



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:56 PM UTC

PDB ID : 5YTO / pdb_00005yto
Title : Crystal Structure of human Superoxide Dismutase I (hSOD1) in complex with a naphthalene-catechol linked compound.
Authors : Padmanabhan, B.; Manjula, R.
Deposited on : 2017-11-19
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/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

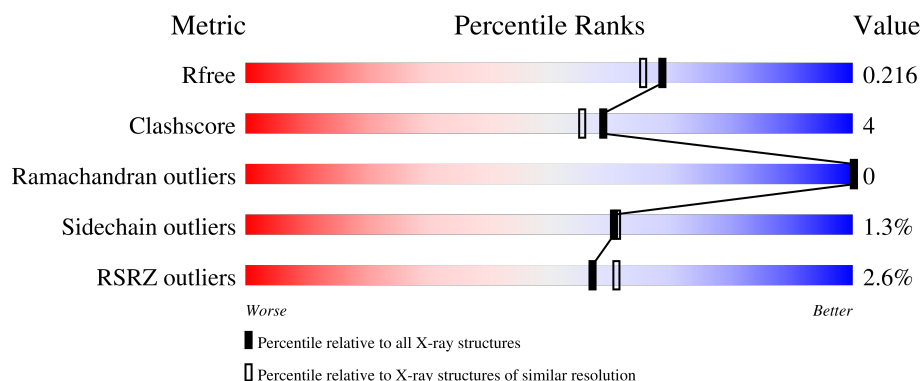
1 Overall quality at a glance

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	83% 14%
1	B	180	79% 6% 14%
1	C	180	79% 7% 14%
1	D	180	81% 6% 14%
1	E	180	83% 14%

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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	202	-	-	X	-
3	GOL	C	202	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12631 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	155	Total	C	N	O	S	0	2	0
			1134	695	206	228	5			
1	B	154	Total	C	N	O	S	0	5	0
			1147	702	209	232	4			
1	C	154	Total	C	N	O	S	0	3	0
			1126	691	204	227	4			
1	D	155	Total	C	N	O	S	0	0	0
			1120	685	205	226	4			
1	E	154	Total	C	N	O	S	0	2	0
			1127	688	206	229	4			
1	F	155	Total	C	N	O	S	0	3	0
			1131	690	207	230	4			
1	G	153	Total	C	N	O	S	0	1	0
			1109	679	203	223	4			
1	H	154	Total	C	N	O	S	0	2	0
			1124	687	205	228	4			
1	I	153	Total	C	N	O	S	0	0	0
			1110	679	203	224	4			
1	J	125	Total	C	N	O	S	0	0	0
			903	558	163	178	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
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
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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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
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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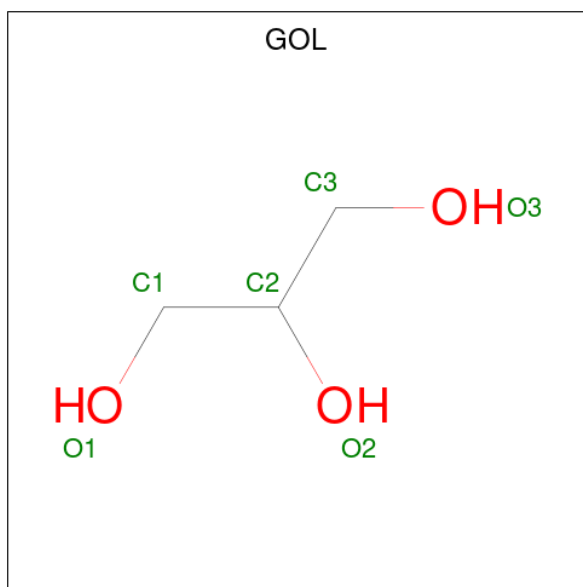
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Chain	Residue	Modelled	Actual	Comment	Reference
I	-15	ASP	-	expression tag	UNP P00441
I	-14	TYR	-	expression tag	UNP P00441
I	-13	ASP	-	expression tag	UNP P00441
I	-12	ILE	-	expression tag	UNP P00441
I	-11	PRO	-	expression tag	UNP P00441
I	-10	THR	-	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).

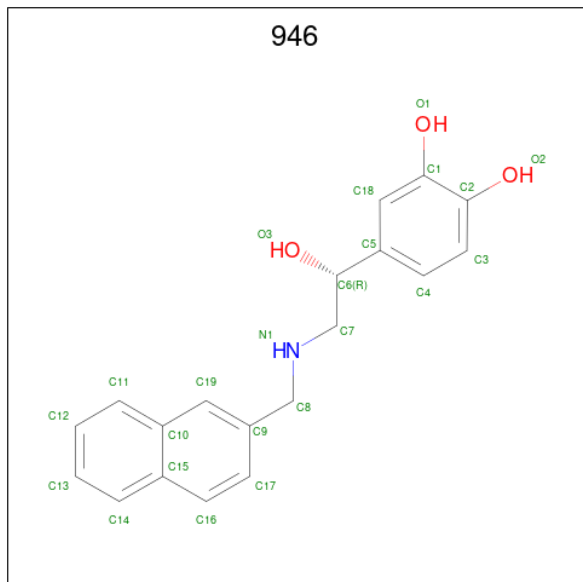
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	E	1	Total Zn 1 1	0	0
2	F	1	Total Zn 1 1	0	0
2	G	1	Total Zn 1 1	0	0
2	H	1	Total Zn 1 1	0	0
2	I	1	Total Zn 1 1	0	0

