



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:20 PM UTC

PDB ID : 7PMN / pdb_00007pmn
EMDB ID : EMD-13539
Title : S. cerevisiae replisome-SCF(Dia2) complex bound to double-stranded DNA
(conformation II)
Authors : Jenkyn-Bedford, M.; Yeeles, J.T.P.; Deegan, T.D.
Deposited on : 2021-09-02
Resolution : 3.20 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:

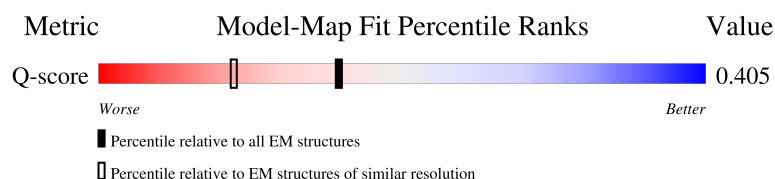
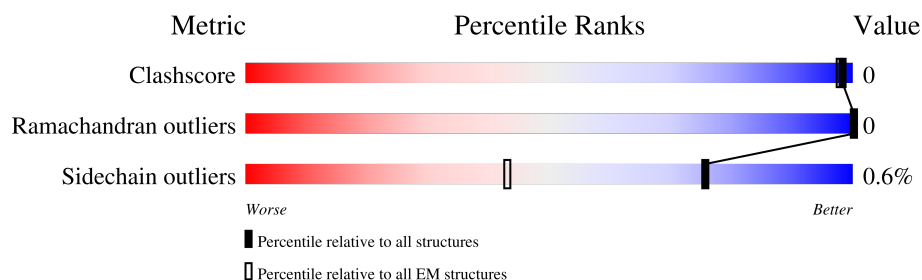
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.20 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	15020 (2.70 - 3.70)

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	5% 75% 24%
2	3	1009	12% 60% 39%
3	4	933	21% 63% 36%
4	5	775	7% 84% 15%

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Mol	Chain	Length	Quality of chain
5	6	1017	
6	7	845	
7	A	208	
8	B	213	
9	C	194	
10	D	294	
11	E	657	
12	F	962	
12	G	962	
12	H	962	
13	I	115	
14	J	122	
15	K	194	
16	L	735	
17	Q	2222	
18	R	689	
19	X	1238	
20	Y	319	

2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 74640 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA replication licensing factor MCM2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	656	Total	C	N	O	S	0	0
			5183	3261	933	971	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	615	Total	C	N	O	S	0	0
			4834	3055	859	907	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	595	Total	C	N	O	S	0	0
			4731	2986	813	904	28		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	660	Total	C	N	O	S	0	0
			5231	3289	912	1007	23		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	641	Total	C	N	O	S	0	0
			5042	3177	886	954	25		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	7	633	Total	C	N	O	S	0	0
			4936	3121	857	932	26		

- Molecule 7 is a protein called DNA replication complex GINS protein PSF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	197	Total	C	N	O	S	0	0
			1611	1012	277	313	9		

- Molecule 8 is a protein called DNA replication complex GINS protein PSF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	192	Total	C	N	O	S	0	0
			1609	1034	285	286	4		

- Molecule 9 is a protein called DNA replication complex GINS protein PSF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	171	Total	C	N	O	S	0	0
			1381	900	223	252	6		

- Molecule 10 is a protein called DNA replication complex GINS protein SLD5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	243	Total	C	N	O	S	0	0
			2004	1276	327	389	12		

- Molecule 11 is a protein called Cell division control protein 45,Cell division control protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	564	Total	C	N	O	S	0	0
			4569	2916	772	867	14		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	167F	ASP	-	expression tag	UNP Q08032
E	167G	TYR	-	expression tag	UNP Q08032
E	167H	LYS	-	expression tag	UNP Q08032
E	167I	ASP	-	expression tag	UNP Q08032
E	167J	ASP	-	expression tag	UNP Q08032
E	167K	ASP	-	expression tag	UNP Q08032
E	167L	GLY	-	expression tag	UNP Q08032
E	167M	ASP	-	expression tag	UNP Q08032
E	167N	TYR	-	expression tag	UNP Q08032
E	167O	LYS	-	expression tag	UNP Q08032

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Chain	Residue	Modelled	Actual	Comment	Reference
E	167P	ASP	-	expression tag	UNP Q08032
E	167Q	ASP	-	expression tag	UNP Q08032

- Molecule 12 is a protein called DNA polymerase alpha-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	424	Total	C	N	O	S	0	0
			3404	2188	564	637	15		
12	G	422	Total	C	N	O	S	0	0
			3380	2172	557	636	15		
12	H	425	Total	C	N	O	S	0	0
			3411	2193	565	638	15		

There are 105 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-34	MET	-	initiating methionine	UNP Q01454
F	-33	LYS	-	expression tag	UNP Q01454
F	-32	ARG	-	expression tag	UNP Q01454
F	-31	ARG	-	expression tag	UNP Q01454
F	-30	TRP	-	expression tag	UNP Q01454
F	-29	LYS	-	expression tag	UNP Q01454
F	-28	LYS	-	expression tag	UNP Q01454
F	-27	ASN	-	expression tag	UNP Q01454
F	-26	PHE	-	expression tag	UNP Q01454
F	-25	ILE	-	expression tag	UNP Q01454
F	-24	ALA	-	expression tag	UNP Q01454
F	-23	VAL	-	expression tag	UNP Q01454
F	-22	SER	-	expression tag	UNP Q01454
F	-21	ALA	-	expression tag	UNP Q01454
F	-20	ALA	-	expression tag	UNP Q01454
F	-19	ASN	-	expression tag	UNP Q01454
F	-18	ARG	-	expression tag	UNP Q01454
F	-17	PHE	-	expression tag	UNP Q01454
F	-16	LYS	-	expression tag	UNP Q01454
F	-15	LYS	-	expression tag	UNP Q01454
F	-14	ILE	-	expression tag	UNP Q01454
F	-13	SER	-	expression tag	UNP Q01454
F	-12	SER	-	expression tag	UNP Q01454
F	-11	SER	-	expression tag	UNP Q01454
F	-10	GLY	-	expression tag	UNP Q01454
F	-9	ALA	-	expression tag	UNP Q01454

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-8	LEU	-	expression tag	UNP Q01454
F	-7	GLU	-	expression tag	UNP Q01454
F	-6	ASN	-	expression tag	UNP Q01454
F	-5	LEU	-	expression tag	UNP Q01454
F	-4	TYR	-	expression tag	UNP Q01454
F	-3	PHE	-	expression tag	UNP Q01454
F	-2	GLN	-	expression tag	UNP Q01454
F	-1	GLY	-	expression tag	UNP Q01454
F	0	GLU	-	expression tag	UNP Q01454
G	-34	MET	-	initiating methionine	UNP Q01454
G	-33	LYS	-	expression tag	UNP Q01454
G	-32	ARG	-	expression tag	UNP Q01454
G	-31	ARG	-	expression tag	UNP Q01454
G	-30	TRP	-	expression tag	UNP Q01454
G	-29	LYS	-	expression tag	UNP Q01454
G	-28	LYS	-	expression tag	UNP Q01454
G	-27	ASN	-	expression tag	UNP Q01454
G	-26	PHE	-	expression tag	UNP Q01454
G	-25	ILE	-	expression tag	UNP Q01454
G	-24	ALA	-	expression tag	UNP Q01454
G	-23	VAL	-	expression tag	UNP Q01454
G	-22	SER	-	expression tag	UNP Q01454
G	-21	ALA	-	expression tag	UNP Q01454
G	-20	ALA	-	expression tag	UNP Q01454
G	-19	ASN	-	expression tag	UNP Q01454
G	-18	ARG	-	expression tag	UNP Q01454
G	-17	PHE	-	expression tag	UNP Q01454
G	-16	LYS	-	expression tag	UNP Q01454
G	-15	LYS	-	expression tag	UNP Q01454
G	-14	ILE	-	expression tag	UNP Q01454
G	-13	SER	-	expression tag	UNP Q01454
G	-12	SER	-	expression tag	UNP Q01454
G	-11	SER	-	expression tag	UNP Q01454
G	-10	GLY	-	expression tag	UNP Q01454
G	-9	ALA	-	expression tag	UNP Q01454
G	-8	LEU	-	expression tag	UNP Q01454
G	-7	GLU	-	expression tag	UNP Q01454
G	-6	ASN	-	expression tag	UNP Q01454
G	-5	LEU	-	expression tag	UNP Q01454
G	-4	TYR	-	expression tag	UNP Q01454
G	-3	PHE	-	expression tag	UNP Q01454
G	-2	GLN	-	expression tag	UNP Q01454

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-1	GLY	-	expression tag	UNP Q01454
G	0	GLU	-	expression tag	UNP Q01454
H	-34	MET	-	initiating methionine	UNP Q01454
H	-33	LYS	-	expression tag	UNP Q01454
H	-32	ARG	-	expression tag	UNP Q01454
H	-31	ARG	-	expression tag	UNP Q01454
H	-30	TRP	-	expression tag	UNP Q01454
H	-29	LYS	-	expression tag	UNP Q01454
H	-28	LYS	-	expression tag	UNP Q01454
H	-27	ASN	-	expression tag	UNP Q01454
H	-26	PHE	-	expression tag	UNP Q01454
H	-25	ILE	-	expression tag	UNP Q01454
H	-24	ALA	-	expression tag	UNP Q01454
H	-23	VAL	-	expression tag	UNP Q01454
H	-22	SER	-	expression tag	UNP Q01454
H	-21	ALA	-	expression tag	UNP Q01454
H	-20	ALA	-	expression tag	UNP Q01454
H	-19	ASN	-	expression tag	UNP Q01454
H	-18	ARG	-	expression tag	UNP Q01454
H	-17	PHE	-	expression tag	UNP Q01454
H	-16	LYS	-	expression tag	UNP Q01454
H	-15	LYS	-	expression tag	UNP Q01454
H	-14	ILE	-	expression tag	UNP Q01454
H	-13	SER	-	expression tag	UNP Q01454
H	-12	SER	-	expression tag	UNP Q01454
H	-11	SER	-	expression tag	UNP Q01454
H	-10	GLY	-	expression tag	UNP Q01454
H	-9	ALA	-	expression tag	UNP Q01454
H	-8	LEU	-	expression tag	UNP Q01454
H	-7	GLU	-	expression tag	UNP Q01454
H	-6	ASN	-	expression tag	UNP Q01454
H	-5	LEU	-	expression tag	UNP Q01454
H	-4	TYR	-	expression tag	UNP Q01454
H	-3	PHE	-	expression tag	UNP Q01454
H	-2	GLN	-	expression tag	UNP Q01454
H	-1	GLY	-	expression tag	UNP Q01454
H	0	GLU	-	expression tag	UNP Q01454

- Molecule 13 is a DNA chain called Leading strand template DNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	I	34	Total	C	N	O	P	
			742	340	161	207	34	
							0	0

- Molecule 14 is a DNA chain called Lagging strand template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	33	Total	C	N	O	P	0	0
			629	298	101	197	33		

- Molecule 15 is a protein called Suppressor of kinetochore protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	137	Total	C	N	O	S	0	0
			1120	709	195	212	4		

- Molecule 16 is a protein called Protein DIA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	475	Total	C	N	O	S	0	0
			3921	2533	654	710	24		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-2	GLY	-	expression tag	UNP Q08496
L	-1	ALA	-	expression tag	UNP Q08496
L	0	GLY	-	expression tag	UNP Q08496

