wwPDB EM Validation Summary Report (i)

Mar 9, 2026 – 04:09 PM UTC

PDB ID	:	9EDT / pdb_00009edt
EMDB ID	:	EMD-47949
Title	:	Tubulin cofactors D,E,G bound to tubulin dimer
Authors	:	Taheri, A.; Al-bassam, J.
Deposited on	:	2024-11-18
Resolution	:	3.70 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 (i) 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 (i)) were used in the production of this report:

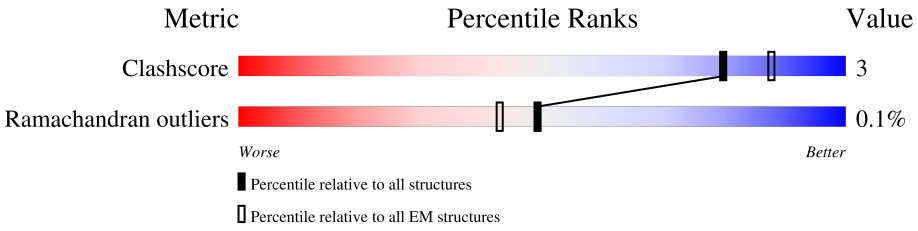
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data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

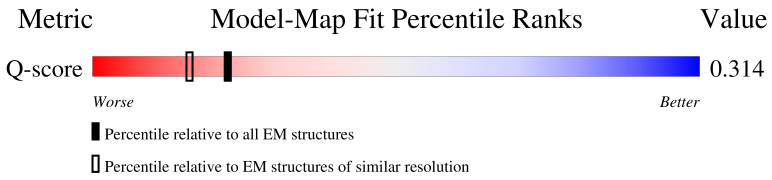
1 Overall quality at a glance (i)

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	-
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 <=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	D	1020	97%
2	G	191	98%
3	A	451	93% 5%
4	B	445	92%
5	F	169	73% 26%

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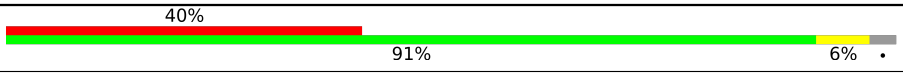
Mol	Chain	Length	Quality of chain
6	E	459	

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 13115 atoms, of which 24 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 Chromosome instability protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	D	1004	4999	2991	1004	1004	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-5	MET	-	initiating methionine	UNP P40987
D	-4	HIS	-	expression tag	UNP P40987
D	-3	HIS	-	expression tag	UNP P40987
D	-2	HIS	-	expression tag	UNP P40987
D	-1	HIS	-	expression tag	UNP P40987
D	0	HIS	-	expression tag	UNP P40987
D	1	HIS	-	expression tag	UNP P40987

- Molecule 2 is a protein called GTP-binding protein CIN4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	G	191	944	562	191	191	0	0

- Molecule 3 is a protein called Tubulin alpha-1A chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	A	429	2114	1256	429	429	0	0

- Molecule 4 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	B	427	2102	1248	427	427	0	0

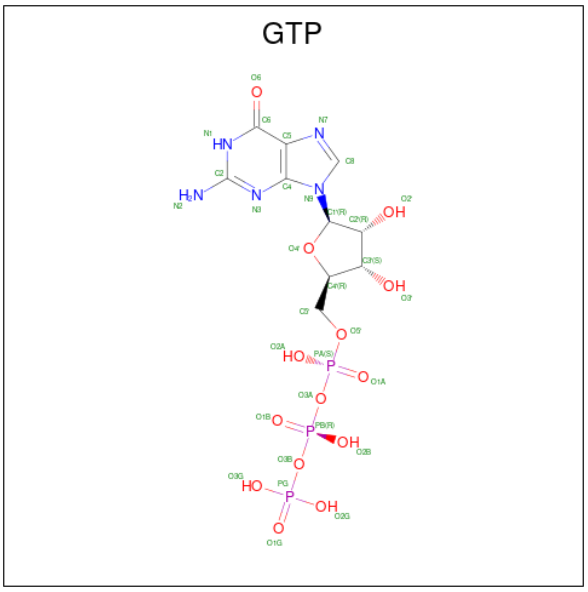
- Molecule 5 is a protein called Designed ankyrin repeat protein – Darpin.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	F	125	Total	C	N	O	0	0
			613	363	125	125		

- Molecule 6 is a protein called Protein PAC2.

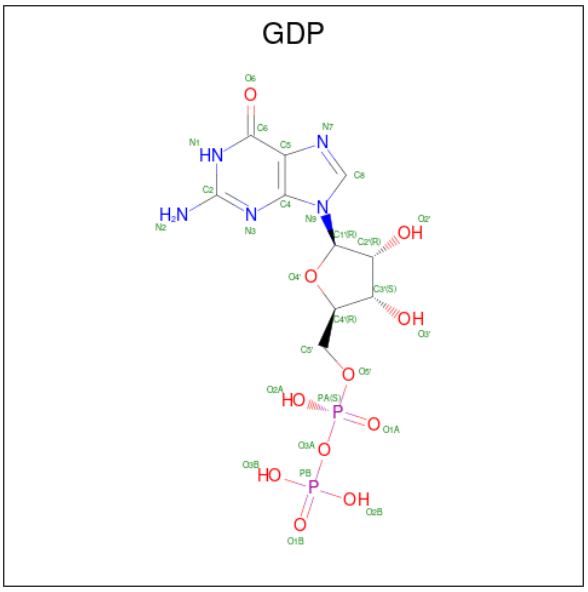
Mol	Chain	Residues	Atoms				AltConf	Trace
6	E	446	Total	C	N	O	0	0
			2227	1335	446	446		

- Molecule 7 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
7	G	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	
7	A	1	Total	C	H	N	O	P	0
			44	10	12	5	14	3	

- Molecule 8 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).



