



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 01:37 PM UTC

PDB ID : 7XX3 / pdb_00007xx3
Title : Crystal structure of human Superoxide Dismutase (SOD1) in complex with a fungal metabolite molecule, Phialomustin B (PB)
Authors : Padmanabhan, B.; Unni, S.
Deposited on : 2022-05-28
Resolution : 1.90 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

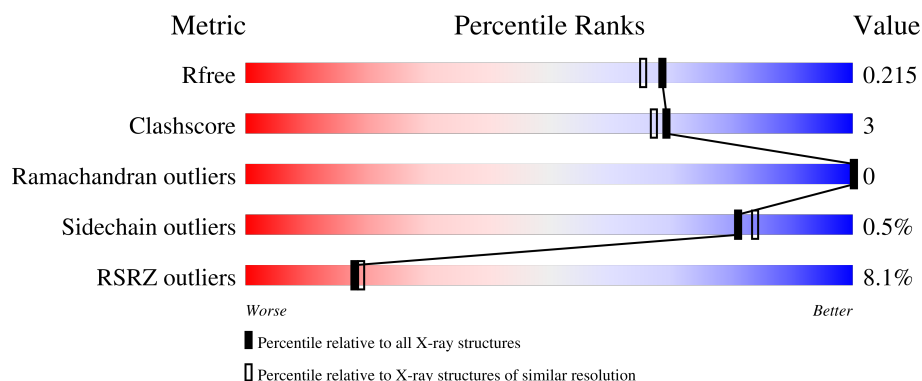
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

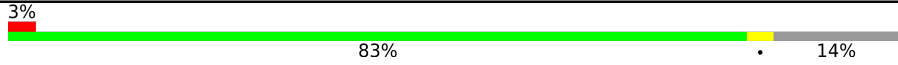
The reported resolution of this entry is 1.90 Å.

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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	180	
1	B	180	
1	C	180	
1	D	180	
1	E	180	

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Mol	Chain	Length	Quality of chain
1	F	180	
1	G	180	
1	H	180	
1	I	180	
1	J	180	

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
3	GOL	A	202	-	-	X	-
3	GOL	B	203	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12385 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 Superoxide dismutase [Cu-Zn].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	154	Total	C	N	O	S	0	3	0
			1139	698	208	229	4			
1	B	154	Total	C	N	O	S	0	2	0
			1134	692	210	228	4			
1	D	154	Total	C	N	O	S	0	1	0
			1119	683	205	227	4			
1	C	153	Total	C	N	O	S	0	5	0
			1146	701	209	232	4			
1	H	154	Total	C	N	O	S	3	3	0
			1125	687	206	228	4			
1	E	153	Total	C	N	O	S	0	3	0
			1128	690	206	228	4			
1	F	153	Total	C	N	O	S	0	1	0
			1118	685	204	225	4			
1	G	152	Total	C	N	O	S	0	1	0
			1111	679	203	225	4			
1	I	153	Total	C	N	O	S	0	2	0
			1122	685	205	228	4			
1	J	126	Total	C	N	O	S	3	1	0
			928	575	167	182	4			

There are 260 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-26	MET	-	initiating methionine	UNP P00441
A	-25	LYS	-	expression tag	UNP P00441
A	-24	HIS	-	expression tag	UNP P00441
A	-23	HIS	-	expression tag	UNP P00441
A	-22	HIS	-	expression tag	UNP P00441
A	-21	HIS	-	expression tag	UNP P00441
A	-20	HIS	-	expression tag	UNP P00441
A	-19	HIS	-	expression tag	UNP P00441
A	-18	PRO	-	expression tag	UNP P00441

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	expression tag	UNP P00441
A	-16	SER	-	expression tag	UNP P00441
A	-15	ASP	-	expression tag	UNP P00441
A	-14	TYR	-	expression tag	UNP P00441
A	-13	ASP	-	expression tag	UNP P00441
A	-12	ILE	-	expression tag	UNP P00441
A	-11	PRO	-	expression tag	UNP P00441
A	-10	THR	-	expression tag	UNP P00441
A	-9	THR	-	expression tag	UNP P00441
A	-8	GLU	-	expression tag	UNP P00441
A	-7	ASN	-	expression tag	UNP P00441
A	-6	LEU	-	expression tag	UNP P00441
A	-5	TYR	-	expression tag	UNP P00441
A	-4	PHE	-	expression tag	UNP P00441
A	-3	GLN	-	expression tag	UNP P00441
A	-2	GLY	-	expression tag	UNP P00441
A	-1	ALA	-	expression tag	UNP P00441
B	-26	MET	-	initiating methionine	UNP P00441
B	-25	LYS	-	expression tag	UNP P00441
B	-24	HIS	-	expression tag	UNP P00441
B	-23	HIS	-	expression tag	UNP P00441
B	-22	HIS	-	expression tag	UNP P00441
B	-21	HIS	-	expression tag	UNP P00441
B	-20	HIS	-	expression tag	UNP P00441
B	-19	HIS	-	expression tag	UNP P00441
B	-18	PRO	-	expression tag	UNP P00441
B	-17	MET	-	expression tag	UNP P00441
B	-16	SER	-	expression tag	UNP P00441
B	-15	ASP	-	expression tag	UNP P00441
B	-14	TYR	-	expression tag	UNP P00441
B	-13	ASP	-	expression tag	UNP P00441
B	-12	ILE	-	expression tag	UNP P00441
B	-11	PRO	-	expression tag	UNP P00441
B	-10	THR	-	expression tag	UNP P00441
B	-9	THR	-	expression tag	UNP P00441
B	-8	GLU	-	expression tag	UNP P00441
B	-7	ASN	-	expression tag	UNP P00441
B	-6	LEU	-	expression tag	UNP P00441
B	-5	TYR	-	expression tag	UNP P00441
B	-4	PHE	-	expression tag	UNP P00441
B	-3	GLN	-	expression tag	UNP P00441
B	-2	GLY	-	expression tag	UNP P00441

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	ALA	-	expression tag	UNP P00441
D	-26	MET	-	initiating methionine	UNP P00441
D	-25	LYS	-	expression tag	UNP P00441
D	-24	HIS	-	expression tag	UNP P00441
D	-23	HIS	-	expression tag	UNP P00441
D	-22	HIS	-	expression tag	UNP P00441
D	-21	HIS	-	expression tag	UNP P00441
D	-20	HIS	-	expression tag	UNP P00441
D	-19	HIS	-	expression tag	UNP P00441
D	-18	PRO	-	expression tag	UNP P00441
D	-17	MET	-	expression tag	UNP P00441
D	-16	SER	-	expression tag	UNP P00441
D	-15	ASP	-	expression tag	UNP P00441
D	-14	TYR	-	expression tag	UNP P00441
D	-13	ASP	-	expression tag	UNP P00441
D	-12	ILE	-	expression tag	UNP P00441
D	-11	PRO	-	expression tag	UNP P00441
D	-10	THR	-	expression tag	UNP P00441
D	-9	THR	-	expression tag	UNP P00441
D	-8	GLU	-	expression tag	UNP P00441
D	-7	ASN	-	expression tag	UNP P00441
D	-6	LEU	-	expression tag	UNP P00441
D	-5	TYR	-	expression tag	UNP P00441
D	-4	PHE	-	expression tag	UNP P00441
D	-3	GLN	-	expression tag	UNP P00441
D	-2	GLY	-	expression tag	UNP P00441
D	-1	ALA	-	expression tag	UNP P00441
C	-26	MET	-	initiating methionine	UNP P00441
C	-25	LYS	-	expression tag	UNP P00441
C	-24	HIS	-	expression tag	UNP P00441
C	-23	HIS	-	expression tag	UNP P00441
C	-22	HIS	-	expression tag	UNP P00441
C	-21	HIS	-	expression tag	UNP P00441
C	-20	HIS	-	expression tag	UNP P00441
C	-19	HIS	-	expression tag	UNP P00441
C	-18	PRO	-	expression tag	UNP P00441
C	-17	MET	-	expression tag	UNP P00441
C	-16	SER	-	expression tag	UNP P00441
C	-15	ASP	-	expression tag	UNP P00441
C	-14	TYR	-	expression tag	UNP P00441
C	-13	ASP	-	expression tag	UNP P00441
C	-12	ILE	-	expression tag	UNP P00441

