



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2025 – 02:24 am BST

PDB ID : 7Z12 / pdb_00007z12
EMDB ID : EMD-14438
Title : VAR2 complex with PAM1.4
Authors : Raghavan, S.S.R.; Wang, K.T.
Deposited on : 2022-02-24
Resolution : 3.00 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

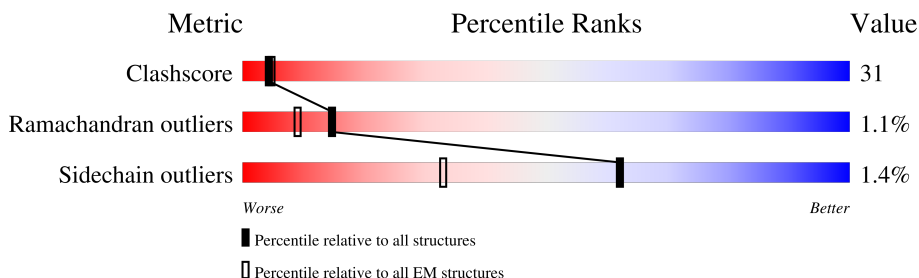
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	B	472	
2	C	233	
3	A	2040	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18352 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 PAM1.4, Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	221	Total	C	N	O	S	0	0
			1650	1042	283	319	6		

- Molecule 2 is a protein called PAM1.4, light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	212	Total	C	N	O	S	0	0
			1631	1021	279	326	5		

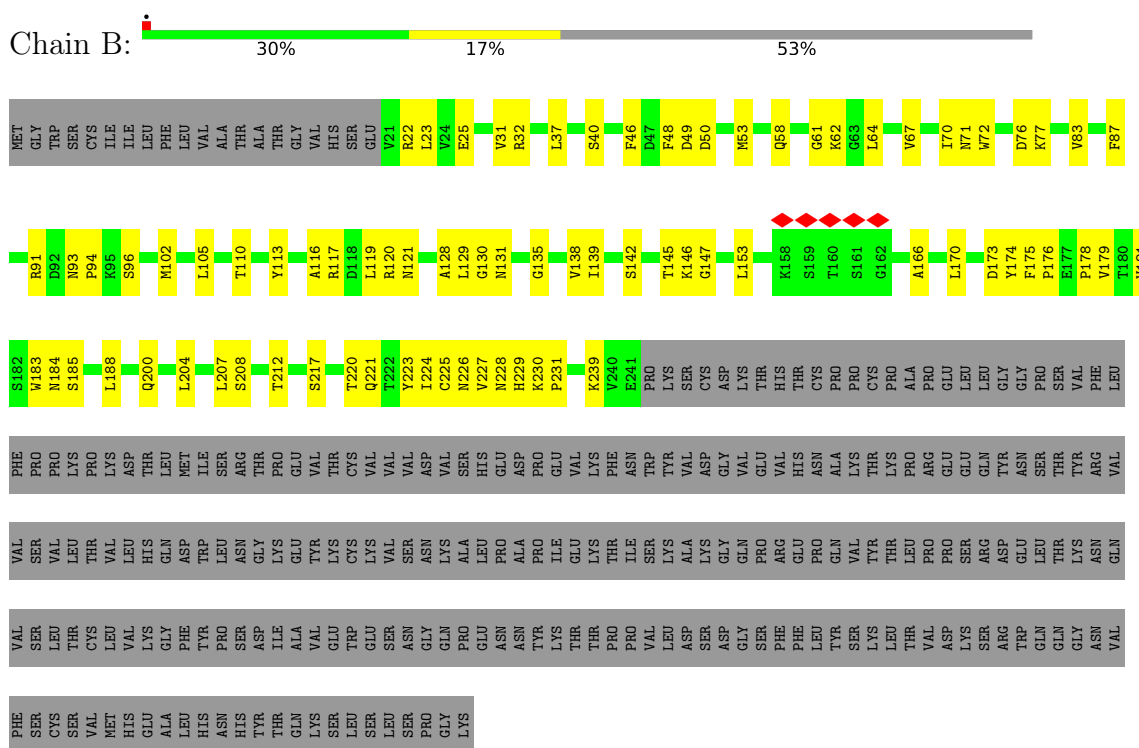
- Molecule 3 is a protein called VAR2CSA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	1853	Total	C	N	O	S	0	0
			15071	9402	2597	2973	99		

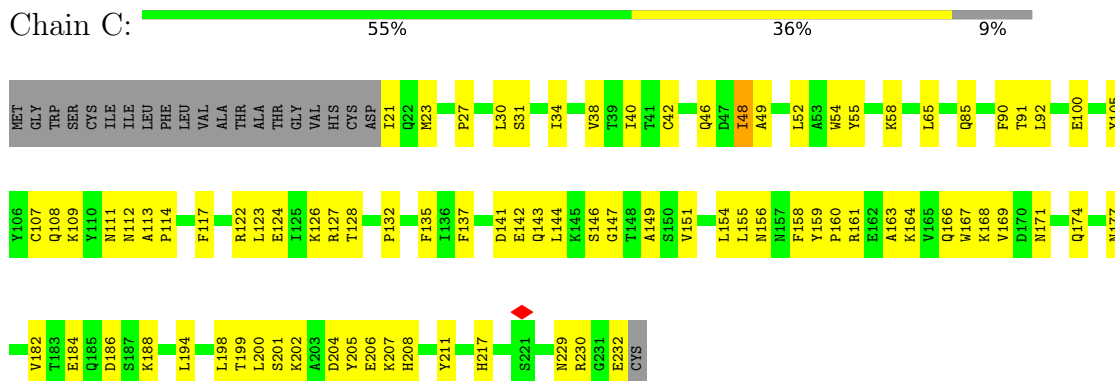
3 Residue-property plots

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.

