



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 11, 2024 – 02:25 PM EST

PDB ID : 2EVV  
Title : Crystal Structure of the PEBP-like Protein of Unknown Function HP0218 from *Helicobacter pylori*  
Authors : Kim, Y.; Xu, X.; Hong, H.; Savchenko, A.; Edwards, A.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2005-11-01  
Resolution : 2.59 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](mailto:validation@mail.wwpdb.org)

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<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>.

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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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

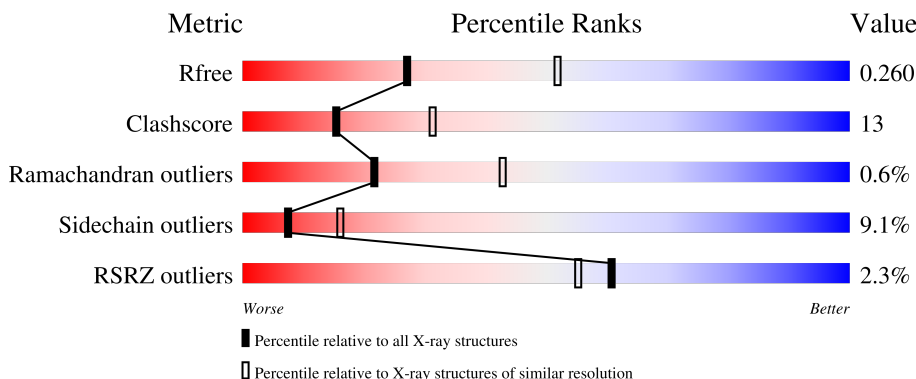
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.59 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))
$R_{free}$	164625	3775 (2.60-2.60)
Clashscore	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)
RSRZ outliers	164620	3775 (2.60-2.60)

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  $\geq 3$ , 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	207	<div> <div>66%</div> <div>18%</div> <div>•</div> <div>13%</div> </div>
1	B	207	<div> <div>2%</div> <div>64%</div> <div>19%</div> <div>•</div> <div>12%</div> </div>
1	C	207	<div> <div>3%</div> <div>69%</div> <div>16%</div> <div>•</div> <div>13%</div> </div>
1	D	207	<div> <div>2%</div> <div>64%</div> <div>19%</div> <div>•</div> <div>13%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6224 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 hypothetical protein HP0218.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	181	Total	C	N	O	S	Se	0	7	0
			1503	961	264	269	1	8			
1	B	182	Total	C	N	O	S	Se	0	4	0
			1486	951	262	265	1	7			
1	C	181	Total	C	N	O	S	Se	0	3	0
			1465	938	254	264	1	8			
1	D	180	Total	C	N	O	S	Se	0	5	0
			1474	942	255	269	1	7			

There are 124 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MSE	-	cloning artifact	UNP O25006
A	-20	GLY	-	cloning artifact	UNP O25006
A	-19	SER	-	cloning artifact	UNP O25006
A	-18	SER	-	cloning artifact	UNP O25006
A	-17	HIS	-	cloning artifact	UNP O25006
A	-16	HIS	-	cloning artifact	UNP O25006
A	-15	HIS	-	cloning artifact	UNP O25006
A	-14	HIS	-	cloning artifact	UNP O25006
A	-13	HIS	-	cloning artifact	UNP O25006
A	-12	HIS	-	cloning artifact	UNP O25006
A	-11	SER	-	cloning artifact	UNP O25006
A	-10	SER	-	cloning artifact	UNP O25006
A	-9	GLY	-	cloning artifact	UNP O25006
A	-8	ARG	-	cloning artifact	UNP O25006
A	-7	GLU	-	cloning artifact	UNP O25006
A	-6	ASN	-	cloning artifact	UNP O25006
A	-5	LEU	-	cloning artifact	UNP O25006
A	-4	TYR	-	cloning artifact	UNP O25006
A	-3	PHE	-	cloning artifact	UNP O25006
A	-2	GLN	-	cloning artifact	UNP O25006
A	-1	GLY	-	cloning artifact	UNP O25006

