



wwPDB EM Validation Summary Report ⓘ

Sep 23, 2026 – 04:19 PM EDT

PDB ID : 11RL / pdb_000011rl
EMDB ID : EMD-75978
Title : CryoEM structure of the human origin recognition complex with DNA and CDC6 protein
Authors : Chouhan, O.P.; Joshua Tor, L.
Deposited on : 2026-03-10
Resolution : 2.80 Å(reported)
Based on initial model : 7JPS

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.dev133
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) : 2.50

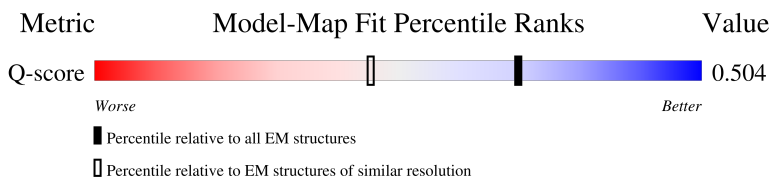
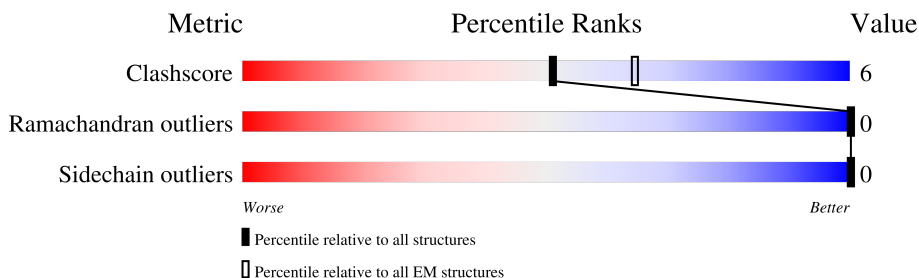
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	577	
2	D	436	
3	H	60	
4	I	60	

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Mol	Chain	Length	Quality of chain
5	A	862	 42% 55%
6	C	712	 68% 17% 15%
7	E	435	 77% 13% 10%
8	G	561	 57% 10% 34%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 21274 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 Origin recognition complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	307	Total	C	N	O	S	0	0
			2500	1604	420	470	6		

- Molecule 2 is a protein called Origin recognition complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	420	Total	C	N	O	S	0	0
			3407	2173	591	622	21		

- Molecule 3 is a DNA chain called DNA (29-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	29	Total	C	N	O	P	0	0
			596	282	105	180	29		

- Molecule 4 is a DNA chain called DNA (29-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	29	Total	C	N	O	P	0	0
			593	279	117	168	29		

- Molecule 5 is a protein called Origin recognition complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	388	Total	C	N	O	S	0	0
			3063	1922	545	572	24		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q13415

- Molecule 6 is a protein called Origin recognition complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	606	Total	C	N	O	S	0	0
			4898	3157	817	896	28		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	GLY	-	expression tag	UNP Q9UBD5

- Molecule 7 is a protein called Origin recognition complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	391	Total	C	N	O	S	0	0
			3176	2073	521	573	9		

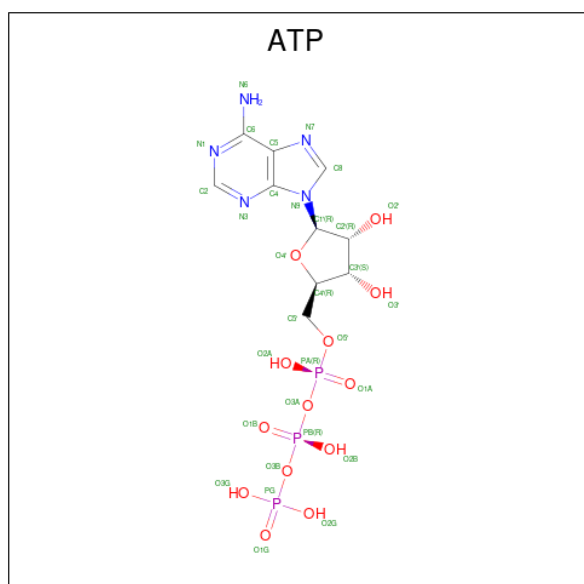
- Molecule 8 is a protein called Cell division control protein 6 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	373	Total	C	N	O	S	0	0
			2913	1838	519	536	20		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	0	GLY	-	expression tag	UNP Q99741

- Molecule 9 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
9	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
9	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
9	E	1	Total	C	N	O	P	0
			31	10	5	13	3	
9	G	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
10	D	1	Total	Mg	0
			1	1	
10	A	1	Total	Mg	0
			1	1	
10	E	1	Total	Mg	0
			1	1	
10	G	1	Total	Mg	0
			1	1	

DG	DG	DG	DG	DC	DC	DT	DG	DC	DC	DT	DG	DC	DC	DT	DG	DC	DA	G1	A2	G3		T9	G10		T17	C18	G19	C20	G21	T22	G23	G24	T25	A26	T27	G28	C29	DG	DG	DC	DC	DC	DG	DG	DG	DG	DA	DC	DC	DA	DT	DA	DC
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Chain I: 23% 25% 52%

DG	DT	DA	DG	DG	DT	DC	DC	DC	DC	DG	DC	DC	G1	C7	A8	C9	G10	G11	G12	A15	C20	A21	G22	C23	A26	C27	T28	C29	DT	DC	DC	DC	DG	DG	DA	DA	DG	DC	DC	DC	CC
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Chain A: 42% 1% 55%

SER	LYS	GLY	GLN	CYS	ASP	GLY
	ARG	LEU	GLU	ASP	GLU	MET
	ASP	SER	SER	SER	ASN	ALA
	ALA	TYR	ALA	ASN	PRO	THR
	GLY	THR	ALA	ILE	TYR	HIS
	GLU	GLU	LYS	ASN	VAL	PRO
	ALA	ASP	GLN	ALA	ALA	THR
	LYS	ASP	CYS	GLU	LYS	ARG
	ALA	LYS	LYS	THR	LEU	LYS
	GLN	LYS	PRO	ILE	LEU	THR
PRO	ASN	ALA	VAL	ILE	GLU	THR
	GLU	SER	ARG	GLY	LEU	ARG
	ALA	PRO	ALA	VAL	PHE	LYS
	GLU	SER	LYS	VAL	ASP	THR
	ARG	HIS	ALA	ARG	ASP	TYR
	SER	ALA	SER	VAL	ASP	SER
	THR	ILE	SER	ILE	SER	TRP
	PRO	ILE	ALA	PRO	ASP	VAL
	HIS	ILE	GLU	LEU	PRO	GLY
	ARG	LEU	SER	SER	GLY	ARG
THR	ILE	ARG	GLU	ALA	PRO	ARG
	VAL	ILE	SER	ALA	PRO	PRO
	SER	THR	GLY	PRO	PRO	PRO
	ARG	ARG	SER	SER	LYS	LEU
	ARG	ILE	TRP	ASP	LYS	LEU
	LYS	ALA	THR	VAL	ARG	ASP
	SER	ALA	ALA	VAL	ALA	ARG
	LEU	SER	VAL	PRO	ARG	LYS
	LEU	VAL	LYS	THR	VAL	LEU
	LYS	THR	LYS	HIS	GLN	TYR
LEU	MET	ILE	VAL	LEU	TRP	TYR
	ASN	ASP	ALA	LYS	PHE	GLN
	SER	ILE	LYS	ASN	VAL	THR
	LEU	ARG	ILE	GLU	ARG	TYR
	HIS	ARG	ILE	LYS	PHE	GLU
	THR	GLU	SER	THR	CYS	THR
	LEU	ARG	SER	LEU	GLU	MET
	THR	THR	SER	PHE	VAL	CYS
	LYS	LEU	ARG	VAL	PRO	VAL
	LYS	GLY	ALA	LYS	ALA	LYS
LYS	ASN	ILE	SER	SER	LYS	GLY
	SER	SER	LYS	TRP	ARG	GLY
	LEU	GLY	ARG	ASN	HIS	CYS
	LYS	GLN	GLN	GLU	LEU	THR
	PRO	ARG	THR	LYS	LEU	THR
	ARG	SER	THR	PHE	GLY	ILE
	THR	SER	THR	ARG	LYS	HIS
	PRO	VAL	SER	PRO	PRO	ILE
	GLU	VAL	ALA	GLN	GLY	GLN
	LYS	ILE	THR	SER	ALA	ILE
R468	A469	A470	A471	A472	A473	A474
	A475	A476	A477	A478	A479	A480
	A481	A482	A483	A484	A485	A486
	A487	A488	A489	A490	A491	A492
	A493	A494	A495	A496	A497	A498
	A499	A500	A501	A502	A503	A504
	A505	A506	A507	A508	A509	A510
	A511	A512	A513	A514	A515	A516
	A517	A518	A519	A520	A521	A522
	A523	A524	A525	A526	A527	A528

