



wwPDB EM Validation Summary Report ⓘ

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PDB ID : 8TQC / pdb_00008tqc
EMDB ID : EMD-41502
Title : Structure of the human CDK8 kinase module
Authors : Chen, S.F.; Chao, T.C.; Kim, H.J.; Tang, H.C.; Khadka, S.; Li, T.; Murakami, K.; Boyer, T.G.; Tsai, K.L.
Deposited on : 2023-08-06
Resolution : 3.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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<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
MolProbity : 4-5-2 with Phenix2.0
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

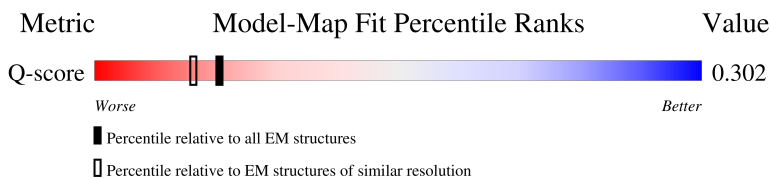
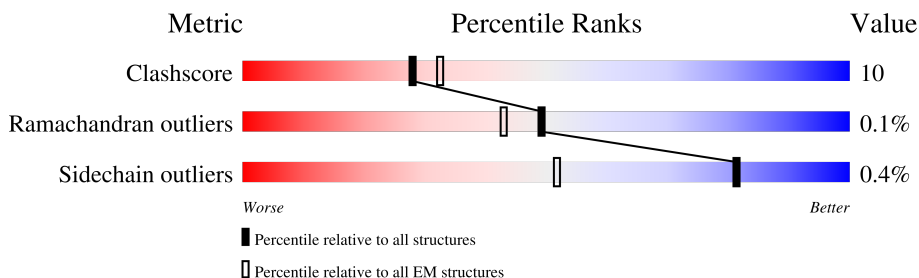
1 Overall quality at a glance

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	C	2177	
2	D	2174	
3	A	464	
4	B	283	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 23620 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 Mediator of RNA polymerase II transcription subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	1400	Total	C	N	O	S	0	0
			11147	7063	1947	2065	72		

- Molecule 2 is a protein called Mediator of RNA polymerase II transcription subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	969	Total	C	N	O	S	0	0
			7714	4945	1310	1393	66		

- Molecule 3 is a protein called Cyclin-dependent kinase 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	313	Total	C	N	O	S	0	0
			2561	1663	439	442	17		

- Molecule 4 is a protein called Cyclin-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	262	Total	C	N	O	S	1	0
			2196	1442	358	379	17		

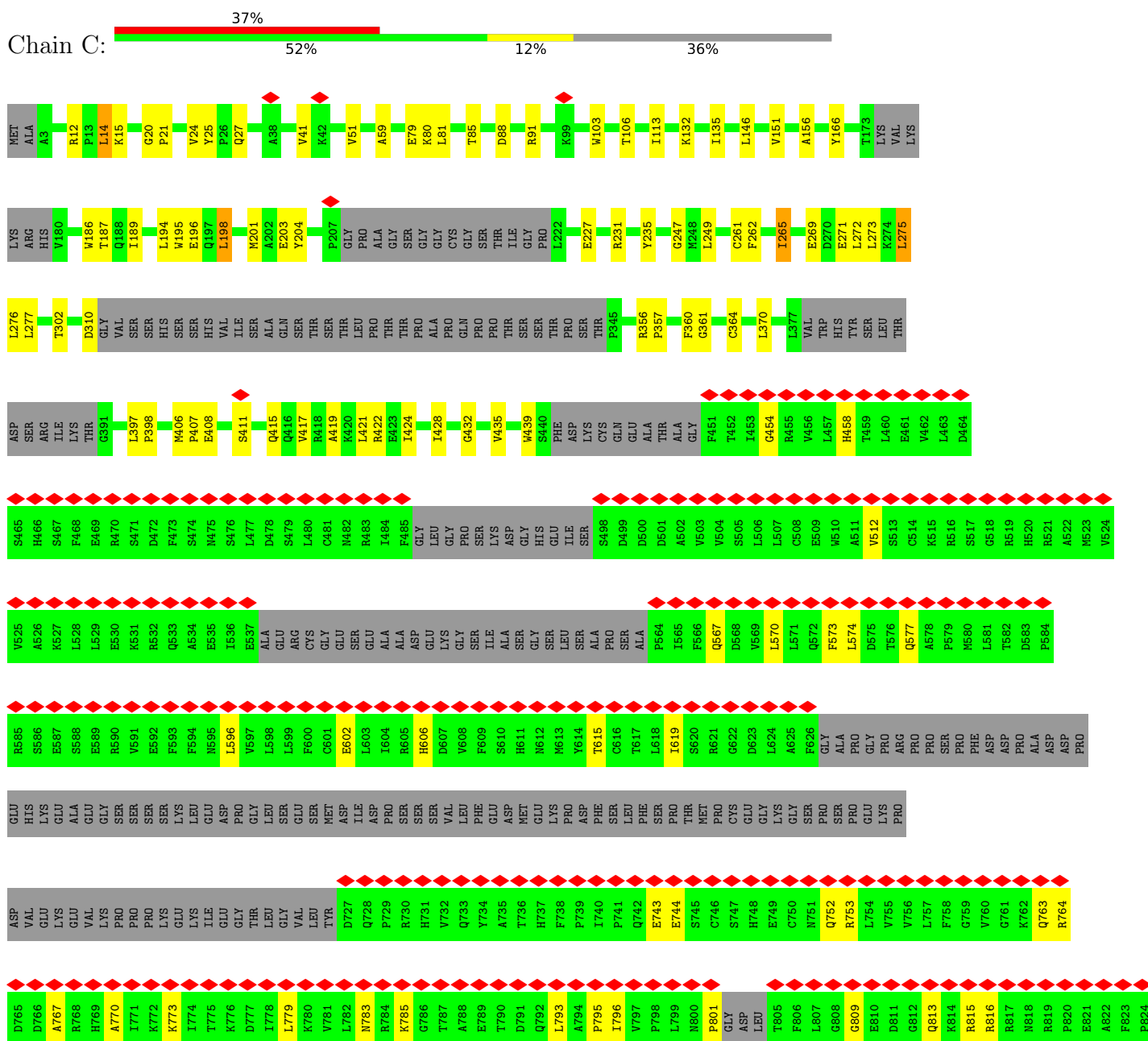
- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	C	1	Total	Zn	0
			1	1	
5	D	1	Total	Zn	0
			1	1	

3 Residue-property plots

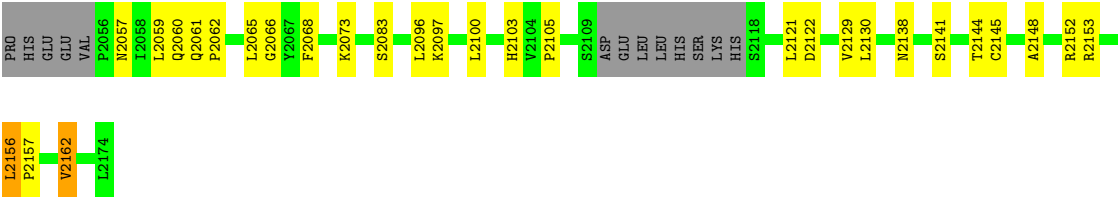
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Mediator of RNA polymerase II transcription subunit 12

