



# Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 12:17 pm BST

PDB ID : 5OIE  
Title : Crystal structure of Mycolicibacterium hassiacum glucosylglycerate hydrolase (MhGgH) E419A variant in complex with serine and glycerol  
Authors : Cereija, T.B.; Macedo-Ribeiro, S.; Pereira, P.J.B.  
Deposited on : 2017-07-18  
Resolution : 2.07 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

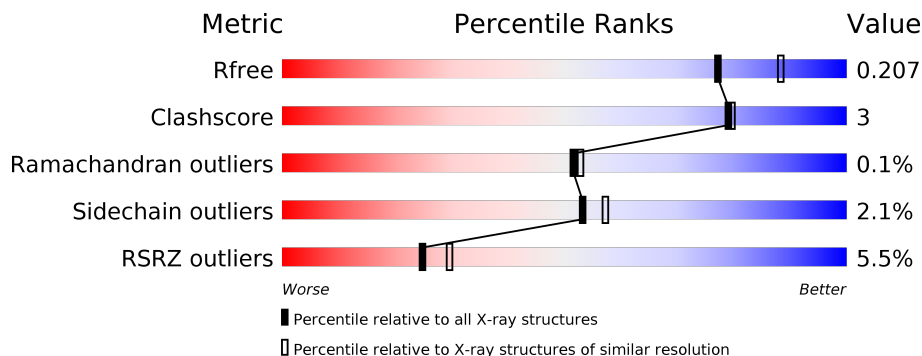
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.07 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	6189 (2.10-2.06)
Clashscore	141614	6738 (2.10-2.06)
Ramachandran outliers	138981	6663 (2.10-2.06)
Sidechain outliers	138945	6664 (2.10-2.06)
RSRZ outliers	127900	6057 (2.10-2.06)

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	448	 3% 94% 5%
1	B	448	 8% 90% 9%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7767 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.

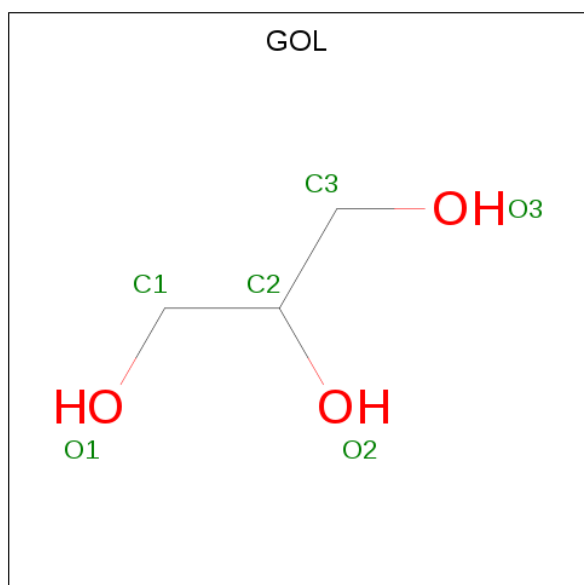
- Molecule 1 is a protein called hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	445	Total 3651	C 2318	N 668	O 652	S 13	0	8	0
1	B	445	Total 3615	C 2299	N 657	O 646	S 13	0	4	0

There are 6 discrepancies between the modelled and reference sequences:

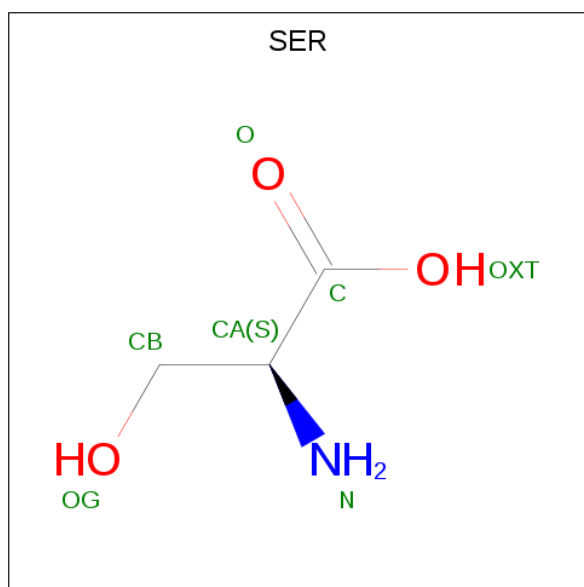
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP K5BDL0
A	0	ALA	-	expression tag	UNP K5BDL0
A	419	ALA	GLU	engineered mutation	UNP K5BDL0
B	-1	GLY	-	expression tag	UNP K5BDL0
B	0	ALA	-	expression tag	UNP K5BDL0
B	419	ALA	GLU	engineered mutation	UNP K5BDL0

