



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 10:25 PM UTC

PDB ID : 8DVF / pdb_00008dvf
EMDB ID : EMD-27737
Title : T4 Bacteriophage primosome with single strand DNA, state 1
Authors : Feng, X.; Li, H.
Deposited on : 2022-07-28
Resolution : 3.30 Å(reported)
Based on initial models : 6QEM, 2AU3, 6N9U

This is a Full wwPDB EM Validation 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

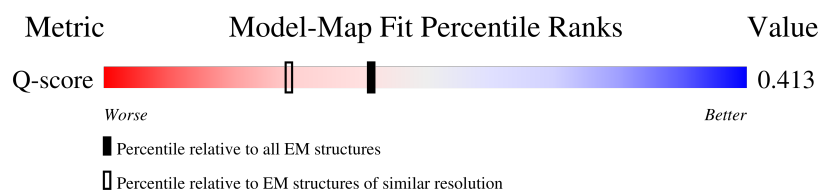
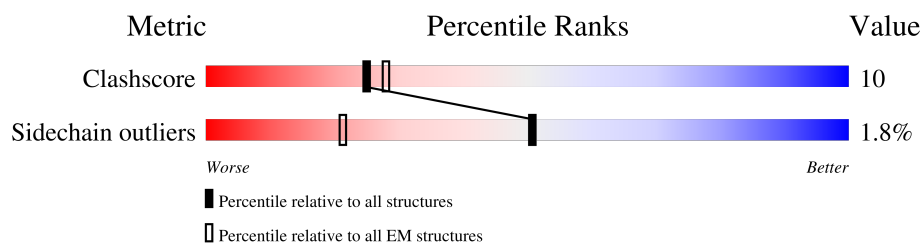
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	A	475	7% 66% 24% 9%
1	B	475	71% 19% 9%
1	C	475	5% 74% 17% 9%
1	D	475	71% 20% 9%
1	E	475	5% 70% 20% 9%

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Mol	Chain	Length	Quality of chain
1	F	475	69% 21% 9%
2	M	12	25% 67% 33%
3	H	342	44% 66% 27% 6%
4	T	5	80% 80% 20%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 23693 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 DnaB-like replicative helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	432	Total	C	N	O	S	0	0
			3424	2179	570	656	19		
1	B	432	Total	C	N	O	S	0	0
			3424	2179	570	656	19		
1	C	432	Total	C	N	O	S	0	0
			3424	2179	570	656	19		
1	D	432	Total	C	N	O	S	0	0
			3424	2179	570	656	19		
1	E	432	Total	C	N	O	S	0	0
			3424	2179	570	656	19		
1	F	432	Total	C	N	O	S	0	0
			3424	2179	570	656	19		

There are 258 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	433	GLN	-	expression tag	UNP P04530
A	434	ASP	-	expression tag	UNP P04530
A	435	SER	-	expression tag	UNP P04530
A	436	THR	-	expression tag	UNP P04530
A	437	PRO	-	expression tag	UNP P04530
A	438	THR	-	expression tag	UNP P04530
A	439	GLU	-	expression tag	UNP P04530
A	440	VAL	-	expression tag	UNP P04530
A	441	ASN	-	expression tag	UNP P04530
A	442	GLU	-	expression tag	UNP P04530
A	443	VAL	-	expression tag	UNP P04530
A	444	ALA	-	expression tag	UNP P04530
A	445	GLY	-	expression tag	UNP P04530
A	446	SER	-	expression tag	UNP P04530
A	447	GLN	-	expression tag	UNP P04530
A	448	GLN	-	expression tag	UNP P04530
A	449	ILE	-	expression tag	UNP P04530
A	450	GLN	-	expression tag	UNP P04530

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Chain	Residue	Modelled	Actual	Comment	Reference
A	451	ALA	-	expression tag	UNP P04530
A	452	GLU	-	expression tag	UNP P04530
A	453	GLN	-	expression tag	UNP P04530
A	454	ASN	-	expression tag	UNP P04530
A	455	ARG	-	expression tag	UNP P04530
A	456	TYR	-	expression tag	UNP P04530
A	457	GLN	-	expression tag	UNP P04530
A	458	ARG	-	expression tag	UNP P04530
A	459	ASN	-	expression tag	UNP P04530
A	460	GLU	-	expression tag	UNP P04530
A	461	SER	-	expression tag	UNP P04530
A	462	THR	-	expression tag	UNP P04530
A	463	ARG	-	expression tag	UNP P04530
A	464	ALA	-	expression tag	UNP P04530
A	465	GLN	-	expression tag	UNP P04530
A	466	LEU	-	expression tag	UNP P04530
A	467	ASP	-	expression tag	UNP P04530
A	468	ALA	-	expression tag	UNP P04530
A	469	LEU	-	expression tag	UNP P04530
A	470	ALA	-	expression tag	UNP P04530
A	471	ASN	-	expression tag	UNP P04530
A	472	GLU	-	expression tag	UNP P04530
A	473	LEU	-	expression tag	UNP P04530
A	474	LYS	-	expression tag	UNP P04530
A	475	PHE	-	expression tag	UNP P04530
B	433	GLN	-	expression tag	UNP P04530
B	434	ASP	-	expression tag	UNP P04530
B	435	SER	-	expression tag	UNP P04530
B	436	THR	-	expression tag	UNP P04530
B	437	PRO	-	expression tag	UNP P04530
B	438	THR	-	expression tag	UNP P04530
B	439	GLU	-	expression tag	UNP P04530
B	440	VAL	-	expression tag	UNP P04530
B	441	ASN	-	expression tag	UNP P04530
B	442	GLU	-	expression tag	UNP P04530
B	443	VAL	-	expression tag	UNP P04530
B	444	ALA	-	expression tag	UNP P04530
B	445	GLY	-	expression tag	UNP P04530
B	446	SER	-	expression tag	UNP P04530
B	447	GLN	-	expression tag	UNP P04530
B	448	GLN	-	expression tag	UNP P04530
B	449	ILE	-	expression tag	UNP P04530

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Chain	Residue	Modelled	Actual	Comment	Reference
B	450	GLN	-	expression tag	UNP P04530
B	451	ALA	-	expression tag	UNP P04530
B	452	GLU	-	expression tag	UNP P04530
B	453	GLN	-	expression tag	UNP P04530
B	454	ASN	-	expression tag	UNP P04530
B	455	ARG	-	expression tag	UNP P04530
B	456	TYR	-	expression tag	UNP P04530
B	457	GLN	-	expression tag	UNP P04530
B	458	ARG	-	expression tag	UNP P04530
B	459	ASN	-	expression tag	UNP P04530
B	460	GLU	-	expression tag	UNP P04530
B	461	SER	-	expression tag	UNP P04530
B	462	THR	-	expression tag	UNP P04530
B	463	ARG	-	expression tag	UNP P04530
B	464	ALA	-	expression tag	UNP P04530
B	465	GLN	-	expression tag	UNP P04530
B	466	LEU	-	expression tag	UNP P04530
B	467	ASP	-	expression tag	UNP P04530
B	468	ALA	-	expression tag	UNP P04530
B	469	LEU	-	expression tag	UNP P04530
B	470	ALA	-	expression tag	UNP P04530
B	471	ASN	-	expression tag	UNP P04530
B	472	GLU	-	expression tag	UNP P04530
B	473	LEU	-	expression tag	UNP P04530
B	474	LYS	-	expression tag	UNP P04530
B	475	PHE	-	expression tag	UNP P04530
C	433	GLN	-	expression tag	UNP P04530
C	434	ASP	-	expression tag	UNP P04530
C	435	SER	-	expression tag	UNP P04530
C	436	THR	-	expression tag	UNP P04530
C	437	PRO	-	expression tag	UNP P04530
C	438	THR	-	expression tag	UNP P04530
C	439	GLU	-	expression tag	UNP P04530
C	440	VAL	-	expression tag	UNP P04530
C	441	ASN	-	expression tag	UNP P04530
C	442	GLU	-	expression tag	UNP P04530
C	443	VAL	-	expression tag	UNP P04530
C	444	ALA	-	expression tag	UNP P04530
C	445	GLY	-	expression tag	UNP P04530
C	446	SER	-	expression tag	UNP P04530
C	447	GLN	-	expression tag	UNP P04530
C	448	GLN	-	expression tag	UNP P04530

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Chain	Residue	Modelled	Actual	Comment	Reference
C	449	ILE	-	expression tag	UNP P04530
C	450	GLN	-	expression tag	UNP P04530
C	451	ALA	-	expression tag	UNP P04530
C	452	GLU	-	expression tag	UNP P04530
C	453	GLN	-	expression tag	UNP P04530
C	454	ASN	-	expression tag	UNP P04530
C	455	ARG	-	expression tag	UNP P04530
C	456	TYR	-	expression tag	UNP P04530
C	457	GLN	-	expression tag	UNP P04530
C	458	ARG	-	expression tag	UNP P04530
C	459	ASN	-	expression tag	UNP P04530
C	460	GLU	-	expression tag	UNP P04530
C	461	SER	-	expression tag	UNP P04530
C	462	THR	-	expression tag	UNP P04530
C	463	ARG	-	expression tag	UNP P04530
C	464	ALA	-	expression tag	UNP P04530
C	465	GLN	-	expression tag	UNP P04530
C	466	LEU	-	expression tag	UNP P04530
C	467	ASP	-	expression tag	UNP P04530
C	468	ALA	-	expression tag	UNP P04530
C	469	LEU	-	expression tag	UNP P04530
C	470	ALA	-	expression tag	UNP P04530
C	471	ASN	-	expression tag	UNP P04530
C	472	GLU	-	expression tag	UNP P04530
C	473	LEU	-	expression tag	UNP P04530
C	474	LYS	-	expression tag	UNP P04530
C	475	PHE	-	expression tag	UNP P04530
D	433	GLN	-	expression tag	UNP P04530
D	434	ASP	-	expression tag	UNP P04530
D	435	SER	-	expression tag	UNP P04530
D	436	THR	-	expression tag	UNP P04530
D	437	PRO	-	expression tag	UNP P04530
D	438	THR	-	expression tag	UNP P04530
D	439	GLU	-	expression tag	UNP P04530
D	440	VAL	-	expression tag	UNP P04530
D	441	ASN	-	expression tag	UNP P04530
D	442	GLU	-	expression tag	UNP P04530
D	443	VAL	-	expression tag	UNP P04530
D	444	ALA	-	expression tag	UNP P04530
D	445	GLY	-	expression tag	UNP P04530
D	446	SER	-	expression tag	UNP P04530
D	447	GLN	-	expression tag	UNP P04530

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Chain	Residue	Modelled	Actual	Comment	Reference
D	448	GLN	-	expression tag	UNP P04530
D	449	ILE	-	expression tag	UNP P04530
D	450	GLN	-	expression tag	UNP P04530
D	451	ALA	-	expression tag	UNP P04530
D	452	GLU	-	expression tag	UNP P04530
D	453	GLN	-	expression tag	UNP P04530
D	454	ASN	-	expression tag	UNP P04530
D	455	ARG	-	expression tag	UNP P04530
D	456	TYR	-	expression tag	UNP P04530
D	457	GLN	-	expression tag	UNP P04530
D	458	ARG	-	expression tag	UNP P04530
D	459	ASN	-	expression tag	UNP P04530
D	460	GLU	-	expression tag	UNP P04530
D	461	SER	-	expression tag	UNP P04530
D	462	THR	-	expression tag	UNP P04530
D	463	ARG	-	expression tag	UNP P04530
D	464	ALA	-	expression tag	UNP P04530
D	465	GLN	-	expression tag	UNP P04530
D	466	LEU	-	expression tag	UNP P04530
D	467	ASP	-	expression tag	UNP P04530
D	468	ALA	-	expression tag	UNP P04530
D	469	LEU	-	expression tag	UNP P04530
D	470	ALA	-	expression tag	UNP P04530
D	471	ASN	-	expression tag	UNP P04530
D	472	GLU	-	expression tag	UNP P04530
D	473	LEU	-	expression tag	UNP P04530
D	474	LYS	-	expression tag	UNP P04530
D	475	PHE	-	expression tag	UNP P04530
E	433	GLN	-	expression tag	UNP P04530
E	434	ASP	-	expression tag	UNP P04530
E	435	SER	-	expression tag	UNP P04530
E	436	THR	-	expression tag	UNP P04530
E	437	PRO	-	expression tag	UNP P04530
E	438	THR	-	expression tag	UNP P04530
E	439	GLU	-	expression tag	UNP P04530
E	440	VAL	-	expression tag	UNP P04530
E	441	ASN	-	expression tag	UNP P04530
E	442	GLU	-	expression tag	UNP P04530
E	443	VAL	-	expression tag	UNP P04530
E	444	ALA	-	expression tag	UNP P04530
E	445	GLY	-	expression tag	UNP P04530
E	446	SER	-	expression tag	UNP P04530

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Chain	Residue	Modelled	Actual	Comment	Reference
E	447	GLN	-	expression tag	UNP P04530
E	448	GLN	-	expression tag	UNP P04530
E	449	ILE	-	expression tag	UNP P04530
E	450	GLN	-	expression tag	UNP P04530
E	451	ALA	-	expression tag	UNP P04530
E	452	GLU	-	expression tag	UNP P04530
E	453	GLN	-	expression tag	UNP P04530
E	454	ASN	-	expression tag	UNP P04530
E	455	ARG	-	expression tag	UNP P04530
E	456	TYR	-	expression tag	UNP P04530
E	457	GLN	-	expression tag	UNP P04530
E	458	ARG	-	expression tag	UNP P04530
E	459	ASN	-	expression tag	UNP P04530
E	460	GLU	-	expression tag	UNP P04530
E	461	SER	-	expression tag	UNP P04530
E	462	THR	-	expression tag	UNP P04530
E	463	ARG	-	expression tag	UNP P04530
E	464	ALA	-	expression tag	UNP P04530
E	465	GLN	-	expression tag	UNP P04530
E	466	LEU	-	expression tag	UNP P04530
E	467	ASP	-	expression tag	UNP P04530
E	468	ALA	-	expression tag	UNP P04530
E	469	LEU	-	expression tag	UNP P04530
E	470	ALA	-	expression tag	UNP P04530
E	471	ASN	-	expression tag	UNP P04530
E	472	GLU	-	expression tag	UNP P04530
E	473	LEU	-	expression tag	UNP P04530
E	474	LYS	-	expression tag	UNP P04530
E	475	PHE	-	expression tag	UNP P04530
F	433	GLN	-	expression tag	UNP P04530
F	434	ASP	-	expression tag	UNP P04530
F	435	SER	-	expression tag	UNP P04530
F	436	THR	-	expression tag	UNP P04530
F	437	PRO	-	expression tag	UNP P04530
F	438	THR	-	expression tag	UNP P04530
F	439	GLU	-	expression tag	UNP P04530
F	440	VAL	-	expression tag	UNP P04530
F	441	ASN	-	expression tag	UNP P04530
F	442	GLU	-	expression tag	UNP P04530
F	443	VAL	-	expression tag	UNP P04530
F	444	ALA	-	expression tag	UNP P04530
F	445	GLY	-	expression tag	UNP P04530

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Chain	Residue	Modelled	Actual	Comment	Reference
F	446	SER	-	expression tag	UNP P04530
F	447	GLN	-	expression tag	UNP P04530
F	448	GLN	-	expression tag	UNP P04530
F	449	ILE	-	expression tag	UNP P04530
F	450	GLN	-	expression tag	UNP P04530
F	451	ALA	-	expression tag	UNP P04530
F	452	GLU	-	expression tag	UNP P04530
F	453	GLN	-	expression tag	UNP P04530
F	454	ASN	-	expression tag	UNP P04530
F	455	ARG	-	expression tag	UNP P04530
F	456	TYR	-	expression tag	UNP P04530
F	457	GLN	-	expression tag	UNP P04530
F	458	ARG	-	expression tag	UNP P04530
F	459	ASN	-	expression tag	UNP P04530
F	460	GLU	-	expression tag	UNP P04530
F	461	SER	-	expression tag	UNP P04530
F	462	THR	-	expression tag	UNP P04530
F	463	ARG	-	expression tag	UNP P04530
F	464	ALA	-	expression tag	UNP P04530
F	465	GLN	-	expression tag	UNP P04530
F	466	LEU	-	expression tag	UNP P04530
F	467	ASP	-	expression tag	UNP P04530
F	468	ALA	-	expression tag	UNP P04530
F	469	LEU	-	expression tag	UNP P04530
F	470	ALA	-	expression tag	UNP P04530
F	471	ASN	-	expression tag	UNP P04530
F	472	GLU	-	expression tag	UNP P04530
F	473	LEU	-	expression tag	UNP P04530
F	474	LYS	-	expression tag	UNP P04530
F	475	PHE	-	expression tag	UNP P04530

- Molecule 2 is a DNA chain called DNA (5'-D(P*TP*TP*TP*TP*TP*TP*TP*TP*TP*TP*TP*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	12	Total	C	N	O	P	0	0
			240	120	24	84	12		