V544	1548	E567	E575	P576	L618	L622	A651	1652	M664	N665	L715	S716	1725	C726	R727	T730	Q737	GLN	LYS	PRO	ASP	SER	F743	G744	F759	E791	E792	R830	E835	L843	R846	D860	GLU
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Chain C: 68% 17% 15%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	130819	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTF correction was done first in WARP during exposure/micrograph pre-processing, and re-corrected during the final refinements/reconstruction of the map in cryoSPARC	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43.2	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.557	Depositor
Minimum map value	-0.134	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	363.88, 363.88, 363.88	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.827, 0.827, 0.827	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: ATP, MG

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	0.10	0/2554	0.24	0/3461
2	D	0.11	0/3472	0.26	0/4683
3	H	0.20	0/666	0.42	0/1027
4	I	0.18	0/666	0.33	0/1024
5	A	0.11	0/3115	0.26	0/4215
6	C	0.12	0/5001	0.28	0/6774
7	E	0.12	0/3252	0.28	0/4420
8	G	0.12	0/2946	0.30	0/3965
All	All	0.12	0/21672	0.28	0/29569

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	2500	0	2475	21	0
2	D	3407	0	3444	40	0
3	H	596	0	328	8	0
4	I	593	0	322	12	0
5	A	3063	0	3087	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	4898	0	4893	76	0
7	E	3176	0	3182	37	0
8	G	2913	0	3035	35	0
9	A	31	0	12	0	0
9	D	31	0	12	1	0
9	E	31	0	12	1	0
9	G	31	0	12	0	0
10	A	1	0	0	0	0
10	D	1	0	0	0	0
10	E	1	0	0	0	0
10	G	1	0	0	0	0
All	All	21274	0	20814	232	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.

The worst 5 of 232 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:C:622:ILE:HD12	6:C:634:LYS:HB2	1.58	0.84
6:C:472:LEU:HD13	6:C:497:PHE:HB3	1.70	0.72
6:C:269:SER:HA	7:E:271:ARG:HH21	1.55	0.71
7:E:9:LEU:H	9:E:501:ATP:HN62	1.36	0.71
6:C:367:ARG:HE	6:C:394:LEU:HD22	1.57	0.69

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	305/577 (53%)	303 (99%)	2 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	418/436 (96%)	410 (98%)	8 (2%)	0	100	100
5	A	384/862 (44%)	379 (99%)	5 (1%)	0	100	100
6	C	592/712 (83%)	583 (98%)	9 (2%)	0	100	100
7	E	383/435 (88%)	375 (98%)	8 (2%)	0	100	100
8	G	365/561 (65%)	361 (99%)	4 (1%)	0	100	100
All	All	2447/3583 (68%)	2411 (98%)	36 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	282/529 (53%)	282 (100%)	0	100	100
2	D	386/403 (96%)	386 (100%)	0	100	100
5	A	339/766 (44%)	339 (100%)	0	100	100
6	C	551/659 (84%)	551 (100%)	0	100	100
7	E	354/399 (89%)	354 (100%)	0	100	100
8	G	322/499 (64%)	322 (100%)	0	100	100
All	All	2234/3255 (69%)	2234 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
6	C	85	GLN
7	E	100	ASN
8	G	474	GLN
7	E	136	ASN
6	C	636	HIS

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 4 are 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	$\# Z > 2$
9	ATP	G	901	10	32,33,33	0.36	0	48,52,52	0.30	0
9	ATP	E	501	10	32,33,33	0.29	0	48,52,52	0.32	0
9	ATP	A	901	10	32,33,33	0.34	0	48,52,52	0.32	0
9	ATP	D	901	10	32,33,33	0.41	0	48,52,52	0.34	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
9	ATP	G	901	10	-	2/22/38/38	0/3/3/3
9	ATP	E	501	10	-	1/22/38/38	0/3/3/3
9	ATP	A	901	10	-	1/22/38/38	0/3/3/3
9	ATP	D	901	10	-	5/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

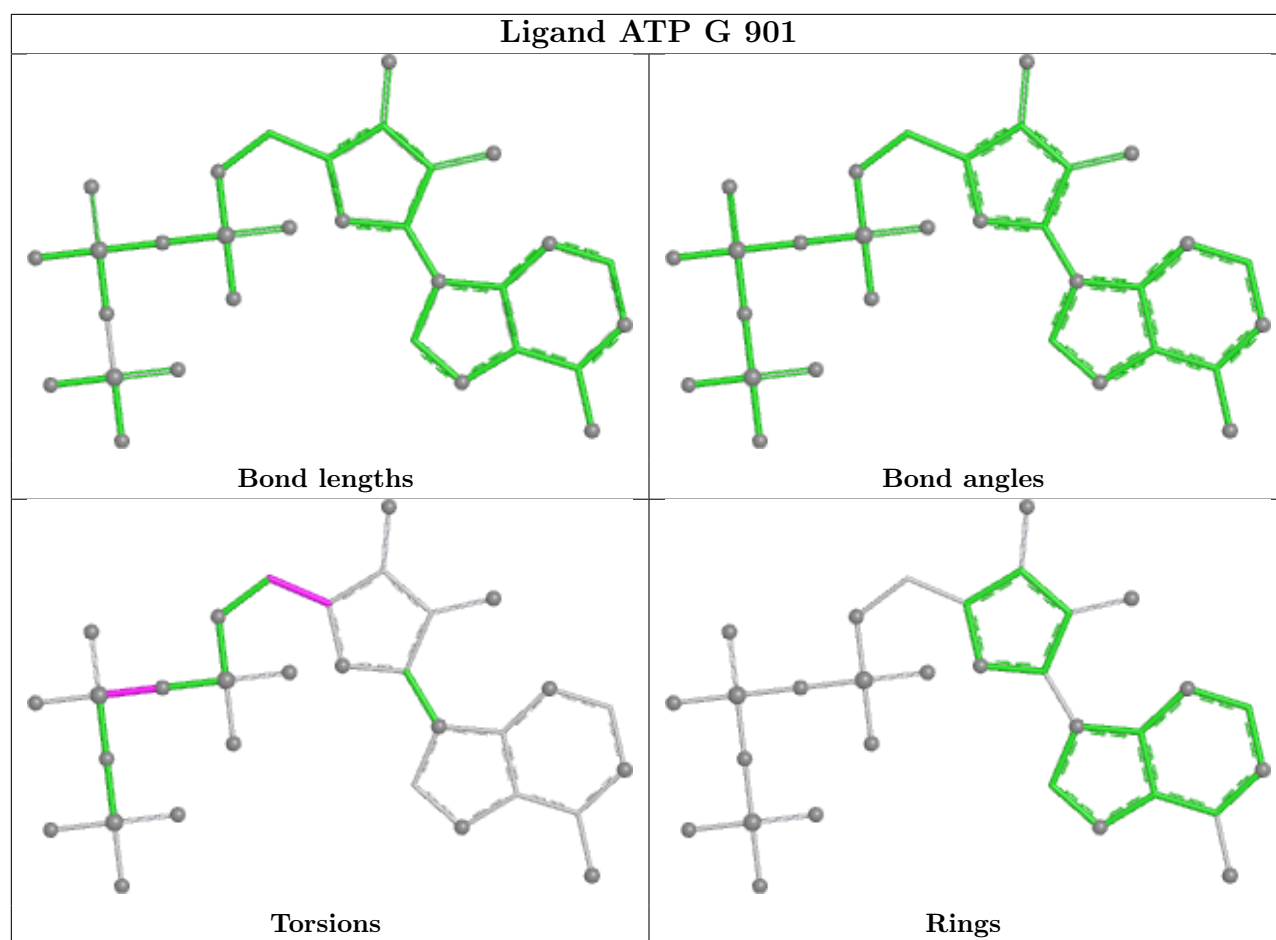
Mol	Chain	Res	Type	Atoms
9	D	901	ATP	C5'-O5'-PA-O1A
9	D	901	ATP	C5'-O5'-PA-O3A
9	E	501	ATP	O4'-C4'-C5'-O5'
9	G	901	ATP	O4'-C4'-C5'-O5'
9	D	901	ATP	PA-O3A-PB-O1B

There are no ring outliers.

