



Full wwPDB EM Validation Report ⓘ

Jan 7, 2025 – 03:21 pm GMT

PDB ID : 9GAP
EMDB ID : EMD-51185
Title : CryoEM structure of influenza A RNP-like particle double-stranded assembled with a 12-mer RNA.
Authors : Chenavier, F.; Ruigrok, R.W.H.; Schoehn, G.; Ballandras-Colas, A.; Crepin, T.
Deposited on : 2024-07-29
Resolution : 4.00 Å(reported)

This is a Full wwPDB EM Validation 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:

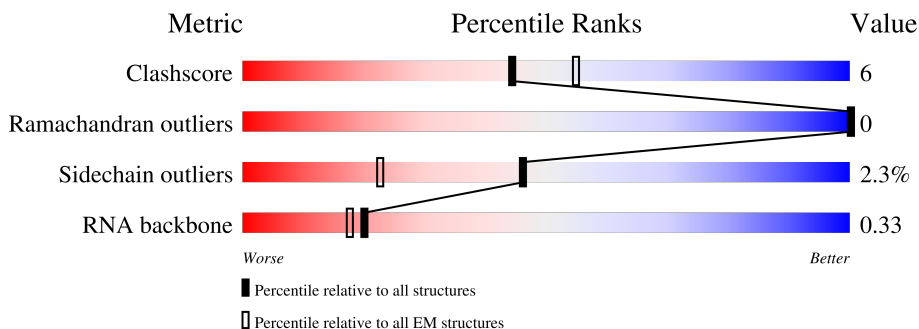
EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

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 4.00 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
RNA backbone	6643	2191

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	12	
1	D	12	
2	A	494	
2	B	494	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 3930 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 RNA chain called RNA (5'-P(UC)6-FAM3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	C	6	Total	C	N	O	P	0	0
			119	54	15	44	6		
1	D	6	Total	C	N	O	P	0	0
			121	54	15	46	6		

- Molecule 2 is a protein called Nucleoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	433	Total	C	N	O	S	0	0
			3436	2125	646	641	24		
2	B	28	Total	C	N	O	S	0	0
			218	139	38	40	1		

There are 20 discrepancies between the modelled and reference sequences:

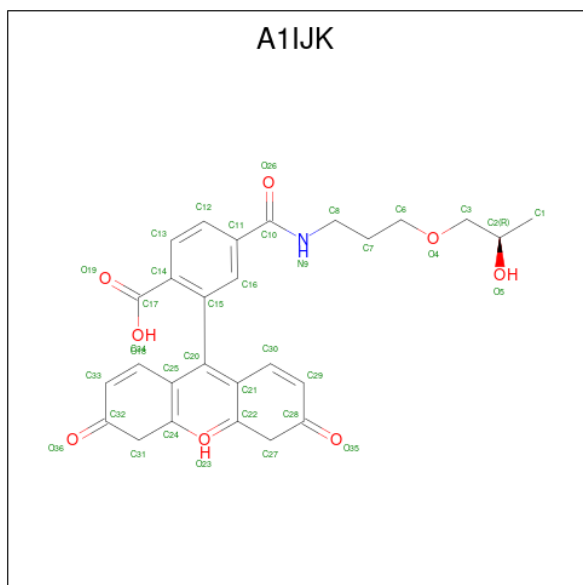
Chain	Residue	Modelled	Actual	Comment	Reference
A	13	HIS	-	expression tag	UNP Q1K9H2
A	14	MET	-	expression tag	UNP Q1K9H2
A	499	LEU	-	expression tag	UNP Q1K9H2
A	500	GLU	-	expression tag	UNP Q1K9H2
A	501	HIS	-	expression tag	UNP Q1K9H2
A	502	HIS	-	expression tag	UNP Q1K9H2
A	503	HIS	-	expression tag	UNP Q1K9H2
A	504	HIS	-	expression tag	UNP Q1K9H2
A	505	HIS	-	expression tag	UNP Q1K9H2
A	506	HIS	-	expression tag	UNP Q1K9H2
B	13	HIS	-	expression tag	UNP Q1K9H2
B	14	MET	-	expression tag	UNP Q1K9H2
B	499	LEU	-	expression tag	UNP Q1K9H2
B	500	GLU	-	expression tag	UNP Q1K9H2
B	501	HIS	-	expression tag	UNP Q1K9H2
B	502	HIS	-	expression tag	UNP Q1K9H2
B	503	HIS	-	expression tag	UNP Q1K9H2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	504	HIS	-	expression tag	UNP Q1K9H2
B	505	HIS	-	expression tag	UNP Q1K9H2
B	506	HIS	-	expression tag	UNP Q1K9H2

- Molecule 3 is 2-[3,6-bis(oxidanylidene)-4,5-dihydroxanthren-9-yl]-4-[3-[(2R)-2-oxidanylpropoxy]propylcarbonyl]benzoic acid (three-letter code: A1IJK) (formula: C₂₇H₂₇NO₈).

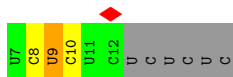
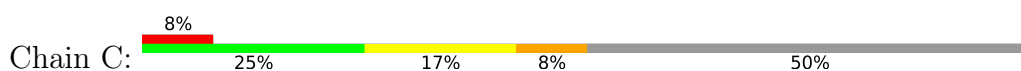


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
3	C	1	36	27	1	8	0

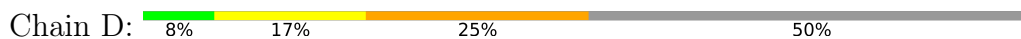
3 Residue-property plots [i](#)

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.

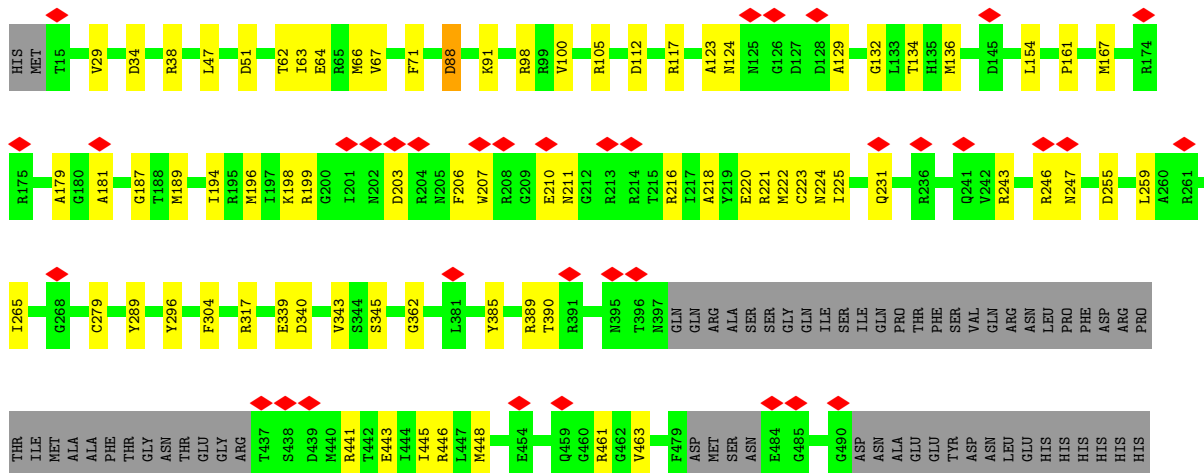
- Molecule 1: RNA (5'-P(UC)6-FAM3')



- Molecule 1: RNA (5'-P(UC)6-FAM3')



- Molecule 2: Nucleoprotein



- Molecule 2: Nucleoprotein



LEU ARG
THR ARG
HIS ASN
MET ASN
MET LYS
TYR TYR
LEU LEU
GLU GLU
HIS HIS
SER HIS
PRO PRO
ASP ASP
ALA ALA
GLY ALA

LEU THR
HIS HIS
MET MET
MET ILE
ILE ILE
LYS LYS
ARG ARG
GLY GLY
HIS HIS
SER SER
ASP ASP
ALA ALA
THR THR
TYR TYR
GLN GLN
ARG ARG
LYS LYS
THR THR
ARG ARG
ALA ALA
GLY GLY
VAL VAL
THR THR
LEU LEU
MET MET
CYS CYS
SER SER
LEU LEU
MET MET
GLY GLY
SER SER
THR THR
LEU LEU
ARG ARG
GLY GLY
ALA ALA
VAL VAL
GLY GLY
ASP ASP
ALA ALA
VAL VAL
LEU LEU
GLY GLY
MET MET
SER SER
THR THR
MET MET
ALA ALA
GLY GLY

