wwPDB EM Validation Summary Report (i)

Oct 19, 2026 – 06:17 PM JST

PDB ID	:	9WJX / pdb_00009wjx
EMDB ID	:	EMD-66033
Title	:	RUVBL1-RUVBL2 complex
Authors	:	Qin, Y.; Xu, G.
Deposited on	:	2025-08-31
Resolution	:	3.50 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:

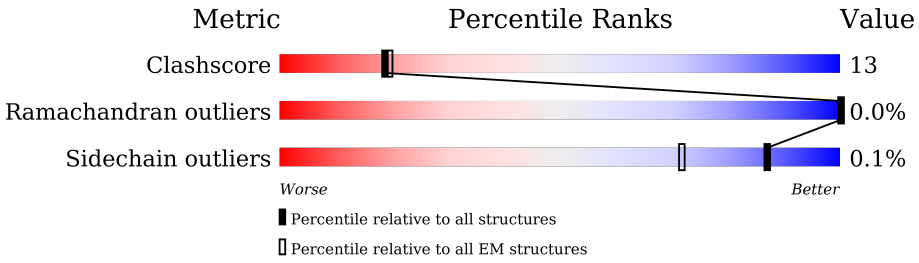
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using 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)	:	2.51

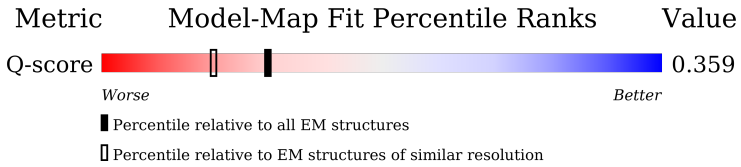
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	456	28% 62% 27% 10%
1	F	456	28% 63% 27% 10%
1	H	456	28% 66% 23% 10%
2	E	466	29% 66% 22% 12%

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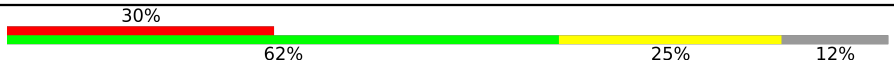
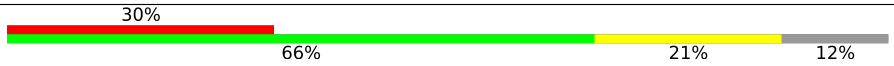
Mol	Chain	Length	Quality of chain
2	G	466	
2	I	466	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 19037 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.

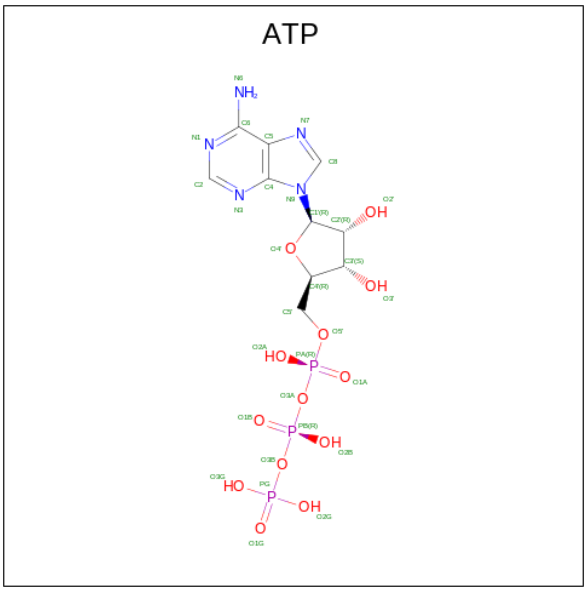
- Molecule 1 is a protein called RuvB-like helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	409	Total	C	N	O	S	0	0
			3130	1981	543	598	8		
1	F	409	Total	C	N	O	S	0	0
			3132	1982	543	599	8		
1	H	409	Total	C	N	O	S	0	0
			3128	1981	542	597	8		

- Molecule 2 is a protein called RuvB-like helicase.

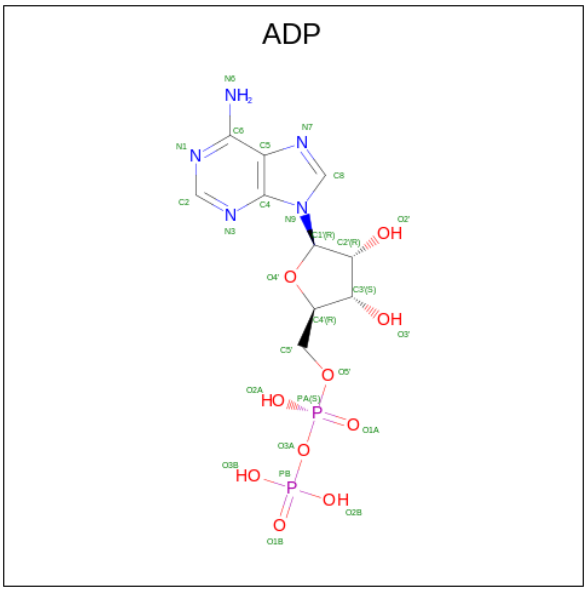
Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	409	Total	C	N	O	S	0	0
			3160	1970	558	613	19		
2	G	409	Total	C	N	O	S	0	0
			3160	1970	558	613	19		
2	I	409	Total	C	N	O	S	0	0
			3153	1964	558	612	19		

- Molecule 3 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
3	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	F	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	H	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



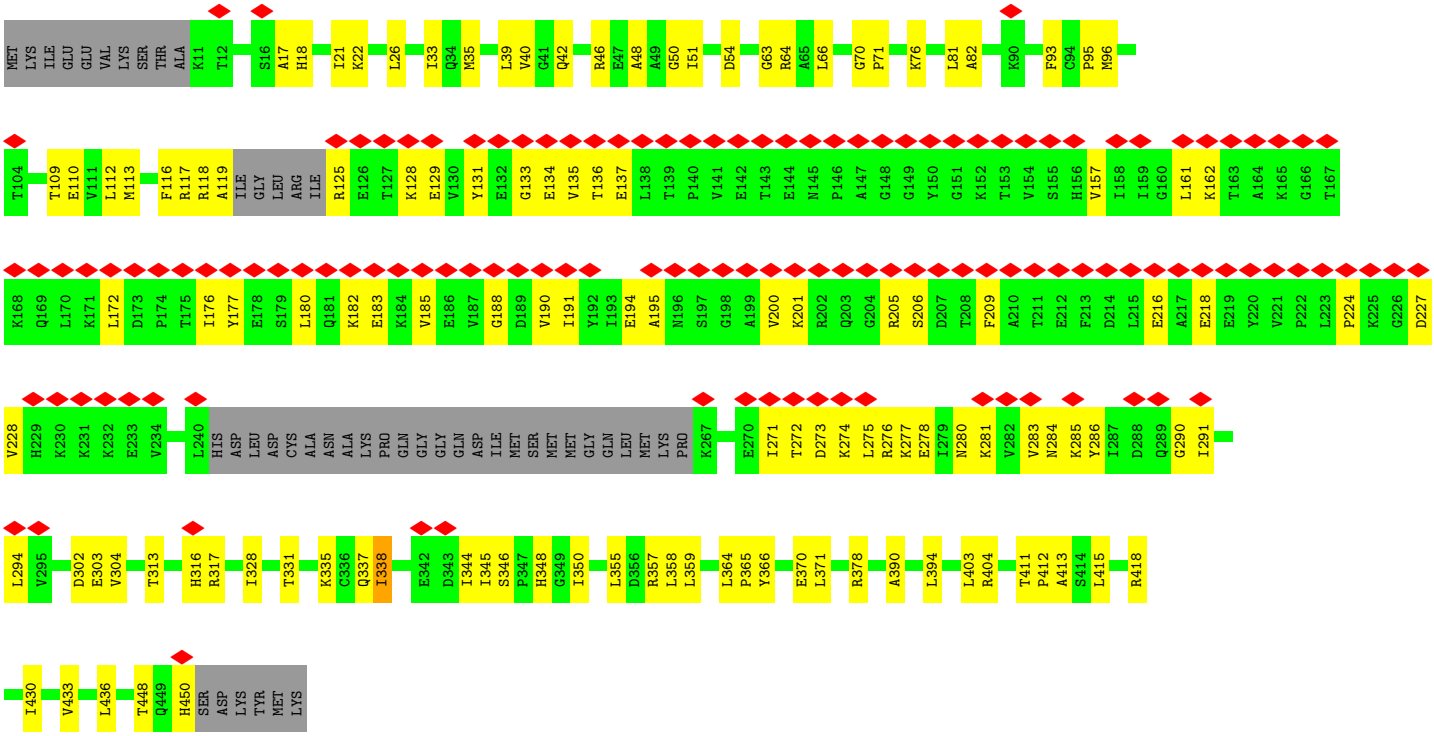
Mol	Chain	Residues	Atoms					AltConf
4	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	G	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	I	1	Total	C	N	O	P	0
			27	10	5	10	2	

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.

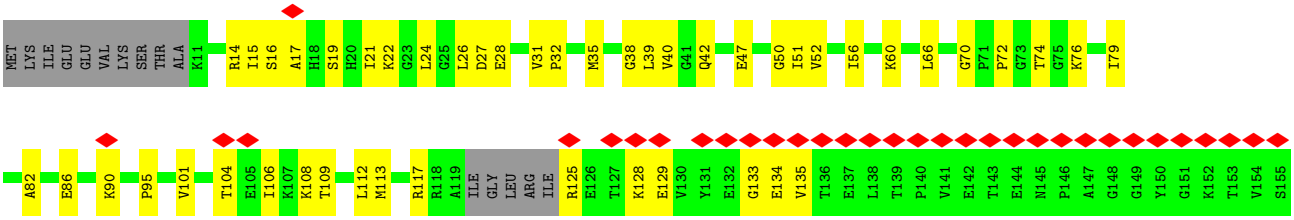
• Molecule 1: RuvB-like helicase

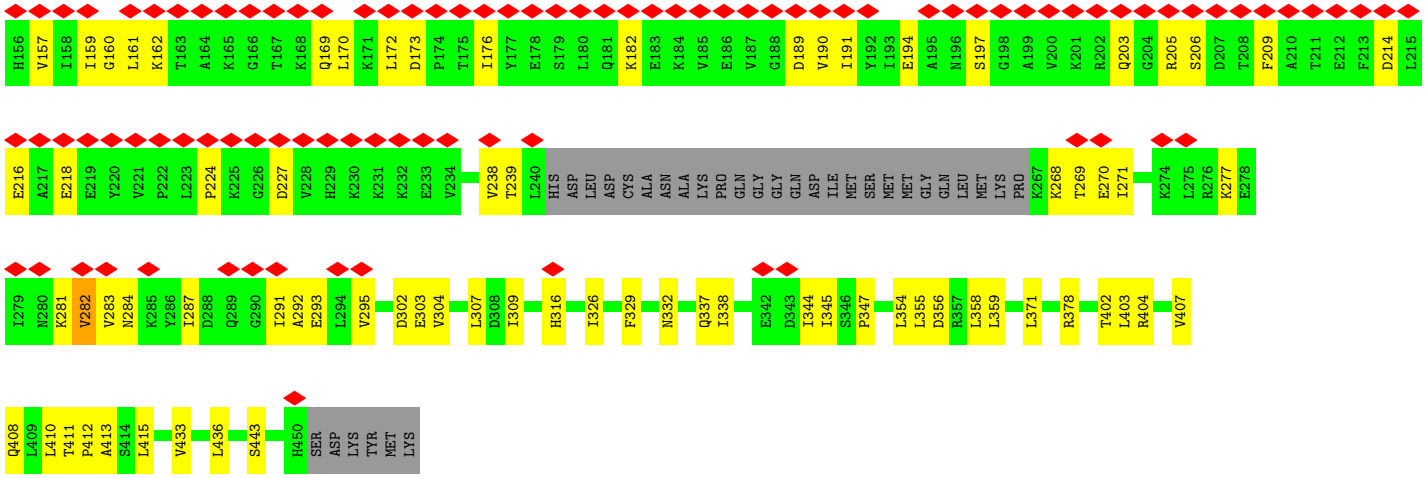
Chain D:



• Molecule 1: RuvB-like helicase

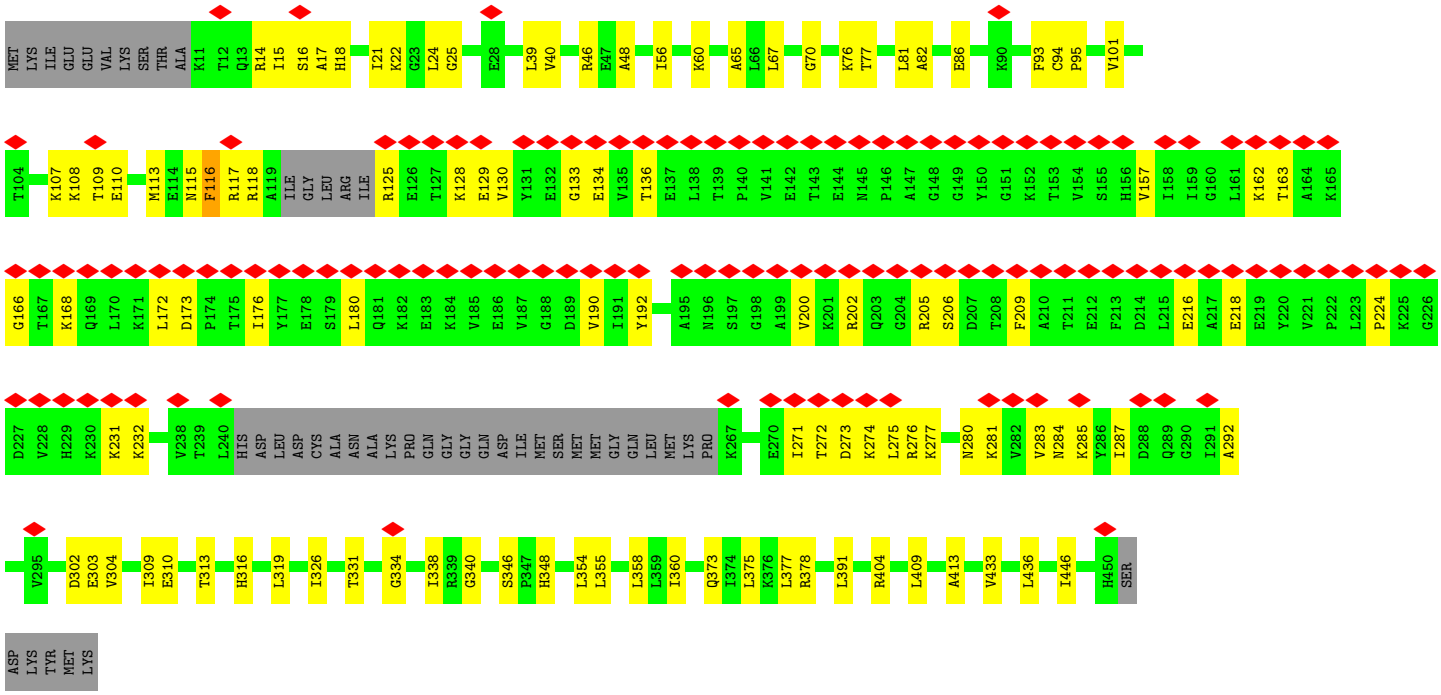
Chain F:





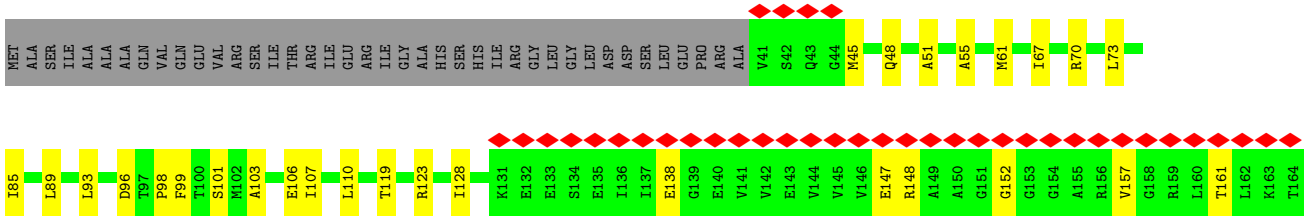
• Molecule 1: RuvB-like helicase

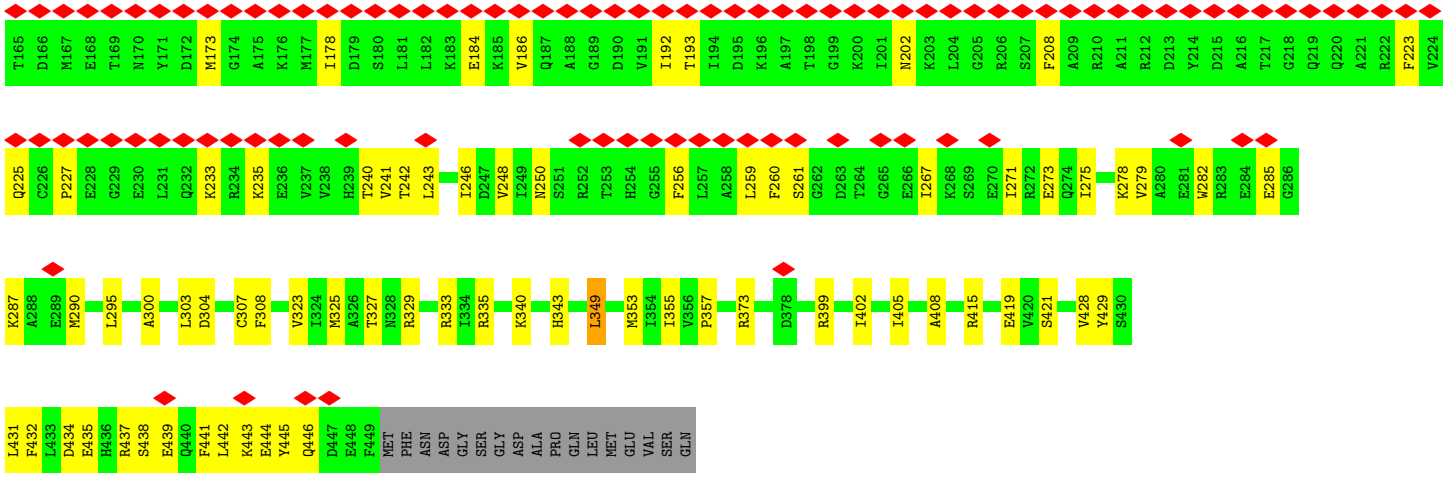
Chain H:



• Molecule 2: RuvB-like helicase

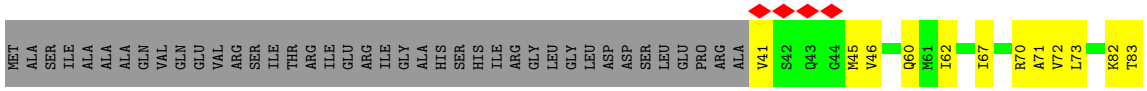
Chain E:

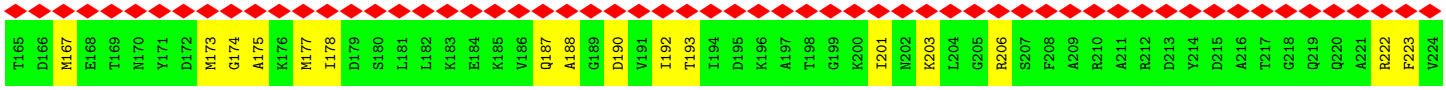


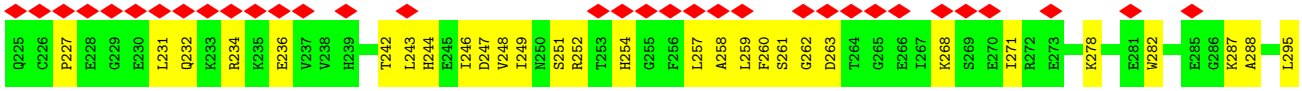


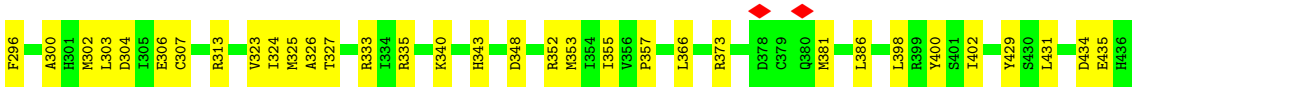
• Molecule 2: RuvB-like helicase

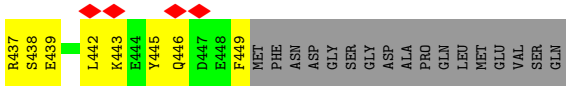
Chain G:





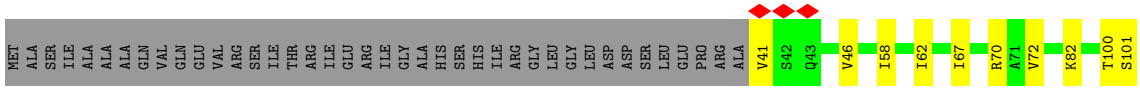


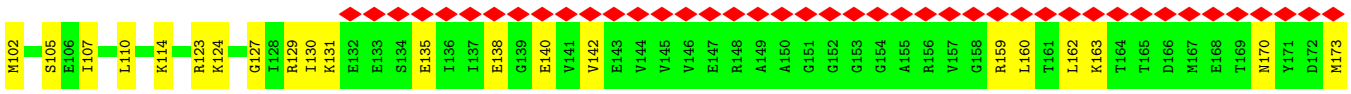


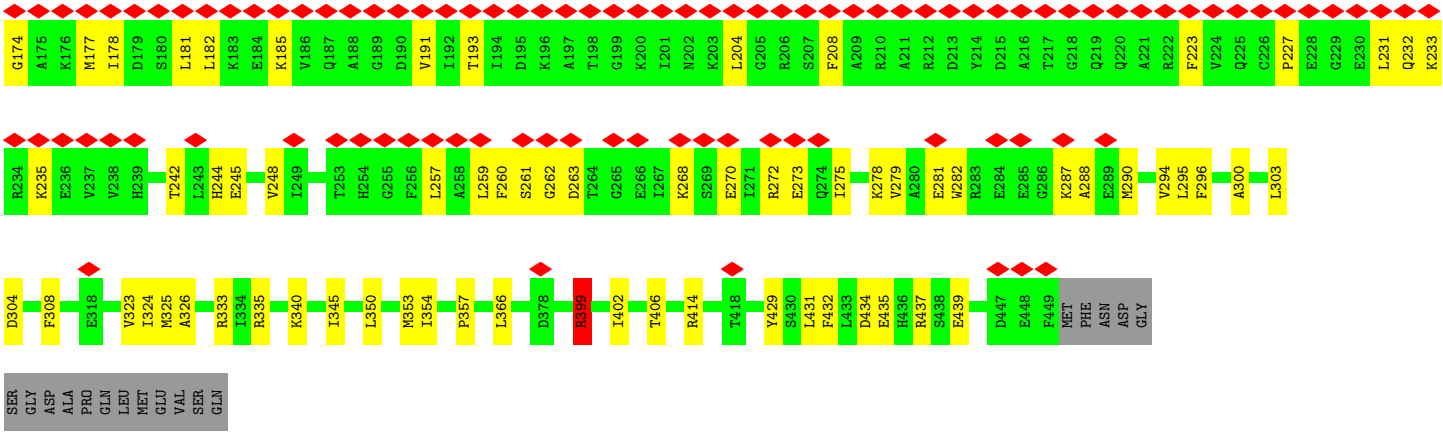


• Molecule 2: RuvB-like helicase

Chain I:






G174 A175 K176 M177 I178 D179 S180 L181 L182 K183 E184 K185 V186 Q187 A188 G189 D190 V191 I192 T193 I194 D195 K196 A197 T198 G199 K200 I201 N202 K203 L204 G205 R206 S207 F208 A209 R210 A211 R212 D213 Y214 D215 A216 T217 G218 Q219 Q220 A221 R222 F223 V224 Q225 C226 P227 E228 G229 E230 L231 Q232 K233
R234 K235 E236 V237 V238 H239 T242 L243 H244 E245 V248 I249 T253 H254 G255 F256 L257 A258 L259 F260 S261 G262 D263 T264 G265 E266 I267 K268 S269 E270 I271 R272 E273 Q274 I275 K278 V279 A280 E281 W282 R283 E284 E285 G286 K287 A288 E289 M290 V294 L295 F296 A300 L303
D304 F308 E318 V323 I324 M325 A326 R333 I334 R335 K340 I345 L350 M353 I354 P357 L366 D378 R389 I402 T406 R414 T418 Y429 S430 L431 F432 L433 D434 E435 H436 R437 S438 E439 D447 E448 F449 MET PHE ASN ASP GLY
SER GLY ASP ALA PRO GLN LEU MET GLU VAL SER GLN

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	357328	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)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	2.315	Depositor
Minimum map value	-1.705	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	428.00003, 428.00003, 428.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, ATP

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	0.13	0/3172	0.34	0/4289
1	F	0.10	0/3174	0.29	0/4292
1	H	0.11	0/3170	0.31	0/4287
2	E	0.09	0/3195	0.26	0/4294
2	G	0.09	0/3195	0.25	0/4294
2	I	0.11	0/3187	0.36	1/4283 (0.0%)
All	All	0.11	0/19093	0.30	1/25739 (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
1	H	0	1
2	I	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})
2	I	399	ARG	CG-CD-NE	-6.59	97.51	112.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	116	PHE	Peptide

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Mol	Chain	Res	Type	Group
2	I	399	ARG	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	3130	0	3245	110	0
1	F	3132	0	3249	92	0
1	H	3128	0	3243	96	0
2	E	3160	0	3220	80	0
2	G	3160	0	3220	104	0
2	I	3153	0	3212	83	0
3	D	31	0	11	3	0
3	F	31	0	11	2	0
3	H	31	0	11	4	0
4	E	27	0	12	0	0
4	G	27	0	12	2	0
4	I	27	0	11	2	0
All	All	19037	0	19457	495	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 13.

The worst 5 of 495 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:H:275:LEU:H	2:G:261:SER:H	0.90	0.89
1:H:275:LEU:N	2:G:261:SER:H	1.74	0.85
1:H:275:LEU:H	2:G:261:SER:N	1.75	0.83
2:I:160:LEU:HD21	2:I:162:LEU:HG	1.59	0.83
1:H:21:ILE:HD11	1:H:82:ALA:HB2	1.61	0.82

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	D	403/456 (88%)	394 (98%)	9 (2%)	0	100 100
1	F	403/456 (88%)	388 (96%)	14 (4%)	1 (0%)	43 74
1	H	403/456 (88%)	391 (97%)	12 (3%)	0	100 100
2	E	403/466 (86%)	397 (98%)	6 (2%)	0	100 100
2	G	403/466 (86%)	395 (98%)	8 (2%)	0	100 100
2	I	403/466 (86%)	391 (97%)	12 (3%)	0	100 100
All	All	2418/2766 (87%)	2356 (97%)	61 (2%)	1 (0%)	100 100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	282	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
1	D	336/377 (89%)	334 (99%)	2 (1%)	78 79
1	F	337/377 (89%)	337 (100%)	0	100 100
1	H	335/377 (89%)	335 (100%)	0	100 100
2	E	340/385 (88%)	339 (100%)	1 (0%)	86 83
2	G	340/385 (88%)	340 (100%)	0	100 100
2	I	339/385 (88%)	339 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2027/2286 (89%)	2024 (100%)	3 (0%)	87 87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	338	ILE
1	D	344	ILE
2	E	349	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	202	ASN
2	E	371	ASN
2	I	440	GLN
2	E	364	GLN
2	E	446	GLN

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

6 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	$\#\|Z\| > 2$
3	ATP	H	501	-	29,33,33	0.29	0	44,52,52	0.50	1 (2%)
3	ATP	F	501	-	29,33,33	0.28	0	44,52,52	0.48	1 (2%)
4	ADP	E	501	-	27,29,29	1.36	4 (14%)	42,45,45	1.97	10 (23%)
3	ATP	D	501	-	29,33,33	0.29	0	44,52,52	0.49	1 (2%)
4	ADP	I	501	-	27,29,29	1.31	3 (11%)	42,45,45	2.11	12 (28%)
4	ADP	G	501	-	27,29,29	1.36	4 (14%)	42,45,45	1.98	10 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ATP	H	501	-	-	10/22/38/38	0/3/3/3
3	ATP	F	501	-	-	9/22/38/38	0/3/3/3
4	ADP	E	501	-	-	5/16/32/32	0/3/3/3
3	ATP	D	501	-	-	9/22/38/38	0/3/3/3
4	ADP	I	501	-	-	10/16/32/32	0/3/3/3
4	ADP	G	501	-	-	6/16/32/32	0/3/3/3

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	501	ADP	C5-C4	4.56	1.47	1.39
4	G	501	ADP	C5-C4	4.54	1.47	1.39
4	I	501	ADP	C5-C4	3.49	1.45	1.39
4	I	501	ADP	C5-C6	3.10	1.49	1.41
4	G	501	ADP	C5-C6	2.70	1.48	1.41

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	I	501	ADP	C5-C4-N3	-6.49	118.28	126.75
4	G	501	ADP	C5-C4-N3	-6.19	118.68	126.75
4	E	501	ADP	C5-C4-N3	-6.15	118.73	126.75
4	G	501	ADP	N3-C4-N9	4.85	135.08	127.08
4	E	501	ADP	N3-C4-N9	4.82	135.03	127.08

There are no chirality outliers.

5 of 49 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	501	ATP	O4'-C4'-C5'-O5'
3	D	501	ATP	C3'-C4'-C5'-O5'
3	F	501	ATP	PB-O3B-PG-O2G
3	F	501	ATP	C3'-C4'-C5'-O5'
3	F	501	ATP	O4'-C1'-N9-C8

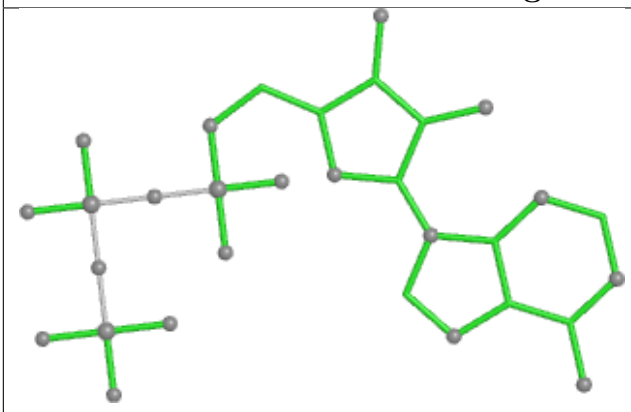
There are no ring outliers.

5 monomers are involved in 13 short contacts:

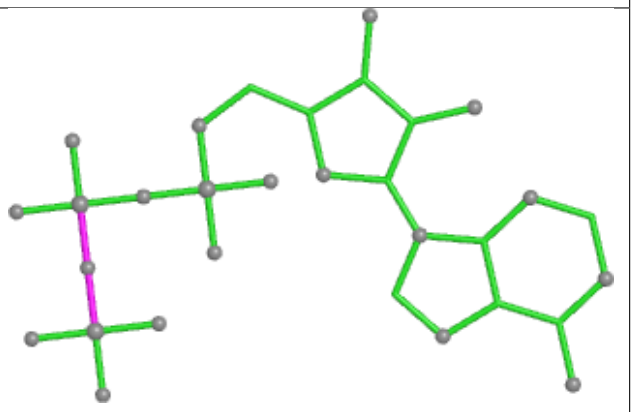
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	501	ATP	4	0
3	F	501	ATP	2	0
3	D	501	ATP	3	0
4	I	501	ADP	2	0
4	G	501	ADP	2	0

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.

