



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 03:13 PM UTC

PDB ID : 7TUI / pdb_00007tui
EMDB ID : EMD-26132
Title : Structure of *C. albicans* FAS in an inhibited state
Authors : Lou, J.W.; Mazhab-Jafari, M.T.
Deposited on : 2022-02-02
Resolution : 2.66 Å (reported)
Based on initial model : 6U5V

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:

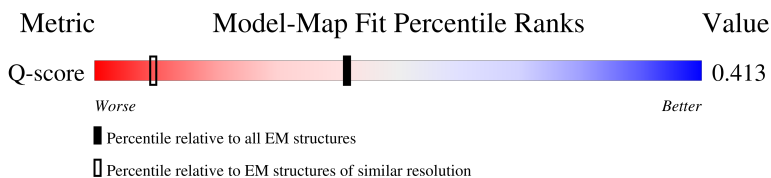
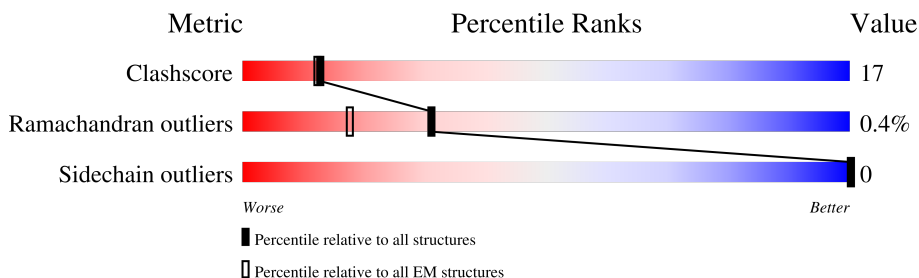
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.49

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 2.66 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	9119 (2.16 - 3.16)

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	1885	<p>11% (red), 54% (green), 22% (yellow), 24% (grey)</p>
2	B	2037	<p>50% (red), 62% (green), 38% (yellow), . (grey)</p>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 27380 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 Fatty acid synthase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1433	11295	7171	1894	2185	45	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	350	VAL	SER	conflict	UNP P43098
A	351	ASP	ARG	conflict	UNP P43098
A	353	ASN	LYS	conflict	UNP P43098
A	354	LYS	GLN	conflict	UNP P43098
A	357	ALA	LEU	conflict	UNP P43098
A	814	THR	PRO	conflict	UNP P43098
A	1067	LYS	GLN	conflict	UNP P43098
A	1124	VAL	ILE	conflict	UNP P43098
A	1445	GLU	LYS	conflict	UNP P43098
A	1743	SER	ASN	conflict	UNP P43098

- Molecule 2 is a protein called Fatty acid synthase subunit beta.

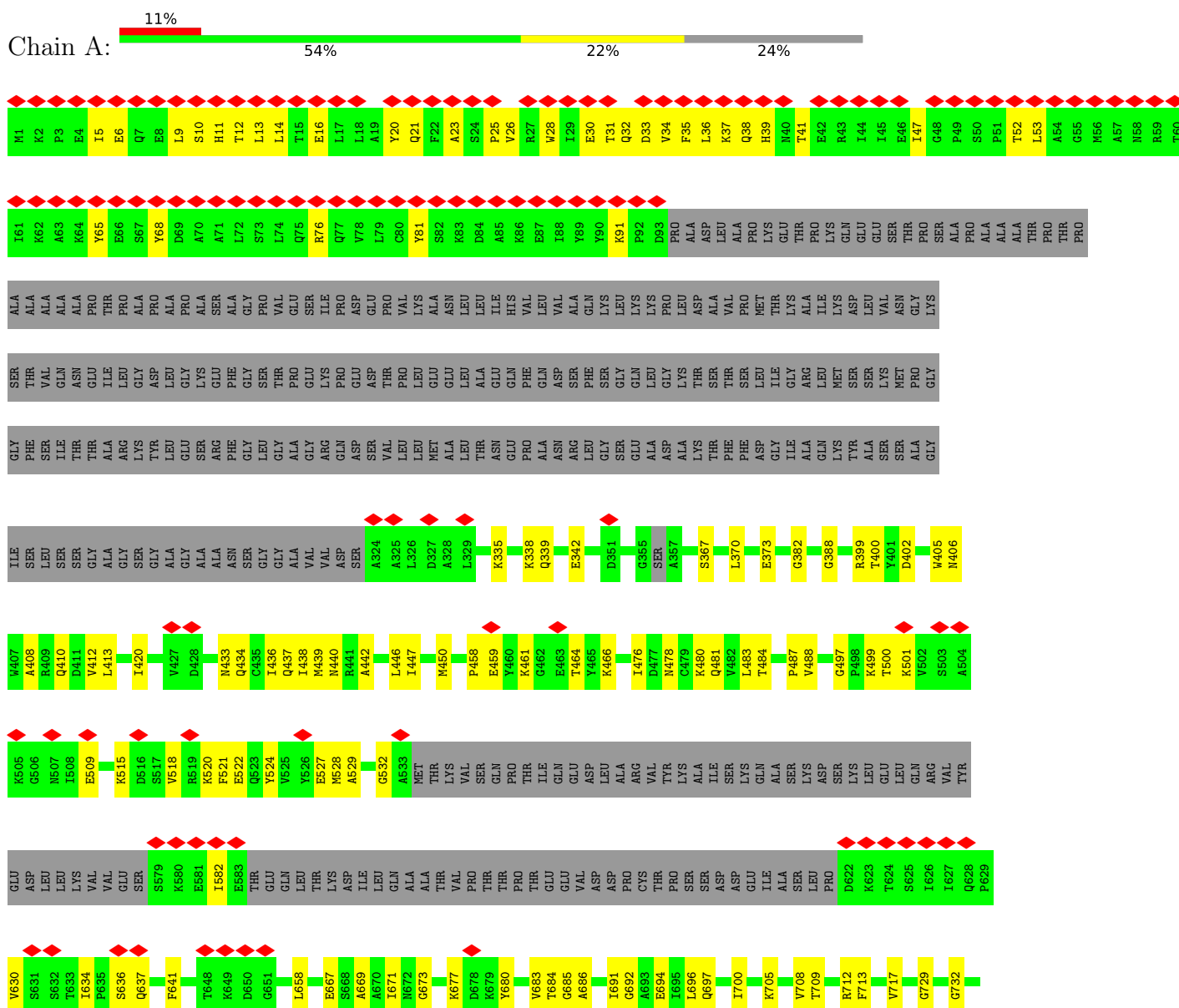
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	2033	16054	10290	2665	3045	54	1	0

