



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 7, 2020 – 01:58 am BST

PDB ID : 6H43  
Title : Flavín-dependent Tryptophan 6-halogenase Thal  
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Deposited on : 2018-07-20  
Resolution : 2.20 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

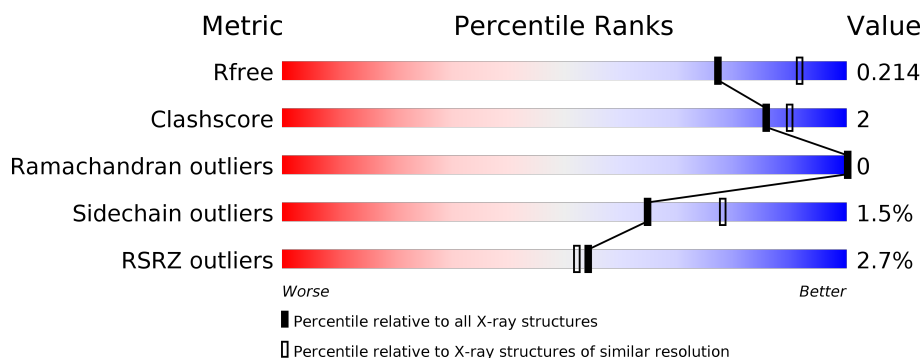
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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))
$R_{free}$	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	534	<div> <div>2%</div> <div> <div></div> <div>92%</div> <div>7%</div> </div> </div>
1	B	534	<div> <div>3%</div> <div> <div></div> <div>91%</div> <div>6%</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8856 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 Tryptophan 6-halogenase Thal.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	528	Total	C	N	O	S	0	3	0
			4238	2704	728	785	21			
1	B	521	Total	C	N	O	S	0	4	0
			4190	2675	724	771	20			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP A1E280
A	-1	ALA	-	expression tag	UNP A1E280
A	0	MET	-	expression tag	UNP A1E280
A	1	GLY	-	expression tag	UNP A1E280
B	-2	GLY	-	expression tag	UNP A1E280
B	-1	ALA	-	expression tag	UNP A1E280
B	0	MET	-	expression tag	UNP A1E280
B	1	GLY	-	expression tag	UNP A1E280

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total K 1 1	0	0

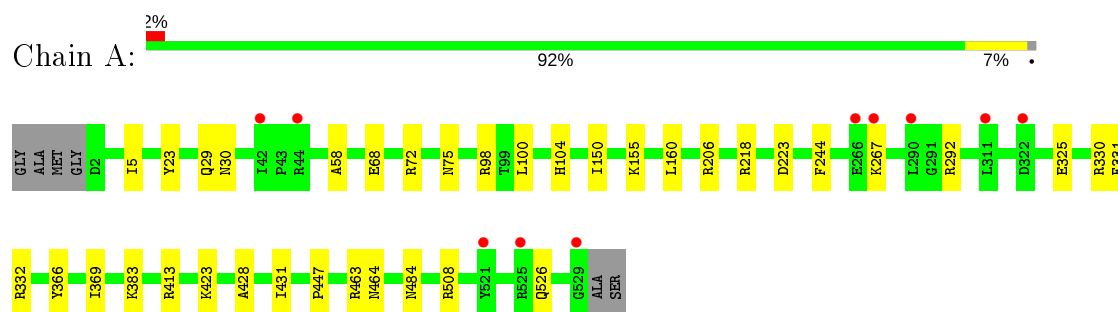
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	189	Total O 189 189	0	0
5	B	130	Total O 130 130	0	0

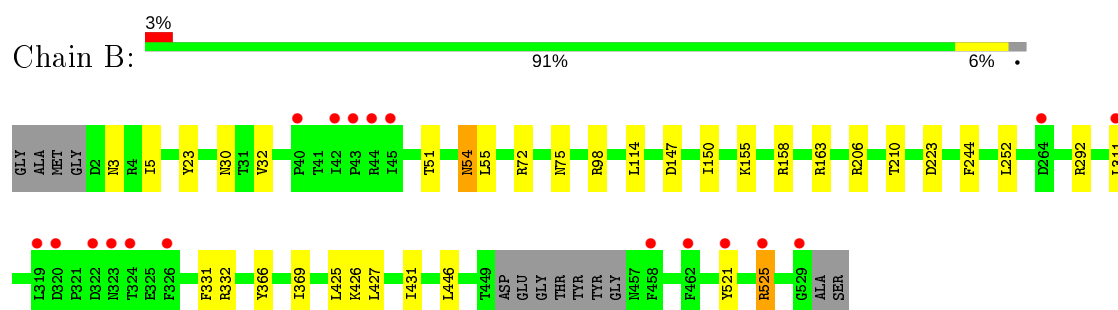
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Tryptophan 6-halogenase Thal