- Molecule 3 is a protein called DNA primase.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	322	Total	C	N	O	S	0	0
			2644	1702	454	475	13		

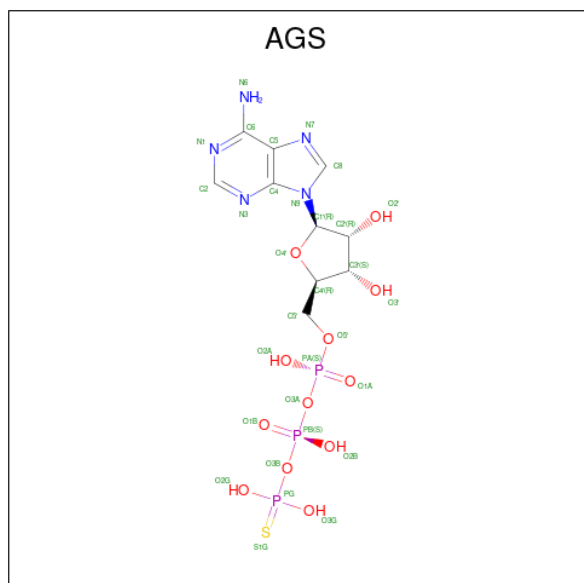
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	1	MET	-	initiating methionine	UNP P04520
H	2	SER	-	expression tag	UNP P04520
H	342	ILE	-	expression tag	UNP P04520

- Molecule 4 is a DNA chain called DNA (5'-D(P*GP*GP*CP*TP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
4	T	5	Total	C	N	O	P	0	0
			105	49	20	31	5		

- Molecule 5 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
5	B	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
5	C	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
5	D	1	Total 31	C 10	N 5	O 12	P 3	S 1	0

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Mol	Chain	Residues	Atoms						AltConf
5	E	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
5	F	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

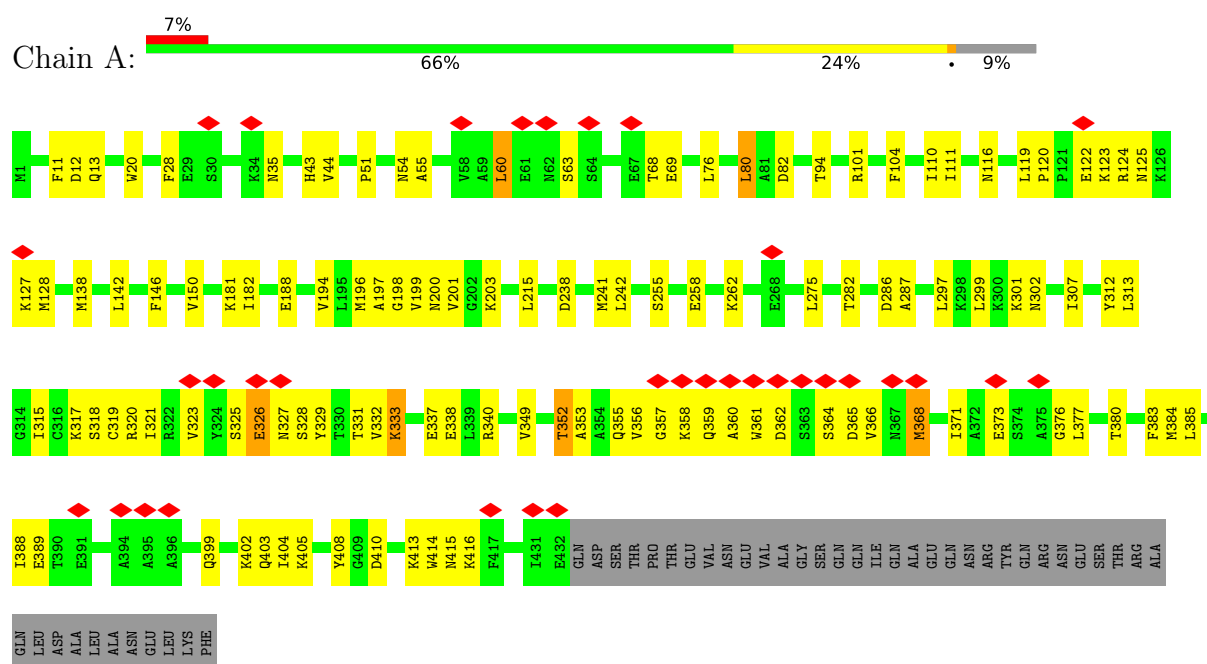
- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
6	B	1	Total	Mg	0
			1	1	
6	C	1	Total	Mg	0
			1	1	
6	D	1	Total	Mg	0
			1	1	
6	E	1	Total	Mg	0
			1	1	
6	F	1	Total	Mg	0
			1	1	

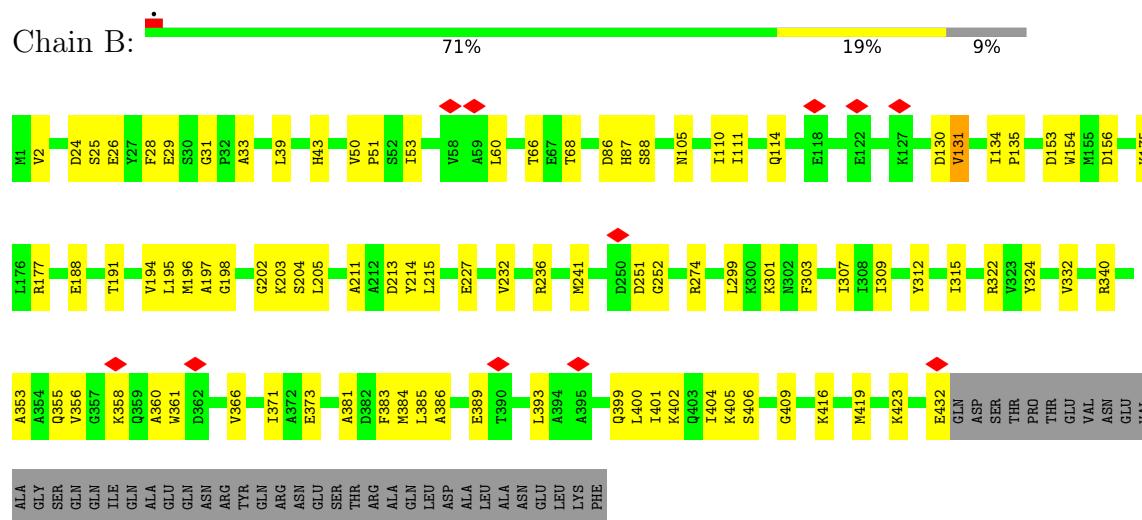
3 Residue-property plots

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: DnaB-like replicative helicase



• Molecule 1: DnaB-like replicative helicase



Chain C:

5% 74% 17% 9%

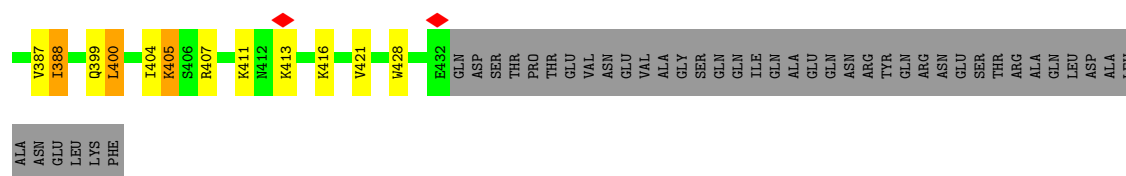
M1 V2 D12 V19 W20 E29 S30 A33 H43 V44 H48 P51 S52 I53 M54 N57 V58 A59 L60 E61 M62 S63 S64 F65 T66 E67 T68 E69 Y70 S71 K74 I77 L80 A81 D82 M103 T107 I110 N116 E122 K126 K127

P129 D130 L142 Y149 D153 W154 M155 D156 R177 I178 L179 I182 E188 T191 L195 M196 A197 G198 V199 N200 K203 M226 E227 R236 I237 D238 L242 D243 V244 I254 K262 K265 E268 T282 A285 D286 T289 F290 R291 N302

I309 V310 G315 R322 V323 G324 S325 V332 A335 E345 T351 T352 V356 G357 K358 D362 D365 E373 D382 L385 A386 V387 I388 A395 L400 I401 K402 Q403 R407 W414 N415 K416 Q426 E432 GLN ASP SER THR PRO THR GLU VAL ASN

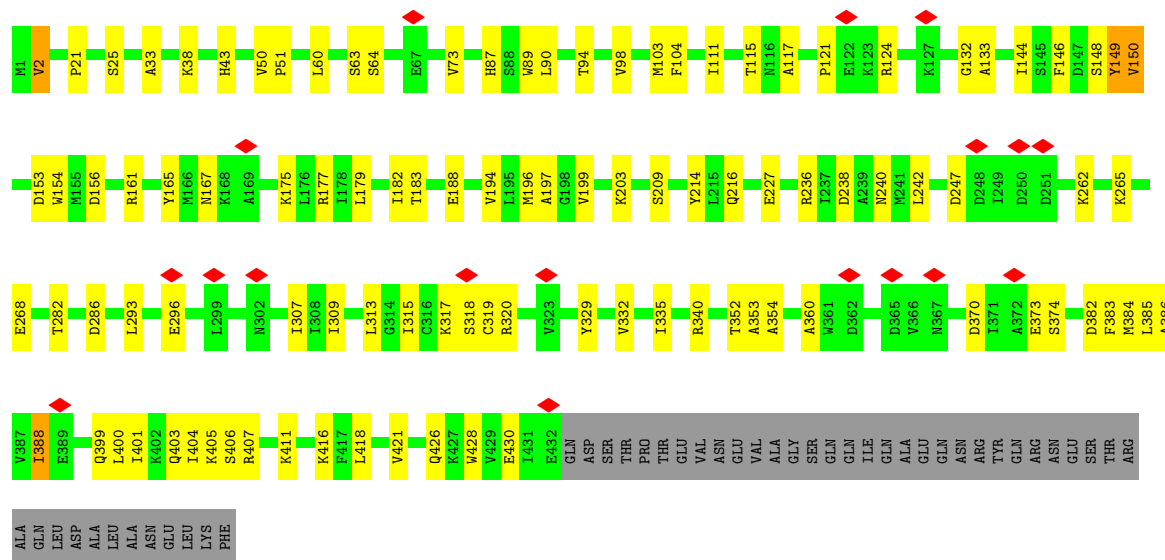
Chain D:

Chain E:



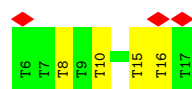
• Molecule 1: DnaB-like replicative helicase

Chain F: 69% 21% 9%



• Molecule 2: DNA (5'-D(P*TP*TP*TP*TP*TP*TP*TP*TP*TP*TP*TP*T)-3')

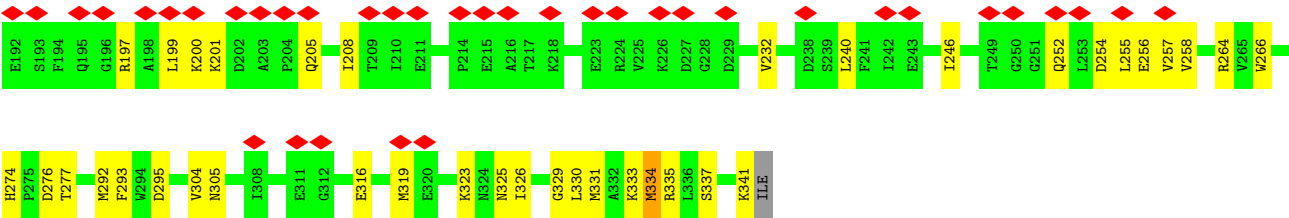
Chain M: 25% 67% 33%



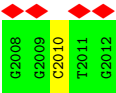
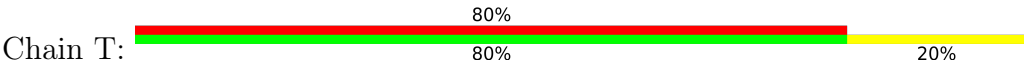
• Molecule 3: DNA primase

Chain H: 44% 66% 27% 6%





• Molecule 4: DNA (5'-D(P*GP*GP*CP*TP*G)-3')



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	124592	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	66	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.090	Depositor
Minimum map value	-0.051	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.012	Depositor
Map size ($\text{\AA}$)	264.96, 264.96, 264.96	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.82799995, 0.82799995, 0.82799995	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: MG, AGS

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	A	0.43	0/3490	0.61	0/4717
1	B	0.22	0/3490	0.37	0/4717
1	C	0.15	0/3490	0.27	0/4717
1	D	0.32	0/3490	0.46	0/4717
1	E	0.27	0/3490	0.39	0/4717
1	F	0.24	0/3490	0.39	0/4717
2	M	0.26	0/263	0.54	0/404
3	H	0.39	0/2712	0.61	0/3662
4	T	0.19	0/117	0.38	0/179
All	All	0.30	0/24032	0.45	0/32547

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	A	3424	0	3429	115	0
1	B	3424	0	3429	72	0
1	C	3424	0	3429	49	0
1	D	3424	0	3429	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	3424	0	3429	74	0
1	F	3424	0	3428	79	0
2	M	240	0	145	3	0
3	H	2644	0	2655	93	0
4	T	105	0	57	1	0
5	B	31	0	12	2	0
5	C	31	0	12	6	0
5	D	31	0	12	1	0
5	E	31	0	12	0	0
5	F	31	0	12	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
All	All	23693	0	23490	494	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 10.