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



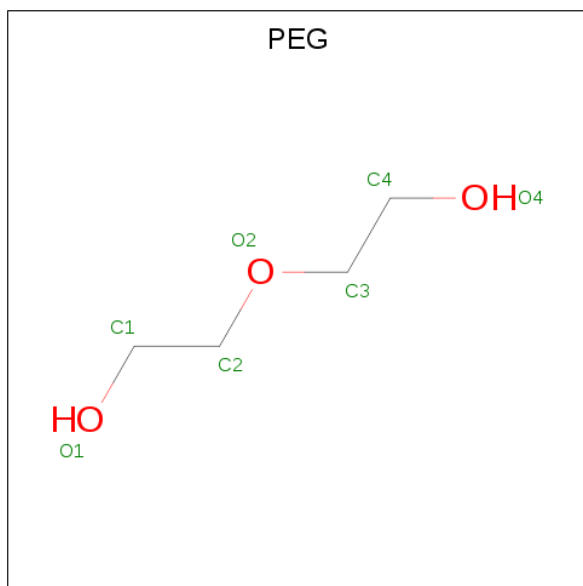
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is SERINE (three-letter code: SER) (formula: C<sub>3</sub>H<sub>7</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			7	3	1	3		
3	B	1	Total	C	N	O	0	0
			7	3	1	3		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 7 4 3	0	0

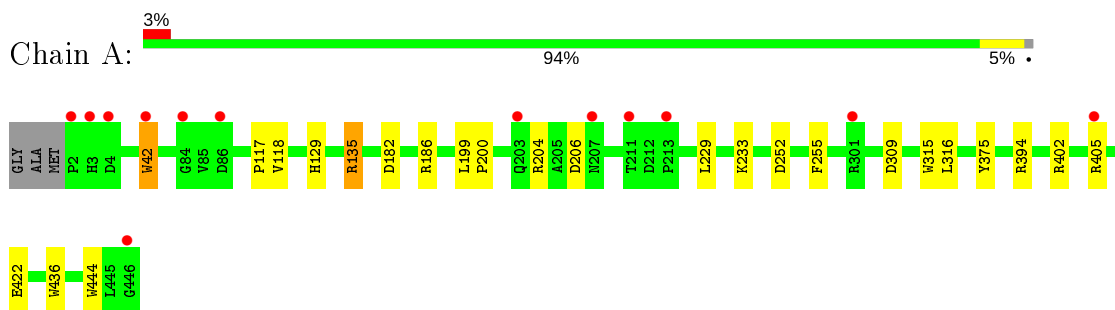
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	253	Total O 253 253	0	1
5	B	167	Total O 167 167	0	0

