



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:16 AM GMT

PDB ID : 3OGS
Title : Complex structure of beta-galactosidase from Trichoderma reesei with IPTG
Authors : Maksimainen, M.; Rouvinen, J.
Deposited on : 2010-08-17
Resolution : 1.75 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

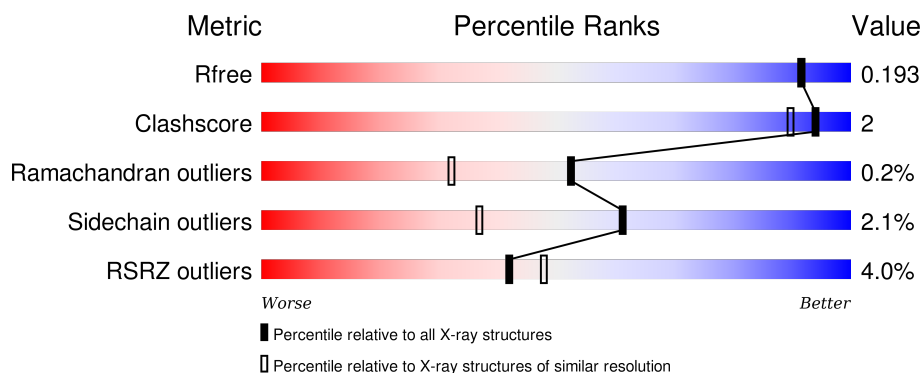
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 1.75 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	1609 (1.76-1.76)
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

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	1003	

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
4	MAN	A	1038	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	A	1041	-	-	-	X
5	NAG	A	1042	-	-	-	X

2 Entry composition [i](#)

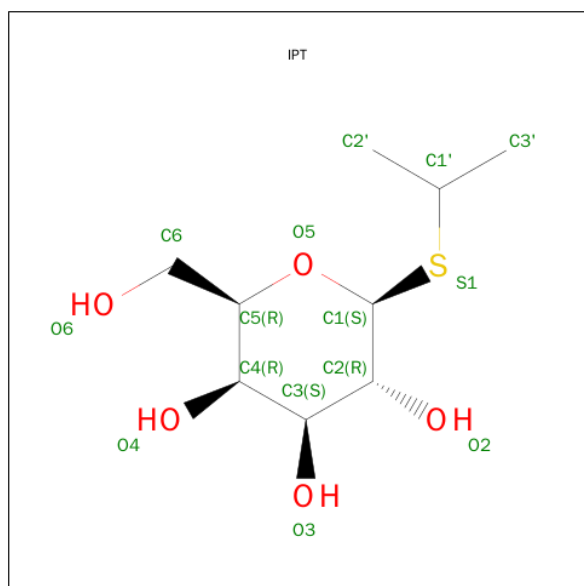
There are 7 unique types of molecules in this entry. The entry contains 8819 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Beta-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	986	Total	C	N	O	S	0	3	0
			7634	4906	1289	1431	8			

- Molecule 2 is ISOPROPYL-1-BETA-D-THIOGALACTOSIDE (three-letter code: IPT) (formula: C₉H₁₈O₅S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			15	9	5	1		

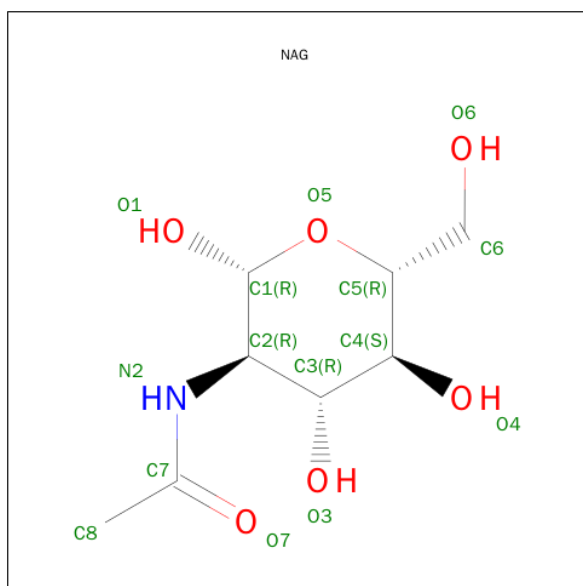
- Molecule 3 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	7	Total	C	N	O	0	0
			83	46	2	35		