- Molecule 17 is a protein called DNA polymerase epsilon catalytic subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	766	Total	C	N	O	S	0	0
			6203	4028	1015	1124	36		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	290	ALA	ASP	variant	UNP P21951
Q	292	ALA	GLU	variant	UNP P21951

- Molecule 18 is a protein called DNA polymerase epsilon subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	552	Total	C	N	O	S	0	0
			4427	2843	759	807	18		

- Molecule 19 is a protein called Topoisomerase 1-associated factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	X	665	Total	C	N	O	S	0	0
			5410	3505	912	974	19		

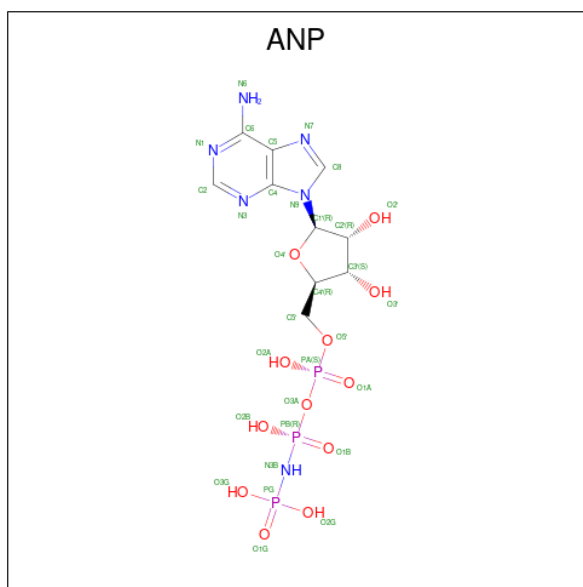
- Molecule 20 is a protein called Chromosome segregation in meiosis protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	98	Total	C	N	O	S	0	0
			791	511	138	138	4		

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 21 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
21	2	1	Total	C	N	O	P	0
			31	10	6	12	3	
21	5	1	Total	C	N	O	P	0
			31	10	6	12	3	

- 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	5	1	Total 1	Mg 1	0

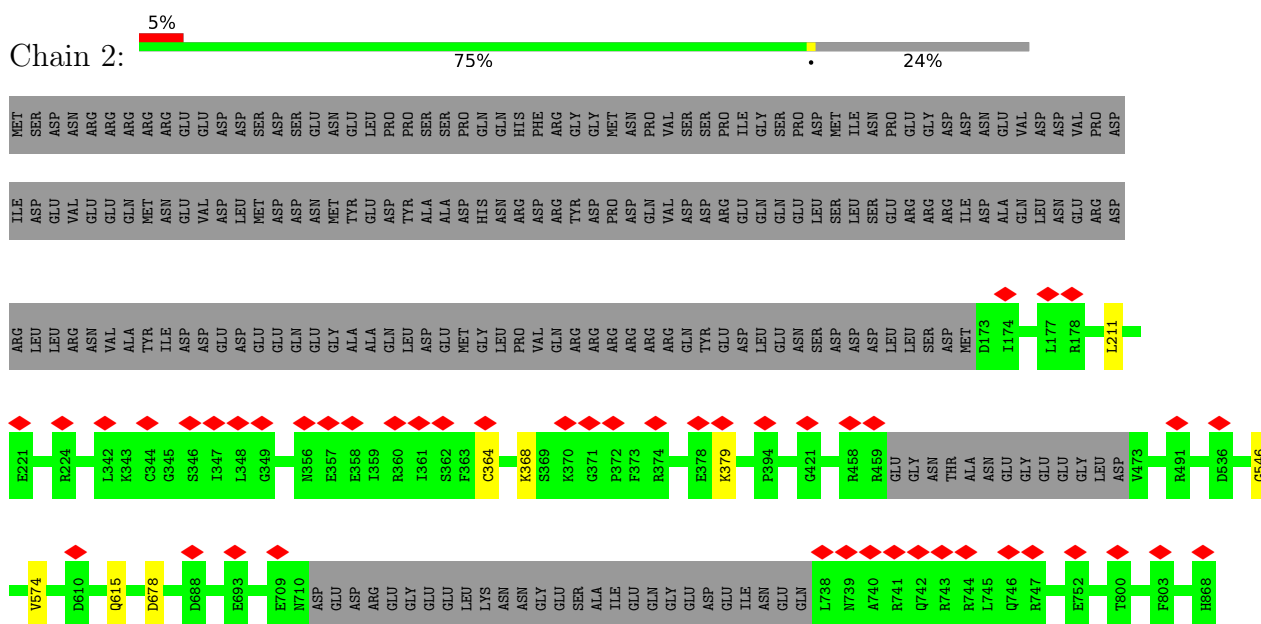
- Molecule 23 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
23	2	1	Total 1	Zn 1	0
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
23	Q	2	Total 2	Zn 2	0

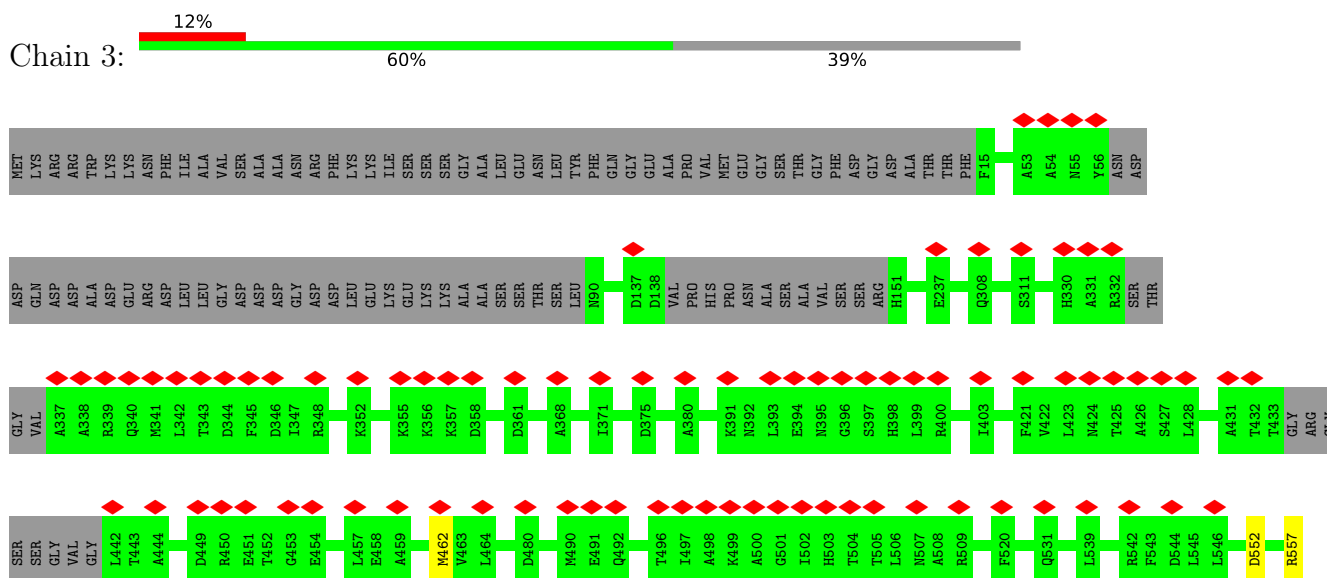
3 Residue-property plots

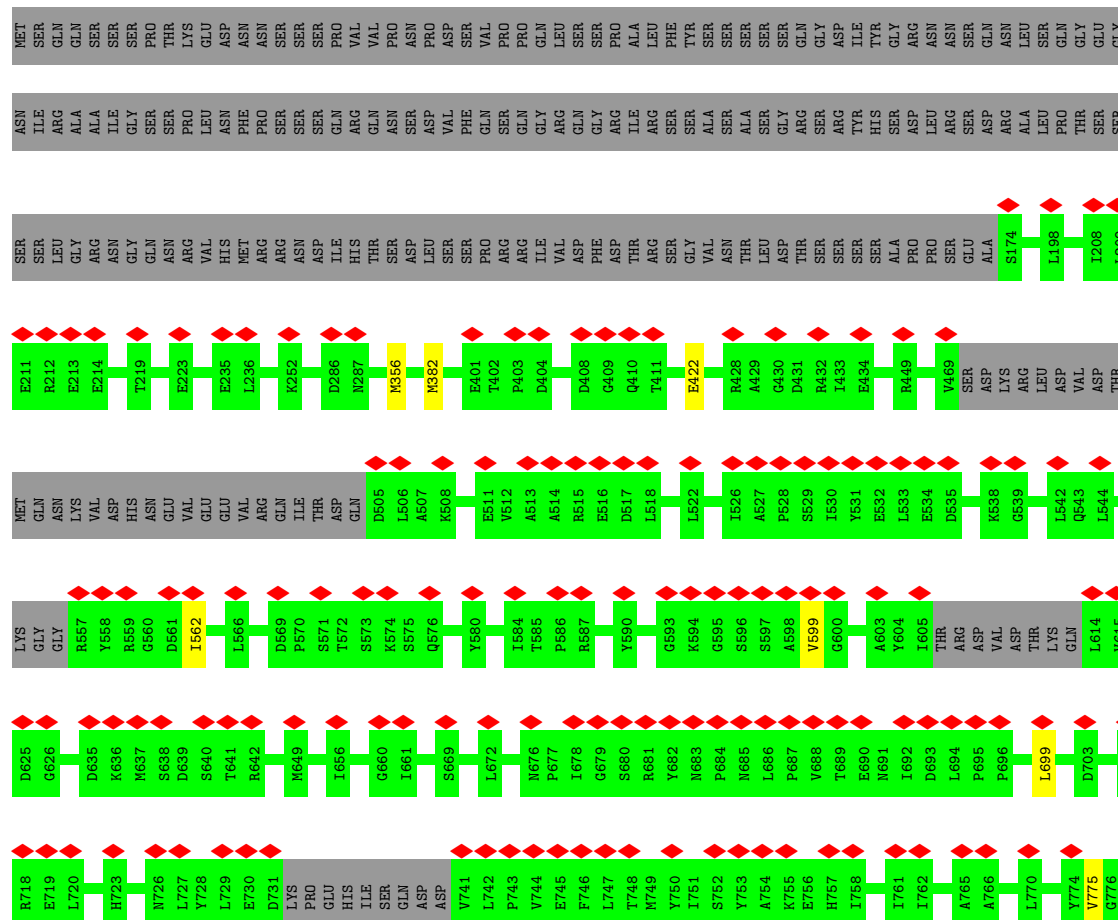
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

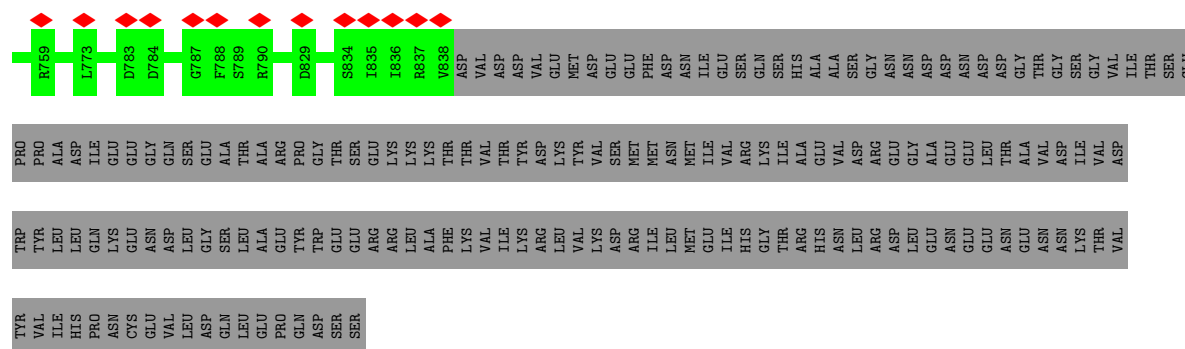
- Molecule 1: DNA replication licensing factor MCM2