LEU ILE
ARG ARG
MET MET
ILE ILE
LYS LYS
ARG ARG
ALA ALA
SER SER
ASP ASP
ASP ASP
PHE PHE
THR THR
TYR TYR
GLY GLY
SER SER
VAL VAL
GLN GLN
ASP ASP
ASN ASN
GLY GLY
ARG ARG
THR THR
PHE PHE
LEU LEU
ILE ILE
SER SER
VAL VAL
VAL VAL
ALA ALA
PRO PRO
GLY GLY
SER SER
THR THR
LEU LEU
MET MET
VAL VAL
SER SER
THR THR
LEU LEU
GLY GLY
ASP ASP
ALA ALA
VAL VAL
GLY GLY
MET MET
SER SER
THR THR
MET MET
ALA ALA
GLY GLY

PHE GLU
THR ASP
SER ILE
LEU ILE
SER ILE
PHE PHE
LEU LEU
ALA ALA
ARG ARG
SER SER
ASP ASP
ASP ASP
ILE ILE
LEU LEU
SER SER
GLN GLN
VAL VAL
TRP TRP
VAL VAL
ALA ALA
HIS HIS
LYS LYS
SER SER
LEU LEU
ARG ARG
GLY GLY
SER SER
VAL VAL
TRP TRP
VAL VAL
ALA ALA
HIS HIS
CYS CYS
SER SER
SER SER
ALA ALA
PRO PRO
PHE PHE
ALA ALA
CYS CYS
TYR TYR
ASP ASP
VAL VAL
SER SER
SER SER
ALA ALA
SER SER
PHE PHE
GLY GLY
TYR TYR
SER SER
LEU LEU
VAL VAL
VAL VAL
SER SER
THR THR
ILE ILE
SER SER
GLY GLY
TYR TYR
ASP ASP
PHE PHE
GLN GLN
VAL VAL
SER SER
THR THR
LEU LEU
SER SER
THR THR
ASN ASN
GLN GLN
SER SER
MET MET
VAL VAL

TYR SER
SER LEU
LEU ILE
SER ILE
ARG ARG
PRO PRO
ASN ASN
GLU GLU
SER SER
ASN ASN
PRO PRO
ALA ALA
HIS HIS
LYS LYS
SER SER
SER SER
GLN GLN
VAL VAL
TRP TRP
VAL VAL
MET MET
ALA ALA
CYS CYS
HIS HIS
SER SER
SER SER
SER SER
ALA ALA
ALA ALA
PHE PHE
GLN GLN
GLN GLN
ASP ASP
SER SER
LEU LEU
SER SER
PHE PHE
SER SER
ILE ILE
SER SER
THR THR
GLY GLY
VAL VAL
VAL VAL
SER SER

THR MET
SER GLU
LEU SER
SER ILE
THR ARG
LEU THR
GLU LEU
LEU LEU
SER SER
SER SER
ALA ALA
TYR TYR
TRP TRP
ALA ALA
ILE ILE
SER SER
THR THR
THR THR
GLN GLN
SER SER
SER SER
GLY GLY
GLY GLY
VAL VAL
SER SER
GLU GLU
LYS LYS
ALA ALA
THR THR
SER SER
SER SER
PRO PRO
ILE ILE
VAL VAL
SER SER
PHE PHE
PRO PRO
GLY GLY
ASP ASP
SER SER
PHE PHE
SER SER
GLY GLY
SER SER
THR THR
LEU LEU
SER SER
THR THR
MET MET
ASP ASP
MET MET

ARG THR
THR GLU
GLU ILE
ILE ILE
ARG ARG
LEU LEU
MET MET
GLU GLU
SER SER
SER SER
ALA ALA
ALA ALA
PRO PRO
GLU GLU
ASP ASP
VAL VAL
SER SER
PHE PHE
GLN GLN
GLY GLY
ARG ARG
SER SER
SER SER
VAL VAL
PHE PHE
GLU GLU
LEU LEU
SER SER
ASP ASP
LYS LYS
ALA ALA
THR THR
SER SER
PRO PRO
ILE ILE
VAL VAL
SER SER
PHE PHE
PRO PRO
SER SER
PHE PHE
ASP ASP
MET MET
SER SER
ASN ASN
GLU GLU
GLY GLY
SER SER
TYR TYR
PHE PHE
PHE PHE
GLY GLY
ASP ASP
ASN ASN
ALA ALA
GLU GLU
GLU GLU
TYR TYR
ASP ASP
ASN ASN
LEU LEU
SER SER
THR THR
MET MET
GLU GLU

HIS
HIS
HIS
HIS
HIS
HIS

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=57.53°, rise=23.87 Å, axial sym=C2	Depositor
Number of segments used	158401	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{Å}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.234	Depositor
Minimum map value	-0.465	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.422	Depositor
Map size (Å)	458.0, 458.0, 458.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.145, 1.145, 1.145	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: A1IJK

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	0.31	0/130	0.85	0/197
1	D	0.97	1/132 (0.8%)	1.02	0/200
2	A	0.27	0/3493	0.54	0/4692
2	B	0.27	0/223	0.54	0/302
All	All	0.32	1/3978 (0.0%)	0.58	0/5391

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	1	U	OP3-P	-10.73	1.48	1.61

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	C	119	0	63	3	0
1	D	121	0	64	2	0
2	A	3436	0	3415	44	0
2	B	218	0	216	6	0
3	C	36	0	0	0	0
All	All	3930	0	3758	48	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 6.

All (48) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:63:ILE:O	2:A:67:VAL:HG23	1.95	0.66
2:A:255:ASP:OD1	2:A:441:ARG:NH1	2.33	0.62
2:A:390:THR:HB	2:B:413:SER:HB2	1.84	0.59
2:A:317:ARG:NH2	2:A:362:GLY:O	2.35	0.59
2:A:216:ARG:HH12	2:A:246:ARG:HA	1.70	0.57
2:A:154:LEU:HD13	2:A:161:PRO:HA	1.87	0.56
2:A:100:VAL:HB	2:A:105:ARG:HH12	1.72	0.55
2:A:91:LYS:NZ	2:A:112:ASP:OD1	2.39	0.55
2:A:132:GLY:O	2:A:136:MET:HG3	2.06	0.55
2:A:47:LEU:O	2:A:98:ARG:NH2	2.41	0.54
1:D:2:C:H2'	1:D:3:U:C6	2.47	0.49
2:A:223:CYS:SG	2:A:243:ARG:HB2	2.52	0.49
2:A:265:ILE:HD12	2:A:448:MET:HE3	1.94	0.49
2:A:339:GLU:HB2	2:B:411:THR:HG22	1.95	0.49
1:C:8:C:H41	2:A:231:GLN:NE2	2.11	0.48
2:A:221:ARG:O	2:A:225:ILE:HG23	2.13	0.47
2:B:407:SER:OG	2:B:408:ILE:N	2.47	0.47
2:A:340:ASP:HB3	2:A:343:VAL:HG12	1.97	0.47
2:A:343:VAL:HG11	2:B:416:ARG:HH11	1.80	0.47
2:B:406:ILE:HD13	2:B:425:ILE:HG12	1.97	0.47
1:C:9:U:C2	2:A:461:ARG:HD3	2.50	0.46
2:A:218:ALA:O	2:A:222:MET:HG3	2.15	0.45
1:C:8:C:H41	2:A:231:GLN:HE22	1.65	0.45
2:A:167:MET:HE1	2:A:187:GLY:HA3	1.97	0.45
2:A:124:ASN:HD22	2:A:129:ALA:HB3	1.82	0.45
2:A:194:ILE:O	2:A:198:LYS:HG2	2.16	0.45
1:D:3:U:H2'	1:D:4:C:C6	2.51	0.45
2:A:29:VAL:HG23	2:A:296:TYR:HB3	2.00	0.44
2:A:64:GLU:HG2	2:A:136:MET:CE	2.48	0.44
2:A:441:ARG:O	2:A:445:ILE:HG13	2.18	0.44
2:A:199:ARG:HG2	2:A:199:ARG:HH11	1.83	0.43
2:A:88:ASP:OD1	2:A:91:LYS:HB2	2.18	0.43
2:A:71:PHE:CE1	2:A:117:ARG:HG2	2.53	0.43
2:A:189:MET:HE3	2:A:189:MET:HB3	1.94	0.43
2:A:259:LEU:HD23	2:A:259:LEU:HA	1.87	0.43
2:A:62:THR:O	2:A:66:MET:HG3	2.18	0.42
2:A:210:GLU:OE1	2:A:211:ASN:N	2.52	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:134:THR:HG21	2:A:179:ALA:HB3	2.03	0.41
2:A:38:ARG:HD2	2:A:123:ALA:O	2.21	0.41
2:A:181:ALA:HB1	2:A:225:ILE:HD12	2.02	0.41
2:A:443:GLU:OE1	2:A:446:ARG:NH2	2.51	0.41
2:A:220:GLU:OE1	2:A:243:ARG:HD3	2.20	0.41
2:A:196:MET:HG2	2:A:207:TRP:CH2	2.56	0.41
2:A:224:ASN:OD1	2:A:243:ARG:NH2	2.53	0.40
2:A:339:GLU:OE2	2:B:416:ARG:NH1	2.54	0.40
2:A:385:TYR:HB3	2:A:463:VAL:HG12	2.04	0.40
2:A:304:PHE:HE2	2:A:389:ARG:HH12	1.69	0.40
2:A:247:ASN:OD1	2:A:247:ASN:N	2.54	0.40

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	
2	A	427/494 (86%)	412 (96%)	15 (4%)	0	100	100
2	B	26/494 (5%)	24 (92%)	2 (8%)	0	100	100
All	All	453/988 (46%)	436 (96%)	17 (4%)	0	100	100

There are no Ramachandran outliers to report.