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-11	PRO	-	expression tag	UNP P00441
C	-10	THR	-	expression tag	UNP P00441
C	-9	THR	-	expression tag	UNP P00441
C	-8	GLU	-	expression tag	UNP P00441
C	-7	ASN	-	expression tag	UNP P00441
C	-6	LEU	-	expression tag	UNP P00441
C	-5	TYR	-	expression tag	UNP P00441
C	-4	PHE	-	expression tag	UNP P00441
C	-3	GLN	-	expression tag	UNP P00441
C	-2	GLY	-	expression tag	UNP P00441
C	-1	ALA	-	expression tag	UNP P00441
H	-26	MET	-	initiating methionine	UNP P00441
H	-25	LYS	-	expression tag	UNP P00441
H	-24	HIS	-	expression tag	UNP P00441
H	-23	HIS	-	expression tag	UNP P00441
H	-22	HIS	-	expression tag	UNP P00441
H	-21	HIS	-	expression tag	UNP P00441
H	-20	HIS	-	expression tag	UNP P00441
H	-19	HIS	-	expression tag	UNP P00441
H	-18	PRO	-	expression tag	UNP P00441
H	-17	MET	-	expression tag	UNP P00441
H	-16	SER	-	expression tag	UNP P00441
H	-15	ASP	-	expression tag	UNP P00441
H	-14	TYR	-	expression tag	UNP P00441
H	-13	ASP	-	expression tag	UNP P00441
H	-12	ILE	-	expression tag	UNP P00441
H	-11	PRO	-	expression tag	UNP P00441
H	-10	THR	-	expression tag	UNP P00441
H	-9	THR	-	expression tag	UNP P00441
H	-8	GLU	-	expression tag	UNP P00441
H	-7	ASN	-	expression tag	UNP P00441
H	-6	LEU	-	expression tag	UNP P00441
H	-5	TYR	-	expression tag	UNP P00441
H	-4	PHE	-	expression tag	UNP P00441
H	-3	GLN	-	expression tag	UNP P00441
H	-2	GLY	-	expression tag	UNP P00441
H	-1	ALA	-	expression tag	UNP P00441
E	-26	MET	-	initiating methionine	UNP P00441
E	-25	LYS	-	expression tag	UNP P00441
E	-24	HIS	-	expression tag	UNP P00441
E	-23	HIS	-	expression tag	UNP P00441
E	-22	HIS	-	expression tag	UNP P00441

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-21	HIS	-	expression tag	UNP P00441
E	-20	HIS	-	expression tag	UNP P00441
E	-19	HIS	-	expression tag	UNP P00441
E	-18	PRO	-	expression tag	UNP P00441
E	-17	MET	-	expression tag	UNP P00441
E	-16	SER	-	expression tag	UNP P00441
E	-15	ASP	-	expression tag	UNP P00441
E	-14	TYR	-	expression tag	UNP P00441
E	-13	ASP	-	expression tag	UNP P00441
E	-12	ILE	-	expression tag	UNP P00441
E	-11	PRO	-	expression tag	UNP P00441
E	-10	THR	-	expression tag	UNP P00441
E	-9	THR	-	expression tag	UNP P00441
E	-8	GLU	-	expression tag	UNP P00441
E	-7	ASN	-	expression tag	UNP P00441
E	-6	LEU	-	expression tag	UNP P00441
E	-5	TYR	-	expression tag	UNP P00441
E	-4	PHE	-	expression tag	UNP P00441
E	-3	GLN	-	expression tag	UNP P00441
E	-2	GLY	-	expression tag	UNP P00441
E	-1	ALA	-	expression tag	UNP P00441
F	-26	MET	-	initiating methionine	UNP P00441
F	-25	LYS	-	expression tag	UNP P00441
F	-24	HIS	-	expression tag	UNP P00441
F	-23	HIS	-	expression tag	UNP P00441
F	-22	HIS	-	expression tag	UNP P00441
F	-21	HIS	-	expression tag	UNP P00441
F	-20	HIS	-	expression tag	UNP P00441
F	-19	HIS	-	expression tag	UNP P00441
F	-18	PRO	-	expression tag	UNP P00441
F	-17	MET	-	expression tag	UNP P00441
F	-16	SER	-	expression tag	UNP P00441
F	-15	ASP	-	expression tag	UNP P00441
F	-14	TYR	-	expression tag	UNP P00441
F	-13	ASP	-	expression tag	UNP P00441
F	-12	ILE	-	expression tag	UNP P00441
F	-11	PRO	-	expression tag	UNP P00441
F	-10	THR	-	expression tag	UNP P00441
F	-9	THR	-	expression tag	UNP P00441
F	-8	GLU	-	expression tag	UNP P00441
F	-7	ASN	-	expression tag	UNP P00441
F	-6	LEU	-	expression tag	UNP P00441

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-5	TYR	-	expression tag	UNP P00441
F	-4	PHE	-	expression tag	UNP P00441
F	-3	GLN	-	expression tag	UNP P00441
F	-2	GLY	-	expression tag	UNP P00441
F	-1	ALA	-	expression tag	UNP P00441
G	-26	MET	-	initiating methionine	UNP P00441
G	-25	LYS	-	expression tag	UNP P00441
G	-24	HIS	-	expression tag	UNP P00441
G	-23	HIS	-	expression tag	UNP P00441
G	-22	HIS	-	expression tag	UNP P00441
G	-21	HIS	-	expression tag	UNP P00441
G	-20	HIS	-	expression tag	UNP P00441
G	-19	HIS	-	expression tag	UNP P00441
G	-18	PRO	-	expression tag	UNP P00441
G	-17	MET	-	expression tag	UNP P00441
G	-16	SER	-	expression tag	UNP P00441
G	-15	ASP	-	expression tag	UNP P00441
G	-14	TYR	-	expression tag	UNP P00441
G	-13	ASP	-	expression tag	UNP P00441
G	-12	ILE	-	expression tag	UNP P00441
G	-11	PRO	-	expression tag	UNP P00441
G	-10	THR	-	expression tag	UNP P00441
G	-9	THR	-	expression tag	UNP P00441
G	-8	GLU	-	expression tag	UNP P00441
G	-7	ASN	-	expression tag	UNP P00441
G	-6	LEU	-	expression tag	UNP P00441
G	-5	TYR	-	expression tag	UNP P00441
G	-4	PHE	-	expression tag	UNP P00441
G	-3	GLN	-	expression tag	UNP P00441
G	-2	GLY	-	expression tag	UNP P00441
G	-1	ALA	-	expression tag	UNP P00441
I	-26	MET	-	initiating methionine	UNP P00441
I	-25	LYS	-	expression tag	UNP P00441
I	-24	HIS	-	expression tag	UNP P00441
I	-23	HIS	-	expression tag	UNP P00441
I	-22	HIS	-	expression tag	UNP P00441
I	-21	HIS	-	expression tag	UNP P00441
I	-20	HIS	-	expression tag	UNP P00441
I	-19	HIS	-	expression tag	UNP P00441
I	-18	PRO	-	expression tag	UNP P00441
I	-17	MET	-	expression tag	UNP P00441
I	-16	SER	-	expression tag	UNP P00441

