



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 06:36 PM UTC

PDB ID : 6SKO / pdb_00006sko
EMDB ID : EMD-10230
Title : Cryo-EM Structure of the Fork Protection Complex Bound to CMG at a Replication Fork - conformation 2 MCM CTD:ssDNA
Authors : Yeeles, J.; Baretic, D.; Jenkyn-Bedford, M.
Deposited on : 2019-08-16
Resolution : 3.40 Å(reported)
Based on initial model : 5U8S

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

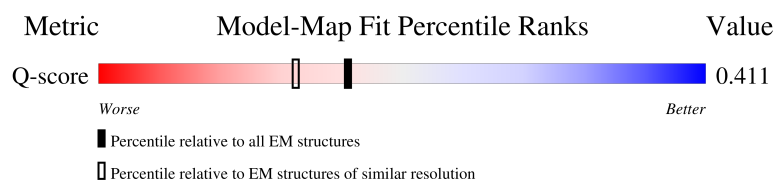
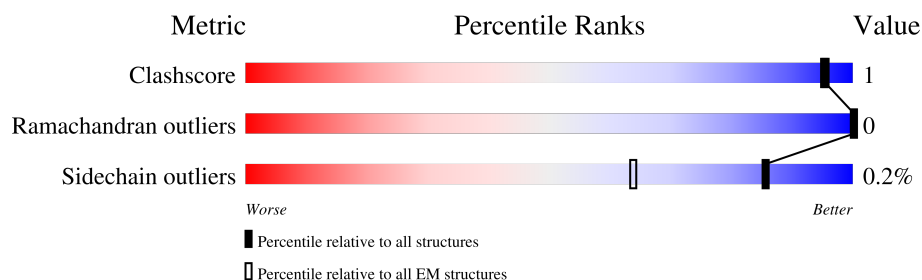
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	6	1017	
2	7	845	
3	2	868	
4	5	775	

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Mol	Chain	Length	Quality of chain
5	3	971	
6	4	933	
7	I	85	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 31618 atoms, of which 15903 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 MCM6.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	6	328	Total	C	H	N	O	S	0	0
			5130	1605	2579	443	490	13		

- Molecule 2 is a protein called DNA replication licensing factor MCM7.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	7	335	Total	C	H	N	O	S	0	0
			5242	1624	2652	448	501	17		

- Molecule 3 is a protein called DNA replication licensing factor MCM2.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	346	Total	C	H	N	O	S	0	0
			5499	1710	2775	492	512	10		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
4	5	280	Total	C	H	N	O	S	0	0
			4460	1383	2276	377	412	12		

- Molecule 5 is a protein called DNA replication licensing factor MCM3.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	3	336	Total	C	H	N	O	S	0	0
			5327	1645	2709	473	491	9		

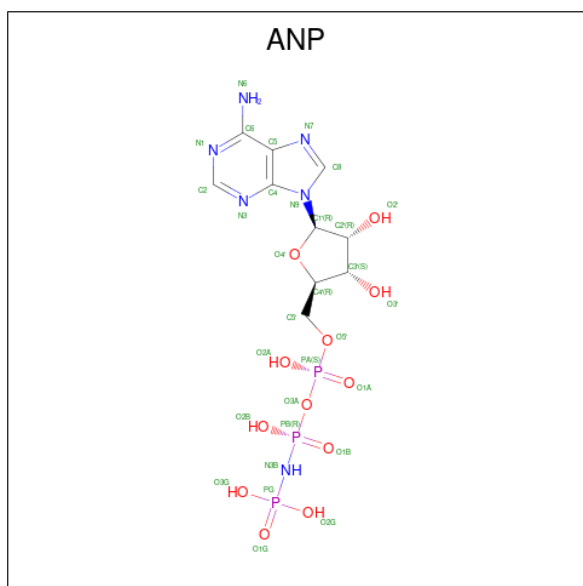
- Molecule 6 is a protein called DNA replication licensing factor MCM4.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	4	330	Total	C	H	N	O	S	0	0
			5223	1622	2655	440	495	11		

- Molecule 7 is a DNA chain called ssDNA, leading-strand template.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	I	16	Total	C	H	N	O	P	0	0
			512	160	192	32	112	16		

- Molecule 8 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
8	6	1	Total	C	H	N	O	P	0
			44	10	13	6	12	3	
8	7	1	Total	C	H	N	O	P	0
			44	10	13	6	12	3	
8	2	1	Total	C	H	N	O	P	0
			44	10	13	6	12	3	
8	3	1	Total	C	H	N	O	P	0
			44	10	13	6	12	3	
8	4	1	Total	C	H	N	O	P	0
			44	10	13	6	12	3	

- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
9	6	1	Total	Mg	0
			1	1	
9	7	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
9	2	1	Total 1	Mg 1	0
9	3	1	Total 1	Mg 1	0
9	4	1	Total 1	Mg 1	0

ASN	ASP	GLY	SER	LEU	ALA	GLU	GLU	TYR	TRP	GLU	ARG	ARG	PHE	LYS	VAL	ILE	LYS	ARG	LEU	VAL	LYS	ASP	ARG	ILE	ILE	GLY	GLY	THR	ARG	HIS	ASN	LEU	ASP	ARG	ASN	GLU	GLU	ASN	GLU	GLU	ASN	GLU	GLU	ASN	GLU	ASP	GLY	THR	VAL	TYR	VAL	ILE	HIS	PRO	HIS	PRO	ASN	ASP	GLU	VAL	ASN
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- Molecule 2: DNA replication licensing factor MCM7



MET SER ALA ALA LEU PRO SER ILE GLN GLN PRO PRO VAL ASP TYR ASN ASN PHE ASN GLU ILE THR THR LYS GLN ASP THR THR LEU LEU SER SER ASP ASP ALA ALA ARG ARG ASN ASN GLU ASN LEU LEU ASP ASP ALA ALA ASN ASN GLN HIS LEU LEU GLU GLU LYS

PRO	LYS	TYR	MET	ALA	ALA	MET	LEU	GLN	LYS	VAL	ALA	ASN	ARG	GLU	LEU	ASN	SER	VAL	ILE	ILE	ASP	LEU	GLN	TYR	GLN	ASN	GLY	LYS	PHE	LEU	LEU	GLN	GLY	THR	GLN	ALA	ALA	ASP	ASP	LEU	VAL	SER	ILE	ILE	ALA	GLN	GLN	ASN	ASN	PHE	THR	GLU	LEU	PHE	CYS	ARG	ALA
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ILE	ASP	ASN	ASN	MET	PRO	LEU	PRO	THR	LYS	GLU	ILE	ASP	TYR	LYS	ASP	ASP	VAL	LEU	ASP	ILE	VAL	LEU	ASN	GLN	ARG	ARG	ARG	LEU	ASN	GLU	ARG	MET	LEU	SER	ASP	ARG	THR	ASN	GLU	ILE	GLU	ARG	SER	GLU	ASN	LEU	MET	ASP	PRO	PRO	SER	SER	MET	ASN	ASP	ALA
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LEU ARG ARG GLU VAL VAL GLU ASP GLU GLU THR GLU LEU PHE PRO PRO ASN LEU LEU THR ARG ARG TYR PHE LEU TYR PHE LYS PRO LEU SER GLN ASN CYS ALA ARG ARG TYR TYR LYS LYS LYS ILE SER SER LYS PRO LEU LEU VAL VAL GLN ILE LYS GLY GLY ASP PHE LEU GLY GLN LEU LEU ILE

VAL	ARG	GLY	ILE	THR	ARG	VAL	VAL	ASP	ASP	LYS	PRO	ALA	ALA	GLU	VAL	ILE	ALA	TYR	THR	CYS	ASP	GLN	CYS	GLY	TYR	GLU	VAL	PHE	GLN	GLU	VAL	VAL	ASN	SER	ARG	THR	PHE	THR	THR	PRO	LEU	SER	SER	GLU	CYS	THR	CYS	GLU	GLN	ASN	SER	GLN	THR	LYS	GLY	GLN	LEU	PHE	THR
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SER THR ARG ALA SER LYS PHE SER SER PHE ALA ALA GLN GLU CYS LYS ILE ILE GLN GLU LEU SER SER GLN GLN VAL VAL PRO PRO VAL VAL GLY HIS ILE ILE HIS VAL VAL ASN GLY THR LEU LEU VAL VAL ARG SER SER LEU SER SER PRO PRO GLY GLY ASP ASP ILE VAL VAL ASP VAL VAL THR THR GLY ILE PHE LEU LEU PRO ALA ALA PRO PRO THR

Residue	Position	Score	Label
THR	1	0.00	
GLY	2	0.00	
PHE	3	0.00	
LYS	4	0.00	
ALA	5	0.00	
LEU	6	0.00	
LYS	7	0.00	
ALA	8	0.00	
GLY	9	0.00	
LEU	10	0.00	
LEU	11	0.00	
THR	12	0.00	
GLU	13	0.00	
THR	14	0.00	
TYR	15	0.00	
LEU	16	0.00	
GLU	17	0.00	
ALA	18	0.00	
GLN	19	0.00	
PHE	20	0.00	
VAL	21	0.00	
ARG	22	0.00	
GLN	23	0.00	
HIS	24	0.00	
LYS	25	0.00	
LYS	26	0.00	
PHE	27	0.00	
ALA	28	0.00	
SER	29	0.00	
PHE	30	0.00	
SER	31	0.00	
LEU	32	0.00	
T394	33	0.00	
E399	34	0.00	
P420	35	0.00	
R451	36	0.00	
N455	37	0.00	
G463	38	0.00	
R479	39	0.00	
V497	40	0.00	
D500	41	0.00	
P501	42	0.00	
V502	43	0.00	
T503	44	0.00	
D504	45	0.00	
E505	46	0.00	
D517	47	0.00	
E525	48	0.00	
F526	49	0.00	

