



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 02:52 AM UTC

PDB ID : 8FND / pdb_00008fnd
EMDB ID : EMD-29309
Title : Structure of E138K HIV-1 intasome with Dolutegravir bound
Authors : Shan, Z.L.; Passos, D.O.; Strutzenberg, T.S.; Li, M.; Lyumkis, D.
Deposited on : 2022-12-27
Resolution : 3.00 Å(reported)

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:

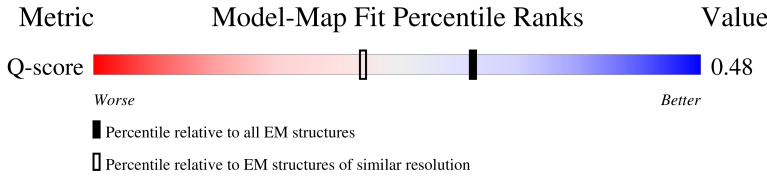
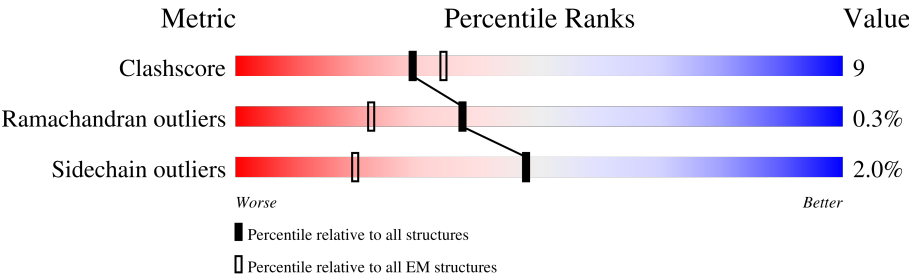
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	364	
1	B	364	
1	C	364	
1	D	364	

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Mol	Chain	Length	Quality of chain
1	G	364	
1	H	364	
1	I	364	
1	J	364	
2	E	27	
2	K	27	
3	F	25	
3	L	25	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	DLU	A	304	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11471 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 Lamina-associated polypeptide 2, isoform alpha,Integrase chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	261	Total	C	N	O	S	0	0
			2035	1307	361	358	9		
1	B	242	Total	C	N	O	S	0	0
			1911	1223	339	342	7		
1	C	66	Total	C	N	O	S	0	0
			543	347	102	93	1		
1	D	47	Total	C	N	O		0	0
			388	251	73	64			
1	G	261	Total	C	N	O	S	0	0
			2035	1307	361	358	9		
1	H	242	Total	C	N	O	S	0	0
			1911	1223	339	342	7		
1	I	66	Total	C	N	O	S	0	0
			543	347	102	93	1		
1	J	47	Total	C	N	O		0	0
			388	251	73	64			

There are 216 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-75	GLY	-	expression tag	UNP P42166
A	-74	SER	-	expression tag	UNP P42166
A	-73	HIS	-	expression tag	UNP P42166
A	-72	MET	-	expression tag	UNP P42166
A	-71	PRO	-	expression tag	UNP P42166
A	-70	LYS	-	expression tag	UNP P42166
A	-69	ARG	-	expression tag	UNP P42166
A	-68	GLY	-	expression tag	UNP P42166
A	-67	ARG	-	expression tag	UNP P42166
A	-66	PRO	-	expression tag	UNP P42166
A	-65	ALA	-	expression tag	UNP P42166
A	-64	ALA	-	expression tag	UNP P42166
A	-63	THR	-	expression tag	UNP P42166

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-62	GLU	-	expression tag	UNP P42166
A	-61	VAL	-	expression tag	UNP P42166
A	-60	LYS	-	expression tag	UNP P42166
A	-59	ILE	-	expression tag	UNP P42166
A	-58	PRO	-	expression tag	UNP P42166
A	-57	LYS	-	expression tag	UNP P42166
A	-56	PRO	-	expression tag	UNP P42166
A	-55	ARG	-	expression tag	UNP P42166
A	-54	GLY	-	expression tag	UNP P42166
A	-17	GLN	ARG	conflict	UNP P42166
A	-2	GLY	-	linker	UNP P42166
A	-1	GLY	-	linker	UNP P42166
A	0	GLY	-	linker	UNP P42166
A	138	LYS	GLU	engineered mutation	UNP P12497
B	-75	GLY	-	expression tag	UNP P42166
B	-74	SER	-	expression tag	UNP P42166
B	-73	HIS	-	expression tag	UNP P42166
B	-72	MET	-	expression tag	UNP P42166
B	-71	PRO	-	expression tag	UNP P42166
B	-70	LYS	-	expression tag	UNP P42166
B	-69	ARG	-	expression tag	UNP P42166
B	-68	GLY	-	expression tag	UNP P42166
B	-67	ARG	-	expression tag	UNP P42166
B	-66	PRO	-	expression tag	UNP P42166
B	-65	ALA	-	expression tag	UNP P42166
B	-64	ALA	-	expression tag	UNP P42166
B	-63	THR	-	expression tag	UNP P42166
B	-62	GLU	-	expression tag	UNP P42166
B	-61	VAL	-	expression tag	UNP P42166
B	-60	LYS	-	expression tag	UNP P42166
B	-59	ILE	-	expression tag	UNP P42166
B	-58	PRO	-	expression tag	UNP P42166
B	-57	LYS	-	expression tag	UNP P42166
B	-56	PRO	-	expression tag	UNP P42166
B	-55	ARG	-	expression tag	UNP P42166
B	-54	GLY	-	expression tag	UNP P42166
B	-17	GLN	ARG	conflict	UNP P42166
B	-2	GLY	-	linker	UNP P42166
B	-1	GLY	-	linker	UNP P42166
B	0	GLY	-	linker	UNP P42166
B	138	LYS	GLU	engineered mutation	UNP P12497
C	-75	GLY	-	expression tag	UNP P42166

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-74	SER	-	expression tag	UNP P42166
C	-73	HIS	-	expression tag	UNP P42166
C	-72	MET	-	expression tag	UNP P42166
C	-71	PRO	-	expression tag	UNP P42166
C	-70	LYS	-	expression tag	UNP P42166
C	-69	ARG	-	expression tag	UNP P42166
C	-68	GLY	-	expression tag	UNP P42166
C	-67	ARG	-	expression tag	UNP P42166
C	-66	PRO	-	expression tag	UNP P42166
C	-65	ALA	-	expression tag	UNP P42166
C	-64	ALA	-	expression tag	UNP P42166
C	-63	THR	-	expression tag	UNP P42166
C	-62	GLU	-	expression tag	UNP P42166
C	-61	VAL	-	expression tag	UNP P42166
C	-60	LYS	-	expression tag	UNP P42166
C	-59	ILE	-	expression tag	UNP P42166
C	-58	PRO	-	expression tag	UNP P42166
C	-57	LYS	-	expression tag	UNP P42166
C	-56	PRO	-	expression tag	UNP P42166
C	-55	ARG	-	expression tag	UNP P42166
C	-54	GLY	-	expression tag	UNP P42166
C	-17	GLN	ARG	conflict	UNP P42166
C	-2	GLY	-	linker	UNP P42166
C	-1	GLY	-	linker	UNP P42166
C	0	GLY	-	linker	UNP P42166
C	138	LYS	GLU	engineered mutation	UNP P12497
D	-75	GLY	-	expression tag	UNP P42166
D	-74	SER	-	expression tag	UNP P42166
D	-73	HIS	-	expression tag	UNP P42166
D	-72	MET	-	expression tag	UNP P42166
D	-71	PRO	-	expression tag	UNP P42166
D	-70	LYS	-	expression tag	UNP P42166
D	-69	ARG	-	expression tag	UNP P42166
D	-68	GLY	-	expression tag	UNP P42166
D	-67	ARG	-	expression tag	UNP P42166
D	-66	PRO	-	expression tag	UNP P42166
D	-65	ALA	-	expression tag	UNP P42166
D	-64	ALA	-	expression tag	UNP P42166
D	-63	THR	-	expression tag	UNP P42166
D	-62	GLU	-	expression tag	UNP P42166
D	-61	VAL	-	expression tag	UNP P42166
D	-60	LYS	-	expression tag	UNP P42166

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-59	ILE	-	expression tag	UNP P42166
D	-58	PRO	-	expression tag	UNP P42166
D	-57	LYS	-	expression tag	UNP P42166
D	-56	PRO	-	expression tag	UNP P42166
D	-55	ARG	-	expression tag	UNP P42166
D	-54	GLY	-	expression tag	UNP P42166
D	-17	GLN	ARG	conflict	UNP P42166
D	-2	GLY	-	linker	UNP P42166
D	-1	GLY	-	linker	UNP P42166
D	0	GLY	-	linker	UNP P42166
D	138	LYS	GLU	engineered mutation	UNP P12497
G	-75	GLY	-	expression tag	UNP P42166
G	-74	SER	-	expression tag	UNP P42166
G	-73	HIS	-	expression tag	UNP P42166
G	-72	MET	-	expression tag	UNP P42166
G	-71	PRO	-	expression tag	UNP P42166
G	-70	LYS	-	expression tag	UNP P42166
G	-69	ARG	-	expression tag	UNP P42166
G	-68	GLY	-	expression tag	UNP P42166
G	-67	ARG	-	expression tag	UNP P42166
G	-66	PRO	-	expression tag	UNP P42166
G	-65	ALA	-	expression tag	UNP P42166
G	-64	ALA	-	expression tag	UNP P42166
G	-63	THR	-	expression tag	UNP P42166
G	-62	GLU	-	expression tag	UNP P42166
G	-61	VAL	-	expression tag	UNP P42166
G	-60	LYS	-	expression tag	UNP P42166
G	-59	ILE	-	expression tag	UNP P42166
G	-58	PRO	-	expression tag	UNP P42166
G	-57	LYS	-	expression tag	UNP P42166
G	-56	PRO	-	expression tag	UNP P42166
G	-55	ARG	-	expression tag	UNP P42166
G	-54	GLY	-	expression tag	UNP P42166
G	-17	GLN	ARG	conflict	UNP P42166
G	-2	GLY	-	linker	UNP P42166
G	-1	GLY	-	linker	UNP P42166
G	0	GLY	-	linker	UNP P42166
G	138	LYS	GLU	engineered mutation	UNP P12497
H	-75	GLY	-	expression tag	UNP P42166
H	-74	SER	-	expression tag	UNP P42166
H	-73	HIS	-	expression tag	UNP P42166
H	-72	MET	-	expression tag	UNP P42166

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-71	PRO	-	expression tag	UNP P42166
H	-70	LYS	-	expression tag	UNP P42166
H	-69	ARG	-	expression tag	UNP P42166
H	-68	GLY	-	expression tag	UNP P42166
H	-67	ARG	-	expression tag	UNP P42166
H	-66	PRO	-	expression tag	UNP P42166
H	-65	ALA	-	expression tag	UNP P42166
H	-64	ALA	-	expression tag	UNP P42166
H	-63	THR	-	expression tag	UNP P42166
H	-62	GLU	-	expression tag	UNP P42166
H	-61	VAL	-	expression tag	UNP P42166
H	-60	LYS	-	expression tag	UNP P42166
H	-59	ILE	-	expression tag	UNP P42166
H	-58	PRO	-	expression tag	UNP P42166
H	-57	LYS	-	expression tag	UNP P42166
H	-56	PRO	-	expression tag	UNP P42166
H	-55	ARG	-	expression tag	UNP P42166
H	-54	GLY	-	expression tag	UNP P42166
H	-17	GLN	ARG	conflict	UNP P42166
H	-2	GLY	-	linker	UNP P42166
H	-1	GLY	-	linker	UNP P42166
H	0	GLY	-	linker	UNP P42166
H	138	LYS	GLU	engineered mutation	UNP P12497
I	-75	GLY	-	expression tag	UNP P42166
I	-74	SER	-	expression tag	UNP P42166
I	-73	HIS	-	expression tag	UNP P42166
I	-72	MET	-	expression tag	UNP P42166
I	-71	PRO	-	expression tag	UNP P42166
I	-70	LYS	-	expression tag	UNP P42166
I	-69	ARG	-	expression tag	UNP P42166
I	-68	GLY	-	expression tag	UNP P42166
I	-67	ARG	-	expression tag	UNP P42166
I	-66	PRO	-	expression tag	UNP P42166
I	-65	ALA	-	expression tag	UNP P42166
I	-64	ALA	-	expression tag	UNP P42166
I	-63	THR	-	expression tag	UNP P42166
I	-62	GLU	-	expression tag	UNP P42166
I	-61	VAL	-	expression tag	UNP P42166
I	-60	LYS	-	expression tag	UNP P42166
I	-59	ILE	-	expression tag	UNP P42166
I	-58	PRO	-	expression tag	UNP P42166
I	-57	LYS	-	expression tag	UNP P42166