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
2	A	366/420 (87%)	358 (98%)	8 (2%)	47 65
2	B	25/420 (6%)	24 (96%)	1 (4%)	27 49
All	All	391/840 (46%)	382 (98%)	9 (2%)	46 64

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	34	ASP
2	A	51	ASP
2	A	88	ASP
2	A	203	ASP
2	A	206	PHE
2	A	279	CYS
2	A	289	TYR
2	A	345	SER
2	B	416	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	5/12 (41%)	2 (40%)	0
1	D	5/12 (41%)	3 (60%)	1 (20%)
All	All	10/24 (41%)	5 (50%)	1 (10%)

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C	9	U
1	C	10	C
1	D	2	C
1	D	4	C
1	D	5	U

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	D	3	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	A1IJK	C	101	1	34,39,39	1.43	7 (20%)	44,55,55	0.81	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
3	A1IJK	C	101	1	-	1/21/59/59	0/4/4/4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	101	A1IJK	C33-C32	-3.75	1.38	1.46
3	C	101	A1IJK	C21-C20	2.91	1.46	1.41
3	C	101	A1IJK	C25-C20	2.77	1.46	1.41
3	C	101	A1IJK	C29-C30	2.55	1.39	1.34
3	C	101	A1IJK	C25-C34	-2.28	1.40	1.44
3	C	101	A1IJK	C21-C30	-2.25	1.40	1.44
3	C	101	A1IJK	C27-C28	2.04	1.44	1.39

There are no bond angle outliers.

There are no chirality outliers.

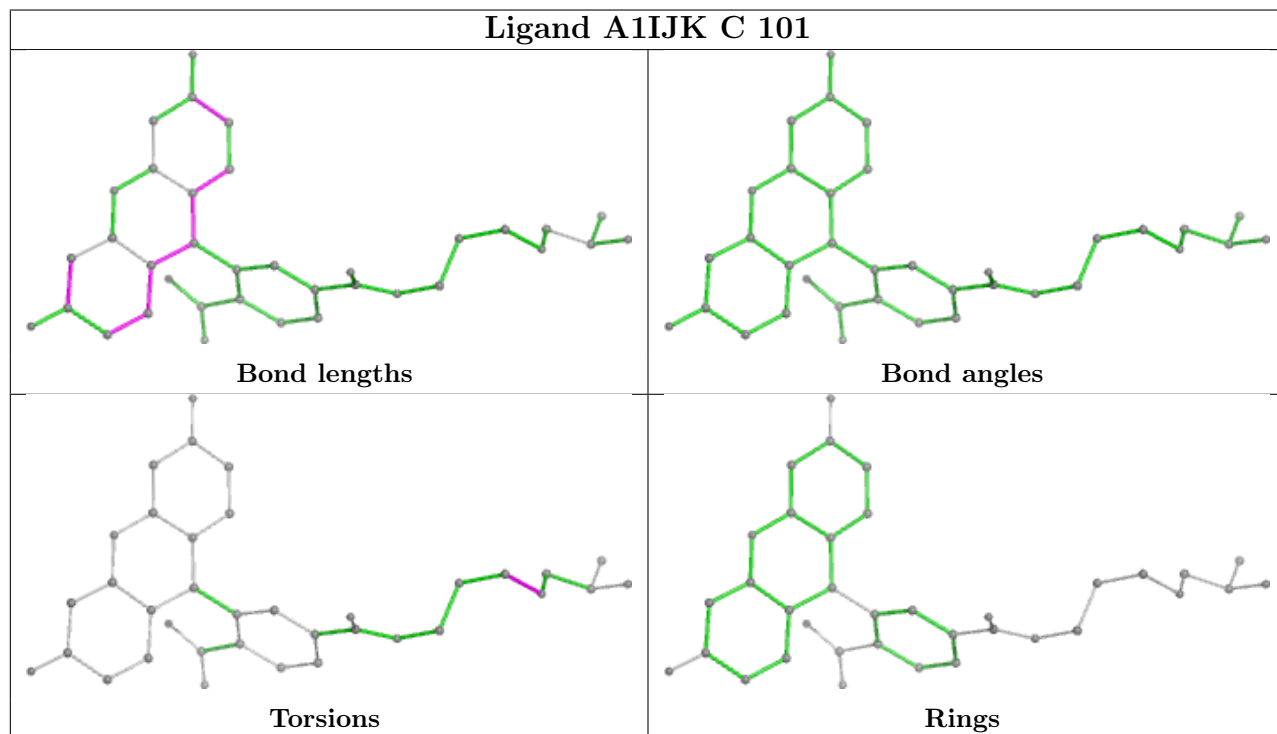
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	101	A1IJK	C7-C6-O4-C3

There are no ring outliers.

No monomer is involved in short contacts.

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.

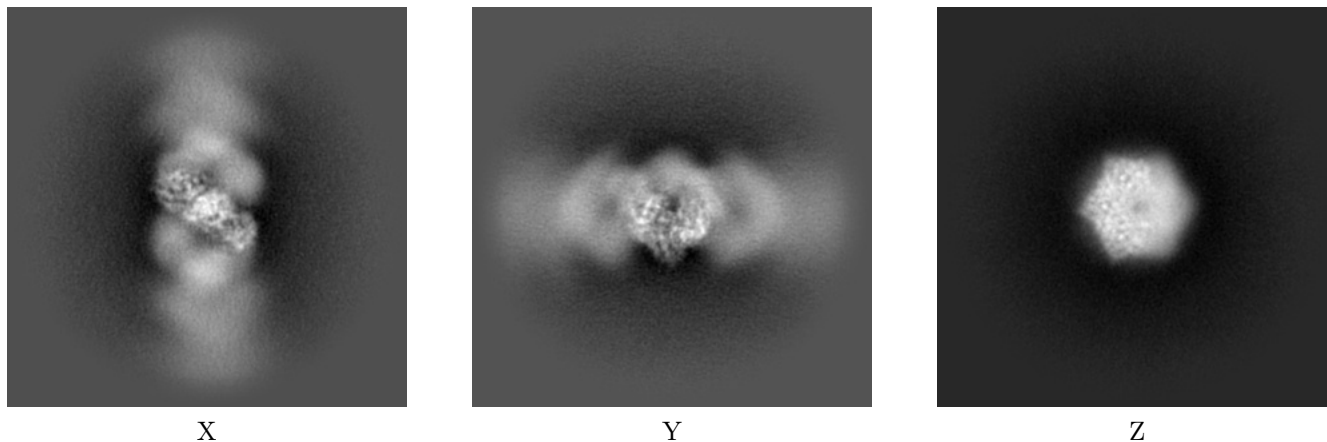
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51185. These allow visual inspection of the internal detail of the map and identification of artifacts.