Amino Acid	Count
E531	1
H538	2
G552	1
I553	2
R560	2
Y574	2
R593	3
F598	2
L612	2
D627	1
LEU	1
ASP	4
F630	1
S640	1
R668	2
K678	1
Q729	4
T730	4
THR	4
ASN	4
LYS	4
SER	4
LYS	4
GLU	4
ASP	4
GLU	4
SER	4
PRO	4
THR	4
THR	4
LYS	4
ILE	4
PHE	4
THR	4
ILE	4
ILE	4
LYS	4
LYS	4
MET	4
LEU	4
GLN	4
GLU	4
THR	4
GLY	4
LYS	4
ASN	4
THR	4

LEU TYR SER TYR GLU ASN ILE VAL LYS THR VAL ARG LEU ARG GLY PHE THR MET LEU GLN LEU LEU SER ASN CYS ILE GLN GLU TYR TYR LEU ASN VAL TRP LEU ILE ASN GLY GLY ASN THR LEU LYS PHE ASP VAL ASP GLY THR MET ASP THR GLN ASP SER LEU VAL SER

THR	PRO	LYS	LEU	ALA	PRO	GLN	THR	THR	ALA	SER	ALA	ASN	VAL	SER	SER	ALA	GLN	ASP	SER	ASP	ILE	ASP	LEU	GLN	ASP	ALA
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- Molecule 3: DNA replication licensing factor MCM2

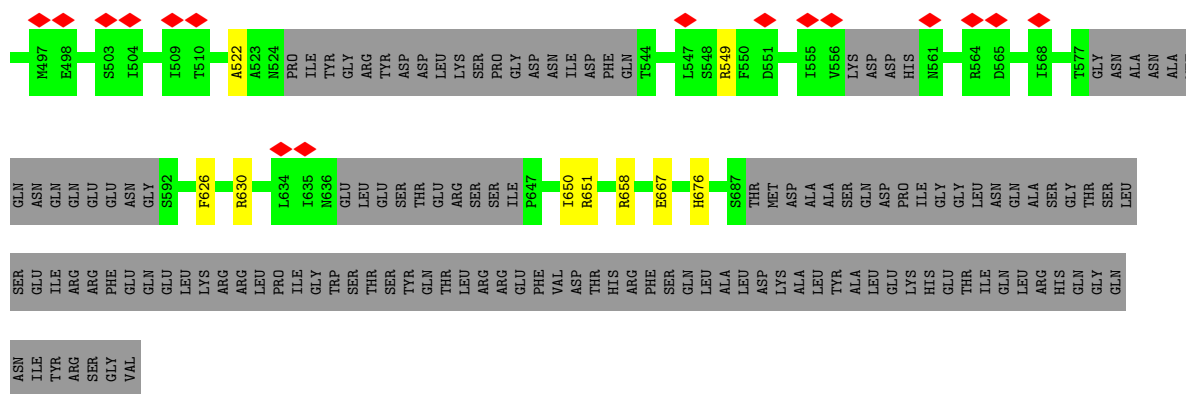


MET	ASP	ASN	ARG	ARG	ARG	ARG	GLU	ASP	ASP	ASP	ASP	SER	SER	SER	SER	PRO	GLN	GLN	GLN	LEU	PRO	PRO	PRO	PRO	SER	SER	SER	GLY	GLY	GLY	MET	ASN	PRO	PRO	VAL	SER	SER	SER	PRO	PRO	ILE	ILE	GLY	GLY	ASP	MET	ILE	ILE	ASN	ASN	PRO	PRO	GLY	GLY	ASP	ASP	ASP	ASP	VAL	VAL	GLY	VAL	ASP	ASP	PRO	PRO	ASP
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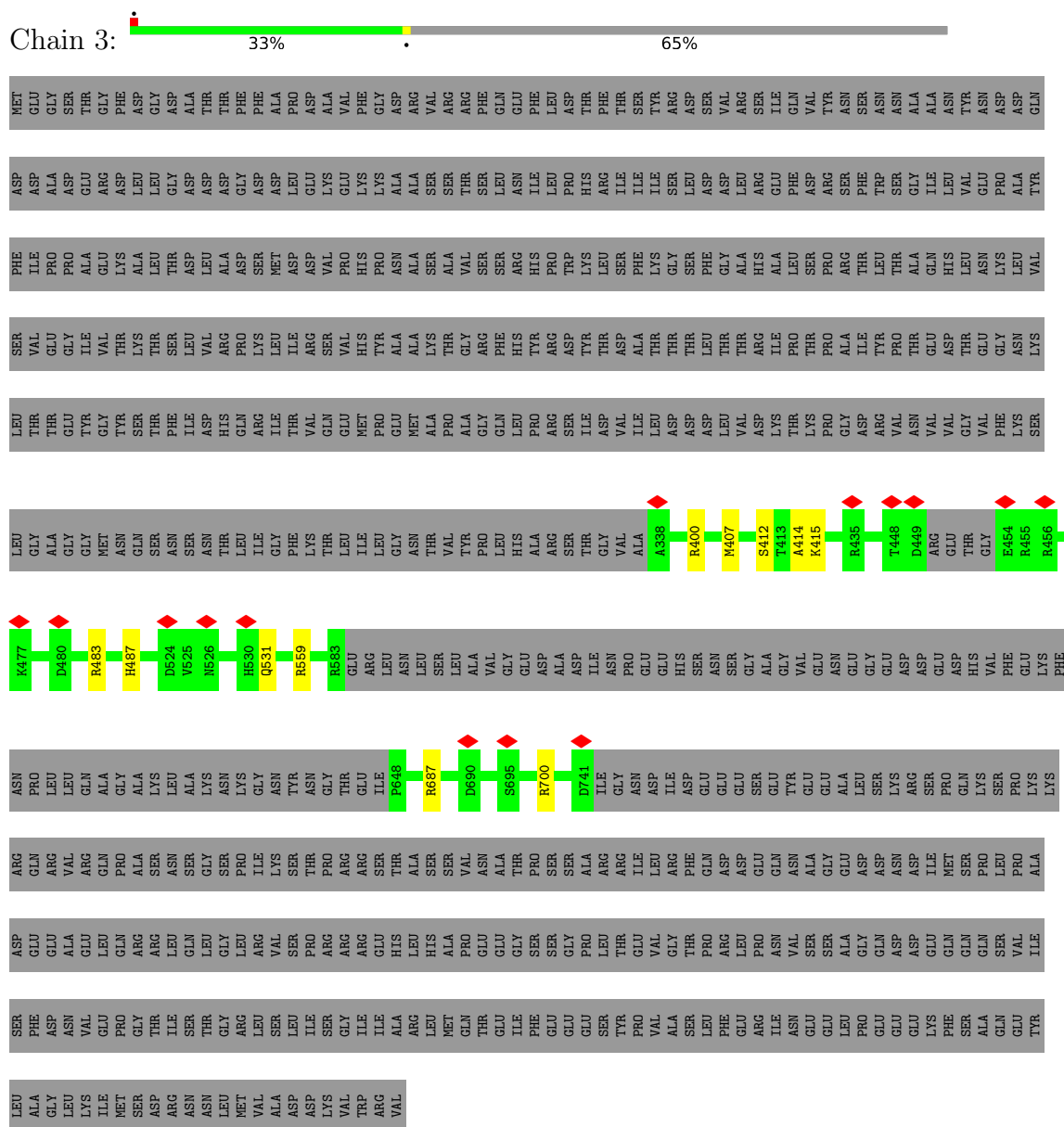
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ARG	LEU	LEU	LEU	ASN	VAL	ALA	TYR	ILE	ASP	ASP	GLU	ASP	GLU	GLN	GLY	ALA	ALA	GLN	LEU	ASP	GLU	MET	GLY	LEU	GLY	PRO	VAL	VAL	GLN	ARG	ARG	ARG	ARG	ARG	GLN	TYR	GLU	ASP	LEU	GLU	GLU	ASN	SER	ASP	ASP	ASP	ASP	ASP	LEU	LEU	ILE	ASP	PRO	ASP	LEU	ARG	GLU	GLY
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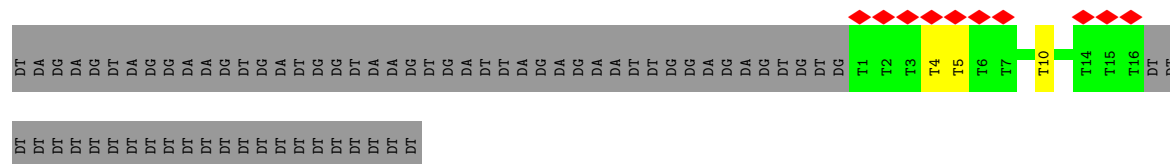
LEU	THR	LEU	LEU	GLU	SER	LEU	SER	ASN	VAL	LYS	ALA	ASN	SER	TYR	SER	SER	GLU	TRP	ILE	THR	GLN	PRO	ASN	ASN	VAL	SER	ARG	THR	ILE	ALA	ARG	GLU	LEU	LYS	SER	PHE	LEU	LEU	GLU	TYR	THR	ASP	GLU	THR	GLY	ARG	SER	VAL	TYR	GLY	ALA	ARG	ILE	THR	THR	LEU	GLY	GLU	GLY	MET	ASN	SER	THR	GLN
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• Molecule 5: DNA replication licensing factor MCM3



• Molecule 6: DNA replication licensing factor MCM4

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	182000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	37	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.071	Depositor
Minimum map value	-0.026	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	377.64, 377.64, 377.64	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.049, 1.049, 1.049	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ANP, 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	6	0.83	0/2586	1.39	14/3485 (0.4%)
2	7	0.79	1/2623 (0.0%)	1.40	9/3541 (0.3%)
3	2	0.87	0/2762	1.52	22/3718 (0.6%)
4	5	0.76	0/2203	1.42	9/2957 (0.3%)
5	3	0.80	0/2652	1.38	5/3587 (0.1%)
6	4	0.75	0/2601	1.35	8/3515 (0.2%)
7	I	0.76	0/351	1.61	2/540 (0.4%)
All	All	0.80	1/15778 (0.0%)	1.42	69/21343 (0.3%)

