



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 01:07 am GMT

PDB ID : 3WIQ
Title : Crystal structure of kojibiose phosphorylase complexed with kojibiose
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Deposited on : 2013-09-24
Resolution : 2.80 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

<http://wwpdb.org/validation/2016/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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

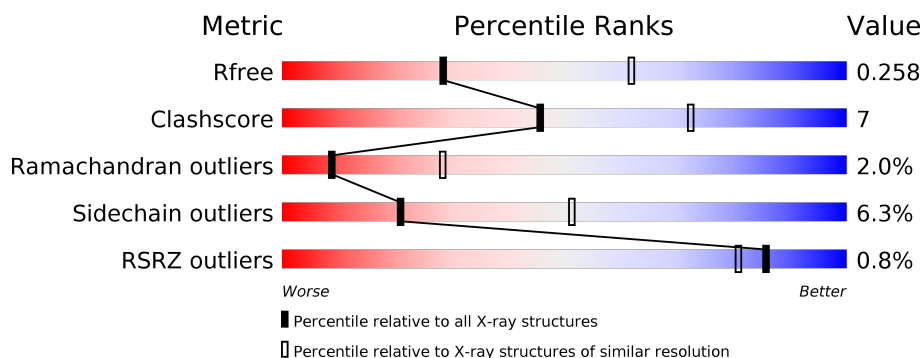
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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 ≥ 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	764	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;">%</div> <div style="position: absolute; top: 10px; left: 0; width: 100%;">78%16%...</div> </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
3	SO4	A	803	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6241 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 Kojibiose phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	751	Total	C	N	O	S	0	0	0
			6148	3960	1013	1154	21			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	757	GLY	-	EXPRESSION TAG	UNP A4XGP2
A	758	SER	-	EXPRESSION TAG	UNP A4XGP2
A	759	HIS	-	EXPRESSION TAG	UNP A4XGP2
A	760	HIS	-	EXPRESSION TAG	UNP A4XGP2
A	761	HIS	-	EXPRESSION TAG	UNP A4XGP2
A	762	HIS	-	EXPRESSION TAG	UNP A4XGP2
A	763	HIS	-	EXPRESSION TAG	UNP A4XGP2
A	764	HIS	-	EXPRESSION TAG	UNP A4XGP2

- Molecule 2 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	2	Total	C	O	0	0
			23	12	11		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

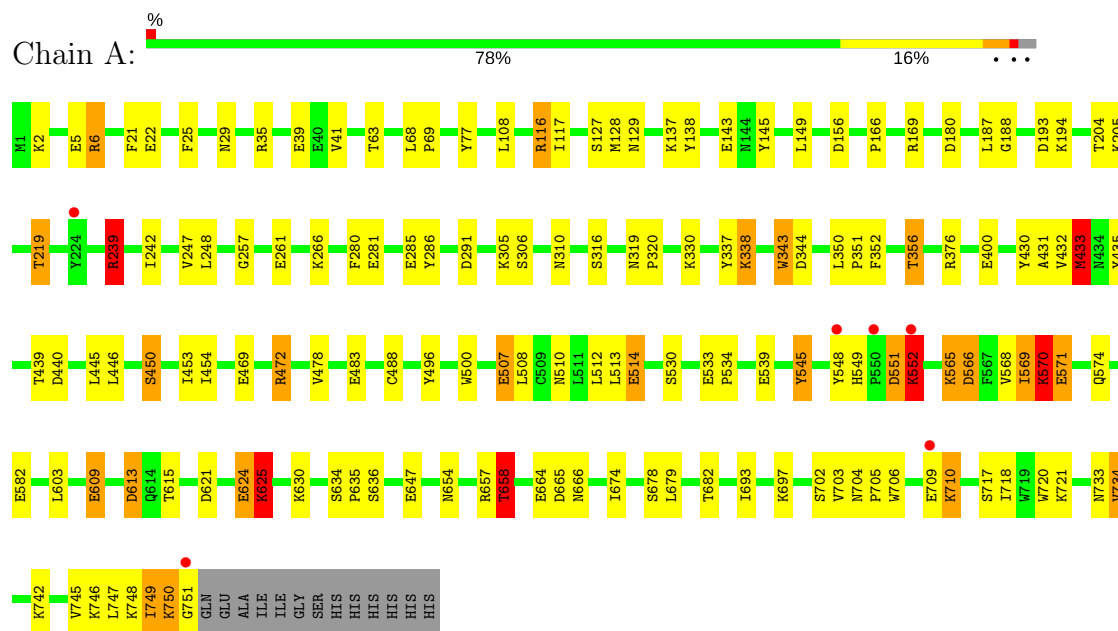
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	65	Total	O	0	0
			65	65		

