



wwPDB EM Validation Summary Report ⓘ

Nov 14, 2024 – 09:28 am GMT

PDB ID : 8RIK
EMDB ID : EMD-19188
Title : Microtubule-associated kinesin-1 tail complex bound to ADP, single-headed state
Authors : Atherton, J.; Chegkazi, M.S.; Steiner, R.A.
Deposited on : 2023-12-18
Resolution : 3.60 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.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) : 2.39

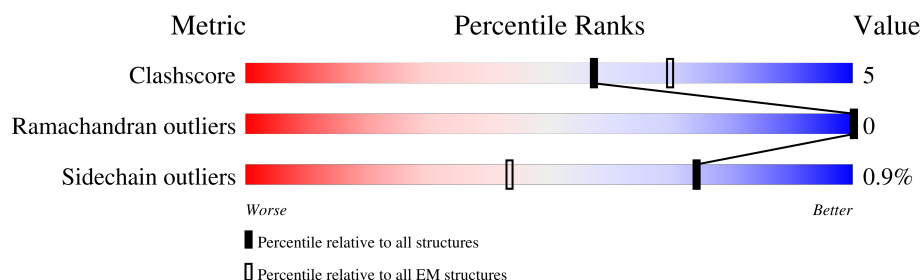
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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

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	B	445	
2	A	451	
3	K	963	
3	T	963	
3	t	963	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 9353 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 Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	426	Total	C	N	O	S	0	0
			3351	2106	575	644	26		

- Molecule 2 is a protein called Tubulin alpha-1B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	428	Total	C	N	O	S	0	0
			3358	2130	571	635	22		

- Molecule 3 is a protein called Kinesin-1 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	312	Total	C	N	O	S	0	0
			2448	1528	421	487	12		
3	T	3	Total	C	N	O		3	0
			24	17	4	3			
3	t	3	Total	C	N	O		3	0
			22	15	4	3			

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



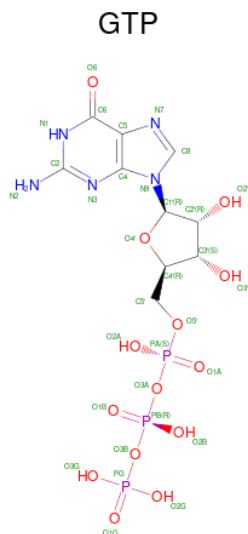
Mol	Chain	Residues	Atoms					AltConf
4	B	1	Total 28	C 10	N 5	O 11	P 2	0

- Molecule 5 is TAXOL (three-letter code: TA1) (formula: $C_{47}H_{51}NO_{14}$).



Mol	Chain	Residues	Atoms				AltConf
5	B	1	Total	C	N	O	0
			62	47	1	14	

- Molecule 6 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{14}\text{P}_3$).

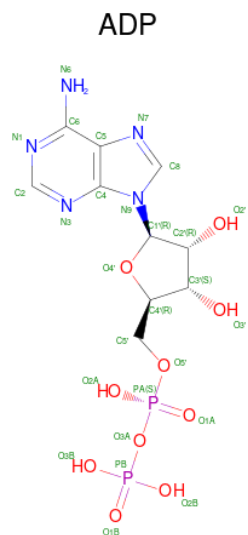


Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total 32	C 10	N 5	O 14	P 3	0

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
7	A	1	Total Mg 1 1	0

- Molecule 8 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{10}\text{P}_2$).

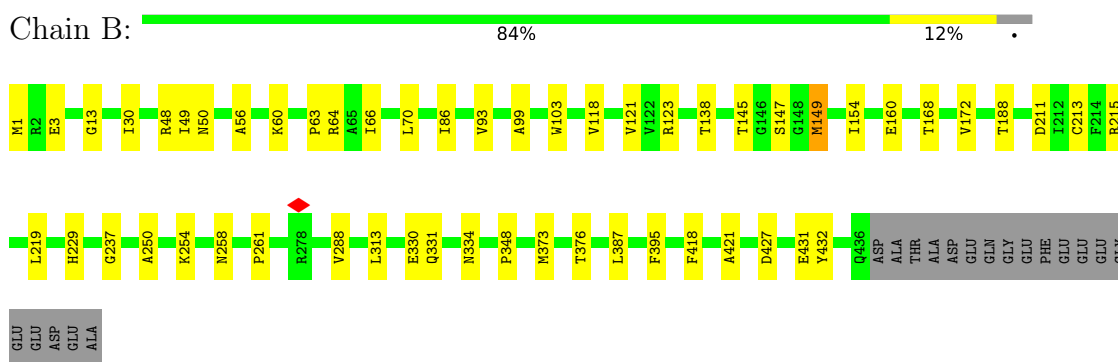


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
8	K	1	27	10	5	10	2	0

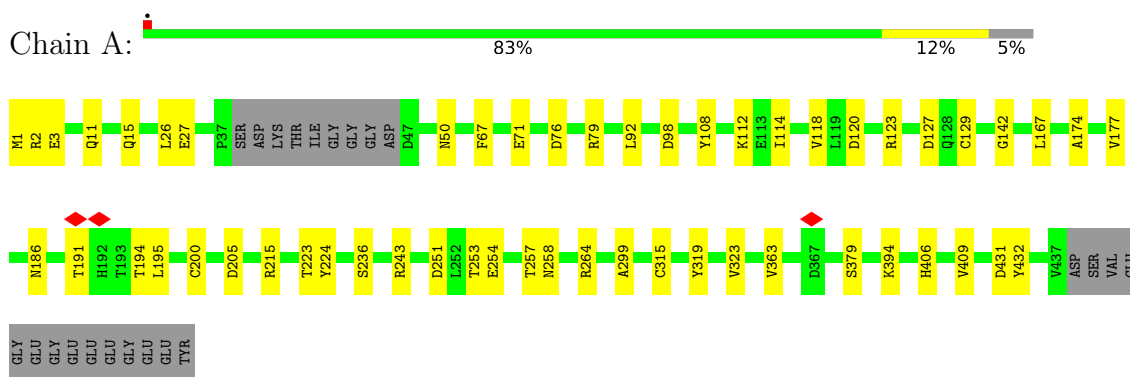
3 Residue-property plots [i](#)

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.

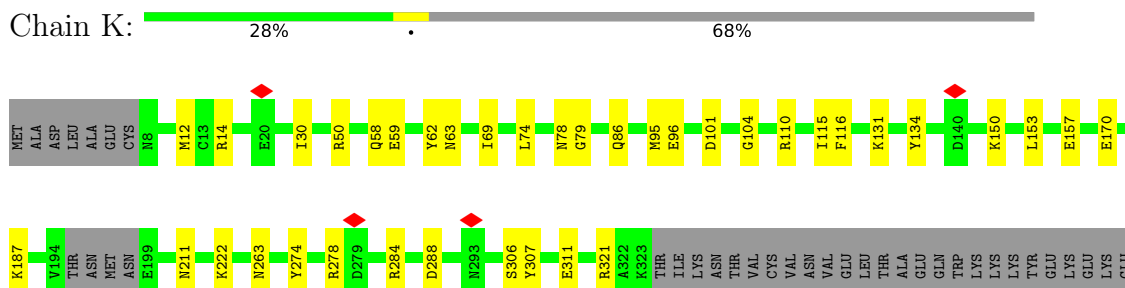
- Molecule 1: Tubulin beta chain



- Molecule 2: Tubulin alpha-1B chain



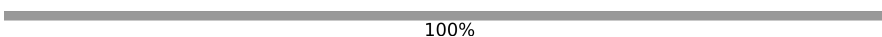
- Molecule 3: Kinesin-1 heavy chain



[illegible]

- Molecule 3: Kinesin-1 heavy chain

Chain T:



C	CYS	LEU	CYS	THR	ASP	SER	VAL	MET
	GLU	GLU	CYS	GLY	THR	MET	THR	ALA
	GLU	ASN	SER	ALA	ILE	ASN	ASN	ALA
	ILE	GLU	PRO	GLU	ASP	GLU	ASP	LEU
	ALA	ASN	SER	GLY	GLU	LEU	CYS	ALA
	LYS	ARG	TYR	VAL	LYS	GLU	LYS	GLY
	LEU	TRP	ASN	LEU	SER	PHE	CYS	ASN
	TYR	ARG	GLU	ASP	ASN	ILE	ILE	LYS
	GLN	GLY	GLU	ALA	HIS	LYS	VAL	VAL
	LEU	THR	THR	LYS	VAL	VAL	ASP	MET
A	ASP	THR	LYS	ASN	ALA	SER	VAL	CYS
	ASP	VAL	SER	ILE	VAL	TYR	VAL	ARG
	LYS	PRO	THR	ASN	THR	PHE	LEU	GLY
	ASP	ILE	LEU	LYS	ASN	GLU	GLY	ASN
	GLU	ASP	LEU	SER	MET	ILE	TYR	PRO
	GLY	GLU	PHE	LEU	ASN	TYR	ASN	LEU
	ILE	GLN	GLY	ALA	HIS	LYS	THR	GLU
	ASN	ASP	ARG	GLY	SER	ILE	PHE	GLY
	GLN	LYS	ALA	GLY	SER	ILE	ALA	VAL
	LEU	GLY	THR	VAL	ASN	ASP	TYR	ASN
S	LEU	ALA	ILE	ILE	HIS	LEU	GLY	ARG
	VAL	ASN	LYS	SER	SER	LEU	GLN	GLY
	GLU	LEU	ASN	ALA	ILE	ASP	THR	ASP
	LYS	GLU	THR	LEU	PHE	VAL	SER	LYS
	LEU	ALA	VAL	ALA	LEU	SER	SER	TYR
	LYS	THR	CYS	GLU	ILE	LYS	GLY	ILE
	THR	THR	VAL	GLY	ASN	THR	LYS	ALA
	GLN	VAL	ASN	THR	VAL	ASN	HIS	GLU
	LYS	ASP	GLU	TYR	GLN	SER	THR	GLN
	ASP	ASP	LEU	VAL	GLU	VAL	MET	GLY
E	GLN	THR	THR	PRO	ASN	HIS	GLU	GLU
	GLU	ILE	ALA	TYR	THR	GLU	GLY	ASP
	LEU	LEU	GLU	ARG	GLN	ASP	LEU	THR
	LEU	THR	GLN	ASP	THR	LYS	VAL	VAL
	LEU	ASN	TRP	SER	GLU	ASN	HIS	VAL
	ALA	ASP	LYS	LYS	GLN	ARG	ASP	ILE
	SER	LYS	LYS	MET	LYS	VAL	PRO	ALA
	THR	PRO	LYS	THR	LEU	PHO	GLU	SER
	ARG	ALA	TYR	ARG	SER	TYR	GLY	LYS
	ARG	THR	GLU	ILE	GLY	VAL	MET	TYR
R	ASP	ILE	GLU	GLY	LYS	GLY	ILE	PHE
	GLN	ASN	ILE	GLN	TYR	GLY	ILE	GLN
	GLY	PHE	ILE	ASN	VAL	PHE	VAL	PHE
	THR	THR	LEU	CYS	GLY	ASP	ASP	SER
	ASN	ASP	ARG	ARG	SER	ILE	ILE	SER
	ARG	ALA	ASN	THR	GLU	THR	THR	THR
	GLN	GLY	ASN	GLY	ASP	GLU	ASN	SER
	ALA	ASN	LYS	GLY	LEU	PHE	GLN	GLN
	GLY	THR	ILE	LYS	GLY	VAL	VAL	GLY
	LEU	THR	LEU	CYS	GLY	CYS	ASP	SER
I	ASN	ASP	ARG	ARG	SER	SER	ILE	SER
	ARG	ALA	ASN	THR	PHO	SER	THR	THR
	GLN	GLY	ASN	GLY	GLU	GLU	ARG	VAL
	ALA	ASN	LYS	GLY	LEU	PHE	GLN	PHE
	GLY	PHE	ILE	ASN	ALA	VAL	GLN	GLN
	LEU	THR	LEU	CYS	GLY	ASP	ASP	SER
	ASN	ASP	ARG	THR	GLU	THR	PRO	ASP
	THR	PRO	LYS	MET	LYS	VAL	GLU	SER
	ARG	ALA	TYR	ARG	SER	TYR	GLY	LYS
	ARG	THR	GLU	ILE	GLY	VAL	MET	TYR
O	ASN	ILE	GLU	GLY	LYS	GLY	ILE	PHE
	ASN	VAL	GLY	GLN	TYR	GLY	ILE	GLN
	GLN	ASN	ILE	ASN	VAL	ASN	GLY	GLY
	GLY	THR	GLY	THR	GLN	VAL	THR	GLY
	GLY	THR	GLY	VAL	GLU	VAL	GLY	GLY
	GLY	THR	THR	PRO	ASN	HIS	GLU	GLU
	GLY	ILE	ALA	TYR	THR	GLU	GLY	ASP
	GLU	LEU	GLU	ARG	GLN	ASP	LEU	THR
	GLU	THR	GLU	ASP	THR	LYS	LEU	VAL
	GLU	THR	THR	GLY	ILE	LYS	THR	THR





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110731	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.073	Depositor
Minimum map value	-0.039	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.013	Depositor
Map size (Å)	259.91998, 259.91998, 259.91998	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.083, 1.083, 1.083	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: ADP, MG, TA1, GTP, GDP

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	B	0.27	0/3426	0.47	0/4641
2	A	0.27	0/3435	0.47	0/4663
3	K	0.27	0/2486	0.47	0/3348
3	T	0.21	0/24	0.38	0/31
3	t	0.24	0/21	0.39	0/26
All	All	0.27	0/9392	0.47	0/12709

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	B	3351	0	3237	35	0
2	A	3358	0	3277	30	0
3	K	2448	0	2416	23	0
3	T	24	0	29	0	0
3	t	22	0	26	0	0
4	B	28	0	12	0	0
5	B	62	0	51	4	0
6	A	32	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	1	0	0	0	0
8	K	27	0	12	0	0
All	All	9353	0	9072	84	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 5.

The worst 5 of 84 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:B:229:HIS:NE2	5:B:502:TA1:O14	2.09	0.85
1:B:145:THR:O	1:B:149:MET:HB2	1.87	0.73
1:B:229:HIS:HB3	5:B:502:TA1:HC71	1.75	0.68
1:B:30:ILE:HD11	1:B:49:ILE:HD11	1.75	0.68
2:A:215:ARG:NH2	2:A:299:ALA:O	2.28	0.67

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	B	424/445 (95%)	414 (98%)	10 (2%)	0	100	100
2	A	424/451 (94%)	405 (96%)	19 (4%)	0	100	100
3	K	308/963 (32%)	296 (96%)	12 (4%)	0	100	100
3	T	1/963 (0%)	1 (100%)	0	0	100	100
3	t	1/963 (0%)	1 (100%)	0	0	100	100
All	All	1158/3785 (31%)	1117 (96%)	41 (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	
1	B	367/381 (96%)	365 (100%)	2 (0%)	86	93
2	A	362/379 (96%)	359 (99%)	3 (1%)	79	88
3	K	276/854 (32%)	272 (99%)	4 (1%)	62	79
3	T	3/854 (0%)	3 (100%)	0	100	100
3	t	2/854 (0%)	2 (100%)	0	100	100
All	All	1010/3322 (30%)	1001 (99%)	9 (1%)	74	87

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	K	134	TYR
3	K	307	TYR
2	A	205	ASP
2	A	432	TYR
3	K	95	MET

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

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

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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
6	GTP	A	501	7	26,34,34	1.03	2 (7%)	32,54,54	1.43	5 (15%)
5	TA1	B	502	-	68,68,68	0.64	1 (1%)	105,105,105	1.09	9 (8%)
8	ADP	K	1001	-	24,29,29	0.94	1 (4%)	29,45,45	1.45	4 (13%)
4	GDP	B	501	-	24,30,30	1.01	2 (8%)	30,47,47	1.19	3 (10%)

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
6	GTP	A	501	7	-	8/18/38/38	0/3/3/3
5	TA1	B	502	-	-	8/41/127/127	0/7/7/7
8	ADP	K	1001	-	-	5/12/32/32	0/3/3/3
4	GDP	B	501	-	-	3/12/32/32	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	501	GTP	C5-C6	-3.43	1.40	1.47
4	B	501	GDP	C6-N1	-2.64	1.33	1.37
8	K	1001	ADP	C5-C4	2.36	1.47	1.40
5	B	502	TA1	C18-C10	2.15	1.62	1.57
6	A	501	GTP	C2-N3	2.09	1.38	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	502	TA1	O08-C20-C21	-4.79	113.06	119.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	K	1001	ADP	PA-O3A-PB	-3.70	120.13	132.83
6	A	501	GTP	PA-O3A-PB	-3.48	120.90	132.83
5	B	502	TA1	C18-C20-C21	3.41	129.23	121.44
4	B	501	GDP	PA-O3A-PB	-3.22	121.77	132.83