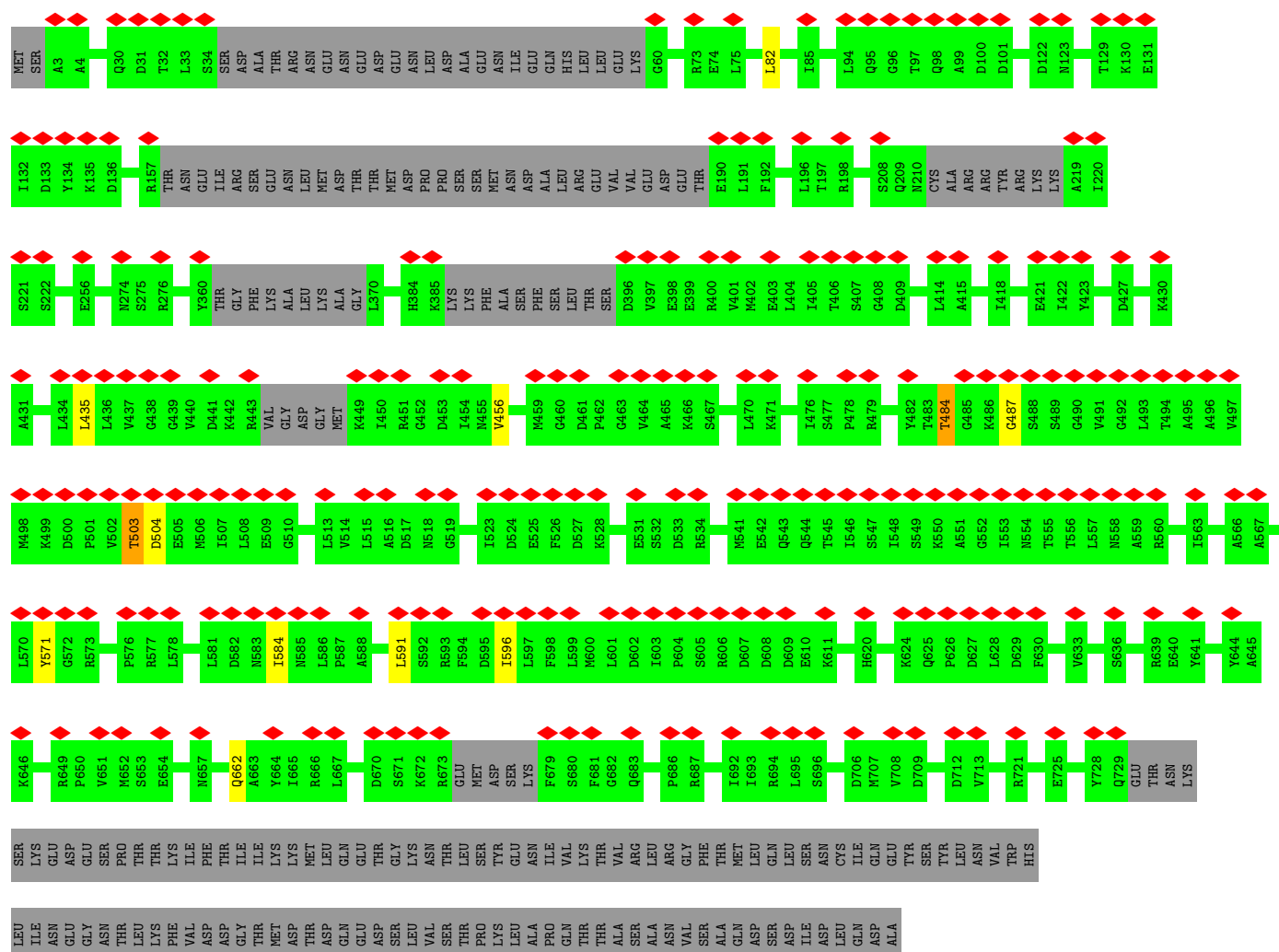
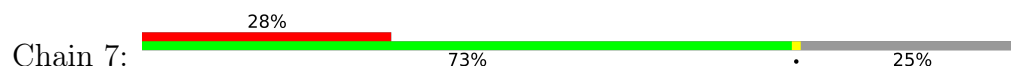
- Molecule 2: DNA replication licensing factor MCM3



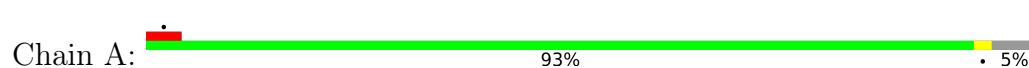


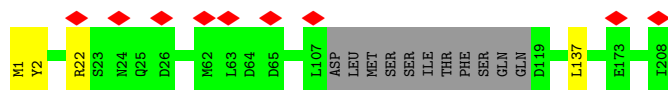


• Molecule 6: DNA replication licensing factor MCM7



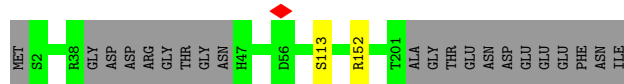
• Molecule 7: DNA replication complex GINS protein PSF1





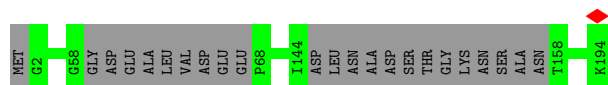
- Molecule 8: DNA replication complex GINS protein PSF2

Chain B: 89% 10%



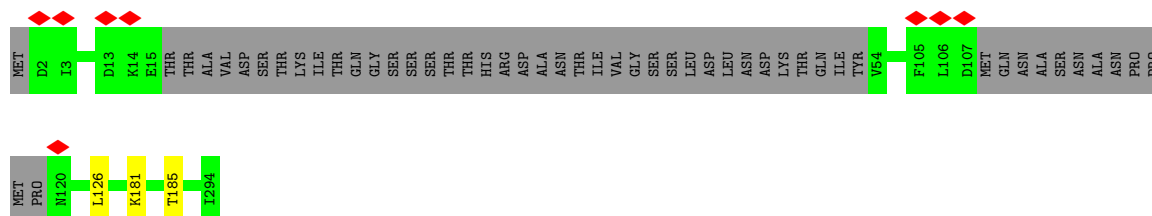
- Molecule 9: DNA replication complex GINS protein PSF3

Chain C: 88% 12%



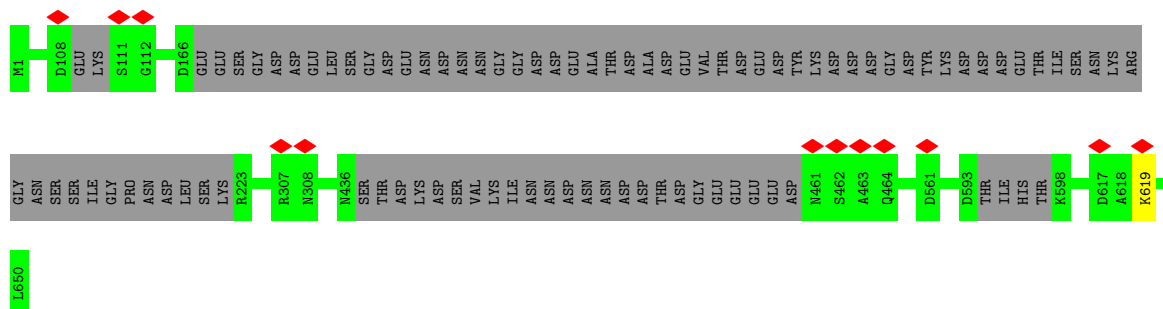
- Molecule 10: DNA replication complex GINS protein SLD5

Chain D: 82% 17%



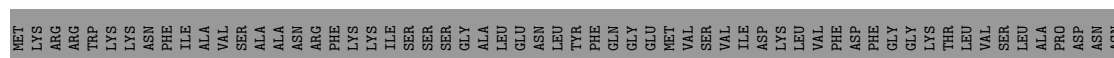
- Molecule 11: Cell division control protein 45,Cell division control protein 45

Chain E: 86% 14%



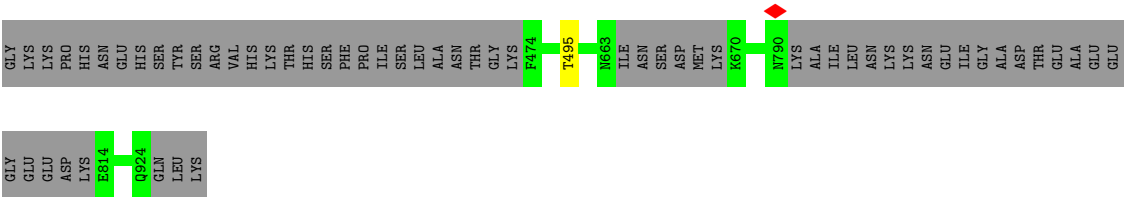
- Molecule 12: DNA polymerase alpha-binding protein

