



wwPDB EM Validation Summary Report ⓘ

Sep 14, 2026 – 01:30 pm BST

PDB ID : 9TU9 / pdb_00009tu9
EMDB ID : EMD-56253
Title : CryoEM structure of DruE:ATPgammaS:DNA from Druantia type III - dimer 2
Authors : Grass, L.M.; Himpich, S.; Hilal, T.; Loll, B.; Wahl, M.C.
Deposited on : 2026-01-08
Resolution : 3.60 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:

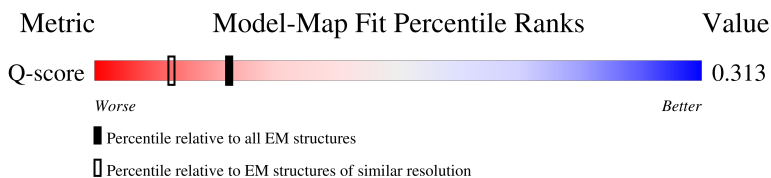
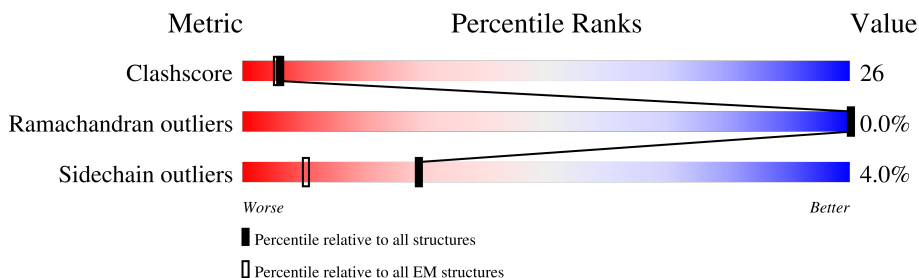
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

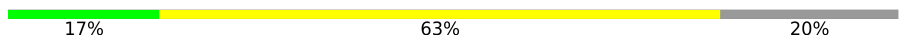
The reported resolution of this entry is 3.60 Å.

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	12797 (3.10 - 4.10)

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	G	30	
3	I	30	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 33663 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	2075	Total	C	N	O	S	0	0
			16471	10380	2939	3080	72		
1	y	2050	Total	C	N	O	S	0	0
			16275	10265	2912	3026	72		

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*GP*AP*CP*CP*GP*TP*CP*GP*GP*AP*AP*GP*AP*GP*AP*CP*TP*AP*TP*CP*GP*AP*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	24	Total	C	N	O	P	0	0
			497	235	98	140	24		

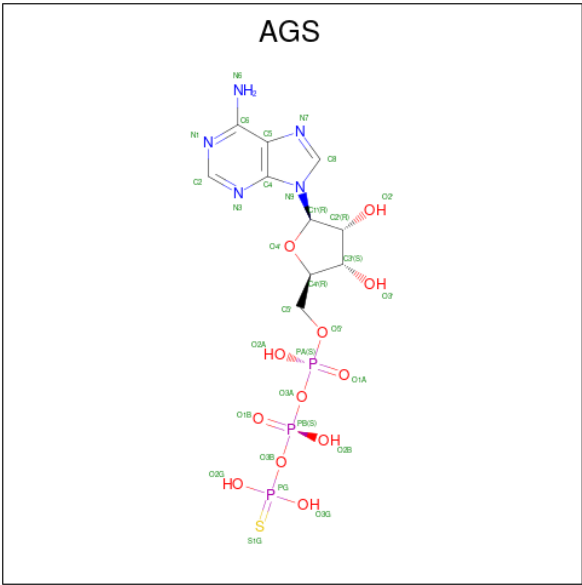
- Molecule 3 is a DNA chain called DNA (5'-D(P*AP*TP*CP*GP*AP*TP*AP*GP*TP*CP*TP*CP*TP*AP*GP*GP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	17	Total	C	N	O	P	0	0
			348	166	62	103	17		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 5 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).

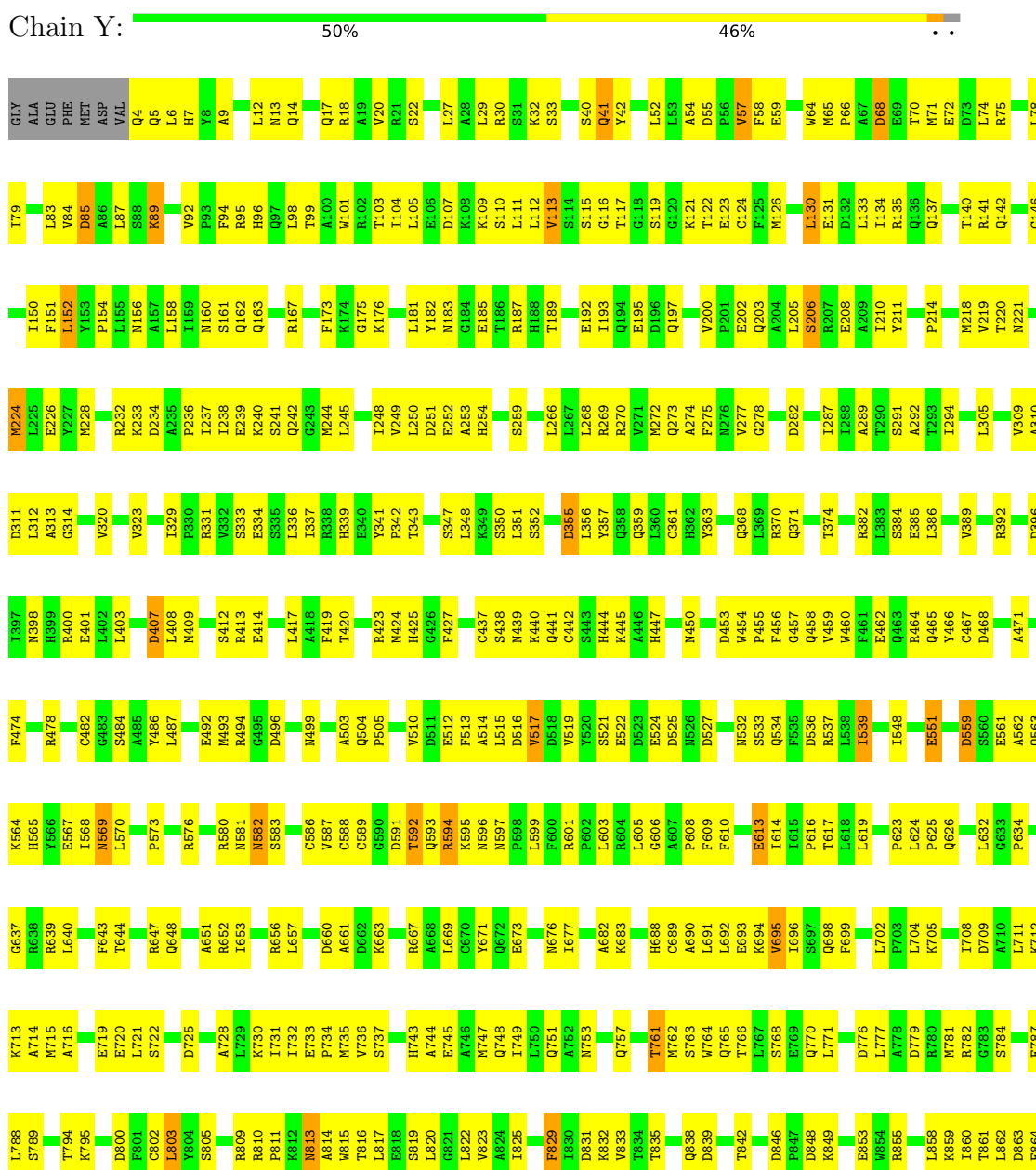


Mol	Chain	Residues	Atoms						AltConf
5	Y	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
5	y	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

