



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:20 PM UTC

PDB ID : 5GAM / pdb_00005gam
EMDB ID : EMD-8011
Title : Foot region of the yeast spliceosomal U4/U6.U5 tri-snRNP
Authors : Nguyen, T.H.D.; Galej, W.P.; Bai, X.C.; Oubridge, C.; Scheres, S.H.W.; Newman, A.J.; Nagai, K.
Deposited on : 2015-12-15
Resolution : 3.70 Å(reported)

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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:

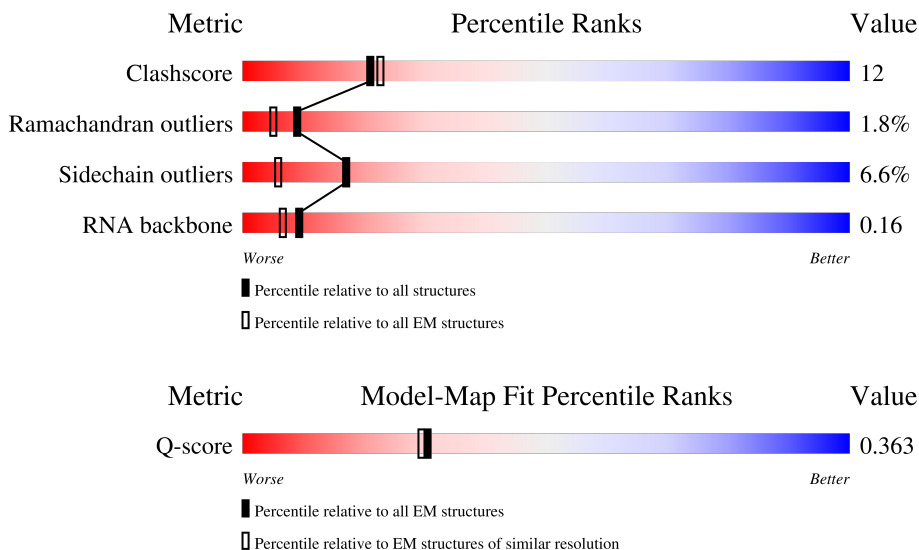
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



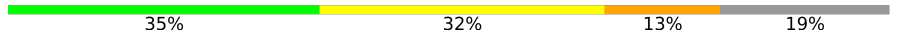




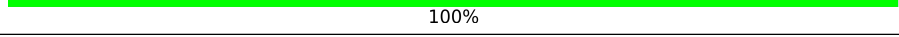

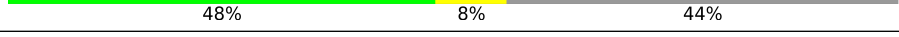
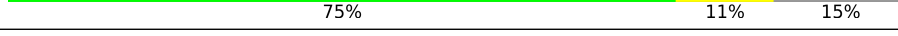
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	U	178	
2	A	735	
3	C	1008	

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Mol	Chain	Length	Quality of chain
4	W	31	 35% 32% 13% 19%
5	b	196	 37% 59%
6	e	94	 60% 20% 20%
7	f	86	 77% 7% 16%
8	g	77	 79% 9% 10%
9	x	18	 100%
10	d	101	 71% 9% 19%
11	h	146	 48% 8% 44%
12	j	110	 75% 11% 15%

2 Entry composition i

There are 13 unique types of molecules in this entry. The entry contains 19123 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 U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	U	141	2999	1342	530	986	141	0	0

- Molecule 2 is a protein called Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	593	4702	3052	817	817	16	0	0

- Molecule 3 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	855	6450	4195	1089	1143	23	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	530	SER	GLU	conflict	UNP P36048
C	531	LYS	ASP	conflict	UNP P36048
C	532	THR	ASP	conflict	UNP P36048

- Molecule 4 is a RNA chain called U6 snRNA, 5' end.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	W	25	532	237	91	179	25	0	0

- Molecule 5 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	b	80	631	403	114	111	3	0	0

- Molecule 6 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	e	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	f	72	Total	C	N	O	S	0	0
			573	368	101	103	1		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	g	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

- Molecule 9 is a protein called Unknown polypeptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	x	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	d	82	Total	C	N	O	S	0	0
			625	399	109	115	2		

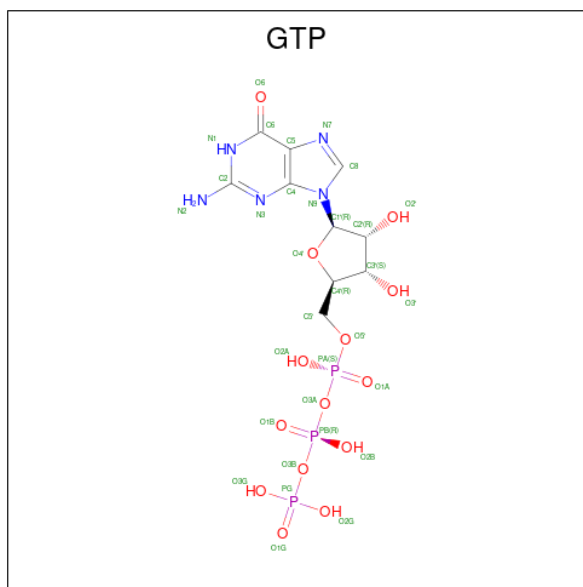
- Molecule 11 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	h	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein Sm D2.

