



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 11:26 PM GMT

PDB ID : 4AD3
Title : Structure of the GH99 endo-alpha-mannosidase from *Bacteroides xyloisolvans* in complex with Glucose-1,3-deoxymannojirimycin
Authors : Thompson, A.J.; Williams, R.J.; Hakki, Z.; Alonzi, D.S.; Wennekes, T.; Gloster, T.M.; Songsrirote, K.; Thomas-Oates, J.E.; Wrodnigg, T.M.; Spreitz, J.; Stuetz, A.E.; Butters, T.D.; Williams, S.J.; Davies, G.J.
Deposited on : 2011-12-21
Resolution : 2.00 Å (reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

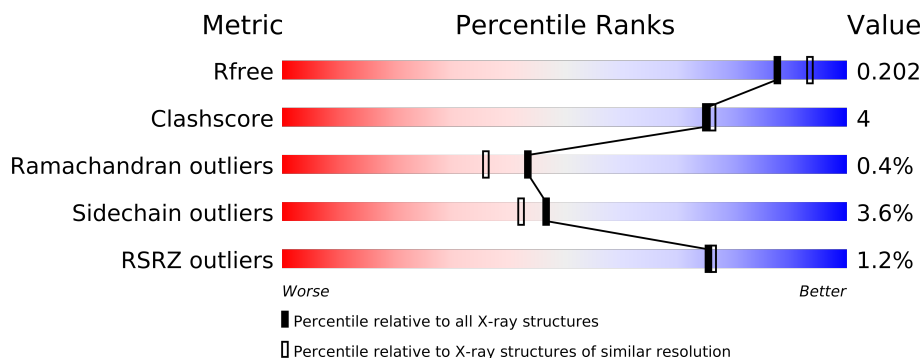
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.00 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}	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (2.00-2.00)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	380	
1	B	380	
1	C	380	
1	D	380	

2 Entry composition i

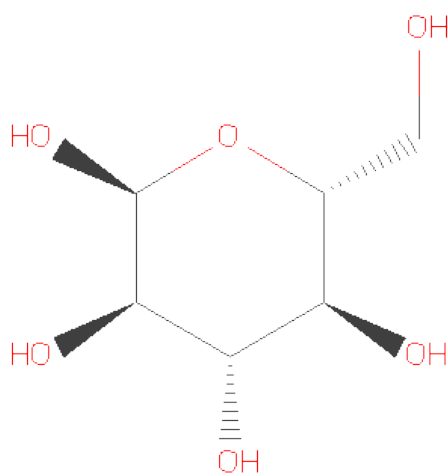
There are 4 unique types of molecules in this entry. The entry contains 12473 atoms, of which 0 are hydrogen and 0 are deuterium.

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 GLYCOSYL HYDROLASE FAMILY 71.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	345	Total	C	N	O	S	0	4	0
			2814	1814	464	528	8			
1	B	346	Total	C	N	O	S	0	5	0
			2838	1831	470	528	9			
1	C	344	Total	C	N	O	S	0	0	0
			2798	1803	464	523	8			
1	D	342	Total	C	N	O	S	0	0	0
			2561	1640	434	479	8			

- Molecule 2 is SUGAR (ALPHA-D-GLUCOSE) (three-letter code: GLC) (formula: C₆H₁₂O₆).



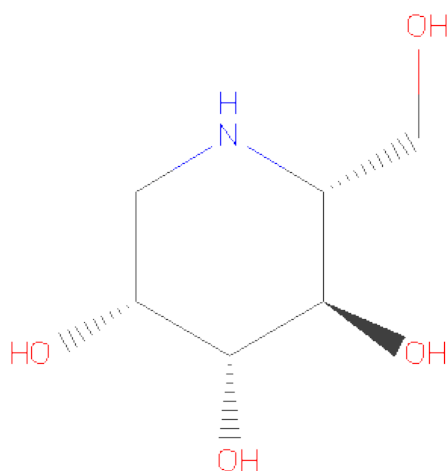
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			11	6	5		
2	B	1	Total	C	O	0	0
			11	6	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			11	6	5		
2	D	1	Total	C	O	0	0
			11	6	5		