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

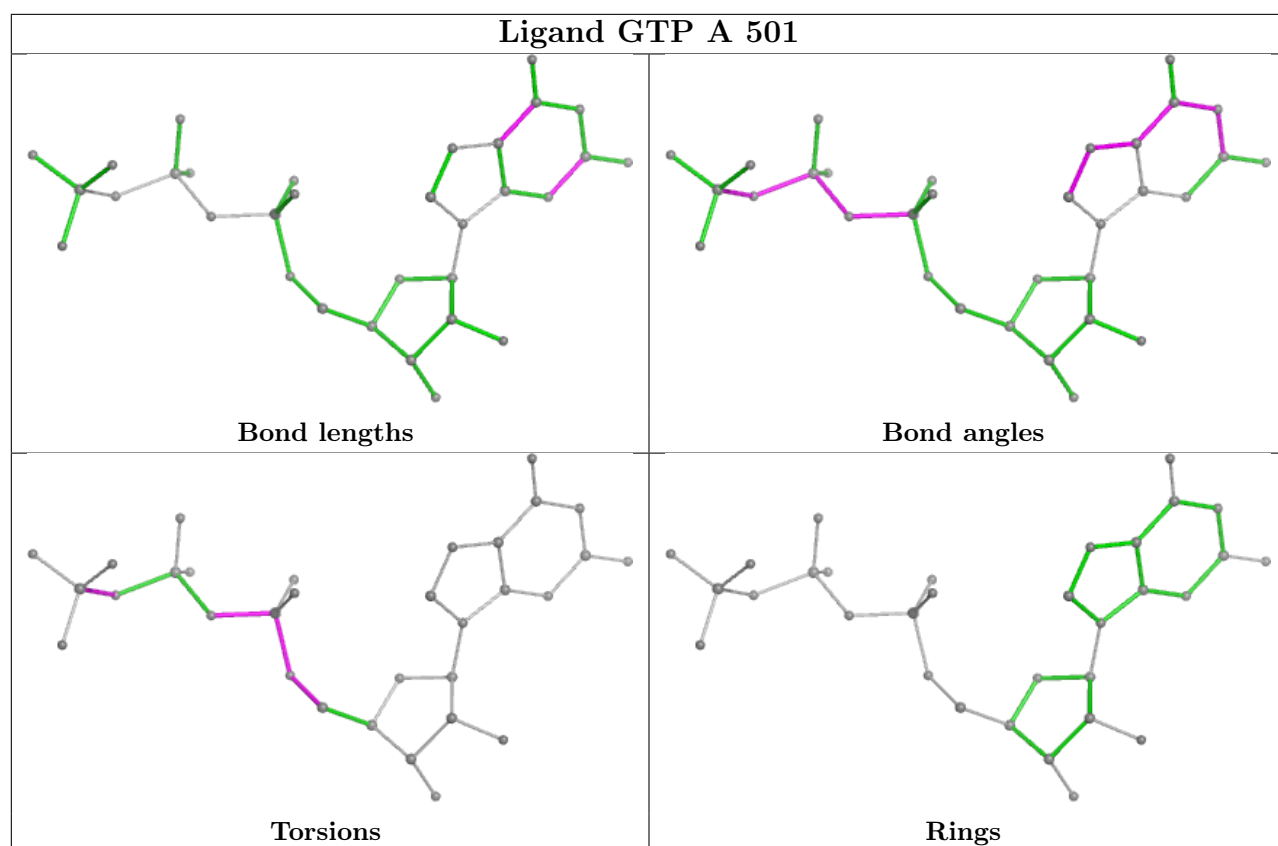
Mol	Chain	Res	Type	Atoms
4	B	501	GDP	C5'-O5'-PA-O1A
4	B	501	GDP	C5'-O5'-PA-O2A
6	A	501	GTP	PB-O3B-PG-O3G
6	A	501	GTP	C5'-O5'-PA-O1A
6	A	501	GTP	C5'-O5'-PA-O2A

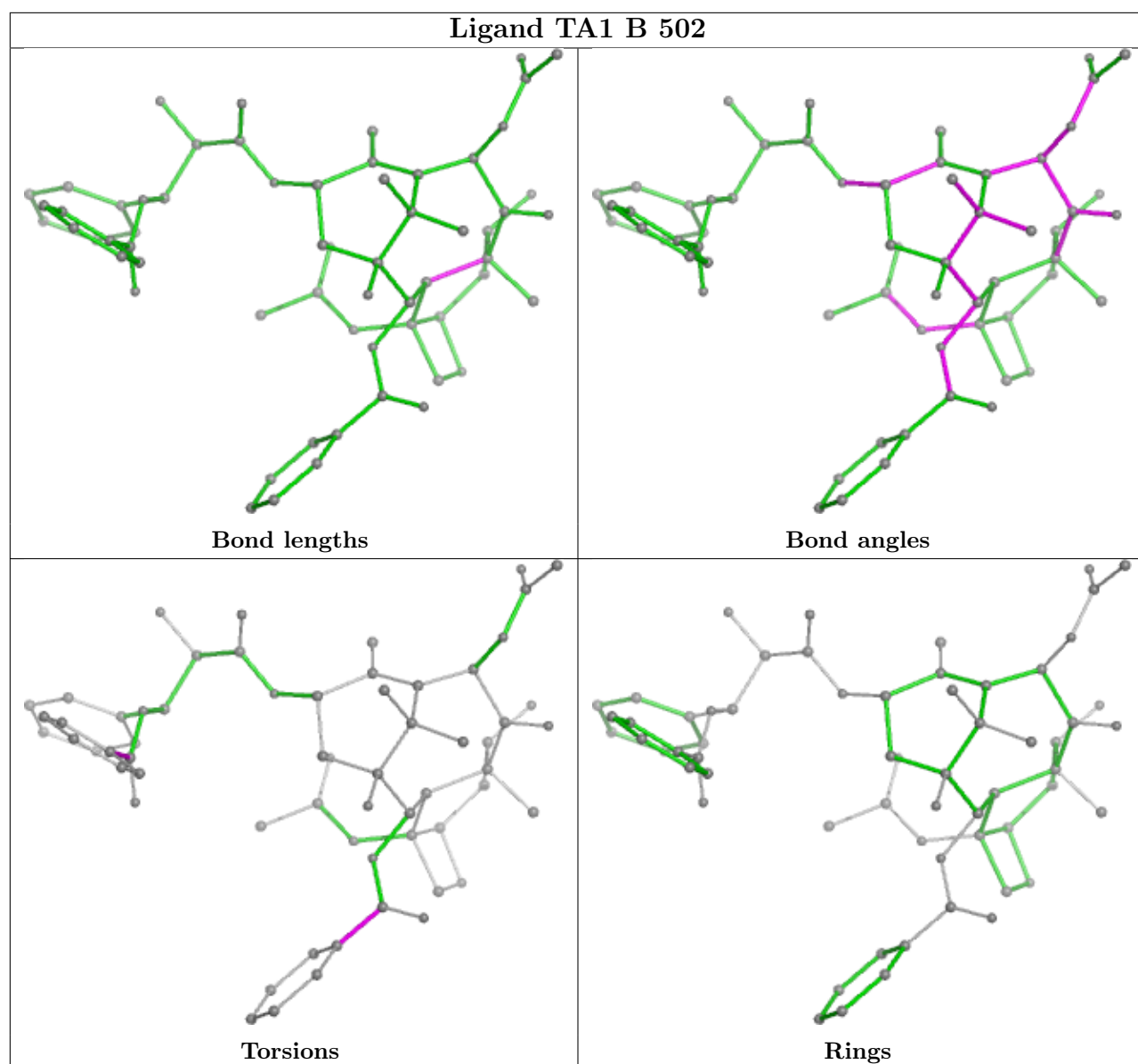
There are no ring outliers.

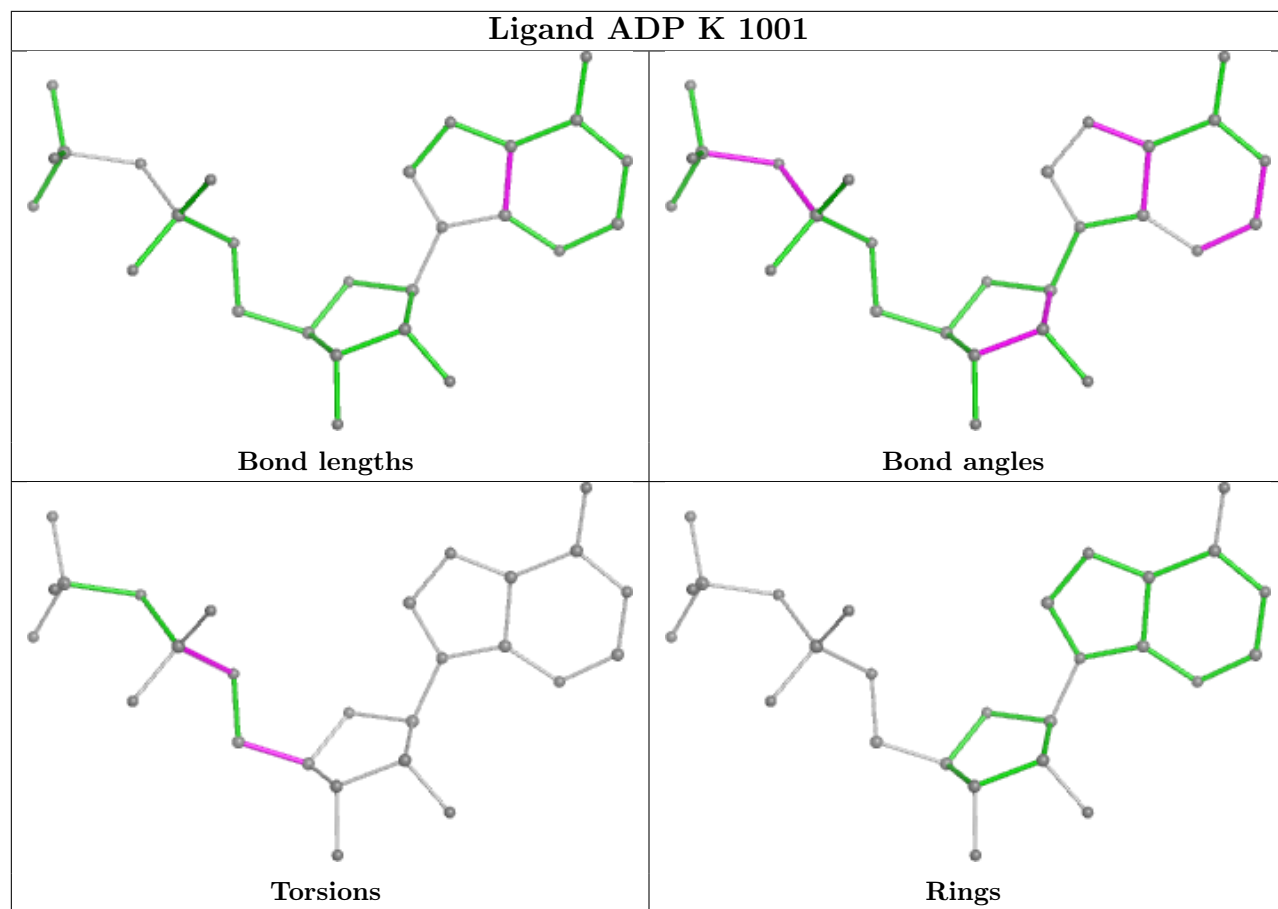
1 monomer is involved in 4 short contacts:

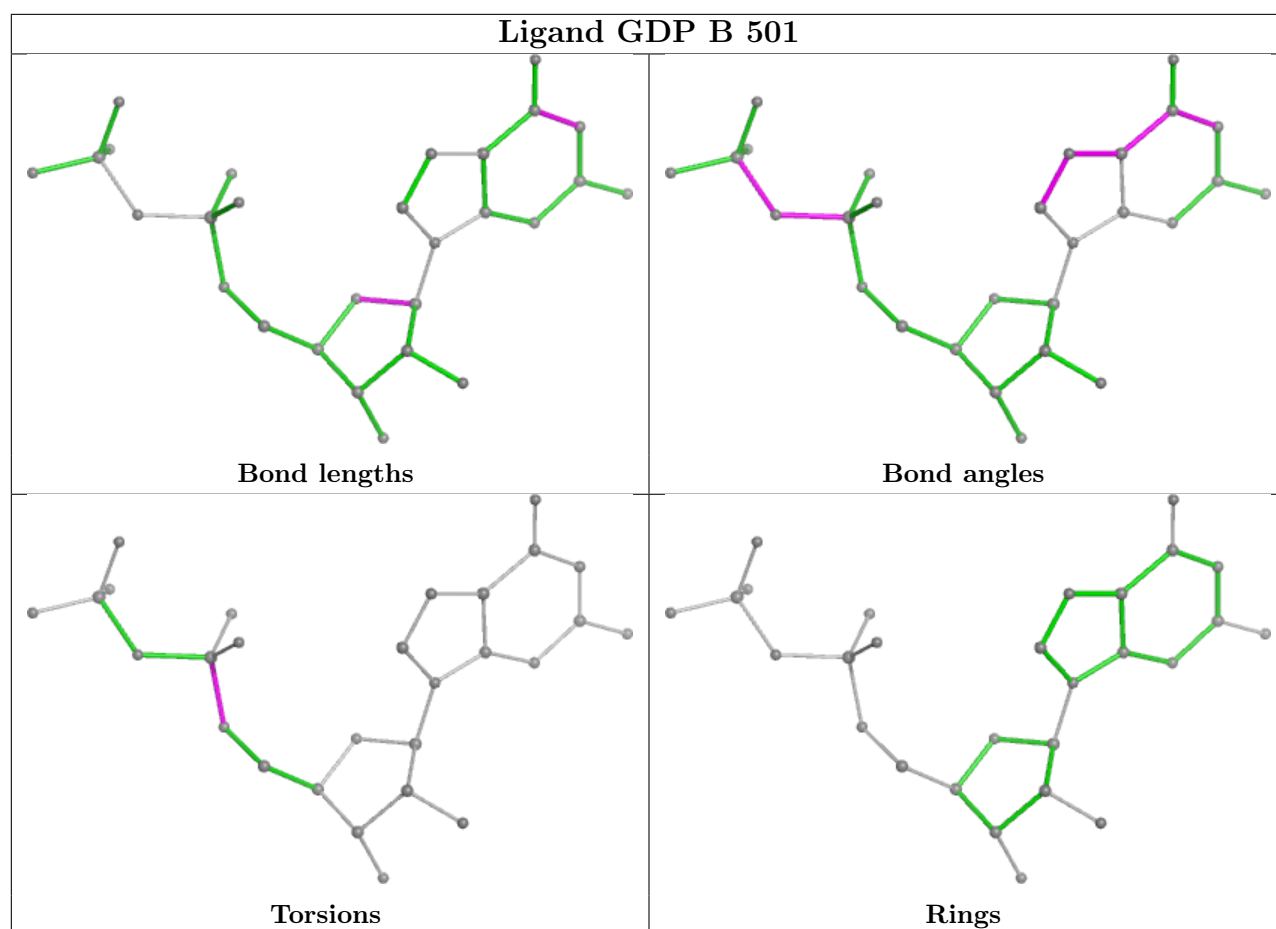
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	502	TA1	4	0

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.

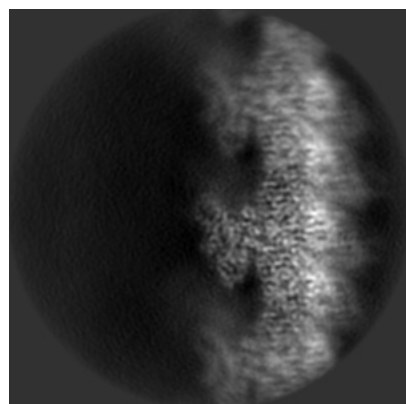
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19188. These allow visual inspection of the internal detail of the map and identification of artifacts.

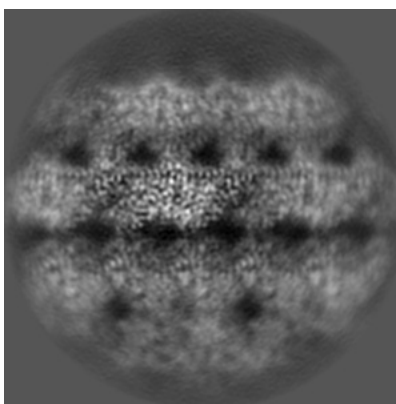
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

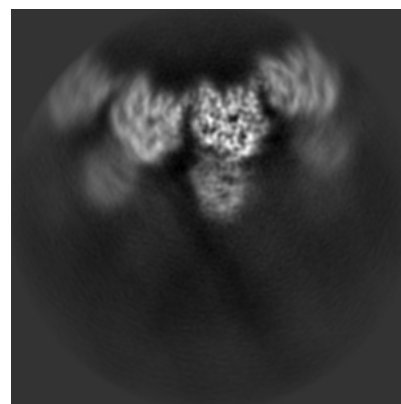
6.1.1 Primary map



X

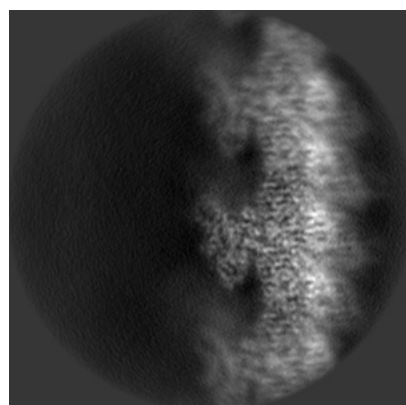


Y

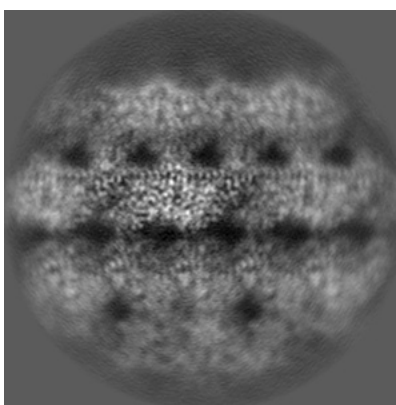


Z

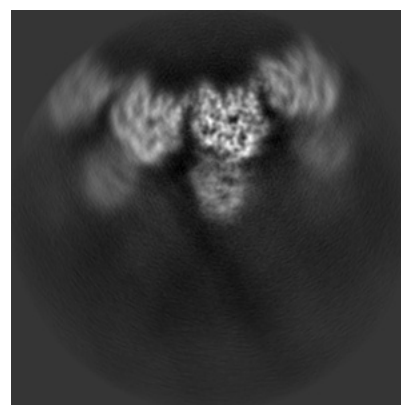
6.1.2 Raw map



X



Y

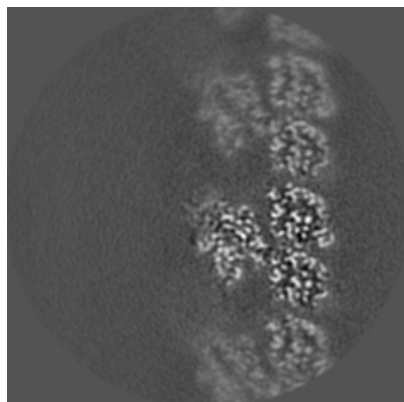


Z

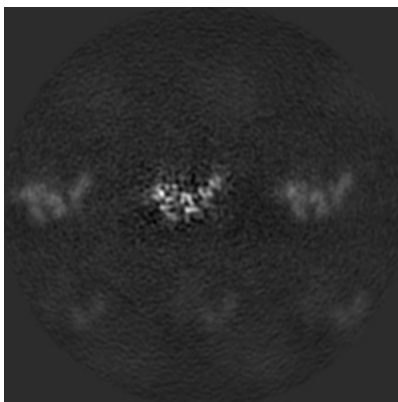
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