All (494) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:282:THR:HG23	1:D:315:ILE:HG23	1.26	1.11
1:E:329:TYR:HA	1:E:374:SER:HB2	1.36	1.02
1:F:64:SER:HG	3:H:3:SER:N	1.62	0.96
1:B:66:THR:HB	3:H:39:VAL:O	1.68	0.92
1:D:17:SER:HB2	1:E:299:LEU:HD21	1.54	0.88
3:H:180:LEU:HG	3:H:199:LEU:HD21	1.56	0.86
1:D:400:LEU:HD11	1:D:416:LYS:HB3	1.61	0.82
1:E:111:ILE:HG21	3:H:331:MET:HB3	1.61	0.81
3:H:325:ASN:HB3	3:H:335:ARG:HH22	1.46	0.79
1:D:194:VAL:HB	1:D:384:MET:HG2	1.63	0.79
1:A:297:LEU:HD23	1:F:150:VAL:HG11	1.65	0.78
1:F:104:PHE:CE2	3:H:330:LEU:HD21	2.18	0.78
1:F:197:ALA:HB3	1:F:203:LYS:HG3	1.66	0.77
1:B:66:THR:CB	3:H:39:VAL:O	2.33	0.77
1:A:196:MET:HB3	1:A:356:VAL:HG12	1.67	0.76
1:E:286:ASP:HB2	1:E:317:LYS:O	1.88	0.74
1:A:104:PHE:HD1	3:H:94:ARG:HG3	1.52	0.74
1:A:122:GLU:HG3	1:A:123:LYS:HG2	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:332:VAL:HG21	1:B:373:GLU:HB3	1.69	0.72
1:B:384:MET:SD	1:B:404:ILE:HD11	2.28	0.72
3:H:7:ILE:HD11	3:H:92:GLU:HB3	1.70	0.72
1:F:286:ASP:HB2	1:F:319:CYS:HB2	1.71	0.72
1:F:405:LYS:HZ1	1:F:407:ARG:HB2	1.53	0.71
1:C:407:ARG:NH2	5:D:501:AGS:S1G	2.63	0.71
1:B:389:GLU:HG2	1:B:399:GLN:HG2	1.73	0.71
1:B:381:ALA:O	1:B:405:LYS:HE3	1.91	0.70
1:C:154:TRP:NE1	1:D:238:ASP:OD1	2.24	0.70
1:B:66:THR:CG2	3:H:39:VAL:O	2.39	0.69
1:A:198:GLY:HA2	1:A:356:VAL:HG22	1.74	0.69
1:A:119:LEU:HG	1:A:120:PRO:HD2	1.73	0.69
1:A:333:LYS:HG2	1:A:376:GLY:HA2	1.74	0.69
1:B:29:GLU:HG2	1:B:33:ALA:HB3	1.74	0.68
1:D:64:SER:HB2	3:H:341:LYS:HZ3	1.58	0.68
1:B:400:LEU:HD11	1:B:416:LYS:HB3	1.75	0.68
3:H:255:LEU:HG	3:H:266:TRP:HZ2	1.59	0.68
1:D:203:LYS:HG2	1:D:353:ALA:HB1	1.75	0.67
1:D:403:GLN:HG2	1:D:406:SER:HB2	1.74	0.67
1:F:405:LYS:NZ	1:F:407:ARG:HB2	2.08	0.67
1:E:282:THR:HG23	1:E:315:ILE:HG23	1.77	0.66
1:C:67:GLU:HA	1:C:70:TYR:HB3	1.77	0.66
1:D:87:HIS:O	1:D:91:VAL:HG23	1.95	0.66
1:C:332:VAL:HG21	1:C:373:GLU:HB3	1.77	0.66
1:A:301:LYS:HZ1	1:F:149:TYR:HA	1.61	0.66
1:A:368:MET:HG3	1:A:404:ILE:HG12	1.78	0.66
1:B:29:GLU:HG3	1:B:31:GLY:H	1.61	0.66
1:F:117:ALA:O	1:F:124:ARG:NH2	2.29	0.65
1:F:352:THR:HG22	1:F:353:ALA:H	1.61	0.65
1:D:175:LYS:NZ	1:D:216:GLN:OE1	2.27	0.64
1:A:76:LEU:O	1:A:80:LEU:HD13	1.98	0.64
1:E:125:ASN:HD21	1:E:127:LYS:HB3	1.62	0.64
1:F:332:VAL:HG21	1:F:373:GLU:HB3	1.79	0.64
1:F:188:GLU:OE1	1:F:407:ARG:NH2	2.31	0.64
3:H:154:TRP:HB2	3:H:181:VAL:HB	1.78	0.64
1:A:301:LYS:O	1:A:302:ASN:ND2	2.30	0.64
3:H:255:LEU:HB3	3:H:264:ARG:NH2	2.13	0.64
1:E:329:TYR:CA	1:E:374:SER:HB2	2.21	0.63
1:C:197:ALA:HB2	1:C:387:VAL:HB	1.80	0.63
1:C:309:ILE:HD13	1:C:351:TRP:HB2	1.81	0.63
3:H:16:LEU:HD12	3:H:33:LEU:HD12	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:340:ARG:HH21	1:F:382:ASP:CG	2.06	0.63
1:A:405:LYS:NZ	5:B:501:AGS:S1G	2.72	0.62
1:B:194:VAL:HB	1:B:384:MET:HG2	1.81	0.62
1:A:329:TYR:O	1:A:332:VAL:HG22	1.99	0.62
1:C:199:VAL:HG13	5:C:501:AGS:S1G	2.38	0.62
1:D:64:SER:HB2	3:H:341:LYS:NZ	2.14	0.62
1:F:175:LYS:NZ	1:F:216:GLN:OE1	2.32	0.62
1:D:154:TRP:NE1	1:E:238:ASP:OD1	2.30	0.62
1:E:244:VAL:HG21	1:E:254:ILE:HD11	1.81	0.62
1:A:28:PHE:O	1:A:101:ARG:NH1	2.33	0.62
1:C:382:ASP:OD1	1:C:407:ARG:NH1	2.32	0.62
3:H:255:LEU:HB3	3:H:264:ARG:HH22	1.64	0.61
1:A:321:ILE:HG23	1:A:323:VAL:H	1.65	0.61
1:E:329:TYR:HA	1:E:374:SER:CB	2.22	0.61
1:D:286:ASP:HB3	1:D:317:LYS:HG3	1.82	0.61
1:A:104:PHE:HD1	3:H:94:ARG:CG	2.14	0.61
1:A:203:LYS:HZ1	1:A:355:GLN:HA	1.65	0.61
3:H:15:ALA:HB1	3:H:77:TYR:HE2	1.65	0.61
1:B:177:ARG:HH22	1:B:432:GLU:HG2	1.66	0.61
1:A:299:LEU:HG	1:F:21:PRO:HB3	1.83	0.60
1:A:119:LEU:HD23	1:A:123:LYS:O	2.01	0.60
1:F:104:PHE:CD2	3:H:330:LEU:HD21	2.35	0.60
1:F:194:VAL:HB	1:F:384:MET:HG2	1.81	0.60
1:B:360:ALA:HB1	1:B:366:VAL:HG22	1.84	0.60
1:E:201:VAL:O	1:E:399:GLN:NE2	2.34	0.60
1:F:313:LEU:HB2	1:F:352:THR:HG21	1.84	0.60
1:E:356:VAL:O	1:E:361:TRP:NE1	2.31	0.60
1:E:197:ALA:HB2	1:E:387:VAL:HB	1.84	0.60
3:H:274:HIS:HE1	3:H:276:ASP:HB2	1.66	0.60
1:F:25:SER:OG	1:F:38:LYS:NZ	2.32	0.60
1:C:244:VAL:HG11	1:C:254:ILE:HD12	1.83	0.59
1:D:243:ASP:OD1	1:D:427:LYS:NZ	2.34	0.59
1:E:165:TYR:O	1:E:168:LYS:NZ	2.34	0.59
1:A:301:LYS:HD3	1:F:150:VAL:HG12	1.83	0.59
1:D:170:ARG:NH1	1:D:188:GLU:OE1	2.35	0.59
1:B:43:HIS:HB2	1:B:60:LEU:HD11	1.84	0.59
1:D:110:ILE:HG13	1:D:134:ILE:HD12	1.83	0.59
1:B:114:GLN:HB2	3:H:94:ARG:HH11	1.66	0.59
1:F:104:PHE:CD2	3:H:330:LEU:HD11	2.38	0.59
1:A:333:LYS:HG2	1:A:376:GLY:CA	2.32	0.59
1:C:236:ARG:NH1	1:C:426:GLN:OE1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:GLN:HG3	1:A:361:TRP:HE1	1.68	0.59
1:F:286:ASP:HB3	1:F:317:LYS:HB3	1.84	0.59
1:F:196:MET:HE2	1:F:404:ILE:HD12	1.85	0.59
1:B:111:ILE:HG22	3:H:90:ILE:HG13	1.84	0.58
3:H:16:LEU:HD13	3:H:35:PHE:CE2	2.38	0.58
1:A:384:MET:HG2	1:A:404:ILE:CG2	2.33	0.58
1:A:238:ASP:OD1	1:F:154:TRP:NE1	2.30	0.58
1:D:415:ASN:HB3	1:D:416:LYS:HZ3	1.67	0.58
1:E:154:TRP:NE1	1:F:238:ASP:OD1	2.36	0.58
1:E:161:ARG:NE	1:F:238:ASP:OD2	2.37	0.58
1:E:227:GLU:HG2	1:E:315:ILE:HD13	1.84	0.58
1:A:383:PHE:HE1	1:A:403:GLN:HE21	1.50	0.58
1:E:30:SER:HA	1:E:34:LYS:HE2	1.86	0.58
1:E:400:LEU:HD21	1:E:416:LYS:HB3	1.86	0.58
1:A:321:ILE:HD13	1:A:331:THR:HG22	1.86	0.58
1:B:39:LEU:HD22	1:B:60:LEU:HB3	1.85	0.58
1:F:383:PHE:CZ	1:F:385:LEU:HD21	2.38	0.57
1:D:110:ILE:HG13	1:D:134:ILE:HG23	1.85	0.57
1:E:111:ILE:HD13	3:H:330:LEU:C	2.29	0.57
3:H:329:GLY:O	3:H:333:LYS:HG3	2.04	0.57
1:D:86:ASP:OD1	1:D:86:ASP:N	2.36	0.57
3:H:274:HIS:CE1	3:H:276:ASP:HB2	2.40	0.57
1:C:388:ILE:HB	1:C:400:LEU:HB3	1.84	0.57
1:D:15:TYR:O	1:D:19:VAL:HG22	2.04	0.57
1:A:203:LYS:HZ1	1:A:355:GLN:CA	2.17	0.57
1:A:286:ASP:HB2	1:A:319:CYS:SG	2.44	0.57
1:A:255:SER:OG	1:A:258:GLU:OE1	2.23	0.57
1:D:15:TYR:CE1	1:D:19:VAL:HG11	2.40	0.56
1:A:319:CYS:H	1:A:338:GLU:CD	2.13	0.56
1:B:154:TRP:NE1	1:C:238:ASP:OD1	2.37	0.56
1:C:403:GLN:NE2	1:C:414:TRP:O	2.32	0.56
1:E:117:ALA:O	1:E:124:ARG:NH2	2.38	0.56
1:A:384:MET:HG2	1:A:404:ILE:HG22	1.85	0.56
1:E:2:VAL:HG21	1:E:33:ALA:HB1	1.88	0.56
1:E:237:ILE:HD13	1:E:275:LEU:HD21	1.87	0.56
1:D:201:VAL:O	1:D:399:GLN:NE2	2.39	0.56
1:C:291:ARG:NH1	1:C:345:GLU:OE1	2.39	0.56
1:D:282:THR:HG23	1:D:315:ILE:CG2	2.18	0.56
1:C:58:VAL:O	1:C:62:ASN:ND2	2.39	0.55
1:F:421:VAL:HG22	1:F:428:TRP:CD1	2.41	0.55
1:E:384:MET:O	1:E:404:ILE:HB	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:53:ILE:O	1:C:57:ASN:ND2	2.39	0.55
1:D:297:LEU:HD12	1:D:303:PHE:HB3	1.88	0.55
1:E:404:ILE:O	1:E:411:LYS:HD2	2.06	0.55
1:D:116:ASN:ND2	1:D:124:ARG:O	2.34	0.55
3:H:84:ASP:N	3:H:84:ASP:OD1	2.38	0.55
3:H:274:HIS:ND1	3:H:277:THR:HG23	2.22	0.55
1:A:360:ALA:HB1	1:A:366:VAL:HG22	1.87	0.55
1:A:364:SER:O	1:A:388:ILE:HG13	2.07	0.55
1:C:53:ILE:HD12	1:C:77:ILE:HD11	1.87	0.55
1:D:383:PHE:HD1	1:D:406:SER:HA	1.72	0.55
1:E:211:ALA:HB2	1:E:309:ILE:HD12	1.89	0.55
1:F:104:PHE:CZ	3:H:330:LEU:HD21	2.41	0.55
1:C:322:ARG:NH1	1:C:325:SER:OG	2.40	0.55
1:A:402:LYS:HG3	1:A:416:LYS:HG3	1.89	0.55
1:D:161:ARG:NE	1:E:238:ASP:OD2	2.40	0.54
1:E:8:HIS:NE2	1:E:85:GLU:OE1	2.39	0.54
1:E:329:TYR:HE1	1:E:375:ALA:HB3	1.73	0.54
1:A:301:LYS:NZ	1:F:148:SER:O	2.41	0.54
1:A:340:ARG:NH2	1:B:227:GLU:O	2.41	0.54
1:D:20:TRP:N	1:D:21:PRO:HD2	2.22	0.54
1:A:150:VAL:H	1:B:301:LYS:HZ3	1.56	0.53
1:F:388:ILE:HB	1:F:400:LEU:HB3	1.91	0.53
3:H:170:THR:O	3:H:172:LYS:NZ	2.42	0.53
1:A:119:LEU:HB3	1:A:124:ARG:HG2	1.90	0.53
1:A:201:VAL:HG13	1:A:399:GLN:HE22	1.74	0.53
1:B:312:TYR:OH	1:B:355:GLN:HB2	2.08	0.53
1:F:133:ALA:HB2	1:F:320:ARG:HG3	1.91	0.53
1:A:196:MET:HB3	1:A:356:VAL:CG1	2.37	0.53
1:A:125:ASN:HD21	1:A:127:LYS:HB3	1.74	0.53
1:B:195:LEU:HD23	1:B:385:LEU:HB2	1.89	0.53
1:E:225:SER:HA	1:E:311:ASP:HB2	1.90	0.53
3:H:149:LYS:HB3	3:H:240:LEU:HD22	1.90	0.53
1:A:282:THR:HG23	1:A:315:ILE:HG23	1.91	0.53
1:B:232:VAL:O	1:B:236:ARG:HG3	2.09	0.52
1:B:404:ILE:HG13	1:B:405:LYS:N	2.24	0.52
1:D:285:ALA:O	1:D:317:LYS:HG2	2.09	0.52
1:B:66:THR:HG21	3:H:39:VAL:O	2.08	0.52
1:E:255:SER:HB2	1:E:258:GLU:OE1	2.09	0.52
1:A:318:SER:HB3	1:A:321:ILE:HG21	1.91	0.52
1:A:358:LYS:O	1:A:361:TRP:HB2	2.10	0.52
1:C:195:LEU:HD23	1:C:385:LEU:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:LYS:NZ	1:F:149:TYR:HA	2.25	0.52
1:A:198:GLY:HA2	1:A:356:VAL:CG2	2.40	0.52
3:H:331:MET:O	3:H:335:ARG:HG3	2.10	0.52
1:A:104:PHE:CD1	3:H:94:ARG:HG3	2.40	0.52
1:C:153:ASP:HB3	1:C:156:ASP:HB2	1.91	0.52
3:H:180:LEU:HB2	3:H:197:ARG:HB3	1.91	0.52
1:A:203:LYS:HE3	1:A:312:TYR:CZ	2.46	0.51
1:A:366:VAL:HG23	1:A:388:ILE:HD11	1.92	0.51
1:D:306:THR:HA	1:D:348:THR:HG22	1.91	0.51
1:A:116:ASN:HD21	1:A:125:ASN:H	1.59	0.51
1:E:39:LEU:HD11	1:E:60:LEU:HD23	1.92	0.51
1:B:312:TYR:HB3	1:B:315:ILE:HG12	1.92	0.51
1:E:245:SER:OG	1:E:247:ASP:OD1	2.22	0.51
3:H:126:ARG:H	3:H:129:LYS:HE2	1.74	0.51
1:A:355:GLN:HG2	1:A:361:TRP:HZ2	1.76	0.51
1:B:399:GLN:O	1:B:419:MET:N	2.42	0.51
1:B:402:LYS:HA	1:B:416:LYS:HD3	1.93	0.51
1:E:154:TRP:HA	1:E:161:ARG:HH12	1.74	0.51
3:H:11:PHE:CZ	3:H:89:TYR:HA	2.45	0.51
3:H:21:LYS:HE3	3:H:48:ASN:HA	1.92	0.51
1:A:94:THR:HG23	1:A:146:PHE:CE2	2.46	0.51
1:E:329:TYR:CG	2:M:8:DT:H4'	2.45	0.51
3:H:127:LEU:HA	3:H:130:LEU:HD12	1.91	0.51
3:H:178:PRO:HB2	3:H:199:LEU:HD12	1.92	0.50
1:A:125:ASN:HD22	1:A:128:MET:HG2	1.76	0.50
1:F:2:VAL:HG21	1:F:33:ALA:HB1	1.93	0.50
1:C:107:THR:O	1:C:110:ILE:HG13	2.11	0.50
3:H:205:GLN:HB3	3:H:208:ILE:HG12	1.93	0.50
1:F:60:LEU:HD13	1:F:73:VAL:HG11	1.93	0.50
3:H:53:TRP:HE1	4:T:2010:DC:H41	1.60	0.50
1:D:242:LEU:HB2	1:D:244:VAL:HG12	1.94	0.50
3:H:255:LEU:HG	3:H:266:TRP:CZ2	2.42	0.50
1:A:197:ALA:O	1:A:355:GLN:NE2	2.45	0.50
1:A:358:LYS:HG2	1:A:361:TRP:CZ3	2.46	0.50
1:C:402:LYS:HD2	1:C:416:LYS:HE2	1.94	0.50
5:C:501:AGS:O5'	5:C:501:AGS:H8	2.12	0.50
1:E:15:TYR:O	1:E:19:VAL:HG22	2.11	0.50
1:F:115:THR:OG1	3:H:337:SER:CB	2.59	0.50
1:A:182:ILE:HG22	1:A:414:TRP:HB2	1.92	0.49
1:B:371:ILE:O	1:C:358:LYS:NZ	2.35	0.49
1:A:383:PHE:HB2	1:A:408:TYR:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:295:ASP:N	3:H:295:ASP:OD1	2.45	0.49
1:B:86:ASP:OD2	1:B:88:SER:OG	2.24	0.49
1:E:111:ILE:HD13	3:H:331:MET:N	2.28	0.49
3:H:116:LYS:NZ	3:H:166:ILE:O	2.40	0.49
3:H:252:GLN:OE1	3:H:257:VAL:HG11	2.12	0.49
1:E:20:TRP:N	1:E:21:PRO:CD	2.76	0.49
1:E:141:ALA:HA	1:E:144:ILE:HD11	1.94	0.49
1:D:171:LYS:NZ	1:D:188:GLU:OE2	2.45	0.49
1:E:332:VAL:HB	1:E:374:SER:HB3	1.93	0.49
1:F:60:LEU:O	1:F:63:SER:OG	2.26	0.49
1:D:177:ARG:HH22	1:D:432:GLU:HB2	1.78	0.49
1:F:161:ARG:HG2	1:F:165:TYR:CZ	2.48	0.49
1:A:371:ILE:HD11	1:A:404:ILE:HD13	1.95	0.49
1:C:177:ARG:HH22	1:C:432:GLU:HG3	1.77	0.49
1:A:384:MET:O	1:A:404:ILE:HG22	2.12	0.49
1:F:360:ALA:HB2	1:F:370:ASP:HB3	1.95	0.49
1:B:111:ILE:O	3:H:94:ARG:NH1	2.45	0.48
1:A:301:LYS:HD3	1:F:150:VAL:CG1	2.43	0.48
1:A:242:LEU:HD22	1:A:262:LYS:HB3	1.95	0.48
1:C:203:LYS:HB2	5:C:501:AGS:O2B	2.14	0.48
1:D:214:TYR:CD2	1:D:307:ILE:HG21	2.48	0.48
1:D:329:TYR:HE1	1:D:375:ALA:HB3	1.78	0.48
1:E:287:ALA:HA	1:E:290:PHE:HB2	1.94	0.48
1:A:383:PHE:CE2	1:A:385:LEU:HG	2.48	0.48
1:E:421:VAL:HG22	1:E:428:TRP:CD1	2.48	0.48
1:F:87:HIS:O	1:F:87:HIS:ND1	2.46	0.48
1:A:150:VAL:H	1:B:301:LYS:NZ	2.11	0.48
