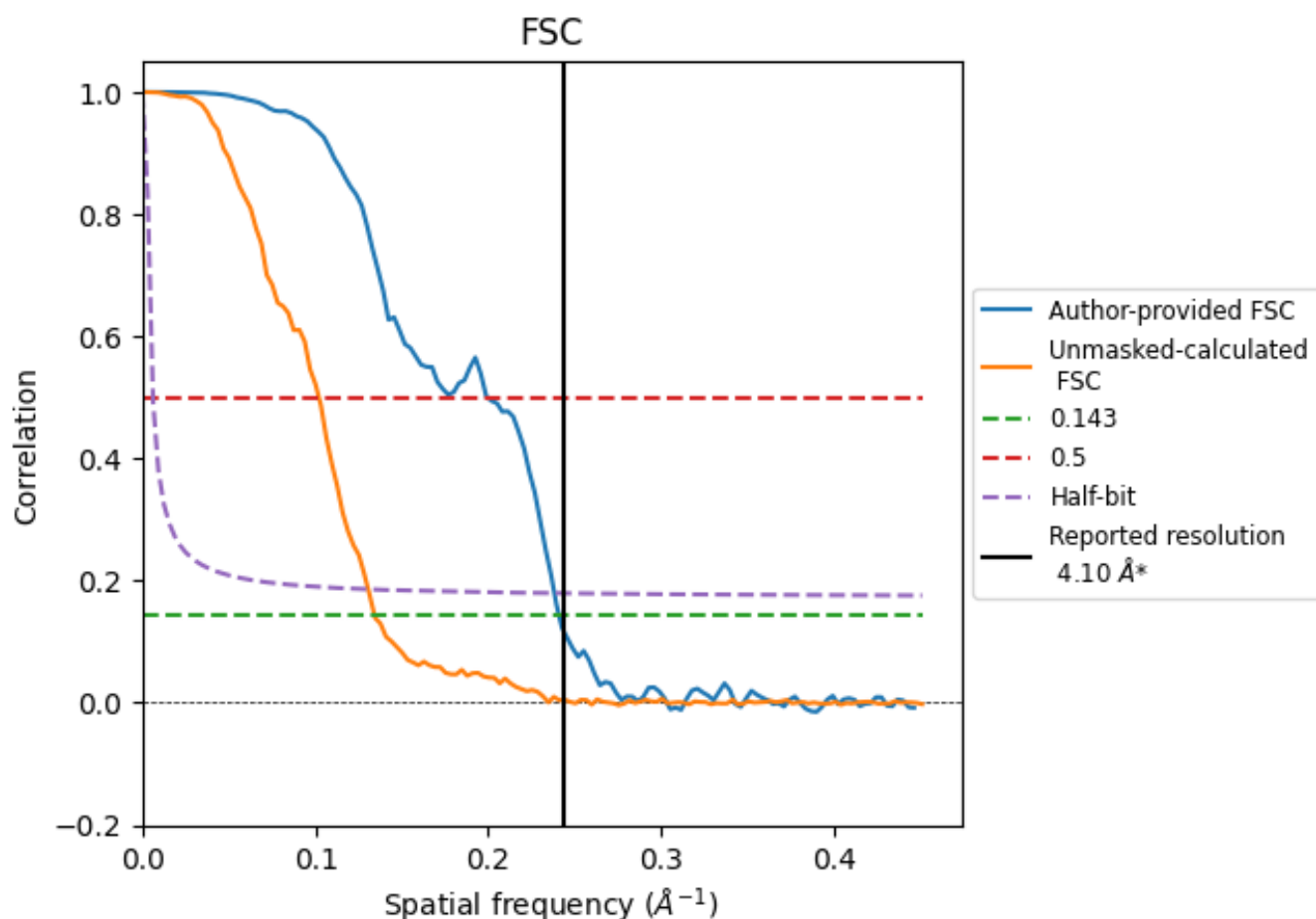


*Reported resolution corresponds to spatial frequency of 0.244 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

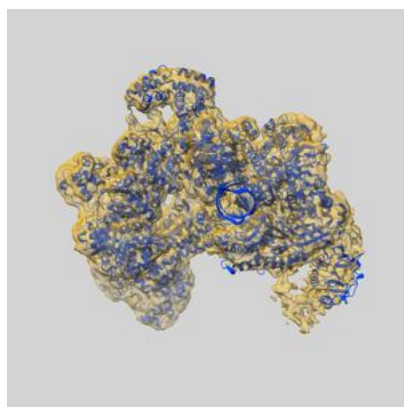
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.15	5.01	4.20
Unmasked-calculated*	7.45	9.79	7.66