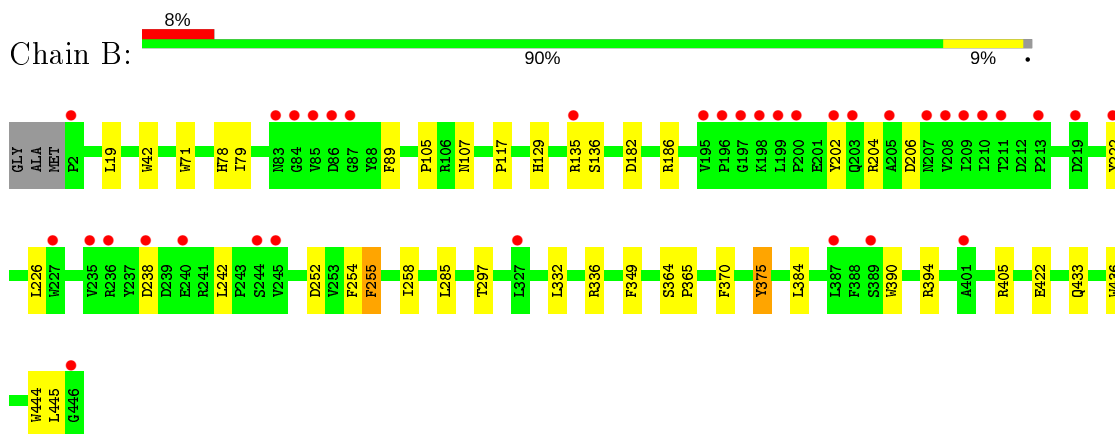
### 3 Residue-property plots [i](#)

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: hydrolase



- Molecule 1: hydrolase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.19Å 159.37Å 88.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.78 - 2.07 48.78 - 2.07	Depositor EDS
% Data completeness (in resolution range)	98.6 (48.78-2.07) 98.6 (48.78-2.07)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.97 (at 2.07Å)	Xtrriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, $R_{free}$	0.167 , 0.208 0.167 , 0.207	Depositor DCC
$R_{free}$ test set	3718 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.9	Xtrriage
Anisotropy	0.368	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 48.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.018 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7767	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.53	0/3761	0.64	0/5125
1	B	0.46	0/3725	0.59	0/5077
All	All	0.50	0/7486	0.62	0/10202

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	3651	0	3524	14	0
1	B	3615	0	3490	23	0
2	A	36	0	48	4	0
2	B	24	0	32	4	0
3	A	7	0	4	2	0
3	B	7	0	4	3	0
4	A	7	0	10	1	0
5	A	253	0	0	0	0
5	B	167	0	0	1	0
All	All	7767	0	7112	40	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 (40) 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)
2:B:501:GOL:HO2	3:B:505:SER:N	1.48	1.09
2:A:501:GOL:HO2	3:A:507:SER:N	1.61	0.96
1:A:129:HIS:CE1	2:B:503:GOL:H2	2.27	0.70
1:A:402:ARG:NH2	2:A:503:GOL:H31	2.10	0.67
1:A:204:ARG:HD2	1:A:206:ASP:OD1	1.97	0.65
1:B:89:PHE:HE2	1:B:226:LEU:HD11	1.63	0.63
1:A:204:ARG:HB2	4:A:508:PEG:H41	1.82	0.62
1:A:405[B]:ARG:HG3	1:A:444:TRP:CD1	2.37	0.60
1:B:332:LEU:HD22	1:B:336:ARG:HD2	1.86	0.56
1:B:129:HIS:HD2	5:B:759:HOH:O	1.88	0.55
2:B:501:GOL:O2	3:B:505:SER:N	2.28	0.55
1:B:19:LEU:HD21	1:B:433:GLN:HB3	1.89	0.54
1:B:204:ARG:HD3	1:B:222:TYR:CG	2.43	0.53
1:B:117:PRO:HD3	1:B:255:PHE:CE2	2.45	0.52
1:B:390:TRP:CH2	1:B:394:ARG:HD2	2.45	0.51
1:B:182:ASP:OD2	3:B:505:SER:HA	2.10	0.51
1:A:315:TRP:CE2	2:A:504:GOL:H11	2.46	0.50
1:A:117:PRO:HD3	1:A:255:PHE:CE1	2.47	0.50
1:B:254:PHE:CE2	1:B:258:ILE:HD11	2.47	0.49
1:B:78:HIS:CE1	1:B:79:ILE:HG13	2.49	0.47
1:B:89:PHE:CZ	1:B:202:TYR:HB2	2.49	0.47
1:B:71:TRP:CD1	1:B:105:PRO:HD3	2.50	0.46
1:B:204:ARG:HD2	1:B:206:ASP:OD1	2.15	0.46
1:B:405:ARG:HG3	1:B:444:TRP:CD1	2.51	0.46
1:B:349:PHE:CZ	1:B:364:SER:HB2	2.52	0.44
1:B:238:ASP:O	1:B:242:LEU:HG	2.18	0.44
1:A:186:ARG:NH1	1:A:252:ASP:OD1	2.43	0.44
1:A:199:LEU:HD12	1:A:200:PRO:HD2	1.99	0.44
1:A:135:ARG:HD2	1:A:135:ARG:HA	1.82	0.44
1:B:226:LEU:HA	1:B:226:LEU:HD23	1.84	0.44
1:A:229:LEU:O	1:A:233:LYS:HG3	2.19	0.43
2:A:503:GOL:H2	1:B:129:HIS:NE2	2.35	0.42
1:B:384:LEU:HA	1:B:384:LEU:HD23	1.87	0.42
1:B:297:THR:O	2:B:504:GOL:H31	2.19	0.41
1:B:365:PRO:HA	1:B:370:PHE:CD1	2.55	0.41
1:A:42:TRP:HB2	1:A:118:VAL:HG21	2.03	0.41
1:A:309:ASP:HB2	1:A:316:LEU:HD21	2.04	0.40
1:B:186:ARG:NH1	1:B:252:ASP:OD1	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:ASP:OD2	3:A:507:SER:HA	2.21	0.40
1:B:445:LEU:HA	1:B:445:LEU:HD23	1.80	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	451/448 (101%)	436 (97%)	15 (3%)	0	100	100
1	B	447/448 (100%)	429 (96%)	17 (4%)	1 (0%)	47	47
All	All	898/896 (100%)	865 (96%)	32 (4%)	1 (0%)	51	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	375	TYR