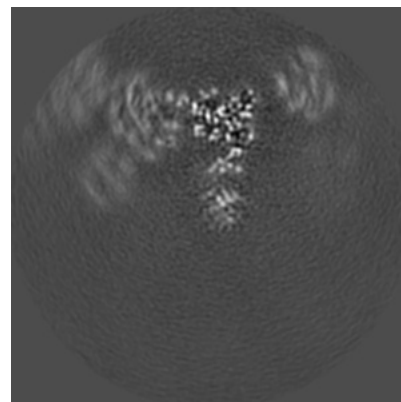
6.2.1 Primary map



X Index: 120

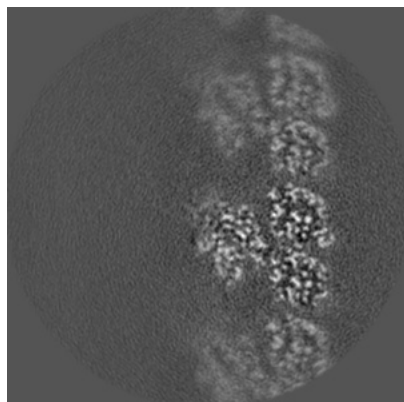


Y Index: 120

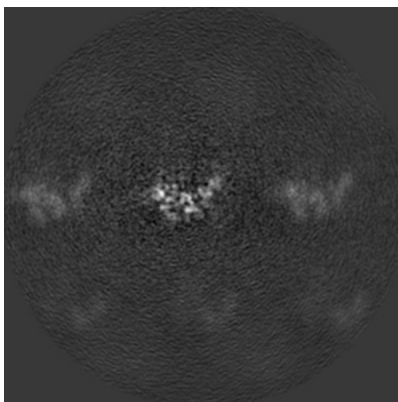


Z Index: 120

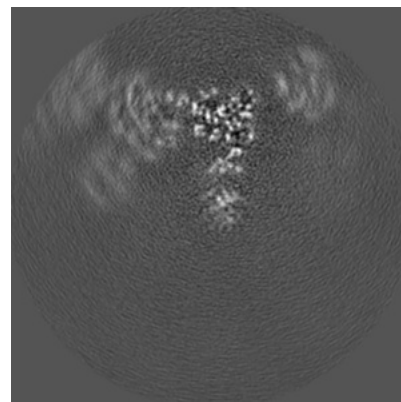
6.2.2 Raw map



X Index: 120



Y Index: 120

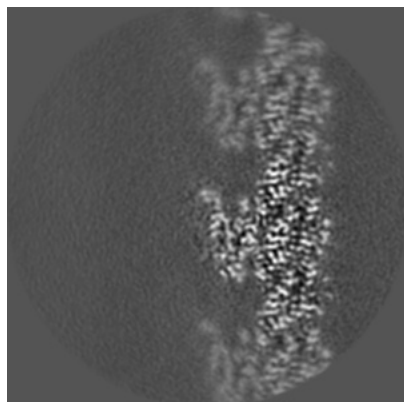


Z Index: 120

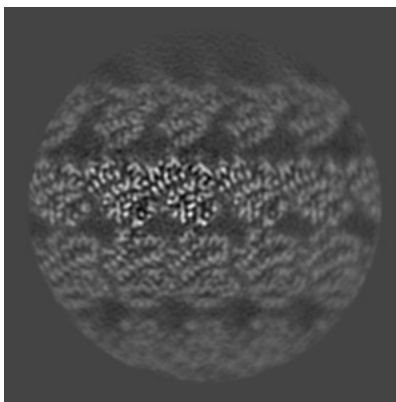
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

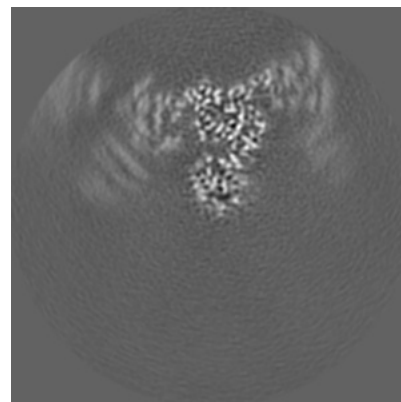
6.3.1 Primary map



X Index: 135

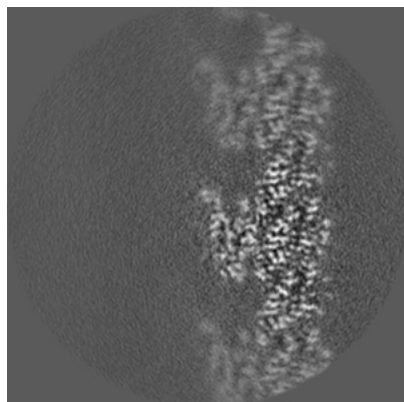


Y Index: 180

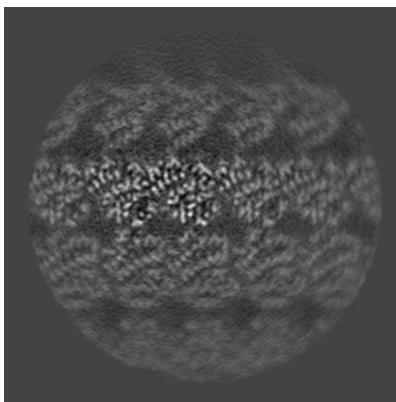


Z Index: 108

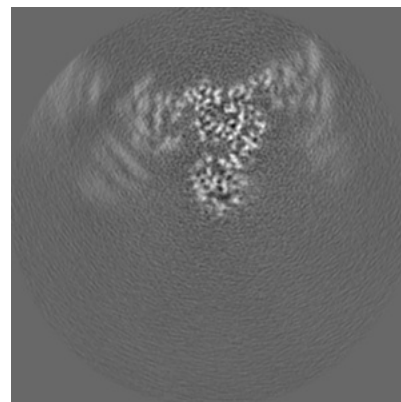
6.3.2 Raw map



X Index: 135



Y Index: 180

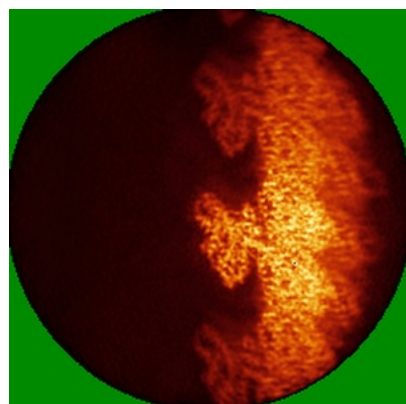


Z Index: 108

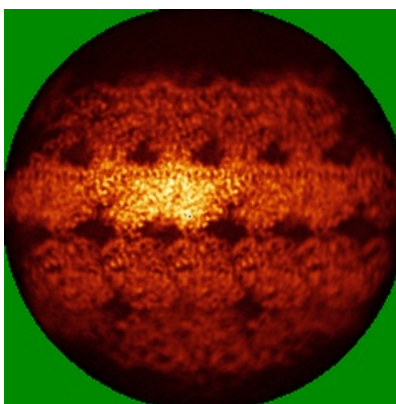
The images above show the largest variance slices of the map in three orthogonal directions.

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

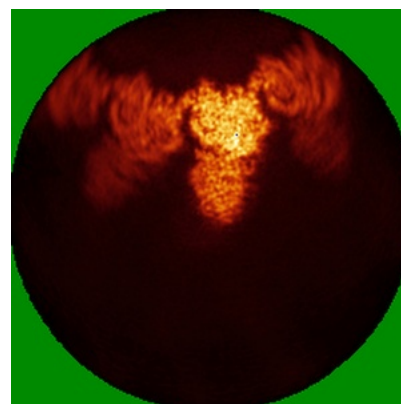
6.4.1 Primary map



X

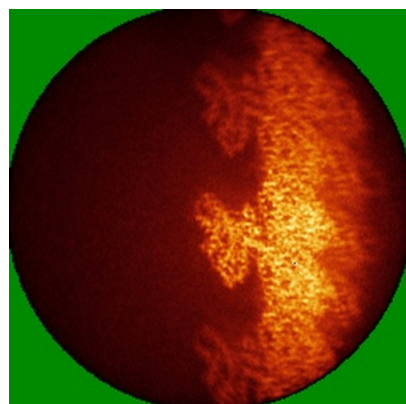


Y

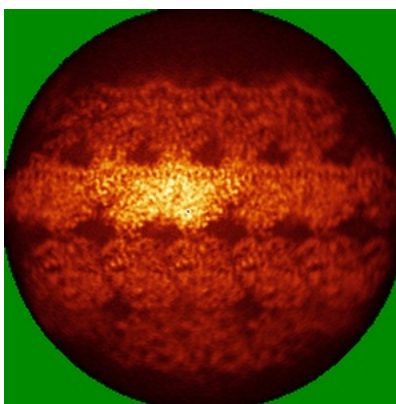


Z

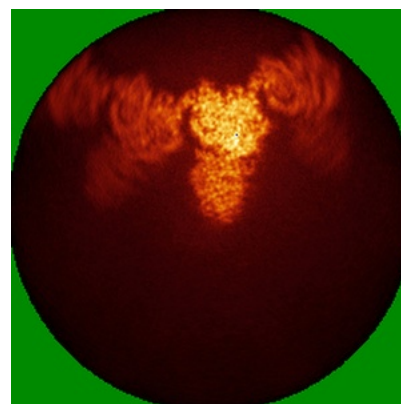
6.4.2 Raw map



X



Y

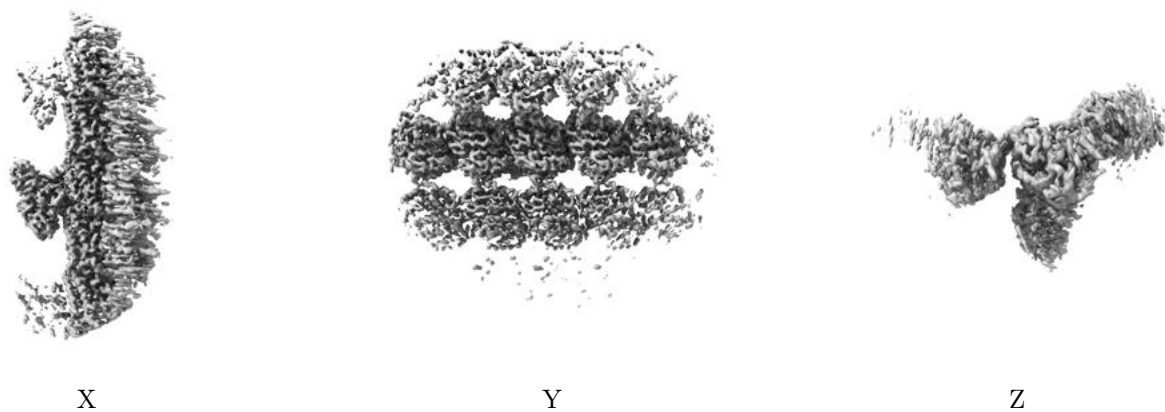


Z

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.