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	6	0	3
2	7	0	7
3	2	0	4
4	5	0	2
5	3	0	2
6	4	0	2
7	I	0	1
All	All	0	21

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	7	593	ARG	CZ-NH2	-5.69	1.26	1.33

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	7	501	PRO	CA-C-N	8.74	130.71	121.97
2	7	501	PRO	C-N-CA	8.74	130.71	121.97
5	3	700	ARG	NE-CZ-NH2	8.54	126.89	119.20
3	2	864	TYR	CA-C-N	8.48	132.00	120.38
3	2	864	TYR	C-N-CA	8.48	132.00	120.38

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	6	566	ARG	Sidechain
1	6	708	ARG	Sidechain
1	6	828	TYR	Sidechain
2	7	451	ARG	Sidechain
2	7	479	ARG	Sidechain

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	6	2551	2579	2573	6	0
2	7	2590	2652	2649	4	0
3	2	2724	2775	2764	8	0
4	5	2184	2276	2269	5	0
5	3	2618	2709	2705	5	0
6	4	2568	2655	2651	4	0
7	I	320	192	193	0	0
8	2	31	13	13	8	0
8	3	31	13	13	3	0
8	4	31	13	13	3	0
8	6	31	13	13	2	0
8	7	31	13	13	2	0
9	2	1	0	0	0	0
9	3	1	0	0	0	0
9	4	1	0	0	0	0
9	6	1	0	0	0	0
9	7	1	0	0	0	0
All	All	15715	15903	15869	32	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 1.

The worst 5 of 32 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)
5:3:412:SER:H	8:3:1500:ANP:HNB1	1.14	0.96
2:7:463:GLY:H	8:7:1500:ANP:HNB1	1.19	0.86
1:6:578:SER:H	8:6:1500:ANP:HNB1	1.31	0.78
6:4:571:SER:H	8:4:1500:ANP:HNB1	1.33	0.75
8:6:1500:ANP:PG	6:4:796:ARG:HH22	2.28	0.56

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	6	322/1017 (32%)	299 (93%)	23 (7%)	0	100	100
2	7	331/845 (39%)	315 (95%)	16 (5%)	0	100	100
3	2	334/868 (38%)	303 (91%)	31 (9%)	0	100	100
4	5	264/775 (34%)	251 (95%)	13 (5%)	0	100	100
5	3	330/971 (34%)	315 (96%)	15 (4%)	0	100	100
6	4	322/933 (34%)	306 (95%)	16 (5%)	0	100	100
All	All	1903/5409 (35%)	1789 (94%)	114 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	6	276/886 (31%)	275 (100%)	1 (0%)	84	83
2	7	287/753 (38%)	287 (100%)	0	100	100
3	2	298/770 (39%)	296 (99%)	2 (1%)	76	78
4	5	242/688 (35%)	242 (100%)	0	100	100
5	3	289/835 (35%)	289 (100%)	0	100	100
6	4	287/848 (34%)	286 (100%)	1 (0%)	86	84
All	All	1679/4780 (35%)	1675 (100%)	4 (0%)	85	85

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	6	693	LEU
3	2	569	GLN
3	2	752	GLU
6	4	578	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
4	5	571	HIS
6	4	651	GLN
4	5	574	ASN
6	4	726	ASN
5	3	682	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 5 are monoatomic - leaving 5 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	ANP	3	1500	9	33,33,33	1.84	7 (21%)	45,52,52	2.24	13 (28%)
8	ANP	2	1500	9	33,33,33	3.47	9 (27%)	45,52,52	1.77	8 (17%)
8	ANP	4	1500	9	33,33,33	1.76	9 (27%)	45,52,52	1.75	8 (17%)
8	ANP	7	1500	9	33,33,33	1.52	7 (21%)	45,52,52	1.36	7 (15%)
8	ANP	6	1500	9	33,33,33	1.37	5 (15%)	45,52,52	2.03	11 (24%)

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	ANP	3	1500	9	-	9/18/38/38	0/3/3/3
8	ANP	2	1500	9	-	4/18/38/38	0/3/3/3
8	ANP	4	1500	9	-	5/18/38/38	0/3/3/3
8	ANP	7	1500	9	-	4/18/38/38	0/3/3/3
8	ANP	6	1500	9	-	6/18/38/38	0/3/3/3

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	2	1500	ANP	PB-O3A	-13.00	1.42	1.59
8	2	1500	ANP	PA-O3A	-12.24	1.46	1.59
8	3	1500	ANP	PB-O3A	-5.61	1.52	1.59

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	3	1500	ANP	PA-O3A	-4.37	1.54	1.59
8	4	1500	ANP	PB-O1B	4.13	1.52	1.46

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	3	1500	ANP	O1B-PB-N3B	-7.90	100.13	111.77
8	2	1500	ANP	O1B-PB-N3B	6.63	121.53	111.77
8	6	1500	ANP	O1G-PG-N3B	-6.62	102.03	111.77
8	6	1500	ANP	O3G-PG-O1G	-5.78	98.95	113.45
8	3	1500	ANP	O2B-PB-O3A	5.24	122.11	104.64

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	6	1500	ANP	PG-N3B-PB-O1B
8	6	1500	ANP	PA-O3A-PB-O2B
8	6	1500	ANP	C5'-O5'-PA-O1A
8	6	1500	ANP	C5'-O5'-PA-O2A
8	6	1500	ANP	C5'-O5'-PA-O3A

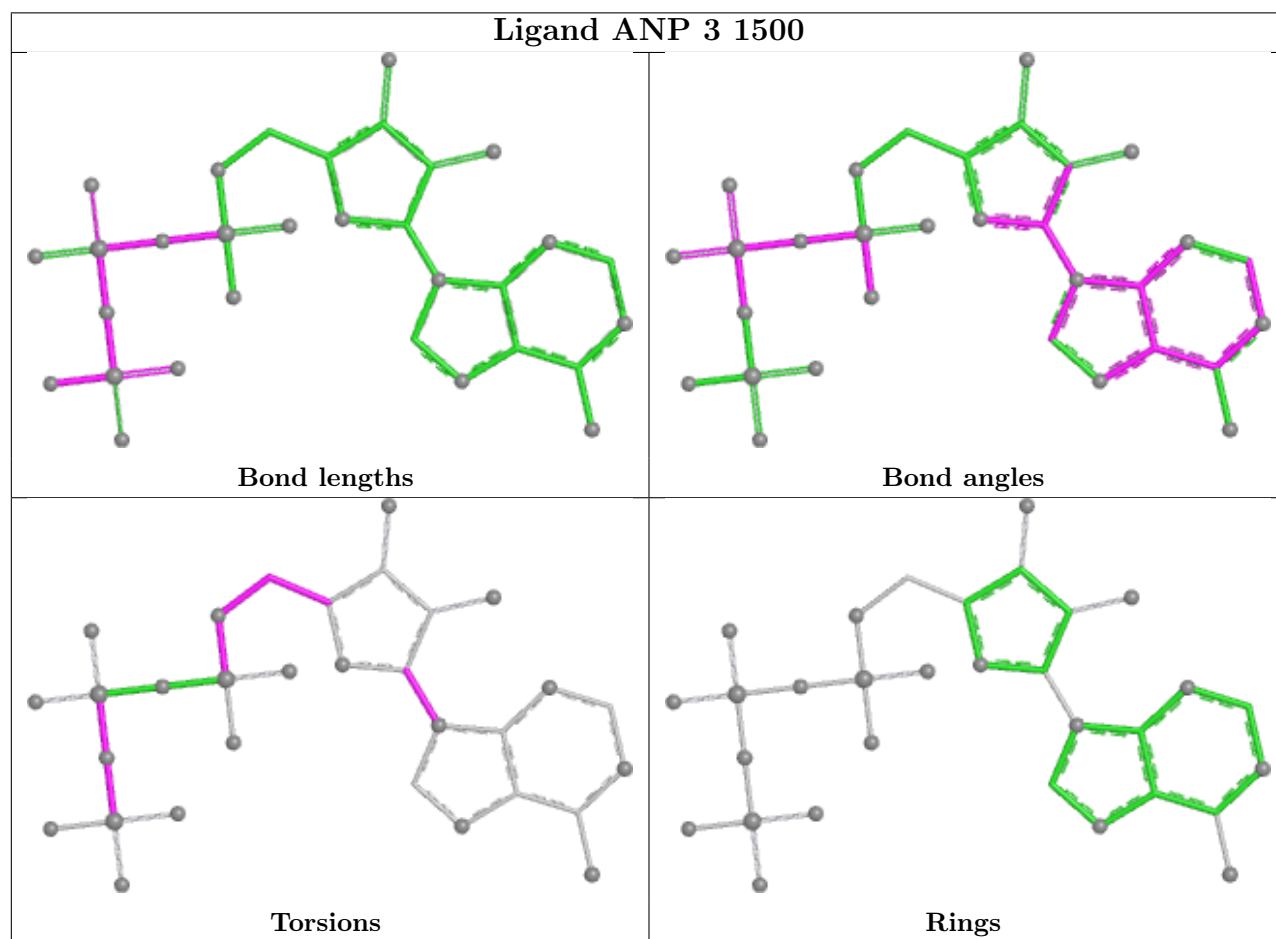
There are no ring outliers.