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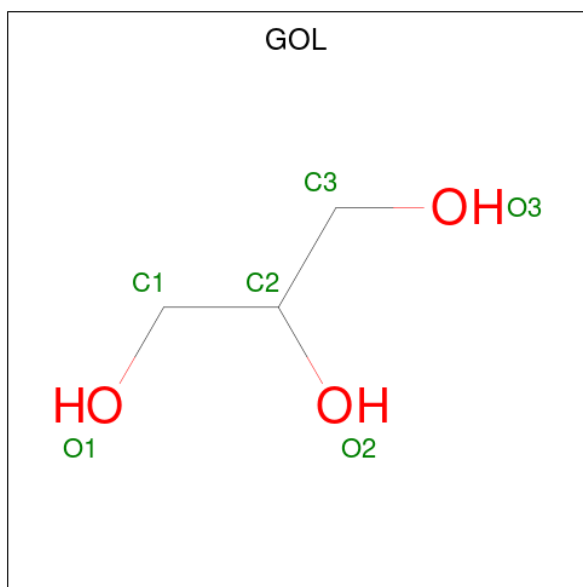
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Chain	Residue	Modelled	Actual	Comment	Reference
I	-15	ASP	-	expression tag	UNP P00441
I	-14	TYR	-	expression tag	UNP P00441
I	-13	ASP	-	expression tag	UNP P00441
I	-12	ILE	-	expression tag	UNP P00441
I	-11	PRO	-	expression tag	UNP P00441
I	-10	THR	-	expression tag	UNP P00441
I	-9	THR	-	expression tag	UNP P00441
I	-8	GLU	-	expression tag	UNP P00441
I	-7	ASN	-	expression tag	UNP P00441
I	-6	LEU	-	expression tag	UNP P00441
I	-5	TYR	-	expression tag	UNP P00441
I	-4	PHE	-	expression tag	UNP P00441
I	-3	GLN	-	expression tag	UNP P00441
I	-2	GLY	-	expression tag	UNP P00441
I	-1	ALA	-	expression tag	UNP P00441
J	-26	MET	-	initiating methionine	UNP P00441
J	-25	LYS	-	expression tag	UNP P00441
J	-24	HIS	-	expression tag	UNP P00441
J	-23	HIS	-	expression tag	UNP P00441
J	-22	HIS	-	expression tag	UNP P00441
J	-21	HIS	-	expression tag	UNP P00441
J	-20	HIS	-	expression tag	UNP P00441
J	-19	HIS	-	expression tag	UNP P00441
J	-18	PRO	-	expression tag	UNP P00441
J	-17	MET	-	expression tag	UNP P00441
J	-16	SER	-	expression tag	UNP P00441
J	-15	ASP	-	expression tag	UNP P00441
J	-14	TYR	-	expression tag	UNP P00441
J	-13	ASP	-	expression tag	UNP P00441
J	-12	ILE	-	expression tag	UNP P00441
J	-11	PRO	-	expression tag	UNP P00441
J	-10	THR	-	expression tag	UNP P00441
J	-9	THR	-	expression tag	UNP P00441
J	-8	GLU	-	expression tag	UNP P00441
J	-7	ASN	-	expression tag	UNP P00441
J	-6	LEU	-	expression tag	UNP P00441
J	-5	TYR	-	expression tag	UNP P00441
J	-4	PHE	-	expression tag	UNP P00441
J	-3	GLN	-	expression tag	UNP P00441
J	-2	GLY	-	expression tag	UNP P00441
J	-1	ALA	-	expression tag	UNP P00441

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	H	1	Total Zn 1 1	0	0
2	E	1	Total Zn 1 1	0	0
2	F	1	Total Zn 1 1	0	0
2	G	1	Total Zn 1 1	0	0
2	I	1	Total Zn 1 1	0	0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



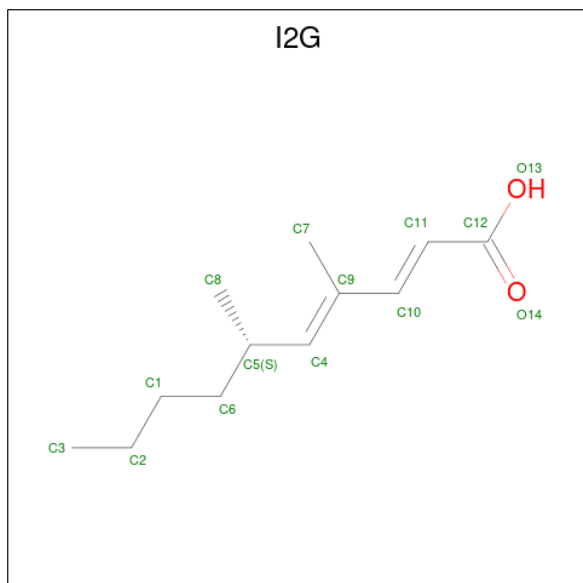
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0

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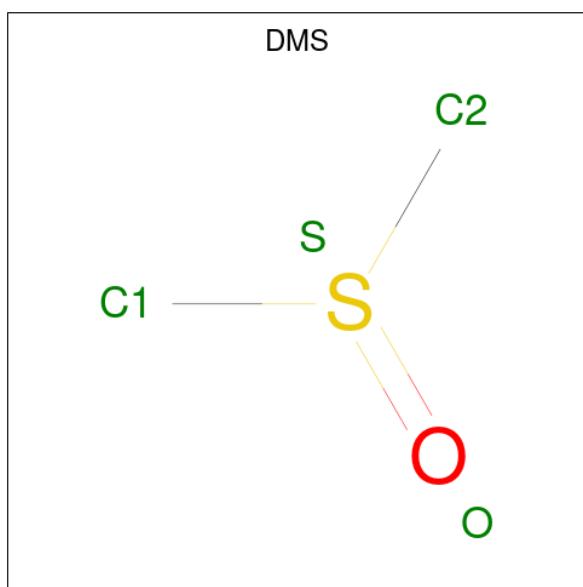
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is (2 {E},4 {E},6 {S})-4,6-dimethyldeca-2,4-dienoic acid (CCD ID: I2G) (formula: C₁₂H₂₀O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			14	12	2		
4	D	1	Total	C	O	0	0
			14	12	2		
4	C	1	Total	C	O	0	0
			14	12	2		
4	I	1	Total	C	O	0	0
			14	12	2		

- Molecule 5 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	E	1	Total	C	O	S	0	0
			4	2	1	1		

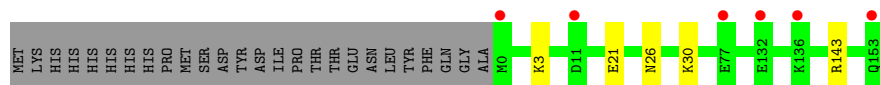
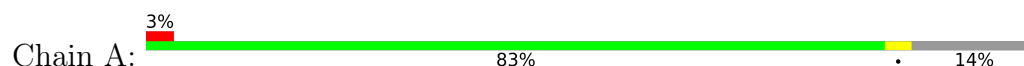
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	147	Total	O	0	1
			148	148		
6	B	171	Total	O	0	2
			173	173		
6	D	116	Total	O	0	0
			116	116		
6	C	163	Total	O	0	0
			163	163		
6	H	111	Total	O	0	2
			113	113		
6	E	160	Total	O	0	1
			161	161		
6	F	66	Total	O	0	0
			66	66		
6	G	82	Total	O	0	0
			82	82		
6	I	125	Total	O	0	2
			127	127		
6	J	67	Total	O	0	0
			67	67		

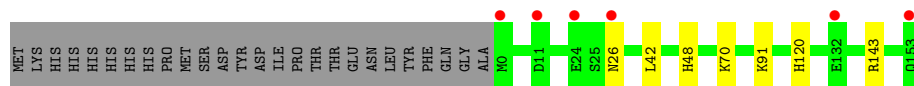
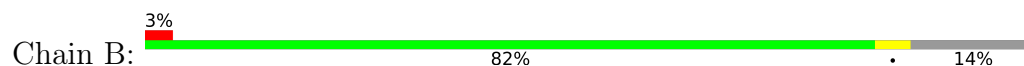
3 Residue-property plots [i](#)

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.

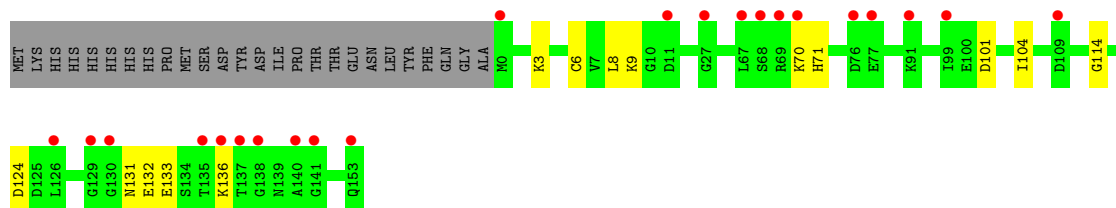
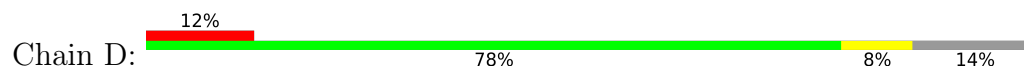
- Molecule 1: Superoxide dismutase [Cu-Zn]



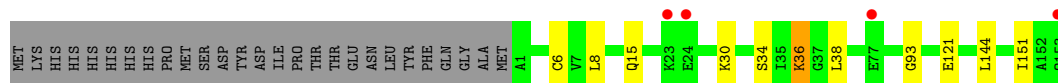
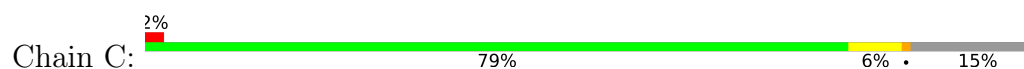
- Molecule 1: Superoxide dismutase [Cu-Zn]