1:A:201:VAL:HG13	1:A:399:GLN:NE2	2.29	0.48
1:A:415:ASN:HB3	1:A:416:LYS:HD2	1.95	0.48
1:B:153:ASP:HB3	1:B:156:ASP:HB2	1.94	0.48
1:C:71:SER:HA	1:C:74:LYS:HG2	1.96	0.48
1:A:321:ILE:HG12	1:A:323:VAL:HG22	1.95	0.48
1:A:326:GLU:CD	1:A:326:GLU:H	2.21	0.48
1:A:410:ASP:HB3	1:A:413:LYS:HD3	1.95	0.48
1:B:405:LYS:HZ3	1:C:200:ASN:HD22	1.61	0.48
1:D:376:GLY:O	1:D:380:THR:HG22	2.14	0.48
1:E:29:GLU:HG3	1:E:30:SER:H	1.79	0.48
1:E:244:VAL:HG13	1:E:245:SER:H	1.78	0.48
3:H:325:ASN:HB3	3:H:335:ARG:NH2	2.22	0.48
1:A:366:VAL:H	1:A:402:LYS:HE2	1.79	0.48
1:B:386:ALA:O	1:B:401:ILE:HA	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:282:THR:HG23	1:C:315:ILE:HB	1.96	0.48
1:F:182:ILE:HG13	1:F:183:THR:HG23	1.96	0.48
1:A:371:ILE:HG22	1:A:373:GLU:N	2.29	0.47
1:D:89:TRP:HE3	1:D:90:LEU:HD22	1.79	0.47
1:F:340:ARG:NH2	1:F:382:ASP:OD1	2.40	0.47
1:A:199:VAL:O	1:A:200:ASN:HB2	2.15	0.47
1:A:241:MET:HE3	1:A:241:MET:HB3	1.74	0.47
1:C:265:LYS:O	1:C:268:GLU:HG2	2.14	0.47
1:B:2:VAL:HG11	1:B:33:ALA:HB1	1.96	0.47
1:D:342:LEU:O	1:D:346:THR:HG22	2.13	0.47
1:C:188:GLU:O	1:C:191:THR:OG1	2.29	0.47
1:F:196:MET:HG2	1:F:354:ALA:HB3	1.97	0.47
1:B:188:GLU:O	1:B:191:THR:OG1	2.28	0.47
1:F:111:ILE:HD13	3:H:334:MET:N	2.30	0.47
3:H:27:ASN:HB2	3:H:30:THR:HG22	1.97	0.47
3:H:32:LYS:HA	3:H:54:TYR:O	2.14	0.47
1:A:356:VAL:CG2	1:A:361:TRP:HD1	2.28	0.47
1:C:2:VAL:HG21	1:C:33:ALA:HB1	1.97	0.47
1:D:198:GLY:HA2	1:D:356:VAL:HG22	1.96	0.47
1:D:312:TYR:CE2	1:D:355:GLN:HG2	2.49	0.47
1:F:329:TYR:HA	1:F:374:SER:HB2	1.95	0.47
1:D:2:VAL:HG21	1:D:33:ALA:HB1	1.95	0.47
3:H:143:ARG:NH1	3:H:305:ASN:OD1	2.48	0.47
1:C:226:MET:HE1	1:C:285:ALA:HB3	1.96	0.47
1:E:245:SER:HB3	1:E:248:ASP:HB2	1.97	0.47
1:D:313:LEU:HB3	1:D:352:THR:HG21	1.97	0.46
3:H:57:ASP:OD1	3:H:57:ASP:N	2.48	0.46
1:B:43:HIS:CG	1:B:51:PRO:HB3	2.50	0.46
1:B:175:LYS:HB2	1:B:213:ASP:HB3	1.97	0.46
1:F:236:ARG:NH1	1:F:426:GLN:OE1	2.48	0.46
1:B:203:LYS:HG2	1:B:353:ALA:HB1	1.96	0.46
1:D:383:PHE:CD1	1:D:406:SER:HA	2.49	0.46
1:E:226:MET:HE1	1:E:285:ALA:HB3	1.97	0.46
1:E:384:MET:HB3	1:E:405:LYS:HB3	1.98	0.46
3:H:316:GLU:HA	3:H:319:MET:HG2	1.97	0.46
1:B:383:PHE:HD1	1:B:406:SER:HA	1.80	0.46
1:C:29:GLU:HG3	1:C:30:SER:H	1.81	0.46
1:F:89:TRP:HE3	1:F:90:LEU:HD22	1.81	0.46
1:A:328:SER:O	1:A:332:VAL:HG13	2.15	0.46
1:A:359:GLN:HA	1:A:362:ASP:OD2	2.15	0.46
1:D:368:MET:HB2	1:D:404:ILE:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:ILE:HG22	1:A:373:GLU:H	1.80	0.46
1:B:236:ARG:HH22	5:B:501:AGS:PA	2.39	0.46
1:F:104:PHE:CE2	3:H:330:LEU:CD2	2.94	0.46
3:H:254:ASP:OD2	3:H:257:VAL:HG13	2.16	0.46
1:B:389:GLU:HA	1:B:393:LEU:HD12	1.96	0.46
3:H:14:ARG:CZ	3:H:85:LEU:HD22	2.46	0.46
1:A:356:VAL:CG2	1:A:361:TRP:CD1	2.99	0.46
1:E:11:PHE:HE2	1:E:80:LEU:HB3	1.80	0.46
1:B:274:ARG:HB2	1:B:303:PHE:HE1	1.81	0.45
1:E:365:ASP:HA	1:E:388:ILE:HD13	1.97	0.45
1:B:130:ASP:OD1	1:B:131:VAL:N	2.44	0.45
1:A:43:HIS:CG	1:A:51:PRO:HB3	2.51	0.45
1:F:179:LEU:HA	1:F:182:ILE:HG12	1.99	0.45
1:F:242:LEU:HD22	1:F:262:LYS:HB3	1.99	0.45
1:D:332:VAL:HG21	1:D:373:GLU:HB3	1.97	0.45
3:H:254:ASP:O	3:H:257:VAL:HG22	2.15	0.45
1:B:196:MET:CE	1:B:404:ILE:HD13	2.46	0.45
1:D:312:TYR:HB3	1:D:315:ILE:HD12	1.98	0.45
1:A:337:GLU:HA	1:A:380:THR:HG21	1.99	0.45
1:B:197:ALA:HB3	1:B:203:LYS:HB2	1.99	0.45
1:E:313:LEU:HD11	1:E:336:ALA:HA	1.97	0.45
2:M:15:DT:H4'	2:M:16:DT:OP1	2.17	0.45
1:F:282:THR:HG23	1:F:315:ILE:HG13	1.99	0.45
1:B:198:GLY:HA2	1:B:356:VAL:HG12	1.98	0.45
3:H:33:LEU:HB2	3:H:54:TYR:HB3	1.98	0.45
1:E:312:TYR:CD1	1:E:313:LEU:N	2.85	0.45
3:H:153:LEU:HD21	3:H:240:LEU:HD11	1.99	0.45
3:H:157:THR:HA	3:H:178:PRO:HA	1.99	0.45
3:H:293:PHE:HB2	3:H:335:ARG:NH2	2.32	0.45
1:D:15:TYR:CE2	1:D:19:VAL:HG21	2.53	0.44
1:C:198:GLY:HA2	1:C:356:VAL:HG22	1.99	0.44
1:E:378:PRO:O	1:F:199:VAL:HG11	2.17	0.44
3:H:232:VAL:HG22	3:H:246:ILE:HG13	1.99	0.44
1:E:407:ARG:NH2	1:F:227:GLU:OE2	2.50	0.44
1:B:196:MET:HE2	1:B:404:ILE:HD13	1.99	0.44
3:H:16:LEU:HD12	3:H:33:LEU:CD1	2.44	0.44
1:B:251:ASP:OD1	1:B:252:GLY:N	2.51	0.44
1:B:405:LYS:HE2	5:C:501:AGS:S1G	2.58	0.44
1:C:179:LEU:HA	1:C:182:ILE:HG12	1.99	0.44
1:B:389:GLU:HB3	1:B:399:GLN:HA	2.00	0.44
1:E:184:LYS:NZ	1:F:247:ASP:OD2	2.34	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:346:THR:HB	1:E:348:THR:HG22	1.99	0.44
1:A:60:LEU:O	1:A:63:SER:OG	2.32	0.44
1:A:138:MET:HE2	1:B:134:ILE:HG21	1.99	0.44
1:F:307:ILE:O	1:F:309:ILE:HG13	2.17	0.44
1:A:356:VAL:HG23	1:A:361:TRP:CD1	2.52	0.44
1:C:103:MET:HE1	1:C:142:LEU:HD13	2.00	0.44
1:D:153:ASP:HB3	1:D:156:ASP:HB2	1.99	0.44
1:D:242:LEU:HD22	1:D:262:LYS:HB3	1.99	0.44
3:H:254:ASP:HB3	3:H:257:VAL:HG22	1.99	0.44
1:C:323:VAL:HG12	1:C:324:TYR:HD2	1.82	0.44
1:D:385:LEU:HD23	1:D:403:GLN:HA	1.99	0.44
1:E:61:GLU:OE1	1:E:70:TYR:OH	2.22	0.44
3:H:201:LYS:HD3	3:H:201:LYS:HA	1.89	0.44
3:H:292:MET:SD	3:H:293:PHE:N	2.90	0.44
1:A:313:LEU:HB2	1:A:352:THR:HG21	2.00	0.43
1:E:332:VAL:HG21	1:E:373:GLU:HB3	2.00	0.43
1:F:265:LYS:O	1:F:268:GLU:HG2	2.18	0.43
1:A:54:ASN:OD1	1:A:55:ALA:N	2.51	0.43
1:A:241:MET:HE2	1:F:154:TRP:CH2	2.53	0.43
1:A:357:GLY:O	1:A:360:ALA:HB3	2.18	0.43
1:D:329:TYR:HB2	2:M:10:DT:H2"	2.00	0.43
1:F:43:HIS:CG	1:F:51:PRO:HB3	2.53	0.43
1:A:94:THR:HG23	1:A:146:PHE:HE2	1.83	0.43
1:A:111:ILE:HD12	3:H:91:PHE:CE1	2.53	0.43
1:A:325:SER:HB3	1:A:328:SER:OG	2.18	0.43
1:A:383:PHE:HE1	1:A:403:GLN:NE2	2.17	0.43
1:B:202:GLY:C	1:B:204:SER:H	2.26	0.43
1:E:20:TRP:N	1:E:21:PRO:HD2	2.32	0.43
1:B:2:VAL:HG13	1:B:28:PHE:HD2	1.82	0.43
1:D:2:VAL:HG23	1:D:28:PHE:HD2	1.82	0.43
1:C:77:ILE:HD13	1:C:80:LEU:HD12	2.01	0.43
1:D:56:LEU:HB3	1:D:77:ILE:HD13	2.01	0.43
1:F:177:ARG:NH1	1:F:430:GLU:OE1	2.52	0.43
1:B:87:HIS:O	1:B:87:HIS:ND1	2.51	0.43
1:B:205:LEU:HD11	1:B:423:LYS:HA	2.01	0.43
1:C:66:THR:HG23	1:C:69:GLU:HG2	2.00	0.43
1:E:22:TYR:O	1:E:23:MET:HG2	2.18	0.43
1:D:20:TRP:O	1:D:21:PRO:C	2.59	0.43
1:E:384:MET:HE3	1:E:384:MET:HB2	1.78	0.43
1:B:24:ASP:OD1	1:B:25:SER:N	2.51	0.43
1:A:142:LEU:HB3	1:B:299:LEU:HD13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:LYS:HE3	1:A:312:TYR:OH	2.18	0.43
1:B:405:LYS:NZ	1:C:200:ASN:HD22	2.16	0.43
1:C:43:HIS:CG	1:C:51:PRO:HB3	2.54	0.43
1:D:415:ASN:C	1:D:416:LYS:HD3	2.44	0.43
1:A:12:ASP:OD1	1:A:13:GLN:N	2.52	0.43
1:A:320:ARG:O	1:B:324:TYR:HB3	2.18	0.43
1:A:377:LEU:HD23	1:A:377:LEU:HA	1.88	0.43
1:D:29:GLU:HG2	1:D:30:SER:H	1.84	0.43
1:E:179:LEU:O	1:E:183:THR:OG1	2.23	0.43
1:F:404:ILE:O	1:F:411:LYS:HE3	2.19	0.43
3:H:156:THR:O	3:H:178:PRO:HA	2.18	0.43
1:A:317:LYS:HE2	1:A:317:LYS:HB3	1.86	0.42
1:A:365:ASP:OD1	1:A:402:LYS:HE2	2.18	0.42
1:C:53:ILE:HG23	1:C:77:ILE:HD11	2.01	0.42
1:D:406:SER:HB3	1:D:411:LYS:HB3	2.01	0.42
1:F:98:VAL:HG12	1:F:144:ILE:HG21	2.01	0.42
1:A:307:ILE:HD13	1:A:349:VAL:HB	2.01	0.42
1:E:332:VAL:HG11	1:E:373:GLU:HB3	2.00	0.42
1:A:20:TRP:CZ2	1:A:44:VAL:HG11	2.53	0.42
1:A:199:VAL:HG22	1:A:200:ASN:OD1	2.19	0.42
1:E:7:SER:HA	1:E:80:LEU:HD23	2.01	0.42
3:H:17:ALA:HA	3:H:22:PHE:CD2	2.54	0.42
1:A:215:LEU:HD22	1:A:275:LEU:HD12	2.01	0.42
1:A:287:ALA:HB3	1:A:338:GLU:HB3	2.01	0.42
1:E:308:ILE:HD12	1:E:348:THR:HG21	2.00	0.42
1:E:340:ARG:NH1	1:E:382:ASP:OD2	2.53	0.42
1:B:111:ILE:CG2	3:H:90:ILE:HG13	2.49	0.42
1:B:214:TYR:CD2	1:B:307:ILE:HG21	2.55	0.42
1:D:385:LEU:HD23	1:D:385:LEU:HA	1.88	0.42
1:E:226:MET:HB3	1:E:315:ILE:HG21	2.00	0.42
3:H:256:GLU:C	3:H:258:VAL:H	2.28	0.42
1:D:43:HIS:CG	1:D:51:PRO:HB3	2.55	0.42
3:H:200:LYS:HB2	3:H:200:LYS:HE3	1.88	0.42
1:A:366:VAL:CG2	1:A:388:ILE:HD11	2.50	0.42
1:E:15:TYR:CE1	1:E:19:VAL:HG11	2.55	0.42
1:C:310:VAL:O	1:C:352:THR:HA	2.20	0.42
1:C:322:ARG:HB3	1:C:325:SER:OG	2.20	0.42
1:F:153:ASP:HB3	1:F:156:ASP:HB3	2.01	0.42
3:H:334:MET:HB2	3:H:334:MET:HE2	1.74	0.42
1:A:196:MET:HE2	1:A:384:MET:SD	2.60	0.41
1:C:20:TRP:CZ2	1:C:44:VAL:HG11	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:178:ILE:HG12	1:D:417:PHE:CD2	2.56	0.41
1:F:318:SER:HA	1:F:335:ILE:HG12	2.01	0.41
3:H:181:VAL:HG12	3:H:183:PRO:HD3	2.02	0.41
1:C:242:LEU:HD22	1:C:262:LYS:HB3	2.02	0.41
1:D:214:TYR:O	1:D:219:HIS:HB2	2.20	0.41
1:F:386:ALA:O	1:F:401:ILE:HA	2.20	0.41
1:B:405:LYS:NZ	5:C:501:AGS:O2G	2.53	0.41
1:C:286:ASP:N	1:C:289:THR:OG1	2.51	0.41
1:D:17:SER:CB	1:E:299:LEU:HD21	2.39	0.41
1:F:209:SER:HA	1:F:240:ASN:ND2	2.34	0.41
3:H:24:GLN:N	3:H:24:GLN:OE1	2.53	0.41
1:B:409:GLY:HA2	5:C:501:AGS:C2	2.50	0.41
1:D:382:ASP:O	1:D:407:ARG:CB	2.69	0.41
1:E:142:LEU:HD13	1:F:132:GLY:HA2	2.01	0.41
1:F:382:ASP:O	1:F:405:LYS:NZ	2.54	0.41
3:H:51:ARG:HD2	3:H:67:ASN:HB2	2.02	0.41
3:H:158:GLU:HB3	3:H:161:LYS:HB3	2.02	0.41
1:A:297:LEU:CD2	1:F:150:VAL:HG11	2.44	0.41
1:F:121:PRO:HA	1:F:124:ARG:HD2	2.02	0.41
3:H:148:ASP:O	3:H:151:LYS:NZ	2.38	0.41
1:A:35:ASN:ND2	1:A:69:GLU:OE1	2.52	0.41
1:B:211:ALA:HB2	1:B:309:ILE:HD12	2.02	0.41
1:D:119:LEU:HG	1:D:120:PRO:HD2	2.01	0.41
1:E:75:THR:O	1:E:78:SER:OG	2.37	0.41
3:H:19:LEU:HD22	3:H:38:PRO:HB3	2.03	0.41
3:H:255:LEU:O	3:H:258:VAL:HB	2.21	0.41
3:H:256:GLU:C	3:H:258:VAL:N	2.77	0.41
1:F:115:THR:OG1	3:H:337:SER:OG	2.30	0.41
1:A:11:PHE:HB3	1:A:82:ASP:CG	2.45	0.41
1:A:383:PHE:HB2	1:A:408:TYR:HE2	1.85	0.41
1:E:2:VAL:HG23	1:E:28:PHE:HD2	1.85	0.41
1:F:115:THR:OG1	3:H:337:SER:HB2	2.21	0.41
1:A:181:LYS:HD3	1:A:414:TRP:CE2	2.56	0.41
1:A:188:GLU:HG3	1:A:408:TYR:CE1	2.56	0.41
1:B:215:LEU:HD23	1:B:241:MET:SD	2.61	0.41
1:D:332:VAL:HB	1:D:374:SER:HB2	2.03	0.41
1:E:174:PHE:C	1:E:176:LEU:H	2.28	0.41
1:F:403:GLN:HE21	1:F:406:SER:CB	2.34	0.41
3:H:323:LYS:O	3:H:326:ILE:HG22	2.21	0.41
1:B:134:ILE:N	1:B:135:PRO:HD2	2.36	0.41
1:D:286:ASP:HB3	1:D:317:LYS:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:360:ALA:O	1:D:363:SER:OG	2.32	0.41
1:A:201:VAL:HG22	1:A:389:GLU:CB	2.49	0.40
1:B:340:ARG:NH1	1:C:227:GLU:O	2.54	0.40
1:D:121:PRO:C	1:D:123:LYS:H	2.29	0.40
1:F:293:LEU:HA	1:F:296:GLU:HG2	2.03	0.40
1:F:383:PHE:HD1	1:F:406:SER:HA	1.86	0.40
1:A:110:ILE:HD11	1:B:110:ILE:HD11	2.02	0.40
1:A:194:VAL:HA	1:A:352:THR:O	2.21	0.40
1:A:352:THR:HG22	1:A:353:ALA:H	1.86	0.40
1:B:358:LYS:HG2	1:B:361:TRP:CE3	2.56	0.40
1:C:116:ASN:HD22	1:C:128:MET:HB3	1.85	0.40
1:D:285:ALA:C	1:D:317:LYS:HG2	2.46	0.40
1:D:382:ASP:O	1:D:407:ARG:HB2	2.21	0.40
1:E:121:PRO:HA	1:E:124:ARG:HG2	2.03	0.40
1:E:413:LYS:HE3	1:E:413:LYS:HB2	1.89	0.40
1:F:214:TYR:CD2	1:F:307:ILE:HG21	2.56	0.40
1:F:401:ILE:O	1:F:416:LYS:HA	2.21	0.40
3:H:200:LYS:H	3:H:200:LYS:HG3	1.77	0.40
3:H:319:MET:O	3:H:323:LYS:HG2	2.21	0.40
1:A:358:LYS:HA	1:A:361:TRP:CD2	2.56	0.40
3:H:134:HIS:HB3	3:H:137:ILE:HG12	2.04	0.40
1:B:26:GLU:O	1:B:105:ASN:ND2	2.41	0.40
1:F:94:THR:HG22	1:F:146:PHE:HZ	1.85	0.40
1:F:352:THR:HG22	1:F:353:ALA:N	2.31	0.40
3:H:12:ALA:O	3:H:16:LEU:HG	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	A	373/410 (91%)	365 (98%)	8 (2%)	47	67
1	B	373/410 (91%)	368 (99%)	5 (1%)	61	74
1	C	373/410 (91%)	372 (100%)	1 (0%)	86	86
1	D	373/410 (91%)	366 (98%)	7 (2%)	50	68
1	E	373/410 (91%)	362 (97%)	11 (3%)	37	62
1	F	373/410 (91%)	364 (98%)	9 (2%)	43	65
3	H	285/304 (94%)	281 (99%)	4 (1%)	59	73
All	All	2523/2764 (91%)	2478 (98%)	45 (2%)	51	70