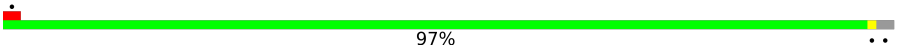
Mol	Chain	Residues	Atoms					AltConf
8	B	1	Total	C	N	O	P	0
			28	10	5	11	2	

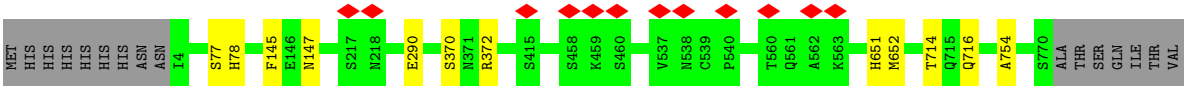
3 Residue-property plots (i)

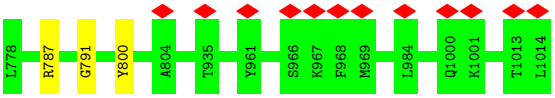
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Chromosome instability protein 1

Chain D:

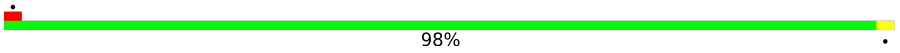


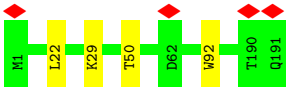




• Molecule 2: GTP-binding protein CIN4

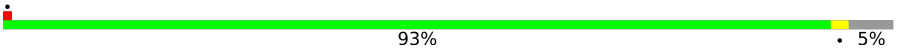
Chain G:

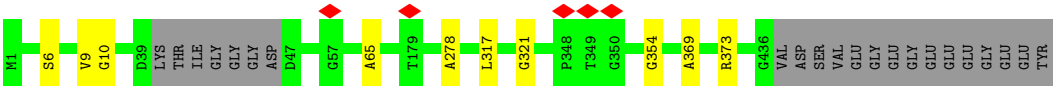




• Molecule 3: Tubulin alpha-1A chain

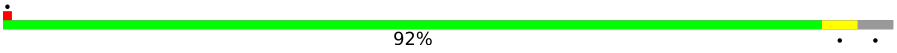
Chain A:

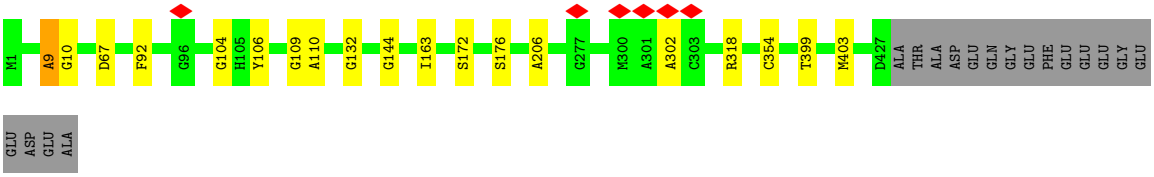




• Molecule 4: Tubulin beta chain

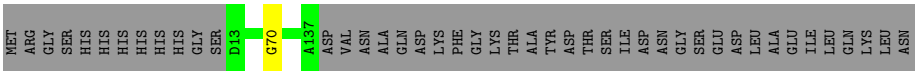
Chain B:





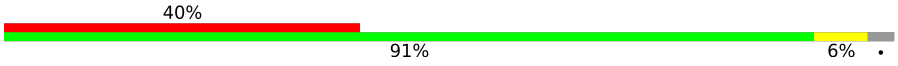
• Molecule 5: Designed ankyrin repeat protein – Darpin

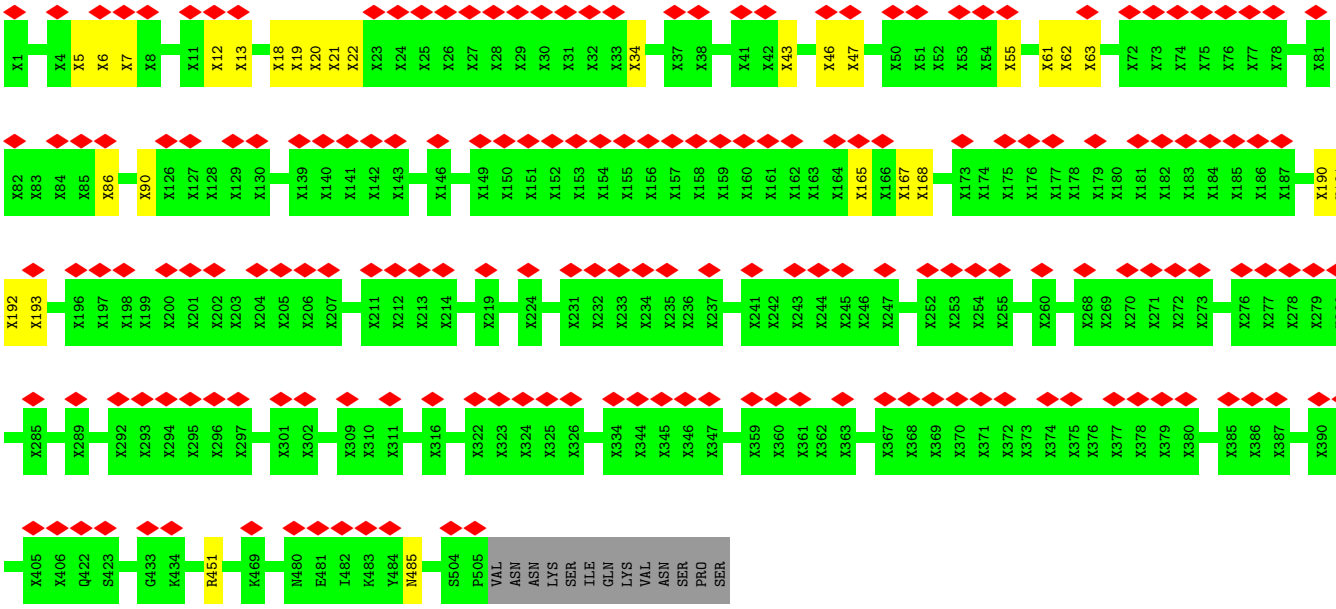
Chain F:



• Molecule 6: Protein PAC2

Chain E:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	275487	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	1.967	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.0343	Depositor
Map size (Å)	529.6, 529.6, 529.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3239999, 1.3239999, 1.3239999	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, 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	D	0.26	0/4997	0.64	1/6980 (0.0%)
2	G	0.25	0/943	0.65	0/1312
3	A	0.26	0/2112	0.65	0/2935
4	B	0.29	0/2101	0.64	0/2920
5	F	0.23	0/612	0.62	0/848
6	E	0.22	0/416	0.57	0/579
All	All	0.26	0/11181	0.64	1/15574 (0.0%)

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
3	A	0	1
4	B	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	290	GLU	N-CA-CB	5.07	118.02	110.22

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	9	VAL	Peptide

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Mol	Chain	Res	Type	Group
4	B	9	ALA	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	D	4999	0	2135	7	0
2	G	944	0	397	3	0
3	A	2114	0	981	4	0
4	B	2102	0	947	10	0
5	F	613	0	315	0	0
6	E	2227	0	544	24	0
7	A	32	12	12	0	0
7	G	32	12	12	2	0
8	B	28	0	12	1	0
All	All	13091	24	5355	49	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 3.