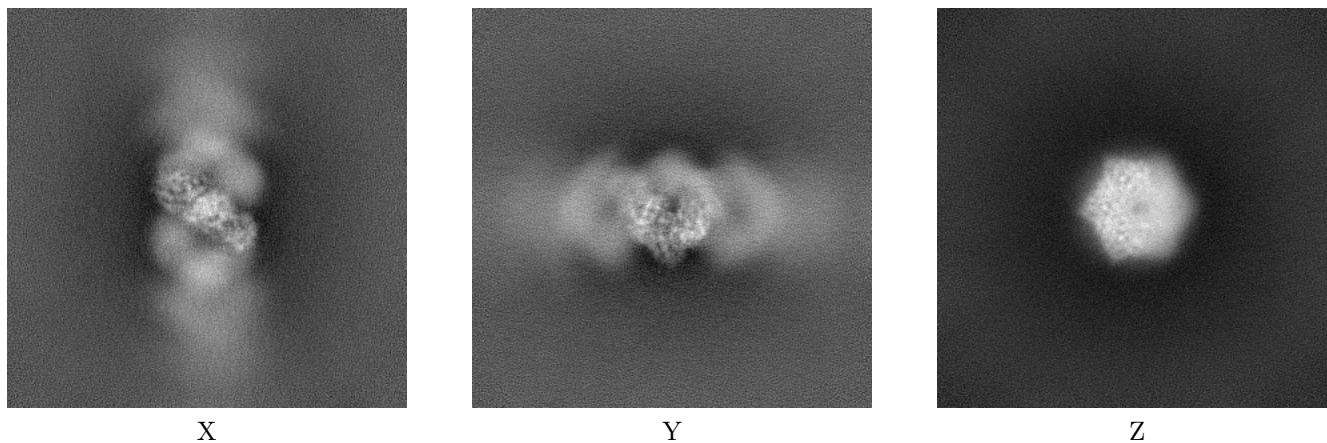
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



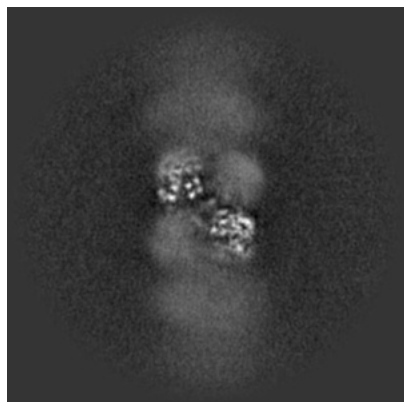
6.1.2 Raw map



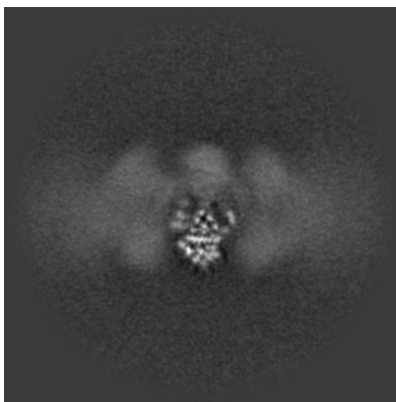
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

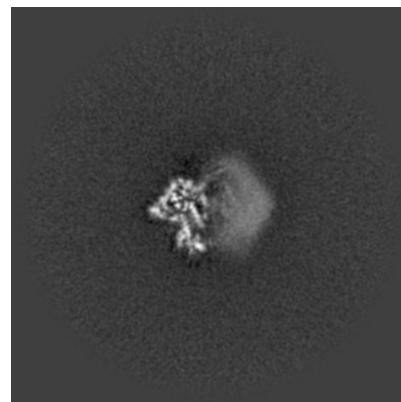
6.2.1 Primary map



X Index: 200

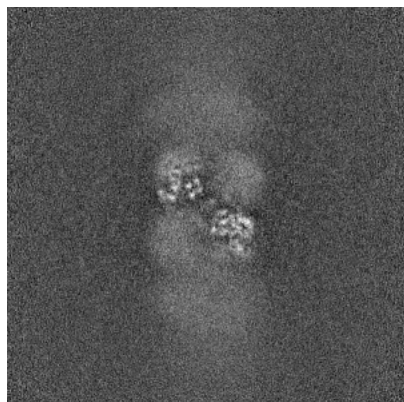


Y Index: 200

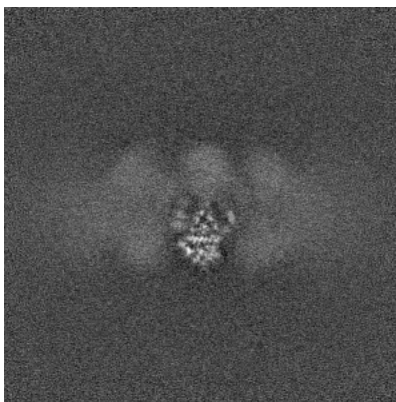


Z Index: 200

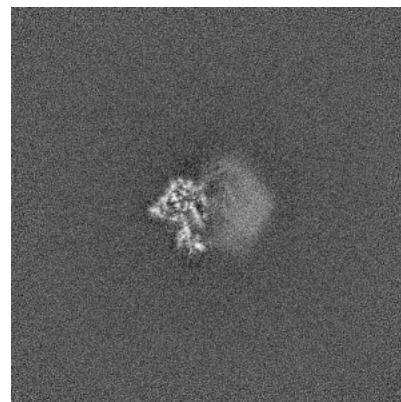
6.2.2 Raw map



X Index: 200



Y Index: 200

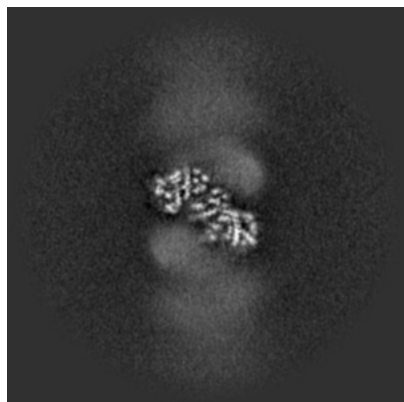


Z Index: 200

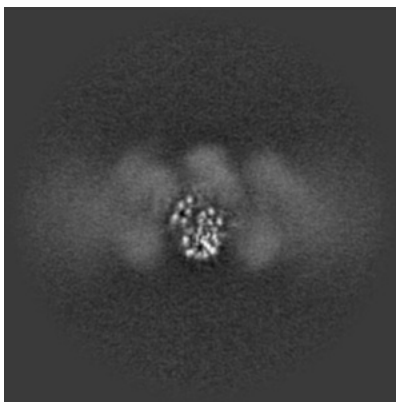
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