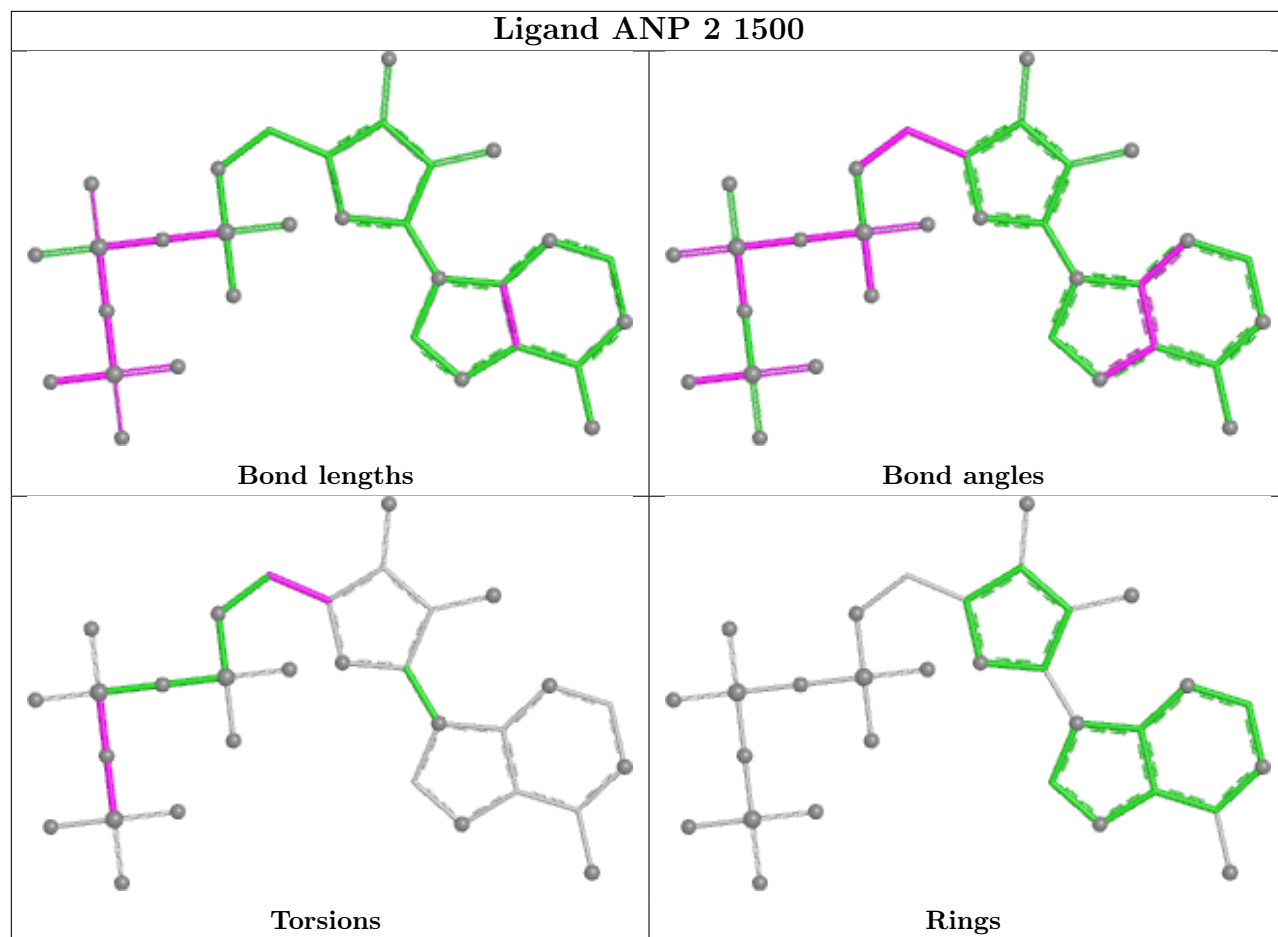
5 monomers are involved in 18 short contacts:

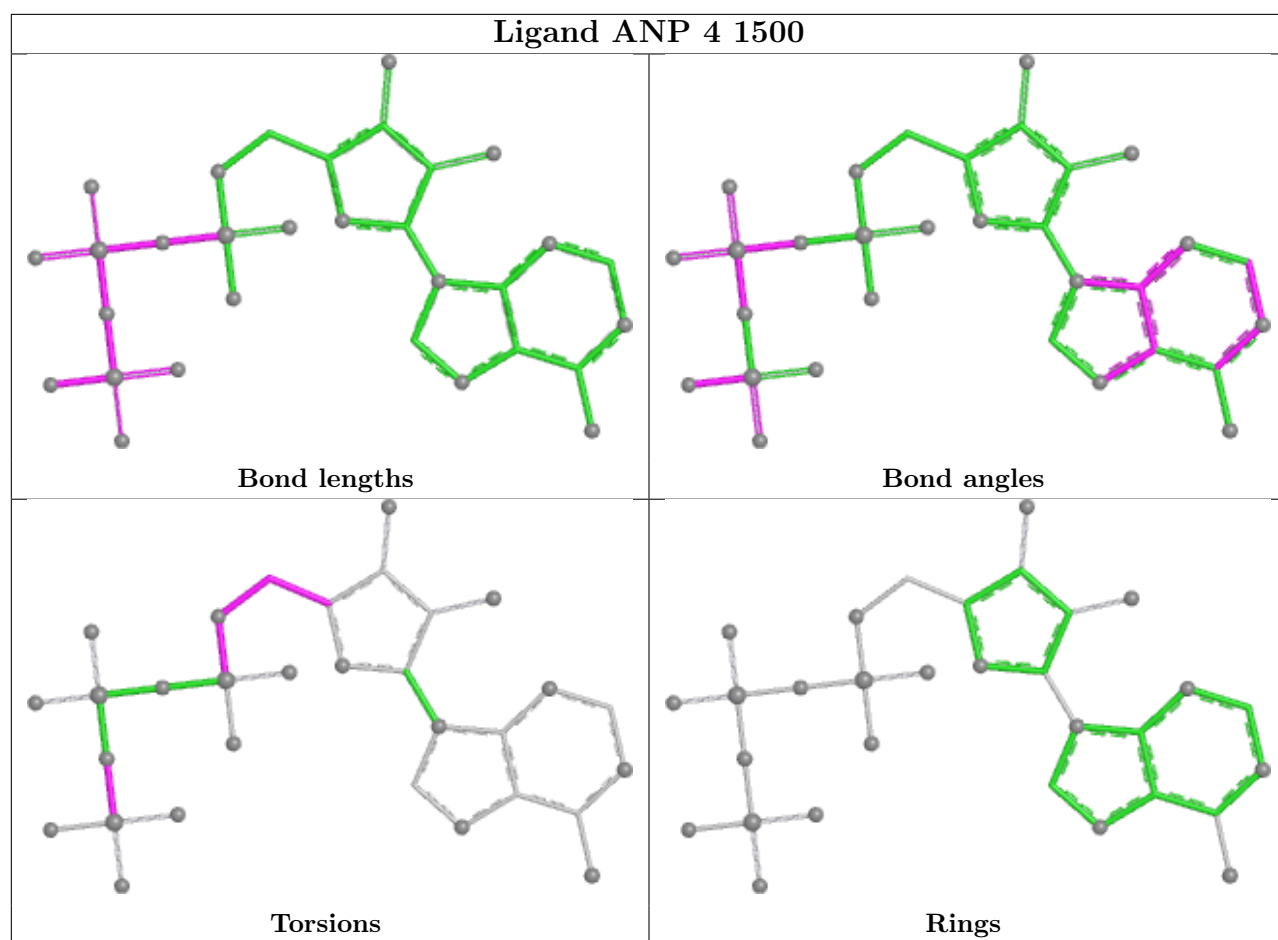
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	3	1500	ANP	3	0
8	2	1500	ANP	8	0
8	4	1500	ANP	3	0
8	7	1500	ANP	2	0
8	6	1500	ANP	2	0

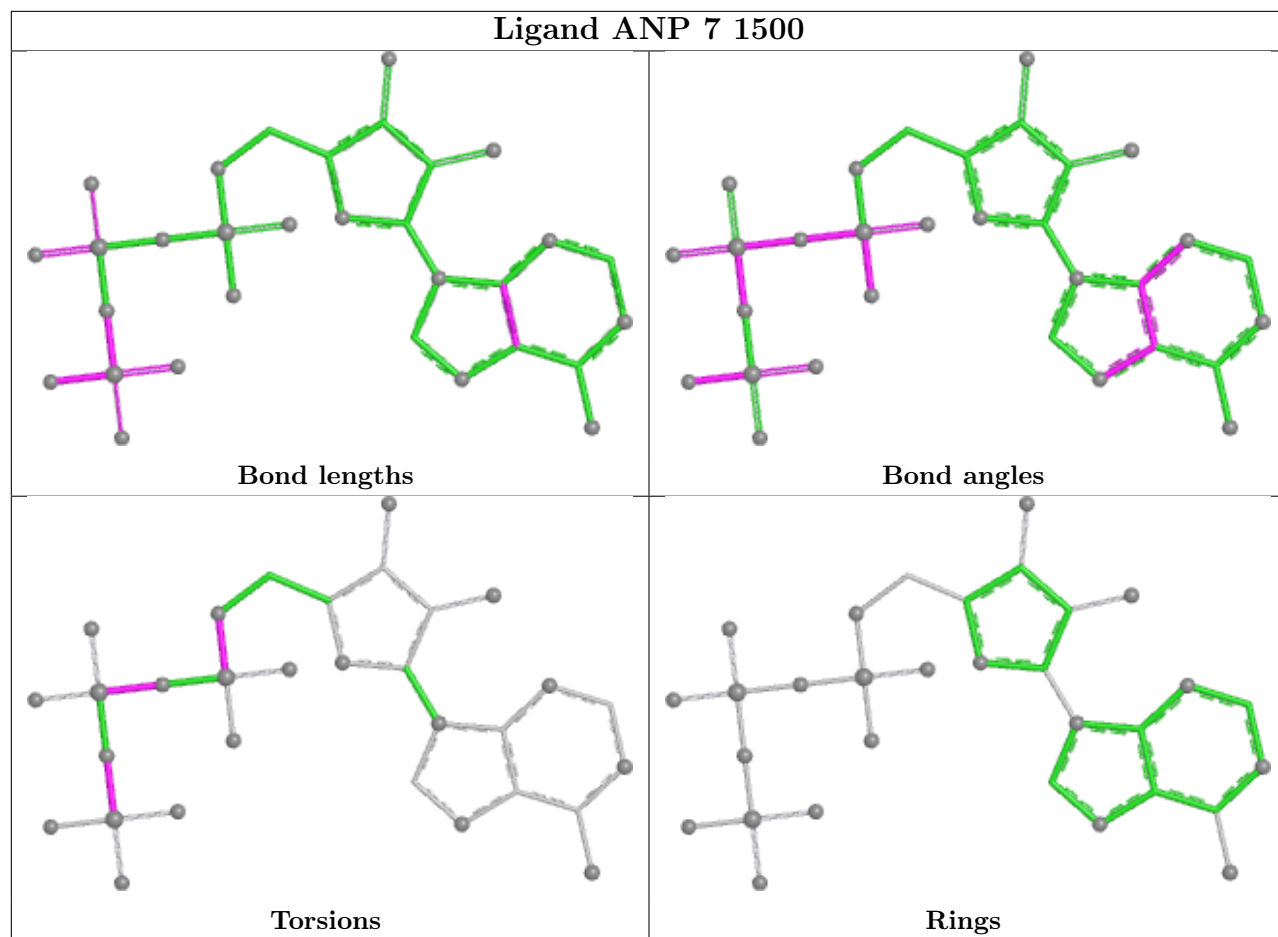
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