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	LEU
1	A	68	THR
1	A	80	LEU
1	A	326	GLU
1	A	327	ASN
1	A	333	LYS
1	A	352	THR
1	A	368	MET
1	B	50	VAL
1	B	53	ILE
1	B	68	THR
1	B	131	VAL
1	B	322	ARG
1	C	19	VAL
1	D	50	VAL
1	D	86	ASP
1	D	119	LEU
1	D	127	LYS
1	D	200	ASN
1	D	297	LEU
1	D	352	THR
1	E	60	LEU
1	E	144	ILE
1	E	152	HIS
1	E	244	VAL
1	E	265	LYS

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Mol	Chain	Res	Type
1	E	293	LEU
1	E	346	THR
1	E	380	THR
1	E	388	ILE
1	E	400	LEU
1	E	405	LYS
1	F	2	VAL
1	F	50	VAL
1	F	103	MET
1	F	149	TYR
1	F	150	VAL
1	F	167	ASN
1	F	388	ILE
1	F	399	GLN
1	F	418	LEU
3	H	92	GLU
3	H	95	LYS
3	H	304	VAL
3	H	334	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	ASN
1	A	167	ASN
1	A	327	ASN
1	A	403	GLN
1	B	62	ASN
1	B	295	ASN
1	B	327	ASN
1	C	200	ASN
1	C	425	ASN
1	D	302	ASN
1	D	412	ASN
1	D	415	ASN
1	F	62	ASN
1	F	288	ASN
3	H	195	GLN
3	H	317	GLN
3	H	325	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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$
5	AGS	E	501	6	32,33,33	0.51	1 (3%)	45,52,52	0.67	1 (2%)
5	AGS	F	501	6	32,33,33	0.51	1 (3%)	45,52,52	0.69	1 (2%)
5	AGS	B	501	6	32,33,33	0.52	1 (3%)	45,52,52	0.68	1 (2%)
5	AGS	D	501	6	32,33,33	0.50	1 (3%)	45,52,52	0.71	1 (2%)
5	AGS	C	501	6	32,33,33	0.66	1 (3%)	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
5	AGS	E	501	6	-	9/21/38/38	0/3/3/3
5	AGS	F	501	6	-	3/21/38/38	0/3/3/3
5	AGS	B	501	6	-	6/21/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	AGS	D	501	6	-	7/21/38/38	0/3/3/3
5	AGS	C	501	6	-	0/21/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	501	AGS	PG-S1G	2.14	1.95	1.90
5	D	501	AGS	PG-S1G	2.12	1.95	1.90
5	E	501	AGS	PG-S1G	2.09	1.95	1.90
5	C	501	AGS	PG-S1G	2.08	1.95	1.90
5	B	501	AGS	PG-S1G	2.07	1.95	1.90

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	501	AGS	PB-O3B-PG	-3.99	118.57	133.17
5	B	501	AGS	PB-O3B-PG	-3.80	119.26	133.17
5	F	501	AGS	PB-O3B-PG	-3.71	119.60	133.17
5	E	501	AGS	PB-O3B-PG	-3.48	120.43	133.17

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	501	AGS	C5'-O5'-PA-O1A
5	B	501	AGS	C5'-O5'-PA-O2A
5	B	501	AGS	C5'-O5'-PA-O3A
5	D	501	AGS	PB-O3B-PG-O2G
5	D	501	AGS	PB-O3B-PG-O3G
5	D	501	AGS	C5'-O5'-PA-O1A
5	E	501	AGS	PB-O3B-PG-O3G
5	E	501	AGS	O4'-C4'-C5'-O5'
5	B	501	AGS	C3'-C4'-C5'-O5'
5	E	501	AGS	C3'-C4'-C5'-O5'
5	B	501	AGS	O4'-C4'-C5'-O5'
5	D	501	AGS	PA-O3A-PB-O1B
5	B	501	AGS	PB-O3A-PA-O5'
5	D	501	AGS	O4'-C4'-C5'-O5'
5	D	501	AGS	C5'-O5'-PA-O3A
5	E	501	AGS	C5'-O5'-PA-O1A
5	E	501	AGS	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
5	E	501	AGS	C5'-O5'-PA-O3A
5	F	501	AGS	C5'-O5'-PA-O1A
5	E	501	AGS	PG-O3B-PB-O1B
5	E	501	AGS	PG-O3B-PB-O2B
5	F	501	AGS	PB-O3A-PA-O2A
5	E	501	AGS	PB-O3B-PG-O2G
5	D	501	AGS	PA-O3A-PB-O2B
5	F	501	AGS	PB-O3A-PA-O1A

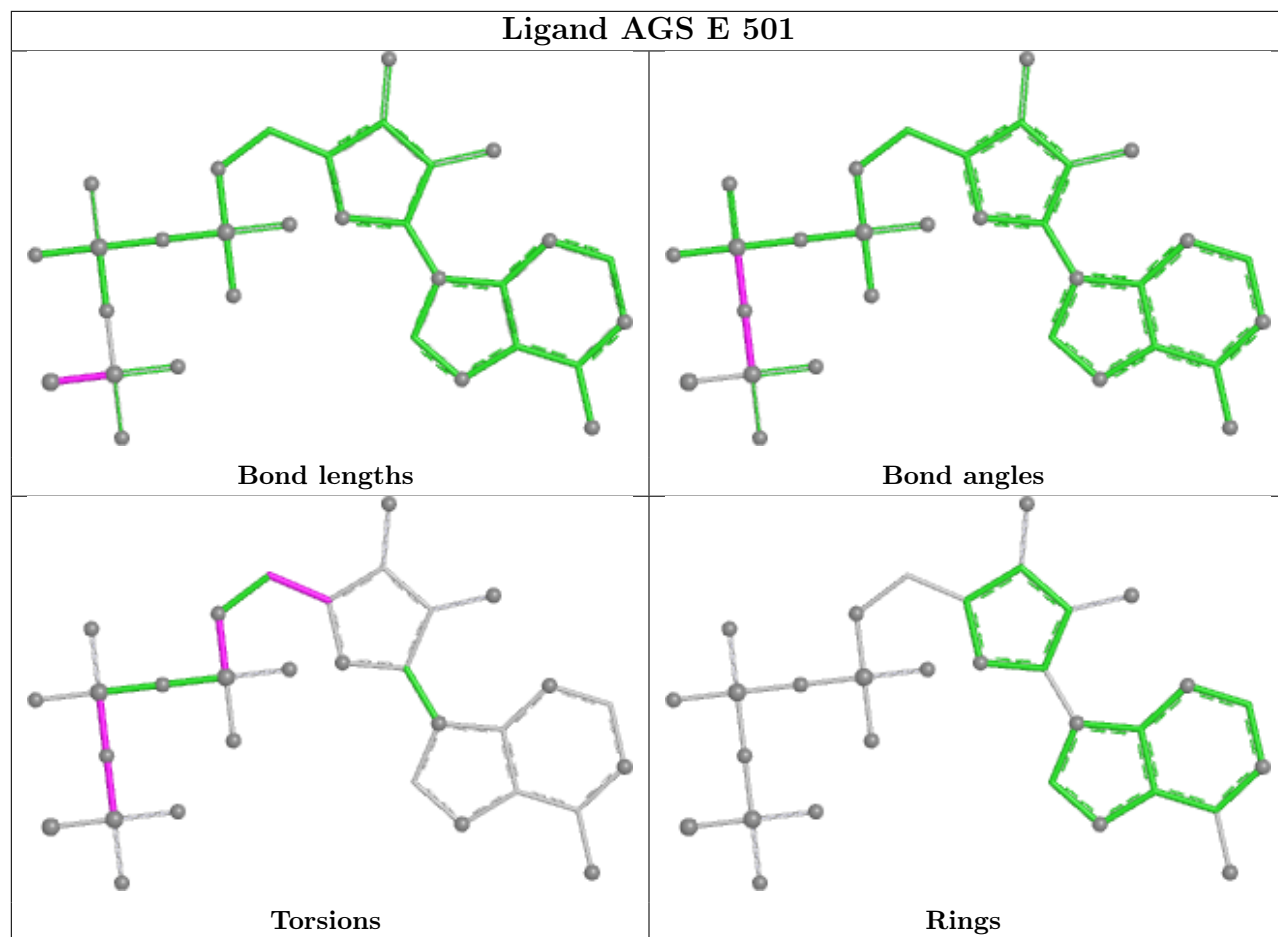
There are no ring outliers.

3 monomers are involved in 9 short contacts:

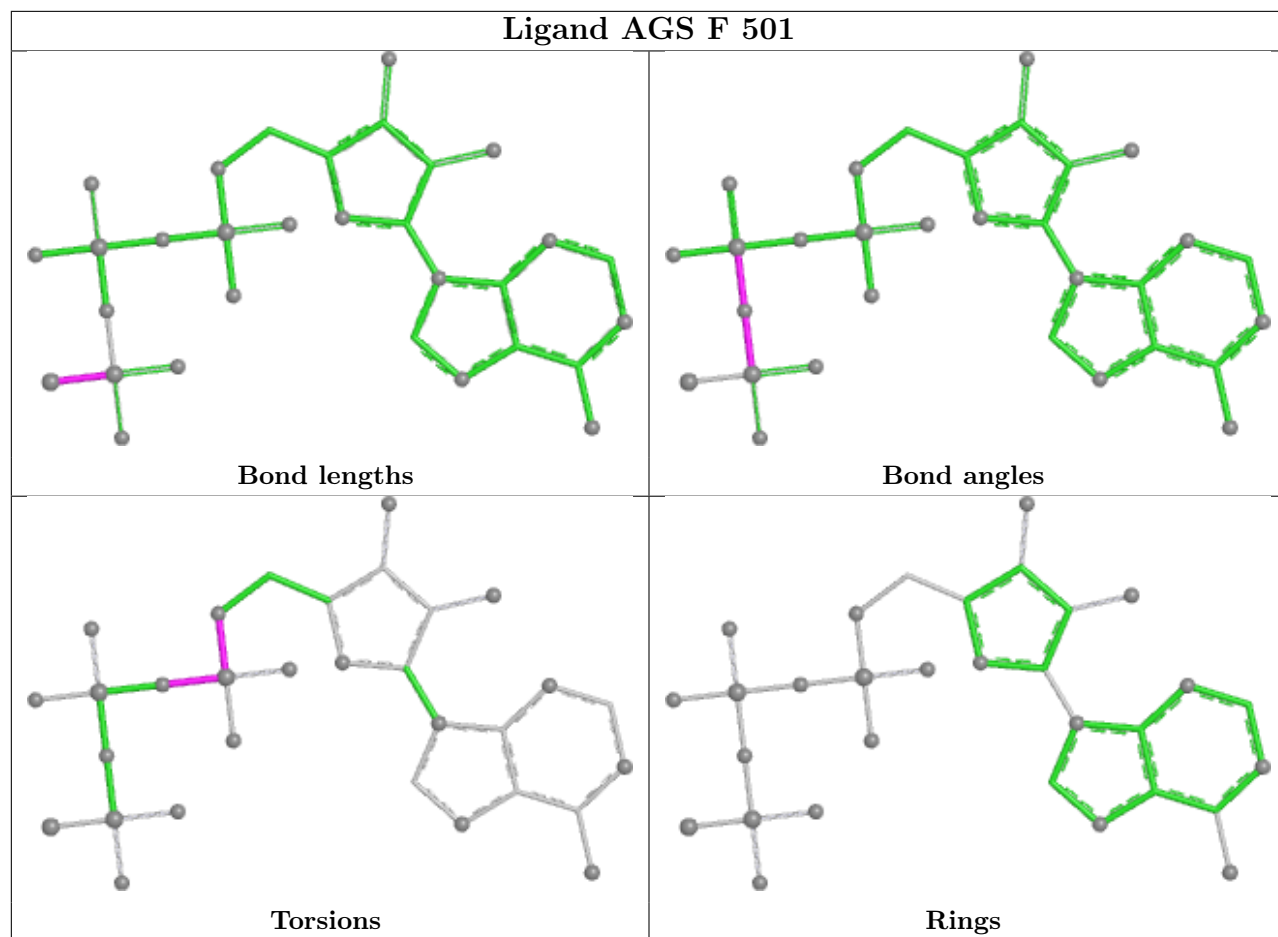
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	501	AGS	2	0
5	D	501	AGS	1	0
5	C	501	AGS	6	0