The worst 5 of 49 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)
6:E:43:UNK:CB	6:E:62:UNK:C	2.00	1.39
6:E:43:UNK:CB	6:E:61:UNK:O	1.98	1.12
6:E:43:UNK:CB	6:E:62:UNK:CA	2.35	1.05
6:E:43:UNK:CB	6:E:62:UNK:HA	2.03	0.88
8:B:501:GDP:C8	8:B:501:GDP:H5'	2.13	0.84

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	D	1000/1020 (98%)	970 (97%)	30 (3%)	0	100 100
2	G	189/191 (99%)	183 (97%)	6 (3%)	0	100 100
3	A	425/451 (94%)	408 (96%)	16 (4%)	1 (0%)	43 72
4	B	425/445 (96%)	416 (98%)	8 (2%)	1 (0%)	43 72
5	F	123/169 (73%)	116 (94%)	6 (5%)	1 (1%)	16 48
6	E	82/459 (18%)	79 (96%)	3 (4%)	0	100 100
All	All	2244/2735 (82%)	2172 (97%)	69 (3%)	3 (0%)	49 78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	10	GLY
4	B	10	GLY
5	F	70	GLY

5.3.2 Protein sidechains

There are no protein residues with a non-rotameric sidechain to report in this entry.

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)

3 ligands are 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	$\#\|Z\| > 2$
7	GTP	A	501	-	33,34,34	2.32	7 (21%)	50,54,54	1.78	12 (24%)
7	GTP	G	501	-	33,34,34	2.39	8 (24%)	50,54,54	1.73	11 (22%)
8	GDP	B	501	-	29,30,30	1.65	6 (20%)	45,47,47	1.59	6 (13%)

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
7	GTP	A	501	-	-	7/22/38/38	0/3/3/3
7	GTP	G	501	-	-	1/22/38/38	0/3/3/3
8	GDP	B	501	-	-	8/16/32/32	0/3/3/3

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	501	GTP	PB-O3A	7.76	1.67	1.59
7	A	501	GTP	PB-O3A	6.95	1.67	1.59
7	G	501	GTP	PA-O5'	6.69	1.85	1.59
7	A	501	GTP	PA-O5'	6.42	1.84	1.59
7	A	501	GTP	PB-O3B	-4.87	1.54	1.59

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	B	501	GDP	O2A-PA-O3A	6.42	124.62	107.27
7	G	501	GTP	O2B-PB-O3A	-5.56	92.24	107.27
7	A	501	GTP	O2B-PB-O3A	-5.38	92.72	107.27
7	G	501	GTP	O3A-PA-O1A	3.43	121.01	110.70
7	A	501	GTP	O3A-PA-O1A	3.42	120.98	110.70

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	501	GTP	C5'-O5'-PA-O3A
7	A	501	GTP	C5'-O5'-PA-O1A
7	A	501	GTP	C5'-O5'-PA-O2A
8	B	501	GDP	PA-O3A-PB-O2B
8	B	501	GDP	C5'-O5'-PA-O3A

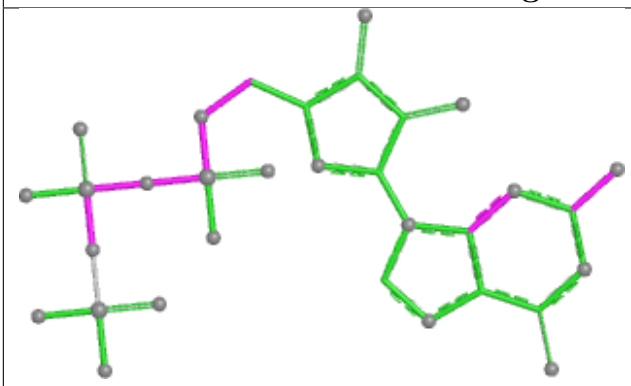
There are no ring outliers.

2 monomers are involved in 3 short contacts:

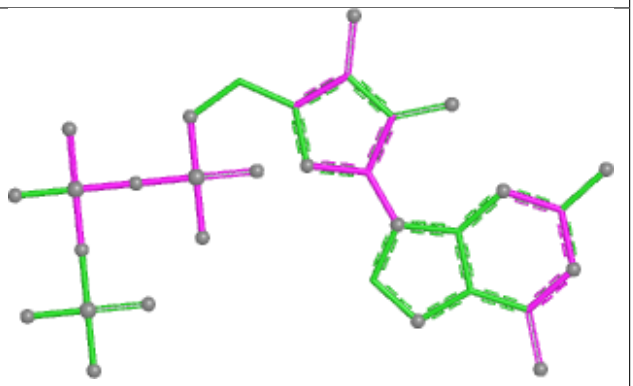
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	G	501	GTP	2	0
8	B	501	GDP	1	0

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 then 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.

