



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 10:11 PM UTC

PDB ID : 7YXX / pdb_00007yxx
EMDB ID : EMD-14368
Title : Cryo-EM structure of USP9X
Authors : Deme, J.C.; Halabelian, L.; Arrowsmith, C.H.; Lea, S.M.; Structural Genomics Consortium (SGC)
Deposited on : 2022-02-16
Resolution : 3.30 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.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

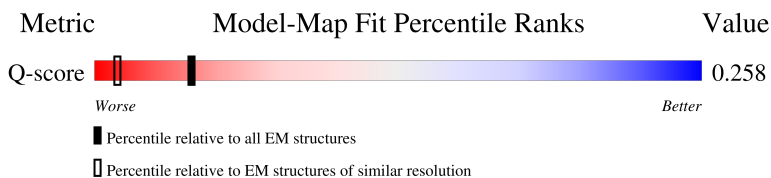
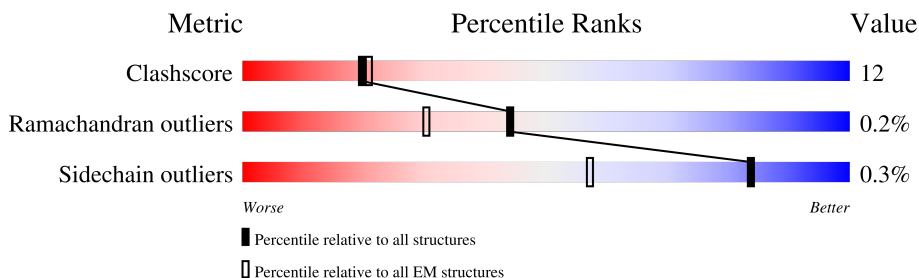
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	2579	
1	B	2579	
1	C	2579	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 42357 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 Probable ubiquitin carboxyl-terminal hydrolase FAF-X.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1754	Total 14155	C 9062	N 2426	O 2571	S 96	1	0
1	B	1754	Total 14155	C 9062	N 2426	O 2571	S 96	1	0
1	C	1741	Total 14047	C 8997	N 2407	O 2547	S 96	1	0

There are 75 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	initiating methionine	UNP Q93008
A	-16	HIS	-	expression tag	UNP Q93008
A	-15	HIS	-	expression tag	UNP Q93008
A	-14	HIS	-	expression tag	UNP Q93008
A	-13	HIS	-	expression tag	UNP Q93008
A	-12	HIS	-	expression tag	UNP Q93008
A	-11	HIS	-	expression tag	UNP Q93008
A	-10	SER	-	expression tag	UNP Q93008
A	-9	SER	-	expression tag	UNP Q93008
A	-8	GLY	-	expression tag	UNP Q93008
A	-7	ARG	-	expression tag	UNP Q93008
A	-6	GLU	-	expression tag	UNP Q93008
A	-5	ASN	-	expression tag	UNP Q93008
A	-4	LEU	-	expression tag	UNP Q93008
A	-3	TYR	-	expression tag	UNP Q93008
A	-2	PHE	-	expression tag	UNP Q93008
A	-1	GLN	-	expression tag	UNP Q93008
A	0	GLY	-	expression tag	UNP Q93008
A	2555	ASP	-	expression tag	UNP Q93008
A	2556	TYR	-	expression tag	UNP Q93008
A	2557	LYS	-	expression tag	UNP Q93008
A	2558	ASP	-	expression tag	UNP Q93008
A	2559	ASP	-	expression tag	UNP Q93008
A	2560	ASP	-	expression tag	UNP Q93008

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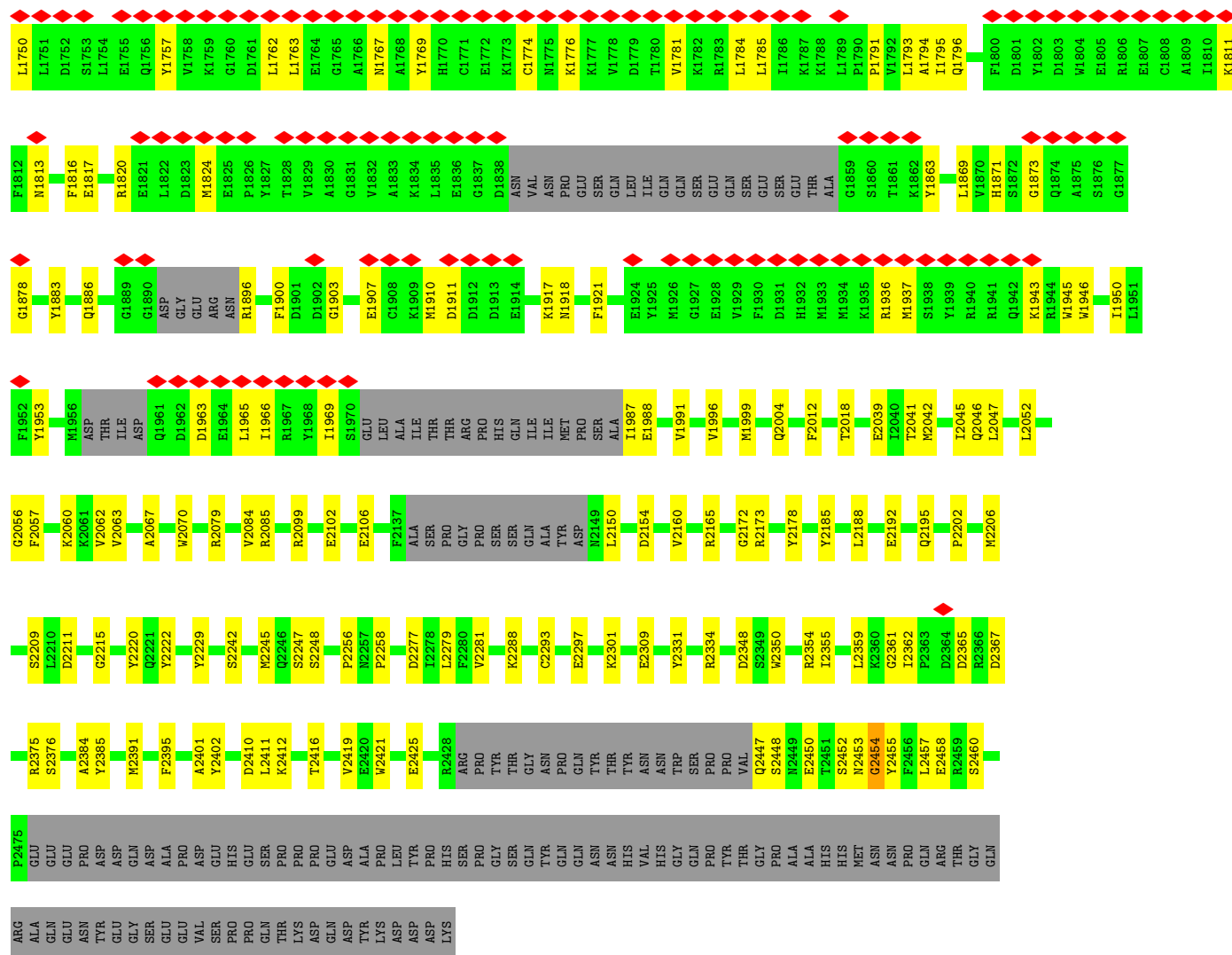
Chain	Residue	Modelled	Actual	Comment	Reference
A	2561	LYS	-	expression tag	UNP Q93008
B	-17	MET	-	initiating methionine	UNP Q93008
B	-16	HIS	-	expression tag	UNP Q93008
B	-15	HIS	-	expression tag	UNP Q93008
B	-14	HIS	-	expression tag	UNP Q93008
B	-13	HIS	-	expression tag	UNP Q93008
B	-12	HIS	-	expression tag	UNP Q93008
B	-11	HIS	-	expression tag	UNP Q93008
B	-10	SER	-	expression tag	UNP Q93008
B	-9	SER	-	expression tag	UNP Q93008
B	-8	GLY	-	expression tag	UNP Q93008
B	-7	ARG	-	expression tag	UNP Q93008
B	-6	GLU	-	expression tag	UNP Q93008
B	-5	ASN	-	expression tag	UNP Q93008
B	-4	LEU	-	expression tag	UNP Q93008
B	-3	TYR	-	expression tag	UNP Q93008
B	-2	PHE	-	expression tag	UNP Q93008
B	-1	GLN	-	expression tag	UNP Q93008
B	0	GLY	-	expression tag	UNP Q93008
B	2555	ASP	-	expression tag	UNP Q93008
B	2556	TYR	-	expression tag	UNP Q93008
B	2557	LYS	-	expression tag	UNP Q93008
B	2558	ASP	-	expression tag	UNP Q93008
B	2559	ASP	-	expression tag	UNP Q93008
B	2560	ASP	-	expression tag	UNP Q93008
B	2561	LYS	-	expression tag	UNP Q93008
C	-17	MET	-	initiating methionine	UNP Q93008
C	-16	HIS	-	expression tag	UNP Q93008
C	-15	HIS	-	expression tag	UNP Q93008
C	-14	HIS	-	expression tag	UNP Q93008
C	-13	HIS	-	expression tag	UNP Q93008
C	-12	HIS	-	expression tag	UNP Q93008
C	-11	HIS	-	expression tag	UNP Q93008
C	-10	SER	-	expression tag	UNP Q93008
C	-9	SER	-	expression tag	UNP Q93008
C	-8	GLY	-	expression tag	UNP Q93008
C	-7	ARG	-	expression tag	UNP Q93008
C	-6	GLU	-	expression tag	UNP Q93008
C	-5	ASN	-	expression tag	UNP Q93008
C	-4	LEU	-	expression tag	UNP Q93008
C	-3	TYR	-	expression tag	UNP Q93008
C	-2	PHE	-	expression tag	UNP Q93008