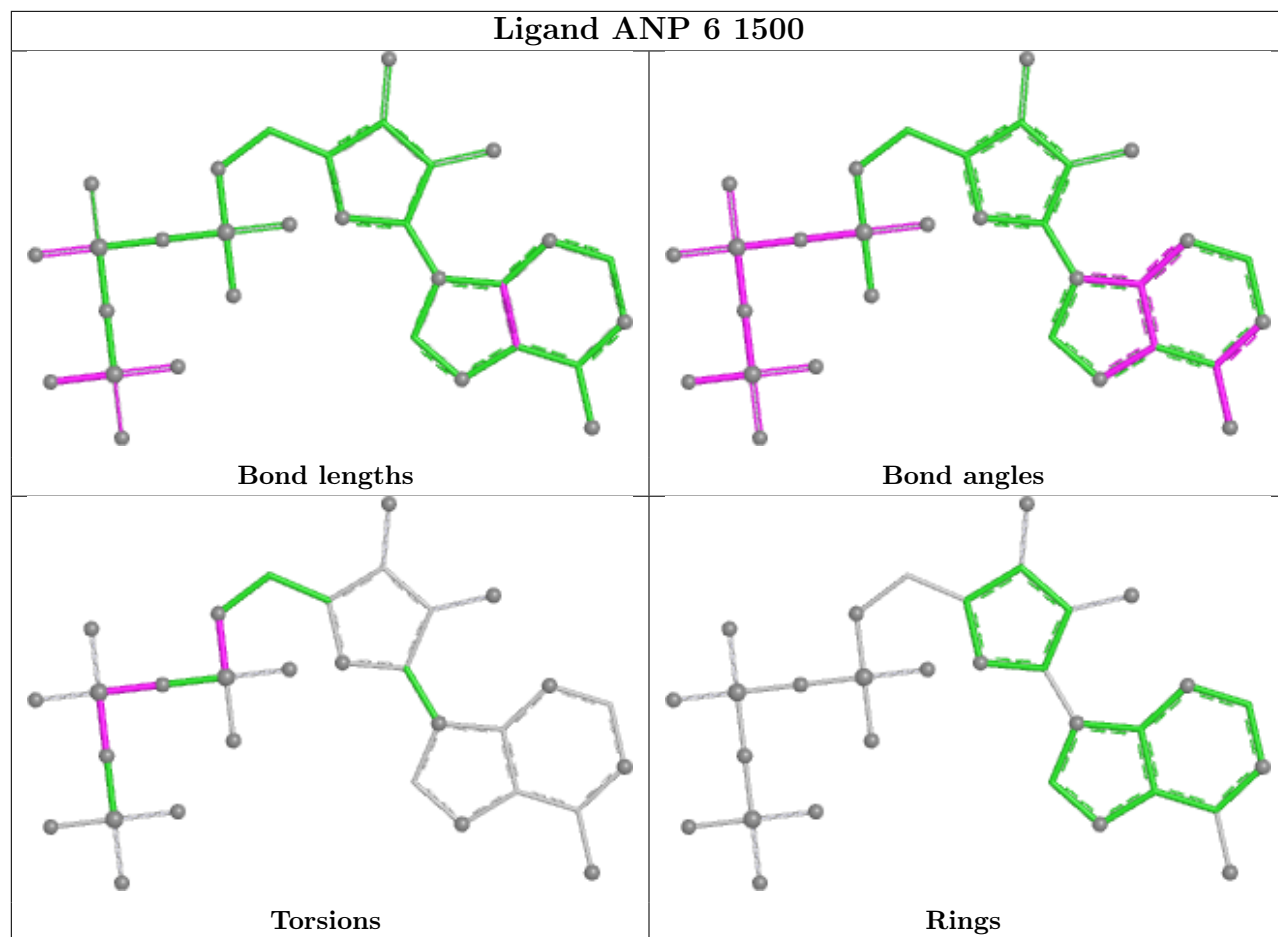
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

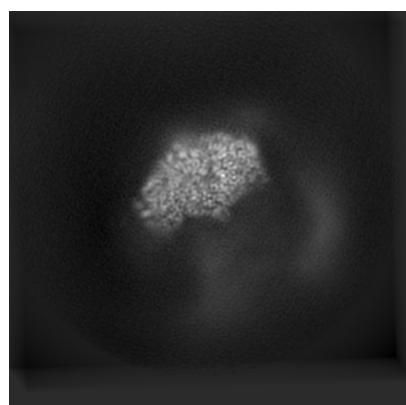
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10230. These allow visual inspection of the internal detail of the map and identification of artifacts.

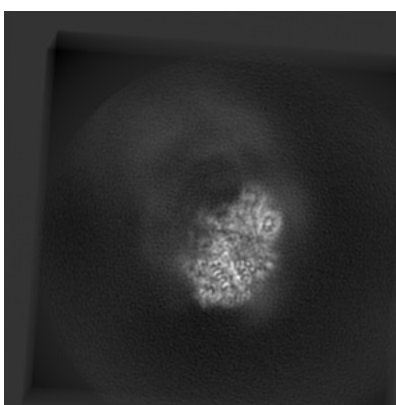
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

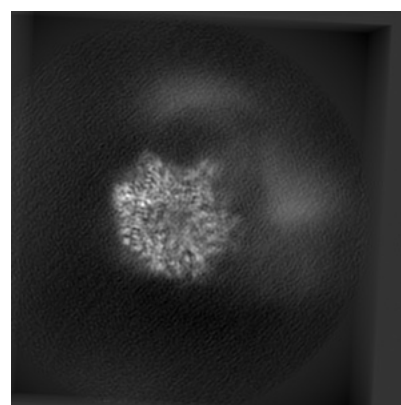
6.1.1 Primary map



X



Y

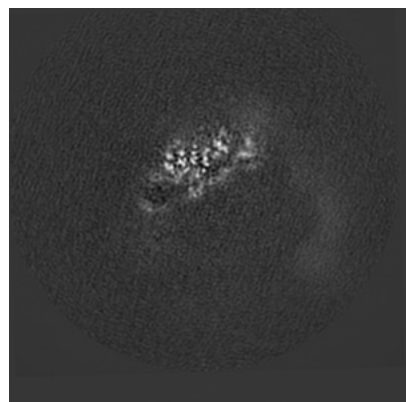


Z

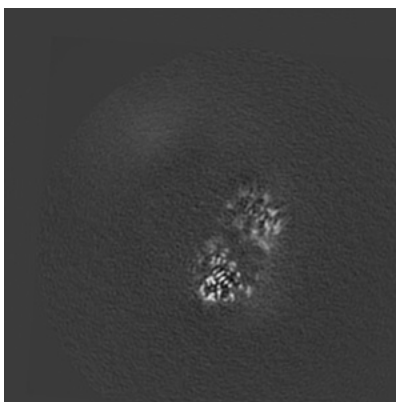
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

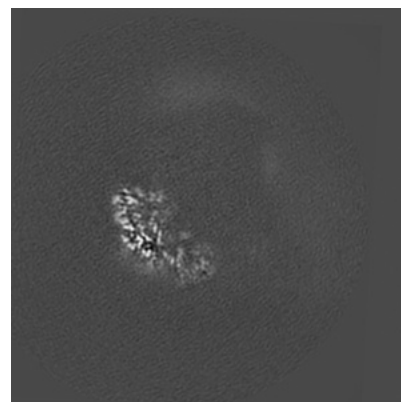
6.2.1 Primary map



X Index: 180



Y Index: 180

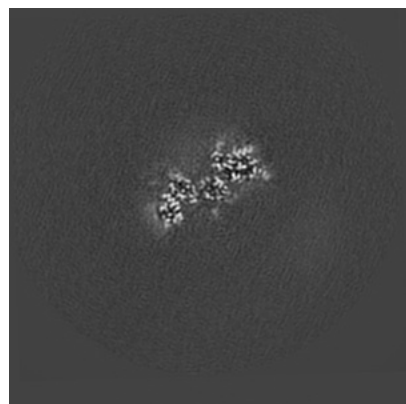


Z Index: 180

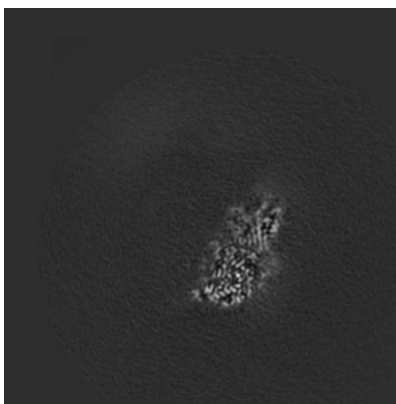
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