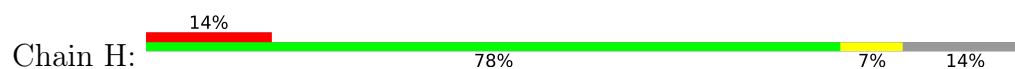
- Molecule 1: Superoxide dismutase [Cu-Zn]

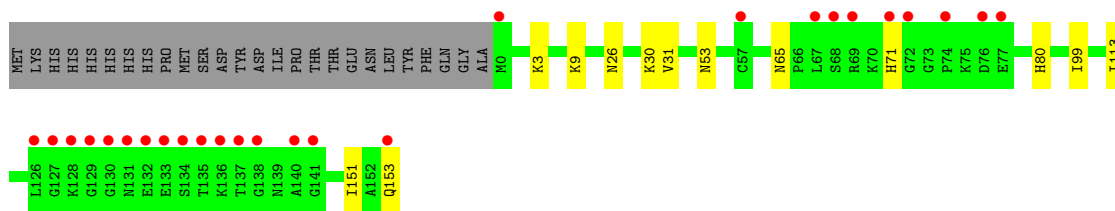


- Molecule 1: Superoxide dismutase [Cu-Zn]

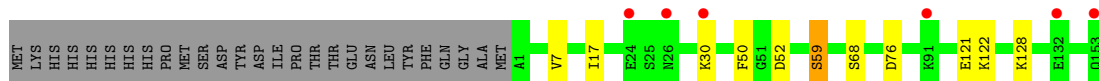
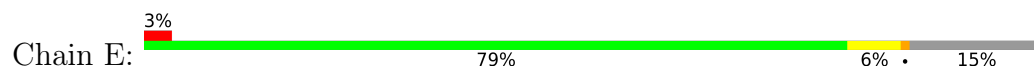


- Molecule 1: Superoxide dismutase [Cu-Zn]

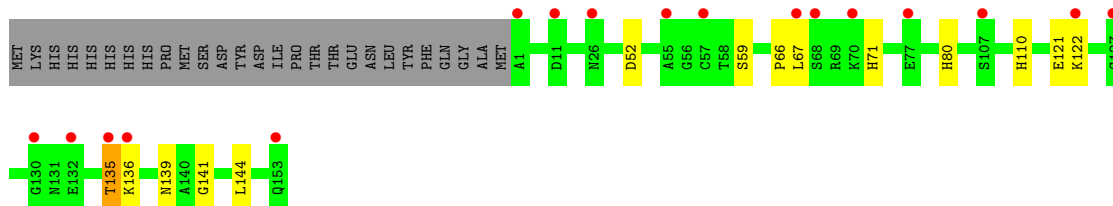
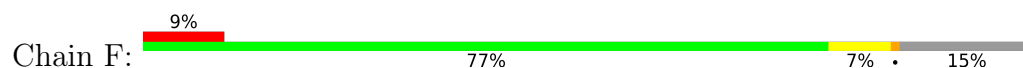




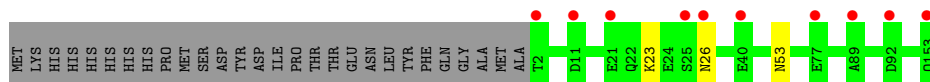
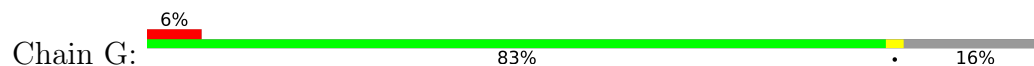
• Molecule 1: Superoxide dismutase [Cu-Zn]



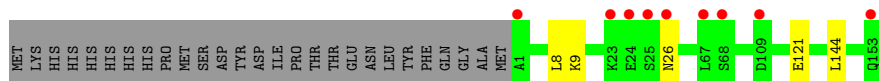
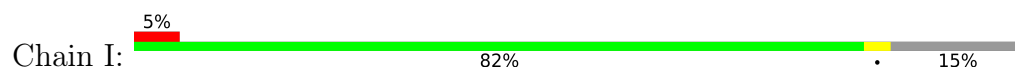
• Molecule 1: Superoxide dismutase [Cu-Zn]



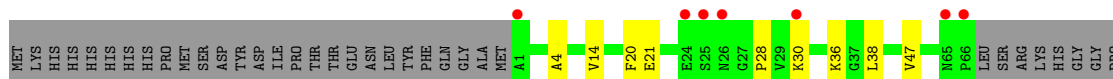
• Molecule 1: Superoxide dismutase [Cu-Zn]

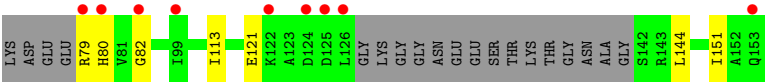


• Molecule 1: Superoxide dismutase [Cu-Zn]



• Molecule 1: Superoxide dismutase [Cu-Zn]





4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	242.44Å 242.44Å 144.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.69 – 1.90 38.69 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.6 (38.69-1.90) 99.9 (38.69-1.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.199 , 0.230 (Not available) , 0.215	Depositor DCC
R_{free} test set	9850 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	27.5	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 40.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12385	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.24% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: I2G, ZN, GOL, DMS

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	0.32	0/1157	0.53	0/1560
1	B	0.45	0/1152	0.60	0/1552
1	C	0.57	2/1164 (0.2%)	0.70	4/1569 (0.3%)
1	D	0.42	0/1137	0.59	0/1534
1	E	0.35	0/1146	0.54	0/1544
1	F	0.35	0/1136	0.52	0/1531
1	G	0.39	0/1129	0.58	0/1521
1	H	0.38	0/1143	0.63	0/1544
1	I	0.30	0/1140	0.52	0/1536
1	J	0.38	0/942	0.61	0/1270
All	All	0.40	2/11246 (0.0%)	0.59	4/15161 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	34[A]	SER	C-N	-9.50	1.21	1.33
1	C	34[B]	SER	C-N	-9.50	1.21	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	34[A]	SER	CA-C-N	7.11	132.87	122.99
1	C	34[A]	SER	C-N-CA	7.11	132.87	122.99
1	C	34[B]	SER	CA-C-N	7.11	132.87	122.99
1	C	34[B]	SER	C-N-CA	7.11	132.87	122.99

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	1139	0	1104	6	0
1	B	1134	0	1096	8	0
1	C	1146	0	1110	7	0
1	D	1119	0	1073	11	0
1	E	1128	0	1090	9	0
1	F	1118	0	1087	8	0
1	G	1111	0	1073	1	0
1	H	1125	0	1072	10	0
1	I	1122	0	1085	3	0
1	J	928	0	907	11	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
3	A	6	0	8	4	0
3	B	18	0	24	4	0
3	D	6	0	8	1	0
4	B	14	0	0	1	0
4	C	14	0	0	1	0
4	D	14	0	0	2	0
4	I	14	0	0	2	0
5	E	4	0	6	0	0
6	A	148	0	0	2	0
6	B	173	0	0	2	0
6	C	163	0	0	3	0
6	D	116	0	0	5	0
6	E	161	0	0	4	0
6	F	66	0	0	0	0
6	G	82	0	0	1	0
6	H	113	0	0	3	0
6	I	127	0	0	1	0
6	J	67	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	12385	0	10743	76	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 3.

