



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:40 AM UTC

PDB ID : 6EYC / pdb_00006eyc
EMDB ID : EMD-6338
Title : Re-refinement of the MCM2-7 double hexamer using ISOLDE
Authors : Croll, T.I.
Deposited on : 2017-11-11
Resolution : 3.80 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

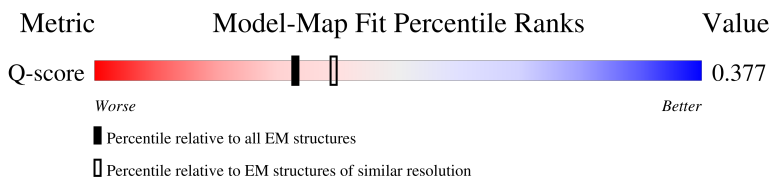
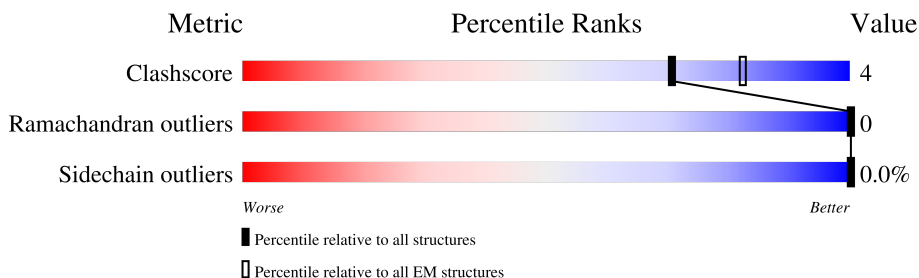
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	2	868	20% 62% 7% 31%
2	3	971	13% 53% 9% 38%
3	4	933	13% 64% 5% 31%
4	5	775	20% 75% 7% 18%

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Mol	Chain	Length	Quality of chain
5	6	1017	18% 57% 39%
6	7	845	13% 73% 8% 18%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 60365 atoms, of which 30301 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 DNA replication licensing factor MCM2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	2	603	Total	C	H	N	O	S	0	0
			9619	3007	4849	850	894	19		

- Molecule 2 is a protein called DNA replication licensing factor MCM3.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	3	605	Total	C	H	N	O	S	0	0
			9561	2990	4816	846	896	13		

- Molecule 3 is a protein called DNA replication licensing factor MCM4.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	4	641	Total	C	H	N	O	S	0	0
			10296	3210	5186	883	989	28		

- Molecule 4 is a protein called Minichromosome maintenance protein 5.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	5	633	Total	C	H	N	O	S	0	0
			9990	3116	5024	855	971	24		

- Molecule 5 is a protein called DNA replication licensing factor MCM6.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	6	616	Total	C	H	N	O	S	0	0
			9794	3072	4920	853	924	25		

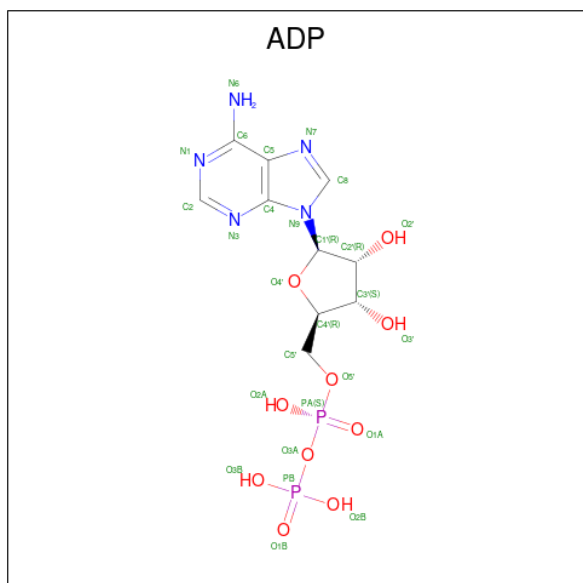
- Molecule 6 is a protein called DNA replication licensing factor MCM7.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	7	689	Total	C	H	N	O	S	0	0
			10938	3419	5506	940	1042	31		

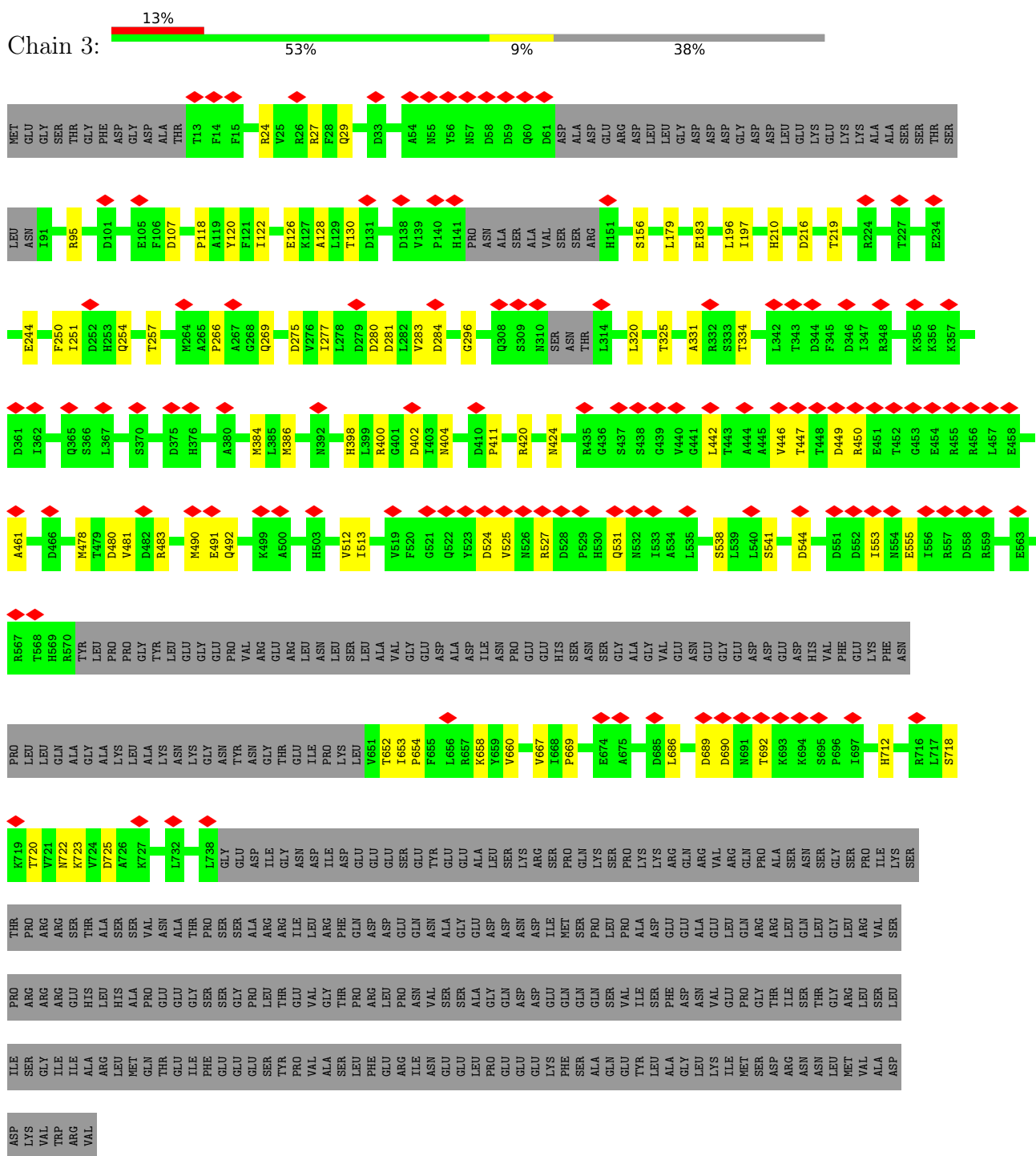
- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
7	2	1	Total	Zn	0
			1	1	
7	4	1	Total	Zn	0
			1	1	
7	5	1	Total	Zn	0
			1	1	
7	6	1	Total	Zn	0
			1	1	
7	7	1	Total	Zn	0
			1	1	

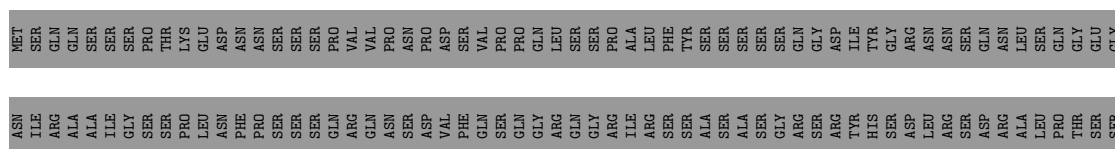
- Molecule 8 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



