



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 04:45 AM UTC

PDB ID : 7QY3 / pdb_00007qy3
Title : Crystal structure of the halohydrin dehalogenase HheG D114C mutant cross-linked with BMOE
Authors : Henke, S.; Blankenfeldt, W.; Schallmeyer, A.
Deposited on : 2022-01-27
Resolution : 2.72 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

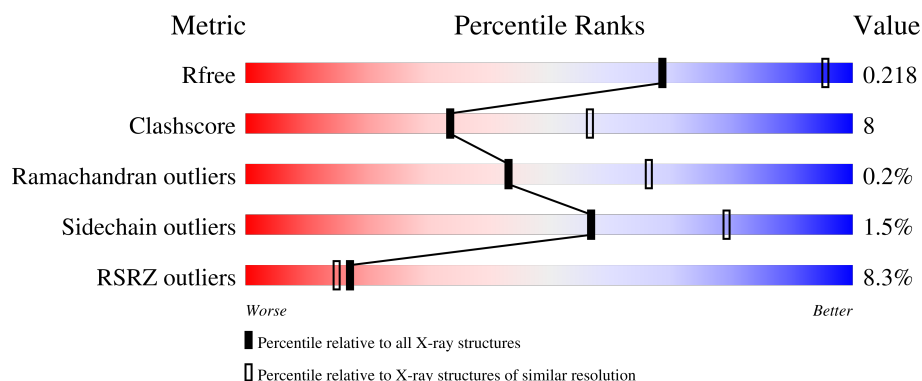
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.72 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (2.74-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	282	0.2% 76% 15% 9%
1	B	282	0.2% 80% 12% 9%
1	C	282	6% 73% 18% 9%
1	D	282	4% 79% 12% 9%
1	E	282	0.2% 82% 10% 9%

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Mol	Chain	Length	Quality of chain
1	F	282	
1	G	282	
1	H	282	
1	I	282	
1	J	282	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 19012 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Putative oxidoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	0	0
			1888	1176	338	360	14			
1	B	258	Total	C	N	O	S	0	1	0
			1905	1187	340	363	15			
1	C	257	Total	C	N	O	S	0	3	0
			1889	1176	334	365	14			
1	D	258	Total	C	N	O	S	0	2	0
			1895	1181	339	359	16			
1	E	258	Total	C	N	O	S	0	1	0
			1899	1182	339	363	15			
1	F	258	Total	C	N	O	S	0	0	0
			1896	1180	339	363	14			
1	G	254	Total	C	N	O	S	0	2	0
			1772	1105	319	334	14			
1	H	254	Total	C	N	O	S	0	0	0
			1815	1132	328	342	13			
1	I	257	Total	C	N	O	S	0	1	0
			1850	1147	334	355	14			
1	J	256	Total	C	N	O	S	0	0	0
			1812	1128	324	347	13			

There are 210 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A0A6C7EF96
A	-18	GLY	-	expression tag	UNP A0A6C7EF96
A	-17	SER	-	expression tag	UNP A0A6C7EF96
A	-16	SER	-	expression tag	UNP A0A6C7EF96
A	-15	HIS	-	expression tag	UNP A0A6C7EF96
A	-14	HIS	-	expression tag	UNP A0A6C7EF96
A	-13	HIS	-	expression tag	UNP A0A6C7EF96
A	-12	HIS	-	expression tag	UNP A0A6C7EF96
A	-11	HIS	-	expression tag	UNP A0A6C7EF96

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	HIS	-	expression tag	UNP A0A6C7EF96
A	-9	SER	-	expression tag	UNP A0A6C7EF96
A	-8	SER	-	expression tag	UNP A0A6C7EF96
A	-7	GLY	-	expression tag	UNP A0A6C7EF96
A	-6	LEU	-	expression tag	UNP A0A6C7EF96
A	-5	VAL	-	expression tag	UNP A0A6C7EF96
A	-4	PRO	-	expression tag	UNP A0A6C7EF96
A	-3	ARG	-	expression tag	UNP A0A6C7EF96
A	-2	GLY	-	expression tag	UNP A0A6C7EF96
A	-1	SER	-	expression tag	UNP A0A6C7EF96
A	0	HIS	-	expression tag	UNP A0A6C7EF96
A	114	CYS	ASP	engineered mutation	UNP A0A6C7EF96
B	-19	MET	-	initiating methionine	UNP A0A6C7EF96
B	-18	GLY	-	expression tag	UNP A0A6C7EF96
B	-17	SER	-	expression tag	UNP A0A6C7EF96
B	-16	SER	-	expression tag	UNP A0A6C7EF96
B	-15	HIS	-	expression tag	UNP A0A6C7EF96
B	-14	HIS	-	expression tag	UNP A0A6C7EF96
B	-13	HIS	-	expression tag	UNP A0A6C7EF96
B	-12	HIS	-	expression tag	UNP A0A6C7EF96
B	-11	HIS	-	expression tag	UNP A0A6C7EF96
B	-10	HIS	-	expression tag	UNP A0A6C7EF96
B	-9	SER	-	expression tag	UNP A0A6C7EF96
B	-8	SER	-	expression tag	UNP A0A6C7EF96
B	-7	GLY	-	expression tag	UNP A0A6C7EF96
B	-6	LEU	-	expression tag	UNP A0A6C7EF96
B	-5	VAL	-	expression tag	UNP A0A6C7EF96
B	-4	PRO	-	expression tag	UNP A0A6C7EF96
B	-3	ARG	-	expression tag	UNP A0A6C7EF96
B	-2	GLY	-	expression tag	UNP A0A6C7EF96
B	-1	SER	-	expression tag	UNP A0A6C7EF96
B	0	HIS	-	expression tag	UNP A0A6C7EF96
B	114	CYS	ASP	engineered mutation	UNP A0A6C7EF96
C	-19	MET	-	initiating methionine	UNP A0A6C7EF96
C	-18	GLY	-	expression tag	UNP A0A6C7EF96
C	-17	SER	-	expression tag	UNP A0A6C7EF96
C	-16	SER	-	expression tag	UNP A0A6C7EF96
C	-15	HIS	-	expression tag	UNP A0A6C7EF96
C	-14	HIS	-	expression tag	UNP A0A6C7EF96
C	-13	HIS	-	expression tag	UNP A0A6C7EF96
C	-12	HIS	-	expression tag	UNP A0A6C7EF96
C	-11	HIS	-	expression tag	UNP A0A6C7EF96

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-10	HIS	-	expression tag	UNP A0A6C7EF96
C	-9	SER	-	expression tag	UNP A0A6C7EF96
C	-8	SER	-	expression tag	UNP A0A6C7EF96
C	-7	GLY	-	expression tag	UNP A0A6C7EF96
C	-6	LEU	-	expression tag	UNP A0A6C7EF96
C	-5	VAL	-	expression tag	UNP A0A6C7EF96
C	-4	PRO	-	expression tag	UNP A0A6C7EF96
C	-3	ARG	-	expression tag	UNP A0A6C7EF96
C	-2	GLY	-	expression tag	UNP A0A6C7EF96
C	-1	SER	-	expression tag	UNP A0A6C7EF96
C	0	HIS	-	expression tag	UNP A0A6C7EF96
C	114	CYS	ASP	engineered mutation	UNP A0A6C7EF96
D	-19	MET	-	initiating methionine	UNP A0A6C7EF96
D	-18	GLY	-	expression tag	UNP A0A6C7EF96
D	-17	SER	-	expression tag	UNP A0A6C7EF96
D	-16	SER	-	expression tag	UNP A0A6C7EF96
D	-15	HIS	-	expression tag	UNP A0A6C7EF96
D	-14	HIS	-	expression tag	UNP A0A6C7EF96
D	-13	HIS	-	expression tag	UNP A0A6C7EF96
D	-12	HIS	-	expression tag	UNP A0A6C7EF96
D	-11	HIS	-	expression tag	UNP A0A6C7EF96
D	-10	HIS	-	expression tag	UNP A0A6C7EF96
D	-9	SER	-	expression tag	UNP A0A6C7EF96
D	-8	SER	-	expression tag	UNP A0A6C7EF96
D	-7	GLY	-	expression tag	UNP A0A6C7EF96
D	-6	LEU	-	expression tag	UNP A0A6C7EF96
D	-5	VAL	-	expression tag	UNP A0A6C7EF96
D	-4	PRO	-	expression tag	UNP A0A6C7EF96
D	-3	ARG	-	expression tag	UNP A0A6C7EF96
D	-2	GLY	-	expression tag	UNP A0A6C7EF96
D	-1	SER	-	expression tag	UNP A0A6C7EF96
D	0	HIS	-	expression tag	UNP A0A6C7EF96
D	114	CYS	ASP	engineered mutation	UNP A0A6C7EF96
E	-19	MET	-	initiating methionine	UNP A0A6C7EF96
E	-18	GLY	-	expression tag	UNP A0A6C7EF96
E	-17	SER	-	expression tag	UNP A0A6C7EF96
E	-16	SER	-	expression tag	UNP A0A6C7EF96
E	-15	HIS	-	expression tag	UNP A0A6C7EF96
E	-14	HIS	-	expression tag	UNP A0A6C7EF96
E	-13	HIS	-	expression tag	UNP A0A6C7EF96
E	-12	HIS	-	expression tag	UNP A0A6C7EF96
E	-11	HIS	-	expression tag	UNP A0A6C7EF96

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-10	HIS	-	expression tag	UNP A0A6C7EF96
E	-9	SER	-	expression tag	UNP A0A6C7EF96
E	-8	SER	-	expression tag	UNP A0A6C7EF96
E	-7	GLY	-	expression tag	UNP A0A6C7EF96
E	-6	LEU	-	expression tag	UNP A0A6C7EF96
E	-5	VAL	-	expression tag	UNP A0A6C7EF96
E	-4	PRO	-	expression tag	UNP A0A6C7EF96
E	-3	ARG	-	expression tag	UNP A0A6C7EF96
E	-2	GLY	-	expression tag	UNP A0A6C7EF96
E	-1	SER	-	expression tag	UNP A0A6C7EF96
E	0	HIS	-	expression tag	UNP A0A6C7EF96
E	114	CYS	ASP	engineered mutation	UNP A0A6C7EF96
F	-19	MET	-	initiating methionine	UNP A0A6C7EF96
F	-18	GLY	-	expression tag	UNP A0A6C7EF96
F	-17	SER	-	expression tag	UNP A0A6C7EF96
F	-16	SER	-	expression tag	UNP A0A6C7EF96
F	-15	HIS	-	expression tag	UNP A0A6C7EF96
F	-14	HIS	-	expression tag	UNP A0A6C7EF96
F	-13	HIS	-	expression tag	UNP A0A6C7EF96
F	-12	HIS	-	expression tag	UNP A0A6C7EF96
F	-11	HIS	-	expression tag	UNP A0A6C7EF96
F	-10	HIS	-	expression tag	UNP A0A6C7EF96
F	-9	SER	-	expression tag	UNP A0A6C7EF96
F	-8	SER	-	expression tag	UNP A0A6C7EF96
F	-7	GLY	-	expression tag	UNP A0A6C7EF96
F	-6	LEU	-	expression tag	UNP A0A6C7EF96
F	-5	VAL	-	expression tag	UNP A0A6C7EF96
F	-4	PRO	-	expression tag	UNP A0A6C7EF96
F	-3	ARG	-	expression tag	UNP A0A6C7EF96
F	-2	GLY	-	expression tag	UNP A0A6C7EF96
F	-1	SER	-	expression tag	UNP A0A6C7EF96
F	0	HIS	-	expression tag	UNP A0A6C7EF96
F	114	CYS	ASP	engineered mutation	UNP A0A6C7EF96
G	-19	MET	-	initiating methionine	UNP A0A6C7EF96
G	-18	GLY	-	expression tag	UNP A0A6C7EF96
G	-17	SER	-	expression tag	UNP A0A6C7EF96
G	-16	SER	-	expression tag	UNP A0A6C7EF96
G	-15	HIS	-	expression tag	UNP A0A6C7EF96
G	-14	HIS	-	expression tag	UNP A0A6C7EF96
G	-13	HIS	-	expression tag	UNP A0A6C7EF96
G	-12	HIS	-	expression tag	UNP A0A6C7EF96
G	-11	HIS	-	expression tag	UNP A0A6C7EF96

