



wwPDB EM Validation Summary Report ⓘ

Apr 6, 2026 – 01:10 AM UTC

PDB ID : 9V3S / pdb_00009v3s
EMDB ID : EMD-64755
Title : Nav1.5 in complex with quinidine-azo
Authors : Huang, Z.; Li, Z.; Liu, S.
Deposited on : 2025-05-22
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.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

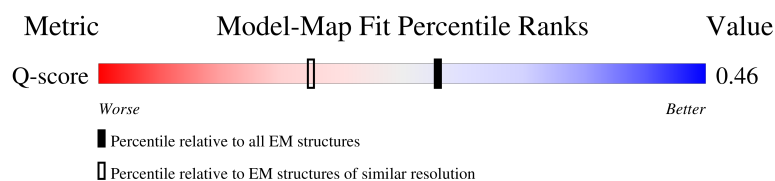
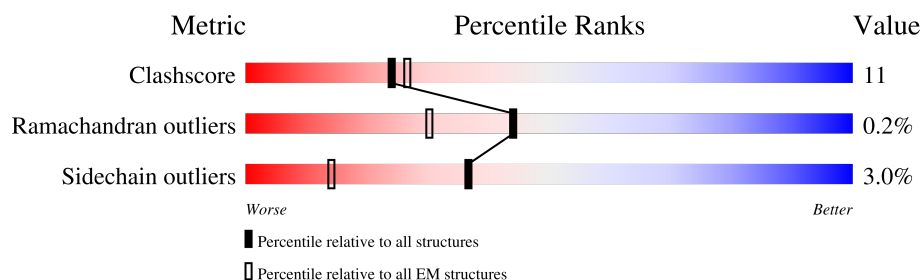
1 Overall quality at a glance

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	1618	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9402 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 Sodium channel protein type 5 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1151	9237	6115	1458	1591	73	0	0

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-42	MET	-	initiating methionine	UNP Q14524
A	-41	ALA	-	expression tag	UNP Q14524
A	-40	SER	-	expression tag	UNP Q14524
A	-39	TRP	-	expression tag	UNP Q14524
A	-38	SER	-	expression tag	UNP Q14524
A	-37	HIS	-	expression tag	UNP Q14524
A	-36	PRO	-	expression tag	UNP Q14524
A	-35	GLN	-	expression tag	UNP Q14524
A	-34	PHE	-	expression tag	UNP Q14524
A	-33	GLU	-	expression tag	UNP Q14524
A	-32	LYS	-	expression tag	UNP Q14524
A	-31	GLY	-	expression tag	UNP Q14524
A	-30	GLY	-	expression tag	UNP Q14524
A	-29	GLY	-	expression tag	UNP Q14524
A	-28	ALA	-	expression tag	UNP Q14524
A	-27	ARG	-	expression tag	UNP Q14524
A	-26	GLY	-	expression tag	UNP Q14524
A	-25	GLY	-	expression tag	UNP Q14524
A	-24	SER	-	expression tag	UNP Q14524
A	-23	GLY	-	expression tag	UNP Q14524
A	-22	GLY	-	expression tag	UNP Q14524
A	-21	GLY	-	expression tag	UNP Q14524
A	-20	SER	-	expression tag	UNP Q14524
A	-19	TRP	-	expression tag	UNP Q14524
A	-18	SER	-	expression tag	UNP Q14524
A	-17	HIS	-	expression tag	UNP Q14524
A	-16	PRO	-	expression tag	UNP Q14524
A	-15	GLN	-	expression tag	UNP Q14524

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	PHE	-	expression tag	UNP Q14524
A	-13	GLU	-	expression tag	UNP Q14524
A	-12	LYS	-	expression tag	UNP Q14524
A	-11	GLY	-	expression tag	UNP Q14524
A	-10	PHE	-	expression tag	UNP Q14524
A	-9	ASP	-	expression tag	UNP Q14524
A	-8	TYR	-	expression tag	UNP Q14524
A	-7	LYS	-	expression tag	UNP Q14524
A	-6	ASP	-	expression tag	UNP Q14524
A	-5	ASP	-	expression tag	UNP Q14524
A	-4	ASP	-	expression tag	UNP Q14524
A	-3	ASP	-	expression tag	UNP Q14524
A	-2	LYS	-	expression tag	UNP Q14524
A	-1	GLY	-	expression tag	UNP Q14524
A	0	THR	-	expression tag	UNP Q14524

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



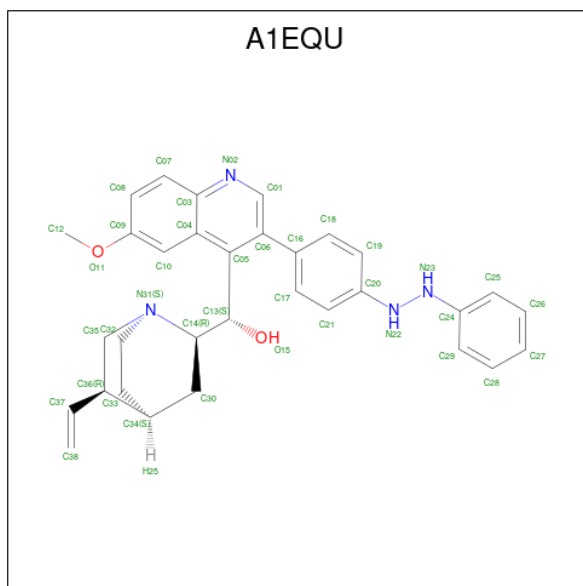
Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 3 is ({S})-[(1 {S},2 {R},4 {S},5 {R})-5-ethenyl-1-azabicyclo[2.2.2]octan-2-yl]-[6-methoxy-3-[4-(2-phenylhydrazinyl)phenyl]quinolin-4-yl]methanol (CCD ID: A1EQU) (formula: C₃₂H₃₄N₄O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			38	32	4	2	