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-56	PRO	-	expression tag	UNP P42166
I	-55	ARG	-	expression tag	UNP P42166
I	-54	GLY	-	expression tag	UNP P42166
I	-17	GLN	ARG	conflict	UNP P42166
I	-2	GLY	-	linker	UNP P42166
I	-1	GLY	-	linker	UNP P42166
I	0	GLY	-	linker	UNP P42166
I	138	LYS	GLU	engineered mutation	UNP P12497
J	-75	GLY	-	expression tag	UNP P42166
J	-74	SER	-	expression tag	UNP P42166
J	-73	HIS	-	expression tag	UNP P42166
J	-72	MET	-	expression tag	UNP P42166
J	-71	PRO	-	expression tag	UNP P42166
J	-70	LYS	-	expression tag	UNP P42166
J	-69	ARG	-	expression tag	UNP P42166
J	-68	GLY	-	expression tag	UNP P42166
J	-67	ARG	-	expression tag	UNP P42166
J	-66	PRO	-	expression tag	UNP P42166
J	-65	ALA	-	expression tag	UNP P42166
J	-64	ALA	-	expression tag	UNP P42166
J	-63	THR	-	expression tag	UNP P42166
J	-62	GLU	-	expression tag	UNP P42166
J	-61	VAL	-	expression tag	UNP P42166
J	-60	LYS	-	expression tag	UNP P42166
J	-59	ILE	-	expression tag	UNP P42166
J	-58	PRO	-	expression tag	UNP P42166
J	-57	LYS	-	expression tag	UNP P42166
J	-56	PRO	-	expression tag	UNP P42166
J	-55	ARG	-	expression tag	UNP P42166
J	-54	GLY	-	expression tag	UNP P42166
J	-17	GLN	ARG	conflict	UNP P42166
J	-2	GLY	-	linker	UNP P42166
J	-1	GLY	-	linker	UNP P42166
J	0	GLY	-	linker	UNP P42166
J	138	LYS	GLU	engineered mutation	UNP P12497

- Molecule 2 is a DNA chain called DNA (27-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	19	Total	C	N	O	P	0	0
			384	185	67	114	18		
2	K	19	Total	C	N	O	P	0	0
			384	185	67	114	18		

- | Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|--------------|----------|---------|----------|---------|---------|-------|
| 3 | F | 17 | Total
371 | C
176 | N
73 | O
104 | P
18 | 1 | 0 |
| 3 | L | 17 | Total
371 | C
176 | N
73 | O
104 | P
18 | 1 | 0 |

- | Mol | Chain | Residues | Atoms | AltConf |
|-----|-------|----------|-----------------|---------|
| 4 | A | 2 | Total Mg
2 2 | 0 |
| 4 | G | 2 | Total Mg
2 2 | 0 |

- | Mol | Chain | Residues | Atoms | AltConf |
|-----|-------|----------|-----------------|---------|
| 5 | A | 1 | Total Zn
1 1 | 0 |
| 5 | G | 1 | Total Zn
1 1 | 0 |

- # DLU
-
- The chemical structure of DLU (1,3-bis(2,4,6-trifluorophenyl)pyrrolidine) is shown. The molecule consists of a central pyrrolidine ring substituted with two 2,4,6-trifluorophenyl groups. The atoms are labeled as follows:
- Central Pyrrolidine Ring:**
 - Nitrogen atoms: NBC (top), NBD (bottom).
 - Carbon atoms: CBA(R) (top-left), CAY (top-right), CAX (bottom-right), CBB(S) (bottom-left), CAO (bottom).
 - Oxygen atoms: OAC (top), OAD (top-right), OAE (top-right), OAB (bottom-right), OAO (bottom-left).
 - Hydrogen atoms: HBB (bottom-left, attached to CBB(S)).
 - 2,4,6-Trifluorophenyl Groups:**
 - Top group (attached to NBC):
 - Carbon atoms: CAW (top), CAZ (top-right), CAY (top-left).
 - Oxygen atoms: OAE (top), OAD (top-right).
 - Bottom group (attached to NBD):
 - Carbon atoms: CAX (bottom-right), CAK (bottom), CAJ (bottom-left), CAI (bottom-right), CAH (bottom-right), CAT (bottom-right).
 - Fluorine atoms: FAG (top-left), FAF (bottom-right).

Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	F	N	O	0
			30	20	2	3	5	
6	G	1	Total	C	F	N	O	0
			30	20	2	3	5	

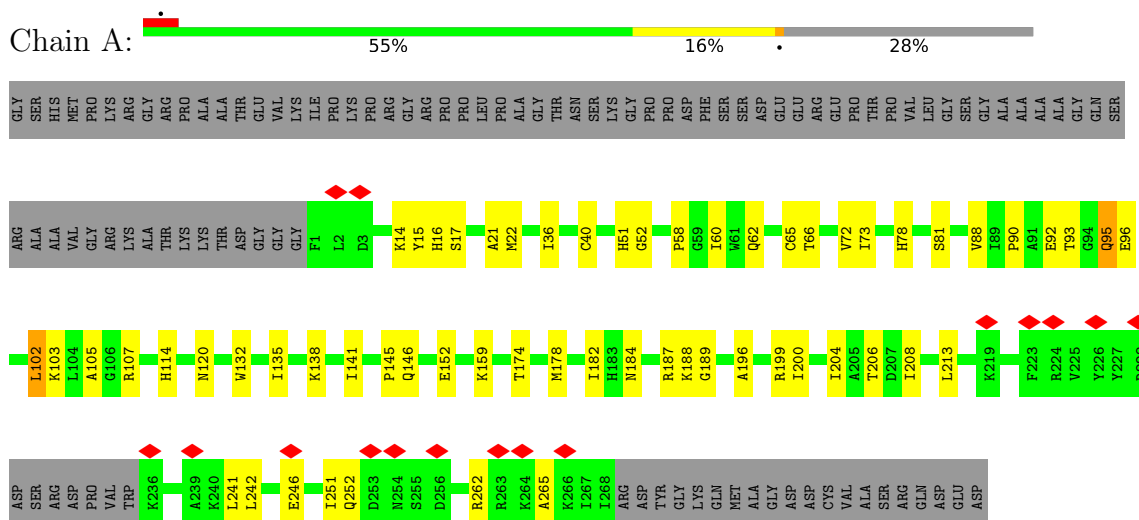
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		AltConf
7	A	35	Total	O	0
			35	35	
7	B	19	Total	O	0
			19	19	
7	D	3	Total	O	0
			3	3	
7	E	5	Total	O	0
			5	5	
7	F	8	Total	O	0
			8	8	
7	G	36	Total	O	0
			36	36	
7	H	19	Total	O	0
			19	19	
7	J	3	Total	O	0
			3	3	
7	K	5	Total	O	0
			5	5	
7	L	8	Total	O	0
			8	8	

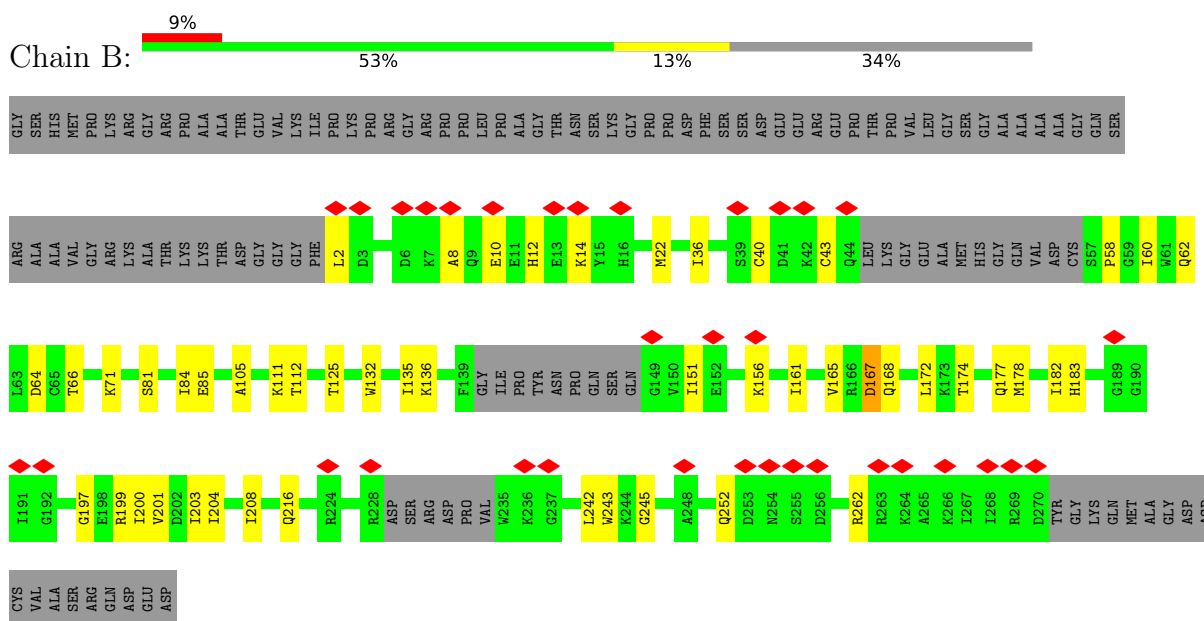
3 Residue-property plots

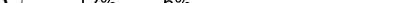
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Lamina-associated polypeptide 2, isoform alpha,Integrase chimera

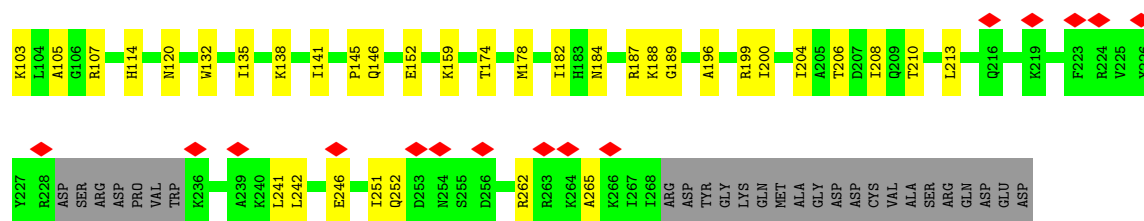


- Molecule 1: Lamina-associated polypeptide 2, isoform alpha,Integrase chimera

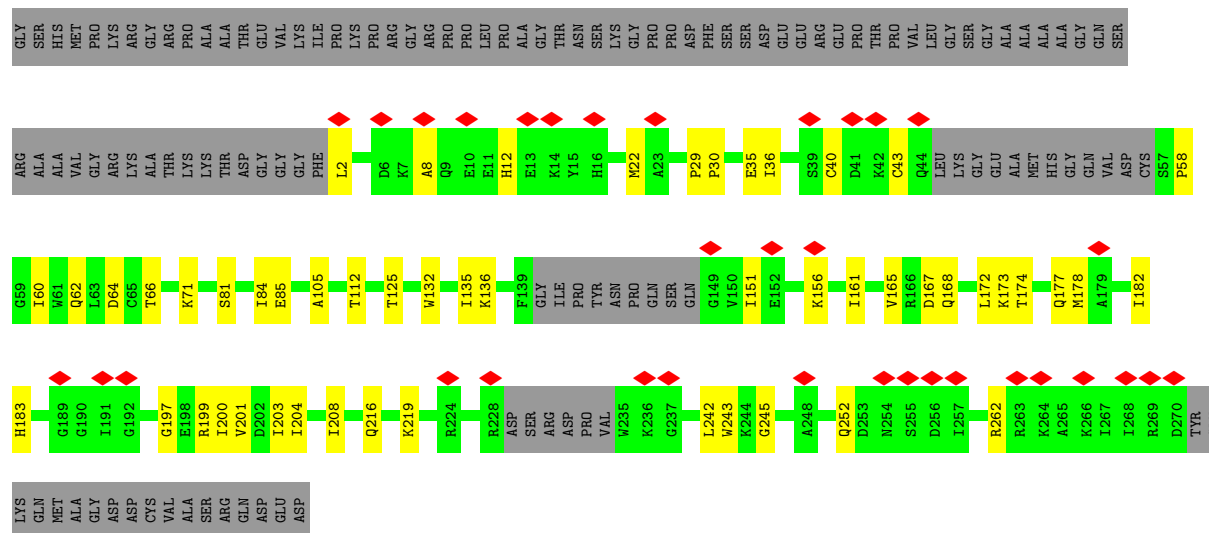


- Chain C:  12% 6% 82%

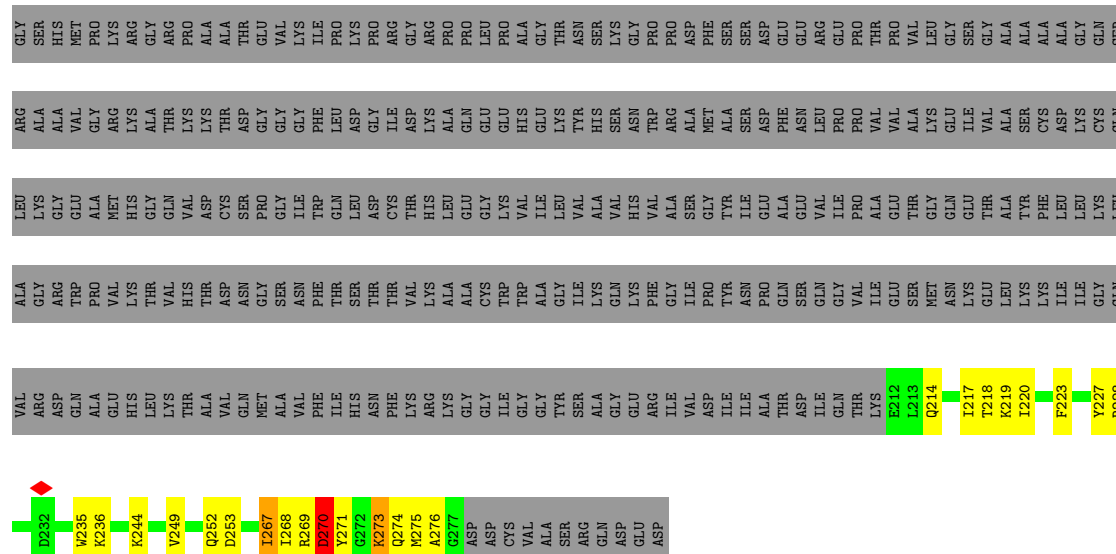




- Molecule 1: Lamina-associated polypeptide 2, isoform alpha,Integrase chimera



- Molecule 1: Lamina-associated polypeptide 2, isoform alpha,Integrase chimera



- Molecule 1: Lamina-associated polypeptide 2, isoform alpha,Integrase chimera

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

D229	S230	G247	V250	V259	V260	P261	R262	R263	K264	T268	ARG	ASP	TYR	GLY	LYS	GLN	MET	ALA	GLY	ASP	ASP	CYS	VAL	ALA	SER	ARG	GLN	ASP	GLU	ASP
------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

