



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 09:15 PM GMT

PDB ID : 4ZW9  
Title : Crystal structure of human GLUT3 bound to D-glucose in the outward-occluded conformation at 1.5 angstrom  
Authors : Deng, D.; Sun, P.C.; Yan, C.Y.; Yan, N.  
Deposited on : 2015-05-19  
Resolution : 1.50 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  
<http://wwpdb.org/validation/2016/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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20026982

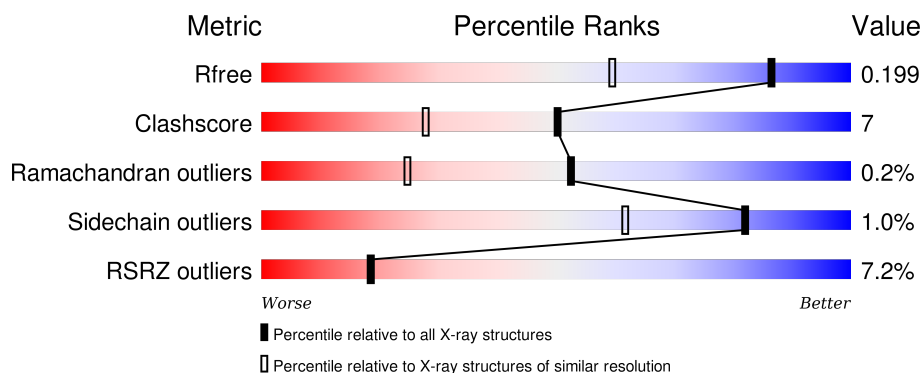
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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))
$R_{free}$	91344	2072 (1.50-1.50)
Clashscore	102246	2274 (1.50-1.50)
Ramachandran outliers	100387	2218 (1.50-1.50)
Sidechain outliers	100360	2216 (1.50-1.50)
RSRZ outliers	91569	2075 (1.50-1.50)

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. 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	518	<div> <div>7%</div> <div>82%</div> <div>8%</div> <div>9%</div> </div>

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	OLC	A	501	-	-	X	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	OLC	A	502	-	-	-	X
2	OLC	A	503	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3838 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.

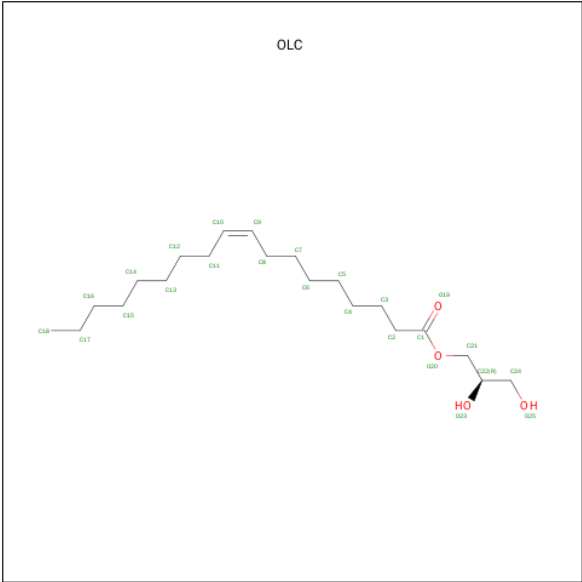
- Molecule 1 is a protein called Solute carrier family 2, facilitated glucose transporter member 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	470	Total	C	N	O	S	0	5	0
			3638	2389	587	641	21			

There are 23 discrepancies between the modelled and reference sequences:

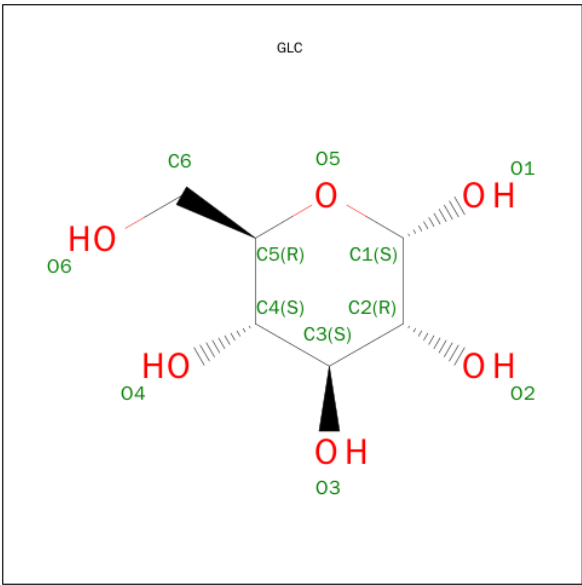
Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	expression tag	UNP P11169
A	-20	HIS	-	expression tag	UNP P11169
A	-19	HIS	-	expression tag	UNP P11169
A	-18	HIS	-	expression tag	UNP P11169
A	-17	HIS	-	expression tag	UNP P11169
A	-16	HIS	-	expression tag	UNP P11169
A	-15	HIS	-	expression tag	UNP P11169
A	-14	HIS	-	expression tag	UNP P11169
A	-13	HIS	-	expression tag	UNP P11169
A	-12	HIS	-	expression tag	UNP P11169
A	-11	HIS	-	expression tag	UNP P11169
A	-10	SER	-	expression tag	UNP P11169
A	-9	GLY	-	expression tag	UNP P11169
A	-8	ASP	-	expression tag	UNP P11169
A	-7	GLU	-	expression tag	UNP P11169
A	-6	VAL	-	expression tag	UNP P11169
A	-5	ASP	-	expression tag	UNP P11169
A	-4	ALA	-	expression tag	UNP P11169
A	-3	GLY	-	expression tag	UNP P11169
A	-2	SER	-	expression tag	UNP P11169
A	-1	GLY	-	expression tag	UNP P11169
A	0	HIS	-	expression tag	UNP P11169
A	43	THR	ASN	engineered mutation	UNP P11169

- Molecule 2 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula: C<sub>21</sub>H<sub>40</sub>O<sub>4</sub>).



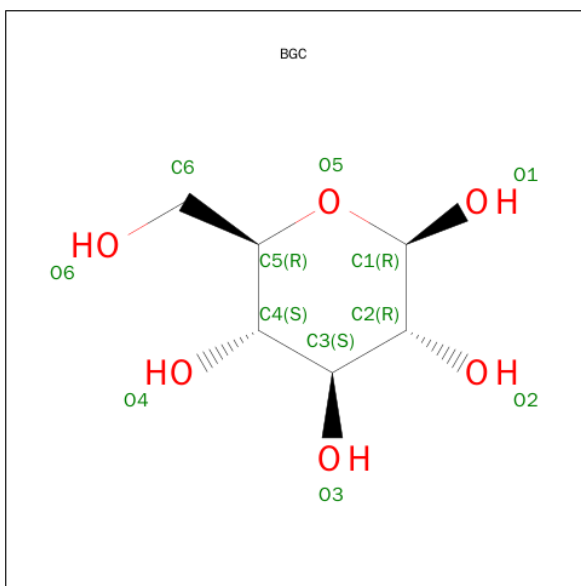
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			25	21	4		
2	A	1	Total	C	O	0	0
			25	21	4		
2	A	1	Total	C	O	0	0
			25	21	4		

- Molecule 3 is ALPHA-D-GLUCOSE (three-letter code: GLC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			12	6	6		

- Molecule 4 is BETA-D-GLUCOSE (three-letter code: BGC) (formula:  $C_6H_{12}O_6$ ).



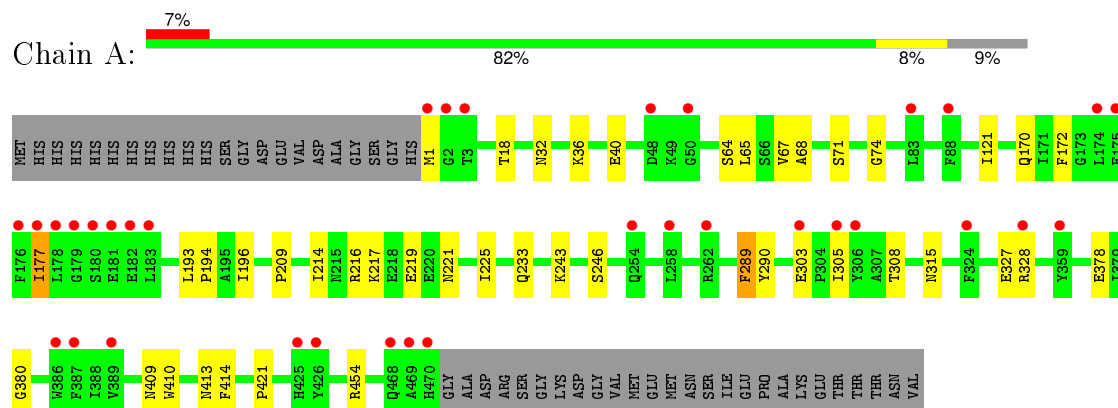
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	1
			12	6	6		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	101	Total	O	0	0
			101	101		