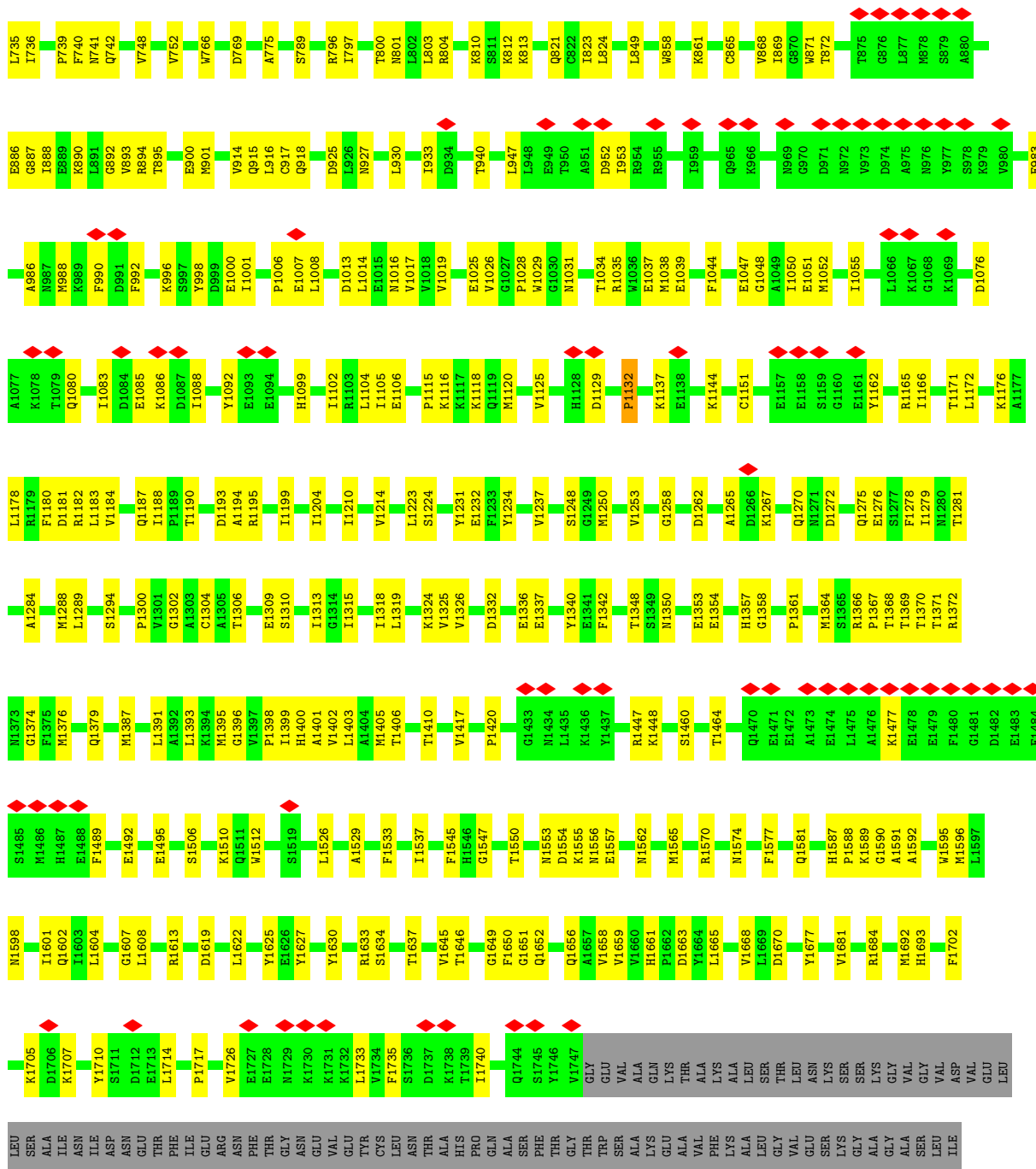
- Molecule 3 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$) (labeled as "Ligand of Interest" by depositor).

3 Residue-property plots

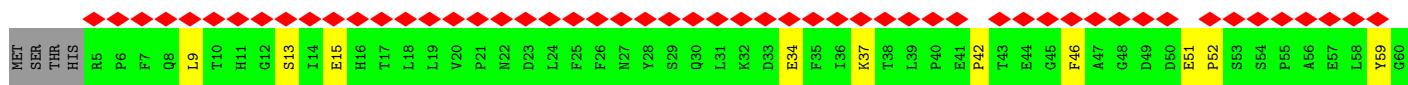
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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