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



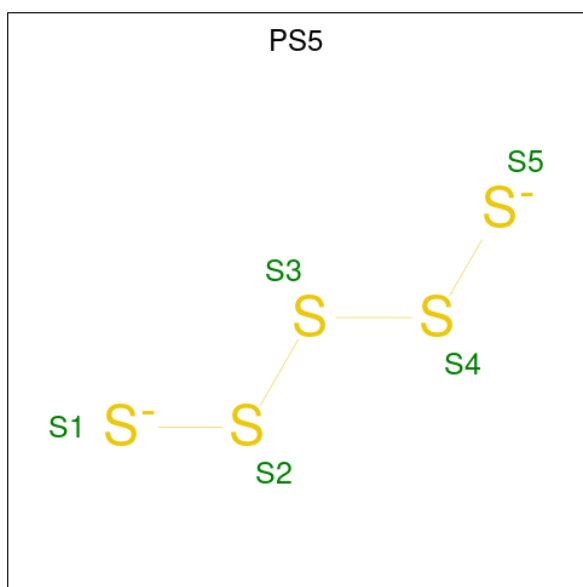
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0

- Molecule 4 is 4-[(1 {R})-2-(naphthalen-2-ylmethylamino)-1-oxidanyl-ethyl]benzene-1,2-diol (CCD ID: 946) (formula: C₁₉H₁₉NO₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			23	19	1	3		
4	D	1	Total	C	O		0	0
			11	8	3			
4	H	1	Total	C	N	O	0	0
			23	19	1	3		

- Molecule 5 is PENTASULFIDE-SULFUR (CCD ID: PS5) (formula: S₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total S 5 5	0	0
5	C	1	Total S 5 5	0	0
5	E	1	Total S 5 5	0	0

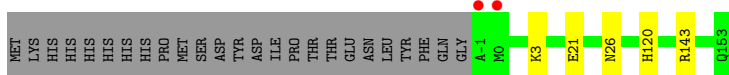
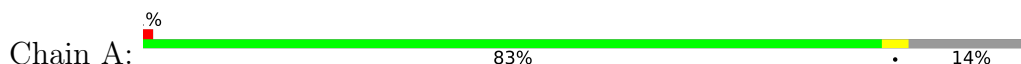
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	172	Total O 175 175	0	3
6	B	218	Total O 220 220	0	2
6	C	182	Total O 185 185	0	3
6	D	145	Total O 146 146	0	1
6	E	187	Total O 187 187	0	0
6	F	129	Total O 131 131	0	2
6	G	109	Total O 109 109	0	0
6	H	122	Total O 122 122	0	0
6	I	142	Total O 143 143	0	1
6	J	83	Total O 83 83	0	0

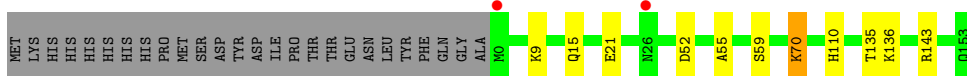
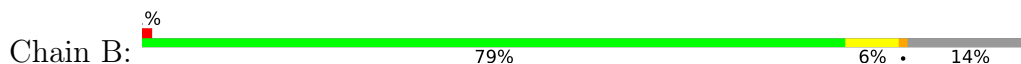
3 Residue-property plots [i](#)

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.

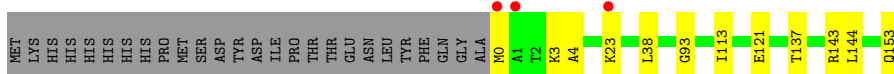
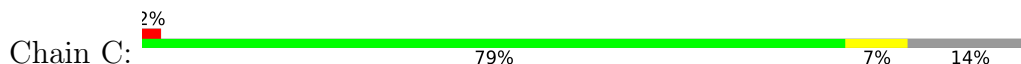
- Molecule 1: Superoxide dismutase [Cu-Zn]



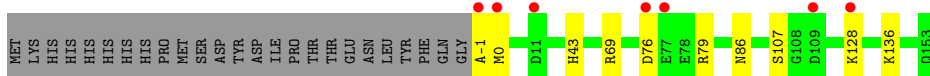
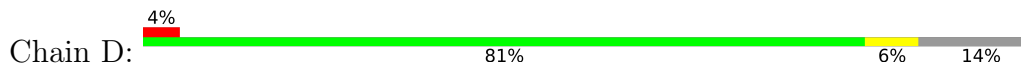
- Molecule 1: Superoxide dismutase [Cu-Zn]