### 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	372/365 (102%)	366 (98%)	6 (2%)	62	67
1	B	368/365 (101%)	358 (97%)	10 (3%)	44	47
All	All	740/730 (101%)	724 (98%)	16 (2%)	53	55

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	TRP
1	A	135	ARG
1	A	375	TYR
1	A	394	ARG
1	A	422	GLU
1	A	436	TRP
1	B	42	TRP
1	B	107[A]	ASN
1	B	107[B]	ASN
1	B	135	ARG
1	B	136	SER
1	B	255	PHE
1	B	285	LEU
1	B	375	TYR
1	B	422	GLU
1	B	436	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

13 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GOL	A	503	-	5,5,5	0.40	0	5,5,5	0.49	0
2	GOL	B	503	-	5,5,5	0.23	0	5,5,5	0.72	0
2	GOL	B	504	-	5,5,5	0.35	0	5,5,5	0.44	0
2	GOL	A	506	-	5,5,5	0.31	0	5,5,5	0.21	0
2	GOL	A	505	-	5,5,5	0.33	0	5,5,5	0.26	0
2	GOL	A	502	-	5,5,5	0.30	0	5,5,5	0.54	0
2	GOL	A	501	-	5,5,5	0.57	0	5,5,5	0.39	0
2	GOL	B	501	-	5,5,5	0.38	0	5,5,5	0.34	0
2	GOL	A	504	-	5,5,5	0.40	0	5,5,5	0.23	0
2	GOL	B	502	-	5,5,5	0.29	0	5,5,5	0.58	0
4	PEG	A	508	-	6,6,6	0.50	0	5,5,5	0.27	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	A	503	-	-	2/4/4/4	-
2	GOL	B	503	-	-	4/4/4/4	-
2	GOL	B	504	-	-	4/4/4/4	-
2	GOL	A	506	-	-	2/4/4/4	-
2	GOL	A	505	-	-	0/4/4/4	-
2	GOL	A	502	-	-	2/4/4/4	-
2	GOL	A	501	-	-	0/4/4/4	-
2	GOL	B	501	-	-	0/4/4/4	-
2	GOL	A	504	-	-	2/4/4/4	-
2	GOL	B	502	-	-	2/4/4/4	-
4	PEG	A	508	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	503	GOL	O1-C1-C2-C3
2	B	503	GOL	O1-C1-C2-C3
2	B	504	GOL	O1-C1-C2-C3
2	A	506	GOL	O1-C1-C2-C3
2	A	502	GOL	O1-C1-C2-C3
2	A	504	GOL	O1-C1-C2-C3
2	B	503	GOL	O2-C2-C3-O3
2	B	504	GOL	O1-C1-C2-O2
2	A	502	GOL	O1-C1-C2-O2
2	A	504	GOL	O1-C1-C2-O2
2	A	503	GOL	O1-C1-C2-O2
2	B	503	GOL	O1-C1-C2-O2
2	A	506	GOL	O1-C1-C2-O2
2	B	504	GOL	O2-C2-C3-O3
2	B	504	GOL	C1-C2-C3-O3
2	B	502	GOL	O1-C1-C2-C3
2	B	503	GOL	C1-C2-C3-O3
2	B	502	GOL	O1-C1-C2-O2