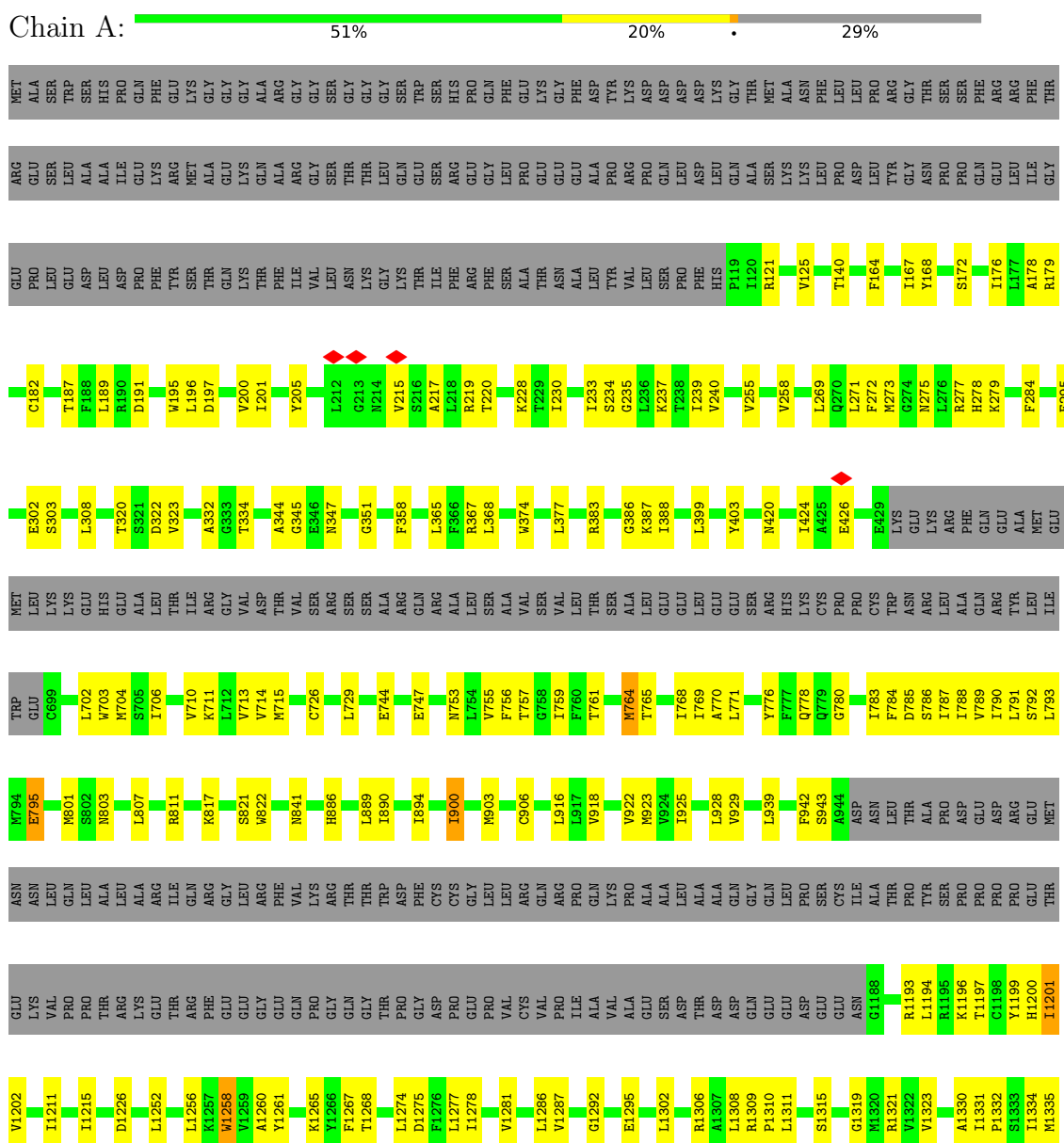
- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Na	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: Sodium channel protein type 5 subunit alpha



THR	VAL	M1645	M1542	M1461	M1336
GLU	SER	L1646	V1543	T1462	V1337
PRO	GLY	L1647	T1544	N1463	L1338
ASP	ASP	M1545	M1546	L1464	L1339
ARG	ARG	M1651	M1547	F1465	V1340
ILE	ILE	M1652	E1548	I1466	C1341
HIS	HIS	S1653	T1549	G1467	L1342
ASP	ASP	L1654	Q1552	V1468	I1343
PHE	PHE	A1656	S1553	I1470	F1344
ASP	ASP	I1660	M1564	D1471	W1345
LEU	LEU	F1669	L1565	N1472	C1363
PHE	PHE	I1673	F1567	Q1475	I1364
ALA	ALA	Y1681	V1568	K1478	N1365
GLU	GLU	Y1685	I1570	E1368	Q1366
THR	THR	E1686	L1582	I1485	E1369
GLY	GLY	A1686	R1583	F1486	N1379
GLY	GLY	M1691	H1584	M1487	N1388
GLN	GLN	C1703	Y1585	T1488	G1391
PHE	PHE	I1707	Y1586	E1489	E1392
ILE	ILE	D1714	M1592	Q1491	L1393
TYR	TYR	G1715	D1595	K1492	Y1394
SER	SER	L1716	F1596	K1493	W1395
VAL	VAL	Y1720	V1597	Y1494	V1400
LEU	LEU	I1723	V1598	K1499	Y1409
SER	SER	T1724	L1601	K1504	V1415
ASP	ASP	G1724	Y1607	K1508	K1419
ALA	ALA	P1725	L1608	P1509	G1420
PHE	PHE	P1726	I1611	R1512	W1421
MET	MET	Y1727	I1612	L1514	M1422
ALA	ALA	C1728	Y1615	N1515	D1430
ALA	ALA	D1729	F1622	S1431	S1431
ASN	ASN	N1734	R1626	Q1518	R1432
PRO	PRO	S1738	L1627	G1519	Q1437
SER	SER	F1752	A1628	F1520	P1438
LYS	LYS	I1758	R1629	I1521	M1443
ILE	ILE	I1762	I1630	I1524	L1444
THR	THR	V1763	G1631	V1525	Y1445
THR	THR	I1766	R1632	Q1528	M1446
LEU	LEU	M1766	I1633	D1531	Y1447
ASN	ASN	Y1767	I1634	V1532	I1448
MET	MET	I1770	R1635	T1533	Y1449
ASP	ASP	E1781	K1641	I1534	F1450
LEU	LEU	SER	G1642	M1535	V1451
PRO	PRO		I1643	I1538	I1454
MET	MET		R1644	F1456	I1455
				G1457	G1457

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	287376	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI SPIRIT	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.725	Depositor
Minimum map value	-2.461	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.077	Depositor
Recommended contour level	0.23	Depositor
Map size (Å)	274.9952, 274.9952, 274.9952	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0742, 1.0742, 1.0742	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: A1EQU, NAG, NA

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	0.16	0/9462	0.42	0/12835

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9237	0	9414	204	0
2	A	126	0	117	2	0
3	A	38	0	0	3	0
4	A	1	0	0	0	0
All	All	9402	0	9531	204	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 11.

The worst 5 of 204 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:A:1345:TRP:HZ2	3:A:1910:A1EQU:C28	1.86	0.88
1:A:1345:TRP:CZ2	3:A:1910:A1EQU:C28	2.58	0.86
1:A:1337:VAL:HG11	1:A:1468:VAL:HG11	1.62	0.81
1:A:1512:ARG:HD2	1:A:1514:LEU:HD23	1.65	0.79
1:A:714:VAL:HG13	1:A:715:MET:HE3	1.67	0.75

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	1145/1618 (71%)	1079 (94%)	64 (6%)	2 (0%)	43 76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	182	CYS
1	A	1553	SER

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	1013/1417 (72%)	983 (97%)	30 (3%)	36 69

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1194	LEU
1	A	1647	LEU
1	A	1286	LEU
1	A	1766	MET
1	A	1490	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1383	GLN
1	A	1476	GLN
1	A	1491	GLN
1	A	278	HIS
1	A	275	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](#)

Of 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	A	1903	1	14,14,15	0.80	0	17,19,21	1.29	1 (5%)
2	NAG	A	1907	1	14,14,15	0.74	0	17,19,21	0.75	0
2	NAG	A	1909	1	14,14,15	0.73	0	17,19,21	0.84	0
2	NAG	A	1908	1	14,14,15	0.68	0	17,19,21	0.81	0
2	NAG	A	1905	1	14,14,15	0.70	0	17,19,21	0.87	1 (5%)
2	NAG	A	1902	1	14,14,15	0.76	0	17,19,21	0.75	0
3	A1EQU	A	1910	-	42,43,43	5.81	17 (40%)	60,61,61	2.29	20 (33%)
2	NAG	A	1904	1	14,14,15	0.75	0	17,19,21	0.93	0
2	NAG	A	1901	1	14,14,15	0.72	0	17,19,21	0.75	0
2	NAG	A	1906	1	14,14,15	0.73	0	17,19,21	0.85	0

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
2	NAG	A	1903	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1907	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1909	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1908	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1905	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1902	1	-	1/6/23/26	0/1/1/1
3	A1EQU	A	1910	-	-	7/21/42/42	0/7/6/6
2	NAG	A	1904	1	-	1/6/23/26	0/1/1/1
2	NAG	A	1901	1	-	1/6/23/26	0/1/1/1
2	NAG	A	1906	1	-	0/6/23/26	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1910	A1EQU	C32-N31	-22.75	1.05	1.47
3	A	1910	A1EQU	C35-N31	-17.05	1.20	1.47
3	A	1910	A1EQU	C36-C34	-10.76	1.35	1.54
3	A	1910	A1EQU	C33-C34	-9.85	1.30	1.53
3	A	1910	A1EQU	C14-N31	-8.74	1.29	1.48

