



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 08:07 am BST

PDB ID : 5NS8  
Title : Crystal structure of beta-glucosidase BglM-G1 mutant H75R from marine metagenome in complex with inhibitor 1-Deoxynojirimycin  
Authors : Mhaindarkar, D.C.; Gasper, R.; Lupilova, N.; Leichert, L.I.; Hofmann, E.  
Deposited on : 2017-04-25  
Resolution : 1.55 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.

---

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

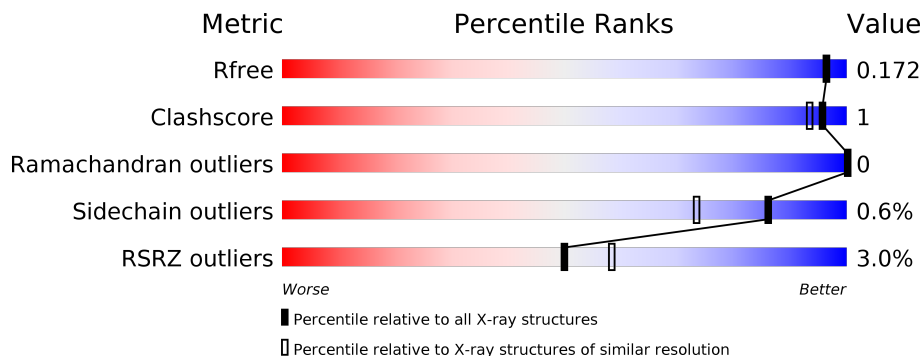
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

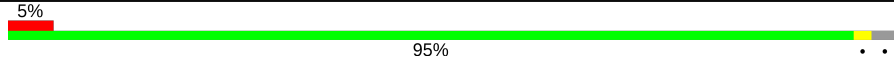
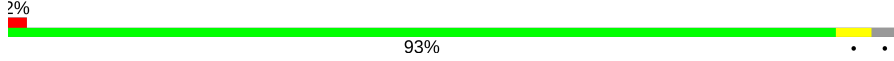
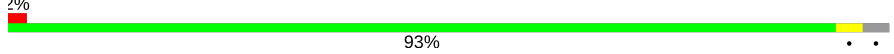
The reported resolution of this entry is 1.55 Å.

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	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (1.56-1.56)

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	454	 5% 95%
1	B	454	 2% 93%
1	C	454	 2% 93%

## 2 Entry composition [i](#)

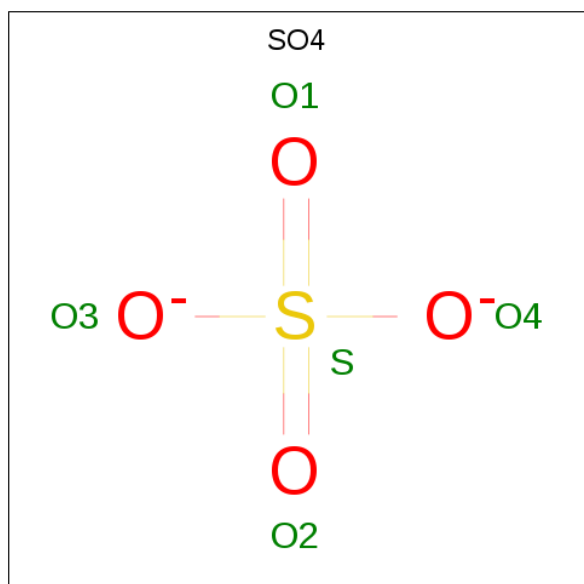
There are 5 unique types of molecules in this entry. The entry contains 22012 atoms, of which 10400 are hydrogens and 0 are deuteriums.

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 beta-glucosidase M - G1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	440	6998	2306	3423	595	661	13	2	7	0
1	B	440	6991	2303	3421	595	659	13	2	6	0
1	C	440	7010	2310	3430	595	661	14	2	8	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



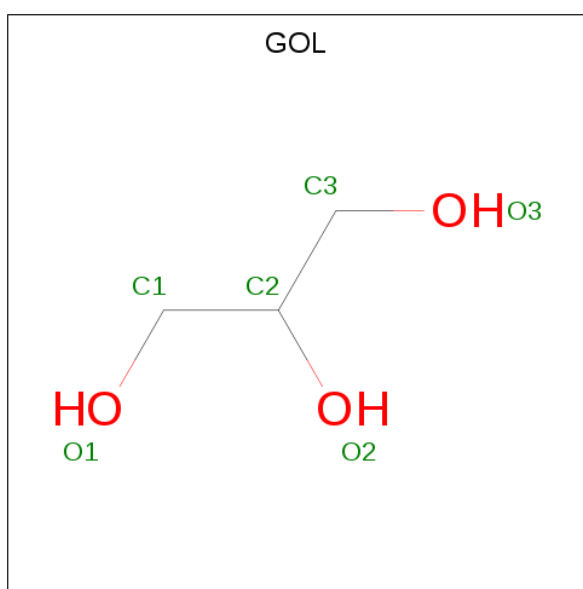
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0
2	B	1	5	4	1	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	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>).