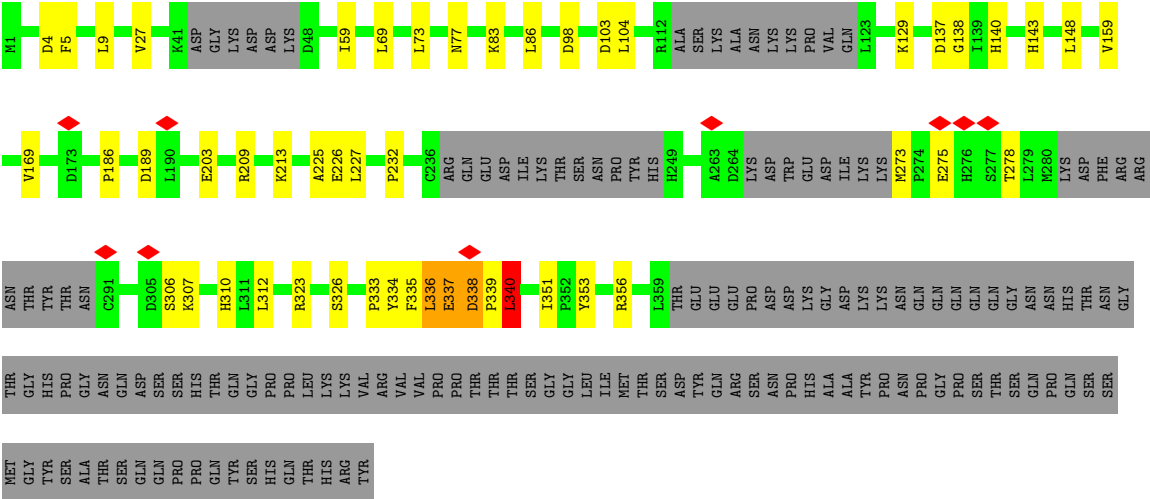


L1583	L1584	M1512	M1585	N1513	TRP	ARG	ARG	ASP	ASP	GLN	LEU	TYR	G1592	G1593	L1594	A1595	ALA	ASP	MET	SER	SER	ILE	SER	GLN	GLY	MET	GLU	GLU	G1541	G1458	S1459	S1460	S1461	R1462	K1463	K1464	E1465	S1550	T1551	Q1552	Q1553	E1556	L1560	L1561	L1562	E1563	I1564	I1565	V1570	D1571	R1636	Q1637	L1638	L1639	Q1644	C1651	E1652	F1657	P1653	T1580	T1581	V1582	K1434	L1435	P1436	T1437	S1438	V1439	Q1440	G1441	H1442	V1443	L1444	E1449	E1450	E1451	E1452	K1453	Q1454	Q1455	H1456	L1457	G1458	S1459	S1460	S1461	R1462	K1463	K1464	E1465	S1550	T1551	Q1552	Q1553	E1556	L1560	L1561	L1562	E1563	I1564	I1565	V1570	D1571	R1636	Q1637	L1638	L1639	Q1644	C1651	E1652	F1657	P1653	T1580	T1581	V1582	L1365	M1366	I1367	K1368	Q1369	T1370	P1371	M1372	M1373	M1374	M1375	M1376	S1377	L1378	L1379	E1388	V1389	F1390	Q1391	Q1392	S1393	A1394	E1395	T1396	GLY	SER	SER	GLY	SER	ALA	ALA	ASN	MET	SER	PRO	SER	SER	LYS	S1419	L1420	E1421	R1422	S1423	G1424	V1425	W1426	L1427	V1428	A1429	P1430	L1335	L1336	L1337	L1338	L1339	L1340	L1341	L1342	L1343	L1344	K1345	R1346	I1347	L1348	Q1349	M1350	L1351	D1352	Q1353	W1354	T1355	M1356	R1357	Q1358	S1359	S1360	L1361	E1362	L1363	Q1364	M1305	D1306	L1307	Q1308	D1309	P1310	V1311	L1312	S1313	S1314	A1315	Q1316	A1317	Q1318	R1319	L1320	M1321	Q1322	L1323	I1324	Y1325	P1326	P1327	H1328	R1329	L1330	L1331	D1332	M1333	E1334	D1335	G1336	E1337	M1338	P1339	Q1340	R1341	Q1342	R1343	I1344	K1345	R1346	I1347	L1348	Q1349	M1350	L1351	D1352	Q1353	W1354	T1355	M1356	R1357	Q1358	S1359	S1360	L1361	E1362	L1363	Q1364	GLY	THR	GLU	LEU	PRO	GLY	ASP	SER	ASN	LYS	P1195	T1196	V1197	I1198	I1199	R1200	S1201	S1202	C1203	D1204	R1205	H1206	L1207	L1208	A1209	A1210	S1211	Q1212	N1213	R1214	I1215	V1216	D1217	G1218	A1219	V1220	F1221	A1222	V1223	L1224	K1225	A1226	V1227	F1228	V1229	L1230	G1231	D1232	ALA	GLU	LEU	LYS	GLY	SER	GLY	PHE	THR	VAL	THR	L1179	F1180	K1181	THR	PRO	GLN	L1125	D1126	S1127	L1128	A1129	T1130	F1131	V1132	L1133	T1134	L1135	T1136	L1137	R1138	R1139	Q1139	C1140	L1141	L1142	L1143	E1144	D1145	L1146	T1147	R1148	C1149	A1150	A1151	T1152	P1153	S1154	L1155	L1156	N1157	A1158	A1159	C1160	S1161	E1162	Q1163	D1164	S1165	E1166	P1167	G1168	A1169	R1170	L1171	T1172	L1173	R1174	T1175	L1176	L1177	H1178	L1179	F1180	K1181	THR	PRO	GLN	F1124	S1123	L1122	D1121	S1120	V1119	L1118	V1117	M1116	C1115	L1114	D1113	L1112	M1111	R1110	F1109	G1108	T1107	E1106	M1105	N1104	S1103	L1043	S1044	E1045	N1046	P1047	G1048	F999	R1049	S1052	Y1051	R1050	C1055	F996	C997	S998	L1053	M1059	H1060	V1061	K1001	N1002	T1003	G1064	V1063	L1062	S1123	L1122	D1121	S1120	V1119	L1118	V1117	M1116	C1115	L1114	D1113	L1112	M1111	R1110	F1109	G1108	T1107	E1106	M1105	N1104	S1103	L1043	S1044	E1045	N1046	P1047	G1048	F999	R1049	S1052	Y1051	R1050	C1055	F996	C997	S998	L1053	M1059	H1060	V1061	K1001	N1002	T1003	G1064	V1063	L1062	S1123	L1122	D1121	S1120	V1119	L1118	V1117	M1116	C1115	L1114	D1113	L1112	M1111	R1110	F1109	G1108	T1107	E1106	M1105	N1104	S1103	L1043	S1044	E1045	N1046	P1047	G1048	F999	R1049	S1052	Y1051	R1050	C1055	F996	C997	S998	L1053	M1059	H1060	V1061	K1001	N1002	T1003	G1064	V1063	L1062	S1123	L1122	D1121	S1120	V1119	L1118	V1117	M1116	C1115	L1114	D1113	L1112	M1111	R1110	F1109	G1108	T1107	E1106	M1105	N1104	S1103	L1043	S1044	E1045	N1046	P1047	G1048	F999	R1049	S1052	Y1051	R1050	C1055	F996	C997	S998	L1053	M1059	H1060	V1061	K1001	N1002	T1003	G1064	V1063	L1062	S1123	L1122	D1121	S1120	V1119	L1118	V1117	M1116	C1115	L1114	D1113	L1112	M1111	R1110	F1109	G1108	T1107	E1106	M1105	N1104	S1103	L1043	S1044	E1045	N1046	P1047	G1048	F999	R1049	S1052	Y1051	R1050	C1055	F996	C997	S998	L1053	M1059	H1060	V1061	K1001	N1002	T1003	G1064	V1063	L1062	S1123	L1122	D1121	S1120	V1119	L1118	V1117	M1116	C1115	L1114	D1113	L1112	M1111	R1110	F1109	G1108	T1107	E1106	M1105	N1104	S1103	L1043	S1044	E1045	N1046	P1047	G1048	F999	R1049	S1052	Y1051	R1050	C1055	F996	C997	S998	L1053	M1059	H1060	V1061	K1001	N1002	T1003	G1064	V1063	L1062	S1123	L1122	D1121	S1120	V1119	L1118	V1117	M1116	C1115	L1114	D1113	L1112	M1111	R1110	F1109	G1108	T1107	E1106	M1105	N1104	S1103	L1043	S1044	E1045	N1046	P1047	G1048	F999	R1049	S1052	Y1051	R1050	C1055	F996	C997	S998	L1053	M1059	H1060	V1061	K1001	N1002	T1003	G1064	V1063	L1062	S1123	L1122	D1121	S1120	V1119	L1118	V1117	M1116	C1115	L1114	D1113	L1112	M1111	R1110	F1109	G1108	T1107	E1106	M1105	N1104	S1103	L1043	S1044	E1045	N1046	P1047	G1048	F999	R1049	S1052	Y1051	R1050	C1055	F996	C997	S998	L1053	M1059	H1060	V1061	K1001	N1002	T1003	G1064	V1063	L1062	S1123	L1122	D1121	S1120	V1119	L1118	V1117	M1116	C1115	L1114	D1113	L1112	M1111	R1110	F1109	G1108	T1107	E1106	M1105	N1104	S1103	L1043	S1044	E1045	N1046	P1047	G1048	F999	R1049	S1052	Y1051	R1050	C1055	F996	C997	S998	L1053	M1059	H1060	V1061	K1001	N1002	T1003	G1064	V1063	L1062	S1123	L1122	D1121	S1120	V1119	L1118	V1117	M1116	C1115	L1114	D1113	L1112	M1111	R1110	F1109	G1108	T1107	E1106	M1105	N1104	S1103	L1043	S1044	E1045	N1046	P1047	G1048	F999	R1049	S1052	Y1051	R1050	C1055	F996	C997	S998	L1053	M1059	H1060	V1061	K1001	N1002	T1003	G1064	V1063	L1062	S1123	L1122	D1121	S1120	V1119	L1118	V1117	M1116	C1115	L1114	D1113	L1112	M1111	R1110	F1109	G1108	T1107	E1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● Molecule 3: Cyclin-dependent kinase 8