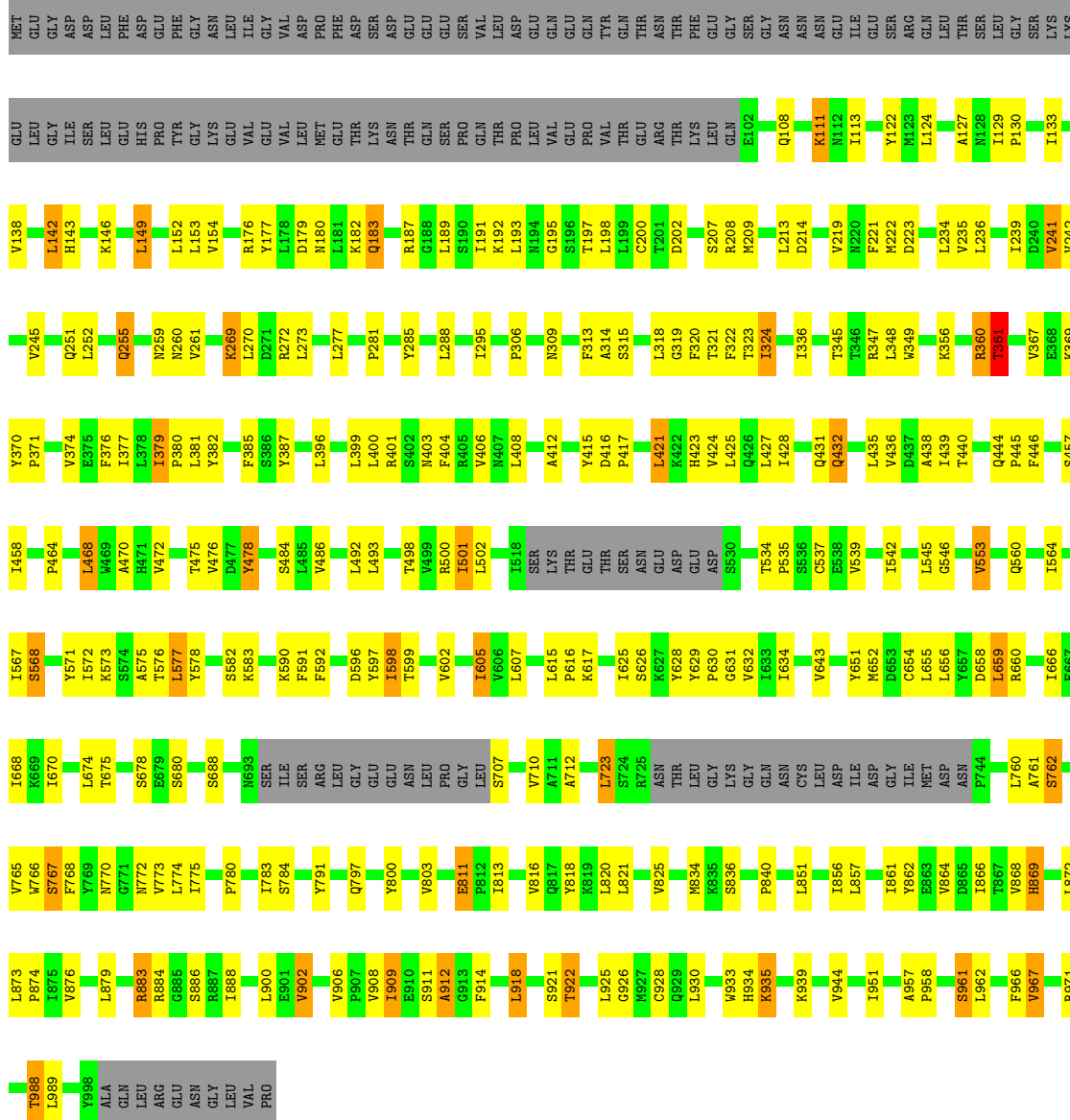
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	j	94	Total	C	N	O	S	0	0
			741	477	141	119	4		

- Molecule 13 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
13	C	1	32	10	5	14	3	0

● Molecule 3: Pre-mRNA-splicing factor SNU114

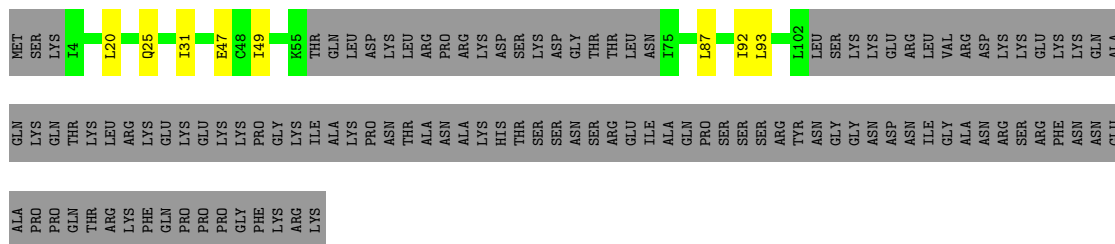


● Molecule 4: U6 snRNA, 5' end



● Molecule 5: Small nuclear ribonucleoprotein-associated protein B





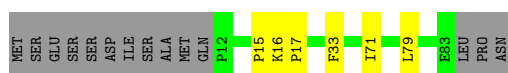
- Molecule 6: Small nuclear ribonucleoprotein E

Chain e: 60% 20% 20%



- Molecule 7: Small nuclear ribonucleoprotein F

Chain f: 77% 7% 16%



- Molecule 8: Small nuclear ribonucleoprotein G

Chain g: 79% 9% 10%



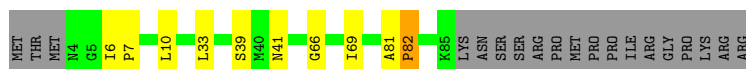
- Molecule 9: Unknown polypeptide

Chain x: 100%

There are no outlier residues recorded for this chain.

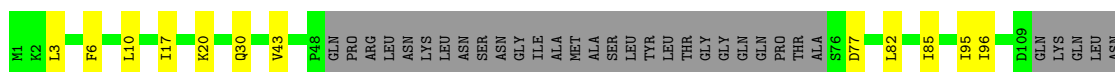
- Molecule 10: Small nuclear ribonucleoprotein Sm D3

Chain d: 71% 9% 19%



- Molecule 11: Small nuclear ribonucleoprotein Sm D1

Chain h: 48% 8% 44%



SER
LEU
ARG
ARG
SER
GLN
GLY
GLN
ILE
ALA
ASN
ASP
PRO
SER
LYS
LYS
ARG
ARG
ARG
ASP
PHE
GLY
ALA
PRO
ALA
ASN
LYS
ARG
PRO
ARG
ARG
GLY
LEU

- Molecule 12: Small nuclear ribonucleoprotein Sm D2

Chain j:  75% 11% 15%

MET
SER
SER
GLN
ILE
ILE
ASP
ARG
PRO
LYS
HIS
GLU
LEU
SER
R15
F24
L48
R49
A60
T77
L94
G98
D99
S100
V101
I102
V103
V104
L105
P108
VAL
GLU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	140155	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	35714	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.194	Depositor
Minimum map value	-0.076	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.012	Depositor
Map size (\AA)	543.39996, 543.39996, 543.39996	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.43, 1.43, 1.43	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: GTP

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	U	0.48	0/3351	0.98	17/5213 (0.3%)
2	A	0.57	1/4840 (0.0%)	1.09	10/6596 (0.2%)
3	C	0.59	0/6590	1.10	9/8975 (0.1%)
4	W	0.43	0/592	0.83	0/918
5	b	0.53	0/636	0.78	0/856
6	e	0.60	0/585	0.87	0/795
7	f	0.62	0/585	0.89	0/791
8	g	0.51	0/532	0.85	0/715
10	d	0.50	0/634	0.91	1/859 (0.1%)
11	h	0.51	0/649	0.78	0/880
12	j	0.57	0/753	0.94	1/1013 (0.1%)
All	All	0.55	1/19747 (0.0%)	1.02	38/27611 (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	A	0	5
3	C	0	4
8	g	0	1
All	All	0	10

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	403	TYR	CA-C	6.86	1.58	1.52

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	C	259	ASN	N-CA-C	9.38	121.27	111.14
3	C	811	GLU	CA-C-N	9.03	129.10	119.89
3	C	811	GLU	C-N-CA	9.03	129.10	119.89
2	A	719	ILE	O-C-N	8.76	126.03	120.42
1	U	95	C	C4'-C3'-O3'	8.70	122.45	109.40

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	460	PRO	Peptide
2	A	464	GLU	Peptide
2	A	466	GLU	Peptide
2	A	553	ASN	Peptide
2	A	556	TYR	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	U	2999	0	1515	107	0
2	A	4702	0	4527	118	0
3	C	6450	0	6420	192	0
4	W	532	0	269	4	0
5	b	631	0	670	4	0
6	e	575	0	597	11	0
7	f	573	0	572	4	0
8	g	529	0	557	4	0
9	x	90	0	20	0	0
10	d	625	0	647	5	0
11	h	644	0	686	6	0
12	j	741	0	778	5	0
13	C	32	0	12	1	0
All	All	19123	0	17270	427	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 427 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:139:LEU:HD13	2:A:193:TYR:CD2	1.31	1.63
2:A:139:LEU:CD1	2:A:193:TYR:CD2	2.15	1.29
1:U:42:A:H3'	1:U:43:G:H5''	1.24	1.15
2:A:139:LEU:HD13	2:A:193:TYR:CE2	1.87	1.08
2:A:139:LEU:CD1	2:A:193:TYR:HD2	1.60	1.07

There are no symmetry-related clashes.