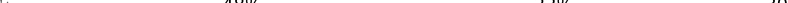
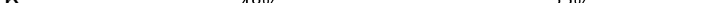
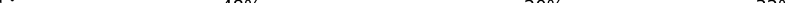
Chain E: 

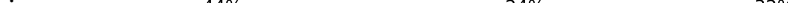
Figure 1 shows the 128-bit input and output of the proposed algorithm. The input is a 128-bit vector with 16 elements: A15, C16, T17, G18, C19, T20, A21, an empty slot, C31, C32, G33, and a greyed-out section (DC, DC, DC, DA, DC, DC, DC, DC, DT). The output is a 128-bit vector with 16 elements: A15, C16, T17, G18, C19, T20, A21, an empty slot, C31, C32, G33, and a greyed-out section (DC, DC, DC, DA, DC, DC, DC, DC, DT). Red diamonds indicate a swap between C31 and G33.

Chain K:  7% 48% 22% 30%

Category	Color	Relative Height
A15	Green	Medium
C16	Green	Medium
T17	Green	Medium
G18	Yellow	Medium
C19	Yellow	Medium
T20	Yellow	Medium
A21	Yellow	Medium
C31	Green	Medium
C32	Yellow	Tallest
G33	Yellow	Second Tallest
DC	Yellow	Medium
DC	Yellow	Medium
DC	Yellow	Medium
DA	Green	Medium
DC	Green	Medium
DC	Green	Medium
DC	Green	Medium
DT	Grey	Shortest

Chain F: 

Category	Count
DA	1
DG	1
DC	1
DG	1
DT	1
DG	1
DG	1
DG	1
C5	1
G6	1
G7	1
G8	1
T17	1
A18	1
A21	1

Chain L: 

DA	DG	DC	DG	DT	DG	DG	DG	C5	G6	G7	G8	T17	A18	G19	C20	A21
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	81551	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	60240	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.045	Depositor
Minimum map value	-0.382	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	318.72, 318.72, 318.72	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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: ZN, MG, DLU

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	0.19	0/2077	0.36	0/2794
1	B	0.18	0/1948	0.35	0/2624
1	C	0.77	2/553 (0.4%)	0.55	0/741
1	D	0.21	0/397	0.41	0/535
1	G	0.19	0/2077	0.36	0/2794
1	H	0.18	0/1948	0.35	0/2624
1	I	0.79	2/553 (0.4%)	0.63	1/741 (0.1%)
1	J	0.21	0/397	0.42	0/535
2	E	0.24	0/429	0.40	0/660
2	K	0.24	0/429	0.40	0/660
3	F	0.23	0/416	0.36	0/637
3	L	0.23	0/416	0.36	0/637
All	All	0.31	4/11640 (0.0%)	0.39	1/15982 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	270	ASP	CA-C	-6.53	1.44	1.52
1	C	270	ASP	CA-C	-6.42	1.44	1.52
1	I	271	TYR	N-CA	-5.66	1.38	1.46
1	C	271	TYR	N-CA	-5.60	1.38	1.46

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	267	ILE	N-CA-C	6.97	118.01	109.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2035	0	2077	53	0
1	B	1911	0	1943	36	0
1	C	543	0	569	17	0
1	D	388	0	406	6	0
1	G	2035	0	2077	51	0
1	H	1911	0	1943	40	0
1	I	543	0	569	20	0
1	J	388	0	406	6	0
2	E	384	0	217	6	0
2	K	384	0	217	5	0
3	F	371	0	203	5	0
3	L	371	0	203	5	0
4	A	2	0	0	0	0
4	G	2	0	0	0	0
5	A	1	0	0	0	0
5	G	1	0	0	0	0
6	A	30	0	18	9	0
6	G	30	0	18	8	0
7	A	35	0	0	0	0
7	B	19	0	0	0	0
7	D	3	0	0	0	0
7	E	5	0	0	0	0
7	F	8	0	0	0	0
7	G	36	0	0	0	0
7	H	19	0	0	1	0
7	J	3	0	0	0	0
7	K	5	0	0	0	0
7	L	8	0	0	0	0
All	All	11471	0	10866	207	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 9.