3 Residue-property plots

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: DEAD/DEAH box helicase

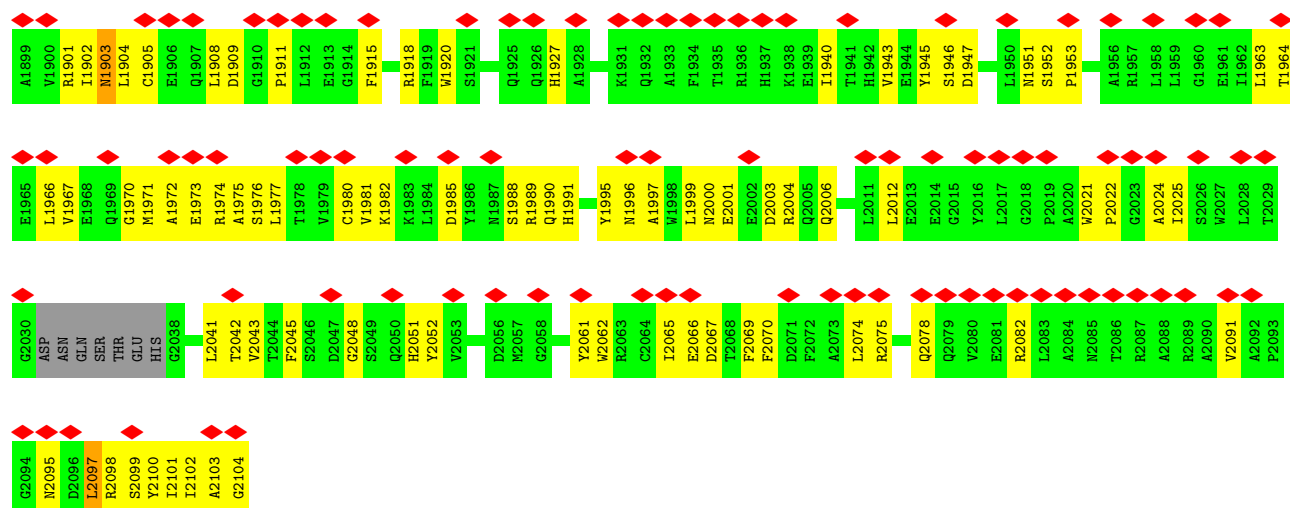


Y2061	L1994	L1922	D1851	L1758	W1668	D1563	V1472	R1395	T1294	C1209	P1123	E1052	L965	F865
C2064	Y1995	Y1923	D1852	V1759	A1669	R1564	S1473	R1396	P1295	K1210	F1124	W1056	K968	I866
I2065	N1996	T1924	A1853	L1760	D1670	Q1565	M1474	S1396	K1298	W1211	A1125	S1057	K969	I867
E2066	W1998	Q1925	A1761	A1761	L1679	M1568	L1478	M1400	Y1307	E1214	M1128	T1058	N869	E868
F2069	W1999	H1926	T1855	P1763	D1680	C1671	R1484	K1403	R1308	S1218	Y1129	D1061	S870	S870
F2070	N2000	H1927	T1856	Q1765	C1681	C1571	Y1485	M1400	R1308	Q1219	L1130	R1062	A871	A871
F2071	E2001	W1930	A1857	Q1766	K1685	H1572	Y1486	Y1404	L1312	L1221	Q1131	D1062	W872	W872
F2072	E2002	W1937	W1862	Q1767	F1686	G1573	Y1487	L1405	E1319	F1223	R1135	K1065	K977	F873
A2073	D2003	K1938	W1862	D1768	C1687	H1576	P1488	E1410	Y1329	W1226	A1136	L1067	N876	N876
L2074	Q2005	E1939	S1865	F1769	H1688	D1578	S1489	E1411	Y1329	F1223	G1437	S1068	E877	E877
E2075	Q2006	I1940	S1868	A1770	H1689	L1579	V1491	S1412	G1330	W1226	R1138	W1069	Q882	Q882
V2076	V2007	T1941	S1868	L1779	C1690	W1580	W1492	D1414	T1338	Q1230	R1139	Y1070	P880	P880
P2077	L2011	H1942	W1871	Q1780	L1691	L1581	W1492	D1414	T1338	Q1230	R1139	Y1070	R881	R881
Q2078	L2012	E1944	W1871	Q1780	L1692	L1581	W1492	D1414	T1338	Q1230	R1139	Y1070	R882	R882
W2080	L2013	Y1945	K1874	S1783	S1693	Y1583	D1497	H1415	D1339	D1232	S1141	E1073	W883	W883
E2081	E2013	S1946	R1875	S1783	S1693	Y1583	D1497	H1415	D1339	D1232	S1141	E1073	W883	W883
R2082	E2014	D1947	T1876	W1788	S1696	D1695	R1502	I1417	E1341	Q1233	A1143	E1074	R886	R886
L2083	E2015	R1948	S1877	E1789	S1696	D1695	R1502	I1417	E1341	Q1233	A1143	E1074	R886	R886
T2086	Y2016	L1950	G1878	L1790	Y1699	D1588	F1505	C1422	E1343	R1240	C1150	A1077	V889	V889
R2087	L2017	L1950	L1879	L1791	Y1700	M1589	F1505	C1422	E1343	R1240	C1150	A1077	V889	V889
A2088	W2021	S1952	F1881	V1792	N1701	E1591	E1509	C1425	L1348	L1242	K1151	Q1078	M891	M891
R2089	P2022	P1953	Q1884	L1796	D1704	L1592	E1510	C1426	L1348	L1242	K1151	Q1078	M891	M891
A2090	A2024	F1954	T1885	L1796	H1706	Q1593	F1512	C1426	L1348	L1242	K1151	Q1078	M891	M891
V2091	I2025	T1955	T1885	L1796	H1706	Q1593	F1512	C1426	L1348	L1242	K1151	Q1078	M891	M891
N2095	T2029	R1957	S1887	L1799	H1707	L1600	F1514	G1429	ALA	G1244	G1156	T1080	Q893	Q893
D2096	G2030	L1958	L1886	L1799	H1707	L1600	F1514	G1429	ALA	G1244	G1156	T1080	Q893	Q893
L2097	ASP	L1959	A1888	D1801	L1708	L1601	F1514	G1429	ALA	G1244	G1156	T1080	Q893	Q893
R2098	ASN	G1960	E1889	S1802	T1710	R1602	F1519	S1432	PRO	S1248	F1160	M1087	Q902	Q902
S2099	GLN	E1961	L1891	S1803	L1711	R1603	G1520	T1433	ASN	L1250	F1161	E1088	R904	R904
Y2100	THR	L1962	L1892	R1804	L1712	R1616	H1521	T1434	GLU	L1251	F1174	E1088	R905	R905
T2101	THR	L1963	L1895	L1807	V1715	V1632	C1526	H1446	GLU	L1251	F1174	E1088	R905	R905
A2103	HIS	L1966	A1899	M1813	R1716	V1632	C1526	H1446	GLU	L1251	F1174	E1088	R905	R905
G2104	G2038	V1967	V1967	L1818	L1717	Q1718	P1538	Q1447	K1368	V1266	M1189	S1102	H336	H336
	R2039	E1968	A1899	L1818	L1717	Q1718	P1538	Q1447	K1368	V1266	M1189	S1102	H336	H336
	E2040	Q1969	R1901	L1818	L1717	Q1718	P1538	Q1447	K1368	V1266	M1189	S1102	H336	H336
L2041	E2040	Q1970	R1901	L1818	L1717	Q1718	P1538	Q1447	K1368	V1266	M1189	S1102	H336	H336
T2042	L2041	M1971	N1903	I1823	P1724	G1642	Q1536	I1446	GLU	M1263	R1186	G1031	E1031	E1031
V2043	L1904	A1972	N1903	I1823	P1724	G1642	Q1536	I1446	GLU	M1263	R1186	G1031	E1031	E1031
V2043	C1905	E1973	C1905	Q1827	Q1727	T1643	P1538	Q1447	K1368	V1266	M1189	S1102	H336	H336
T2044	E1906	R1974	E1906	L1828	Y1728	T1643	P1538	Q1447	K1368	V1266	M1189	S1102	H336	H336
F2045	Q1907	A1975	Q1907	M1829	Y1728	T1643	P1538	Q1447	K1368	V1266	M1189	S1102	H336	H336
S2046	Q1907	S1976	Q1907	Q1830	D1731	F1649	T1541	V1451	P1375	W1270	L1195	E1106	V941	V941
D2047	D1909	L1908	L1908	Q1830	D1731	F1649	T1541	V1451	P1375	W1270	L1195	E1106	V941	V941
G2048	G1910	G1910	G1910	W1835	S1733	Y1651	N1547	R1453	R1379	L1277	L1197	M1107	N942	N942
H2051	P1911	V1981	P1911	W1835	S1733	Y1651	N1547	R1453	R1379	L1277	L1197	M1107	N942	N942
Y2052	L1912	K1982	L1912	Q1838	R1735	G1659	R1590	V1458	A1382	I1281	L1198	D1110	L944	L944
V2053	E1913	K1983	L1912	Q1838	R1735	G1659	R1590	V1458	A1382	I1281	L1198	D1110	L944	L944
L2054	G1914	T1940	E1913	V1839	T1737	G1659	R1590	V1458	A1382	I1281	L1198	D1110	L944	L944
G1916	F1915	R1841	G1914	V1839	T1737	G1659	R1590	V1458	A1382	I1281	L1198	D1110	L944	L944
S1917	G1916	R1841	G1914	V1839	T1737	G1659	R1590	V1458	A1382	I1281	L1198	D1110	L944	L944
H1991	G1916	R1841	G1914	V1839	T1737	G1659	R1590	V1458	A1382	I1281	L1198	D1110	L944	L944
G2058	S1917	G1916	G1916	G1843	R1743	L1664	L1557	I1464	V1387	K1285	D1203	L1046	V948	V948
L2059	H1919	D1992	H1919	Q1844	Y1753	L1665	L1558	I1469	L1389	W1291	T1205	Q1048	W949	W949
S2060	A1993	A1993	A1993	S1845	Y1753	D1666	L1558	I1469	L1389	W1291	T1205	Q1048	W949	W949