● Molecule 4: Cyclin-C



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	122015	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 ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.098	Depositor
Minimum map value	-0.047	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0115	Depositor
Map size (Å)	376.67517, 376.67517, 376.67517	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0701, 1.0701, 1.0701	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	C	0.16	0/11361	0.42	2/15364 (0.0%)
2	D	0.13	0/7895	0.34	2/10703 (0.0%)
3	A	0.11	0/2627	0.34	2/3542 (0.1%)
4	B	0.11	0/2253	0.30	0/3051
All	All	0.14	0/24136	0.37	6/32660 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	20	GLY	CA-C-N	8.33	125.74	119.66
1	C	20	GLY	C-N-CA	8.33	125.74	119.66
3	A	340	LEU	CA-C-N	7.05	127.08	119.89
3	A	340	LEU	C-N-CA	7.05	127.08	119.89
2	D	1365	SER	N-CA-C	6.00	119.84	111.74

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	C	11147	0	11175	252	0
2	D	7714	0	7627	144	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	2561	0	2578	51	0
4	B	2196	0	2233	52	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
All	All	23620	0	23613	453	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 10.

The worst 5 of 453 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:338:ASP:HB3	3:A:339:PRO:CD	1.56	1.34
3:A:333:PRO:HA	3:A:336:LEU:HD23	1.26	1.15
3:A:338:ASP:CB	3:A:339:PRO:HD2	1.74	1.14
3:A:338:ASP:CB	3:A:339:PRO:CD	2.28	1.09
1:C:1616:LEU:O	1:C:1620:LEU:HG	1.55	1.07

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	C	1366/2177 (63%)	1320 (97%)	46 (3%)	0	100	100
2	D	923/2174 (42%)	884 (96%)	38 (4%)	1 (0%)	48	79
3	A	301/464 (65%)	294 (98%)	6 (2%)	1 (0%)	36	67
4	B	261/283 (92%)	258 (99%)	3 (1%)	0	100	100
All	All	2851/5098 (56%)	2756 (97%)	93 (3%)	2 (0%)	49	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	338	ASP
2	D	2156	LEU

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	1247/1916 (65%)	1242 (100%)	5 (0%)	84	83
2	D	869/1918 (45%)	867 (100%)	2 (0%)	87	87
3	A	277/412 (67%)	274 (99%)	3 (1%)	65	73
4	B	241/258 (93%)	241 (100%)	0	100	100
All	All	2634/4504 (58%)	2624 (100%)	10 (0%)	81	83

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	336	LEU
3	A	337	GLU
3	A	340	LEU
1	C	275	LEU
1	C	1585	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1575	ASN
4	B	49	GLN
1	C	1729	HIS
2	D	2138	ASN
1	C	1644	GLN

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 2 ligands modelled in this entry, 2 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.

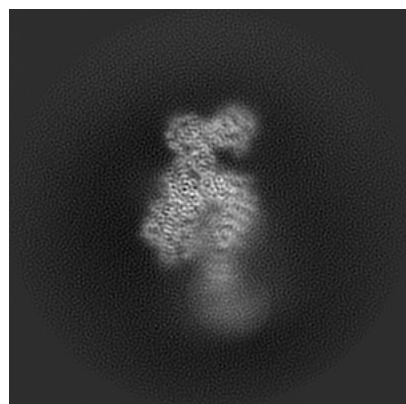
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41502. These allow visual inspection of the internal detail of the map and identification of artifacts.

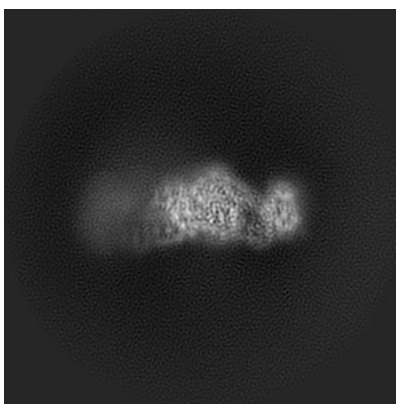
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