All (207) 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:B:216:GLN:HE22	1:C:276:ALA:HA	1.41	0.84
1:A:146:GLN:HG3	6:A:304:DLU:FAF	1.68	0.84
1:H:216:GLN:HE22	1:I:276:ALA:HA	1.42	0.82
1:H:242:LEU:HD11	1:H:252:GLN:HB2	1.63	0.81
1:G:200:ILE:O	1:G:204:ILE:HD12	1.80	0.81
1:B:12:HIS:NE2	1:B:40:CYS:SG	2.52	0.81
1:B:242:LEU:HD11	1:B:252:GLN:HB2	1.62	0.81
1:A:200:ILE:O	1:A:204:ILE:HD12	1.80	0.81
1:H:12:HIS:NE2	1:H:40:CYS:SG	2.52	0.80
1:G:146:GLN:HG3	6:G:304:DLU:FAF	1.73	0.78
1:G:78:HIS:ND1	1:G:81:SER:OG	2.17	0.78
1:A:78:HIS:ND1	1:A:81:SER:OG	2.17	0.77
1:A:66:THR:OG1	1:A:159:LYS:NZ	2.19	0.75
1:G:66:THR:OG1	1:G:159:LYS:NZ	2.19	0.75
1:H:8:ALA:HB1	1:H:22:MET:HE3	1.71	0.73
1:G:145:PRO:HB2	6:G:304:DLU:CAJ	2.18	0.73
1:A:145:PRO:HB2	6:A:304:DLU:CAJ	2.19	0.73
1:A:189:GLY:O	1:A:199:ARG:NH2	2.22	0.73
1:B:71:LYS:HD2	1:B:172:LEU:HD23	1.71	0.72
1:G:189:GLY:O	1:G:199:ARG:NH2	2.22	0.72
1:H:71:LYS:HD2	1:H:172:LEU:HD23	1.71	0.72
1:B:8:ALA:HB1	1:B:22:MET:HE3	1.71	0.71
1:B:197:GLY:O	1:B:201:VAL:HG23	1.91	0.71
1:A:146:GLN:CG	6:A:304:DLU:FAF	2.30	0.70
1:H:197:GLY:O	1:H:201:VAL:HG23	1.90	0.69
1:G:93:THR:HG22	1:G:95:GLN:H	1.57	0.69
1:A:145:PRO:HB2	6:A:304:DLU:CAU	2.23	0.68
1:A:93:THR:HG22	1:A:95:GLN:H	1.57	0.68
1:G:145:PRO:HB2	6:G:304:DLU:CAU	2.26	0.66
3:F:17:DT:H2"	3:F:18:DA:C8	2.31	0.66
3:L:17:DT:H2"	3:L:18:DA:C8	2.32	0.65
1:G:107:ARG:NH2	1:H:177:GLN:OE1	2.30	0.65
1:A:107:ARG:NH2	1:B:177:GLN:OE1	2.30	0.64
1:G:146:GLN:CG	6:G:304:DLU:FAF	2.35	0.64
1:H:216:GLN:NE2	1:I:276:ALA:HA	2.13	0.64
1:G:262:ARG:NH1	1:G:265:ALA:O	2.32	0.63
1:G:204:ILE:O	1:G:208:ILE:HG13	1.99	0.62
1:H:245:GLY:O	1:H:262:ARG:NH1	2.32	0.62
1:B:245:GLY:O	1:B:262:ARG:NH1	2.32	0.62
1:G:213:LEU:HD21	1:I:219:LYS:HE2	1.81	0.62
1:A:262:ARG:NH1	1:A:265:ALA:O	2.32	0.62
1:A:241:LEU:HA	1:A:251:ILE:HG22	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:241:LEU:HA	1:G:251:ILE:HG22	1.82	0.61
1:A:213:LEU:HD21	1:C:219:LYS:HE2	1.81	0.61
1:B:216:GLN:NE2	1:C:276:ALA:HA	2.12	0.61
1:A:58:PRO:O	1:A:78:HIS:NE2	2.29	0.61
1:D:250:VAL:HG22	1:D:259:VAL:HG22	1.83	0.61
1:A:204:ILE:O	1:A:208:ILE:HG13	1.99	0.60
1:H:12:HIS:NE2	1:H:43:CYS:SG	2.74	0.60
1:B:12:HIS:NE2	1:B:43:CYS:SG	2.74	0.60
1:C:228:ARG:HD3	1:C:235:TRP:CE2	2.37	0.60
1:A:72:VAL:HG11	1:A:92:GLU:HG3	1.84	0.60
1:I:228:ARG:HD3	1:I:235:TRP:CE2	2.37	0.59
1:J:250:VAL:HG22	1:J:259:VAL:HG22	1.83	0.59
1:G:72:VAL:HG11	1:G:92:GLU:HG3	1.84	0.58
1:G:246:GLU:OE1	1:I:252:GLN:NE2	2.37	0.58
1:I:214:GLN:O	1:I:218:THR:HG23	2.04	0.58
1:C:214:GLN:O	1:C:218:THR:HG23	2.04	0.58
1:A:246:GLU:OE1	1:C:252:GLN:NE2	2.37	0.57
1:B:216:GLN:OE1	1:C:276:ALA:HB2	2.06	0.56
1:G:58:PRO:O	1:G:78:HIS:NE2	2.29	0.56
1:A:52:GLY:HA3	2:E:17:DT:H1'	1.88	0.56
1:C:228:ARG:HD3	1:C:235:TRP:CD2	2.41	0.56
1:C:274:GLN:HB3	1:C:275:MET:HE2	1.88	0.55
1:I:228:ARG:HD3	1:I:235:TRP:CD2	2.41	0.55
1:A:22:MET:HE1	1:A:36:ILE:HB	1.88	0.55
1:B:167:ASP:OD1	1:B:167:ASP:N	2.38	0.55
1:H:167:ASP:OD1	1:H:167:ASP:N	2.38	0.55
1:H:216:GLN:OE1	1:I:276:ALA:HB2	2.06	0.55
1:I:274:GLN:HB3	1:I:275:MET:HE2	1.89	0.55
6:A:304:DLU:OAB	3:F:21[B]:DA:O4'	2.24	0.54
1:G:22:MET:HE1	1:G:36:ILE:HB	1.88	0.54
1:G:52:GLY:HA3	2:K:17:DT:H1'	1.88	0.54
1:A:103:LYS:O	1:A:107:ARG:HG2	2.08	0.54
1:H:60:ILE:HD13	1:H:112:THR:HB	1.90	0.54
1:B:60:ILE:HD13	1:B:112:THR:HB	1.90	0.53
6:A:304:DLU:OAB	3:F:21[A]:DA:H3'	2.08	0.53
1:G:141:ILE:HG21	1:J:261:PRO:HD3	1.90	0.53
1:G:103:LYS:O	1:G:107:ARG:HG2	2.08	0.53
1:A:141:ILE:HG21	1:D:261:PRO:HD3	1.91	0.53
1:G:90:PRO:HD2	1:G:96:GLU:OE2	2.09	0.53
1:G:16:HIS:CE1	1:G:40:CYS:SG	3.02	0.52
1:A:90:PRO:HD2	1:A:96:GLU:OE2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:51:HIS:CD2	2:K:18:DG:H5''	2.45	0.52
1:H:174:THR:O	1:H:178:MET:HG3	2.10	0.52
1:B:58:PRO:HB3	1:B:203:ILE:HG22	1.91	0.52
1:A:16:HIS:CE1	1:A:40:CYS:SG	3.02	0.52
1:B:174:THR:O	1:B:178:MET:HG3	2.10	0.51
1:H:58:PRO:HB3	1:H:203:ILE:HG22	1.92	0.51
1:A:51:HIS:CD2	2:E:18:DG:H5''	2.45	0.51
2:E:20:DT:H2''	2:E:21:DA:C8	2.46	0.51
1:A:184:ASN:HA	1:A:196:ALA:HB3	1.92	0.51
2:K:20:DT:H2''	2:K:21:DA:C8	2.46	0.51
1:B:62:GLN:HB3	1:B:151:ILE:HD13	1.93	0.51
1:H:62:GLN:HB3	1:H:151:ILE:HD13	1.93	0.50
1:G:184:ASN:HA	1:G:196:ALA:HB3	1.92	0.50
1:A:21:ALA:HA	1:G:188:LYS:HD2	1.93	0.50
1:B:156:LYS:NZ	1:B:156:LYS:HB3	2.27	0.49
1:B:60:ILE:CD1	1:B:112:THR:HB	2.43	0.49
1:A:14:LYS:NZ	1:H:132:TRP:O	2.45	0.49
1:B:81:SER:O	1:B:199:ARG:NH1	2.46	0.49
1:H:81:SER:O	1:H:199:ARG:NH1	2.46	0.49
1:C:227:TYR:OH	1:C:253:ASP:OD2	2.22	0.49
1:I:244:LYS:HD2	1:I:267:ILE:HD12	1.95	0.49
1:H:60:ILE:CD1	1:H:112:THR:HB	2.43	0.48
1:A:188:LYS:HD2	1:G:21:ALA:HA	1.94	0.48
1:B:165:VAL:HG23	1:B:168:GLN:NE2	2.29	0.48
1:A:16:HIS:O	1:G:187:ARG:NH1	2.46	0.48
1:G:152:GLU:HB3	6:G:304:DLU:FAG	2.03	0.48
1:B:84:ILE:HD12	1:B:183:HIS:CD2	2.49	0.48
1:H:156:LYS:NZ	1:H:156:LYS:HB3	2.27	0.48
1:H:165:VAL:HG23	1:H:168:GLN:NE2	2.28	0.48
1:A:187:ARG:NH1	1:G:16:HIS:O	2.47	0.48
1:G:138:LYS:HD2	1:G:138:LYS:HA	1.58	0.47
1:A:152:GLU:HB3	6:A:304:DLU:FAG	2.04	0.47
1:H:84:ILE:HD12	1:H:183:HIS:CD2	2.49	0.47
1:H:219:LYS:NZ	7:H:302:HOH:O	2.47	0.47
1:G:200:ILE:HG12	1:G:204:ILE:HD11	1.96	0.47
1:A:174:THR:O	1:A:178:MET:HG3	2.15	0.47
1:I:227:TYR:OH	1:I:253:ASP:OD2	2.22	0.47
1:A:103:LYS:HB3	1:A:103:LYS:HE3	1.62	0.46
1:B:216:GLN:NE2	1:C:275:MET:O	2.49	0.46
1:D:229:ASP:OD1	1:D:230:SER:N	2.48	0.46
1:G:206:THR:HG23	1:I:223:PHE:CD1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:161:ILE:O	1:B:165:VAL:HG12	2.15	0.46
1:D:228:ARG:NH2	1:D:264:LYS:HG2	2.30	0.46
1:G:73:ILE:HG12	1:G:88:VAL:HG22	1.97	0.46
1:J:228:ARG:NH2	1:J:264:LYS:HG2	2.30	0.46
1:B:105:ALA:HB2	1:B:135:ILE:HD11	1.98	0.46
1:G:174:THR:O	1:G:178:MET:HG3	2.15	0.46
1:H:161:ILE:O	1:H:165:VAL:HG12	2.15	0.46
1:H:216:GLN:NE2	1:I:275:MET:O	2.49	0.46
1:B:132:TRP:O	1:G:14:LYS:NZ	2.46	0.46
1:G:103:LYS:HB3	1:G:103:LYS:HE3	1.62	0.46
1:A:146:GLN:NE2	6:A:304:DLU:HAH	2.30	0.46
1:A:200:ILE:HG12	1:A:204:ILE:HD11	1.96	0.46
1:A:73:ILE:HG12	1:A:88:VAL:HG22	1.97	0.45
1:A:206:THR:HG23	1:C:223:PHE:CD1	2.51	0.45
1:I:273:LYS:O	1:I:274:GLN:C	2.59	0.45
1:B:197:GLY:O	1:B:200:ILE:HG22	2.17	0.45
1:D:247:GLY:H	1:D:262:ARG:HD3	1.82	0.45
1:J:247:GLY:H	1:J:262:ARG:HD3	1.82	0.45
1:H:105:ALA:HB2	1:H:135:ILE:HD11	1.98	0.45
1:A:146:GLN:CD	6:A:304:DLU:FAF	2.50	0.45
1:H:197:GLY:O	1:H:200:ILE:HG22	2.17	0.45
1:I:217:ILE:O	1:I:220:ILE:HG22	2.17	0.45
1:H:136:LYS:HE3	1:H:136:LYS:HB3	1.72	0.44
1:B:111:LYS:HA	1:B:111:LYS:HD2	1.78	0.44
1:A:65:CYS:SG	1:A:120:ASN:ND2	2.91	0.44
1:B:136:LYS:HE3	1:B:136:LYS:HB3	1.72	0.44
1:C:217:ILE:O	1:C:220:ILE:HG22	2.17	0.44
1:G:65:CYS:SG	1:G:120:ASN:ND2	2.91	0.44
3:F:18:DA:OP1	1:J:263:ARG:HD2	2.18	0.43
2:E:31:DC:H2"	2:E:32:DC:C6	2.54	0.43
1:G:132:TRP:CZ2	1:H:178:MET:HE3	2.54	0.43
1:A:60:ILE:HD13	1:A:60:ILE:HA	1.90	0.43
1:B:204:ILE:O	1:B:208:ILE:HG13	2.19	0.43
1:C:273:LYS:O	1:C:274:GLN:C	2.59	0.43
1:D:263:ARG:HD2	3:L:18:DA:OP1	2.18	0.43
1:G:105:ALA:HB2	1:G:135:ILE:HD11	2.01	0.43
1:G:102:LEU:HD12	1:G:102:LEU:HA	1.78	0.43
2:K:31:DC:H2"	2:K:32:DC:C6	2.54	0.43
1:A:208:ILE:HG13	1:A:208:ILE:H	1.68	0.43
1:A:102:LEU:HD12	1:A:102:LEU:HA	1.78	0.42
1:A:132:TRP:CZ2	1:B:178:MET:HE3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:GLN:HB3	2:E:18:DG:O5'	2.19	0.42
1:H:204:ILE:O	1:H:208:ILE:HG13	2.19	0.42
1:C:270:ASP:HB3	1:C:273:LYS:HG3	2.02	0.42
1:H:22:MET:HE1	1:H:36:ILE:HG21	2.02	0.42
1:A:138:LYS:HD2	1:A:138:LYS:HA	1.58	0.42
1:G:146:GLN:HB3	2:K:18:DG:O5'	2.19	0.42
1:G:242:LEU:HD11	1:G:252:GLN:HB2	2.01	0.42
1:A:182:ILE:HG12	1:G:15:TYR:HB3	2.02	0.42
1:A:242:LEU:HD11	1:A:252:GLN:HB2	2.01	0.42
1:I:273:LYS:C	1:I:275:MET:N	2.76	0.42
1:B:2:LEU:HD21	1:B:243:TRP:HZ3	1.85	0.42
1:B:22:MET:HE1	1:B:36:ILE:HG21	2.02	0.42
1:J:229:ASP:OD1	1:J:230:SER:N	2.48	0.42
1:A:105:ALA:HB2	1:A:135:ILE:HD11	2.01	0.42
3:F:7:DG:H2''	3:F:8:DG:H5'	2.02	0.41
1:A:15:TYR:HB3	1:G:182:ILE:HG12	2.02	0.41
1:G:146:GLN:NE2	6:G:304:DLU:HAH	2.35	0.41
1:G:107:ARG:HD2	1:H:85:GLU:CD	2.46	0.41
1:G:132:TRP:CE2	1:H:178:MET:HE3	2.56	0.41
1:A:51:HIS:HD2	2:E:18:DG:H5''	1.85	0.41
1:G:146:GLN:CD	6:G:304:DLU:FAF	2.53	0.41
1:H:22:MET:HE3	1:H:22:MET:HB3	1.89	0.41
1:H:2:LEU:HD21	1:H:243:TRP:HZ3	1.85	0.41
1:G:210:THR:OG1	1:I:244:LYS:HE2	2.21	0.41
1:I:227:TYR:CE2	1:I:236:LYS:HG3	2.56	0.41
1:I:270:ASP:HB3	1:I:273:LYS:HG3	2.03	0.41
3:L:7:DG:H2''	3:L:8:DG:H5'	2.02	0.41
1:A:62:GLN:HG2	1:A:114:HIS:HB3	2.02	0.41
1:A:132:TRP:CE2	1:B:178:MET:HE3	2.56	0.41
1:C:227:TYR:CE2	1:C:236:LYS:HG3	2.56	0.41
1:C:244:LYS:HD2	1:C:267:ILE:HD12	2.03	0.41
3:L:18:DA:H2''	3:L:19:DG:C8	2.56	0.41
1:H:64:ASP:HB2	1:H:151:ILE:HG12	2.03	0.41
1:A:107:ARG:HD2	1:B:85:GLU:CD	2.46	0.40
1:B:10:GLU:O	1:B:14:LYS:HG3	2.22	0.40
1:H:30:PRO:HG2	1:I:275:MET:HA	2.03	0.40
1:H:60:ILE:HD13	1:H:60:ILE:HA	1.84	0.40
1:G:62:GLN:HG2	1:G:114:HIS:HB3	2.02	0.40
6:G:304:DLU:HANA	3:L:20:DC:H2'	2.02	0.40
1:B:64:ASP:HB2	1:B:151:ILE:HG12	2.04	0.40
1:H:29:PRO:HA	1:H:30:PRO:HD3	2.00	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:35:GLU:OE2	1:H:252:GLN:NE2	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	257/364 (71%)	252 (98%)	5 (2%)	0	100	100
1	B	234/364 (64%)	232 (99%)	2 (1%)	0	100	100
1	C	64/364 (18%)	61 (95%)	1 (2%)	2 (3%)	3	19
1	D	45/364 (12%)	42 (93%)	3 (7%)	0	100	100
1	G	257/364 (71%)	252 (98%)	5 (2%)	0	100	100
1	H	234/364 (64%)	232 (99%)	2 (1%)	0	100	100
1	I	64/364 (18%)	60 (94%)	2 (3%)	2 (3%)	3	19
1	J	45/364 (12%)	42 (93%)	3 (7%)	0	100	100
All	All	1200/2912 (41%)	1173 (98%)	23 (2%)	4 (0%)	37	70

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	270	ASP
1	I	270	ASP
1	I	268	ILE
1	C	268	ILE

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	A	217/294 (74%)	214 (99%)	3 (1%)	59	80
1	B	202/294 (69%)	198 (98%)	4 (2%)	48	76
1	C	57/294 (19%)	53 (93%)	4 (7%)	14	44
1	D	41/294 (14%)	41 (100%)	0	100	100
1	G	217/294 (74%)	215 (99%)	2 (1%)	70	85
1	H	202/294 (69%)	198 (98%)	4 (2%)	48	76
1	I	57/294 (19%)	53 (93%)	4 (7%)	14	44
1	J	41/294 (14%)	41 (100%)	0	100	100
All	All	1034/2352 (44%)	1013 (98%)	21 (2%)	48	76

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	SER
1	A	95	GLN
1	A	102	LEU
1	B	66	THR
1	B	125	THR
1	B	167	ASP
1	B	182	ILE
1	C	249	VAL
1	C	269	ARG
1	C	270	ASP
1	C	273	LYS
1	G	17	SER
1	G	102	LEU
1	H	66	THR
1	H	125	THR
1	H	173	LYS
1	H	182	ILE
1	I	249	VAL
1	I	269	ARG

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Mol	Chain	Res	Type
1	I	270	ASP
1	I	273	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	221	GLN
1	C	216	GLN
1	C	222	ASN
1	G	9	GLN
1	G	221	GLN
1	I	216	GLN
1	I	222	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 8 ligands modelled in this entry, 6 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
6	DLU	A	304	4	30,33,33	4.85	15 (50%)	34,49,49	2.08	12 (35%)
6	DLU	G	304	4	30,33,33	4.84	15 (50%)	34,49,49	2.04	10 (29%)

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
6	DLU	A	304	4	-	4/9/35/35	0/4/4/4
6	DLU	G	304	4	-	4/9/35/35	0/4/4/4

