



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:14 PM UTC

PDB ID : 8B9C / pdb_00008b9c
EMDB ID : EMD-15924
Title : S. cerevisiae pol alpha - replisome complex
Authors : Jones, M.L.; Yeeles, J.T.P.
Deposited on : 2022-10-05
Resolution : 4.60 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.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

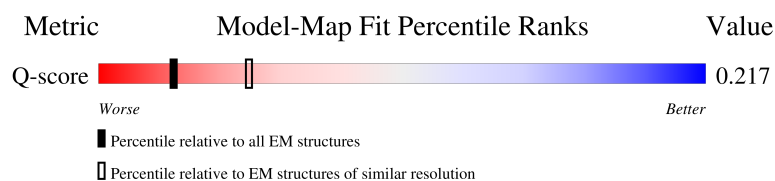
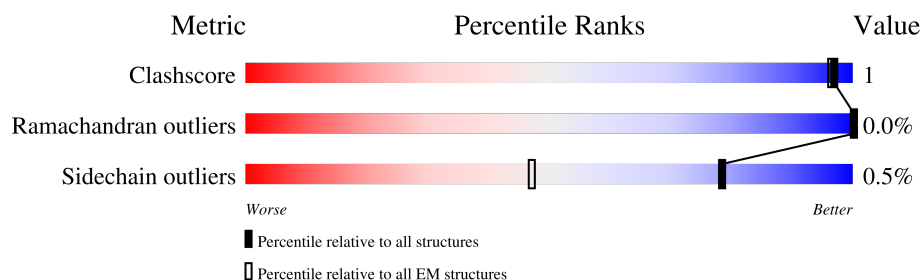
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	
2	3	1009	
3	4	933	
4	5	775	

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Mol	Chain	Length	Quality of chain
5	6	1017	
6	7	845	
7	A	528	
8	B	705	
9	C	208	
10	D	213	
11	E	217	
12	F	294	
13	G	657	
14	P	1109	
15	Q	84	
16	R	106	
17	S	444	
18	X	1238	
19	Y	319	
20	J	1468	

2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 118037 atoms, of which 59070 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	568	Total	C	H	N	O	S	0	0
			9140	2857	4606	810	853	14		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	3	613	Total	C	H	N	O	S	0	0
			9653	3023	4861	853	903	13		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	-37	MET	-	initiating methionine	UNP P24279
3	-36	LYS	-	expression tag	UNP P24279
3	-35	ARG	-	expression tag	UNP P24279
3	-34	ARG	-	expression tag	UNP P24279
3	-33	TRP	-	expression tag	UNP P24279
3	-32	LYS	-	expression tag	UNP P24279
3	-31	LYS	-	expression tag	UNP P24279
3	-30	ASN	-	expression tag	UNP P24279
3	-29	PHE	-	expression tag	UNP P24279
3	-28	ILE	-	expression tag	UNP P24279
3	-27	ALA	-	expression tag	UNP P24279
3	-26	VAL	-	expression tag	UNP P24279
3	-25	SER	-	expression tag	UNP P24279
3	-24	ALA	-	expression tag	UNP P24279
3	-23	ALA	-	expression tag	UNP P24279
3	-22	ASN	-	expression tag	UNP P24279
3	-21	ARG	-	expression tag	UNP P24279
3	-20	PHE	-	expression tag	UNP P24279
3	-19	LYS	-	expression tag	UNP P24279
3	-18	LYS	-	expression tag	UNP P24279
3	-17	ILE	-	expression tag	UNP P24279

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Chain	Residue	Modelled	Actual	Comment	Reference
3	-16	SER	-	expression tag	UNP P24279
3	-15	SER	-	expression tag	UNP P24279
3	-14	SER	-	expression tag	UNP P24279
3	-13	GLY	-	expression tag	UNP P24279
3	-12	ALA	-	expression tag	UNP P24279
3	-11	LEU	-	expression tag	UNP P24279
3	-10	GLU	-	expression tag	UNP P24279
3	-9	ASN	-	expression tag	UNP P24279
3	-8	LEU	-	expression tag	UNP P24279
3	-7	TYR	-	expression tag	UNP P24279
3	-6	PHE	-	expression tag	UNP P24279
3	-5	GLN	-	expression tag	UNP P24279
3	-4	GLY	-	expression tag	UNP P24279
3	-3	GLU	-	expression tag	UNP P24279
3	-2	ALA	-	expression tag	UNP P24279
3	-1	PRO	-	expression tag	UNP P24279
3	0	VAL	-	expression tag	UNP P24279

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

Mol	Chain	Residues	Atoms						AltConf	Trace
3	4	628	Total	C	H	N	O	S	0	0
			10055	3145	5065	855	961	29		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
4	5	533	Total	C	H	N	O	S	0	0
			8560	2670	4347	724	798	21		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	6	623	Total	C	H	N	O	S	0	0
			9908	3112	4980	860	931	25		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
6	7	656	Total	C	H	N	O	S	0	0
			10387	3257	5233	885	983	29		

- Molecule 7 is a protein called DNA primase large subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	A	258	Total	C	H	N	O	S	0	0
			4382	1412	2197	363	405	5		

- Molecule 8 is a protein called DNA polymerase alpha subunit B.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	B	561	Total	C	H	N	O	S	0	0
			8944	2859	4464	758	852	11		

- Molecule 9 is a protein called DNA replication complex GINS protein PSF1.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	C	195	Total	C	H	N	O	S	0	0
			3202	1004	1603	275	311	9		

- Molecule 10 is a protein called DNA replication complex GINS protein PSF2.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	D	188	Total	C	H	N	O	S	0	0
			3191	1010	1620	275	282	4		

- Molecule 11 is a protein called DNA replication complex GINS protein PSF3.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	E	171	Total	C	H	N	O	S	0	0
			2775	899	1396	221	252	7		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-22	MET	-	initiating methionine	UNP Q12146
E	-21	GLY	-	expression tag	UNP Q12146
E	-20	SER	-	expression tag	UNP Q12146
E	-19	SER	-	expression tag	UNP Q12146
E	-18	HIS	-	expression tag	UNP Q12146
E	-17	HIS	-	expression tag	UNP Q12146
E	-16	HIS	-	expression tag	UNP Q12146
E	-15	HIS	-	expression tag	UNP Q12146
E	-14	HIS	-	expression tag	UNP Q12146
E	-13	HIS	-	expression tag	UNP Q12146
E	-12	SER	-	expression tag	UNP Q12146

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-11	SER	-	expression tag	UNP Q12146
E	-10	GLY	-	expression tag	UNP Q12146
E	-9	LEU	-	expression tag	UNP Q12146
E	-8	VAL	-	expression tag	UNP Q12146
E	-7	PRO	-	expression tag	UNP Q12146
E	-6	ARG	-	expression tag	UNP Q12146
E	-5	GLY	-	expression tag	UNP Q12146
E	-4	SER	-	expression tag	UNP Q12146
E	-3	HIS	-	expression tag	UNP Q12146
E	-2	MET	-	expression tag	UNP Q12146
E	-1	ALA	-	expression tag	UNP Q12146
E	0	SER	-	expression tag	UNP Q12146

- Molecule 12 is a protein called DNA replication complex GINS protein SLD5.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	F	224	Total	C	H	N	O	S	0	0
			3709	1179	1861	305	352	12		

- Molecule 13 is a protein called Cell division control protein 45.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	G	565	Total	C	H	N	O	S	0	0
			9185	2929	4598	776	868	14		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	167G	TYR	-	linker	UNP Q08032
G	167H	LYS	-	linker	UNP Q08032
G	167I	ASP	-	linker	UNP Q08032
G	167J	ASP	-	linker	UNP Q08032
G	167K	ASP	-	linker	UNP Q08032
G	167L	GLY	-	linker	UNP Q08032
G	167M	ASP	-	linker	UNP Q08032
G	167N	TYR	-	linker	UNP Q08032
G	167O	LYS	-	linker	UNP Q08032
G	167P	ASP	-	linker	UNP Q08032
G	167Q	ASP	-	linker	UNP Q08032

- Molecule 14 is a protein called Mediator of replication checkpoint protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	P	50	Total	C	H	N	O	S	0	0
			805	258	397	68	81	1		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	1097	ASP	-	expression tag	UNP P25588
P	1098	TYR	-	expression tag	UNP P25588
P	1099	LYS	-	expression tag	UNP P25588
P	1100	ASP	-	expression tag	UNP P25588
P	1101	ASP	-	expression tag	UNP P25588
P	1102	ASP	-	expression tag	UNP P25588
P	1103	GLY	-	expression tag	UNP P25588
P	1104	ASP	-	expression tag	UNP P25588
P	1105	TYR	-	expression tag	UNP P25588
P	1106	LYS	-	expression tag	UNP P25588
P	1107	ASP	-	expression tag	UNP P25588
P	1108	ASP	-	expression tag	UNP P25588
P	1109	ASP	-	expression tag	UNP P25588

- Molecule 15 is a DNA chain called Leading strand.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	Q	35	Total	C	H	N	O	P	0	0
			1128	350	406	112	225	35		

- Molecule 16 is a DNA chain called Lagging strand.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	R	21	Total	C	H	N	O	P	0	0
			656	202	237	71	125	21		

- Molecule 17 is a protein called DNA primase small subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	S	391	Total	C	H	N	O	S	0	0
			6428	2055	3201	561	595	16		

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	-34	MET	-	initiating methionine	UNP P10363

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Chain	Residue	Modelled	Actual	Comment	Reference
S	-33	LYS	-	expression tag	UNP P10363
S	-32	ARG	-	expression tag	UNP P10363
S	-31	ARG	-	expression tag	UNP P10363
S	-30	TRP	-	expression tag	UNP P10363
S	-29	LYS	-	expression tag	UNP P10363
S	-28	LYS	-	expression tag	UNP P10363
S	-27	ASN	-	expression tag	UNP P10363
S	-26	PHE	-	expression tag	UNP P10363
S	-25	ILE	-	expression tag	UNP P10363
S	-24	ALA	-	expression tag	UNP P10363
S	-23	VAL	-	expression tag	UNP P10363
S	-22	SER	-	expression tag	UNP P10363
S	-21	ALA	-	expression tag	UNP P10363
S	-20	ALA	-	expression tag	UNP P10363
S	-19	ASN	-	expression tag	UNP P10363
S	-18	ARG	-	expression tag	UNP P10363
S	-17	PHE	-	expression tag	UNP P10363
S	-16	LYS	-	expression tag	UNP P10363
S	-15	LYS	-	expression tag	UNP P10363
S	-14	ILE	-	expression tag	UNP P10363
S	-13	SER	-	expression tag	UNP P10363
S	-12	SER	-	expression tag	UNP P10363
S	-11	SER	-	expression tag	UNP P10363
S	-10	GLY	-	expression tag	UNP P10363
S	-9	ALA	-	expression tag	UNP P10363
S	-8	LEU	-	expression tag	UNP P10363
S	-7	GLU	-	expression tag	UNP P10363
S	-6	ASN	-	expression tag	UNP P10363
S	-5	LEU	-	expression tag	UNP P10363
S	-4	TYR	-	expression tag	UNP P10363
S	-3	PHE	-	expression tag	UNP P10363
S	-2	GLN	-	expression tag	UNP P10363
S	-1	GLY	-	expression tag	UNP P10363
S	0	GLU	-	expression tag	UNP P10363

- Molecule 18 is a protein called Topoisomerase 1-associated factor 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	X	665	Total	C	H	N	O	S	0	0
			10978	3506	5563	911	979	19		

- Molecule 19 is a protein called Chromosome segregation in meiosis protein 3.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	Y	92	Total	C	H	N	O	S	0	0
			1575	496	806	139	131	3		

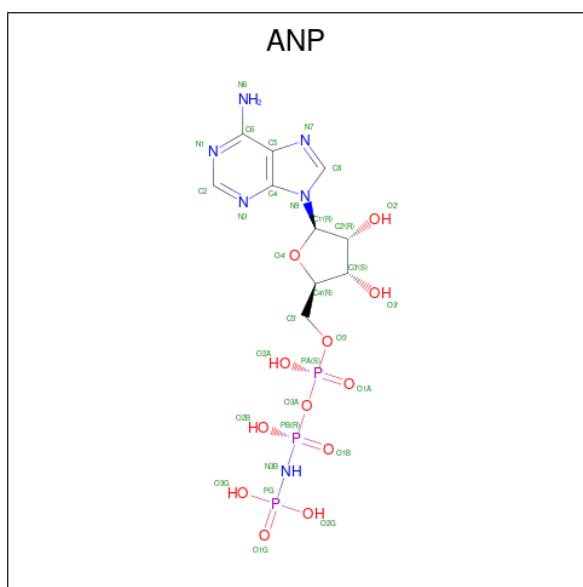
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	-1	GLY	-	expression tag	UNP Q04659
Y	0	GLU	-	expression tag	UNP Q04659

- Molecule 20 is a protein called DNA polymerase alpha catalytic subunit A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	J	198	Total	C	H	N	O	S	0	0
			3192	1018	1577	271	312	14		

- Molecule 21 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃) (labeled as "Ligand of Interest" by depositor).