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	cloning artifact	UNP O25006
A	1	MSE	MET	modified residue	UNP O25006
A	7	MSE	MET	modified residue	UNP O25006
A	67	MSE	MET	modified residue	UNP O25006
A	88	MSE	MET	modified residue	UNP O25006
A	89	MSE	MET	modified residue	UNP O25006
A	128	MSE	MET	modified residue	UNP O25006
A	163	MSE	MET	modified residue	UNP O25006
A	184	GLY	-	cloning artifact	UNP O25006
A	185	SER	-	cloning artifact	UNP O25006
B	-21	MSE	-	cloning artifact	UNP O25006
B	-20	GLY	-	cloning artifact	UNP O25006
B	-19	SER	-	cloning artifact	UNP O25006
B	-18	SER	-	cloning artifact	UNP O25006
B	-17	HIS	-	cloning artifact	UNP O25006
B	-16	HIS	-	cloning artifact	UNP O25006
B	-15	HIS	-	cloning artifact	UNP O25006
B	-14	HIS	-	cloning artifact	UNP O25006
B	-13	HIS	-	cloning artifact	UNP O25006
B	-12	HIS	-	cloning artifact	UNP O25006
B	-11	SER	-	cloning artifact	UNP O25006
B	-10	SER	-	cloning artifact	UNP O25006
B	-9	GLY	-	cloning artifact	UNP O25006
B	-8	ARG	-	cloning artifact	UNP O25006
B	-7	GLU	-	cloning artifact	UNP O25006
B	-6	ASN	-	cloning artifact	UNP O25006
B	-5	LEU	-	cloning artifact	UNP O25006
B	-4	TYR	-	cloning artifact	UNP O25006
B	-3	PHE	-	cloning artifact	UNP O25006
B	-2	GLN	-	cloning artifact	UNP O25006
B	-1	GLY	-	cloning artifact	UNP O25006
B	0	HIS	-	cloning artifact	UNP O25006
B	1	MSE	MET	modified residue	UNP O25006
B	7	MSE	MET	modified residue	UNP O25006
B	67	MSE	MET	modified residue	UNP O25006
B	88	MSE	MET	modified residue	UNP O25006
B	89	MSE	MET	modified residue	UNP O25006
B	128	MSE	MET	modified residue	UNP O25006
B	163	MSE	MET	modified residue	UNP O25006
B	184	GLY	-	cloning artifact	UNP O25006
B	185	SER	-	cloning artifact	UNP O25006
C	-21	MSE	-	cloning artifact	UNP O25006

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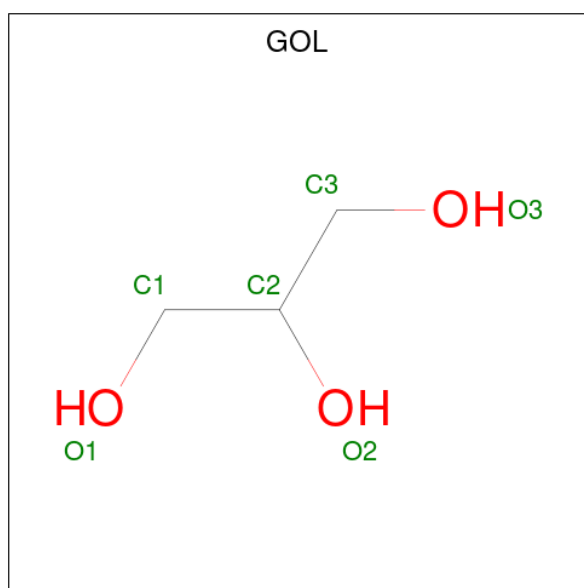
Chain	Residue	Modelled	Actual	Comment	Reference
C	-20	GLY	-	cloning artifact	UNP O25006
C	-19	SER	-	cloning artifact	UNP O25006
C	-18	SER	-	cloning artifact	UNP O25006
C	-17	HIS	-	cloning artifact	UNP O25006
C	-16	HIS	-	cloning artifact	UNP O25006
C	-15	HIS	-	cloning artifact	UNP O25006
C	-14	HIS	-	cloning artifact	UNP O25006
C	-13	HIS	-	cloning artifact	UNP O25006
C	-12	HIS	-	cloning artifact	UNP O25006
C	-11	SER	-	cloning artifact	UNP O25006
C	-10	SER	-	cloning artifact	UNP O25006
C	-9	GLY	-	cloning artifact	UNP O25006
C	-8	ARG	-	cloning artifact	UNP O25006
C	-7	GLU	-	cloning artifact	UNP O25006
C	-6	ASN	-	cloning artifact	UNP O25006
C	-5	LEU	-	cloning artifact	UNP O25006
C	-4	TYR	-	cloning artifact	UNP O25006
C	-3	PHE	-	cloning artifact	UNP O25006
C	-2	GLN	-	cloning artifact	UNP O25006
C	-1	GLY	-	cloning artifact	UNP O25006
C	0	HIS	-	cloning artifact	UNP O25006
C	1	MSE	MET	modified residue	UNP O25006
C	7	MSE	MET	modified residue	UNP O25006
C	67	MSE	MET	modified residue	UNP O25006
C	88	MSE	MET	modified residue	UNP O25006
C	89	MSE	MET	modified residue	UNP O25006
C	128	MSE	MET	modified residue	UNP O25006
C	163	MSE	MET	modified residue	UNP O25006
C	184	GLY	-	cloning artifact	UNP O25006
C	185	SER	-	cloning artifact	UNP O25006
D	-21	MSE	-	cloning artifact	UNP O25006
D	-20	GLY	-	cloning artifact	UNP O25006
D	-19	SER	-	cloning artifact	UNP O25006
D	-18	SER	-	cloning artifact	UNP O25006
D	-17	HIS	-	cloning artifact	UNP O25006
D	-16	HIS	-	cloning artifact	UNP O25006
D	-15	HIS	-	cloning artifact	UNP O25006
D	-14	HIS	-	cloning artifact	UNP O25006
D	-13	HIS	-	cloning artifact	UNP O25006
D	-12	HIS	-	cloning artifact	UNP O25006
D	-11	SER	-	cloning artifact	UNP O25006
D	-10	SER	-	cloning artifact	UNP O25006