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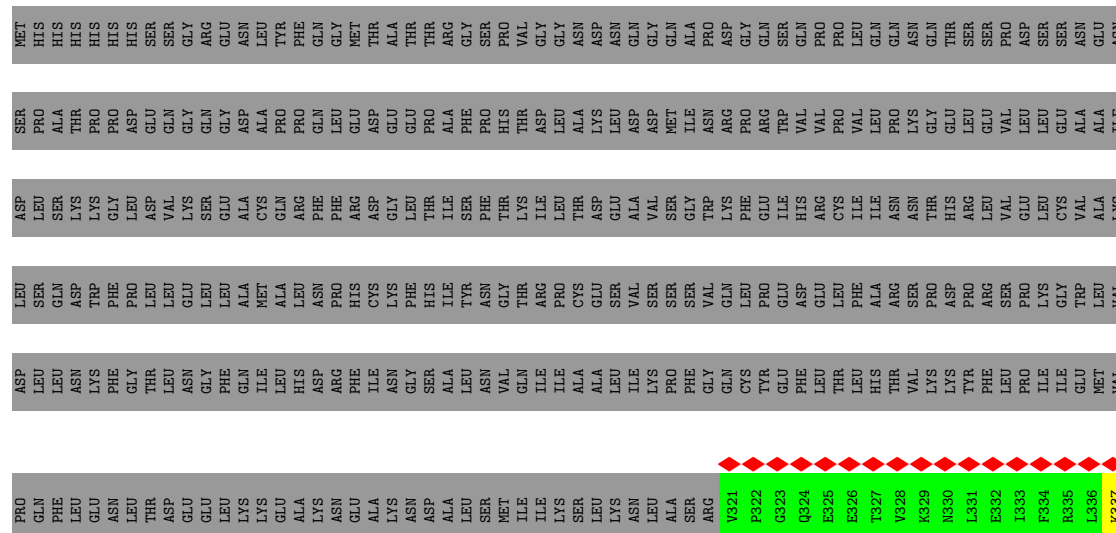
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	GLN	-	expression tag	UNP Q93008
C	0	GLY	-	expression tag	UNP Q93008
C	2555	ASP	-	expression tag	UNP Q93008
C	2556	TYR	-	expression tag	UNP Q93008
C	2557	LYS	-	expression tag	UNP Q93008
C	2558	ASP	-	expression tag	UNP Q93008
C	2559	ASP	-	expression tag	UNP Q93008
C	2560	ASP	-	expression tag	UNP Q93008
C	2561	LYS	-	expression tag	UNP Q93008





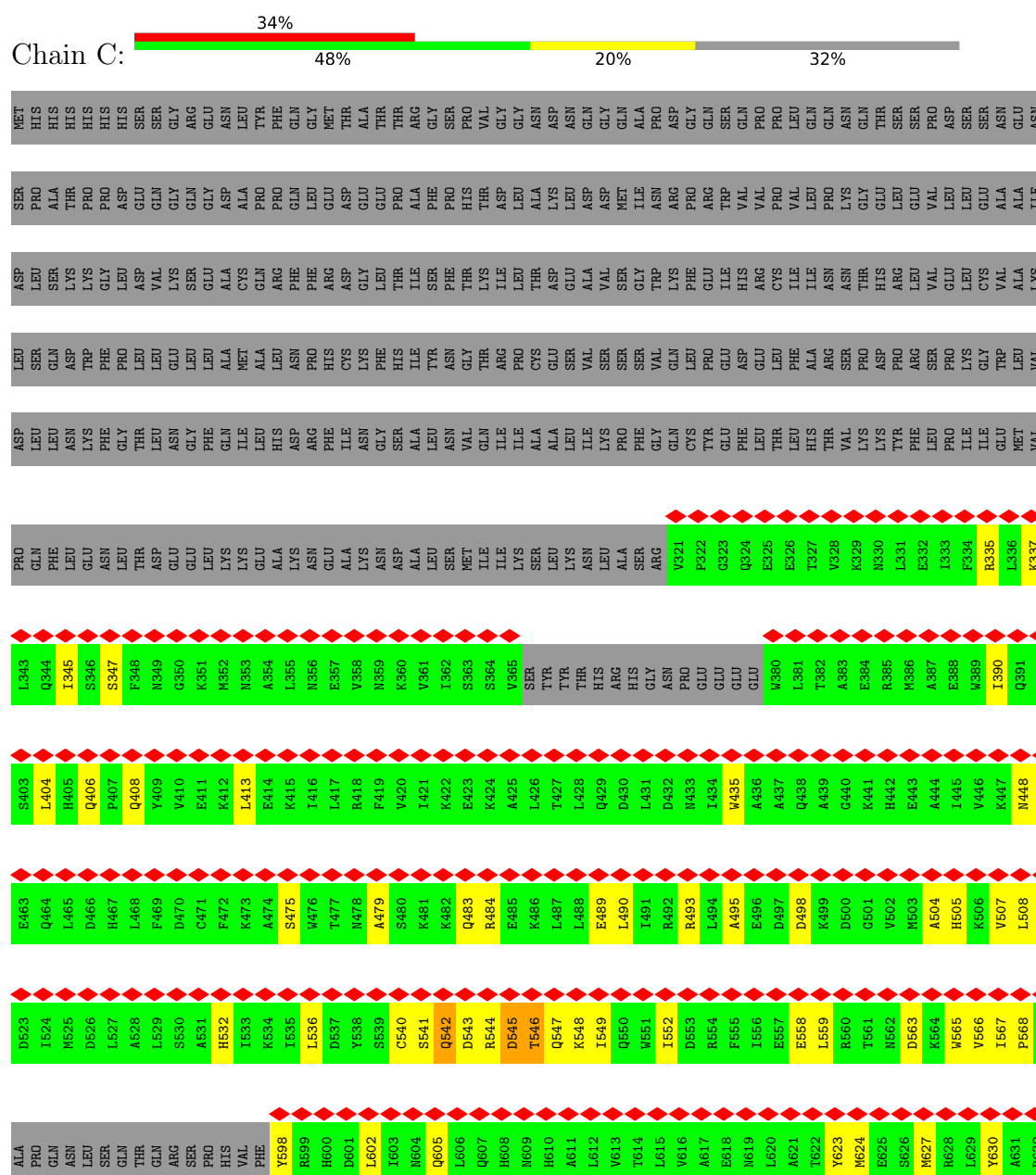
• Molecule 1: Probable ubiquitin carboxyl-terminal hydrolase FAF-X