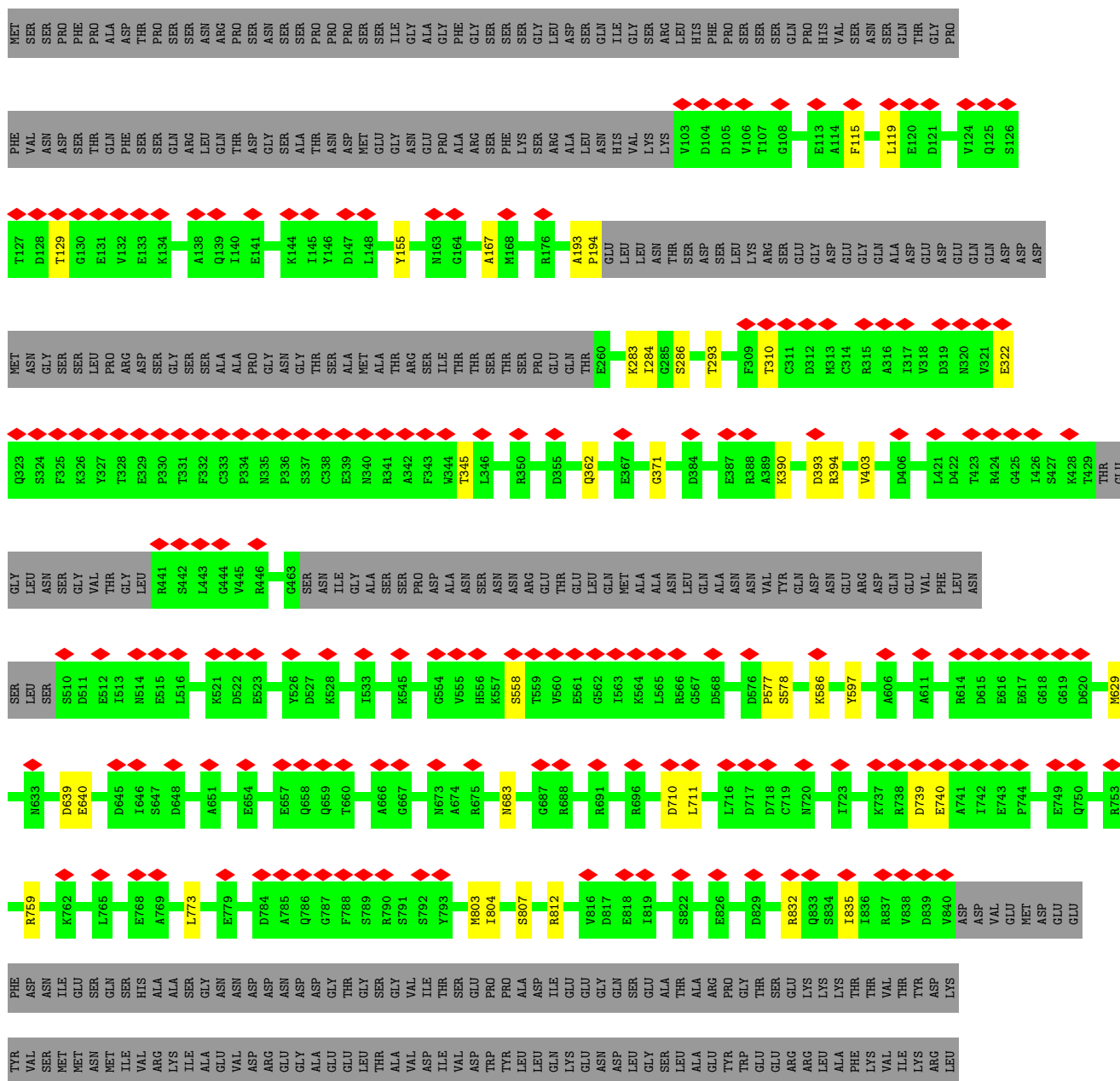
Mol	Chain	Residues	Atoms					AltConf
8	2	1	Total	C	N	O	P	0
			27	10	5	10	2	
8	3	1	Total	C	N	O	P	0
			27	10	5	10	2	
8	3	1	Total	C	N	O	P	0
			27	10	5	10	2	
8	4	1	Total	C	N	O	P	0
			27	10	5	10	2	
8	5	1	Total	C	N	O	P	0
			27	10	5	10	2	
8	6	1	Total	C	N	O	P	0
			27	10	5	10	2	



• Molecule 3: DNA replication licensing factor MCM4

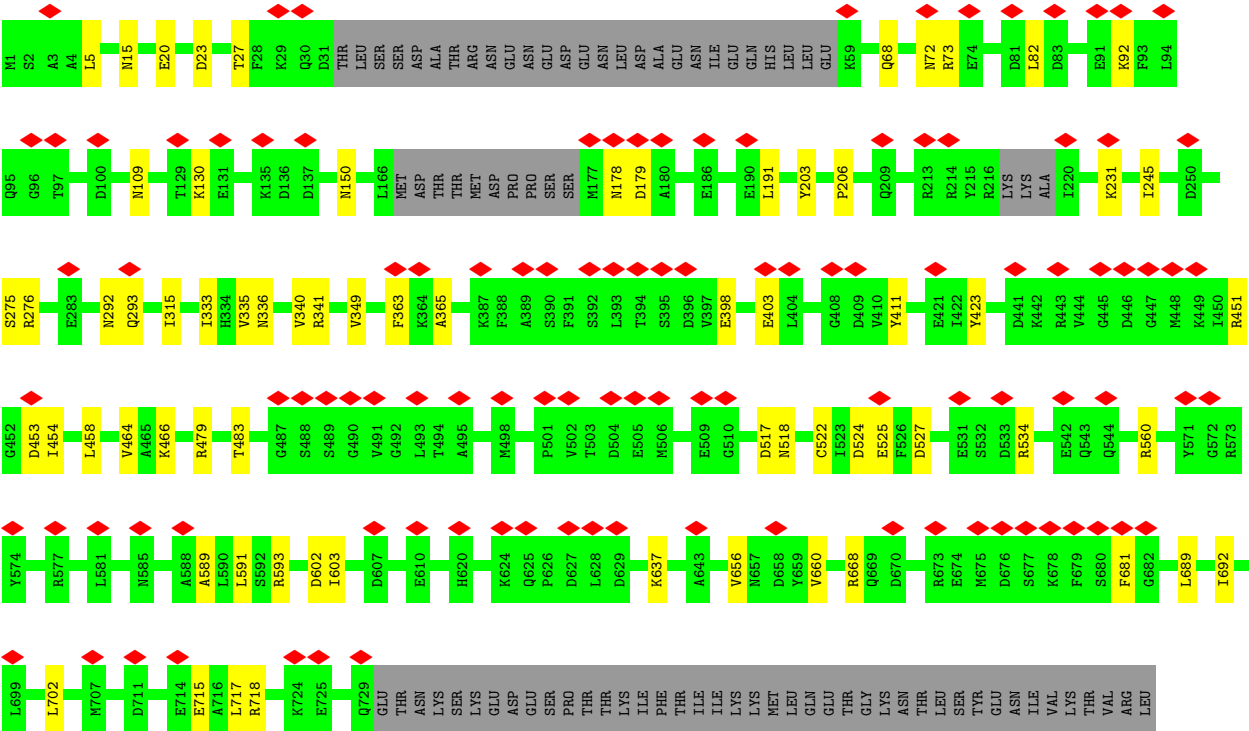


- Molecule 5: DNA replication licensing factor MCM6



VAL	LYS	ASP	ARG	ILE	LEU	MET	GLU	ILE	HIS	GLY	THR	ARG	HIS	ASN	LEU	ARG	ASP	LEU	GLU	ASN	ASN	GLU	GLU	ASN	GLU	ASN	GLU	VAL	GLN	ASP	GLN	LEU	GLU	PRO	GLN	ASP	SER	SER
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● Molecule 6: DNA replication licensing factor MCM7