- Molecule 3 is 1-DEOXYMANNOJIRIMYCIN (three-letter code: DMJ) (formula: $C_6H_{13}NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			11	6	1	4		
3	B	1	Total	C	N	O	0	0
			11	6	1	4		
3	C	1	Total	C	N	O	0	0
			11	6	1	4		
3	D	1	Total	C	N	O	0	0
			11	6	1	4		

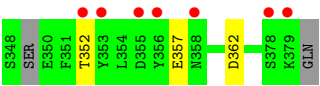
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	417	Total	O	0	0
			417	417		
4	B	443	Total	O	0	0
			443	443		
4	C	387	Total	O	0	0
			387	387		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	127	Total 127	O 127	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	222.48Å 222.48Å 84.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.49 – 2.00 46.49 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.49-2.00) 96.2 (46.49-2.00)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.6.0086	Depositor
R, R_{free}	0.175 , 0.202 0.175 , 0.202	Depositor DCC
R_{free} test set	7754 reflections (5.23%)	DCC
Wilson B-factor (Å ²)	27.6	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.2	EDS
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 155896 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12473	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.34% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DMJ, GLC

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	0.63	0/2918	0.63	0/3977
1	B	0.62	0/2945	0.63	2/4011 (0.0%)
1	C	0.64	0/2890	0.65	2/3936 (0.1%)
1	D	0.50	0/2643	0.57	2/3621 (0.1%)
All	All	0.60	0/11396	0.62	6/15545 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	121	LEU	CA-CB-CG	6.57	130.41	115.30
1	B	136	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	C	293	ARG	NE-CZ-NH2	-5.55	117.53	120.30
1	D	296	PRO	N-CA-CB	5.46	109.85	103.30
1	B	136	ARG	NE-CZ-NH1	5.05	122.82	120.30
1	C	376	ARG	NE-CZ-NH2	-5.02	117.79	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2814	0	2657	21	0
1	B	2838	0	2697	11	0
1	C	2798	0	2649	29	0
1	D	2561	0	2223	25	1
2	A	11	0	10	0	0
2	B	11	0	10	0	0
2	C	11	0	10	0	0
2	D	11	0	10	0	0
3	A	11	0	12	0	0
3	B	11	0	12	0	0
3	C	11	0	12	0	0
3	D	11	0	12	0	0
4	A	417	0	0	8	0
4	B	443	0	0	2	0
4	C	387	0	0	11	0
4	D	127	0	0	2	0
All	All	12473	0	10314	85	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (85) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:59:ARG:HD2	4:A:2019:HOH:O	1.55	1.04
1:A:347:THR:HG22	4:A:2376:HOH:O	1.63	0.97
1:C:265:THR:CG2	4:C:2275:HOH:O	2.15	0.93
1:C:68:ASP:H	1:C:75:GLN:HE22	1.17	0.92
1:C:60:HIS:HD2	1:C:335:HIS:HE1	1.22	0.85
1:C:60:HIS:HD2	1:C:335:HIS:CE1	1.94	0.84
1:C:265:THR:HG23	4:C:2275:HOH:O	1.76	0.83
1:B:85:GLU:HG2	4:B:2396:HOH:O	1.80	0.81
1:D:68:ASP:H	1:D:75:GLN:HE22	1.29	0.80
1:D:313:ALA:O	1:D:317:LYS:HG3	1.86	0.76
1:C:220:THR:CG2	1:C:222:TYR:H	1.99	0.74
1:C:220:THR:HG23	1:C:222:TYR:H	1.54	0.72
1:C:275:LYS:HG3	4:C:2281:HOH:O	1.88	0.72
1:C:60:HIS:CD2	1:C:335:HIS:HE1	2.07	0.72
1:C:198:TYR:HD2	4:C:2221:HOH:O	1.76	0.69
1:D:339:GLN:H	1:D:339:GLN:NE2	1.92	0.66
1:D:263:THR:HB	1:D:266:ASN:ND2	2.11	0.66
1:D:264:PRO:HB2	1:D:317:LYS:HD3	1.78	0.65