- Molecule 4 is a polymer of unknown type called SUGAR (9-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	9	Total	C	N	O	0	0
			105	58	2	45		

- Molecule 5 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	2	Total	C	N	O	0	0
			28	16	2	10		

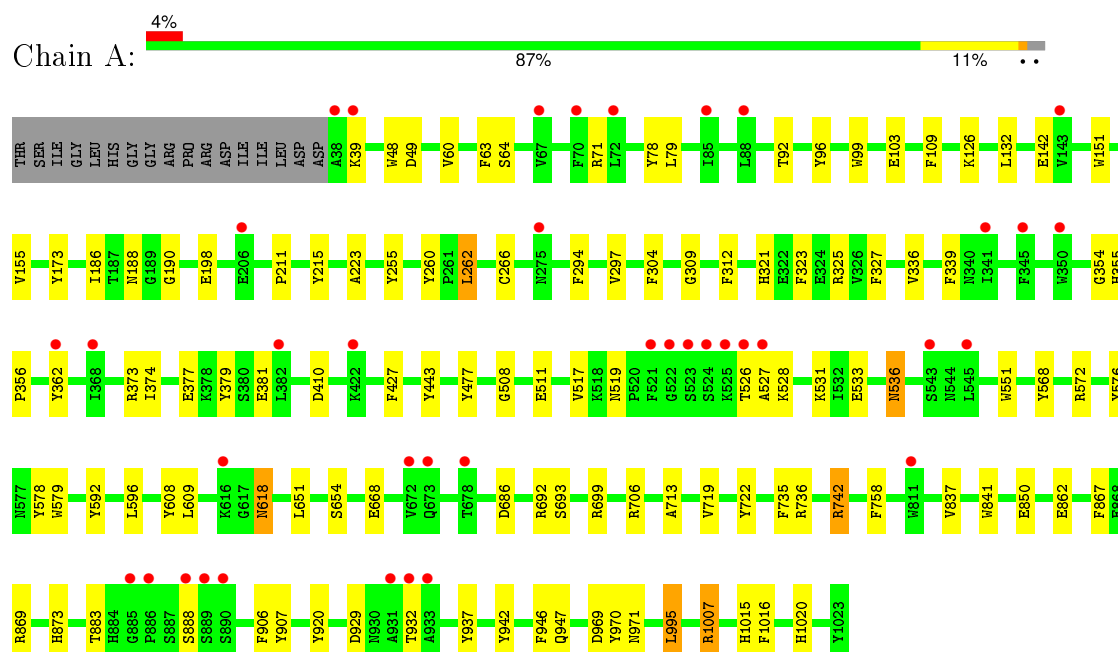
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	926	Total	O	0	0
			926	926		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Beta-galactosidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	69.50 Å 70.30 Å 82.40 Å 108.50° 97.80° 114.40°	Depositor
Resolution (Å)	43.54 – 1.75 43.54 – 1.75	Depositor EDS
% Data completeness (in resolution range)	95.0 (43.54-1.75) 77.3 (43.54-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.28 (at 1.75 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.145 , 0.200 0.159 , 0.193	Depositor DCC
R_{free} test set	5893 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	18.2	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 64.6	EDS
Estimated twinning fraction	0.019 for k,h,-h-k-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 117858 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8819	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, BMA, NAG, IPT, MAN

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	1.78	85/7862 (1.1%)	0.99	18/10715 (0.2%)