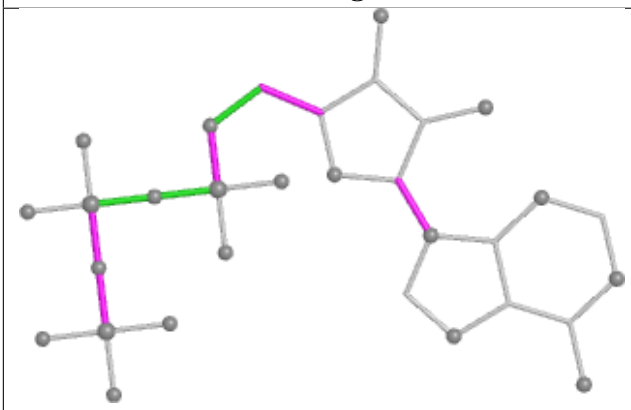
Ligand ATP H 501



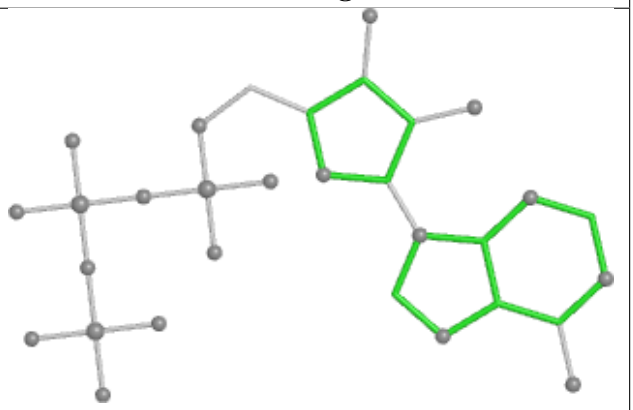
Bond lengths



Bond angles

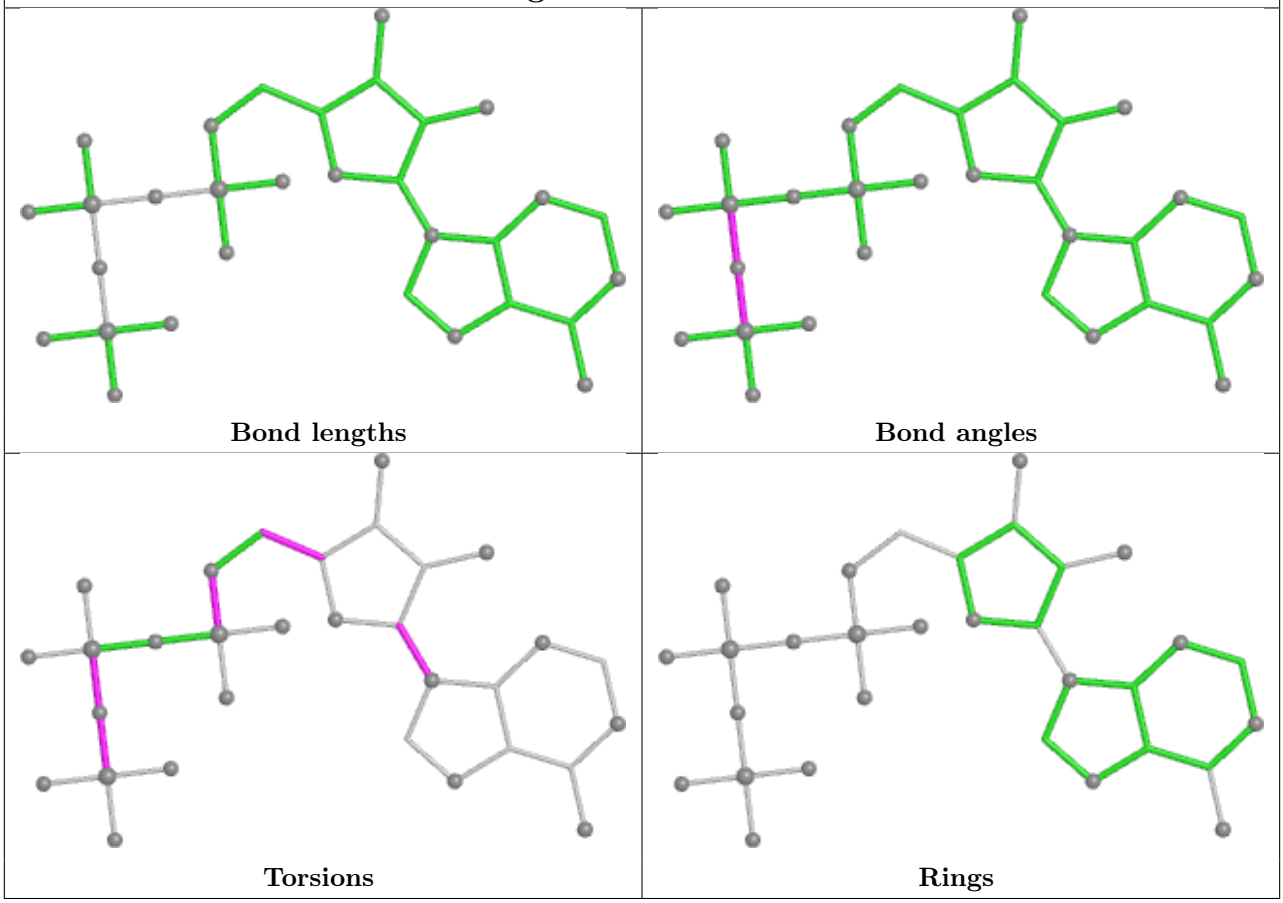


Torsions

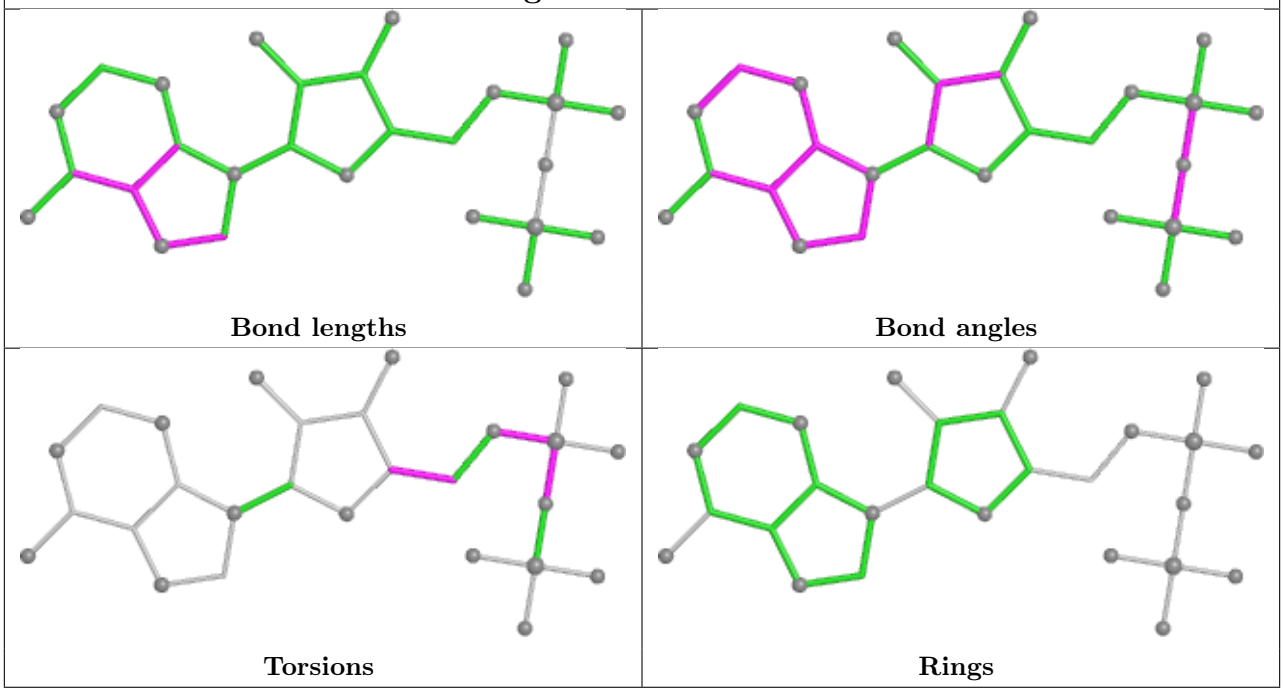


Rings

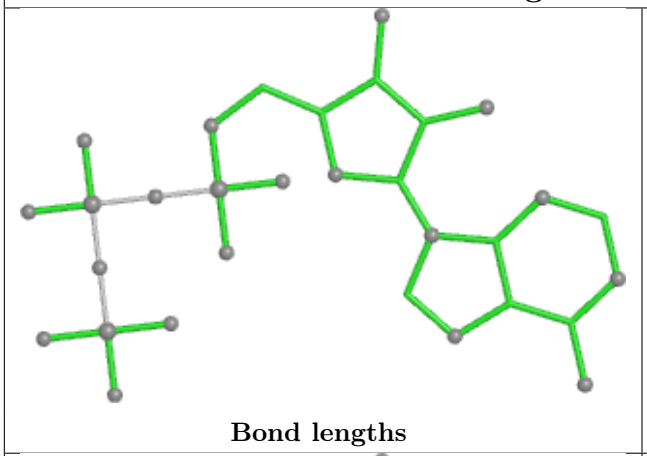
Ligand ATP F 501



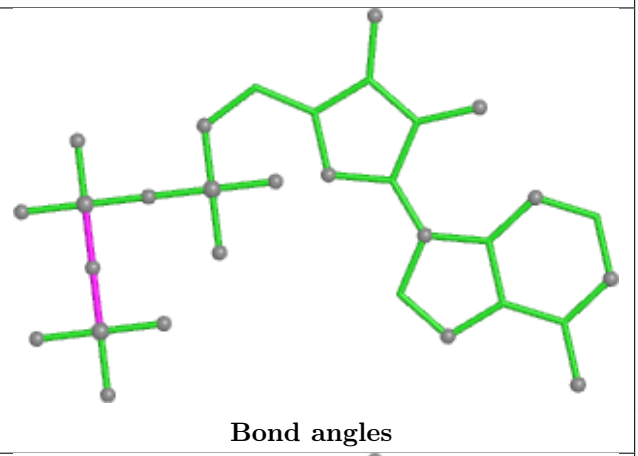
Ligand ADP E 501



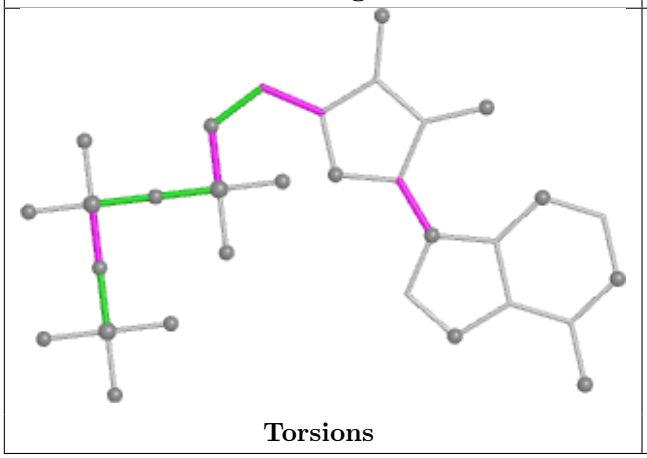
Ligand ATP D 501



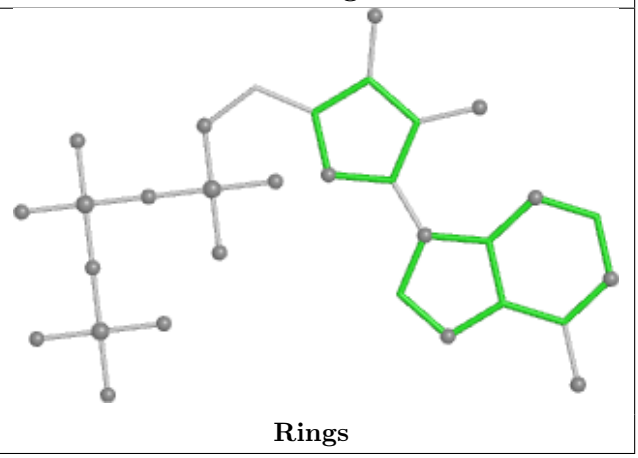
Bond lengths



Bond angles

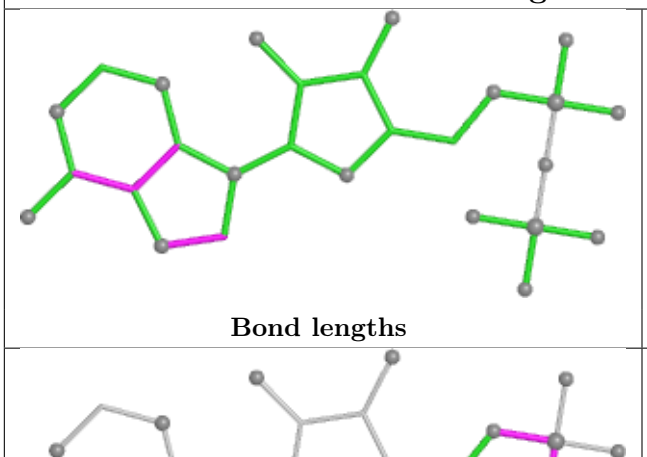


Torsions

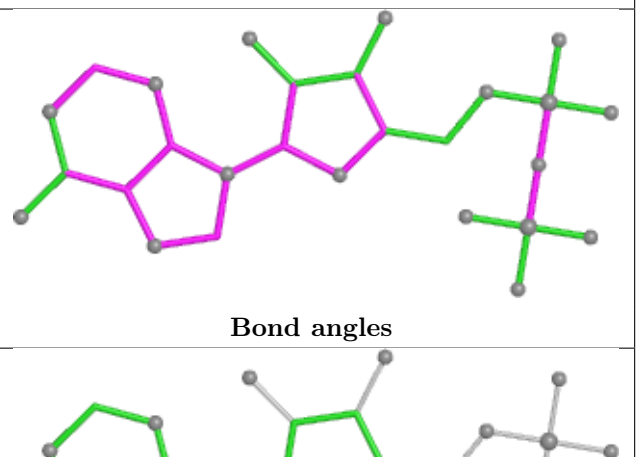


Rings

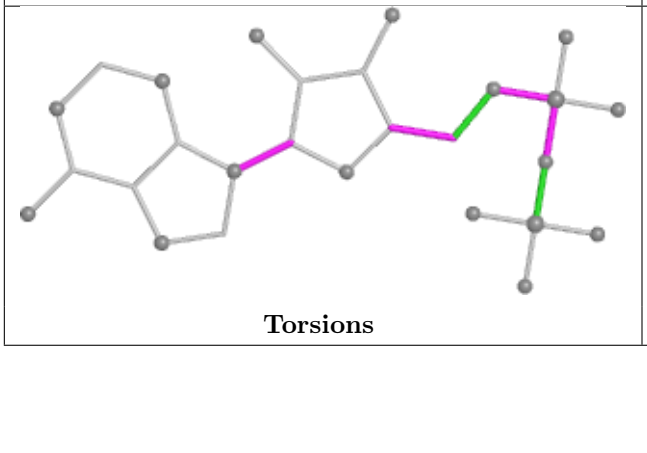
Ligand ADP I 501



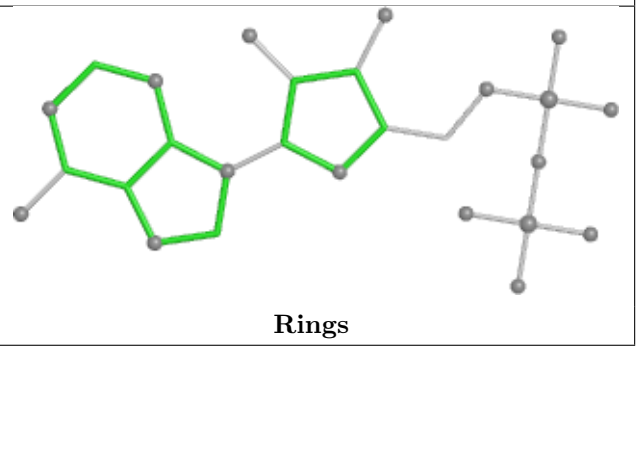
Bond lengths



Bond angles

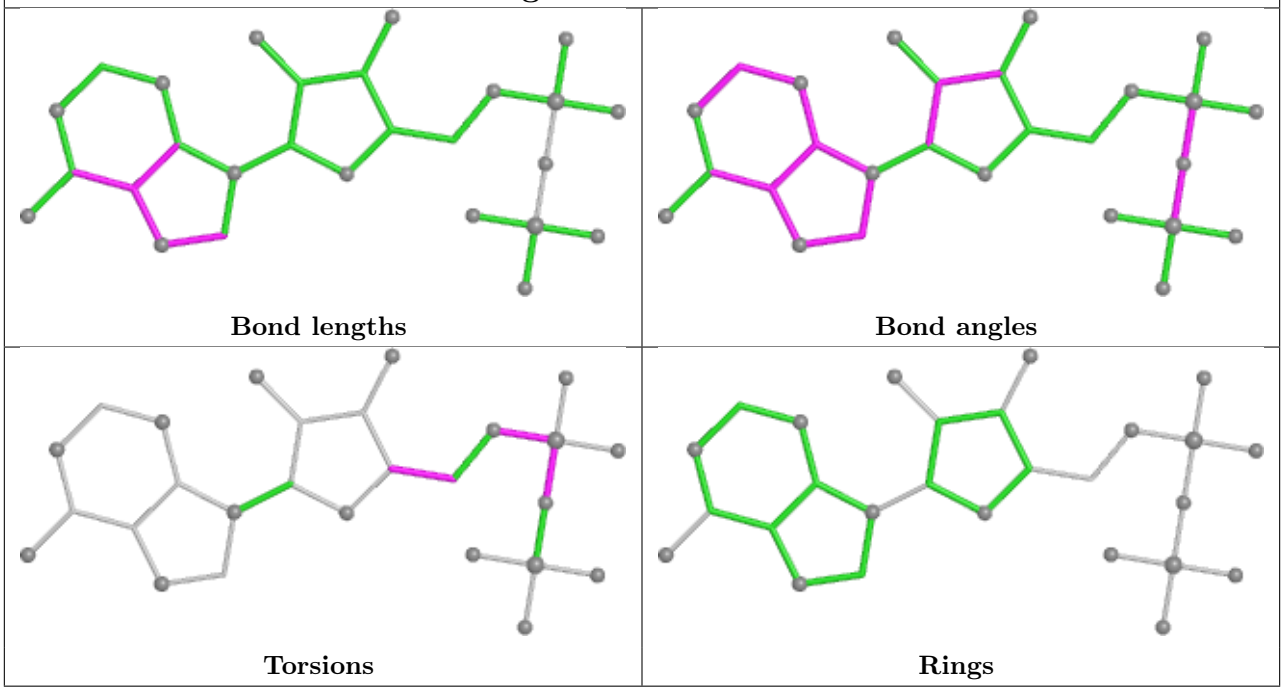


Torsions



Rings

Ligand ADP G 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
2	I	2
2	E	2
2	G	2