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	G	304	DLU	CAO-NBD	15.79	1.60	1.46
6	A	304	DLU	CAO-NBD	15.78	1.60	1.46
6	G	304	DLU	CAY-CAW	13.01	1.53	1.36
6	A	304	DLU	CAY-CAW	12.98	1.53	1.36
6	A	304	DLU	CAR-NAP	7.80	1.46	1.33
6	G	304	DLU	CAR-NAP	7.74	1.46	1.33
6	A	304	DLU	CAK-NBD	6.93	1.50	1.37
6	G	304	DLU	CAK-NBD	6.86	1.50	1.37
6	G	304	DLU	CBA-NBC	-6.22	1.42	1.48
6	A	304	DLU	CBA-NBC	-6.19	1.42	1.48
6	A	304	DLU	CAK-CAX	5.16	1.51	1.38
6	G	304	DLU	CAK-CAX	5.11	1.51	1.38
6	A	304	DLU	CAS-NBC	-4.82	1.31	1.36
6	G	304	DLU	CAS-NBC	-4.80	1.31	1.36
6	A	304	DLU	CAY-CAS	4.63	1.54	1.43
6	G	304	DLU	CAY-CAS	4.62	1.54	1.43
6	A	304	DLU	OAD-CAZ	-3.99	1.14	1.23
6	G	304	DLU	OAD-CAZ	-3.97	1.14	1.23
6	A	304	DLU	OAE-CAW	3.81	1.46	1.33
6	G	304	DLU	OAE-CAW	3.79	1.46	1.33
6	A	304	DLU	CAX-CAR	2.75	1.57	1.49
6	G	304	DLU	CAX-CAR	2.72	1.57	1.49
6	A	304	DLU	OAC-CAS	-2.68	1.17	1.23
6	G	304	DLU	OAC-CAS	-2.63	1.17	1.23
6	A	304	DLU	CAM-CBA	-2.55	1.47	1.53
6	G	304	DLU	CAM-CBA	-2.55	1.47	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	304	DLU	CAM-CAL	2.35	1.59	1.51
6	G	304	DLU	CAM-CAL	2.33	1.59	1.51
6	A	304	DLU	CAI-CAV	-2.19	1.36	1.39
6	G	304	DLU	CAI-CAV	-2.11	1.36	1.39

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	304	DLU	CAV-CAN-NAP	-5.98	101.10	113.15
6	G	304	DLU	CAV-CAN-NAP	-5.81	101.43	113.15
6	A	304	DLU	CAM-CBA-NBC	-3.58	105.99	109.42
6	G	304	DLU	CAM-CBA-NBC	-3.48	106.09	109.42
6	G	304	DLU	OAC-CAS-CAY	-3.43	119.35	126.38
6	A	304	DLU	OAC-CAS-CAY	-3.41	119.38	126.38
6	A	304	DLU	OAB-CAR-NAP	-3.23	117.52	123.35
6	G	304	DLU	CAA-CBA-CAM	-3.22	106.75	112.74
6	A	304	DLU	CAA-CBA-CAM	-3.17	106.83	112.74
6	G	304	DLU	OAB-CAR-NAP	-3.11	117.74	123.35
6	A	304	DLU	CAX-CAR-NAP	2.52	122.03	116.67
6	G	304	DLU	CAX-CAR-NAP	2.50	122.00	116.67
6	A	304	DLU	CAH-CAT-CAJ	-2.48	119.95	123.23
6	G	304	DLU	CAU-CAJ-CAT	2.45	119.28	116.67
6	G	304	DLU	CAH-CAT-CAJ	-2.43	120.02	123.23
6	A	304	DLU	CAU-CAJ-CAT	2.40	119.23	116.67
6	A	304	DLU	CAI-CAH-CAT	2.39	120.83	118.38
6	G	304	DLU	CAI-CAH-CAT	2.22	120.66	118.38
6	G	304	DLU	CAJ-CAU-CAV	-2.05	120.60	123.76
6	A	304	DLU	CAJ-CAU-CAV	-2.04	120.61	123.76
6	A	304	DLU	OAQ-CAL-CAM	2.04	114.54	110.75
6	A	304	DLU	CAK-CAX-CAZ	-2.01	118.16	120.44

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	304	DLU	OAB-CAR-CAX-CAZ
6	G	304	DLU	OAB-CAR-CAX-CAZ
6	A	304	DLU	NAP-CAR-CAX-CAZ
6	G	304	DLU	NAP-CAR-CAX-CAZ
6	A	304	DLU	OAB-CAR-CAX-CAK
6	G	304	DLU	OAB-CAR-CAX-CAK
6	A	304	DLU	NAP-CAR-CAX-CAK

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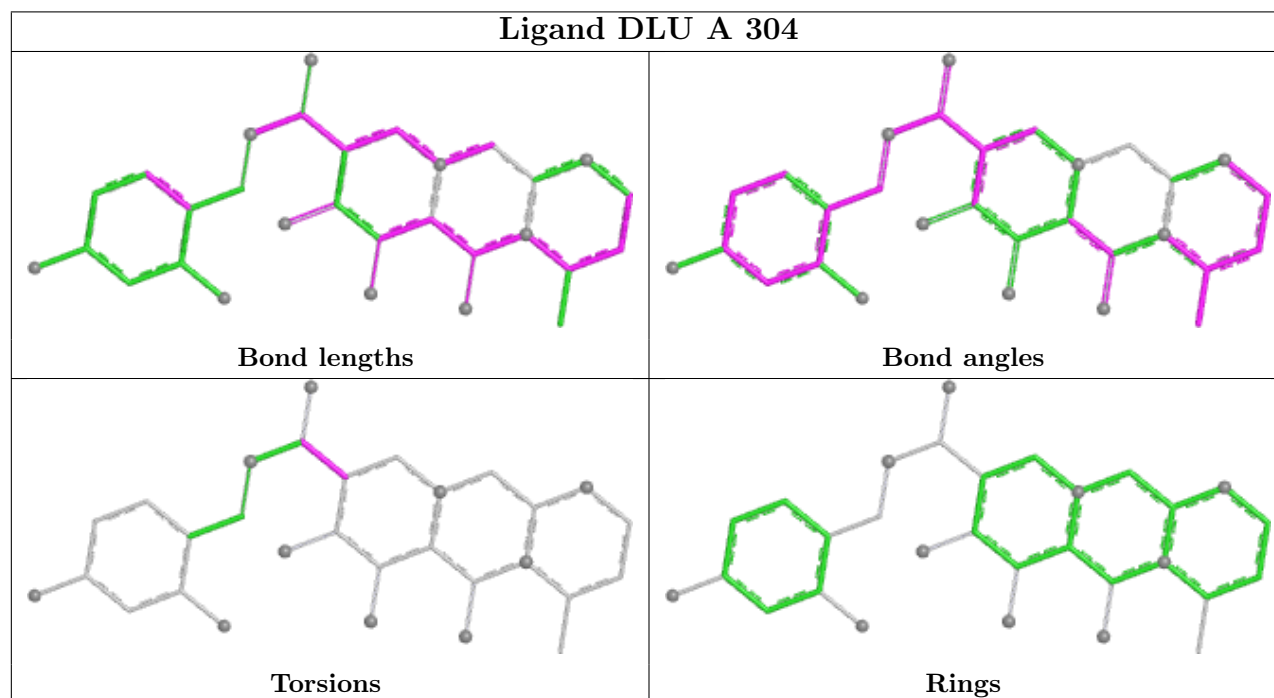
Mol	Chain	Res	Type	Atoms
6	G	304	DLU	NAP-CAR-CAX-CAK

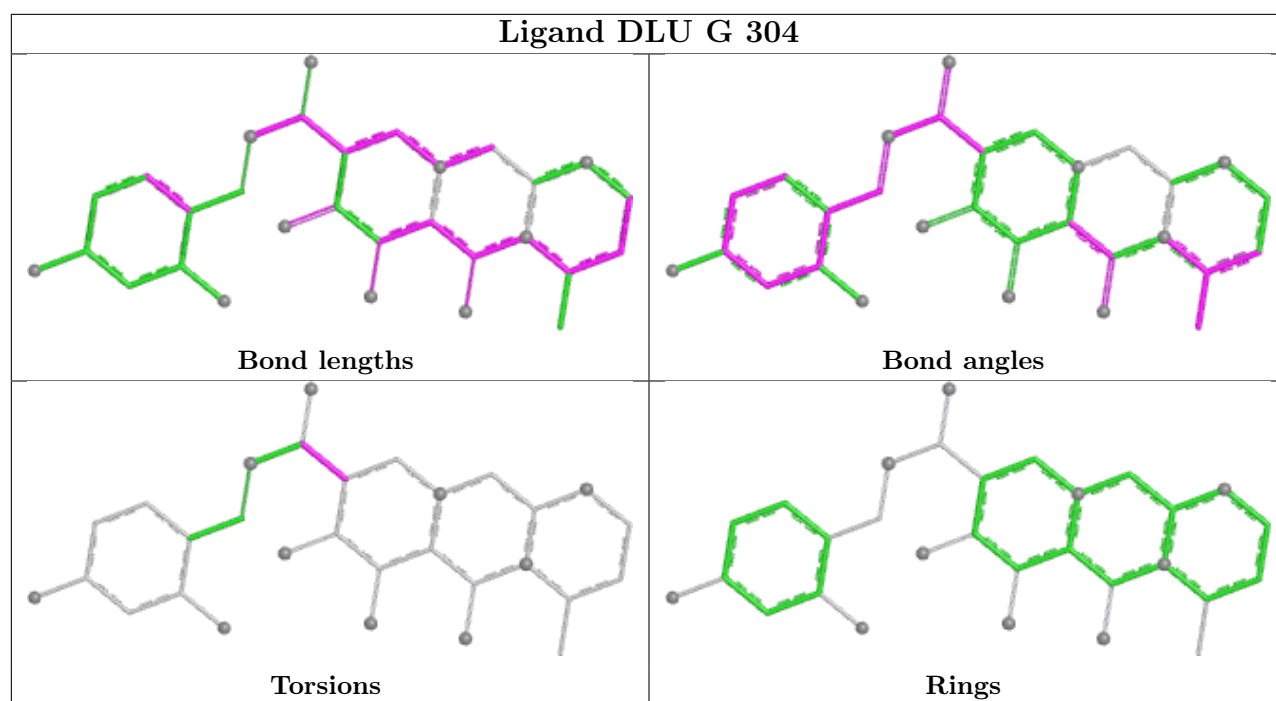
There are no ring outliers.

2 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	304	DLU	9	0
6	G	304	DLU	8	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.

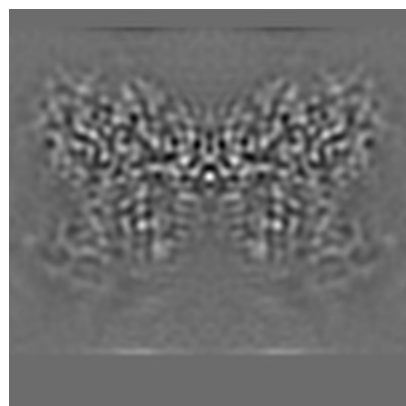
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29309. These allow visual inspection of the internal detail of the map and identification of artifacts.

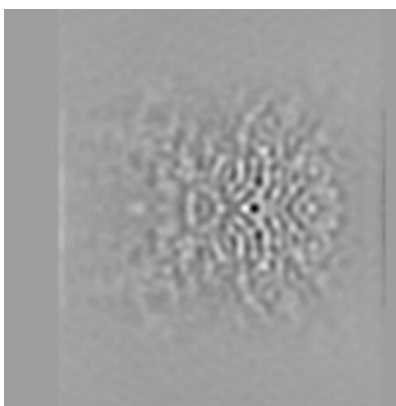
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