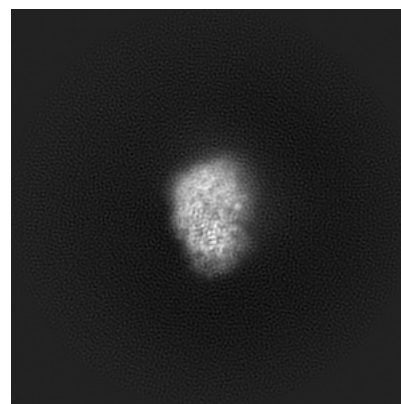
6.1.1 Primary map



X

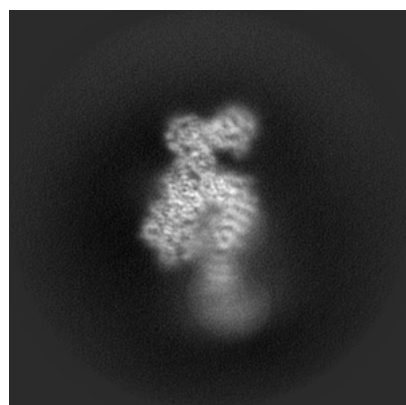


Y

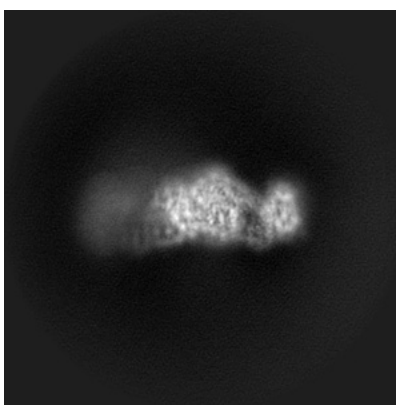


Z

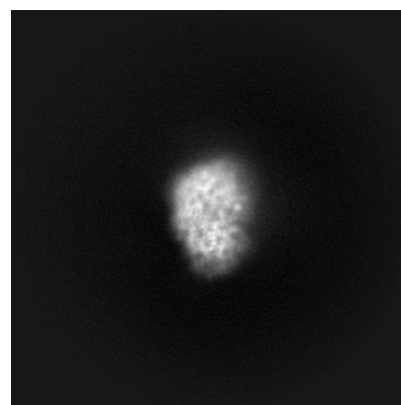
6.1.2 Raw map



X



Y

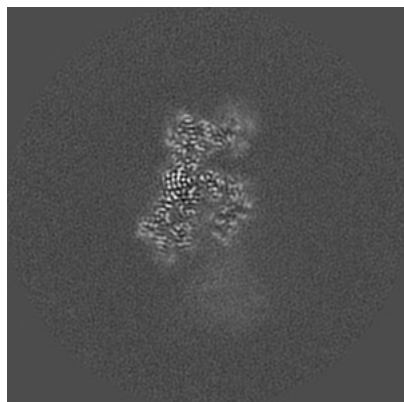


Z

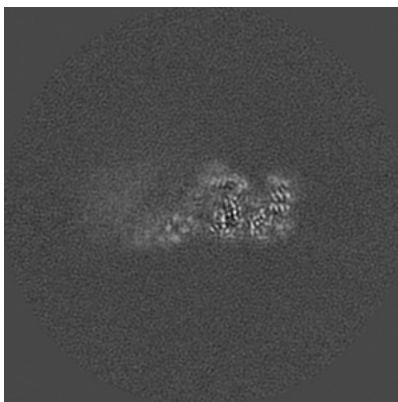
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

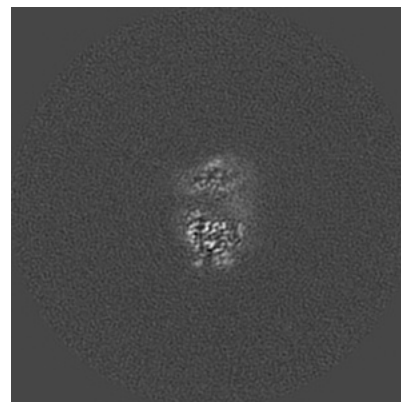
6.2.1 Primary map



X Index: 176

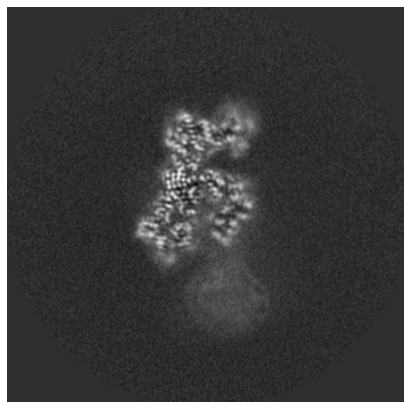


Y Index: 176

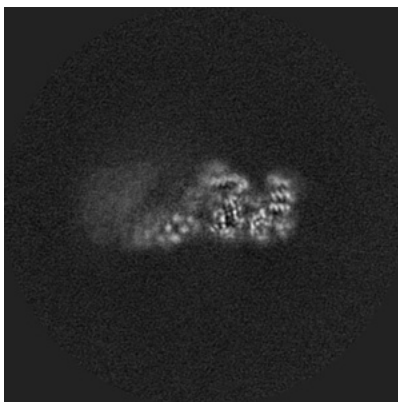


Z Index: 176

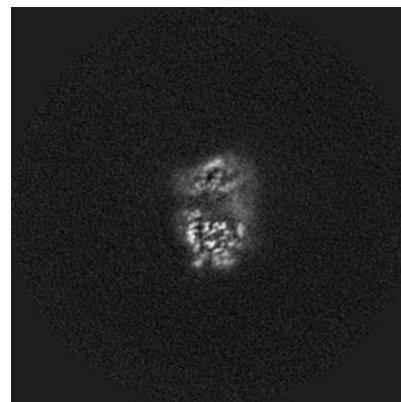
6.2.2 Raw map



X Index: 176



Y Index: 176

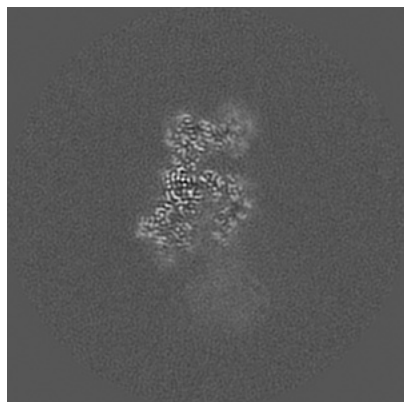


Z Index: 176

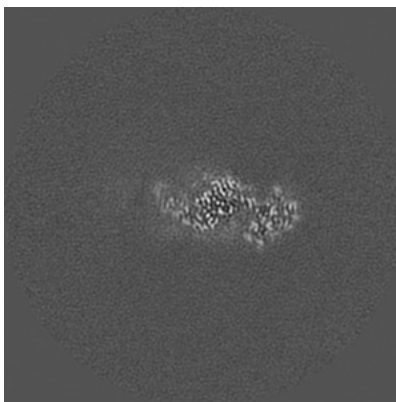
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