1:D:45:TYR:HB3	1:D:121:LEU:HD13	1.79	0.65
1:B:316:ARG:HH21	1:C:358:ASN:HD21	1.47	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:107:THR:HG22	4:C:2056:HOH:O	1.99	0.62
1:C:85:GLU:HG2	4:C:2349:HOH:O	2.01	0.61
1:A:60:HIS:ND1	1:A:335:HIS:HE1	1.98	0.61
1:C:293:ARG:HD3	1:C:351:PHE:CE1	2.36	0.60
1:A:339:GLN:H	1:A:339:GLN:NE2	2.00	0.58
1:D:287:PRO:HB2	1:D:305:ARG:NH1	2.19	0.58
1:C:68:ASP:N	1:C:75:GLN:HE22	1.96	0.57
1:D:337:GLY:HA2	1:D:339:GLN:HE22	1.69	0.56
1:D:63:HIS:HD2	1:D:64:ALA:O	1.88	0.55
1:C:347:THR:HG22	4:C:2344:HOH:O	2.05	0.55
1:A:90:ASN:HD21	1:A:293:ARG:H	1.52	0.54
1:C:60:HIS:CD2	1:C:335:HIS:CE1	2.85	0.54
1:D:339:GLN:H	1:D:339:GLN:HE21	1.55	0.54
1:A:293:ARG:HD2	4:A:2329:HOH:O	2.07	0.54
1:A:60:HIS:ND1	1:A:335:HIS:CE1	2.77	0.52
1:A:337:GLY:HA2	1:A:339:GLN:HE22	1.73	0.52
1:C:220:THR:HG22	1:C:222:TYR:H	1.74	0.51
1:A:293:ARG:HD3	1:A:351:PHE:CE1	2.44	0.51
1:A:88:ALA:O	1:A:335:HIS:HD2	1.93	0.51
1:D:341:GLU:HG2	1:D:342:PRO:HD2	1.92	0.51
1:D:293:ARG:HB2	4:D:2027:HOH:O	2.10	0.51
1:C:337:GLY:HA2	1:C:339:GLN:HE22	1.76	0.50
1:C:293:ARG:HD2	4:C:2301:HOH:O	2.10	0.50
1:B:337:GLY:HA2	1:B:339:GLN:HE22	1.77	0.50
1:B:380:GLN:NE2	4:B:2441:HOH:O	2.46	0.49
1:B:339:GLN:H	1:B:339:GLN:NE2	2.11	0.49
1:A:86:SER:HB2	1:A:350:GLU:HG3	1.95	0.49
1:D:347:THR:HB	1:D:352:THR:HG22	1.95	0.47
1:C:68:ASP:H	1:C:75:GLN:NE2	1.99	0.47
1:A:245:HIS:HD2	4:A:2280:HOH:O	1.96	0.47
1:A:268[A]:VAL:HG13	4:A:2296:HOH:O	2.15	0.47
1:D:228:GLY:O	1:D:249:PHE:HA	2.14	0.47
1:D:162:ASN:O	1:D:166:LEU:HB2	2.17	0.45
1:D:286:GLY:O	1:D:314:MET:HE3	2.17	0.45
1:A:145:ASP:HB2	1:A:182:ALA:HB2	1.99	0.45
1:D:287:PRO:O	1:D:305:ARG:HD2	2.16	0.45
1:D:134:ALA:HB1	1:D:176:ARG:HH21	1.81	0.45
1:C:316:ARG:NH2	4:C:2327:HOH:O	2.46	0.45
1:C:88:ALA:O	1:C:335:HIS:HD2	1.99	0.45
1:C:293:ARG:HD3	1:C:351:PHE:CZ	2.53	0.44
1:A:266:ASN:ND2	4:A:2300:HOH:O	2.51	0.44
1:D:362:ASP:HA	4:D:2117:HOH:O	2.16	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:88:ALA:O	1:D:335:HIS:HD2	2.01	0.44
1:D:45:TYR:CB	1:D:121:LEU:HD13	2.47	0.43
1:D:310:TYR:CE2	1:D:314:MET:HE2	2.53	0.43
1:B:313:ALA:O	1:B:317:LYS:HD3	2.18	0.43
1:C:76:ASN:CG	1:C:76:ASN:O	2.56	0.42
1:A:245:HIS:HE1	4:A:2122:HOH:O	2.02	0.42
1:A:230:TRP:C	1:A:230:TRP:CD1	2.92	0.42
1:B:289:TYR:CE2	1:B:336[B]:GLU:HB2	2.54	0.42
1:C:265:THR:HB	4:C:2269:HOH:O	2.20	0.42
1:B:90:ASN:HD21	1:B:293:ARG:H	1.68	0.42
1:A:162:ASN:O	1:A:166:LEU:HB2	2.19	0.41
1:B:228:GLY:O	1:B:249:PHE:HA	2.21	0.41
1:A:52:GLU:HB2	1:A:58:TYR:CE2	2.55	0.41
1:C:339:GLN:H	1:C:339:GLN:NE2	2.19	0.41
1:C:76:ASN:HB2	4:C:2040:HOH:O	2.20	0.41
1:B:102:ASP:HA	1:B:103:PRO:HD2	1.96	0.41
1:D:68:ASP:HA	1:D:69:PRO:HD3	1.93	0.41
1:C:93:PRO:HA	1:C:334:TRP:CH2	2.57	0.40
1:D:263:THR:HB	1:D:266:ASN:HD22	1.82	0.40
1:B:289:TYR:CE2	1:B:336[A]:GLU:HB3	2.56	0.40
1:A:189:LYS:HD2	4:A:2093:HOH:O	2.20	0.40
1:D:121:LEU:C	1:D:121:LEU:HD12	2.42	0.40
1:A:228:GLY:O	1:A:249:PHE:HA	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:187:ASP:O	1:D:219:ASN:ND2[6_554]	2.04	0.16