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1910	A1EQU	C20-N22-N23	6.60	136.81	119.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1910	A1EQU	C24-N23-N22	6.59	136.79	119.14
3	A	1910	A1EQU	C30-C14-N31	-5.90	104.27	110.50
3	A	1910	A1EQU	C01-C06-C16	-5.13	112.15	119.56
3	A	1910	A1EQU	O15-C13-C14	3.87	117.58	109.69

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

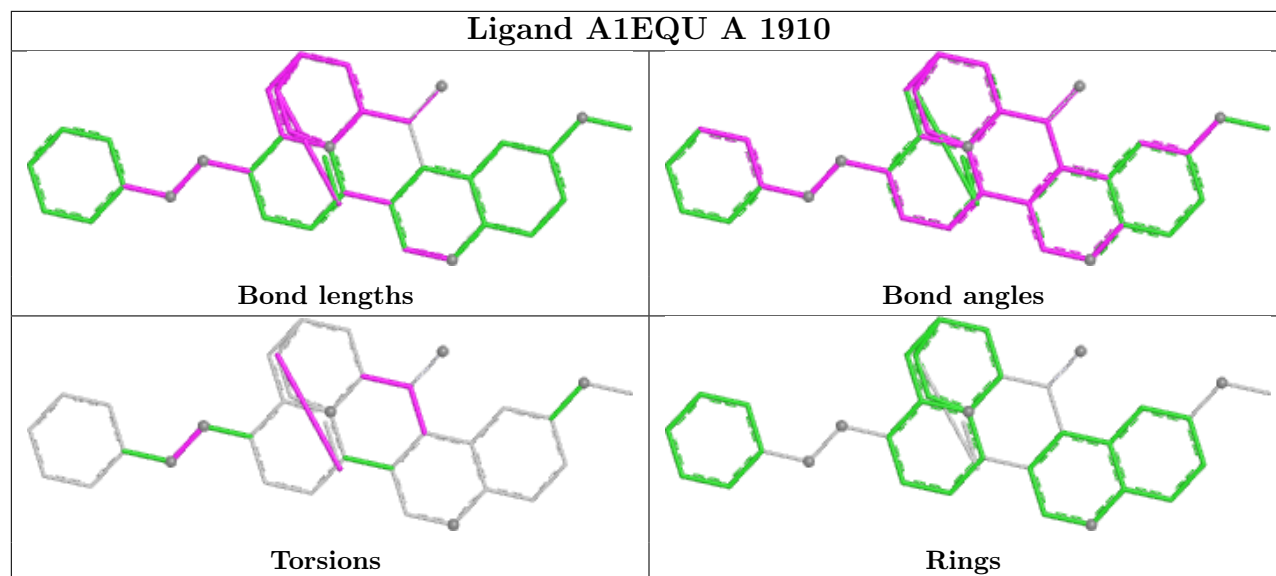
Mol	Chain	Res	Type	Atoms
3	A	1910	A1EQU	C05-C13-C14-C30
3	A	1910	A1EQU	O15-C13-C14-C30
3	A	1910	A1EQU	O15-C13-C14-N31
3	A	1910	A1EQU	C20-N22-N23-C24
2	A	1901	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1909	NAG	2	0
3	A	1910	A1EQU	3	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.

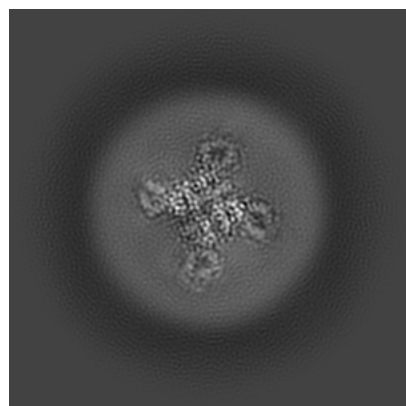
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64755. These allow visual inspection of the internal detail of the map and identification of artifacts.

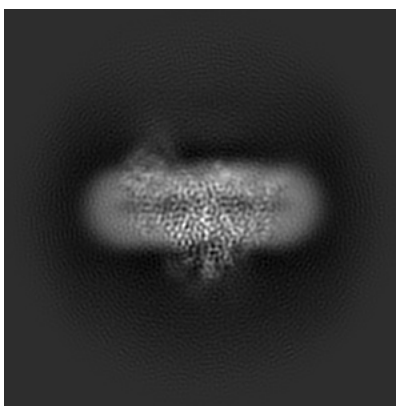
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

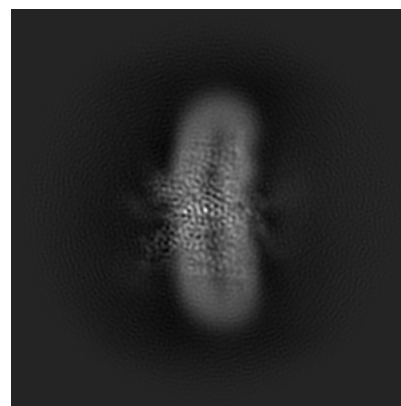
6.1.1 Primary map



X

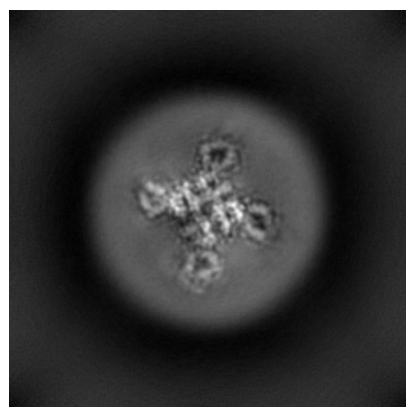


Y

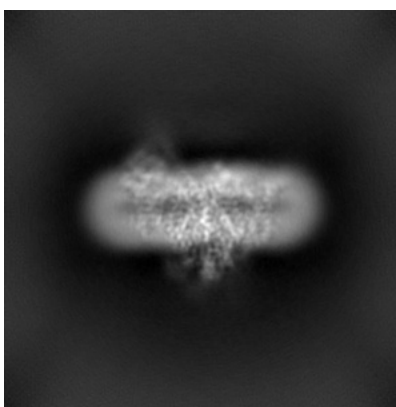


Z

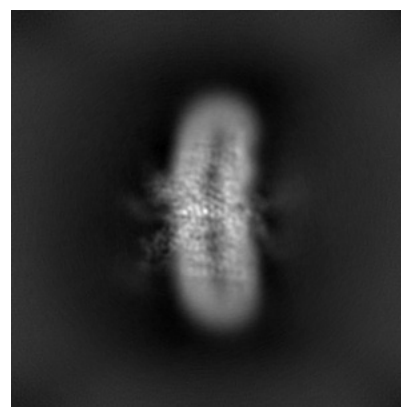
6.1.2 Raw map



X



Y

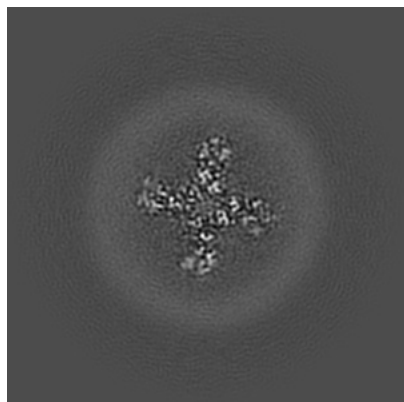


Z

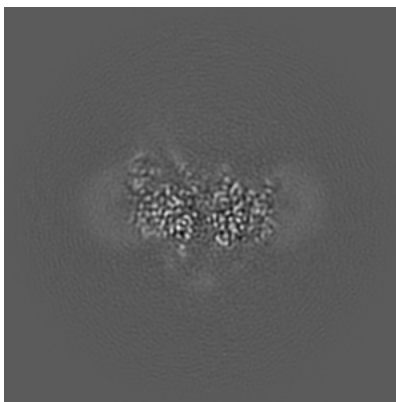
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