There are no ring outliers.

7 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	503	GOL	2	0
2	B	503	GOL	1	0
2	B	504	GOL	1	0
2	A	501	GOL	1	0
2	B	501	GOL	2	0
2	A	504	GOL	1	0
4	A	508	PEG	1	0

## 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, 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	445/448 (99%)	0.27	13 (2%) 51 56	25, 41, 65, 108	0
1	B	445/448 (99%)	0.45	36 (8%) 12 15	28, 49, 81, 123	0
All	All	890/896 (99%)	0.36	49 (5%) 25 30	25, 45, 76, 123	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	85	VAL	4.3
1	B	199	LEU	4.1
1	B	198	LYS	3.6
1	B	209	ILE	3.6
1	B	211	THR	3.4
1	B	196	PRO	3.4
1	B	202	TYR	3.3
1	B	240	GLU	3.2
1	B	197	GLY	3.2
1	B	446	GLY	3.2
1	B	86	ASP	3.0
1	B	236	ARG	2.9
1	B	203	GLN	2.8
1	B	227	TRP	2.8
1	B	87	GLY	2.7
1	A	211	THR	2.7
1	B	135	ARG	2.7
1	B	387	LEU	2.7
1	A	2	PRO	2.6
1	B	208	VAL	2.6
1	B	84	GLY	2.6
1	B	245	VAL	2.6
1	A	86	ASP	2.6
1	A	207	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	83	ASN	2.6
1	B	222	TYR	2.5
1	B	219	ASP	2.5
1	B	210	ILE	2.5
1	A	42	TRP	2.4
1	B	2	PRO	2.4
1	A	4	ASP	2.4
1	B	200	PRO	2.4
1	A	405[A]	ARG	2.3
1	A	213	PRO	2.3
1	B	238	ASP	2.2
1	B	235	VAL	2.2
1	A	84	GLY	2.2
1	A	3	HIS	2.2
1	A	446	GLY	2.2
1	B	213	PRO	2.1
1	A	203	GLN	2.1
1	B	244	SER	2.1
1	B	389[A]	SER	2.1
1	A	301	ARG	2.1
1	B	195	VAL	2.1
1	B	401	ALA	2.0
1	B	207	ASN	2.0
1	B	205	ALA	2.0
1	B	327	LEU	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( $\text{\AA}^2$ )	Q<0.9
4	PEG	A	508	7/7	0.55	0.33	77,88,90,91	0
2	GOL	B	501	6/6	0.70	0.24	68,71,75,75	0
2	GOL	A	505	6/6	0.76	0.30	81,84,88,91	0
2	GOL	A	506	6/6	0.78	0.23	80,81,84,88	0
2	GOL	B	503	6/6	0.86	0.29	49,67,69,72	0
2	GOL	A	501	6/6	0.87	0.17	50,55,58,60	0
2	GOL	A	503	6/6	0.87	0.17	60,69,74,76	0
2	GOL	B	502	6/6	0.88	0.36	56,63,66,68	0
3	SER	A	507	7/7	0.90	0.17	44,45,54,57	0
2	GOL	B	504	6/6	0.91	0.18	68,72,76,77	0
3	SER	B	505	7/7	0.93	0.21	47,53,61,62	0
2	GOL	A	502	6/6	0.94	0.18	48,52,64,69	0
2	GOL	A	504	6/6	0.95	0.19	71,73,78,83	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.