All (76) 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:143:ARG:HH21	3:B:203:GOL:H32	1.42	0.81
1:A:3:LYS:NZ	1:A:21:GLU:OE2	2.18	0.76
1:C:30:LYS:NZ	6:C:302:HOH:O	2.18	0.76
1:H:53[B]:ASN:OD1	6:H:301:HOH:O	2.03	0.75
1:J:36[B]:LYS:O	6:J:201:HOH:O	2.05	0.74
1:J:36[A]:LYS:O	6:J:201:HOH:O	2.08	0.72
1:F:122:LYS:NZ	1:F:139:ASN:O	2.24	0.70
1:A:143:ARG:HH21	3:A:202:GOL:H2	1.58	0.67
1:B:91:LYS:NZ	6:B:302:HOH:O	2.25	0.67
1:B:70:LYS:NZ	6:B:301:HOH:O	2.25	0.67
1:E:52:ASP:O	1:E:59:SER:HB2	1.96	0.66
1:B:48:HIS:HE1	3:B:203:GOL:H11	1.60	0.65
1:E:76:ASP:OD2	6:E:301:HOH:O	2.15	0.65
1:J:38:LEU:HG	6:J:201:HOH:O	1.97	0.65
1:J:14:VAL:HG13	6:J:201:HOH:O	1.97	0.64
1:I:8:LEU:O	1:I:9:LYS:HD3	1.99	0.63
1:F:52:ASP:O	1:F:59:SER:HB2	2.01	0.61
1:C:6:CYS:O	6:C:301:HOH:O	2.15	0.60
1:D:9:LYS:HE2	4:D:202:I2G:C8	2.31	0.60
1:C:15:GLN:HG2	1:C:36:LYS:HE3	1.85	0.58
1:C:8:LEU:HG	6:C:301:HOH:O	2.03	0.58
1:I:26:ASN:ND2	6:I:301:HOH:O	2.26	0.57
1:E:128:LYS:NZ	6:E:301:HOH:O	2.21	0.57
1:E:121:GLU:HG2	1:E:122:LYS:HG2	1.88	0.56
1:E:17:ILE:HG23	6:E:302:HOH:O	2.04	0.56
1:A:143:ARG:NH2	3:A:202:GOL:H2	2.21	0.55
1:D:8:LEU:HG	6:D:301:HOH:O	2.07	0.55
1:B:48:HIS:CE1	3:B:203:GOL:H11	2.41	0.55
1:H:9:LYS:NZ	6:H:303:HOH:O	2.41	0.54
1:B:42:LEU:HD11	4:C:202:I2G:C8	2.38	0.53
1:B:120:HIS:HE1	3:B:203:GOL:H2	1.73	0.53
4:I:202:I2G:C7	4:I:202:I2G:C8	2.86	0.53
1:D:114:GLY:O	1:C:151[B]:ILE:HG22	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:ASN:HA	1:H:26:ASN:HA	1.94	0.50
1:J:4:ALA:HB3	1:J:20:PHE:HB2	1.94	0.49
1:J:47:VAL:HB	1:J:82:GLY:HA3	1.93	0.49
1:J:113:ILE:HD13	1:J:151:ILE:HG12	1.94	0.49
1:F:135:THR:HG22	1:F:136:LYS:HE3	1.95	0.48
1:D:132:GLU:OE2	1:D:136:LYS:NZ	2.45	0.48
1:C:121:GLU:HA	1:C:144:LEU:HD11	1.96	0.48
1:F:71:HIS:HB2	1:F:80:HIS:CE1	2.49	0.47
1:H:3:LYS:NZ	1:H:153:GLN:O	2.37	0.47
1:J:21:GLU:HG2	1:J:30:LYS:HE3	1.96	0.47
1:D:131:ASN:ND2	1:D:133:GLU:H	2.13	0.46
4:B:202:I2G:C6	4:B:202:I2G:C7	2.93	0.46
1:F:67:LEU:HD21	1:F:110:HIS:NE2	2.31	0.45
1:J:121:GLU:HA	1:J:144:LEU:HD11	1.99	0.45
1:B:26:ASN:ND2	1:E:68:SER:HB2	2.31	0.45
1:D:101:ASP:O	6:D:302:HOH:O	2.21	0.45
1:D:71:HIS:HE2	1:D:124:ASP:CG	2.24	0.44
1:D:101:ASP:OD2	1:D:104:ILE:HG12	2.17	0.44
3:A:202:GOL:H32	6:A:374:HOH:O	2.16	0.44
1:H:30:LYS:HE2	6:H:372:HOH:O	2.17	0.44
1:D:6:CYS:O	6:D:301:HOH:O	2.21	0.44
1:H:65:ASN:CG	1:H:80:HIS:HD2	2.26	0.43
1:G:53:ASN:HB2	6:G:362:HOH:O	2.17	0.43
1:C:38:LEU:O	1:C:93:GLY:HA2	2.18	0.43
1:A:30:LYS:NZ	6:A:301:HOH:O	2.32	0.43
1:I:121:GLU:HA	1:I:144:LEU:HD11	2.01	0.43
1:E:7:VAL:HG22	6:E:302:HOH:O	2.18	0.43
1:A:143:ARG:HE	3:A:202:GOL:H2	1.85	0.42
4:D:202:I2G:C8	4:D:202:I2G:C7	2.97	0.42
1:J:28:PRO:HD3	6:J:218:HOH:O	2.18	0.42
1:J:79:ARG:HB2	1:J:80:HIS:H	1.62	0.42
1:F:66:PRO:HG2	1:F:67:LEU:HD22	2.01	0.42
1:D:131:ASN:HD21	1:D:133:GLU:HB3	1.85	0.42
1:H:113[B]:ILE:HD13	1:H:151:ILE:HG12	2.01	0.42
1:F:121:GLU:HA	1:F:144:LEU:HD11	2.02	0.41
1:H:71:HIS:HB2	1:H:80:HIS:CE1	2.55	0.41
1:D:3:LYS:HE3	6:D:339:HOH:O	2.20	0.41
4:I:202:I2G:C7	4:I:202:I2G:C6	2.98	0.41
3:D:203:GOL:O2	6:D:303:HOH:O	2.21	0.41
1:H:31:VAL:HB	1:H:99:ILE:HB	2.03	0.40
1:H:153:GLN:HB2	1:E:50:PHE:CZ	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:122:LYS:HE3	1:F:141:GLY:HA3	2.03	0.40
1:E:30:LYS:HA	1:E:30:LYS:HD2	1.77	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	155/180 (86%)	155 (100%)	0	0	100	100
1	B	154/180 (86%)	154 (100%)	0	0	100	100
1	C	156/180 (87%)	155 (99%)	1 (1%)	0	100	100
1	D	153/180 (85%)	149 (97%)	4 (3%)	0	100	100
1	E	154/180 (86%)	154 (100%)	0	0	100	100
1	F	152/180 (84%)	149 (98%)	3 (2%)	0	100	100
1	G	151/180 (84%)	150 (99%)	1 (1%)	0	100	100
1	H	155/180 (86%)	155 (100%)	0	0	100	100
1	I	153/180 (85%)	152 (99%)	1 (1%)	0	100	100
1	J	121/180 (67%)	120 (99%)	1 (1%)	0	100	100
All	All	1504/1800 (84%)	1493 (99%)	11 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	121/143 (85%)	121 (100%)	0	100	100
1	B	120/143 (84%)	120 (100%)	0	100	100
1	C	123/143 (86%)	122 (99%)	1 (1%)	73	75
1	D	118/143 (82%)	117 (99%)	1 (1%)	73	75
1	E	120/143 (84%)	119 (99%)	1 (1%)	73	75
1	F	119/143 (83%)	118 (99%)	1 (1%)	73	75
1	G	119/143 (83%)	117 (98%)	2 (2%)	53	52
1	H	118/143 (82%)	118 (100%)	0	100	100
1	I	120/143 (84%)	120 (100%)	0	100	100
1	J	100/143 (70%)	100 (100%)	0	100	100
All	All	1178/1430 (82%)	1172 (100%)	6 (0%)	81	84

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	70	LYS
1	C	36	LYS
1	E	59	SER
1	F	135	THR
1	G	23	LYS
1	G	26	ASN

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

Mol	Chain	Res	Type
1	D	110	HIS
1	D	131	ASN
1	H	19	ASN
1	E	53	ASN
1	F	15	GLN
1	F	53	ASN
1	I	53	ASN
1	J	53	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 9 are monoatomic - leaving 10 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	$\# Z > 2$
3	GOL	D	203	-	5,5,5	0.94	0	5,5,5	0.93	0
3	GOL	B	205	-	5,5,5	1.04	0	5,5,5	1.03	0
4	I2G	I	202	-	13,13,13	0.68	0	14,15,15	1.78	2 (14%)
4	I2G	B	202	-	13,13,13	0.68	0	14,15,15	1.78	2 (14%)
3	GOL	B	204	-	5,5,5	0.95	0	5,5,5	0.95	0
4	I2G	D	202	-	13,13,13	0.69	0	14,15,15	1.77	2 (14%)
5	DMS	E	201	-	3,3,3	0.69	0	3,3,3	0.91	0
3	GOL	B	203	-	5,5,5	0.83	0	5,5,5	0.94	0
4	I2G	C	202	-	13,13,13	0.68	0	14,15,15	1.79	2 (14%)
3	GOL	A	202	-	5,5,5	0.95	0	5,5,5	1.16	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
3	GOL	D	203	-	-	4/4/4/4	-
3	GOL	B	205	-	-	0/4/4/4	-
4	I2G	I	202	-	-	4/13/13/13	-
4	I2G	B	202	-	-	10/13/13/13	-
3	GOL	B	204	-	-	2/4/4/4	-
4	I2G	D	202	-	-	5/13/13/13	-
3	GOL	B	203	-	-	2/4/4/4	-
4	I2G	C	202	-	-	1/13/13/13	-
3	GOL	A	202	-	-	0/4/4/4	-