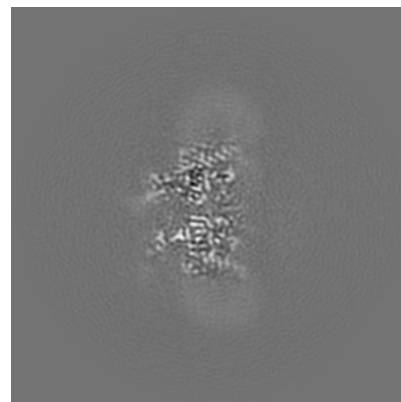
6.2.1 Primary map



X Index: 128

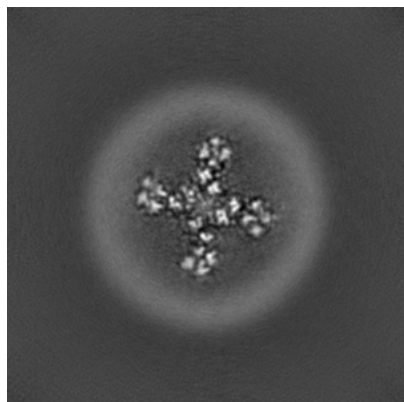


Y Index: 128

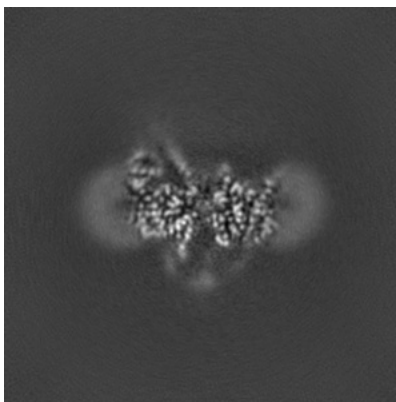


Z Index: 128

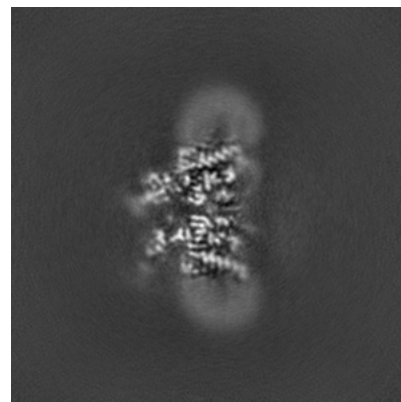
6.2.2 Raw map



X Index: 128



Y Index: 128

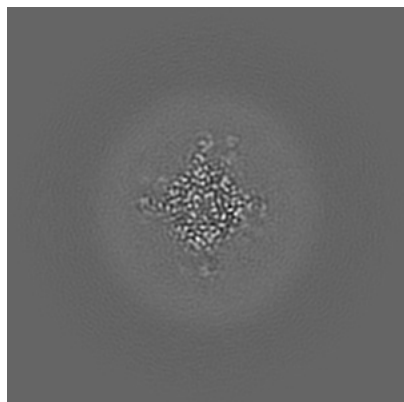


Z Index: 128

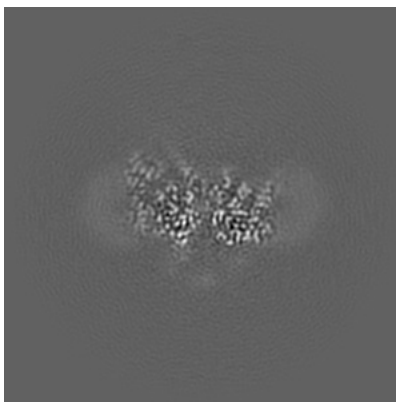
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

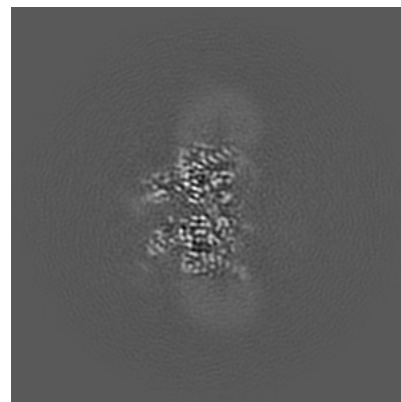
6.3.1 Primary map



X Index: 116

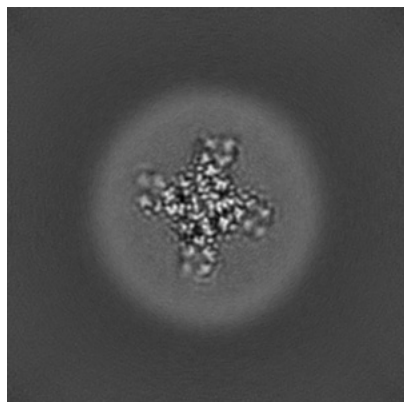


Y Index: 126

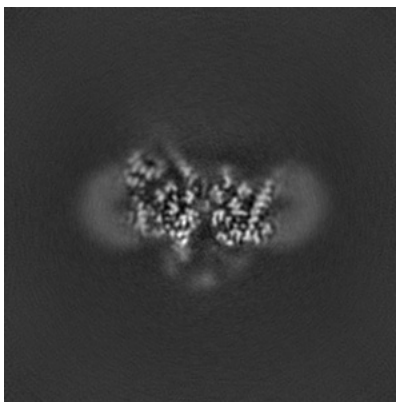


Z Index: 129

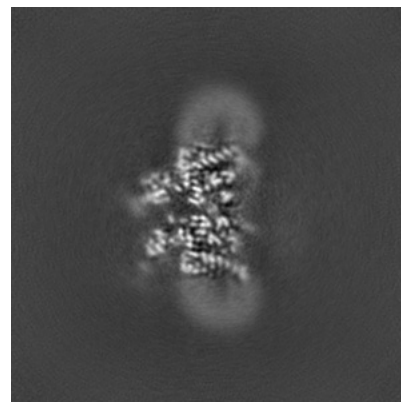
6.3.2 Raw map



X Index: 119



Y Index: 126

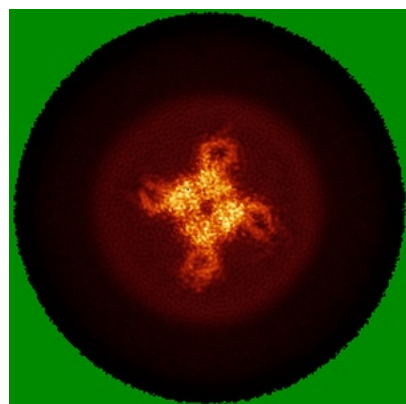


Z Index: 129

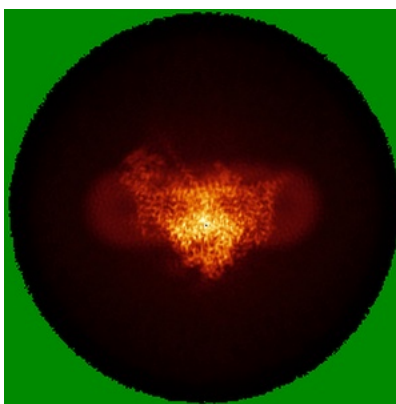
The images above show the largest variance slices of the map in three orthogonal directions.