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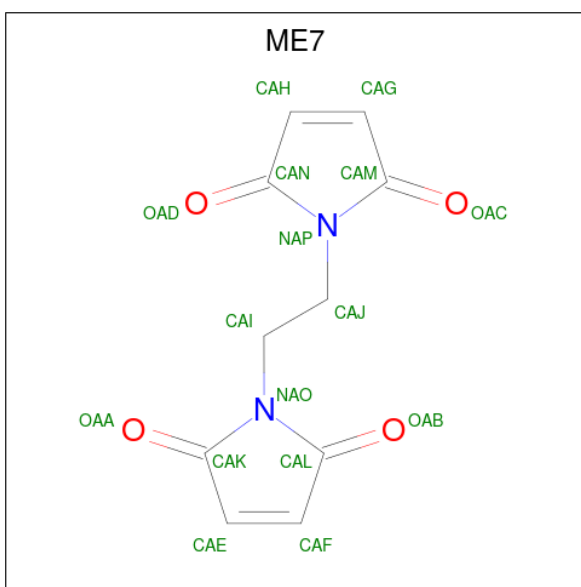
Chain	Residue	Modelled	Actual	Comment	Reference
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G	-9	SER	-	expression tag	UNP A0A6C7EF96
G	-8	SER	-	expression tag	UNP A0A6C7EF96
G	-7	GLY	-	expression tag	UNP A0A6C7EF96
G	-6	LEU	-	expression tag	UNP A0A6C7EF96
G	-5	VAL	-	expression tag	UNP A0A6C7EF96
G	-4	PRO	-	expression tag	UNP A0A6C7EF96
G	-3	ARG	-	expression tag	UNP A0A6C7EF96
G	-2	GLY	-	expression tag	UNP A0A6C7EF96
G	-1	SER	-	expression tag	UNP A0A6C7EF96
G	0	HIS	-	expression tag	UNP A0A6C7EF96
G	114	CYS	ASP	engineered mutation	UNP A0A6C7EF96
H	-19	MET	-	initiating methionine	UNP A0A6C7EF96
H	-18	GLY	-	expression tag	UNP A0A6C7EF96
H	-17	SER	-	expression tag	UNP A0A6C7EF96
H	-16	SER	-	expression tag	UNP A0A6C7EF96
H	-15	HIS	-	expression tag	UNP A0A6C7EF96
H	-14	HIS	-	expression tag	UNP A0A6C7EF96
H	-13	HIS	-	expression tag	UNP A0A6C7EF96
H	-12	HIS	-	expression tag	UNP A0A6C7EF96
H	-11	HIS	-	expression tag	UNP A0A6C7EF96
H	-10	HIS	-	expression tag	UNP A0A6C7EF96
H	-9	SER	-	expression tag	UNP A0A6C7EF96
H	-8	SER	-	expression tag	UNP A0A6C7EF96
H	-7	GLY	-	expression tag	UNP A0A6C7EF96
H	-6	LEU	-	expression tag	UNP A0A6C7EF96
H	-5	VAL	-	expression tag	UNP A0A6C7EF96
H	-4	PRO	-	expression tag	UNP A0A6C7EF96
H	-3	ARG	-	expression tag	UNP A0A6C7EF96
H	-2	GLY	-	expression tag	UNP A0A6C7EF96
H	-1	SER	-	expression tag	UNP A0A6C7EF96
H	0	HIS	-	expression tag	UNP A0A6C7EF96
H	114	CYS	ASP	engineered mutation	UNP A0A6C7EF96
I	-19	MET	-	initiating methionine	UNP A0A6C7EF96
I	-18	GLY	-	expression tag	UNP A0A6C7EF96
I	-17	SER	-	expression tag	UNP A0A6C7EF96
I	-16	SER	-	expression tag	UNP A0A6C7EF96
I	-15	HIS	-	expression tag	UNP A0A6C7EF96
I	-14	HIS	-	expression tag	UNP A0A6C7EF96
I	-13	HIS	-	expression tag	UNP A0A6C7EF96
I	-12	HIS	-	expression tag	UNP A0A6C7EF96
I	-11	HIS	-	expression tag	UNP A0A6C7EF96

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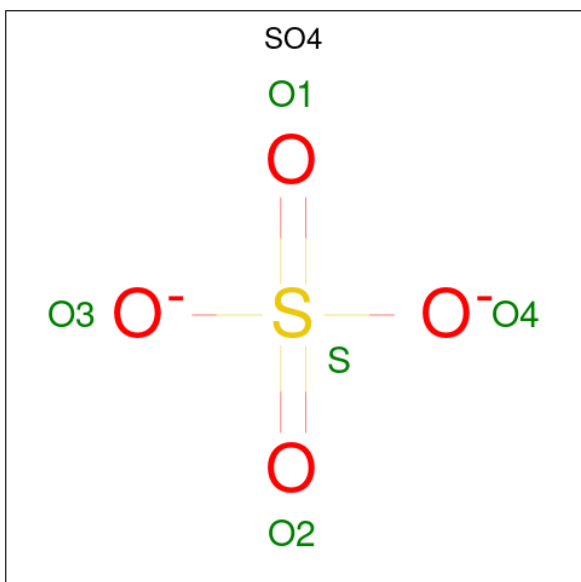
Chain	Residue	Modelled	Actual	Comment	Reference
I	-10	HIS	-	expression tag	UNP A0A6C7EF96
I	-9	SER	-	expression tag	UNP A0A6C7EF96
I	-8	SER	-	expression tag	UNP A0A6C7EF96
I	-7	GLY	-	expression tag	UNP A0A6C7EF96
I	-6	LEU	-	expression tag	UNP A0A6C7EF96
I	-5	VAL	-	expression tag	UNP A0A6C7EF96
I	-4	PRO	-	expression tag	UNP A0A6C7EF96
I	-3	ARG	-	expression tag	UNP A0A6C7EF96
I	-2	GLY	-	expression tag	UNP A0A6C7EF96
I	-1	SER	-	expression tag	UNP A0A6C7EF96
I	0	HIS	-	expression tag	UNP A0A6C7EF96
I	114	CYS	ASP	engineered mutation	UNP A0A6C7EF96
J	-19	MET	-	initiating methionine	UNP A0A6C7EF96
J	-18	GLY	-	expression tag	UNP A0A6C7EF96
J	-17	SER	-	expression tag	UNP A0A6C7EF96
J	-16	SER	-	expression tag	UNP A0A6C7EF96
J	-15	HIS	-	expression tag	UNP A0A6C7EF96
J	-14	HIS	-	expression tag	UNP A0A6C7EF96
J	-13	HIS	-	expression tag	UNP A0A6C7EF96
J	-12	HIS	-	expression tag	UNP A0A6C7EF96
J	-11	HIS	-	expression tag	UNP A0A6C7EF96
J	-10	HIS	-	expression tag	UNP A0A6C7EF96
J	-9	SER	-	expression tag	UNP A0A6C7EF96
J	-8	SER	-	expression tag	UNP A0A6C7EF96
J	-7	GLY	-	expression tag	UNP A0A6C7EF96
J	-6	LEU	-	expression tag	UNP A0A6C7EF96
J	-5	VAL	-	expression tag	UNP A0A6C7EF96
J	-4	PRO	-	expression tag	UNP A0A6C7EF96
J	-3	ARG	-	expression tag	UNP A0A6C7EF96
J	-2	GLY	-	expression tag	UNP A0A6C7EF96
J	-1	SER	-	expression tag	UNP A0A6C7EF96
J	0	HIS	-	expression tag	UNP A0A6C7EF96
J	114	CYS	ASP	engineered mutation	UNP A0A6C7EF96

- Molecule 2 is 1,1'-ethane-1,2-diylbis(1H-pyrrole-2,5-dione) (CCD ID: ME7) (formula: C₁₀H₈N₂O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			16	10	2	4		
2	B	1	Total	C	N	O	0	0
			16	10	2	4		
2	G	1	Total	C	N	O	0	0
			16	10	2	4		
2	H	1	Total	C	N	O	0	0
			16	10	2	4		
2	I	1	Total	C	N	O	0	0
			16	10	2	4		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	E	1	Total O S 5 4 1	0	0
3	E	1	Total O S 5 4 1	0	0
3	E	1	Total O S 5 4 1	0	0
3	E	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0
3	G	1	Total O S 5 4 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		

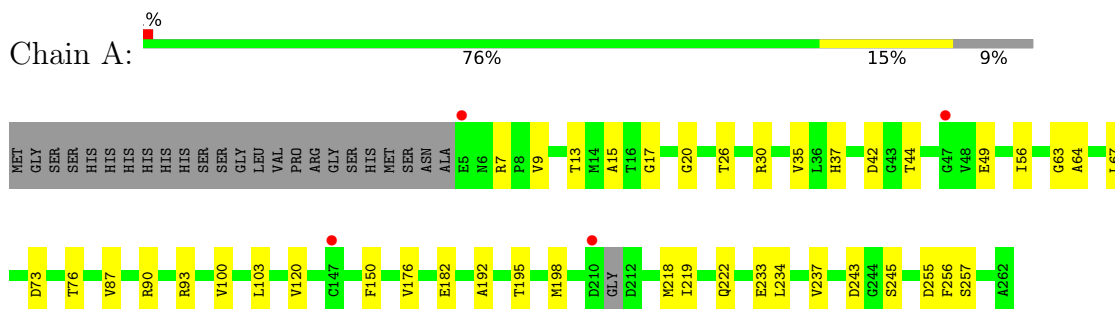
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	29	Total	O	0	0
			29	29		
4	B	19	Total	O	0	0
			19	19		
4	C	13	Total	O	0	0
			13	13		
4	D	21	Total	O	0	0
			21	21		
4	E	25	Total	O	0	0
			25	25		
4	F	29	Total	O	0	0
			29	29		
4	G	5	Total	O	0	0
			5	5		
4	H	2	Total	O	0	0
			2	2		
4	I	10	Total	O	0	0
			10	10		
4	J	3	Total	O	0	0
			3	3		

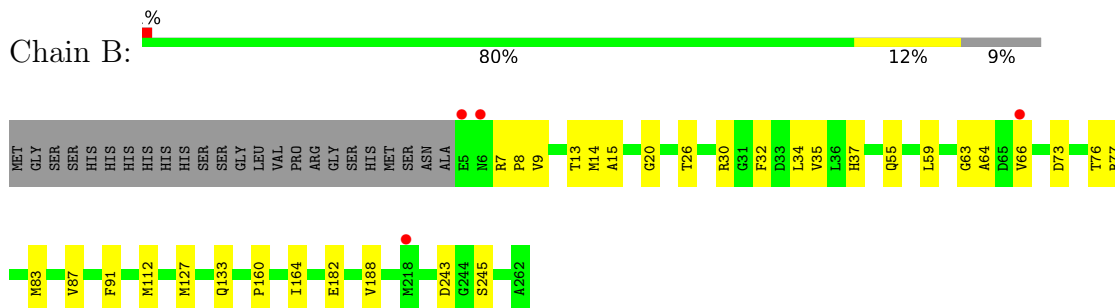
3 Residue-property plots

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

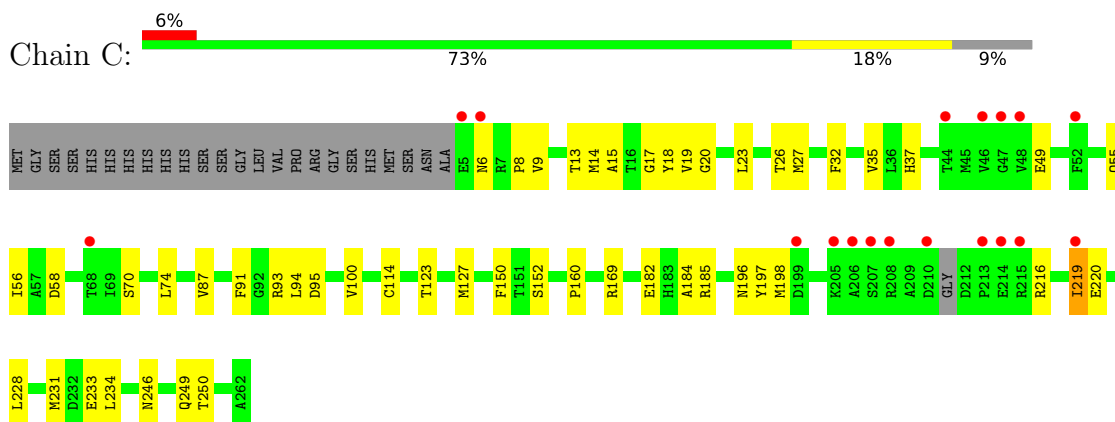
- Molecule 1: Putative oxidoreductase



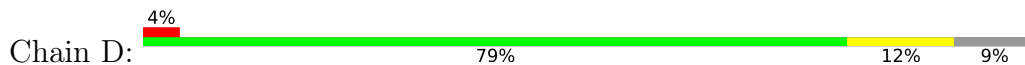
- Molecule 1: Putative oxidoreductase

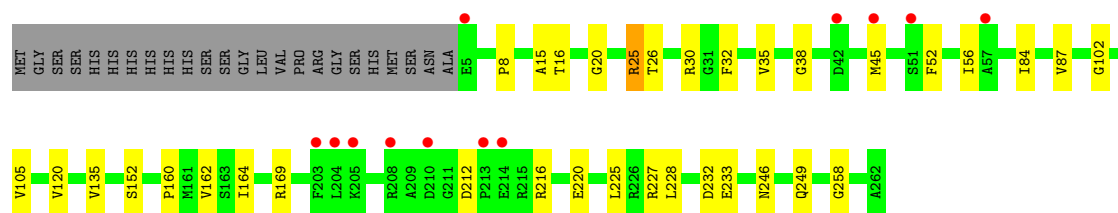


- Molecule 1: Putative oxidoreductase

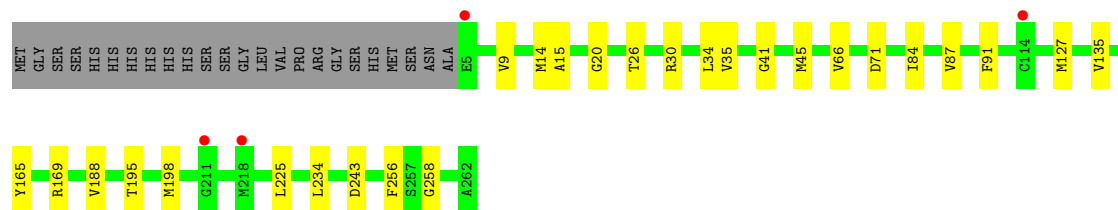
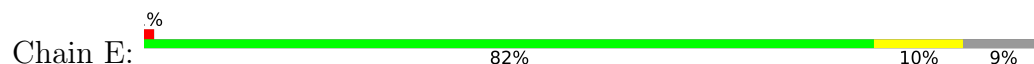