● Molecule 2: Fatty acid synthase subunit beta



E1926	H1927	L1928	Y1929	E1930	I1931	I1932	D1933	E1934	V1935	A1936	A1937	K1938	S1939	L1940	A1941	Q1942	P1943	Q1944	P1945	I1946	D1947	L1948	E1949	R1950	G1951	F1952	A1953	I1954	I1955	P1956	L1957	K1958	L1959	S1960	K1961	L1962	P1963	F1964	H1965	S1966	S1967	Y1968	L1969	M1970	S1971	G1972	V1973	K1974	P1975	Q1916	Q1917	Q1918	M1919	S1920	I1921	E1922	K1923	V1924	P1925
V1866	A1867	M1868	K1869	T1870	K1871	W1872	L1873	L1874	E1875	L1876	V1877	M1878	I1879	M1880	V1881	E1882	M1883	Q1884	Q1885	V1886	V1887	A1888	A1889	G1890	D1891	L1892	R1893	A1894	L1895	D1896	L1897	L1898	T1899	N1900	V1901	L1902	M1903	V1904	L1905	I1907	M1908	K1909	I1910	D1911	I1912	V1913	K1914	L1915	Q1916	E1917	Q1918	M1919	S1920	I1921	E1922	K1923	V1924	P1925	
L1806	A1807	M1808	M1810	P1811	E1812	E1813	S1814	L1815	L1816	D1817	V1818	I1819	F1820	Y1821	R1822	M1824	T1825	M1826	Q1827	Y1828	A1829	V1830	R1831	R1832	E1833	E1834	L1835	G1836	R1837	S1838	Y1839	G1841	M1842	L1843	A1844	V1845	M1846	P1847	S1848	R1849	V1850	S1851	A1852	T1853	F1854	F1855	D1856	S1857	A1858	L1859	R1860	F1861	V1862	D1864	E1865				
A1733	L1734	K1735	S1736	E1737	K1738	I1739	F1740	K1741	D1742	I1743	T1756	G1757	L1758	L1759	S1760	A1761	T1762	Q1763	F1764	Q1765	Q1766	L1769	T1770	L1771	E1772	E1773	K1774	A1775	A1776	F1777	D1778	D1779	I1780	K1781	S1782	K1783	G1784	L1785	I1786	P1787	S1788	D1789	M1790	M1791	F1792	H1795	S1796	L1797	G1798	E1799	Y1800	S1801	A1802	L1803	S1804	S1805			
L1638	E1641	A1642	E1643	I1644	E1645	Q1646	P1647	T1648	V1652	F1653	T1654	G1655	Q1656	G1657	S1658	Q1659	M1663	G1664	M1665	E1672	V1677	D1682	R1683	H1684	F1685	M1688	I1689	L1694	D1695	L1696	V1697	P1701	G1709	G1713	M1719	M1723	M1724	F1725	E1726	T1727	I1728	G1729	E1634	E1635	P1636	V1637													
D1488	Y1489	V1499	T1500	D1501	Y1502	S1503	R1505	M1506	K1508	T1509	I1510	E1511	E1512	S1513	V1514	I1515	F1516	E1517	M1518	A1519	I1520	F1521	S1523	S1524	G1525	E1526	K1531	A1532	F1533	G1534	T1535	M1536	E1537	P1538	I1549	H1550	V1551	S1552	F1555	A1556	A1557	K1560	L1561	P1562	M1569														
S1423	A1424	K1425	D1426	L1427	A1428	R1431	V1435	F1436	E1439	K1440	D1441	V1442	Q1443	F1444	D1445	V1446	L1447	T1448	F1449	R1450	C1451	E1452	S1453	T1454	Y1455	K1456	F1457	S1458	A1459	A1460	M1461	V1462	Y1463	S1464	K1467	T1468	T1469	G1470	Q1471	V1472	L1473	L1474	L1475	L1476	E1477	T1478	E1479	Q1481	Q1482	Y1483	Y1484	G1485	V1486	V1487					
P1351	L1352	K1353	K1354	V1357	K1361	A1362	E1363	I1364	K1365	A1366	V1367	L1368	P1371	S1372	G1373	K1374	L1375	V1376	E1377	V1378	V1379	G1380	R1384	E1385	G1386	K1387	P1388	V1389	M1390	E1391	V1392	T1393	S1394	Q1395	Y1398	E1401	Y1402	N1403	D1404	M1407	Q1410	E1414	T1415	V1416	Q1418	V1419	A1420	F1421	K1422										
S1284	E1285	F1286	T1287	H1288	A1289	I1290	G1291	M1292	K1293	C1294	D1295	A1296	V1297	R1300	P1301	G1302	K1303	A1304	T1305	L1306	A1307	P1308	M1309	D1310	F1311	A1312	I1313	V1314	G1315	H1316	V1317	I1321	I1324	F1325	P1326	V1329	D1330	G1331	L1332	L1333	L1334	H1338	M1341	G1342	Y1343	K1344	M1345	I1346	T1347	G1348	A1349	A1350							
V1198	K1199	P1200	M1201	T1202	I1203	H1210	R1211	T1212	A1213	D1214	T1215	M1216	P1217	V1218	I1219	Y1224	M1227	D1230	G1231	L1232	A1233	P1234	D1241	I1246	K1247	E1248	K1252	L1253	M1254	S1257	S1258	M1263	D1264	I1265	M1266	V1267	A1270	I1271	L1272	G1273	D1274	E1275	I1276	M1277	I1278	S1279	S1280	Q1281											
P1121	N1122	K1123	Q1124	E1125	L1130	A1131	G1132	T1133	E1134	L1135	L1138	Q1139	I1142	R1146	I1147	H1153	N1156	P1157	L1158	H1159	D1160	I1161	L1162	T1163	P1164	A1165	I1172	D1173	K1174	K1175	T1176	K1177	K1178	T1180	A1181	F1182	E1183	N1184	I1185	K1186	M1187	D1188	L1189	L1190	P1191	V1192	M1193	E1194	Q1111	E1115	I1116	D1117	S1118	E1119	L1120				

K1986	S1987	S1988	V1989	K1990	P1991	D1993	L1994	I1995	K1996	K1997	Y1998	I1999	P2000	N2001	L2002	T2003	A2004	K2005	P2006	F2007	E2008	L2009	T2010	K2011	E2012	Y2013	F2014	Q2015	S2016	Y2017	Y2018	D2019	L2020	T2021	K2022	S2023	E2024	K2025	I2026	K2027	S2028	I2029	L2030	D2031	N2032	K2033	E2034	Q2035	Y2036	E2037
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D3	Depositor
Number of particles used	252339	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	6.743	Depositor
Minimum map value	-4.396	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.273	Depositor
Recommended contour level	0.8	Depositor
Map size (\AA)	333.72, 333.72, 333.72	wwPDB
Map dimensions	324, 324, 324	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.03, 1.03, 1.03	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: FMN

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	0.24	0/11522	0.49	1/15575 (0.0%)
2	B	0.21	0/16423	0.55	4/22279 (0.0%)
All	All	0.22	0/27945	0.53	5/37854 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	1969	LEU	CA-C-N	6.75	134.44	121.54
2	B	1969	LEU	C-N-CA	6.75	134.44	121.54
1	A	1132	PRO	CA-N-CD	-6.30	103.18	112.00
2	B	2034	GLU	CB-CA-C	-5.85	109.28	117.23
2	B	743	LYS	N-CA-C	-5.66	106.05	114.64

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	1810	MET	Peptide
2	B	1929	TYR	Peptide
2	B	1982	LYS	Peptide

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	11295	0	11214	308	0
2	B	16054	0	16025	625	0
3	B	31	0	19	4	0
All	All	27380	0	27258	905	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 17.

The worst 5 of 905 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)
2:B:1780:ILE:HA	2:B:1783:LYS:HB2	1.54	0.88
2:B:1571:SER:HB3	2:B:1638:LEU:HD11	1.58	0.85
2:B:1620:GLY:HA2	2:B:1786:ILE:HB	1.57	0.85
1:A:709:THR:HG23	1:A:740:PHE:HB3	1.60	0.84
2:B:573:LEU:HB2	2:B:1096:PRO:HG3	1.61	0.83

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	1425/1885 (76%)	1383 (97%)	42 (3%)	0	100	100
2	B	2032/2037 (100%)	1824 (90%)	194 (10%)	14 (1%)	18	30
All	All	3457/3922 (88%)	3207 (93%)	236 (7%)	14 (0%)	31	45

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1032	VAL
2	B	1477	PRO
2	B	1580	GLU
2	B	1970	MET
2	B	1974	LYS

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	1220/1579 (77%)	1220 (100%)	0	100	100
2	B	1780/1784 (100%)	1780 (100%)	0	100	100
All	All	3000/3363 (89%)	3000 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1403	ASN
2	B	1550	HIS
2	B	1827	GLN
1	A	1470	GLN
1	A	1432	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](#)

1 ligand 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
3	FMN	B	2101	-	33,33,33	1.08	2 (6%)	48,50,50	1.22	7 (14%)

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
3	FMN	B	2101	-	-	3/18/18/18	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2101	FMN	C4A-N5	3.47	1.38	1.30
3	B	2101	FMN	C10-N1	2.46	1.38	1.33

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2101	FMN	C4-N3-C2	-3.11	120.12	125.64
3	B	2101	FMN	C4'-C3'-C2'	-2.74	109.02	113.57
3	B	2101	FMN	C4A-C4-N3	2.69	120.10	113.25
3	B	2101	FMN	O4-C4-C4A	-2.51	119.90	126.53
3	B	2101	FMN	C4A-C10-N10	2.46	120.00	116.48

There are no chirality outliers.