- Molecule 1: Probable ubiquitin carboxyl-terminal hydrolase FAF-X



L1508	D1412	H1324	A1248	I1232	V1126	A1065	GLU	PRO	GLY	L523	M763	K703	ARG
N1515	D1413	S1325	S1263	K1066	M1229	K1066	SER	ALA	LYS	K824	D764	L704	LEU
V1520	V1414	T1327	L1254	LEU	CYS	LEU	CYS	ASP	HIS	A825	D765	M705	GLY
D1521	K1415	V1328	L1256	GLU	PRO	GLY	PRO	ARG	SER	S826	L766	G706	ARG
S1522	I1426	R1329	Q1256	SER	VAL	SER	VAL	LYS	PHE	Y827	E767	D707	TYR
L1523	L1427	Q1330	L1257	LEU	ILE	LEU	ILE	LEU	VAL	D828	L768	E708	SER
T1524	H1430	V1331	P1260	PRO	MET	SER	S1012	GLN	VAL	T829	I769	P709	
E1525	G1431	A1332	N1261	SER	F1135	PRO	LEU	ASN	ASN	L830	G770	D710	
M1526	V1433	Q1333	E1262	GLN	L1136	SER	H1013	LEU	GLN	C831	L771	L711	
Y1527	T1434	F1336	E1263	LEU	P1137	SER	H1014	LEU	GLY	VAL	D772	D712	
T1531	K1435	M1339	T1264	ALA	P1138	SER	P1015	LYS	ASP	LEU	Y773	P713	
A1532	E1436	R1342	T1265	GLN	M1138	SER	R1016	ASP	ARG	GLY	L774	D714	
I1533	L1437	C1343	E1266	LEU	A1139	SER	Y1017	LYS	VAL	ASP	W775	I715	
T1534	L1438	Q1344	Y1268	GLN	D1140	SER	I1018	LEU	ASP	LYS	R776	N716	
E1537	Q1441	R1348	E1269	ILE	M1141	SER	S1019	THR	ASP	SER	V777	K717	
A1538	K1445	F1353	K1270	PRO	E1142	PRO	F1020	ALA	LEU	VAL	V778	D718	
L1539	K1446	N1271	T1271	ASN	T1143	PRO	Q1087	LYS	TRP	ASN	I779	F719	
T1540	F1447	N1272	A1273	SER	R1144	SER	S1084	THR	LEU	GLY	Q780	F720	
E1541	E1482	T1274	G1274	SER	R1145	SER	Q1085	GLN	SER	A843	S781	E721	
V1548	A1456	D1276	D1276	CYS	G1146	GLY	A1086	ILE	THR	Q844	D783	S722	
R1551	N1457	L1279	E1280	LEU	Y1147	LEU	S1086	ASP	THR	E946	D784	V724	
K1554	L1458	V1360	D1281	ARG	L1149	LEU	Q1087	ASP	ILE	A947	I785	L725	
F1555	I1459	L1361	E1282	ASN	M1150	ARG	Y1090	ASP	GLY	V948	A786	Q726	
F1556	L1462	S1363	Q1283	SER	A1151	ARG	T1091	PRO	SER	R849	S787	G668	
L1559	I1467	R1366	C1286	ARG	K1153	LEU	E1093	SER	VAL	M850	R788	Q669	
K1560	Y1474	A1369	E1287	ALA	I1154	LEU	V1094	PRO	ARG	R852	A789	L670	
N1561	M1478	K1370	E1290	GLN	K1156	LEU	V1095	ASP	ARG	M853	I790	L671	
A1562	R1479	H1371	V1291	ILE	L1157	LEU	Y1096	SER	CYS	L854	D791	S730	
A1564	ASN	D1374	M1292	SER	L1158	GLY	A1097	SER	ILE	T855	L792	L731	
T1565	GLY	Y1375	T1293	ASP	L1159	LEU	L1098	ASP	LEU	R794	L732	L732	
C1566	LEU	F1376	L1294	GLU	L1159	LEU	D1038	SER	ASN	L857	L793	T733	
Y1567	PRO	T1377	L1295	ALA	A1161	ALA	G1039	SER	LYS	E858	K794	E734	
Q1573	ALA	L1378	F1296	SER	I1162	ALA	R1041	GLY	ASN	E859	I796	N735	
Q1574	GLN	H1381	A1297	ARG	G1163	GLY	V1042	PRO	VAL	Y860	Y797	K678	
I1585	ALA	L1383	P1234	ARG	G1165	LEU	L1043	GLY	ALA	I861	T798	M737	
I1588	P1490	A1386	M1233	VAL	HIS	ASP	M1044	ASN	HIS	N862	N799	K738	
E1589	V1491	Y1387	D1235	ALA	VAL	ASP	K1045	GLY	LYS	E863	L800	F740	
G1590	I1498	N1388	V1238	ALA	VAL	S1110	M1046	THR	THR	D865	G801	E741	
T1591	N1499	K1308	I1239	ALA	GLU	S1111	M1047	PHE	ASP	R803	P802	R742	
G1592	A1500	S1389	R1240	ALA	VAL	D1112	P1048	VAL	ASP	L804	F743	F743	
SER	G1501	N1390	A1241	ALA	GLU	F1113	P1049	GLY	VAL	Q805	F744	E686	
ASP	F1502	I1391	I1242	CYS	VAL	Q1114	D1050	GLY	HIS	V806	K745	K745	
VAL	E1503	I1404	Q1243	GLN	PRO	F1115	S1051	ASN	GLY	A746	A746	N687	
ASP	L1504	K1408	K1244	PRO	GLY	H1116	T1052	PRO	LEU	N807	V747	A688	
ASP			I1245	GLY	VAL	H1117	T1053	GLU	ASP	Q808	N748	V689	
MET			I1246	GLU	GLY	F1117	T1054	THR	ILE	V809	C749	Y690	
			W1247	GLY	GLY	L1118	E1055	LEU	ILE	V810	R750	L691	
				VAL	VAL	K1119	E1056	PRO	LEU	E751	C692	C692	
				ASN	VAL	S1120	L1057	MET	PRO	H812	E752	D693	
				MET	PRO	G1121	R1058	ARG	SER	E813	K753	E695	
				THR	THR	L1122	A1059	ALA	ALA	D814	L754	A696	
				GLN	GLN	L1123	C1061	PHE	PHE	F815	V755	A696	
						P1124	I1062	ARG	ARG	I816	A756	C697	
						L1125	D1063			Q817	K757	F698	
							H1064			S818	R758	K699	
										F820	A760	W700	
										C819	R759	Y701	
										D821	M762	S702	



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	330000	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 ($e^-/\text{\AA}^2$)	56.7	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.330	Depositor
Minimum map value	-0.608	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.034	Depositor
Recommended contour level	0.221	Depositor
Map size (Å)	372.73602, 372.73602, 372.73602	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8320001, 0.8320001, 0.8320001	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	A	0.15	0/14461	0.35	3/19559 (0.0%)
1	B	0.16	0/14461	0.39	0/19559
1	C	0.16	0/14351	0.38	2/19411 (0.0%)
All	All	0.16	0/43273	0.37	5/58529 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2402	TYR	N-CA-C	-6.54	107.17	114.62
1	C	2404	ILE	N-CA-C	-5.41	107.16	111.81
1	C	1902	ASP	CB-CA-C	-5.36	110.37	116.54
1	A	1258	PHE	CA-C-N	5.09	131.86	121.48
1	A	1258	PHE	C-N-CA	5.09	131.86	121.48

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	A	14155	0	14051	346	0
1	B	14155	0	14051	350	0
1	C	14047	0	13957	366	0
All	All	42357	0	42059	1054	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 12.

The worst 5 of 1054 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:C:2413:ARG:O	1:C:2416:THR:HG22	1.31	1.24
1:C:1521:ASP:O	1:C:1524:THR:HG22	1.38	1.20
1:B:540:CYS:HB2	1:B:544:ARG:HA	1.29	1.07
1:C:1789:LEU:HB3	1:C:1863:TYR:OH	1.58	1.02
1:A:1265:THR:HA	1:A:1268:TYR:CD2	2.02	0.95

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	1721/2579 (67%)	1631 (95%)	86 (5%)	4 (0%)	43	71
1	B	1721/2579 (67%)	1631 (95%)	90 (5%)	0	100	100
1	C	1708/2579 (66%)	1614 (94%)	88 (5%)	6 (0%)	30	60
All	All	5150/7737 (67%)	4876 (95%)	264 (5%)	10 (0%)	44	71

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	544	ARG
1	A	2454	GLY
1	C	2365	ASP
1	C	546	THR
1	C	1348	ARG

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	A	1544/2286 (68%)	1539 (100%)	5 (0%)	86	86
1	B	1544/2286 (68%)	1542 (100%)	2 (0%)	88	90
1	C	1532/2286 (67%)	1527 (100%)	5 (0%)	86	86
All	All	4620/6858 (67%)	4608 (100%)	12 (0%)	84	86

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	542	GLN
1	C	545	ASP
1	C	1357	LEU
1	C	1354	ILE
1	A	547	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1640	ASN
1	B	2221	GLN
1	C	2180	ASN
1	B	1729	HIS
1	B	2011	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

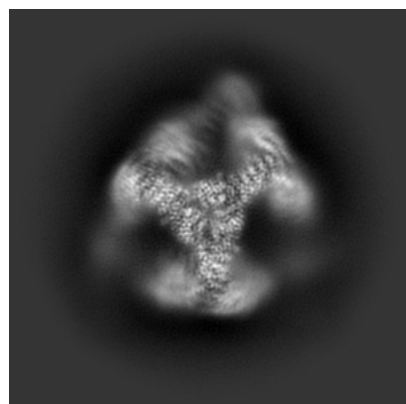
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14368. These allow visual inspection of the internal detail of the map and identification of artifacts.