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	347/380 (91%)	335 (96%)	11 (3%)	1 (0%)	50 44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	349/380 (92%)	339 (97%)	9 (3%)	1 (0%)	50	44
1	C	342/380 (90%)	331 (97%)	10 (3%)	1 (0%)	50	44
1	D	338/380 (89%)	325 (96%)	11 (3%)	2 (1%)	33	24
All	All	1376/1520 (90%)	1330 (97%)	41 (3%)	5 (0%)	43	36

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	252	TYR
1	A	252	TYR
1	B	252	TYR
1	C	252	TYR
1	D	357	GLU

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	296/328 (90%)	290 (98%)	6 (2%)	68	69
1	B	299/328 (91%)	290 (97%)	9 (3%)	53	50
1	C	294/328 (90%)	282 (96%)	12 (4%)	41	35
1	D	233/328 (71%)	220 (94%)	13 (6%)	30	22
All	All	1122/1312 (86%)	1082 (96%)	40 (4%)	47	42

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	TRP
1	A	166	LEU
1	A	206	GLU
1	A	315	TYR
1	A	333	GLU
1	A	339	GLN
1	B	48	TRP

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Mol	Chain	Res	Type
1	B	268	VAL
1	B	293	ARG
1	B	315	TYR
1	B	316	ARG
1	B	317	LYS
1	B	333	GLU
1	B	339	GLN
1	B	374	LYS
1	C	48	TRP
1	C	76	ASN
1	C	131	GLU
1	C	135	LYS
1	C	206	GLU
1	C	220	THR
1	C	242	LEU
1	C	250	TYR
1	C	265	THR
1	C	315	TYR
1	C	333	GLU
1	C	339	GLN
1	D	48	TRP
1	D	121	LEU
1	D	139	LEU
1	D	166	LEU
1	D	173	LEU
1	D	197	SER
1	D	250	TYR
1	D	275	LYS
1	D	305	ARG
1	D	315	TYR
1	D	317	LYS
1	D	333	GLU
1	D	339	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	ASN
1	A	169	ASN
1	A	179	ASN
1	A	243	ASN
1	A	245	HIS