ARG	GLY	PHE	THR	MET	LEU	GLN	LEU	SER	ASN	CYS	ILE	GLN	GLU	TYR	TYR	LEU	ASN	VAL	TRP	HIS	LEU	ILE	ASN	GLU	GLY	ASN	THR	LEU	LYS	PHE	VAL	ASP	GLY	THR	MET	ASP	THR	GLN	ASP	SER	LEU	VAL	SER	THR	PRO	LYS	LEU	SER	ALA	PRO	GLU	ASN	THR	THR	VAL	LYS	THR	SER	ALA
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ASN	VAL	SER	GLN	ASP	SER	ASP	ASP	GLN	ASP	ALA
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	85365	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	22	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	32.028	Depositor
Minimum map value	-16.136	Depositor
Average map value	-0.058	Depositor
Map value standard deviation	0.697	Depositor
Recommended contour level	5	Depositor
Map size ($\text{\AA}$)	396.00003, 396.00003, 396.00003	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.32, 1.32, 1.32	Depositor

5 Model quality

5.1 Standard geometry

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

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	2	0.28	0/4852	0.67	0/6551
2	3	0.31	0/4827	0.71	2/6545 (0.0%)
3	4	0.29	0/5185	0.72	3/7009 (0.0%)
4	5	0.29	0/5037	0.65	2/6809 (0.0%)
5	6	0.29	0/4954	0.68	0/6683
6	7	0.30	0/5514	0.69	0/7450
All	All	0.29	0/30369	0.69	7/41047 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	4	0	1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3	652	THR	CA-C-N	7.69	127.81	120.43
2	3	652	THR	C-N-CA	7.69	127.81	120.43
3	4	468	LYS	CB-CA-C	6.07	123.49	110.21
4	5	266	PRO	CB-CA-C	5.96	121.40	111.56
4	5	266	PRO	N-CA-C	5.83	124.48	112.47

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	4	552	PHE	Peptide

5.2 Too-close contacts

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	2	4770	4849	4834	38	0
2	3	4745	4816	4793	53	0
3	4	5110	5186	5171	33	0
4	5	4966	5024	5011	36	0
5	6	4874	4920	4909	25	0
6	7	5432	5506	5496	45	0
7	2	1	0	0	0	0
7	4	1	0	0	0	0
7	5	1	0	0	0	0
7	6	1	0	0	0	0
7	7	1	0	0	0	0
8	2	27	0	12	1	0
8	3	54	0	24	4	0
8	4	27	0	12	4	0
8	5	27	0	12	1	0
8	6	27	0	12	2	0
All	All	30064	30301	30286	213	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 4.

The worst 5 of 213 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)
1:2:353:GLN:NE2	1:2:357:GLU:O	2.15	0.79
1:2:588:GLU:OE2	4:5:273:ASN:ND2	2.16	0.78
4:5:409:ASP:O	4:5:658:ARG:NH1	2.18	0.77
2:3:404:ASN:ND2	2:3:490:MET:SD	2.57	0.77
2:3:284:ASP:OD2	6:7:231:LYS:NZ	2.18	0.76

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	597/868 (69%)	552 (92%)	45 (8%)	0	100	100
2	3	595/971 (61%)	559 (94%)	36 (6%)	0	100	100
3	4	635/933 (68%)	591 (93%)	44 (7%)	0	100	100
4	5	621/775 (80%)	576 (93%)	45 (7%)	0	100	100
5	6	608/1017 (60%)	571 (94%)	37 (6%)	0	100	100
6	7	681/845 (81%)	645 (95%)	36 (5%)	0	100	100
All	All	3737/5409 (69%)	3494 (94%)	243 (6%)	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	2	528/770 (69%)	528 (100%)	0	100	100
2	3	523/835 (63%)	523 (100%)	0	100	100
3	4	582/848 (69%)	581 (100%)	1 (0%)	87	87
4	5	566/688 (82%)	566 (100%)	0	100	100
5	6	537/886 (61%)	537 (100%)	0	100	100
6	7	609/753 (81%)	609 (100%)	0	100	100
All	All	3345/4780 (70%)	3344 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	4	284	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
4	5	581	ASN
6	7	554	ASN
4	5	585	ASN
5	6	700	ASN
2	3	569	HIS

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 [i](#)

Of 11 ligands modelled in this entry, 5 are monoatomic - leaving 6 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	$\# Z > 2$
8	ADP	3	2002	-	28,29,29	1.39	4 (14%)	43,45,45	1.91	8 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	ADP	3	2001	-	28,29,29	1.43	5 (17%)	43,45,45	1.83	10 (23%)
8	ADP	4	1002	-	28,29,29	1.36	4 (14%)	43,45,45	1.92	11 (25%)
8	ADP	6	1102	-	28,29,29	1.44	5 (17%)	43,45,45	1.96	7 (16%)
8	ADP	2	902	-	28,29,29	1.41	4 (14%)	43,45,45	1.84	10 (23%)
8	ADP	5	802	-	28,29,29	1.37	4 (14%)	43,45,45	1.86	8 (18%)

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
8	ADP	3	2002	-	-	4/16/32/32	0/3/3/3
8	ADP	3	2001	-	-	3/16/32/32	0/3/3/3
8	ADP	4	1002	-	-	2/16/32/32	0/3/3/3
8	ADP	6	1102	-	-	5/16/32/32	0/3/3/3
8	ADP	2	902	-	-	4/16/32/32	0/3/3/3
8	ADP	5	802	-	-	3/16/32/32	0/3/3/3

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	6	1102	ADP	C5-C4	4.86	1.47	1.39
8	3	2002	ADP	C5-C4	4.68	1.47	1.39
8	2	902	ADP	C5-C4	4.67	1.47	1.39
8	3	2001	ADP	C5-C4	4.61	1.47	1.39
8	4	1002	ADP	C5-C4	4.57	1.47	1.39

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	6	1102	ADP	C5-C4-N3	-6.83	117.31	126.72
8	3	2002	ADP	C5-C4-N3	-6.36	117.97	126.72
8	5	802	ADP	C5-C4-N3	-6.11	118.31	126.72
8	3	2001	ADP	C5-C4-N3	-6.01	118.44	126.72
8	4	1002	ADP	C5-C4-N3	-5.98	118.49	126.72