All (3) torsion outliers are listed below:

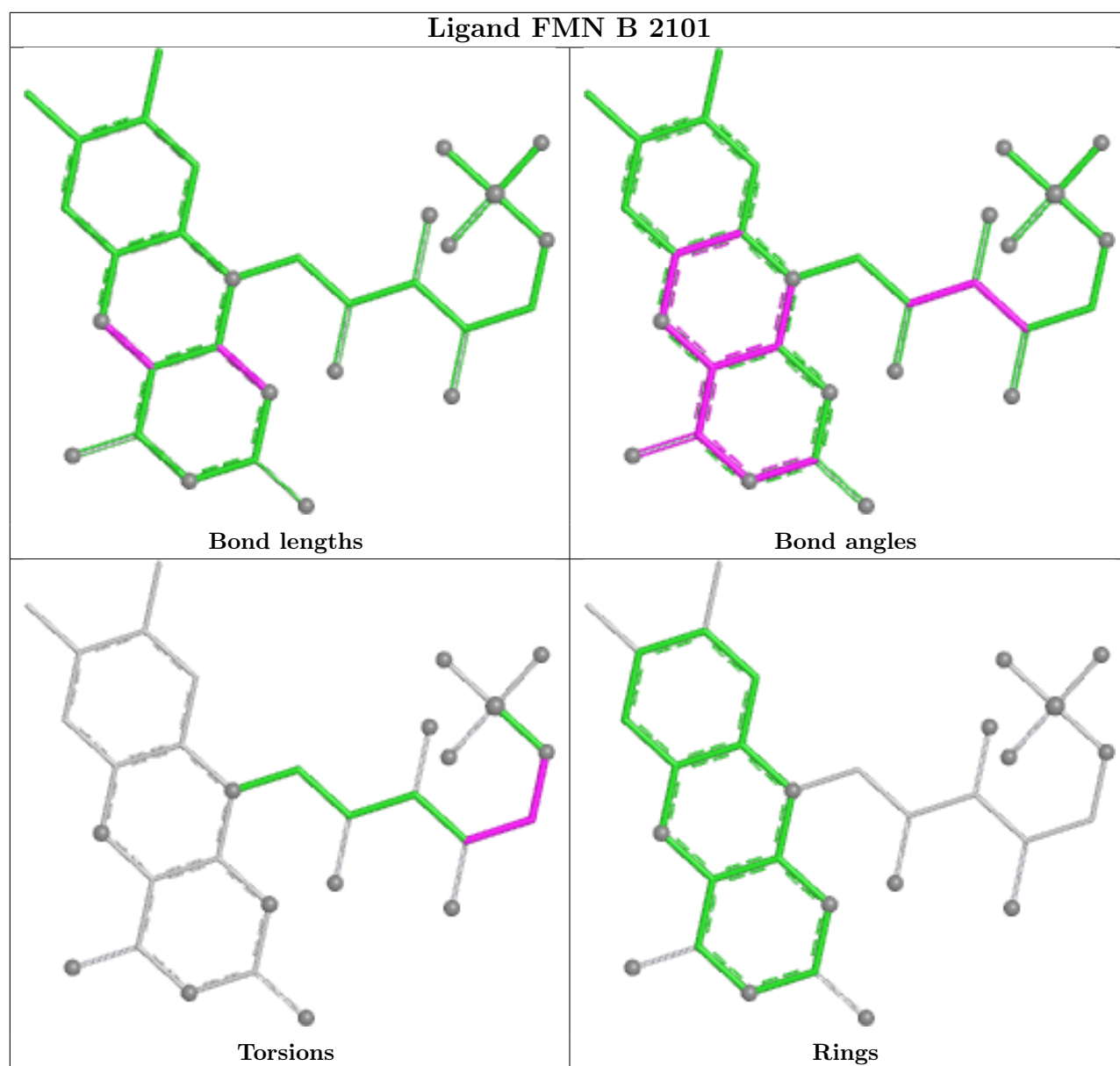
Mol	Chain	Res	Type	Atoms
3	B	2101	FMN	C3'-C4'-C5'-O5'
3	B	2101	FMN	O4'-C4'-C5'-O5'
3	B	2101	FMN	C4'-C5'-O5'-P

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	2101	FMN	4	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.

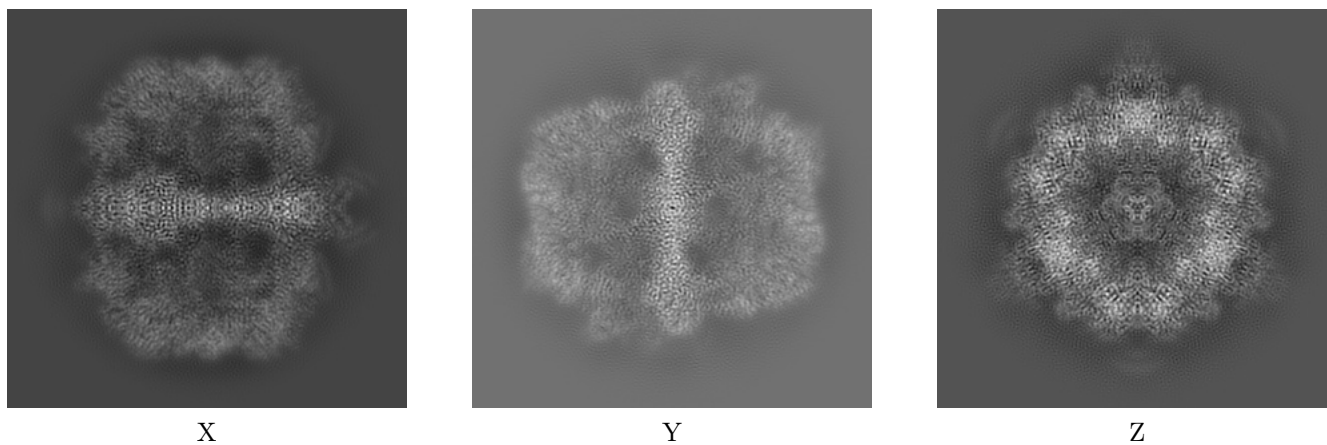
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26132. 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](#)