- Molecule 22 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
22	2	1	Total 1	Mg 1	0
22	4	1	Total 1	Mg 1	0
22	5	1	Total 1	Mg 1	0
22	7	1	Total 1	Mg 1	0

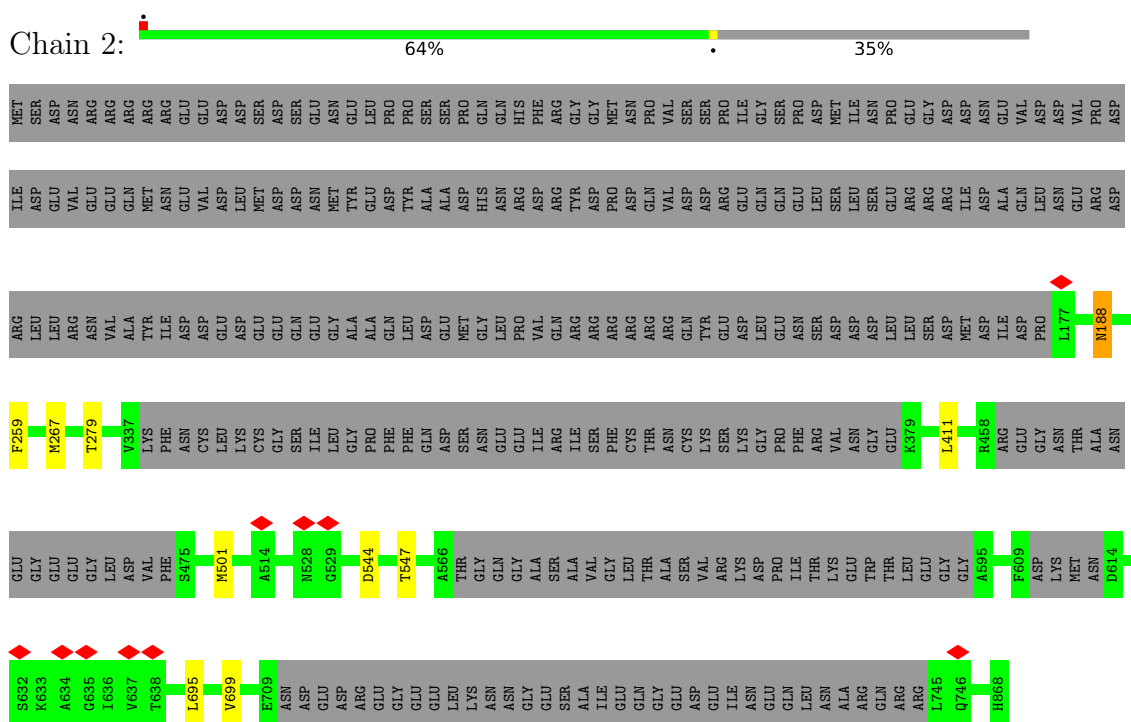
- Molecule 23 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
23	4	1	Total 1	Zn 1	0
23	5	1	Total 1	Zn 1	0
23	6	1	Total 1	Zn 1	0
23	7	1	Total 1	Zn 1	0

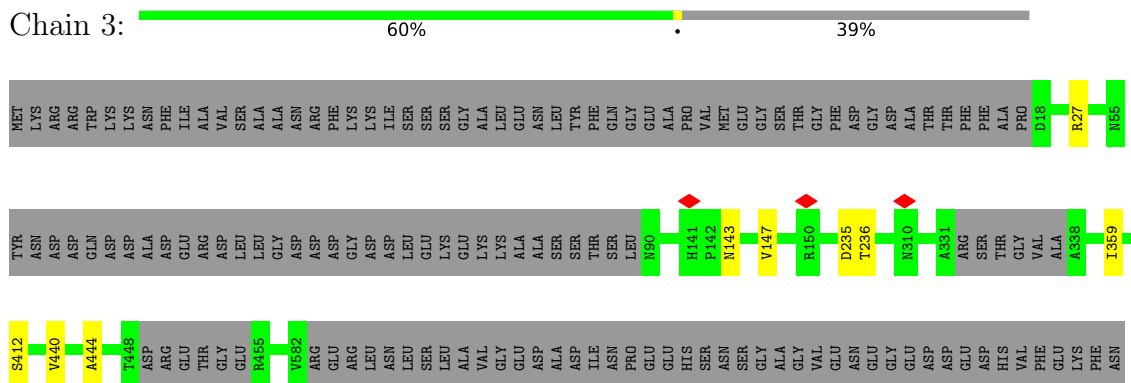
3 Residue-property plots

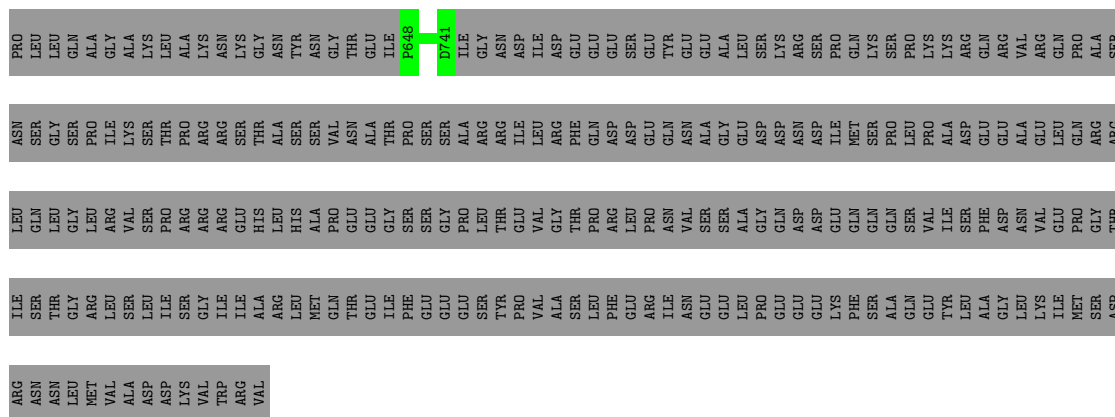
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: DNA replication licensing factor MCM2

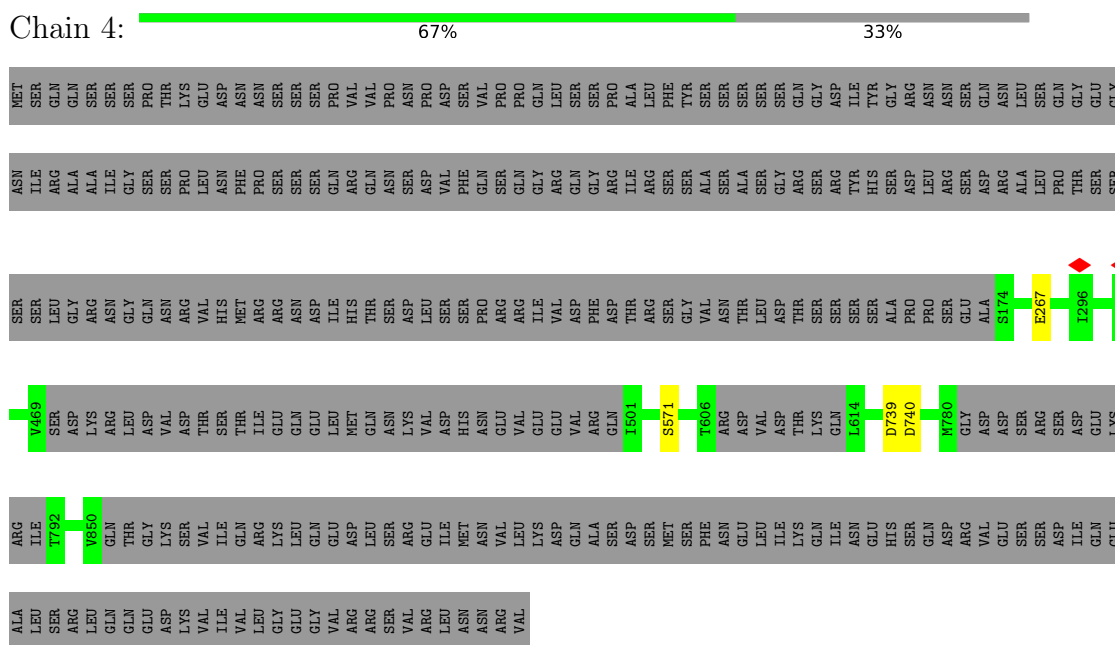


- Molecule 2: DNA replication licensing factor MCM3

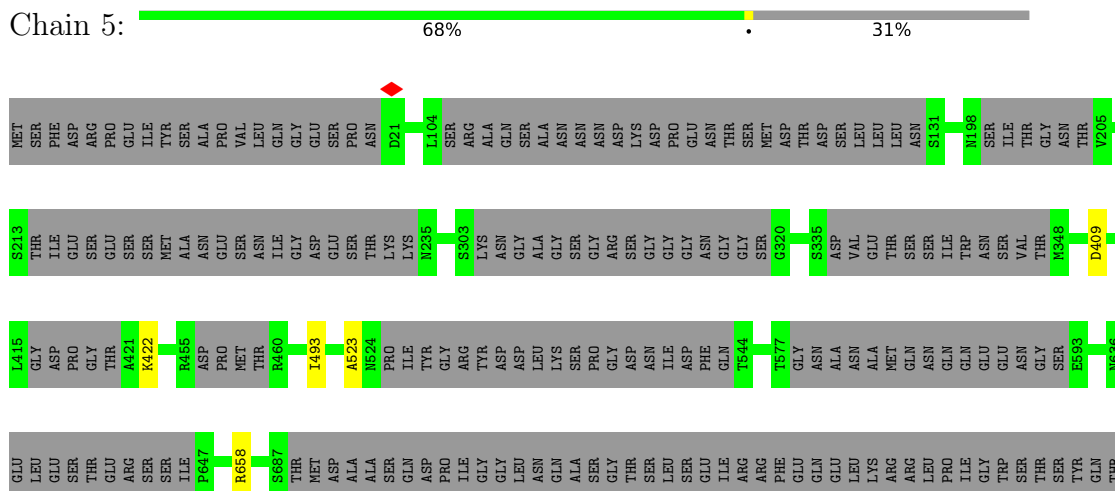




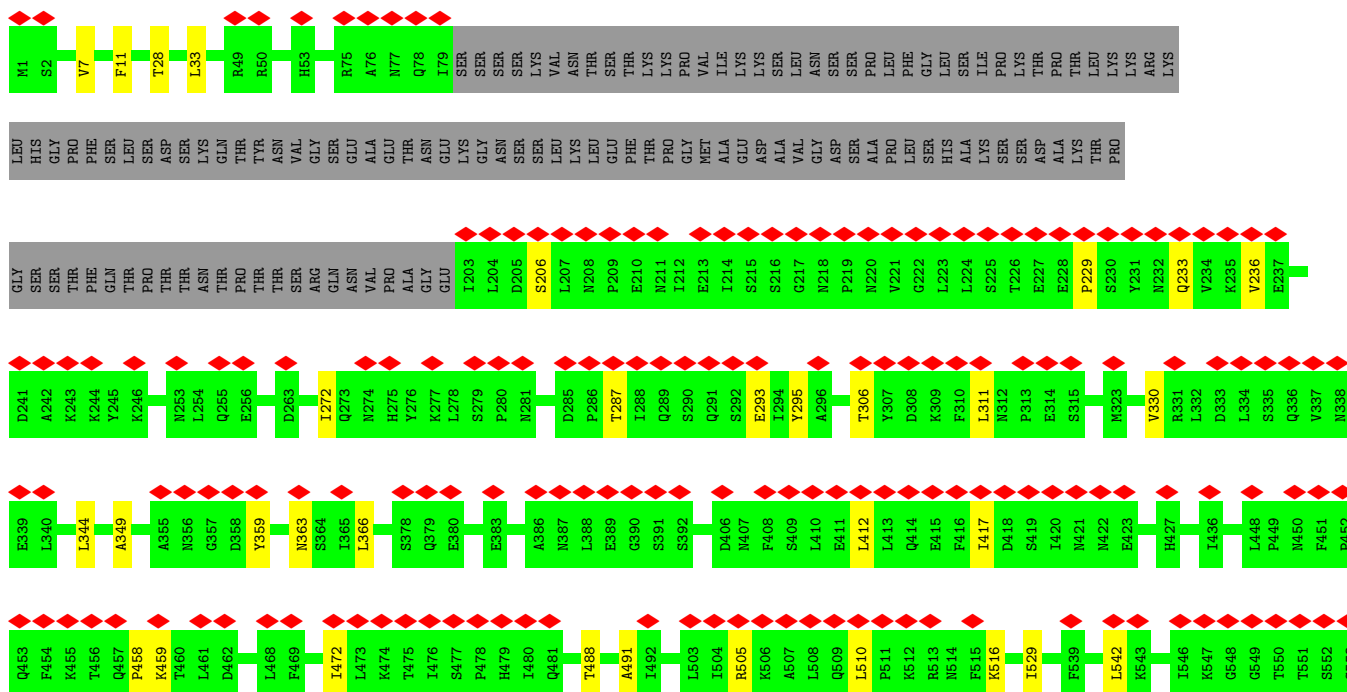
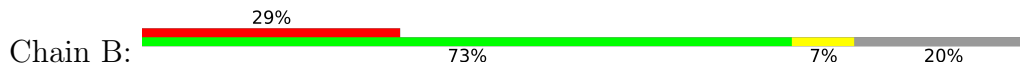
- Molecule 3: DNA replication licensing factor MCM4

