



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 2, 2025 – 12:16 am BST

PDB ID : 2WVX / pdb\_00002wvx  
Title : Structure of the Family GH92 Inverting Mannosidase BT3990 from Bacteroides  
thetaiotaomicron VPI-5482  
Authors : Suits, M.D.L.; Zhu, Y.; Thompson, A.; Gilbert, H.J.; Davies, G.J.  
Deposited on : 2009-10-21  
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](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 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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
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) : 2.42

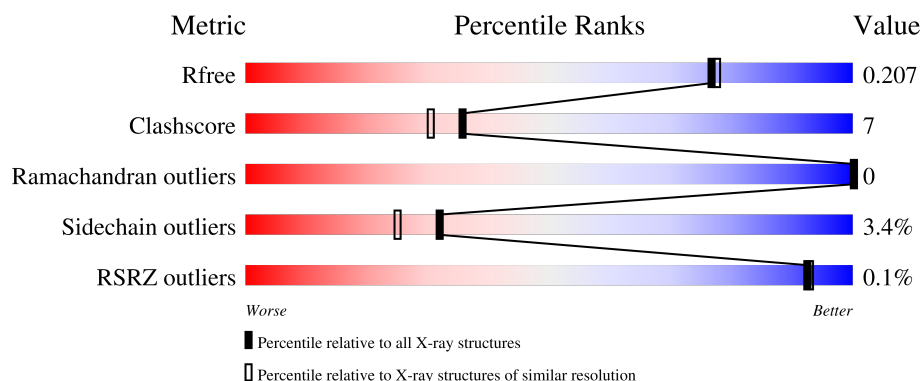
# 1 Overall quality at a glance

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))
$R_{free}$	164625	7293 (1.90-1.90)
Clashscore	180529	8090 (1.90-1.90)
Ramachandran outliers	177936	8022 (1.90-1.90)
Sidechain outliers	177891	8022 (1.90-1.90)
RSRZ outliers	164620	7292 (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  $\geq 3$ , 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	744	 88% 10% ..
1	C	744	 86% 12% ..
1	D	744	 87% 11% ..
2	B	744	 86% 11% ..

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 25973 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 PUTATIVE ALPHA-1,2-MANNOSIDASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	736	Total	C	N	O	S	Se	0	2	0
			5932	3801	974	1124	6	27			
1	C	736	Total	C	N	O	S	Se	0	6	0
			5972	3831	976	1129	6	30			
1	D	736	Total	C	N	O	S	Se	0	4	0
			5973	3831	982	1126	6	28			

- Molecule 2 is a protein called PUTATIVE ALPHA-1,2-MANNOSIDASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	737	Total	C	N	O	S	Se	0	5	0
			5974	3833	982	1124	6	29			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	216	GLN	ASN	conflict	UNP Q8A0N1

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		
3	B	1	Total	Ca	0	0
			1	1		
3	C	1	Total	Ca	0	0
			1	1		
3	D	1	Total	Ca	0	0
			1	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

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

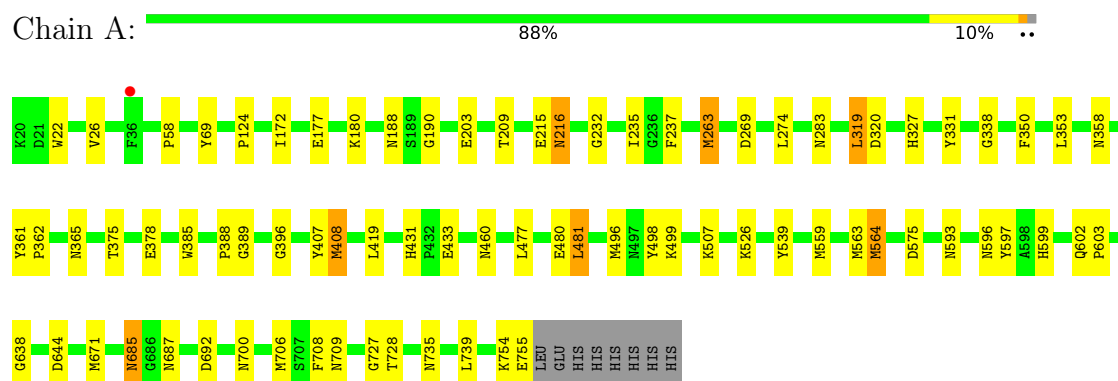
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	529	Total	O	0	0
			529	529		
5	B	463	Total	O	0	0
			463	463		
5	C	531	Total	O	0	0
			531	531		
5	D	499	Total	O	0	0
			499	499		