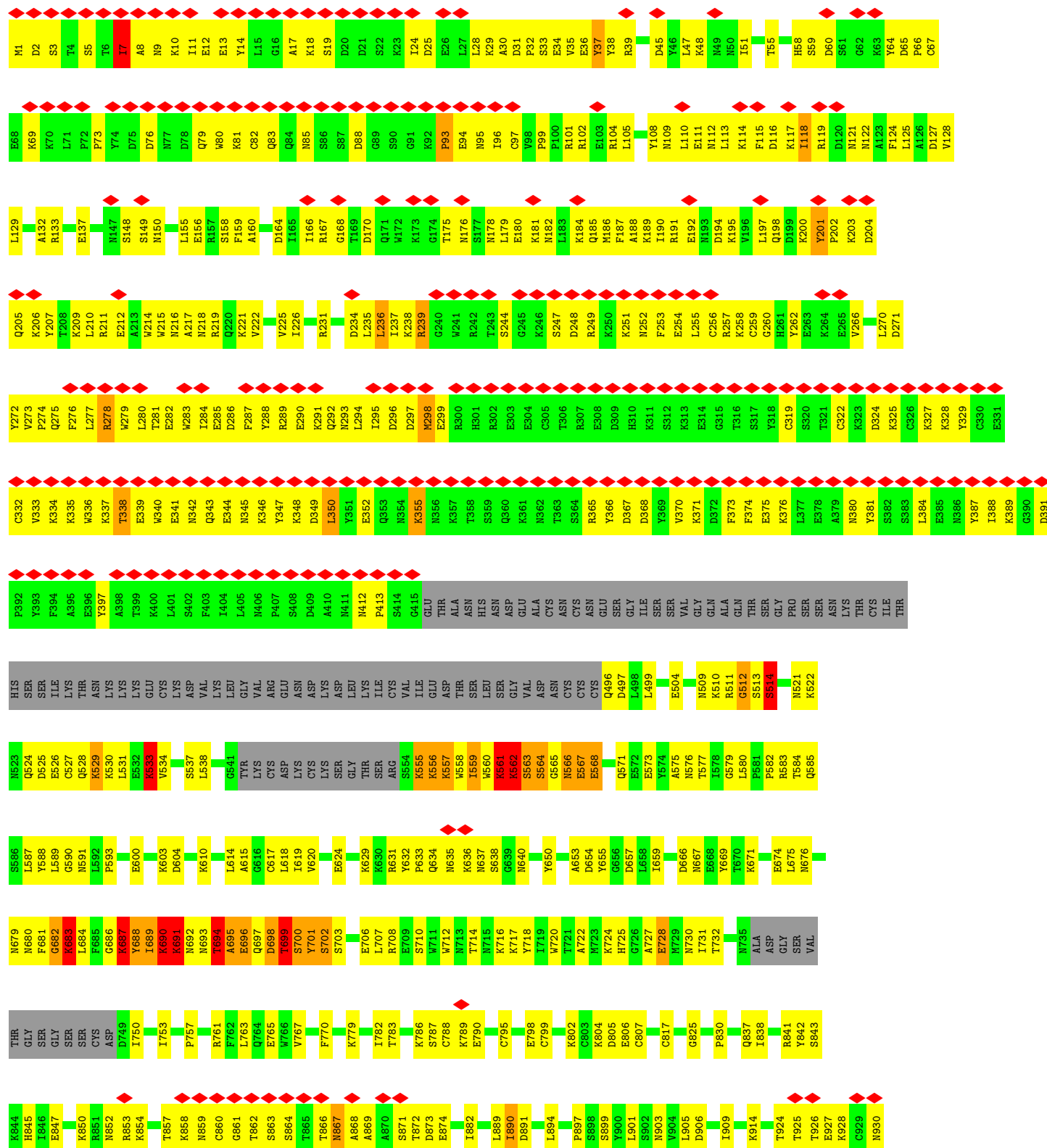
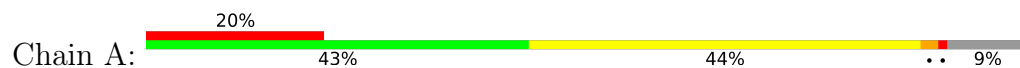
• Molecule 1: PAM1.4, Heavy Chain