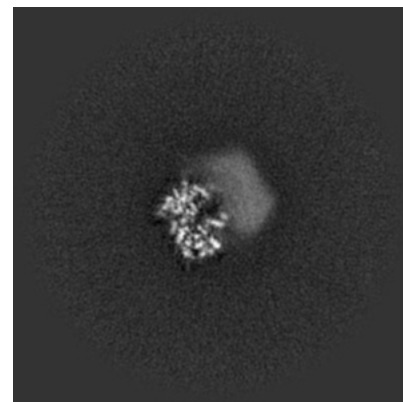
6.3.1 Primary map



X Index: 185

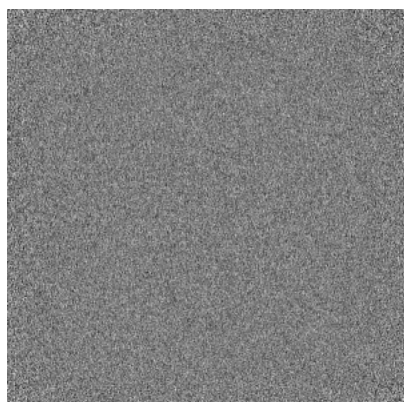


Y Index: 208

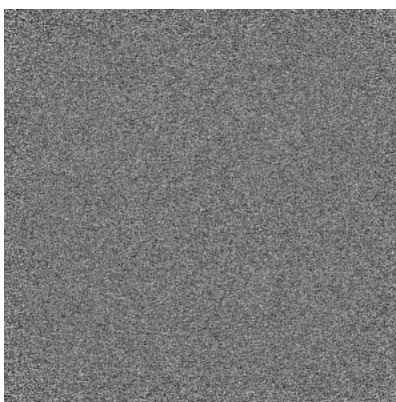


Z Index: 210

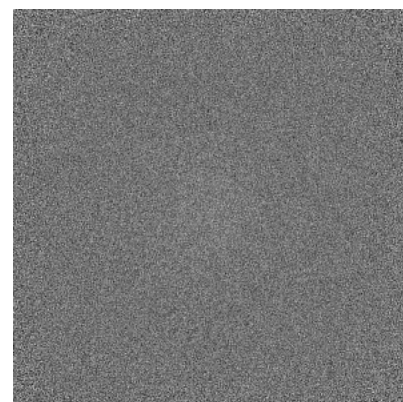
6.3.2 Raw map



X Index: 0



Y Index: 0

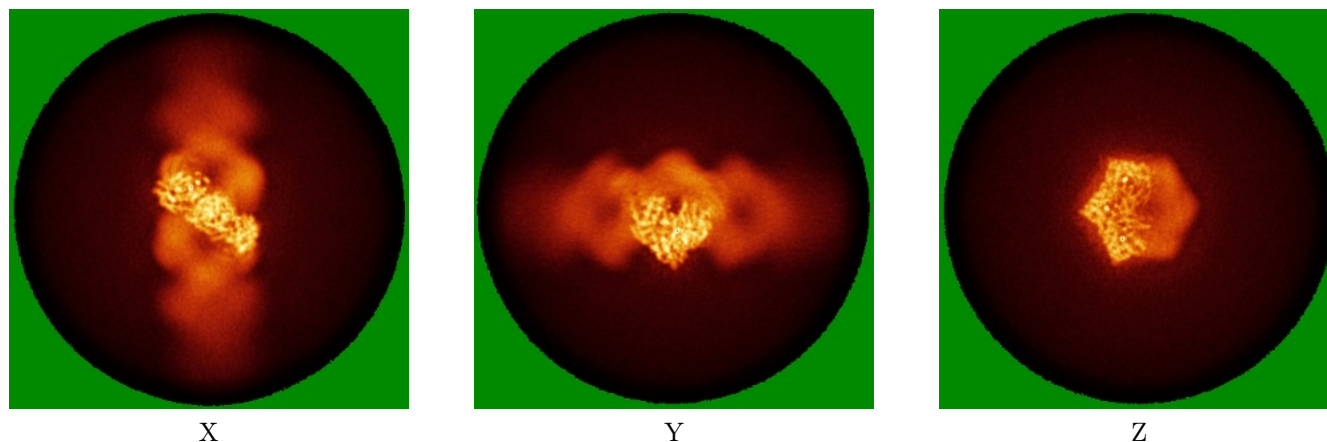


Z Index: 399

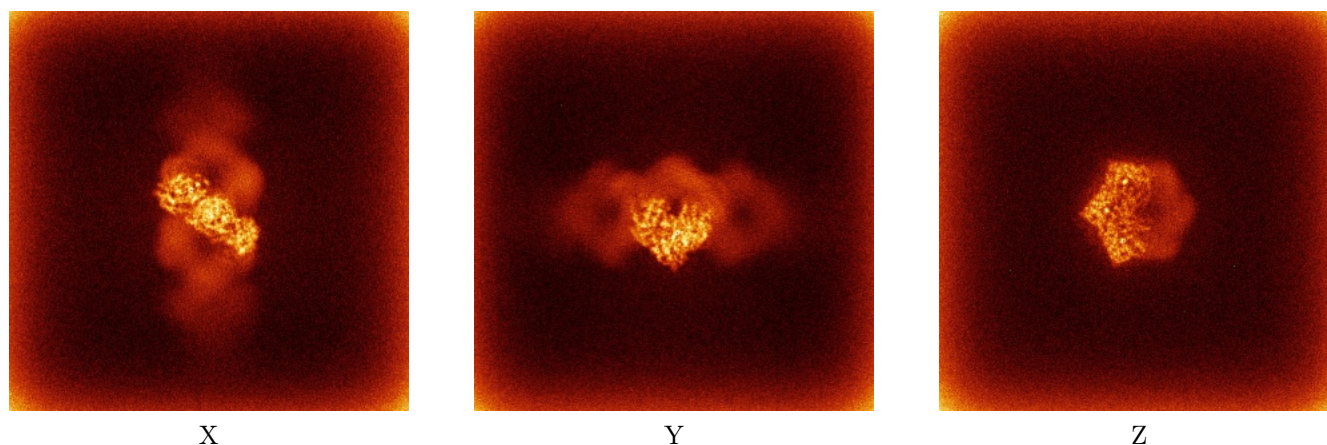
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



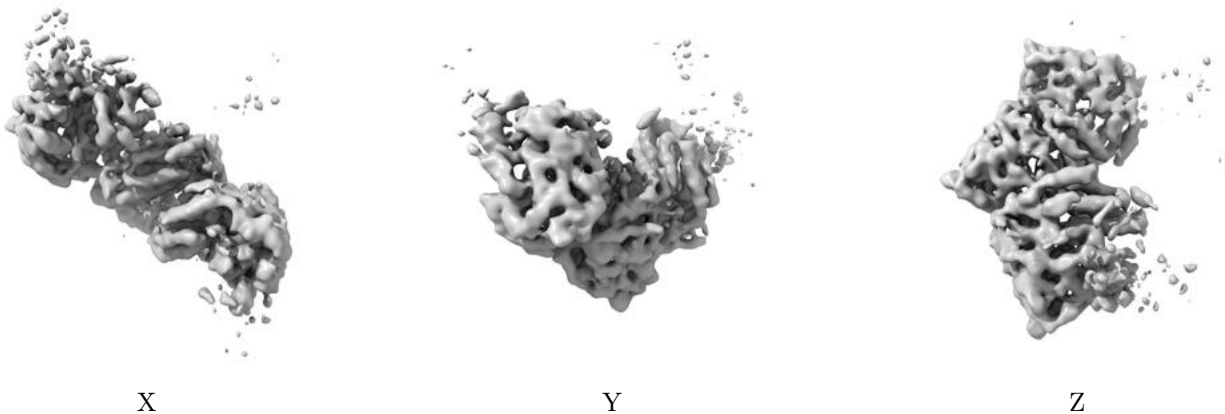
6.4.2 Raw map



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.

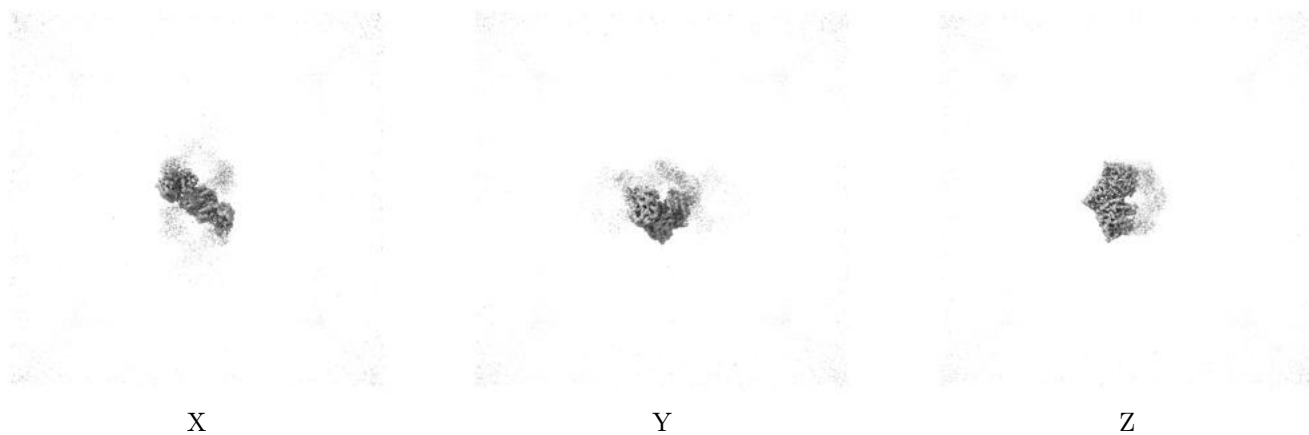
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.422. 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.

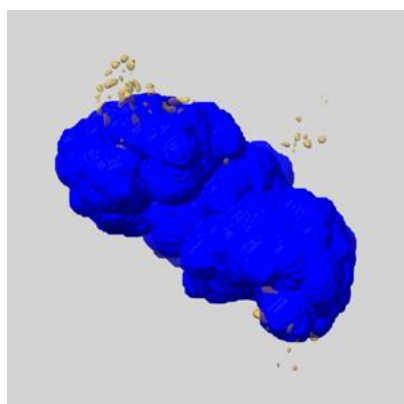
6.6 Mask visualisation [i](#)

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

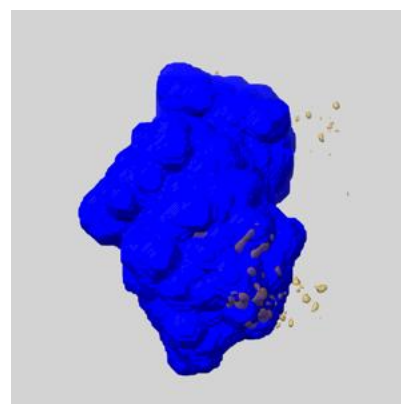
6.6.1 emd_51185_msk_1.map [i](#)