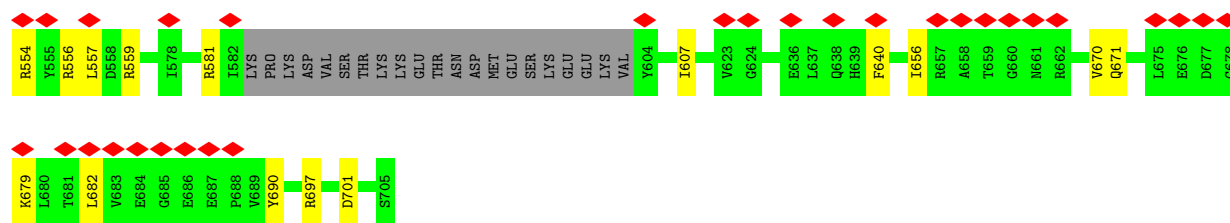


- Molecule 4: Minichromosome maintenance protein 5



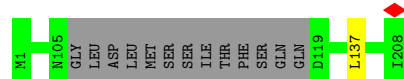
- Molecule 8: DNA polymerase alpha subunit B





- Molecule 9: DNA replication complex GINS protein PSF1

Chain C: 93% 6%



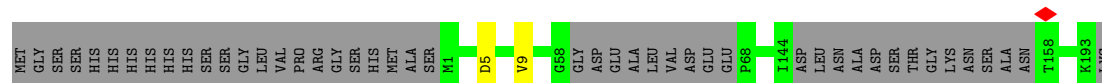
- Molecule 10: DNA replication complex GINS protein PSF2

Chain D: 86% 12%



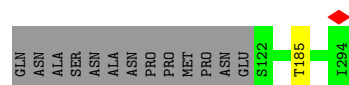
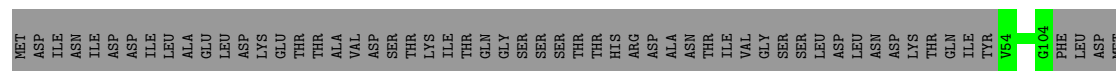
- Molecule 11: DNA replication complex GINS protein PSF3

Chain E: 78% 21%



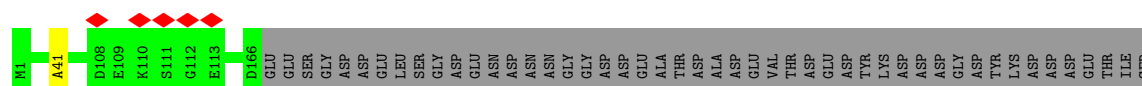
- Molecule 12: DNA replication complex GINS protein SLD5

Chain F: 76% 24%



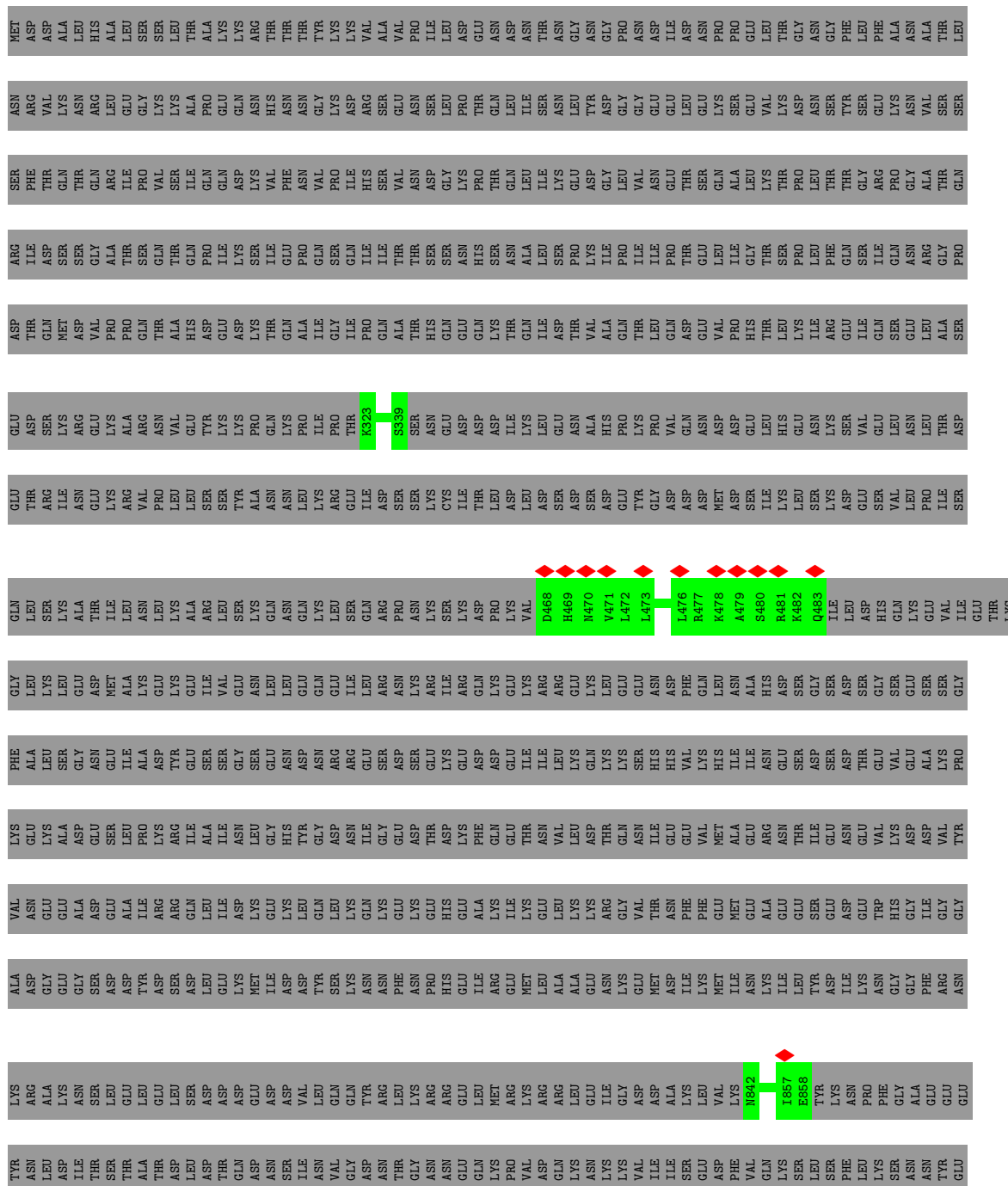
- Molecule 13: Cell division control protein 45

Chain G: 85% 14%





Chain P: 5% 95%

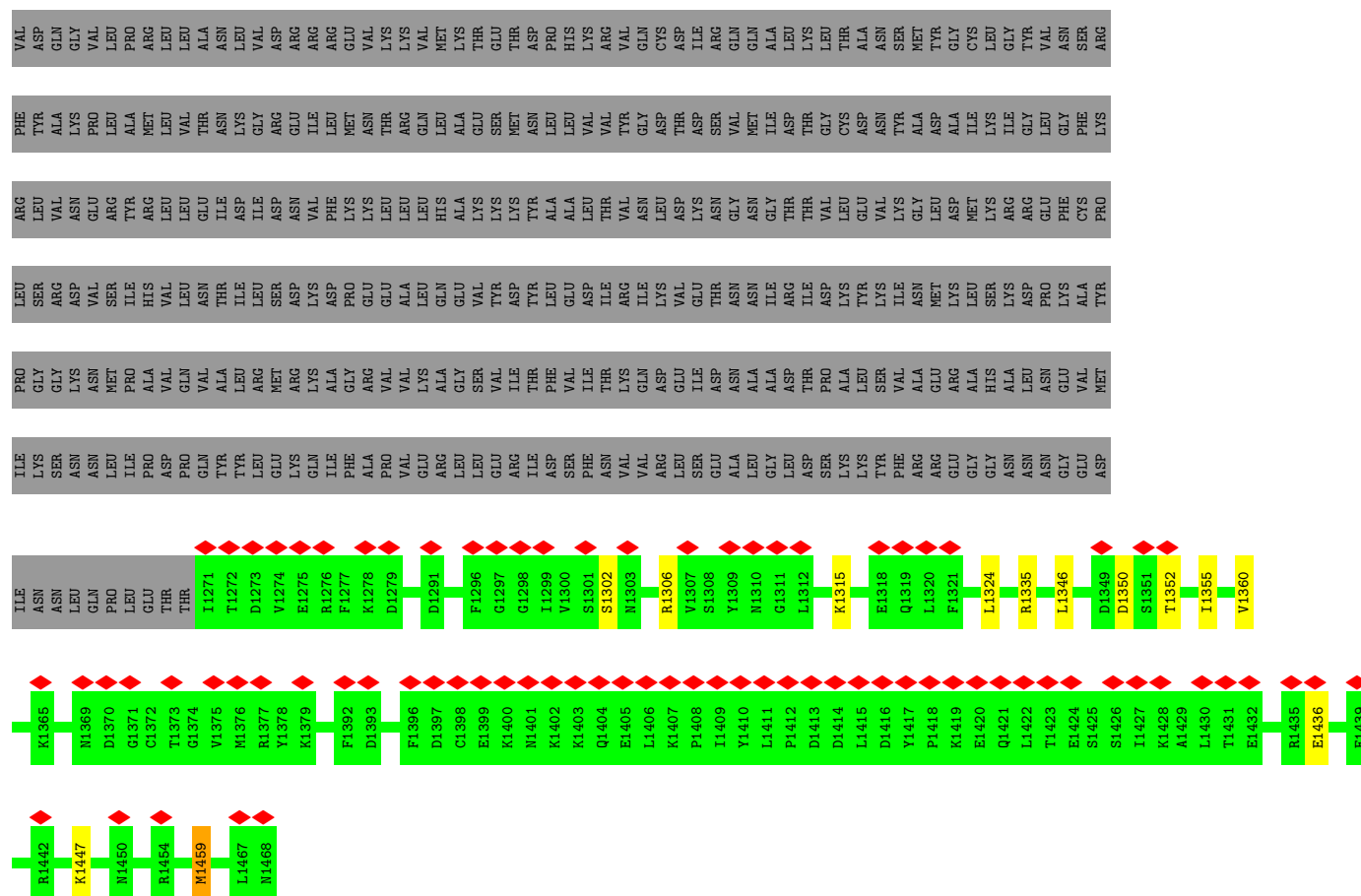


MET	GLY	LYS	GLY	GLY	GLY	MET	THR	GLU	GLU	ASP	VAL	GLN	LEU	ILE	GLN	SER	LEU	GLU	GLU	TRP	GLU	MET	ASN	ASP	ASP	ILE	GLY	GLN	HIS	THR	HIS	TYR	ASP	ASP	LEU	LEU	PRO	GLY	GLY	ASP	ASP	GLU	GLU	PHE	GLY	VAL	ASP	GLN	ASP	ASP	GLU	LEU	ASP	ALA	MET	LYS	GLU	GLU	MET	GLY	PHE
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- Molecule 20: DNA polymerase alpha catalytic subunit A



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53964	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 ($e^-/\text{\AA}^2$)	39.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	11.148	Depositor
Minimum map value	-6.107	Depositor
Average map value	0.035	Depositor
Map value standard deviation	0.305	Depositor
Recommended contour level	1.68	Depositor
Map size (Å)	498.80597, 498.80597, 498.80597	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.2673, 2.2673, 2.2673	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ANP, ZN, 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	2	0.30	0/4608	0.47	0/6221
2	3	0.21	0/4877	0.43	0/6616
3	4	0.23	0/5066	0.44	0/6850
4	5	0.23	0/4265	0.43	0/5750
5	6	0.23	0/5008	0.42	0/6755
6	7	0.23	1/5235 (0.0%)	0.44	2/7077 (0.0%)
7	A	0.19	0/2228	0.39	0/2993
8	B	0.19	0/4579	0.36	0/6211
9	C	0.21	0/1619	0.41	0/2178
10	D	0.22	0/1603	0.43	0/2170
11	E	0.21	0/1412	0.41	0/1910
12	F	0.21	0/1884	0.41	0/2545
13	G	0.21	0/4672	0.41	0/6320
14	P	0.24	0/413	0.45	0/547
15	Q	0.35	0/804	0.68	0/1240
16	R	0.37	0/467	0.59	0/715
17	S	0.18	0/3304	0.36	0/4462
18	X	0.27	0/5519	0.52	0/7441
19	Y	0.26	0/785	0.51	0/1050
20	J	0.18	0/1647	0.36	0/2220
All	All	0.23	1/59995 (0.0%)	0.44	2/81271 (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	2	0	1
5	6	0	1
6	7	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
18	X	0	2
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	7	627	ASP	C-N	5.77	1.41	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	7	627	ASP	CA-C-N	5.98	132.96	121.54
6	7	627	ASP	C-N-CA	5.98	132.96	121.54