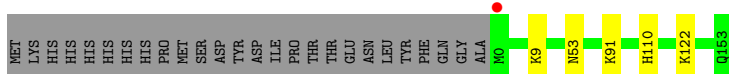
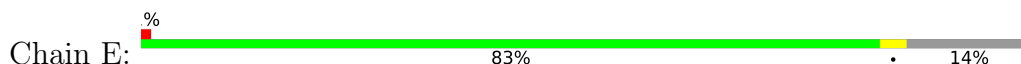
- Molecule 1: Superoxide dismutase [Cu-Zn]



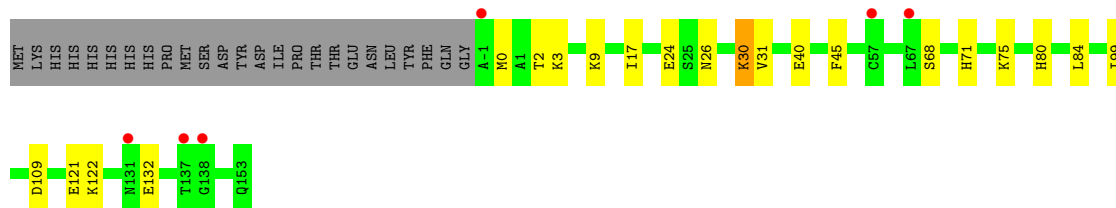
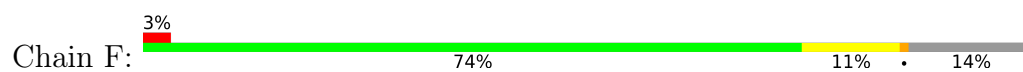
- Molecule 1: Superoxide dismutase [Cu-Zn]



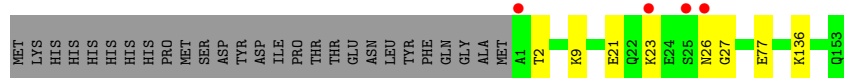
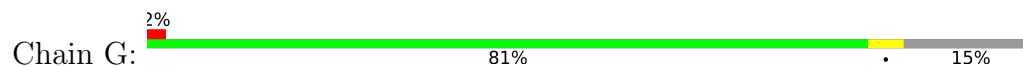
- Molecule 1: Superoxide dismutase [Cu-Zn]



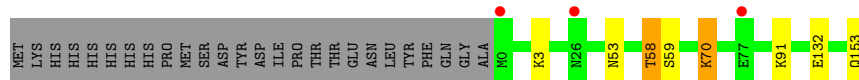
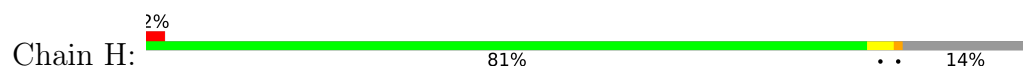
- Molecule 1: Superoxide dismutase [Cu-Zn]



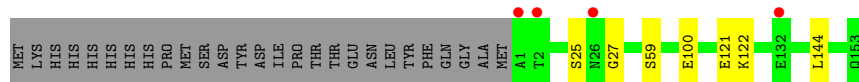
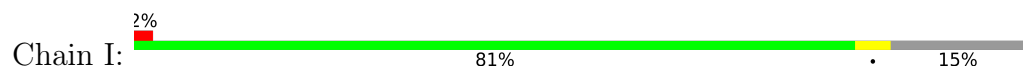
- Molecule 1: Superoxide dismutase [Cu-Zn]



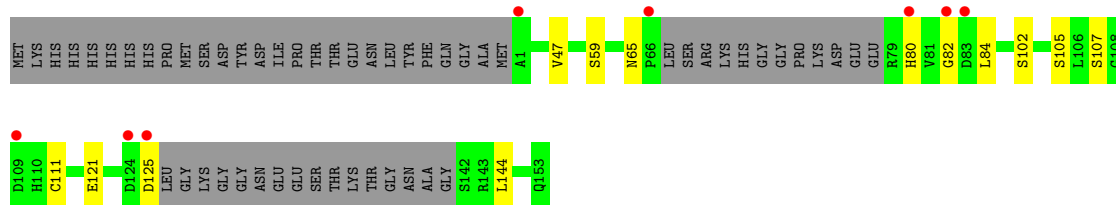
- Molecule 1: Superoxide dismutase [Cu-Zn]



- 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	243.94Å 243.94Å 144.78Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.90 20.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.4 (20.00-1.90) 99.3 (20.00-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.179 , 0.215 0.180 , 0.216	Depositor DCC
R_{free} test set	9697 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.310	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12631	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.93% 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: ZN, GOL, 946, PS5