- Molecule 1: Solute carrier family 2, facilitated glucose transporter member 3



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.34Å 118.13Å 51.34Å 90.00° 102.67° 90.00°	Depositor
Resolution (Å)	30.23 – 1.50 30.23 – 1.50	Depositor EDS
% Data completeness (in resolution range)	98.6 (30.23-1.50) 98.6 (30.23-1.50)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.25 (at 1.50Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.184 , 0.199 0.187 , 0.199	Depositor DCC
$R_{free}$ test set	4233 reflections (5.05%)	DCC
Wilson B-factor (Å <sup>2</sup> )	17.3	Xtriage
Anisotropy	0.780	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.44 , 75.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 88083 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3838	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.50% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GLC, OLC, BGC

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	0.39	0/3722	0.52	1/5050 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	216	ARG	NE-CZ-NH2	-6.20	117.20	120.30

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	3638	0	3744	52	0
2	A	75	0	119	37	0
3	A	12	0	12	0	0
4	A	12	0	12	0	0
5	A	101	0	0	2	0
All	All	3838	0	3887	53	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.

All (53) 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:32:ASN:HD22	2:A:501:OLC:H6A	1.12	1.10
1:A:71:SER:OG	2:A:502:OLC:H5A	1.53	1.07
1:A:305:ILE:HD13	2:A:501:OLC:H13	1.46	0.95
1:A:32:ASN:OD1	2:A:501:OLC:C24	2.18	0.91
1:A:32:ASN:OD1	2:A:501:OLC:H24A	1.77	0.85
1:A:170:GLN:HE21	2:A:501:OLC:H9	1.42	0.84
1:A:32:ASN:OD1	2:A:501:OLC:H24	1.81	0.80
1:A:32:ASN:ND2	2:A:501:OLC:H6A	1.93	0.78
1:A:32:ASN:ND2	2:A:501:OLC:H3A	1.99	0.78
1:A:32:ASN:HD22	2:A:501:OLC:C6	1.96	0.75
1:A:305:ILE:HD13	2:A:501:OLC:C13	2.23	0.65
1:A:68:ALA:HB2	2:A:502:OLC:H11	1.79	0.64
1:A:71:SER:HG	2:A:502:OLC:H5A	1.58	0.62
1:A:71:SER:OG	2:A:502:OLC:C5	2.40	0.61
1:A:233:GLN:H	1:A:233:GLN:CD	2.02	0.61
1:A:32:ASN:HD22	2:A:501:OLC:H3A	1.66	0.58
1:A:414:PHE:HA	2:A:502:OLC:H9	1.84	0.58
1:A:289:PHE:HB3	2:A:501:OLC:H2	1.88	0.55
1:A:221:ASN:O	1:A:225:ILE:HG12	2.08	0.54
1:A:64[B]:SER:HB2	2:A:502:OLC:H13A	1.90	0.53
1:A:305:ILE:CD1	2:A:501:OLC:H11A	2.38	0.53
1:A:196:ILE:HG22	2:A:503:OLC:H16A	1.91	0.53
1:A:410:TRP:HA	2:A:502:OLC:H22	1.90	0.53
1:A:18:THR:OG1	2:A:503:OLC:H24	2.09	0.52
1:A:172:PHE:HA	1:A:177:ILE:HG21	1.90	0.52
1:A:454:ARG:NH1	5:A:605:HOH:O	2.39	0.51
1:A:308:THR:HG21	2:A:501:OLC:C9	2.41	0.51
1:A:209:PRO:HG3	1:A:225:ILE:HG21	1.93	0.50
1:A:305:ILE:CD1	2:A:501:OLC:H13	2.32	0.49
1:A:32:ASN:CG	2:A:501:OLC:H24	2.33	0.48
1:A:36:LYS:O	1:A:40:GLU:HG3	2.13	0.48
1:A:64[A]:SER:HB3	2:A:502:OLC:H13A	1.95	0.48
1:A:219:GLU:OE1	1:A:243:LYS:HE2	2.15	0.47
1:A:32:ASN:HD21	2:A:501:OLC:H3A	1.80	0.47
1:A:327:GLU:HB2	1:A:328:ARG:NH1	2.30	0.46
1:A:413:ASN:HB2	2:A:502:OLC:O23	2.15	0.46
1:A:209:PRO:HG3	1:A:225:ILE:CG2	2.46	0.46
1:A:65:LEU:HG	1:A:121:ILE:HD12	1.98	0.46
1:A:290:TYR:CD1	2:A:501:OLC:H22	2.51	0.45
1:A:421:PRO:HG2	2:A:502:OLC:H15A	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:THR:HG21	2:A:501:OLC:C8	2.47	0.44
1:A:315:ASN:ND2	1:A:378:GLU:OE2	2.50	0.43
1:A:36:LYS:HA	1:A:36:LYS:HD3	1.76	0.43
1:A:214:ILE:HG23	1:A:246:SER:HA	1.99	0.43
2:A:502:OLC:H16	2:A:502:OLC:H13	1.63	0.43
1:A:217:LYS:NZ	5:A:610:HOH:O	2.51	0.43
1:A:305:ILE:CD1	2:A:501:OLC:C13	2.93	0.42
1:A:67:VAL:HG13	2:A:501:OLC:O25	2.19	0.42
1:A:74:GLY:HA3	1:A:410:TRP:CE3	2.54	0.42
1:A:409:ASN:OD1	2:A:502:OLC:H24A	2.20	0.42
1:A:305:ILE:CD1	2:A:501:OLC:C11	2.99	0.41
1:A:410:TRP:CE3	2:A:502:OLC:H21	2.56	0.41
1:A:193:LEU:HB2	1:A:194:PRO:HD3	2.02	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	473/518 (91%)	467 (99%)	5 (1%)	1 (0%)	52	25