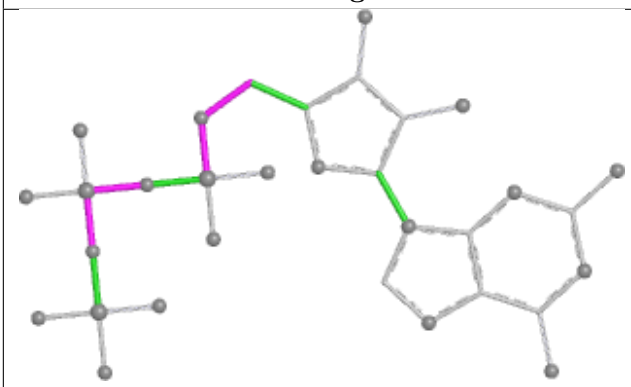
Ligand GTP A 501



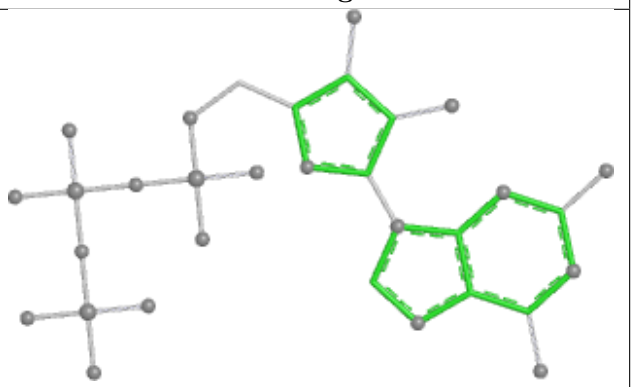
Bond lengths



Bond angles

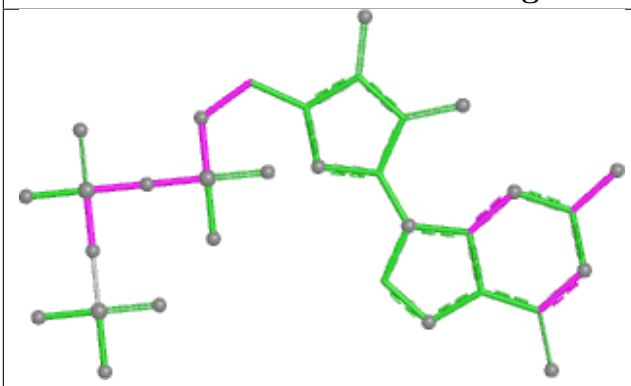


Torsions

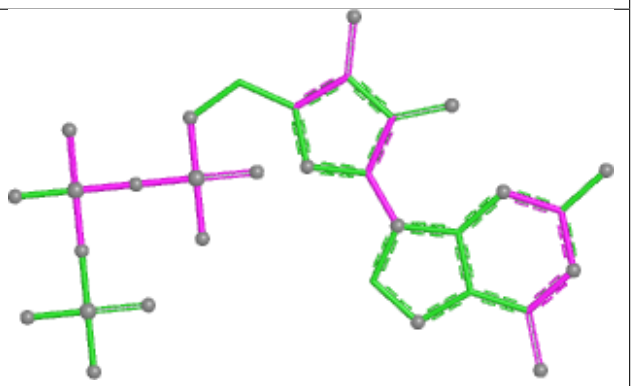


Rings

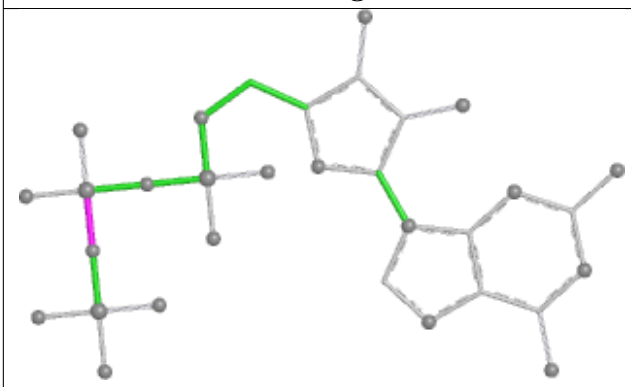
Ligand GTP G 501



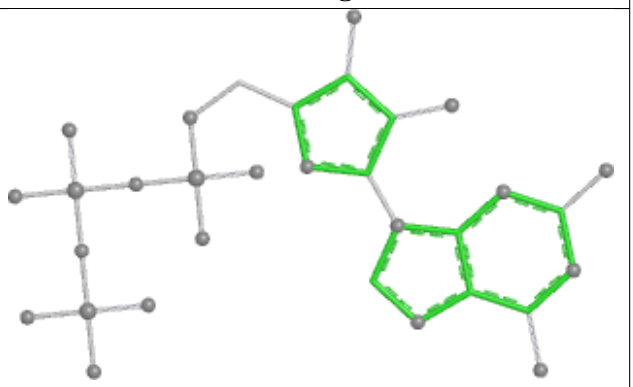
Bond lengths



Bond angles

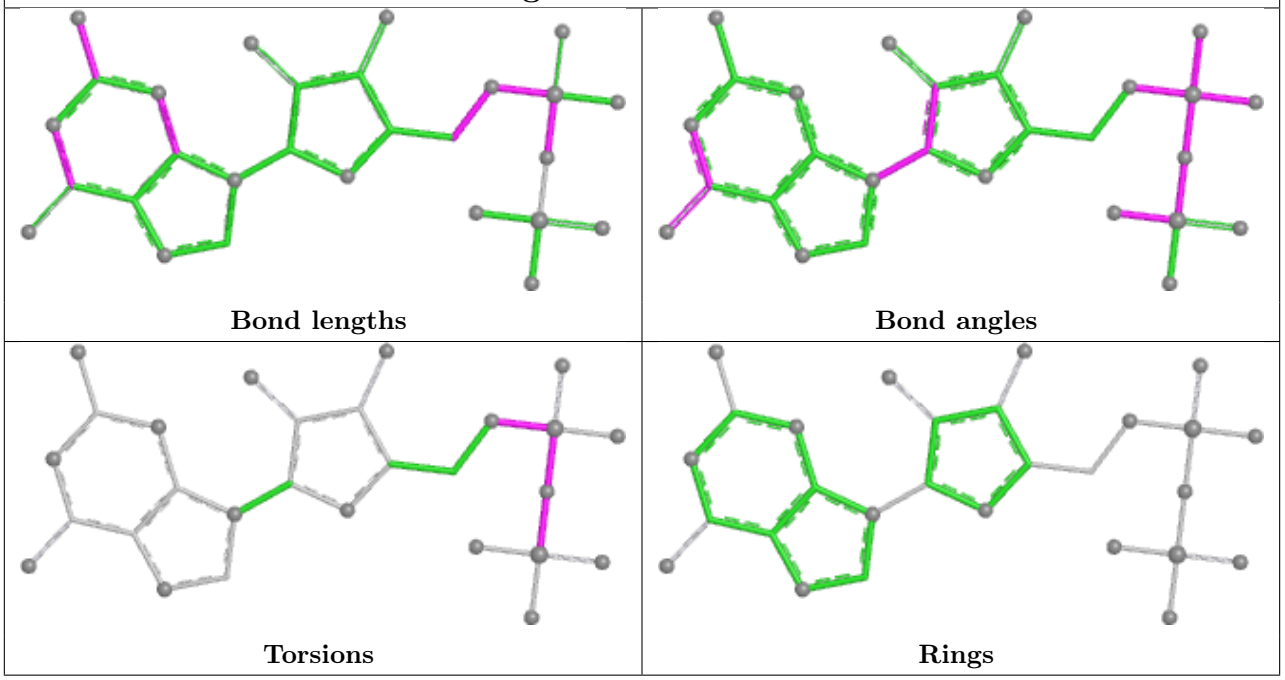


Torsions



Rings

Ligand GDP B 501



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	E	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	406:UNK	C	422:GLN	N	24.65
1	E	90:UNK	C	126:UNK	N	15.74
1	E	334:UNK	C	344:UNK	N	10.05

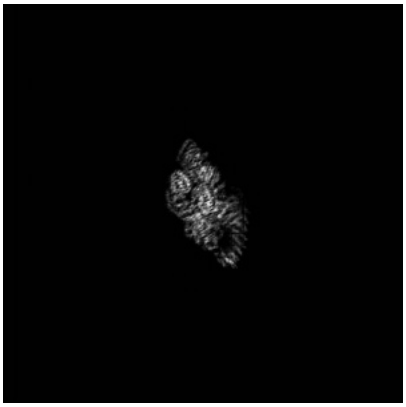
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-47949. These allow visual inspection of the internal detail of the map and identification of artifacts.