Chain F: 44% 56%

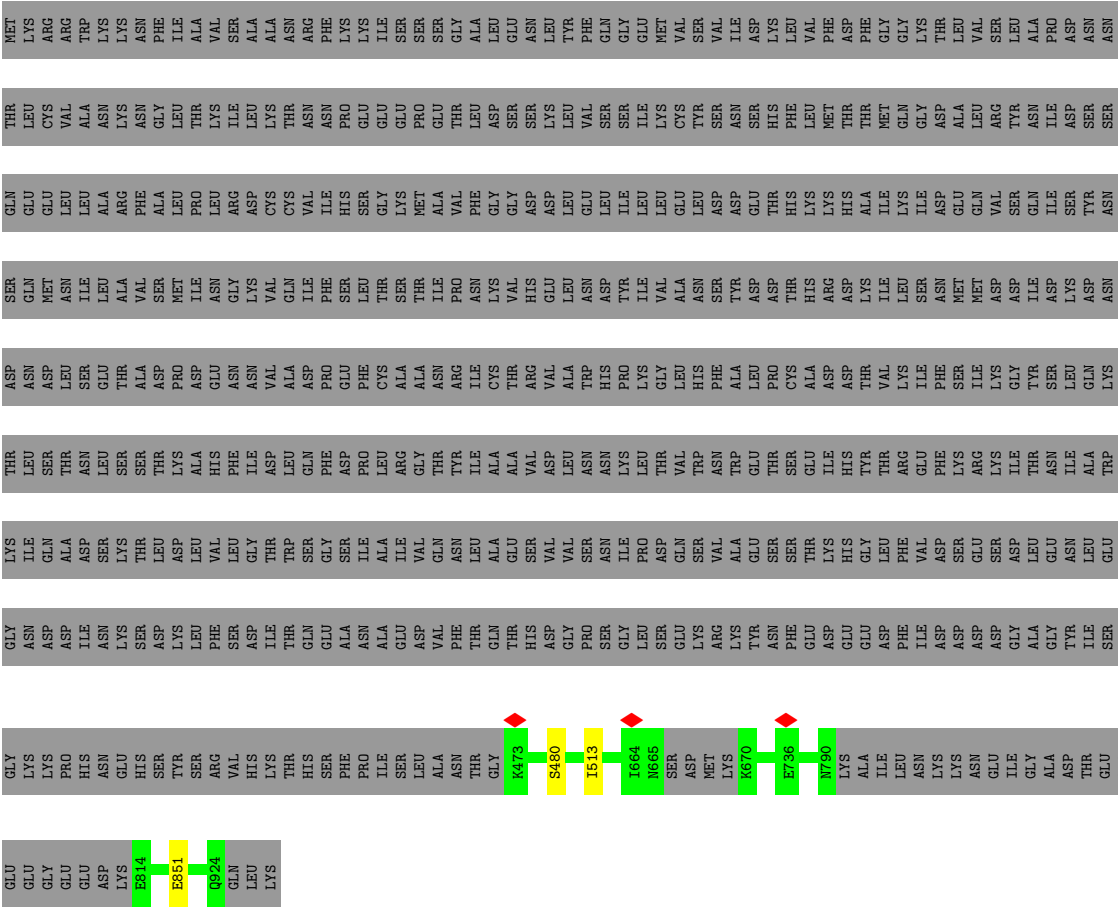




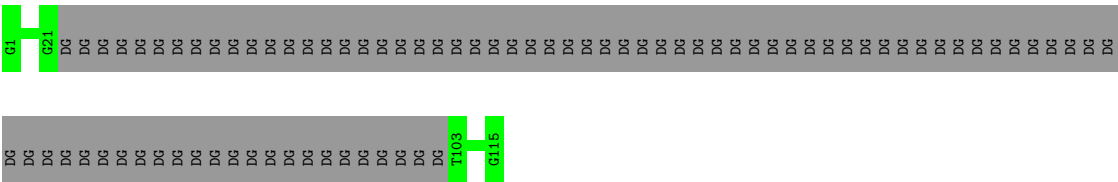
GLY	LYS	THR	ASP	SER	GLN	THR	THR	GLY	THR	MET
ASN	ILE	LEU	ASN	GLN	ASN	LEU	GLN	GLN	GLY	LYS
ASP	ASN	SER	ASP	ASP	ASN	SER	MET	GLU	CYS	ARG
ILE	ALA	THR	ASN	SER	ILE	LEU	ASN	LEU	VAL	TRP
ASN	SER	LEU	GLU	LEU	LEU	GLU	LEU	ALA	ASN	LYS
LYS	THR	SER	THR	LYS	THR	SER	ALA	ARG	LYS	LYS
SER	LEU	THR	ALA	ASP	VAL	THR	VAL	PHE	ASN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



● Molecule 12: DNA polymerase alpha-binding protein

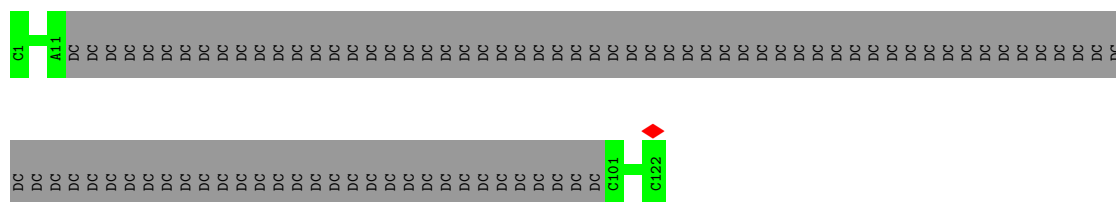


● Molecule 13: Leading strand template DNA

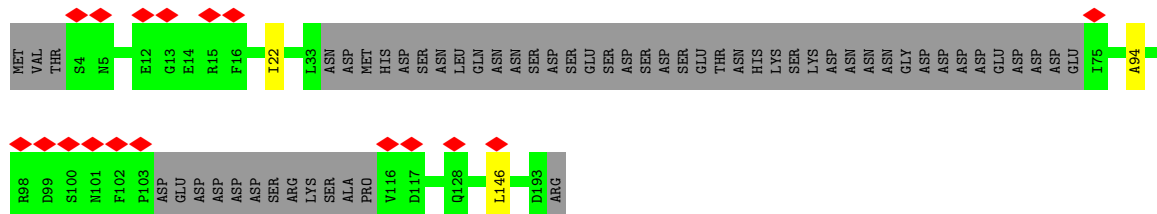


● Molecule 14: Lagging strand template DNA

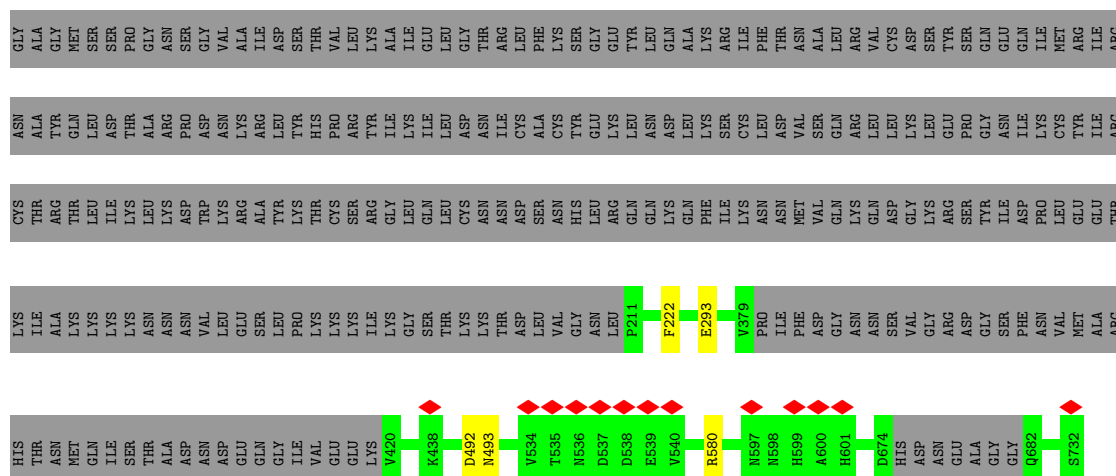




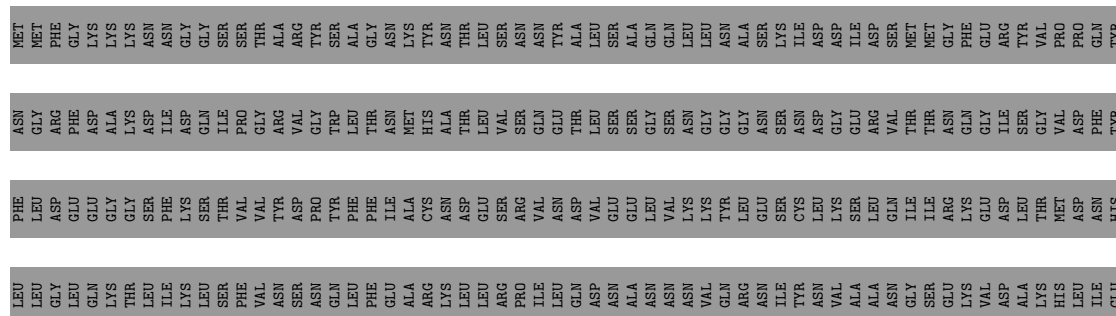
• Molecule 15: Suppressor of kinetochore protein 1



• Molecule 16: Protein DIA2

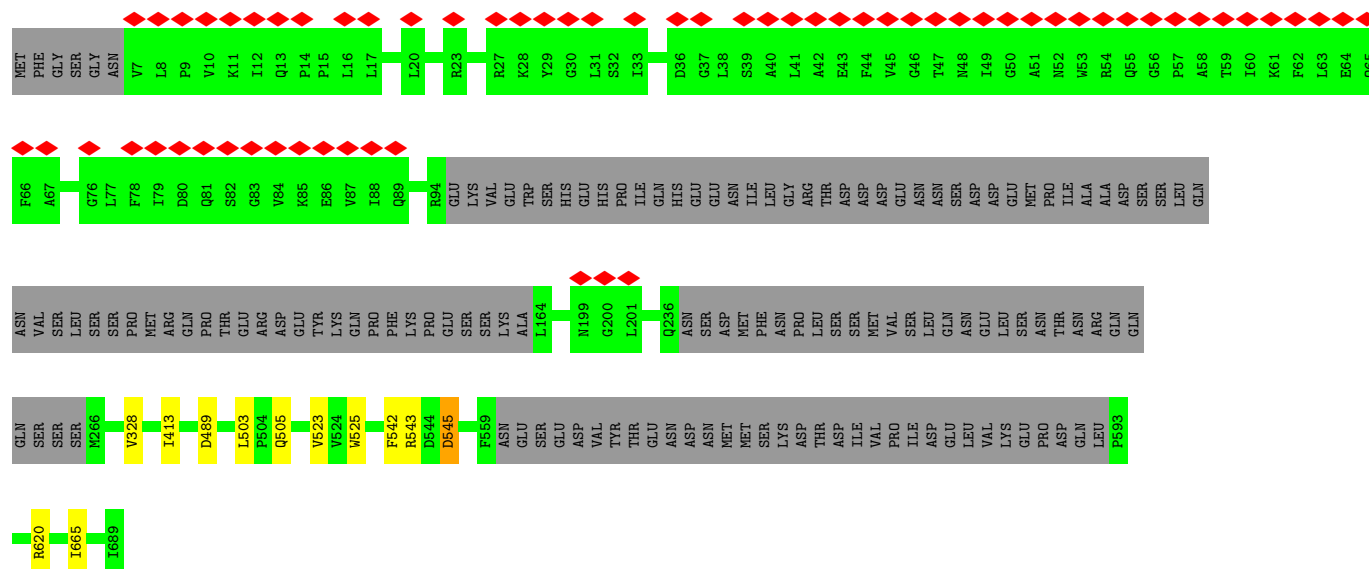
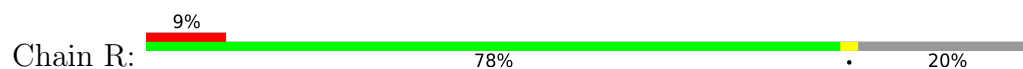