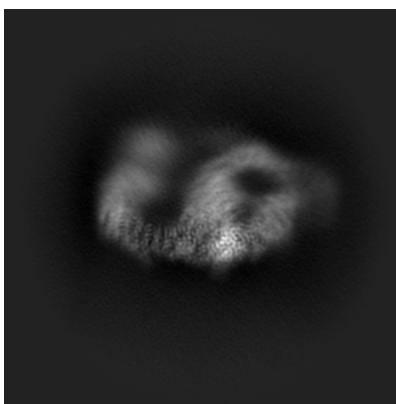
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

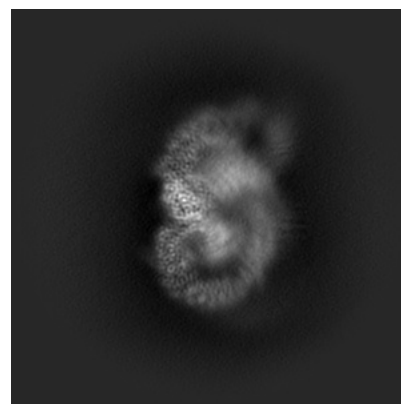
6.1.1 Primary map



X

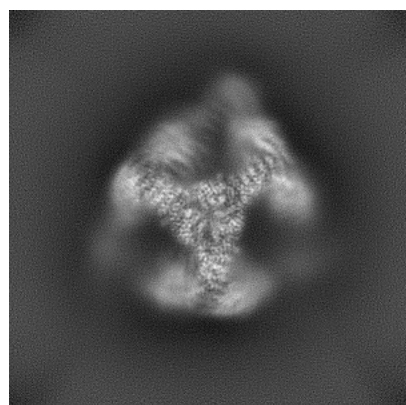


Y

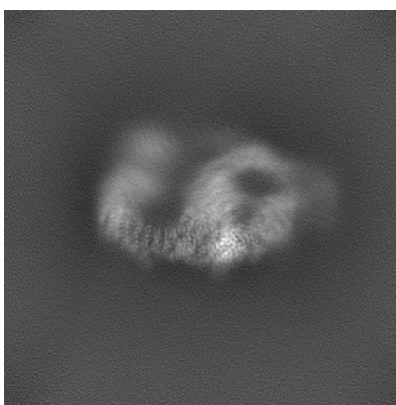


Z

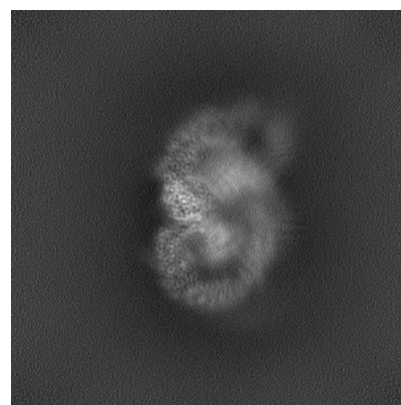
6.1.2 Raw map



X



Y

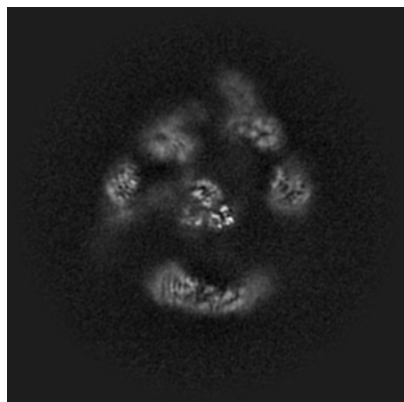


Z

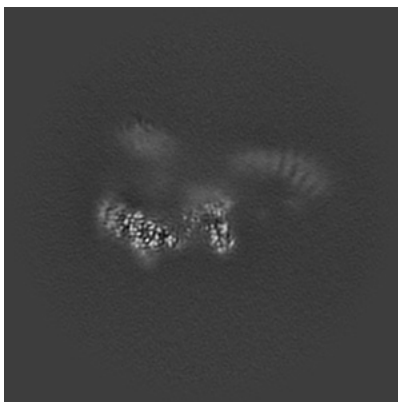
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

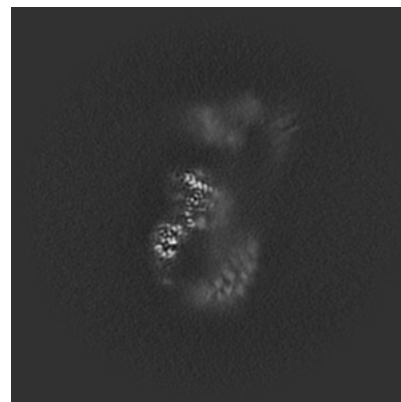
6.2.1 Primary map



X Index: 224

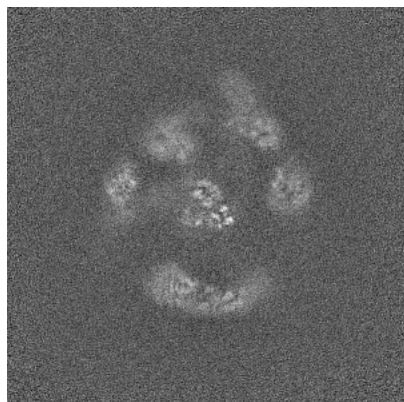


Y Index: 224

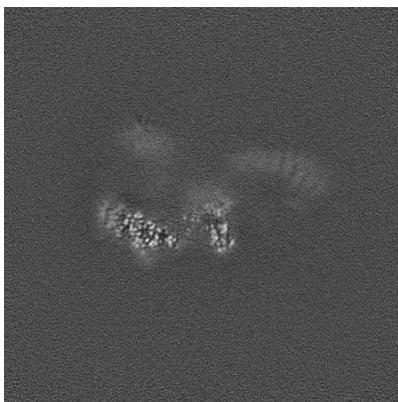


Z Index: 224

6.2.2 Raw map



X Index: 224



Y Index: 224

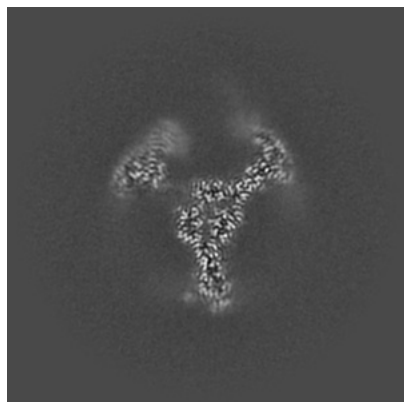


Z Index: 224

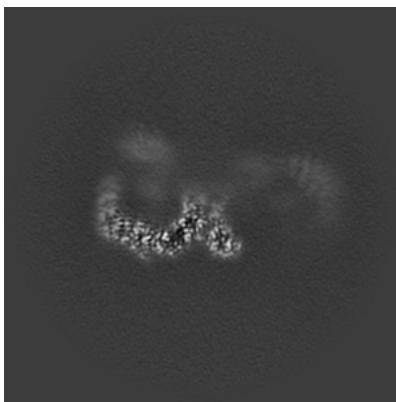
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