Chain y: 13% 48% 48%

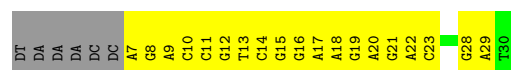






- Molecule 2: DNA (5'-D(P*AP*GP*AP*CP*CP*GP*TP*CP*GP*GP*AP*AP*GP*AP*GP*A P*CP*TP*AP*TP*CP*GP*AP*T)-3')

Chain G: 17% 63% 20%



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

Chain I: 13% 43% 43%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27507	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	0.374	Depositor
Minimum map value	0.000	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	319.488, 319.488, 319.488	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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: AGS, 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	Y	0.33	0/16840	0.42	0/22830
1	y	0.17	0/16641	0.35	0/22555
2	G	0.29	0/559	0.45	0/861
3	I	0.25	0/389	0.41	0/598
All	All	0.26	0/34429	0.39	0/46844

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	16471	0	16231	822	0
1	y	16275	0	16083	867	0
2	G	497	0	269	39	0
3	I	348	0	193	23	0
4	Y	5	0	0	0	0
4	y	5	0	0	0	0
5	Y	31	0	12	6	0
5	y	31	0	12	3	0
All	All	33663	0	32800	1721	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 26.

The worst 5 of 1721 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:1529:CYS:SG	1:Y:1554:HIS:CD2	2.49	1.05
1:y:1622:LYS:HZ3	1:y:1671:VAL:HA	1.29	0.96
2:G:21:DG:N2	3:I:10:DC:O2	2.00	0.92
1:Y:65:MET:HE3	1:Y:66:PRO:HD2	1.51	0.92
2:G:21:DG:N1	3:I:10:DC:N3	2.19	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	2069/2108 (98%)	1919 (93%)	149 (7%)	1 (0%)	100	100
1	y	2042/2108 (97%)	1934 (95%)	108 (5%)	0	100	100
All	All	4111/4216 (98%)	3853 (94%)	257 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Y	1208	SER

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	Y	1768/1795 (98%)	1683 (95%)	85 (5%)	23	50
1	y	1746/1795 (97%)	1691 (97%)	55 (3%)	34	58
All	All	3514/3590 (98%)	3374 (96%)	140 (4%)	29	54

5 of 140 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	y	1169	THR
1	y	1251	THR
1	y	1574	HIS
1	Y	1201	VAL
1	Y	1153	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	y	1083	GLN
1	y	1688	HIS
1	y	1128	ASN
1	y	1576	HIS
1	y	1805	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 10 are monoatomic - leaving 2 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	$\# Z > 2$
5	AGS	y	2206	-	29,33,33	0.47	1 (3%)	39,52,52	0.75	1 (2%)
5	AGS	Y	2206	-	29,33,33	0.46	0	39,52,52	0.75	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
5	AGS	y	2206	-	-	7/21/38/38	0/3/3/3
5	AGS	Y	2206	-	-	6/21/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	y	2206	AGS	PG-S1G	2.09	1.95	1.90

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	Y	2206	AGS	PA-O3A-PB	-3.90	119.45	132.83
5	y	2206	AGS	PA-O3A-PB	-3.76	119.93	132.83

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

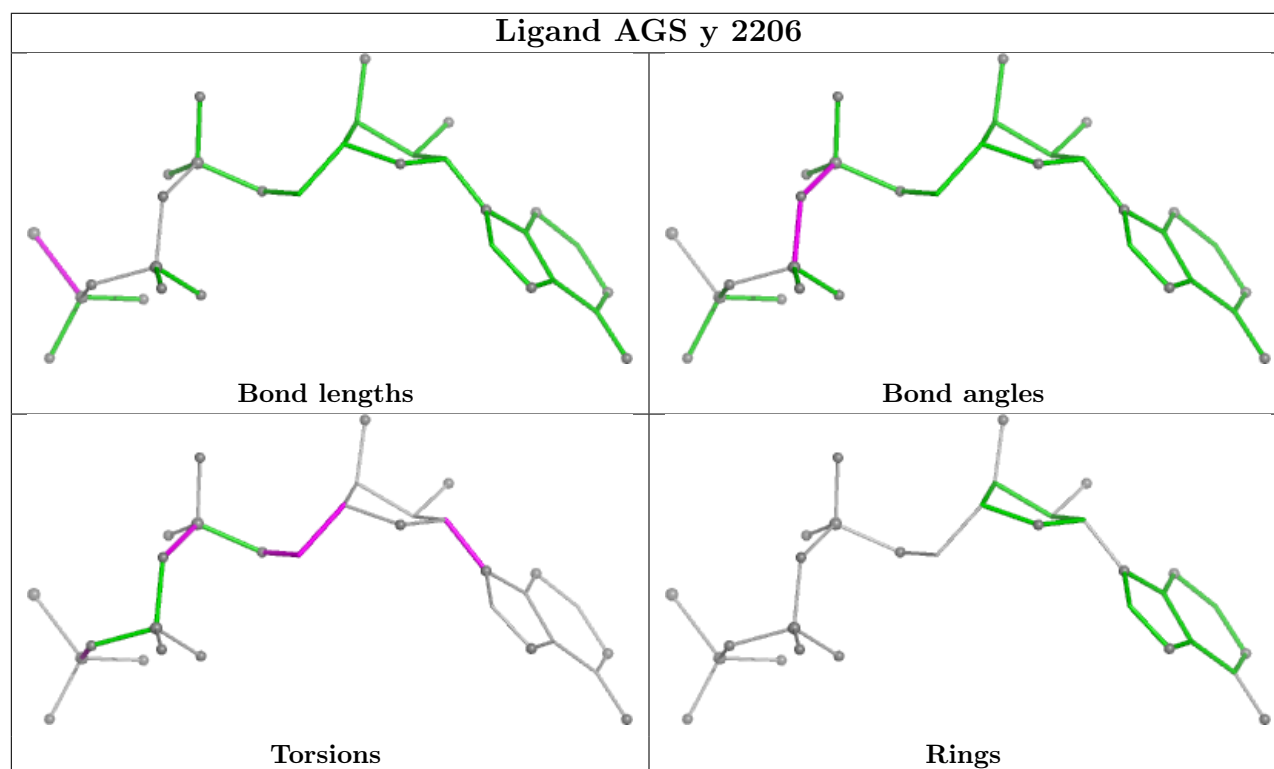
Mol	Chain	Res	Type	Atoms
5	Y	2206	AGS	C5'-O5'-PA-O2A
5	y	2206	AGS	PB-O3B-PG-O2G
5	y	2206	AGS	PB-O3B-PG-O3G
5	Y	2206	AGS	O4'-C4'-C5'-O5'
5	y	2206	AGS	O4'-C4'-C5'-O5'

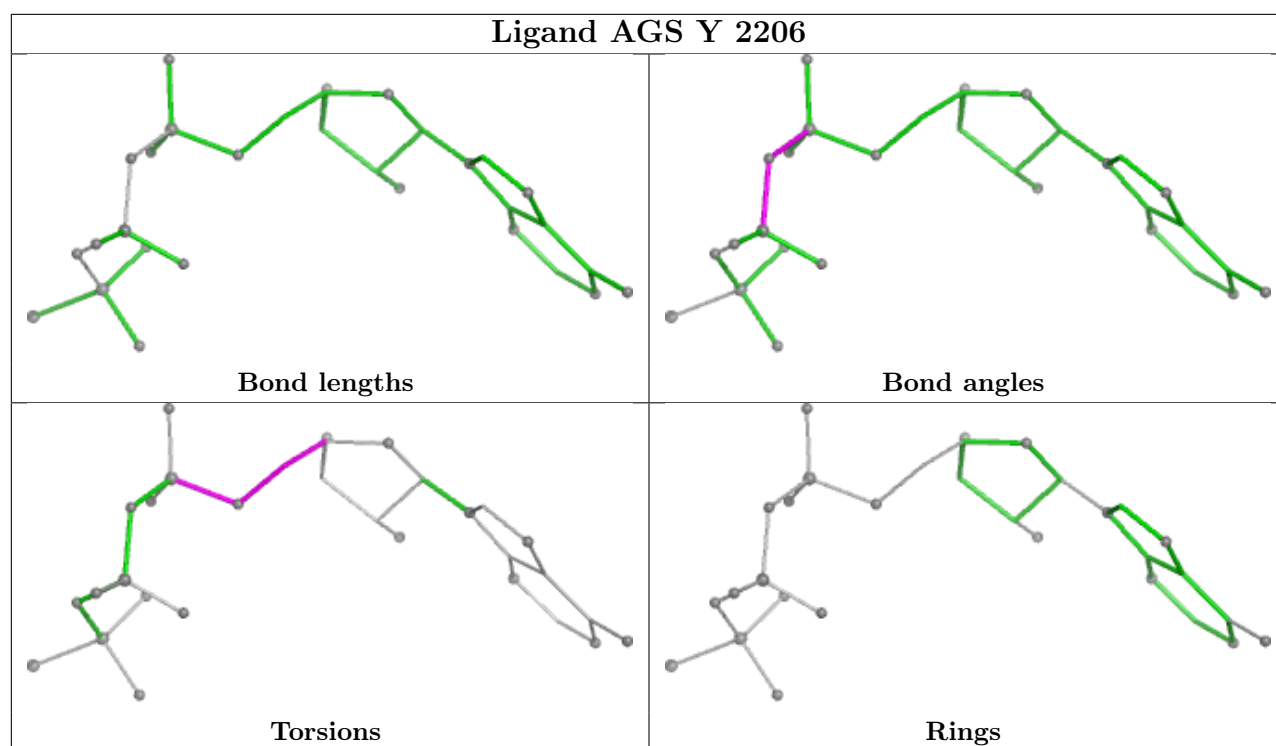
There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	y	2206	AGS	3	0
5	Y	2206	AGS	6	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.