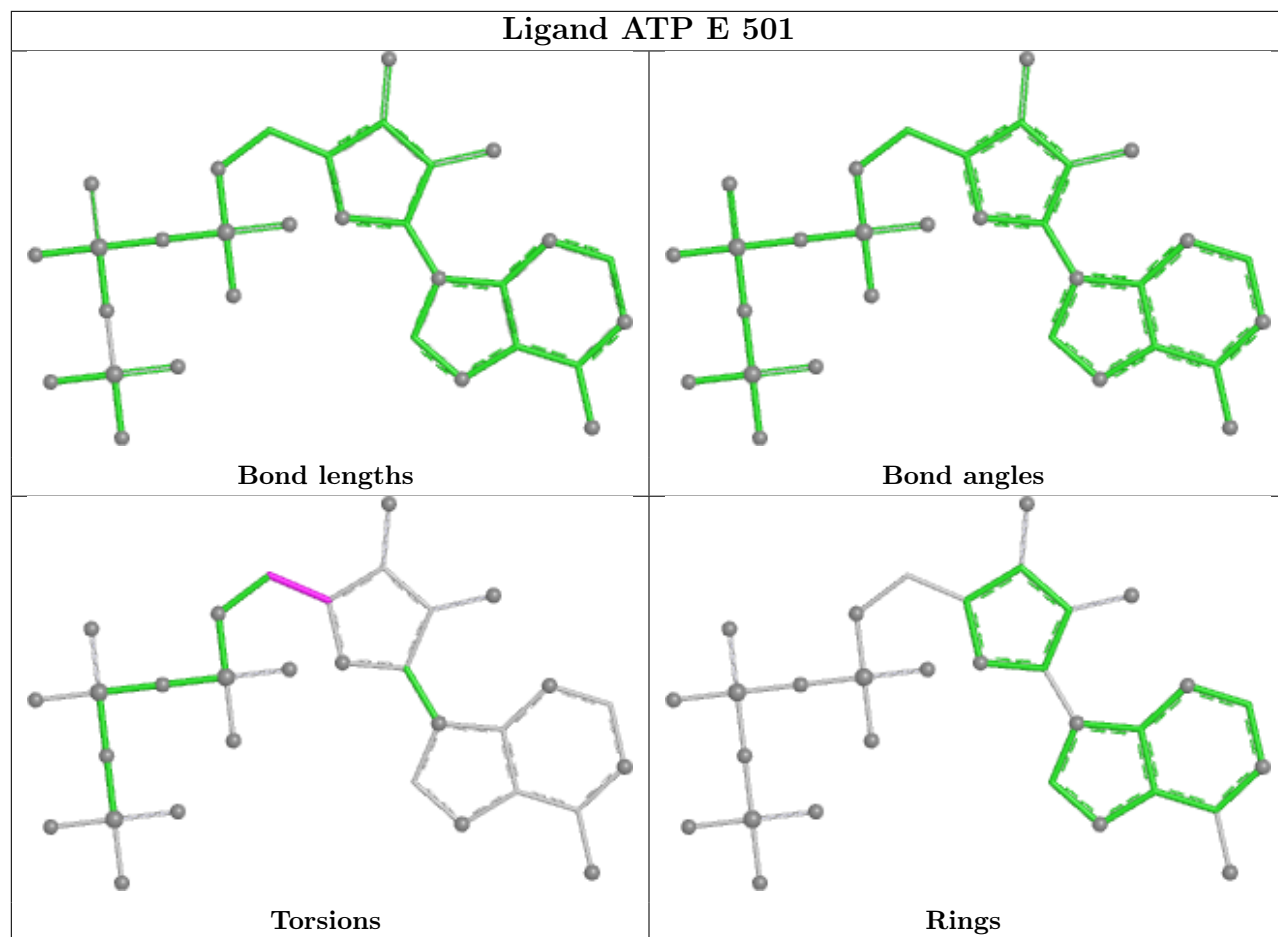
2 monomers are involved in 2 short contacts:

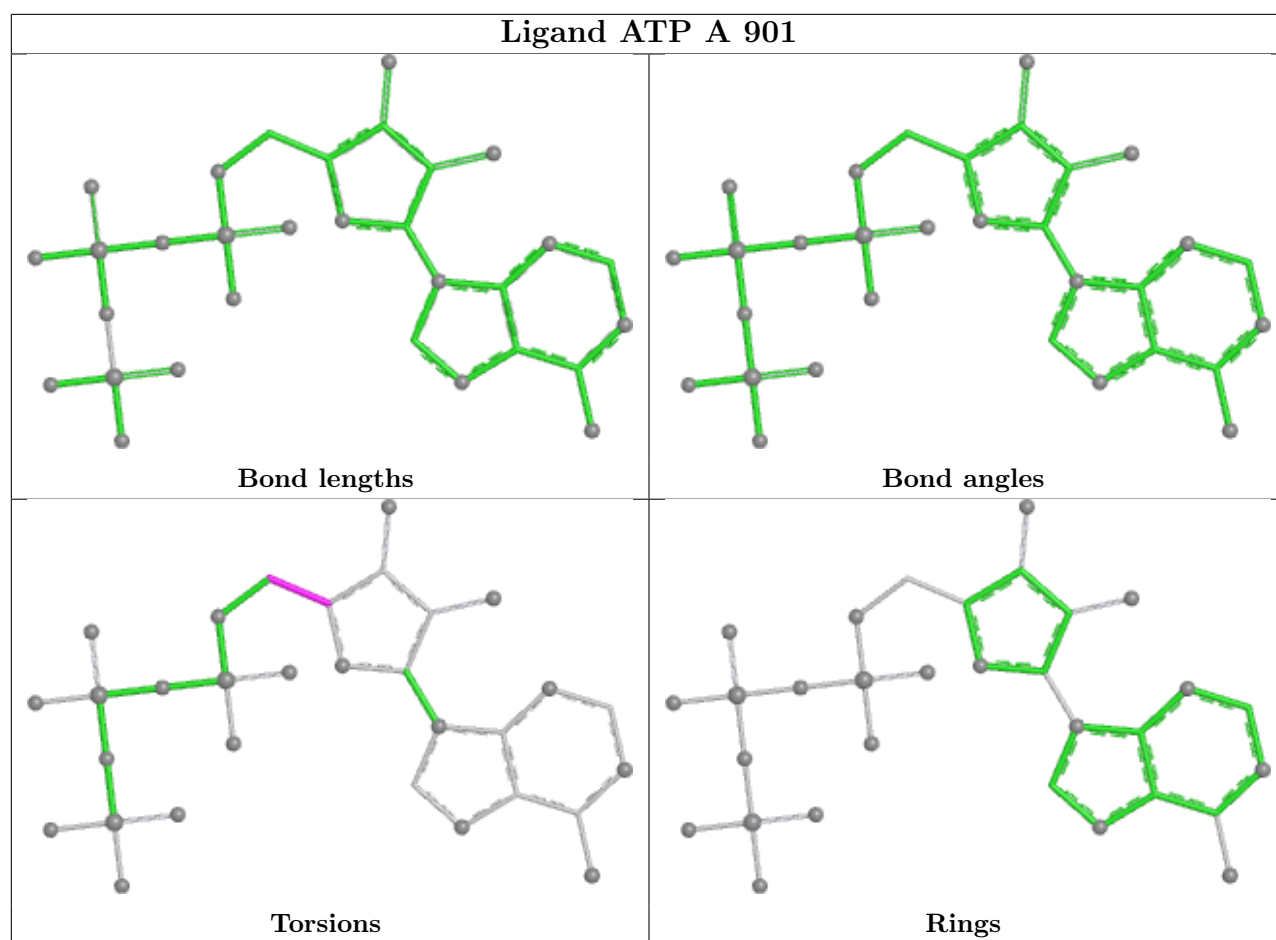
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	E	501	ATP	1	0
9	D	901	ATP	1	0

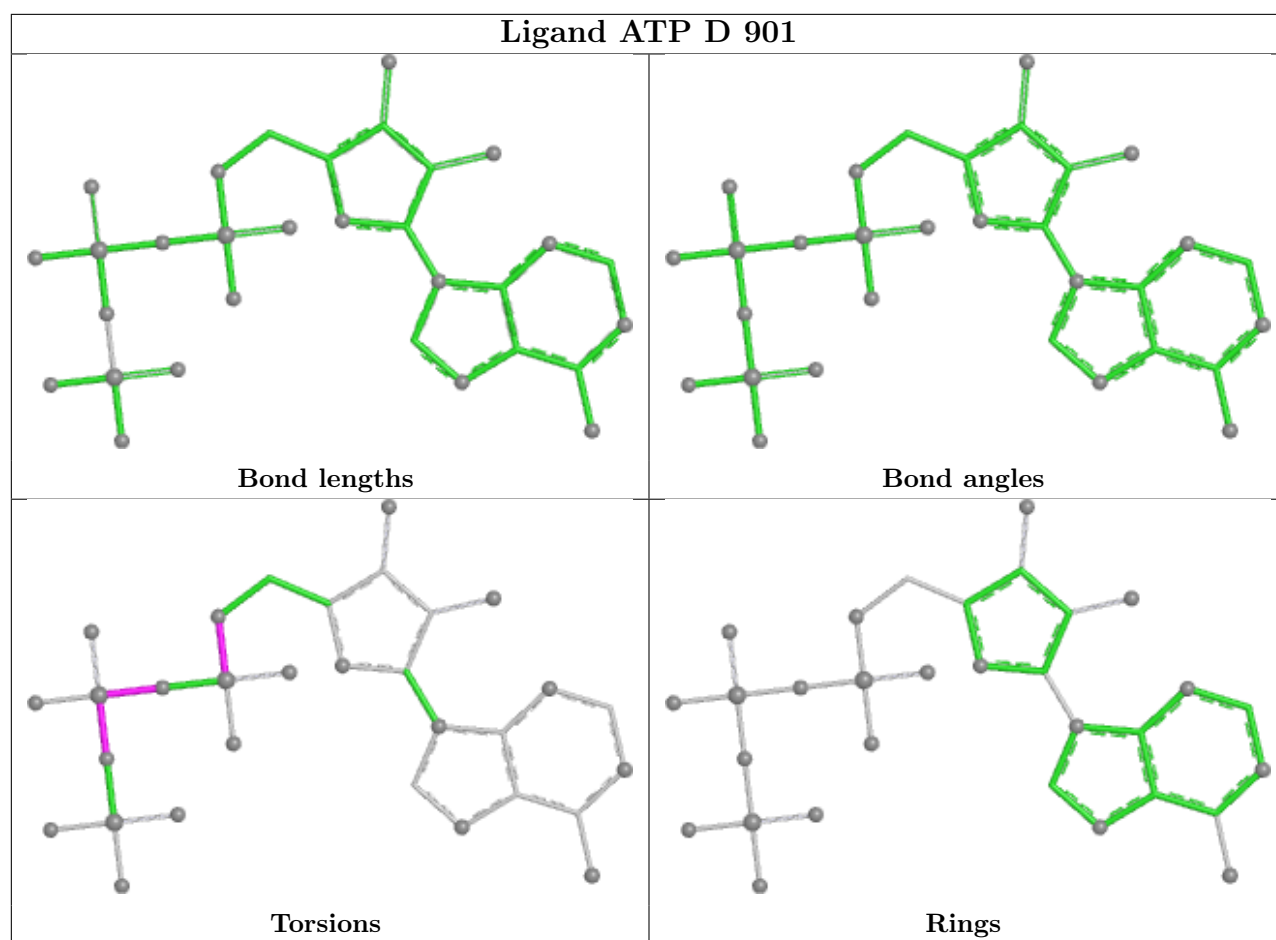
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