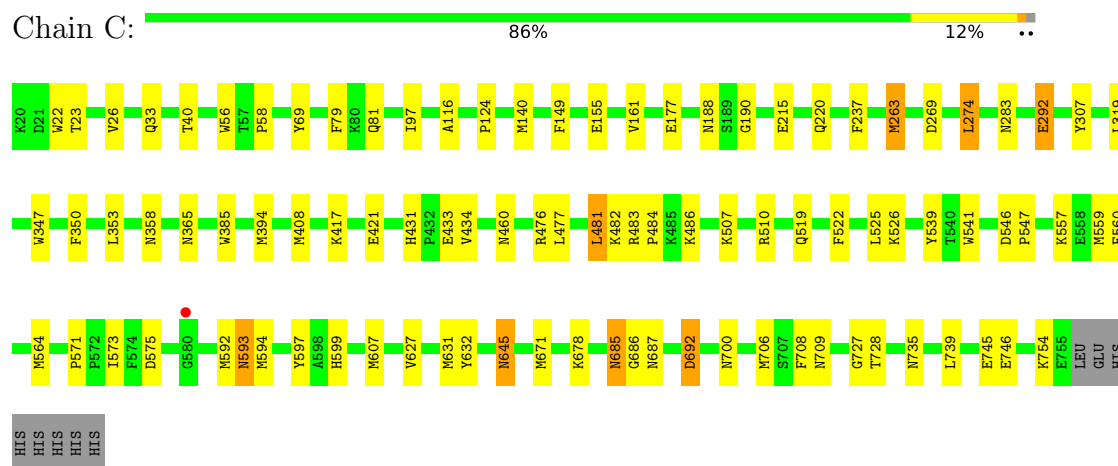
### 3 Residue-property plots

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.

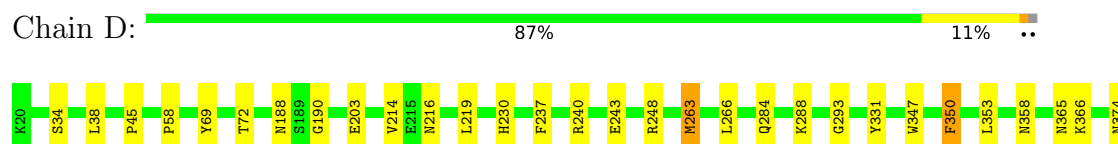
#### • Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE

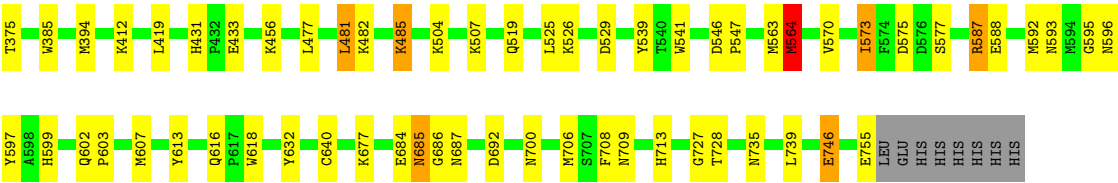


#### • Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE

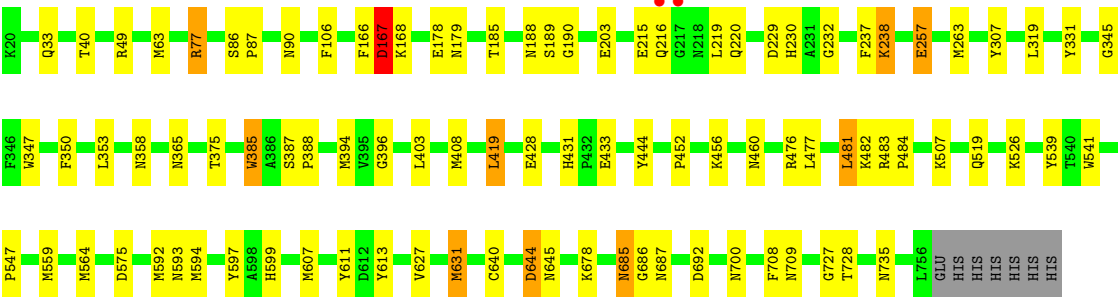
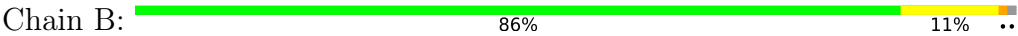


#### • Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE





• Molecule 2: PUTATIVE ALPHA-1,2-MANNOSIDASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.23Å 190.95Å 135.10Å 90.00° 96.97° 90.00°	Depositor
Resolution (Å)	133.63 – 1.90 133.63 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.5 (133.63-1.90) 97.5 (133.63-1.90)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.70 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.4.0077	Depositor
R, $R_{free}$	0.155 , 0.186 0.181 , 0.207	Depositor DCC
$R_{free}$ test set	12380 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.1	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 34.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	25973	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	8.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% 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: CA, GOL

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	0.81	2/6086 (0.0%)	0.70	3/8226 (0.0%)
1	C	0.81	2/6141 (0.0%)	0.68	1/8292 (0.0%)
1	D	0.77	0/6136	0.69	2/8283 (0.0%)
2	B	0.74	3/6136 (0.0%)	0.67	3/8282 (0.0%)
All	All	0.78	7/24499 (0.0%)	0.68	9/33083 (0.0%)

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
2	B	0	2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	167	ASP	C-N	8.19	1.52	1.34
1	A	638	GLY	C-O	-6.14	1.13	1.23
1	C	116	ALA	CA-CB	-6.01	1.39	1.52
2	B	428	GLU	CB-CG	-5.86	1.41	1.52
2	B	396	GLY	C-O	-5.74	1.14	1.23

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	564	MSE	CG-SE-CE	-9.49	78.02	98.90
2	B	167	ASP	CA-C-N	-8.91	97.61	117.20
1	D	564	MSE	CG-SE-CE	-7.92	81.47	98.90
1	C	263	MSE	CG-SE-CE	-6.38	84.87	98.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	77	ARG	NE-CZ-NH2	-5.95	117.32	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	167	ASP	Mainchain

## 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	5932	0	5528	80	0
1	C	5972	0	5606	86	0
1	D	5973	0	5627	74	0
2	B	5974	0	5623	94	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	24	0	32	0	0
4	B	24	0	32	0	0
4	C	24	0	32	0	0
4	D	24	0	32	3	0
5	A	529	0	0	4	0
5	B	463	0	0	5	0
5	C	531	0	0	6	0
5	D	499	0	0	6	0
All	All	25973	0	22512	334	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 7.

The worst 5 of 334 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:63:MSE:CE	2:B:166:PHE:HA	1.12	1.57
2:B:63:MSE:CE	2:B:166:PHE:CA	1.90	1.48
2:B:592:MSE:HE2	2:B:631[B]:MSE:SE	1.64	1.46
1:A:496:MSE:CE	1:A:499:LYS:HE3	1.41	1.44
2:B:63:MSE:HE1	2:B:166:PHE:CA	1.51	1.37

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	736/744 (99%)	716 (97%)	20 (3%)	0	100	100
1	C	740/744 (100%)	719 (97%)	21 (3%)	0	100	100
1	D	738/744 (99%)	718 (97%)	20 (3%)	0	100	100
2	B	740/744 (100%)	722 (98%)	18 (2%)	0	100	100
All	All	2954/2976 (99%)	2875 (97%)	79 (3%)	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	623/616 (101%)	604 (97%)	19 (3%)	36	30
1	C	632/616 (103%)	612 (97%)	20 (3%)	34	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	633/616 (103%)	607 (96%)	26 (4%)	26	19
2	B	631/616 (102%)	608 (96%)	23 (4%)	30	23
All	All	2519/2464 (102%)	2431 (96%)	88 (4%)	32	24

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	645[B]	ASN
1	D	456	LYS
1	C	692	ASP
1	D	263[A]	MSE
1	D	519	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	188	ASN
1	D	264	ASN
1	D	599	HIS
2	B	431	HIS
2	B	374	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](#)