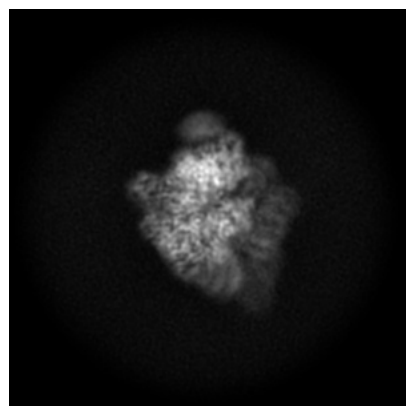
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-56253. These allow visual inspection of the internal detail of the map and identification of artifacts.

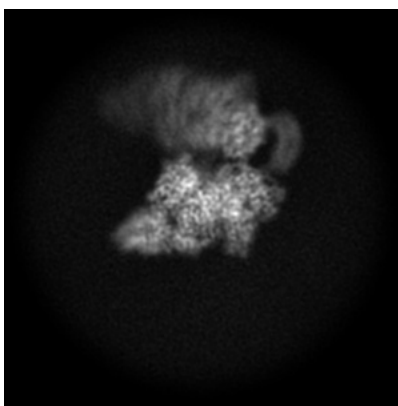
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

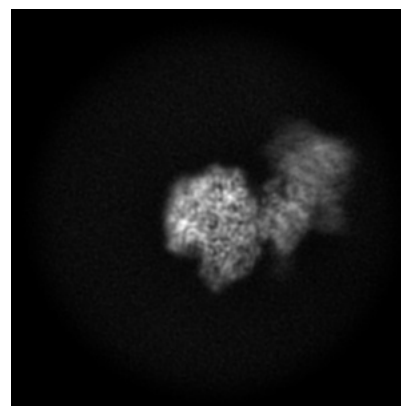
6.1.1 Primary map



X

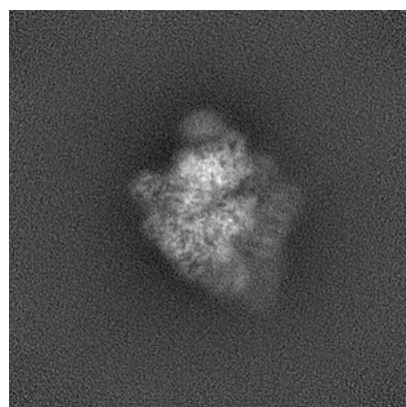


Y

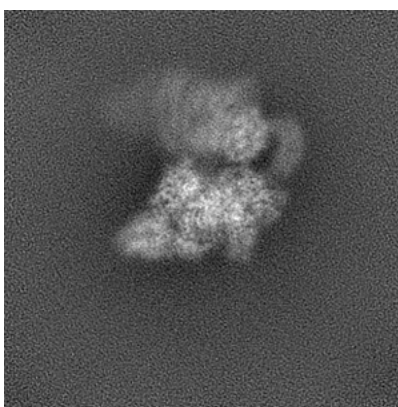


Z

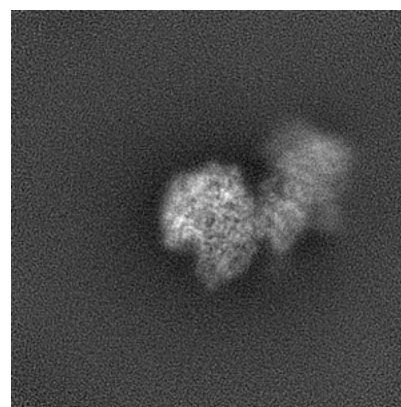
6.1.2 Raw map



X



Y

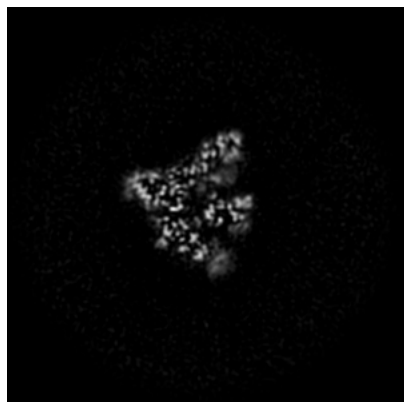


Z

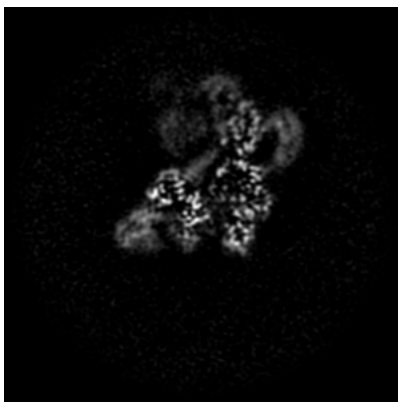
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

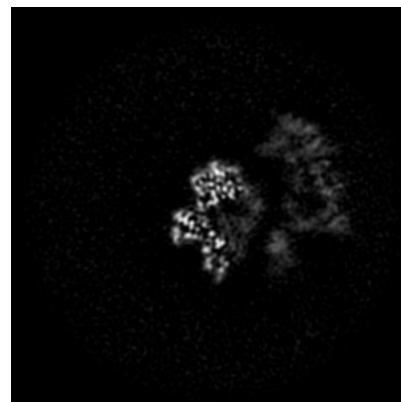
6.2.1 Primary map



X Index: 144

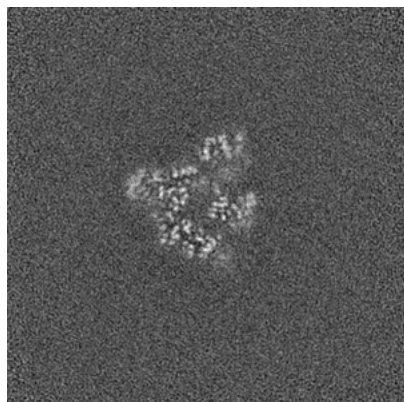


Y Index: 144

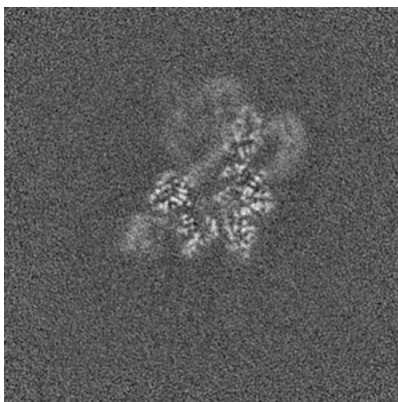


Z Index: 144

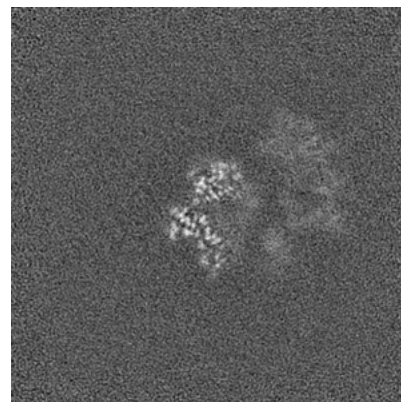
6.2.2 Raw map



X Index: 144



Y Index: 144

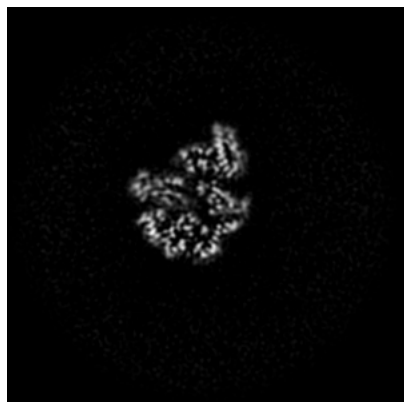


Z Index: 144

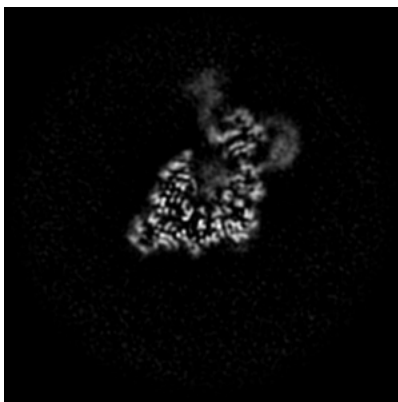
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