Ligand ATP E 501







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.

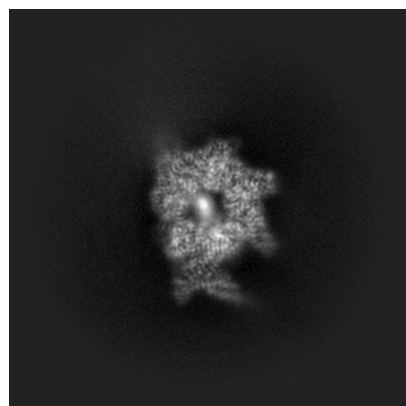
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75978. These allow visual inspection of the internal detail of the map and identification of artifacts.

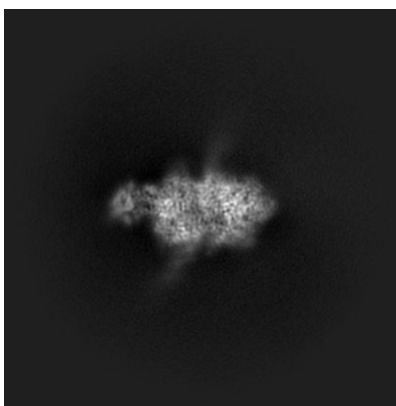
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

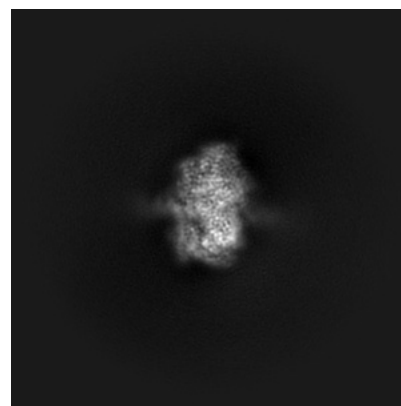
6.1.1 Primary map



X

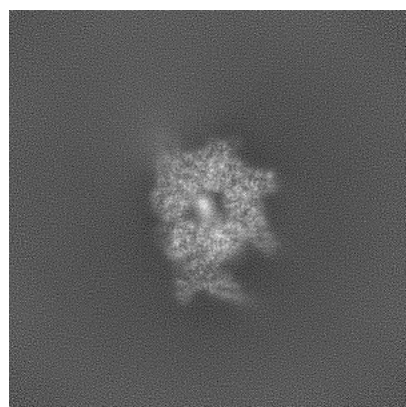


Y

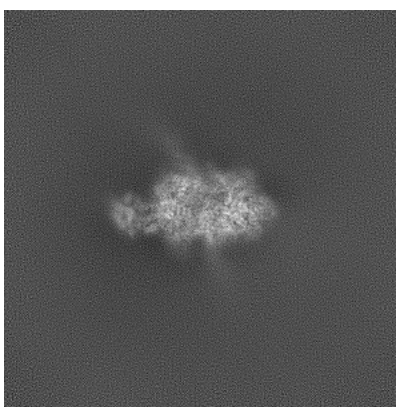


Z

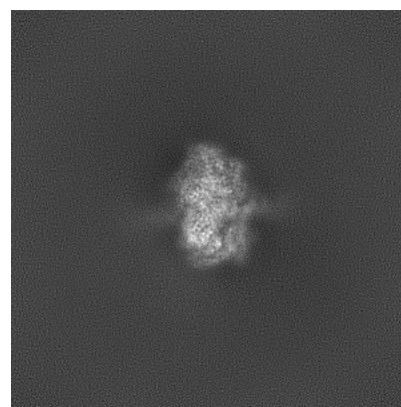
6.1.2 Raw map



X



Y

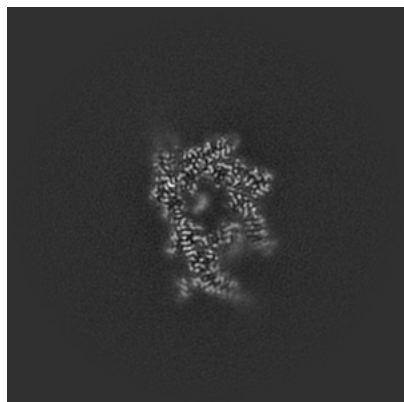


Z

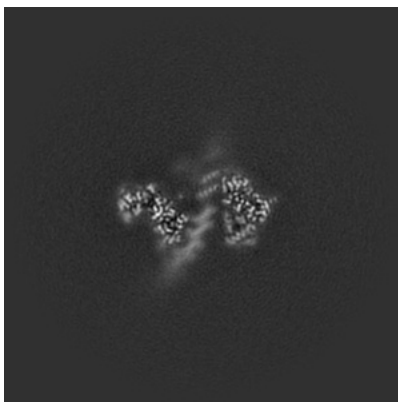
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

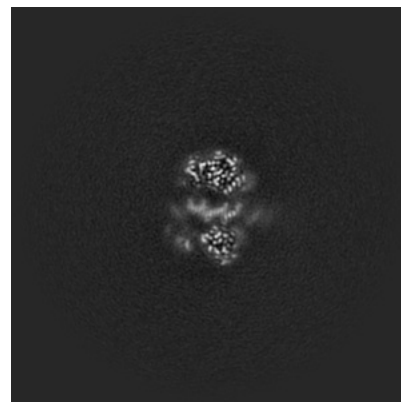
6.2.1 Primary map



X Index: 220

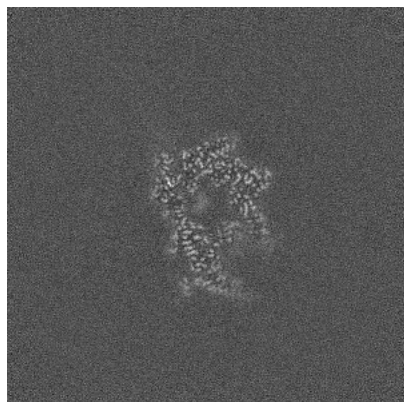


Y Index: 220

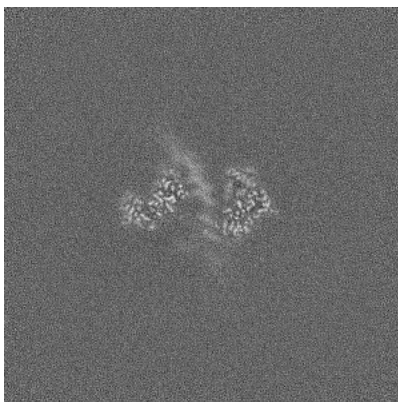


Z Index: 220

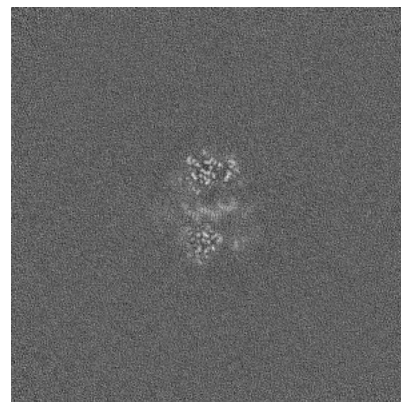
6.2.2 Raw map



X Index: 220



Y Index: 220

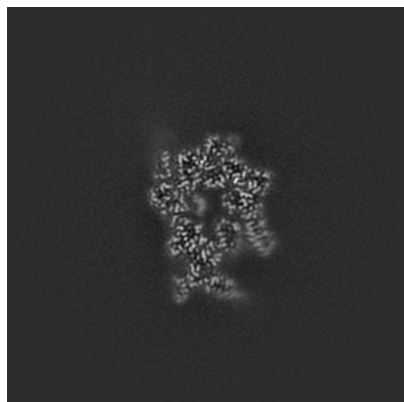


Z Index: 220

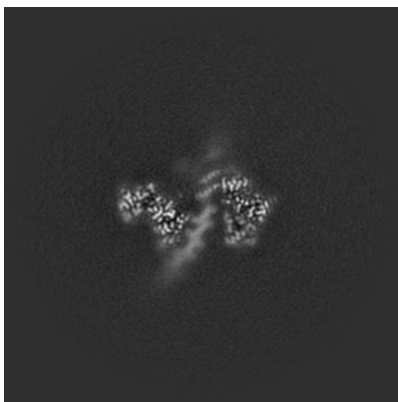
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