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2	411	LEU	Peptide
5	6	737	LYS	Mainchain
6	7	210	ASN	Mainchain
6	7	627	ASP	Mainchain
6	7	81	ASP	Mainchain

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	2	4534	4606	4599	4	0
2	3	4792	4861	4857	4	0
3	4	4990	5065	5057	3	0
4	5	4213	4347	4335	2	0
5	6	4928	4980	4970	1	0
6	7	5154	5233	5224	5	0
7	A	2185	2197	2194	1	0
8	B	4480	4464	4461	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	C	1599	1603	1601	1	0
10	D	1571	1620	1618	2	0
11	E	1379	1396	1397	1	0
12	F	1848	1861	1859	1	0
13	G	4587	4598	4594	2	0
14	P	408	397	394	0	0
15	Q	722	406	408	0	0
16	R	419	237	238	0	0
17	S	3227	3201	3199	5	0
18	X	5415	5563	5556	15	0
19	Y	769	806	805	1	0
20	J	1615	1577	1576	9	0
21	2	31	13	13	0	0
21	3	31	13	13	1	0
21	4	31	13	13	1	0
21	7	31	13	13	0	0
22	2	1	0	0	0	0
22	4	1	0	0	0	0
22	5	1	0	0	0	0
22	7	1	0	0	0	0
23	4	1	0	0	0	0
23	5	1	0	0	0	0
23	6	1	0	0	0	0
23	7	1	0	0	0	0
All	All	58967	59070	58994	77	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 77 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)
8:B:488:THR:O	20:J:1335:ARG:NH2	2.16	0.78
18:X:207:ASN:O	18:X:211:ASN:ND2	2.18	0.77
8:B:236:VAL:O	8:B:516:LYS:NZ	2.27	0.67
8:B:417:ILE:HD12	8:B:472:ILE:HG22	1.79	0.65
8:B:459:LYS:NZ	20:J:1436:GLU:OE2	2.30	0.64

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	556/868 (64%)	546 (98%)	10 (2%)	0	100	100
2	3	603/1009 (60%)	587 (97%)	16 (3%)	0	100	100
3	4	620/933 (66%)	605 (98%)	15 (2%)	0	100	100
4	5	511/775 (66%)	494 (97%)	17 (3%)	0	100	100
5	6	611/1017 (60%)	602 (98%)	9 (2%)	0	100	100
6	7	648/845 (77%)	635 (98%)	13 (2%)	0	100	100
7	A	252/528 (48%)	247 (98%)	4 (2%)	1 (0%)	30	67
8	B	555/705 (79%)	544 (98%)	11 (2%)	0	100	100
9	C	191/208 (92%)	189 (99%)	2 (1%)	0	100	100
10	D	184/213 (86%)	182 (99%)	2 (1%)	0	100	100
11	E	165/217 (76%)	164 (99%)	1 (1%)	0	100	100
12	F	220/294 (75%)	216 (98%)	4 (2%)	0	100	100
13	G	557/657 (85%)	540 (97%)	17 (3%)	0	100	100
14	P	44/1109 (4%)	42 (96%)	2 (4%)	0	100	100
17	S	389/444 (88%)	380 (98%)	9 (2%)	0	100	100
18	X	651/1238 (53%)	640 (98%)	11 (2%)	0	100	100
19	Y	90/319 (28%)	87 (97%)	3 (3%)	0	100	100
20	J	196/1468 (13%)	194 (99%)	2 (1%)	0	100	100
All	All	7043/12847 (55%)	6894 (98%)	148 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	A	255	GLN

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	503/770 (65%)	500 (99%)	3 (1%)	78	80
2	3	530/866 (61%)	528 (100%)	2 (0%)	84	82
3	4	568/848 (67%)	568 (100%)	0	100	100
4	5	482/688 (70%)	481 (100%)	1 (0%)	87	85
5	6	545/886 (62%)	542 (99%)	3 (1%)	78	80
6	7	578/753 (77%)	578 (100%)	0	100	100
7	A	246/488 (50%)	244 (99%)	2 (1%)	73	77
8	B	508/637 (80%)	507 (100%)	1 (0%)	87	85
9	C	181/193 (94%)	181 (100%)	0	100	100
10	D	178/198 (90%)	177 (99%)	1 (1%)	78	80
11	E	155/192 (81%)	155 (100%)	0	100	100
12	F	216/279 (77%)	216 (100%)	0	100	100
13	G	510/592 (86%)	509 (100%)	1 (0%)	87	85
14	P	47/1015 (5%)	47 (100%)	0	100	100
17	S	357/402 (89%)	357 (100%)	0	100	100
18	X	546/1125 (48%)	533 (98%)	13 (2%)	43	63
19	Y	72/286 (25%)	70 (97%)	2 (3%)	38	59
20	J	185/1334 (14%)	183 (99%)	2 (1%)	65	74
All	All	6407/11552 (56%)	6376 (100%)	31 (0%)	78	81

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	X	99	CYS
19	Y	92	ILE
18	X	180	ILE
20	J	1306	ARG
18	X	516	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
3	4	400	GLN
18	X	160	GLN
5	6	659	GLN
20	J	1316	HIS
13	G	55	GLN

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 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
21	ANP	3	1500	22	33,33,33	0.93	4 (12%)	45,52,52	0.63	0
21	ANP	7	901	22	33,33,33	1.02	4 (12%)	45,52,52	0.61	0
21	ANP	4	1001	22	33,33,33	0.94	4 (12%)	45,52,52	0.49	0
21	ANP	2	1500	22	33,33,33	0.94	4 (12%)	45,52,52	0.64	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	ANP	3	1500	22	-	5/18/38/38	0/3/3/3
21	ANP	7	901	22	-	3/18/38/38	0/3/3/3
21	ANP	4	1001	22	-	6/18/38/38	0/3/3/3
21	ANP	2	1500	22	-	7/18/38/38	0/3/3/3

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	7	901	ANP	PB-O3A	-3.63	1.54	1.59
21	4	1001	ANP	PB-O3A	-2.63	1.55	1.59
21	3	1500	ANP	PB-O3A	-2.54	1.55	1.59
21	2	1500	ANP	PG-O1G	2.49	1.50	1.46
21	4	1001	ANP	PG-O1G	2.48	1.49	1.46

There are no bond angle outliers.

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
21	2	1500	ANP	PB-N3B-PG-O1G
21	2	1500	ANP	PG-N3B-PB-O1B
21	2	1500	ANP	O4'-C1'-N9-C8
21	2	1500	ANP	O4'-C1'-N9-C4
21	3	1500	ANP	PB-N3B-PG-O1G

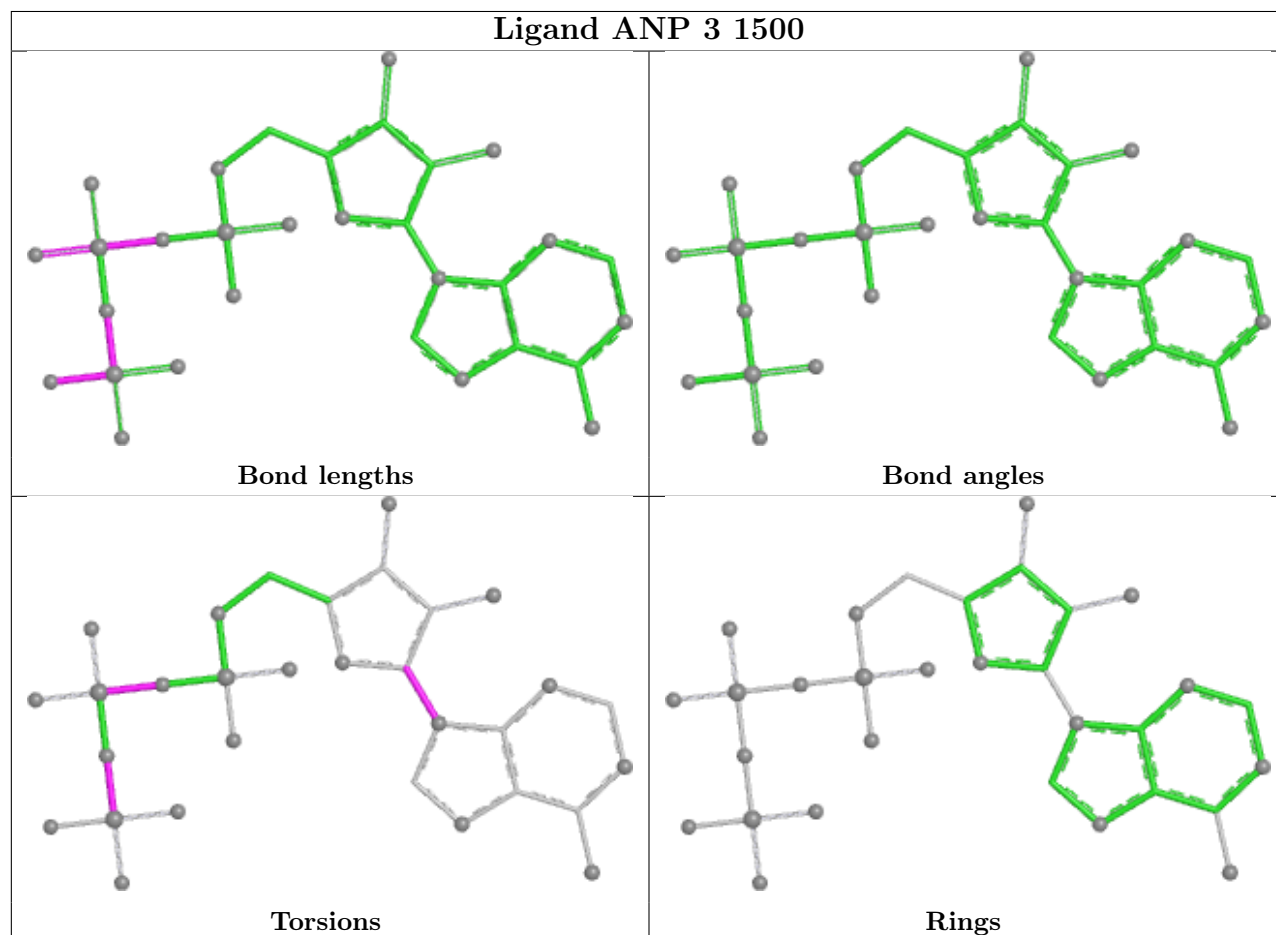
There are no ring outliers.

2 monomers are involved in 2 short contacts:

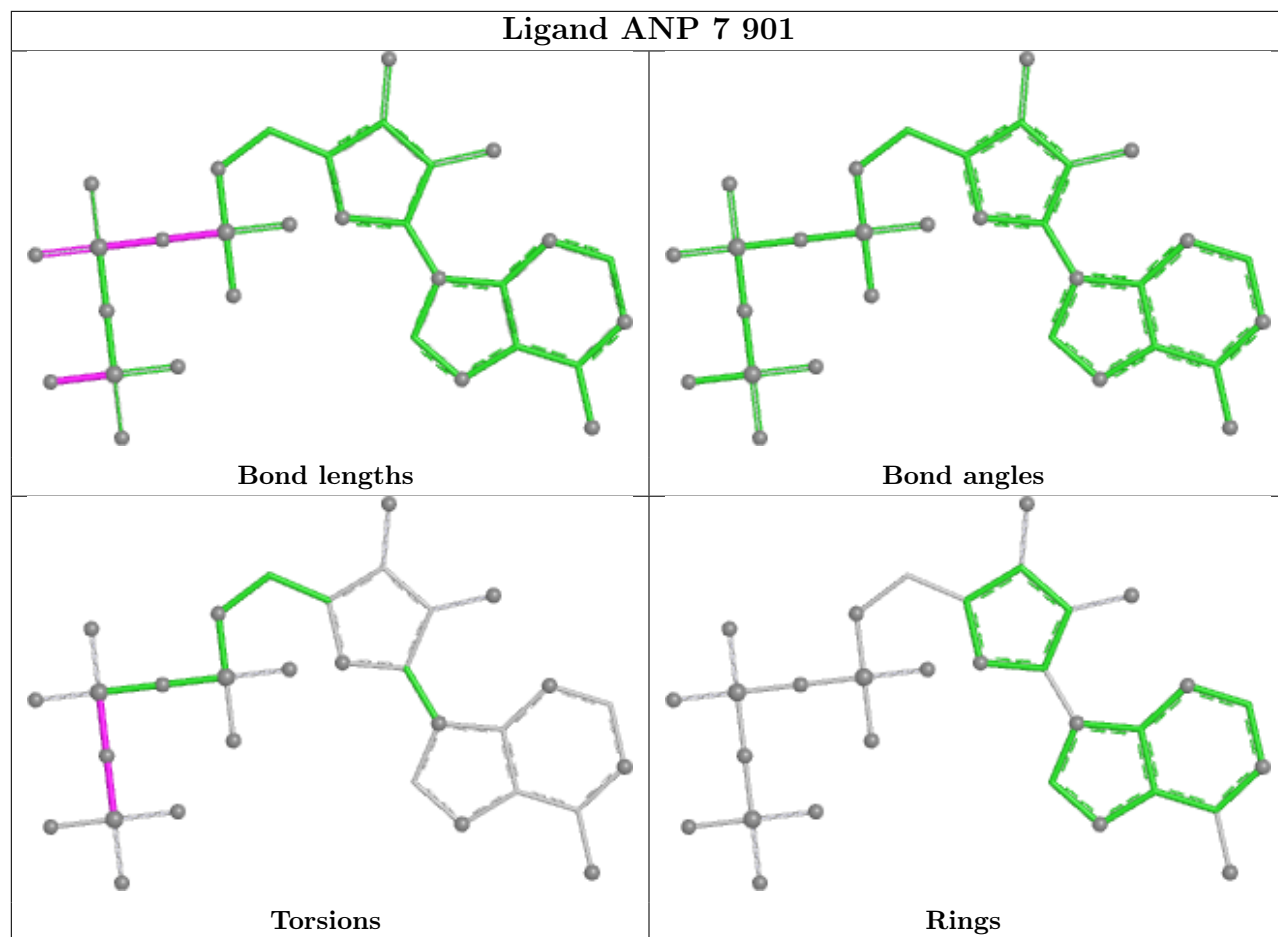
Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	3	1500	ANP	1	0
21	4	1001	ANP	1	0