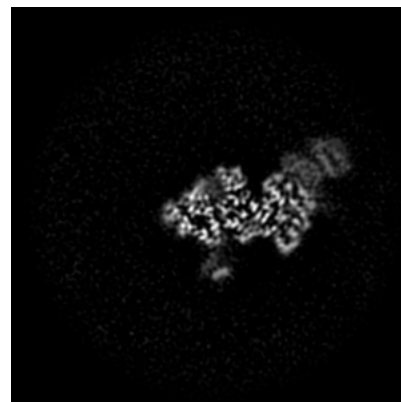
6.3.1 Primary map



X Index: 157

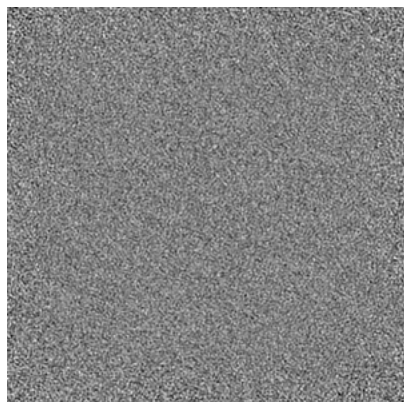


Y Index: 129

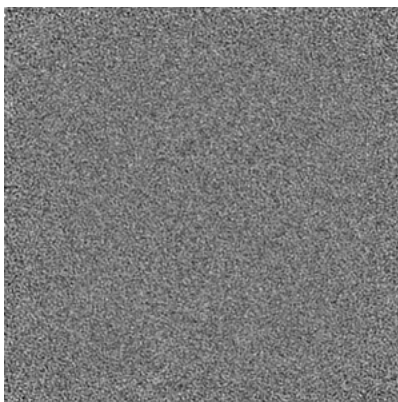


Z Index: 170

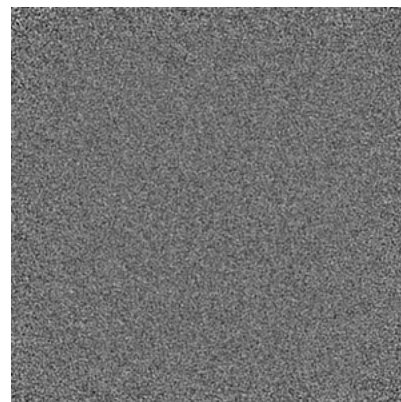
6.3.2 Raw map



X Index: 0



Y Index: 0

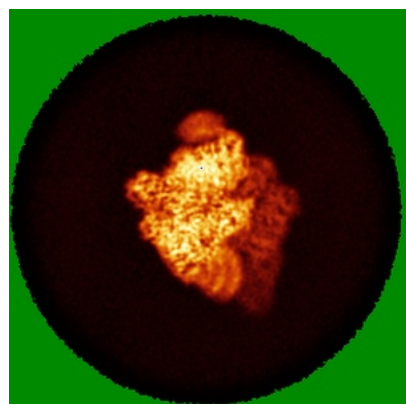


Z Index: 0

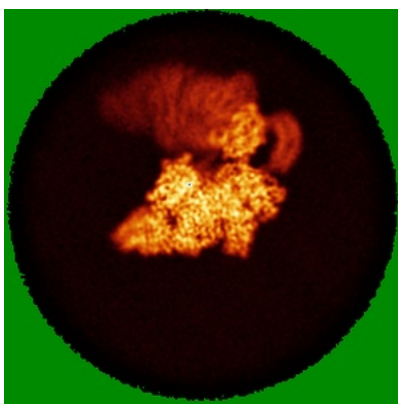
The images above show the largest variance slices of the map in three orthogonal directions.

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

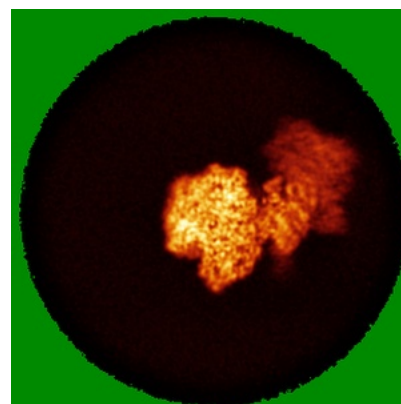
6.4.1 Primary map



X

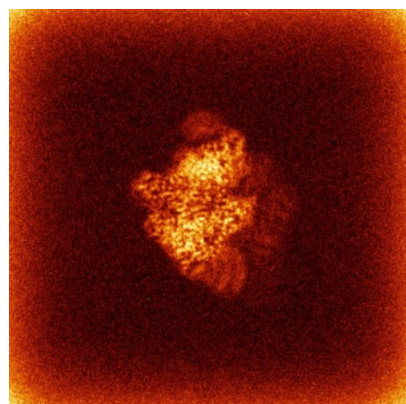


Y

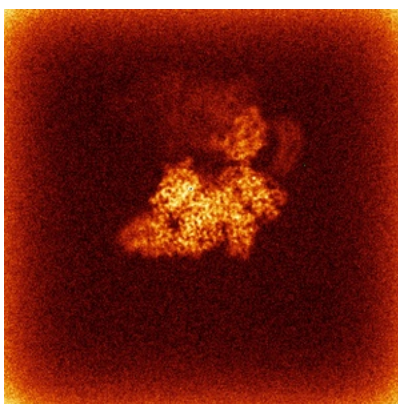


Z

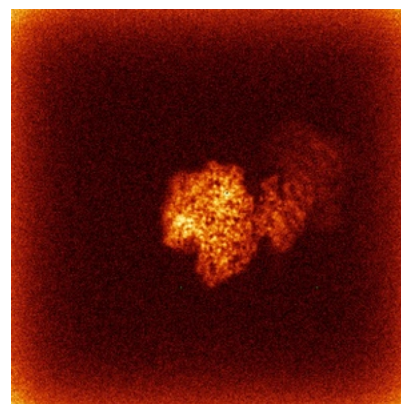
6.4.2 Raw map



X



Y

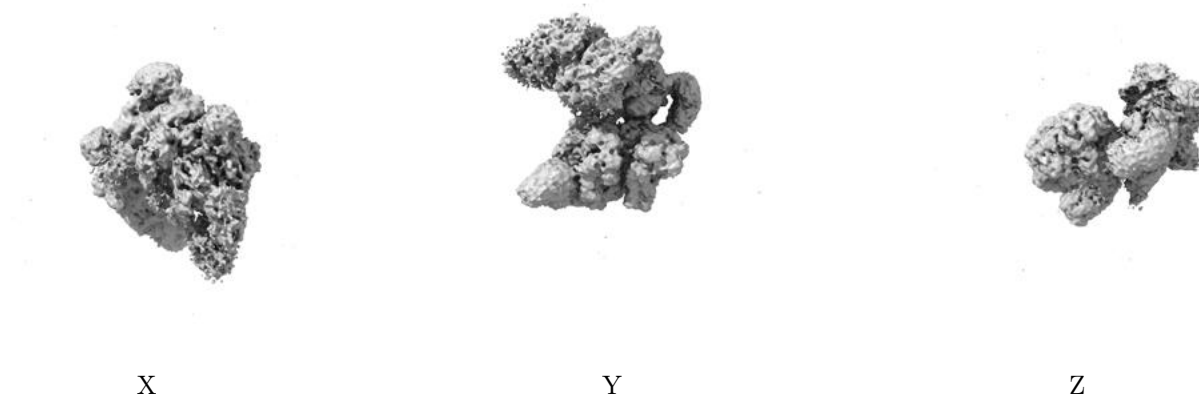


Z

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.