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-9	GLY	-	cloning artifact	UNP O25006
D	-8	ARG	-	cloning artifact	UNP O25006
D	-7	GLU	-	cloning artifact	UNP O25006
D	-6	ASN	-	cloning artifact	UNP O25006
D	-5	LEU	-	cloning artifact	UNP O25006
D	-4	TYR	-	cloning artifact	UNP O25006
D	-3	PHE	-	cloning artifact	UNP O25006
D	-2	GLN	-	cloning artifact	UNP O25006
D	-1	GLY	-	cloning artifact	UNP O25006
D	0	HIS	-	cloning artifact	UNP O25006
D	1	MSE	MET	modified residue	UNP O25006
D	7	MSE	MET	modified residue	UNP O25006
D	67	MSE	MET	modified residue	UNP O25006
D	88	MSE	MET	modified residue	UNP O25006
D	89	MSE	MET	modified residue	UNP O25006
D	128	MSE	MET	modified residue	UNP O25006
D	163	MSE	MET	modified residue	UNP O25006
D	184	GLY	-	cloning artifact	UNP O25006
D	185	SER	-	cloning artifact	UNP O25006

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

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

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

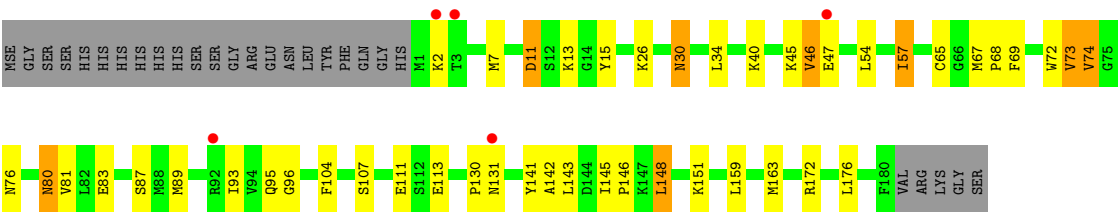
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	81	Total	O	0	0
			81	81		
4	B	72	Total	O	0	0
			72	72		
4	C	53	Total	O	0	0
			53	53		
4	D	61	Total	O	0	0
			61	61		



- Molecule 1: hypothetical protein HP0218







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.31Å 102.27Å 143.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.75 – 2.59 45.75 – 2.59	Depositor EDS
% Data completeness (in resolution range)	97.1 (45.75-2.59) 97.0 (45.75-2.59)	Depositor EDS
$R_{merge}$	0.19	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.72 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.2.0000	Depositor
R, $R_{free}$	0.219 , 0.262 0.219 , 0.260	Depositor DCC
$R_{free}$ test set	4630 reflections (10.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.5	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 40.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.010 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6224	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.59	0/1532	0.69	0/2054
1	B	0.60	0/1516	0.70	0/2035
1	C	0.59	0/1494	0.68	0/2006
1	D	0.61	0/1504	0.68	0/2021
All	All	0.60	0/6046	0.69	0/8116

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	22	GLY	Peptide

### 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	1503	0	1500	30	0
1	B	1486	0	1488	46	0
1	C	1465	0	1457	38	0
1	D	1474	0	1457	57	0
2	A	6	0	8	1	0
2	B	6	0	8	1	0
2	C	6	0	8	0	0
2	D	6	0	8	1	0
3	B	5	0	0	0	0
4	A	81	0	0	5	0
4	B	72	0	0	3	0
4	C	53	0	0	1	0
4	D	61	0	0	4	0
All	All	6224	0	5934	159	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 13.