X



Y

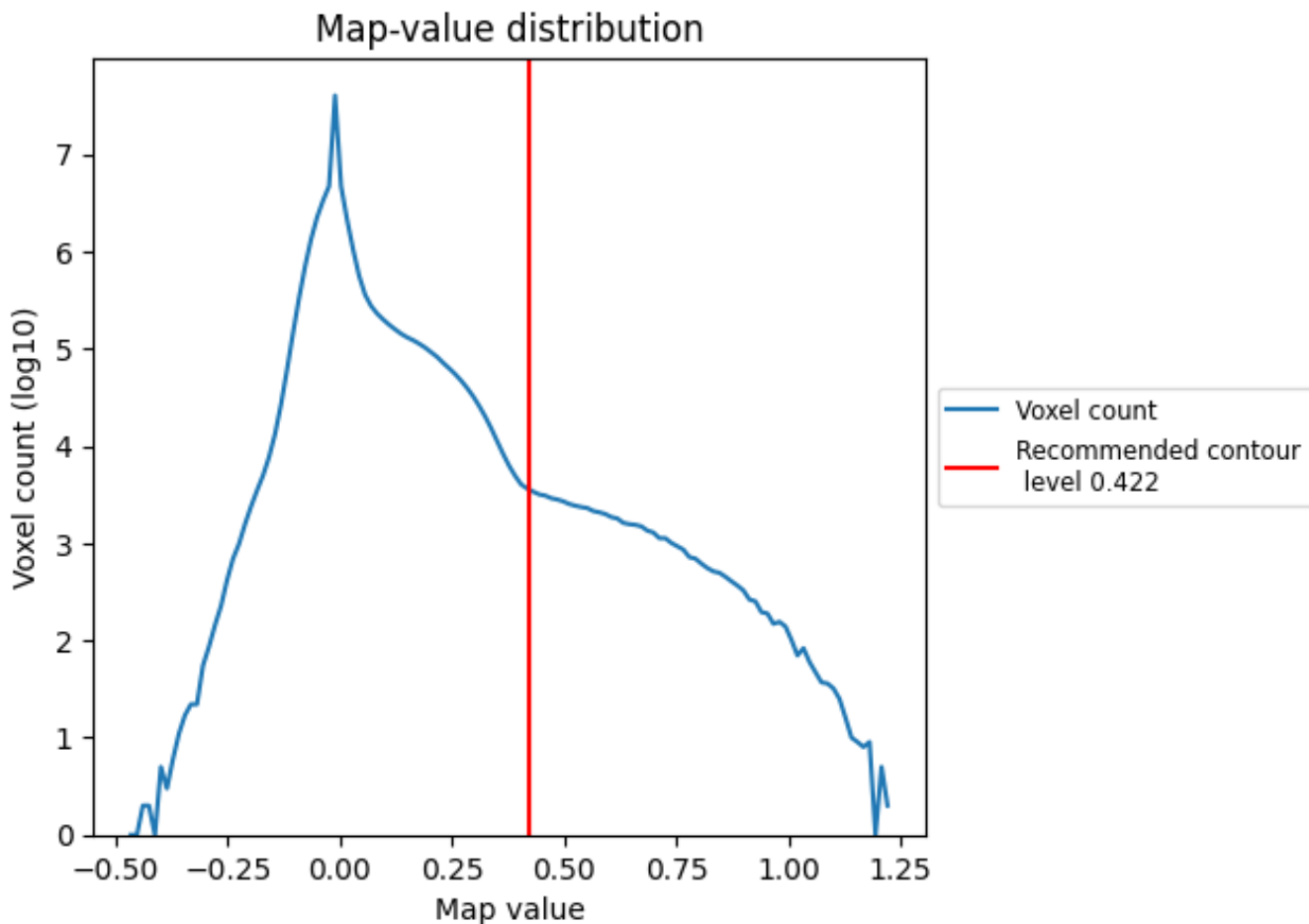


Z

7 Map analysis [i](#)

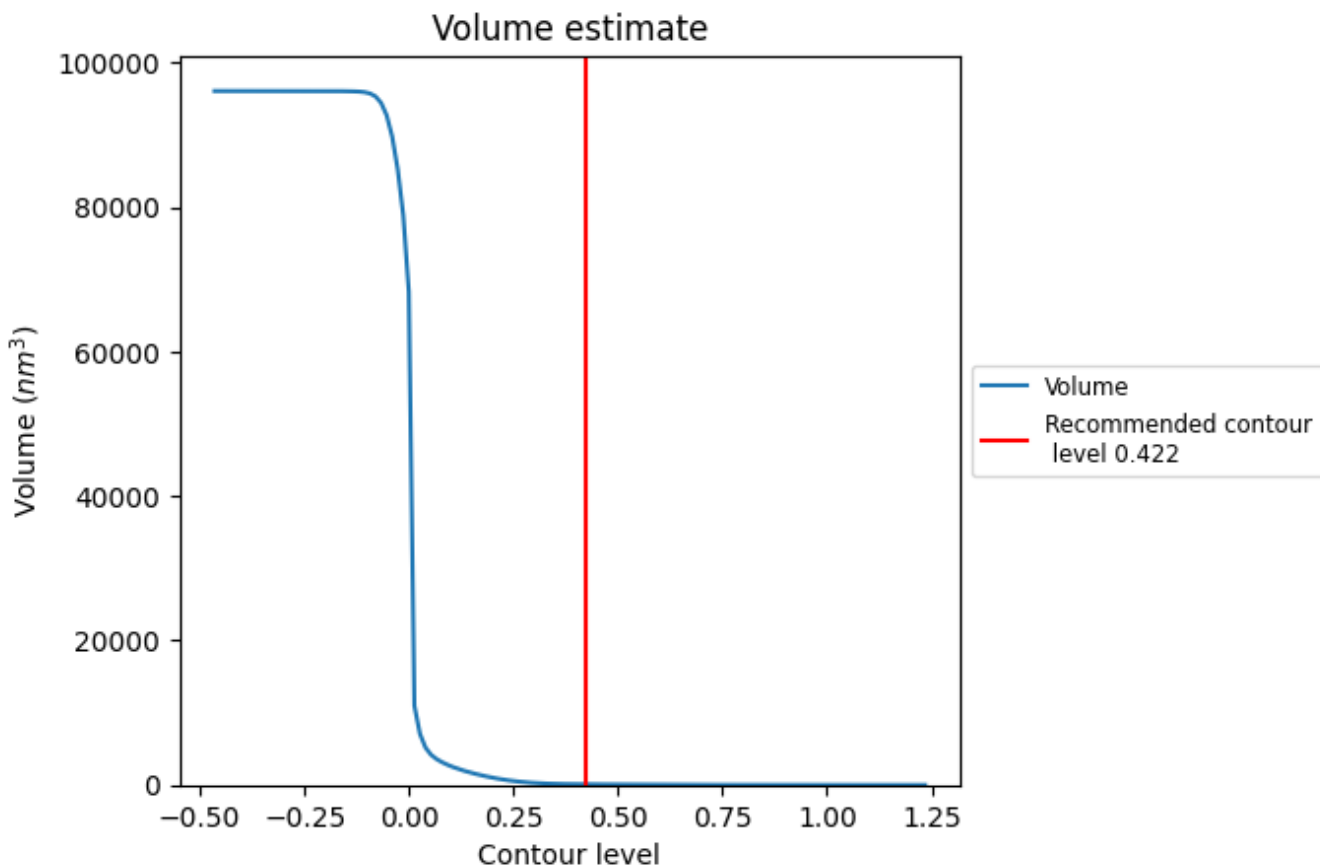
This section contains the results of statistical analysis of the map.

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.

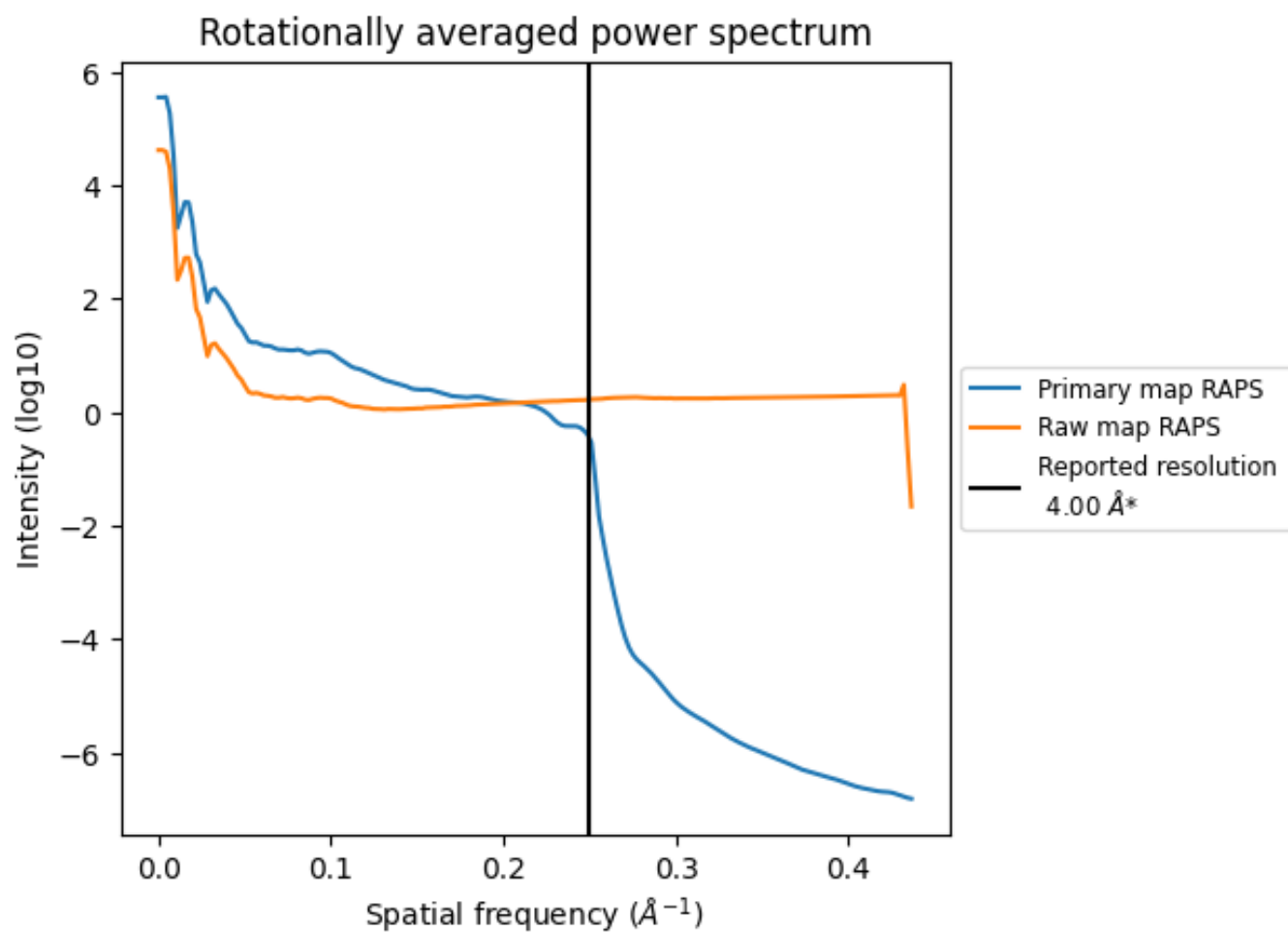
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 91 nm^3 ; this corresponds to an approximate mass of 83 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