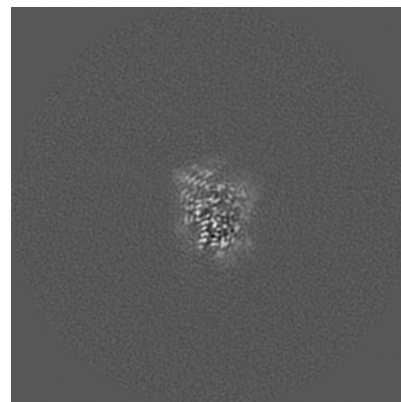
6.3.1 Primary map



X Index: 175

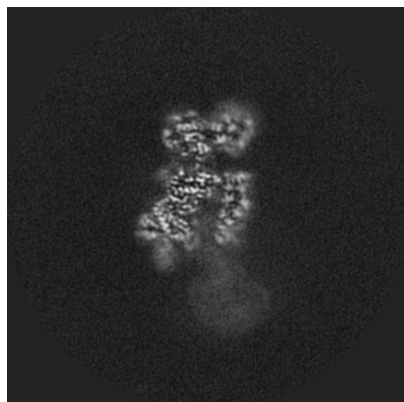


Y Index: 158

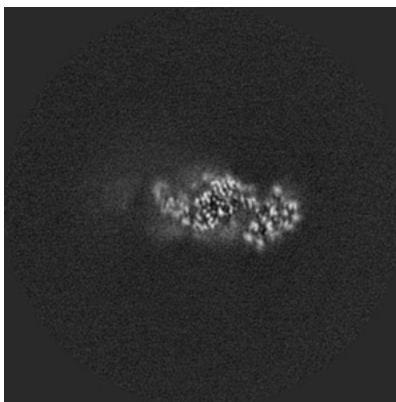


Z Index: 192

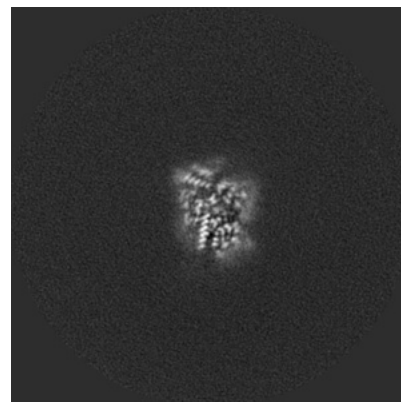
6.3.2 Raw map



X Index: 171



Y Index: 158

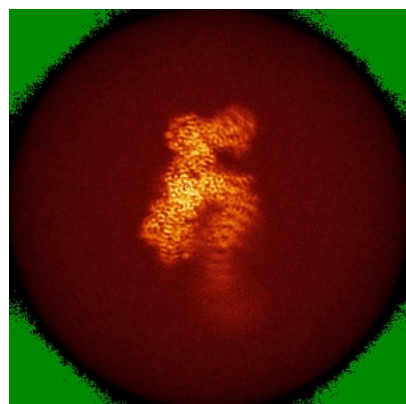


Z Index: 191

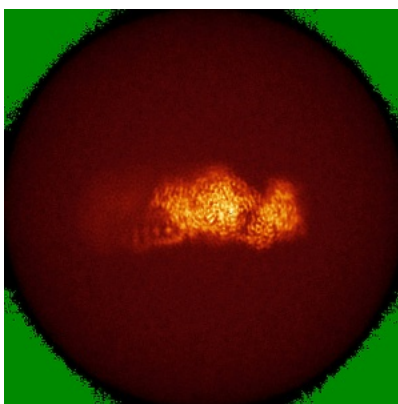
The images above show the largest variance slices of the map in three orthogonal directions.

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

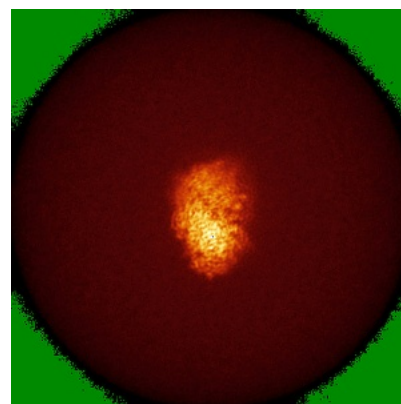
6.4.1 Primary map



X



Y

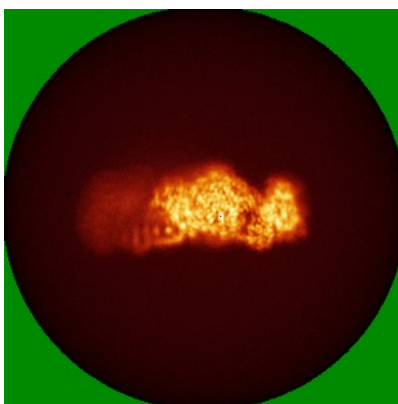


Z

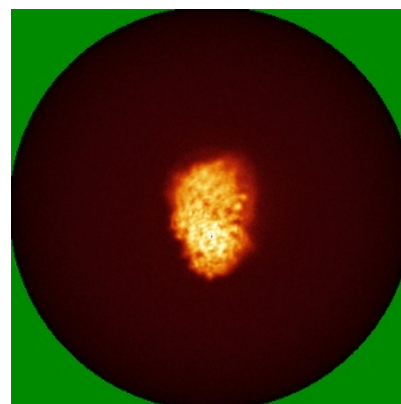
6.4.2 Raw map



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



X



Y



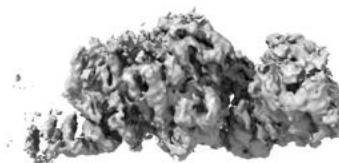
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0115. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

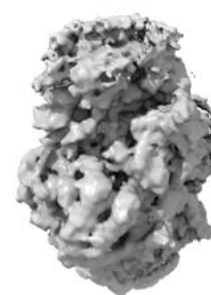
6.5.2 Raw map



X



Y



Z

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.

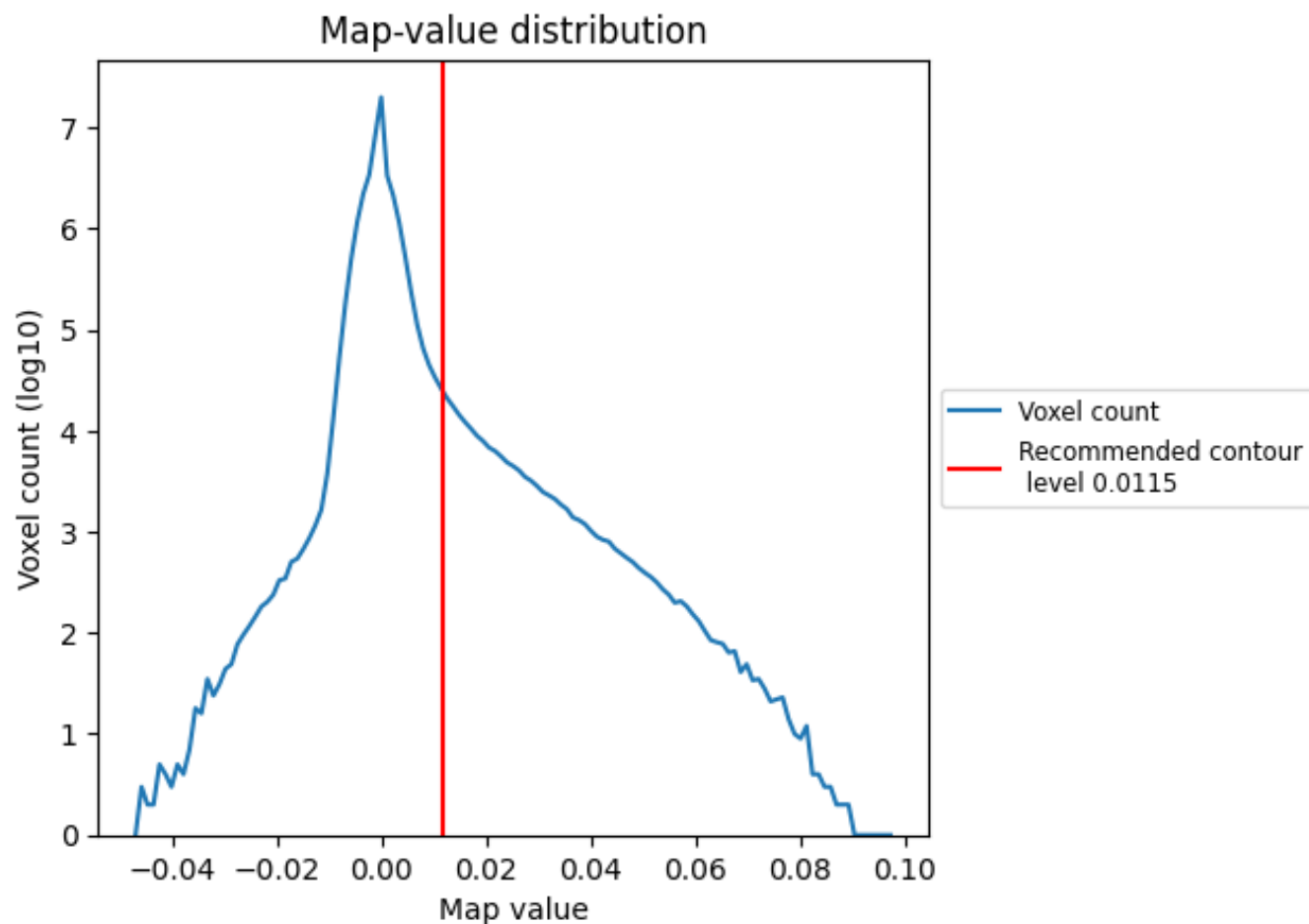
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