#### • Molecule 1: Tryptophan 6-halogenase Thal



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	139.47Å 139.47Å 142.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.89 – 2.20 49.84 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.89-2.20) 100.0 (49.84-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.03 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, $R_{free}$	0.170 , 0.211 0.176 , 0.214	Depositor DCC
$R_{free}$ test set	3990 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.1	Xtriage
Anisotropy	0.201	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 42.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.033 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8856	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GOL, K, PO4

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	0.59	0/4353	0.72	0/5910
1	B	0.58	0/4308	0.73	0/5846
All	All	0.58	0/8661	0.73	0/11756

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	A	0	6
1	B	0	4
All	All	0	10

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	206	ARG	Sidechain
1	A	218	ARG	Sidechain
1	A	463	ARG	Sidechain
1	A	508	ARG	Sidechain
1	A	72	ARG	Sidechain
1	A	98	ARG	Sidechain
1	B	158	ARG	Sidechain
1	B	163	ARG	Sidechain
1	B	525	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	B	98	ARG	Sidechain

## 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	4238	0	4086	16	0
1	B	4190	0	4060	21	0
2	A	10	0	0	0	0
2	B	20	0	0	0	0
3	A	54	0	72	3	0
3	B	24	0	32	3	0
4	A	1	0	0	0	0
5	A	189	0	0	0	0
5	B	130	0	0	1	0
All	All	8856	0	8250	37	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 2.

All (37) 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:54:ASN:ND2	1:B:366:TYR:OH	2.10	0.85
1:A:30:ASN:ND2	3:A:607:GOL:H31	2.05	0.71
1:A:413:ARG:O	1:A:423:LYS:NZ	2.31	0.62
1:A:244:PHE:CE2	1:A:332:ARG:HG2	2.34	0.61
1:B:244:PHE:CE2	1:B:332:ARG:HG2	2.36	0.60
1:B:252:LEU:HG	1:B:425:LEU:HD11	1.83	0.59
1:B:427:LEU:HD22	1:B:431:ILE:CG2	2.33	0.59
1:B:427:LEU:HD22	1:B:431:ILE:HG21	1.85	0.56
1:B:150:ILE:HG23	1:B:155:LYS:HB2	1.88	0.56
1:A:30:ASN:HD22	3:A:607:GOL:H31	1.71	0.56
1:B:72:ARG:HG2	1:B:72:ARG:HH21	1.72	0.54
1:A:58:ALA:HB1	1:A:366:TYR:CZ	2.46	0.50
1:B:210:THR:HA	3:B:606:GOL:H12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:ILE:HG23	1:A:155:LYS:HB2	1.93	0.49
1:A:75[A]:ASN:ND2	1:A:292:ARG:NH1	2.61	0.48
1:A:29:GLN:HA	3:A:607:GOL:C1	2.44	0.48
1:B:5:ILE:HG23	1:B:223:ASP:HB2	1.96	0.47
1:A:5:ILE:HG23	1:A:223:ASP:HB2	1.97	0.46
1:B:521:TYR:CZ	1:B:525:ARG:HD2	2.50	0.46
1:A:447:PRO:HA	1:A:464:ASN:ND2	2.31	0.46
1:B:75[A]:ASN:ND2	1:B:292:ARG:NH1	2.64	0.45
1:A:160:LEU:O	1:A:526:GLN:NE2	2.50	0.45
1:A:75[A]:ASN:ND2	1:A:292:ARG:HH12	2.15	0.45
1:B:3[B]:ASN:HA	1:B:3[B]:ASN:HD22	1.67	0.45
1:B:54:ASN:C	1:B:54:ASN:HD22	2.19	0.45
1:B:51:THR:HB	5:B:799:HOH:O	2.17	0.44
1:A:75[A]:ASN:HD22	1:A:292:ARG:NH1	2.16	0.44
1:B:114:LEU:HD23	1:B:114:LEU:HA	1.84	0.43
1:B:54:ASN:HD22	1:B:55:LEU:N	2.17	0.43
1:B:23:TYR:CD1	1:B:369:ILE:HG22	2.54	0.43
1:B:30:ASN:ND2	3:B:608:GOL:O1	2.51	0.43
1:B:446:LEU:HD12	1:B:446:LEU:HA	1.87	0.42
1:A:428:ALA:O	1:A:431:ILE:HG22	2.21	0.41
1:B:75[A]:ASN:HD22	1:B:292:ARG:NH1	2.18	0.41
1:A:100:LEU:HD12	1:A:104:HIS:HB2	2.02	0.41
1:B:32:VAL:O	3:B:608:GOL:H2	2.21	0.41
1:A:23:TYR:CD1	1:A:369:ILE:HG22	2.56	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	529/534 (99%)	516 (98%)	13 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	521/534 (98%)	508 (98%)	13 (2%)	0	100	100
All	All	1050/1068 (98%)	1024 (98%)	26 (2%)	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	446/445 (100%)	439 (98%)	7 (2%)	62	76
1	B	442/445 (99%)	436 (99%)	6 (1%)	67	80
All	All	888/890 (100%)	875 (98%)	13 (2%)	65	78