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.45 differs from the reported value 4.1 by more than 10 %

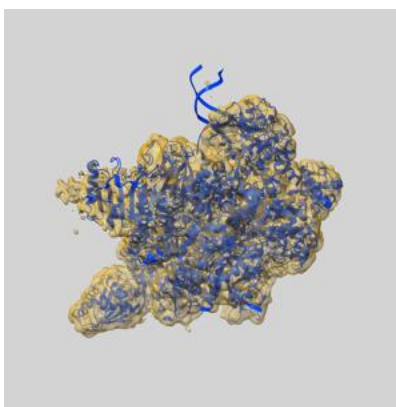
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-56256 and PDB model 9TUC. Per-residue inclusion information can be found in section [3](#) on page [6](#).

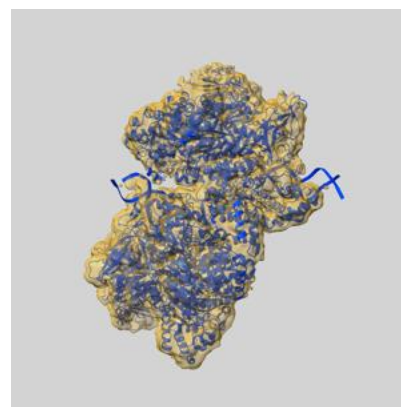
9.1 Map-model overlay [i](#)



X



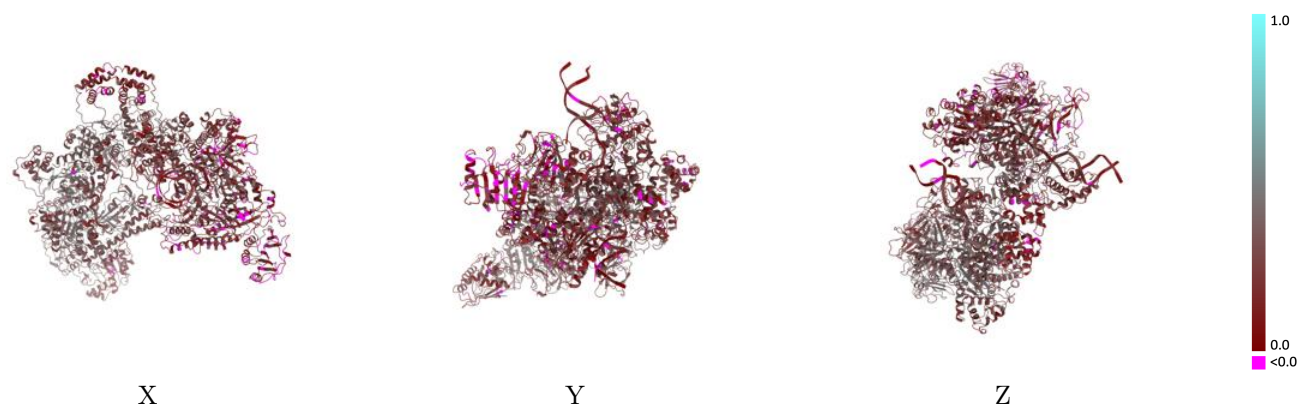
Y



Z

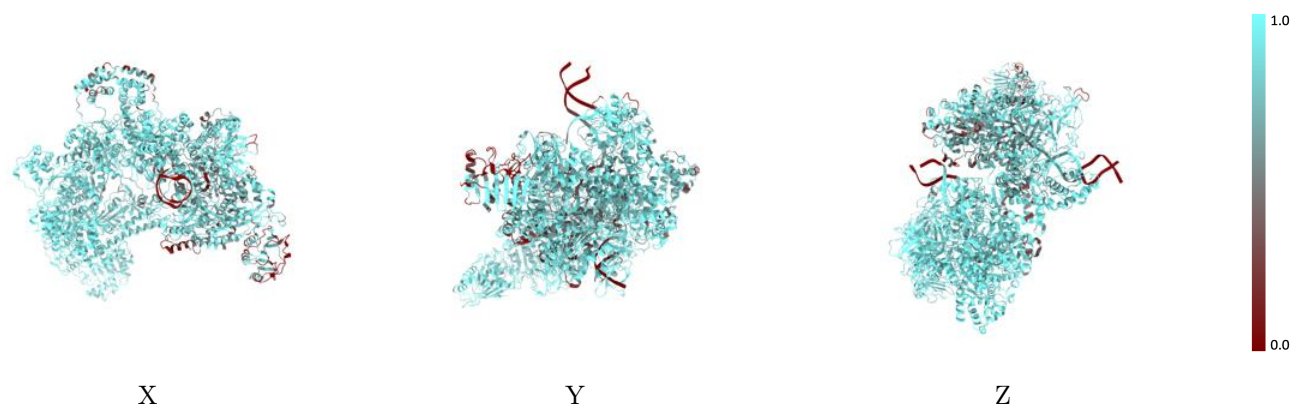
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