• Molecule 2: PAM1.4, light Chain



● Molecule 3: VAR2CSA



R1853	T1755	L1655	N1556	R1465	V1394	G1332	L1271	E1206	N1130	ASP	G996	K931
I1854	I1756	E1656	D1557	L1466	G1395	K1333	L1272	S1207	K1131	GLU	Y997	E932
E1855	Q1757	T1657	N1558	L1467	G1396	N1334	C1273	T1208	G1132	THR	K998	R933
M1859	Q1758	I1660	I1559	Y1468	S1396	D1335	G1274	D1209	Q1134	LVS	N999	D934
Y1863	W1761	I1661	E1560	G1470	T1397	P1336	E1275	T1210	N1135	VAL	D1000	K935
D1762	D1762	A1662	N1471	N1471	E1399	L1339	L1277	N1211	K1136	ARG	N1001	S936
A1763	A1763	E1663	I1472	I1472	N1400	P1340	W1278	T1212	K1137	GLY	E1002	K937
W1764	M1763	E1664	N1473	N1473	V1401	K1341	D1279	N1213	V1138	GLY	E1003	S938
Q1765	Q1765	E1665	A1475	A1475	N1402	G1342	K1280	N1214	W1139	THR	C1005	Q939
Y1768	V1768	Y1667	C1476	C1476	A1403	F1343	S1281	S1215	S1140	GLU	K1006	S940
K1769	Y1770	L1668	T1477	T1477	W1404	C1344	Y1282	E1216	L1441	ASP	Y1007	S941
Y1770	Q1572	I1573	I1478	I1478	W1405	E1345	Y1283	E1217	K1138	GLY	N1008	D942
Q1578	Q1578	Q1578	N1479	N1479	G1407	H1346	Y1284	T1217	N1142	ASN	G1009	T943
Y1581	Y1581	K1481	K1480	K1480	I1408	Q1347	R1285	S1218	F1146	ASN	V1010	L944
K1583	K1583	N1482	E1409	E1409	S1350	Q1348	C1219	C1219	F1147	ASN	D1011	L944
Y1584	Y1584	E1483	R1410	R1410	F1351	N1352	D1220	D1220	S1148	THR	V1012	V945
E1588	E1588	K1484	E1411	E1411	W1413	D1353	L1221	N1222	W1150	GLN	T1015	V946
K1589	K1589	K1485	D1414	D1414	W1415	Y1354	N1289	A1223	I1154	GLY	T1016	V947
K1590	K1590	S1489	A1416	A1416	N1356	K1355	N1290	A1223	Q1155	THR	R1018	N948
Y1594	Y1594	Q1493	R1417	R1417	M1357	N1357	D1291	N1225	K1156	GLY	N1019	V949
C1595	C1595	K1496	C1418	C1418	I1358	L1358	E1294	Y1226	N1159	THR	N1020	S951
K1599	K1599	I1497	A1419	A1419	L1359	L1359	L1295	I1227	G1160	GLY	S1021	P952
K1612	K1612	I1497	I1420	I1420	G1360	G1360	K1297	R1228	E1162	GLY	G1026	L953
N1615	N1615	Q1499	T1421	T1421	T1361	T1361	E1298	G1229	W1162	GLY	Y1017	T956
G1616	G1616	A1500	K1422	K1422	S1362	S1362	K1299	C1230	S1163	GLY	R1018	P957
R1617	R1617	N1364	I1423	I1423	N1363	N1363	K1300	Q1231	I1164	GLY	G1026	Y958
P1626	P1626	K1501	N1424	N1424	N1364	N1364	K1301	Y1235	I1165	GLY	V1029	Y960
R1627	R1627	K1502	K1425	K1425	I1365	I1365	N1302	D1236	K1166	GLY	M1033	C964
Q1629	Q1629	R1503	N1427	N1427	I1369	I1369	A1303	G1237	N1167	GLY	E1041	Q965
Q1630	Q1630	K1504	K1432	K1432	G1370	G1370	I1304	Y1236	W1103	GLY	I1042	C966
L1633	L1633	Y1511	F1432	F1432	E1371	E1371	K1305	G1240	K1106	GLY	I1045	K967
Y1634	Y1634	Y1519	E1436	E1436	K1371	K1371	E1307	F1241	I1107	GLY	Q1045	I968
E1635	E1635	D1520	C1437	C1437	L1372	L1372	E1307	G1242	N1108	GLY	T1046	P969
L1636	L1636	Q1522	P1442	P1442	K1373	K1373	T1308	K1243	D1109	GLY	T1046	T970
P1637	P1637	K1525	G1444	G1444	E1374	E1374	E1309	E1243	W1110	GLY	E1047	N971
T1638	T1638	Y1526	N1445	N1445	D1375	D1375	L1310	E1246	W1111	GLY	Y1049	E972
T1639	T1639	Y1530	G1444	G1444	I1376	I1376	L1311	K1251	G1112	GLY	M1050	C975
I1640	I1640	L1538	N1446	N1446	K1377	K1377	Y1312	K1252	K1113	GLY	T1051	R978
K1642	K1642	L1538	Q1449	Q1449	E1381	E1381	H1315	C1251	K1114	GLY	N1052	K979
E1645	E1645	N1542	F1454	F1454	K1382	K1382	D1316	K1252	D1116	GLY	M1054	E980
K1649	K1649	Y1543	E1456	E1456	G1383	G1383	T1317	D1253	Y1118	GLY	T1055	Y981
E1652	E1652	C1546	K1457	K1457	K1384	K1384	G1318	T1254	K1120	GLY	S1056	M982
Q1657	Q1657	N1550	W1457	W1457	P1385	P1385	T1319	T1255	F1121	GLY	C1057	N983
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	A1320	T1256	N1197	GLY	T1058	Q984
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	I1321	T1256	A1198	GLY	D1059	W985
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	I1322	T1256	E1199	GLY	S1123	S986
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	I1323	T1256	K1200	GLY	K1124	C987
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1324	T1256	Q1125	GLY	Q1125	Q988
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1325	T1256	I1126	GLY	LVS	S989
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1326	T1256	Y1127	GLY	VAL	Q988
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1327	T1256	D1128	GLY	ASP	N982
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1328	T1256	A1129	GLY	GLU	Q983
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1329	T1256	K1201	GLY	GLU	Q984
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1330	T1256	C1202	GLY	VAL	Q985
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1331	T1256	K1203	GLY	ASP	R991
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1331	T1256	E1129	GLY	GLU	T992
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1331	T1256	K1205	GLY	VAL	M993
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1331	T1256	K1205	GLY	VAL	K994
Q1657	Q1657	N1550	W1457	W1457	Q1386	Q1386	K1331	T1256	K1205	GLY	VAL	R995

LYS	ASP	LYS	THR	LYS	LEU	ASP	GLU	LEU	ASP	GLU	ASP	TRP	ASN	ASP	MET	ASP	LEU	ARG	GLY	THR	TYR	ASN	LYS	HIS	LYS	GLY	VAL	LEU	ILE	PRO																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	50000	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.352	Depositor
Minimum map value	-0.906	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	366.08002, 366.08002, 366.08002	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	B	0.29	0/1688	0.47	0/2297
2	C	0.27	0/1665	0.45	0/2263
3	A	0.34	0/15370	0.67	15/20668 (0.1%)
All	All	0.33	0/18723	0.64	15/25228 (0.1%)

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	C	0	1
3	A	0	31
All	All	0	32

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1203	LYS	N-CA-C	7.88	127.59	110.80
3	A	562	LYS	CB-CA-C	-7.25	95.99	110.42
3	A	694	THR	CB-CA-C	-7.08	106.54	115.89
3	A	7	ILE	N-CA-C	-6.92	106.56	113.20
3	A	701	TYR	CB-CA-C	6.75	119.97	109.84

There are no chirality outliers.

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	201	TYR	Peptide
3	A	236	LEU	Peptide
3	A	239	ARG	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
3	A	37	TYR	Peptide
2	C	48	ILE	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	B	1650	0	1628	61	0
2	C	1631	0	1599	65	0
3	A	15071	0	14624	1014	0
All	All	18352	0	17851	1130	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 31.

The worst 5 of 1130 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:924:THR:HA	3:A:946:VAL:O	1.27	1.31
3:A:251:LYS:HB3	3:A:566:ASN:HB2	1.21	1.12
3:A:325:LYS:O	3:A:329:TYR:HB2	1.60	0.99
3:A:1050:MET:HE3	3:A:1198:ALA:HA	1.45	0.97
3:A:83:GLN:HB3	3:A:95:ASN:HD21	1.28	0.97

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	B	219/472 (46%)	205 (94%)	14 (6%)	0	100	100
2	C	210/233 (90%)	189 (90%)	21 (10%)	0	100	100
3	A	1843/2040 (90%)	1512 (82%)	305 (16%)	26 (1%)	9	37
All	All	2272/2745 (83%)	1906 (84%)	340 (15%)	26 (1%)	15	44

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	563	SER
3	A	566	ASN
3	A	683	LYS
3	A	690	LYS
3	A	699	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	B	181/411 (44%)	180 (99%)	1 (1%)	84	93
2	C	184/201 (92%)	184 (100%)	0	100	100
3	A	1674/1839 (91%)	1647 (98%)	27 (2%)	58	82
All	All	2039/2451 (83%)	2011 (99%)	28 (1%)	62	83

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	687	LYS
3	A	1980	ILE
3	A	691	LYS
3	A	890	ILE
3	A	690	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	1765	GLN
3	A	1787	HIS
3	A	773	GLN
3	A	769	ASN
3	A	1864	ASN

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](#)

There are no ligands in this entry.

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.