- Molecule 1: Putative oxidoreductase

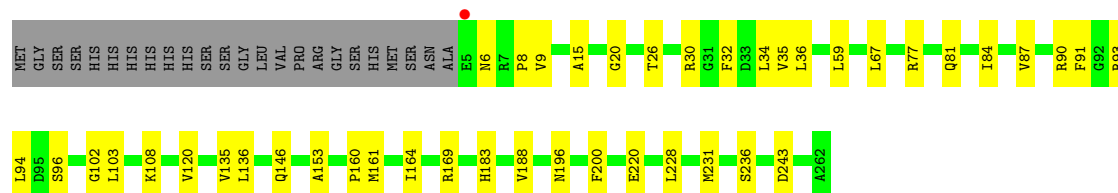
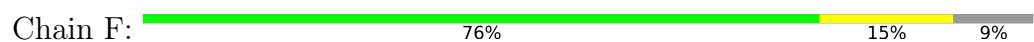




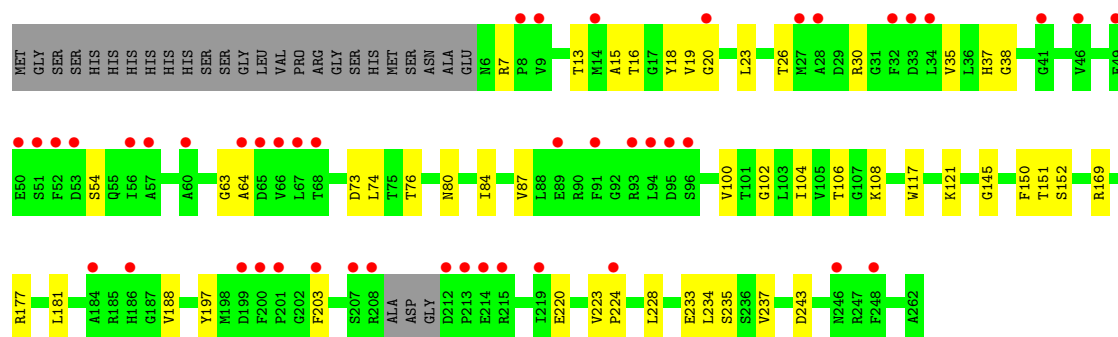
● Molecule 1: Putative oxidoreductase



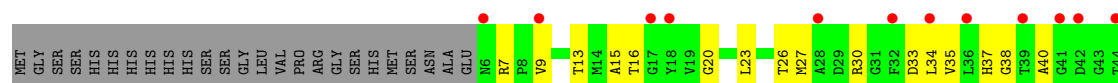
● Molecule 1: Putative oxidoreductase

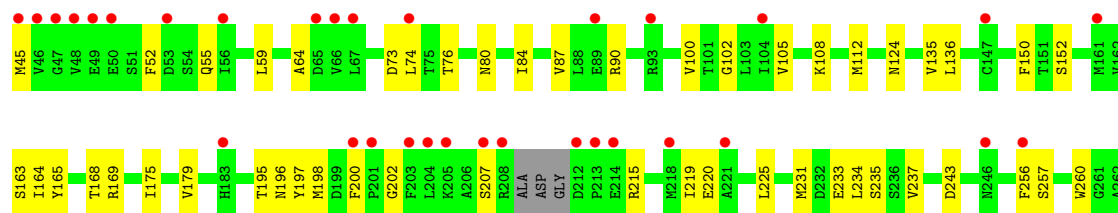


● Molecule 1: Putative oxidoreductase

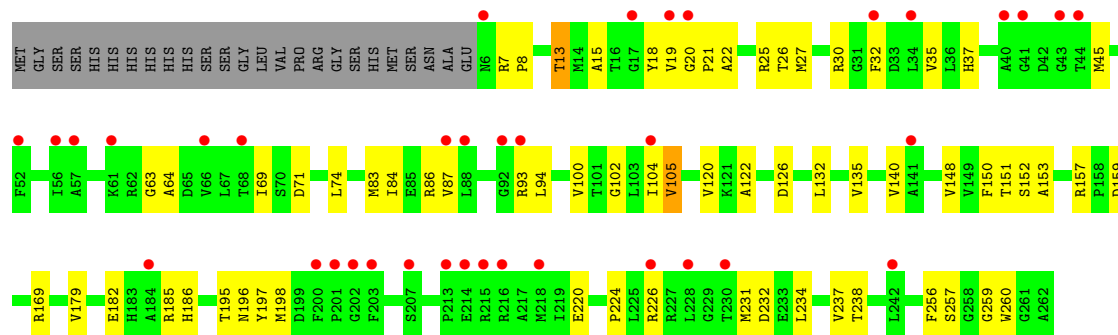


● Molecule 1: Putative oxidoreductase

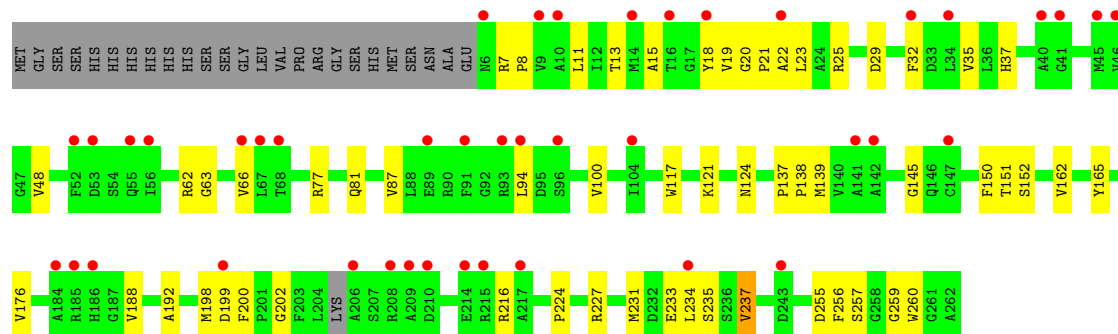




● Molecule 1: Putative oxidoreductase



● Molecule 1: Putative oxidoreductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	195.08Å 195.08Å 195.06Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	56.31 – 2.72 56.31 – 2.73	Depositor EDS
% Data completeness (in resolution range)	99.9 (56.31-2.72) 99.9 (56.31-2.73)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 2.73Å)	Xtriage
Refinement program	PHENIX 1.20-4459	Depositor
R, R_{free}	0.211 , 0.252 0.216 , 0.218	Depositor DCC
R_{free} test set	5589 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	57.3	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 54.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19012	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ME7, SO4

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	0.10	0/1918	0.30	0/2596
1	B	0.11	0/1939	0.29	0/2623
1	C	0.14	0/1928	0.35	0/2614
1	D	0.10	0/1932	0.30	0/2616
1	E	0.10	0/1933	0.28	0/2617
1	F	0.10	0/1927	0.29	0/2609
1	G	0.11	0/1806	0.31	0/2456
1	H	0.12	0/1844	0.33	0/2502
1	I	0.12	0/1884	0.31	0/2556
1	J	0.12	0/1842	0.31	0/2501
All	All	0.11	0/18953	0.31	0/25690

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

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	1888	0	1849	27	0
1	B	1905	0	1877	22	0
1	C	1889	0	1837	31	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1895	0	1862	22	0
1	E	1899	0	1863	15	0
1	F	1896	0	1857	22	0
1	G	1772	0	1667	28	0
1	H	1815	0	1745	44	0
1	I	1850	0	1763	41	0
1	J	1812	0	1705	36	0
2	A	16	0	7	0	1
2	B	16	0	7	0	0
2	G	16	0	7	0	0
2	H	16	0	7	0	0
2	I	16	0	8	0	0
3	A	25	0	0	0	0
3	B	15	0	0	0	0
3	C	15	0	0	0	0
3	D	15	0	0	0	0
3	E	20	0	0	0	0
3	F	15	0	0	0	0
3	G	15	0	0	0	0
3	H	10	0	0	0	0
3	I	15	0	0	0	0
3	J	10	0	0	0	0
4	A	29	0	0	0	0
4	B	19	0	0	0	0
4	C	13	0	0	0	0
4	D	21	0	0	1	0
4	E	25	0	0	0	0
4	F	29	0	0	0	0
4	G	5	0	0	0	0
4	H	2	0	0	0	0
4	I	10	0	0	1	0
4	J	3	0	0	0	0
All	All	19012	0	18061	283	1

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 8.