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

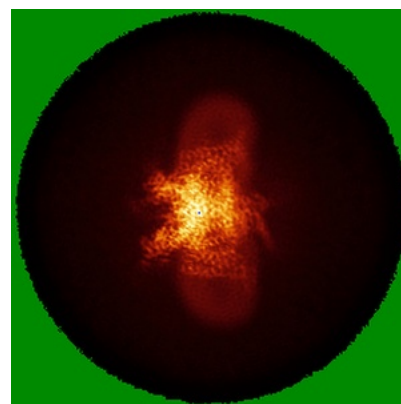
6.4.1 Primary map



X

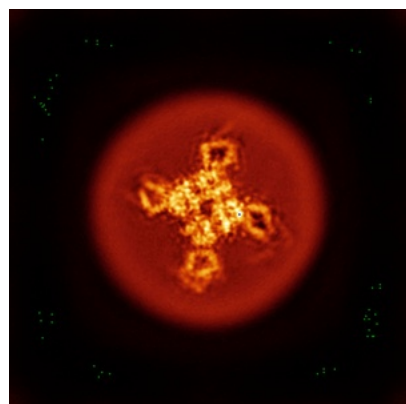


Y

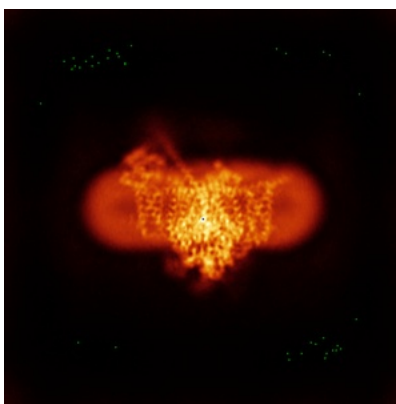


Z

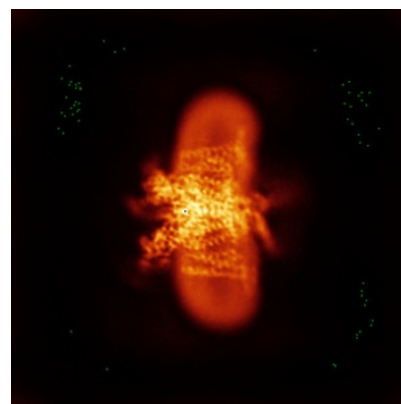
6.4.2 Raw map



X



Y

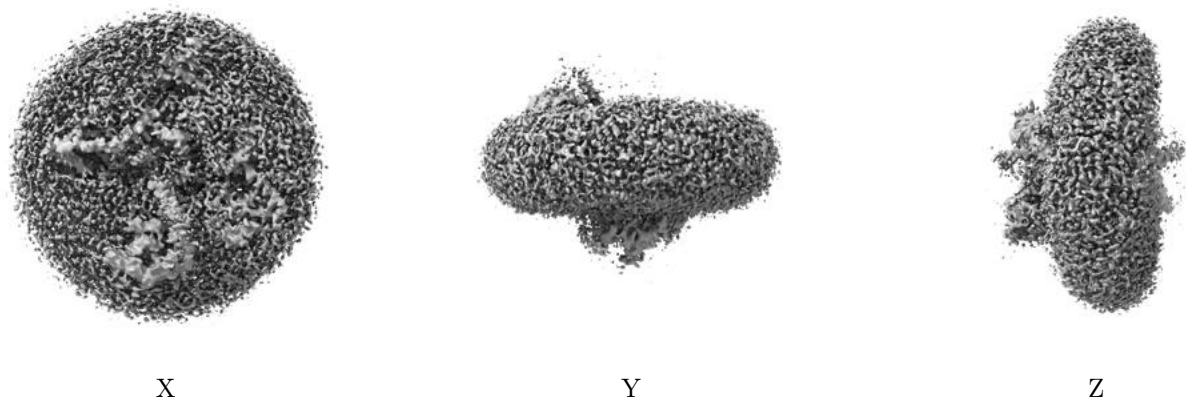


Z

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.

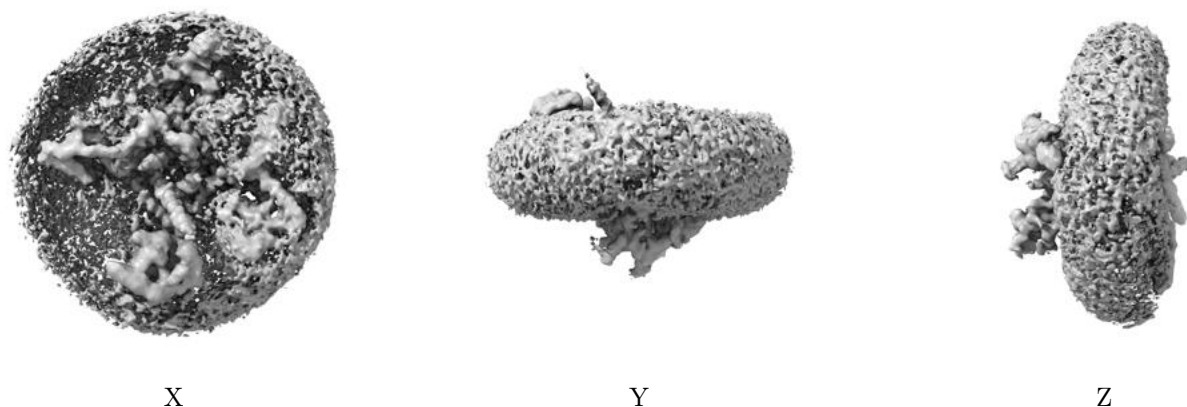
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.23. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

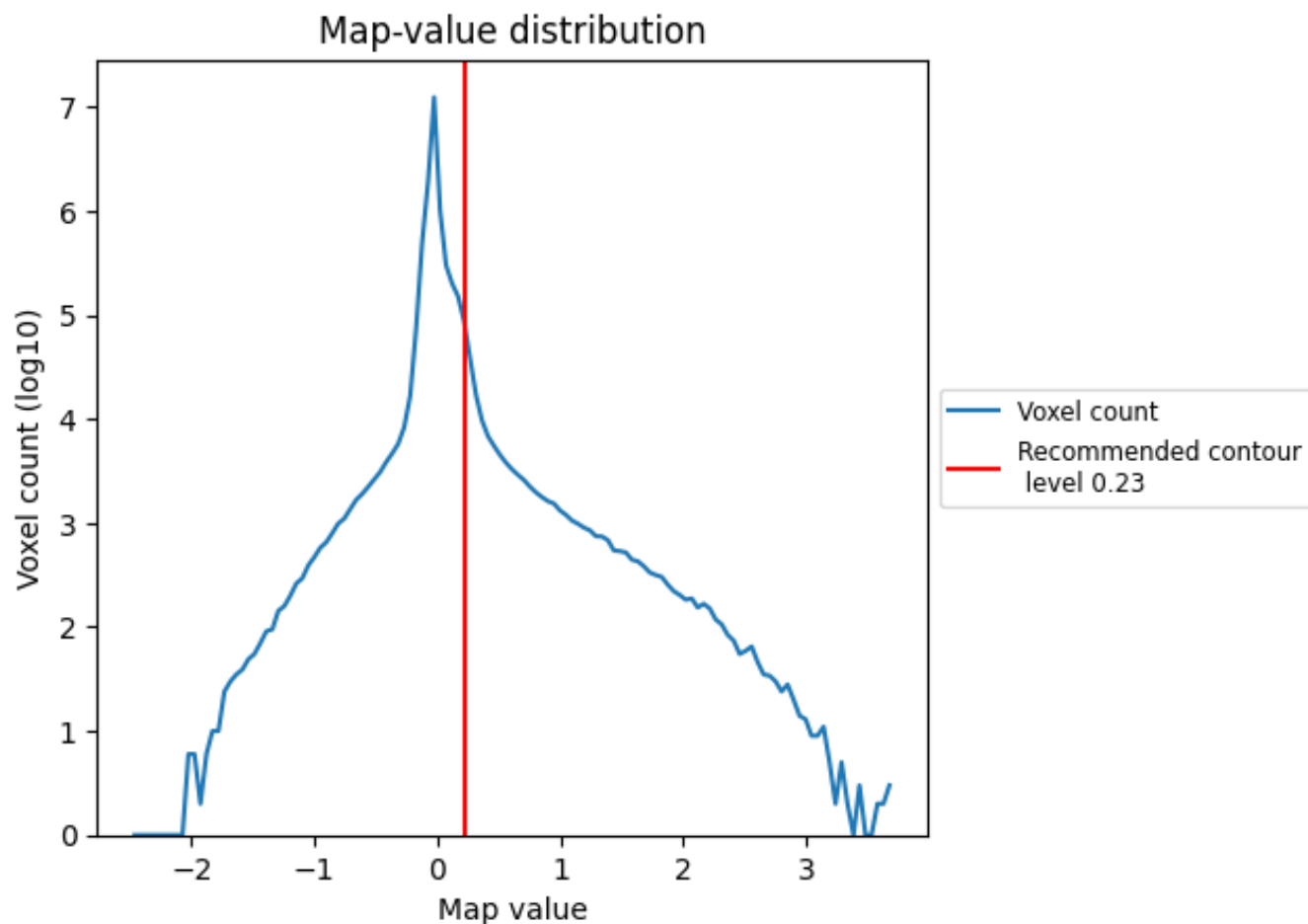
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