5.3 Torsion angles [\(i\)](#)

5.3.1 Protein backbone [\(i\)](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	587/735 (80%)	511 (87%)	67 (11%)	9 (2%)	8	36
3	C	847/1008 (84%)	730 (86%)	93 (11%)	24 (3%)	4	27
5	b	76/196 (39%)	69 (91%)	7 (9%)	0	100	100
6	e	71/94 (76%)	66 (93%)	5 (7%)	0	100	100
7	f	70/86 (81%)	62 (89%)	6 (9%)	2 (3%)	3	26
8	g	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
10	d	80/101 (79%)	72 (90%)	7 (9%)	1 (1%)	9	38
11	h	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
12	j	92/110 (84%)	86 (94%)	6 (6%)	0	100	100
All	All	1966/2553 (77%)	1734 (88%)	196 (10%)	36 (2%)	9	34

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	247	PRO
2	A	615	LEU
3	C	269	LYS

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Mol	Chain	Res	Type
3	C	356	LYS
3	C	367	VAL

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	482/677 (71%)	453 (94%)	29 (6%)	17 44
3	C	673/910 (74%)	613 (91%)	60 (9%)	9 33
5	b	70/176 (40%)	69 (99%)	1 (1%)	59 70
6	e	65/83 (78%)	60 (92%)	5 (8%)	12 38
7	f	63/77 (82%)	62 (98%)	1 (2%)	55 68
8	g	58/66 (88%)	56 (97%)	2 (3%)	32 55
10	d	69/89 (78%)	68 (99%)	1 (1%)	59 70
11	h	77/129 (60%)	74 (96%)	3 (4%)	28 53
12	j	79/103 (77%)	73 (92%)	6 (8%)	12 38
All	All	1636/2310 (71%)	1528 (93%)	108 (7%)	17 42

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	537	CYS
3	C	762	SER
11	h	20	LYS
3	C	576	THR
3	C	659	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	514	GLN
5	b	91	GLN

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Mol	Chain	Res	Type
3	C	557	HIS
3	C	693	ASN
6	e	86	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	U	139/178 (78%)	82 (58%)	23 (16%)
4	W	24/31 (77%)	11 (45%)	4 (16%)
All	All	163/209 (77%)	93 (57%)	27 (16%)

5 of 93 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	U	5	A
1	U	7	C
1	U	8	U
1	U	9	U
1	U	10	U

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	U	83	C
1	U	127	U
4	W	25	C
1	U	114	G
1	U	128	A

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

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
13	GTP	C	1101	-	33,34,34	1.18	4 (12%)	50,54,54	1.77	8 (16%)

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
13	GTP	C	1101	-	-	3/22/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	C	1101	GTP	C5-C4	2.86	1.46	1.38
13	C	1101	GTP	C5-N7	-2.82	1.33	1.39
13	C	1101	GTP	PA-O3A	2.34	1.62	1.59
13	C	1101	GTP	C6-N1	-2.19	1.34	1.38

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	C	1101	GTP	C5-C4-N3	-6.27	118.42	128.39
13	C	1101	GTP	C2-N3-C4	5.29	121.42	112.30
13	C	1101	GTP	N9-C4-N3	5.07	136.10	125.95
13	C	1101	GTP	O6-C6-C5	-3.20	118.08	126.53
13	C	1101	GTP	C5-C6-N1	2.31	119.14	113.25

There are no chirality outliers.

All (3) torsion outliers are listed below:

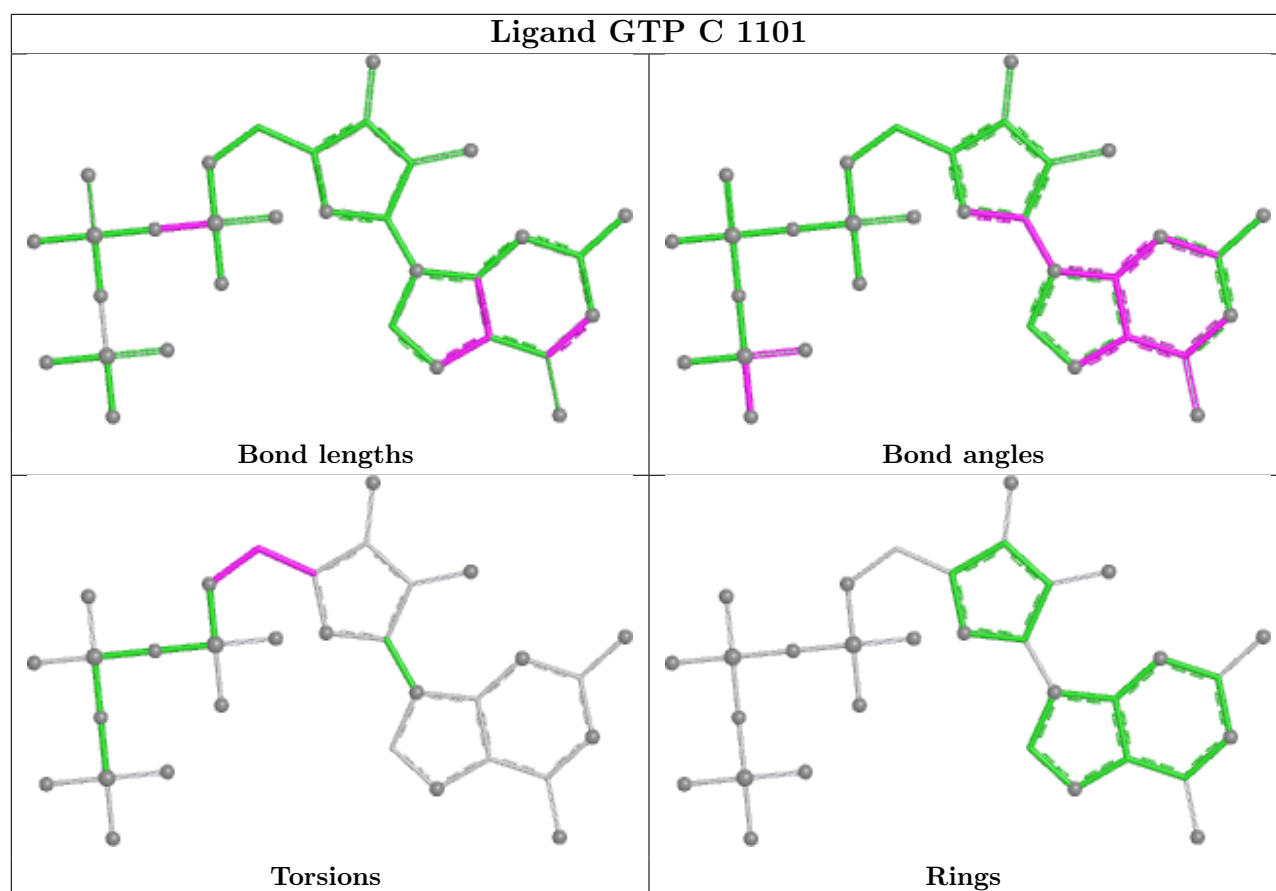
Mol	Chain	Res	Type	Atoms
13	C	1101	GTP	O4'-C4'-C5'-O5'
13	C	1101	GTP	C3'-C4'-C5'-O5'
13	C	1101	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	C	1101	GTP	1	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.