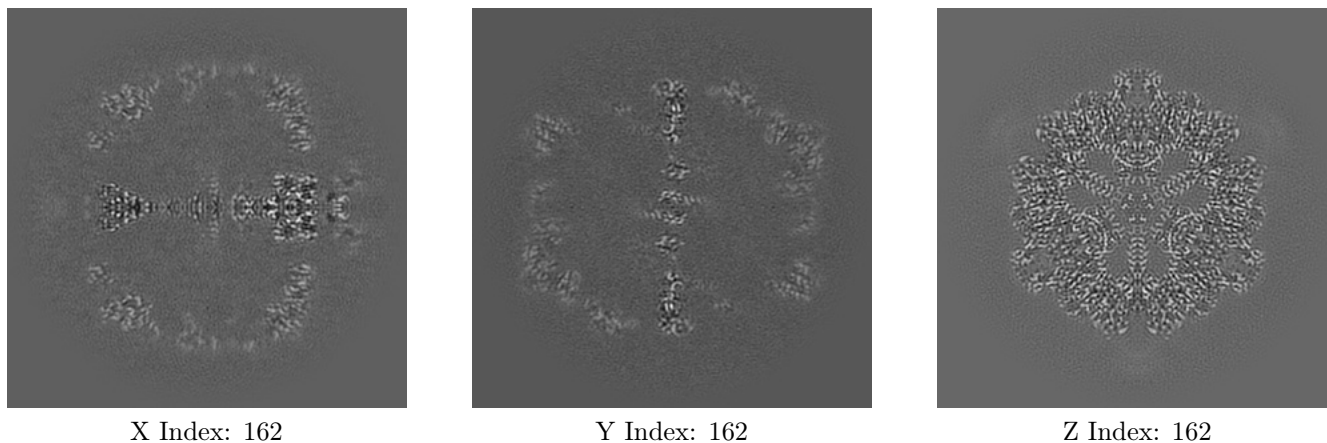
6.1.1 Primary map



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

6.2 Central slices [i](#)

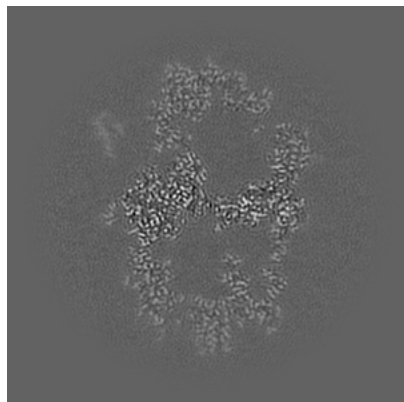
6.2.1 Primary map



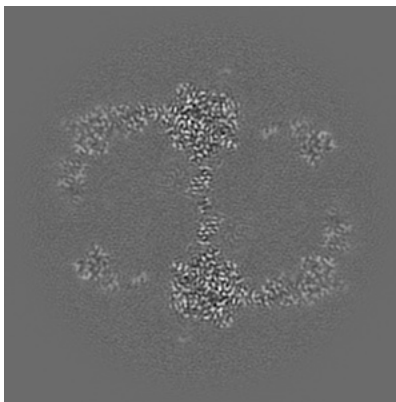
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

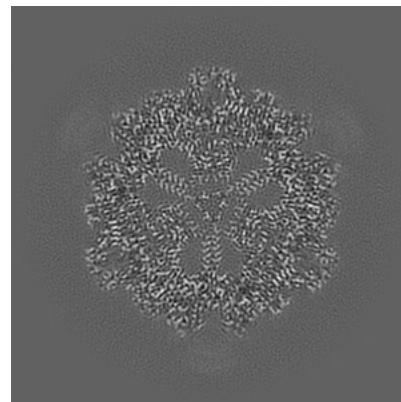
6.3.1 Primary map



X Index: 99



Y Index: 134

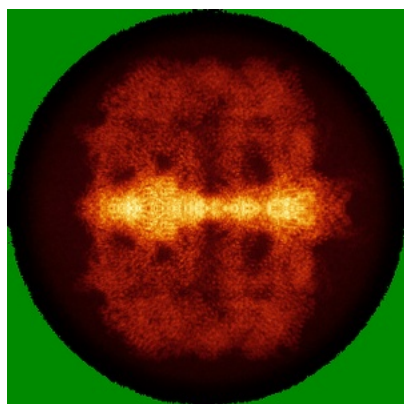


Z Index: 163

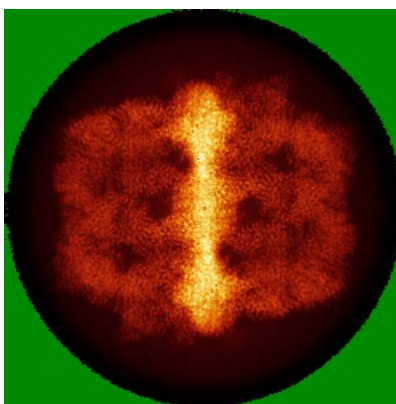
The images above show the largest variance slices of the map in three orthogonal directions.