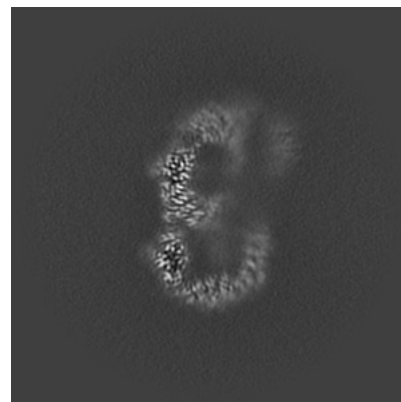
6.3.1 Primary map



X Index: 196

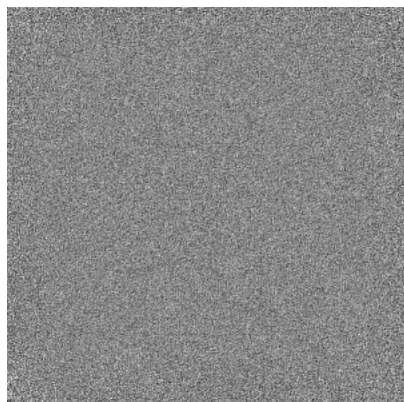


Y Index: 237

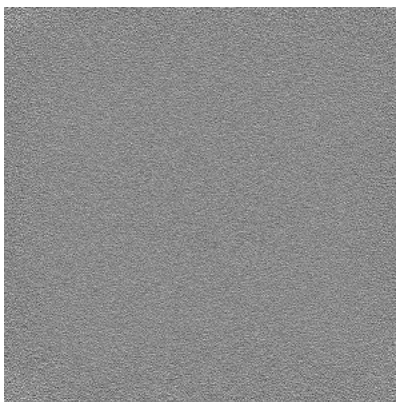


Z Index: 248

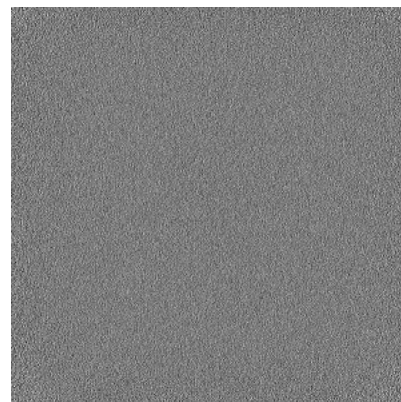
6.3.2 Raw map



X Index: 0



Y Index: 0



Z Index: 0

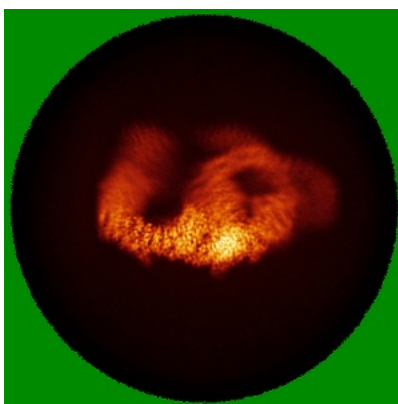
The images above show the largest variance slices of the map in three orthogonal directions.

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

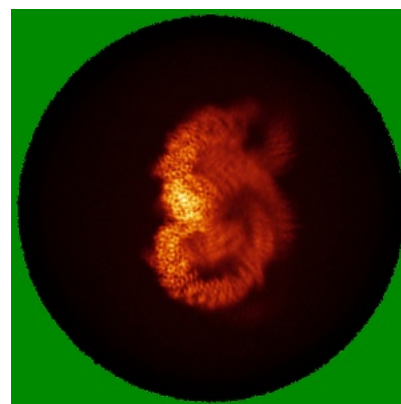
6.4.1 Primary map



X

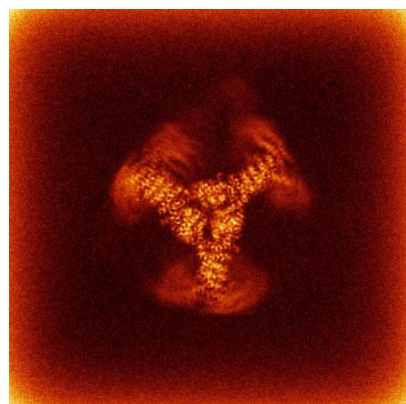


Y



Z

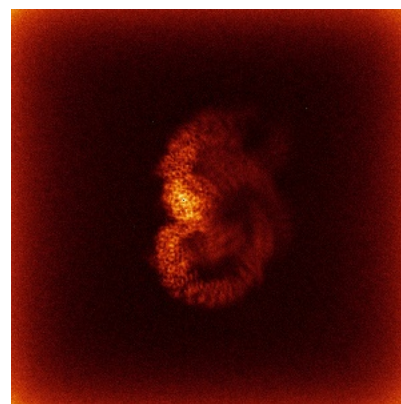
6.4.2 Raw map



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.

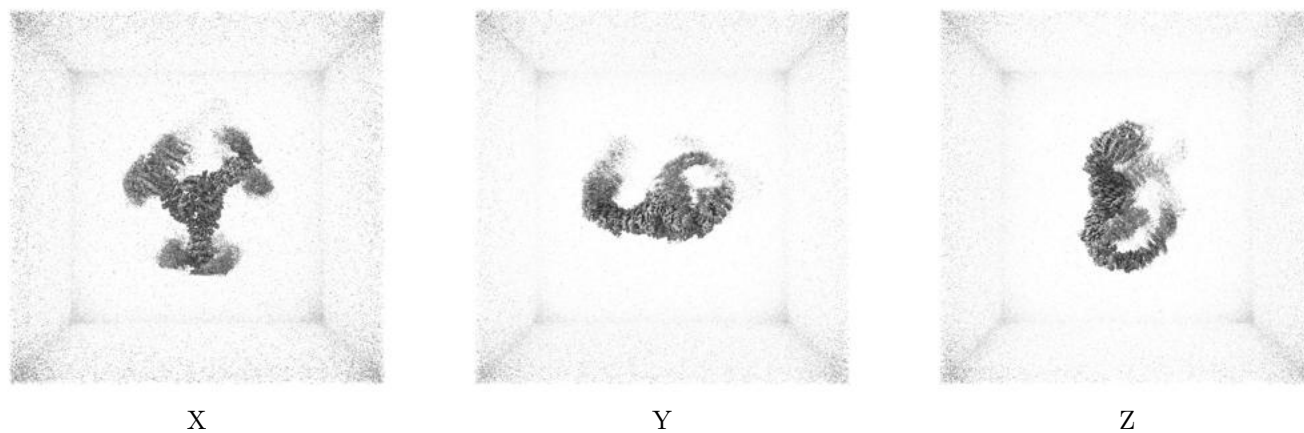
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.221. 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.

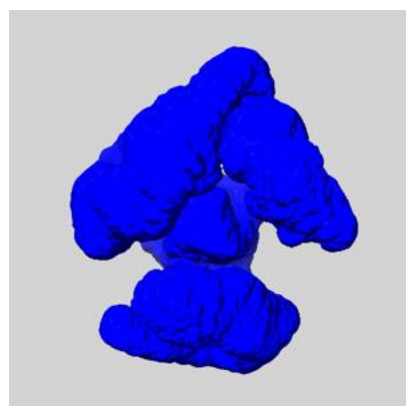
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

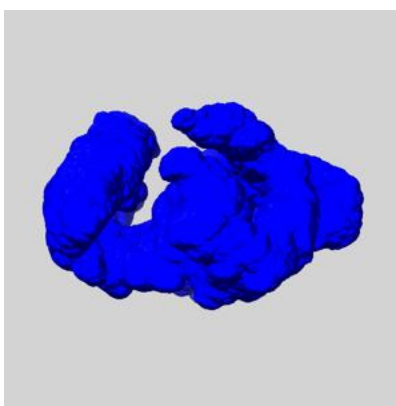
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

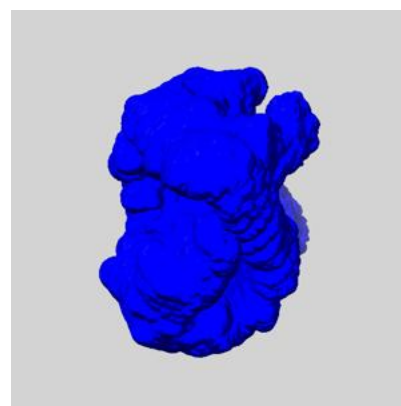
6.6.1 emd_14368_msk_1.map [i](#)