• Molecule 17: DNA polymerase epsilon catalytic subunit A

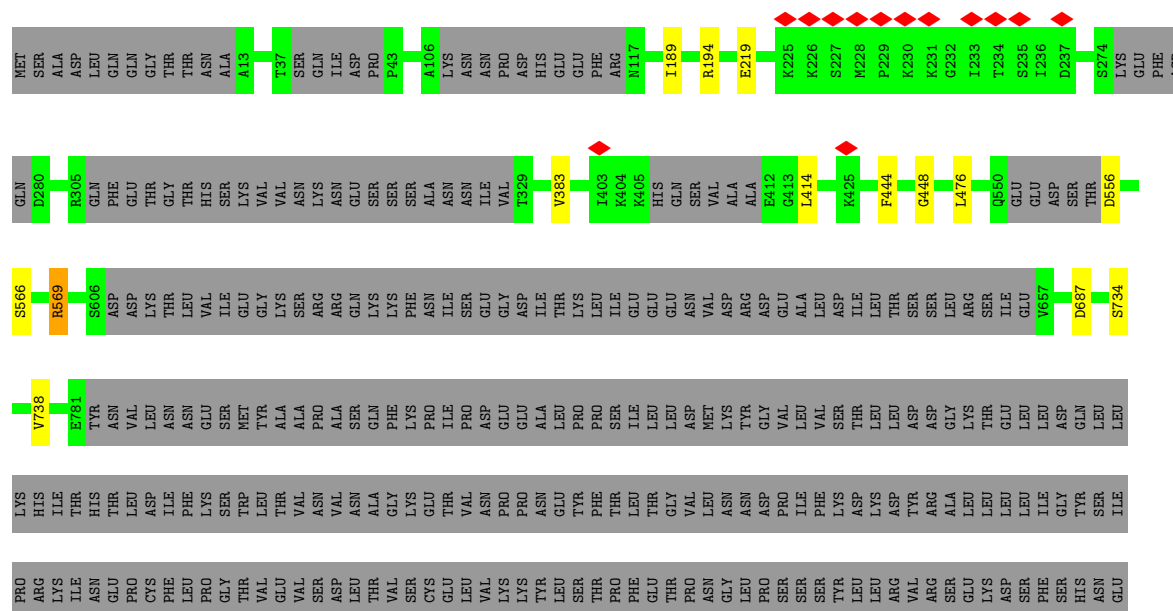




- Molecule 18: DNA polymerase epsilon subunit B



- Molecule 19: Topoisomerase 1-associated factor 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	369254	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 ($e^-/\text{\AA}^2$)	38.8	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	63.838	Depositor
Minimum map value	-32.137	Depositor
Average map value	0.038	Depositor
Map value standard deviation	1.533	Depositor
Recommended contour level	6.82	Depositor
Map size (Å)	398.55997, 398.55997, 398.55997	wwPDB
Map dimensions	376, 376, 376	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.32	0/5272	0.53	0/7122
2	3	0.28	0/4918	0.52	0/6668
3	4	0.28	0/4801	0.53	0/6488
4	5	0.30	0/5303	0.54	0/7155
5	6	0.29	0/5125	0.54	0/6916
6	7	0.29	0/5010	0.53	0/6779
7	A	0.26	0/1631	0.51	0/2194
8	B	0.25	0/1642	0.48	0/2221
9	C	0.27	0/1414	0.46	0/1911
10	D	0.26	0/2040	0.47	0/2755
11	E	0.25	0/4653	0.49	0/6297
12	F	0.24	0/3489	0.49	0/4724
12	G	0.26	0/3465	0.50	0/4696
12	H	0.27	0/3496	0.51	0/4735
13	I	0.36	0/839	0.75	0/1303
14	J	0.53	0/694	0.92	0/1053
15	K	0.30	0/1139	0.55	0/1539
16	L	0.34	0/3996	0.58	0/5395
17	Q	0.28	0/6332	0.54	0/8548
18	R	0.30	0/4526	0.58	0/6125
19	X	0.27	0/5512	0.52	0/7426
20	Y	0.32	0/807	0.53	0/1084
All	All	0.29	0/76104	0.54	0/103134

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

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Mol	Chain	#Chirality outliers	#Planarity outliers
18	R	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2	678	ASP	Peptide
18	R	489	ASP	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	5183	0	5225	2	0
2	3	4834	0	4903	2	0
3	4	4731	0	4796	3	0
4	5	5231	0	5303	7	0
5	6	5042	0	5045	3	0
6	7	4936	0	4970	3	0
7	A	1611	0	1615	2	0
8	B	1609	0	1662	1	0
9	C	1381	0	1394	0	0
10	D	2004	0	2001	2	0
11	E	4569	0	4556	0	0
12	F	3404	0	3352	2	0
12	G	3380	0	3310	0	0
12	H	3411	0	3355	1	0
13	I	742	0	379	0	0
14	J	629	0	365	0	0
15	K	1120	0	1111	1	0
16	L	3921	0	4025	1	0
17	Q	6203	0	6270	6	0
18	R	4427	0	4480	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	X	5410	0	5573	4	0
20	Y	791	0	811	0	0
21	2	31	0	13	1	0
21	5	31	0	13	2	0
22	2	1	0	0	0	0
22	5	1	0	0	0	0
23	2	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
23	Q	2	0	0	0	0
All	All	74640	0	74527	48	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 0.

The worst 5 of 48 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)
12:F:584:THR:OG1	12:F:622:ASN:O	2.08	0.70
19:X:566:SER:O	19:X:569:ARG:NH1	2.25	0.69
18:R:543:ARG:NH1	18:R:545:ASP:OD1	2.28	0.67
18:R:413:ILE:HD13	18:R:665:ILE:HD12	1.85	0.56
1:2:546:GLY:H	21:2:1500:ANP:HNB1	1.54	0.55

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	2	650/868 (75%)	630 (97%)	20 (3%)	0	100	100
2	3	603/1009 (60%)	585 (97%)	18 (3%)	0	100	100
3	4	583/933 (62%)	565 (97%)	18 (3%)	0	100	100
4	5	644/775 (83%)	626 (97%)	18 (3%)	0	100	100
5	6	631/1017 (62%)	608 (96%)	23 (4%)	0	100	100
6	7	617/845 (73%)	594 (96%)	23 (4%)	0	100	100
7	A	193/208 (93%)	186 (96%)	7 (4%)	0	100	100
8	B	188/213 (88%)	184 (98%)	4 (2%)	0	100	100
9	C	165/194 (85%)	164 (99%)	1 (1%)	0	100	100
10	D	237/294 (81%)	234 (99%)	3 (1%)	0	100	100
11	E	554/657 (84%)	539 (97%)	15 (3%)	0	100	100
12	F	418/962 (44%)	409 (98%)	9 (2%)	0	100	100
12	G	416/962 (43%)	404 (97%)	12 (3%)	0	100	100
12	H	419/962 (44%)	408 (97%)	11 (3%)	0	100	100
15	K	131/194 (68%)	124 (95%)	7 (5%)	0	100	100
16	L	469/735 (64%)	450 (96%)	19 (4%)	0	100	100
17	Q	740/2222 (33%)	721 (97%)	19 (3%)	0	100	100
18	R	544/689 (79%)	525 (96%)	19 (4%)	0	100	100
19	X	649/1238 (52%)	637 (98%)	12 (2%)	0	100	100
20	Y	96/319 (30%)	95 (99%)	1 (1%)	0	100	100
All	All	8947/15296 (58%)	8688 (97%)	259 (3%)	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	569/770 (74%)	565 (99%)	4 (1%)	76	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	3	532/866 (61%)	530 (100%)	2 (0%)	84	86
3	4	537/848 (63%)	534 (99%)	3 (1%)	78	84
4	5	591/688 (86%)	589 (100%)	2 (0%)	86	88
5	6	553/886 (62%)	548 (99%)	5 (1%)	70	81
6	7	545/753 (72%)	537 (98%)	8 (2%)	57	76
7	A	182/193 (94%)	181 (100%)	1 (0%)	81	85
8	B	182/198 (92%)	182 (100%)	0	100	100
9	C	154/173 (89%)	154 (100%)	0	100	100
10	D	234/279 (84%)	233 (100%)	1 (0%)	84	86
11	E	507/592 (86%)	506 (100%)	1 (0%)	87	89
12	F	375/854 (44%)	374 (100%)	1 (0%)	86	88
12	G	372/854 (44%)	371 (100%)	1 (0%)	86	88
12	H	375/854 (44%)	373 (100%)	2 (0%)	81	85
15	K	124/179 (69%)	123 (99%)	1 (1%)	73	82
16	L	456/686 (66%)	453 (99%)	3 (1%)	76	83
17	Q	701/2012 (35%)	700 (100%)	1 (0%)	88	91
18	R	498/629 (79%)	496 (100%)	2 (0%)	84	86
19	X	607/1125 (54%)	600 (99%)	7 (1%)	63	79
20	Y	85/286 (30%)	85 (100%)	0	100	100
All	All	8179/13725 (60%)	8134 (99%)	45 (1%)	76	84

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	G	495	THR
17	Q	1484	ILE
12	H	480	SER
16	L	222	PHE
18	R	545	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
11	E	141	GLN

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Mol	Chain	Res	Type
19	X	703	GLN
12	H	665	ASN
19	X	665	ASN
18	R	361	ASN

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, 9 are monoatomic - leaving 2 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	2	1500	22	33,33,33	1.04	5 (15%)	45,52,52	0.52	0
21	ANP	5	1500	22	33,33,33	1.01	4 (12%)	45,52,52	0.50	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	2	1500	22	-	4/18/38/38	0/3/3/3
21	ANP	5	1500	22	-	5/18/38/38	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	2	1500	ANP	PB-O3A	-3.27	1.55	1.59
21	5	1500	ANP	PB-O3A	-3.06	1.55	1.59
21	5	1500	ANP	PG-O1G	2.49	1.50	1.46
21	2	1500	ANP	PG-O1G	2.44	1.49	1.46
21	2	1500	ANP	PG-N3B	2.29	1.69	1.63

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

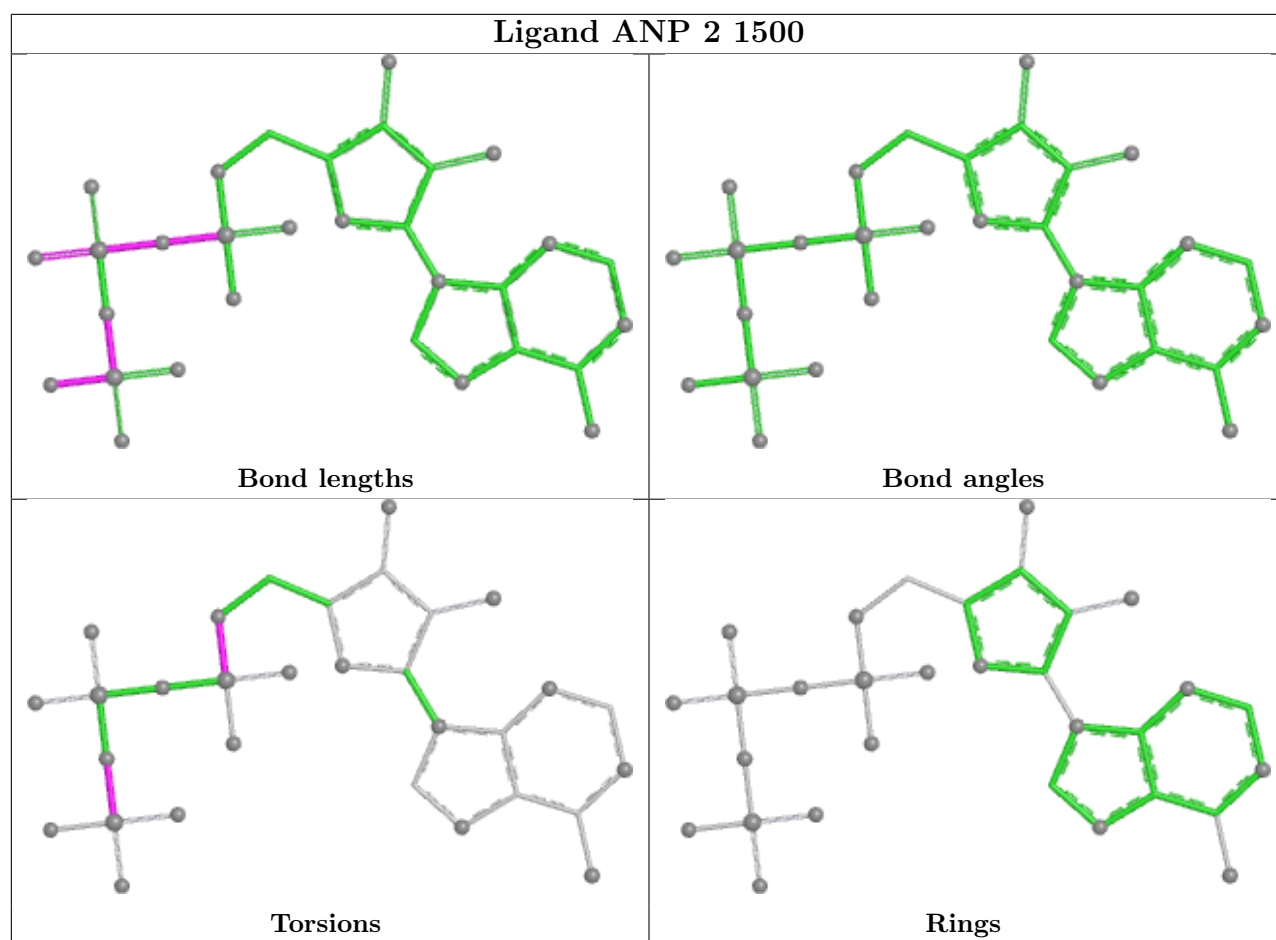
Mol	Chain	Res	Type	Atoms
21	2	1500	ANP	PB-N3B-PG-O1G
21	2	1500	ANP	C5'-O5'-PA-O2A
21	2	1500	ANP	C5'-O5'-PA-O3A
21	5	1500	ANP	PB-N3B-PG-O1G
21	5	1500	ANP	PA-O3A-PB-O1B