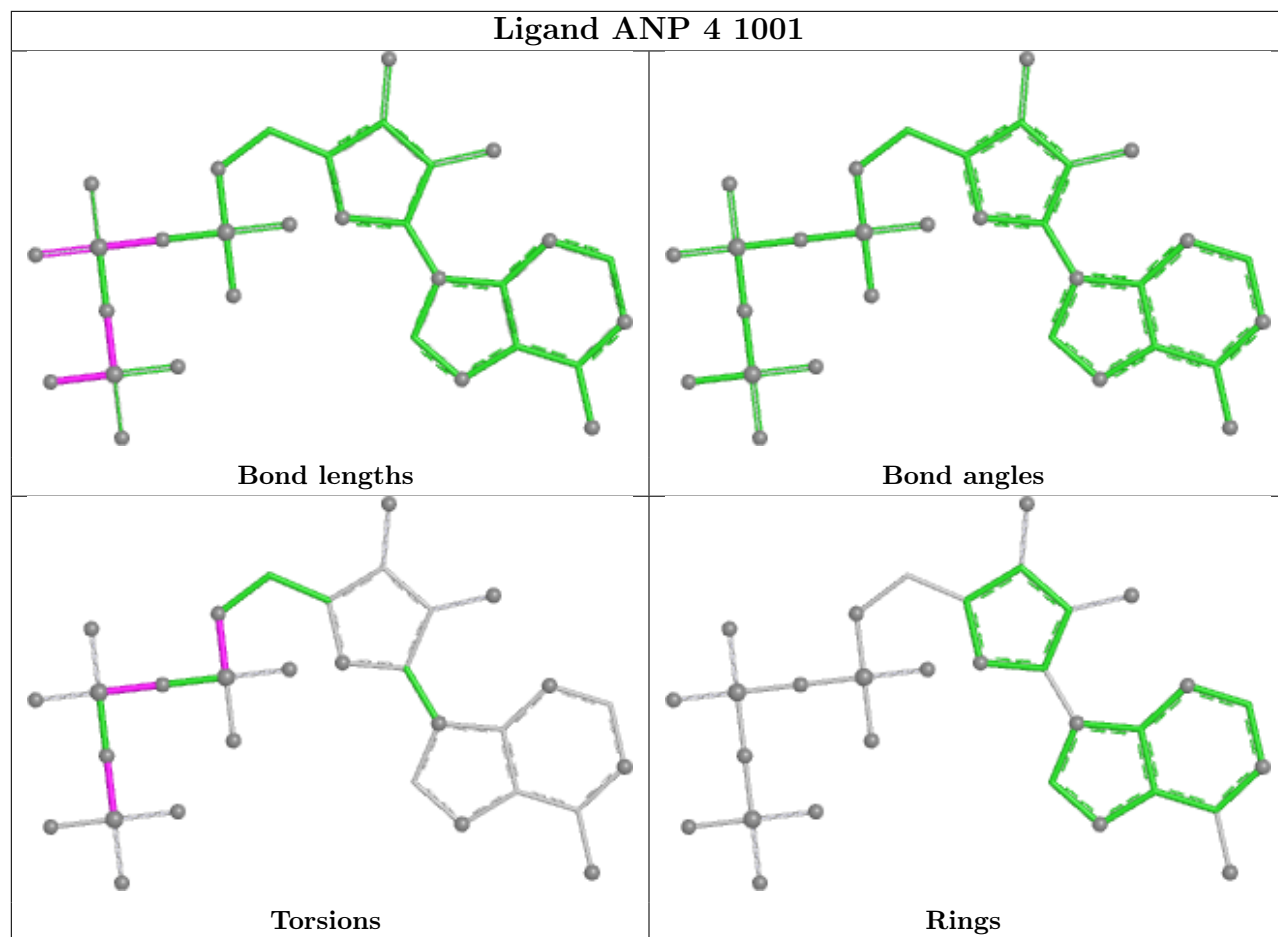
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

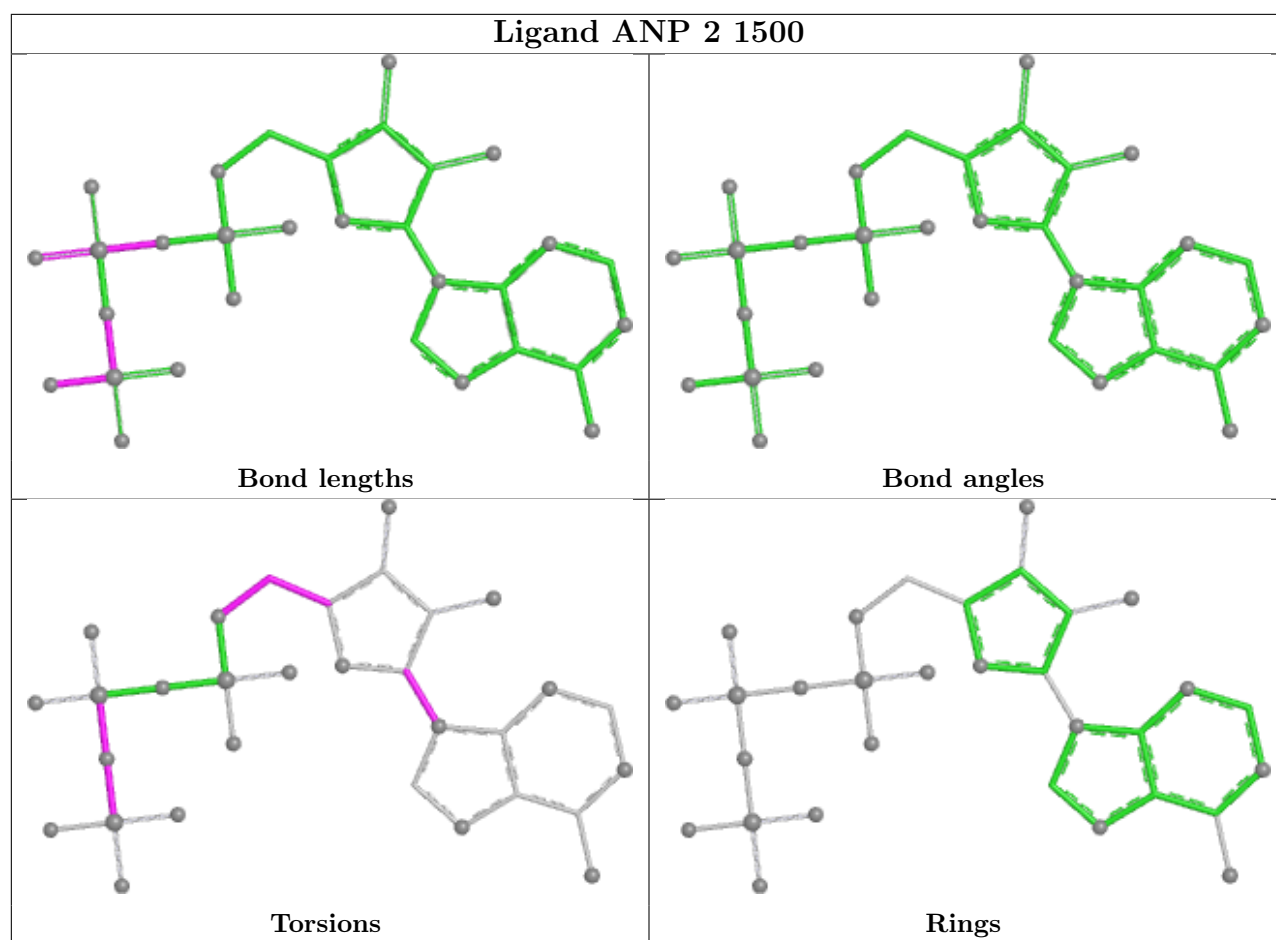
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



Ligand ANP 7 901







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.

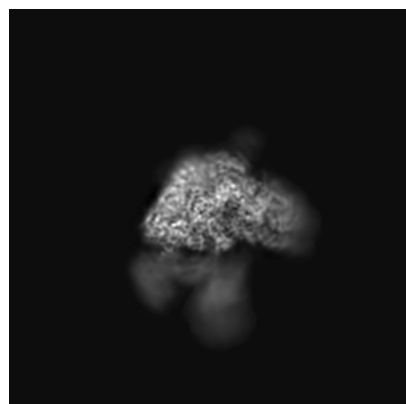
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15924. These allow visual inspection of the internal detail of the map and identification of artifacts.

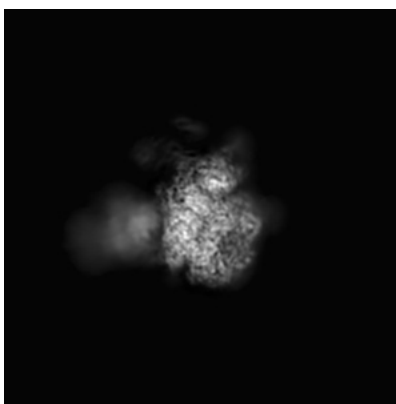
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

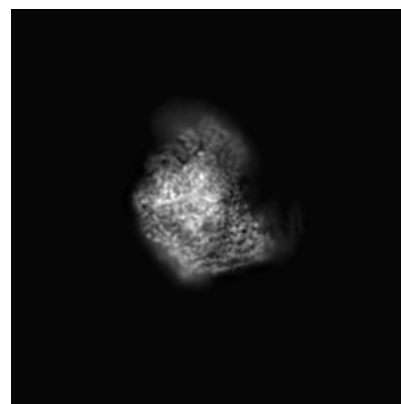
6.1.1 Primary map



X

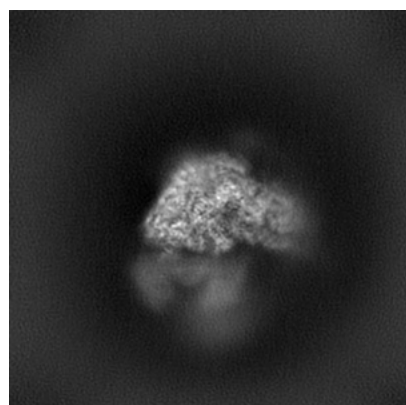


Y

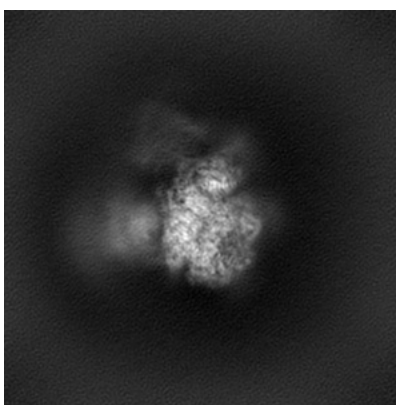


Z

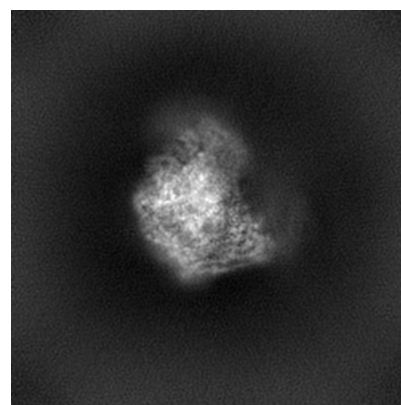
6.1.2 Raw map



X



Y

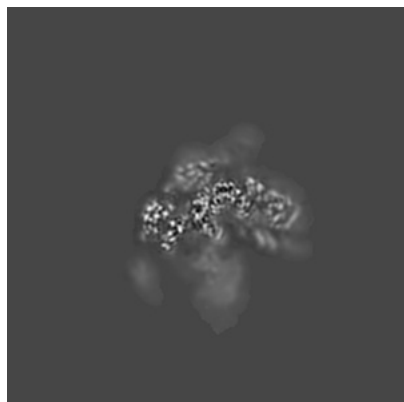


Z

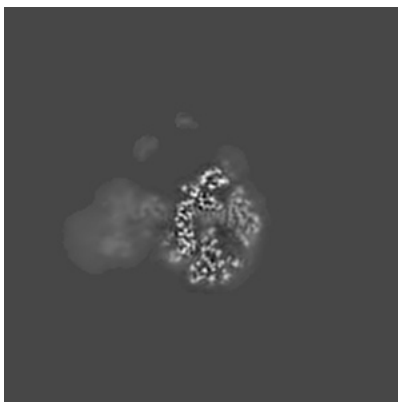
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