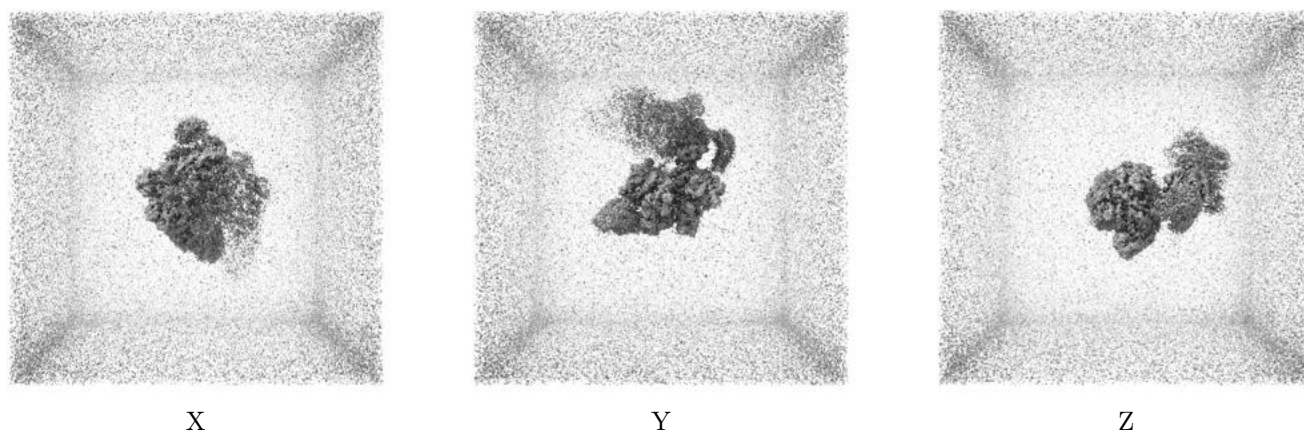
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. 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.

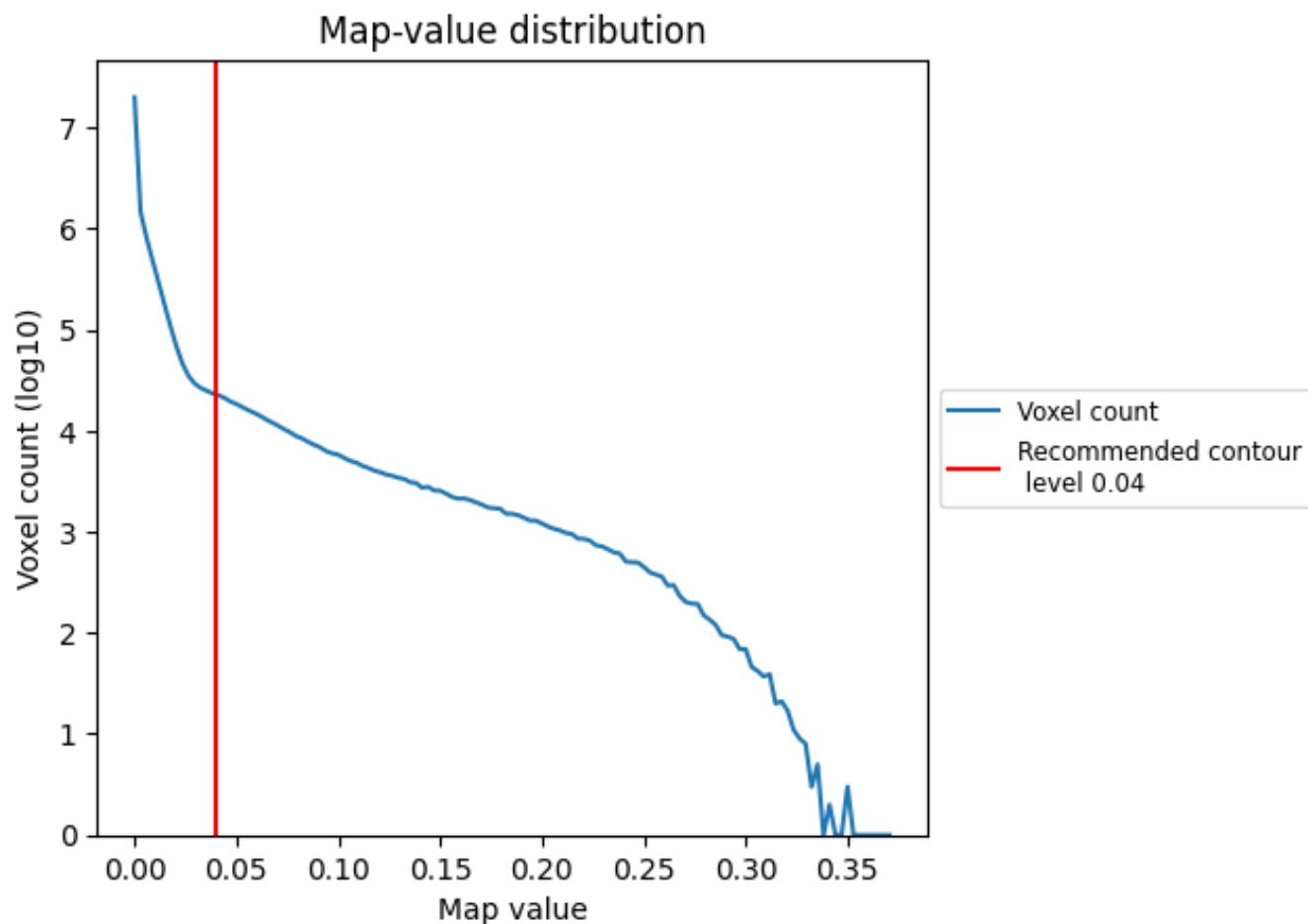
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

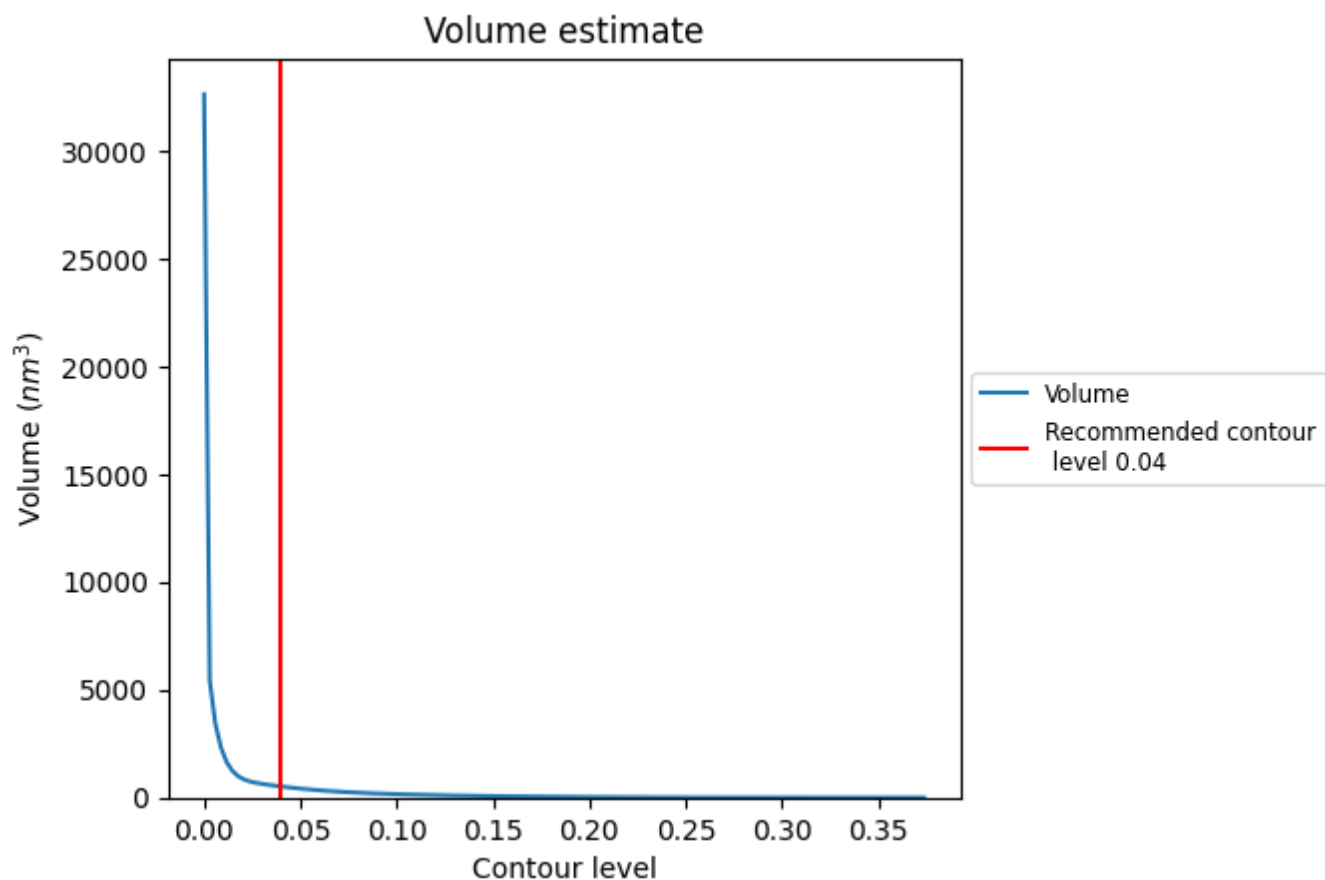
This section contains the results of statistical analysis of the map.