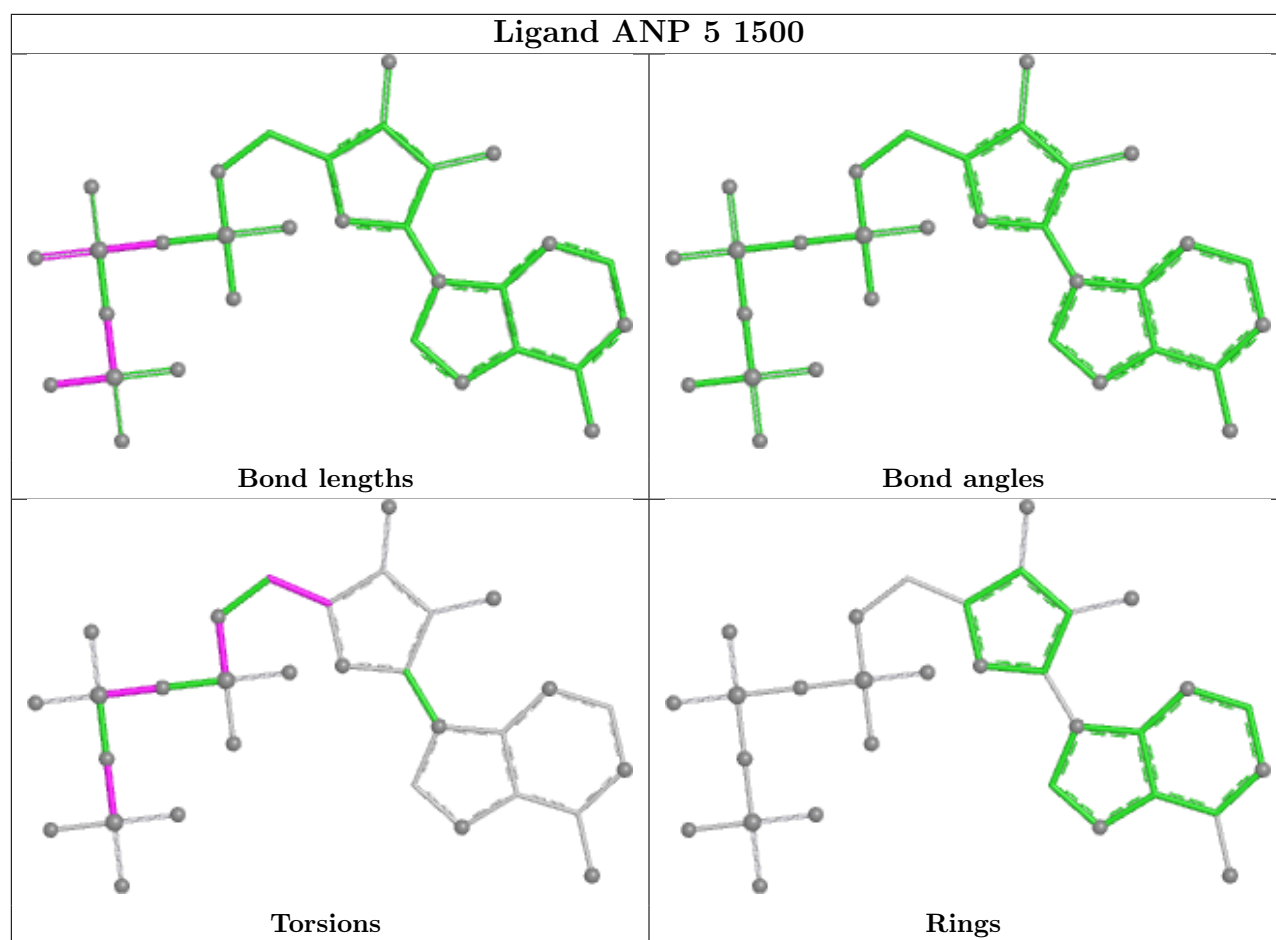
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	2	1500	ANP	1	0
21	5	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.

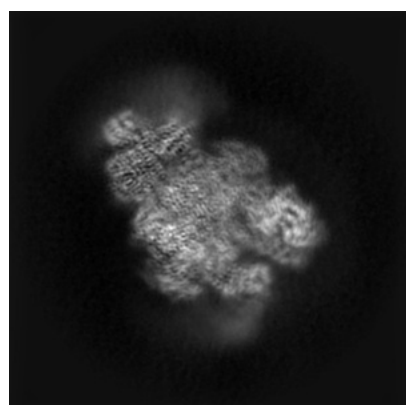
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13539. These allow visual inspection of the internal detail of the map and identification of artifacts.

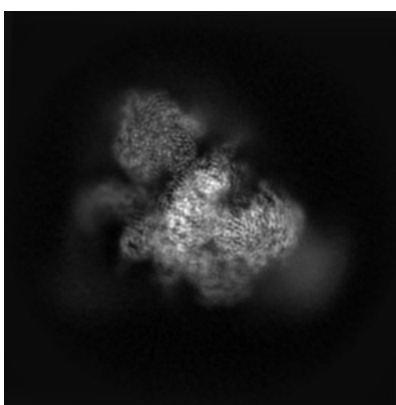
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

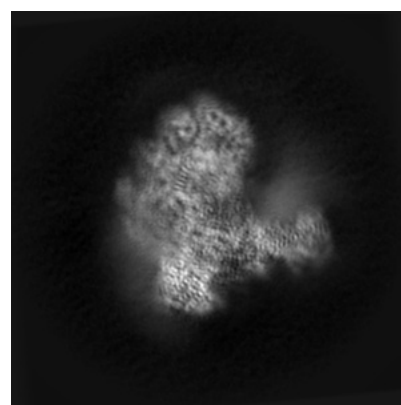
6.1.1 Primary map



X



Y

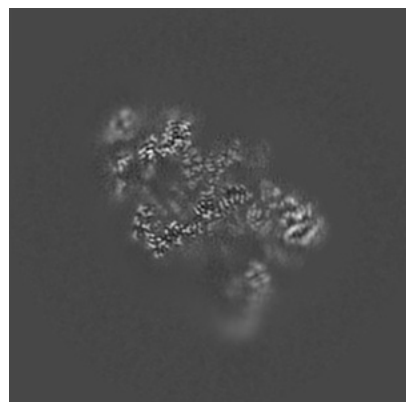


Z

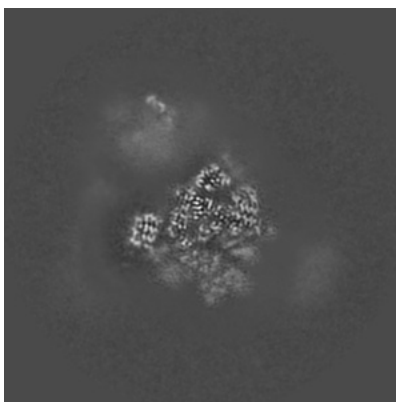
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

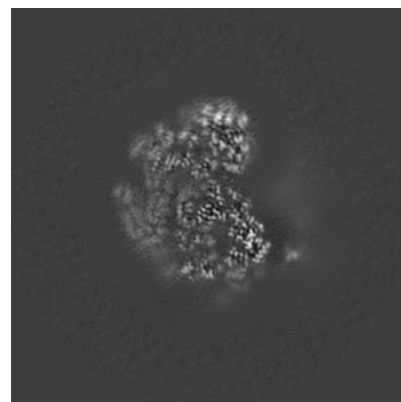
6.2.1 Primary map



X Index: 188



Y Index: 188

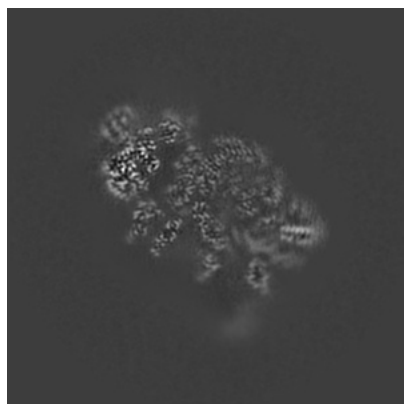


Z Index: 188

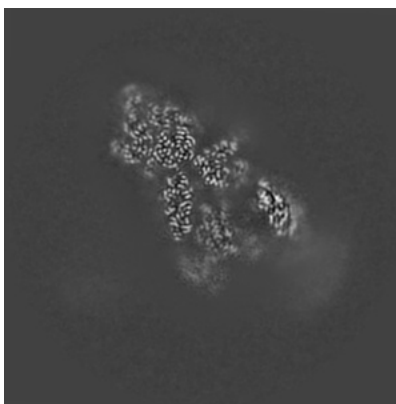
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

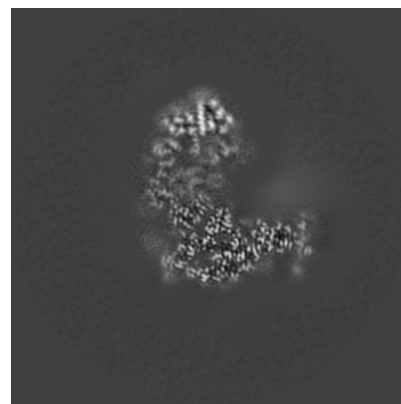
6.3.1 Primary map



X Index: 178



Y Index: 155

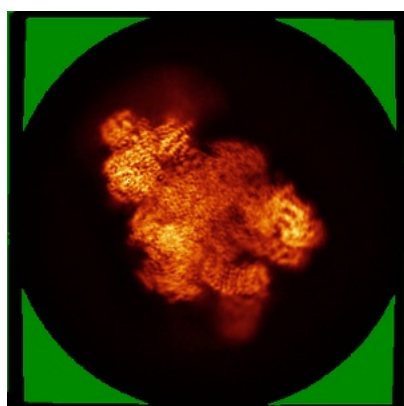


Z Index: 167

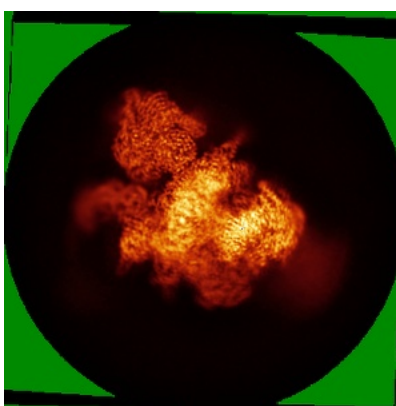
The images above show the largest variance slices of the map in three orthogonal directions.