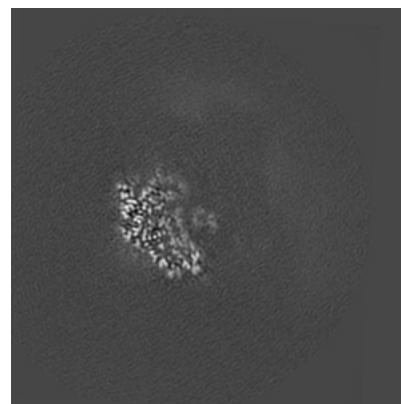
6.3.1 Primary map



X Index: 123



Y Index: 193

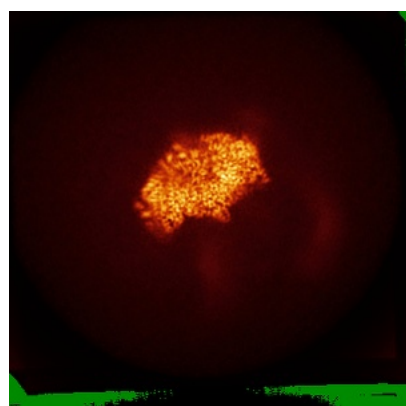


Z Index: 193

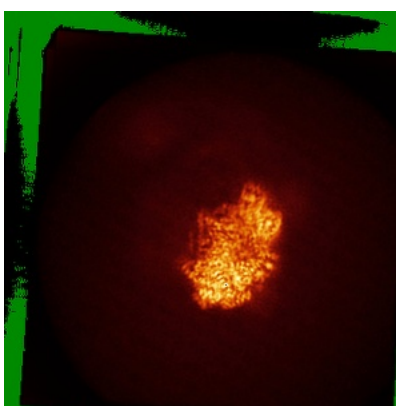
The images above show the largest variance slices of the map in three orthogonal directions.

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

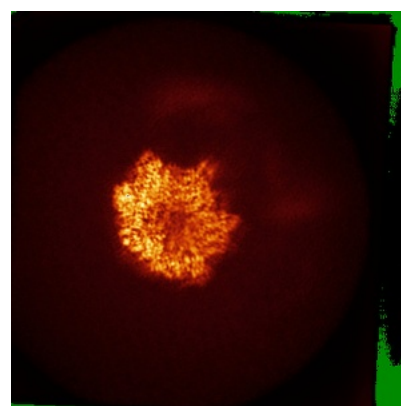
6.4.1 Primary map



X



Y

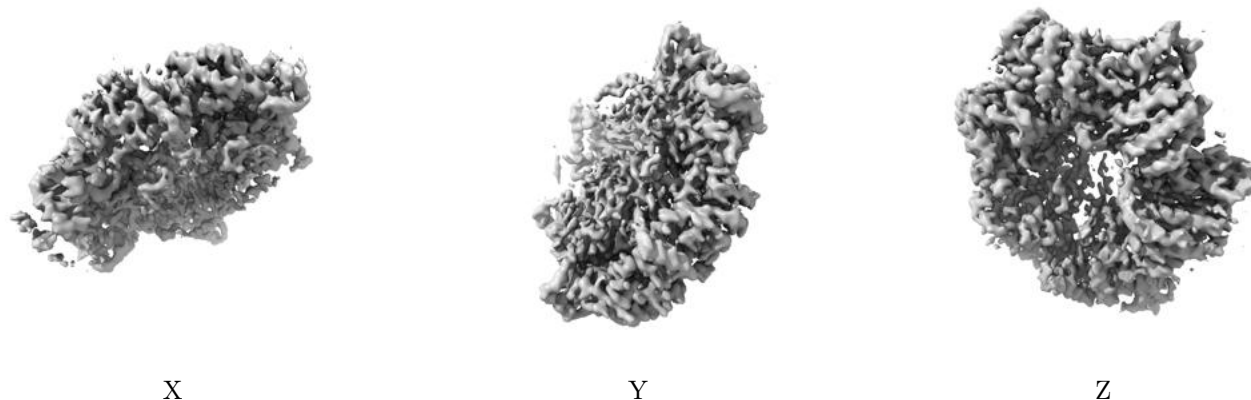


Z

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 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

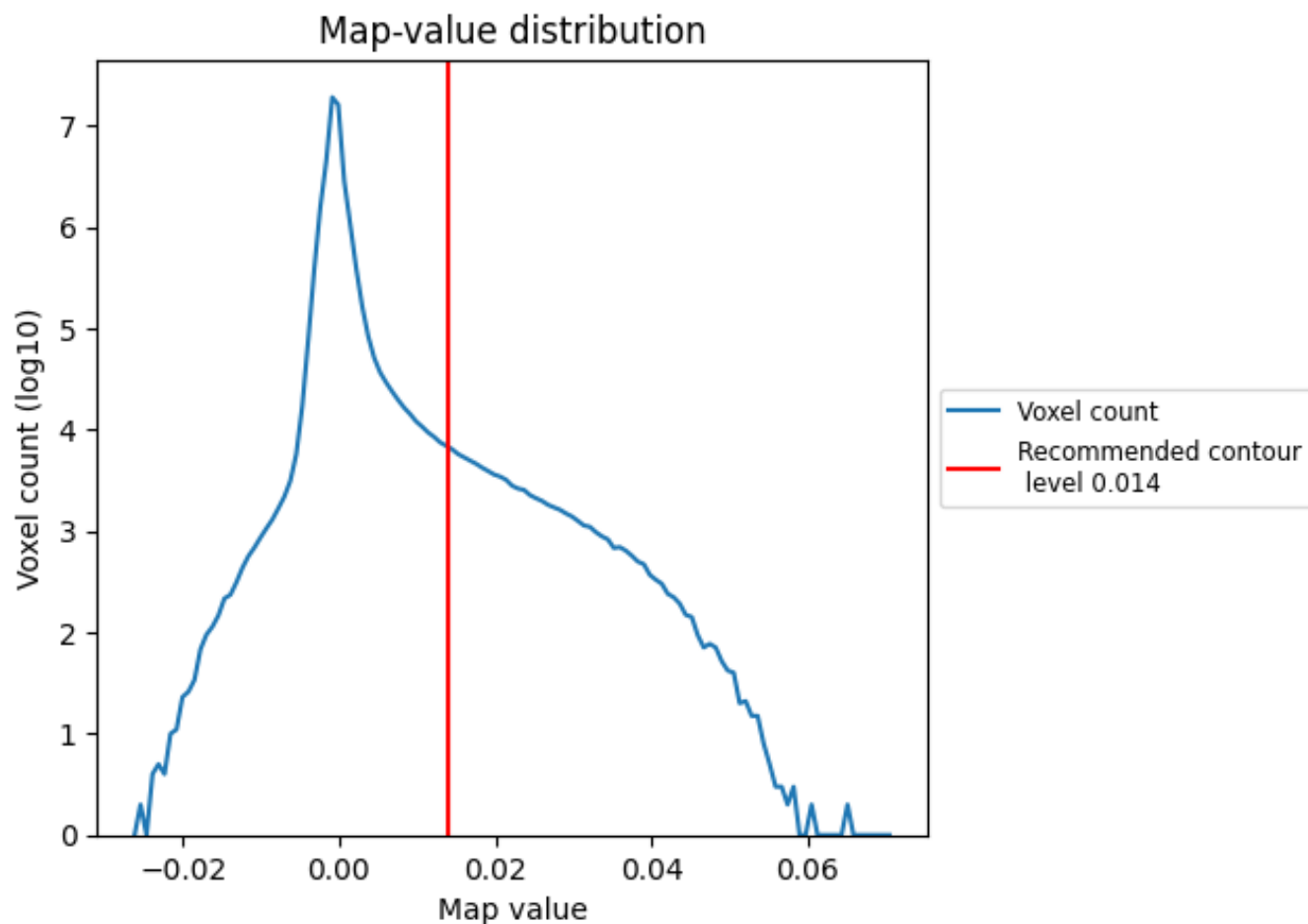
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