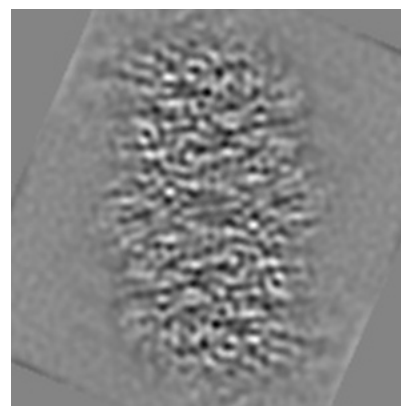
6.1.1 Primary map



X

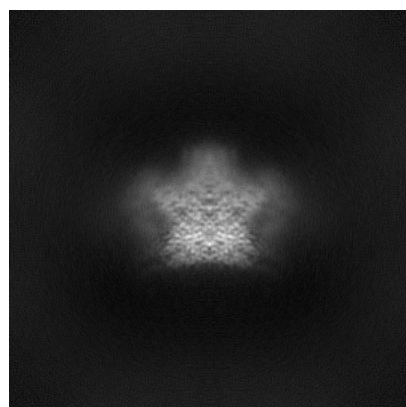


Y

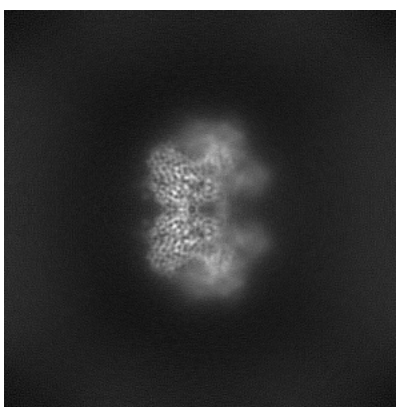


Z

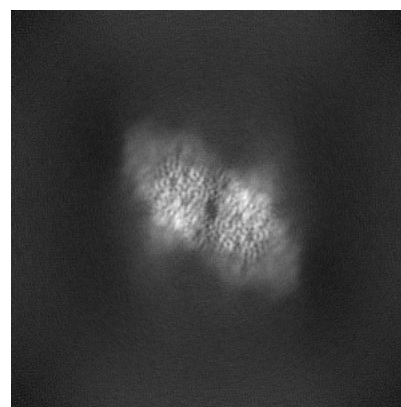
6.1.2 Raw map



X



Y

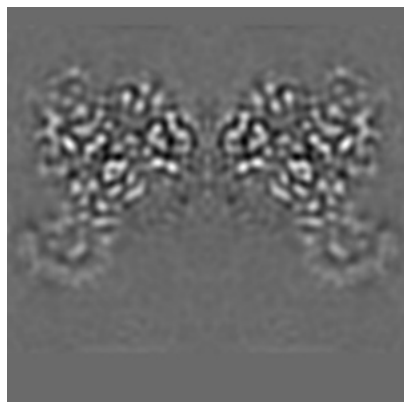


Z

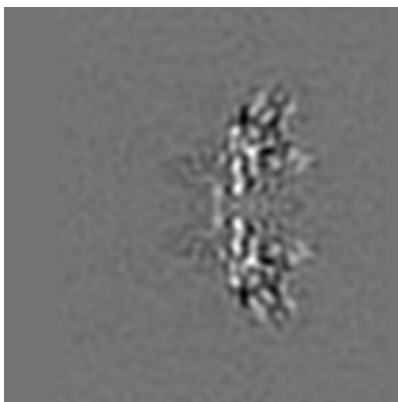
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

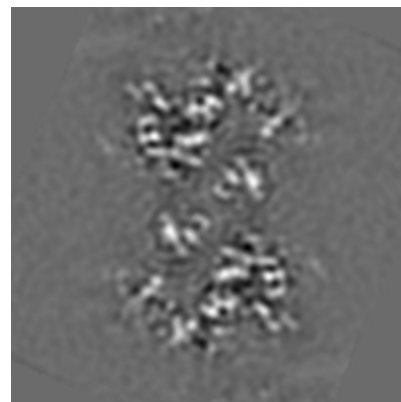
6.2.1 Primary map



X Index: 160



Y Index: 160

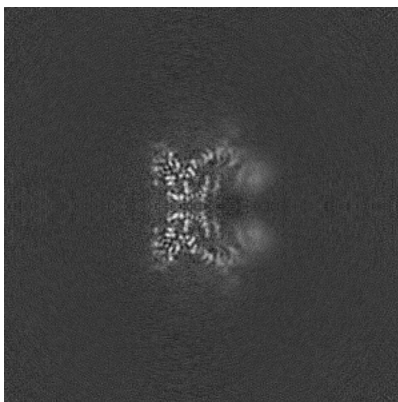


Z Index: 160

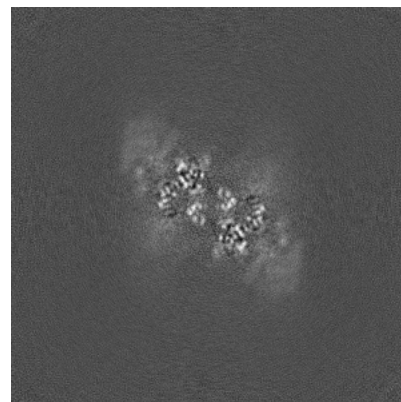
6.2.2 Raw map



X Index: 192



Y Index: 192

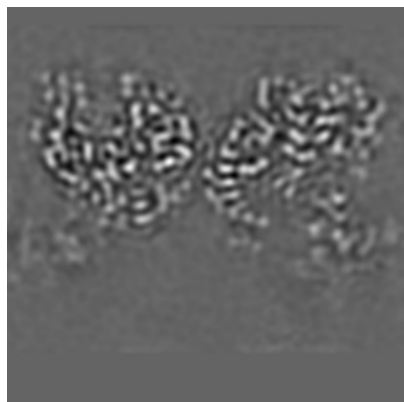


Z Index: 192

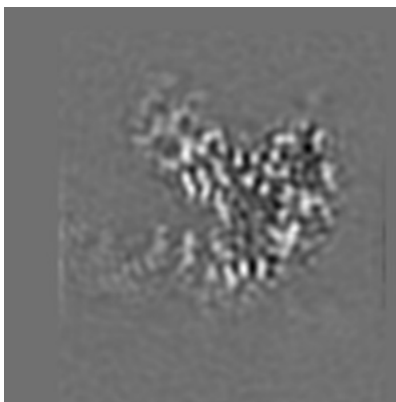
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

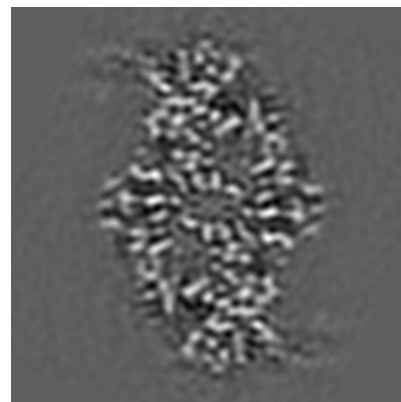
6.3.1 Primary map



X Index: 172

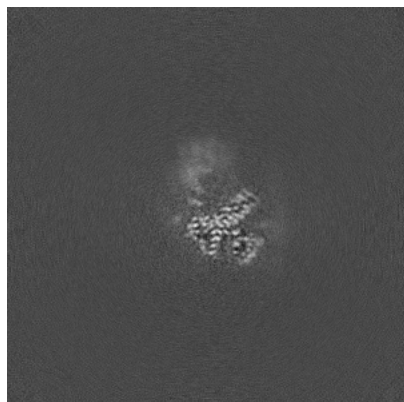


Y Index: 106

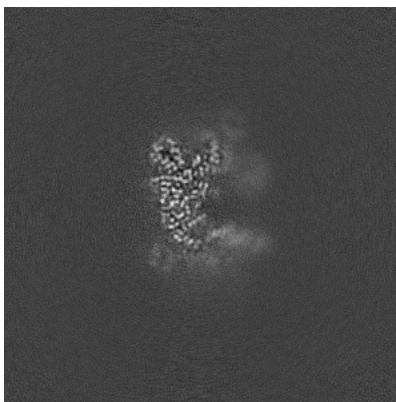


Z Index: 207

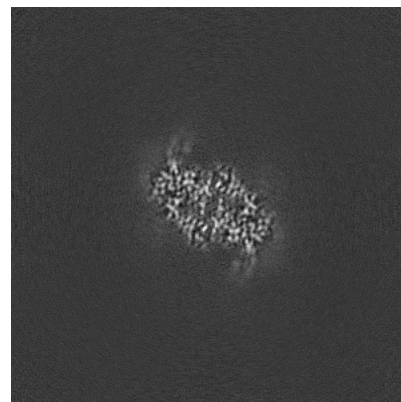
6.3.2 Raw map



X Index: 161



Y Index: 177

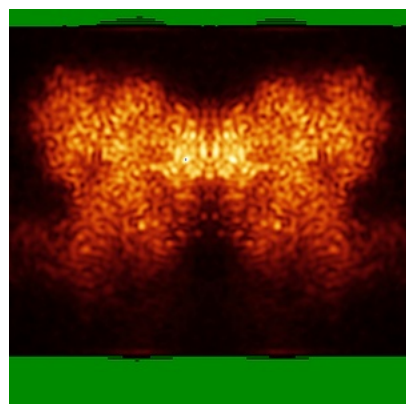


Z Index: 166

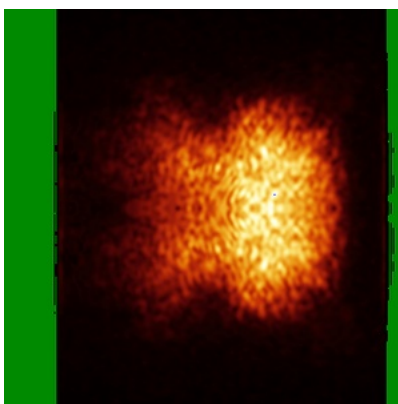
The images above show the largest variance slices of the map in three orthogonal directions.

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

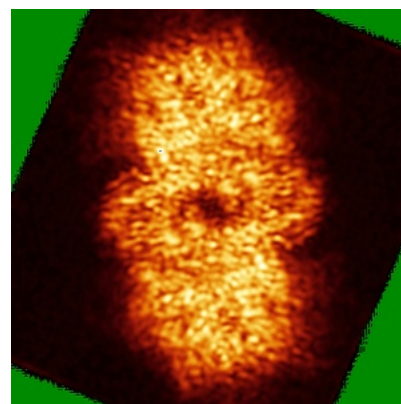
6.4.1 Primary map



X

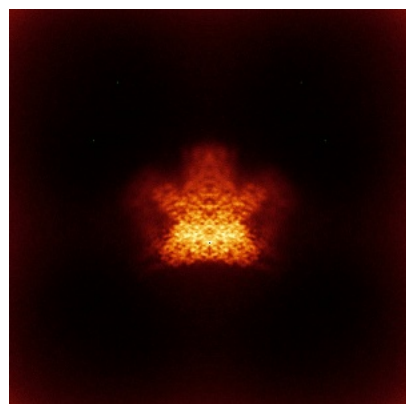


Y

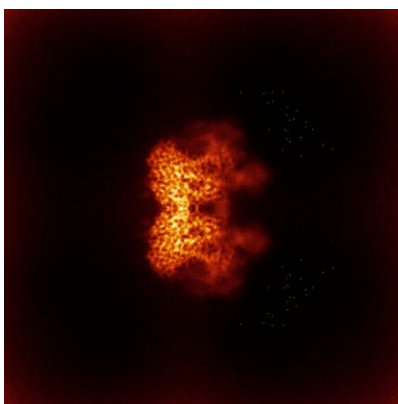


Z

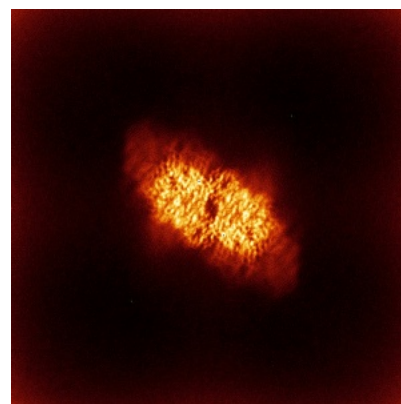
6.4.2 Raw map



X



Y



Z

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

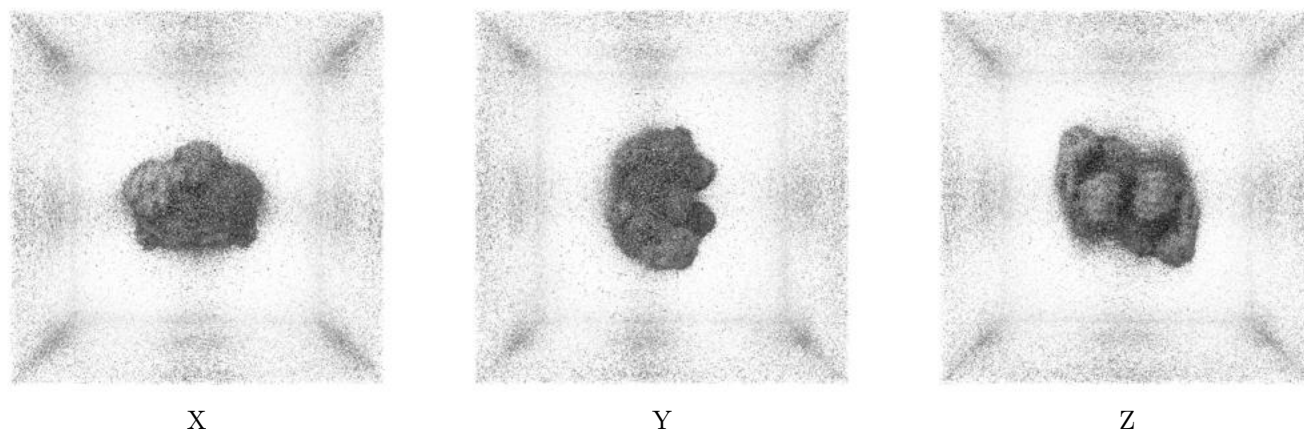
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

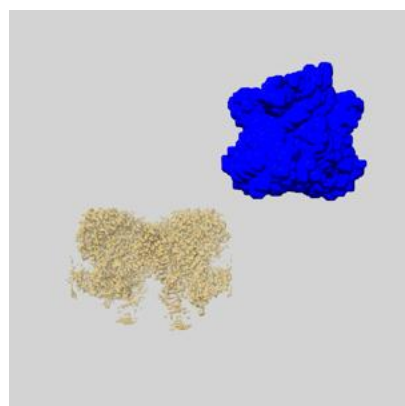
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