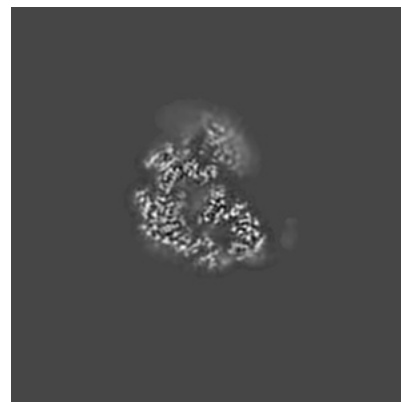
6.2.1 Primary map



X Index: 110

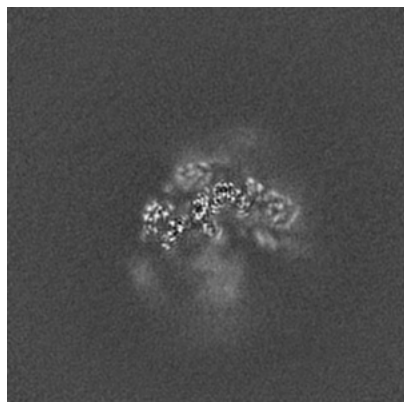


Y Index: 110

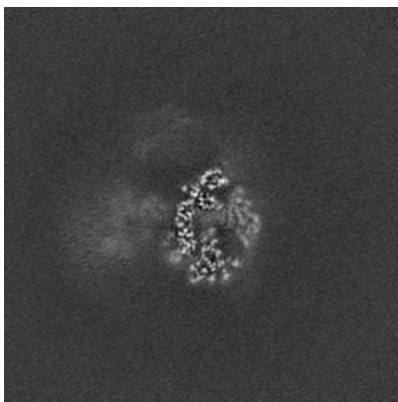


Z Index: 110

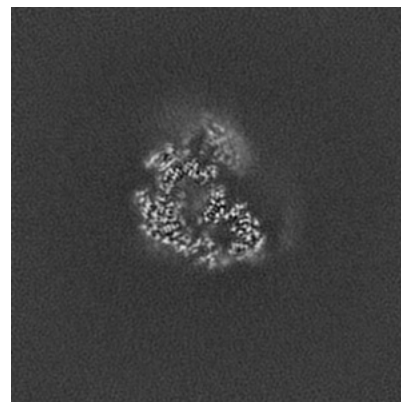
6.2.2 Raw map



X Index: 110



Y Index: 110

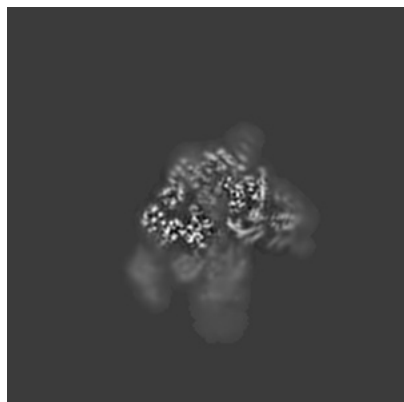


Z Index: 110

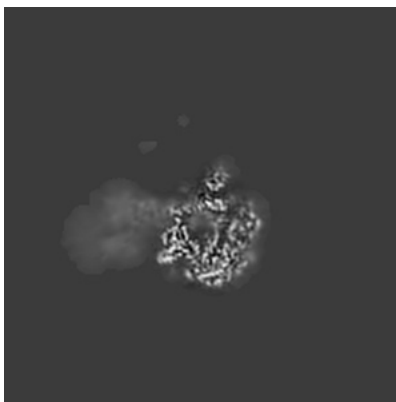
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

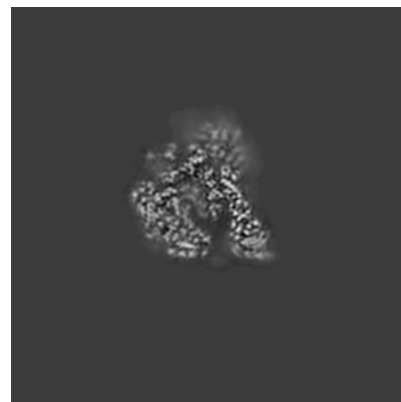
6.3.1 Primary map



X Index: 104

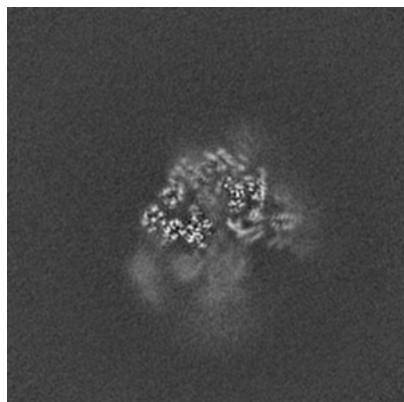


Y Index: 114

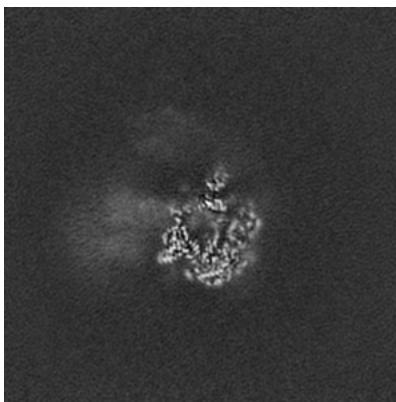


Z Index: 115

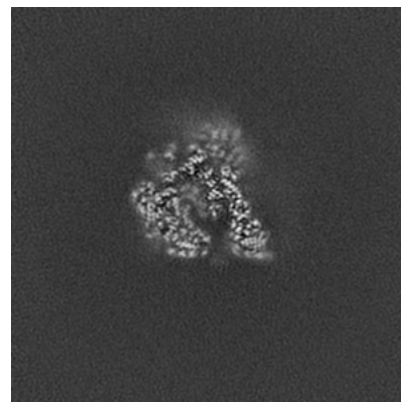
6.3.2 Raw map



X Index: 104



Y Index: 114

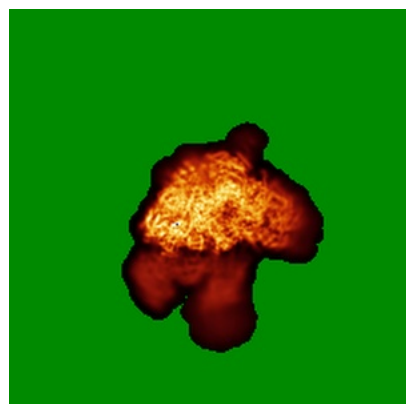


Z Index: 115

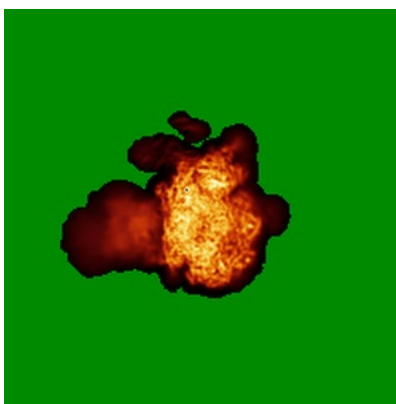
The images above show the largest variance slices of the map in three orthogonal directions.

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

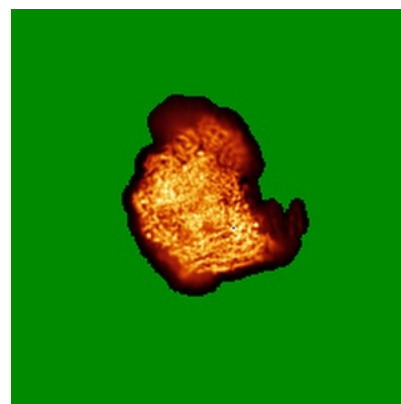
6.4.1 Primary map



X

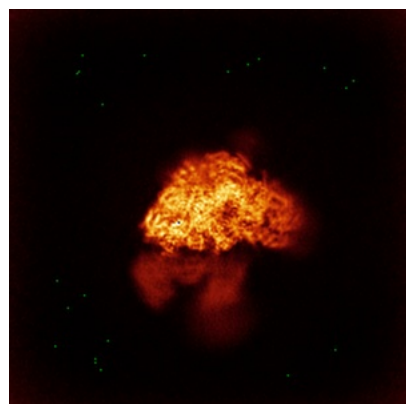


Y

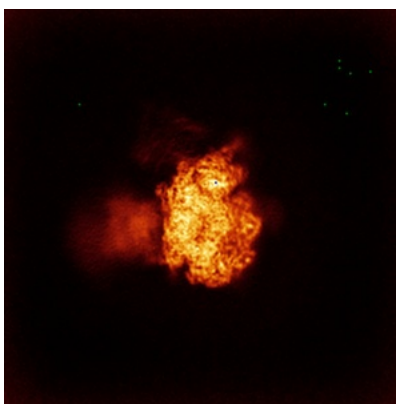


Z

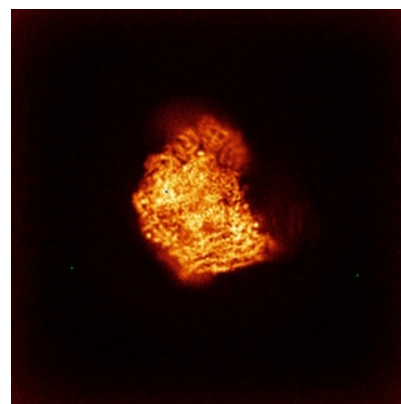
6.4.2 Raw map



X



Y

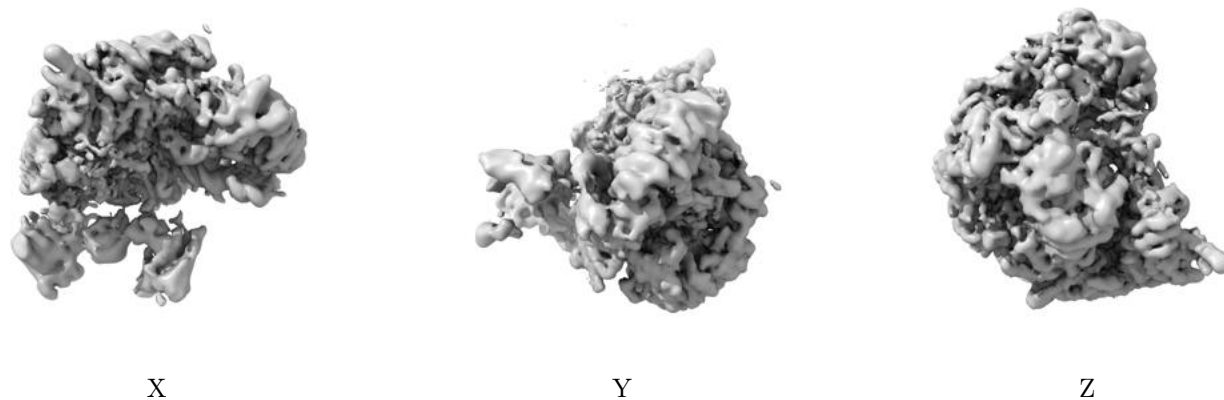


Z

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

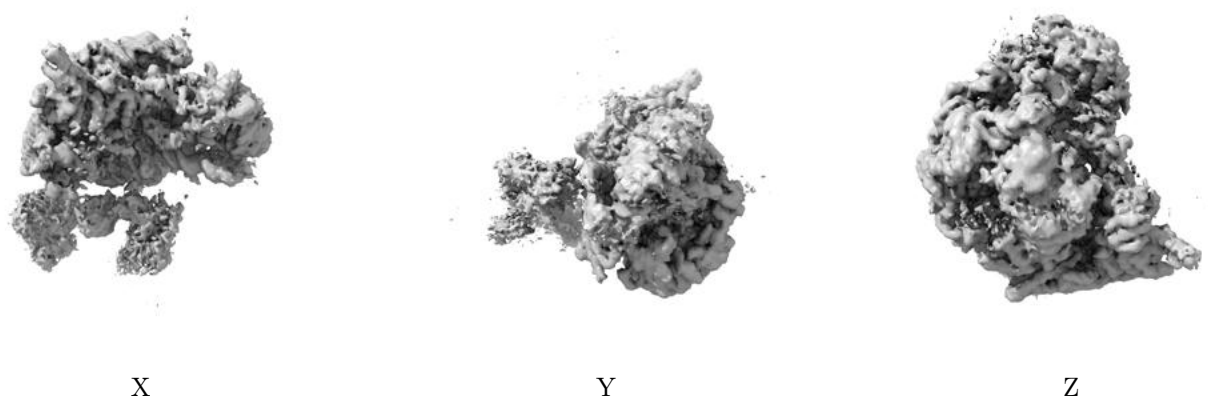
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.68. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