3 Residue-property plots

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: Kojibiose phosphorylase



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	192.51Å 192.51Å 202.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.13 – 2.80 48.13 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.6 (48.13-2.80) 98.6 (48.13-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.37 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.204 , 0.259 0.206 , 0.258	Depositor DCC
R_{free} test set	2330 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	55.9	Xtriage
Anisotropy	0.083	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 38.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.000 for -l,-k,-h 0.000 for -h,l,k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6241	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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: GLC, BGC, 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	0.85	1/6289 (0.0%)	0.96	10/8497 (0.1%)

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	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	507	GLU	CD-OE1	5.23	1.31	1.25

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	116	ARG	NE-CZ-NH1	-6.64	116.98	120.30
1	A	239	ARG	NE-CZ-NH2	6.25	123.42	120.30
1	A	625	LYS	CD-CE-NZ	6.23	126.02	111.70
1	A	666	ASN	CB-CA-C	-5.67	99.07	110.40
1	A	658	THR	N-CA-CB	5.46	120.67	110.30
1	A	665	ASP	CB-CG-OD2	-5.34	113.49	118.30
1	A	625	LYS	CA-CB-CG	5.10	124.63	113.40
1	A	566	ASP	CB-CG-OD1	5.09	122.88	118.30
1	A	376	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	A	433	MET	CB-CG-SD	5.07	127.61	112.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	551	ASP	Peptide
1	A	749	ILE	Peptide