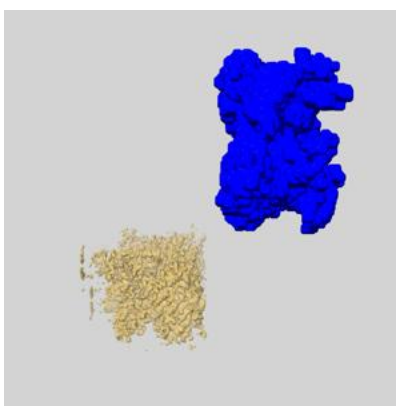
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

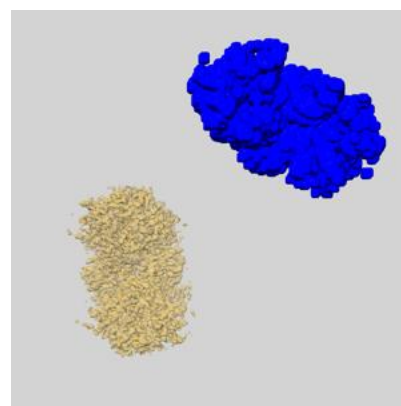
6.6.1 emd_29309_msk_1.map [i](#)



X



Y

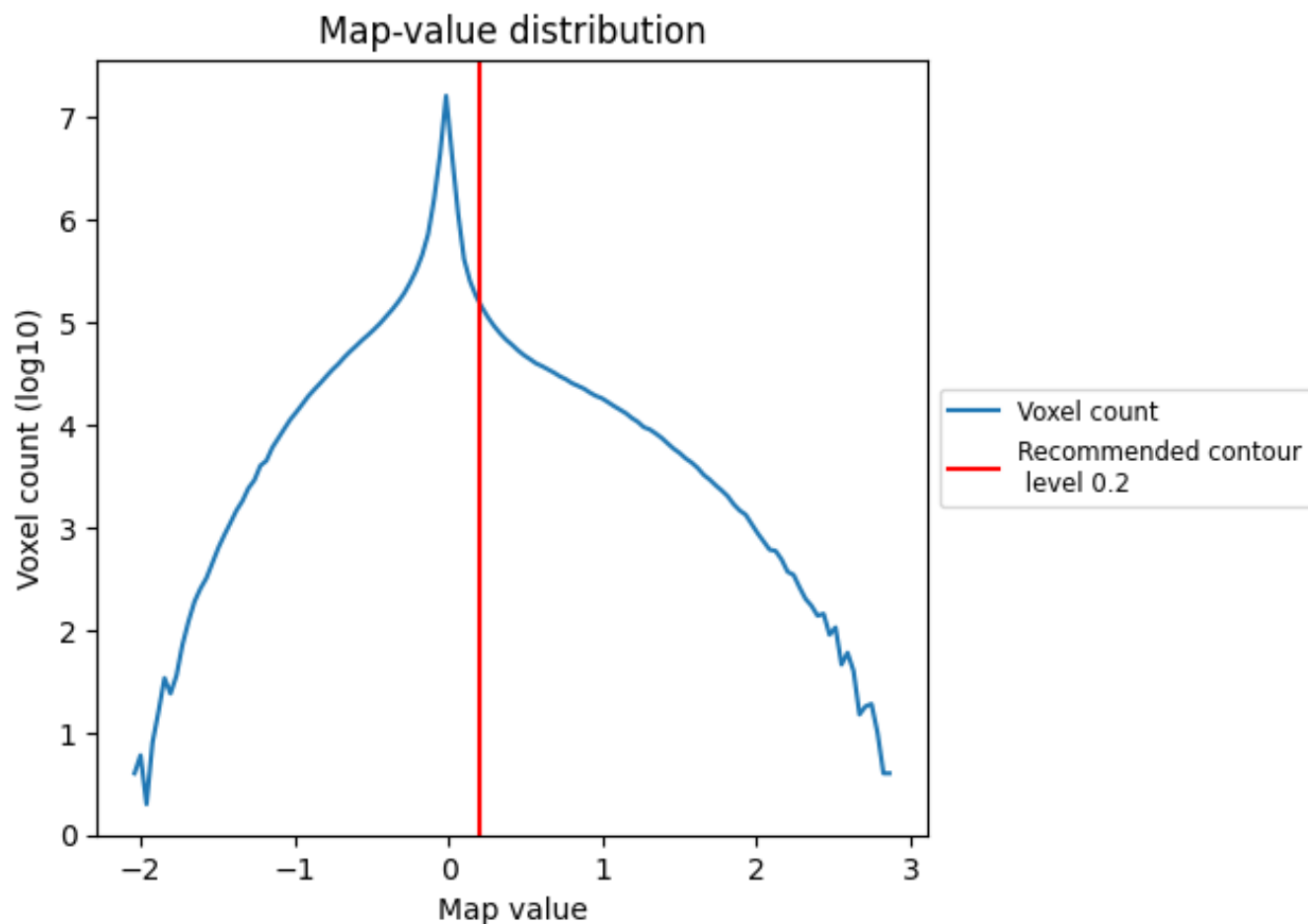


Z

7 Map analysis [i](#)

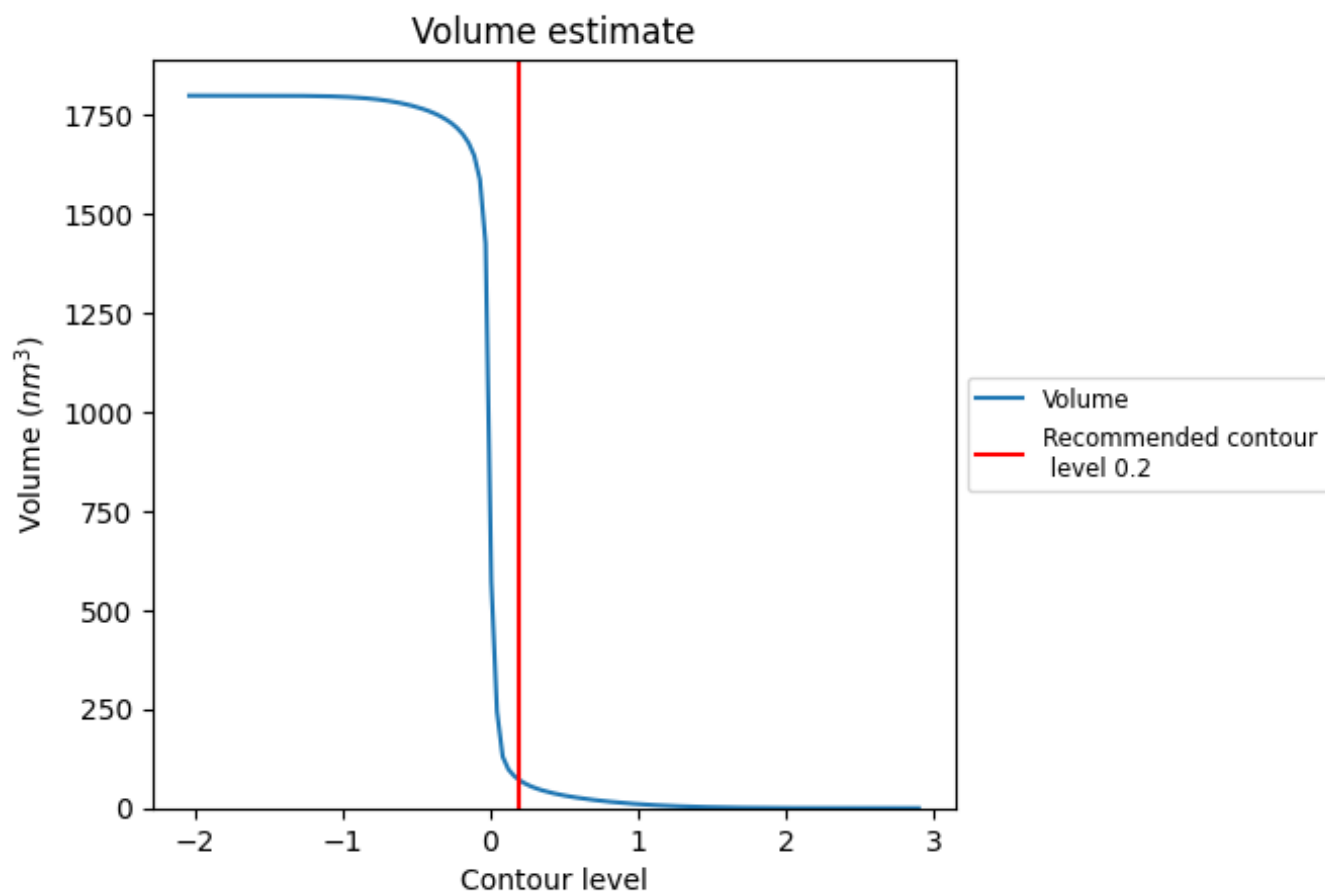
This section contains the results of statistical analysis of the map.

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.

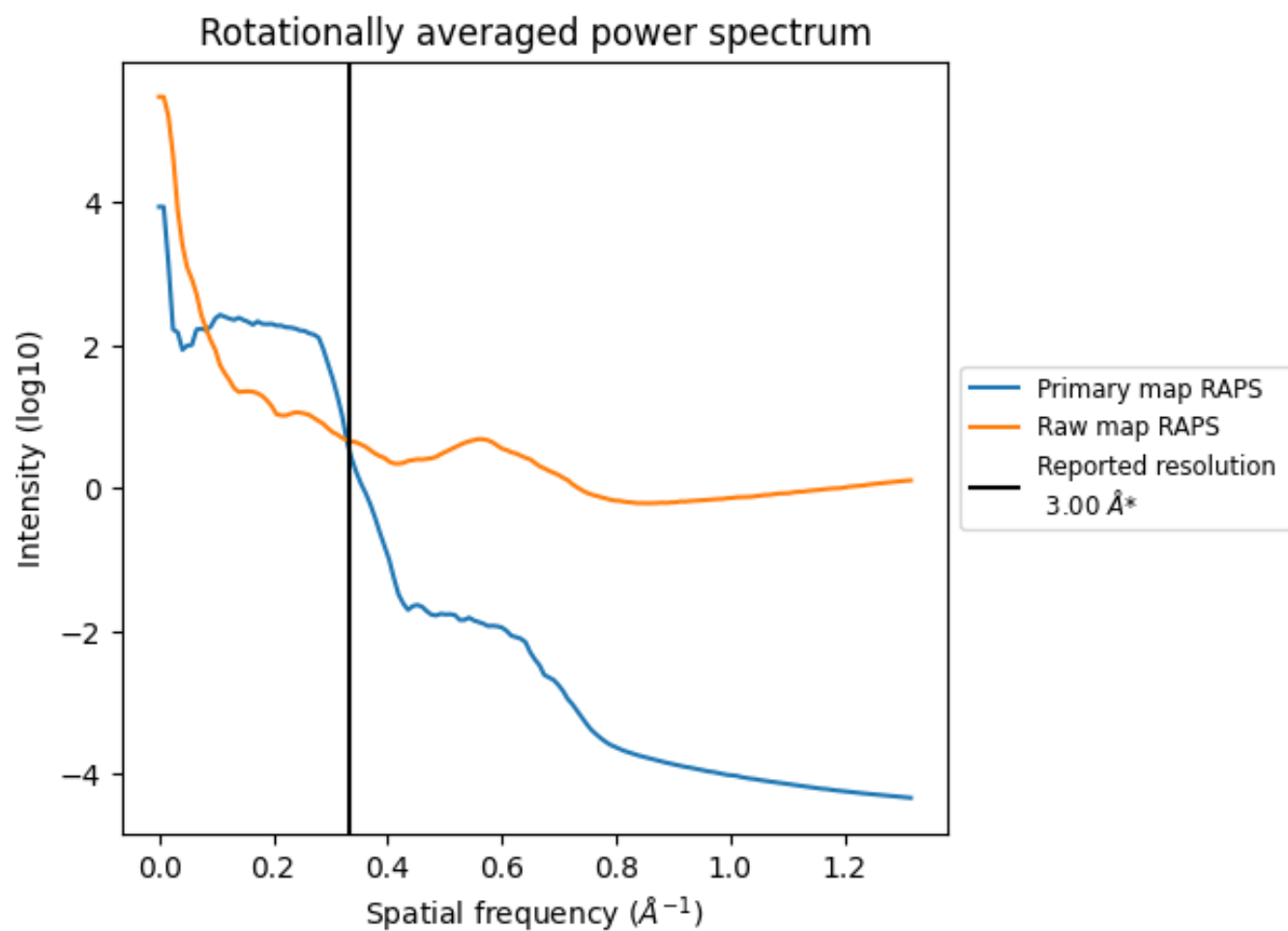
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 70 nm^3 ; this corresponds to an approximate mass of 63 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 ⓘ