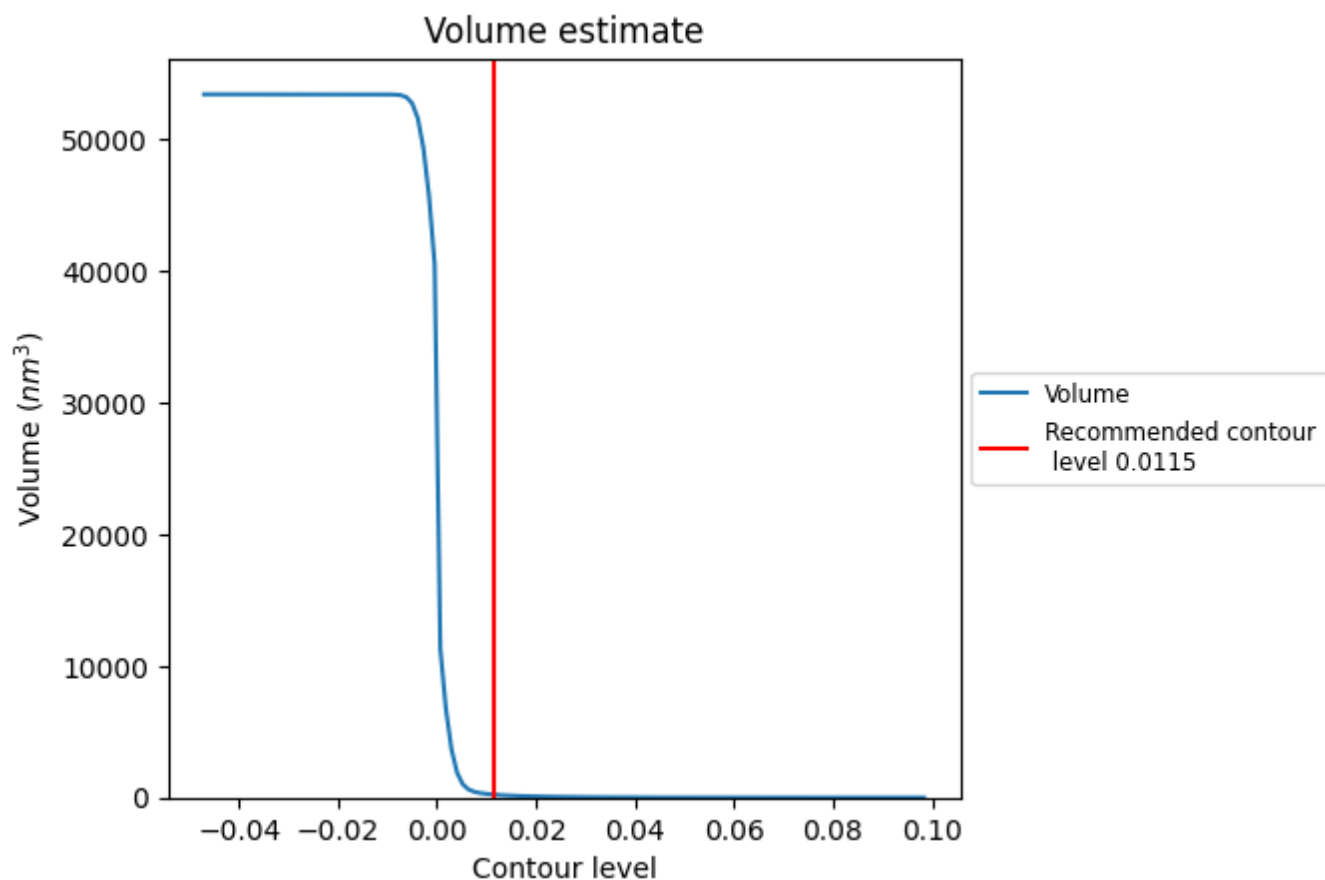
This section contains the results of statistical analysis of the map.

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.

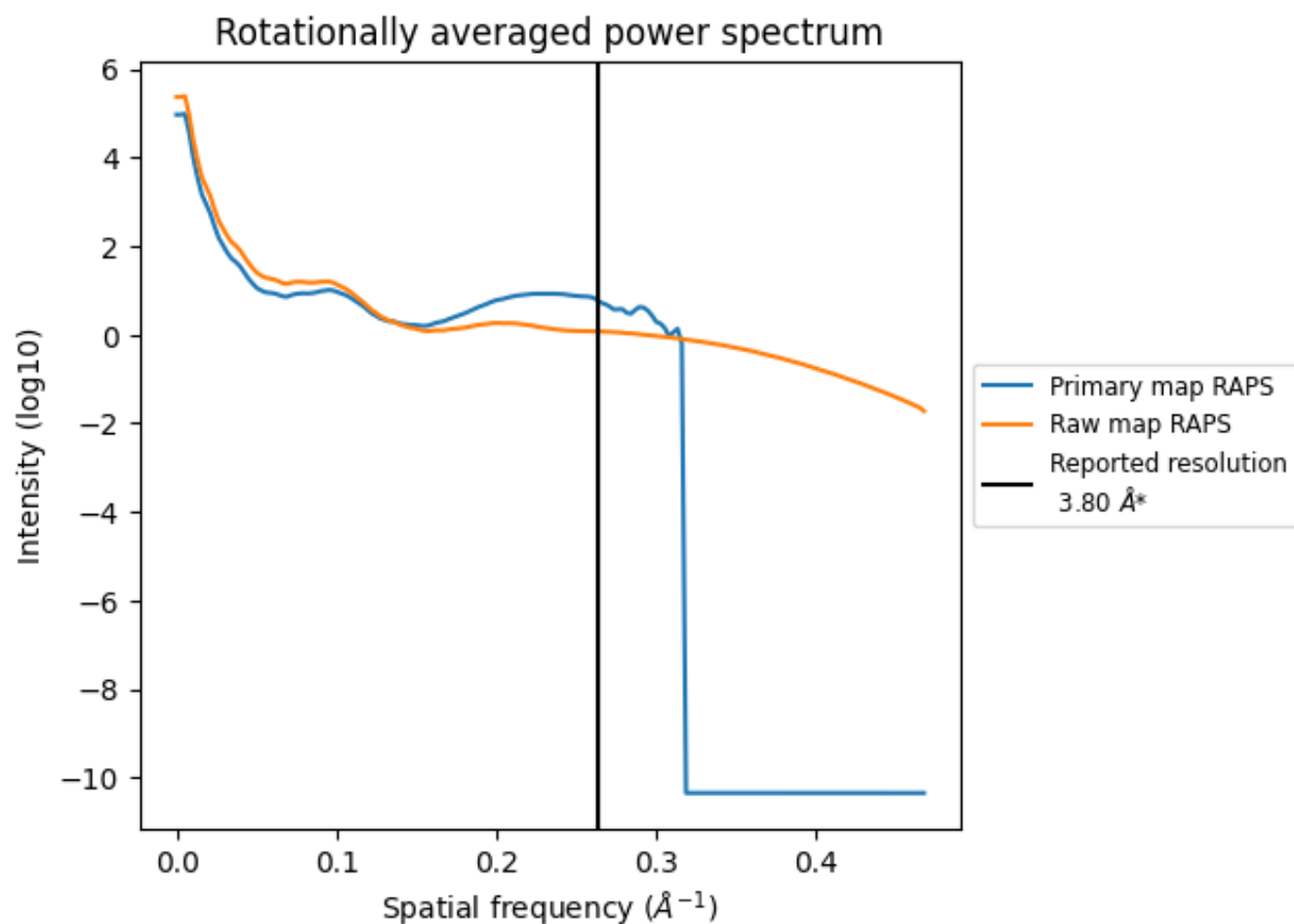
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 222 nm^3 ; this corresponds to an approximate mass of 201 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 ⓘ