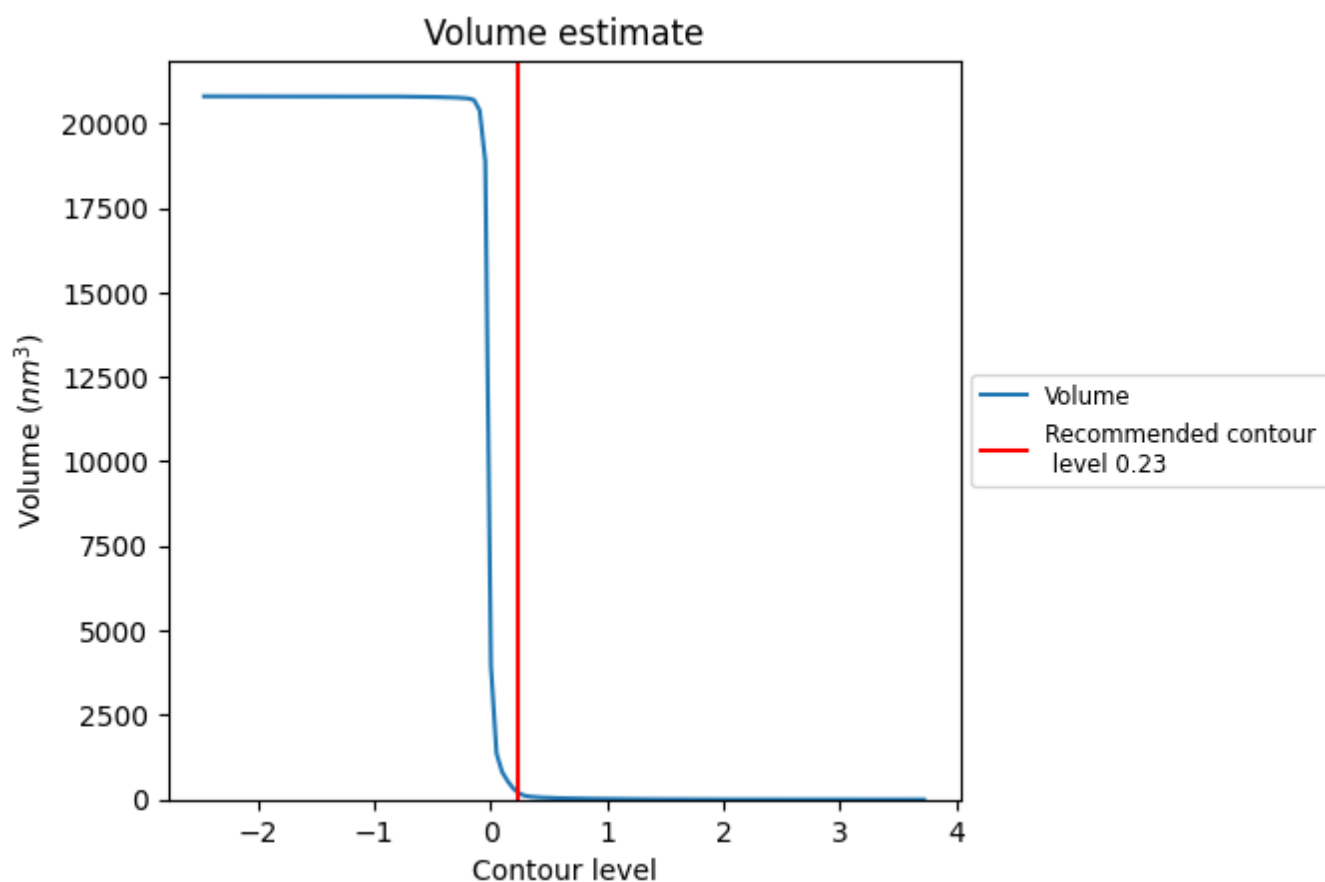
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

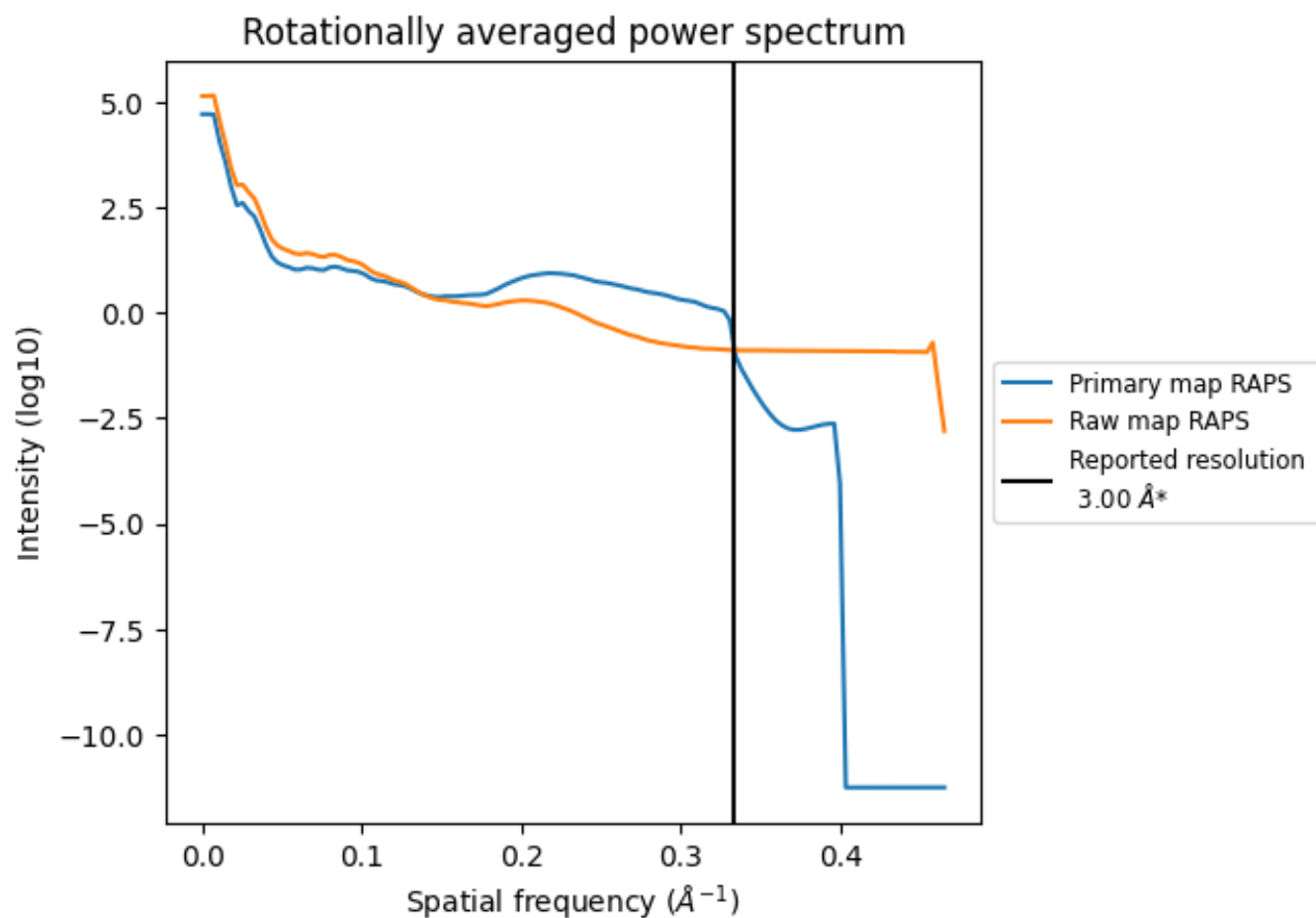
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 229 nm^3 ; this corresponds to an approximate mass of 207 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 ⓘ

