



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:19 PM UTC

PDB ID : 5GR2 / pdb_00005gr2
Title : Crystal structure of branching enzyme L541A mutant from *Cyanothece* sp. ATCC 51142
Authors : Suzuki, R.; Suzuki, E.
Deposited on : 2016-08-08
Resolution : 1.95 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

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>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

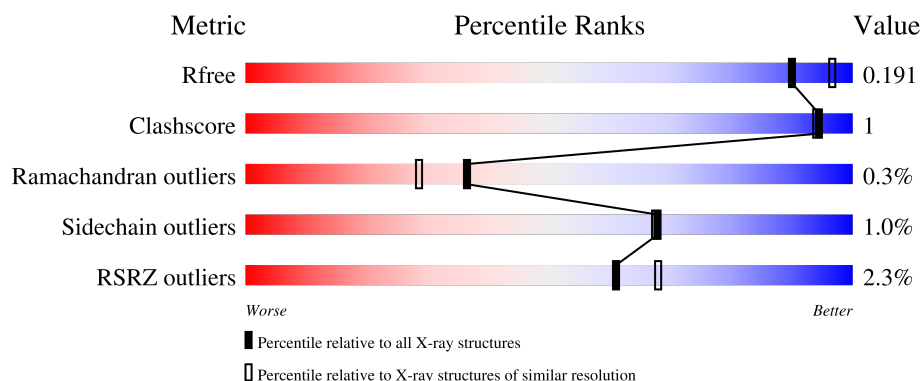
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

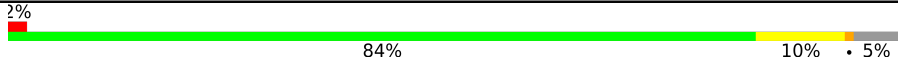
The reported resolution of this entry is 1.95 Å.

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}	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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 ≥ 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	793	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	A	801	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7077 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 1,4-alpha-glucan branching enzyme GlgB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	755	Total	C	N	O	S	0	1	0
			6276	4058	1043	1151	24			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP B1WPM8
A	-18	GLY	-	expression tag	UNP B1WPM8
A	-17	SER	-	expression tag	UNP B1WPM8
A	-16	SER	-	expression tag	UNP B1WPM8
A	-15	HIS	-	expression tag	UNP B1WPM8
A	-14	HIS	-	expression tag	UNP B1WPM8
A	-13	HIS	-	expression tag	UNP B1WPM8
A	-12	HIS	-	expression tag	UNP B1WPM8
A	-11	HIS	-	expression tag	UNP B1WPM8
A	-10	HIS	-	expression tag	UNP B1WPM8
A	-9	SER	-	expression tag	UNP B1WPM8
A	-8	SER	-	expression tag	UNP B1WPM8
A	-7	GLY	-	expression tag	UNP B1WPM8
A	-6	LEU	-	expression tag	UNP B1WPM8
A	-5	VAL	-	expression tag	UNP B1WPM8
A	-4	PRO	-	expression tag	UNP B1WPM8
A	-3	ARG	-	expression tag	UNP B1WPM8
A	-2	GLY	-	expression tag	UNP B1WPM8
A	-1	SER	-	expression tag	UNP B1WPM8
A	0	HIS	-	expression tag	UNP B1WPM8
A	541	ALA	LEU	engineered mutation	UNP B1WPM8