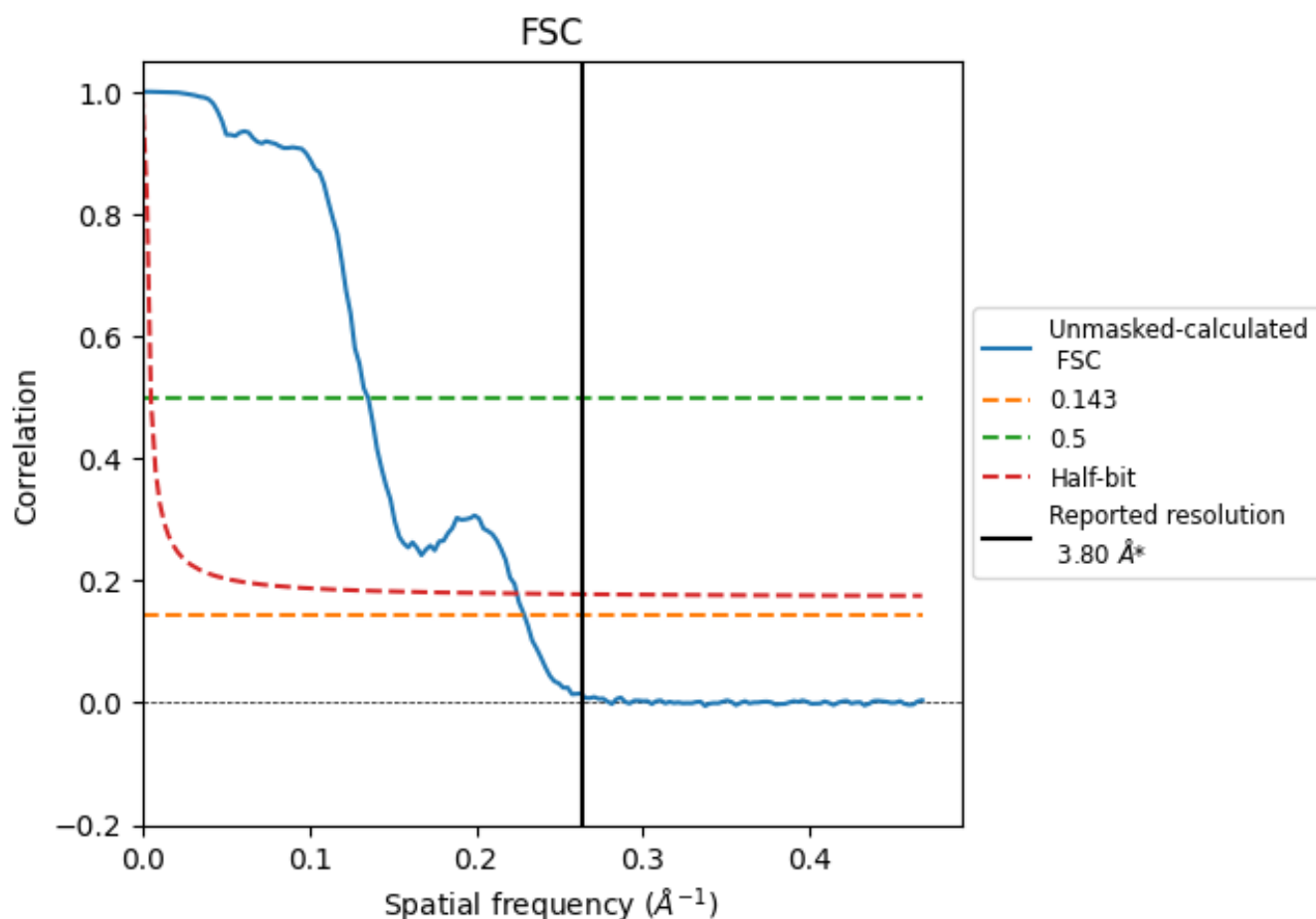


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

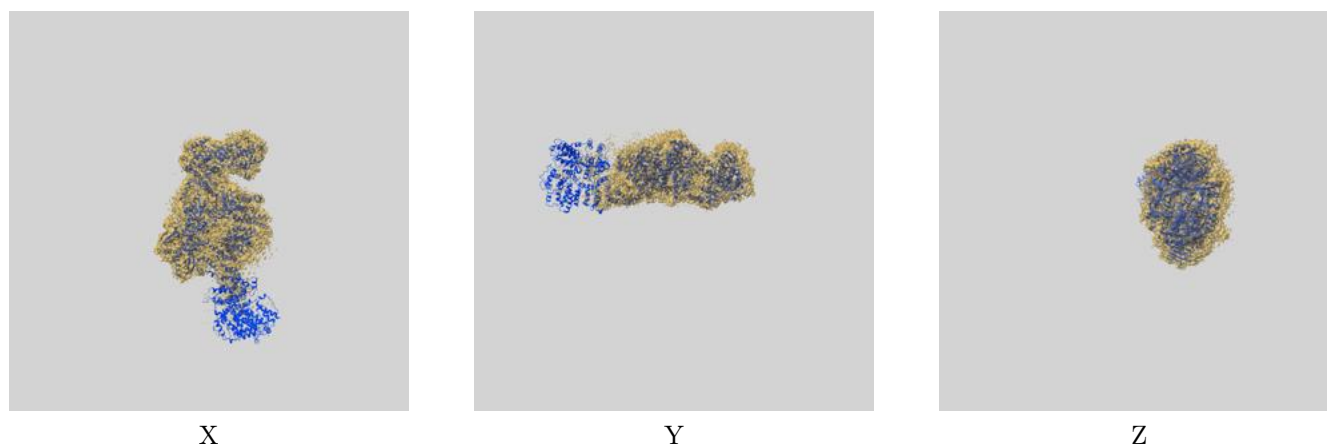
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.37	7.40	4.46

*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 4.37 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