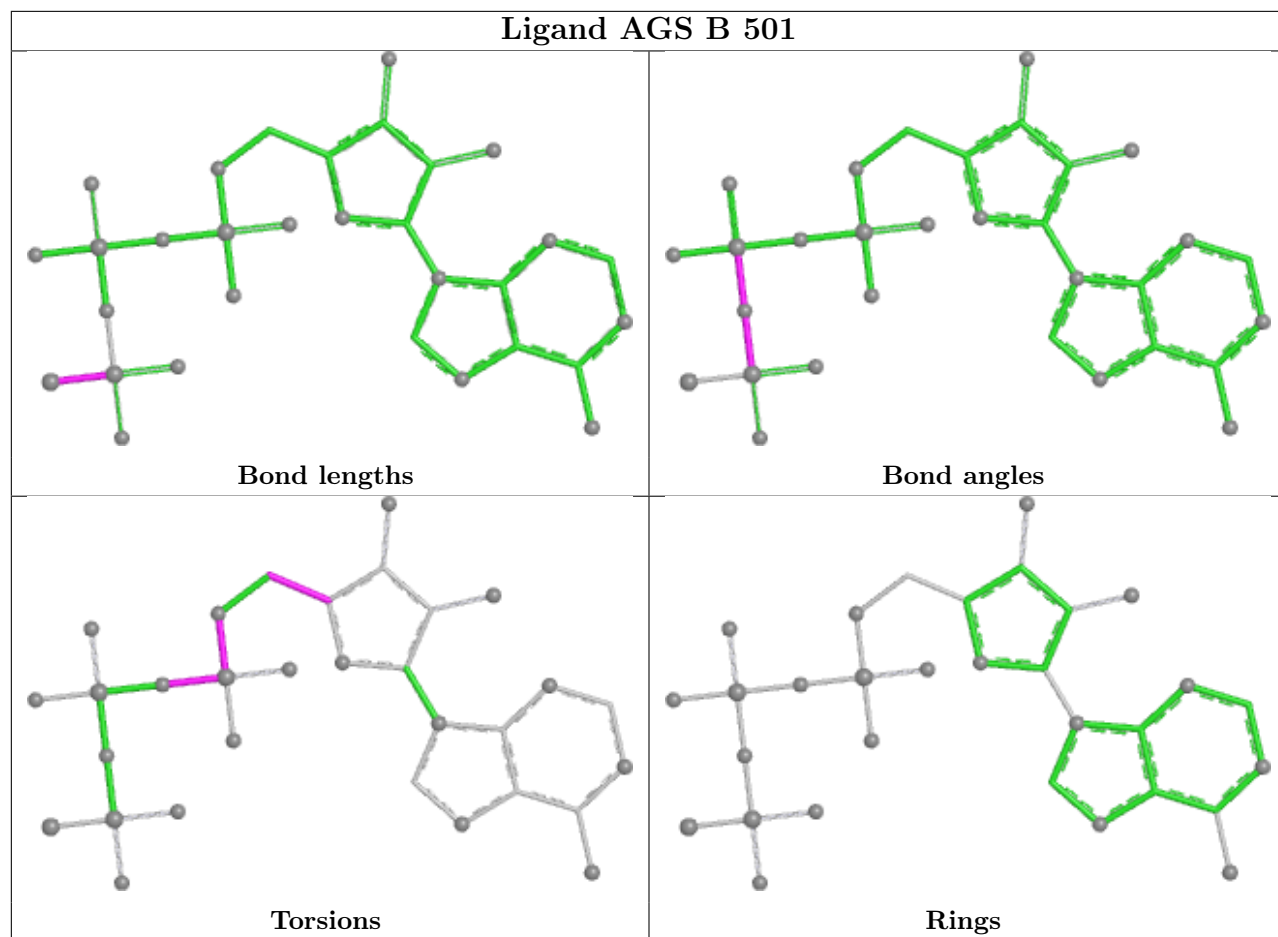
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

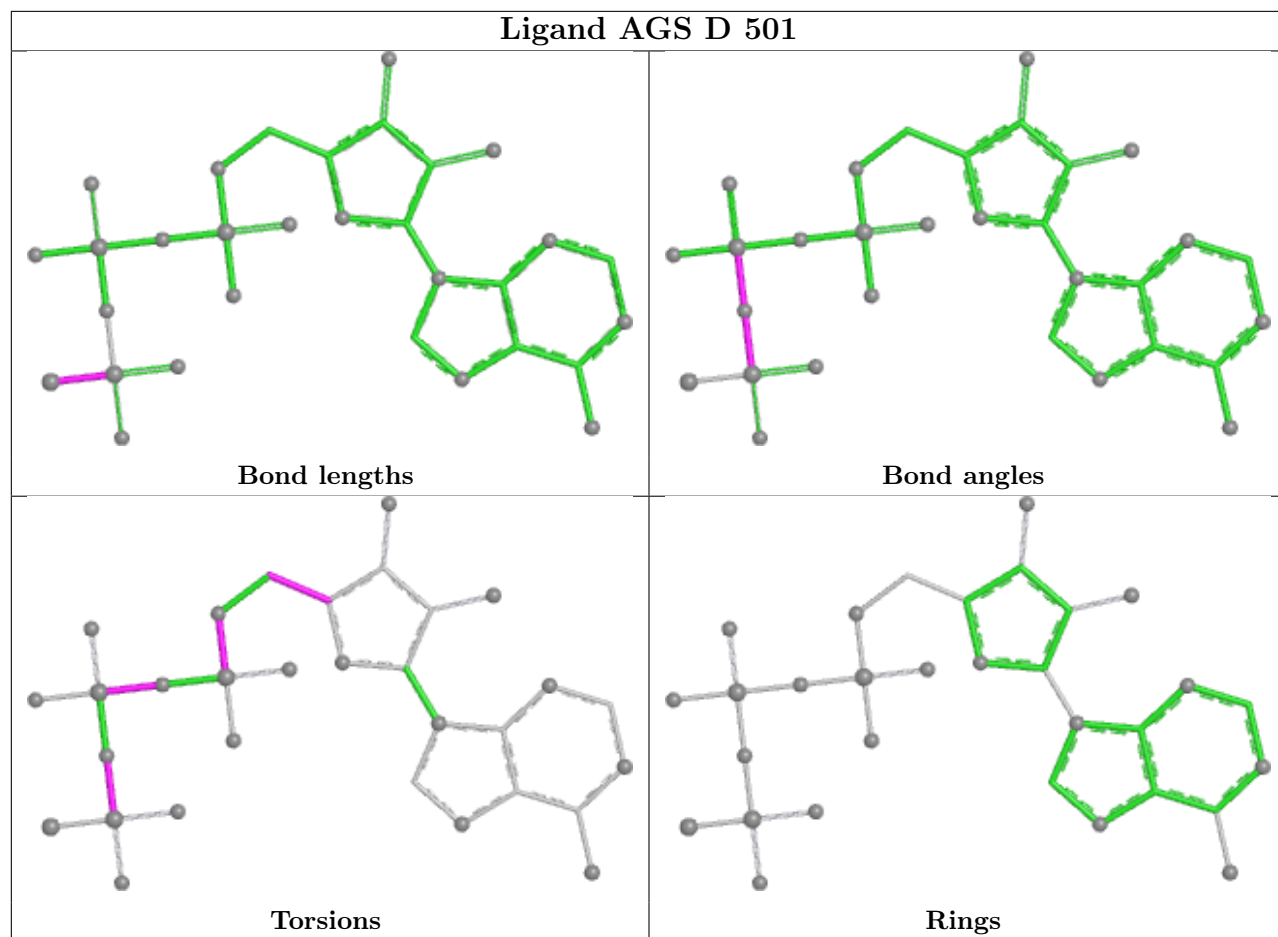
Ligand AGS E 501

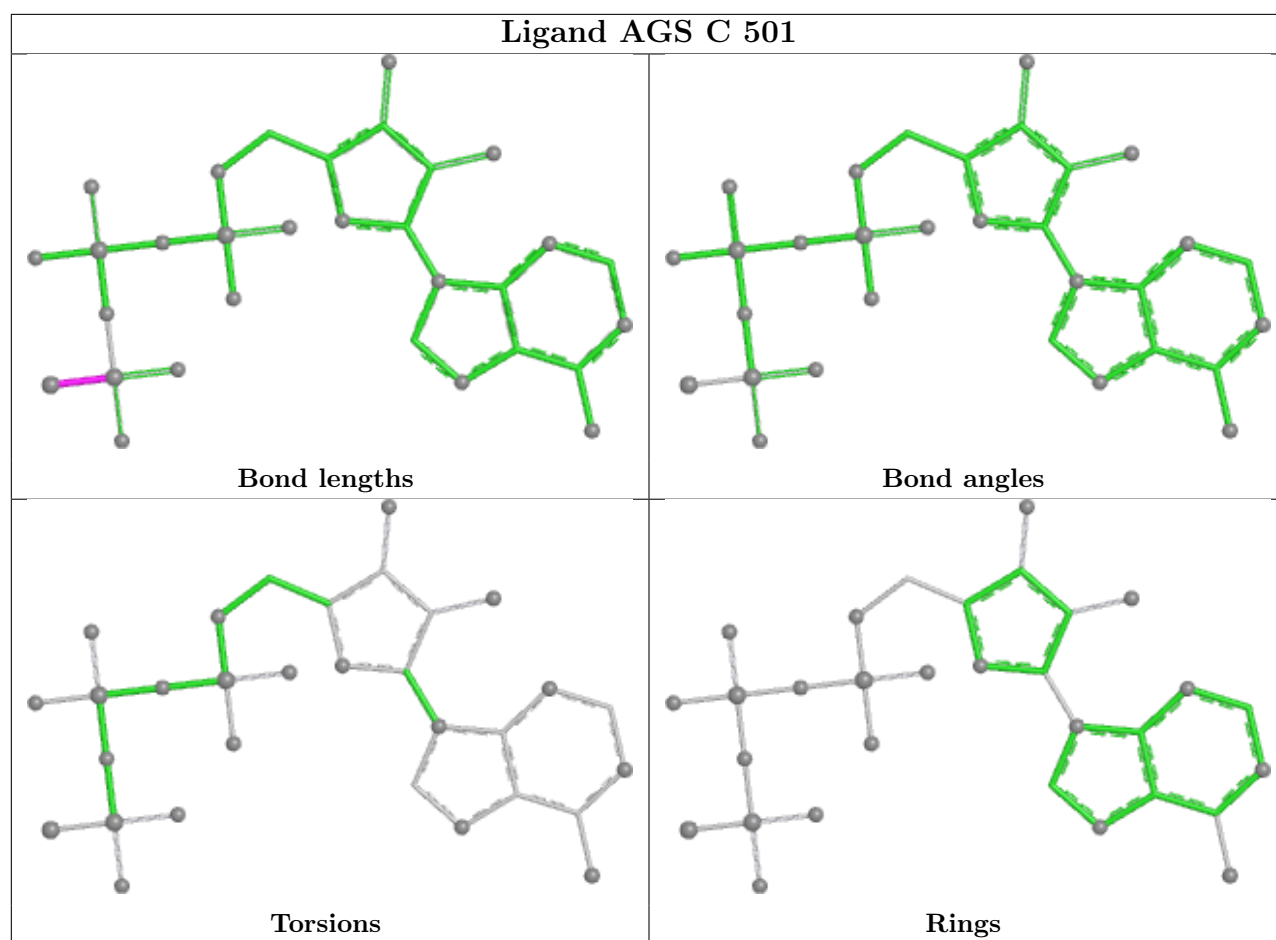


Ligand AGS F 501









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.

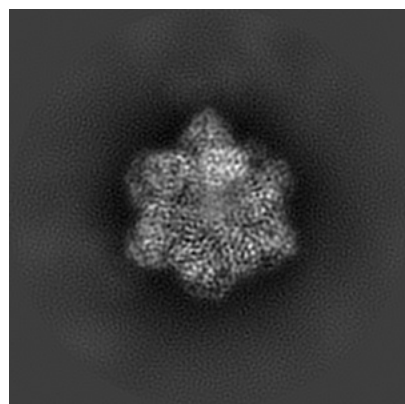
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27737. These allow visual inspection of the internal detail of the map and identification of artifacts.

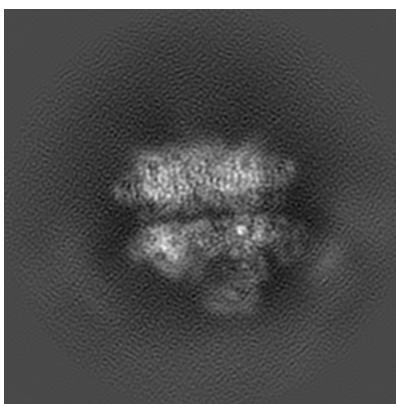
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

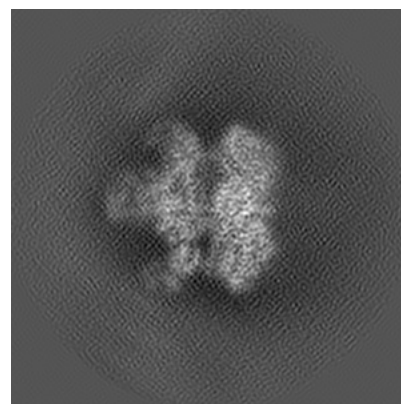
6.1.1 Primary map



X

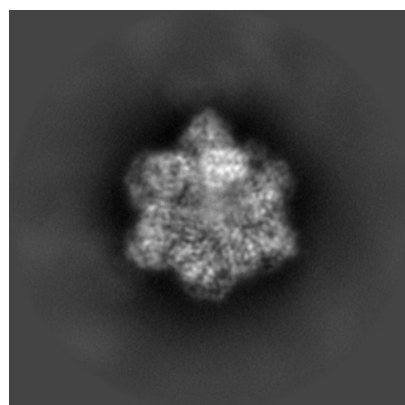


Y

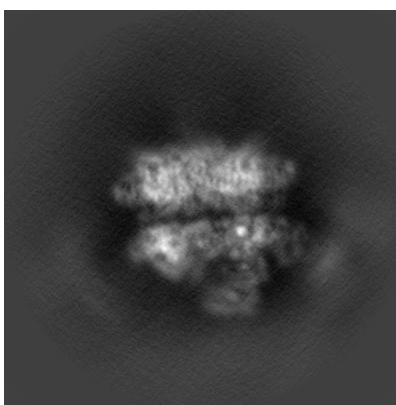


Z

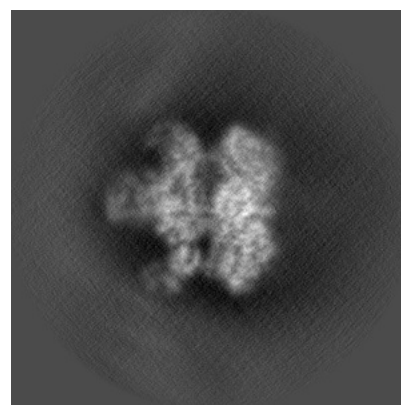
6.1.2 Raw map



X



Y

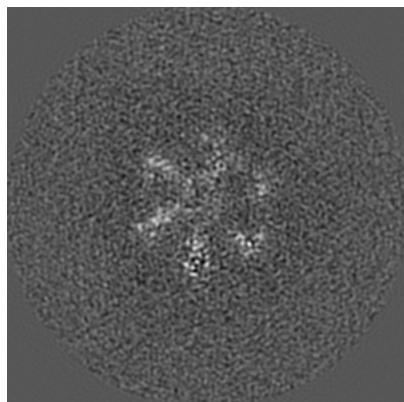


Z

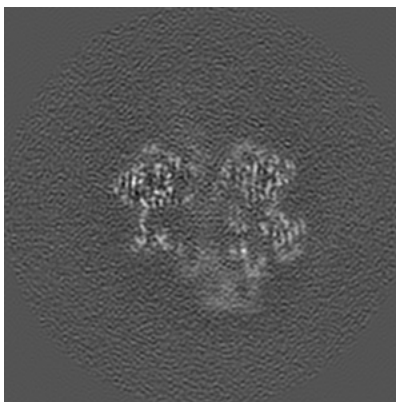
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