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	Mg	0	0
			4	4		

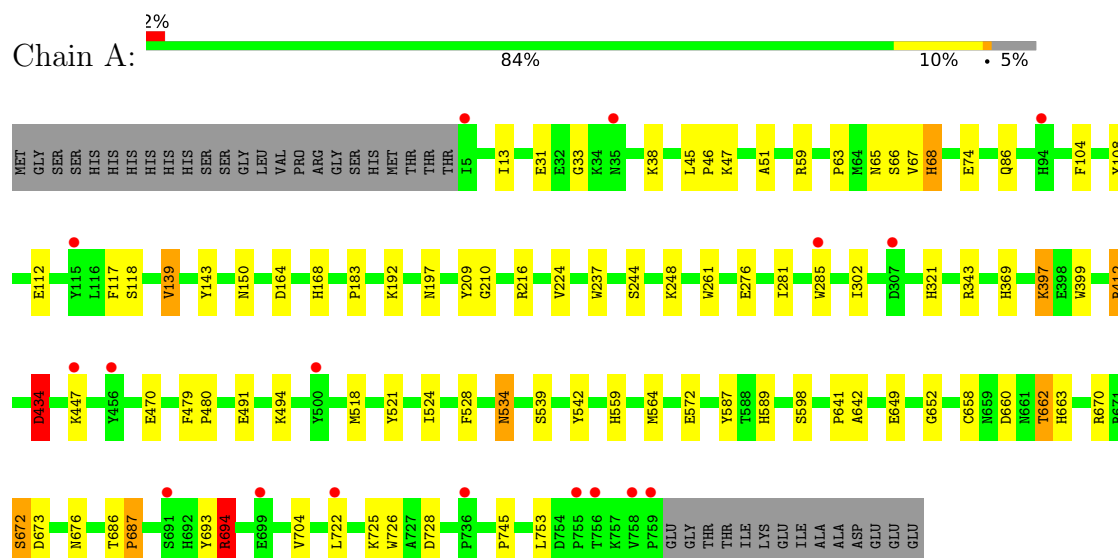
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	767	Total	O	0	0
			767	767		

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: 1,4-alpha-glucan branching enzyme GlgB



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	133.48Å 133.48Å 184.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.19 – 1.95 46.19 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.5 (46.19-1.95) 99.5 (46.19-1.95)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	10.72 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.154 , 0.180 0.167 , 0.191	Depositor DCC
R_{free} test set	6077 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	22.5	Xtriage
Anisotropy	0.007	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7077	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: MG, 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	1.64	60/6499 (0.9%)	1.27	26/8844 (0.3%)

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	1

All (60) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	216	ARG	CA-C	8.62	1.61	1.53
1	A	480	PRO	C-O	-8.54	1.13	1.23
1	A	369	HIS	CA-C	-8.39	1.42	1.52
1	A	672	SER	CA-C	8.35	1.61	1.53
1	A	660	ASP	CA-C	7.96	1.62	1.53
1	A	662	THR	CB-CG2	-7.92	1.26	1.52
1	A	276	GLU	CA-C	-7.88	1.43	1.52
1	A	649	GLU	N-CA	7.61	1.55	1.45
1	A	112	GLU	CA-C	7.40	1.62	1.52
1	A	480	PRO	C-N	-7.39	1.22	1.33
1	A	673	ASP	N-CA	6.75	1.54	1.46
1	A	564	MET	SD-CE	-6.72	1.62	1.79
1	A	104	PHE	CA-C	-6.63	1.44	1.52
1	A	51	ALA	C-O	6.54	1.31	1.23
1	A	753	LEU	N-CA	6.33	1.54	1.46
1	A	663	HIS	CA-C	6.32	1.60	1.52
1	A	676	ASN	CA-C	6.17	1.61	1.52
1	A	726	TRP	CA-CB	6.14	1.62	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	434	ASP	N-CA	6.13	1.53	1.45
1	A	302	ILE	CA-C	5.96	1.58	1.52
1	A	524	ILE	N-CA	5.96	1.53	1.46
1	A	521	TYR	CA-C	-5.92	1.45	1.52
1	A	117	PHE	N-CA	5.92	1.53	1.46
1	A	559	HIS	CA-C	-5.88	1.45	1.53
1	A	65	ASN	CG-ND2	-5.82	1.21	1.33
1	A	209	TYR	C-N	5.74	1.38	1.33
1	A	139	VAL	C-O	5.66	1.29	1.24
1	A	210	GLY	N-CA	-5.63	1.39	1.45
1	A	224	VAL	C-O	-5.62	1.18	1.24
1	A	343	ARG	CZ-NH2	-5.57	1.26	1.33
1	A	66	SER	CA-C	-5.52	1.45	1.52
1	A	704	VAL	CA-C	5.50	1.58	1.52
1	A	321	HIS	CA-C	5.49	1.58	1.52
1	A	74	GLU	CG-CD	5.46	1.65	1.52
1	A	261	TRP	C-O	5.43	1.30	1.24
1	A	51	ALA	CA-C	-5.42	1.46	1.52
1	A	693	TYR	CA-C	-5.42	1.46	1.52
1	A	164	ASP	CA-C	5.37	1.59	1.52
1	A	559	HIS	CA-CB	5.34	1.61	1.53
1	A	397	LYS	N-CA	5.31	1.52	1.46
1	A	13	ILE	N-CA	5.29	1.52	1.46
1	A	641	PRO	CA-CB	5.29	1.61	1.53
1	A	67	VAL	C-O	5.26	1.29	1.24
1	A	237	TRP	N-CA	5.26	1.52	1.46
1	A	534	ASN	CA-C	5.22	1.59	1.52
1	A	59	ARG	CA-C	5.19	1.59	1.53
1	A	587	TYR	CA-C	5.19	1.59	1.52
1	A	399	TRP	CA-C	-5.19	1.45	1.52
1	A	168	HIS	C-O	5.08	1.28	1.23
1	A	480	PRO	CA-C	5.07	1.58	1.52
1	A	63	PRO	CA-CB	5.05	1.60	1.53
1	A	86	GLN	N-CA	-5.05	1.39	1.45
1	A	745	PRO	CA-CB	-5.05	1.47	1.53
1	A	722	LEU	CA-C	-5.04	1.47	1.53
1	A	150	ASN	CA-C	-5.04	1.45	1.52
1	A	285	TRP	CA-CB	-5.03	1.44	1.53
1	A	589	HIS	CA-C	-5.02	1.47	1.53
1	A	192	LYS	N-CA	-5.02	1.39	1.45
1	A	244	SER	CA-C	-5.02	1.46	1.52
1	A	412	ARG	CZ-NH2	5.01	1.40	1.33