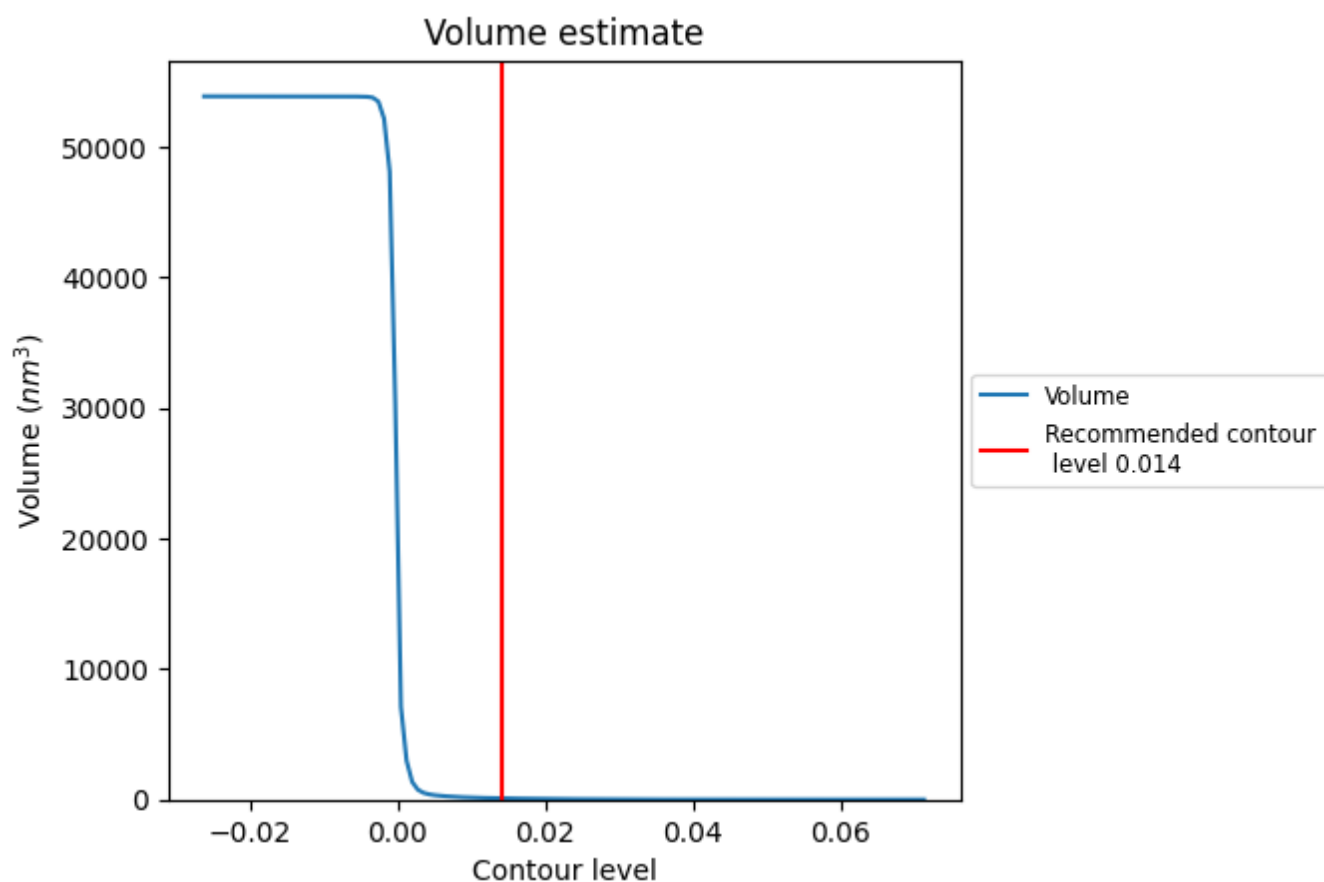
This section contains the results of statistical analysis of the map.

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.

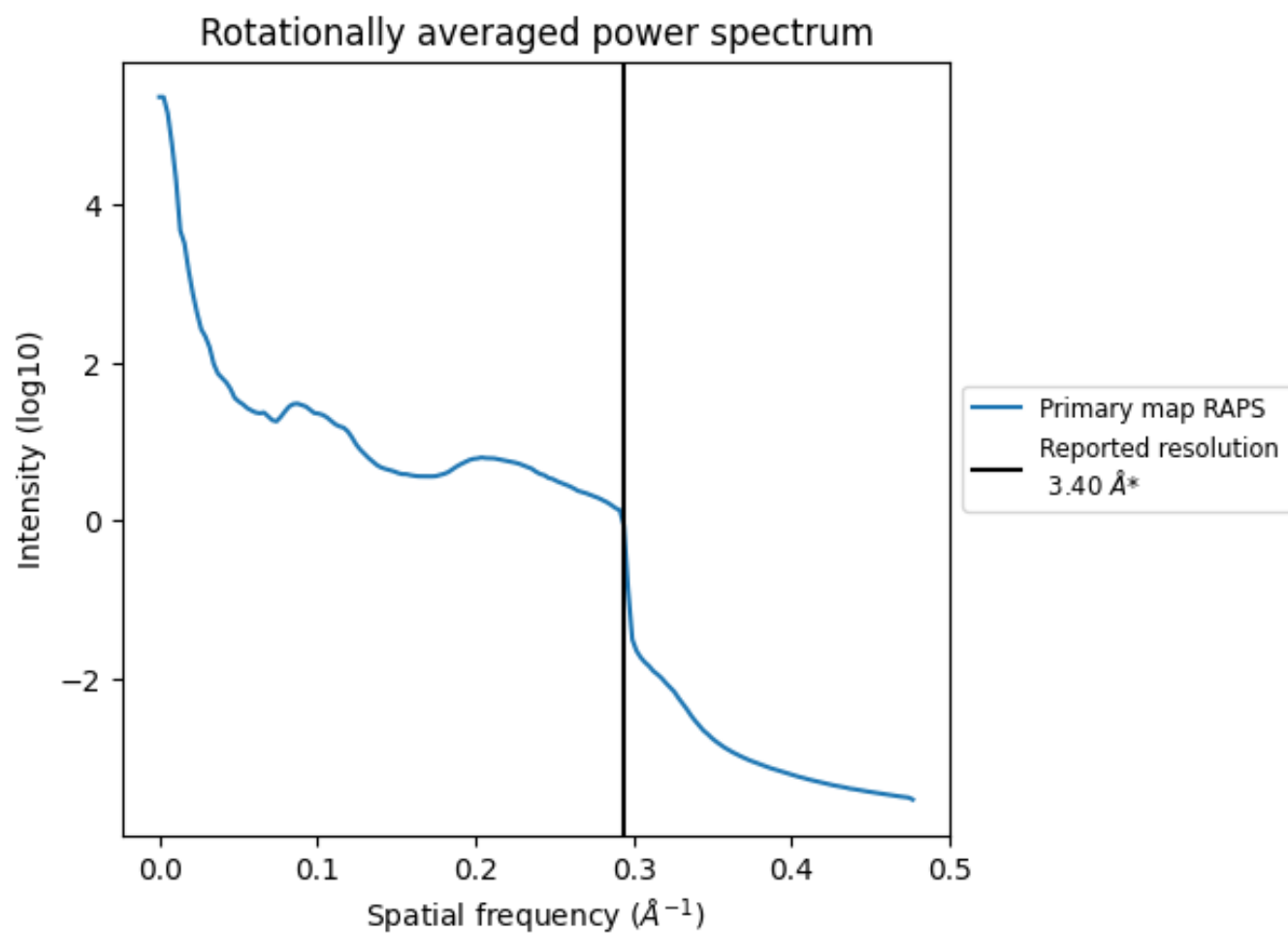
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 97 nm^3 ; this corresponds to an approximate mass of 88 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 ⓘ

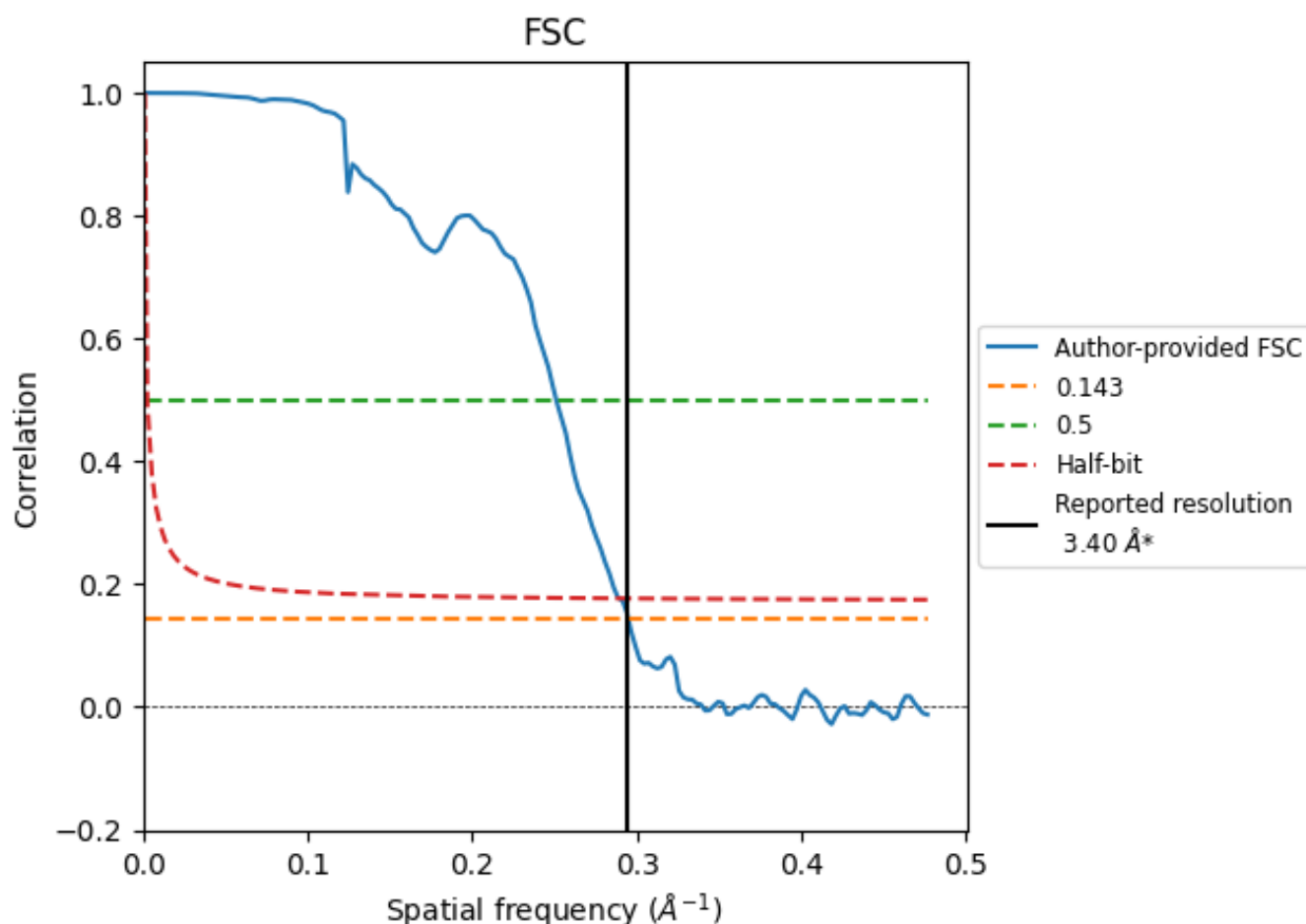


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

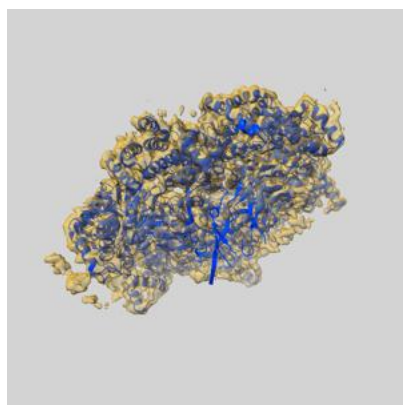
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.39	3.98	3.46
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