All (283) 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:H:198:MET:HE2	1:H:234:LEU:HD12	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:198:MET:HE2	1:I:234:LEU:HD12	1.55	0.87
1:G:30:ARG:NH1	1:G:243:ASP:OD2	2.10	0.83
1:J:22:ALA:HA	1:J:25:ARG:HD2	1.61	0.82
1:J:150:PHE:HZ	1:J:234:LEU:HD21	1.50	0.76
1:I:195:THR:HG21	1:I:234:LEU:HD11	1.68	0.75
1:I:7:ARG:NH1	1:I:63:GLY:O	2.20	0.73
1:B:182:GLU:HG3	1:C:160:PRO:HB3	1.71	0.72
1:A:218:MET:HE2	1:A:219:ILE:HD13	1.73	0.71
1:B:77:ARG:NH1	1:B:133:GLN:OE1	2.23	0.71
1:J:137:PRO:HG2	1:J:138:PRO:HD3	1.74	0.69
1:H:200:PHE:HB3	1:H:231:MET:HE3	1.75	0.69
1:I:195:THR:HG22	1:I:256:PHE:HB3	1.75	0.68
1:C:56:ILE:H	1:C:56:ILE:HD12	1.58	0.68
1:H:207:SER:O	1:H:215:ARG:NH1	2.26	0.68
1:G:7:ARG:NH1	1:G:63:GLY:O	2.28	0.67
1:H:124:ASN:HD21	1:H:165:TYR:HD1	1.42	0.66
1:B:35:VAL:HG11	1:B:87:VAL:HG22	1.78	0.65
1:I:15:ALA:HA	1:I:20:GLY:HA3	1.77	0.65
1:F:200:PHE:HB3	1:F:231:MET:HE3	1.79	0.65
1:C:19:VAL:HG22	1:C:23:LEU:HB2	1.79	0.64
1:D:227:ARG:NH2	1:D:233:GLU:OE1	2.30	0.64
1:I:69:ILE:HD12	1:I:83:MET:HG3	1.79	0.64
1:H:35:VAL:HG21	1:H:87:VAL:HG22	1.80	0.64
1:B:160:PRO:HB3	1:C:182:GLU:HG3	1.80	0.63
1:G:35:VAL:HG11	1:G:87:VAL:HG23	1.80	0.63
1:D:56:ILE:HD12	1:D:56:ILE:H	1.64	0.63
1:A:7:ARG:NH2	1:A:64:ALA:HA	2.14	0.62
1:B:7:ARG:NH1	1:B:63:GLY:O	2.34	0.61
1:G:104:ILE:HD11	1:G:106:THR:HG23	1.81	0.61
1:I:19:VAL:HA	1:I:231:MET:HE2	1.81	0.61
1:J:150:PHE:CZ	1:J:234:LEU:HD21	2.35	0.61
1:J:19:VAL:HB	1:J:234:LEU:HD13	1.83	0.61
1:B:55:GLN:O	1:B:59:LEU:HG	2.00	0.61
1:A:26:THR:O	1:A:30:ARG:HD2	2.01	0.60
1:G:150:PHE:CE2	1:G:234:LEU:HD21	2.36	0.60
1:H:15:ALA:HA	1:H:20:GLY:HA3	1.82	0.60
1:I:257:SER:HB2	1:I:260:TRP:HB3	1.83	0.60
1:F:35:VAL:HG11	1:F:87:VAL:HG22	1.84	0.60
1:D:220:GLU:HG2	1:D:228:LEU:HD13	1.82	0.60
1:H:7:ARG:HH12	1:H:64:ALA:HA	1.67	0.59
1:G:150:PHE:HE2	1:G:234:LEU:HD21	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:139:MET:HB3	1:J:188:VAL:HG11	1.84	0.59
1:H:195:THR:HG21	1:H:234:LEU:HD11	1.84	0.59
1:J:15:ALA:N	1:J:37:HIS:O	2.31	0.59
1:J:117:TRP:CE2	1:J:121:LYS:HD2	2.38	0.58
1:H:16:THR:HG23	1:H:38:GLY:HA3	1.85	0.58
1:H:26:THR:HG22	1:H:30:ARG:HE	1.68	0.58
1:H:237:VAL:HG21	1:H:256:PHE:HE2	1.68	0.58
1:B:7:ARG:HH12	1:B:64:ALA:HA	1.68	0.58
1:D:25:ARG:NH1	4:D:401:HOH:O	2.36	0.58
1:G:220:GLU:HG3	1:G:228:LEU:HD13	1.85	0.58
1:G:7:ARG:HH12	1:G:64:ALA:HA	1.67	0.57
1:H:30:ARG:NH1	1:H:243:ASP:OD2	2.37	0.57
1:J:19:VAL:HG22	1:J:23:LEU:HB2	1.85	0.57
1:A:35:VAL:HG11	1:A:87:VAL:HG22	1.87	0.57
1:H:74:LEU:HD12	1:H:74:LEU:H	1.70	0.57
1:J:87:VAL:HG11	1:J:94:LEU:HD13	1.85	0.57
1:C:220:GLU:HG2	1:C:228:LEU:HD13	1.87	0.56
1:F:26:THR:O	1:F:30:ARG:HG2	2.04	0.56
1:A:67:LEU:HD12	1:A:90:ARG:HB2	1.88	0.56
1:J:124:ASN:HD21	1:J:165:TYR:HD1	1.50	0.56
1:D:26:THR:O	1:D:30:ARG:HG2	2.05	0.56
1:I:7:ARG:HH12	1:I:64:ALA:HA	1.71	0.56
1:H:74:LEU:O	1:H:80:ASN:ND2	2.37	0.55
1:J:77:ARG:HE	1:J:81:GLN:HG3	1.71	0.55
1:F:108:LYS:HG2	1:F:161:MET:HE1	1.89	0.55
1:B:14:MET:HE3	1:B:127:MET:HE1	1.89	0.55
1:G:15:ALA:HA	1:G:20:GLY:HA3	1.89	0.54
1:G:151:THR:OG1	1:G:152:SER:N	2.40	0.54
1:H:37:HIS:NE2	1:H:74:LEU:HD11	2.23	0.54
1:J:29:ASP:OD1	1:J:62:ARG:HD3	2.08	0.53
1:I:18:TYR:HH	1:I:195:THR:HG1	1.56	0.53
1:D:35:VAL:HG11	1:D:87:VAL:HG22	1.89	0.53
1:E:14:MET:HE3	1:E:127:MET:HE1	1.90	0.53
1:F:8:PRO:HA	1:F:93:ARG:HH11	1.72	0.53
1:G:18:TYR:CD2	1:G:19:VAL:HG12	2.43	0.53
1:A:198:MET:HE2	1:A:234:LEU:HD22	1.91	0.53
1:I:35:VAL:HG11	1:I:87:VAL:HG22	1.90	0.53
1:D:15:ALA:HA	1:D:20:GLY:HA3	1.91	0.52
1:C:8:PRO:HB2	1:C:32:PHE:CE2	2.45	0.52
1:I:151:THR:OG1	1:I:152:SER:N	2.43	0.52
1:A:13:THR:HA	1:A:37:HIS:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:184:ALA:HB2	1:C:250:THR:HG21	1.92	0.52
1:H:55:GLN:O	1:H:59:LEU:HD23	2.10	0.52
1:J:13:THR:HA	1:J:37:HIS:HB3	1.91	0.52
1:G:73:ASP:OD2	1:G:76:THR:HG23	2.10	0.51
1:J:151:THR:OG1	1:J:152:SER:N	2.39	0.51
1:H:257:SER:HB2	1:H:260:TRP:HB3	1.91	0.51
1:C:17:GLY:HA2	1:C:49:GLU:OE2	2.09	0.51
1:I:132:LEU:HD13	1:I:179:VAL:HG11	1.91	0.51
1:J:227:ARG:HH22	1:J:233:GLU:CD	2.18	0.51
1:H:215:ARG:O	1:H:219:ILE:HG12	2.10	0.51
1:I:84:ILE:HD11	1:I:135:VAL:HG12	1.92	0.51
1:I:100:VAL:HA	1:I:150:PHE:HB2	1.93	0.51
1:C:246:ASN:ND2	1:C:249:GLN:OE1	2.40	0.51
1:I:27:MET:O	1:I:32:PHE:HB2	2.11	0.51
1:B:15:ALA:HA	1:B:20:GLY:HA3	1.93	0.51
1:C:216:ARG:O	1:C:220:GLU:HG3	2.11	0.50
1:C:15:ALA:HA	1:C:20:GLY:HA3	1.93	0.50
1:E:198:MET:HE2	1:E:234:LEU:HD22	1.93	0.50
1:C:18:TYR:HA	1:C:231:MET:HE3	1.94	0.49
1:C:93:ARG:HD3	1:C:95:ASP:OD2	2.12	0.49
1:C:198:MET:HE2	1:C:234:LEU:HD22	1.94	0.49
1:C:6:ASN:OD1	1:C:6:ASN:O	2.30	0.49
1:C:35:VAL:HG11	1:C:87:VAL:HG22	1.94	0.49
1:I:157:ARG:NH2	1:I:159:ASP:OD2	2.45	0.49
1:C:27:MET:O	1:C:32:PHE:HB2	2.13	0.49
1:A:7:ARG:HH22	1:A:64:ALA:HA	1.77	0.49
1:C:87:VAL:HG11	1:C:94:LEU:HD13	1.95	0.49
1:C:100:VAL:HA	1:C:150:PHE:HB2	1.94	0.49
1:A:218:MET:HE3	1:A:222:GLN:NE2	2.28	0.48
1:J:18:TYR:CD2	1:J:19:VAL:HG12	2.47	0.48
1:J:200:PHE:HB3	1:J:231:MET:HE3	1.95	0.48
1:E:34:LEU:HB2	1:E:66:VAL:HG22	1.96	0.48
1:E:35:VAL:HG11	1:E:87:VAL:HG22	1.95	0.48
1:D:246:ASN:ND2	1:D:249:GLN:OE1	2.44	0.48
1:E:9:VAL:HG21	1:E:91:PHE:HB3	1.95	0.48
1:E:225:LEU:HD12	1:E:258:GLY:HA2	1.96	0.48
1:B:7:ARG:NH1	1:B:64:ALA:HA	2.28	0.48
1:H:100:VAL:HA	1:H:150:PHE:HB2	1.96	0.48
1:I:185:ARG:HG3	4:I:401:HOH:O	2.13	0.48
1:A:42:ASP:OD2	1:A:42:ASP:C	2.57	0.48
1:G:16:THR:HG23	1:G:38:GLY:HA3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:18:TYR:CD2	1:I:19:VAL:HG22	2.49	0.48
1:A:7:ARG:NH2	1:A:63:GLY:O	2.47	0.48
1:B:73:ASP:OD2	1:B:76:THR:HG23	2.14	0.48
1:G:13:THR:HA	1:G:37:HIS:HB3	1.96	0.48
1:G:117:TRP:O	1:G:121:LYS:HG3	2.14	0.48
1:A:30:ARG:HH11	1:A:30:ARG:HG2	1.78	0.47
1:A:42:ASP:OD2	1:A:44:THR:N	2.46	0.47
1:I:153:ALA:HB3	1:I:196:ASN:HB2	1.96	0.47
1:H:52:PHE:H	1:H:52:PHE:HD1	1.61	0.47
1:A:15:ALA:HA	1:A:20:GLY:HA3	1.96	0.47
1:B:13:THR:HA	1:B:37:HIS:HB3	1.96	0.47
1:H:33:ASP:C	1:H:34:LEU:HD12	2.40	0.47
1:H:40:ALA:HA	1:H:52:PHE:CE1	2.50	0.47
1:E:15:ALA:HA	1:E:20:GLY:HA3	1.96	0.47
1:I:18:TYR:HD2	1:I:19:VAL:HG22	1.79	0.47
1:H:152:SER:HB3	1:H:169:ARG:HG3	1.96	0.47
1:A:255:ASP:OD1	1:A:257:SER:OG	2.28	0.47
1:I:102:GLY:HA3	1:I:169:ARG:NH2	2.30	0.47
1:I:231:MET:HA	1:I:231:MET:HE3	1.96	0.47
1:F:84:ILE:HD11	1:F:135:VAL:HG12	1.97	0.46
1:G:100:VAL:HA	1:G:150:PHE:HB2	1.96	0.46
1:A:195:THR:HG22	1:A:256:PHE:HB3	1.98	0.46
1:A:176:VAL:HG11	1:A:192:ALA:HB2	1.96	0.46
1:H:175:ILE:O	1:H:179:VAL:HG23	2.15	0.46
1:D:152:SER:HB3	1:D:169:ARG:HG3	1.98	0.46
1:D:216:ARG:O	1:D:220:GLU:HG3	2.15	0.46
1:D:227:ARG:HH22	1:D:233:GLU:CD	2.21	0.46
1:C:13:THR:HA	1:C:37:HIS:HB3	1.98	0.46
1:F:136:LEU:HD13	1:F:183:HIS:CE1	2.51	0.46
1:G:26:THR:HG21	1:G:235:SER:HB2	1.98	0.46
1:J:15:ALA:HA	1:J:20:GLY:HA3	1.97	0.46
1:A:67:LEU:HD12	1:A:90:ARG:CB	2.46	0.45
1:C:9:VAL:HG21	1:C:91:PHE:HB3	1.98	0.45
1:E:26:THR:O	1:E:30:ARG:HG2	2.17	0.45
1:F:220:GLU:HG2	1:F:228:LEU:HD13	1.97	0.45
1:F:102:GLY:HA3	1:F:169:ARG:NH2	2.31	0.45
1:C:55:GLN:O	1:C:58:ASP:N	2.49	0.45
1:J:8:PRO:HB2	1:J:32:PHE:CE2	2.52	0.45
1:J:62:ARG:HG3	1:J:62:ARG:HH11	1.82	0.45
1:A:233:GLU:O	1:A:237:VAL:HG23	2.17	0.45
1:F:153:ALA:HB3	1:F:196:ASN:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:224:PRO:HG2	1:I:259:GLY:C	2.42	0.45
1:D:8:PRO:HB2	1:D:32:PHE:CE2	2.52	0.45
1:J:199:ASP:OD2	1:J:216:ARG:NH2	2.50	0.45
1:C:14:MET:HG3	1:C:100:VAL:HB	1.99	0.44
1:J:198:MET:HE2	1:J:234:LEU:HD12	1.99	0.44
1:J:227:ARG:NH2	1:J:233:GLU:OE1	2.48	0.44
1:G:74:LEU:O	1:G:80:ASN:ND2	2.50	0.44
1:H:200:PHE:O	1:H:202:GLY:N	2.51	0.44
1:C:196:ASN:OD1	1:C:197:TYR:N	2.50	0.44
1:F:30:ARG:NH1	1:F:243:ASP:OD2	2.46	0.44
1:G:108:LYS:HB3	1:G:108:LYS:HE3	1.70	0.44
1:I:22:ALA:O	1:I:26:THR:HG22	2.18	0.44
1:A:17:GLY:HA2	1:A:49:GLU:OE2	2.16	0.44
1:A:100:VAL:HA	1:A:150:PHE:HB2	2.00	0.44
1:B:8:PRO:HB2	1:B:32:PHE:CE2	2.52	0.44
1:D:84:ILE:HD11	1:D:135:VAL:HG12	2.00	0.44
1:F:9:VAL:HG21	1:F:91:PHE:HB3	2.00	0.44
1:H:45:MET:HE2	1:H:45:MET:HA	2.00	0.44
1:I:237:VAL:HG21	1:I:256:PHE:HE2	1.82	0.44
1:J:100:VAL:HA	1:J:150:PHE:HB2	1.99	0.44
1:B:30:ARG:HD3	1:B:30:ARG:N	2.32	0.44
1:E:41:GLY:HA3	1:E:45:MET:HG3	1.99	0.44
1:E:30:ARG:NH1	1:E:243:ASP:OD2	2.51	0.44
1:G:197:TYR:HA	1:G:203:PHE:CZ	2.53	0.44
1:I:45:MET:HA	1:I:45:MET:HE3	1.99	0.44
1:I:71:ASP:OD1	1:I:86:ARG:NH1	2.49	0.44
1:C:70:SER:O	1:C:70:SER:OG	2.36	0.43
1:H:200:PHE:HB3	1:H:231:MET:CE	2.47	0.43
1:H:73:ASP:OD2	1:H:76:THR:HG23	2.17	0.43
1:I:21:PRO:O	1:I:25:ARG:HG3	2.18	0.43
1:I:196:ASN:OD1	1:I:197:TYR:N	2.50	0.43
1:A:182:GLU:HG3	1:D:160:PRO:HB3	2.00	0.43
1:F:15:ALA:HA	1:F:20:GLY:HA3	2.00	0.43
1:I:122:ALA:O	1:I:126:ASP:HB2	2.17	0.43
1:D:102:GLY:HA3	1:D:169:ARG:NH2	2.33	0.43
1:G:84:ILE:O	1:G:87:VAL:HG12	2.17	0.43
1:I:74:LEU:HD23	1:I:74:LEU:HA	1.83	0.43
1:G:26:THR:O	1:G:30:ARG:HG2	2.19	0.43
1:D:232:ASP:OD2	1:D:232:ASP:N	2.50	0.43
1:A:56:ILE:HD12	1:A:56:ILE:H	1.82	0.43
1:B:30:ARG:NH1	1:B:243:ASP:OD2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:8:PRO:HB2	1:F:32:PHE:CE2	2.54	0.43
1:G:177:ARG:O	1:G:181:LEU:HG	2.19	0.43
1:F:77:ARG:O	1:F:81:GLN:HG2	2.18	0.43
1:I:232:ASP:OD1	1:I:232:ASP:N	2.52	0.43
1:J:145:GLY:N	1:J:188:VAL:HG12	2.34	0.43
1:A:9:VAL:HG23	1:A:93:ARG:HG3	2.01	0.42
1:D:16:THR:HG23	1:D:38:GLY:HA3	2.01	0.42
1:E:71:ASP:OD1	1:E:71:ASP:N	2.52	0.42
1:I:27:MET:HA	1:I:30:ARG:HD2	2.01	0.42
1:F:67:LEU:HB2	1:F:90:ARG:HD2	2.01	0.42
1:G:233:GLU:O	1:G:237:VAL:HG23	2.19	0.42
1:A:73:ASP:OD2	1:A:76:THR:HG23	2.20	0.42
1:H:37:HIS:HE2	1:H:74:LEU:HD11	1.84	0.42
1:H:196:ASN:OD1	1:H:197:TYR:N	2.53	0.42
1:I:220:GLU:O	1:I:226:ARG:HA	2.20	0.42
1:J:257:SER:HB2	1:J:260:TRP:HB3	2.00	0.42
1:B:34:LEU:O	1:B:66:VAL:HA	2.19	0.42
1:C:123:THR:HA	1:C:127:MET:HE3	2.01	0.42
1:F:34:LEU:HD13	1:F:59:LEU:HD13	2.02	0.42
1:H:108:LYS:HE3	1:H:108:LYS:HB3	1.69	0.42
1:I:8:PRO:HA	1:I:93:ARG:HH11	1.85	0.42
1:D:52:PHE:O	1:D:56:ILE:HD12	2.20	0.42
1:E:34:LEU:O	1:E:66:VAL:HA	2.20	0.42
1:H:102:GLY:HA3	1:H:169:ARG:NH2	2.35	0.42
1:H:195:THR:HG22	1:H:256:PHE:HB3	2.02	0.42
1:H:164:ILE:O	1:H:168:THR:OG1	2.27	0.42
1:J:150:PHE:HZ	1:J:234:LEU:CD2	2.27	0.42
1:F:120:VAL:HG11	1:F:164:ILE:HD12	2.01	0.41
1:H:112:MET:SD	1:H:164:ILE:HD11	2.60	0.41
1:H:233:GLU:O	1:H:237:VAL:HG23	2.20	0.41
1:J:255:ASP:OD2	1:J:257:SER:OG	2.35	0.41
1:B:9:VAL:HG21	1:B:91:PHE:HB3	2.02	0.41
1:C:219:ILE:HD13	1:C:219:ILE:HA	1.88	0.41
1:F:87:VAL:HG11	1:F:94:LEU:HD13	2.02	0.41
1:J:200:PHE:O	1:J:202:GLY:N	2.53	0.41
1:J:237:VAL:HG11	1:J:256:PHE:CE2	2.55	0.41
1:C:27:MET:HE3	1:C:27:MET:HB3	1.86	0.41
1:H:84:ILE:HD11	1:H:135:VAL:HG12	2.01	0.41
1:G:145:GLY:O	1:G:188:VAL:HA	2.20	0.41
1:H:23:LEU:HD12	1:H:27:MET:HG2	2.02	0.41
1:H:34:LEU:HD22	1:H:59:LEU:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:90:ARG:O	1:H:90:ARG:NE	2.54	0.41
1:I:104:ILE:HG13	1:I:105:VAL:N	2.35	0.41
1:J:7:ARG:NH1	1:J:63:GLY:O	2.54	0.41
1:H:9:VAL:HA	1:H:33:ASP:O	2.20	0.41
1:G:19:VAL:HG22	1:G:23:LEU:HB2	2.03	0.41
1:A:245:SER:O	1:C:233:GLU:HG2	2.21	0.41
1:B:35:VAL:HG21	1:B:87:VAL:HG13	2.02	0.41
1:F:160:PRO:O	1:F:161:MET:HB2	2.21	0.41
1:A:30:ARG:NH1	1:A:243:ASP:OD2	2.53	0.41
1:C:74:LEU:HD23	1:C:74:LEU:HA	1.68	0.41
1:D:120:VAL:HG11	1:D:164:ILE:HD12	2.02	0.41
1:D:225:LEU:HD12	1:D:258:GLY:HA2	2.03	0.41
1:E:84:ILE:HD11	1:E:135:VAL:HG12	2.02	0.41
1:F:96:SER:HA	1:F:146:GLN:O	2.21	0.41
1:G:102:GLY:HA3	1:G:169:ARG:NH2	2.36	0.41
1:I:13:THR:HA	1:I:37:HIS:HB3	2.02	0.41
1:I:87:VAL:HG11	1:I:94:LEU:HD13	2.03	0.41
1:B:83:MET:O	1:B:87:VAL:HG23	2.20	0.41
1:H:13:THR:HA	1:H:37:HIS:HB3	2.03	0.41
1:J:35:VAL:HG11	1:J:87:VAL:HG22	2.02	0.41
1:D:45:MET:HE3	1:D:45:MET:HA	2.03	0.40
1:J:224:PRO:HG2	1:J:259:GLY:C	2.46	0.40
1:B:26:THR:OG1	1:B:30:ARG:NE	2.52	0.40
1:E:165:TYR:O	1:E:169:ARG:HG2	2.21	0.40
1:E:195:THR:HG22	1:E:256:PHE:HB3	2.03	0.40
1:F:34:LEU:HB3	1:F:36:LEU:HD21	2.04	0.40
1:G:223:VAL:HG12	1:G:224:PRO:O	2.21	0.40
1:I:140:VAL:HG13	1:I:186:HIS:CG	2.56	0.40
1:J:176:VAL:HG11	1:J:192:ALA:HB2	2.03	0.40
1:H:34:LEU:CD2	1:H:59:LEU:HD12	2.51	0.40
1:I:148:VAL:HG11	1:I:238:THR:HG23	2.03	0.40
1:B:112:MET:SD	1:B:164:ILE:HD11	2.61	0.40
1:B:245:SER:O	1:D:233:GLU:HG2	2.22	0.40
1:C:152:SER:HB3	1:C:169:ARG:HG3	2.03	0.40
1:H:237:VAL:HG21	1:H:256:PHE:CE2	2.53	0.40
1:J:11:LEU:HD12	1:J:87:VAL:HG21	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114[B]:CYS:SG	2:A:301:ME7:CAF[2_565]	2.01	0.19