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

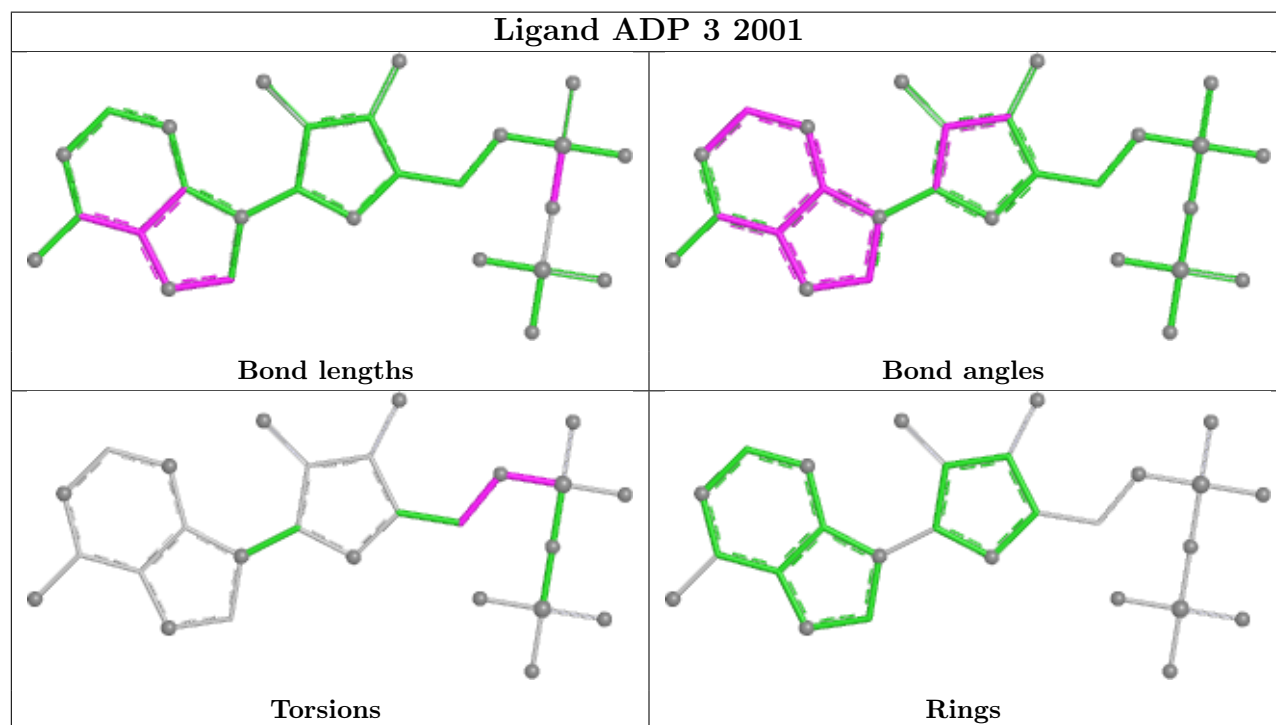
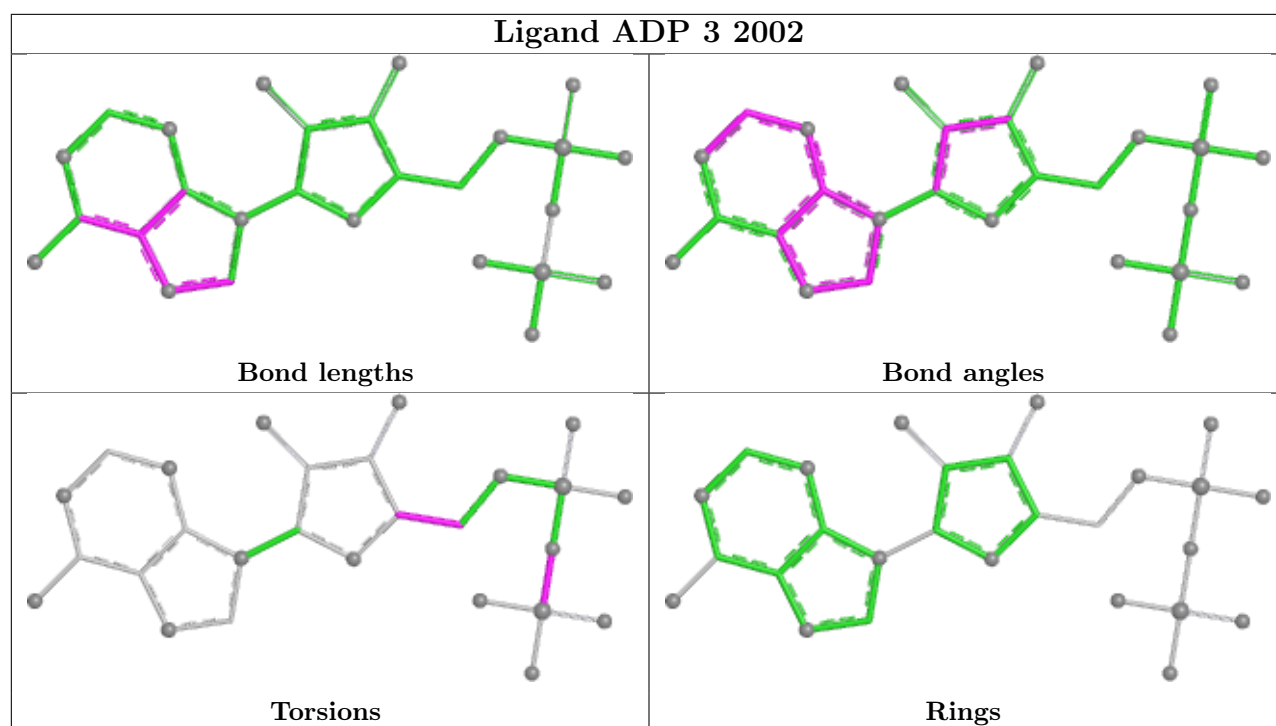
Mol	Chain	Res	Type	Atoms
8	2	902	ADP	C5'-O5'-PA-O2A
8	2	902	ADP	C5'-O5'-PA-O3A
8	3	2001	ADP	C5'-O5'-PA-O1A
8	3	2001	ADP	C5'-O5'-PA-O3A
8	3	2002	ADP	C3'-C4'-C5'-O5'

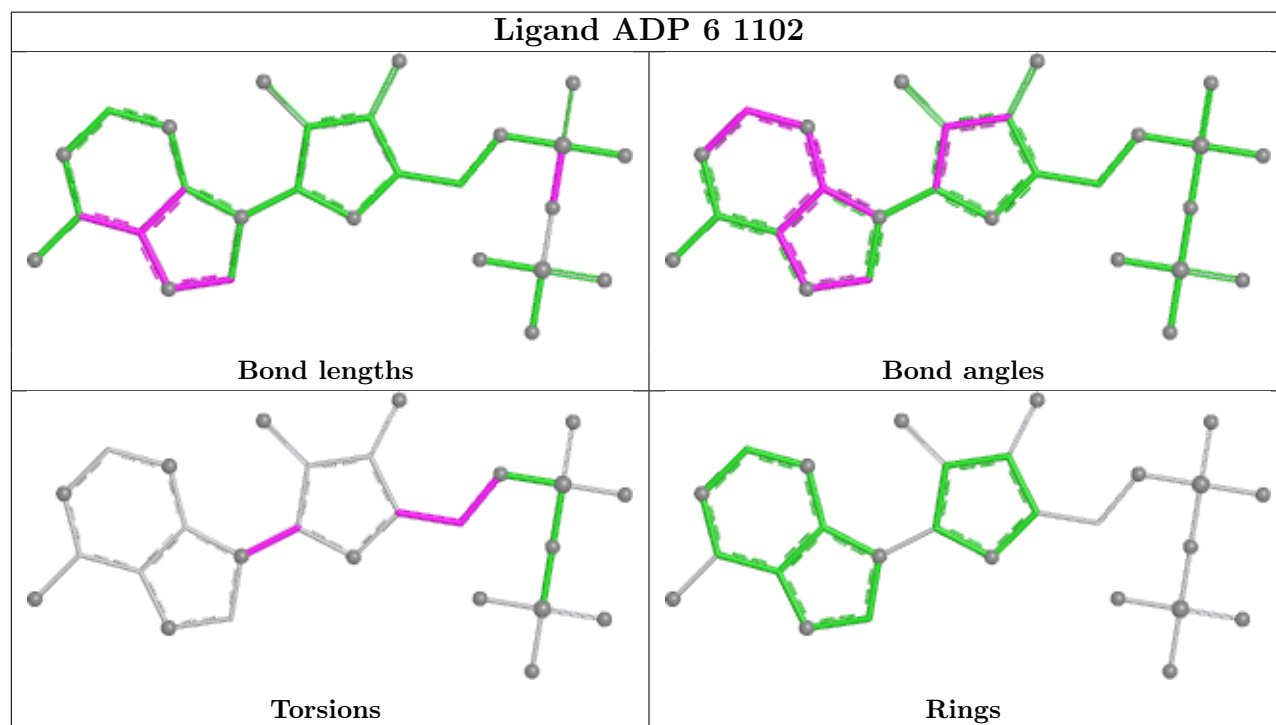
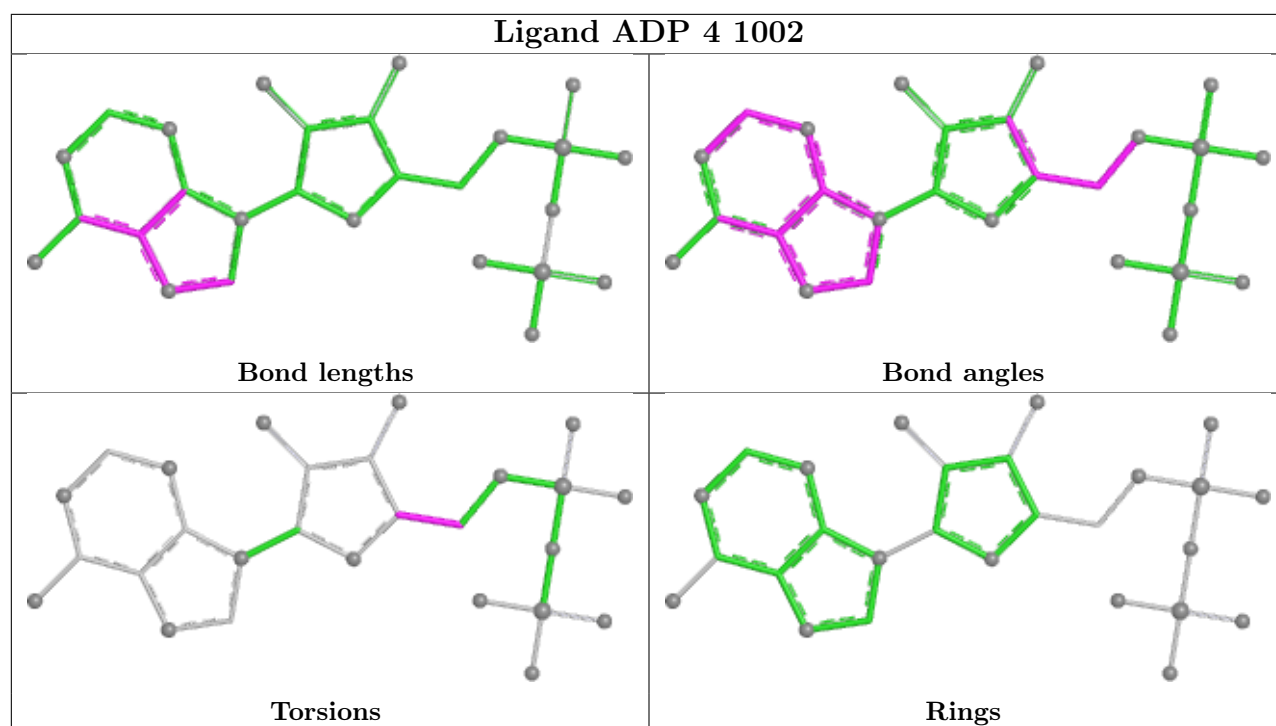
There are no ring outliers.