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

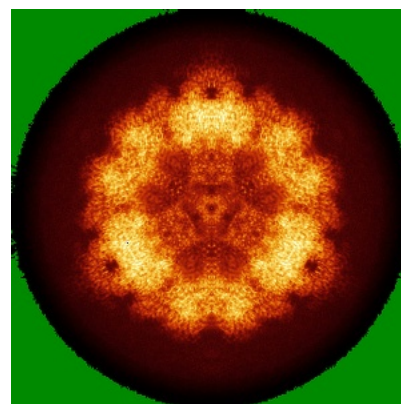
6.4.1 Primary map



X



Y

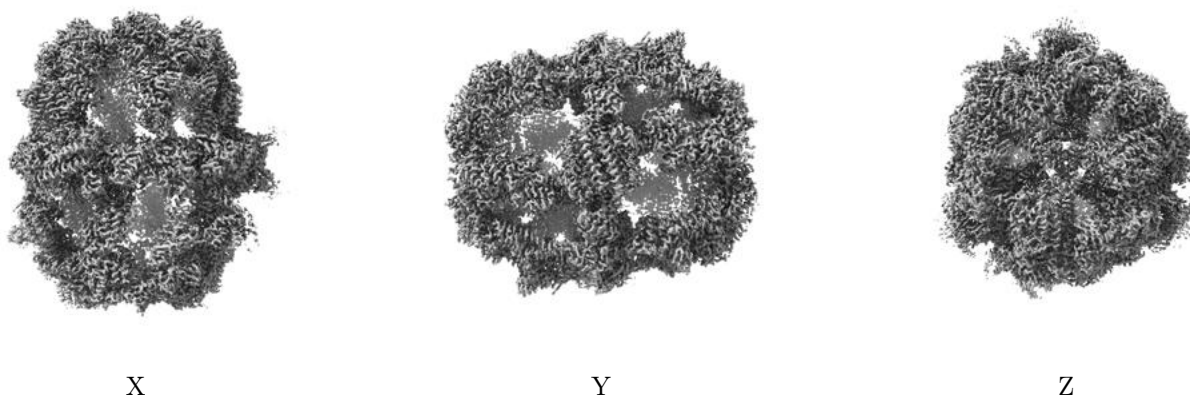


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

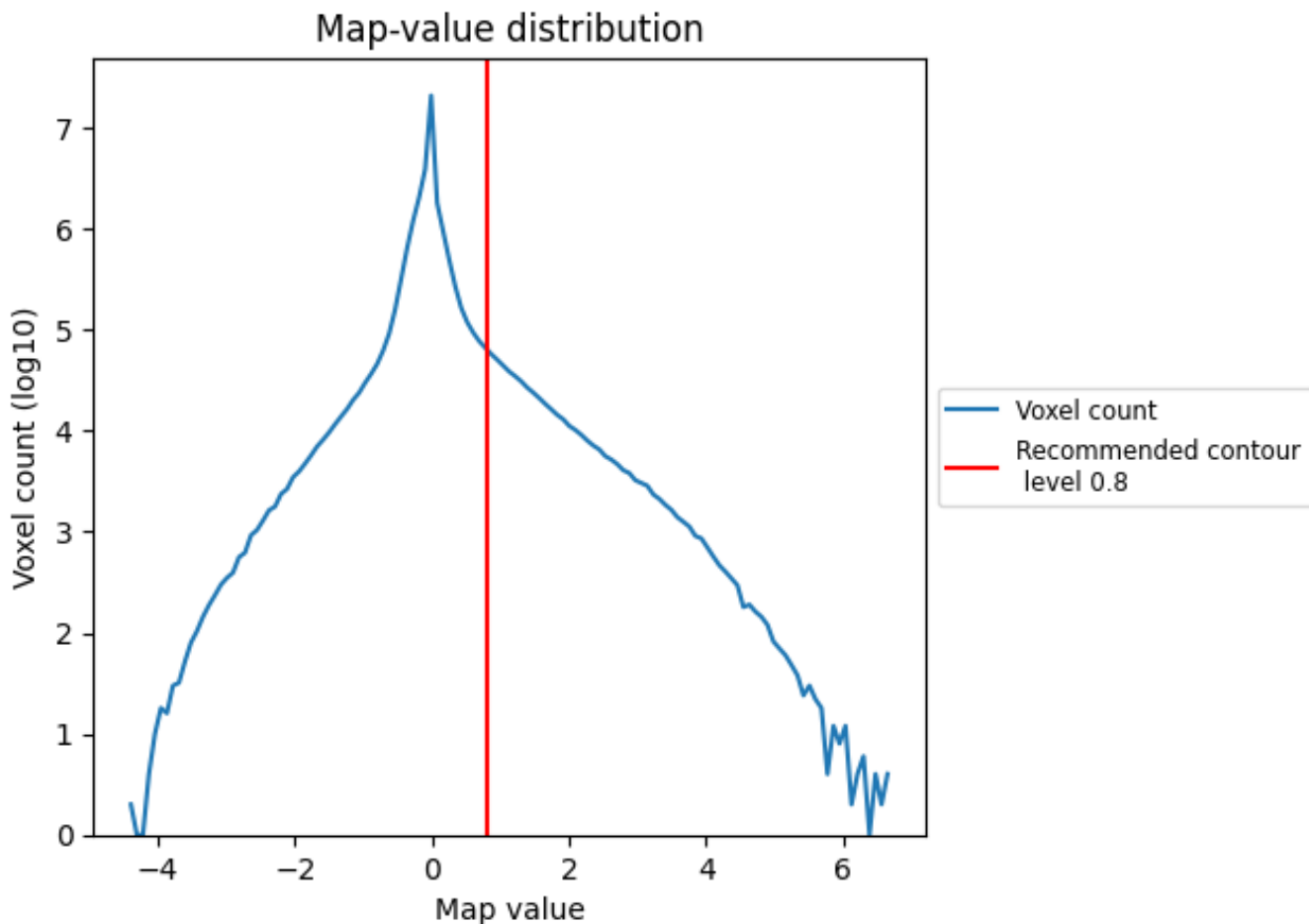
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

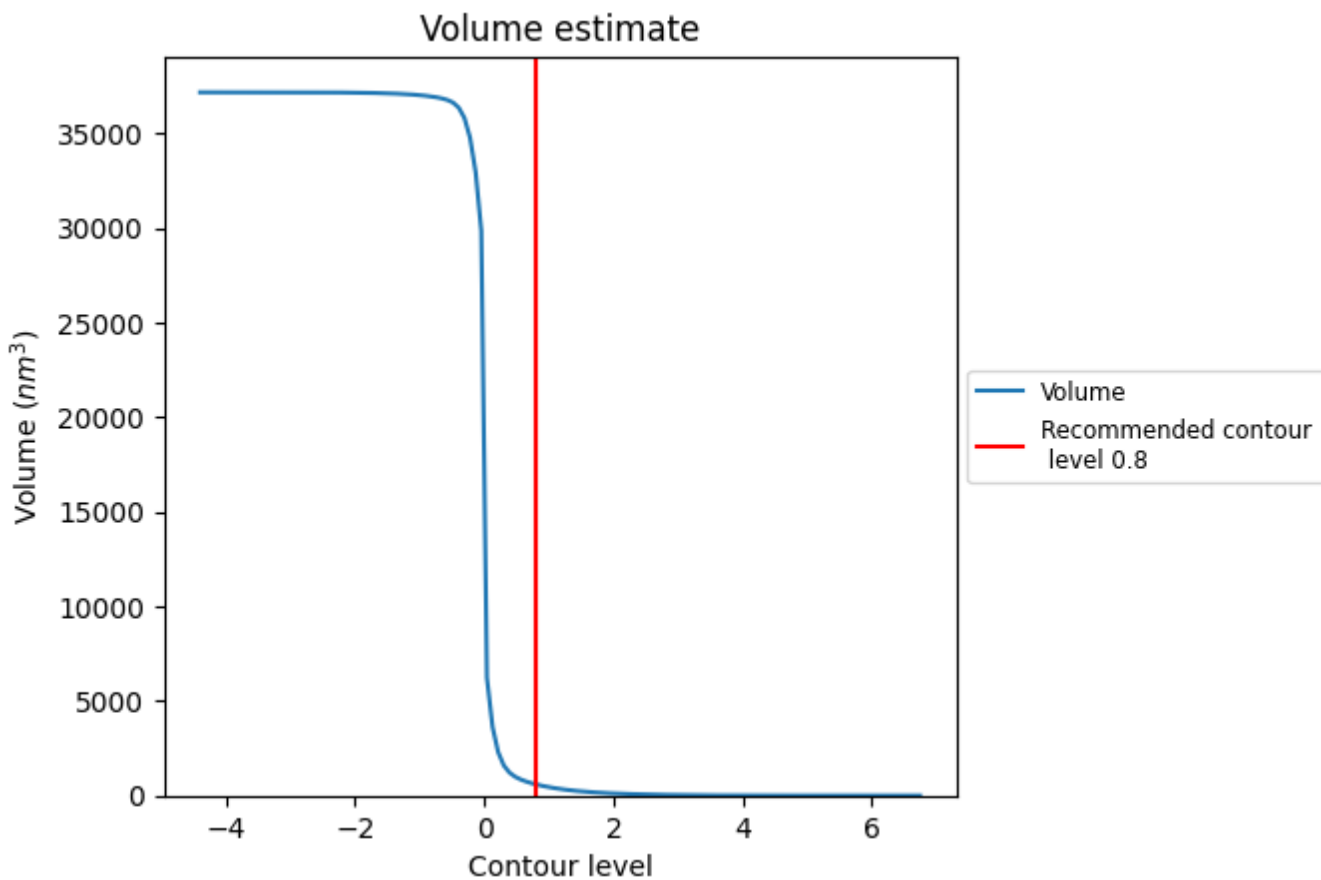
This section contains the results of statistical analysis of the map.