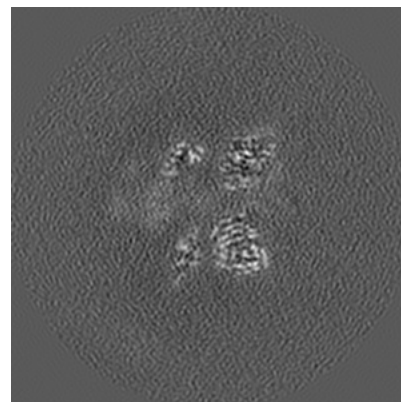
6.2.1 Primary map



X Index: 160

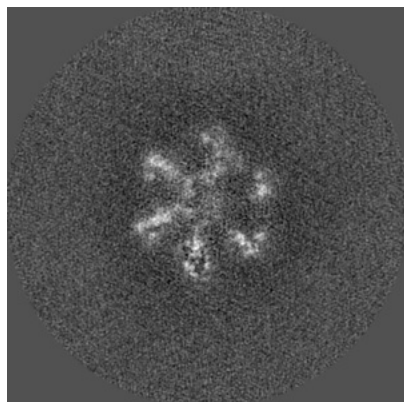


Y Index: 160

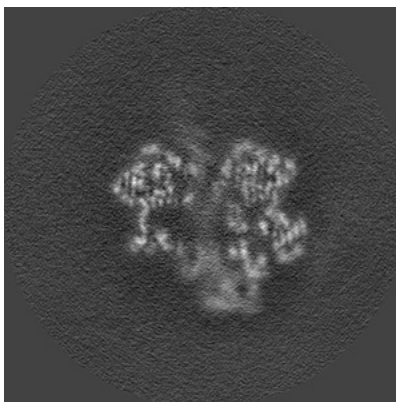


Z Index: 160

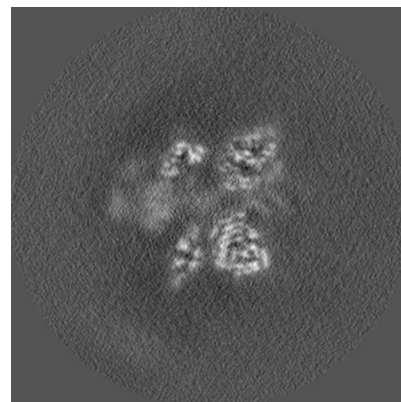
6.2.2 Raw map



X Index: 160



Y Index: 160

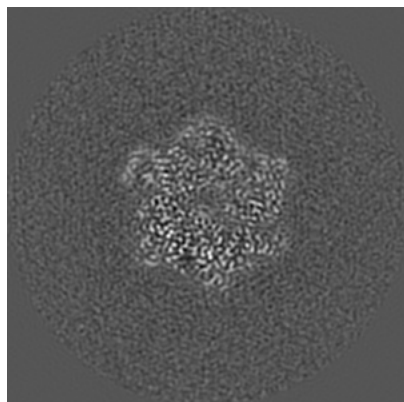


Z Index: 160

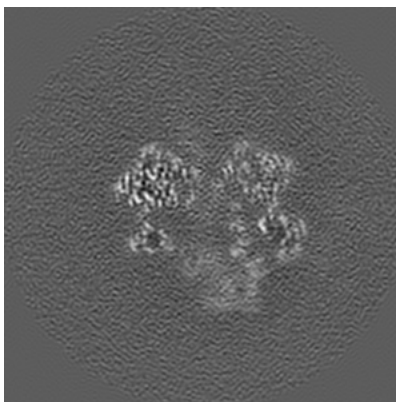
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

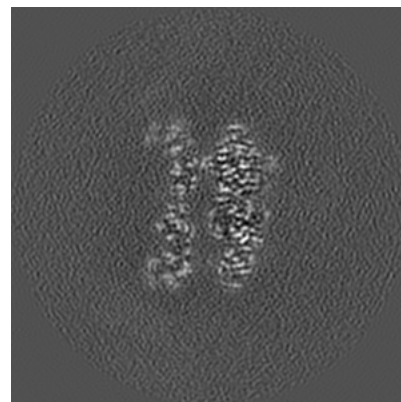
6.3.1 Primary map



X Index: 186

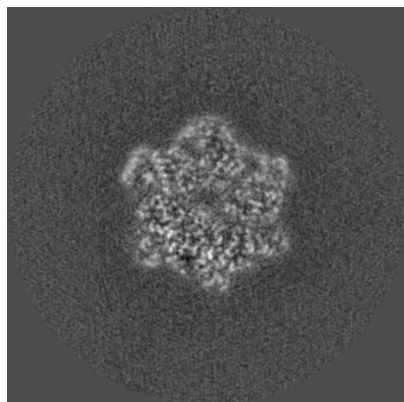


Y Index: 158

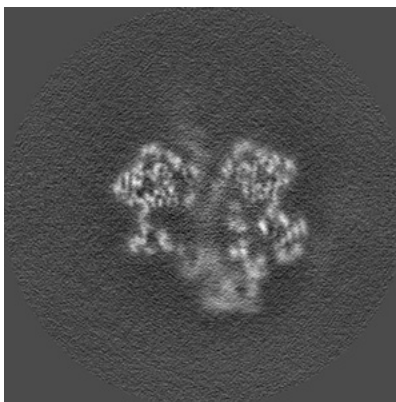


Z Index: 129

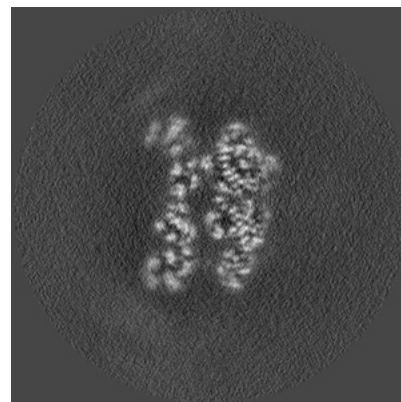
6.3.2 Raw map



X Index: 186



Y Index: 159

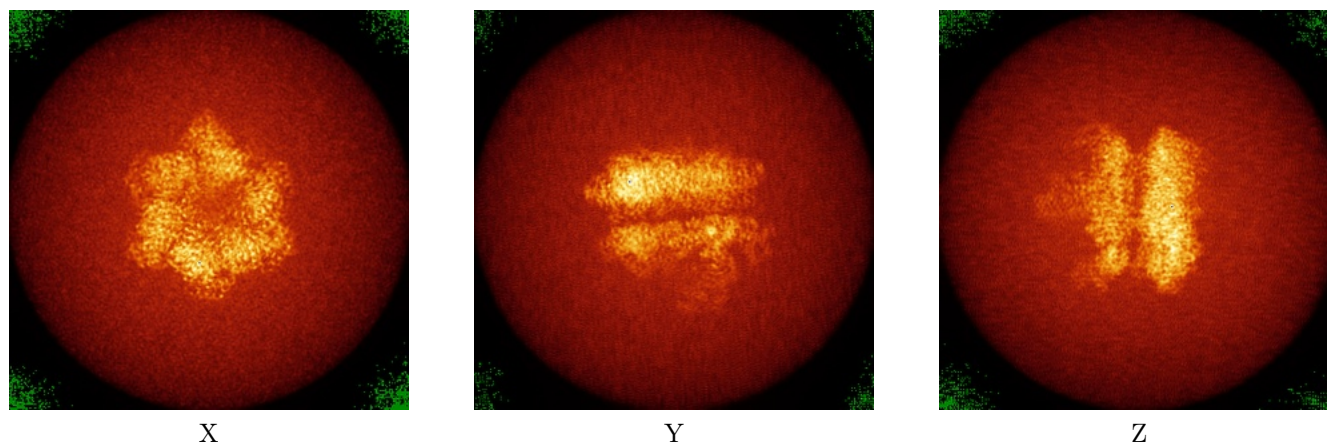


Z Index: 128

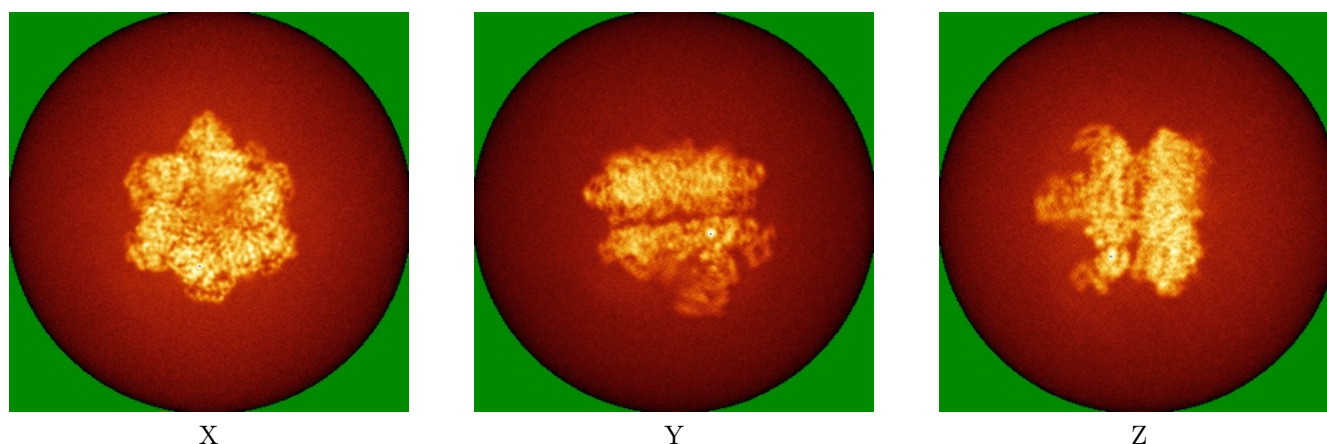
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

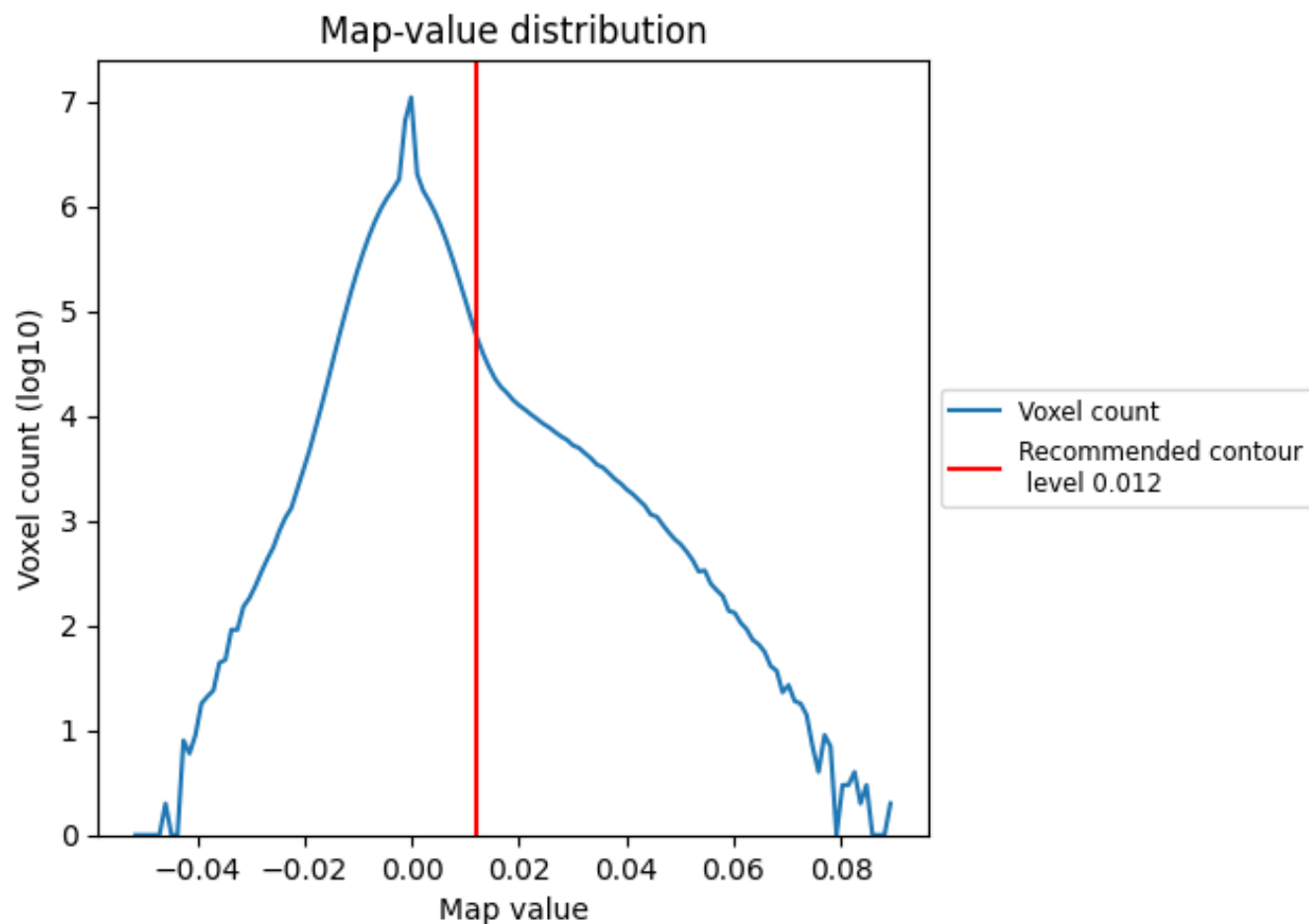
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

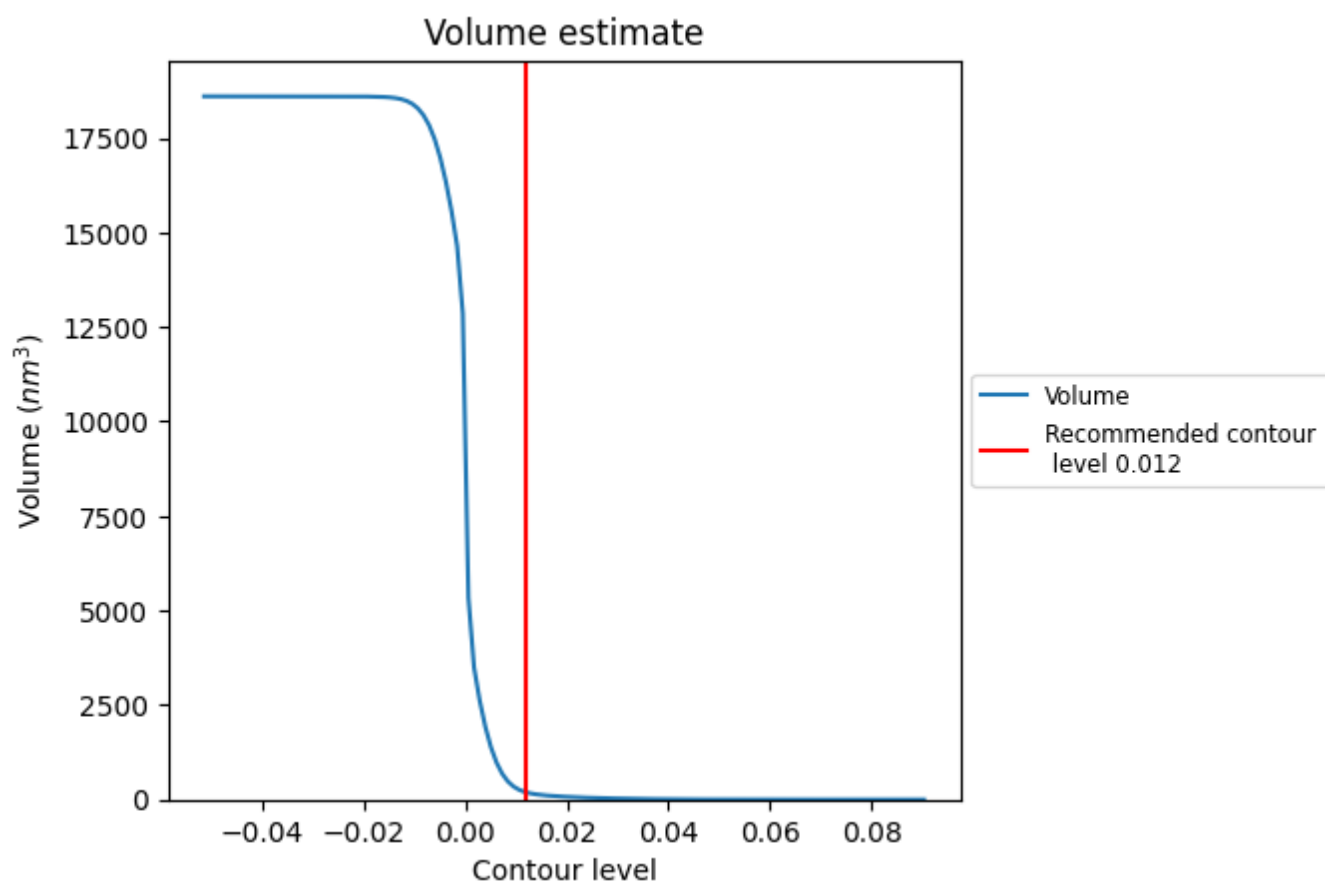
This section contains the results of statistical analysis of the map.

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.