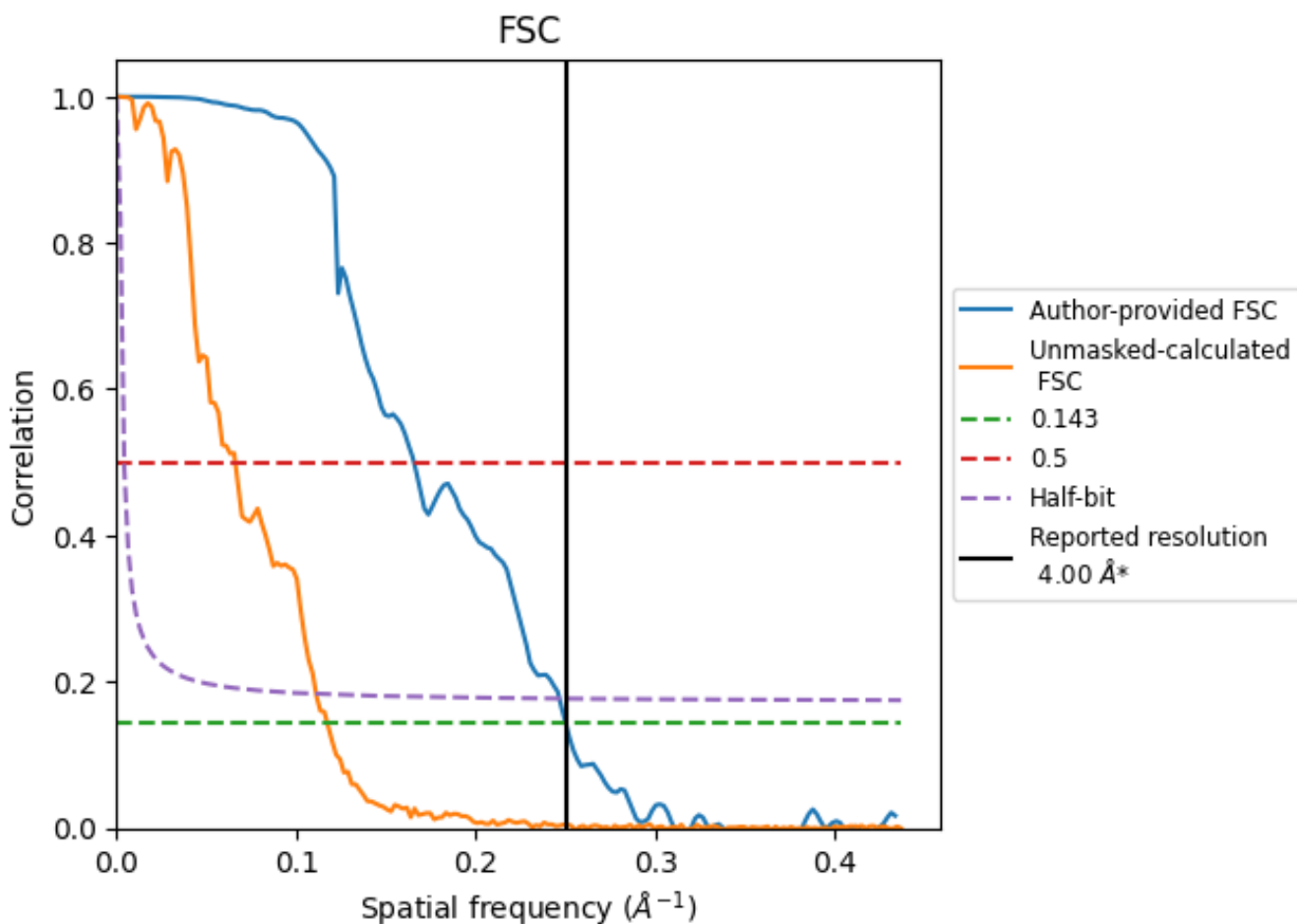


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.00	6.04	4.06
Unmasked-calculated*	8.52	15.13	9.00

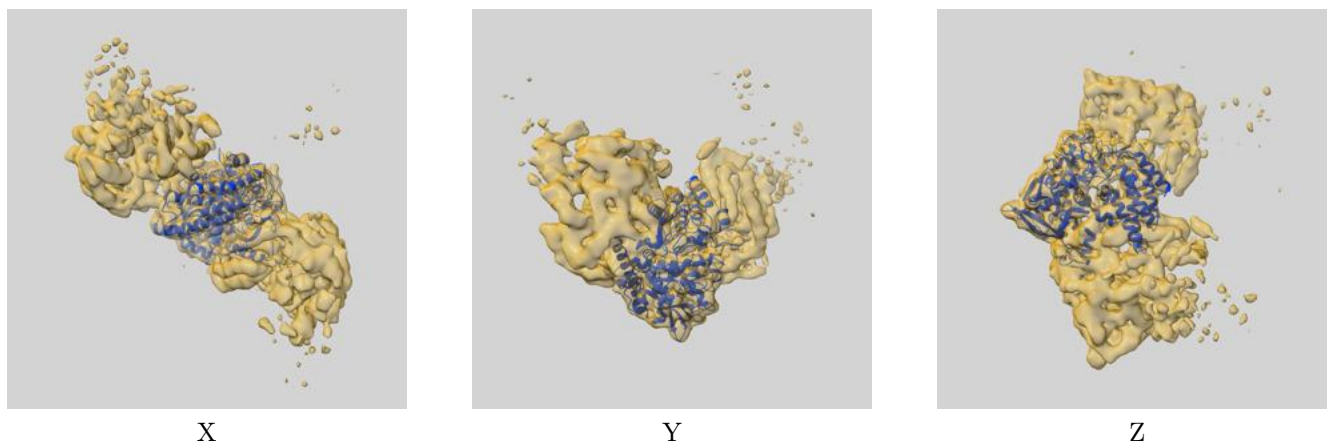
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.52 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