All (85) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	260	TYR	CD1-CE1	8.49	1.52	1.39
1	A	937	TYR	CD1-CE1	8.14	1.51	1.39
1	A	109	PHE	CE2-CZ	7.80	1.52	1.37
1	A	103	GLU	CB-CG	7.63	1.66	1.52
1	A	362	TYR	CE2-CZ	7.43	1.48	1.38
1	A	920	TYR	CD2-CE2	7.30	1.50	1.39
1	A	377	GLU	CB-CG	7.20	1.65	1.52
1	A	551	TRP	CB-CG	7.18	1.63	1.50
1	A	719	VAL	CB-CG2	6.89	1.67	1.52
1	A	578	TYR	CG-CD1	6.88	1.48	1.39
1	A	906	PHE	CE1-CZ	6.80	1.50	1.37
1	A	942	TYR	CD2-CE2	6.67	1.49	1.39
1	A	443	TYR	CD1-CE1	6.66	1.49	1.39
1	A	151	TRP	CE3-CZ3	6.65	1.49	1.38
1	A	937	TYR	CD2-CE2	6.65	1.49	1.39
1	A	99	TRP	CG-CD1	6.57	1.46	1.36
1	A	142	GLU	CB-CG	6.53	1.64	1.52
1	A	477	TYR	CD1-CE1	6.47	1.49	1.39
1	A	96	TYR	CD1-CE1	6.37	1.49	1.39
1	A	304	PHE	CD1-CE1	6.26	1.51	1.39
1	A	443	TYR	CD2-CE2	6.24	1.48	1.39
1	A	568	TYR	CD1-CE1	6.21	1.48	1.39
1	A	427	PHE	CE1-CZ	6.21	1.49	1.37
1	A	592	TYR	CG-CD2	6.18	1.47	1.39
1	A	722	TYR	CE1-CZ	6.18	1.46	1.38
1	A	266	CYS	CB-SG	6.16	1.92	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1016	PHE	CE2-CZ	6.02	1.48	1.37
1	A	294	PHE	CE1-CZ	6.01	1.48	1.37
1	A	758	PHE	CE2-CZ	5.96	1.48	1.37
1	A	379	TYR	CD1-CE1	5.93	1.48	1.39
1	A	850	GLU	CG-CD	5.91	1.60	1.51
1	A	477	TYR	CG-CD1	5.91	1.46	1.39
1	A	309	GLY	N-CA	5.90	1.54	1.46
1	A	568	TYR	CD2-CE2	5.88	1.48	1.39
1	A	354	GLY	N-CA	5.88	1.54	1.46
1	A	533	GLU	CG-CD	5.87	1.60	1.51
1	A	970	TYR	CD1-CE1	5.83	1.48	1.39
1	A	517	VAL	CB-CG1	5.82	1.65	1.52
1	A	155	VAL	CB-CG1	5.82	1.65	1.52
1	A	339	PHE	CD1-CE1	5.77	1.50	1.39
1	A	946	PHE	CE2-CZ	5.71	1.48	1.37
1	A	579	TRP	CZ3-CH2	5.63	1.49	1.40
1	A	907	TYR	CE2-CZ	5.60	1.45	1.38
1	A	592	TYR	CD2-CE2	5.57	1.47	1.39
1	A	198	GLU	CG-CD	5.53	1.60	1.51
1	A	592	TYR	CE1-CZ	5.52	1.45	1.38
1	A	841	TRP	CG-CD1	5.52	1.44	1.36
1	A	381	GLU	CB-CG	5.49	1.62	1.52
1	A	592	TYR	CE2-CZ	5.48	1.45	1.38
1	A	735	PHE	CE2-CZ	5.44	1.47	1.37
1	A	722	TYR	CD1-CE1	5.44	1.47	1.39
1	A	260	TYR	CD2-CE2	5.43	1.47	1.39
1	A	78	TYR	CD1-CE1	5.41	1.47	1.39
1	A	327	PHE	CE2-CZ	5.40	1.47	1.37
1	A	336	VAL	CB-CG1	5.40	1.64	1.52
1	A	841	TRP	CD2-CE2	5.38	1.47	1.41
1	A	578	TYR	CD1-CE1	5.37	1.47	1.39
1	A	576	TYR	CD1-CE1	5.37	1.47	1.39
1	A	869	ARG	CZ-NH1	5.34	1.40	1.33
1	A	215	TYR	CD2-CE2	5.32	1.47	1.39
1	A	970	TYR	CD2-CE2	5.31	1.47	1.39
1	A	255	TYR	CE2-CZ	5.30	1.45	1.38
1	A	48	TRP	CB-CG	5.26	1.59	1.50
1	A	312	PHE	CG-CD1	5.25	1.46	1.38
1	A	294	PHE	CD2-CE2	5.22	1.49	1.39
1	A	508	GLY	N-CA	5.22	1.53	1.46
1	A	841	TRP	CZ3-CH2	5.20	1.48	1.40
1	A	862	GLU	CG-CD	5.20	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	867	PHE	CE2-CZ	5.19	1.47	1.37
1	A	356	PRO	N-CA	5.15	1.55	1.47
1	A	867	PHE	CE1-CZ	5.15	1.47	1.37
1	A	173	TYR	CE2-CZ	5.14	1.45	1.38
1	A	297	VAL	CB-CG1	5.13	1.63	1.52
1	A	362	TYR	CD1-CE1	5.13	1.47	1.39
1	A	608	TYR	CD2-CE2	5.13	1.47	1.39
1	A	654	SER	CB-OG	5.13	1.49	1.42
1	A	713	ALA	CA-CB	5.13	1.63	1.52
1	A	568	TYR	CE2-CZ	5.11	1.45	1.38
1	A	132	LEU	C-O	5.11	1.33	1.23
1	A	339	PHE	CE1-CZ	5.10	1.47	1.37
1	A	223	ALA	CA-CB	5.08	1.63	1.52
1	A	381	GLU	CD-OE2	5.04	1.31	1.25
1	A	920	TYR	CG-CD2	5.03	1.45	1.39
1	A	99	TRP	CE3-CZ3	5.03	1.47	1.38
1	A	511	GLU	CD-OE1	5.01	1.31	1.25