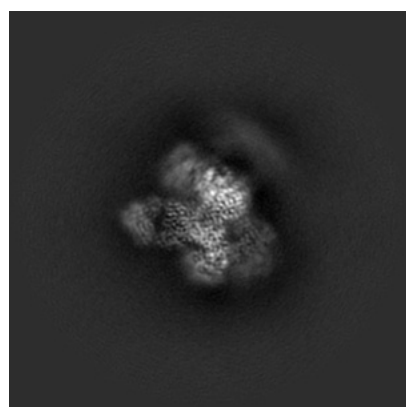
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14438. These allow visual inspection of the internal detail of the map and identification of artifacts.

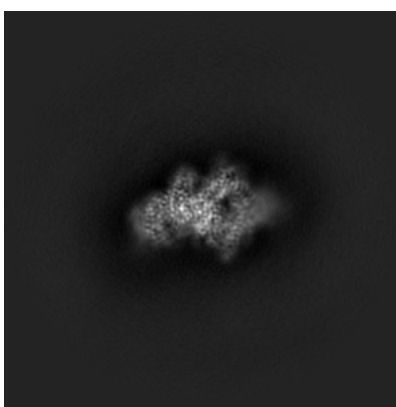
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

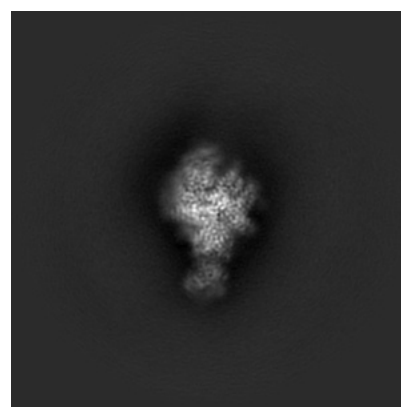
6.1.1 Primary map



X



Y

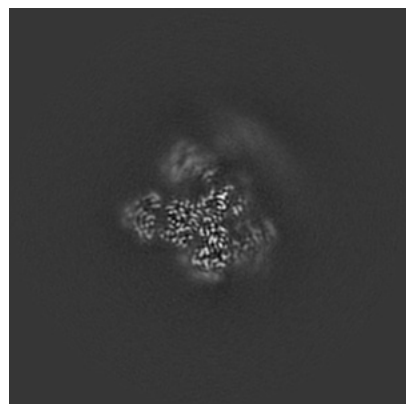


Z

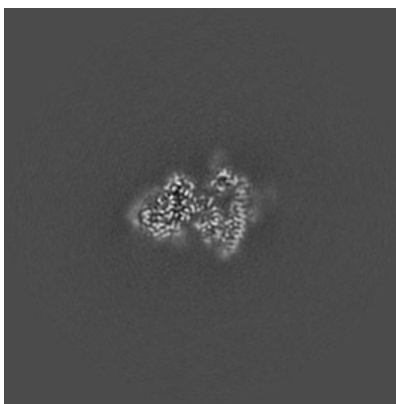
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

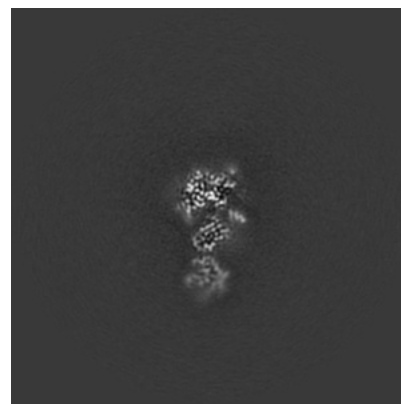
6.2.1 Primary map



X Index: 220



Y Index: 220

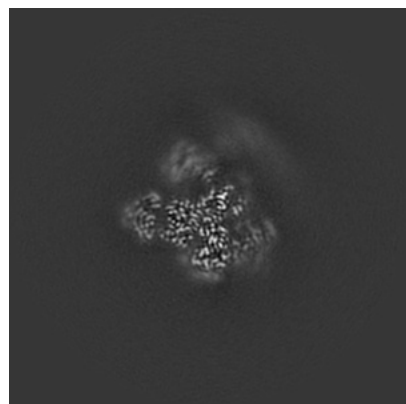


Z Index: 220

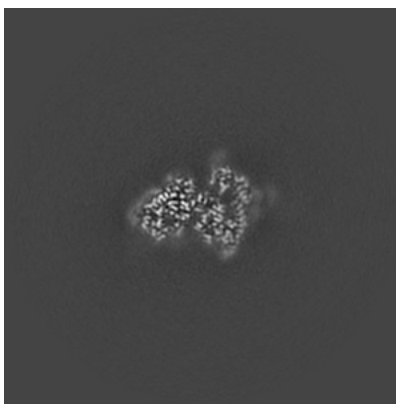
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

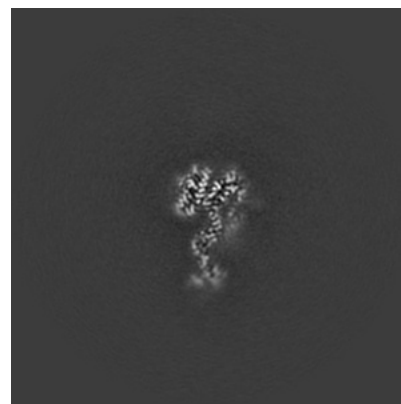
6.3.1 Primary map



X Index: 220



Y Index: 223

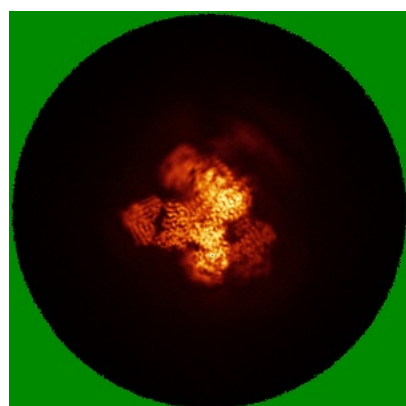


Z Index: 225

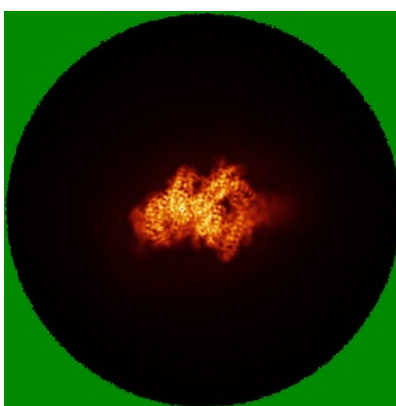
The images above show the largest variance slices of the map in three orthogonal directions.