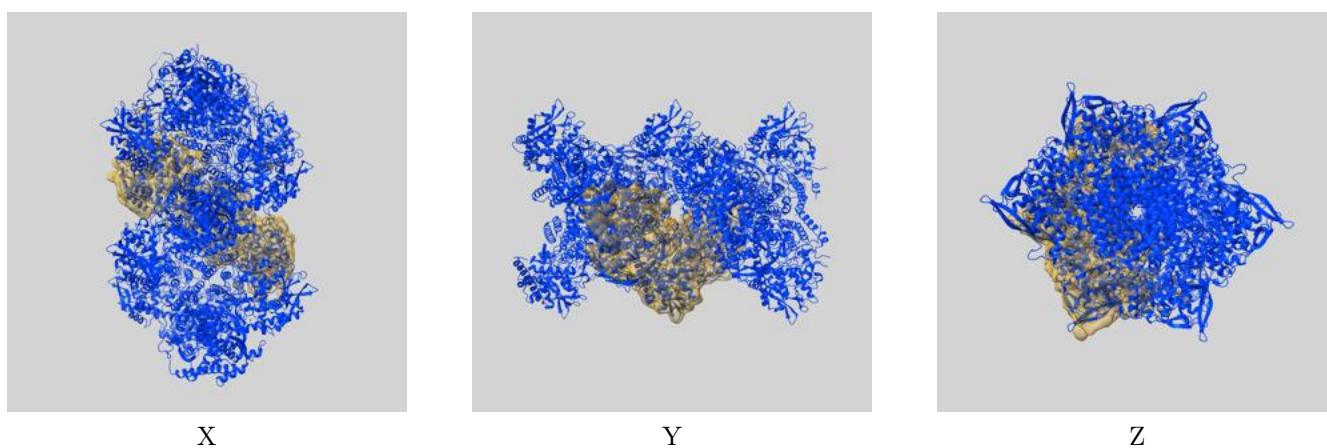
This section contains information regarding the fit between EMDB map EMD-51185 and PDB model 9GAP. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

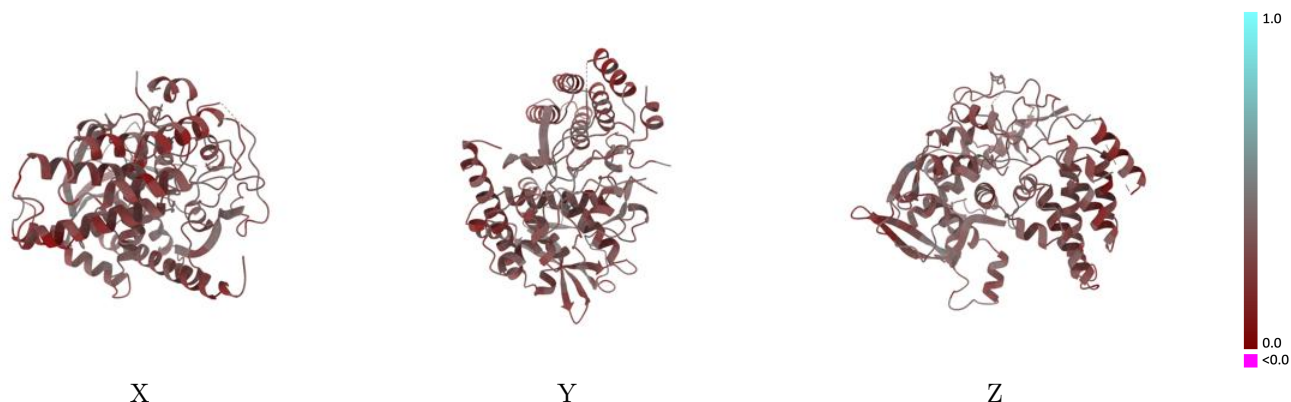


9.1.2 Map-model assembly overlay [i](#)



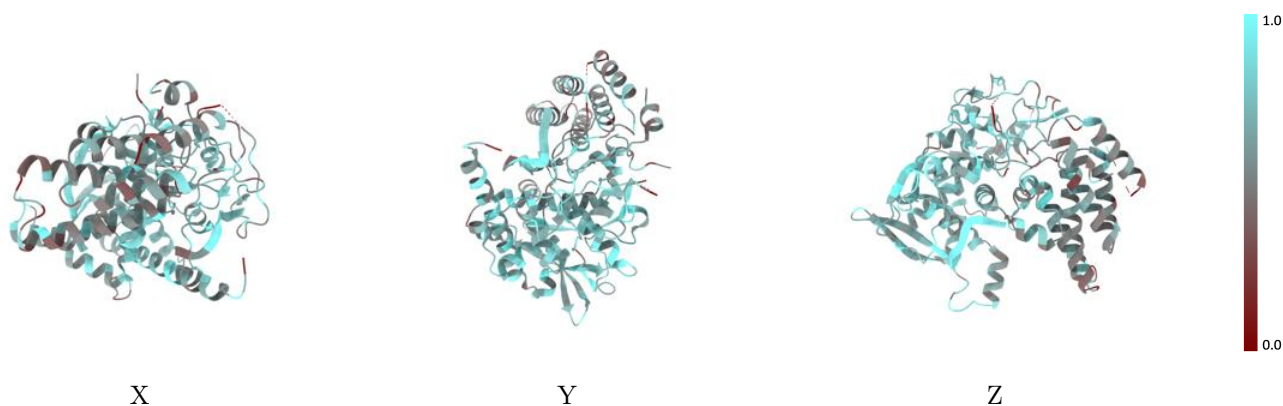
The images above show the 3D surface view of the map at the recommended contour level 0.422 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



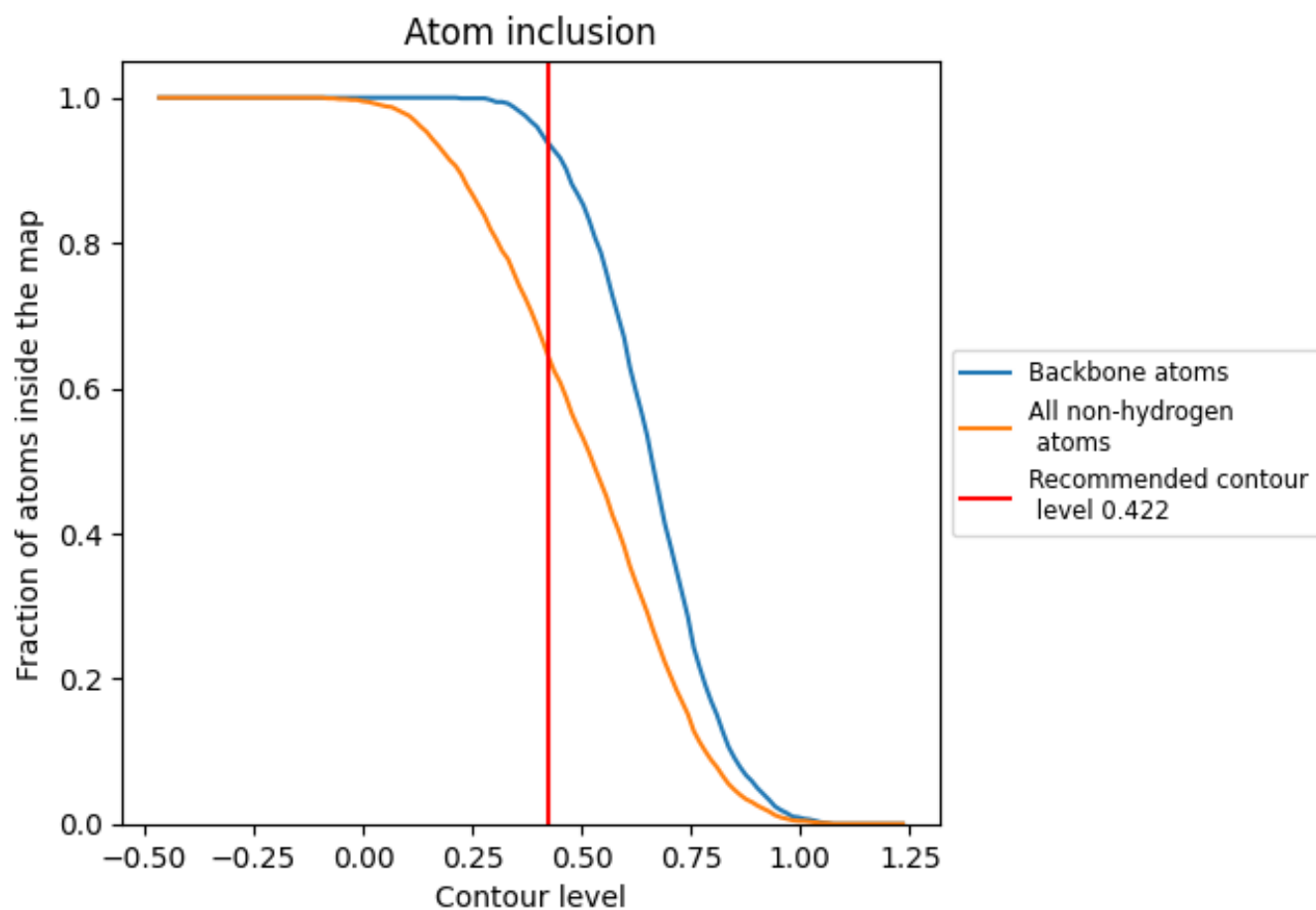
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.422).











9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.422) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6470	 0.3030
A	 0.6460	 0.2970
B	 0.5790	 0.3280
C	 0.5480	 0.3350
D	 0.9170	 0.3840