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	202	I2G	C5-C4-C9	-4.50	120.44	128.13
4	I	202	I2G	C5-C4-C9	-4.48	120.47	128.13
4	B	202	I2G	C5-C4-C9	-4.45	120.53	128.13
4	D	202	I2G	C5-C4-C9	-4.42	120.58	128.13
4	C	202	I2G	C11-C10-C9	-4.24	119.96	126.23
4	B	202	I2G	C11-C10-C9	-4.22	119.98	126.23
4	I	202	I2G	C11-C10-C9	-4.21	120.00	126.23
4	D	202	I2G	C11-C10-C9	-4.20	120.02	126.23

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	203	GOL	O1-C1-C2-C3
3	B	204	GOL	O1-C1-C2-C3
3	D	203	GOL	C1-C2-C3-O3
4	B	202	I2G	C9-C4-C5-C6
4	B	202	I2G	C9-C4-C5-C8
4	D	202	I2G	C9-C4-C5-C6
4	I	202	I2G	C9-C4-C5-C6
4	I	202	I2G	C9-C4-C5-C8
4	I	202	I2G	C11-C10-C9-C4
4	I	202	I2G	C11-C10-C9-C7
4	D	202	I2G	C10-C11-C12-O13
4	B	202	I2G	C10-C11-C12-O13
4	B	202	I2G	C10-C11-C12-O14
4	D	202	I2G	C10-C11-C12-O14

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Mol	Chain	Res	Type	Atoms
4	B	202	I2G	C11-C10-C9-C7
4	B	202	I2G	C11-C10-C9-C4
3	D	203	GOL	O1-C1-C2-C3
3	B	203	GOL	O1-C1-C2-O2
3	B	204	GOL	O1-C1-C2-O2
3	D	203	GOL	O2-C2-C3-O3
4	D	202	I2G	C9-C4-C5-C8
4	B	202	I2G	C8-C5-C6-C1
4	B	202	I2G	C4-C5-C6-C1
4	C	202	I2G	C6-C1-C2-C3
3	D	203	GOL	O1-C1-C2-O2
4	B	202	I2G	C2-C1-C6-C5
4	D	202	I2G	C8-C5-C6-C1
4	B	202	I2G	C6-C1-C2-C3

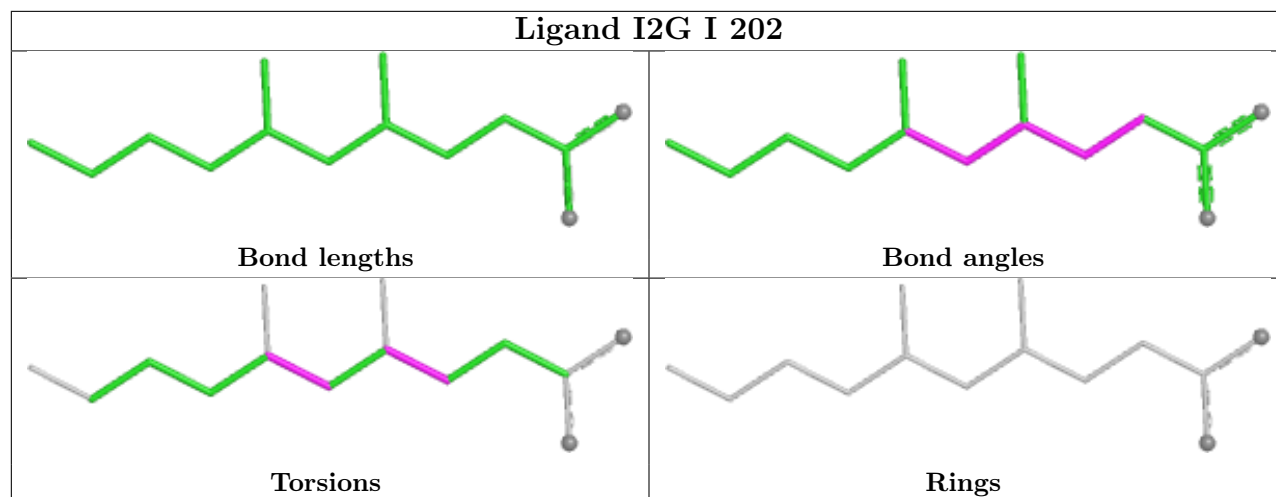
There are no ring outliers.

7 monomers are involved in 15 short contacts:

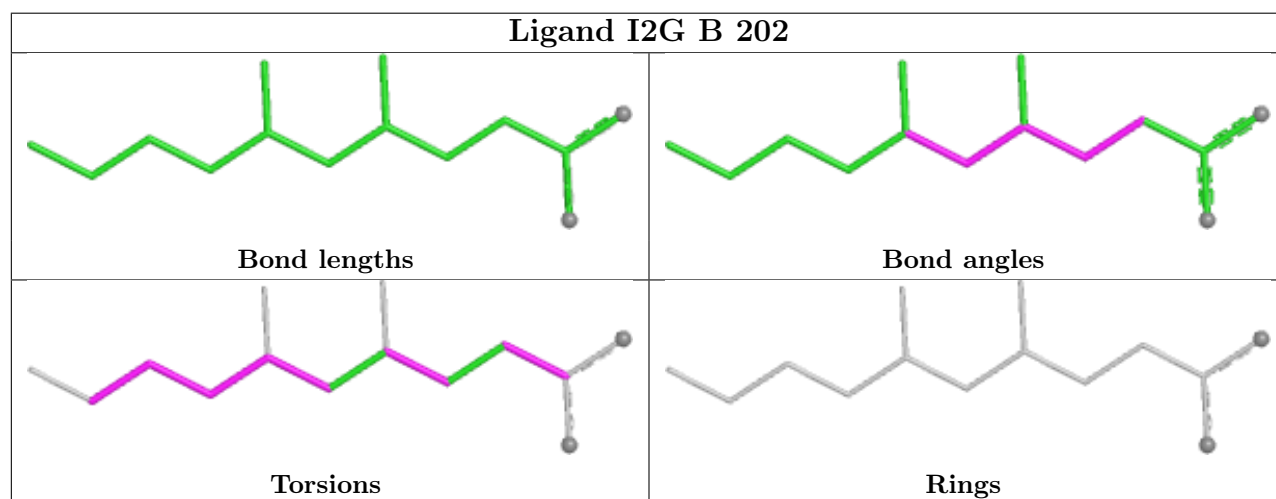
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	203	GOL	1	0
4	I	202	I2G	2	0
4	B	202	I2G	1	0
4	D	202	I2G	2	0
3	B	203	GOL	4	0
4	C	202	I2G	1	0
3	A	202	GOL	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