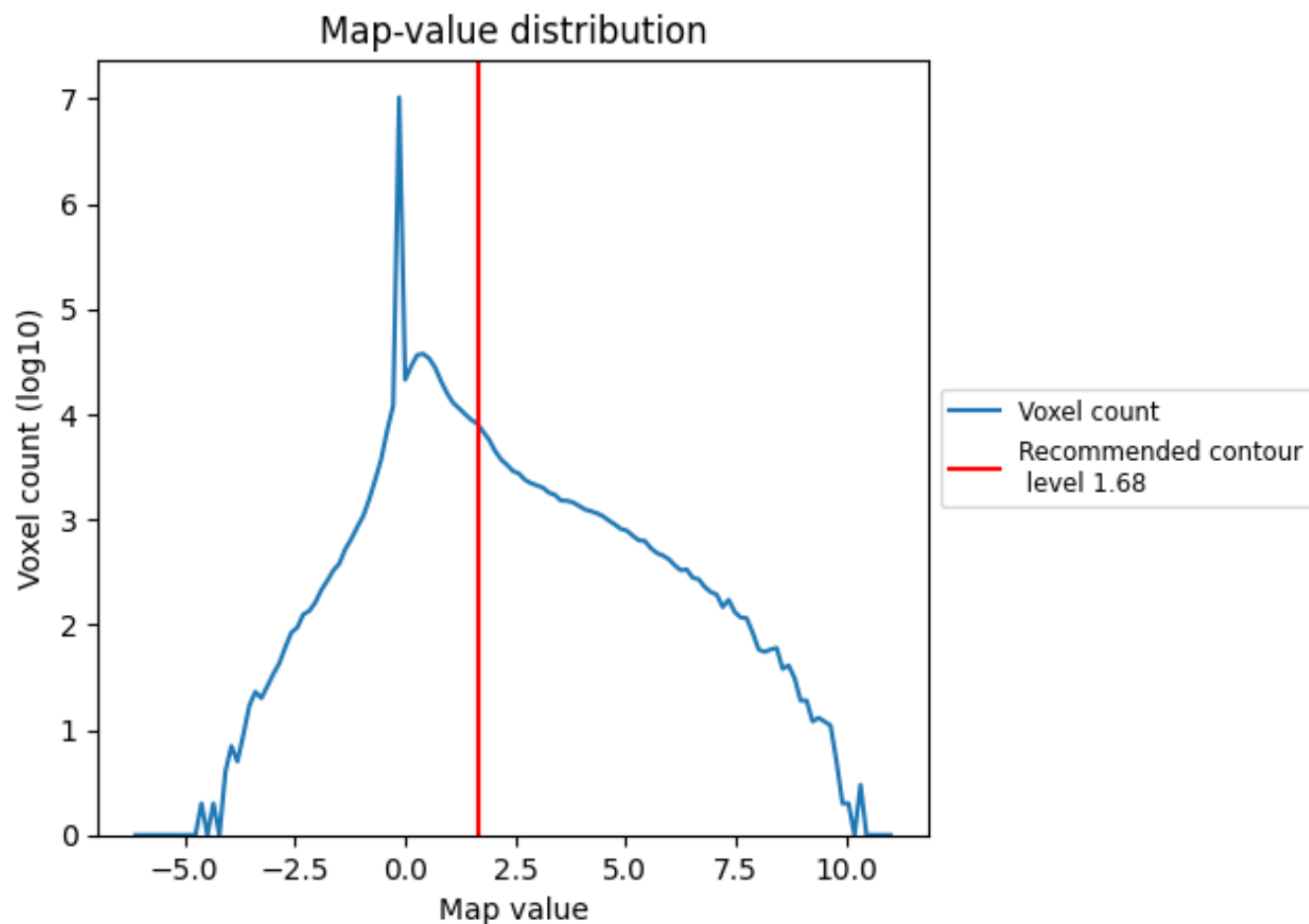
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

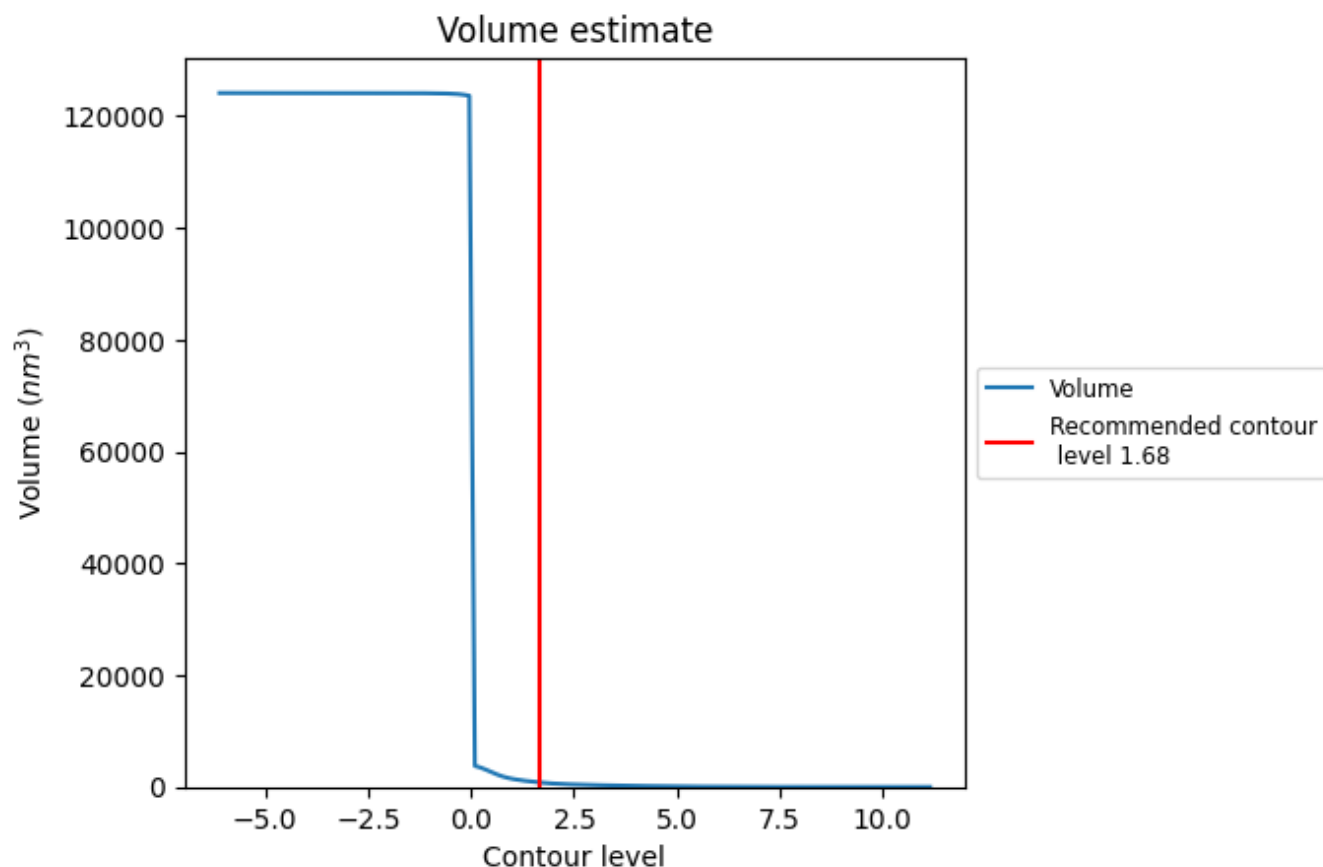
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

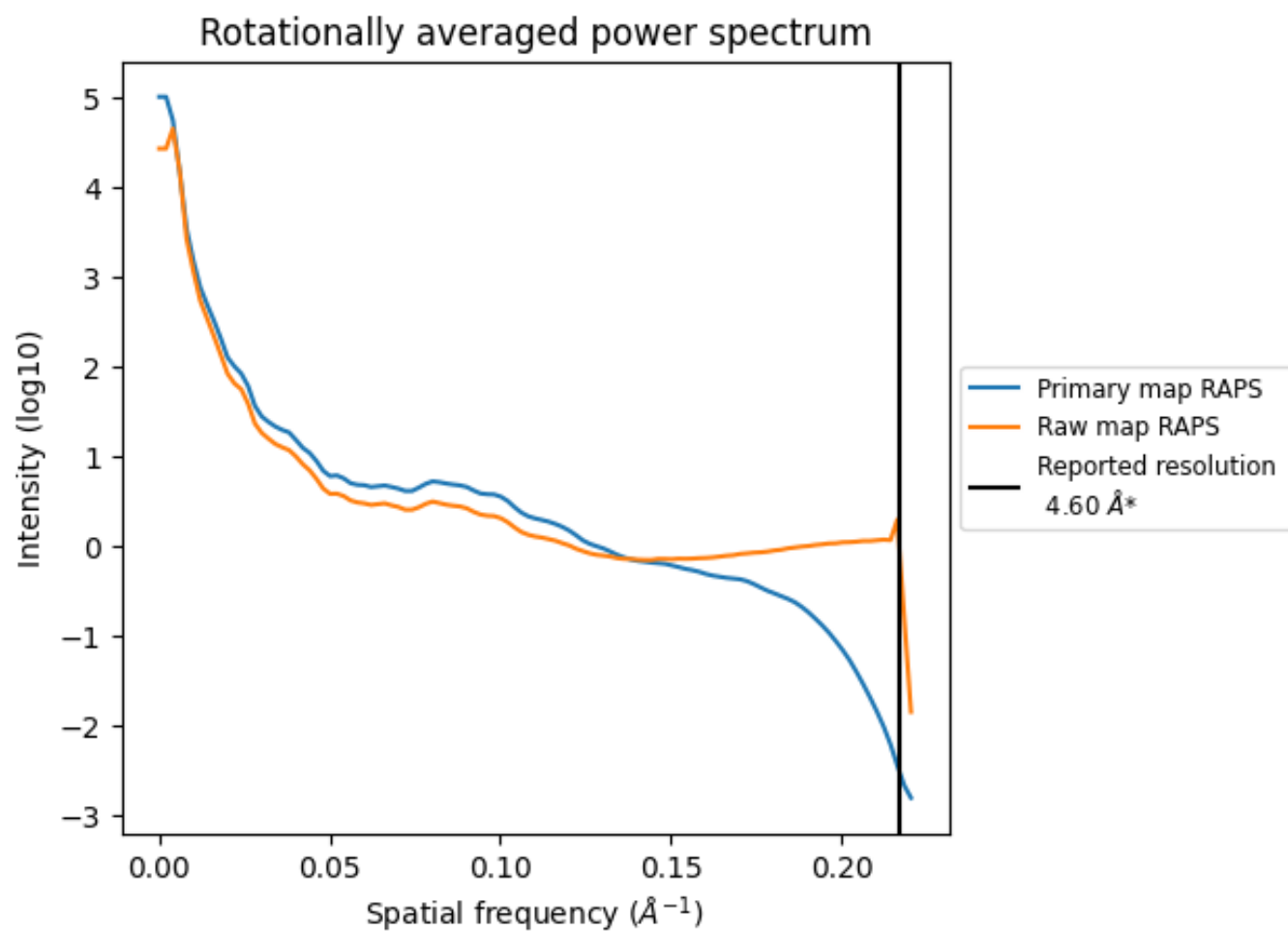
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 800 nm^3 ; this corresponds to an approximate mass of 723 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 ⓘ