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	694	ARG	NE-CZ-NH2	-8.57	111.48	119.20
1	A	74	GLU	CG-CD-OE2	7.45	135.54	118.40
1	A	412	ARG	NE-CZ-NH1	-7.42	114.08	121.50
1	A	118	SER	CA-CB-OG	-7.21	96.67	111.10
1	A	694	ARG	NE-CZ-NH1	7.18	128.68	121.50
1	A	491	GLU	N-CA-C	6.97	121.17	112.24
1	A	480	PRO	CA-C-N	-6.46	111.93	122.20
1	A	480	PRO	C-N-CA	-6.46	111.93	122.20
1	A	658	CYS	CB-CA-C	6.30	121.18	110.85
1	A	74	GLU	CG-CD-OE1	-6.24	104.06	118.40
1	A	694	ARG	CD-NE-CZ	6.04	132.86	124.40
1	A	528	PHE	N-CA-C	6.00	120.45	113.18
1	A	412	ARG	NE-CZ-NH2	6.00	124.60	119.20
1	A	33	GLY	N-CA-C	-5.98	104.38	112.57
1	A	68	HIS	N-CA-C	5.86	123.28	110.80
1	A	479	PHE	CA-C-N	-5.83	114.26	120.03
1	A	479	PHE	C-N-CA	-5.83	114.26	120.03
1	A	694	ARG	CG-CD-NE	-5.74	99.38	112.00
1	A	572	GLU	N-CA-C	-5.69	104.98	111.07
1	A	662	THR	N-CA-CB	-5.63	101.56	110.28
1	A	45	LEU	CA-C-N	-5.60	114.01	119.78
1	A	45	LEU	C-N-CA	-5.60	114.01	119.78
1	A	687	PRO	N-CA-C	5.45	120.35	114.68
1	A	67	VAL	N-CA-CB	5.17	119.64	111.99
1	A	74	GLU	N-CA-C	5.11	117.15	109.23
1	A	480	PRO	O-C-N	-5.04	116.85	123.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	694	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	6276	0	5859	15	0
2	A	30	0	40	1	0
3	A	4	0	0	0	0
4	A	767	0	0	4	0
All	All	7077	0	5899	16	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 (16) 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:A:518:MET:HE2	1:A:518:MET:HA	1.86	0.57
1:A:434:ASP:OD1	4:A:901:HOH:O	2.18	0.56
1:A:397:LYS:NZ	4:A:920:HOH:O	2.48	0.47
1:A:31:GLU:OE1	1:A:38:LYS:HE2	2.14	0.47
1:A:46:PRO:O	1:A:47:LYS:HB2	2.15	0.46
1:A:494:LYS:NZ	4:A:912:HOH:O	2.44	0.45
2:A:801:GOL:H2	4:A:948:HOH:O	2.16	0.45
1:A:197:ASN:C	1:A:197:ASN:OD1	2.61	0.43
1:A:694:ARG:NH2	1:A:728:ASP:OD2	2.50	0.43
1:A:642:ALA:HA	1:A:672:SER:HB2	2.01	0.42
1:A:652:GLY:O	1:A:670:ARG:HA	2.20	0.42
1:A:108:TYR:HA	1:A:143:TYR:CZ	2.55	0.42
1:A:139:VAL:HG11	1:A:183:PRO:HB3	2.02	0.41
1:A:539:SER:HA	1:A:542:TYR:CE2	2.56	0.41
1:A:686:THR:HB	1:A:687:PRO:HD2	2.03	0.40
1:A:412:ARG:HD2	1:A:470:GLU:OE1	2.20	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	754/793 (95%)	734 (97%)	18 (2%)	2 (0%)	36	28