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

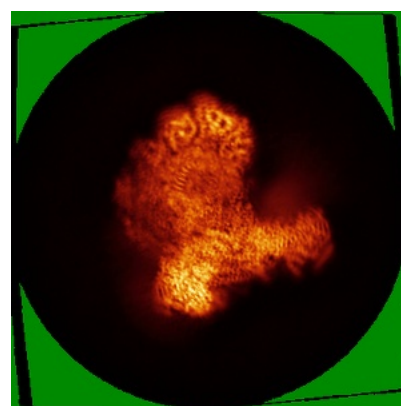
6.4.1 Primary map



X



Y



Z

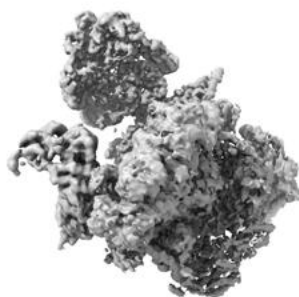
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 6.82. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

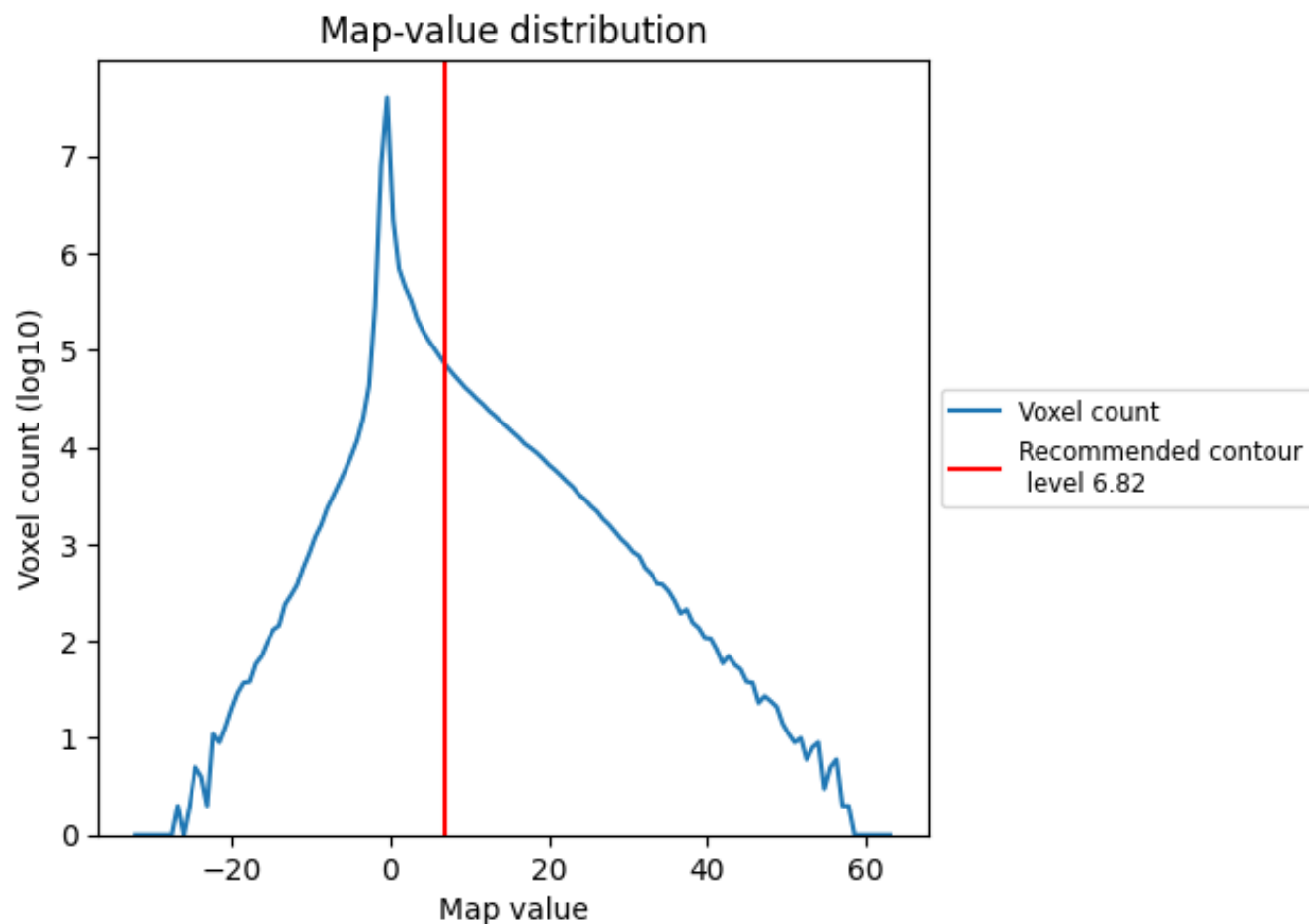
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

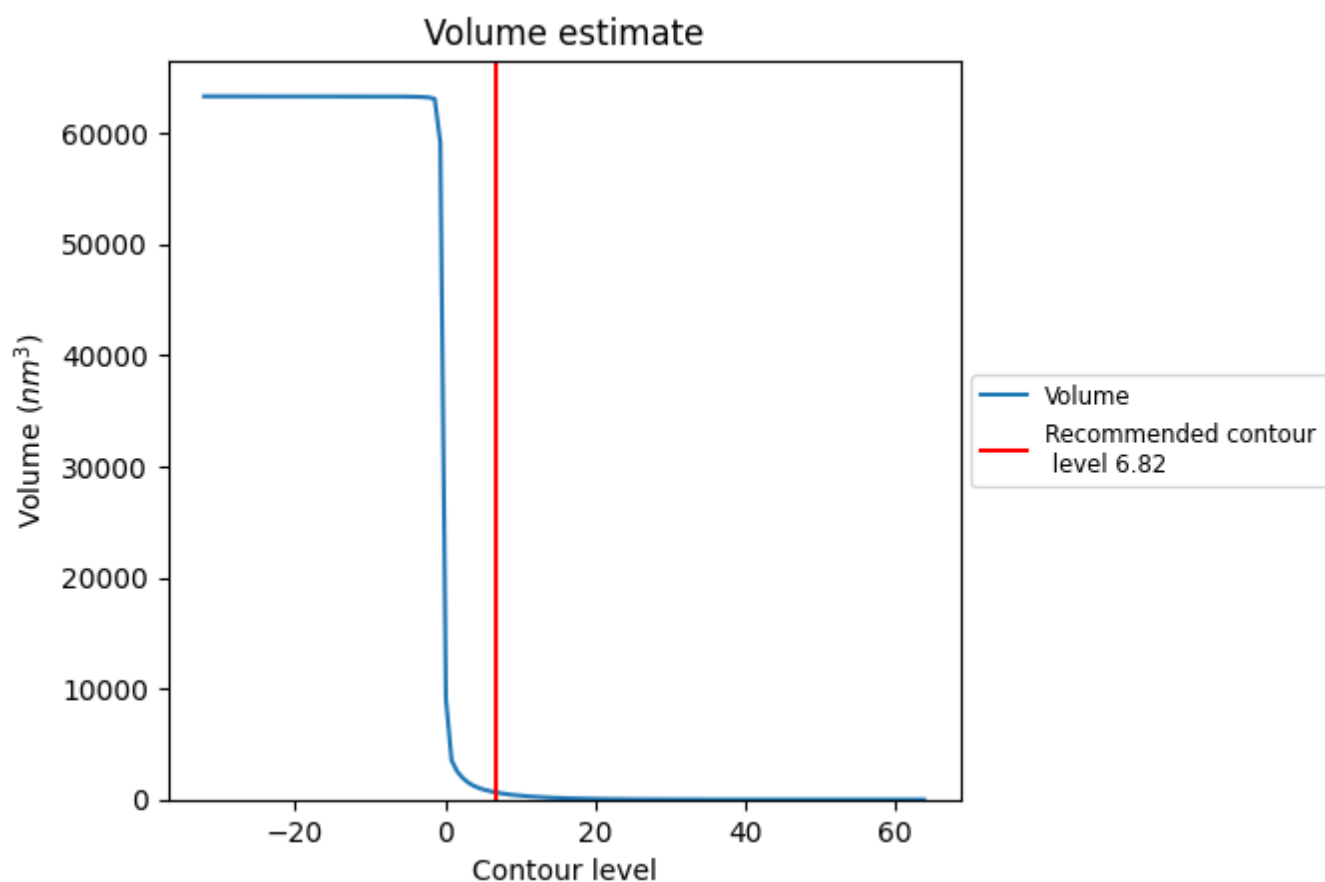
This section contains the results of statistical analysis of the map.

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.

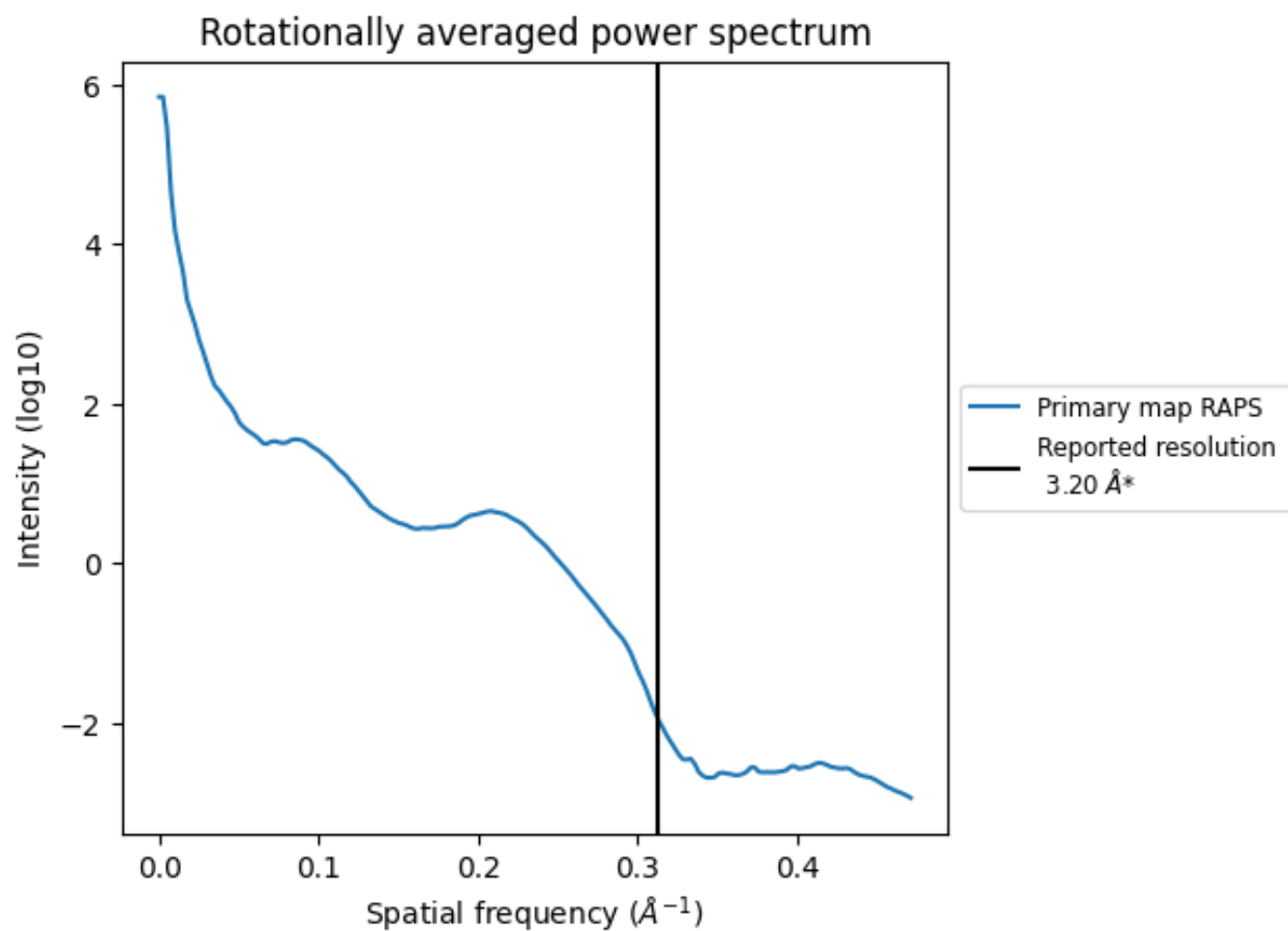
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 634 nm³; this corresponds to an approximate mass of 572 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 0.312 $\text{\AA}^{-1}$