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.

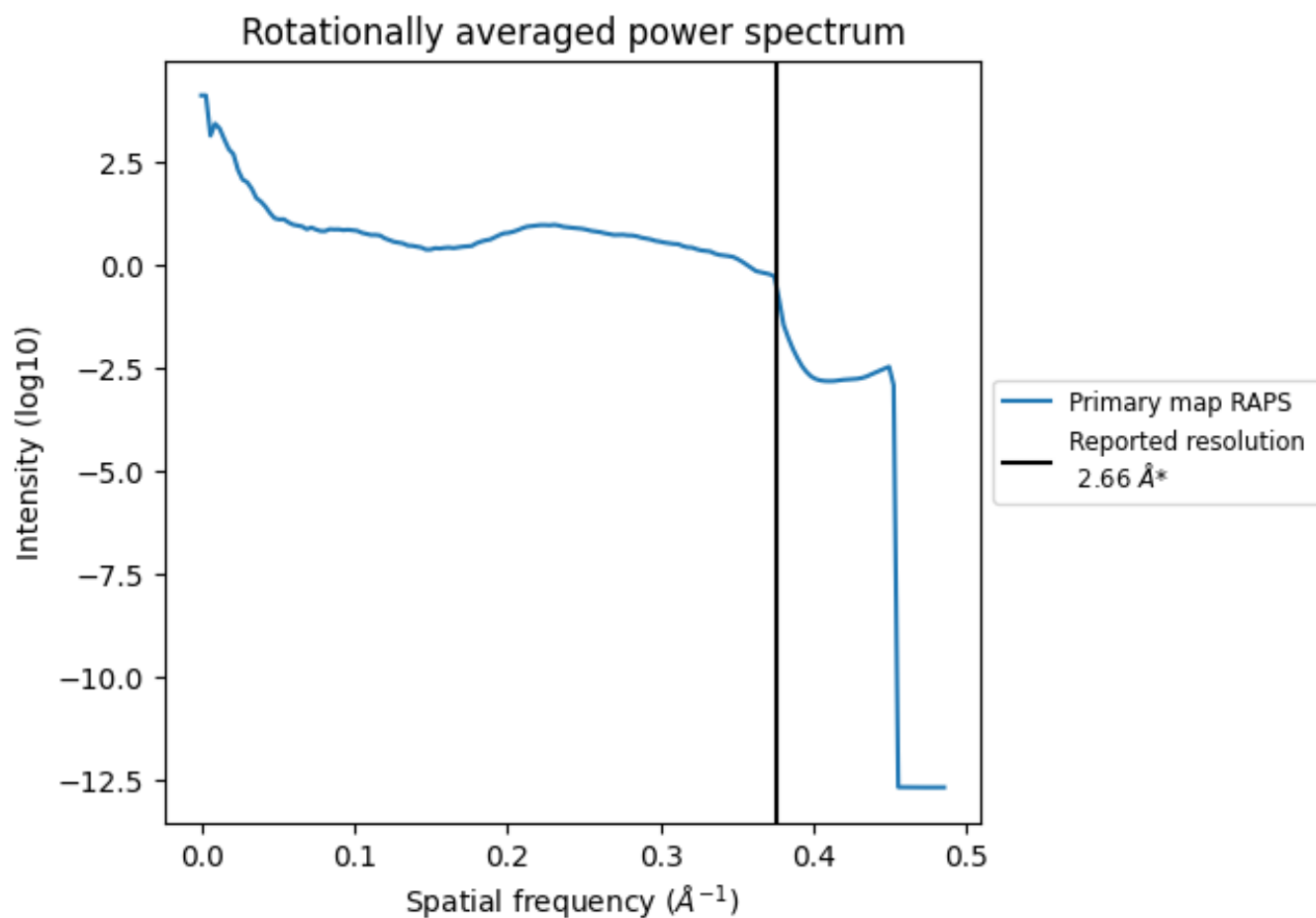
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 593 nm³; this corresponds to an approximate mass of 536 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 0.376 Å⁻¹

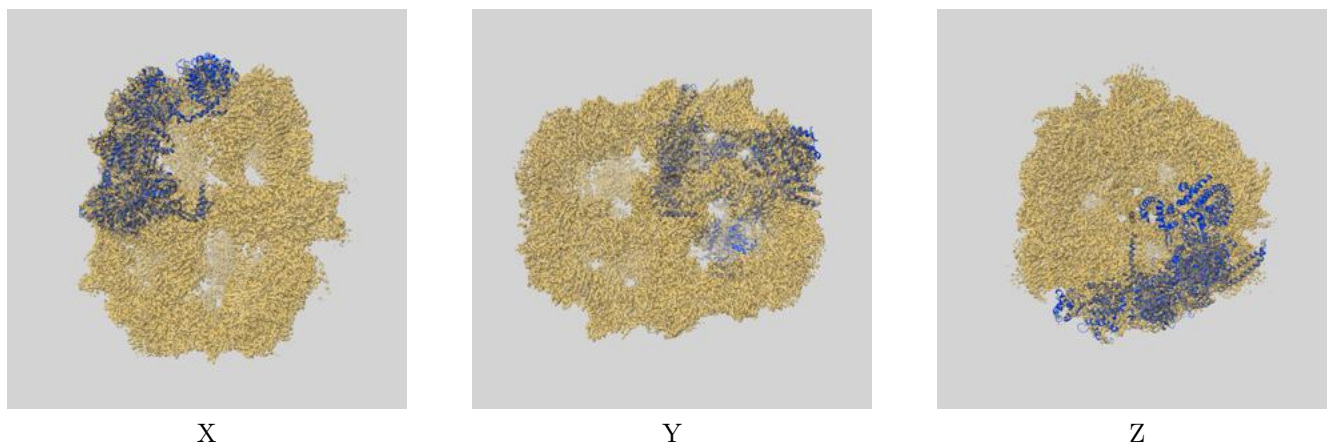
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