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	241:VAL	C	242:THR	N	4.18
1	I	127:GLY	C	128:ILE	N	4.02
1	E	127:GLY	C	128:ILE	N	3.76
1	E	241:VAL	C	242:THR	N	3.76
1	G	127:GLY	C	128:ILE	N	3.68

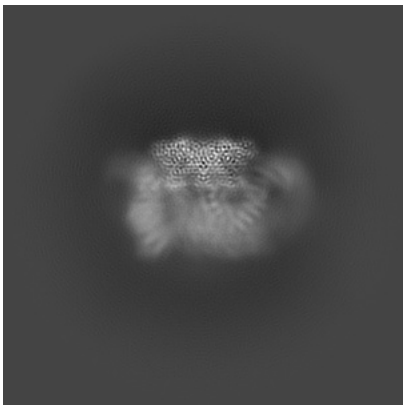
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-66033. These allow visual inspection of the internal detail of the map and identification of artifacts.

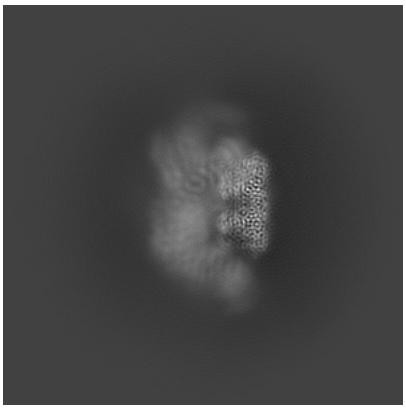
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

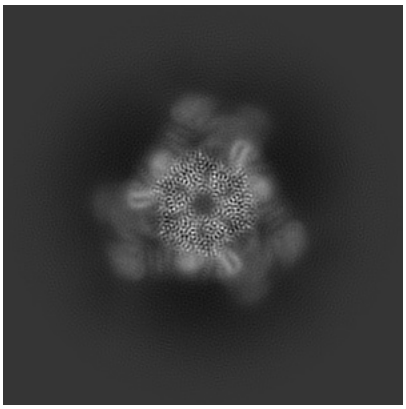
6.1.1 Primary map



X

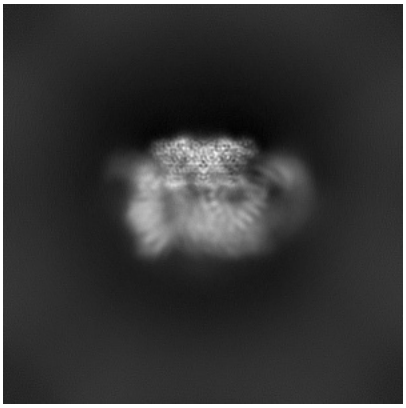


Y

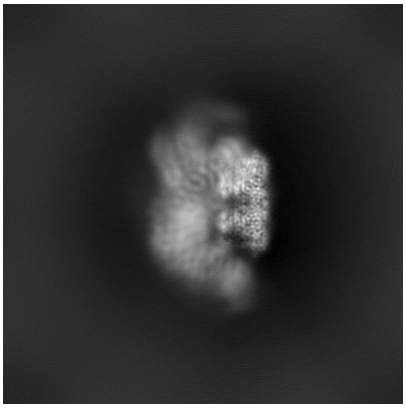


Z

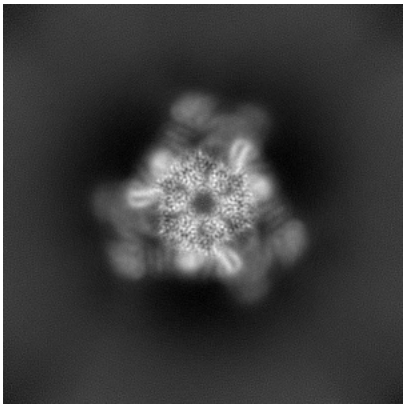
6.1.2 Raw map



X



Y



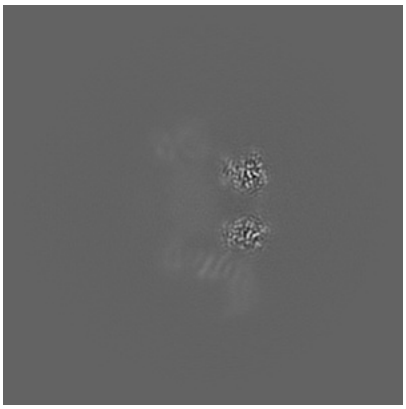
Z

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

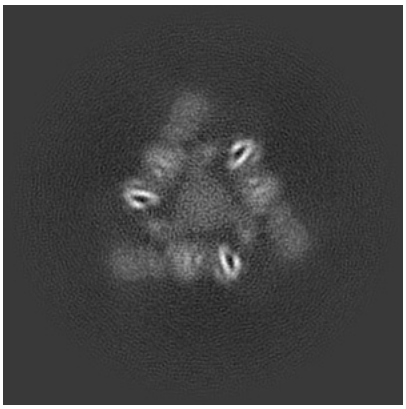
6.2 Central slices (i)