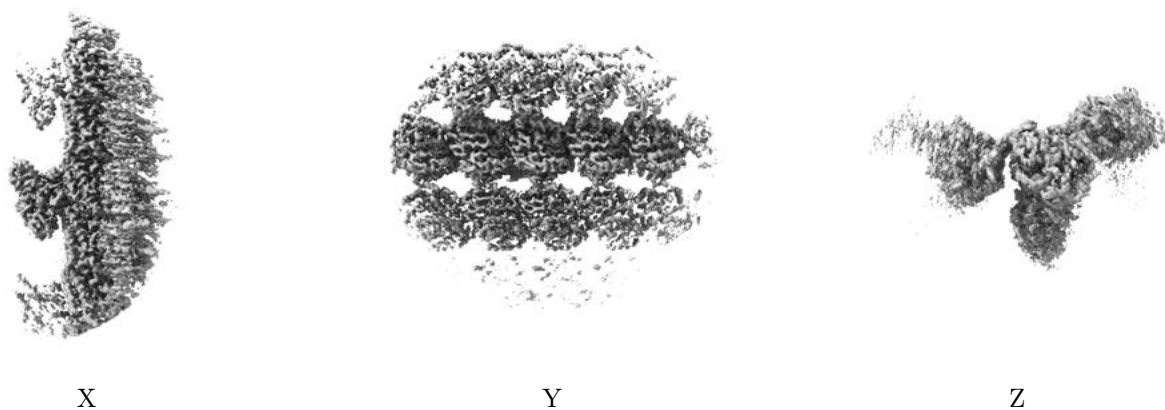
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.013. 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.

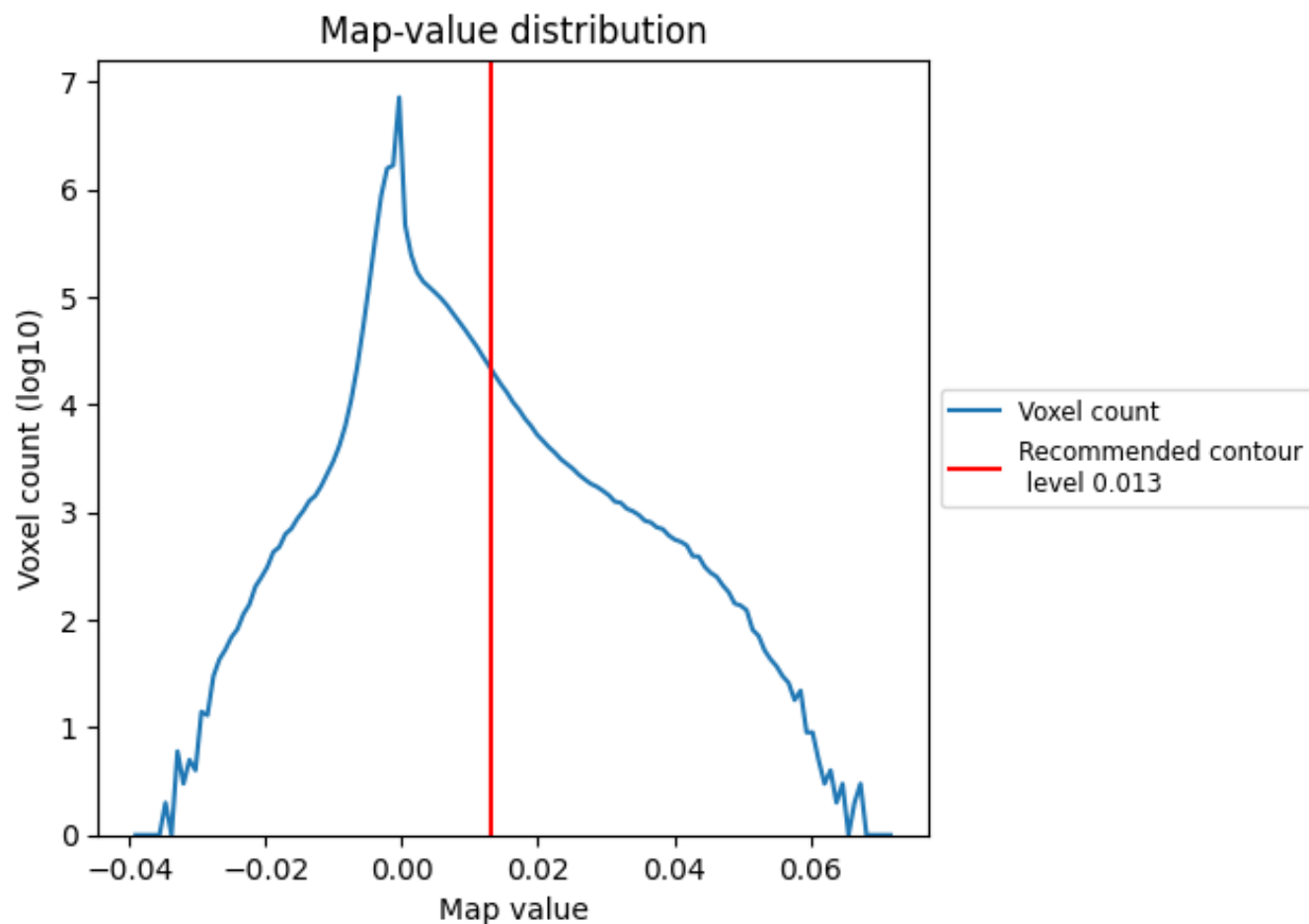
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

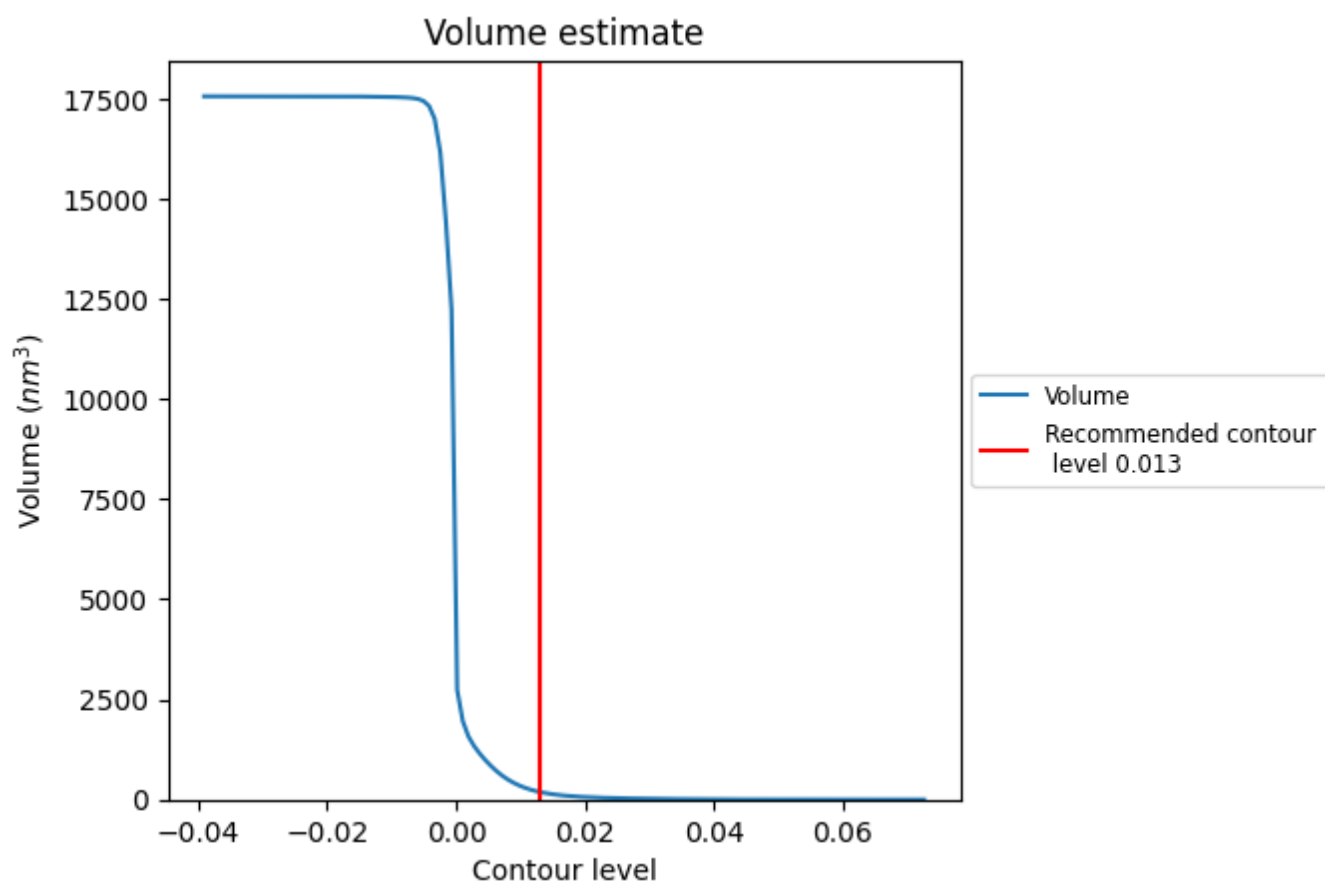
This section contains the results of statistical analysis of the map.