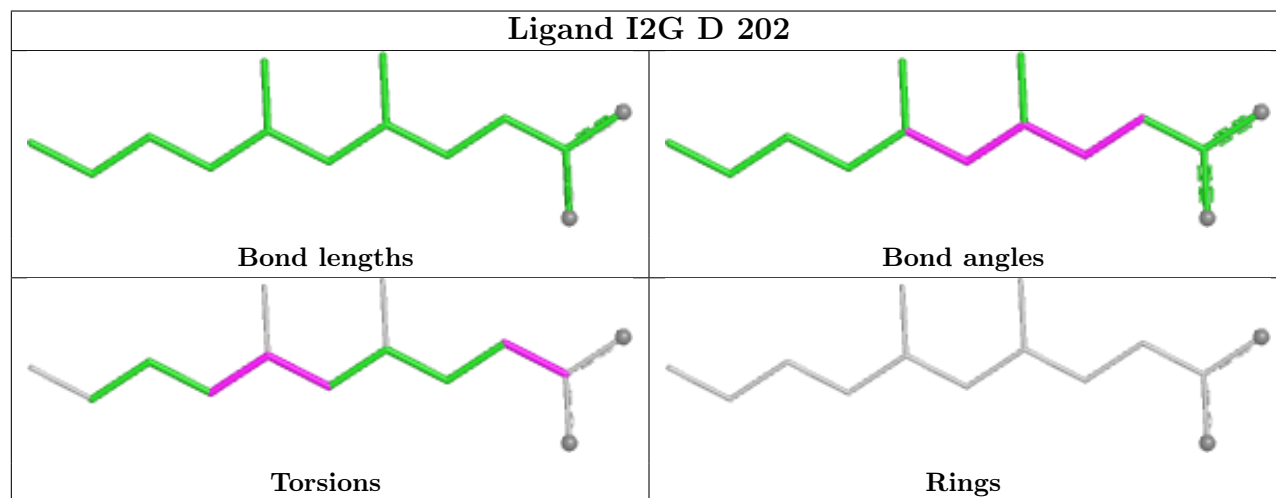
Ligand I2G I 202

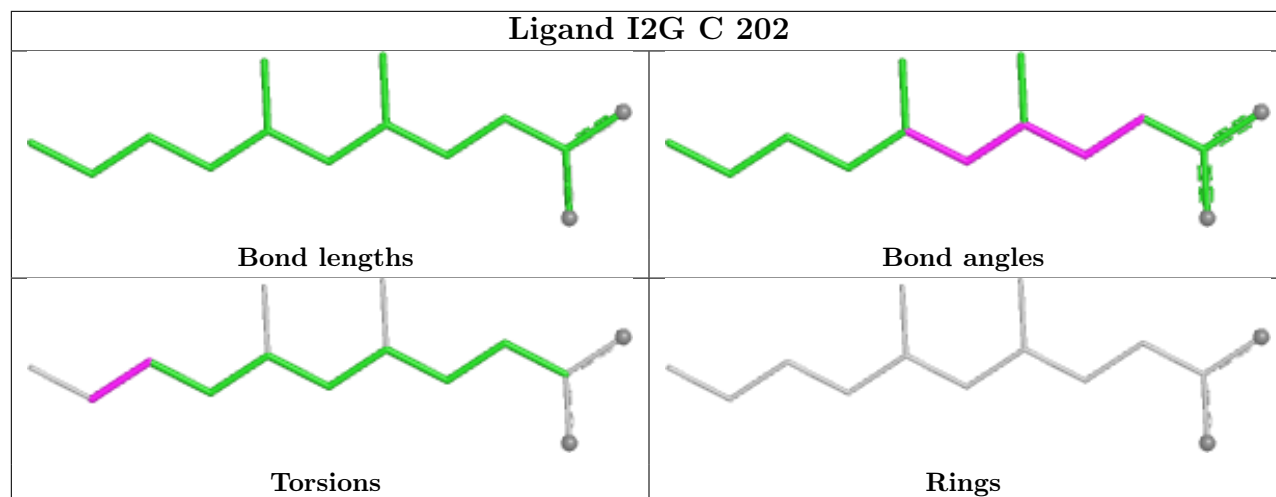


Ligand I2G B 202



Ligand I2G D 202





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	154/180 (85%)	0.10	6 (3%) 43 46	10, 26, 42, 53	3 (1%)
1	B	154/180 (85%)	-0.07	6 (3%) 43 46	12, 22, 39, 49	2 (1%)
1	C	153/180 (85%)	-0.18	4 (2%) 57 61	11, 22, 37, 48	5 (3%)
1	D	154/180 (85%)	0.86	22 (14%) 6 6	14, 32, 52, 58	1 (0%)
1	E	153/180 (85%)	-0.03	6 (3%) 43 46	10, 23, 38, 50	3 (1%)
1	F	153/180 (85%)	0.94	17 (11%) 10 11	16, 40, 55, 60	1 (0%)
1	G	152/180 (84%)	0.75	10 (6%) 24 26	16, 37, 52, 59	1 (0%)
1	H	154/180 (85%)	0.89	26 (16%) 4 4	11, 33, 57, 61	4 (2%)
1	I	153/180 (85%)	0.37	9 (5%) 28 30	14, 30, 48, 58	2 (1%)
1	J	126/180 (70%)	0.85	16 (12%) 8 8	17, 35, 52, 61	2 (1%)
All	All	1506/1800 (83%)	0.44	122 (8%) 18 19	10, 30, 51, 61	24 (1%)

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	126	LEU	5.7
1	G	26	ASN	4.9
1	A	132	GLU	4.7
1	H	137	THR	4.4
1	C	77	GLU	4.3
1	F	130	GLY	4.3
1	G	25	SER	4.2
1	F	55	ALA	4.2
1	J	24	GLU	4.0
1	D	130	GLY	3.9
1	H	127	GLY	3.8
1	H	135	THR	3.8
1	J	26	ASN	3.8

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Mol	Chain	Res	Type	RSRZ
1	J	82	GLY	3.7
1	J	1	ALA	3.7
1	B	0	MET	3.6
1	C	153	GLN	3.6
1	H	129	GLY	3.5
1	F	135	THR	3.4
1	I	153	GLN	3.4
1	D	67	LEU	3.4
1	J	125	ASP	3.4
1	I	1	ALA	3.4
1	H	67	LEU	3.4
1	B	132	GLU	3.4
1	B	26	ASN	3.4
1	F	26	ASN	3.4
1	D	0	MET	3.3
1	D	76	ASP	3.3
1	H	134	SER	3.3
1	F	67	LEU	3.2
1	E	26	ASN	3.2
1	A	0	MET	3.1
1	H	140	ALA	3.1
1	D	153	GLN	3.1
1	J	79	ARG	3.1
1	D	11	ASP	3.1
1	I	23	LYS	3.1
1	H	69	ARG	3.0
1	G	153	GLN	3.0
1	H	131	ASN	3.0
1	E	153	GLN	3.0
1	H	74	PRO	3.0
1	D	99	ILE	3.0
1	H	132	GLU	2.9
1	I	25	SER	2.9
1	D	126	LEU	2.9
1	H	126	LEU	2.9
1	D	68	SER	2.8
1	I	24	GLU	2.8
1	B	11	ASP	2.8
1	J	25	SER	2.8
1	D	77	GLU	2.7
1	F	11	ASP	2.7
1	J	124	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	I	67	LEU	2.7
1	H	136	LYS	2.7
1	D	109	ASP	2.7
1	H	76	ASP	2.7
1	D	129	GLY	2.6
1	H	141	GLY	2.6
1	D	135	THR	2.6
1	G	2	THR	2.6
1	G	11	ASP	2.6
1	F	77	GLU	2.6
1	A	77	GLU	2.6
1	J	99	ILE	2.5
1	H	68	SER	2.5
1	H	0	MET	2.5
1	H	77	GLU	2.5
1	B	153	GLN	2.5
1	F	107	SER	2.5
1	B	24	GLU	2.5
1	G	77	GLU	2.5
1	F	57	CYS	2.4
1	C	23	LYS	2.4
1	I	109	ASP	2.4
1	J	66	PRO	2.4
1	G	21	GLU	2.4
1	D	27	GLY	2.4
1	J	80	HIS	2.4
1	E	91	LYS	2.4
1	A	153	GLN	2.4
1	H	138	GLY	2.4
1	A	136	LYS	2.4
1	A	11	ASP	2.3
1	H	130	GLY	2.3
1	D	91	LYS	2.3
1	H	133	GLU	2.3
1	D	70	LYS	2.3
1	D	69	ARG	2.3
1	H	72	GLY	2.3
1	I	26	ASN	2.3
1	J	122	LYS	2.2
1	F	127	GLY	2.2
1	I	68	SER	2.2
1	H	71	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	92	ASP	2.2
1	F	132	GLU	2.1
1	J	30	LYS	2.1
1	D	138	GLY	2.1
1	H	128	LYS	2.1
1	C	24	GLU	2.1
1	G	40	GLU	2.1
1	H	57	CYS	2.1
1	J	65	ASN	2.1
1	F	153	GLN	2.1
1	J	153	GLN	2.1
1	F	70	LYS	2.1
1	F	122	LYS	2.1
1	D	141	GLY	2.1
1	F	1	ALA	2.1
1	G	89	ALA	2.1
1	E	24	GLU	2.0
1	F	68	SER	2.0
1	D	137	THR	2.0
1	D	140	ALA	2.0
1	E	132	GLU	2.0
1	D	136	LYS	2.0
1	E	30	LYS	2.0
1	F	136	LYS	2.0
1	H	153	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