X



Y

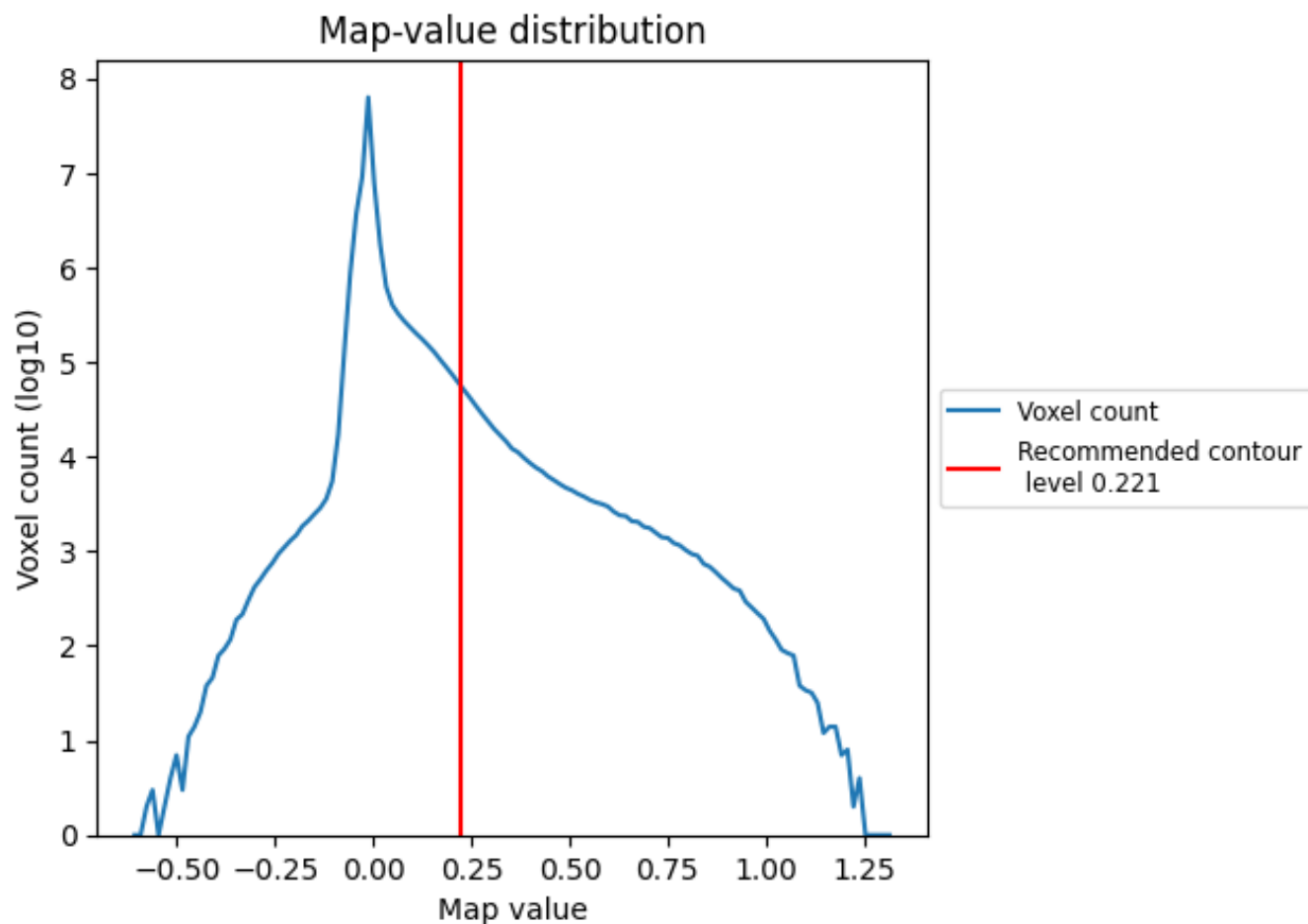


Z

7 Map analysis [i](#)

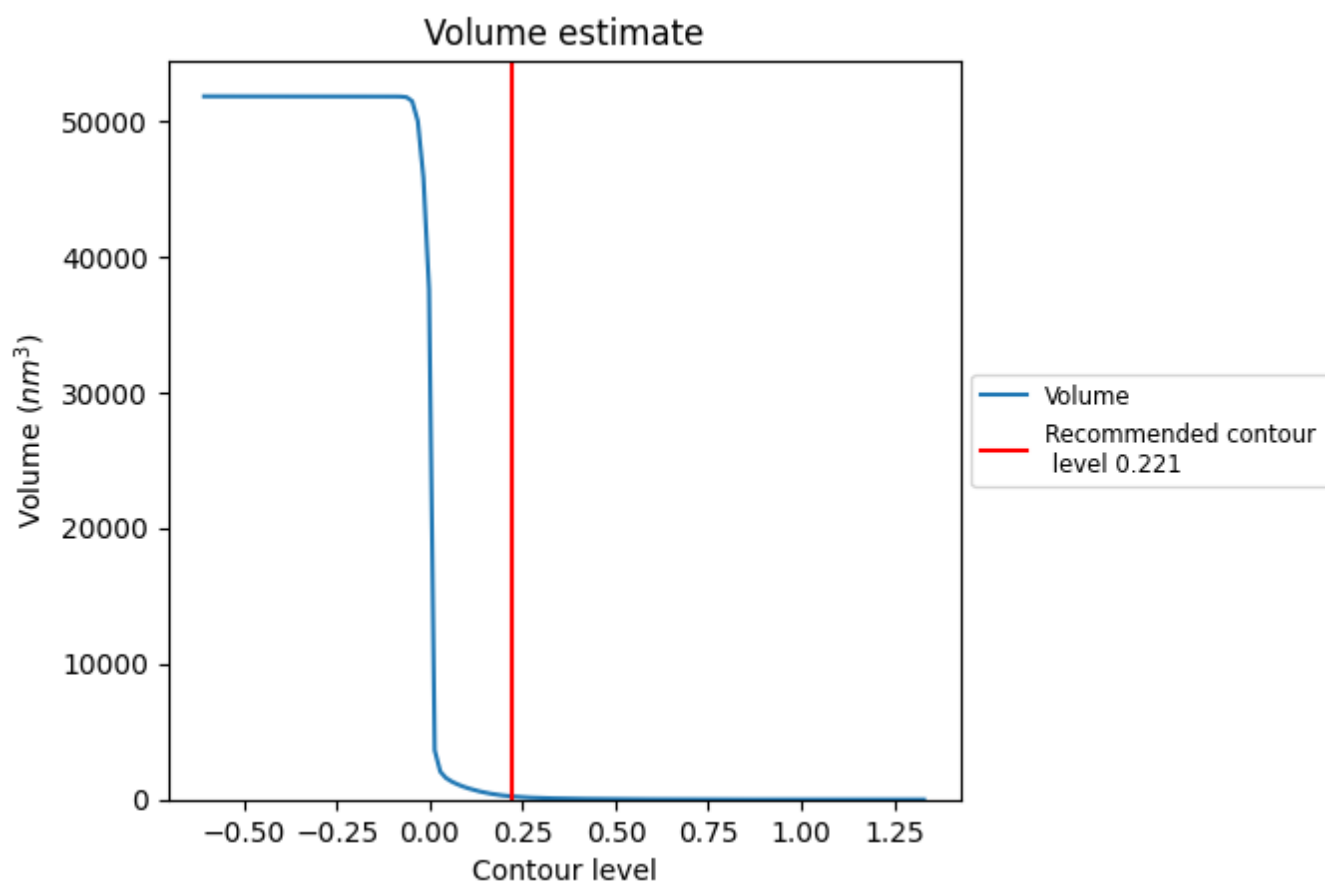
This section contains the results of statistical analysis of the map.

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.