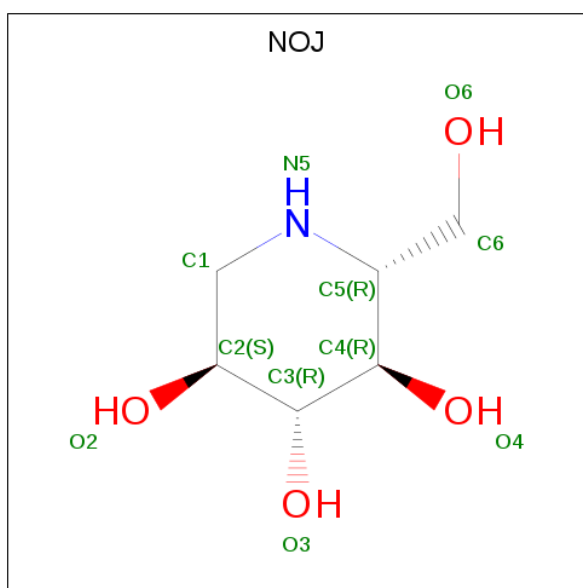
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			13	3	7	3		
3	B	1	Total	C	H	O	0	0
			12	3	6	3		
3	B	1	Total	C	H	O	0	0
			12	3	6	3		
3	B	1	Total	C	H	O	0	0
			13	3	7	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
3	B	1	Total	C	H	O	0	0
			12	3	6	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	C	1	Total	C	H	O	0	0
			14	3	8	3		
3	C	1	Total	C	H	O	0	0
			14	3	8	3		
3	C	1	Total	C	H	O	0	0
			13	3	7	3		

- Molecule 4 is 1-DEOXYNOJIRIMYCIN (three-letter code: NOJ) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	H	N			O
4	A	1	Total	C	H	N	O	0	0
			24	6	13	1	4		
4	B	1	Total	C	H	N	O	0	0
			24	6	13	1	4		
4	C	1	Total	C	H	N	O	0	0
			24	6	13	1	4		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	186	Total	O	0	0
			186	186		

Continued on next page...

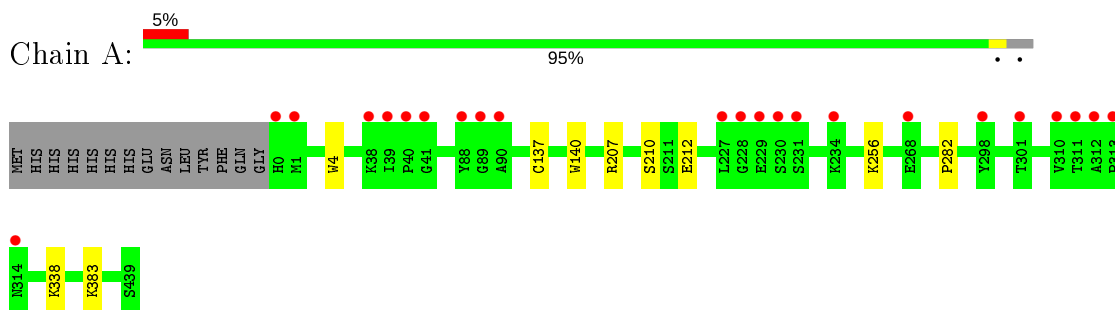
*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	B	299	Total 299	O 299	0	0
5	C	262	Total 262	O 262	0	0

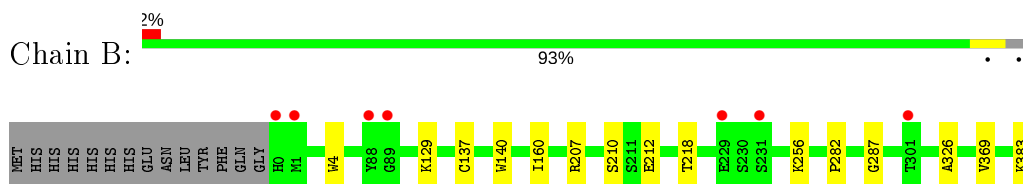
### 3 Residue-property plots [i](#)

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.