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	GLU
1	A	267	LYS
1	A	325	GLU
1	A	330	ARG
1	A	331	PHE
1	A	383	LYS
1	A	484	ASN
1	B	54	ASN
1	B	147	ASP
1	B	206	ARG
1	B	311	LEU
1	B	331	PHE
1	B	426	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	ASN
1	A	526	GLN
1	B	30	ASN
1	B	54	ASN
1	B	133	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 20 ligands modelled in this entry, 1 is monoatomic - leaving 19 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	$\# Z  > 2$
2	PO4	B	604	-	4,4,4	0.75	0	6,6,6	1.00	0
2	PO4	A	602	-	4,4,4	1.15	0	6,6,6	0.57	0
2	PO4	B	603	-	4,4,4	0.73	0	6,6,6	0.42	0
3	GOL	A	606	-	5,5,5	0.12	0	5,5,5	0.85	0
3	GOL	B	608	-	5,5,5	0.53	0	5,5,5	0.79	0
3	GOL	A	608	-	5,5,5	0.83	0	5,5,5	1.05	0
3	GOL	A	605	-	5,5,5	0.19	0	5,5,5	0.92	0
3	GOL	B	605	-	5,5,5	0.47	0	5,5,5	0.52	0
2	PO4	B	601	-	4,4,4	0.95	0	6,6,6	0.32	0
2	PO4	B	602	-	4,4,4	0.81	0	6,6,6	1.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GOL	B	606	-	5,5,5	0.84	0	5,5,5	1.00	0
3	GOL	A	610	-	5,5,5	0.39	0	5,5,5	0.86	0
3	GOL	A	604	-	5,5,5	0.86	0	5,5,5	0.57	0
3	GOL	A	603	-	5,5,5	0.41	0	5,5,5	0.77	0
2	PO4	A	601	-	4,4,4	1.00	0	6,6,6	0.85	0
3	GOL	A	607	-	5,5,5	0.59	0	5,5,5	0.90	0
3	GOL	B	607	-	5,5,5	0.46	0	5,5,5	1.04	0
3	GOL	A	609	-	5,5,5	0.57	0	5,5,5	1.14	0
3	GOL	A	611	-	5,5,5	0.85	0	5,5,5	0.97	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	A	606	-	-	0/4/4/4	-
3	GOL	B	608	-	-	2/4/4/4	-
3	GOL	A	608	-	-	2/4/4/4	-
3	GOL	A	605	-	-	4/4/4/4	-
3	GOL	B	605	-	-	2/4/4/4	-
3	GOL	B	606	-	-	2/4/4/4	-
3	GOL	A	610	-	-	2/4/4/4	-
3	GOL	A	604	-	-	0/4/4/4	-
3	GOL	A	603	-	-	4/4/4/4	-
3	GOL	A	607	-	-	4/4/4/4	-
3	GOL	B	607	-	-	2/4/4/4	-
3	GOL	A	609	-	-	4/4/4/4	-
3	GOL	A	611	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	607	GOL	O1-C1-C2-C3
3	A	607	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
3	A	607	GOL	O2-C2-C3-O3
3	A	605	GOL	C1-C2-C3-O3
3	A	605	GOL	O2-C2-C3-O3
3	B	605	GOL	O1-C1-C2-C3
3	B	606	GOL	O1-C1-C2-C3
3	A	603	GOL	C1-C2-C3-O3
3	A	609	GOL	C1-C2-C3-O3
3	A	609	GOL	O2-C2-C3-O3
3	B	608	GOL	C1-C2-C3-O3
3	A	608	GOL	C1-C2-C3-O3
3	A	603	GOL	O1-C1-C2-C3
3	B	607	GOL	O1-C1-C2-C3
3	A	609	GOL	O1-C1-C2-C3
3	A	611	GOL	O1-C1-C2-C3