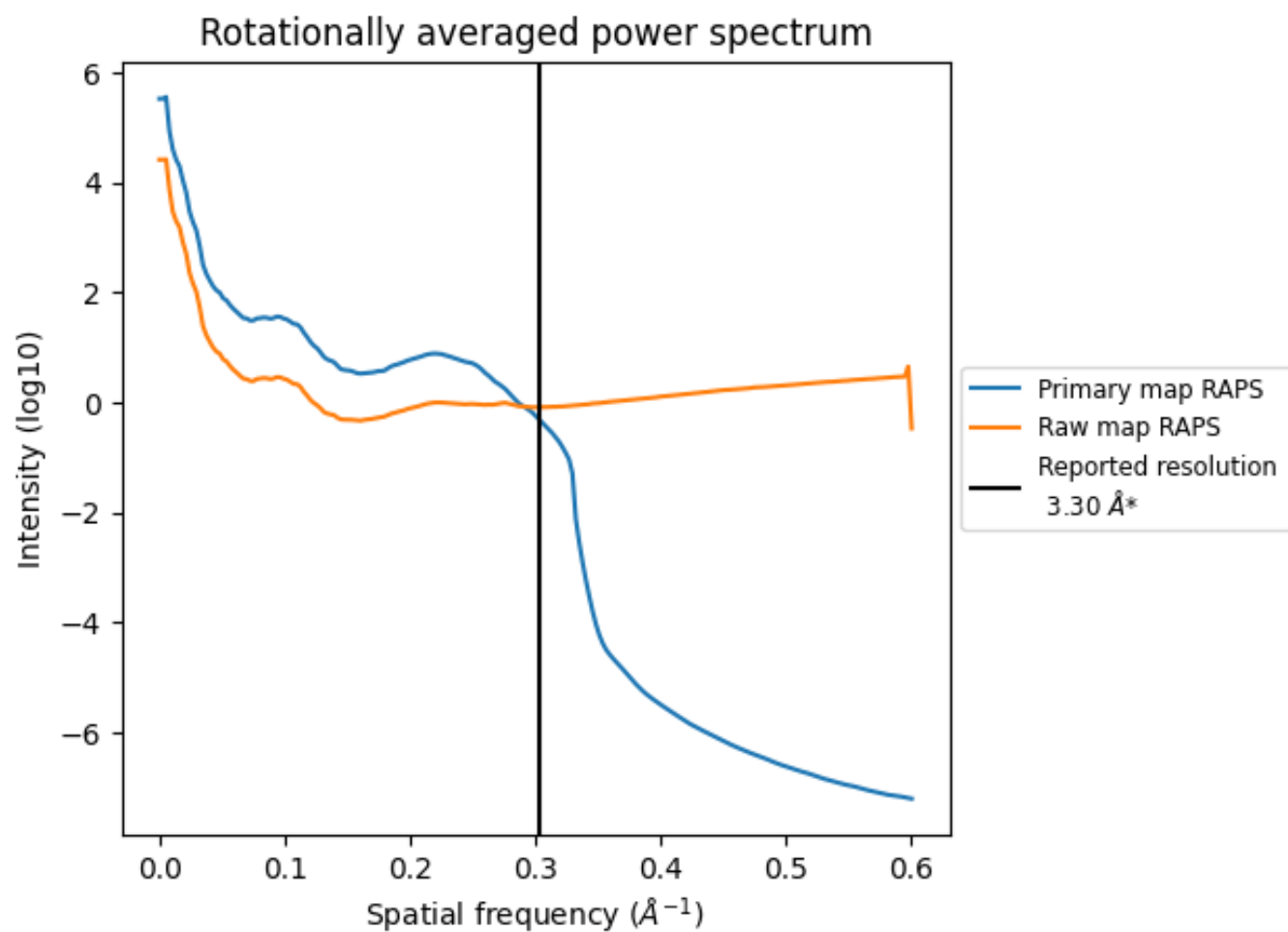
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 235 nm³; this corresponds to an approximate mass of 212 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 ⓘ

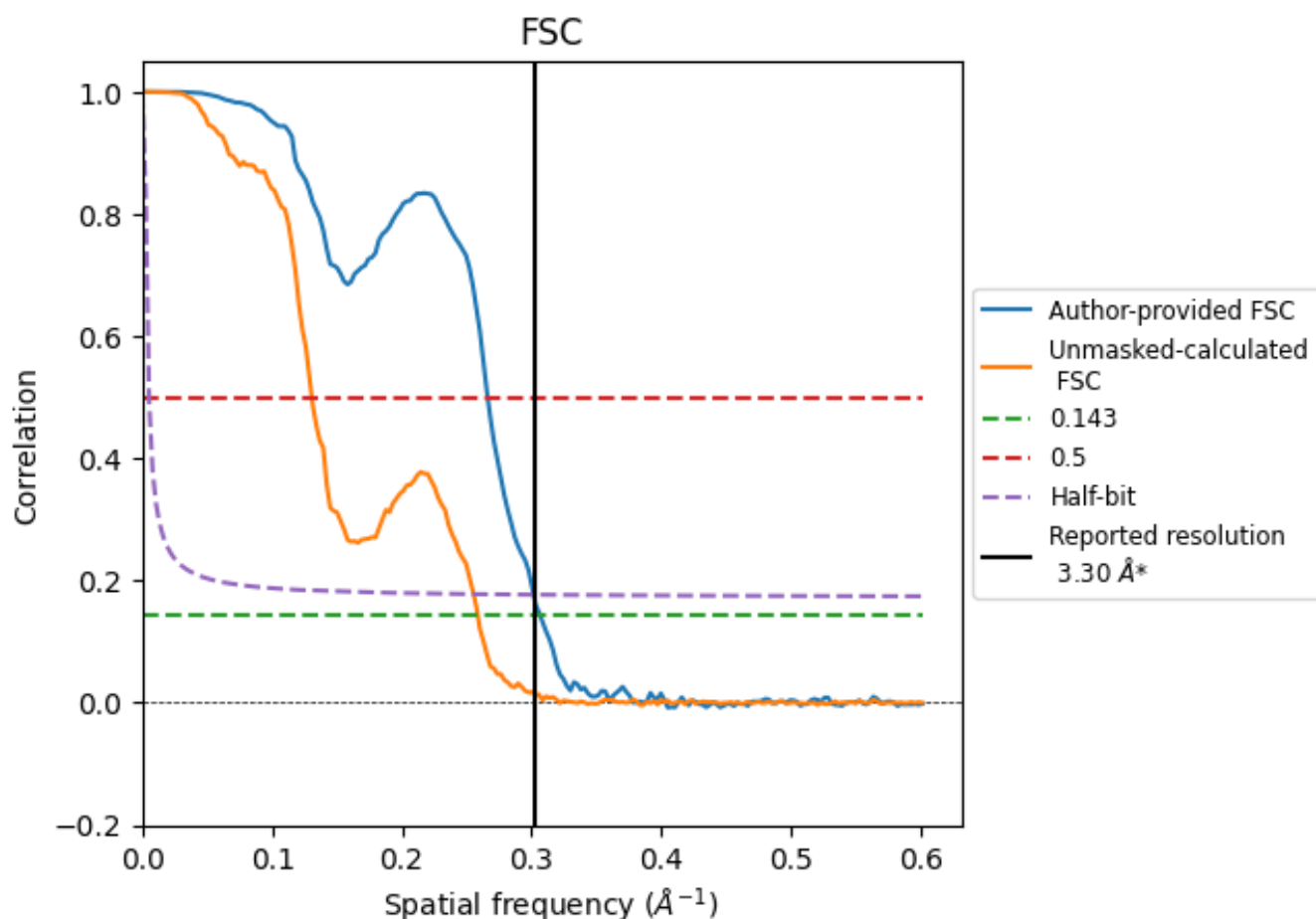


*Reported resolution corresponds to spatial frequency of $0.303 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.303 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

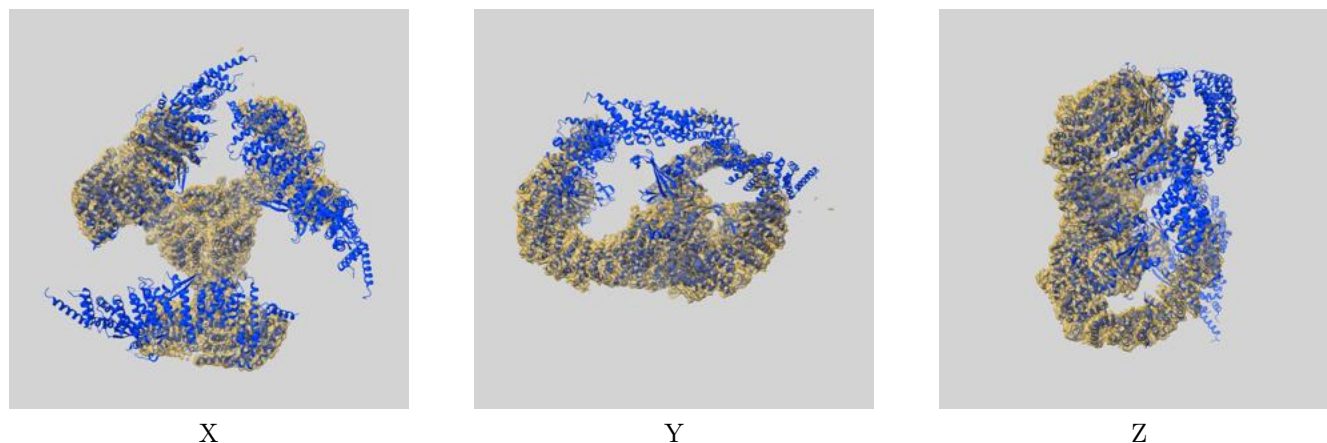
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.26	3.76	3.32
Unmasked-calculated*	3.87	7.65	3.92