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

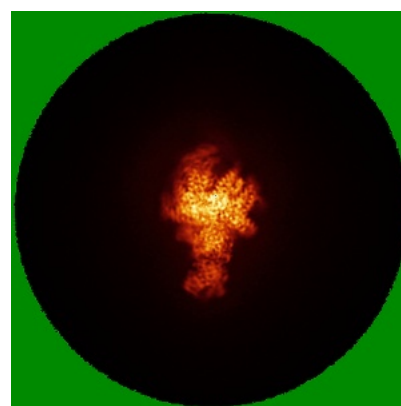
6.4.1 Primary map



X



Y

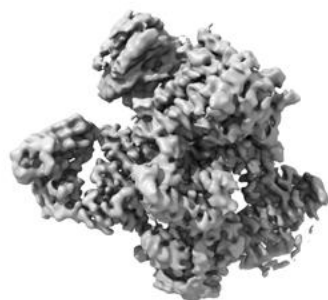


Z

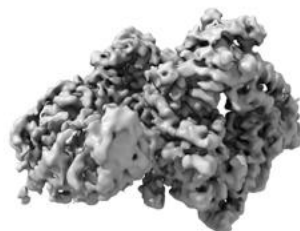
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

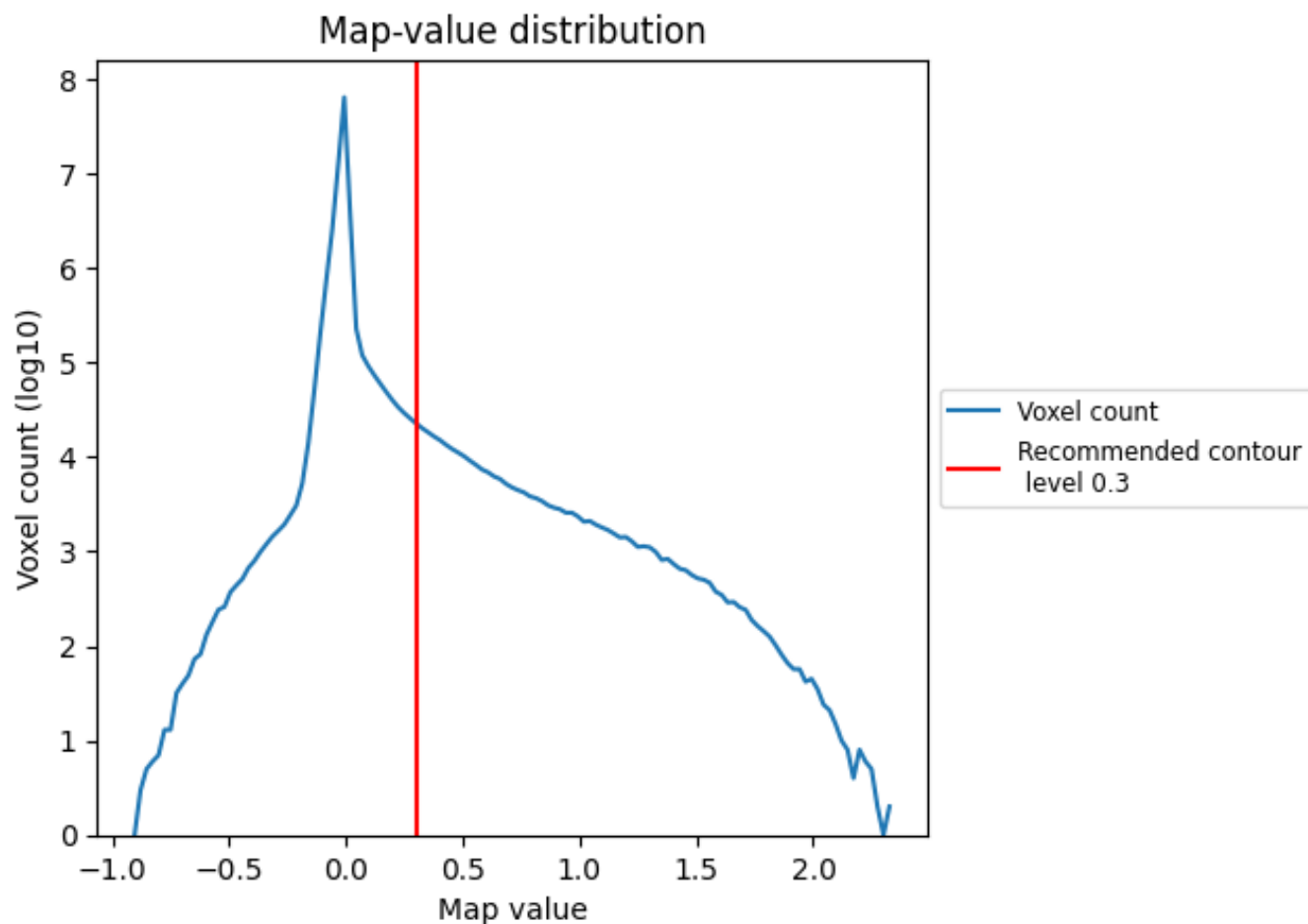
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