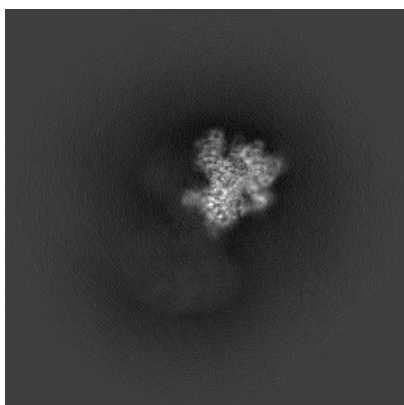
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8011. These allow visual inspection of the internal detail of the map and identification of artifacts.

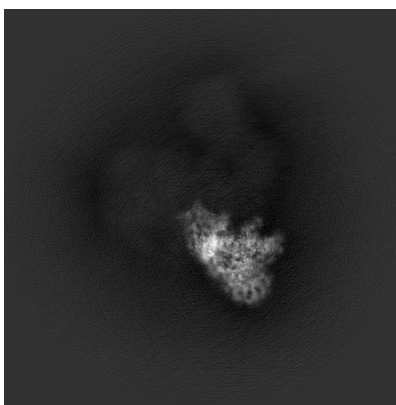
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

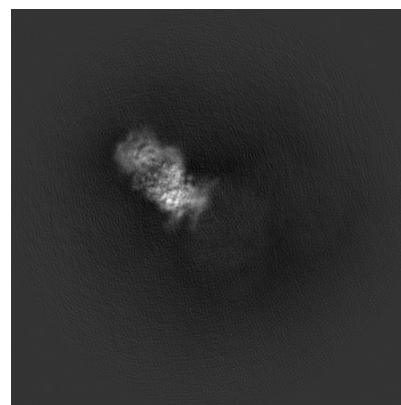
6.1.1 Primary map



X



Y

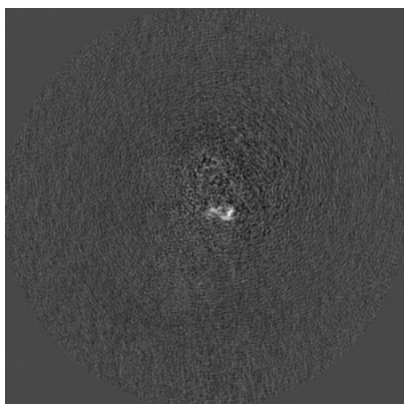


Z

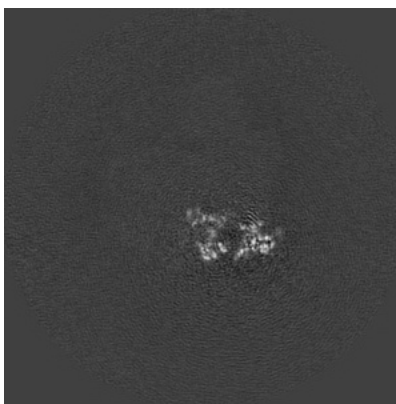
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

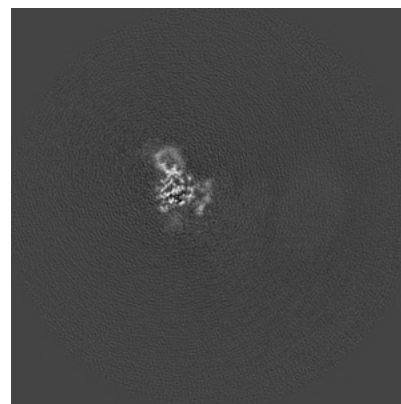
6.2.1 Primary map



X Index: 190



Y Index: 190

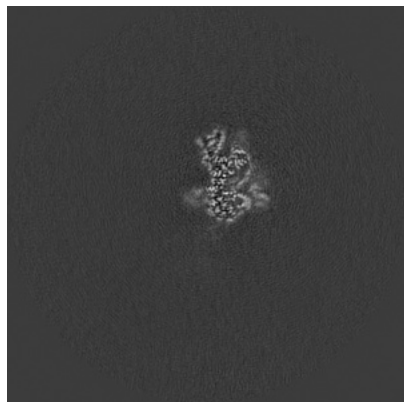


Z Index: 190

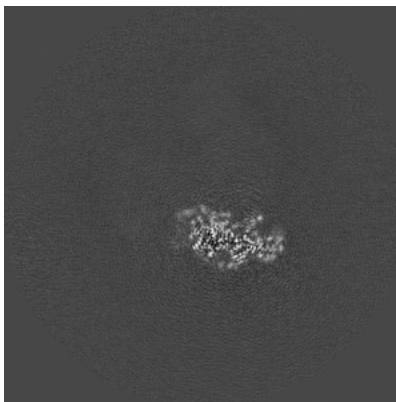
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

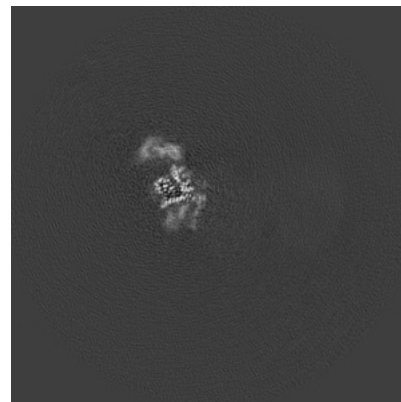
6.3.1 Primary map



X Index: 156



Y Index: 198

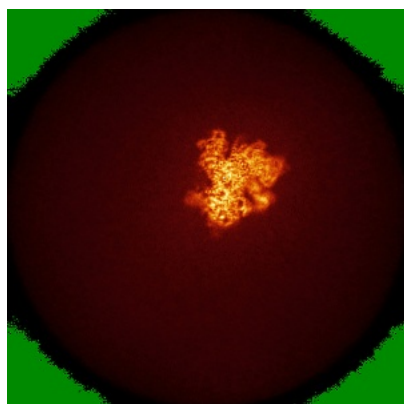


Z Index: 199

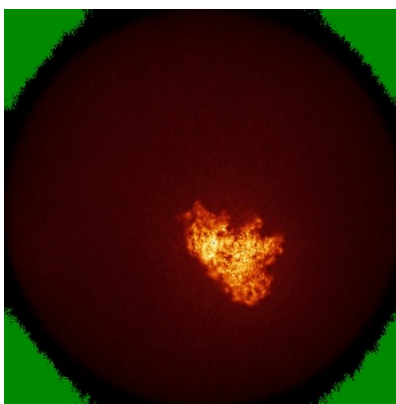
The images above show the largest variance slices of the map in three orthogonal directions.