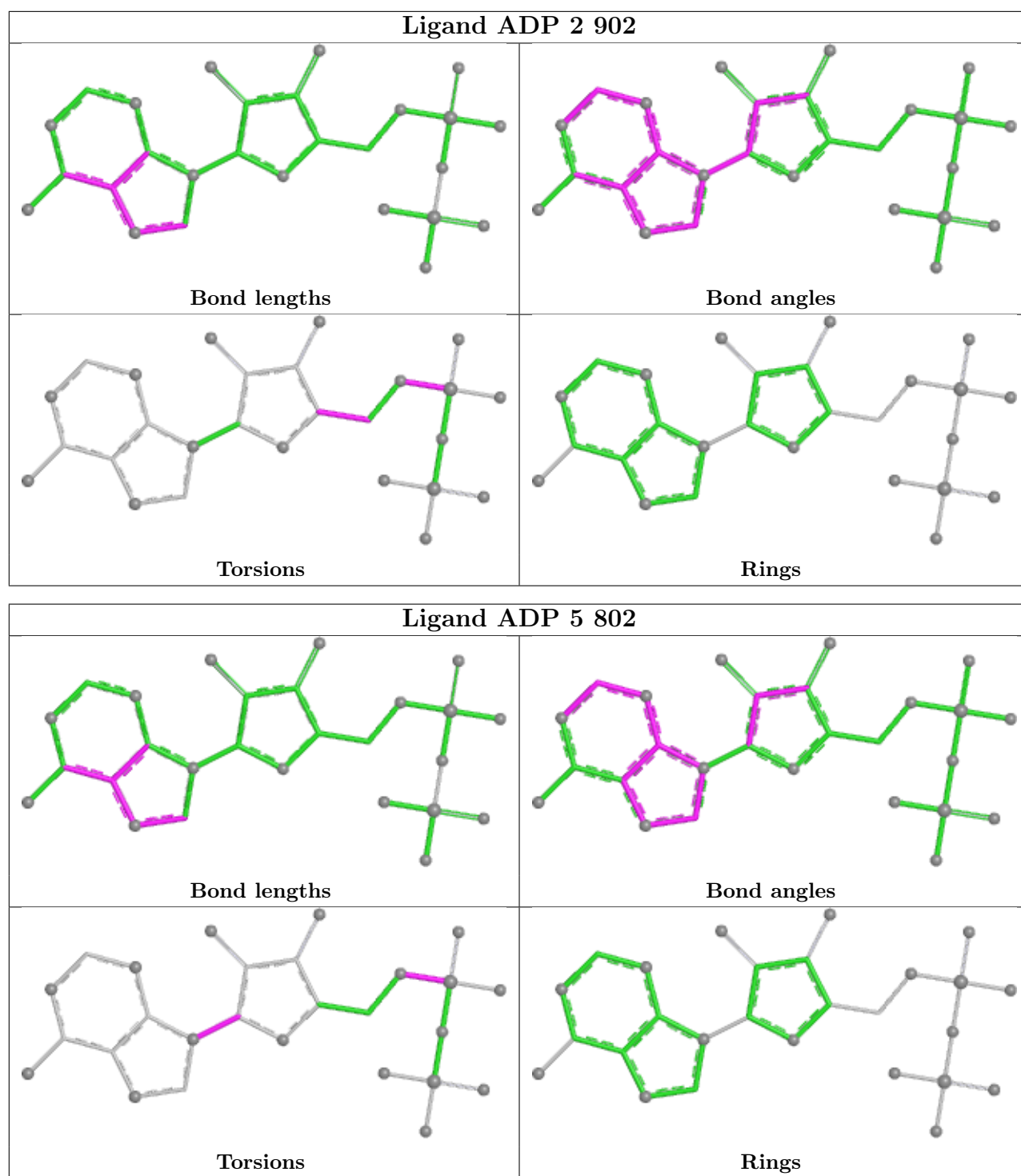
6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	3	2002	ADP	2	0
8	3	2001	ADP	2	0
8	4	1002	ADP	4	0
8	6	1102	ADP	2	0
8	2	902	ADP	1	0
8	5	802	ADP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

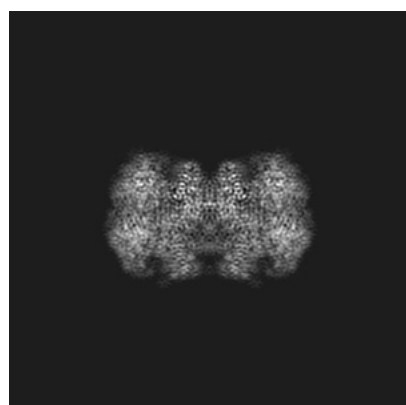
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6338. These allow visual inspection of the internal detail of the map and identification of artifacts.

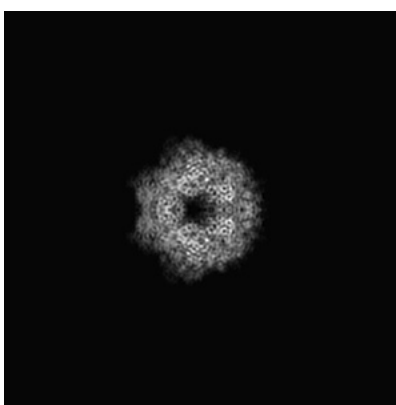
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

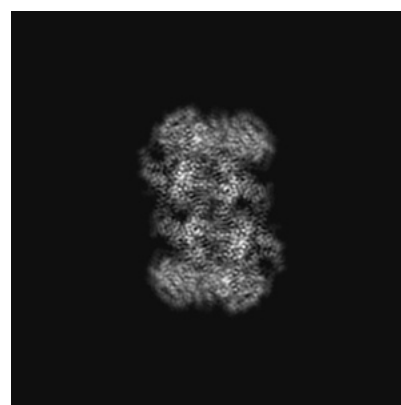
6.1.1 Primary map



X



Y



Z

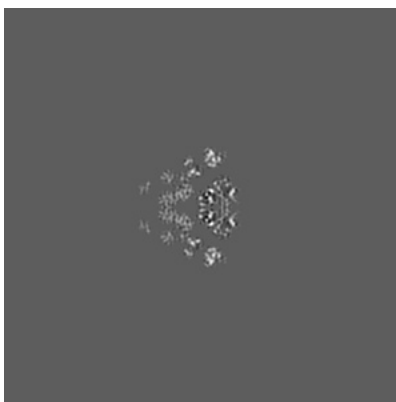
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

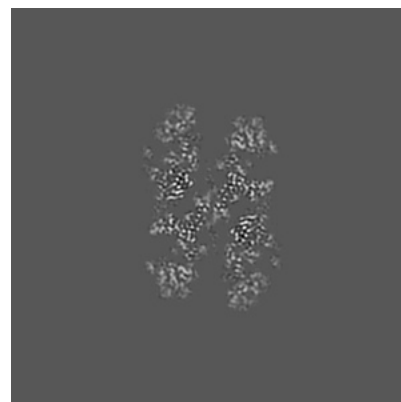
6.2.1 Primary map



X Index: 150



Y Index: 150

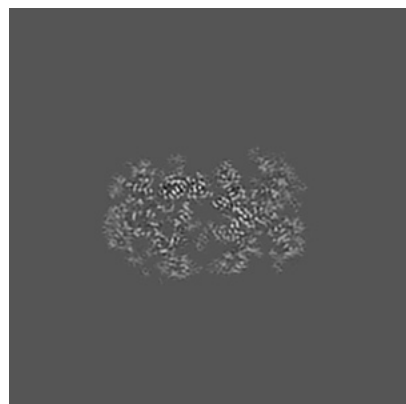


Z Index: 150

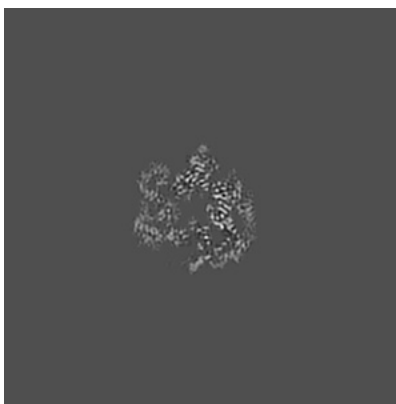
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