*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 3.87 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

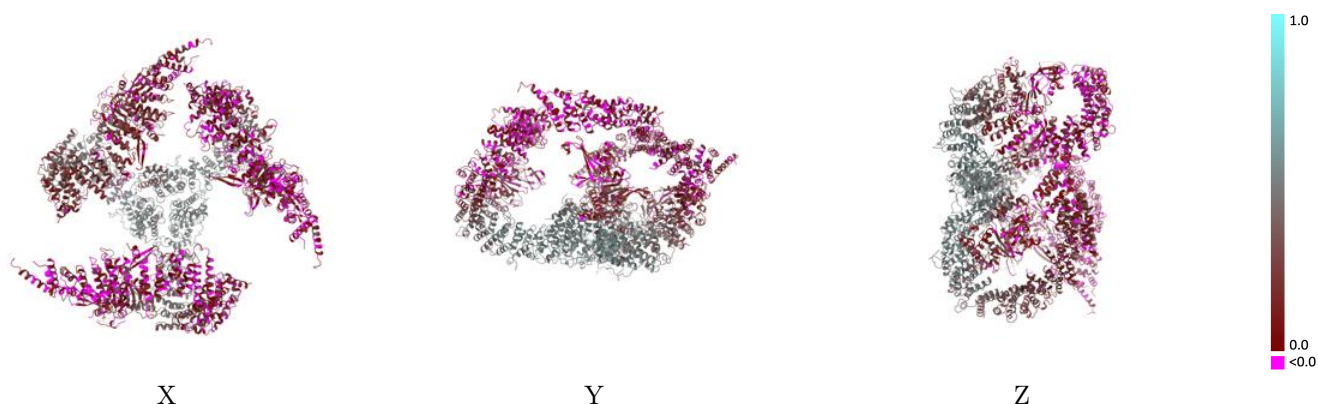
This section contains information regarding the fit between EMDB map EMD-14368 and PDB model 7YXX. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



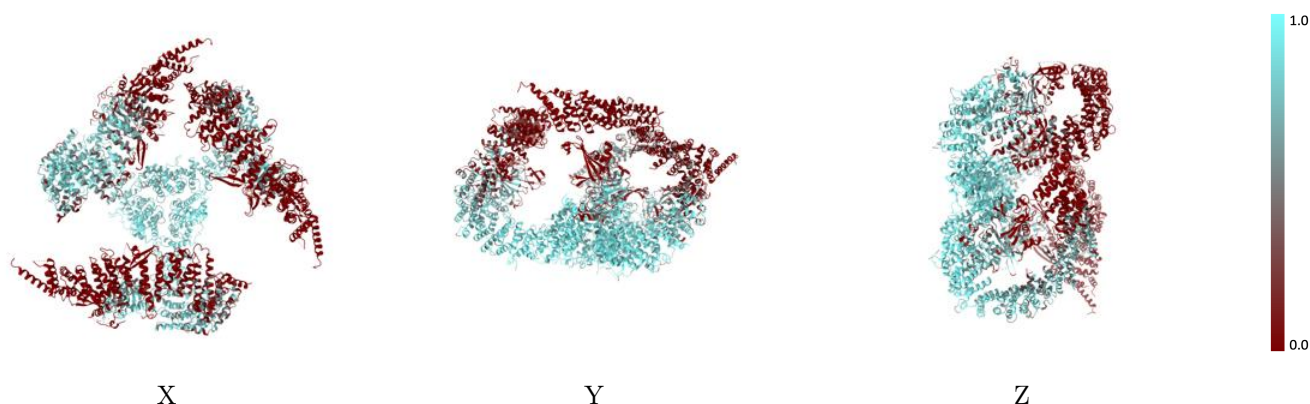
The images above show the 3D surface view of the map at the recommended contour level 0.221 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



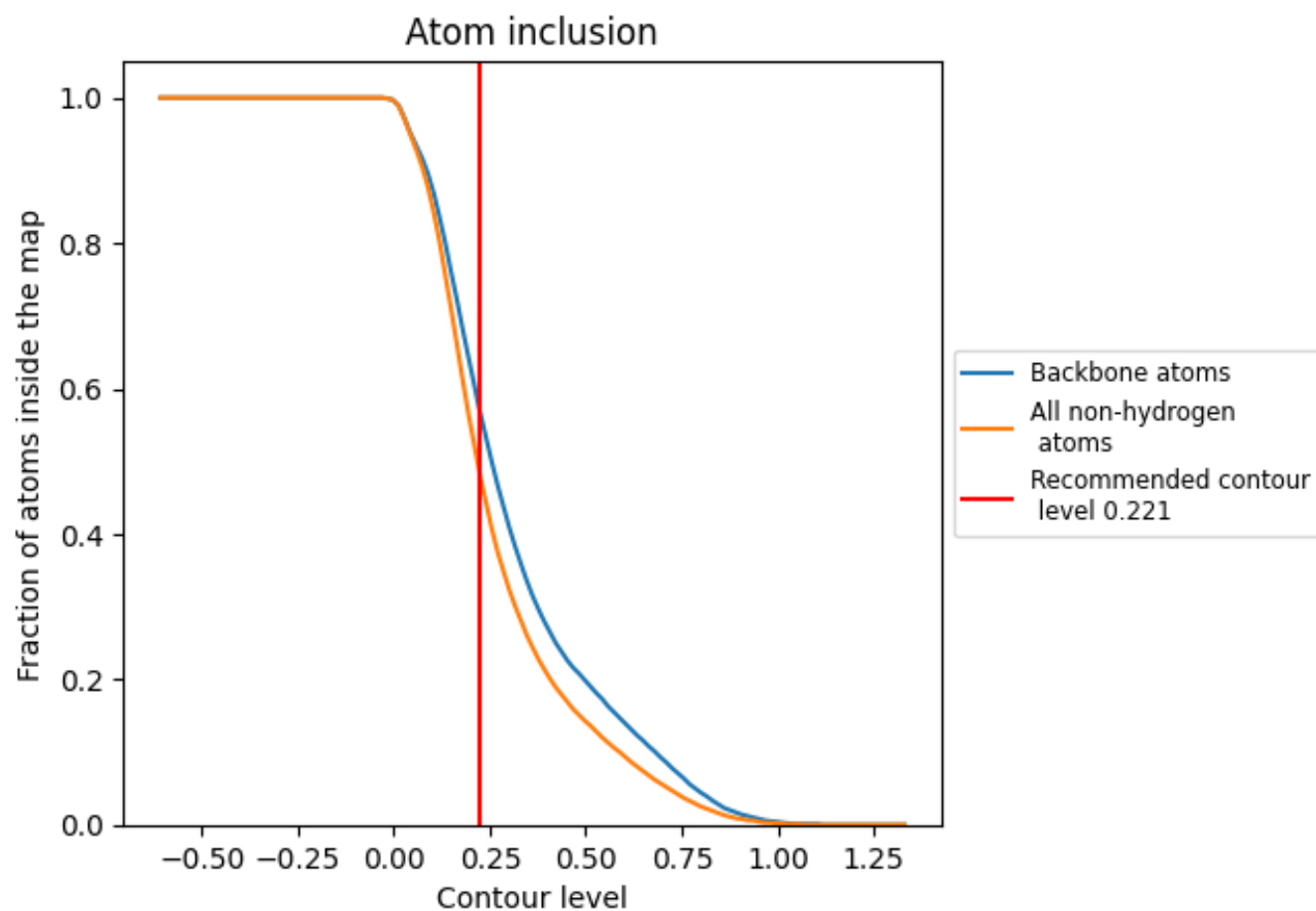
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.221).

9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 49% 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 (0.221) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4900	0.2580
A	0.5790	0.3010
B	0.4570	0.2330
C	0.4330	0.2400