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	380	GLY

### 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	394/428 (92%)	390 (99%)	4 (1%)	82	62

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	177	ILE
1	A	289	PHE
1	A	303	GLU

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](#)

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	OLC	A	501	-	24,24,24	1.19	2 (8%)	25,25,25	1.12	1 (4%)
2	OLC	A	502	-	24,24,24	0.90	1 (4%)	25,25,25	0.87	1 (4%)
2	OLC	A	503	-	24,24,24	0.89	1 (4%)	25,25,25	1.37	4 (16%)
3	GLC	A	504[A]	-	12,12,12	0.73	0	17,17,17	1.03	1 (5%)
4	BGC	A	505[B]	-	12,12,12	0.42	0	17,17,17	0.51	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	OLC	A	501	-	-	0/24/24/24	0/0/0/0
2	OLC	A	502	-	-	0/24/24/24	0/0/0/0
2	OLC	A	503	-	-	0/24/24/24	0/0/0/0
3	GLC	A	504[A]	-	-	0/2/22/22	0/1/1/1
4	BGC	A	505[B]	-	-	0/2/22/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	OLC	O19-C1	-2.10	1.16	1.22
2	A	503	OLC	O20-C1	3.64	1.44	1.33
2	A	501	OLC	O20-C1	3.89	1.44	1.33
2	A	502	OLC	O20-C1	4.20	1.45	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	503	OLC	O20-C1-O19	-2.45	117.08	123.51
2	A	503	OLC	C3-C2-C1	-2.37	104.31	113.57
2	A	503	OLC	C6-C7-C8	-2.28	104.53	113.79
3	A	504[A]	GLC	C1-O5-C5	2.43	118.19	113.54
2	A	502	OLC	O20-C1-C2	2.70	120.17	111.85
2	A	503	OLC	O20-C1-C2	3.57	122.85	111.85
2	A	501	OLC	O20-C1-C2	3.61	122.95	111.85

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 37 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	OLC	22	0
2	A	502	OLC	13	0
2	A	503	OLC	2	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	470/518 (90%)	0.29	34 (7%) 18 18	15, 22, 38, 50	9 (1%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	176	PHE	14.9
1	A	179	GLY	9.3
1	A	177	ILE	8.6
1	A	181	GLU	8.1
1	A	426	TYR	6.9
1	A	2	GLY	5.9
1	A	175	GLU	5.7
1	A	470	HIS	5.5
1	A	83	LEU	4.8
1	A	306	TYR	4.7
1	A	258	LEU	4.3
1	A	468	GLN	3.9
1	A	178	LEU	3.8
1	A	469	ALA	3.7
1	A	425	HIS	3.5
1	A	1	MET	3.4
1	A	48	ASP	3.3
1	A	180	SER	3.3
1	A	305	ILE	3.2
1	A	324	PHE	3.2
1	A	386	TRP	3.1
1	A	328	ARG	3.1
1	A	50	GLY	3.1
1	A	262	ARG	3.1
1	A	3	THR	3.0
1	A	182	GLU	2.6
1	A	359	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	389	VAL	2.4
1	A	174	LEU	2.4
1	A	303	GLU	2.4
1	A	387	PHE	2.3
1	A	254	GLN	2.3
1	A	183	LEU	2.3
1	A	88	PHE	2.2

## 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	OLC	A	503	25/25	0.66	0.22	9.89	30,31,33,33	0
2	OLC	A	502	25/25	0.61	0.32	8.98	27,29,32,32	0
2	OLC	A	501	25/25	0.49	0.32	6.86	32,33,36,36	0
4	BGC	A	505[B]	12/12	0.97	0.14	1.25	17,18,18,18	12
3	GLC	A	504[A]	12/12	0.96	0.14	1.06	17,18,18,18	12

## 6.5 Other polymers [i](#)

There are no such residues in this entry.