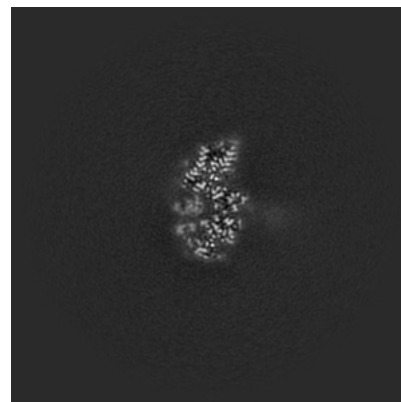
6.3.1 Primary map



X Index: 225

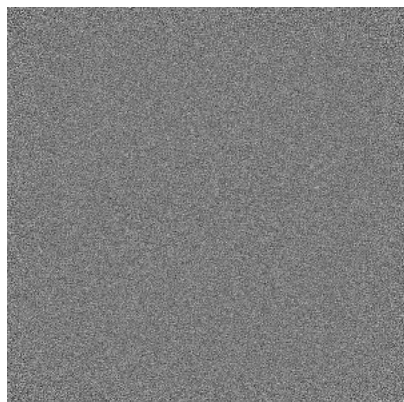


Y Index: 219

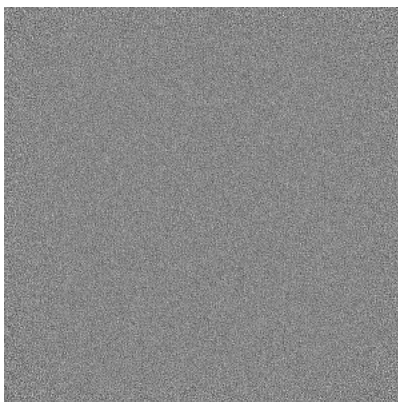


Z Index: 247

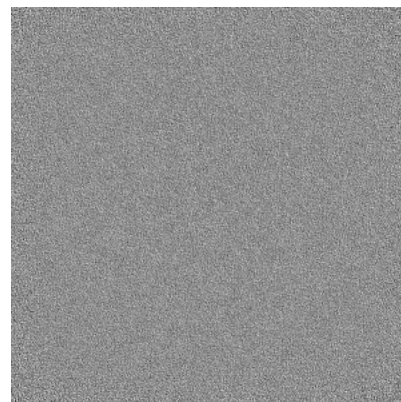
6.3.2 Raw map



X Index: 0



Y Index: 0

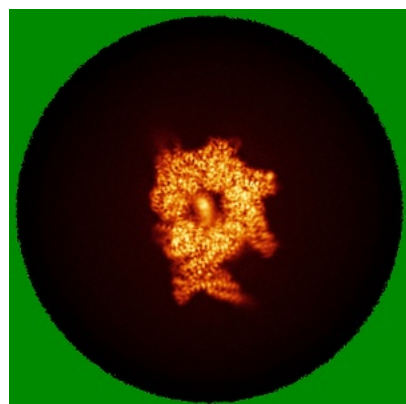


Z Index: 0

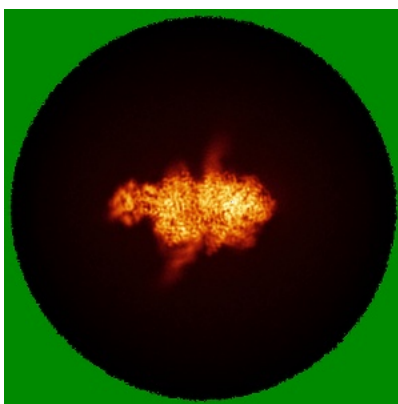
The images above show the largest variance slices of the map in three orthogonal directions.

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

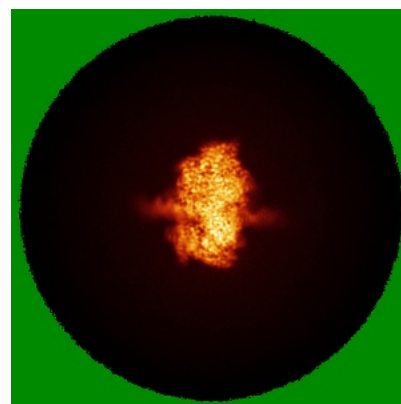
6.4.1 Primary map



X

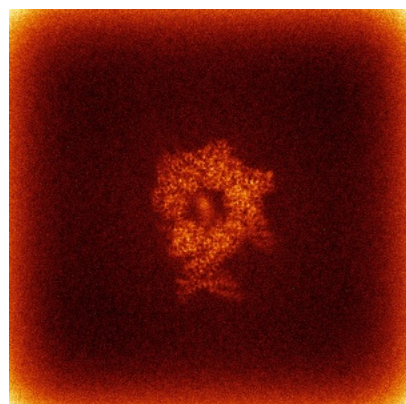


Y

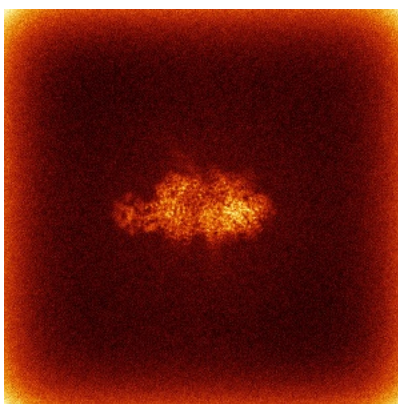


Z

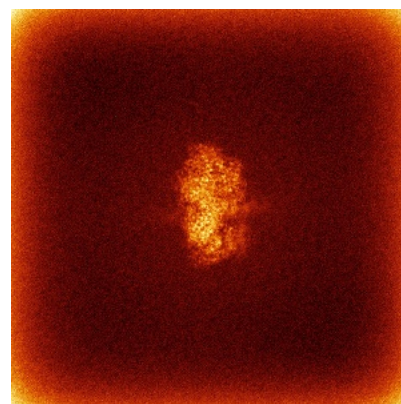
6.4.2 Raw map



X



Y

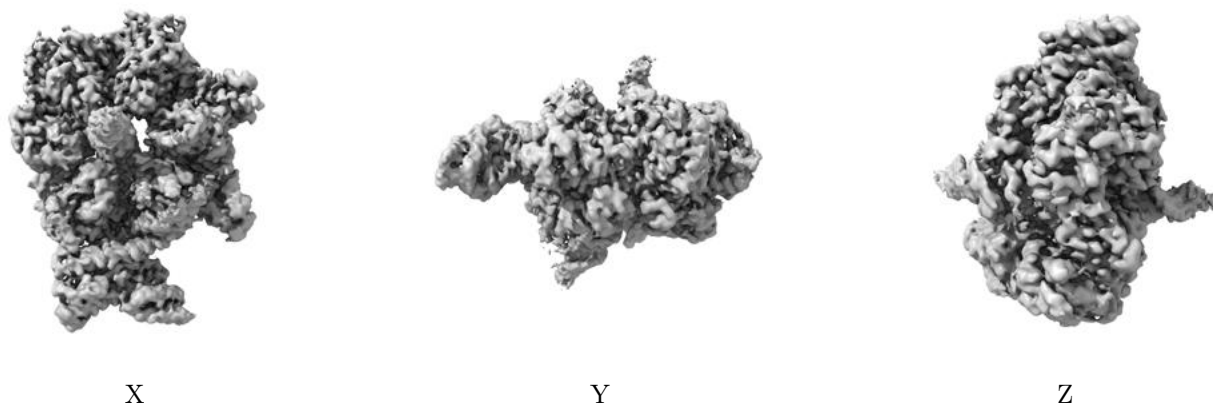


Z

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.