6.2.1 Primary map

X Index: 200



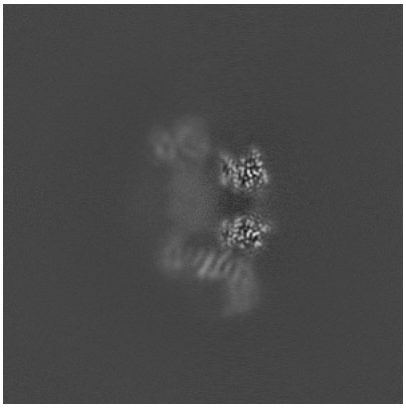
Y Index: 200



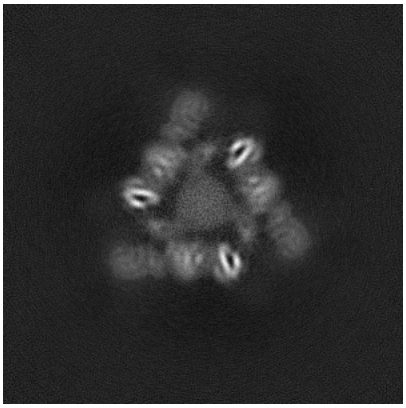
Z Index: 200

6.2.2 Raw map

X Index: 200



Y Index: 200



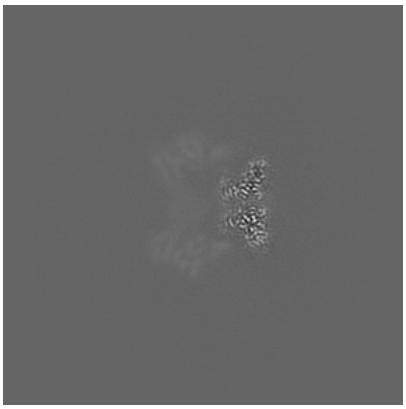
Z Index: 200

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

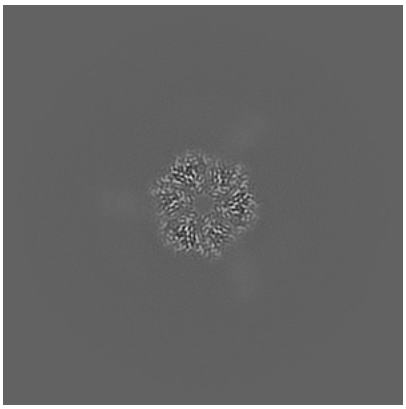
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 185

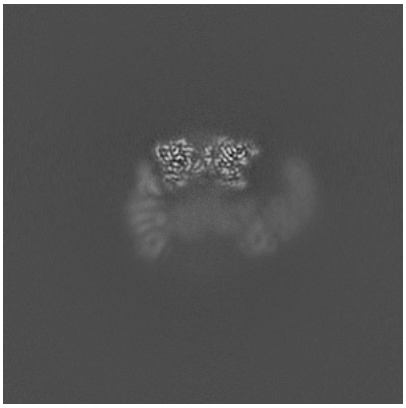


Y Index: 227

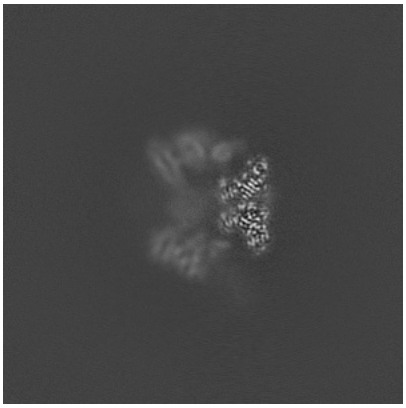


Z Index: 250

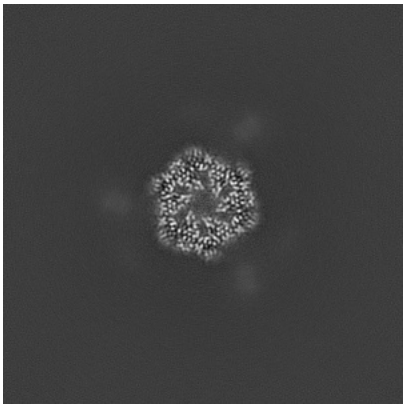
6.3.2 Raw map



X Index: 185



Y Index: 225

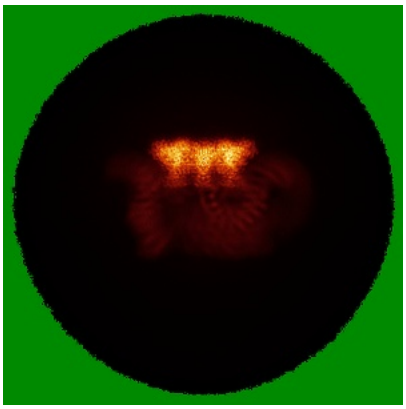


Z Index: 255

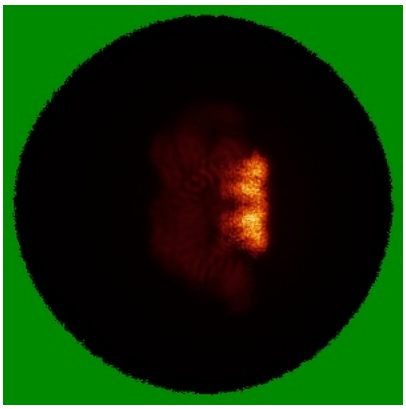
The images above show the largest variance slices of the map in three orthogonal directions.

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

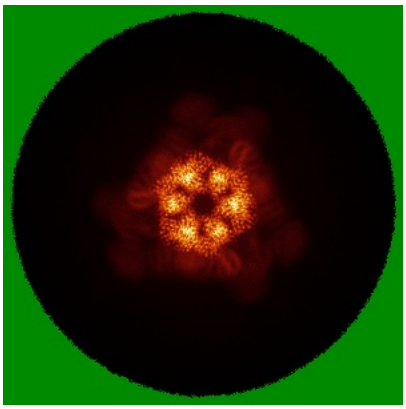
6.4.1 Primary map



X

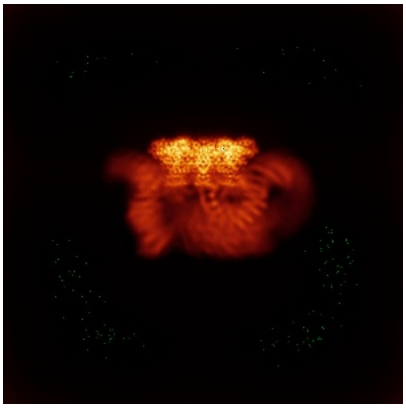


Y

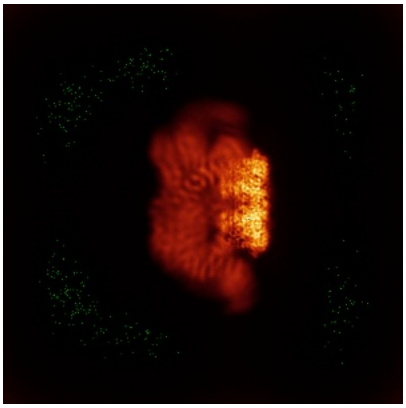


Z

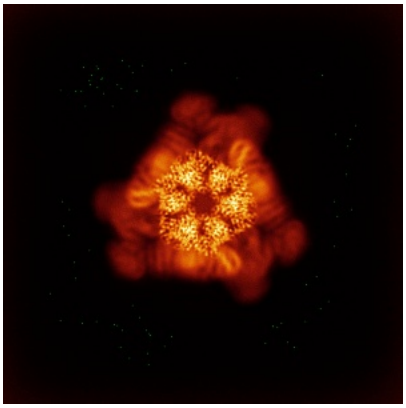
6.4.2 Raw map



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

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.18. 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

X Y Z

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.

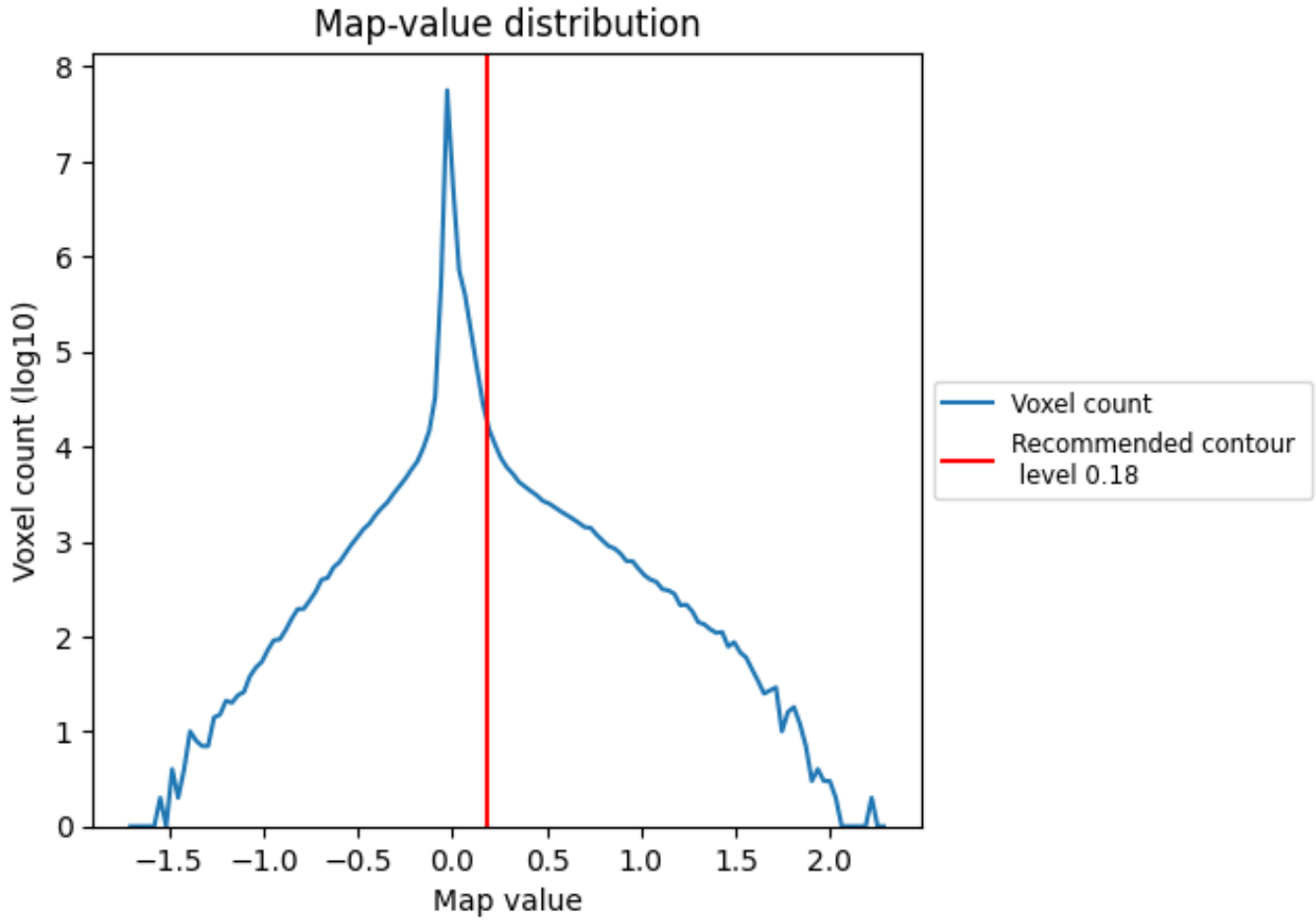
6.6 Mask visualisation (i)