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	6148	0	6079	89	0
2	A	23	0	21	1	0
3	A	5	0	0	0	0
4	A	65	0	0	1	0
All	All	6241	0	6100	89	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 (89) 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:5:GLU:O	1:A:6:ARG:HB2	1.62	0.97
1:A:352:PHE:O	1:A:356:THR:HB	1.67	0.94
1:A:733:ASN:HA	1:A:750:LYS:HE2	1.65	0.78
1:A:5:GLU:O	1:A:6:ARG:CB	2.30	0.77
1:A:750:LYS:CB	1:A:751:GLY:HA3	2.22	0.70
1:A:636:SER:HB3	1:A:658:THR:HG21	1.76	0.68
1:A:750:LYS:HB3	1:A:751:GLY:HA3	1.75	0.68
1:A:248:LEU:HD12	1:A:248:LEU:N	2.11	0.65
1:A:247:VAL:C	1:A:248:LEU:HD12	2.18	0.64
1:A:430:TYR:HA	1:A:500:TRP:CH2	2.33	0.63
1:A:21:PHE:O	1:A:25:PHE:HB2	1.97	0.63
1:A:709:GLU:O	1:A:710:LYS:CB	2.47	0.63
1:A:286:TYR:OH	1:A:316:SER:OG	2.14	0.62
1:A:750:LYS:CB	1:A:751:GLY:CA	2.78	0.61
1:A:239:ARG:HG3	1:A:239:ARG:HH21	1.66	0.61
1:A:747:LEU:HG	1:A:749:ILE:HD11	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:704:ASN:N	1:A:705:PRO:HD3	2.16	0.60
1:A:286:TYR:HH	1:A:316:SER:HG	1.47	0.59
1:A:29:ASN:HA	1:A:128:MET:HE2	1.85	0.58
1:A:337:TYR:C	1:A:338:LYS:HG2	2.23	0.58
1:A:128:MET:HE3	1:A:316:SER:HA	1.85	0.57
1:A:709:GLU:O	1:A:710:LYS:HB2	2.04	0.57
1:A:472:ARG:HD3	1:A:545:TYR:HA	1.86	0.57
1:A:703:VAL:HG12	1:A:705:PRO:HD3	1.85	0.57
1:A:117:ILE:HG22	1:A:143:GLU:HG3	1.86	0.57
1:A:39:GLU:OE2	1:A:138:TYR:OH	2.22	0.57
1:A:257:GLY:N	4:A:924:HOH:O	2.38	0.55
1:A:204:THR:HG22	1:A:205:LYS:N	2.22	0.55
1:A:551:ASP:O	1:A:552:LYS:HB2	2.07	0.55
1:A:450:SER:O	1:A:454:ILE:HG13	2.07	0.54
1:A:239:ARG:HH21	1:A:239:ARG:CG	2.20	0.54
1:A:63:THR:HG22	1:A:400:GLU:CD	2.30	0.52
1:A:749:ILE:HG22	1:A:750:LYS:H	1.73	0.52
1:A:352:PHE:CZ	1:A:356:THR:HG21	2.45	0.52
1:A:624:GLU:HG3	1:A:625:LYS:N	2.24	0.51
1:A:310:ASN:HA	1:A:679:LEU:HD22	1.92	0.51
1:A:248:LEU:N	1:A:248:LEU:CD1	2.72	0.51
1:A:6:ARG:O	1:A:305:LYS:NZ	2.43	0.51
1:A:634:SER:O	1:A:635:PRO:C	2.50	0.50
1:A:344:ASP:OD1	2:A:801:GLC:O6	2.25	0.49
1:A:187:LEU:C	1:A:187:LEU:HD23	2.33	0.49
1:A:29:ASN:HA	1:A:128:MET:CE	2.43	0.49
1:A:352:PHE:CE2	1:A:356:THR:HG21	2.49	0.48
1:A:350:LEU:HD23	1:A:431:ALA:HB1	1.95	0.48
1:A:68:LEU:HB3	1:A:69:PRO:HD2	1.96	0.48
1:A:116:ARG:HB3	1:A:145:TYR:CD2	2.49	0.47
1:A:193:ASP:O	1:A:194:LYS:HB2	2.16	0.47
1:A:720:TRP:CD1	1:A:745:VAL:HG21	2.49	0.46
1:A:747:LEU:HD12	1:A:748:LYS:H	1.80	0.46
1:A:350:LEU:HB3	1:A:351:PRO:HD3	1.98	0.46
1:A:22:GLU:HB3	1:A:35:ARG:NH2	2.31	0.46
1:A:570:LYS:O	1:A:571:GLU:HB2	2.16	0.46
1:A:129:ASN:HB3	1:A:285:GLU:HG3	1.97	0.45
1:A:187:LEU:HD23	1:A:188:GLY:N	2.32	0.45
1:A:621:ASP:OD1	1:A:647:GLU:OE2	2.34	0.45
1:A:569:ILE:O	1:A:570:LYS:O	2.35	0.45
1:A:734:VAL:O	1:A:734:VAL:CG2	2.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:533:GLU:HB2	1:A:534:PRO:HD3	1.98	0.44
1:A:432:VAL:HB	1:A:453:ILE:HD11	1.98	0.44
1:A:749:ILE:HG22	1:A:750:LYS:N	2.32	0.44
1:A:750:LYS:HB2	1:A:751:GLY:CA	2.47	0.44
1:A:548:TYR:HB3	1:A:549:HIS:CA	2.48	0.44
1:A:496:TYR:CD1	1:A:603:LEU:HD21	2.52	0.44
1:A:204:THR:CG2	1:A:205:LYS:N	2.82	0.43
1:A:166:PRO:HA	1:A:169:ARG:NH1	2.33	0.43
1:A:433:MET:HG2	1:A:433:MET:O	2.16	0.43
1:A:435:TYR:CE1	1:A:439:THR:HG21	2.54	0.43
1:A:180:ASP:HB2	1:A:219:THR:HG21	2.01	0.43
1:A:533:GLU:N	1:A:534:PRO:CD	2.82	0.42
1:A:750:LYS:HB2	1:A:751:GLY:C	2.40	0.42
1:A:343:TRP:O	1:A:344:ASP:C	2.56	0.42
1:A:156:ASP:OD1	1:A:156:ASP:C	2.58	0.42
1:A:137:LYS:HA	1:A:242:ILE:O	2.20	0.42
1:A:749:ILE:O	1:A:750:LYS:C	2.59	0.41
1:A:445:LEU:O	1:A:450:SER:OG	2.38	0.41
1:A:613:ASP:N	1:A:613:ASP:OD1	2.50	0.41
1:A:108:LEU:HD23	1:A:108:LEU:HA	1.89	0.41
1:A:77:TYR:O	1:A:149:LEU:HA	2.21	0.41
1:A:630:LYS:HD3	1:A:630:LYS:HA	1.78	0.41
1:A:654:ASN:OD1	1:A:657:ARG:NH2	2.54	0.41
1:A:280:PHE:O	1:A:281:GLU:C	2.59	0.41
1:A:330:LYS:HA	1:A:674:ILE:O	2.21	0.41
1:A:446:LEU:HD23	1:A:512:LEU:HD21	2.03	0.40
1:A:128:MET:CE	1:A:316:SER:HA	2.50	0.40
1:A:319:ASN:HA	1:A:320:PRO:HD2	1.88	0.40
1:A:510:ASN:O	1:A:514:GLU:HG2	2.21	0.40
1:A:565:LYS:HG3	1:A:566:ASP:N	2.36	0.40
1:A:717:SER:O	1:A:718:ILE:HG23	2.20	0.40
1:A:658:THR:HB	1:A:682:THR:OG1	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	749/764 (98%)	688 (92%)	46 (6%)	15 (2%)	9	28