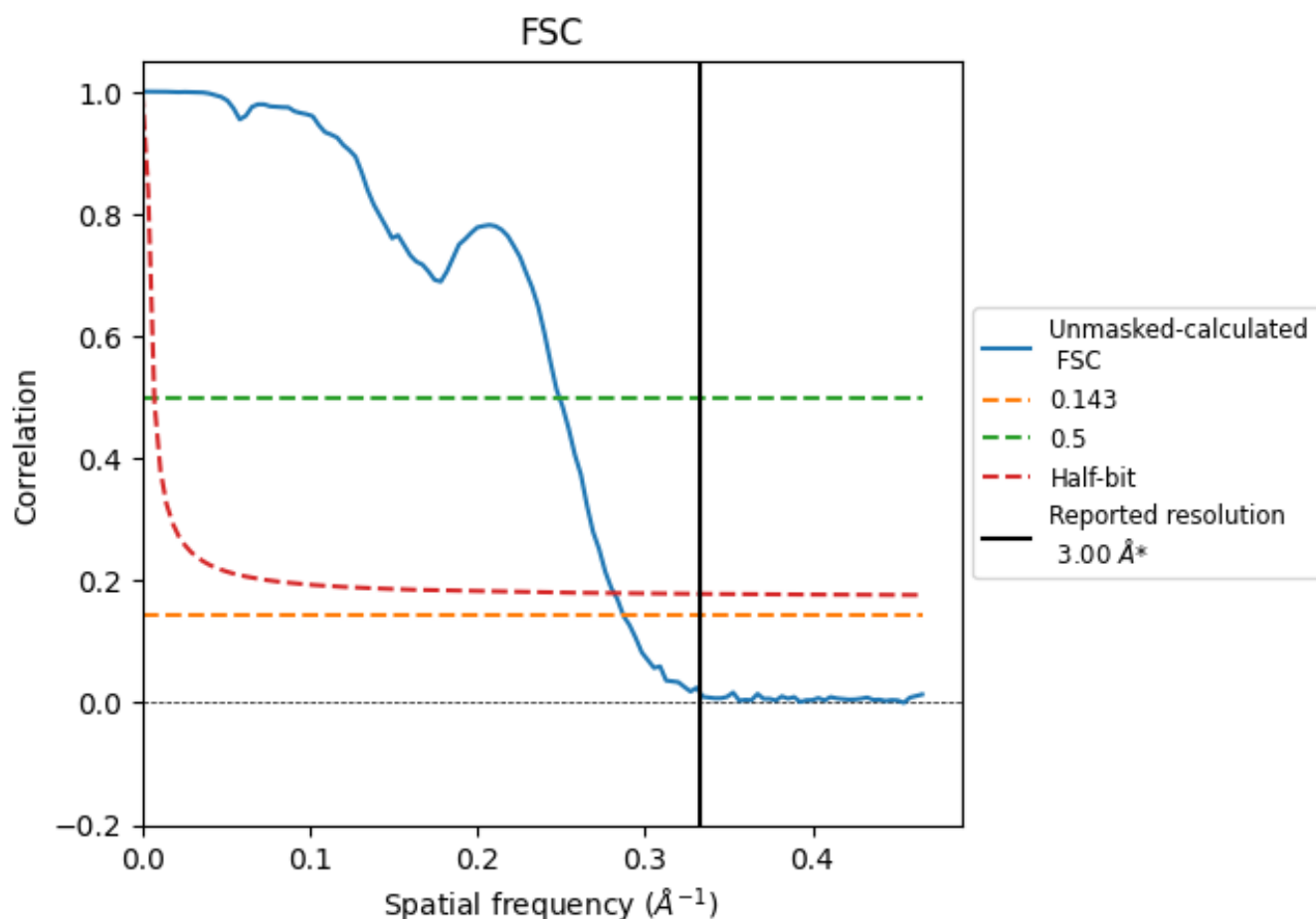


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 \AA^{-1}

8.2 Resolution estimates [i](#)

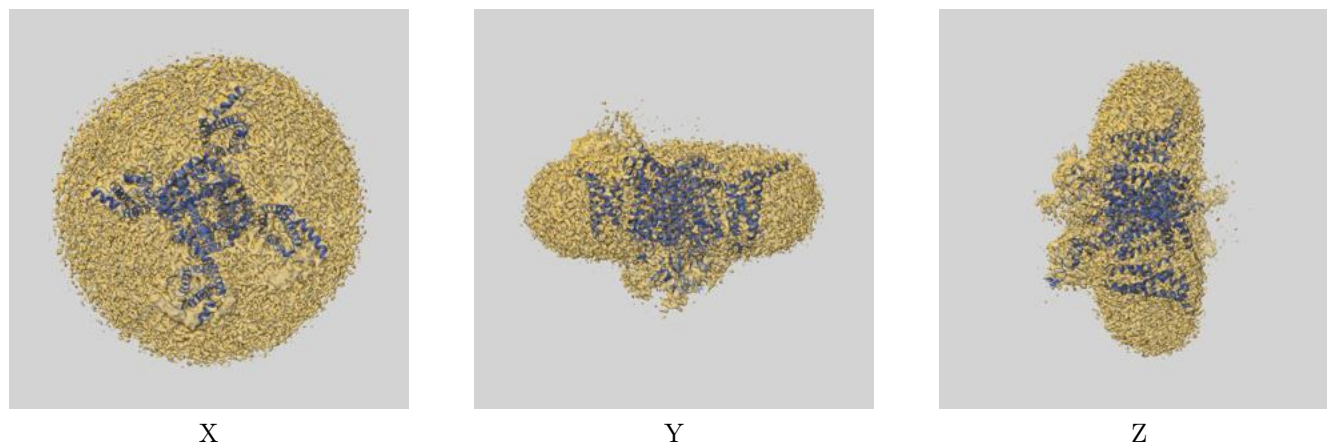
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.48	4.02	3.55

*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 3.48 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