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	1.09	0/1155	1.05	0/1556
1	B	1.15	0/1168	1.07	0/1573
1	C	1.09	0/1153	1.00	0/1554
1	D	1.14	1/1138 (0.1%)	1.11	2/1534 (0.1%)
1	E	1.13	0/1145	1.04	0/1543
1	F	1.07	1/1149 (0.1%)	1.06	0/1551
1	G	0.96	0/1127	1.00	3/1519 (0.2%)
1	H	0.94	0/1142	0.96	0/1539
1	I	1.00	0/1128	1.03	2/1520 (0.1%)
1	J	0.86	0/917	0.98	1/1239 (0.1%)
All	All	1.05	2/11222 (0.0%)	1.03	8/15128 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	86	ASN	CA-C	-5.08	1.46	1.52
1	F	17	ILE	C-O	5.05	1.29	1.24

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	43	HIS	CA-C-N	6.67	126.32	119.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	43	HIS	C-N-CA	6.67	126.32	119.92
1	G	2	THR	N-CA-C	-5.38	107.38	114.31
1	G	27	GLY	CA-C-N	5.31	125.21	119.85
1	G	27	GLY	C-N-CA	5.31	125.21	119.85

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	26	ASN	Peptide

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	1134	0	1106	11	0
1	B	1147	0	1114	13	0
1	C	1126	0	1100	12	0
1	D	1120	0	1084	9	0
1	E	1127	0	1087	6	0
1	F	1131	0	1083	13	0
1	G	1109	0	1073	6	0
1	H	1124	0	1083	6	0
1	I	1110	0	1077	4	0
1	J	903	0	869	8	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	10	0
3	B	6	0	8	8	0
3	C	6	0	8	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	23	0	0	2	0
4	D	11	0	0	0	0
4	H	23	0	0	1	0
5	B	5	0	0	0	0
5	C	5	0	0	0	0
5	E	5	0	0	0	0
6	A	175	0	0	1	1
6	B	220	0	0	4	0
6	C	185	0	0	6	1
6	D	146	0	0	7	1
6	E	187	0	0	7	0
6	F	131	0	0	6	0
6	G	109	0	0	2	1
6	H	122	0	0	5	0
6	I	143	0	0	3	0
6	J	83	0	0	4	0
All	All	12631	0	10700	94	2

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 4.

The worst 5 of 94 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)
3:C:202:GOL:H11	6:C:345:HOH:O	1.46	1.15
1:C:143:ARG:HH21	3:C:202:GOL:H2	1.00	1.13
1:D:69:ARG:HB2	6:D:301:HOH:O	1.45	1.12
1:B:143:ARG:HE	3:B:202:GOL:H12	1.11	1.11
1:F:109:ASP:HB3	6:F:396:HOH:O	1.48	1.09

All (2) 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)
6:C:446:HOH:O	6:D:411:HOH:O[10_664]	2.12	0.08
6:A:449:HOH:O	6:G:382:HOH:O[2_655]	2.15	0.05

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	157/180 (87%)	157 (100%)	0	0	100	100
1	C	155/180 (86%)	153 (99%)	2 (1%)	0	100	100
1	D	153/180 (85%)	151 (99%)	2 (1%)	0	100	100
1	E	154/180 (86%)	154 (100%)	0	0	100	100
1	F	156/180 (87%)	154 (99%)	2 (1%)	0	100	100
1	G	152/180 (84%)	150 (99%)	2 (1%)	0	100	100
1	H	154/180 (86%)	150 (97%)	4 (3%)	0	100	100
1	I	151/180 (84%)	151 (100%)	0	0	100	100
1	J	119/180 (66%)	114 (96%)	5 (4%)	0	100	100
All	All	1506/1800 (84%)	1489 (99%)	17 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	123/143 (86%)	122 (99%)	1 (1%)	73	75
1	C	121/143 (85%)	120 (99%)	1 (1%)	73	75
1	D	118/143 (82%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	120/143 (84%)	119 (99%)	1 (1%)	73	75
1	F	119/143 (83%)	115 (97%)	4 (3%)	32	25
1	G	117/143 (82%)	117 (100%)	0	100	100
1	H	119/143 (83%)	115 (97%)	4 (3%)	32	25
1	I	118/143 (82%)	117 (99%)	1 (1%)	73	75
1	J	96/143 (67%)	93 (97%)	3 (3%)	35	29
All	All	1172/1430 (82%)	1157 (99%)	15 (1%)	61	61