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	253/282 (90%)	242 (96%)	11 (4%)	0	100	100
1	B	257/282 (91%)	250 (97%)	7 (3%)	0	100	100
1	C	256/282 (91%)	244 (95%)	11 (4%)	1 (0%)	30	52
1	D	258/282 (92%)	244 (95%)	13 (5%)	1 (0%)	30	52
1	E	257/282 (91%)	248 (96%)	9 (4%)	0	100	100
1	F	256/282 (91%)	246 (96%)	9 (4%)	1 (0%)	30	52
1	G	252/282 (89%)	236 (94%)	16 (6%)	0	100	100
1	H	250/282 (89%)	234 (94%)	16 (6%)	0	100	100
1	I	256/282 (91%)	242 (94%)	14 (6%)	0	100	100
1	J	252/282 (89%)	234 (93%)	17 (7%)	1 (0%)	30	52
All	All	2547/2820 (90%)	2420 (95%)	123 (5%)	4 (0%)	43	66

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	6	ASN
1	D	212	ASP
1	C	185	ARG
1	J	21	PRO

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 X-ray entries followed by that with respect to entries of similar

resolution.

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	192/217 (88%)	190 (99%)	2 (1%)	68	85
1	B	195/217 (90%)	194 (100%)	1 (0%)	81	91
1	C	193/217 (89%)	191 (99%)	2 (1%)	68	85
1	D	193/217 (89%)	190 (98%)	3 (2%)	55	78
1	E	194/217 (89%)	193 (100%)	1 (0%)	81	91
1	F	193/217 (89%)	190 (98%)	3 (2%)	55	78
1	G	165/217 (76%)	164 (99%)	1 (1%)	78	90
1	H	176/217 (81%)	170 (97%)	6 (3%)	32	60
1	I	181/217 (83%)	177 (98%)	4 (2%)	45	72
1	J	172/217 (79%)	167 (97%)	5 (3%)	37	65
All	All	1854/2170 (85%)	1826 (98%)	28 (2%)	57	79

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	LEU
1	A	120	VAL
1	B	188	VAL
1	C	26	THR
1	C	219	ILE
1	D	25	ARG
1	D	105	VAL
1	D	162	VAL
1	E	188	VAL
1	F	103	LEU
1	F	188	VAL
1	F	236	SER
1	G	54	SER
1	H	105	VAL
1	H	136	LEU
1	H	163	SER
1	H	220	GLU
1	H	225	LEU
1	H	235	SER
1	I	13	THR

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Mol	Chain	Res	Type
1	I	105	VAL
1	I	120	VAL
1	I	182	GLU
1	J	48	VAL
1	J	66	VAL
1	J	162	VAL
1	J	235	SER
1	J	237	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	252	GLN
1	C	6	ASN
1	C	55	GLN
1	C	133	GLN
1	C	183	HIS
1	D	252	GLN
1	E	6	ASN
1	F	252	GLN
1	G	252	GLN
1	H	183	HIS
1	H	222	GLN
1	I	183	HIS
1	I	252	GLN
1	J	81	GLN
1	J	124	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

36 ligands are modelled in this entry.

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	$\# Z > 2$
2	ME7	H	301	1	17,17,17	0.18	0	24,24,24	0.21	0
2	ME7	A	301	1	17,17,17	0.18	0	24,24,24	0.20	0
2	ME7	B	301	1	17,17,17	0.17	0	24,24,24	0.24	0
3	SO4	I	304	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	D	301	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	I	302	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	F	302	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	B	303	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	A	303	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	C	301	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	E	303	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	D	302	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	E	302	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	E	304	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	F	303	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	J	302	-	4,4,4	0.23	0	6,6,6	0.08	0
2	ME7	I	301	-	17,17,17	0.20	0	24,24,24	0.22	0
3	SO4	G	303	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	G	304	-	4,4,4	0.24	0	6,6,6	0.08	0
2	ME7	G	301	1	17,17,17	0.18	0	24,24,24	0.21	0
3	SO4	A	304	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	A	302	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	H	303	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	G	302	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	J	301	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	B	302	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	H	302	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	B	304	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	A	305	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	D	303	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	E	301	-	4,4,4	0.23	0	6,6,6	0.09	0
3	SO4	I	303	-	4,4,4	0.24	0	6,6,6	0.07	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	A	306	-	4,4,4	0.24	0	6,6,6	0.09	0
3	SO4	F	301	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	C	303	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	C	302	-	4,4,4	0.22	0	6,6,6	0.11	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
2	ME7	H	301	1	-	2/5/31/31	0/2/2/2
2	ME7	A	301	1	-	0/5/31/31	0/2/2/2
2	ME7	B	301	1	-	0/5/31/31	0/2/2/2
2	ME7	I	301	-	-	0/5/31/31	0/2/2/2
2	ME7	G	301	1	-	0/5/31/31	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	301	ME7	CAJ-CAI-NAO-CAL
2	H	301	ME7	CAJ-CAI-NAO-CAK

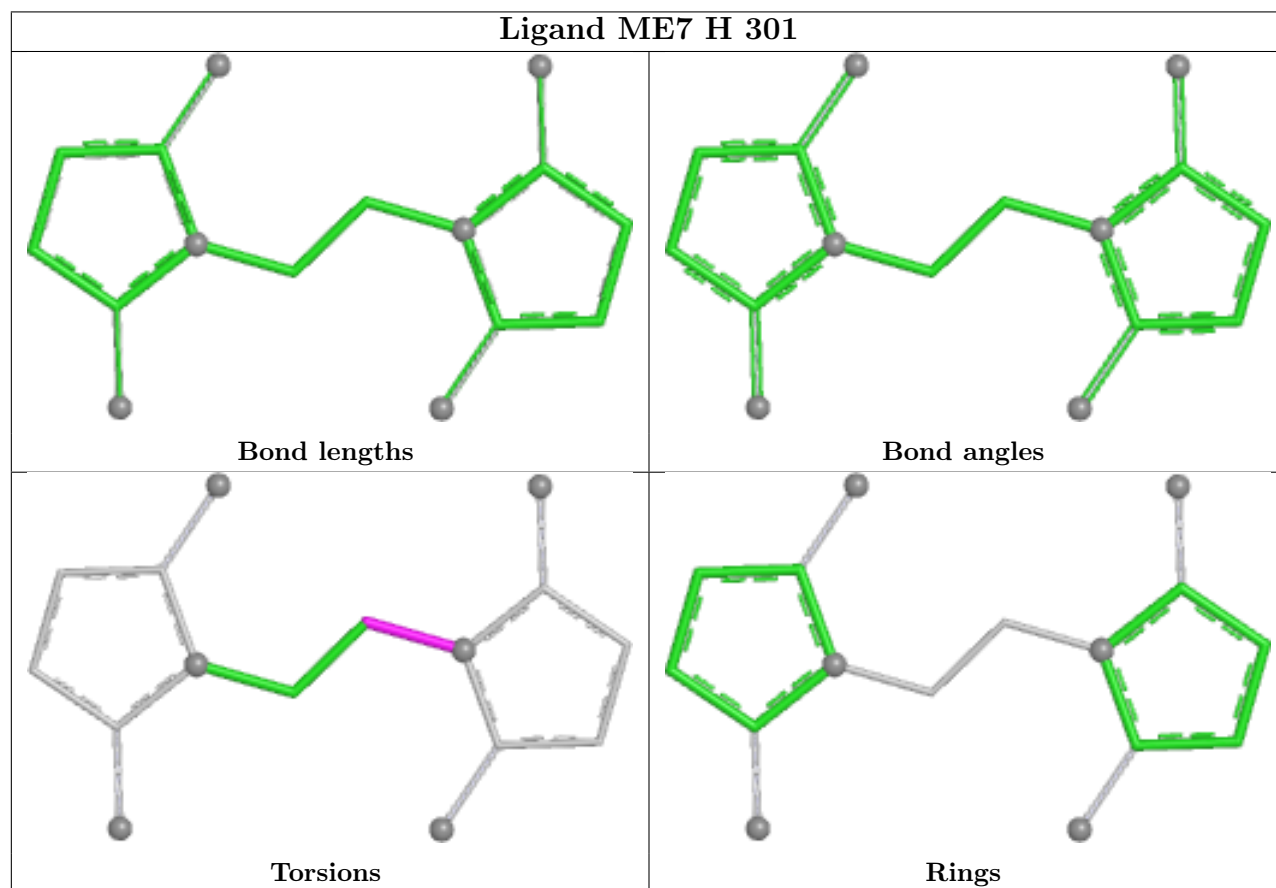
There are no ring outliers.