The worst 5 of 159 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:53:ALA:HB3	1:B:163:MSE:CE	1.63	1.26
1:D:141:TYR:CB	1:D:163:MSE:HE1	1.68	1.23
1:C:85:ASN:HD21	1:C:88[B]:MSE:HE2	1.05	1.09
1:D:141:TYR:HB2	1:D:163:MSE:HE1	1.34	1.05
1:B:72:TRP:HE1	1:B:95:GLN:HE21	1.08	0.97

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	186/207 (90%)	176 (95%)	8 (4%)	2 (1%)	12	26
1	B	184/207 (89%)	173 (94%)	10 (5%)	1 (0%)	25	47
1	C	182/207 (88%)	172 (94%)	9 (5%)	1 (0%)	25	47
1	D	183/207 (88%)	174 (95%)	8 (4%)	1 (0%)	25	47
All	All	735/828 (89%)	695 (95%)	35 (5%)	5 (1%)	22	38

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	11	ASP
1	D	11	ASP
1	A	26[A]	LYS
1	A	26[B]	LYS
1	C	11	ASP

### 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	163/170 (96%)	148 (91%)	15 (9%)	7	15
1	B	161/170 (95%)	146 (91%)	15 (9%)	7	15
1	C	159/170 (94%)	145 (91%)	14 (9%)	8	17
1	D	160/170 (94%)	144 (90%)	16 (10%)	6	13
All	All	643/680 (95%)	583 (91%)	60 (9%)	7	15

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	172	ARG
1	D	81	VAL
1	C	45	LYS
1	D	80	ASN
1	D	176	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	76	ASN
1	D	80	ASN
1	D	139	GLN
1	B	85	ASN
1	B	80	ASN

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

5 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	D	304	-	5,5,5	0.43	0	5,5,5	0.71	0
3	SO4	B	305	-	4,4,4	0.30	0	6,6,6	0.21	0
2	GOL	C	303	-	5,5,5	0.46	0	5,5,5	0.24	0
2	GOL	B	302	-	5,5,5	0.53	0	5,5,5	0.79	0
2	GOL	A	301	-	5,5,5	0.40	0	5,5,5	0.30	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	D	304	-	-	2/4/4/4	-
2	GOL	C	303	-	-	4/4/4/4	-
2	GOL	B	302	-	-	2/4/4/4	-
2	GOL	A	301	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	302	GOL	O1-C1-C2-O2
2	B	302	GOL	O1-C1-C2-C3
2	C	303	GOL	O1-C1-C2-C3
2	C	303	GOL	C1-C2-C3-O3
2	A	301	GOL	O2-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	304	GOL	1	0
2	B	302	GOL	1	0
2	A	301	GOL	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	174/207 (84%)	-0.04	1 (0%) 85 83	9, 24, 36, 48	6 (3%)
1	B	175/207 (84%)	0.07	4 (2%) 61 55	11, 25, 41, 54	4 (2%)
1	C	174/207 (84%)	0.10	6 (3%) 48 42	10, 27, 40, 53	2 (1%)
1	D	173/207 (83%)	0.04	5 (2%) 54 48	9, 27, 42, 56	5 (2%)
All	All	696/828 (84%)	0.04	16 (2%) 61 55	9, 26, 41, 56	17 (2%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	181	VAL	4.0
1	B	182	ARG	3.9
1	C	111[A]	GLU	3.2
1	B	45[A]	LYS	3.2
1	C	47	GLU	2.9

### 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 monosaccharides 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
3	SO4	B	305	5/5	0.68	0.27	109,109,110,110	0
2	GOL	D	304	6/6	0.77	0.20	36,40,41,41	0
2	GOL	A	301	6/6	0.82	0.22	37,40,41,41	0
2	GOL	C	303	6/6	0.85	0.17	37,41,42,44	0
2	GOL	B	302	6/6	0.87	0.16	36,38,41,41	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.