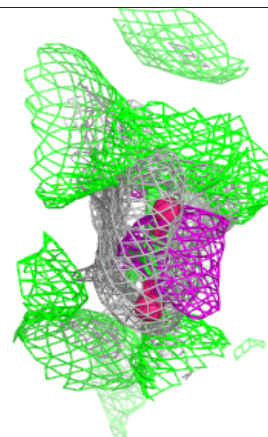
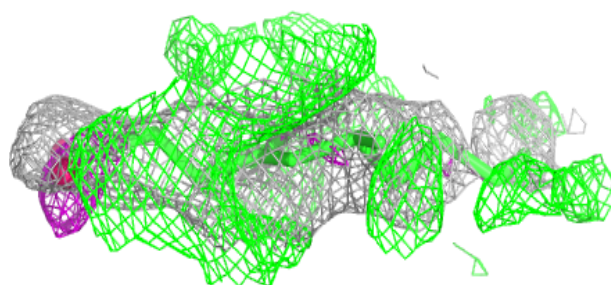
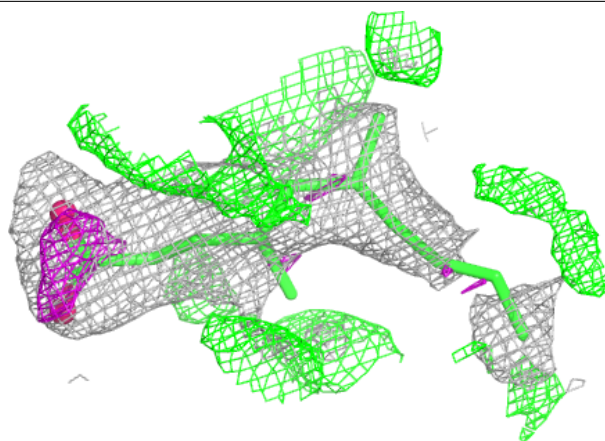
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	I2G	B	202	14/14	0.56	0.28	42,50,56,56	0
4	I2G	I	202	14/14	0.57	0.29	34,49,58,59	0
4	I2G	C	202	14/14	0.58	0.32	30,47,50,55	0
4	I2G	D	202	14/14	0.59	0.25	29,46,54,57	0
5	DMS	E	201	4/4	0.64	0.28	42,42,53,65	0
3	GOL	B	203	6/6	0.67	0.22	29,46,46,51	0
3	GOL	B	204	6/6	0.71	0.20	46,52,56,58	0
3	GOL	A	202	6/6	0.72	0.20	44,49,53,57	0
3	GOL	B	205	6/6	0.75	0.18	48,53,56,58	0
3	GOL	D	203	6/6	0.76	0.17	47,51,53,59	0
2	ZN	H	201	1/1	0.91	0.29	49,49,49,49	0
2	ZN	F	201	1/1	0.95	0.11	53,53,53,53	0
2	ZN	D	201	1/1	0.96	0.10	45,45,45,45	0
2	ZN	G	201	1/1	0.97	0.10	48,48,48,48	0
2	ZN	A	201	1/1	0.98	0.08	54,54,54,54	0
2	ZN	B	201	1/1	0.99	0.06	26,26,26,26	0
2	ZN	I	201	1/1	0.99	0.09	52,52,52,52	0
2	ZN	E	202	1/1	0.99	0.07	37,37,37,37	0
2	ZN	C	201	1/1	0.99	0.13	48,48,48,48	0

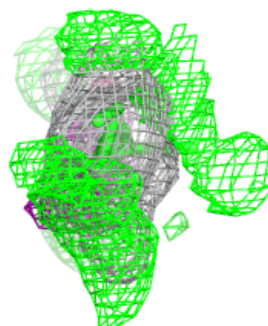
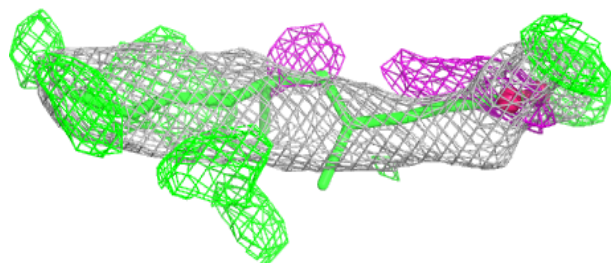
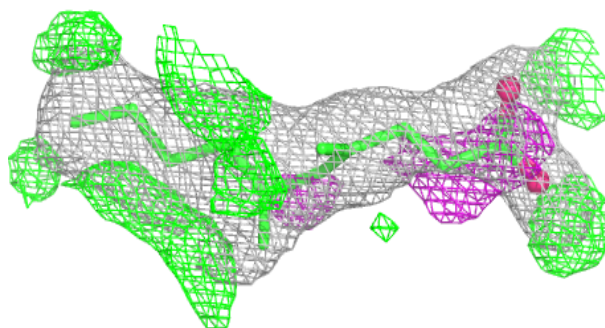
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around I2G B 202:

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

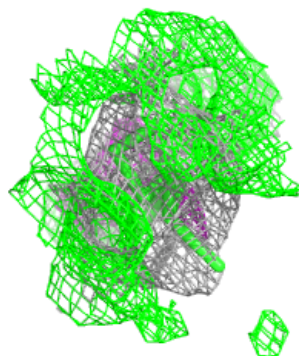
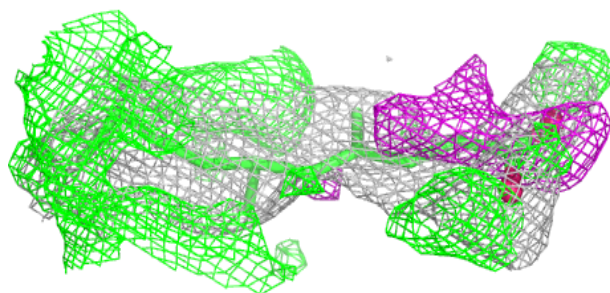
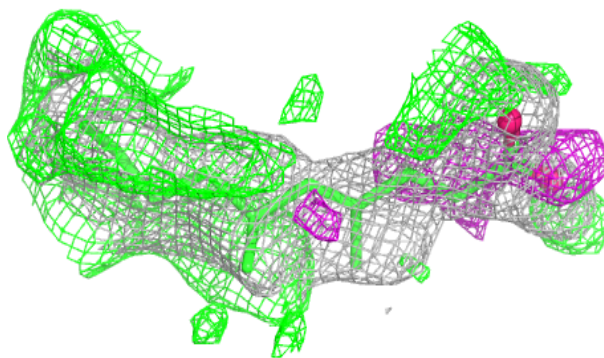
**Electron density around I2G I 202:**

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

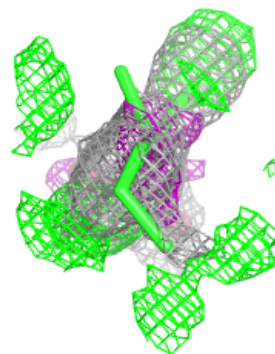
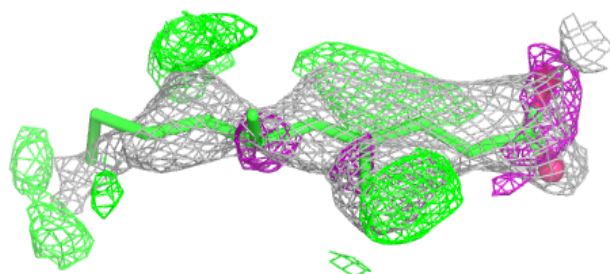
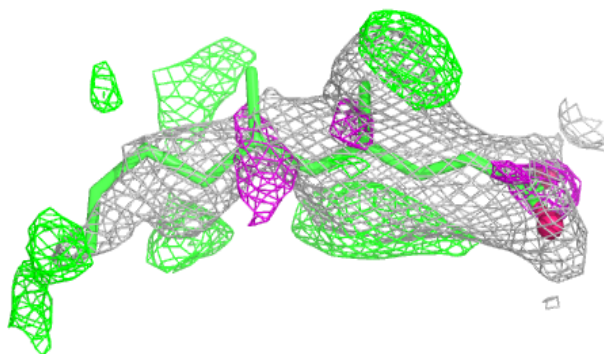


Electron density around I2G C 202:

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

**Electron density around I2G D 202:**

$2mF_o-DF_c$ (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.