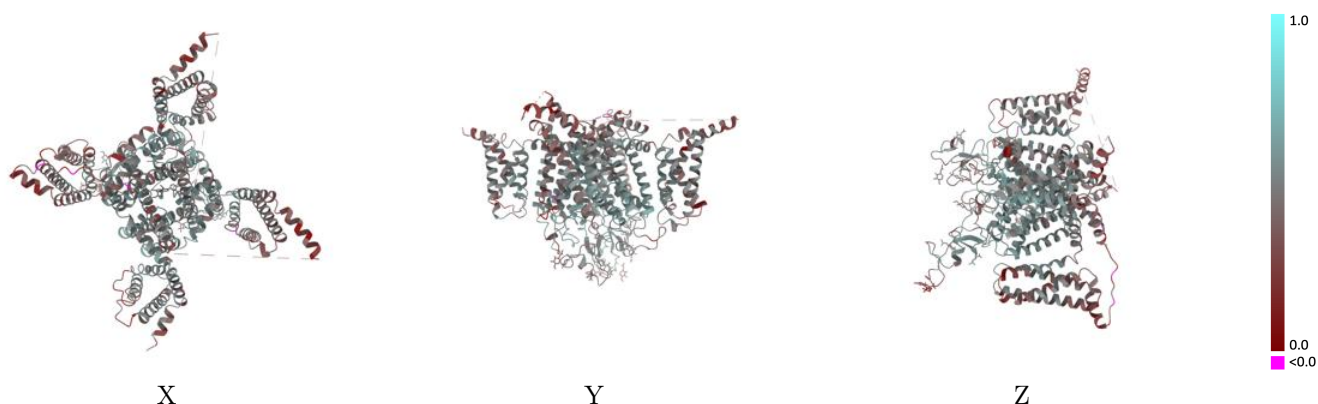
This section contains information regarding the fit between EMDB map EMD-64755 and PDB model 9V3S. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



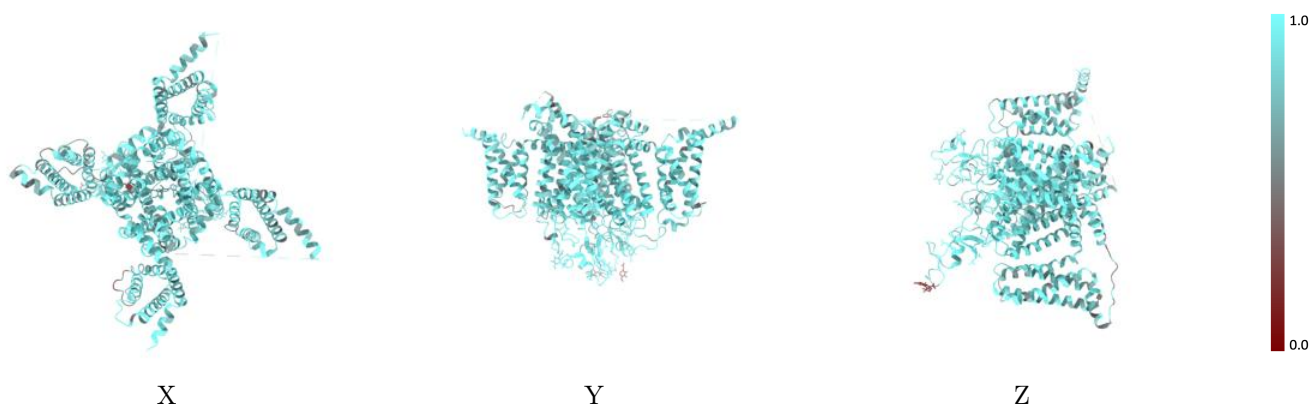
The images above show the 3D surface view of the map at the recommended contour level 0.23 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



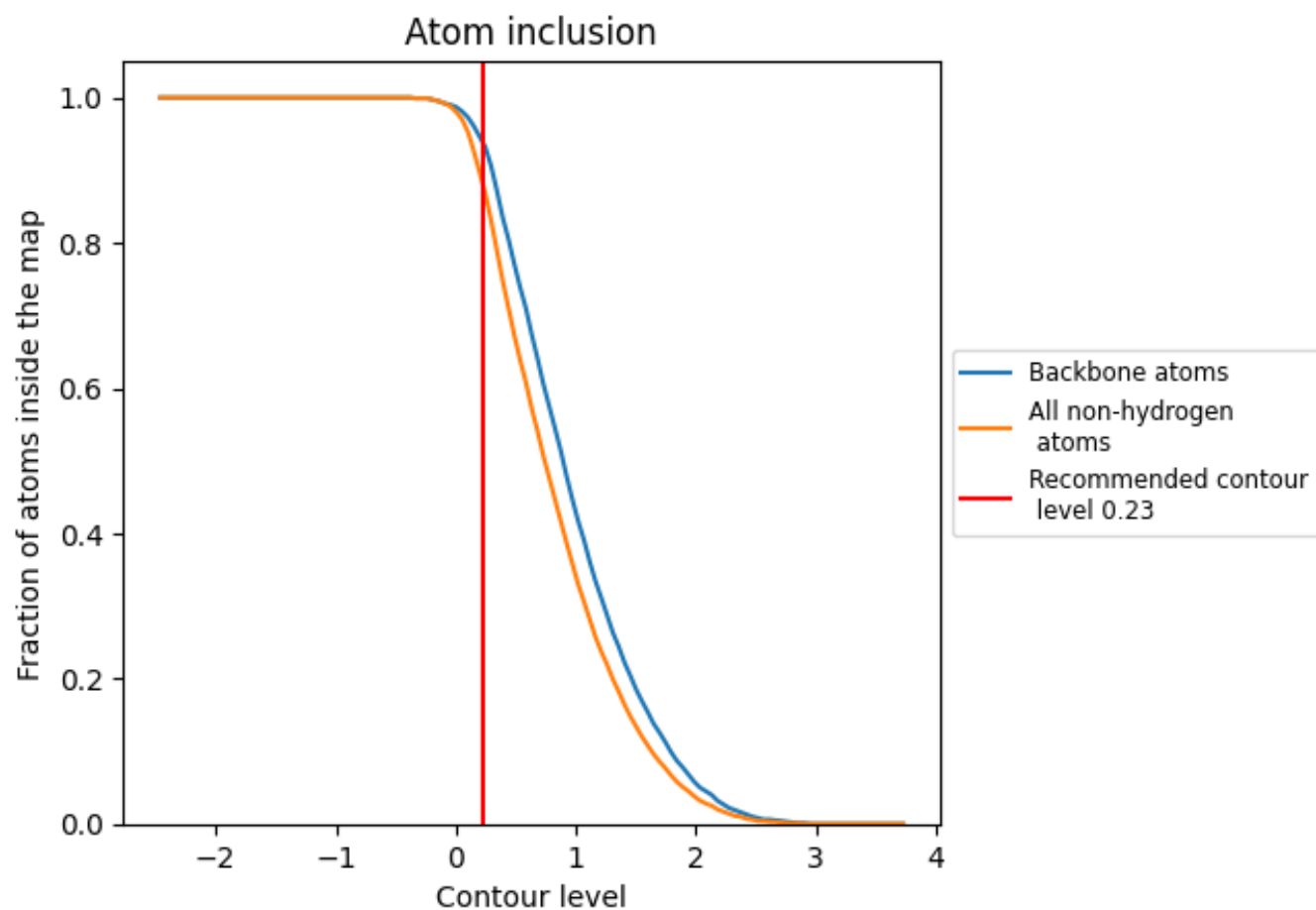
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.23).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 88% 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 (0.23) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8780	<div><div></div></div> 0.4600
A	<div><div></div></div> 0.8780	<div><div></div></div> 0.4600