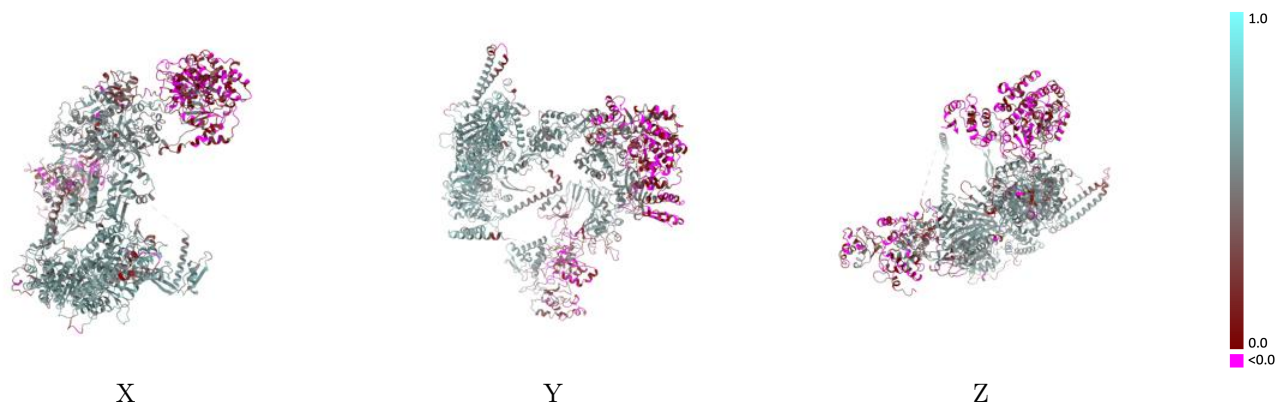
This section contains information regarding the fit between EMDB map EMD-26132 and PDB model 7TUI. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



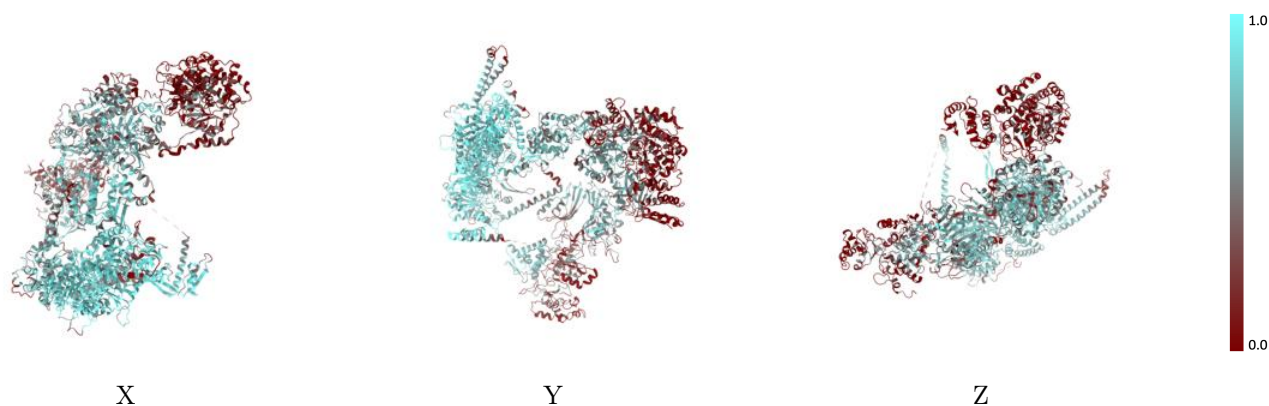
The images above show the 3D surface view of the map at the recommended contour level 0.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



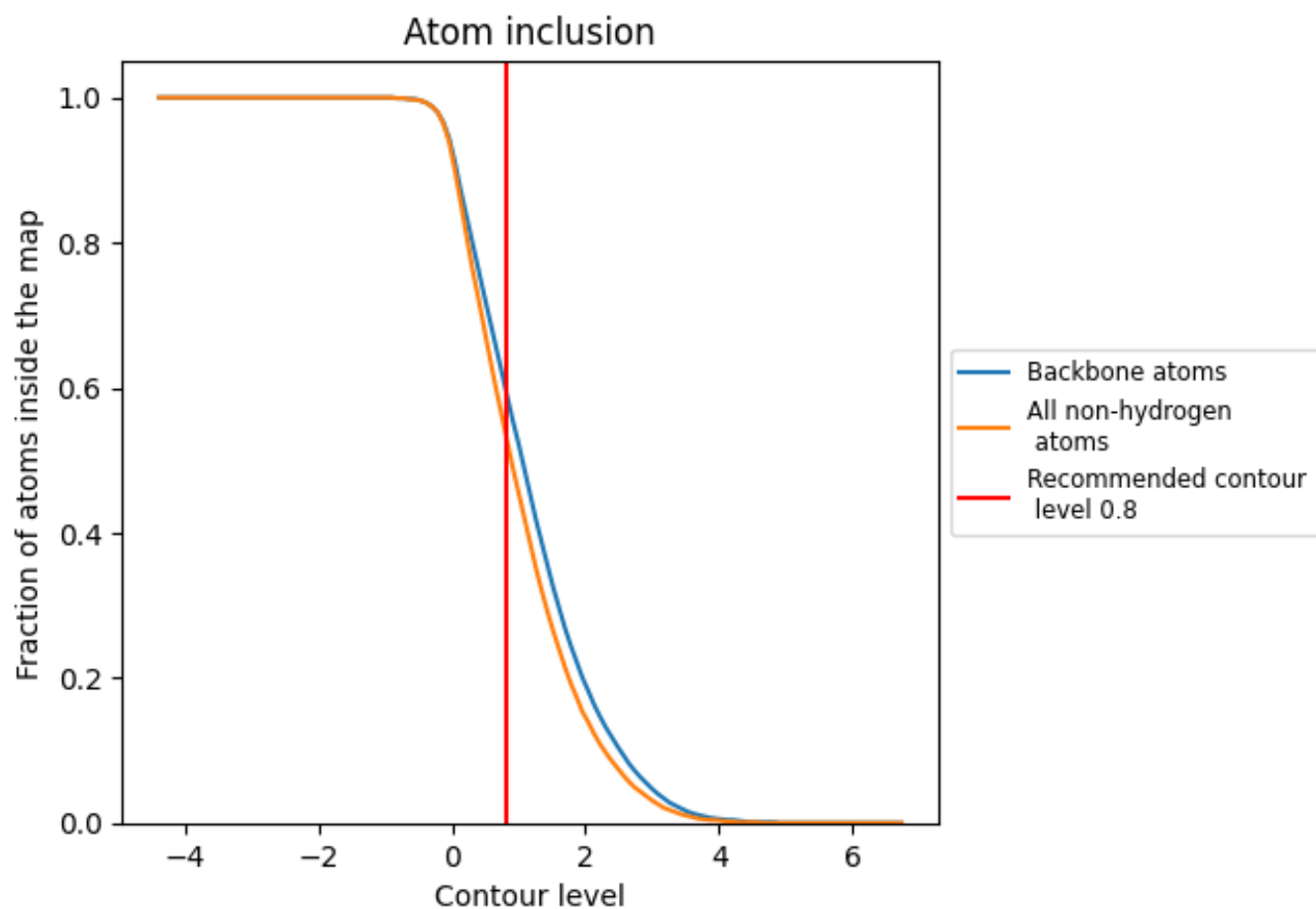
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.8).







9.4 Atom inclusion [i](#)



At the recommended contour level, 60% of all backbone atoms, 54% 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 (0.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5370	 0.4130
A	 0.7220	 0.5220
B	 0.4070	 0.3370