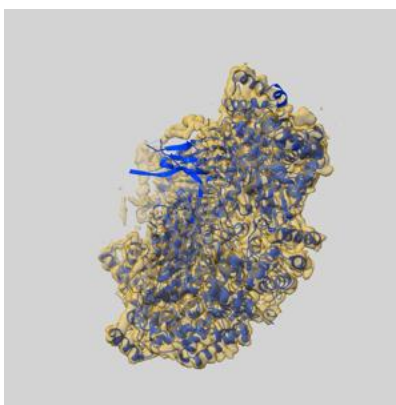
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10230 and PDB model 6SKO. Per-residue inclusion information can be found in section [3](#) on page [7](#).

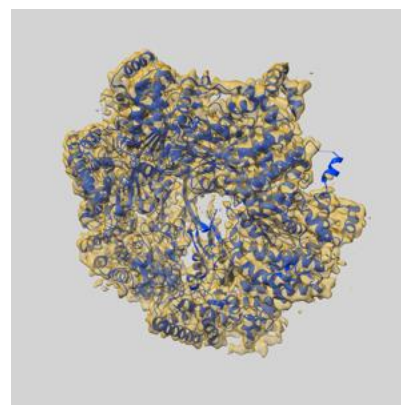
9.1 Map-model overlay [i](#)



X



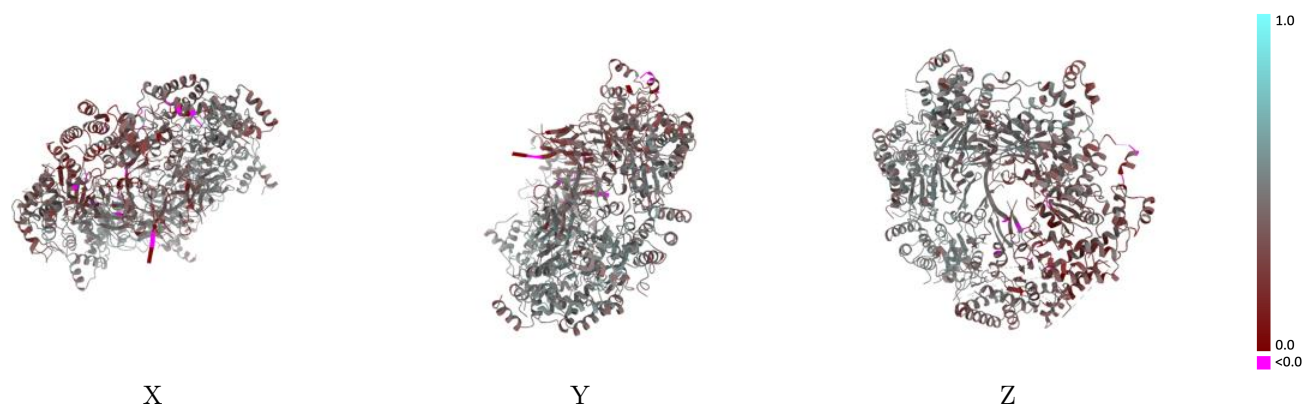
Y



Z

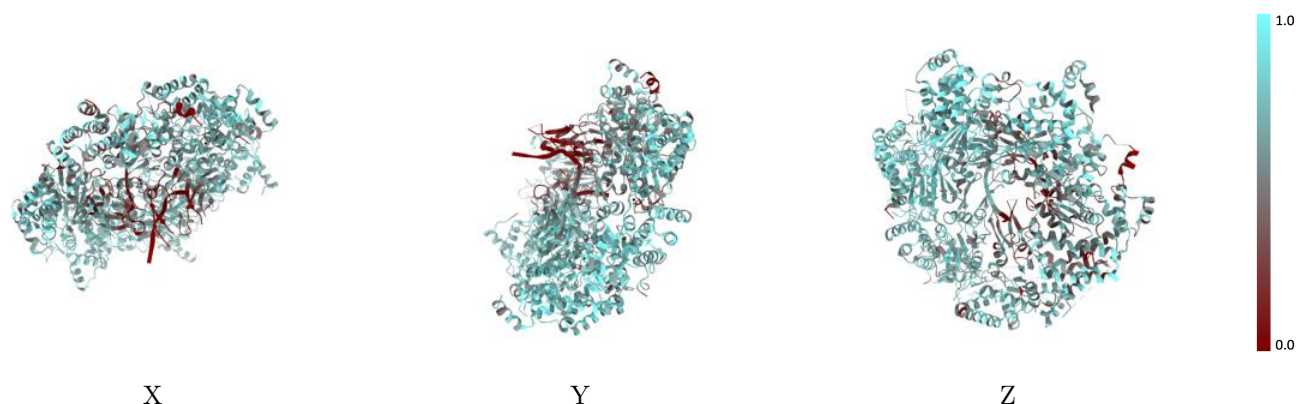
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



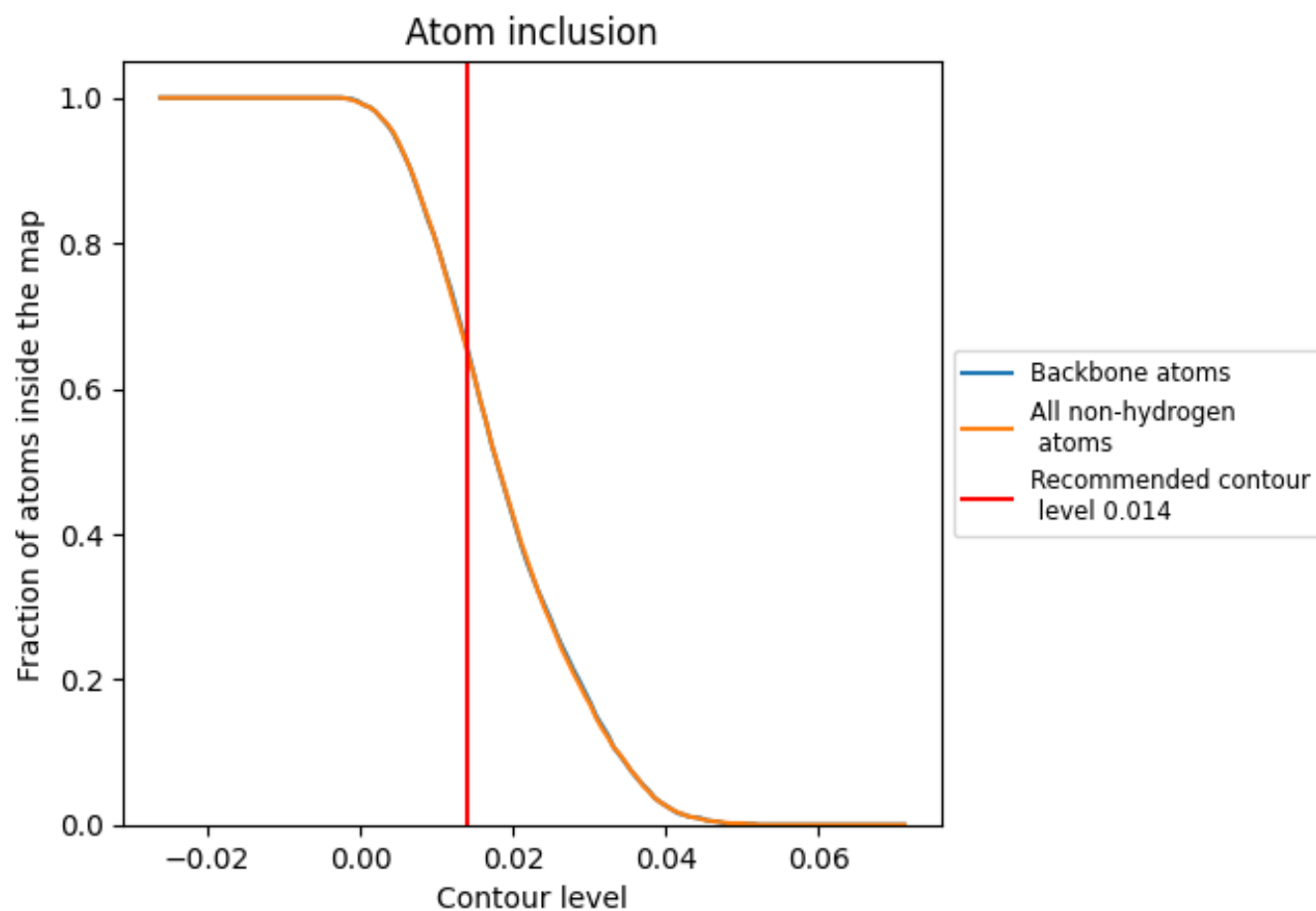
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 65% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6510	0.4110
2	0.5320	0.3080
3	0.7380	0.4690
4	0.7350	0.4670
5	0.6150	0.3570
6	0.6410	0.4100
7	0.7610	0.4640
I	0.2840	0.3080

1.0

0.0

<0.0