3	B	605	GOL	O1-C1-C2-O2
3	B	606	GOL	O1-C1-C2-O2
3	A	607	GOL	O1-C1-C2-O2
3	A	605	GOL	O1-C1-C2-O2
3	A	608	GOL	O2-C2-C3-O3
3	A	603	GOL	O2-C2-C3-O3
3	B	607	GOL	O1-C1-C2-O2
3	A	609	GOL	O1-C1-C2-O2
3	A	603	GOL	O1-C1-C2-O2
3	A	610	GOL	O2-C2-C3-O3
3	A	605	GOL	O1-C1-C2-C3
3	A	610	GOL	C1-C2-C3-O3
3	B	608	GOL	O2-C2-C3-O3
3	A	611	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	608	GOL	2	0
3	B	606	GOL	1	0
3	A	607	GOL	3	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	528/534 (98%)	-0.38	10 (1%) 66 65	30, 43, 70, 127	0
1	B	521/534 (97%)	-0.21	18 (3%) 44 42	35, 49, 80, 146	0
All	All	1049/1068 (98%)	-0.30	28 (2%) 54 52	30, 46, 76, 146	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	42	ILE	10.6
1	B	43	PRO	6.7
1	A	42	ILE	5.1
1	B	40	PRO	4.1
1	B	44	ARG	3.7
1	B	319	LEU	3.6
1	B	529	GLY	3.6
1	B	322	ASP	3.5
1	A	266	GLU	3.4
1	B	326	PHE	3.3
1	A	529	GLY	3.3
1	B	458	PHE	3.3
1	A	311	LEU	3.2
1	B	45	ILE	3.1
1	B	462	PHE	3.1
1	B	320	ASP	2.9
1	B	311	LEU	2.9
1	B	264	ASP	2.6
1	A	290	LEU	2.6
1	A	521	TYR	2.4
1	B	525	ARG	2.4
1	A	267	LYS	2.4
1	B	323	ASN	2.3
1	A	525	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	322	ASP	2.2
1	B	521	TYR	2.1
1	A	44	ARG	2.0
1	B	324	THR	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	GOL	A	607	6/6	0.70	0.36	76,94,97,100	0
2	PO4	B	604	5/5	0.78	0.19	66,69,82,88	5
2	PO4	B	602	5/5	0.81	0.24	50,60,67,70	5
3	GOL	A	605	6/6	0.83	0.15	66,70,74,75	0
3	GOL	B	607	6/6	0.83	0.24	73,76,86,101	0
3	GOL	A	611	6/6	0.84	0.15	61,75,82,90	0
2	PO4	B	603	5/5	0.86	0.31	89,100,107,108	5
3	GOL	B	606	6/6	0.86	0.17	57,74,78,86	0
3	GOL	A	609	6/6	0.87	0.21	63,80,91,94	0
3	GOL	A	608	6/6	0.87	0.17	41,54,56,59	0
3	GOL	A	610	6/6	0.89	0.19	65,82,83,85	0
3	GOL	B	605	6/6	0.91	0.14	63,76,84,87	0
3	GOL	A	606	6/6	0.91	0.20	51,63,65,68	6
3	GOL	B	608	6/6	0.93	0.13	47,67,68,78	0
2	PO4	A	602	5/5	0.93	0.12	69,82,86,90	0
3	GOL	A	603	6/6	0.93	0.11	61,78,80,82	0
2	PO4	B	601	5/5	0.94	0.13	73,81,85,87	0
3	GOL	A	604	6/6	0.97	0.10	46,55,56,63	0
4	K	A	612	1/1	0.98	0.07	42,42,42,42	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	A	601	5/5	0.99	0.06	48,53,54,54	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.