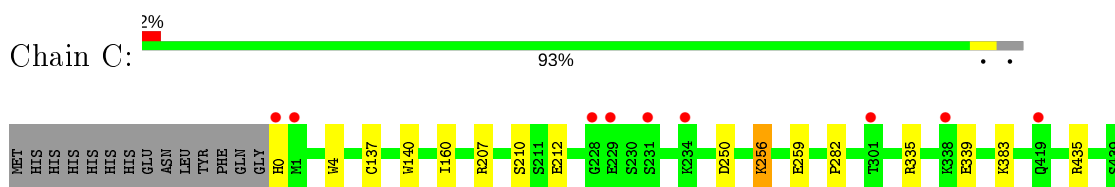
- Molecule 1: beta-glucosidase M - G1



- Molecule 1: beta-glucosidase M - G1



- Molecule 1: beta-glucosidase M - G1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	137.75Å 137.75Å 97.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.70 – 1.55 48.70 – 1.55	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.70-1.55) 100.0 (48.70-1.55)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.20 (at 1.55Å)	Xtrriage
Refinement program	PHENIX dev_2621	Depositor
R, $R_{free}$	0.161 , 0.172 0.161 , 0.172	Depositor DCC
$R_{free}$ test set	13201 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.0	Xtrriage
Anisotropy	0.047	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.45 , 45.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.018 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	22012	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% 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, NOJ

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	0.29	0/3712	0.51	0/5038
1	B	0.32	0/3704	0.55	0/5027
1	C	0.31	0/3720	0.54	0/5048
All	All	0.31	0/11136	0.53	0/15113

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	3575	3423	3428	5	0
1	B	3570	3421	3424	10	0
1	C	3580	3430	3437	10	0
2	A	10	0	0	0	0
2	B	15	0	0	0	0
2	C	10	0	0	0	0
3	A	18	23	24	0	0
3	B	36	41	48	1	0
3	C	18	23	24	1	0
4	A	11	13	13	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	11	13	13	0	0
4	C	11	13	13	0	0
5	A	186	0	0	0	0
5	B	299	0	0	2	0
5	C	262	0	0	5	0
All	All	11612	10400	10424	23	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 1.

All (23) 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:C:210:SER:OG	1:C:212[A]:GLU:OE2	1.91	0.88
1:C:339:GLU:OE1	5:C:601:HOH:O	1.94	0.85
1:C:335:ARG:NH2	5:C:601:HOH:O	2.12	0.82
1:C:207[B]:ARG:NH2	1:C:282:PRO:O	2.20	0.74
1:B:210:SER:OG	1:B:212[A]:GLU:OE2	2.07	0.73
1:C:339:GLU:OE2	5:C:603:HOH:O	2.11	0.67
1:A:210:SER:OG	1:A:212[A]:GLU:OE2	2.13	0.67
1:B:207[B]:ARG:NH2	1:B:282:PRO:O	2.29	0.63
1:B:129:LYS:NZ	5:B:602:HOH:O	2.33	0.60
1:A:207[B]:ARG:NH2	1:A:282:PRO:O	2.30	0.58
1:A:383:LYS:HE3	1:C:4:TRP:CE2	2.43	0.53
1:B:4:TRP:CE2	1:C:383:LYS:HE3	2.44	0.52
1:B:326:ALA:HB3	3:B:507:GOL:H12	1.92	0.52
3:C:505:GOL:O3	5:C:602:HOH:O	2.07	0.50
1:A:4:TRP:CE2	1:B:383:LYS:HE3	2.49	0.48
1:C:137:CYS:HA	1:C:140:TRP:CE3	2.52	0.44
1:C:160:ILE:HD12	5:C:631:HOH:O	2.18	0.44
1:B:160:ILE:HD12	5:B:627:HOH:O	2.17	0.44
1:B:137:CYS:HA	1:B:140:TRP:CE3	2.54	0.43
1:A:137:CYS:HA	1:A:140:TRP:CE3	2.55	0.42
1:B:369:VAL:HG22	1:B:428:SER:HA	2.02	0.41
1:B:218:THR:HA	1:B:287:GLY:O	2.20	0.41
1:C:250:ASP:OD2	1:C:256:LYS:NZ	2.41	0.41