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Mol	Chain	Res	Type
1	A	266	ASN
1	A	335	HIS
1	A	339	GLN
1	B	70	ASN
1	B	90	ASN
1	B	169	ASN
1	B	339	GLN
1	B	380	GLN
1	C	60	HIS
1	C	75	GLN
1	C	90	ASN
1	C	335	HIS
1	C	339	GLN
1	C	358	ASN
1	D	63	HIS
1	D	75	GLN
1	D	219	ASN
1	D	266	ASN
1	D	335	HIS
1	D	339	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

8 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	GLC	A	500	3	10,11,12	0.69	0	11,15,17	1.46	1 (9%)
3	DMJ	A	501	2	11,11,11	0.69	0	15,15,15	1.31	2 (13%)
2	GLC	B	500	3	10,11,12	0.66	0	11,15,17	1.36	1 (9%)
3	DMJ	B	501	2	11,11,11	0.60	0	15,15,15	1.29	2 (13%)
2	GLC	C	500	3	10,11,12	0.77	0	11,15,17	0.59	0
3	DMJ	C	501	2	11,11,11	0.67	0	15,15,15	1.37	1 (6%)
2	GLC	D	500	3	10,11,12	0.90	1 (10%)	11,15,17	0.67	0
3	DMJ	D	501	2	11,11,11	0.60	0	15,15,15	1.56	1 (6%)

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	500	3	-	0/2/19/22	0/1/1/1
3	DMJ	A	501	2	-	0/2/19/19	0/1/1/1
2	GLC	B	500	3	-	0/2/19/22	0/1/1/1
3	DMJ	B	501	2	-	0/2/19/19	0/1/1/1
2	GLC	C	500	3	-	0/2/19/22	0/1/1/1
3	DMJ	C	501	2	-	0/2/19/19	0/1/1/1
2	GLC	D	500	3	-	0/2/19/22	0/1/1/1
3	DMJ	D	501	2	-	0/2/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	GLC	O5-C5	-2.06	1.41	1.45

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	501	DMJ	C1-N5-C5	5.22	119.73	110.79
3	C	501	DMJ	C1-N5-C5	4.65	118.75	110.79
2	A	500	GLC	O5-C5-C6	4.14	111.33	106.98
2	B	500	GLC	O5-C5-C6	3.61	110.77	106.98
3	A	501	DMJ	C1-N5-C5	3.60	116.95	110.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	DMJ	C1-N5-C5	3.55	116.86	110.79
3	A	501	DMJ	C2-C1-N5	-2.34	106.26	111.18
3	B	501	DMJ	C2-C1-N5	-2.27	106.41	111.18

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	345/380 (90%)	-0.59	4 (1%) 75 76	17, 24, 38, 71	0
1	B	346/380 (91%)	-0.59	0 100 100	16, 23, 37, 55	0
1	C	344/380 (90%)	-0.66	0 100 100	16, 23, 39, 59	0
1	D	342/380 (90%)	0.26	12 (3%) 42 41	28, 49, 67, 78	0
All	All	1377/1520 (90%)	-0.40	16 (1%) 75 76	16, 26, 57, 78	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	73	SER	3.8
1	D	347	THR	3.7
1	D	352	THR	3.5
1	D	353	TYR	3.0
1	D	378	SER	2.9
1	D	73	SER	2.9
1	D	358	ASN	2.8
1	D	356	TYR	2.7
1	D	212	GLY	2.6
1	D	355	ASP	2.4
1	A	70	ASN	2.3
1	A	71	GLY	2.3
1	D	69	PRO	2.2
1	A	72	GLY	2.1
1	D	346	TYR	2.1
1	D	379	LYS	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates 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. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	GLC	D	500	11/12	0.13	1.63	38,39,41,42	0
3	DMJ	B	501	11/11	0.12	0.60	19,21,21,22	0
2	GLC	C	500	11/12	0.10	0.56	22,24,27,28	0
3	DMJ	C	501	11/11	0.10	0.55	20,21,22,22	0
3	DMJ	A	501	11/11	0.07	-0.08	20,22,23,23	0
3	DMJ	D	501	11/11	0.11	-0.18	37,38,39,41	0
2	GLC	B	500	11/12	0.09	-0.30	20,22,24,24	0
2	GLC	A	500	11/12	0.06	-1.27	23,25,28,30	0

6.5 Other polymers

There are no such residues in this entry.