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.

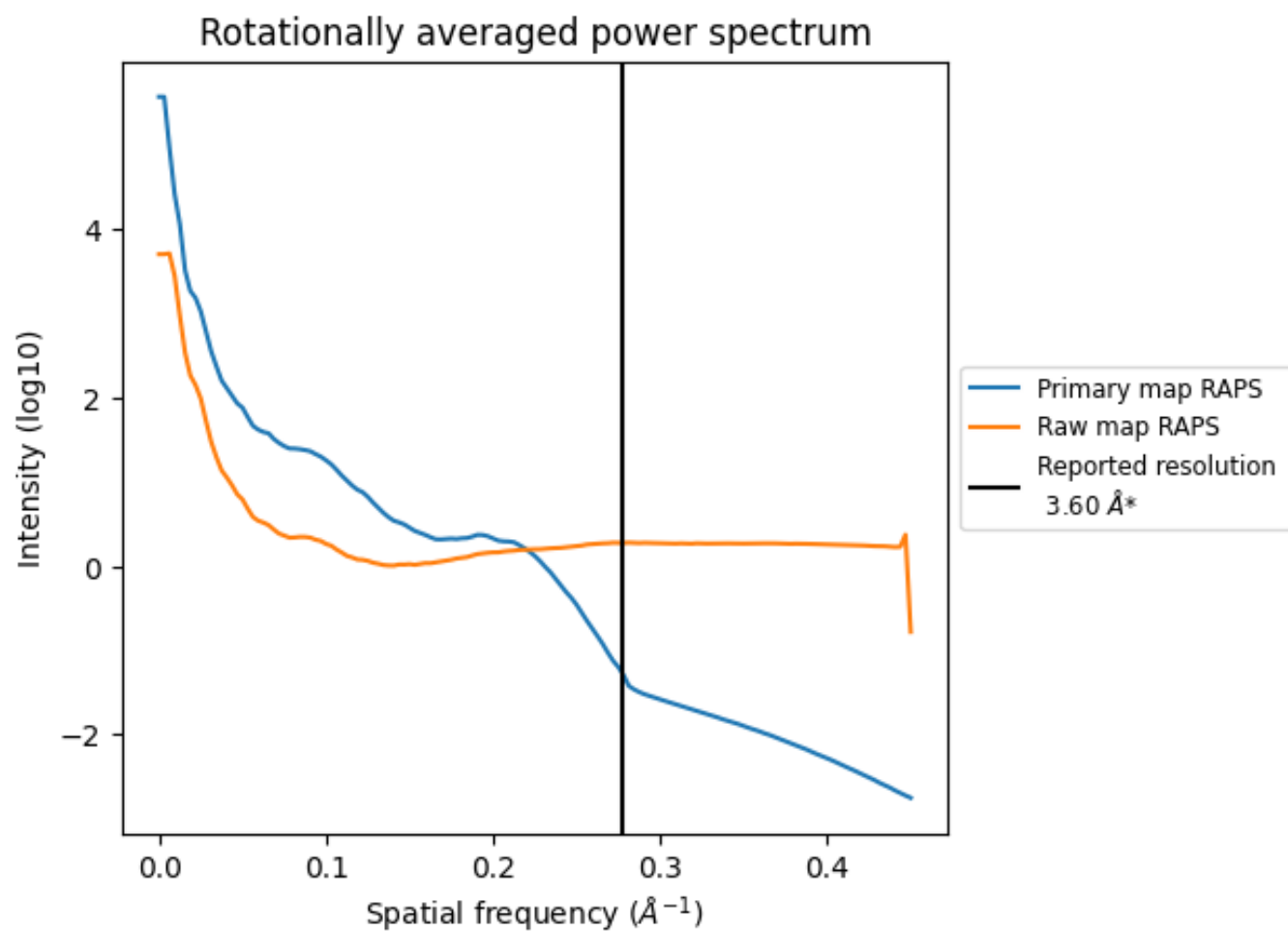
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 512 nm^3 ; this corresponds to an approximate mass of 463 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 ⓘ

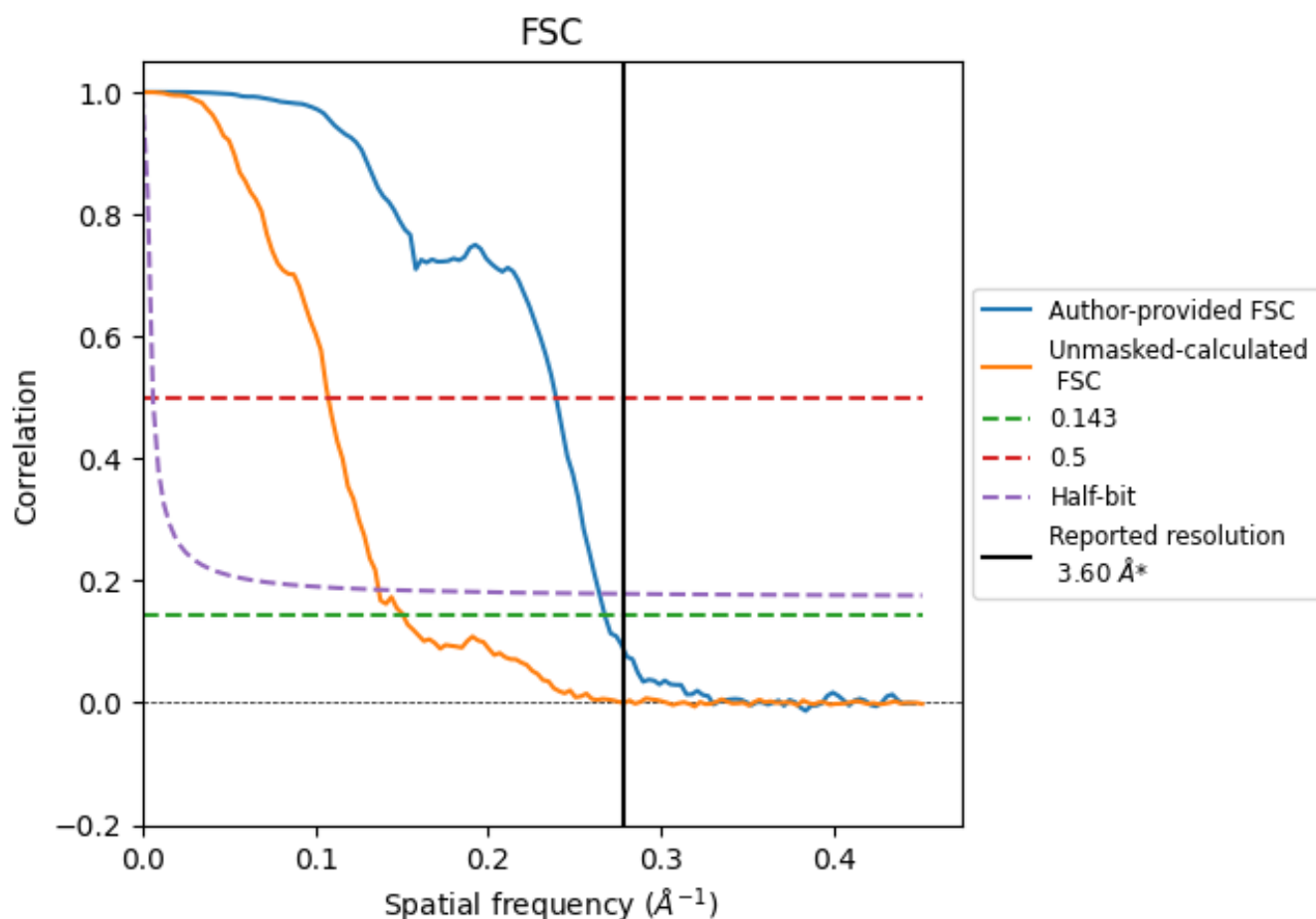


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 $0.278 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

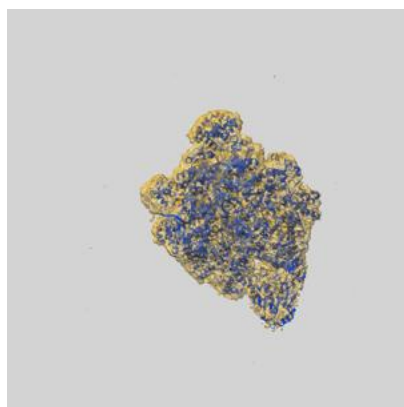
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.74	4.18	3.79
Unmasked-calculated*	6.63	9.31	7.32

*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 6.63 differs from the reported value 3.6 by more than 10 %

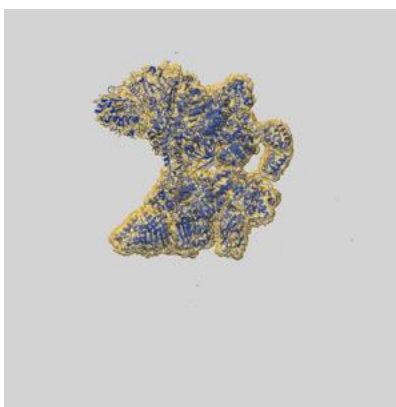
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-56253 and PDB model 9TU9. Per-residue inclusion information can be found in section [3](#) on page [5](#).