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	445/454 (98%)	435 (98%)	10 (2%)	0	100	100
1	B	444/454 (98%)	435 (98%)	9 (2%)	0	100	100
1	C	446/454 (98%)	436 (98%)	10 (2%)	0	100	100
All	All	1335/1362 (98%)	1306 (98%)	29 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	373/379 (98%)	371 (100%)	2 (0%)	88	78
1	B	372/379 (98%)	371 (100%)	1 (0%)	92	85
1	C	374/379 (99%)	370 (99%)	4 (1%)	73	53
All	All	1119/1137 (98%)	1112 (99%)	7 (1%)	86	73

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	256	LYS
1	A	338	LYS
1	B	256	LYS
1	C	0	HIS
1	C	256	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	259	GLU
1	C	435	ARG

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](#)

22 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	SO4	A	502	-	4,4,4	0.15	0	6,6,6	0.05	0
3	GOL	A	504	-	5,5,5	0.91	0	5,5,5	0.95	0
3	GOL	C	503	-	5,5,5	0.97	0	5,5,5	0.94	0
2	SO4	A	501	-	4,4,4	0.13	0	6,6,6	0.06	0
2	SO4	B	501	-	4,4,4	0.20	0	6,6,6	0.36	0
3	GOL	B	507	-	5,5,5	0.94	0	5,5,5	0.89	0
2	SO4	C	502	-	4,4,4	0.12	0	6,6,6	0.12	0
4	NOJ	C	506	-	11,11,11	0.96	0	13,15,15	1.90	4 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	C	501	-	4,4,4	0.14	0	6,6,6	0.05	0
3	GOL	B	504	-	5,5,5	1.07	0	5,5,5	0.98	0
4	NOJ	A	506	-	11,11,11	1.12	1 (9%)	13,15,15	1.81	2 (15%)
2	SO4	B	503	-	4,4,4	0.15	0	6,6,6	0.05	0
3	GOL	A	505	-	5,5,5	0.90	0	5,5,5	0.91	0
3	GOL	B	509	-	5,5,5	1.02	0	5,5,5	0.86	0
2	SO4	B	502	-	4,4,4	0.14	0	6,6,6	0.05	0
4	NOJ	B	510	-	11,11,11	1.00	1 (9%)	13,15,15	1.75	3 (23%)
3	GOL	B	506	-	5,5,5	1.11	0	5,5,5	0.86	0
3	GOL	C	504	-	5,5,5	0.97	0	5,5,5	0.91	0
3	GOL	A	503	-	5,5,5	0.99	0	5,5,5	1.03	0
3	GOL	B	508	-	5,5,5	1.40	0	5,5,5	0.42	0
3	GOL	C	505	-	5,5,5	1.00	0	5,5,5	0.93	0
3	GOL	B	505	-	5,5,5	0.99	0	5,5,5	0.99	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	B	509	-	-	0/4/4/4	-
4	NOJ	C	506	-	-	0/2/19/19	0/1/1/1
3	GOL	C	504	-	-	2/4/4/4	-
3	GOL	A	503	-	-	0/4/4/4	-
3	GOL	A	504	-	-	0/4/4/4	-
3	GOL	C	503	-	-	0/4/4/4	-
3	GOL	A	505	-	-	0/4/4/4	-
3	GOL	B	507	-	-	2/4/4/4	-
3	GOL	B	504	-	-	0/4/4/4	-
3	GOL	B	508	-	-	4/4/4/4	-
3	GOL	B	506	-	-	4/4/4/4	-
3	GOL	C	505	-	-	3/4/4/4	-
4	NOJ	A	506	-	-	0/2/19/19	0/1/1/1
4	NOJ	B	510	-	-	0/2/19/19	0/1/1/1
3	GOL	B	505	-	-	0/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	506	NOJ	C1-N5	2.41	1.50	1.47

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	510	NOJ	C1-N5	2.24	1.50	1.47

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	510	NOJ	C1-N5-C5	4.56	119.47	109.61
4	A	506	NOJ	C1-N5-C5	4.34	119.00	109.61
4	C	506	NOJ	C1-C2-C3	3.85	114.85	110.33
4	A	506	NOJ	C1-C2-C3	3.76	114.74	110.33
4	C	506	NOJ	C1-N5-C5	3.65	117.51	109.61
4	B	510	NOJ	C1-C2-C3	3.03	113.89	110.33
4	C	506	NOJ	O2-C2-C1	-2.62	104.50	109.61
4	C	506	NOJ	C3-C4-C5	-2.61	107.19	111.02
4	B	510	NOJ	O3-C3-C2	-2.43	105.33	109.99