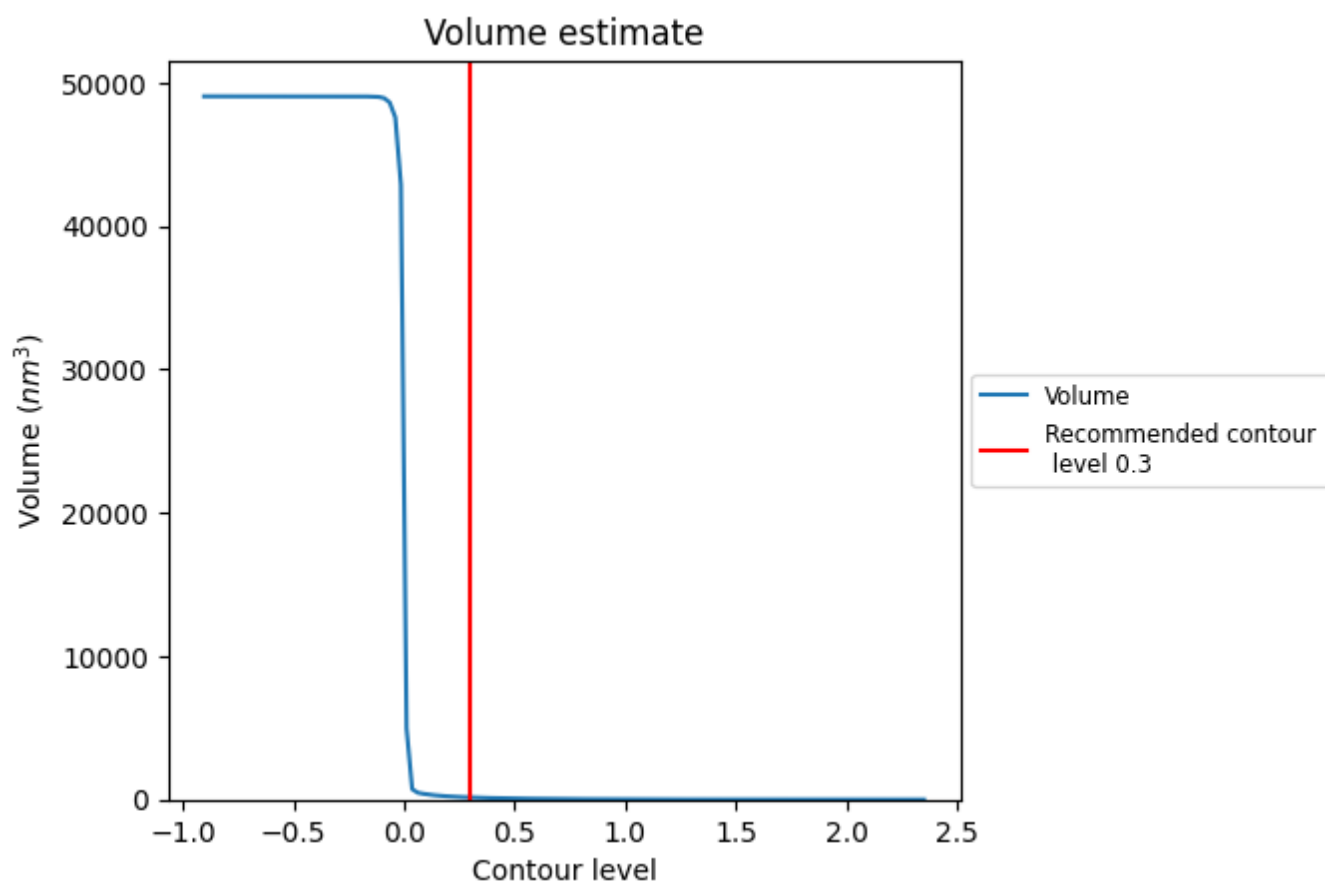
This section contains the results of statistical analysis of the map.

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.

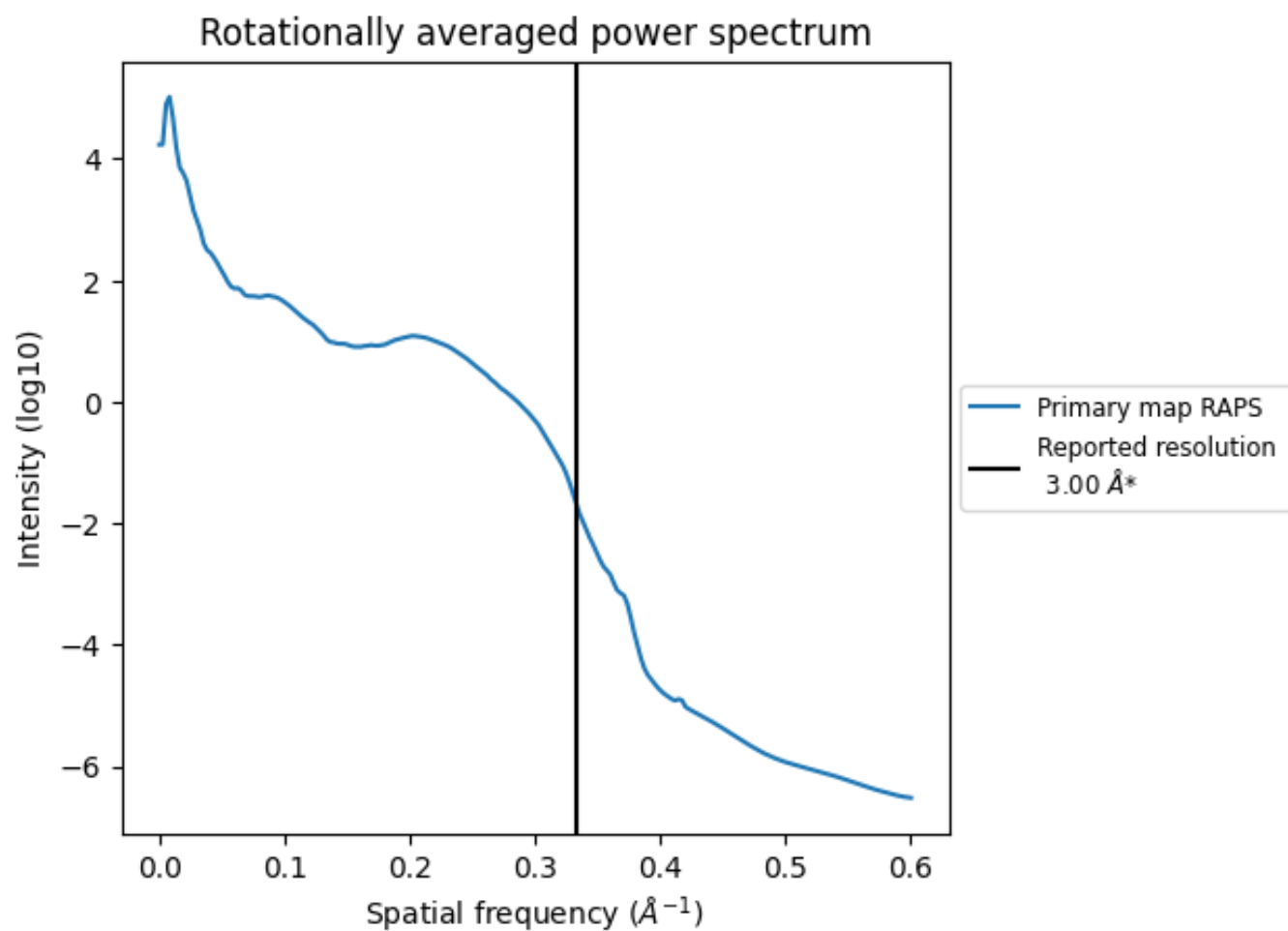
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 149 nm^3 ; this corresponds to an approximate mass of 134 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 ⓘ