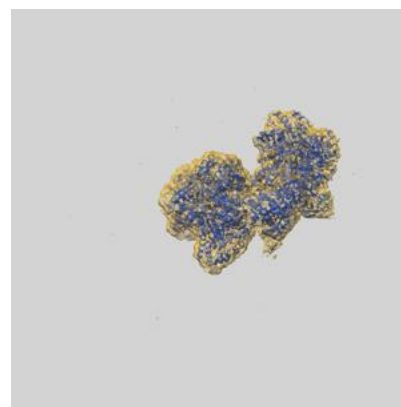
9.1 Map-model overlay [i](#)



X



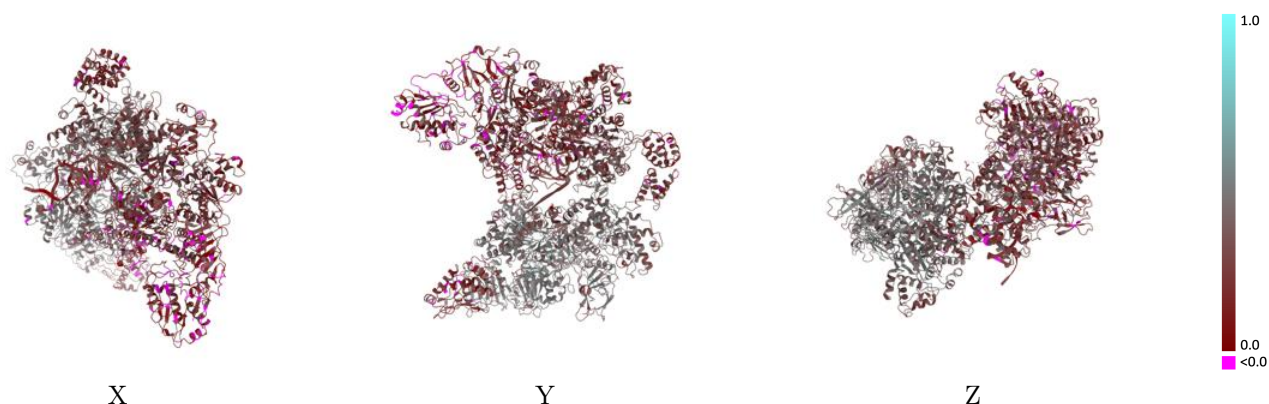
Y



Z

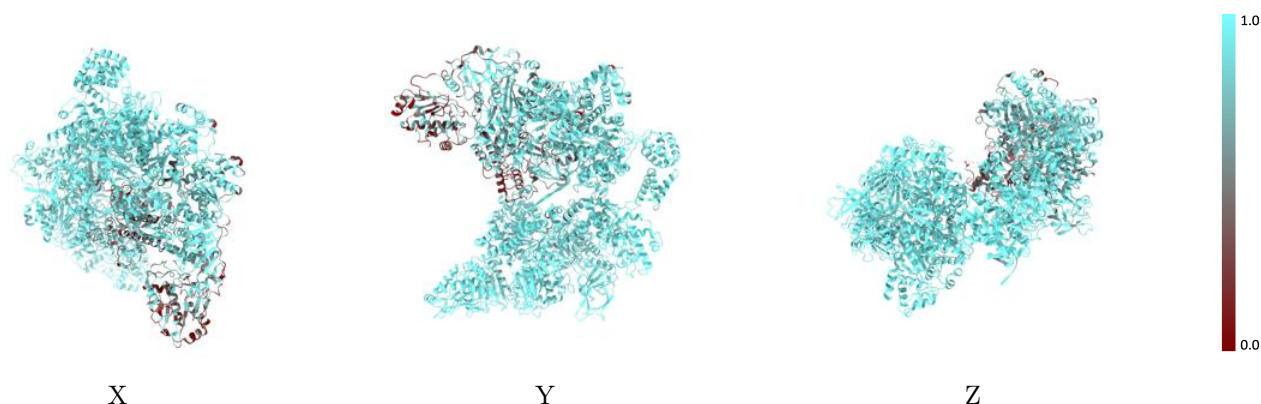
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



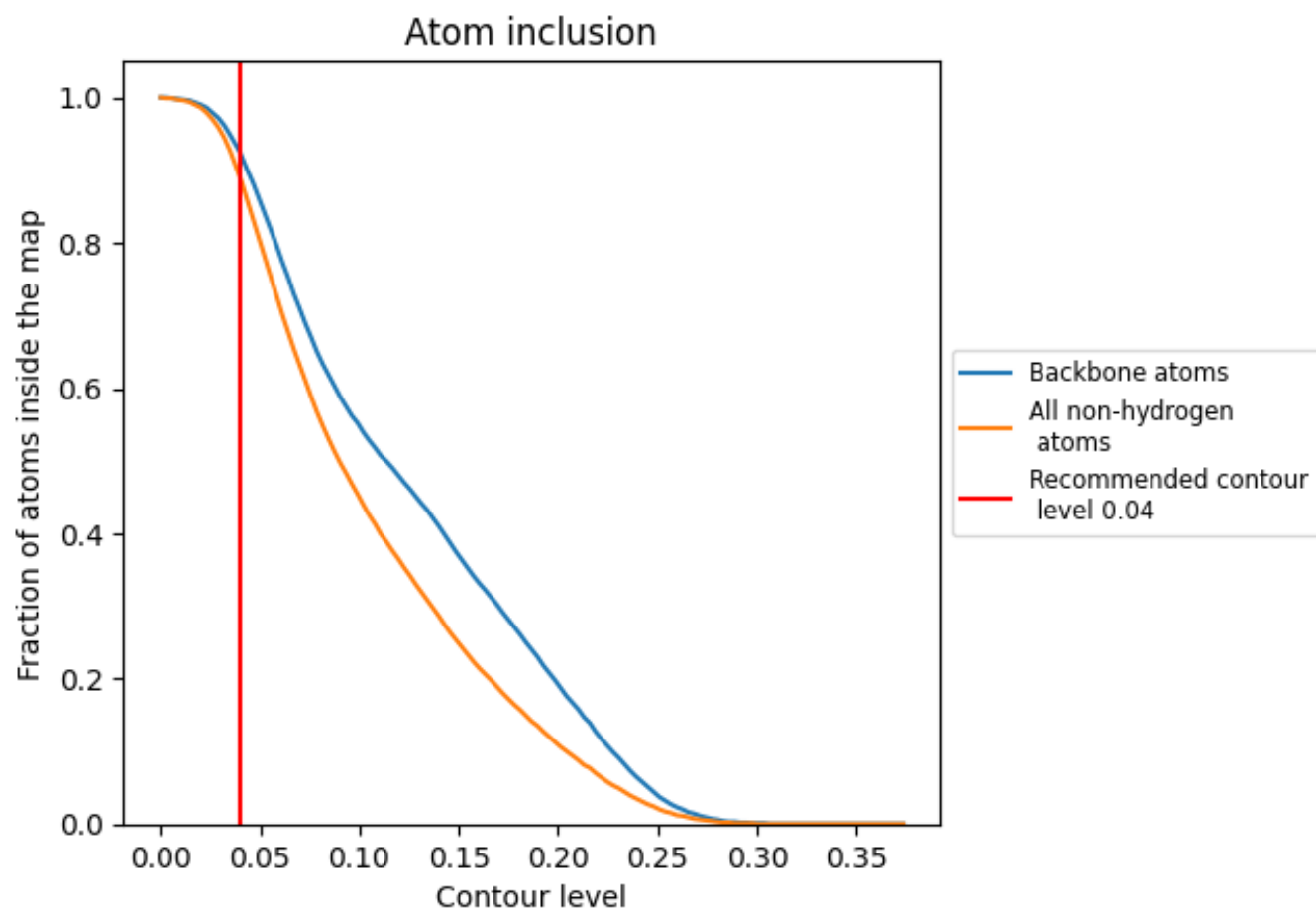
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8910	0.3130
G	0.9380	0.2590
I	0.9400	0.2340
Y	0.9890	0.3870
y	0.7890	0.2420