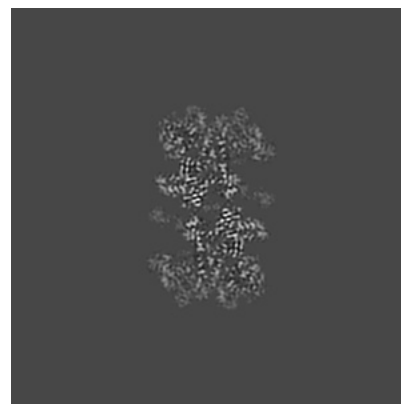
6.3.1 Primary map



X Index: 166



Y Index: 169

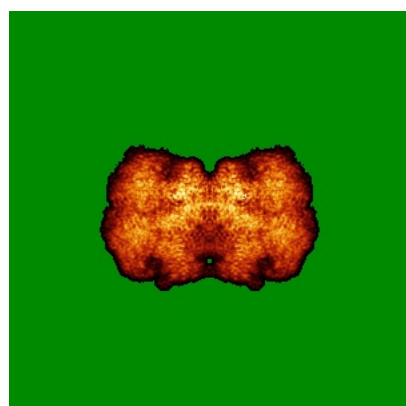


Z Index: 166

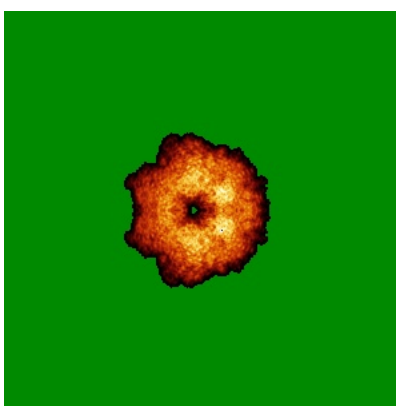
The images above show the largest variance slices of the map in three orthogonal directions.

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

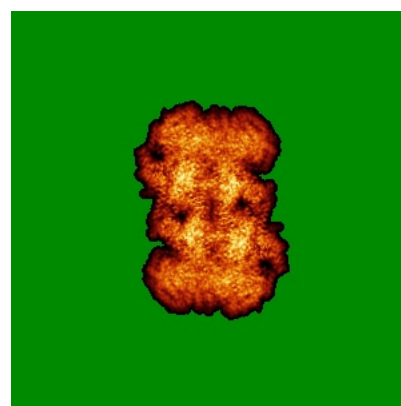
6.4.1 Primary map



X



Y

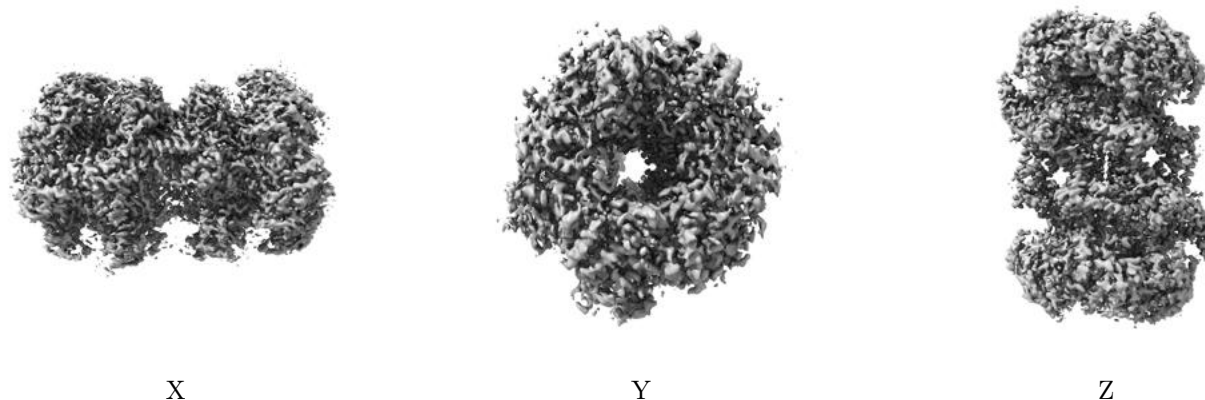


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

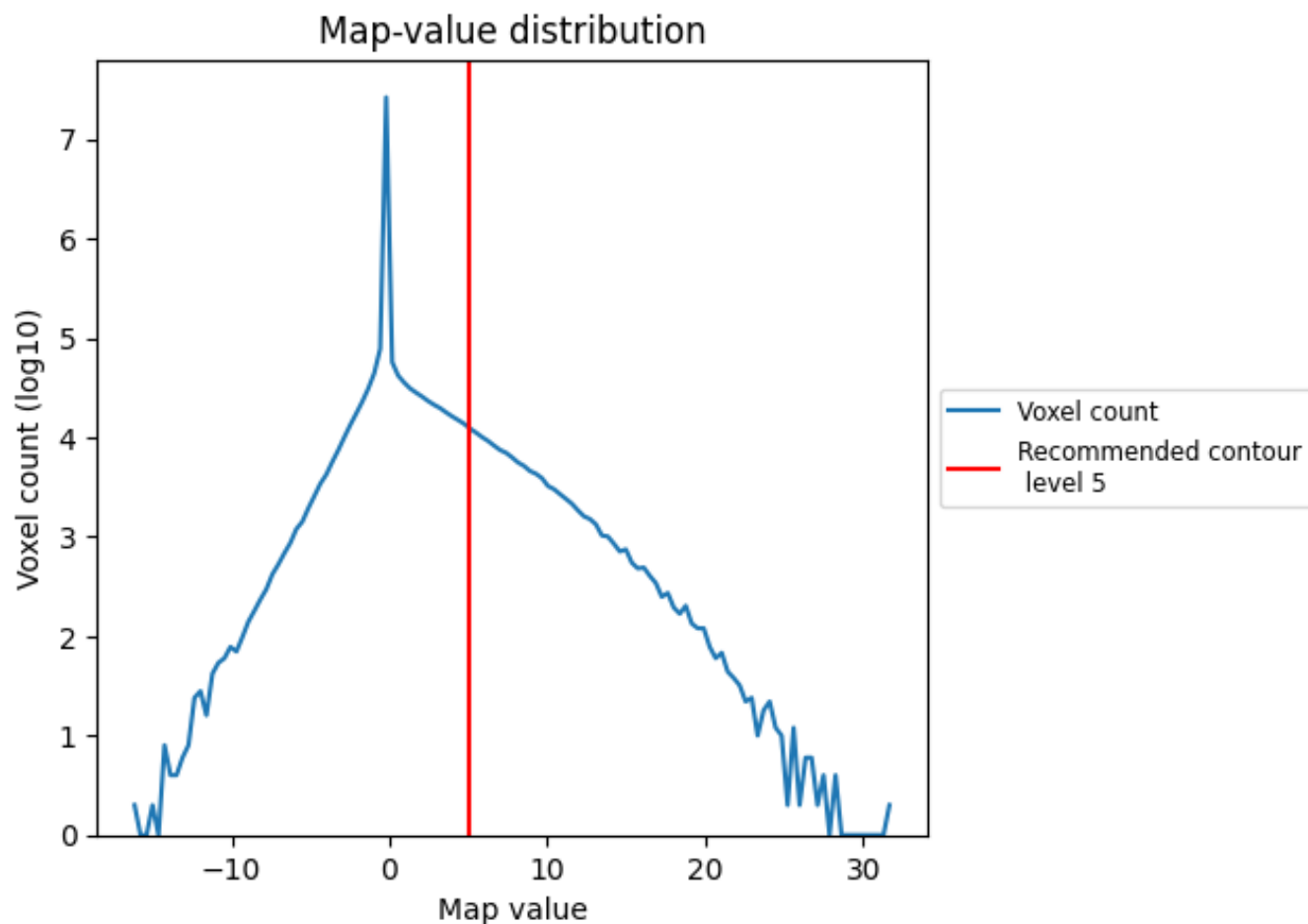
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