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	68	HIS
1	A	598	SER

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	668/699 (96%)	661 (99%)	7 (1%)	68	67

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

Mol	Chain	Res	Type
1	A	248	LYS
1	A	281	ILE
1	A	434	ASP
1	A	447	LYS
1	A	534	ASN
1	A	662	THR
1	A	725	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	16	ASN
1	A	19	HIS
1	A	231	GLN
1	A	286	ASN
1	A	534	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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	GOL	A	803	-	5,5,5	0.36	0	5,5,5	0.85	0
2	GOL	A	801	-	5,5,5	1.44	1 (20%)	5,5,5	2.62	3 (60%)
2	GOL	A	802	-	5,5,5	0.88	0	5,5,5	0.81	0
2	GOL	A	804	-	5,5,5	1.25	0	5,5,5	0.91	0
2	GOL	A	805	-	5,5,5	0.36	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
2	GOL	A	803	-	-	0/4/4/4	-
2	GOL	A	801	-	-	3/4/4/4	-
2	GOL	A	802	-	-	0/4/4/4	-
2	GOL	A	804	-	-	0/4/4/4	-
2	GOL	A	805	-	-	3/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	GOL	O2-C2	2.44	1.50	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	GOL	O2-C2-C3	3.99	125.70	109.18
2	A	801	GOL	O1-C1-C2	3.29	125.17	110.38
2	A	801	GOL	C3-C2-C1	-2.26	103.50	111.80

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	GOL	C1-C2-C3-O3
2	A	801	GOL	O2-C2-C3-O3
2	A	805	GOL	C1-C2-C3-O3
2	A	805	GOL	O1-C1-C2-O2
2	A	801	GOL	O1-C1-C2-O2
2	A	805	GOL	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	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, 95th 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 ²)	Q<0.9
1	A	755/793 (95%)	-0.15	17 (2%) 61 68	14, 22, 42, 76	1 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	759	PRO	7.0
1	A	758	VAL	6.5
1	A	285	TRP	3.4
1	A	456	TYR	3.1
1	A	756	THR	2.9
1	A	35	ASN	2.7
1	A	755	PRO	2.7
1	A	722	LEU	2.5
1	A	115	TYR	2.5
1	A	500	TYR	2.5
1	A	447	LYS	2.5
1	A	307	ASP	2.4
1	A	736	PRO	2.4
1	A	699	GLU	2.1
1	A	691	SER	2.1
1	A	94	HIS	2.1
1	A	5	ILE	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 oligosaccharides in this entry.

6.4 Ligands

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, 95th 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 ²)	Q<0.9
3	MG	A	809	1/1	0.80	0.13	51,51,51,51	0
2	GOL	A	801	6/6	0.82	0.18	35,36,45,52	0
2	GOL	A	803	6/6	0.91	0.14	35,51,57,58	0
3	MG	A	806	1/1	0.95	0.13	48,48,48,48	0
2	GOL	A	805	6/6	0.95	0.11	26,39,48,56	0
2	GOL	A	804	6/6	0.96	0.11	26,41,43,46	0
2	GOL	A	802	6/6	0.96	0.08	36,37,38,39	0
3	MG	A	807	1/1	0.97	0.03	22,22,22,22	0
3	MG	A	808	1/1	0.98	0.10	31,31,31,31	0

6.5 Other polymers

There are no such residues in this entry.