1 monomer is involved in 1 short contact:

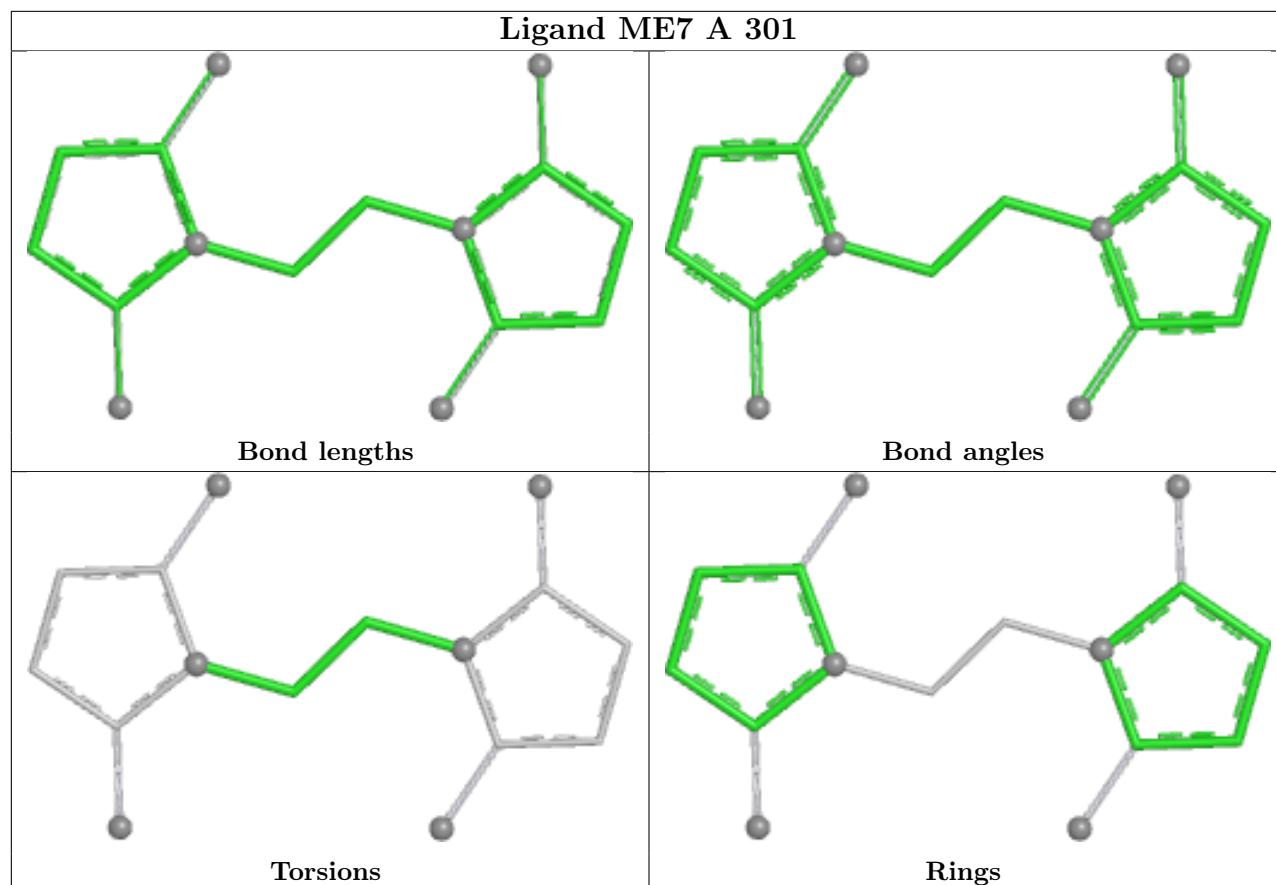
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	ME7	0	1

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

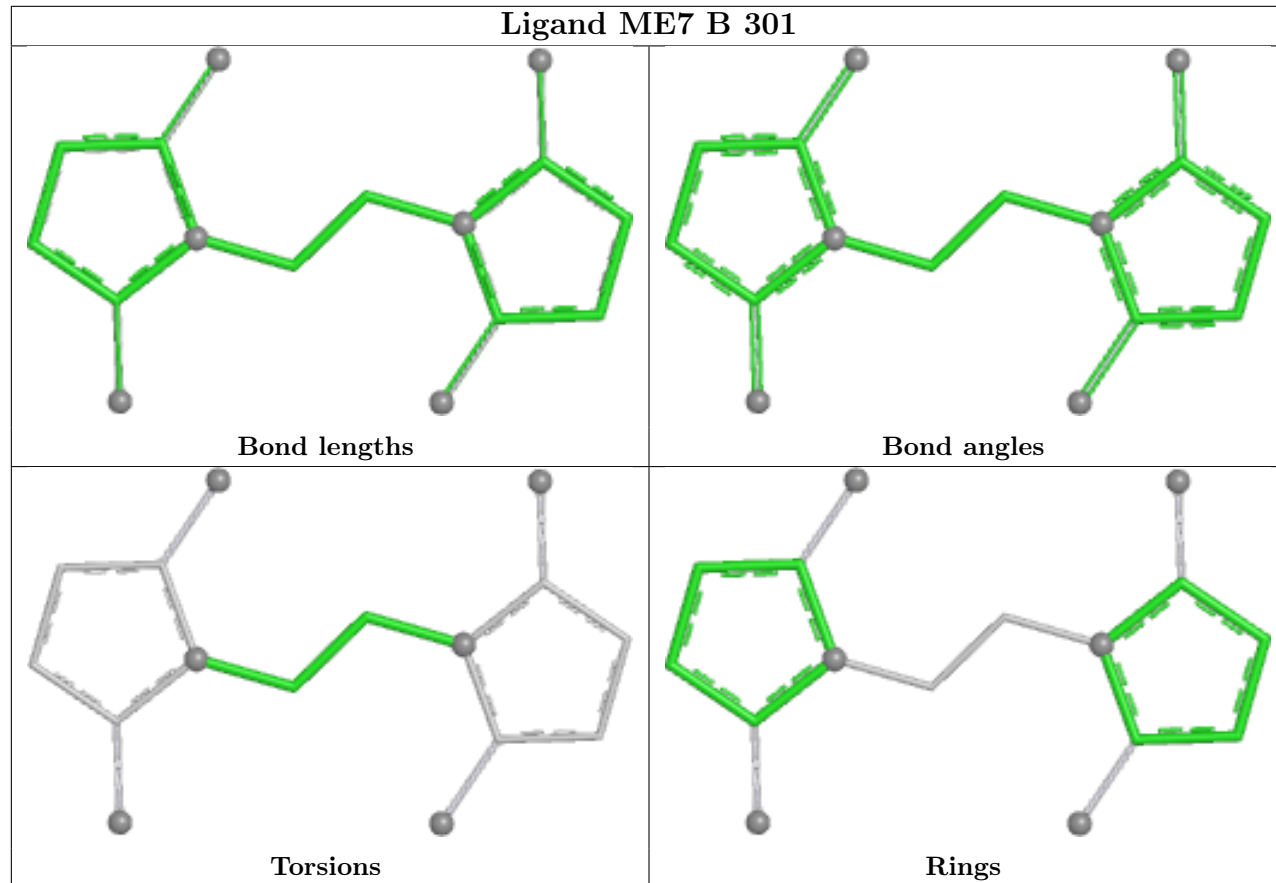
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