Of 20 ligands modelled in this entry, 4 are monoatomic - leaving 16 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
4	GOL	D	803	-	5,5,5	0.35	0	5,5,5	0.08	0
4	GOL	A	802	-	5,5,5	0.35	0	5,5,5	0.41	0
4	GOL	A	804	-	5,5,5	0.53	0	5,5,5	0.42	0
4	GOL	C	804	-	5,5,5	0.29	0	5,5,5	0.70	0
4	GOL	A	803	-	5,5,5	0.37	0	5,5,5	0.20	0
4	GOL	B	804	-	5,5,5	0.35	0	5,5,5	0.50	0
4	GOL	B	805	-	5,5,5	0.31	0	5,5,5	0.43	0
4	GOL	B	803	-	5,5,5	0.42	0	5,5,5	0.95	0
4	GOL	C	805	-	5,5,5	0.43	0	5,5,5	0.35	0
4	GOL	D	805	-	5,5,5	0.36	0	5,5,5	0.60	0
4	GOL	C	802	-	5,5,5	0.22	0	5,5,5	0.52	0
4	GOL	D	806	-	5,5,5	0.26	0	5,5,5	0.64	0
4	GOL	C	803	-	5,5,5	0.42	0	5,5,5	0.54	0
4	GOL	B	802	-	5,5,5	0.25	0	5,5,5	0.58	0
4	GOL	A	805	-	5,5,5	0.27	0	5,5,5	0.57	0
4	GOL	D	804	1	5,5,5	0.23	0	5,5,5	0.62	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
4	GOL	D	803	-	-	0/4/4/4	-
4	GOL	A	802	-	-	2/4/4/4	-
4	GOL	A	804	-	-	0/4/4/4	-
4	GOL	C	804	-	-	2/4/4/4	-
4	GOL	A	803	-	-	0/4/4/4	-
4	GOL	B	804	-	-	1/4/4/4	-
4	GOL	B	805	-	-	0/4/4/4	-
4	GOL	B	803	-	-	3/4/4/4	-
4	GOL	C	805	-	-	0/4/4/4	-
4	GOL	D	805	-	-	2/4/4/4	-
4	GOL	C	802	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	D	806	-	-	2/4/4/4	-
4	GOL	C	803	-	-	0/4/4/4	-
4	GOL	B	802	-	-	0/4/4/4	-
4	GOL	A	805	-	-	2/4/4/4	-
4	GOL	D	804	1	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	805	GOL	C1-C2-C3-O3
4	B	803	GOL	O1-C1-C2-C3
4	B	803	GOL	C1-C2-C3-O3
4	D	804	GOL	O1-C1-C2-C3
4	D	805	GOL	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	804	GOL	3	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	709/744 (95%)	-0.65	1 (0%) 92 93	2, 7, 16, 26	2 (0%)
1	C	709/744 (95%)	-0.67	1 (0%) 92 93	2, 7, 15, 26	3 (0%)
1	D	709/744 (95%)	-0.55	0 100 100	2, 7, 16, 28	3 (0%)
2	B	710/744 (95%)	-0.26	2 (0%) 90 91	3, 8, 15, 25	3 (0%)
All	All	2837/2976 (95%)	-0.53	4 (0%) 92 93	2, 7, 16, 28	11 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	217	GLY	2.9
2	B	216	GLN	2.4
1	A	36	PHE	2.3
1	C	580	GLY	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 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
4	GOL	D	804	6/6	0.77	0.13	18,19,23,26	0
4	GOL	A	805	6/6	0.87	0.10	21,22,22,23	0
4	GOL	D	806	6/6	0.87	0.10	23,24,25,25	0
4	GOL	C	804	6/6	0.91	0.09	14,21,23,25	0
4	GOL	D	805	6/6	0.92	0.07	9,11,14,20	0
4	GOL	A	804	6/6	0.92	0.09	11,12,14,19	0
4	GOL	B	805	6/6	0.93	0.07	13,14,15,15	0
4	GOL	B	803	6/6	0.94	0.08	12,13,15,19	0
4	GOL	B	804	6/6	0.94	0.07	14,18,19,20	0
4	GOL	C	805	6/6	0.94	0.10	9,14,16,20	0
4	GOL	C	803	6/6	0.95	0.06	11,14,16,17	0
4	GOL	D	803	6/6	0.96	0.06	10,14,16,17	0
4	GOL	B	802	6/6	0.96	0.05	14,15,15,17	0
3	CA	D	801	1/1	0.96	0.10	25,25,25,25	0
4	GOL	C	802	6/6	0.96	0.05	9,12,13,14	0
4	GOL	A	803	6/6	0.97	0.06	15,16,17,17	0
3	CA	A	801	1/1	0.97	0.08	23,23,23,23	0
4	GOL	A	802	6/6	0.97	0.05	7,12,14,15	0
3	CA	C	801	1/1	0.98	0.07	19,19,19,19	0
3	CA	B	801	1/1	0.98	0.11	26,26,26,26	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.