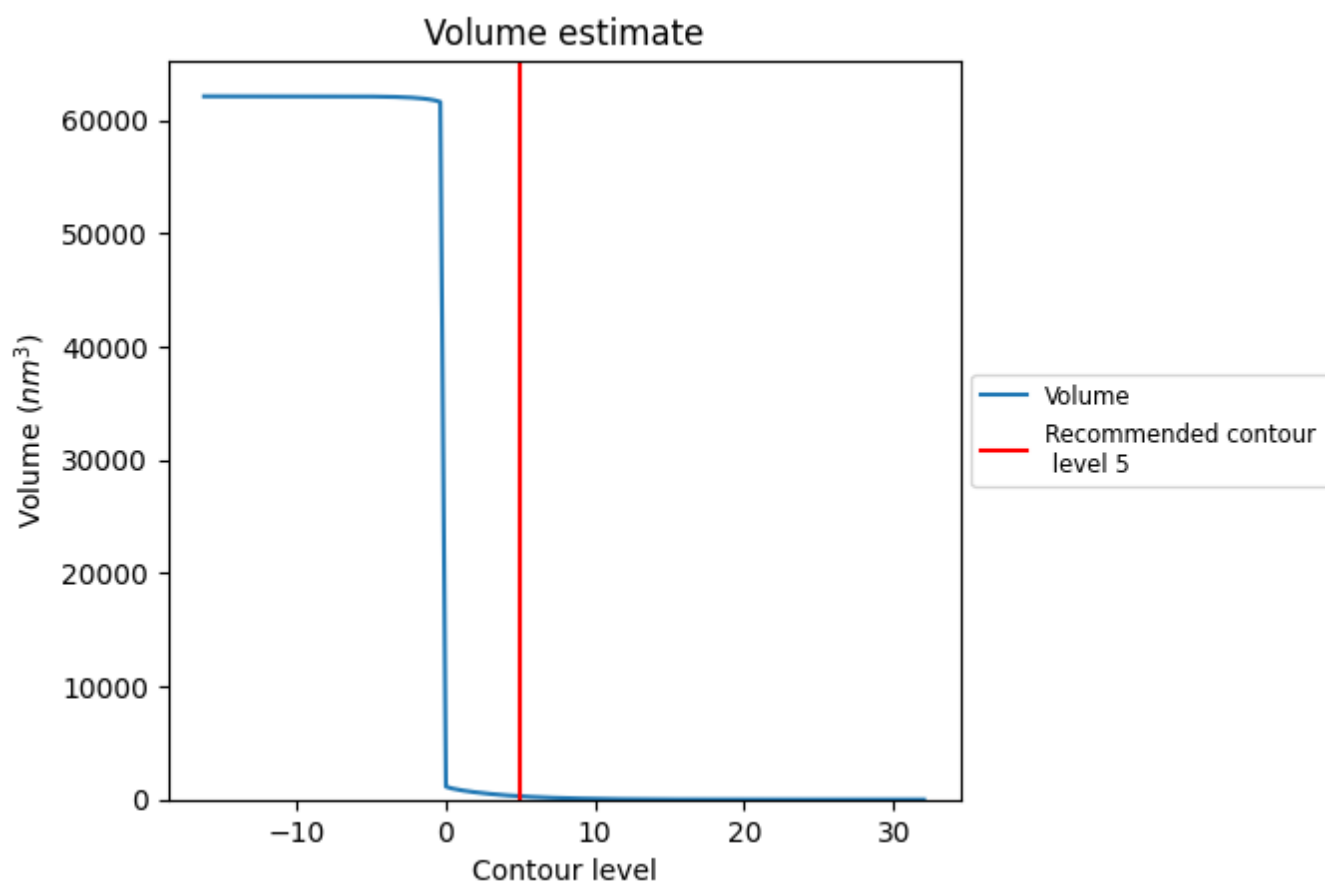
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

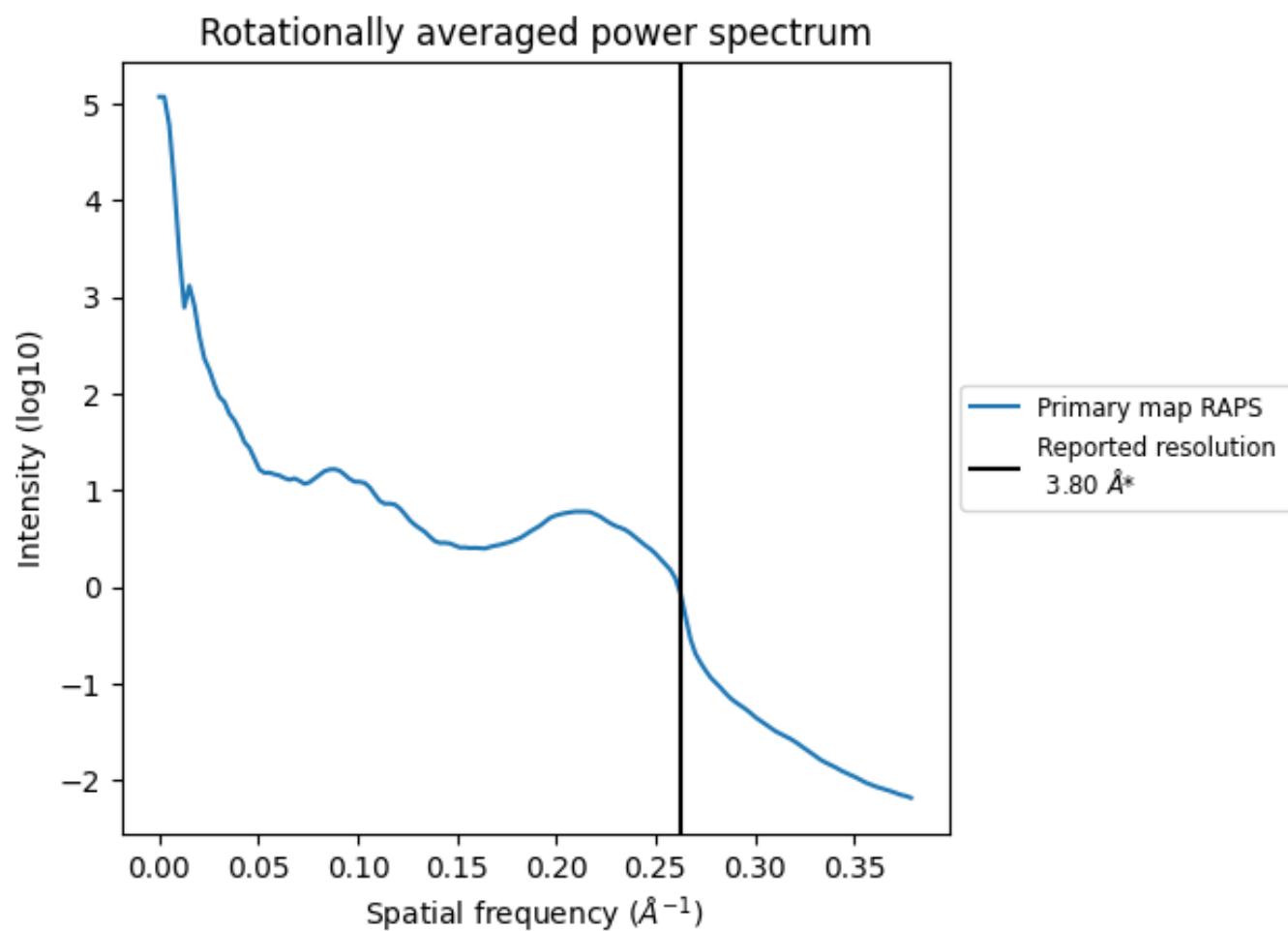
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 292 nm³; this corresponds to an approximate mass of 264 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 0.263 Å⁻¹

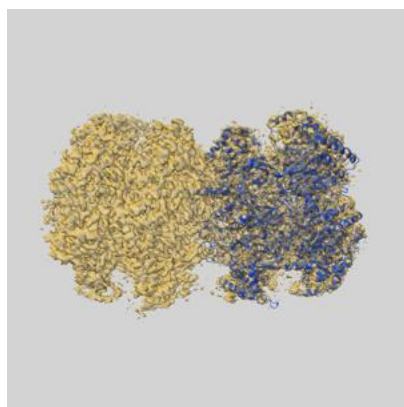
8 Fourier-Shell correlation

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

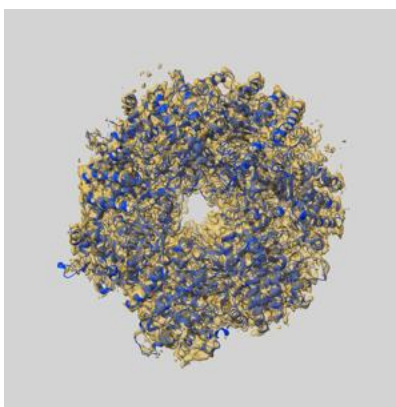
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6338 and PDB model 6EYC. Per-residue inclusion information can be found in section 3 on page 6.