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

7 Map analysis

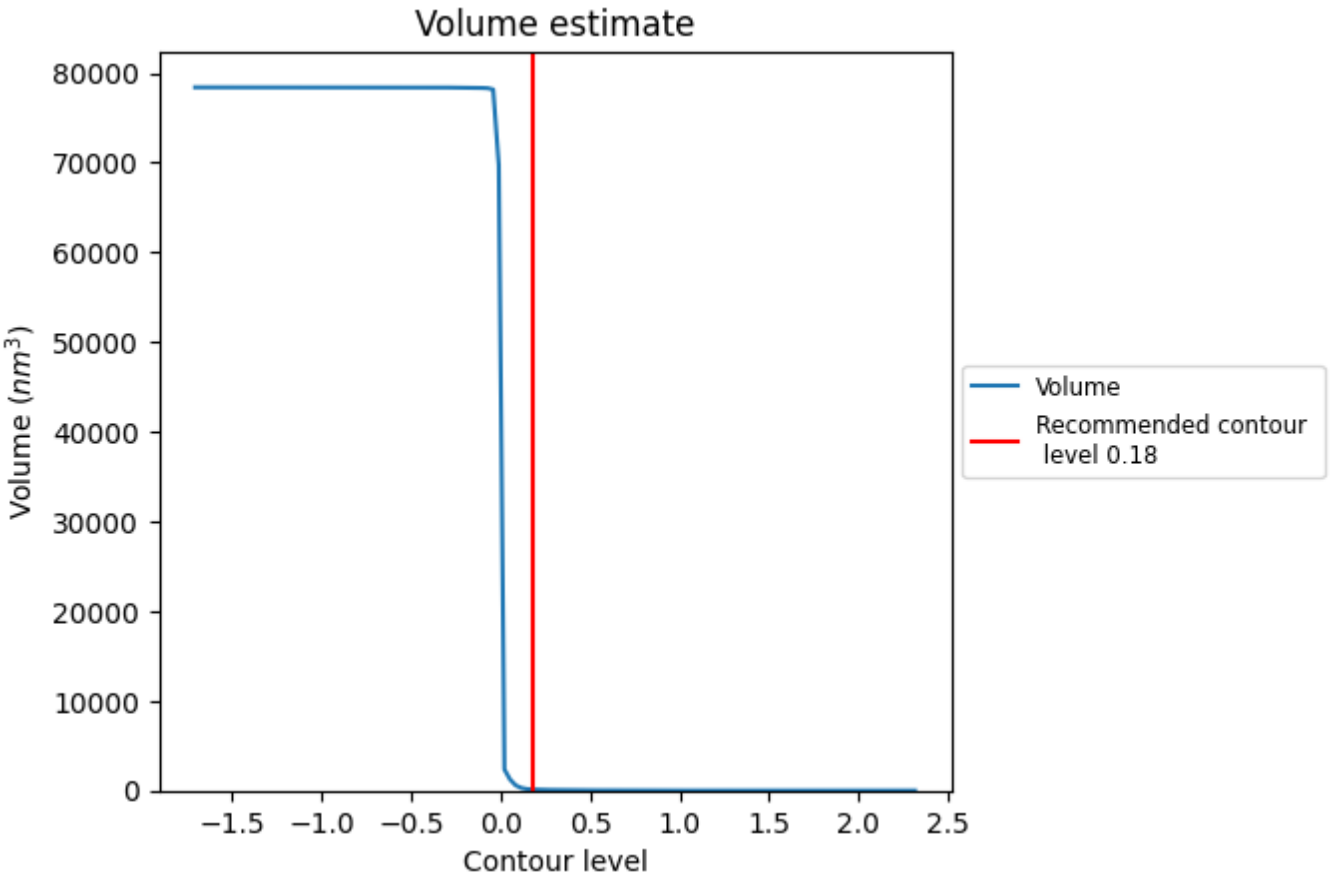
This section contains the results of statistical analysis of the map.

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.

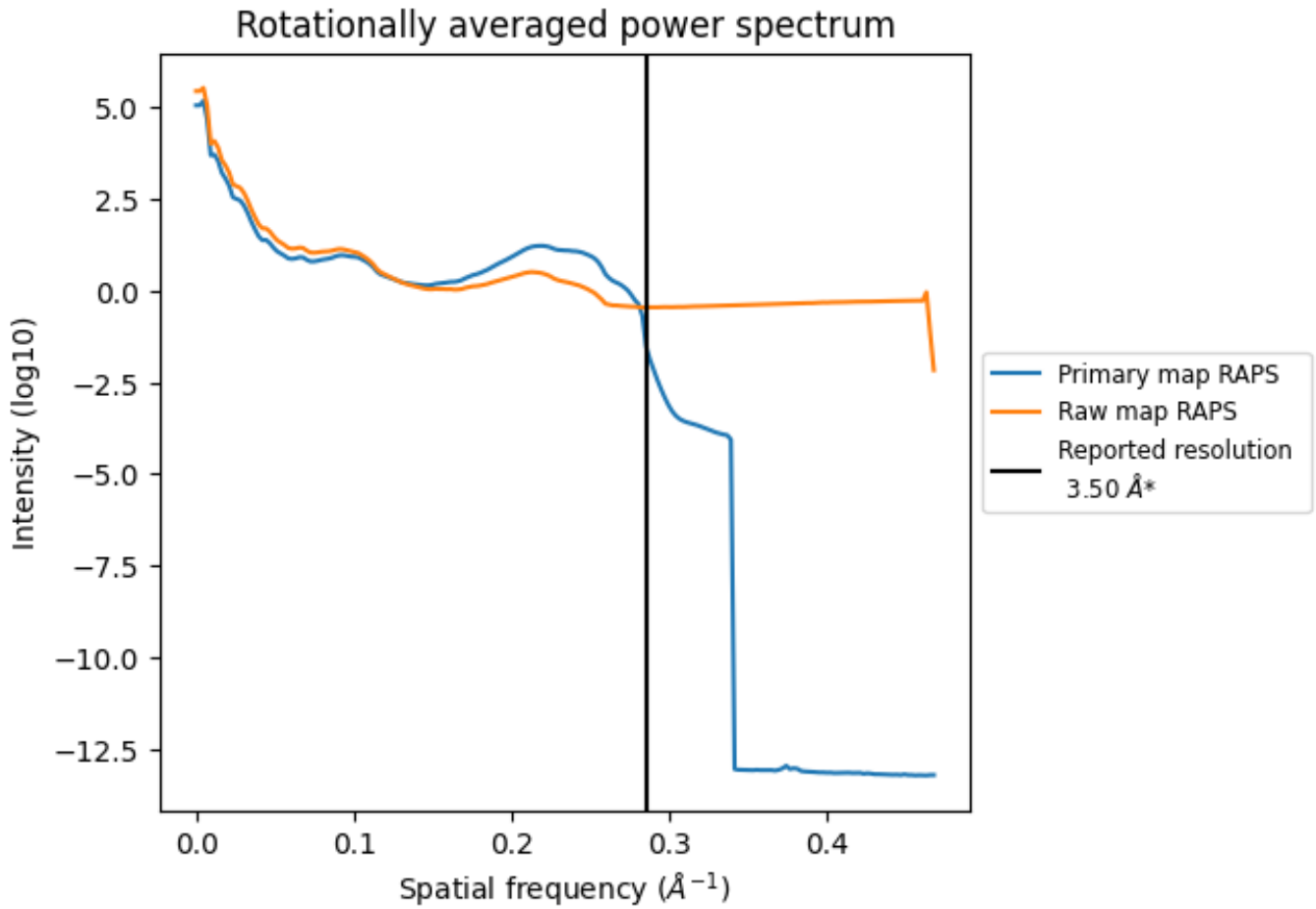
7.2 Volume estimate (i)



The volume at the recommended contour level is 119 nm^3; this corresponds to an approximate mass of 107 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)