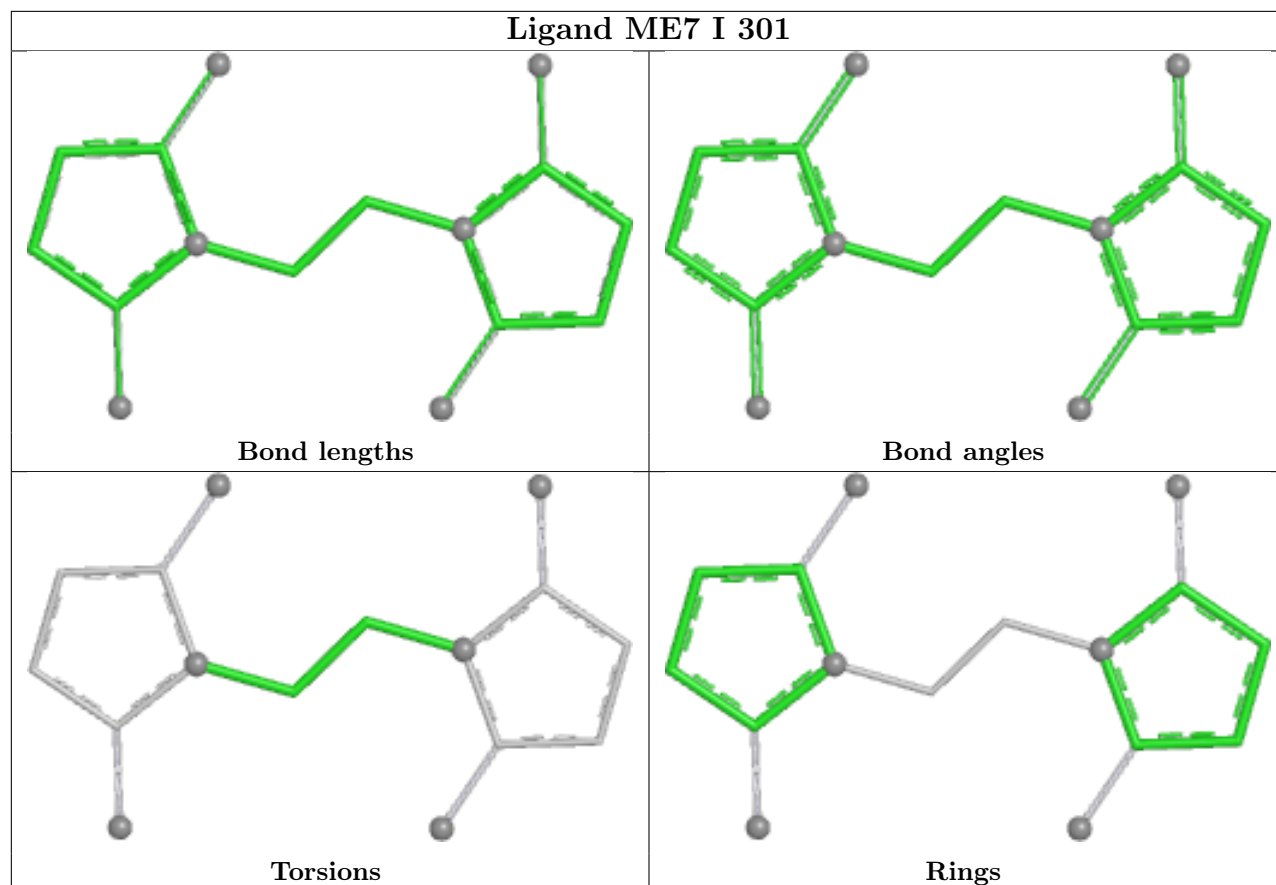
Ligand ME7 A 301



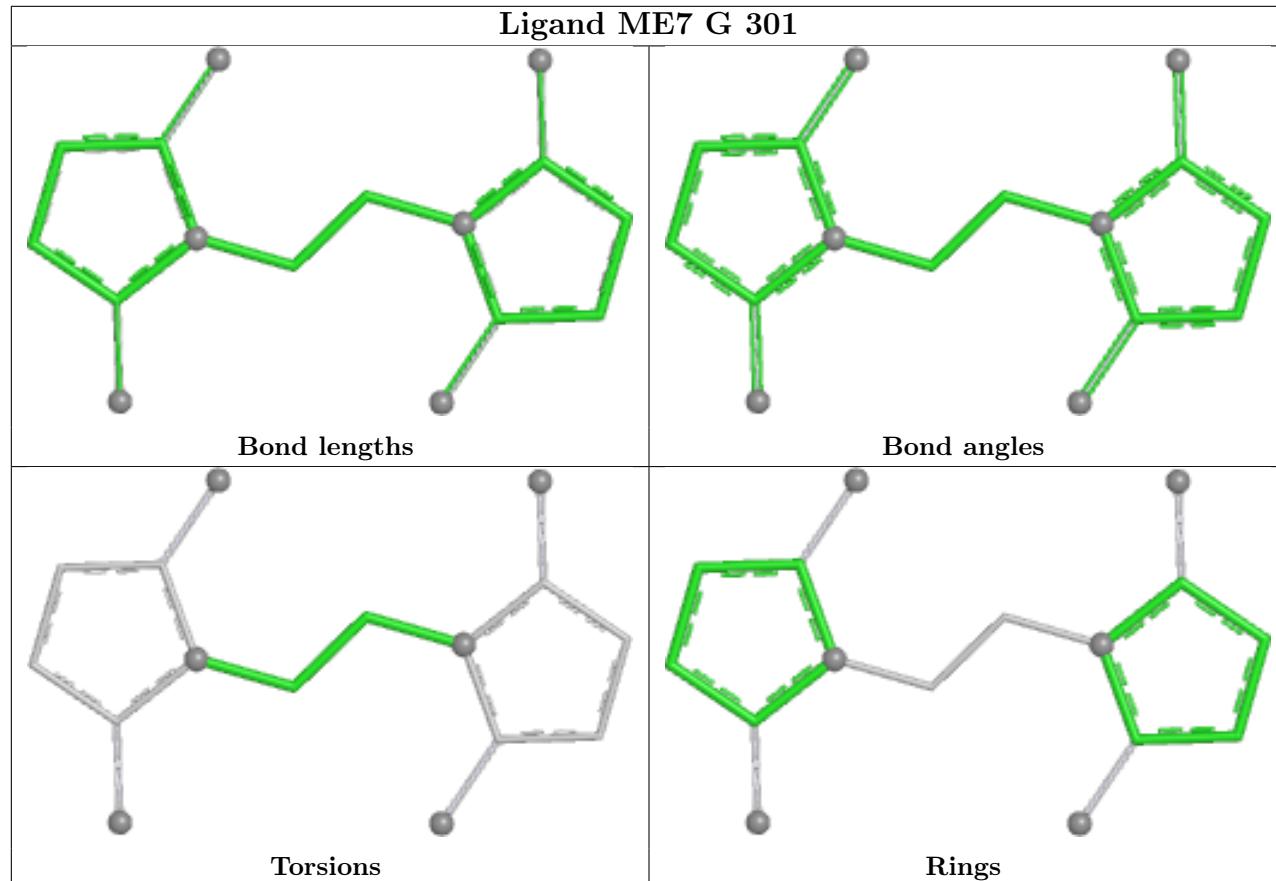
Ligand ME7 B 301



Ligand ME7 I 301



Ligand ME7 G 301



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 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	257/282 (91%)	0.14	4 (1%)	70 68	40, 62, 97, 124	0
1	B	258/282 (91%)	-0.08	4 (1%)	70 68	36, 54, 82, 141	1 (0%)
1	C	257/282 (91%)	0.31	18 (7%)	22 20	36, 62, 112, 164	3 (1%)
1	D	258/282 (91%)	0.14	12 (4%)	36 33	37, 57, 116, 141	2 (0%)
1	E	258/282 (91%)	-0.27	4 (1%)	70 68	33, 49, 80, 105	1 (0%)
1	F	258/282 (91%)	-0.24	1 (0%)	88 88	33, 48, 85, 117	0
1	G	254/282 (90%)	1.06	46 (18%)	3 3	44, 80, 133, 156	2 (0%)
1	H	254/282 (90%)	1.10	44 (17%)	4 4	56, 83, 132, 160	0
1	I	257/282 (91%)	0.88	37 (14%)	6 5	45, 80, 132, 162	1 (0%)
1	J	256/282 (90%)	1.10	42 (16%)	4 4	58, 88, 131, 168	0
All	All	2567/2820 (91%)	0.41	212 (8%)	17 15	33, 66, 122, 168	10 (0%)

All (212) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	34	LEU	6.0
1	J	93	ARG	5.4
1	G	68	THR	5.3
1	G	199	ASP	5.3
1	G	219	ILE	4.9
1	D	5	GLU	4.6
1	G	212	ASP	4.6
1	G	66	VAL	4.5
1	J	6	ASN	4.5
1	H	201	PRO	4.4
1	H	65	ASP	4.3
1	H	32	PHE	4.3
1	D	210	ASP	4.3

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Mol	Chain	Res	Type	RSRZ
1	J	210	ASP	4.3
1	G	200	PHE	4.3
1	G	53	ASP	4.2
1	J	52	PHE	4.2
1	J	34	LEU	4.2
1	I	17	GLY	4.1
1	A	5	GLU	4.0
1	B	5	GLU	3.9
1	G	208	ARG	3.8
1	J	66	VAL	3.8
1	G	51	SER	3.8
1	C	47	GLY	3.8
1	D	204	LEU	3.7
1	I	68	THR	3.7
1	J	53	ASP	3.7
1	J	185	ARG	3.7
1	I	207	SER	3.7
1	H	213	PRO	3.6
1	H	66	VAL	3.6
1	G	52	PHE	3.5
1	G	50	GLU	3.5
1	G	65	ASP	3.4
1	H	93	ARG	3.4
1	J	68	THR	3.4
1	G	8	PRO	3.3
1	I	216	ARG	3.3
1	G	67	LEU	3.3
1	H	89	GLU	3.3
1	G	32	PHE	3.3
1	I	214	GLU	3.2
1	G	215	ARG	3.2
1	F	5	GLU	3.2
1	E	114	CYS	3.2
1	H	41	GLY	3.2
1	G	60	ALA	3.2
1	A	147	CYS	3.1
1	C	219	ILE	3.1
1	G	93	ARG	3.1
1	H	246	ASN	3.1
1	H	53	ASP	3.1
1	I	215	ARG	3.1
1	H	74	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	G	89	GLU	3.1
1	I	213	PRO	3.1
1	I	40	ALA	3.1
1	I	57	ALA	3.1
1	G	201	PRO	3.0
1	J	32	PHE	3.0
1	J	56	ILE	3.0
1	H	48	VAL	3.0
1	H	204	LEU	3.0
1	G	207	SER	3.0
1	H	218	MET	3.0
1	C	213	PRO	2.9
1	H	45	MET	2.9
1	J	67	LEU	2.9
1	J	91	PHE	2.9
1	A	210	ASP	2.9
1	G	33	ASP	2.9
1	C	68	THR	2.9
1	D	205	LYS	2.9
1	H	207	SER	2.8
1	I	6	ASN	2.8
1	J	94	LEU	2.8
1	I	52	PHE	2.8
1	H	200	PHE	2.8
1	C	46	VAL	2.8
1	H	17	GLY	2.7
1	B	218[A]	MET	2.7
1	H	42	ASP	2.7
1	J	184	ALA	2.7
1	J	147	CYS	2.7
1	I	88	LEU	2.7
1	G	64	ALA	2.7
1	J	46	VAL	2.7
1	H	203	PHE	2.7
1	J	209	ALA	2.7
1	H	147	CYS	2.6
1	A	47	GLY	2.6
1	C	205	LYS	2.6
1	E	211	GLY	2.6
1	G	20	GLY	2.6
1	G	57	ALA	2.6
1	G	224	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	H	28	ALA	2.6
1	J	206	ALA	2.6
1	J	55	GLN	2.6
1	I	226	ARG	2.6
1	J	215	ARG	2.6
1	G	214	GLU	2.6
1	I	32	PHE	2.6
1	G	14	MET	2.5
1	H	34	LEU	2.5
1	J	18	TYR	2.5
1	H	9	VAL	2.5
1	J	142	ALA	2.5
1	G	56	ILE	2.5
1	H	183	HIS	2.5
1	C	6	ASN	2.5
1	J	234	LEU	2.5
1	H	46	VAL	2.5
1	G	91	PHE	2.5
1	I	203	PHE	2.5
1	H	205	LYS	2.5
1	G	96	SER	2.5
1	I	228	LEU	2.5
1	D	213	PRO	2.4
1	G	213	PRO	2.4
1	I	218	MET	2.4
1	H	18	TYR	2.4
1	I	87	VAL	2.4
1	D	208	ARG	2.4
1	H	44	THR	2.4
1	G	94	LEU	2.4
1	H	39	THR	2.4
1	C	210	ASP	2.4
1	C	48	VAL	2.4
1	G	46	VAL	2.4
1	C	208	ARG	2.4
1	I	184	ALA	2.4
1	H	67	LEU	2.4
1	H	161	MET	2.4
1	I	19	VAL	2.4
1	G	28	ALA	2.4
1	H	56	ILE	2.3
1	J	186	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	H	49	GLU	2.3
1	I	20	GLY	2.3
1	C	215	ARG	2.3
1	G	248	PHE	2.3
1	C	5	GLU	2.3
1	H	50	GLU	2.3
1	D	203	PHE	2.3
1	H	36	LEU	2.3
1	J	45	MET	2.3
1	D	214	GLU	2.3
1	H	208	ARG	2.3
1	I	43	GLY	2.3
1	G	9	VAL	2.3
1	D	57	ALA	2.3
1	H	104	ILE	2.3
1	I	141	ALA	2.3
1	B	6	ASN	2.3
1	I	56	ILE	2.2
1	J	217	ALA	2.2
1	I	61	LYS	2.2
1	H	6	ASN	2.2
1	C	207	SER	2.2
1	G	41	GLY	2.2
1	E	218	MET	2.2
1	G	184	ALA	2.2
1	H	221	ALA	2.2
1	J	14	MET	2.2
1	J	40	ALA	2.2
1	D	42	ASP	2.2
1	J	141	ALA	2.2
1	J	16	THR	2.2
1	G	95	ASP	2.2
1	I	34	LEU	2.2
1	C	52	PHE	2.2
1	I	200	PHE	2.2
1	H	214	GLU	2.2
1	J	89	GLU	2.2
1	I	230	THR	2.2
1	I	201	PRO	2.2
1	J	243	ASP	2.2
1	G	203	PHE	2.2
1	H	256	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	J	10	ALA	2.1
1	C	214	GLU	2.1
1	G	49	GLU	2.1
1	I	93	ARG	2.1
1	J	208	ARG	2.1
1	J	41	GLY	2.1
1	D	51	SER	2.1
1	J	214	GLU	2.1
1	I	41	GLY	2.1
1	I	92	GLY	2.1
1	J	199	ASP	2.1
1	J	96	SER	2.1
1	C	206	ALA	2.1
1	C	199	ASP	2.1
1	H	212	ASP	2.1
1	D	45	MET	2.1
1	G	186	HIS	2.1
1	H	47	GLY	2.1
1	I	202	GLY	2.1
1	B	66	VAL	2.1
1	I	66	VAL	2.1
1	E	5	GLU	2.0
1	G	27	MET	2.0
1	I	242	LEU	2.0
1	J	104	ILE	2.0
1	J	9	VAL	2.0
1	J	22	ALA	2.0
1	C	44	THR	2.0
1	I	44	THR	2.0
1	G	246	ASN	2.0
1	I	104	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

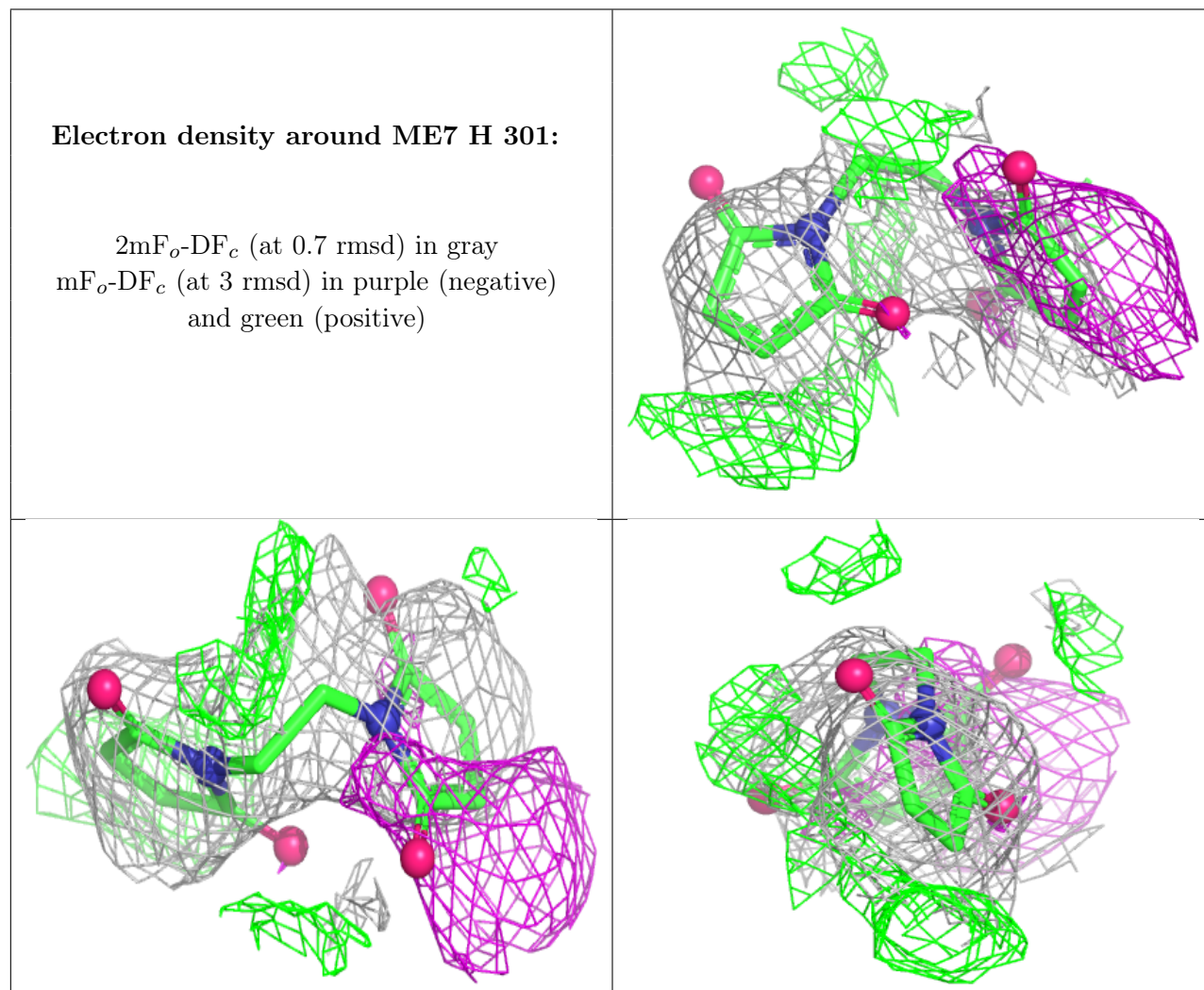
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