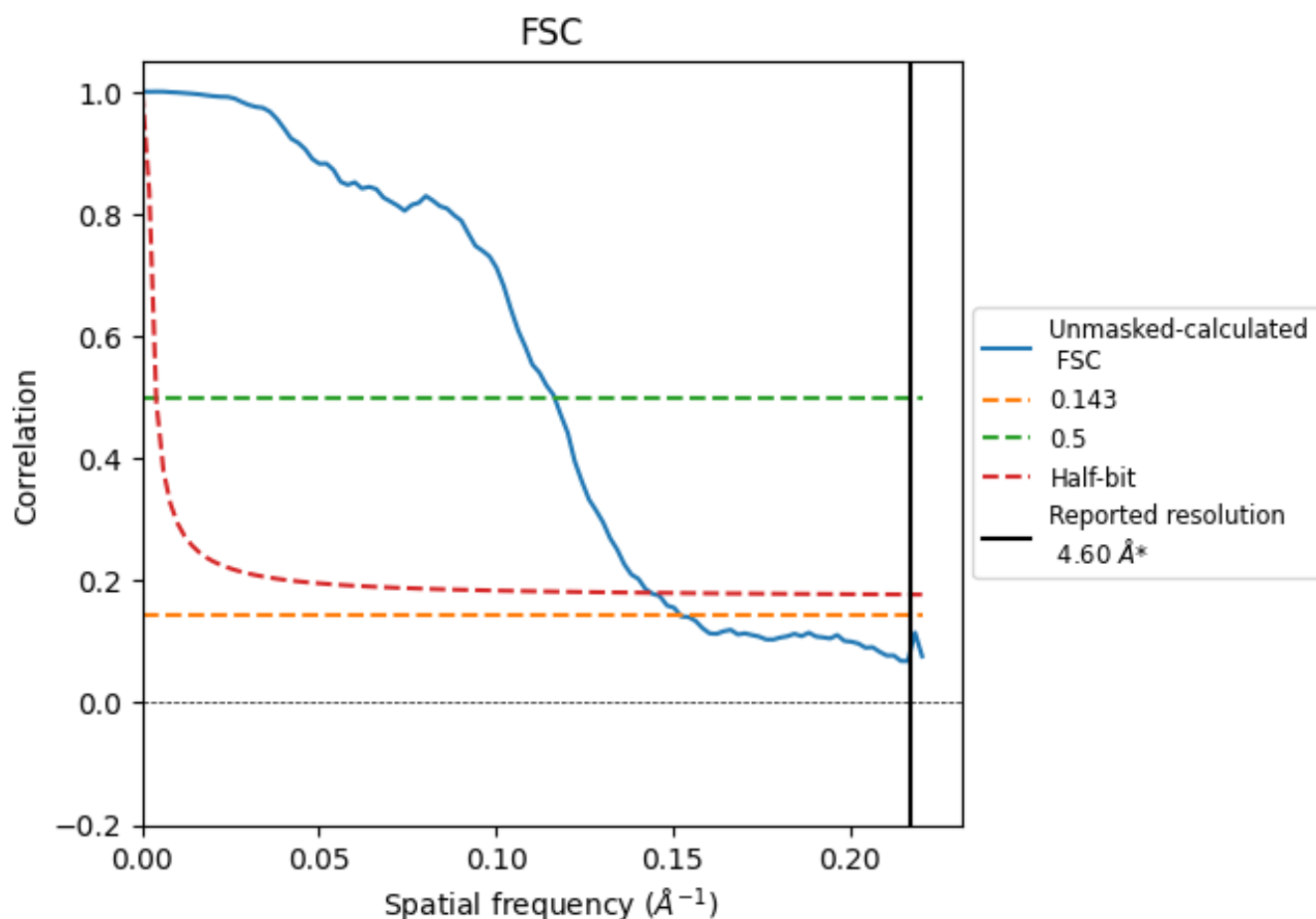


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

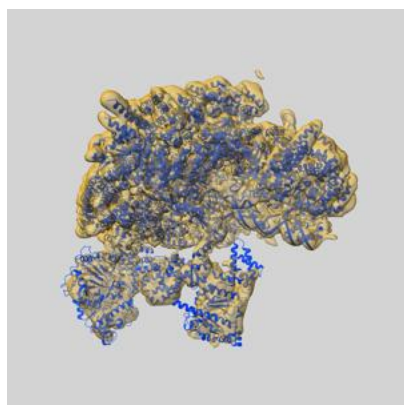
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.57	8.58	6.95

*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 6.57 differs from the reported value 4.6 by more than 10 %

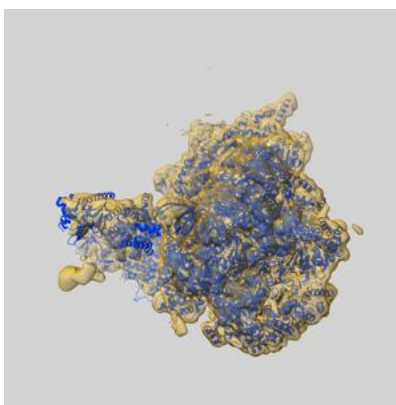
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15924 and PDB model 8B9C. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

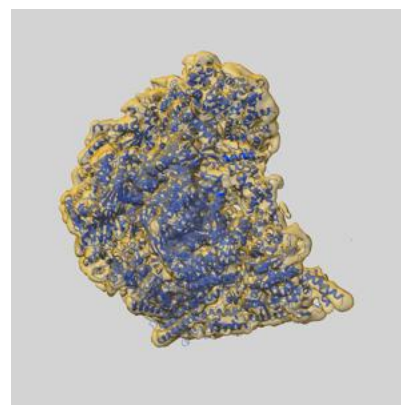
9.1 Map-model overlay [i](#)



X



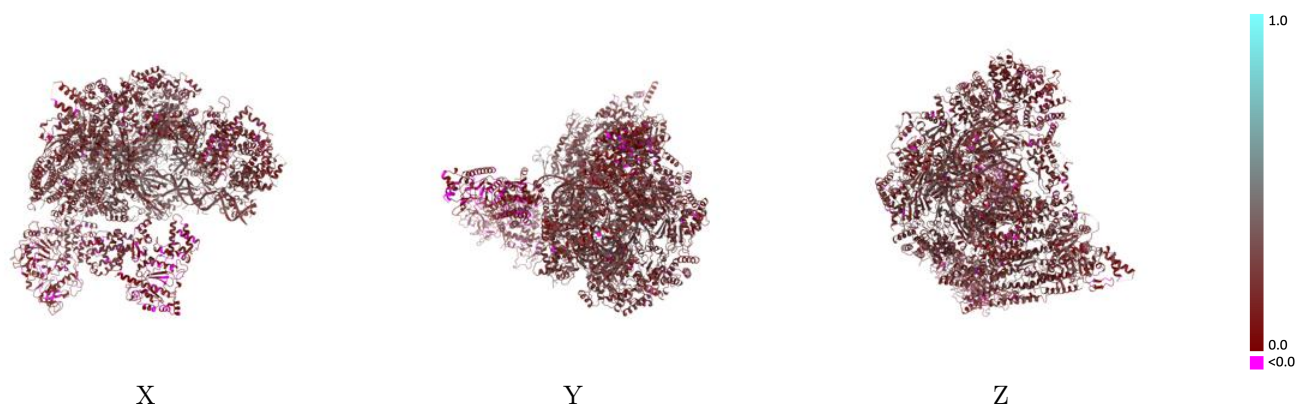
Y



Z

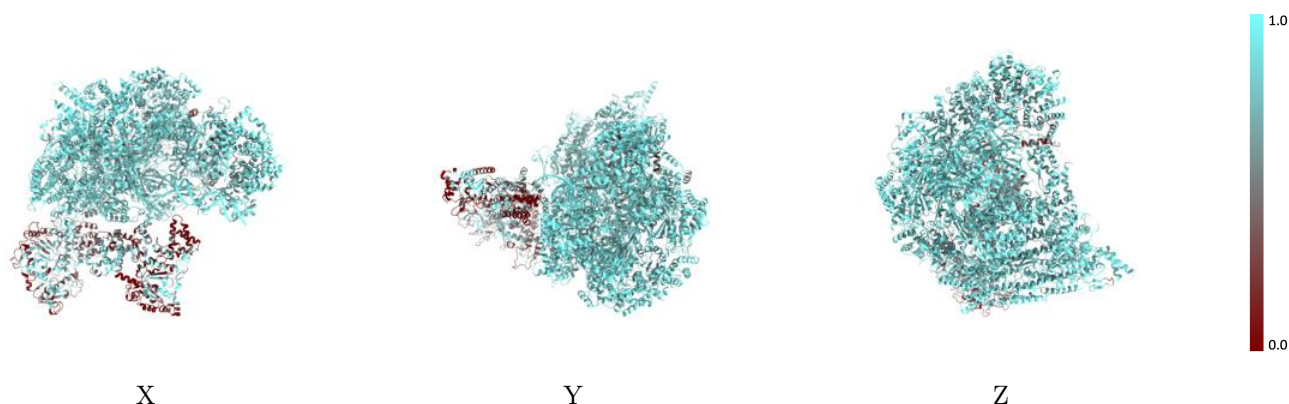
The images above show the 3D surface view of the map at the recommended contour level 1.68 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



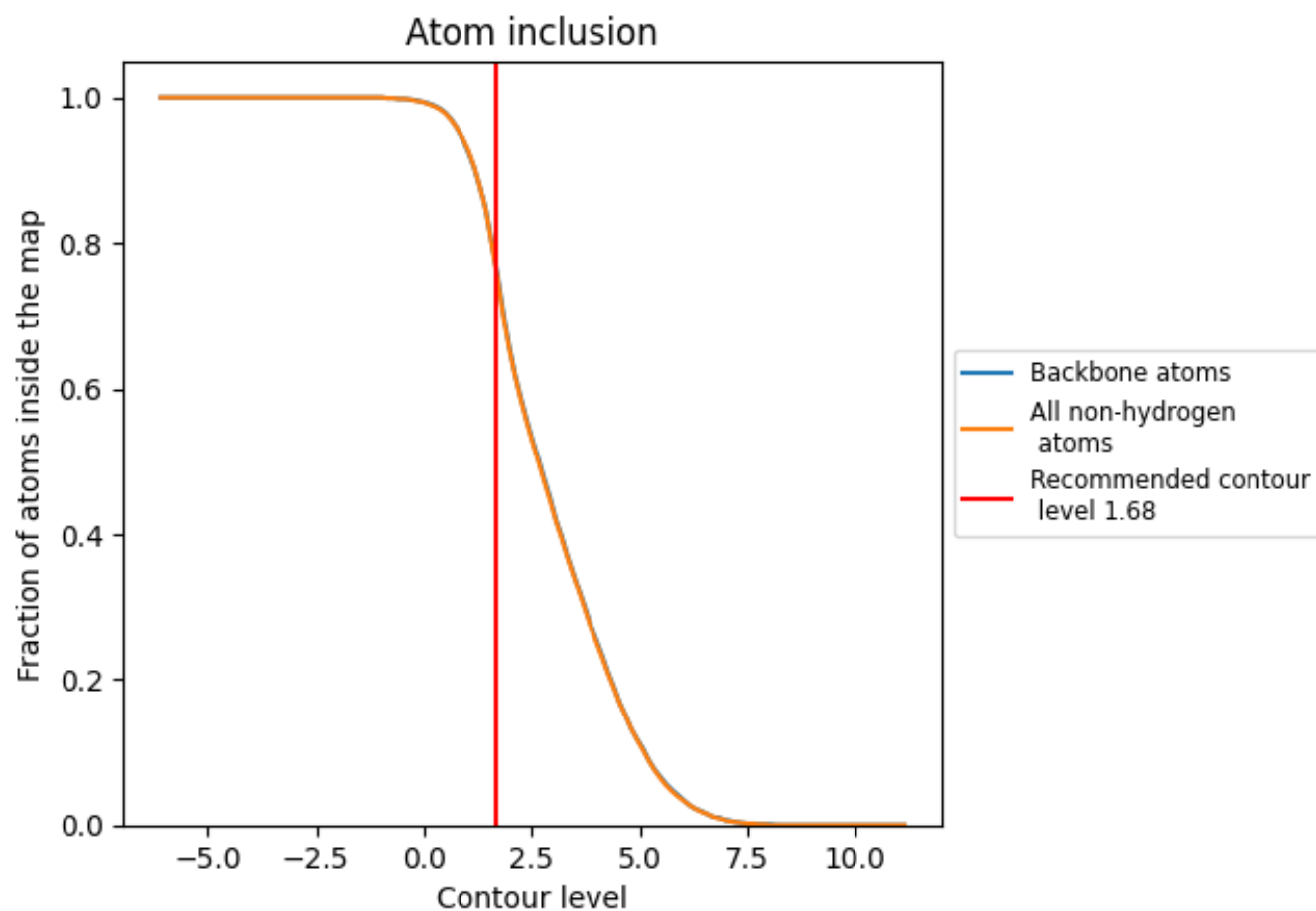
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.68).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 76% 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 (1.68) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7640	 0.2170
2	 0.8490	 0.2240
3	 0.8560	 0.2750
4	 0.8520	 0.2470
5	 0.8620	 0.2670
6	 0.8370	 0.2390
7	 0.8570	 0.2610
A	 0.5200	 0.1350
B	 0.5550	 0.1250
C	 0.8470	 0.2350
D	 0.8180	 0.2520
E	 0.8270	 0.2590
F	 0.8450	 0.2450
G	 0.8410	 0.2320
J	 0.4830	 0.1310
P	 0.6480	 0.1770
Q	 0.9290	 0.2870
R	 0.9550	 0.2820
S	 0.3190	 0.0690
X	 0.7880	 0.1960
Y	 0.8170	 0.2260