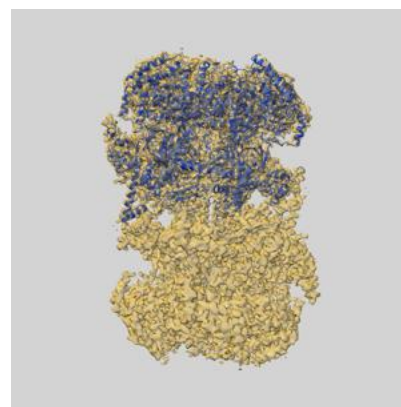
9.1 Map-model overlay [i](#)



X



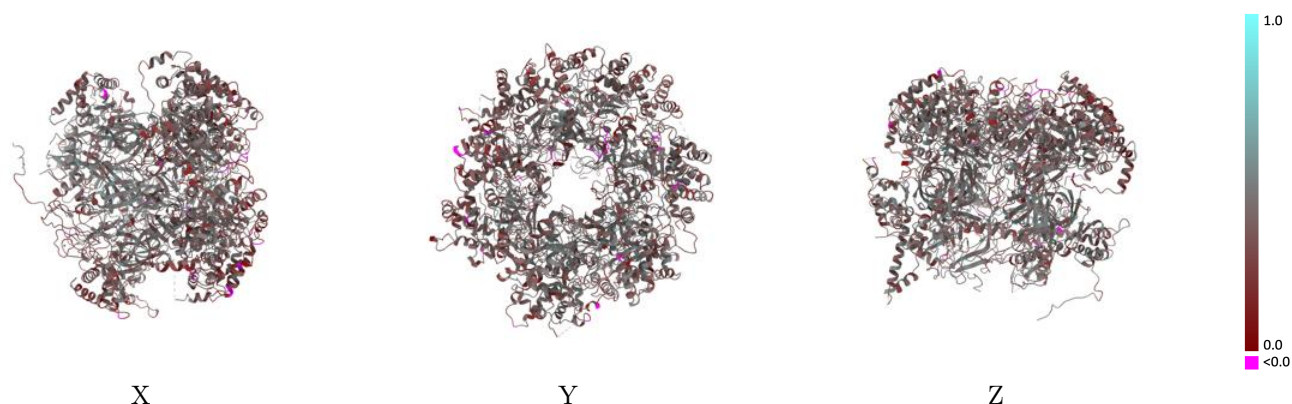
Y



Z

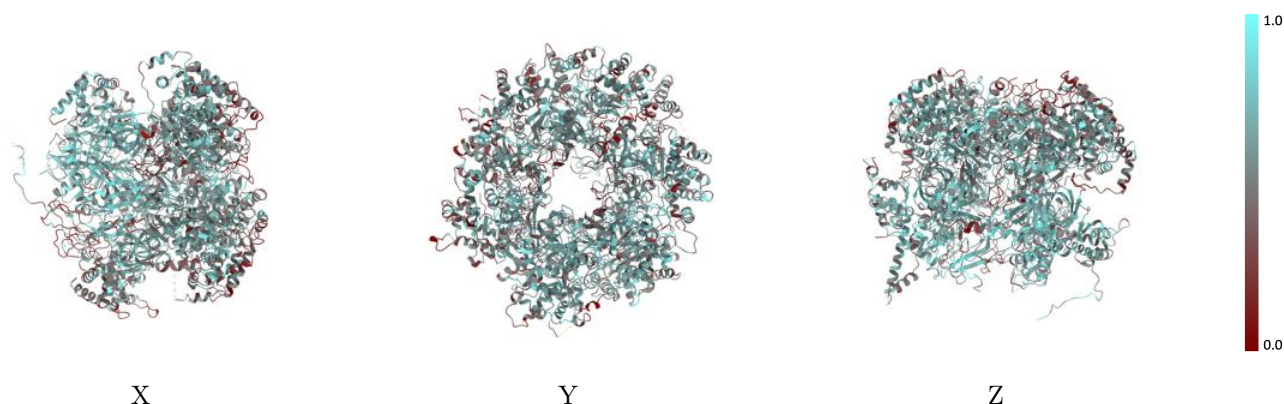
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



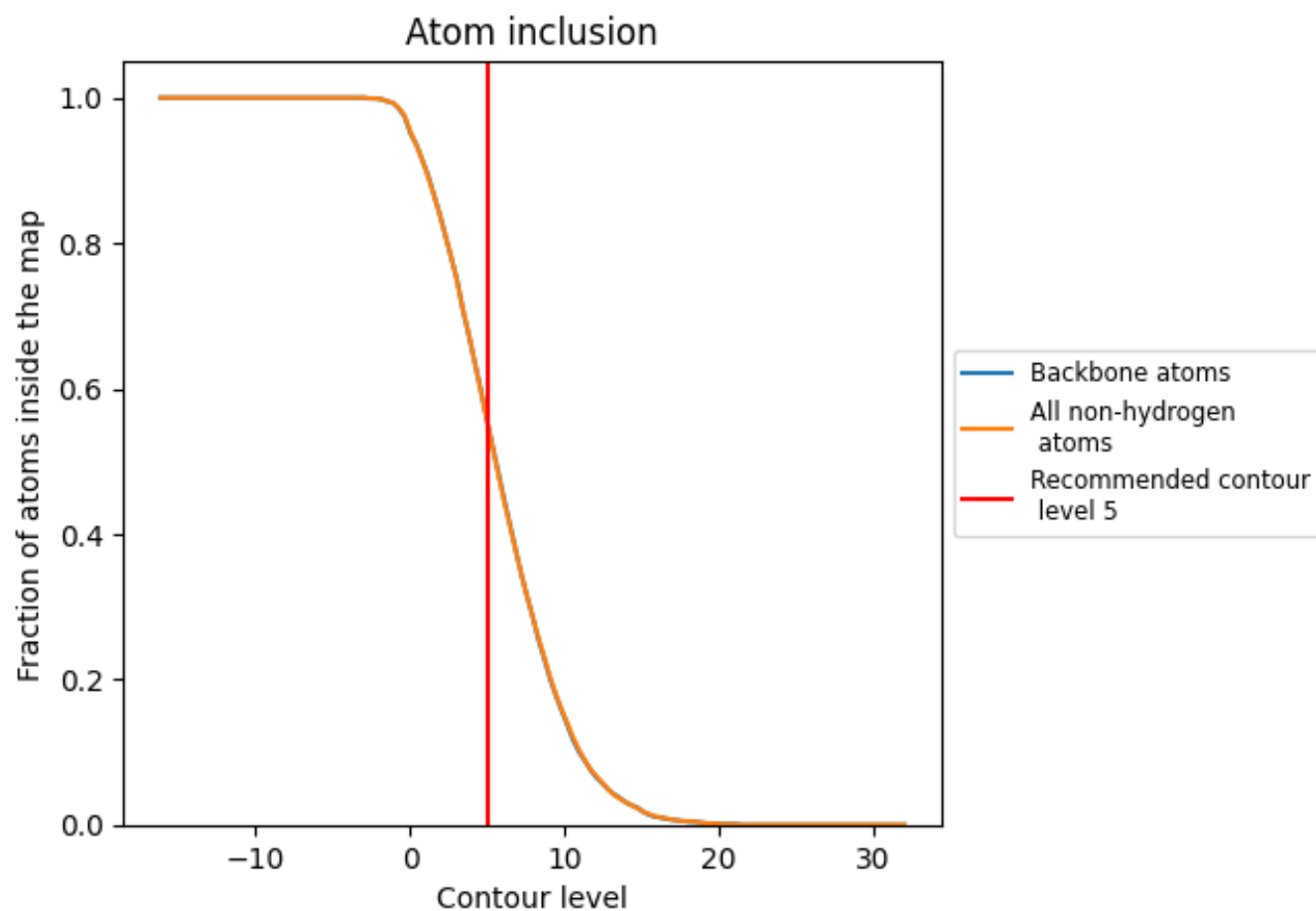
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 56% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5550	0.3770
2	0.5210	0.3540
3	0.5860	0.3890
4	0.5850	0.3920
5	0.5550	0.3790
6	0.4910	0.3470
7	0.6110	0.4000

1.0

0.0

<0.0