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

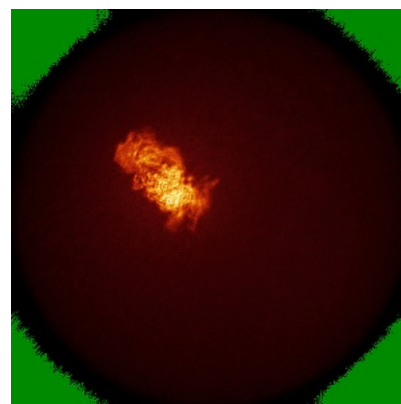
6.4.1 Primary map



X



Y

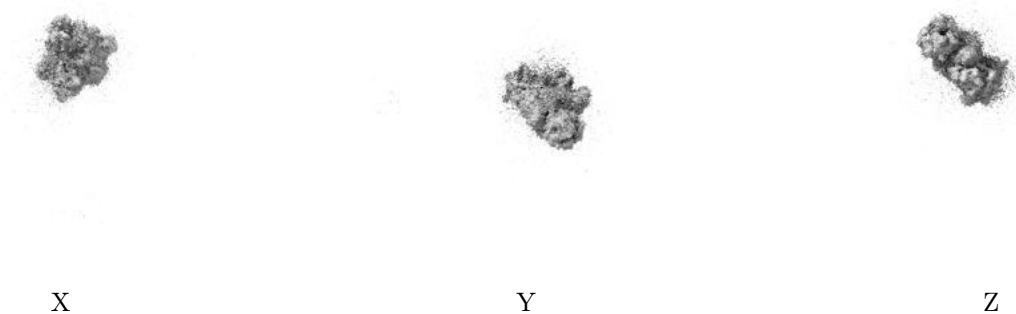


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

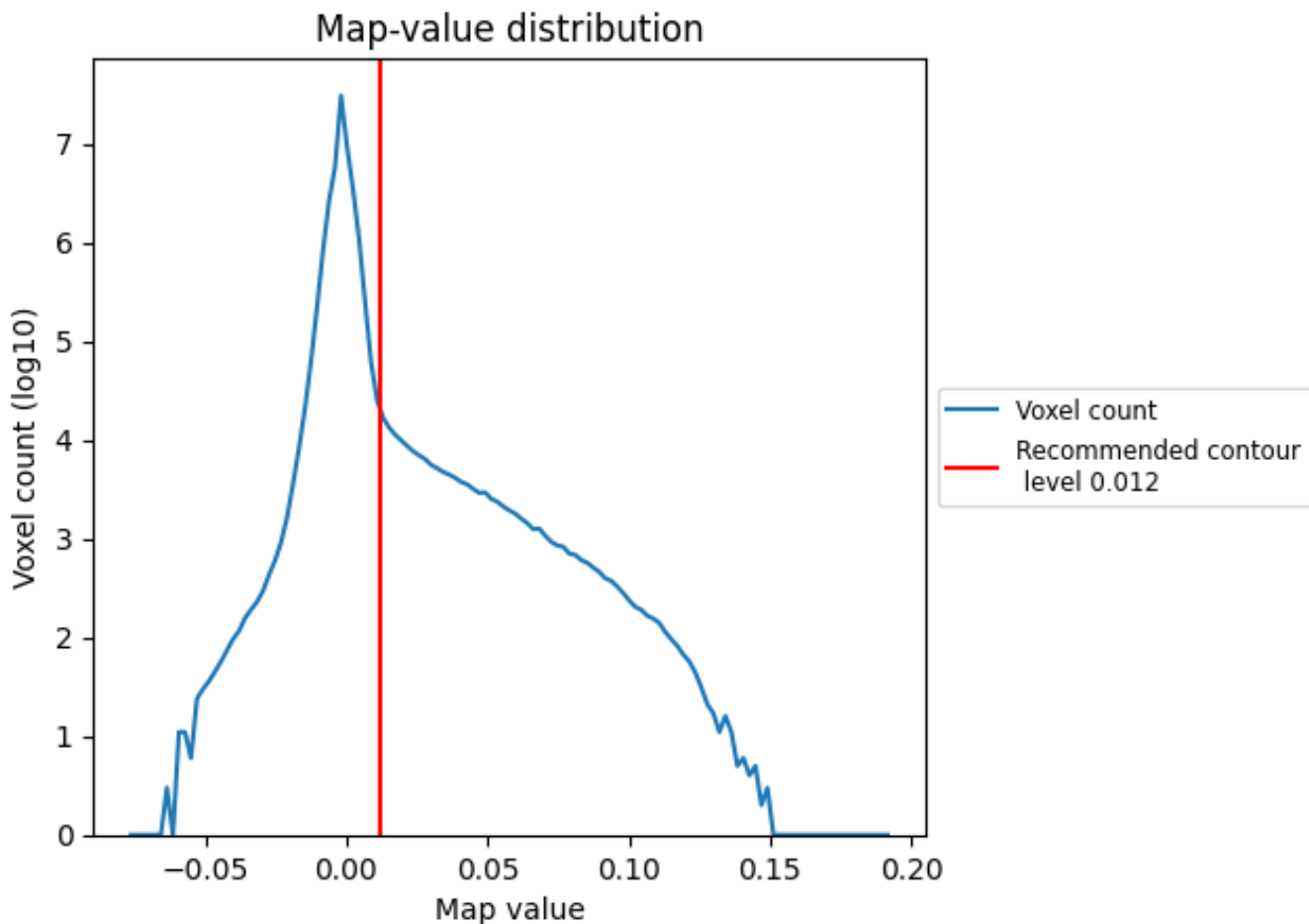
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