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	869	ARG	NE-CZ-NH1	9.01	124.80	120.30
1	A	869	ARG	NE-CZ-NH2	-8.48	116.06	120.30
1	A	49	ASP	CB-CG-OD1	8.34	125.81	118.30
1	A	572	ARG	NE-CZ-NH1	6.96	123.78	120.30
1	A	373	ARG	NE-CZ-NH1	6.36	123.48	120.30
1	A	995	LEU	CA-CB-CG	6.20	129.56	115.30
1	A	572	ARG	NE-CZ-NH2	-6.12	117.24	120.30
1	A	686	ASP	CB-CG-OD1	5.83	123.55	118.30
1	A	71	ARG	NE-CZ-NH2	-5.78	117.41	120.30
1	A	969	ASP	CB-CG-OD1	5.69	123.42	118.30
1	A	929	ASP	CB-CG-OD1	5.61	123.35	118.30
1	A	995	LEU	CB-CG-CD2	5.28	119.97	111.00
1	A	71	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	A	736	ARG	NE-CZ-NH2	-5.23	117.68	120.30
1	A	325	ARG	NE-CZ-NH2	-5.17	117.71	120.30
1	A	699	ARG	NE-CZ-NH1	-5.16	117.72	120.30
1	A	339	PHE	CB-CG-CD2	-5.06	117.26	120.80
1	A	410	ASP	CB-CG-OD1	5.05	122.85	118.30

There are no chirality outliers.

There are no planarity outliers.

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	7634	0	7435	26	0
2	A	15	0	18	0	0
3	A	83	0	70	0	0
4	A	105	0	88	2	0
5	A	28	0	26	0	0
6	A	28	0	25	0	0
7	A	926	0	0	15	0
All	All	8819	0	7662	28	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 2.