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	58	THR
1	J	84	LEU
1	H	59	SER
1	J	102	SER
1	I	25	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	19	ASN
1	J	53	ASN
1	H	19	ASN
1	J	65	ASN
1	I	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 18 ligands modelled in this entry, 9 are monoatomic - leaving 9 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PS5	C	203	-	2,4,4	0.67	0	1,3,3	1.63	0
5	PS5	E	202	-	2,4,4	0.67	0	1,3,3	1.52	0
4	946	H	202	-	25,25,25	1.58	5 (20%)	34,34,34	1.38	4 (11%)
3	GOL	C	202	-	5,5,5	0.49	0	5,5,5	1.08	0
5	PS5	B	204	-	2,4,4	0.38	0	1,3,3	0.53	0
4	946	B	203	-	25,25,25	1.09	1 (4%)	34,34,34	1.24	3 (8%)
4	946	D	202	-	11,11,25	1.33	1 (9%)	15,15,34	0.78	0
3	GOL	A	202	-	5,5,5	0.34	0	5,5,5	0.93	0
3	GOL	B	202	-	5,5,5	0.43	0	5,5,5	0.78	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PS5	C	203	-	-	2/2/2/2	-
5	PS5	E	202	-	-	2/2/2/2	-
4	946	H	202	-	-	4/10/10/10	0/3/3/3
3	GOL	C	202	-	-	2/4/4/4	-
5	PS5	B	204	-	-	2/2/2/2	-
4	946	B	203	-	-	4/10/10/10	0/3/3/3
4	946	D	202	-	-	2/4/4/10	0/1/1/3
3	GOL	A	202	-	-	0/4/4/4	-
3	GOL	B	202	-	-	4/4/4/4	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	202	946	C5-C6	-3.43	1.46	1.51
4	H	202	946	O2-C2	-2.68	1.30	1.36
4	H	202	946	C2-C1	-2.60	1.35	1.40
4	H	202	946	C3-C2	-2.40	1.35	1.39
4	B	203	946	C7-N1	2.39	1.51	1.47

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	202	946	C7-C6-C5	4.42	120.17	110.95
4	B	203	946	C6-C7-N1	3.92	118.33	110.90
4	H	202	946	C6-C7-N1	-3.12	104.98	110.90
4	B	203	946	C9-C8-N1	2.81	121.64	112.79
4	H	202	946	O3-C6-C5	-2.56	104.88	111.05

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	202	GOL	O1-C1-C2-C3
3	B	202	GOL	C1-C2-C3-O3
4	B	203	946	O3-C6-C7-N1
4	B	203	946	C5-C6-C7-N1
4	H	202	946	O3-C6-C7-N1

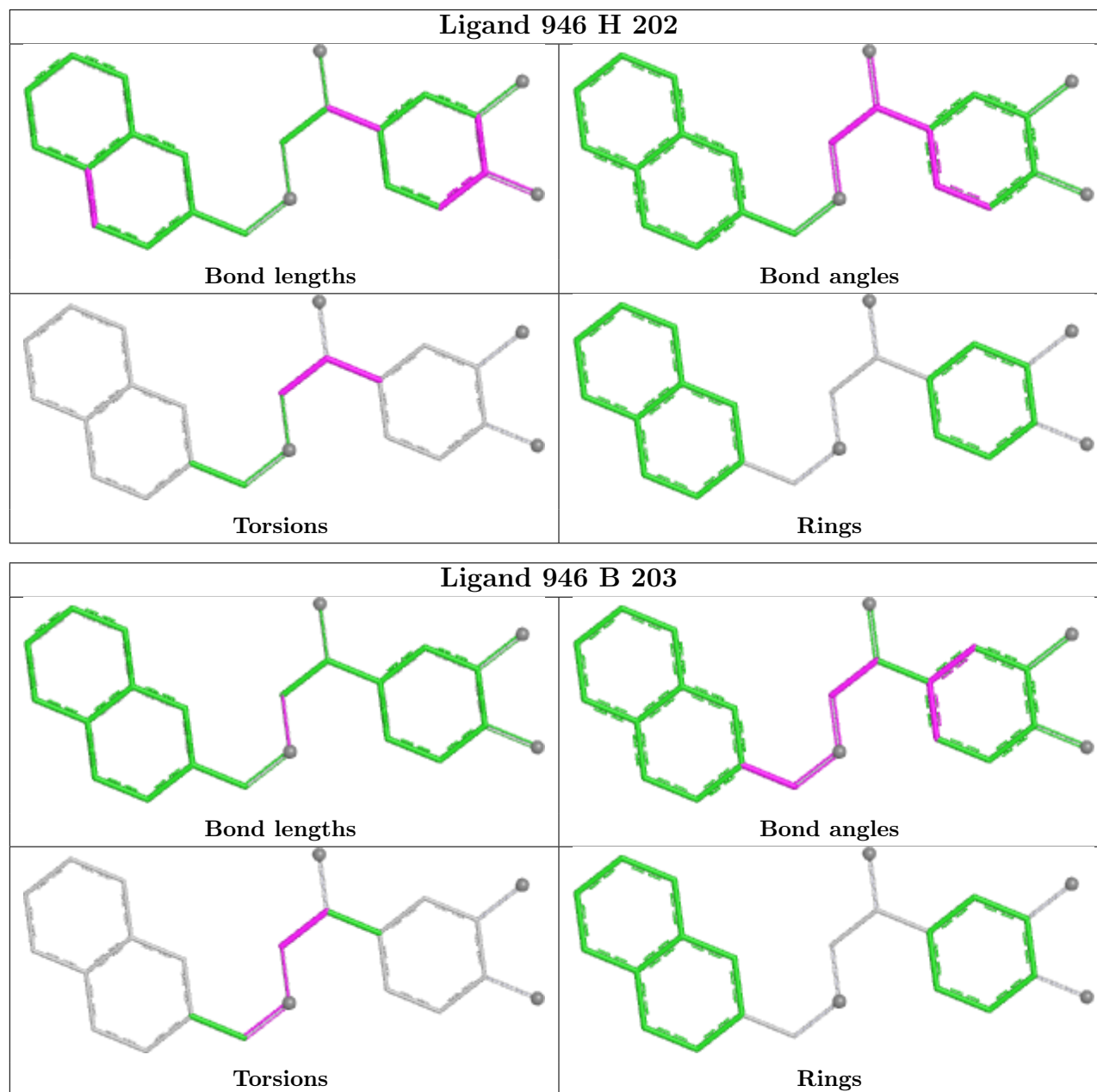
There are no ring outliers.