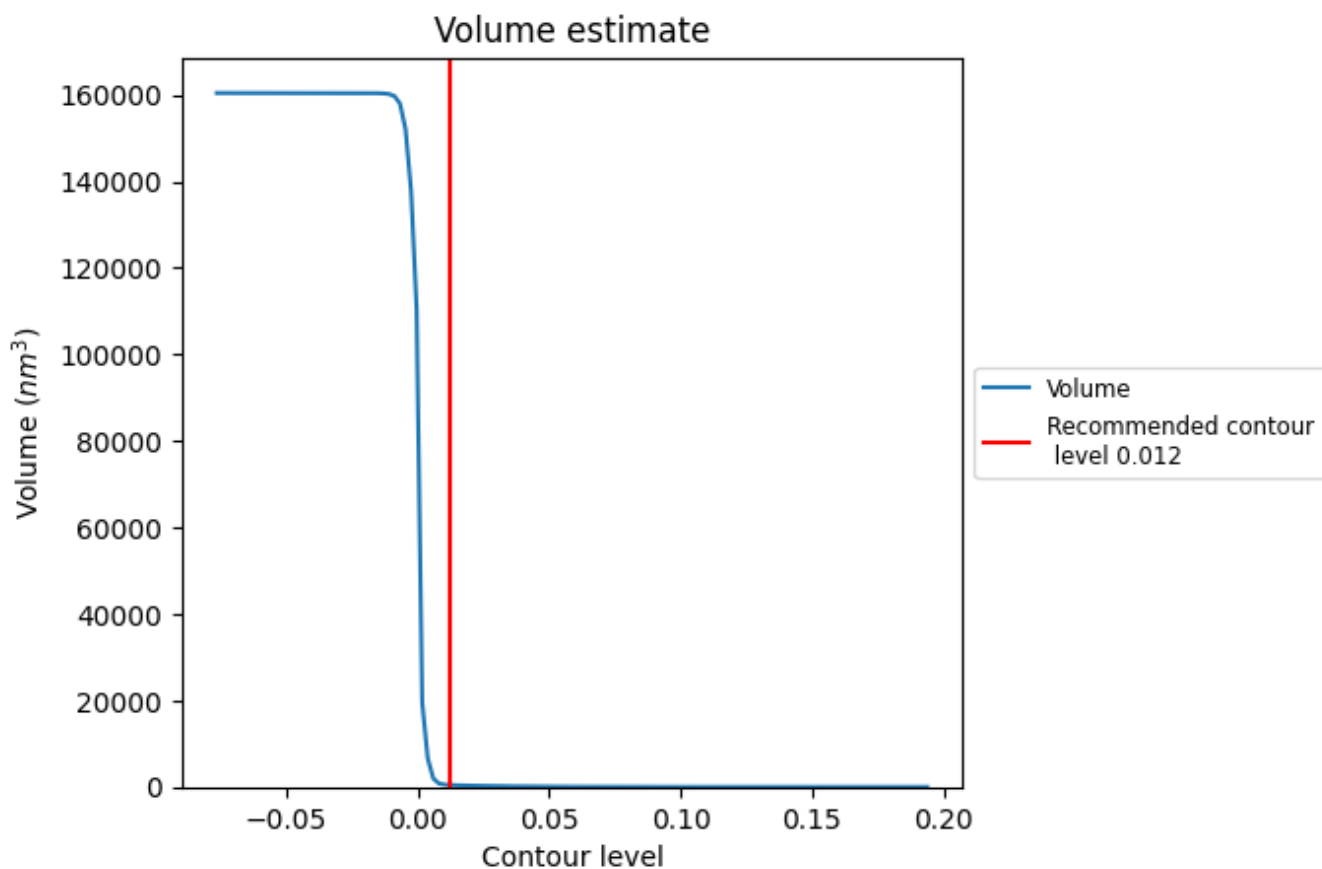
This section contains the results of statistical analysis of the map.

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.

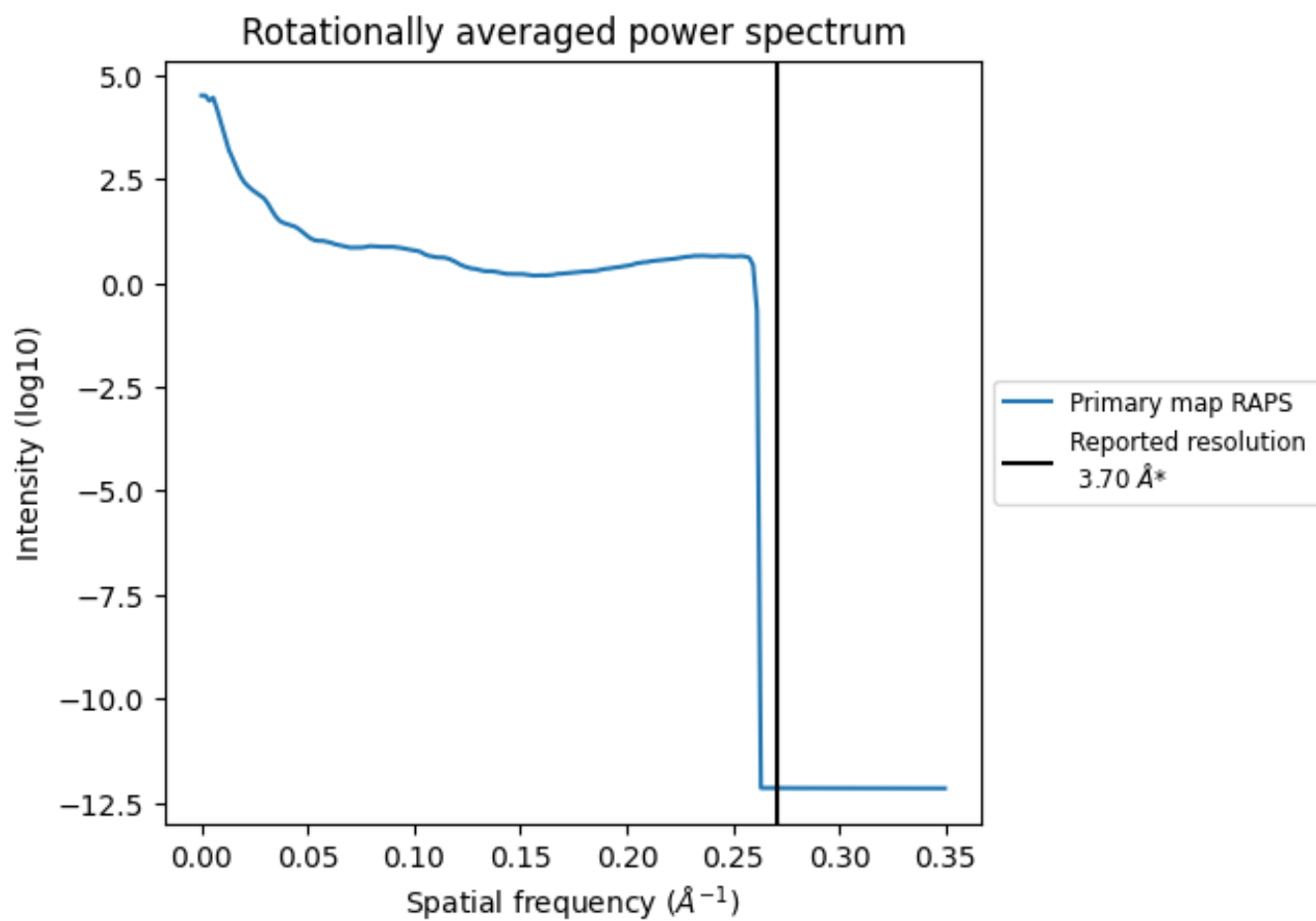
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 467 nm^3 ; this corresponds to an approximate mass of 422 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](#)