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	569	ILE
1	A	570	LYS
1	A	609	GLU
1	A	750	LYS
1	A	6	ARG
1	A	545	TYR
1	A	552	LYS
1	A	710	LYS
1	A	469	GLU
1	A	706	TRP
1	A	625	LYS
1	A	721	LYS
1	A	291	ASP
1	A	571	GLU
1	A	41	VAL

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	665/676 (98%)	623 (94%)	42 (6%)	21	51

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	127	SER

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Mol	Chain	Res	Type
1	A	219	THR
1	A	239	ARG
1	A	261	GLU
1	A	266	LYS
1	A	306	SER
1	A	338	LYS
1	A	343	TRP
1	A	356	THR
1	A	433	MET
1	A	440	ASP
1	A	450	SER
1	A	472	ARG
1	A	478	VAL
1	A	483	GLU
1	A	488	CYS
1	A	507	GLU
1	A	508	LEU
1	A	513	LEU
1	A	514	GLU
1	A	530	SER
1	A	539	GLU
1	A	552	LYS
1	A	565	LYS
1	A	568	VAL
1	A	570	LYS
1	A	574	GLN
1	A	582	GLU
1	A	609	GLU
1	A	613	ASP
1	A	615	THR
1	A	624	GLU
1	A	658	THR
1	A	664	GLU
1	A	678	SER
1	A	693	ILE
1	A	697	LYS
1	A	702	SER
1	A	734	VAL
1	A	742	LYS
1	A	746	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	667	GLN

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 ⓘ

2 carbohydrates 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	GLC	A	801	2	11,11,12	0.83	0	13,15,17	2.00	5 (38%)
2	BGC	A	802	2	12,12,12	0.48	0	17,17,17	1.66	3 (17%)

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	GLC	A	801	2	-	0/2/19/22	0/1/1/1
2	BGC	A	802	2	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	802	BGC	C1-C2-C3	-4.13	103.20	110.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	GLC	C2-C3-C4	-3.00	105.65	110.88
2	A	802	BGC	O5-C1-C2	-2.41	106.04	110.04
2	A	801	GLC	O5-C1-C2	-2.12	107.47	110.79
2	A	801	GLC	O4-C4-C3	2.78	116.41	110.36
2	A	802	BGC	O2-C2-C1	3.09	116.17	109.75
2	A	801	GLC	O3-C3-C4	3.40	117.75	110.36
2	A	801	GLC	C1-O5-C5	3.47	116.94	112.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	GLC	1	0

5.6 Ligand geometry

1 ligand is 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	$\# Z > 2$
3	SO4	A	803	-	4,4,4	0.96	0	6,6,6	1.08	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	SO4	A	803	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	751/764 (98%)	-0.39	6 (0%) 86 81	35, 52, 82, 150	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	548	TYR	6.9
1	A	709	GLU	3.0
1	A	552	LYS	2.8
1	A	751	GLY	2.4
1	A	224	TYR	2.3
1	A	550	PRO	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](#)

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, 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	LLDF	B-factors(Å ²)	Q<0.9
2	BGC	A	802	12/12	0.97	0.13	-0.14	47,55,59,71	0
2	GLC	A	801	11/12	0.98	0.13	-0.91	40,45,54,54	0

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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	SO4	A	803	5/5	0.93	0.22	2.19	55,55,74,83	0

6.5 Other polymers [i](#)

There are no such residues in this entry.