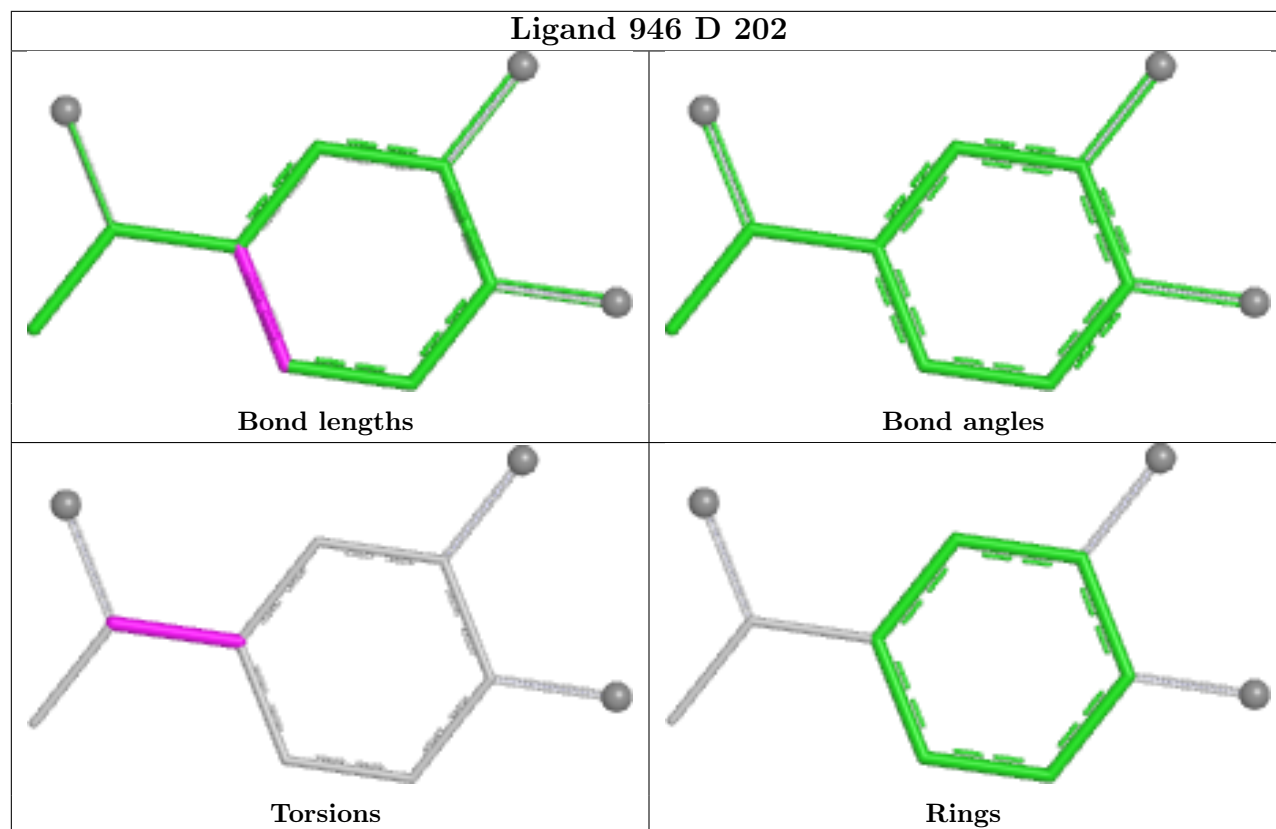
5 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	202	946	1	0
3	C	202	GOL	9	0
4	B	203	946	2	0
3	A	202	GOL	10	0
3	B	202	GOL	8	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 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	155/180 (86%)	-0.25	2 (1%) 75 78	8, 24, 42, 62	2 (1%)
1	B	154/180 (85%)	-0.50	2 (1%) 75 78	8, 19, 37, 54	5 (3%)
1	C	154/180 (85%)	-0.52	3 (1%) 66 70	11, 19, 36, 53	3 (1%)
1	D	155/180 (86%)	0.27	7 (4%) 38 40	17, 29, 52, 63	0
1	E	154/180 (85%)	-0.41	1 (0%) 85 87	10, 21, 36, 52	2 (1%)
1	F	155/180 (86%)	0.52	6 (3%) 43 46	15, 33, 53, 73	3 (1%)
1	G	153/180 (85%)	0.13	4 (2%) 57 61	16, 32, 54, 65	1 (0%)
1	H	154/180 (85%)	0.12	3 (1%) 66 70	18, 33, 52, 66	2 (1%)
1	I	153/180 (85%)	-0.07	4 (2%) 57 61	19, 28, 47, 69	0
1	J	125/180 (69%)	0.67	8 (6%) 25 27	26, 37, 61, 71	0
All	All	1512/1800 (84%)	-0.02	40 (2%) 57 61	8, 28, 51, 73	18 (1%)