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.

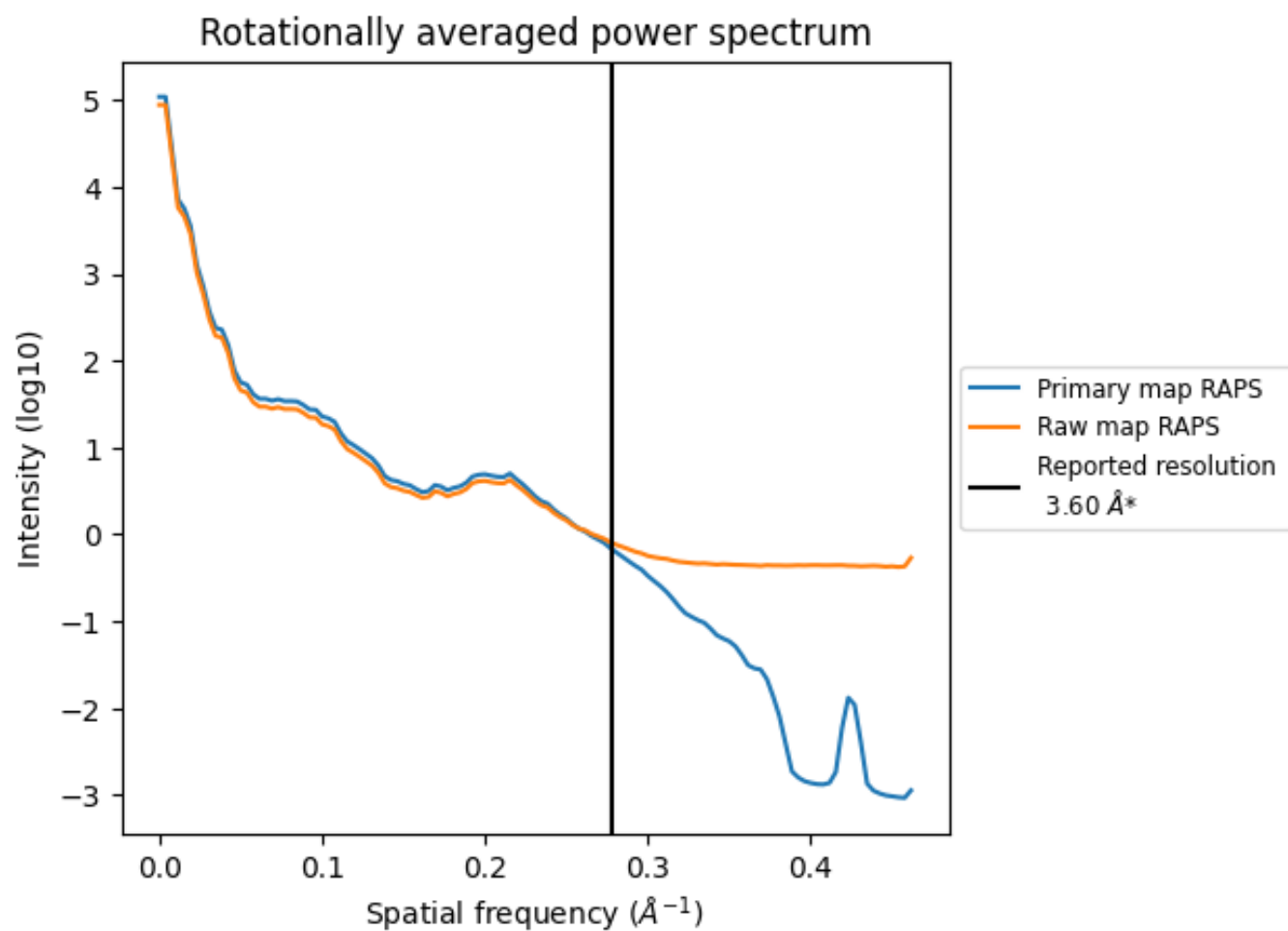
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 190 nm³; this corresponds to an approximate mass of 171 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 ⓘ

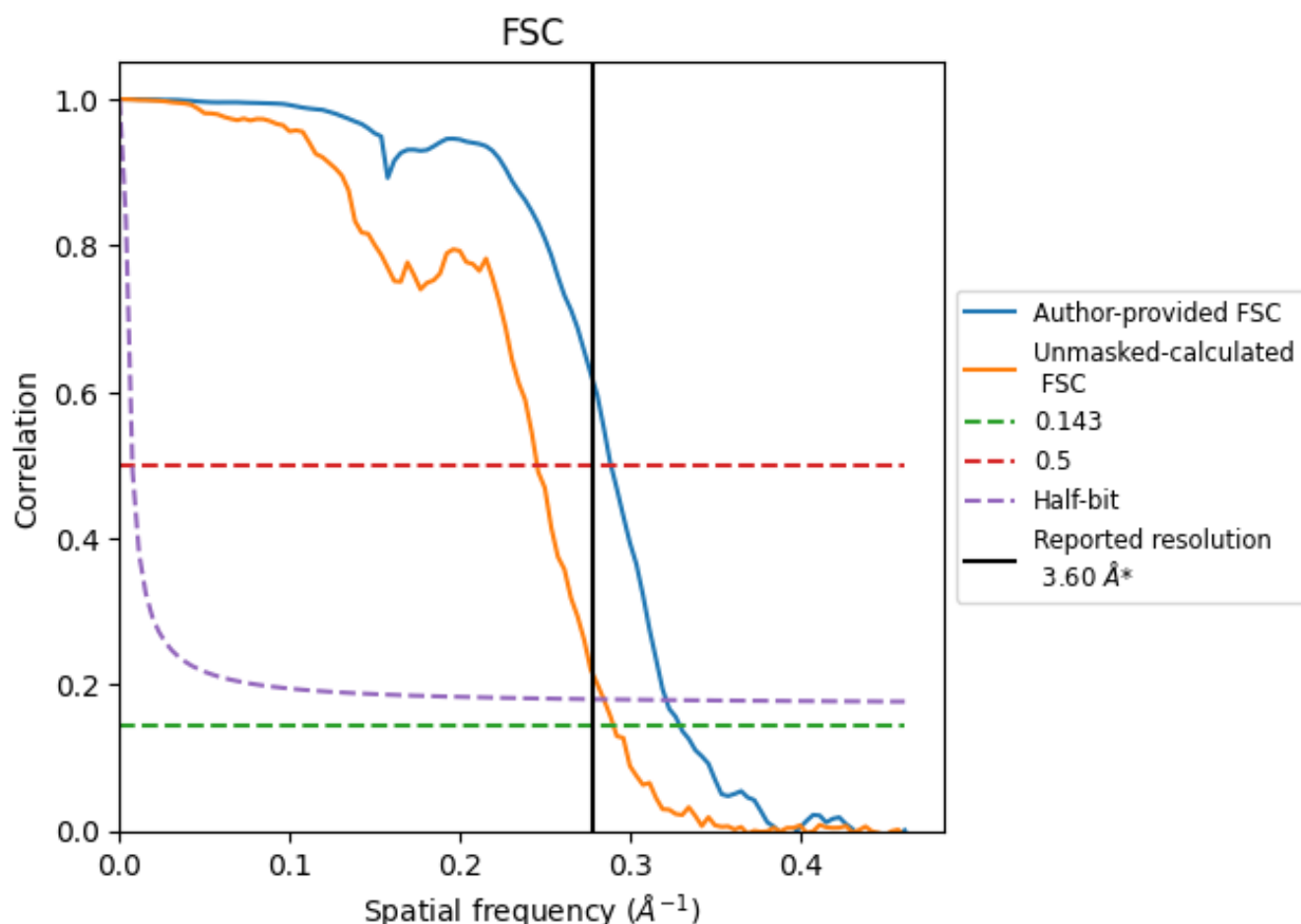


*Reported resolution corresponds to spatial frequency of 0.278 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 \AA^{-1}