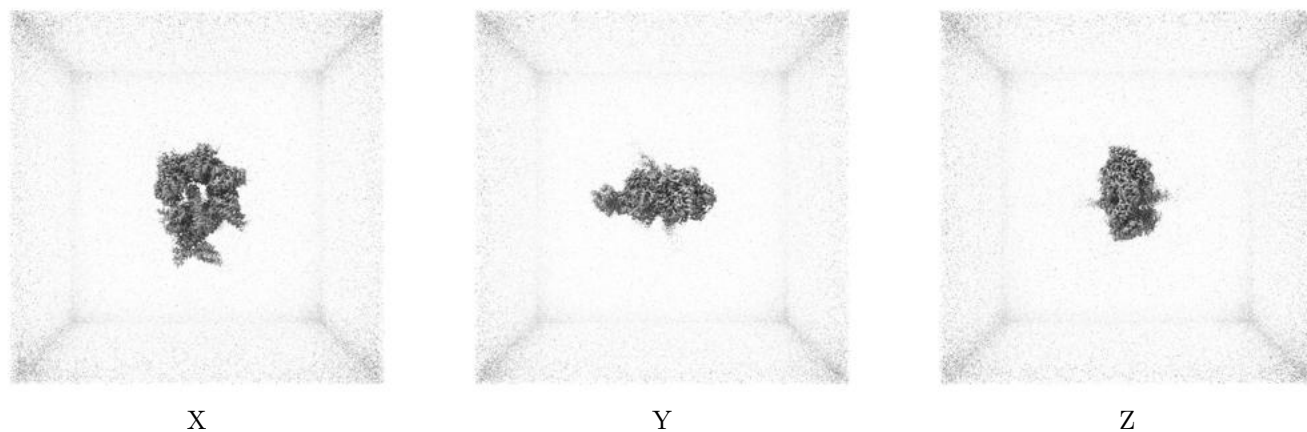
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

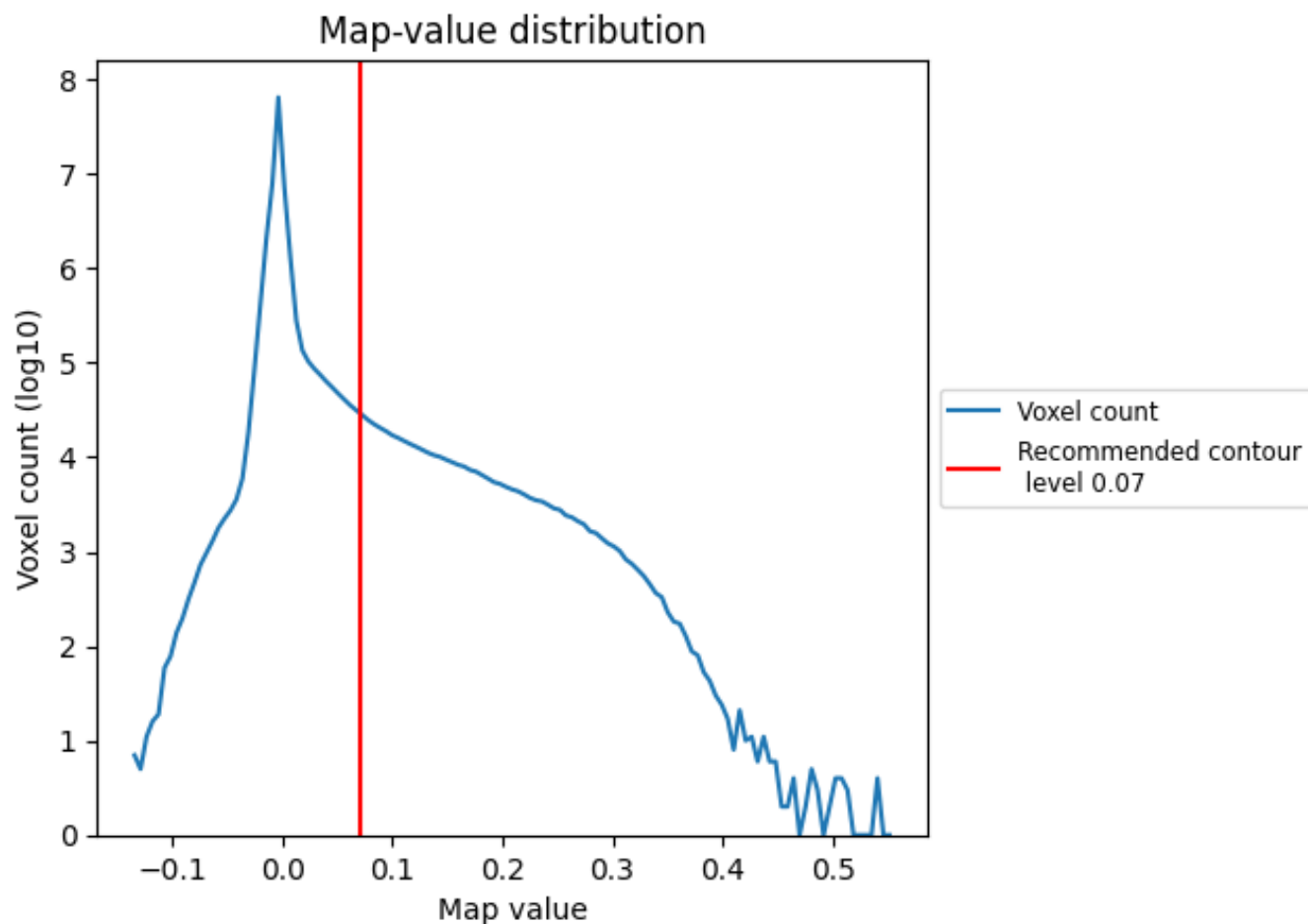
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

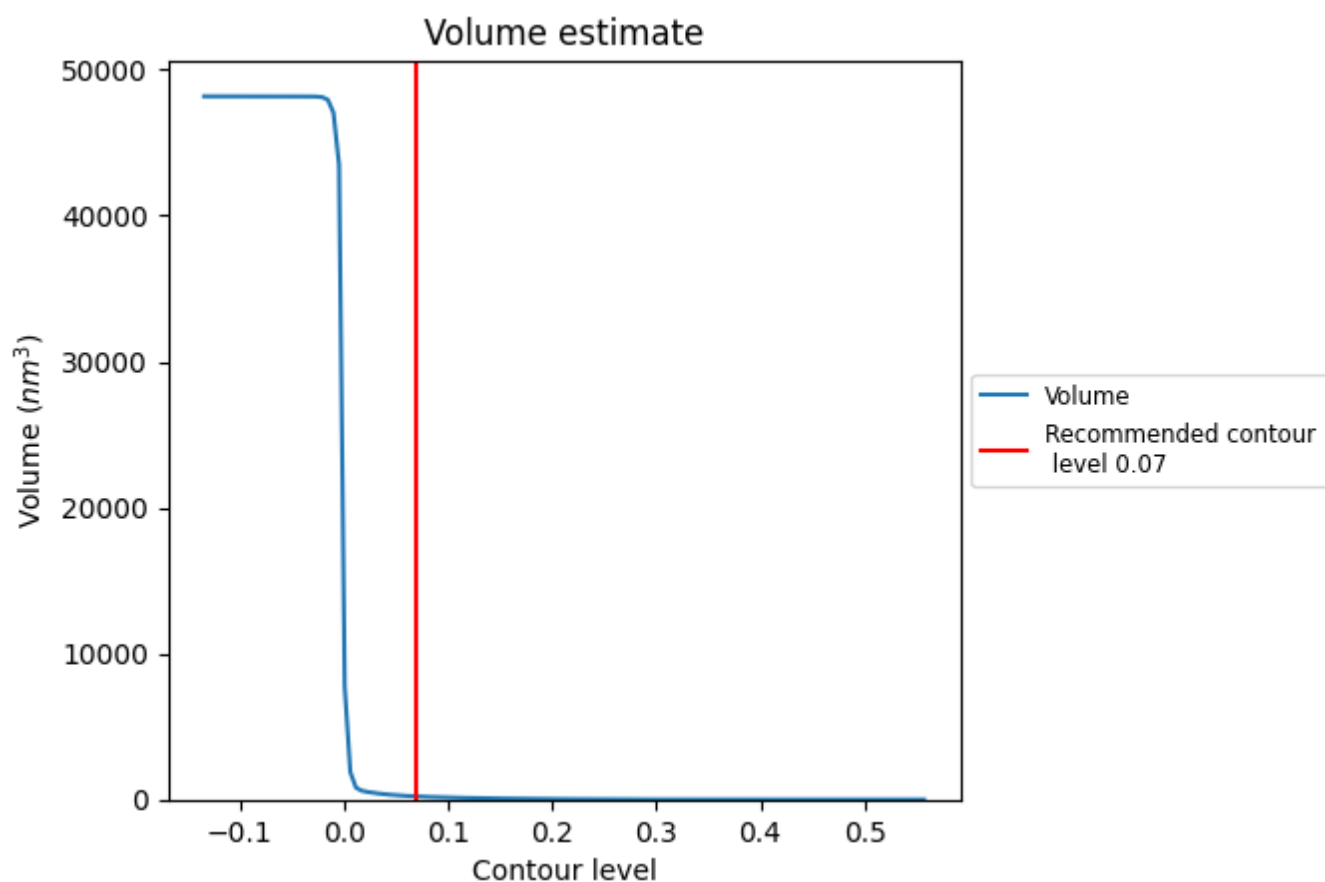
This section contains the results of statistical analysis of the map.