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	66	PRO	5.9
1	A	-1	ALA	5.4
1	D	-1	ALA	5.4
1	F	-1	ALA	4.6
1	J	1	ALA	4.6

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 ⓘ

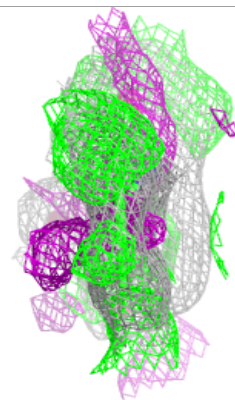
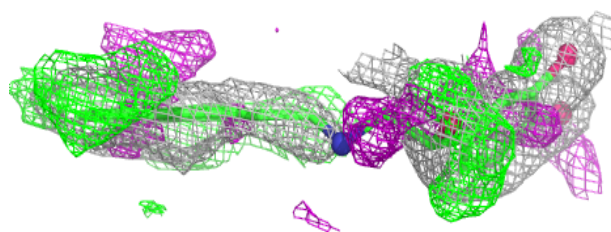
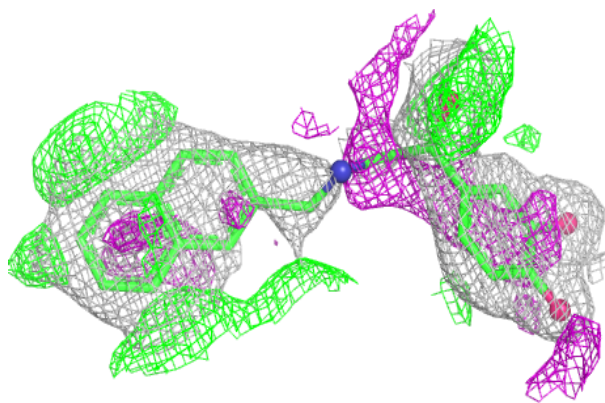
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	946	B	203	23/23	0.68	0.23	32,58,69,74	0
4	946	D	202	11/23	0.69	0.20	34,48,57,58	0
4	946	H	202	23/23	0.70	0.21	41,50,80,81	0
5	PS5	C	203	5/5	0.76	0.15	62,62,68,69	5
5	PS5	B	204	5/5	0.77	0.14	55,67,69,70	5
5	PS5	E	202	5/5	0.77	0.15	64,65,74,78	5
3	GOL	A	202	6/6	0.90	0.11	40,50,52,58	0
3	GOL	B	202	6/6	0.90	0.14	37,37,47,49	0
3	GOL	C	202	6/6	0.90	0.18	37,43,48,49	0
2	ZN	F	201	1/1	0.96	0.11	40,40,40,40	0
2	ZN	H	201	1/1	0.97	0.04	35,35,35,35	0
2	ZN	D	201	1/1	0.97	0.05	34,34,34,34	0
2	ZN	A	201	1/1	0.99	0.10	34,34,34,34	0
2	ZN	I	201	1/1	1.00	0.03	29,29,29,29	0
2	ZN	E	201	1/1	1.00	0.06	24,24,24,24	0
2	ZN	C	201	1/1	1.00	0.05	23,23,23,23	0
2	ZN	G	201	1/1	1.00	0.01	27,27,27,27	0
2	ZN	B	201	1/1	1.00	0.06	24,24,24,24	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.