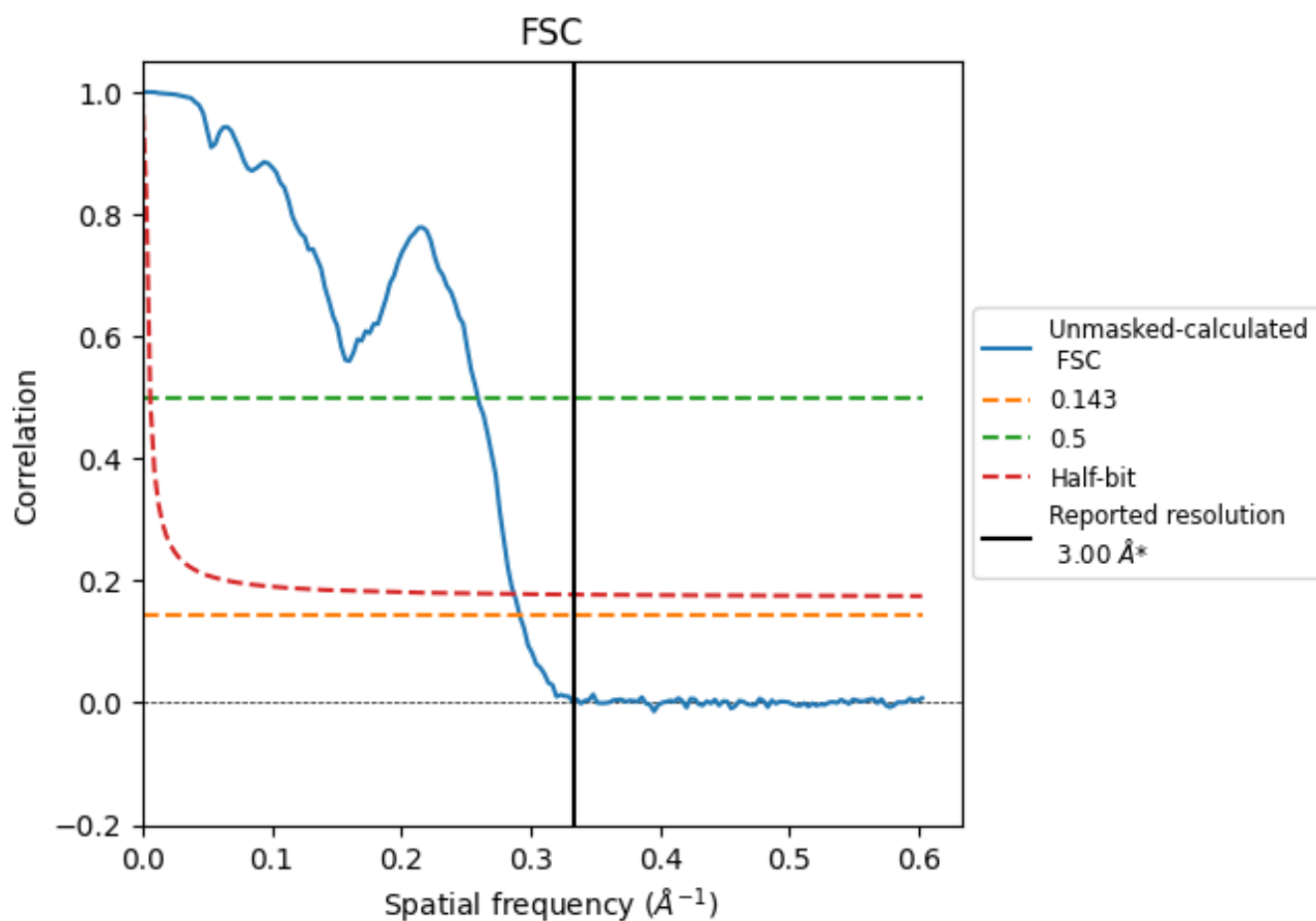


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

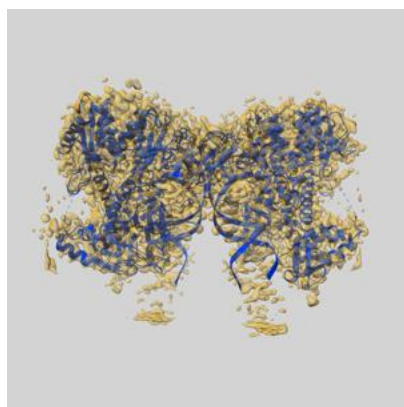
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.43	3.86	3.48

*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 3.43 differs from the reported value 3.0 by more than 10 %

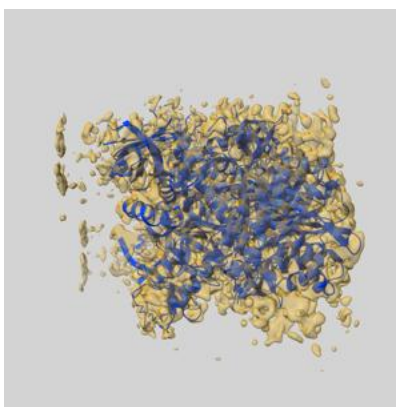
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29309 and PDB model 8FND. Per-residue inclusion information can be found in section 3 on page 12.

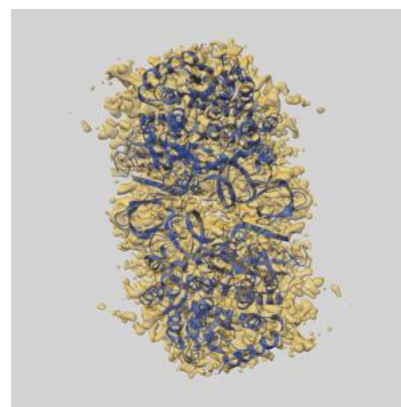
9.1 Map-model overlay [i](#)



X



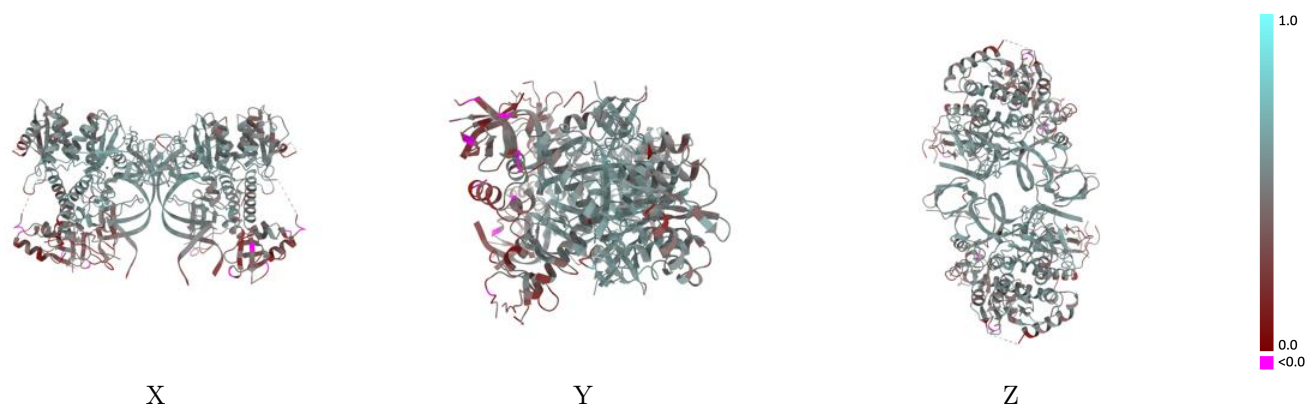
Y



Z

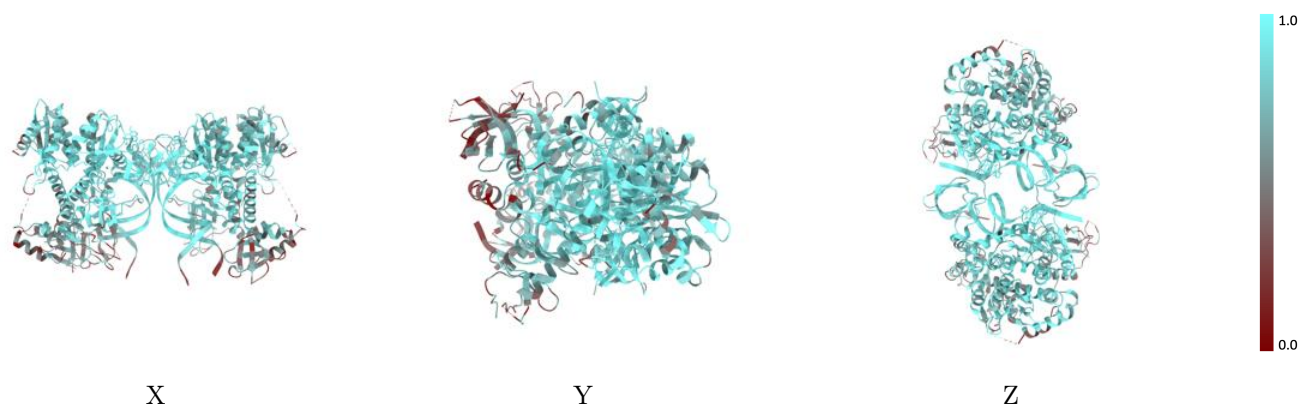
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



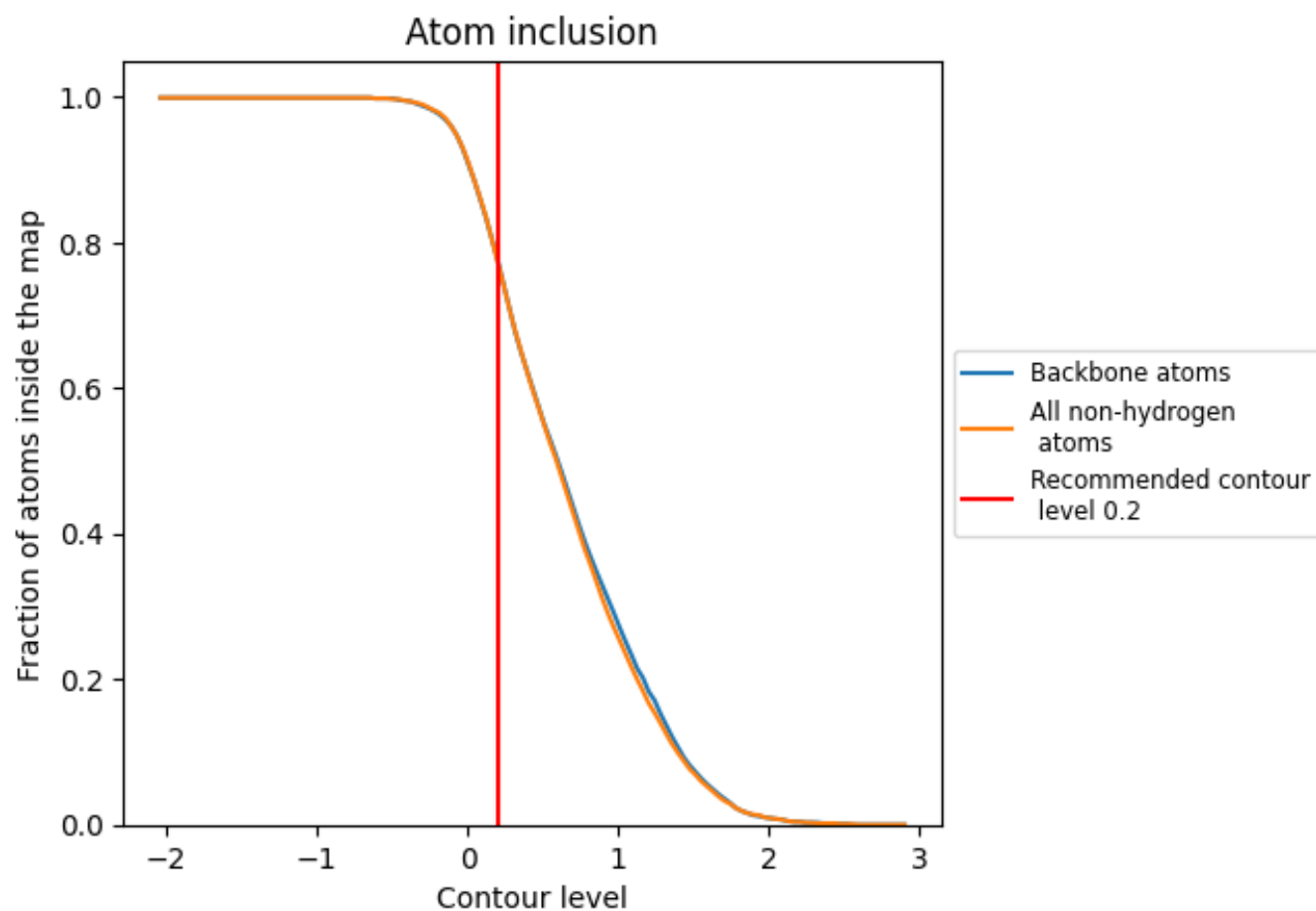
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 77% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7740	0.4800
A	0.8110	0.4960
B	0.6850	0.4250
C	0.8230	0.5060
D	0.8560	0.5300
E	0.8440	0.5310
F	0.7890	0.4980
G	0.8030	0.5000
H	0.7030	0.4330
I	0.8210	0.5130
J	0.8610	0.5230
K	0.8570	0.5290
L	0.8170	0.5070