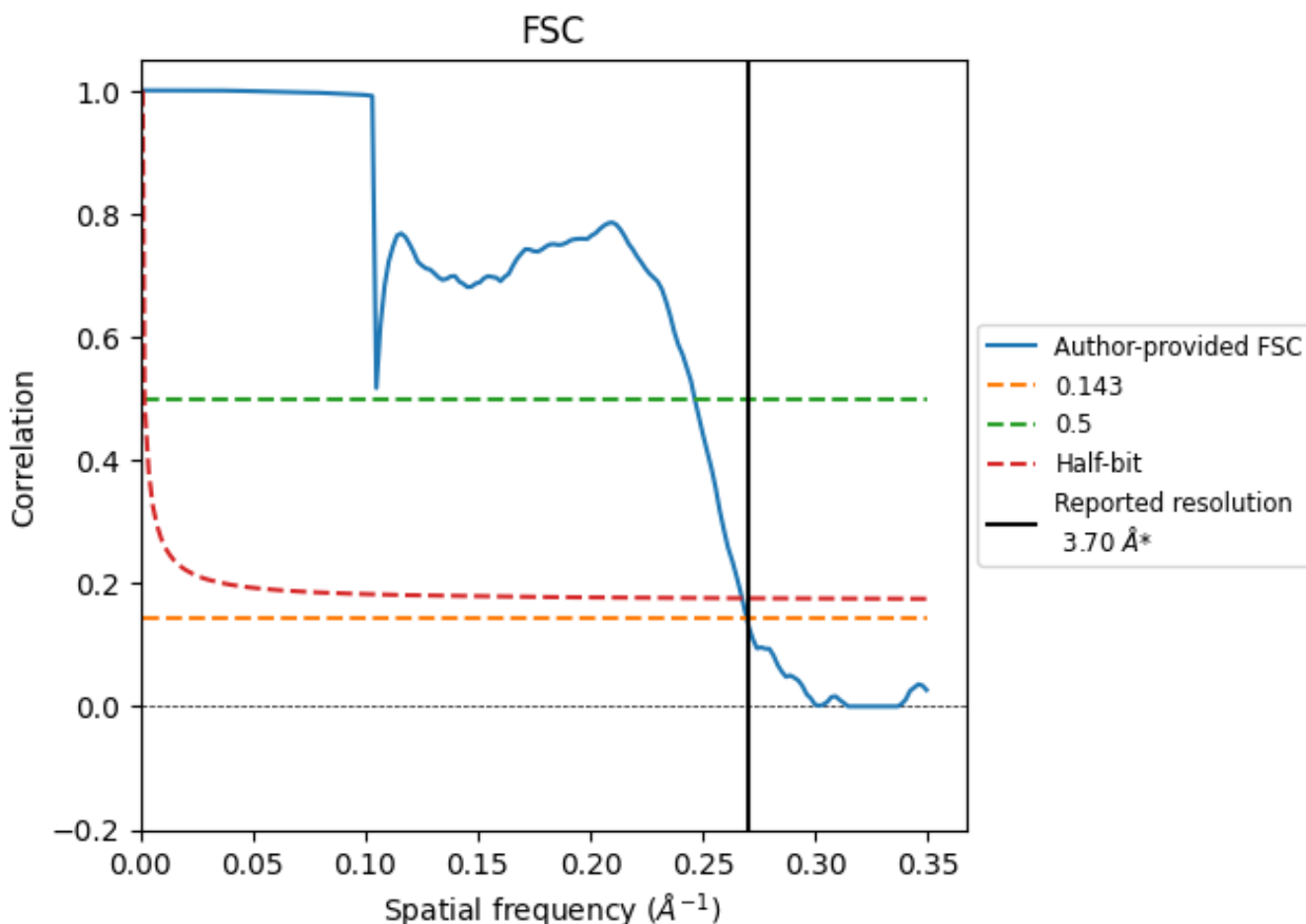


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

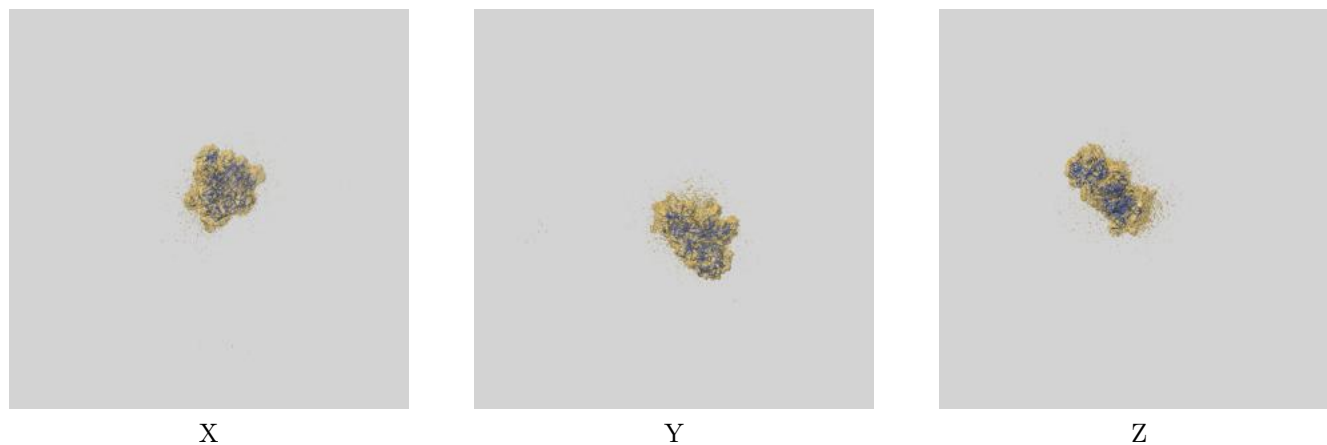
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.71	4.06	3.74
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