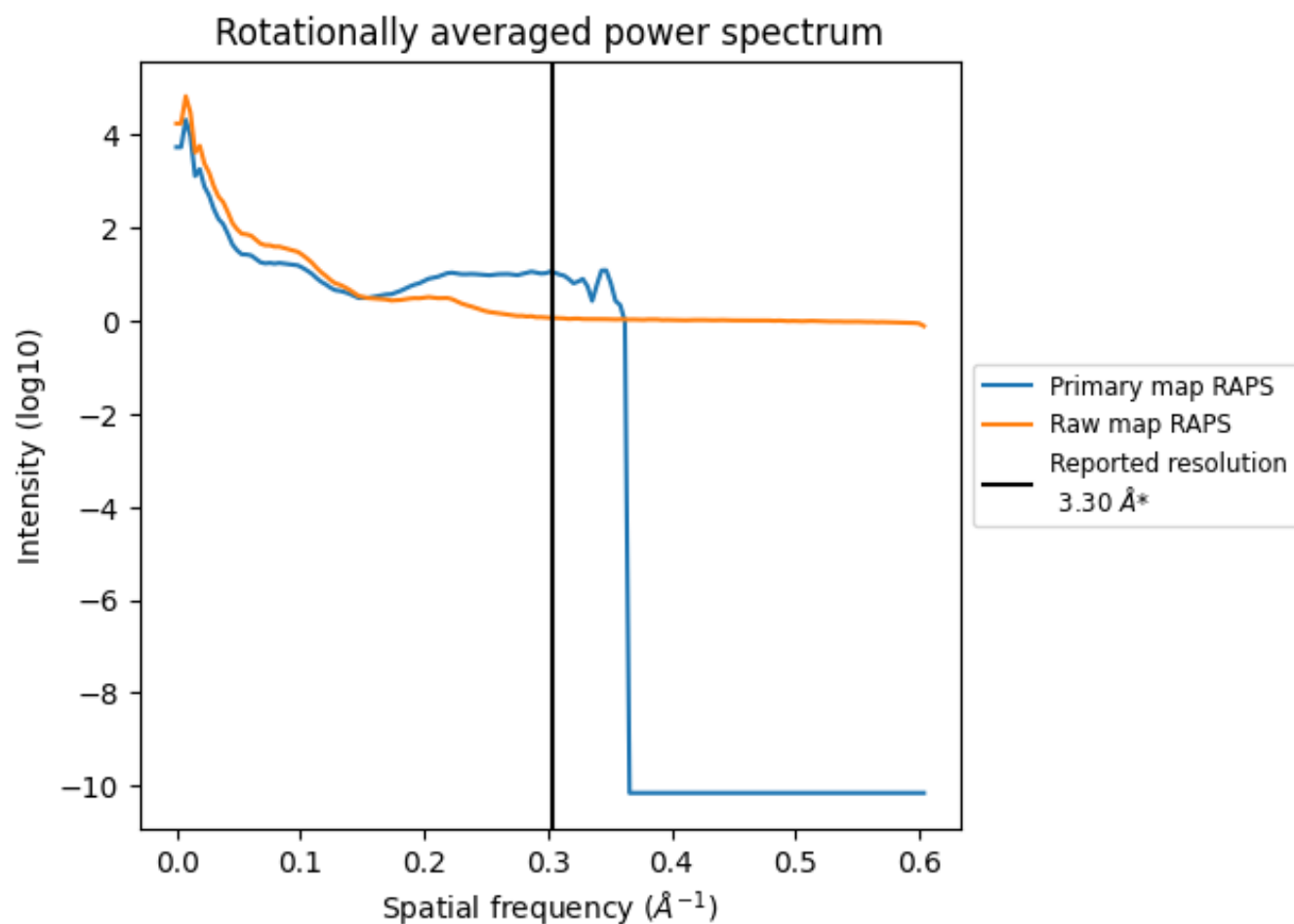
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 191 nm³; this corresponds to an approximate mass of 173 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 ⓘ

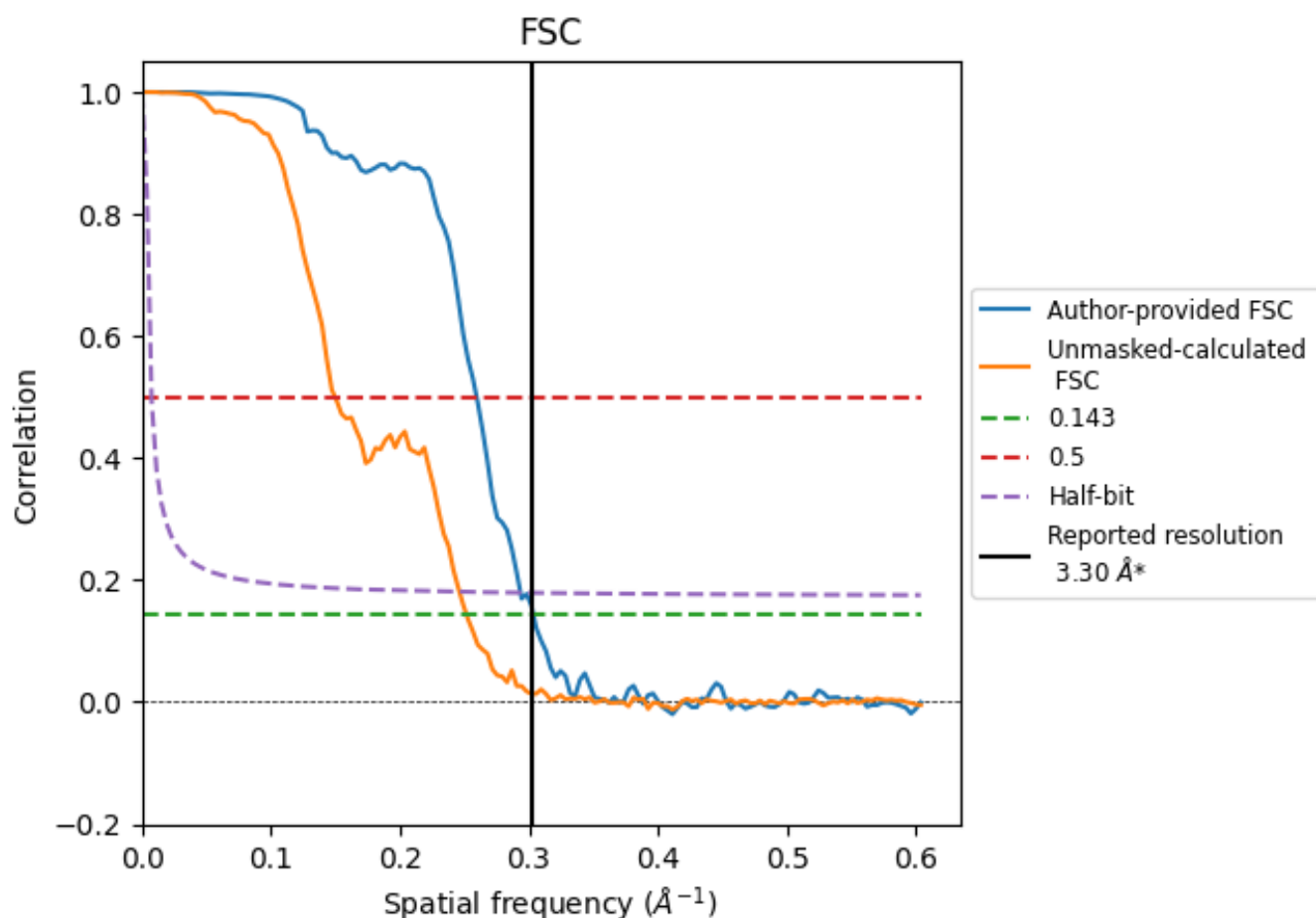


*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

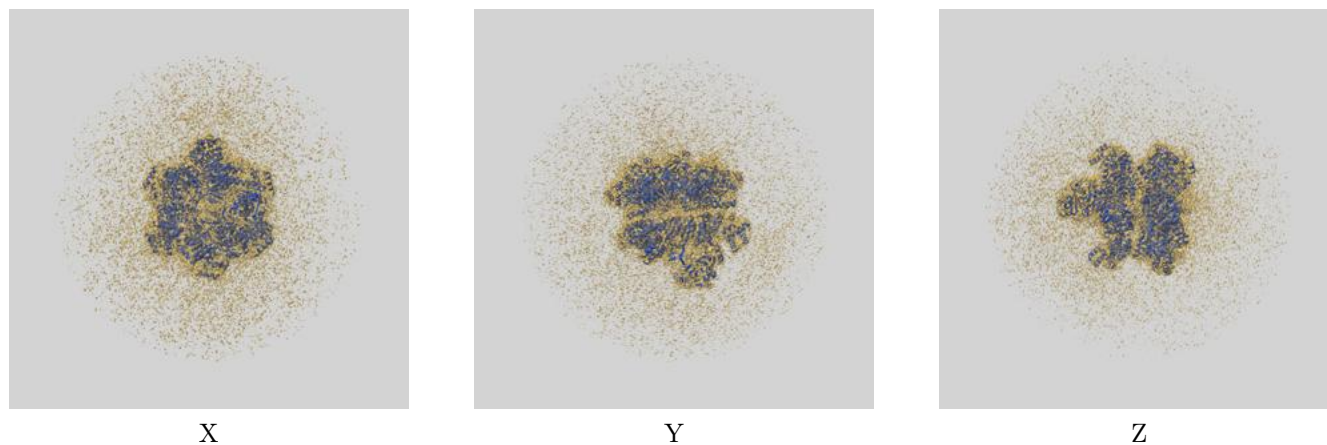
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.29	3.85	3.41
Unmasked-calculated*	3.97	6.68	4.06

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.97 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

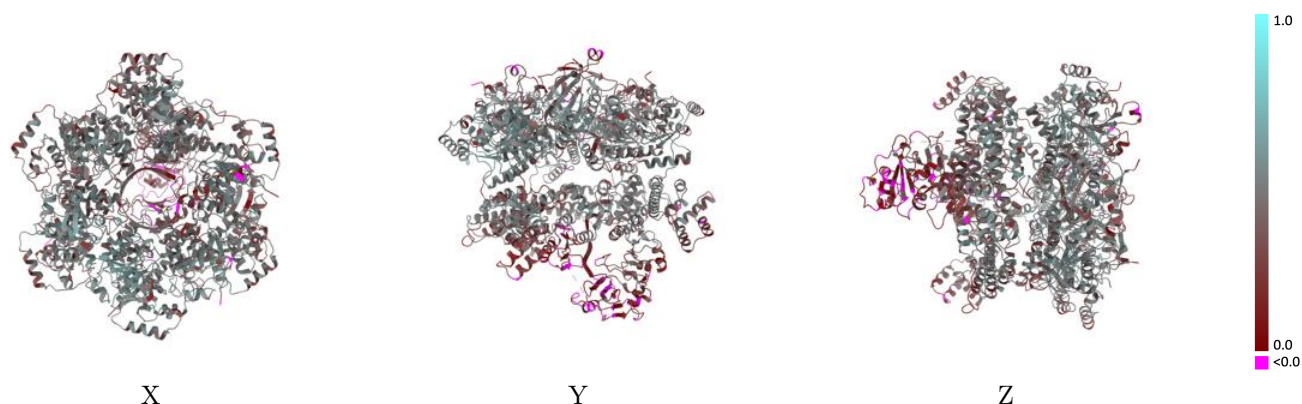
This section contains information regarding the fit between EMDB map EMD-27737 and PDB model 8DVF. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



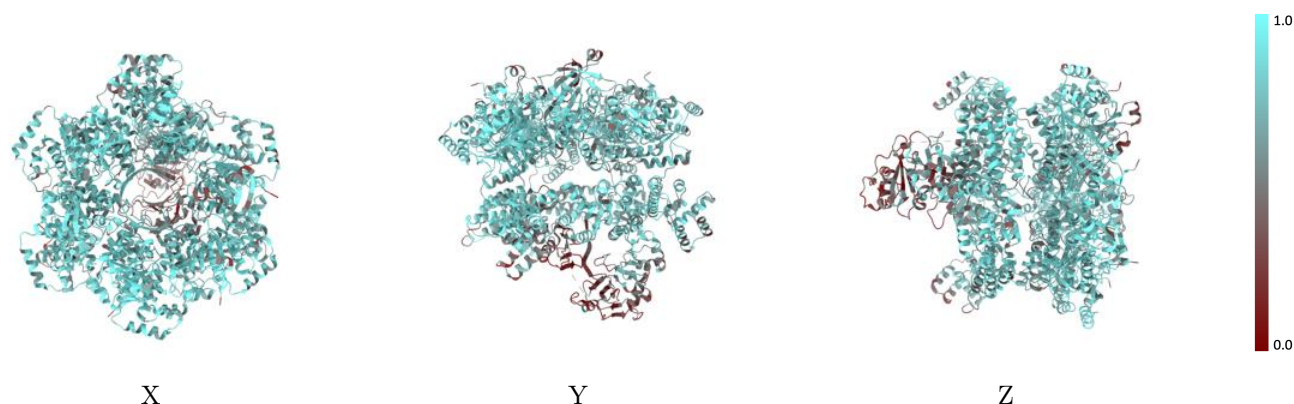
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



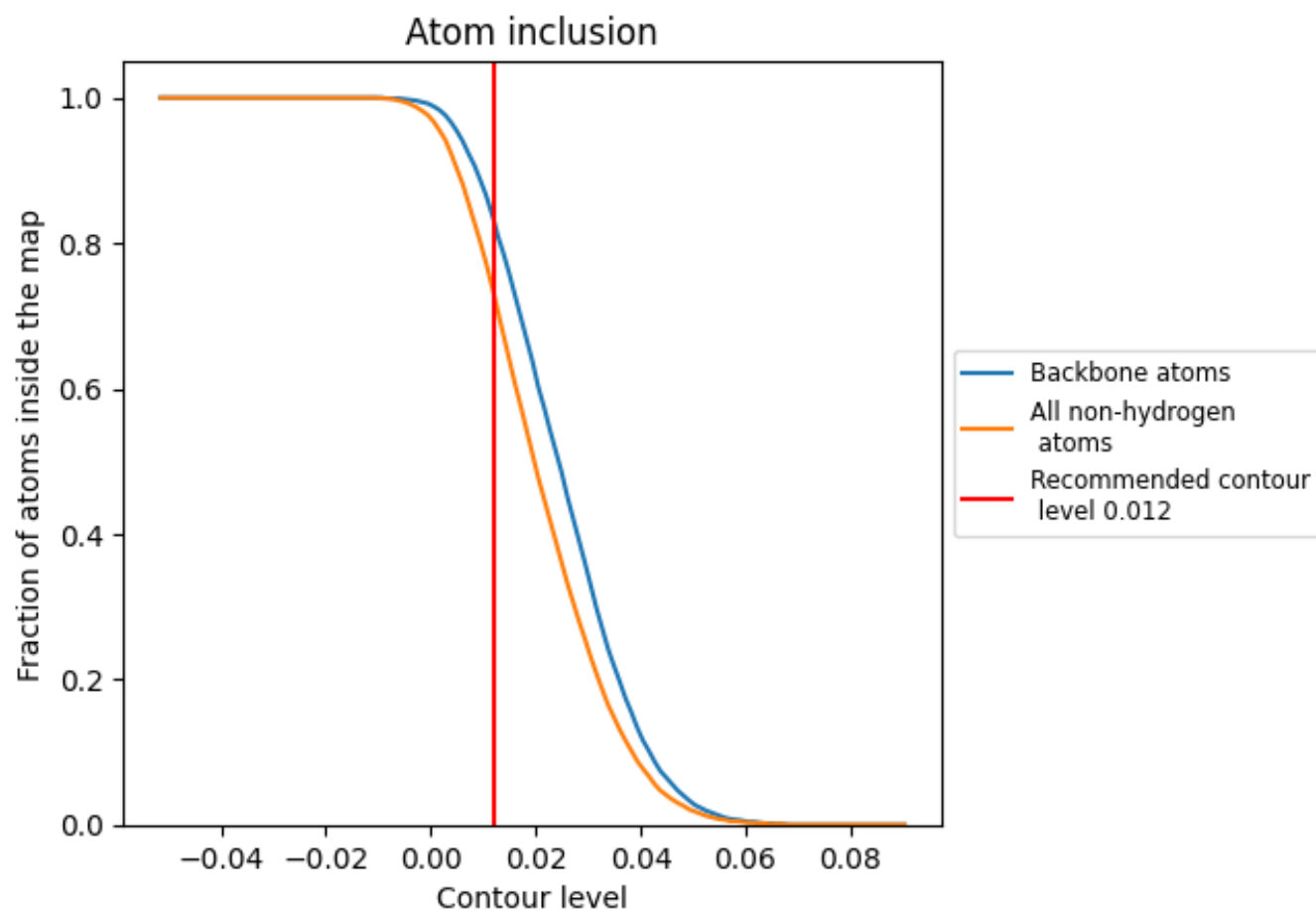
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.012).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 73% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7320	0.4130
A	0.7250	0.4130
B	0.8020	0.4660
C	0.7940	0.4590
D	0.7970	0.4550
E	0.7570	0.4310
F	0.7590	0.4360
H	0.4390	0.1980
M	0.5960	0.2900
T	0.3050	0.1580

1.0

0.0

<0.0