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	507	GOL	C1-C2-C3-O3
3	B	506	GOL	C1-C2-C3-O3
3	C	504	GOL	C1-C2-C3-O3
3	B	508	GOL	O1-C1-C2-C3
3	B	508	GOL	C1-C2-C3-O3
3	B	507	GOL	O2-C2-C3-O3
3	B	508	GOL	O1-C1-C2-O2
3	B	508	GOL	O2-C2-C3-O3
3	B	506	GOL	O2-C2-C3-O3
3	C	504	GOL	O2-C2-C3-O3
3	C	505	GOL	O1-C1-C2-O2
3	B	506	GOL	O1-C1-C2-O2
3	C	505	GOL	C1-C2-C3-O3
3	B	506	GOL	O1-C1-C2-C3
3	C	505	GOL	O1-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	507	GOL	1	0
3	C	505	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

### 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	440/454 (96%)	0.02	23 (5%) 27 31	16, 26, 50, 90	0
1	B	440/454 (96%)	-0.23	7 (1%) 72 77	14, 18, 36, 91	0
1	C	440/454 (96%)	-0.23	9 (2%) 65 71	14, 20, 40, 86	0
All	All	1320/1362 (96%)	-0.15	39 (2%) 50 58	14, 21, 43, 91	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	10.0
1	C	1	MET	9.6
1	C	0	HIS	7.7
1	A	1	MET	7.3
1	A	0	HIS	6.8
1	B	0	HIS	6.2
1	A	313	PRO	5.6
1	A	227	LEU	5.2
1	A	314	ASN	5.1
1	A	88	TYR	4.8
1	A	312	ALA	4.3
1	A	229	GLU	4.3
1	A	310	VAL	4.3
1	A	40	PRO	4.0
1	C	229	GLU	3.9
1	A	301	THR	3.5
1	B	88	TYR	3.5
1	A	298	TYR	3.4
1	A	311	THR	3.3
1	A	268	GLU	3.2
1	A	231	SER	3.2
1	B	229	GLU	3.0
1	A	228	GLY	2.9

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	230	SER	2.9
1	B	231	SER	2.8
1	C	231	SER	2.7
1	C	338	LYS	2.6
1	A	38	LYS	2.5
1	A	39	ILE	2.5
1	A	90	ALA	2.5
1	A	89	GLY	2.4
1	C	234	LYS	2.3
1	C	301	THR	2.2
1	C	228	GLY	2.2
1	A	41	GLY	2.2
1	C	419	GLN	2.2
1	B	301	THR	2.1
1	B	89	GLY	2.1
1	A	234	LYS	2.1

## 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	B	507	6/6	0.57	0.24	49,66,76,79	0
3	GOL	A	504	6/6	0.66	0.28	58,70,80,81	0
3	GOL	B	504	6/6	0.67	0.23	32,41,49,49	0
3	GOL	C	504	6/6	0.67	0.28	37,50,64,69	0
3	GOL	B	508	6/6	0.69	0.20	37,50,59,59	0
2	SO4	B	502	5/5	0.76	0.22	98,100,102,102	0
3	GOL	C	503	6/6	0.78	0.23	38,49,59,61	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	GOL	A	503	6/6	0.81	0.14	32,38,41,41	0
3	GOL	B	505	6/6	0.82	0.19	30,41,56,56	0
2	SO4	A	502	5/5	0.84	0.17	85,85,88,91	0
3	GOL	B	506	6/6	0.85	0.16	26,35,48,48	0
2	SO4	A	501	5/5	0.86	0.20	82,82,84,86	0
3	GOL	C	505	6/6	0.90	0.13	38,49,58,59	0
2	SO4	C	501	5/5	0.92	0.20	67,71,72,74	0
3	GOL	A	505	6/6	0.93	0.12	25,35,48,48	0
2	SO4	B	503	5/5	0.93	0.16	65,65,67,69	0
4	NOJ	C	506	11/11	0.95	0.09	17,23,30,31	0
3	GOL	B	509	6/6	0.96	0.06	19,23,26,26	0
4	NOJ	A	506	11/11	0.96	0.08	22,28,36,37	0
4	NOJ	B	510	11/11	0.96	0.09	15,21,28,28	0
2	SO4	C	502	5/5	0.98	0.08	29,32,34,34	0
2	SO4	B	501	5/5	0.99	0.08	23,23,27,29	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.