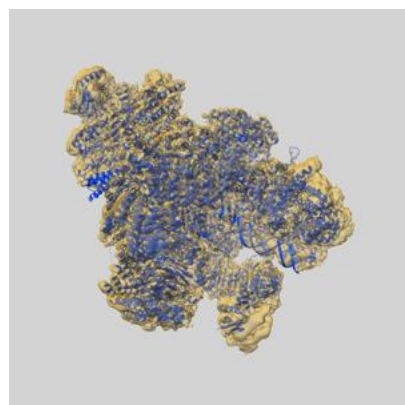
8 Fourier-Shell correlation

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

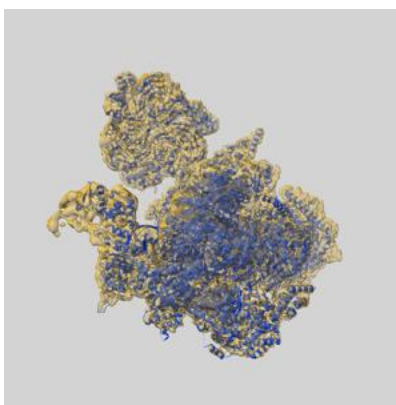
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13539 and PDB model 7PMN. Per-residue inclusion information can be found in section [3](#) on page [13](#).

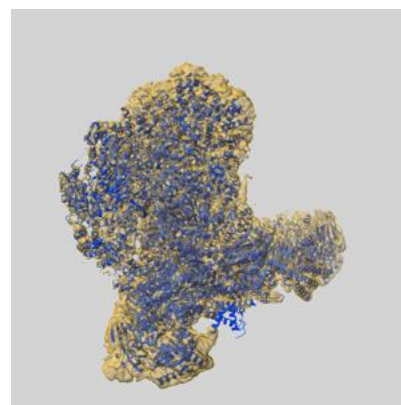
9.1 Map-model overlay [i](#)



X



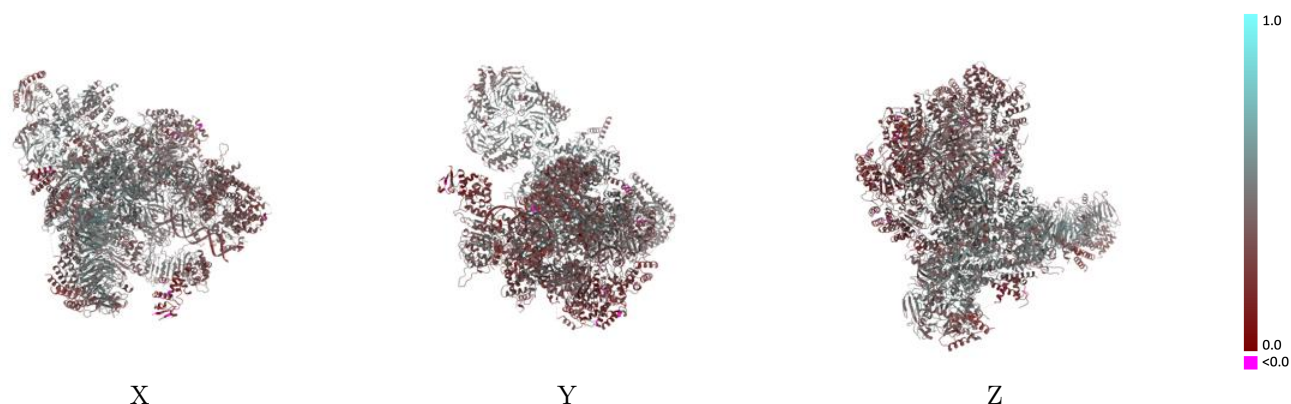
Y



Z

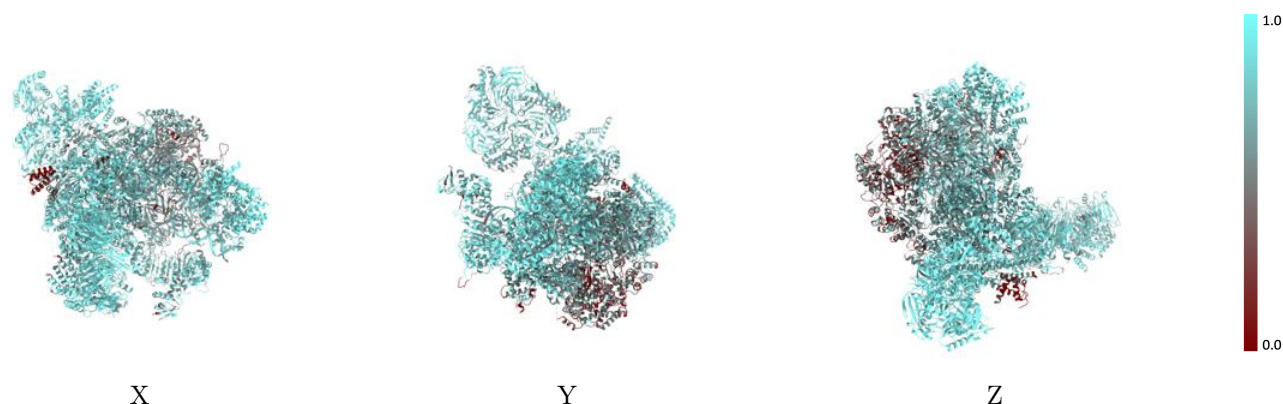
The images above show the 3D surface view of the map at the recommended contour level 6.82 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



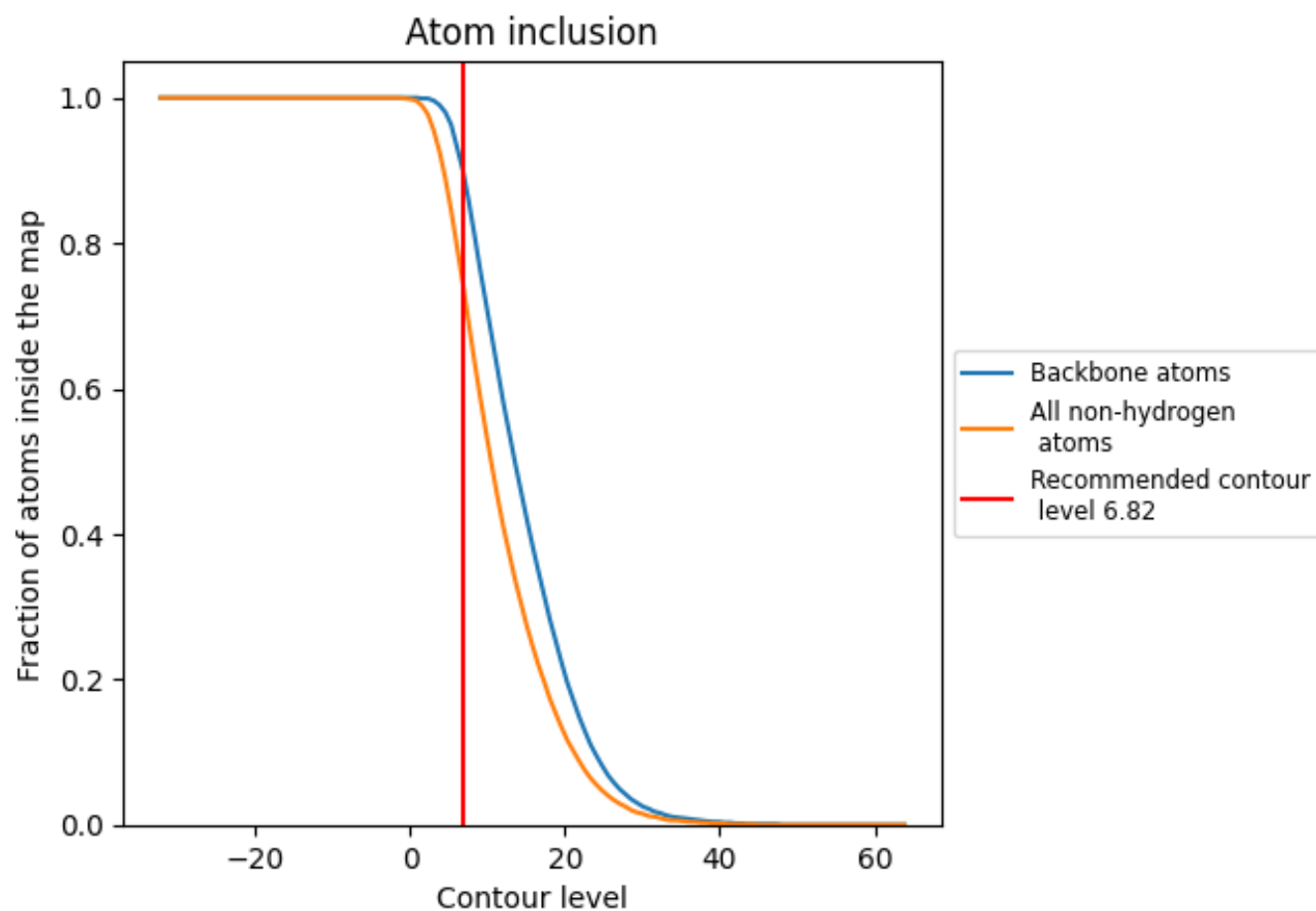
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (6.82).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 75% 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 (6.82) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7470	 0.4050
2	 0.7050	 0.4320
3	 0.6070	 0.3800
4	 0.5210	 0.3290
5	 0.7190	 0.4490
6	 0.6410	 0.3910
7	 0.4810	 0.3160
A	 0.7590	 0.4320
B	 0.8580	 0.5190
C	 0.8280	 0.4800
D	 0.8090	 0.4700
E	 0.8280	 0.4730
F	 0.8310	 0.4760
G	 0.8340	 0.4300
H	 0.8310	 0.4330
I	 0.8500	 0.2960
J	 0.8000	 0.2850
K	 0.7120	 0.1960
L	 0.7930	 0.3830
Q	 0.9130	 0.4280
R	 0.8110	 0.4440
X	 0.8670	 0.3340
Y	 0.8180	 0.3180