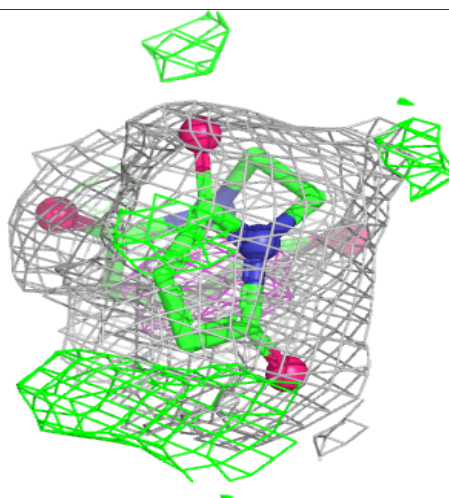
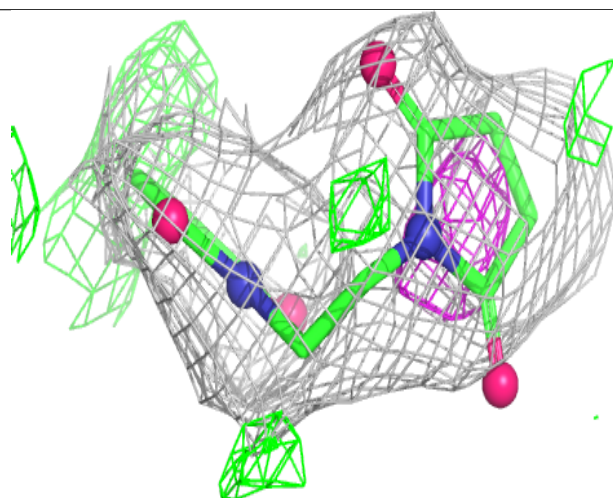
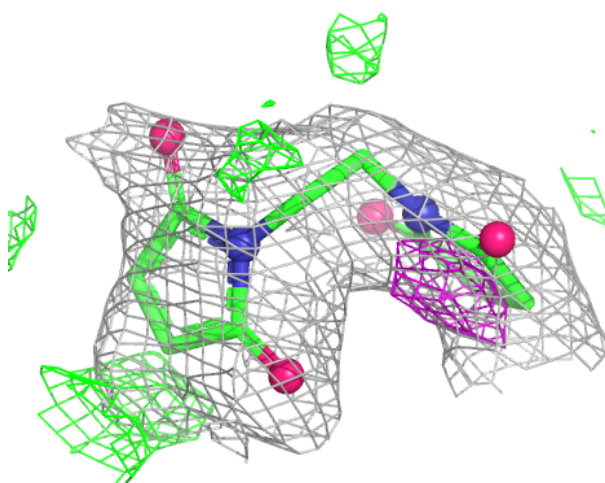
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ME7	H	301	16/16	0.52	0.35	90,107,117,118	0
3	SO4	I	302	5/5	0.60	0.18	96,106,132,134	0
3	SO4	G	304	5/5	0.61	0.16	84,103,132,140	0
3	SO4	C	302	5/5	0.65	0.18	86,89,119,133	0
3	SO4	F	303	5/5	0.65	0.19	96,97,106,142	0
3	SO4	E	304	5/5	0.71	0.14	93,110,127,140	0
2	ME7	A	301	16/16	0.72	0.19	64,82,90,91	0
3	SO4	E	303	5/5	0.72	0.20	83,99,125,141	0
3	SO4	J	301	5/5	0.72	0.17	104,120,128,151	0
3	SO4	I	304	5/5	0.73	0.17	109,119,131,147	0
2	ME7	B	301	16/16	0.73	0.20	74,79,89,90	0
2	ME7	I	301	16/16	0.75	0.22	79,92,100,106	0
2	ME7	G	301	16/16	0.75	0.19	62,80,88,90	0
3	SO4	H	303	5/5	0.75	0.17	107,108,131,193	0
3	SO4	A	305	5/5	0.77	0.38	70,95,106,122	0
3	SO4	D	303	5/5	0.77	0.16	111,115,116,143	0
3	SO4	C	301	5/5	0.78	0.18	97,98,99,136	0
3	SO4	H	302	5/5	0.78	0.12	102,111,116,138	0
3	SO4	J	302	5/5	0.78	0.15	86,107,143,184	0
3	SO4	I	303	5/5	0.79	0.12	100,107,118,138	0
3	SO4	G	302	5/5	0.79	0.11	87,110,116,138	0
3	SO4	C	303	5/5	0.82	0.16	90,103,127,148	0
3	SO4	B	304	5/5	0.82	0.18	93,94,108,135	0
3	SO4	A	304	5/5	0.83	0.11	92,96,112,131	0
3	SO4	A	303	5/5	0.84	0.14	89,99,121,138	0
3	SO4	G	303	5/5	0.85	0.15	107,115,128,144	0
3	SO4	F	302	5/5	0.88	0.18	81,84,94,128	0
3	SO4	E	302	5/5	0.88	0.19	84,84,92,129	0
3	SO4	B	303	5/5	0.89	0.20	78,82,94,127	0
3	SO4	D	301	5/5	0.90	0.24	77,85,112,122	0
3	SO4	D	302	5/5	0.90	0.28	85,89,95,125	0
3	SO4	A	306	5/5	0.91	0.12	97,102,107,173	0
3	SO4	E	301	5/5	0.92	0.21	65,73,79,92	0
3	SO4	A	302	5/5	0.92	0.29	75,77,97,106	0
3	SO4	F	301	5/5	0.93	0.20	63,69,95,97	0
3	SO4	B	302	5/5	0.94	0.21	61,64,86,87	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



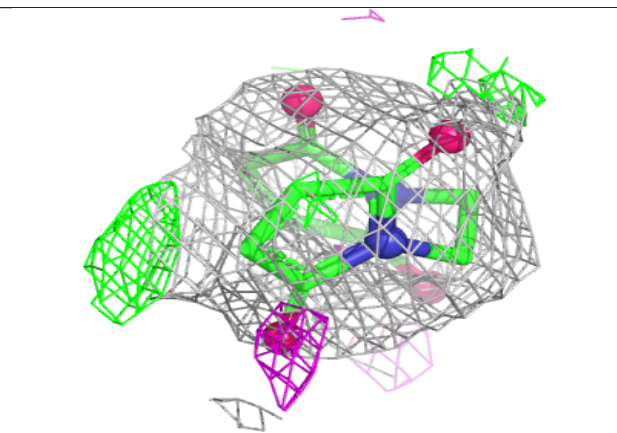
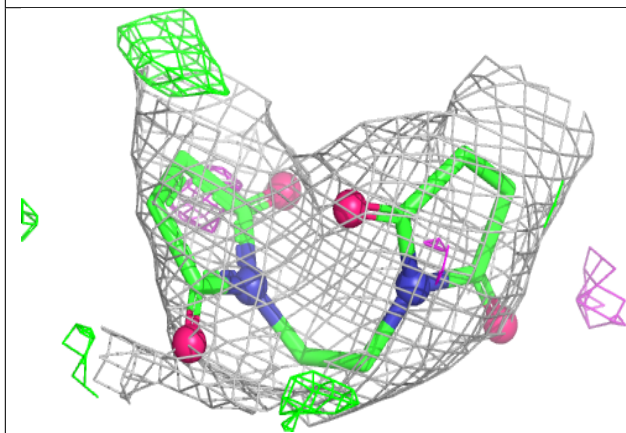
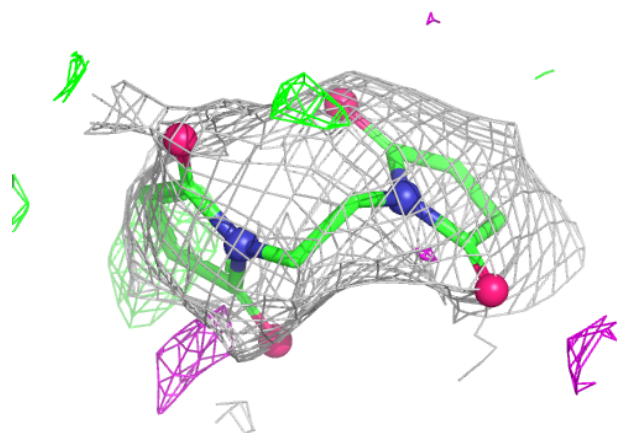
Electron density around ME7 A 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

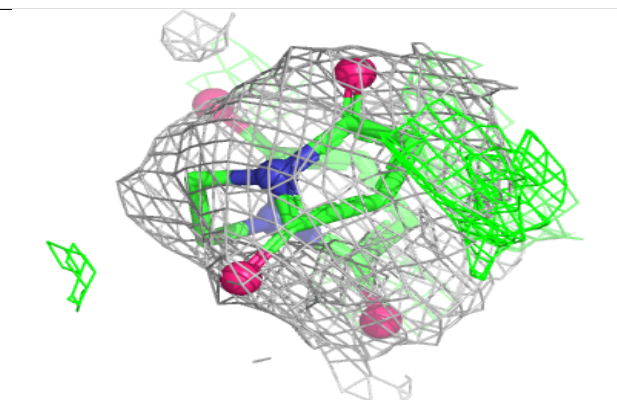
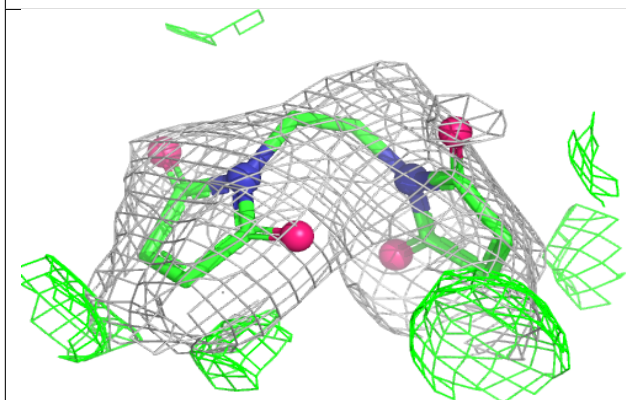
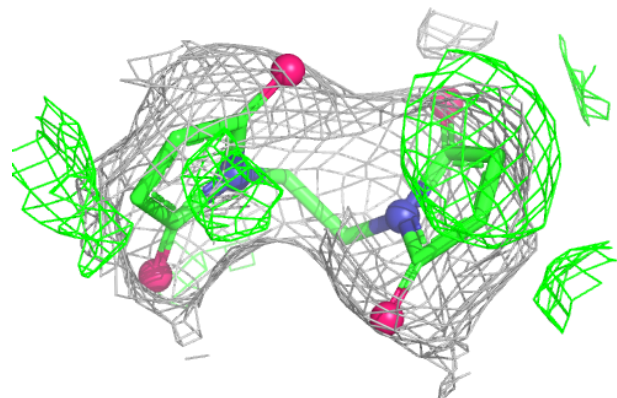


Electron density around ME7 B 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

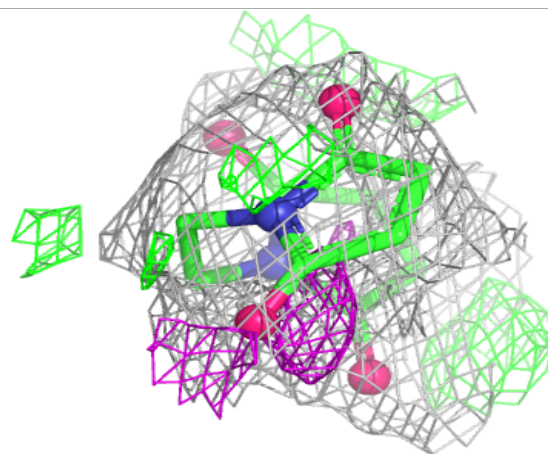
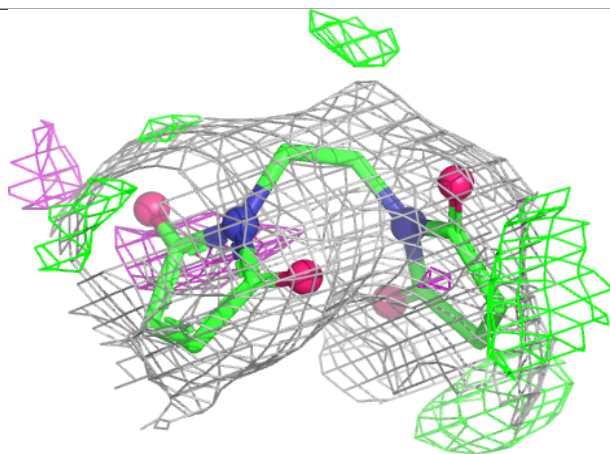
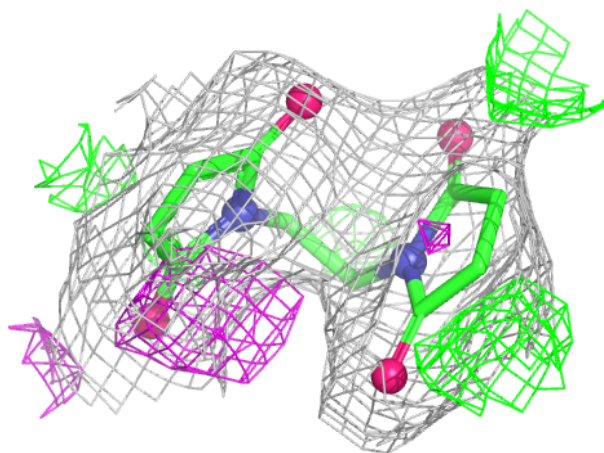
**Electron density around ME7 I 301:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ME7 G 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.