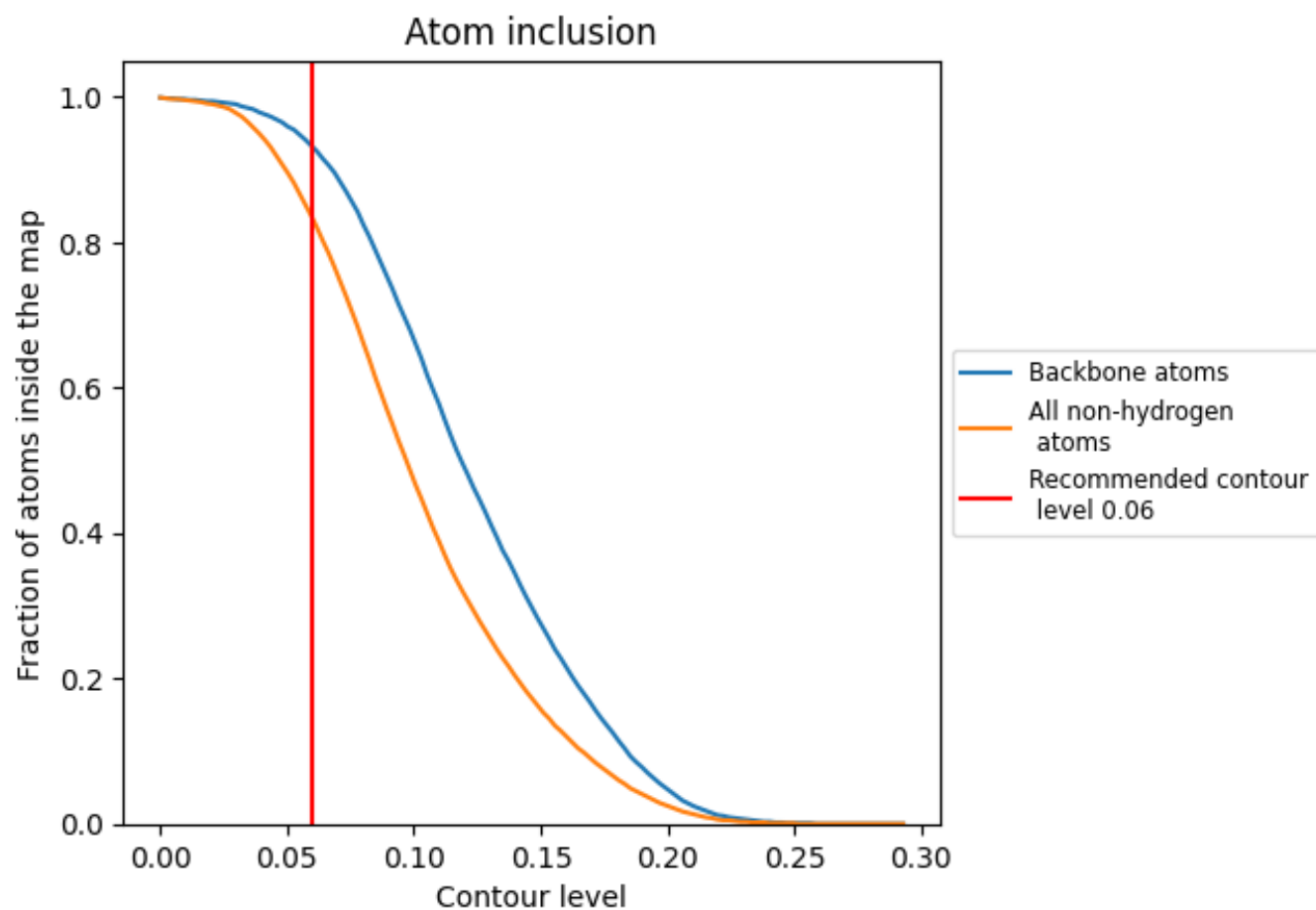
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8330	0.2590
G	0.5540	0.1140
I	0.5690	0.1540
Y	0.9270	0.3110
g	0.4130	0.1840
i	0.4770	0.1950
y	0.7620	0.2100

1.0

0.0

<0.0