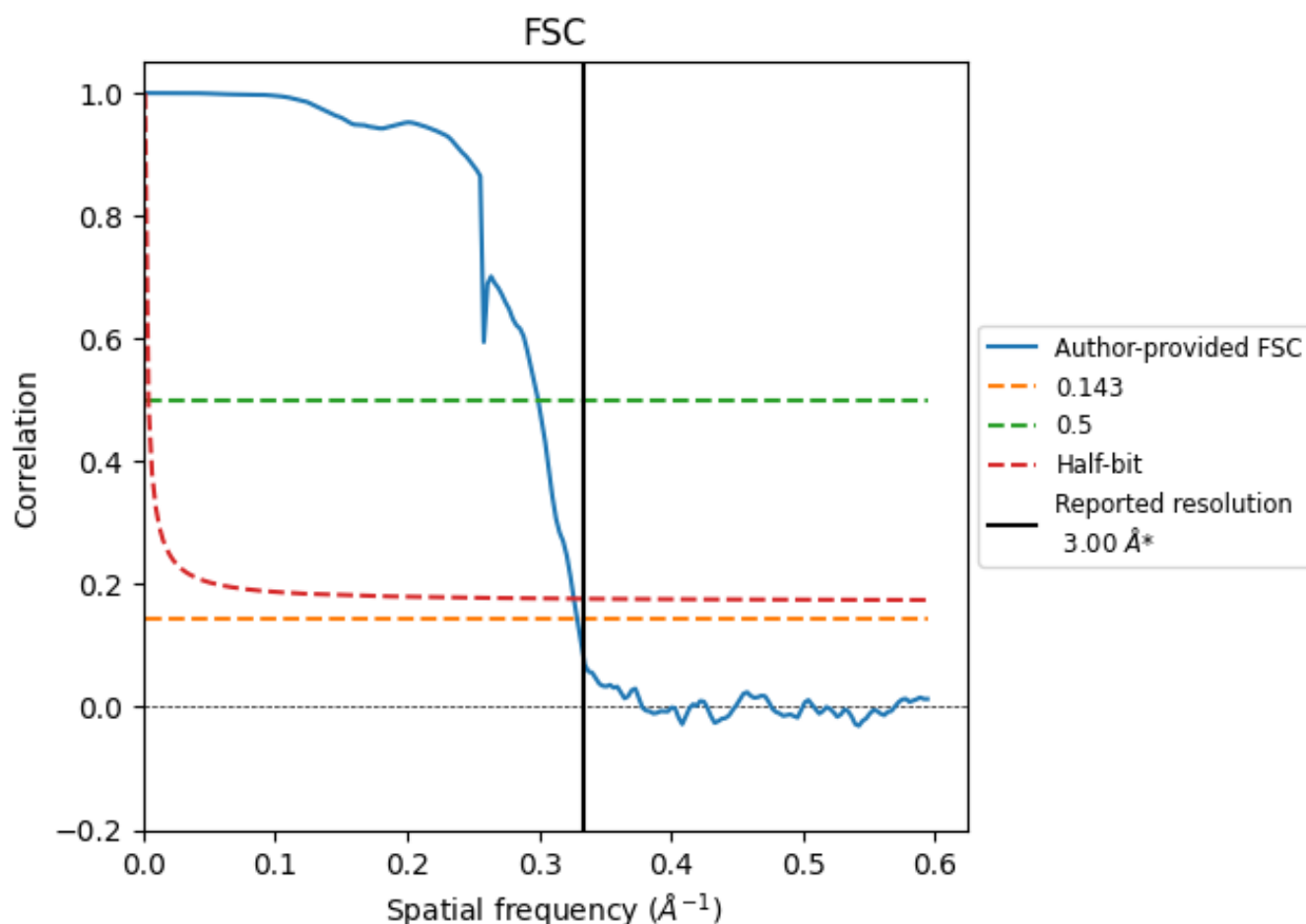


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

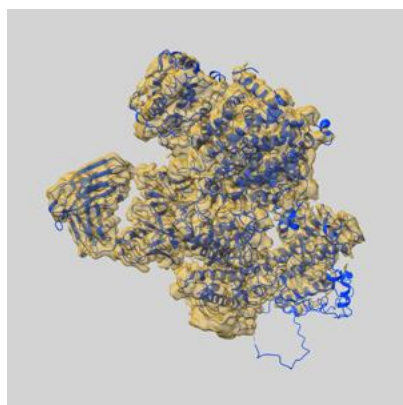
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.34	3.06
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

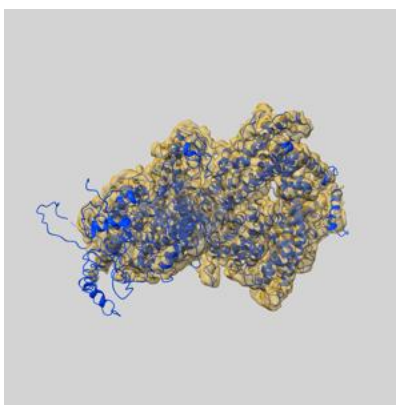
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14438 and PDB model 7Z12. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

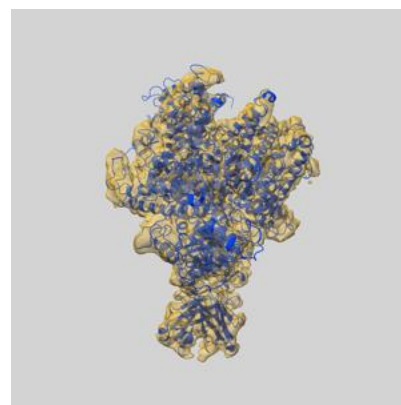
9.1 Map-model overlay [i](#)