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.

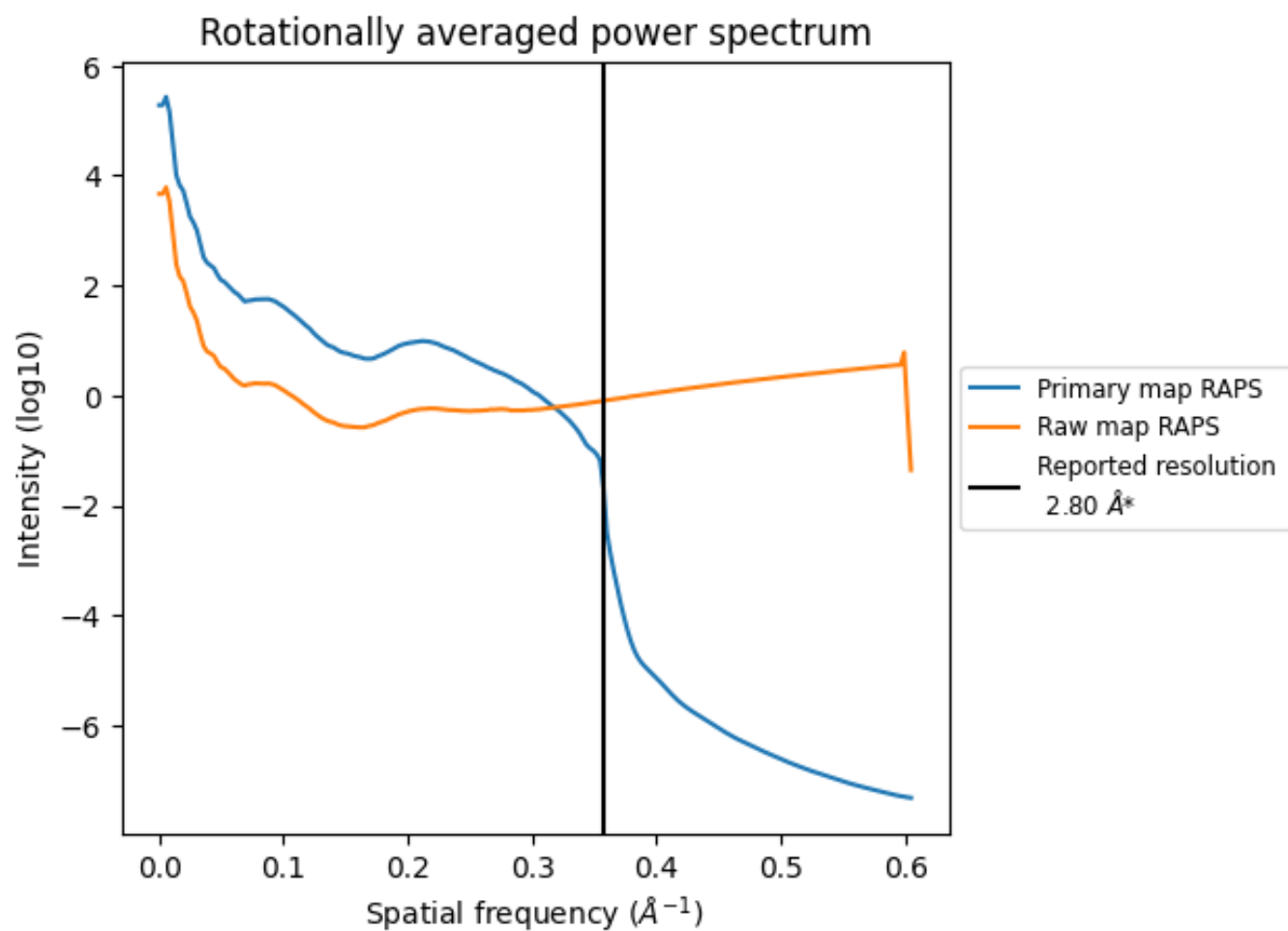
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 214 nm³; this corresponds to an approximate mass of 193 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 ⓘ

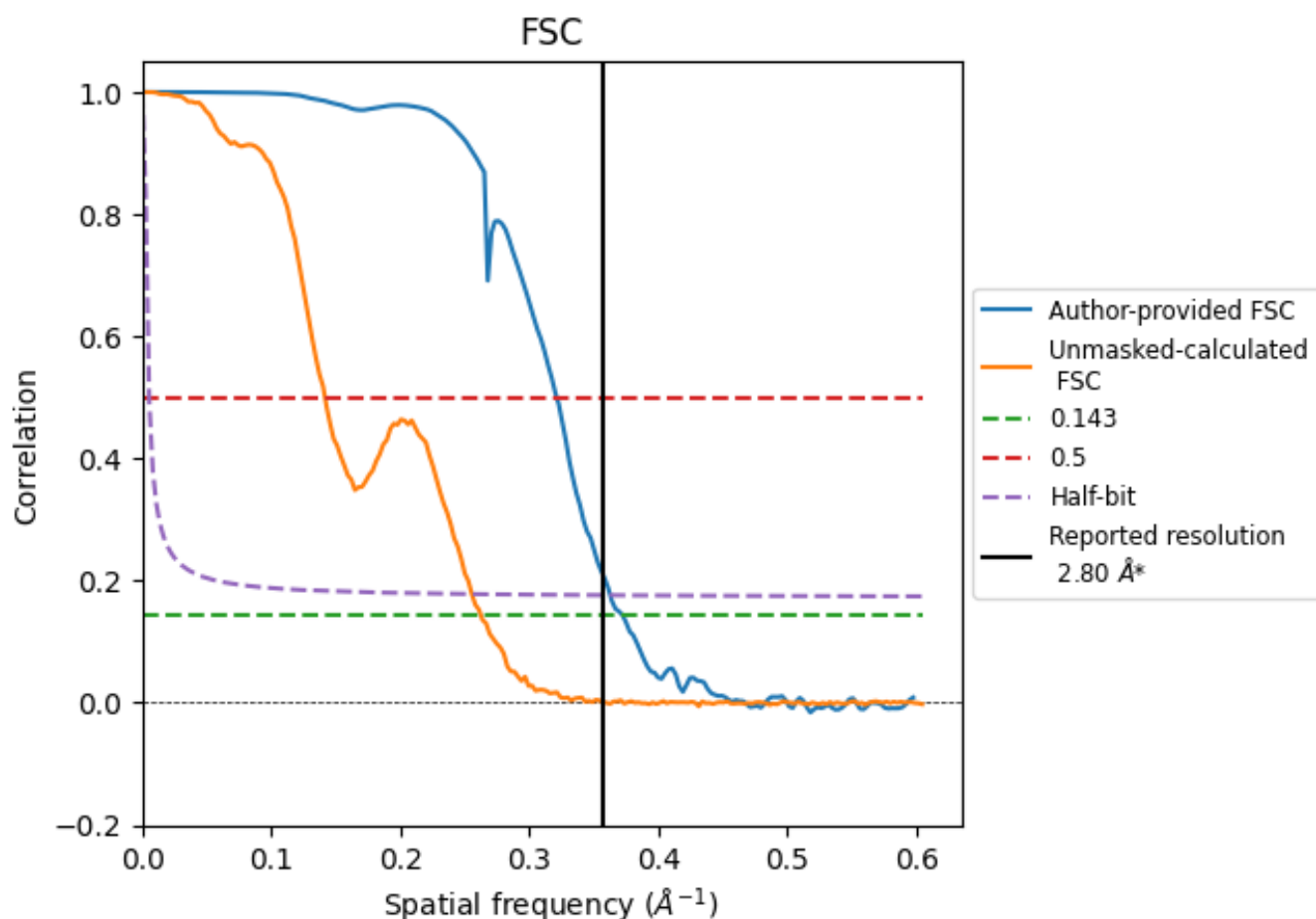


*Reported resolution corresponds to spatial frequency of 0.357 $\text{\AA}^{-1}$

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 $0.357 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	2.80	-
Author-provided FSC curve	2.68	3.11	2.76
Unmasked-calculated*	3.81	7.06	3.91

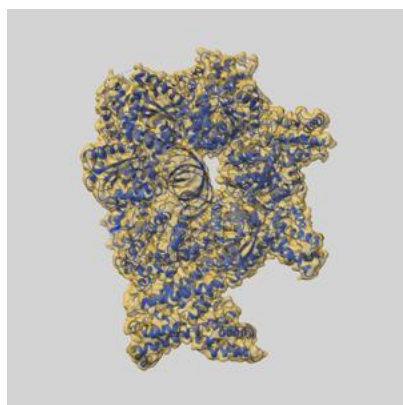
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.5 CUT-OFF 3.11 differs from the reported value 2.8 by more than 10 %

The value from deposited half-maps intersecting FSC 0.5 CUT-OFF 7.06 differs from the reported value 2.8 by more than 10 %

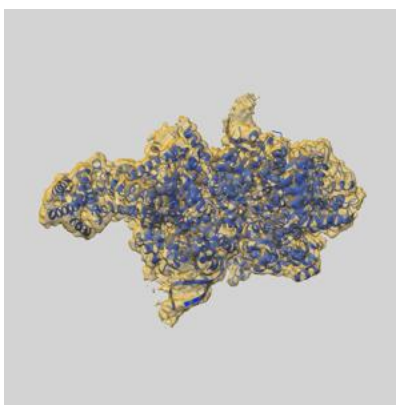
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-75978 and PDB model 11RL. Per-residue inclusion information can be found in section [3](#) on page [7](#).