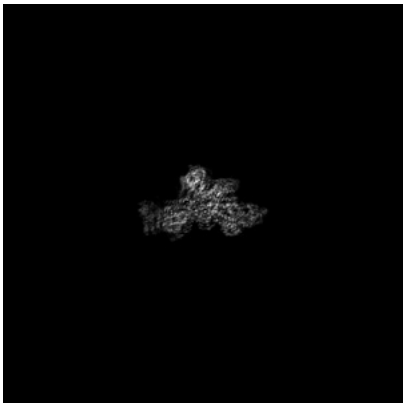
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

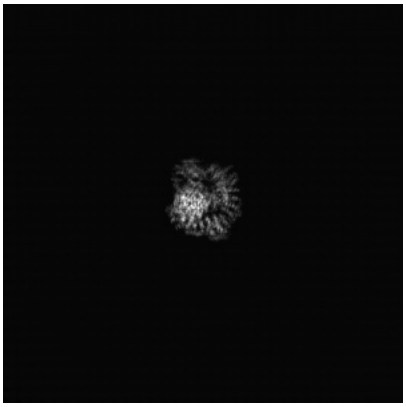
6.1.1 Primary map



X



Y



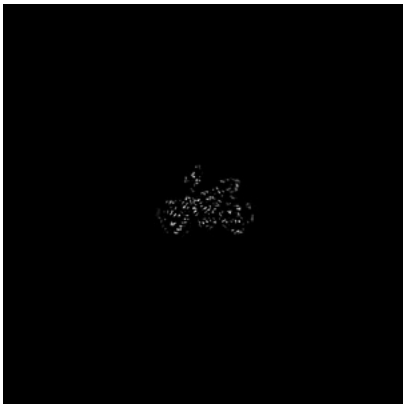
Z

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

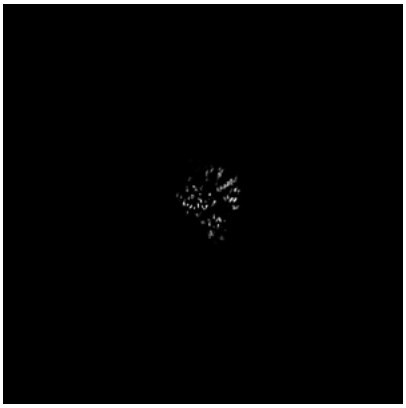
6.2 Central slices

6.2.1 Primary map

X Index: 200



Y Index: 200



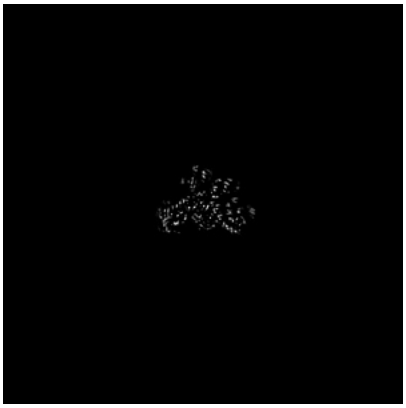
Z Index: 200

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

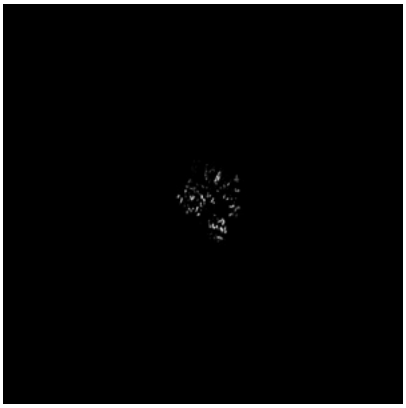
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 191



Y Index: 203

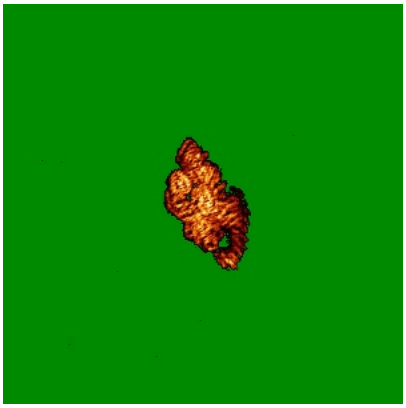


Z Index: 198

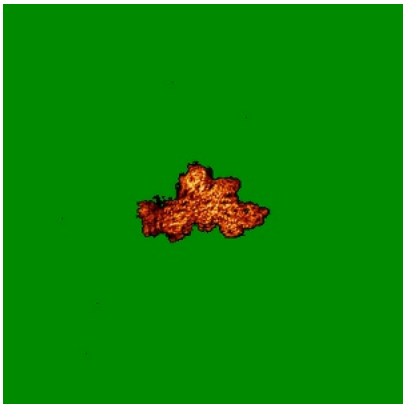
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

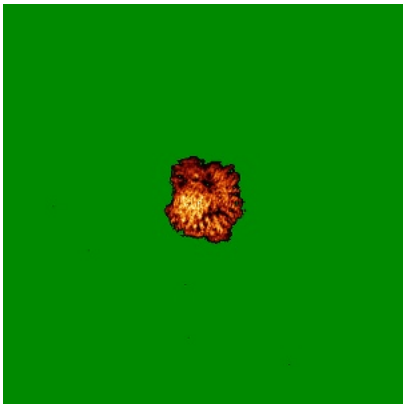
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0343. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