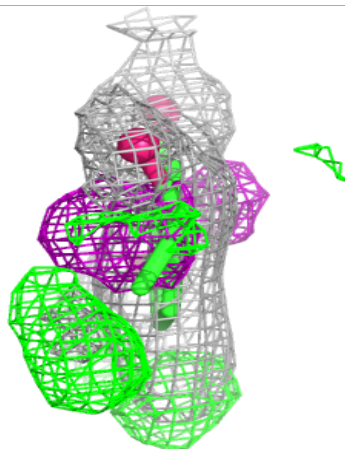
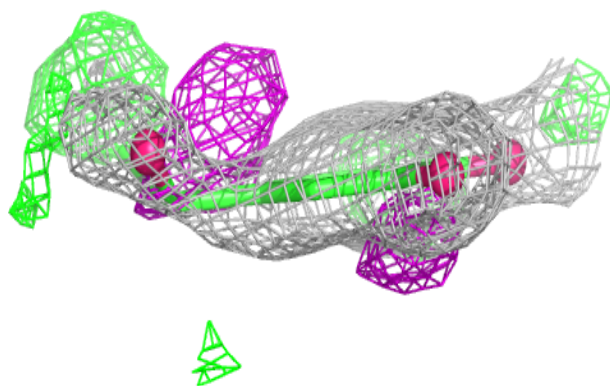
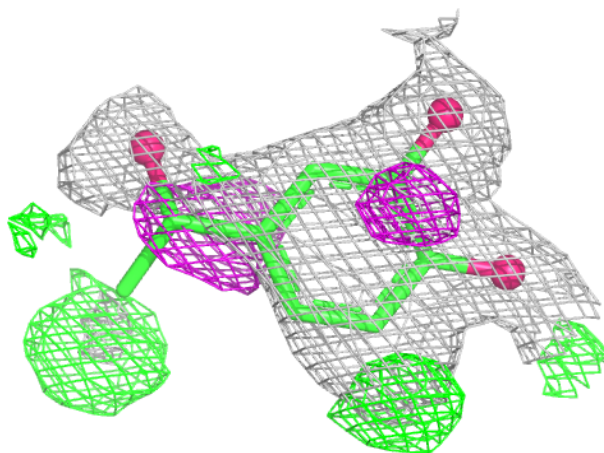
Electron density around 946 B 203:

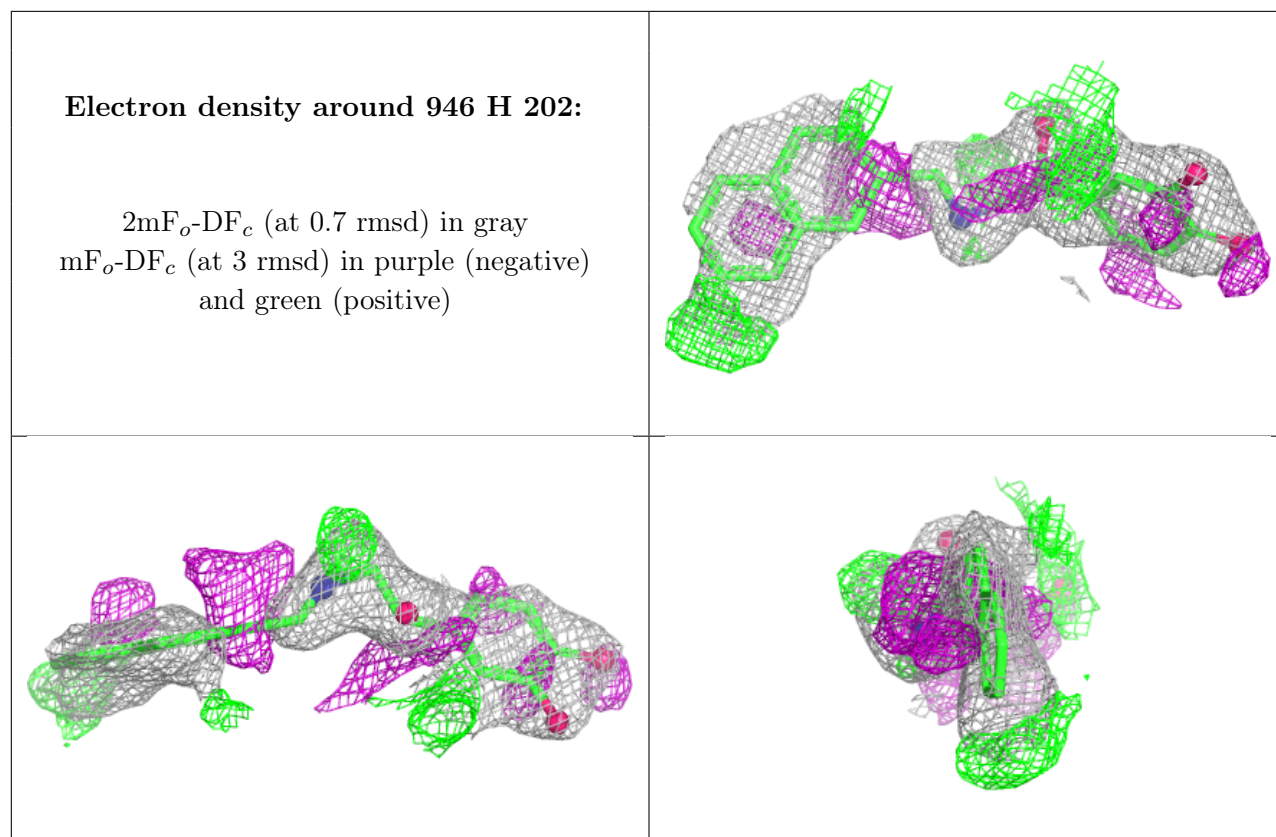
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 946 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.