All (28) 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:1020:HIS:HB2	7:A:1807:HOH:O	1.20	1.34
1:A:188:ASN:HB3	7:A:1881:HOH:O	1.48	1.14
1:A:531:LYS:HB3	7:A:1575:HOH:O	1.62	0.97
1:A:971:ASN:HB3	7:A:1816:HOH:O	1.67	0.95
4:A:1040:GLC:H61	7:A:1952:HOH:O	1.79	0.82
1:A:971:ASN:ND2	7:A:1816:HOH:O	2.21	0.67
1:A:536:ASN:OD1	1:A:536:ASN:C	2.33	0.66
1:A:971:ASN:CB	7:A:1816:HOH:O	2.36	0.64
1:A:692:ARG:NH1	7:A:1666:HOH:O	2.30	0.64
1:A:706:ARG:NH1	7:A:1805:HOH:O	2.34	0.60
1:A:262:LEU:HD22	1:A:323:PHE:CE1	2.41	0.56
1:A:262:LEU:HD22	1:A:323:PHE:CD1	2.42	0.54
1:A:321:HIS:HD2	7:A:1189:HOH:O	1.91	0.53
1:A:668:GLU:HB3	7:A:1882:HOH:O	2.12	0.49
1:A:60[B]:VAL:HG11	1:A:596:LEU:CD1	2.43	0.48
1:A:1007:ARG:HD2	7:A:1607:HOH:O	2.12	0.48
1:A:651:LEU:N	1:A:651:LEU:HD23	2.28	0.48
1:A:883:THR:HG21	7:A:1721:HOH:O	2.14	0.48
1:A:651:LEU:H	1:A:651:LEU:HD23	1.80	0.47
1:A:79:LEU:HD22	1:A:126:LYS:HD3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:SER:HA	1:A:92:THR:O	2.18	0.43
4:A:1040:GLC:C6	7:A:1952:HOH:O	2.53	0.43
1:A:742:ARG:HG3	1:A:837:VAL:HG22	2.01	0.42
1:A:873:HIS:H	1:A:873:HIS:CD2	2.38	0.42
1:A:618:ASN:C	1:A:618:ASN:HD22	2.23	0.42
1:A:883:THR:CG2	7:A:1721:HOH:O	2.67	0.41
1:A:374:ILE:HD11	1:A:609:LEU:HB2	2.03	0.41
1:A:186:ILE:HA	1:A:190:GLY:O	2.21	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	987/1003 (98%)	957 (97%)	28 (3%)	2 (0%)	52 32

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	527	ALA
1	A	519	ASN

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	808/819 (99%)	791 (98%)	17 (2%)	61 37

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LYS
1	A	63	PHE
1	A	211	PRO
1	A	262	LEU
1	A	355	HIS
1	A	526	THR
1	A	528	LYS
1	A	536	ASN
1	A	618	ASN
1	A	693	SER
1	A	742	ARG
1	A	888	SER
1	A	932	THR
1	A	947	GLN
1	A	995	LEU
1	A	1007	ARG
1	A	1015	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	225	ASN
1	A	321	HIS
1	A	412	GLN
1	A	618	ASN
1	A	836	ASN
1	A	873	HIS
1	A	884	HIS
1	A	1015	HIS