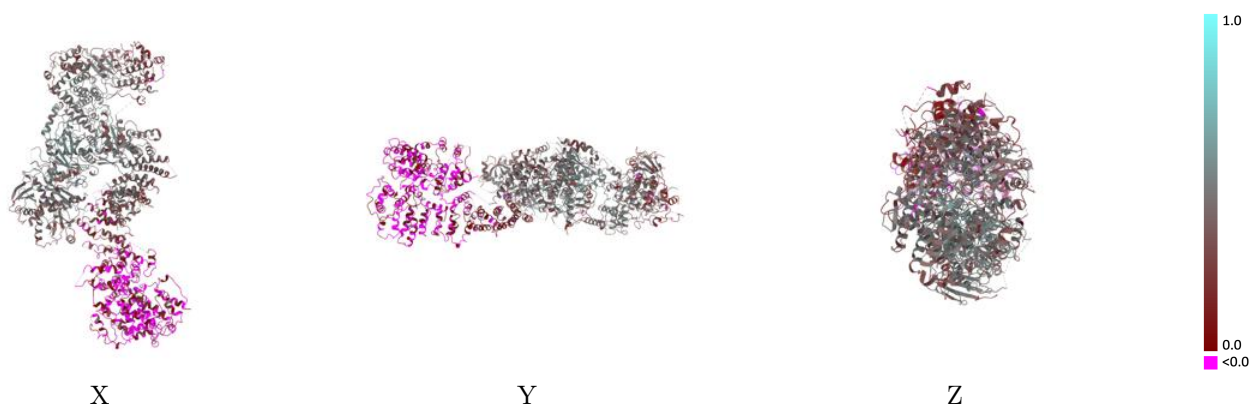
This section contains information regarding the fit between EMDB map EMD-41502 and PDB model 8TQC. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



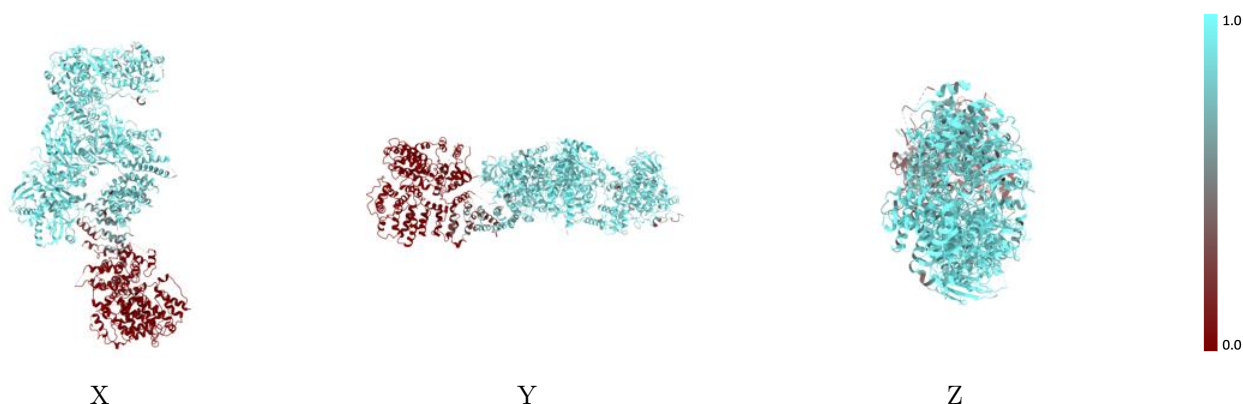
The images above show the 3D surface view of the map at the recommended contour level 0.0115 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



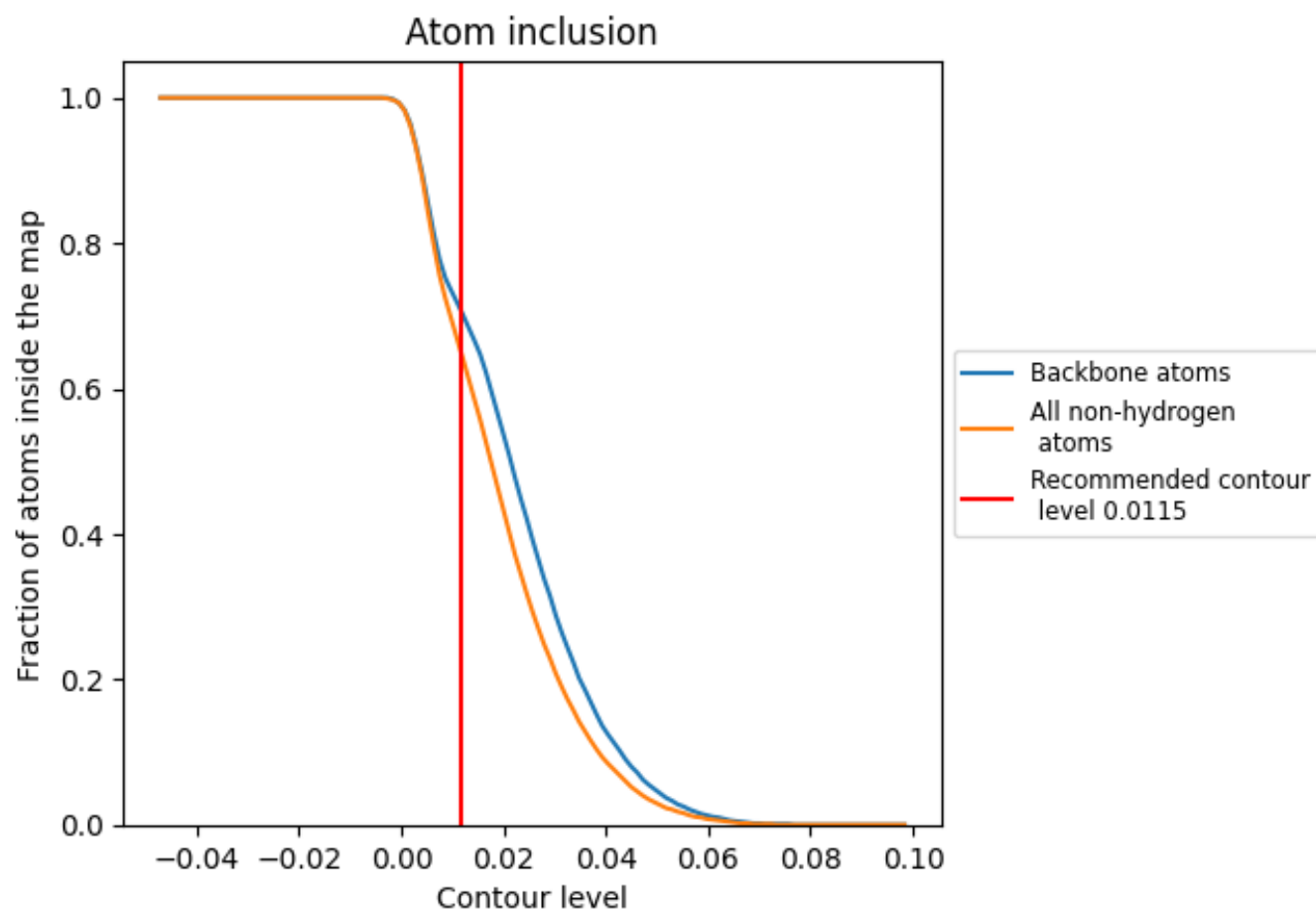
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0115).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 65% 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 (0.0115) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6540	0.3020
A	0.8470	0.3370
B	0.8980	0.4320
C	0.3800	0.1570
D	0.9170	0.4620