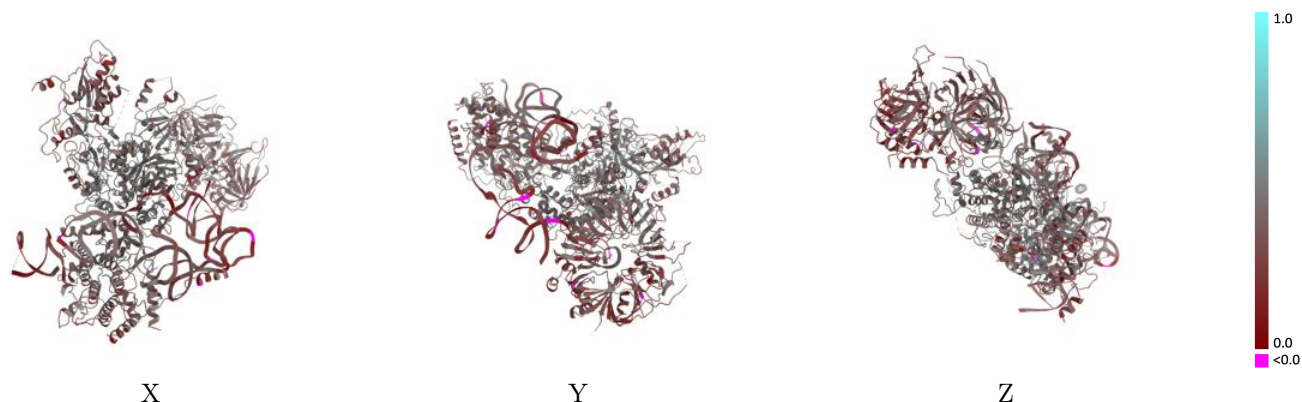
This section contains information regarding the fit between EMDB map EMD-8011 and PDB model 5GAM. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



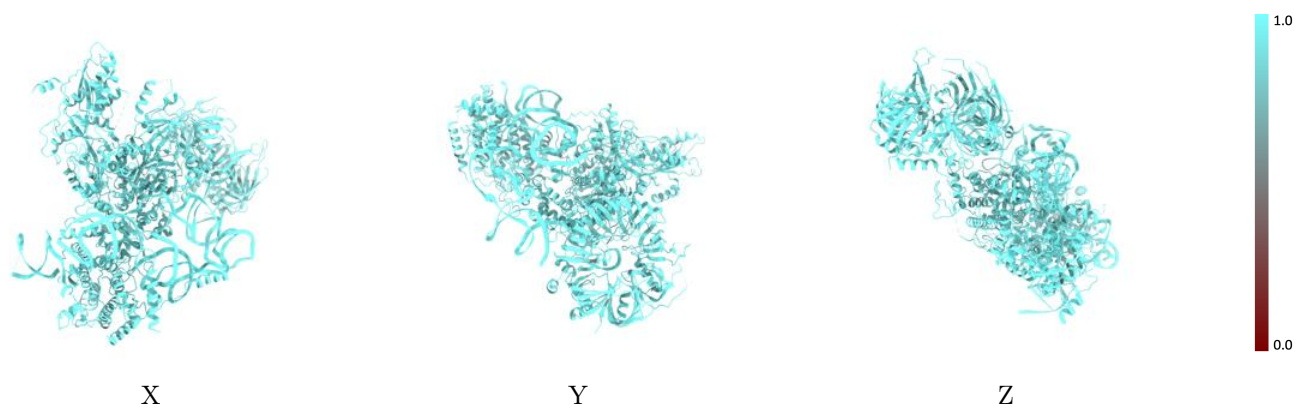
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



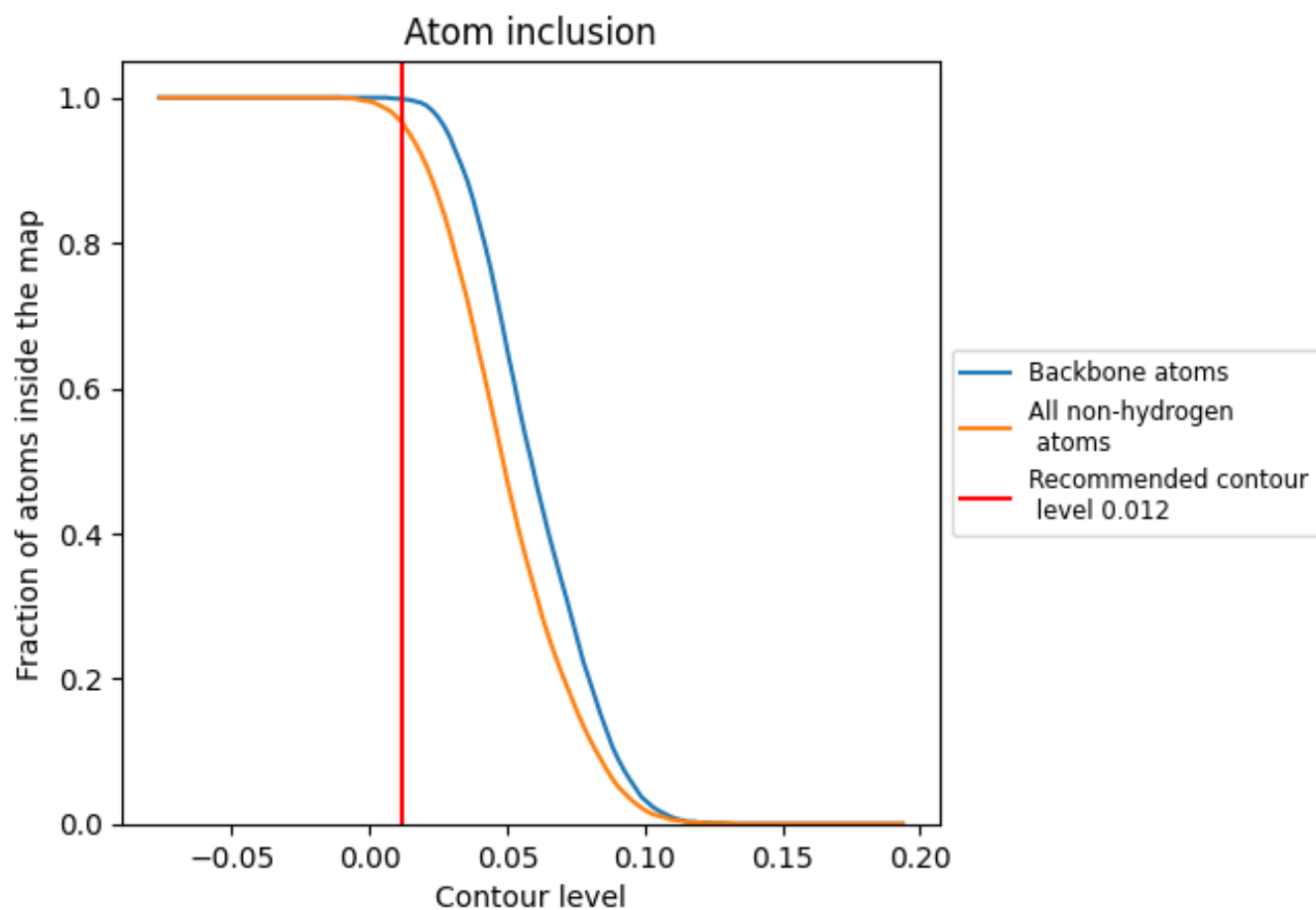
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.012).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 96% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9650	 0.3630
A	 0.9590	 0.3960
C	 0.9630	 0.4090
U	 0.9930	 0.2850
W	 0.9960	 0.2480
b	 0.9270	 0.3790
d	 0.9470	 0.4150
e	 0.9510	 0.2850
f	 0.9680	 0.2620
g	 0.9540	 0.3430
h	 0.9320	 0.2970
j	 0.9640	 0.2950
x	 1.0000	 0.3890