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 ⓘ

18 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$
3	NAG	A	1025	1,3	14,14,15	1.23	1 (7%)	15,19,21	1.59	3 (20%)
3	NAG	A	1026	3	14,14,15	1.02	0	15,19,21	0.82	0
3	BMA	A	1027	3	11,11,12	1.54	2 (18%)	14,15,17	1.19	2 (14%)
3	MAN	A	1028	3	11,11,12	1.61	2 (18%)	14,15,17	1.58	2 (14%)
3	MAN	A	1029	3	11,11,12	1.26	2 (18%)	14,15,17	1.63	4 (28%)
3	MAN	A	1030	3	11,11,12	0.64	0	14,15,17	1.54	4 (28%)
3	MAN	A	1031	3	11,11,12	1.28	2 (18%)	14,15,17	2.12	4 (28%)
4	NAG	A	1032	1,4	14,14,15	1.81	2 (14%)	15,19,21	1.53	4 (26%)
4	NAG	A	1033	4	14,14,15	0.76	0	15,19,21	1.45	2 (13%)
4	BMA	A	1034	4	11,11,12	1.05	0	14,15,17	1.45	2 (14%)
4	MAN	A	1035	4	11,11,12	0.87	0	14,15,17	1.95	2 (14%)
4	MAN	A	1036	4	11,11,12	0.61	0	14,15,17	1.05	0
4	MAN	A	1037	4	11,11,12	1.23	1 (9%)	14,15,17	2.37	5 (35%)
4	MAN	A	1038	4	11,11,12	0.94	0	14,15,17	1.90	5 (35%)
4	MAN	A	1039	4	11,11,12	0.95	1 (9%)	14,15,17	2.38	5 (35%)
4	GLC	A	1040	4	11,11,12	0.67	0	14,15,17	2.91	4 (28%)
6	NAG	A	1043	1,6	14,14,15	0.55	0	15,19,21	1.67	6 (40%)
6	NAG	A	1044	6	14,14,15	0.61	0	15,19,21	1.12	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
3	NAG	A	1025	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1026	3	-	0/6/23/26	0/1/1/1
3	BMA	A	1027	3	-	0/2/19/22	0/1/1/1
3	MAN	A	1028	3	-	0/2/19/22	0/1/1/1
3	MAN	A	1029	3	-	0/2/19/22	0/1/1/1
3	MAN	A	1030	3	-	0/2/19/22	0/1/1/1
3	MAN	A	1031	3	-	0/2/19/22	0/1/1/1
4	NAG	A	1032	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1033	4	-	0/6/23/26	0/1/1/1
4	BMA	A	1034	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1035	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1036	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1037	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1038	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1039	4	-	0/2/19/22	0/1/1/1
4	GLC	A	1040	4	-	0/2/19/22	0/1/1/1
6	NAG	A	1043	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	1044	6	-	0/6/23/26	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1031	MAN	O5-C1	-2.40	1.39	1.43
3	A	1025	NAG	C2-N2	2.01	1.49	1.46
3	A	1028	MAN	C6-C5	2.26	1.60	1.51
3	A	1029	MAN	C2-C3	2.29	1.55	1.52
3	A	1029	MAN	O2-C2	2.42	1.48	1.43
4	A	1039	MAN	C2-C3	2.45	1.55	1.52
3	A	1027	BMA	C2-C3	2.60	1.56	1.52
4	A	1032	NAG	C3-C2	2.63	1.58	1.52
4	A	1037	MAN	C2-C3	2.67	1.56	1.52
3	A	1027	BMA	O4-C4	2.69	1.49	1.43
3	A	1031	MAN	C2-C3	2.90	1.56	1.52
3	A	1028	MAN	C2-C3	3.06	1.56	1.52
4	A	1032	NAG	C1-C2	5.33	1.59	1.52