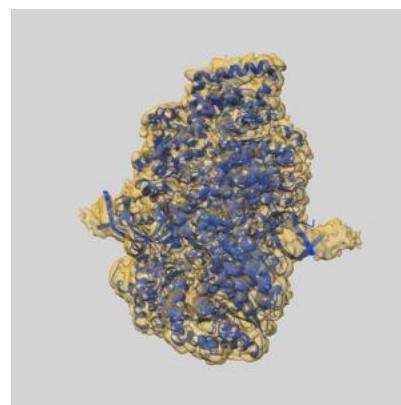
9.1 Map-model overlay [i](#)



X



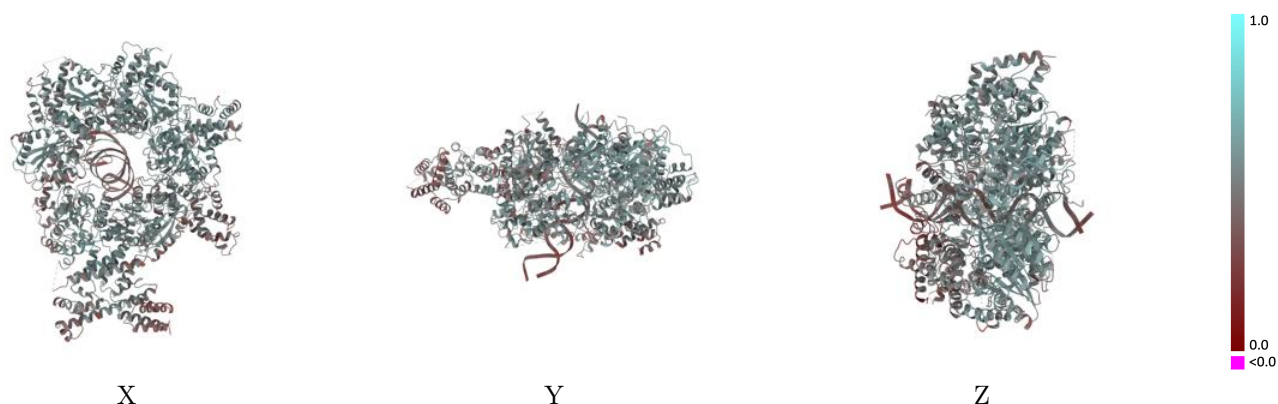
Y



Z

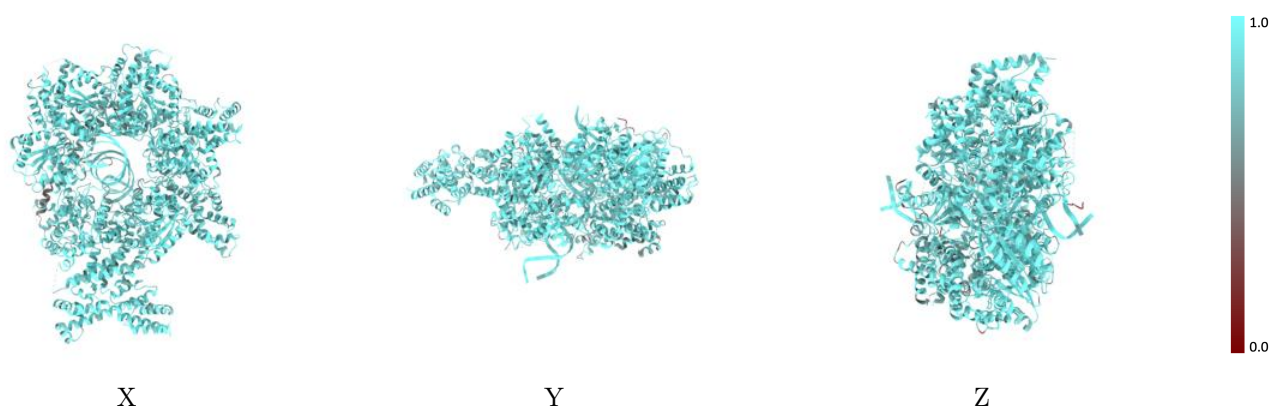
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



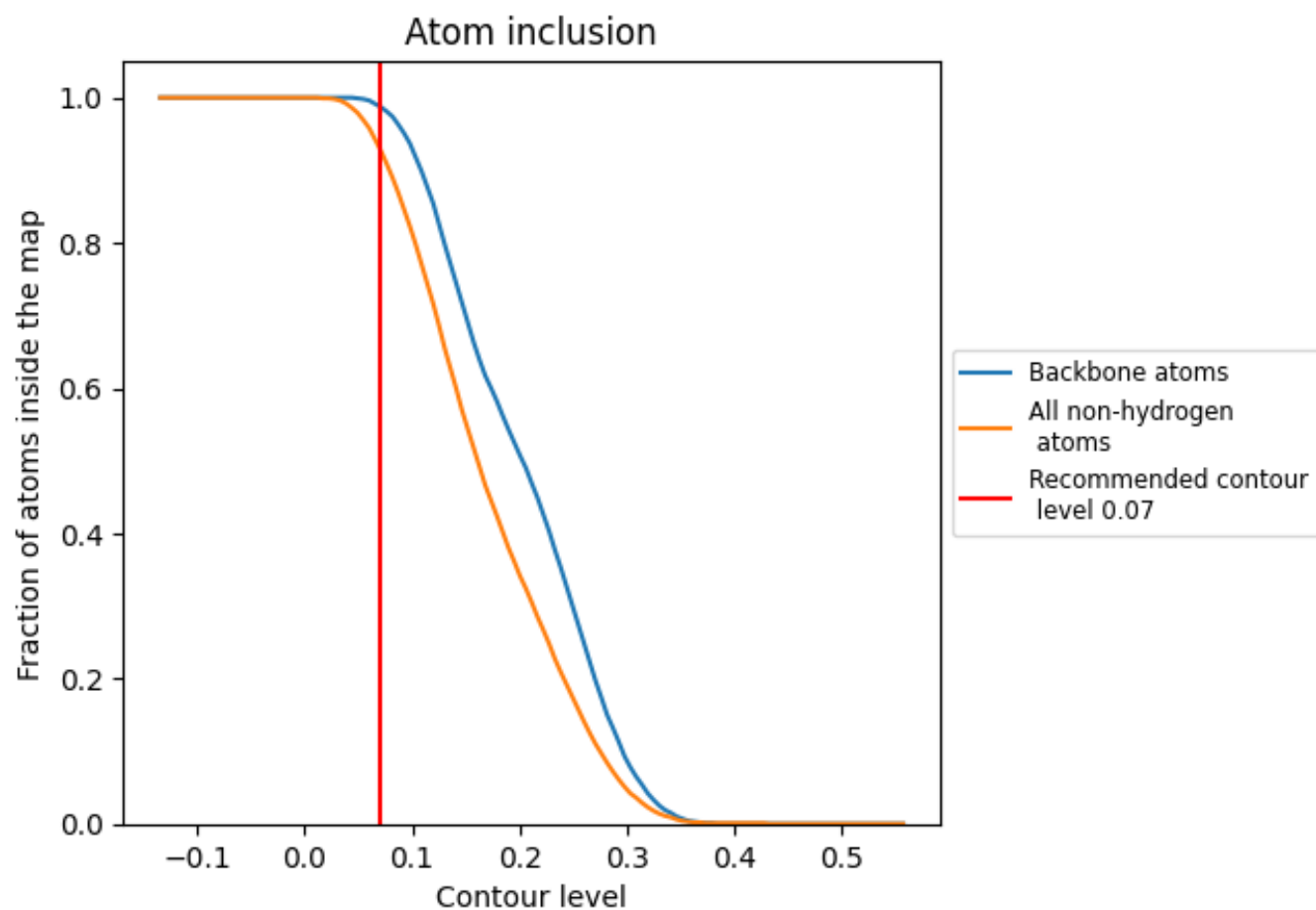
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion ⓘ



At the recommended contour level, 99% of all backbone atoms, 93% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9300	0.5040
A	0.9440	0.5520
B	0.9010	0.4860
C	0.9300	0.4830
D	0.9470	0.5420
E	0.9410	0.5190
G	0.9050	0.4960
H	0.9400	0.3760
I	0.9510	0.3480

1.0

0.0

<0.0