X



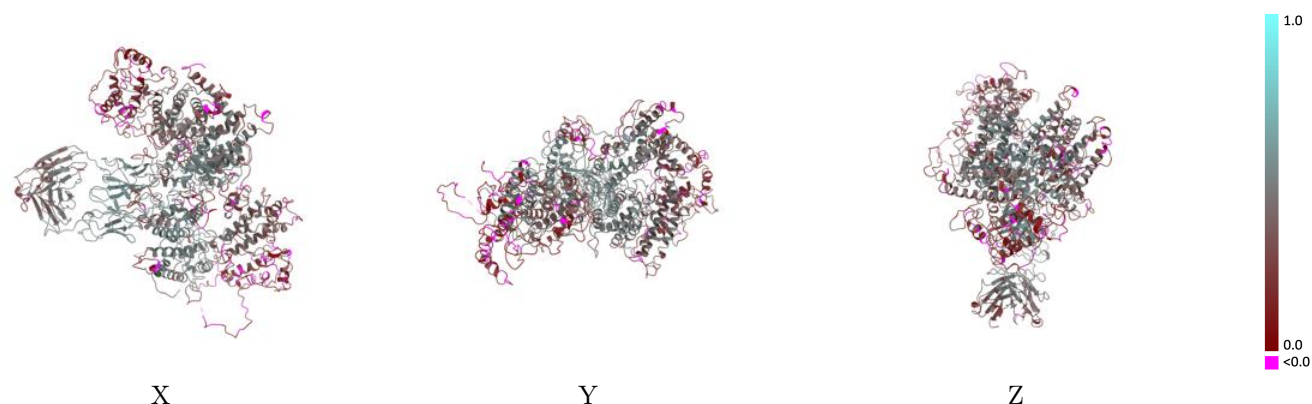
Y



Z

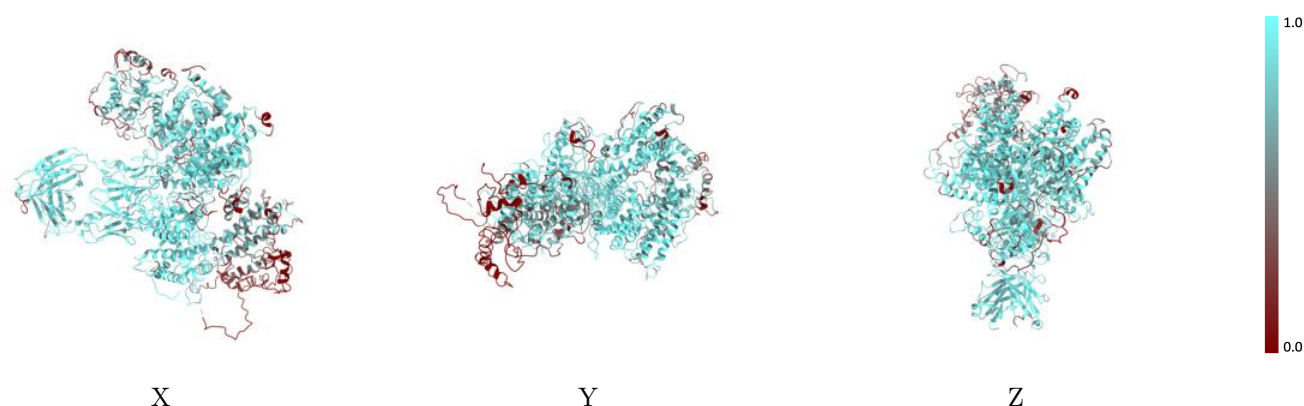
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



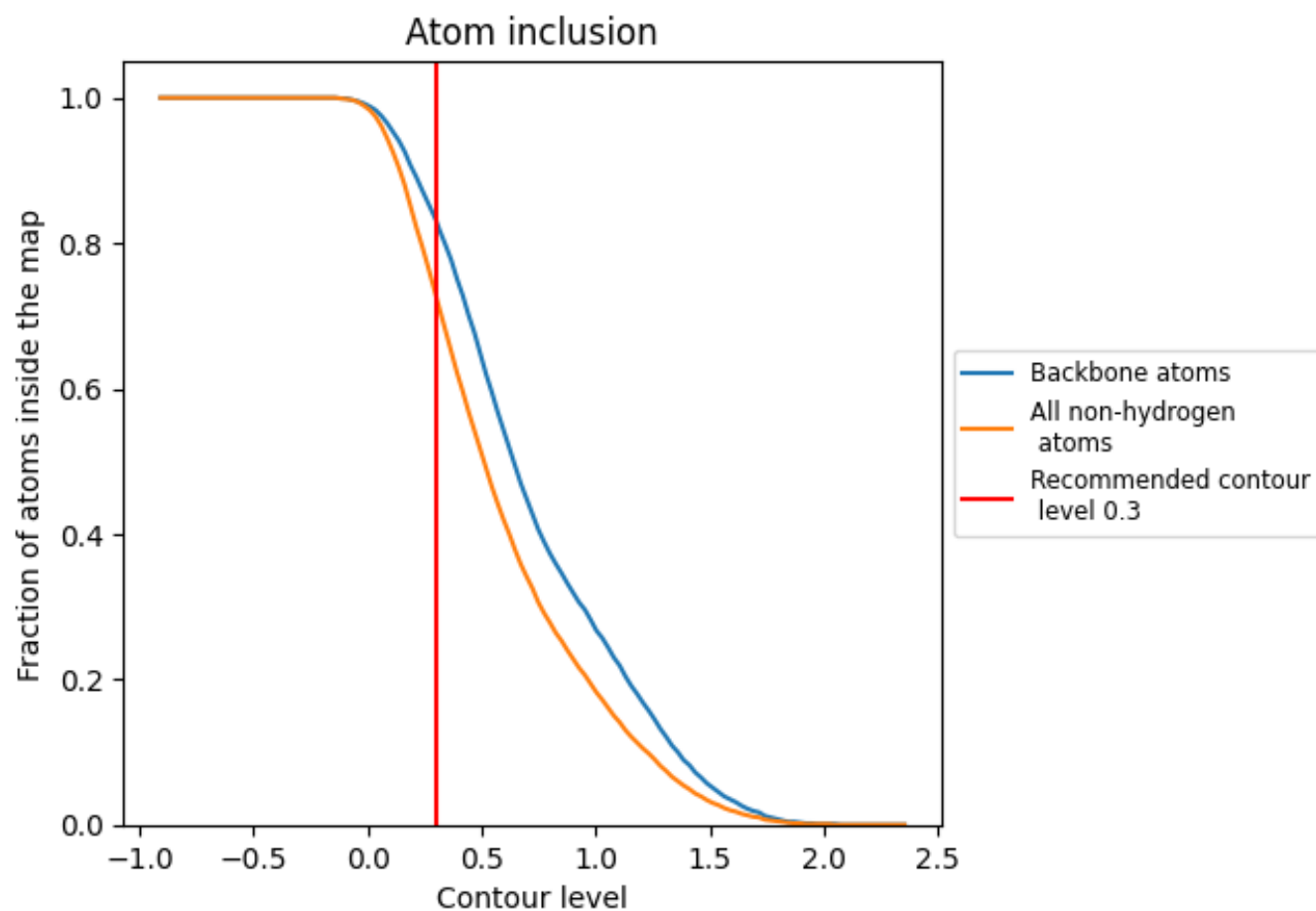
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion ⓘ



At the recommended contour level, 83% of all backbone atoms, 73% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7280	<div></div> 0.3620
A	<div></div> 0.6940	<div></div> 0.3360
B	<div></div> 0.8900	<div></div> 0.4880
C	<div></div> 0.8770	<div></div> 0.4750