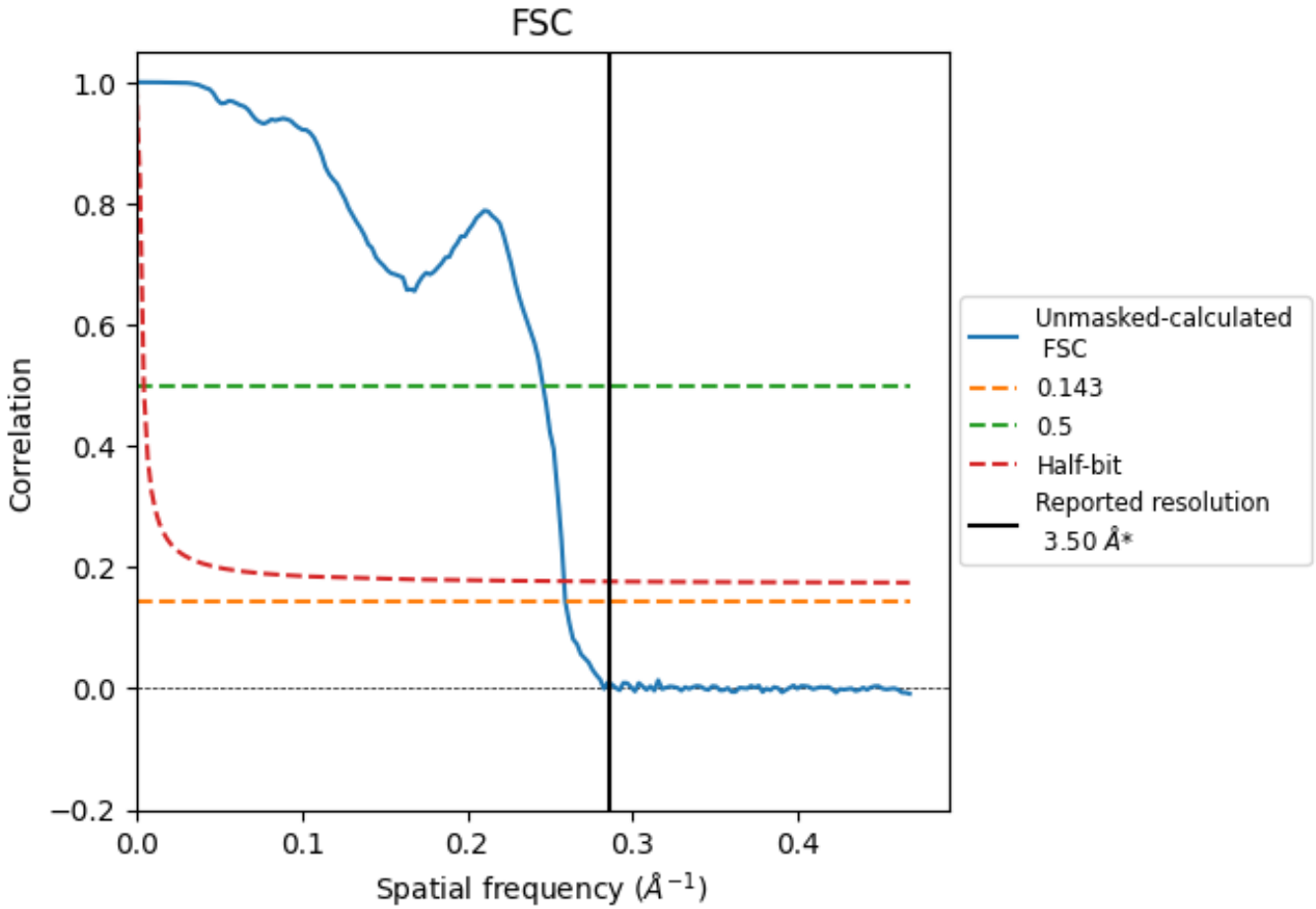


*Reported resolution corresponds to spatial frequency of 0.286 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.286 Å^{-1}

8.2 Resolution estimates (i)

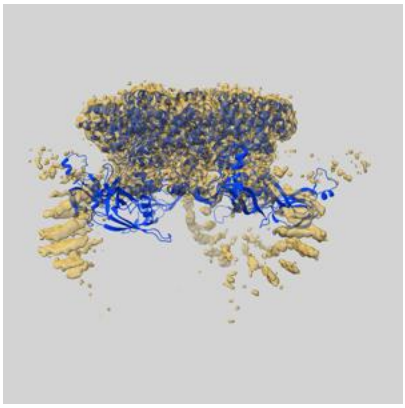
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.86	4.07	3.87

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.86 differs from the reported value 3.5 by more than 10 %

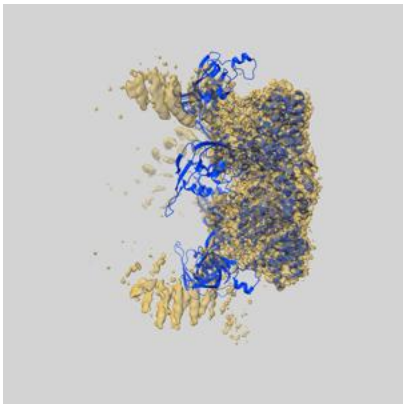
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-66033 and PDB model 9WJX. Per-residue inclusion information can be found in section 3 on page 7.

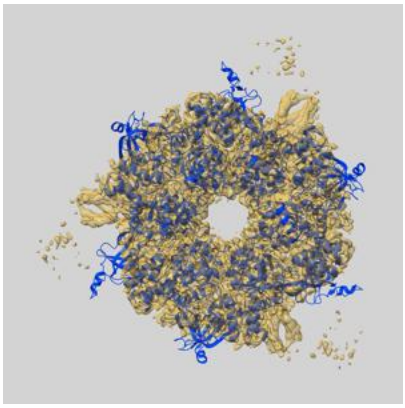
9.1 Map-model overlay



X



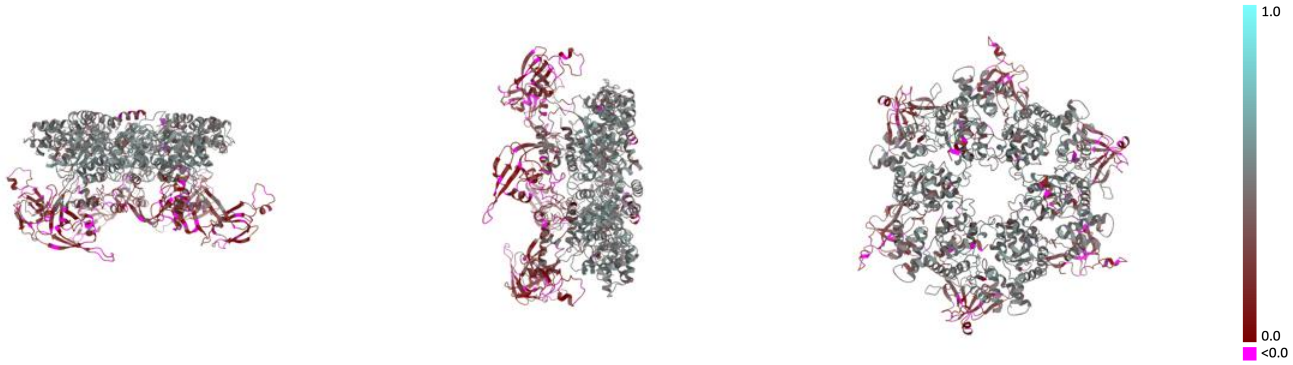
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.18 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.

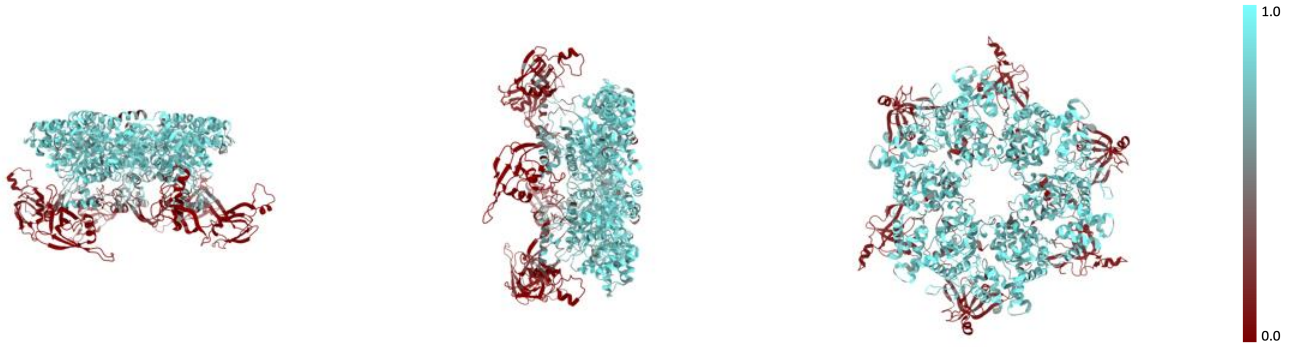
9.2 Q-score mapped to coordinate model (i)



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.

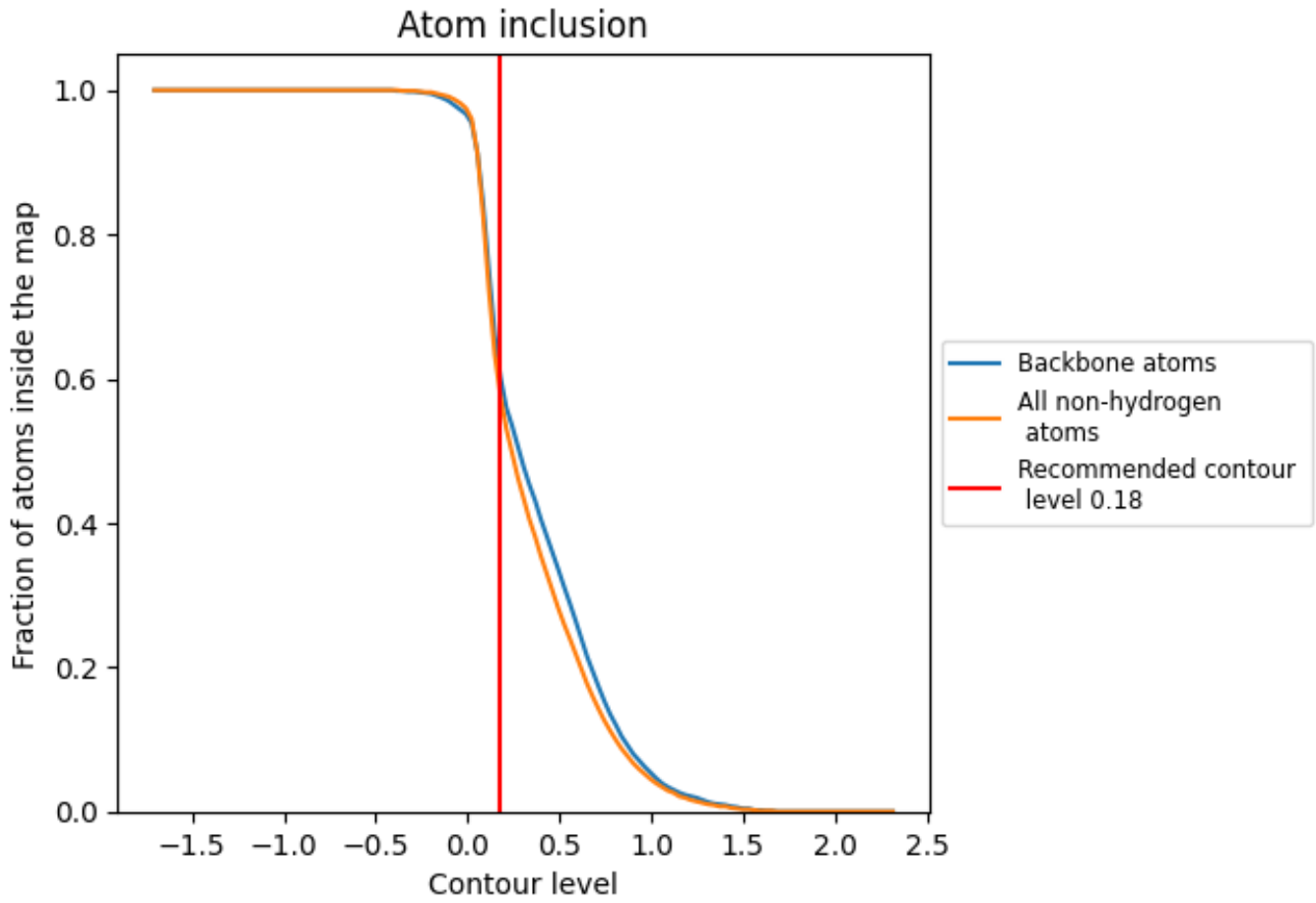
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.18).

9.4 Atom inclusion (i)



At the recommended contour level, 60% of all backbone atoms, 57% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5740	0.3590
D	0.5860	0.3650
E	0.5620	0.3530
F	0.5900	0.3650
G	0.5630	0.3540
H	0.5770	0.3640
I	0.5650	0.3530