8.2 Resolution estimates [i](#)

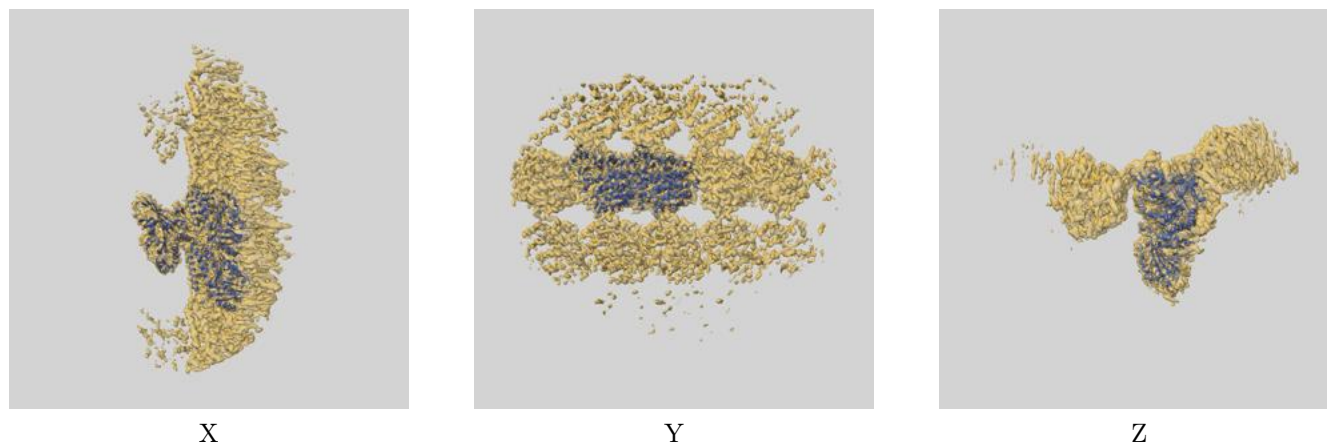
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.03	3.46	3.11
Unmasked-calculated*	3.44	4.07	3.51

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.03 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

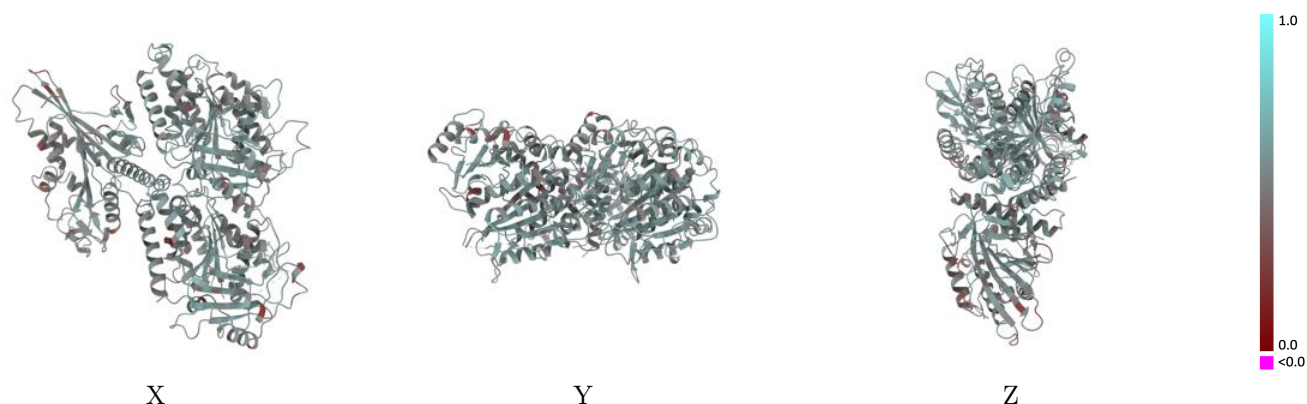
This section contains information regarding the fit between EMDB map EMD-19188 and PDB model 8RIK. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



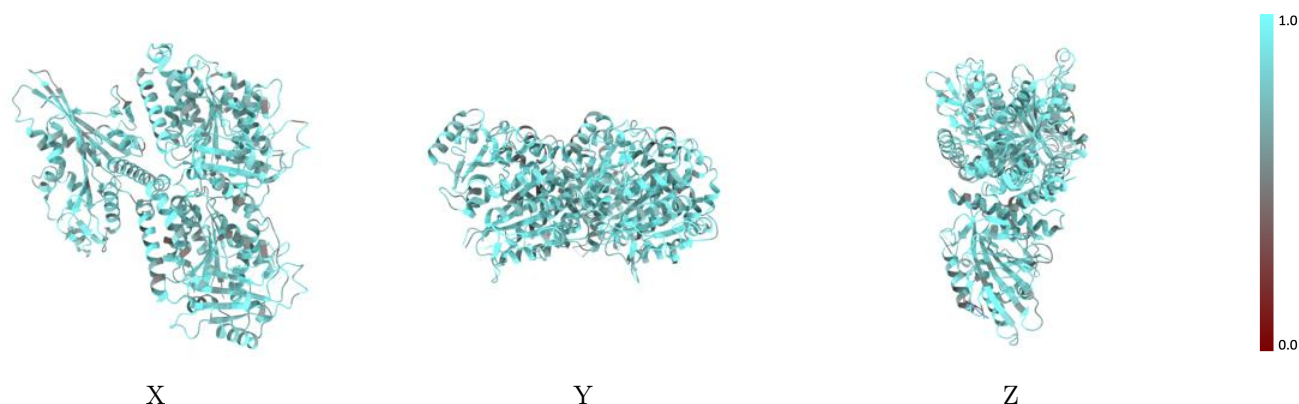
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



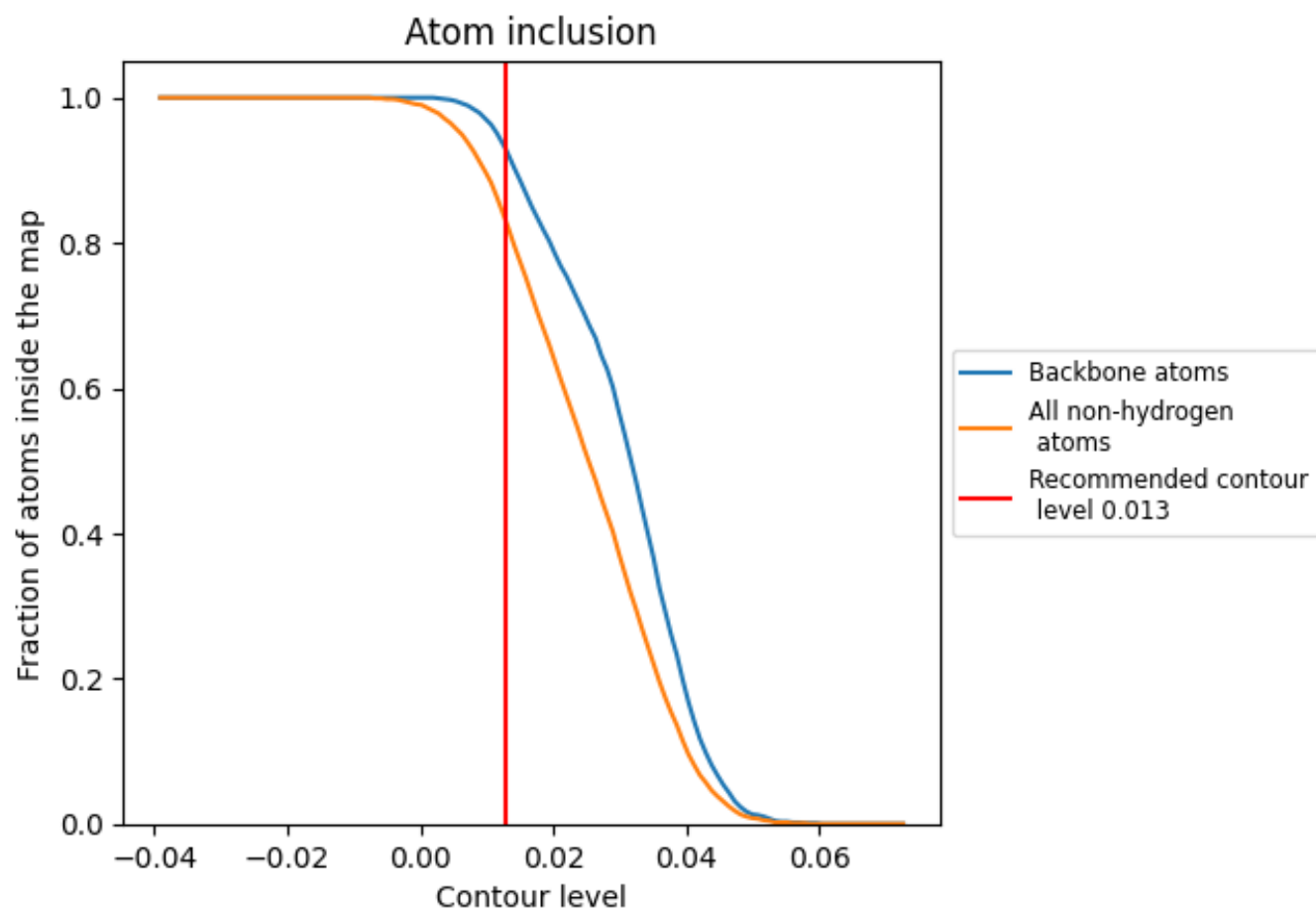
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 83% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8270	<div></div> 0.5250
A	<div></div> 0.8300	<div></div> 0.5310
B	<div></div> 0.8380	<div></div> 0.5380
K	<div></div> 0.8140	<div></div> 0.4990
T	<div></div> 0.3750	<div></div> 0.3960