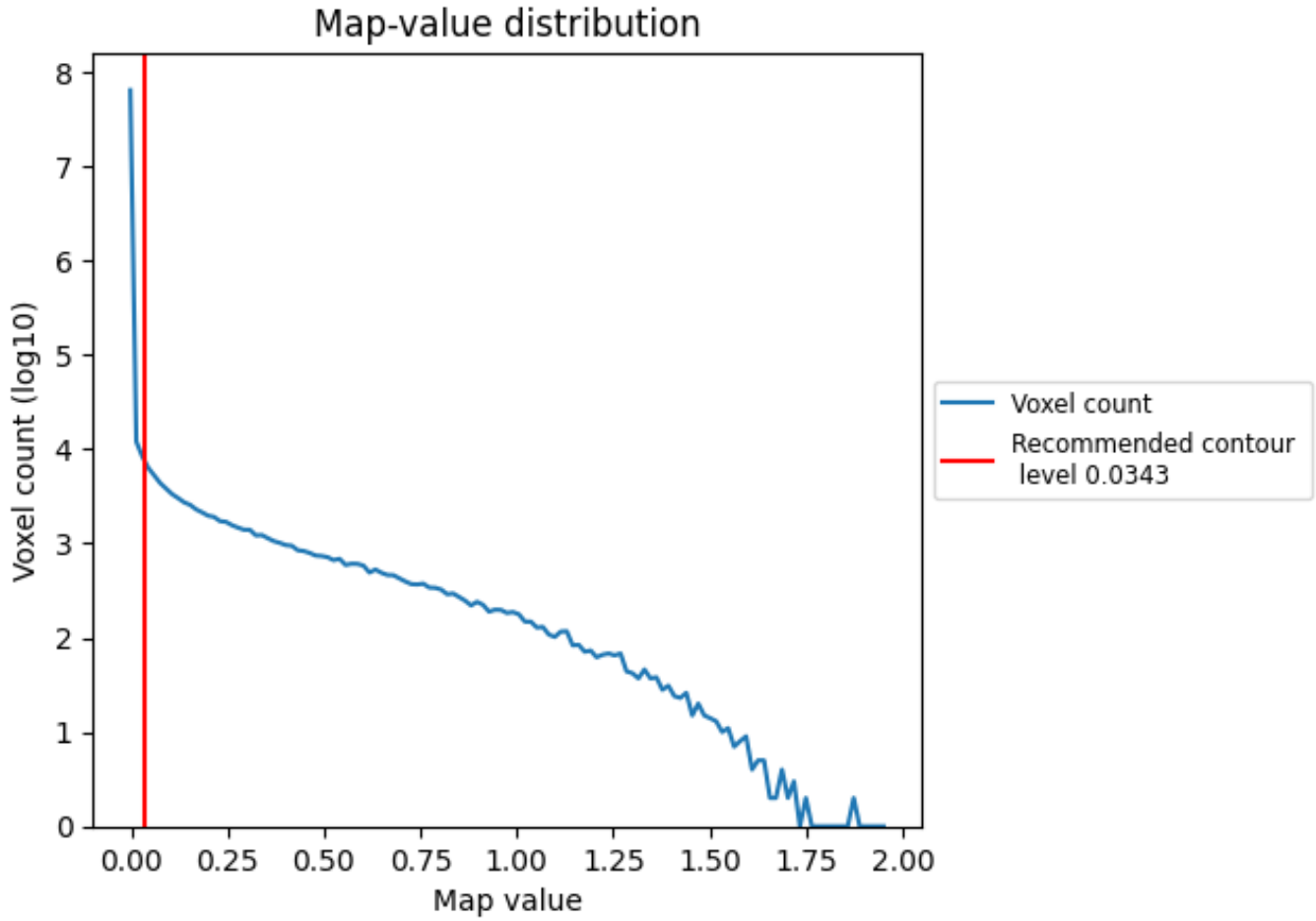
6.6 Mask visualisation (i)

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

7 Map analysis

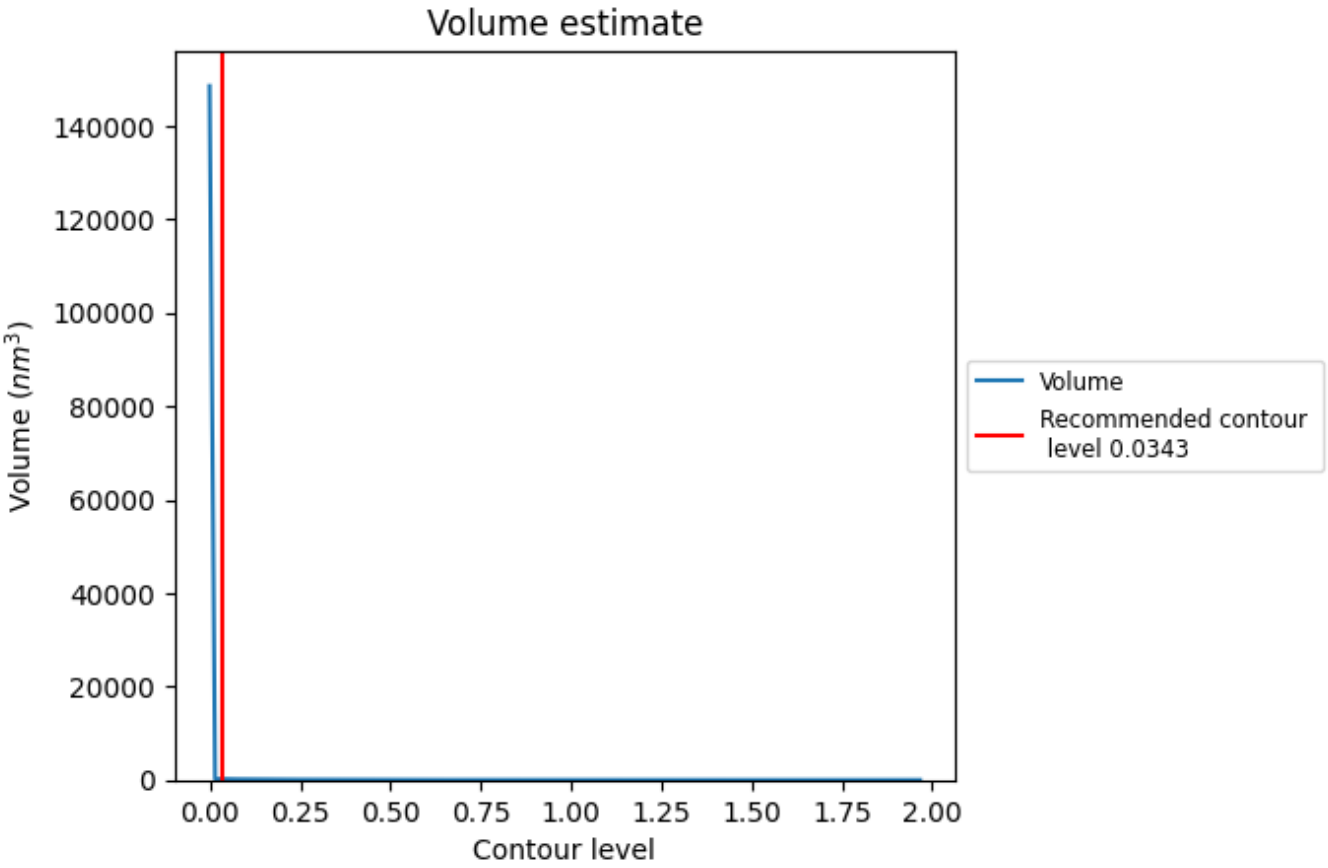
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

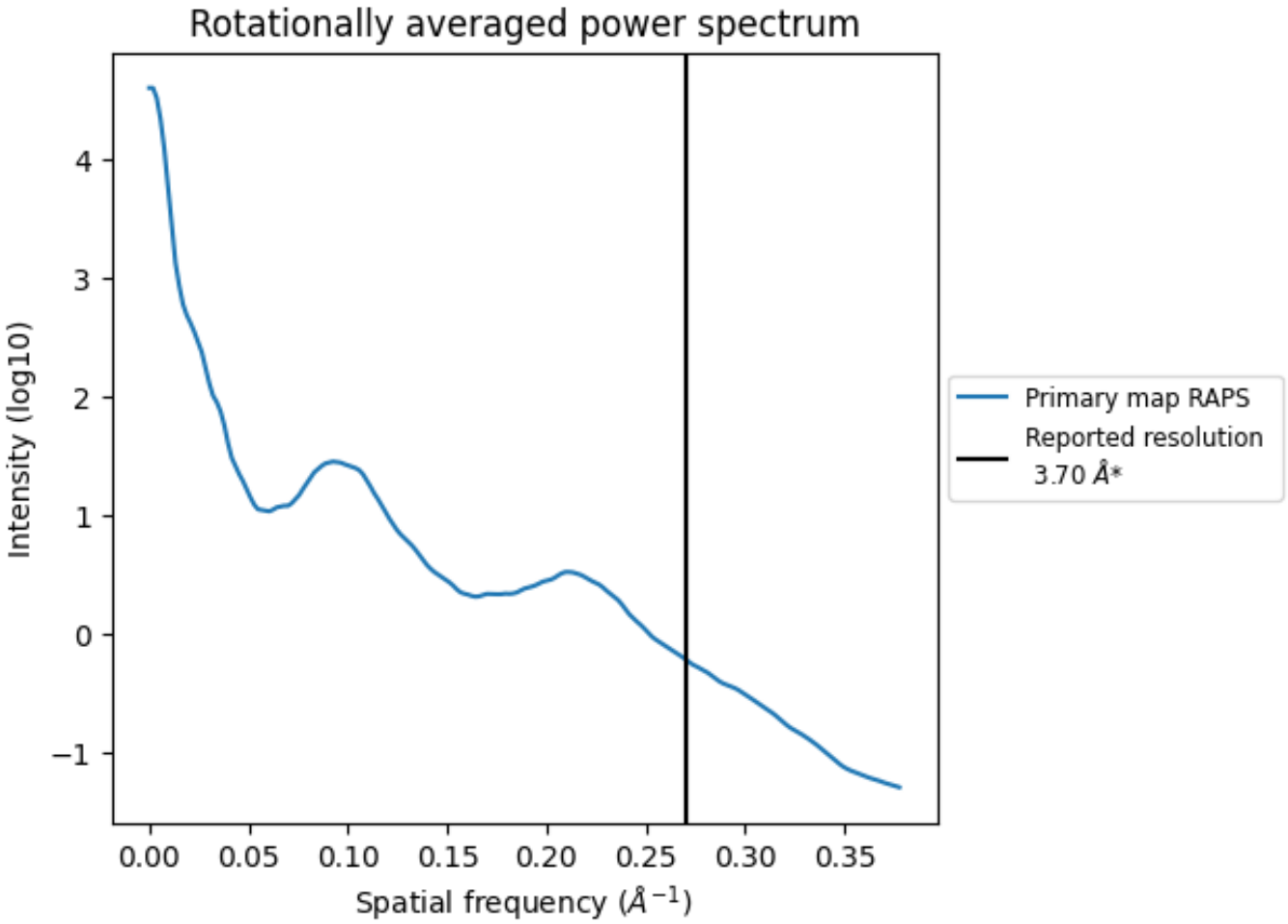
7.2 Volume estimate (i)



The volume at the recommended contour level is 188 nm^3; this corresponds to an approximate mass of 170 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}

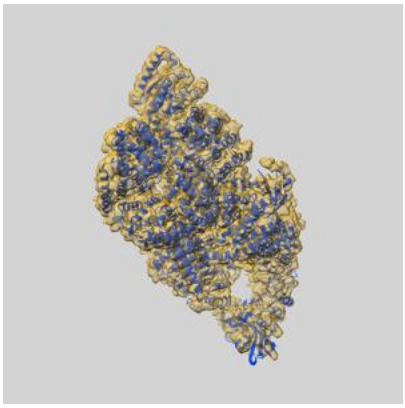
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

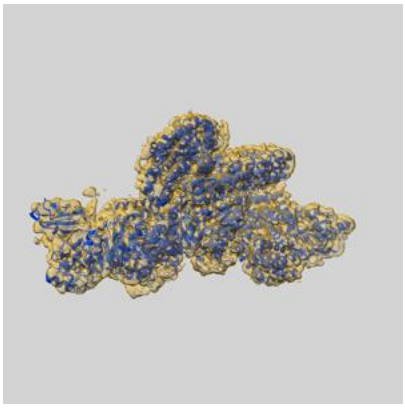
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-47949 and PDB model 9EDT. Per-residue inclusion information can be found in section 3 on page 7.

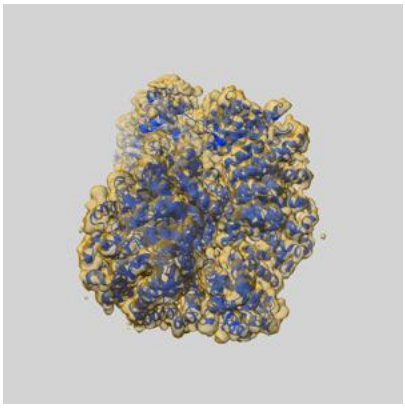
9.1 Map-model overlay



X



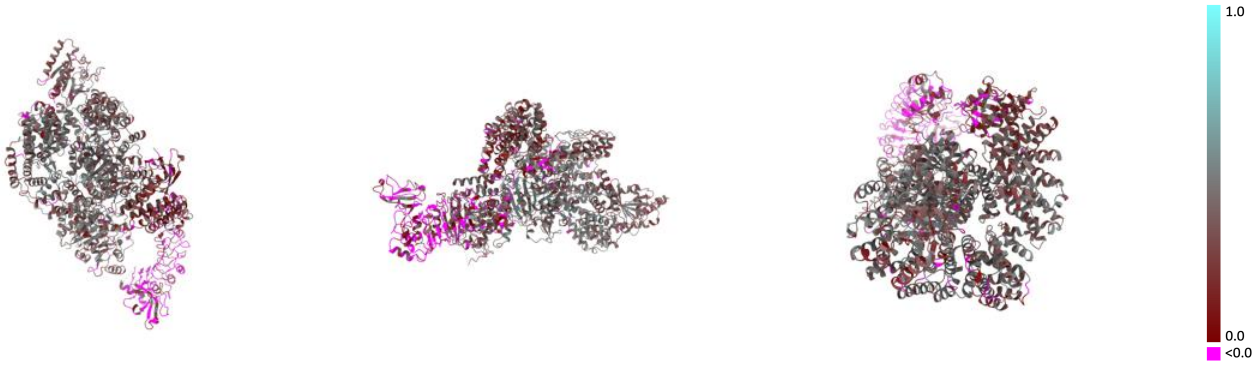
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0343 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.

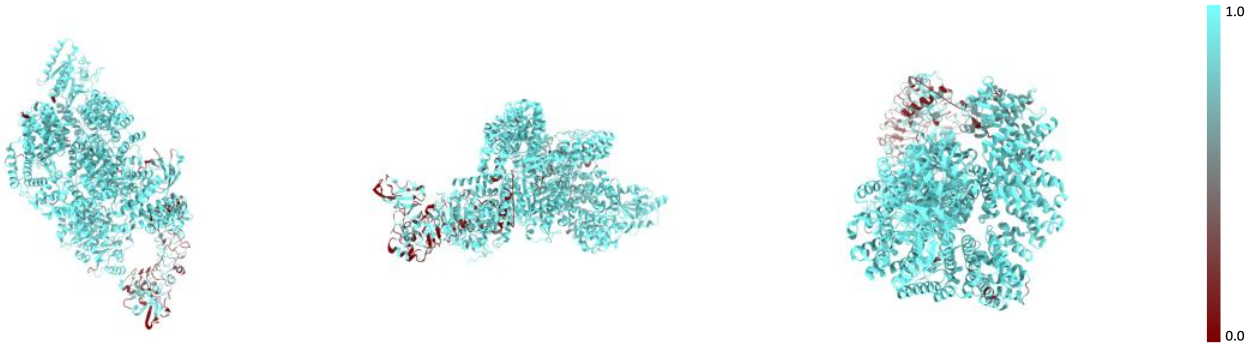
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

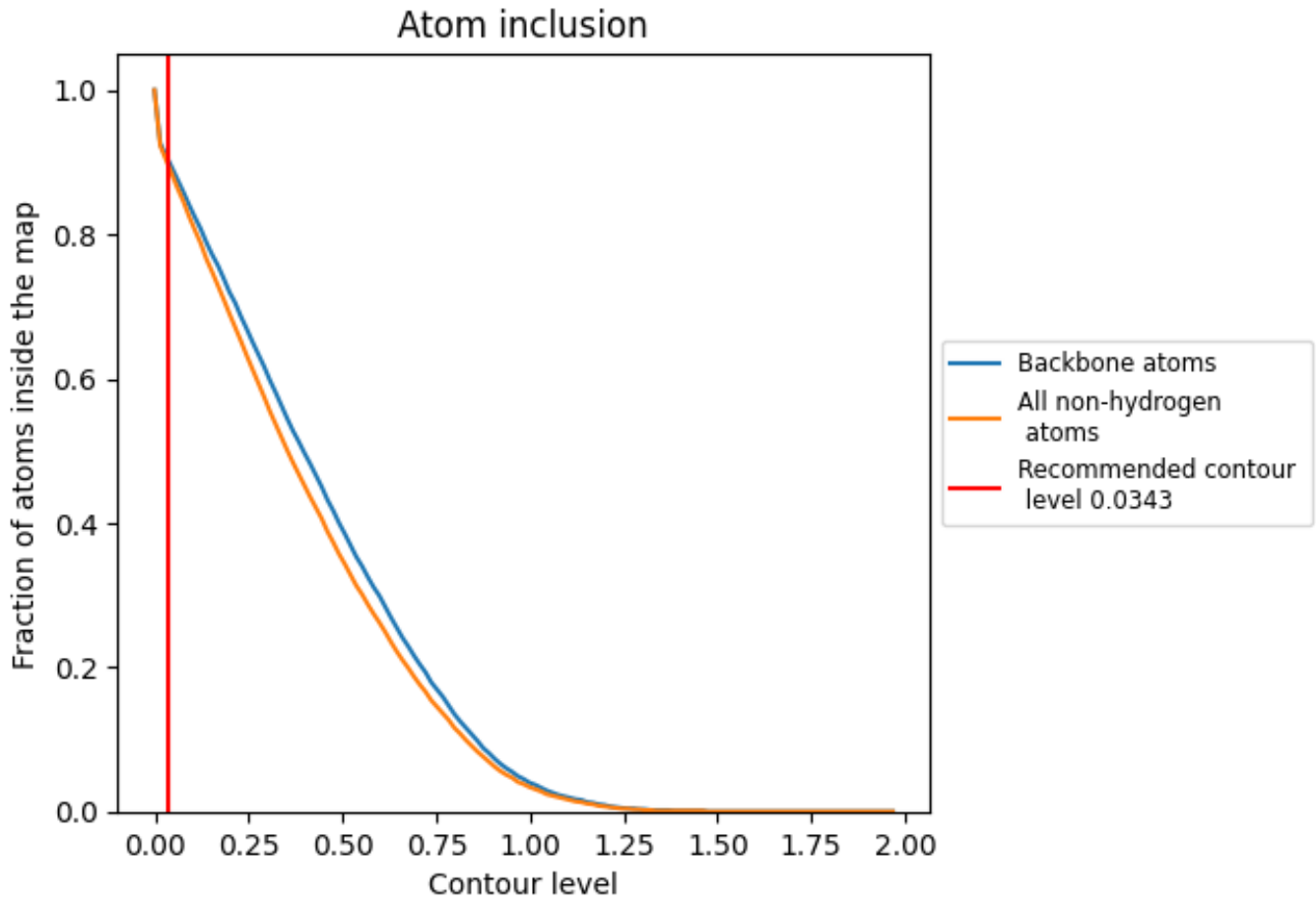
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.0343).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 90% 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 (0.0343) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8970	0.3140
A	0.9650	0.3560
B	0.9710	0.4240
D	0.9620	0.3610
E	0.5690	0.0480
F	0.9770	0.3780
G	0.9550	0.3030