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1037	MAN	C6-C5-C4	-6.57	96.82	113.02
4	A	1039	MAN	O3-C3-C4	-4.35	100.55	110.34
4	A	1039	MAN	O2-C2-C1	-3.92	101.34	109.21
4	A	1040	GLC	O3-C3-C2	-3.40	103.85	110.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1028	MAN	O2-C2-C3	-3.23	103.63	110.12
3	A	1027	BMA	O4-C4-C3	-2.92	103.76	110.34
4	A	1034	BMA	O3-C3-C4	-2.92	103.77	110.34
3	A	1031	MAN	C6-C5-C4	-2.82	106.06	113.02
3	A	1030	MAN	O2-C2-C3	-2.72	104.64	110.12
4	A	1033	NAG	O7-C7-C8	-2.67	117.16	122.06
3	A	1029	MAN	O6-C6-C5	-2.64	102.61	111.33
6	A	1043	NAG	C3-C4-C5	-2.62	105.63	110.20
6	A	1043	NAG	O3-C3-C2	-2.60	103.96	109.11
3	A	1027	BMA	O3-C3-C2	-2.51	105.47	110.00
4	A	1038	MAN	O2-C2-C3	-2.48	105.13	110.12
4	A	1032	NAG	C6-C5-C4	-2.47	106.92	113.02
3	A	1030	MAN	O6-C6-C5	-2.45	103.25	111.33
4	A	1037	MAN	C2-C3-C4	-2.42	106.94	111.04
3	A	1030	MAN	C2-C3-C4	-2.31	107.11	111.04
3	A	1030	MAN	O5-C1-C2	-2.28	107.16	110.86
4	A	1038	MAN	C1-C2-C3	-2.24	106.89	109.54
6	A	1043	NAG	C2-N2-C7	-2.11	120.33	123.04
3	A	1031	MAN	O5-C1-C2	-2.09	107.47	110.86
6	A	1043	NAG	C4-C3-C2	2.01	114.35	111.23
6	A	1043	NAG	C1-O5-C5	2.07	114.87	112.25
4	A	1037	MAN	O5-C1-C2	2.10	114.26	110.86
3	A	1025	NAG	O5-C5-C6	2.15	111.99	107.35
4	A	1038	MAN	O5-C5-C6	2.19	112.09	107.35
4	A	1032	NAG	C8-C7-N2	2.22	120.36	116.11
3	A	1025	NAG	C1-O5-C5	2.23	115.08	112.25
6	A	1044	NAG	C1-O5-C5	2.27	115.13	112.25
4	A	1037	MAN	O4-C4-C3	2.27	115.46	110.34
4	A	1040	GLC	O5-C5-C6	2.28	112.29	107.35
3	A	1031	MAN	O3-C3-C2	2.32	114.18	110.00
4	A	1032	NAG	C3-C2-N2	2.36	116.21	110.56
4	A	1039	MAN	O2-C2-C3	2.38	114.91	110.12
3	A	1029	MAN	O2-C2-C1	2.45	114.13	109.21
4	A	1039	MAN	C1-C2-C3	2.48	112.47	109.54
3	A	1029	MAN	O3-C3-C2	2.51	114.54	110.00
4	A	1038	MAN	O2-C2-C1	3.05	115.33	109.21
4	A	1033	NAG	C1-O5-C5	3.17	116.27	112.25
4	A	1032	NAG	C2-N2-C7	3.17	127.11	123.04
3	A	1025	NAG	C4-C3-C2	3.44	116.58	111.23
3	A	1028	MAN	C1-O5-C5	3.47	116.66	112.25
4	A	1034	BMA	O3-C3-C2	3.49	116.31	110.00
6	A	1043	NAG	O5-C5-C6	3.54	115.01	107.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1029	MAN	C1-O5-C5	3.54	116.75	112.25
4	A	1035	MAN	O3-C3-C2	3.63	116.55	110.00
4	A	1037	MAN	C3-C4-C5	3.71	116.66	110.20
4	A	1038	MAN	C1-O5-C5	4.19	117.57	112.25
4	A	1035	MAN	O5-C5-C6	4.69	117.51	107.35
4	A	1039	MAN	O3-C3-C2	4.89	118.83	110.00
3	A	1031	MAN	C1-O5-C5	5.95	119.80	112.25
4	A	1040	GLC	C1-C2-C3	6.04	116.68	109.54
4	A	1040	GLC	C1-O5-C5	7.53	121.81	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1040	GLC	2	0

5.6 Ligand geometry

3 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	IPT	A	1024	-	15,15,15	1.25	1 (6%)	19,21,21	1.54	3 (15%)
5	NAG	A	1041	1	14,14,15	0.55	0	15,19,21	2.19	1 (6%)
5	NAG	A	1042	1	14,14,15	0.52	0	15,19,21	1.87	5 (33%)

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	IPT	A	1024	-	-	0/6/26/26	0/1/1/1
5	NAG	A	1041	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1042	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1024	IPT	C4-C5	3.08	1.59	1.53

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1042	NAG	O3-C3-C2	-3.21	102.75	109.11
5	A	1042	NAG	O7-C7-C8	-3.00	116.55	122.06
2	A	1024	IPT	O2-C2-C3	-2.58	104.54	110.34
2	A	1024	IPT	O4-C4-C3	-2.21	105.37	110.34
5	A	1042	NAG	O6-C6-C5	-2.19	104.10	111.33
5	A	1042	NAG	C8-C7-N2	2.09	120.11	116.11
5	A	1042	NAG	C1-O5-C5	3.89	117.19	112.25
2	A	1024	IPT	C1-O5-C5	4.01	120.39	112.74
5	A	1041	NAG	C1-O5-C5	7.77	122.11	112.25

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 ⓘ

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	986/1003 (98%)	0.03	39 (3%)	42 48	10, 17, 33, 64	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	933	ALA	8.4
1	A	526	THR	7.7
1	A	932	THR	6.5
1	A	525	LYS	6.5
1	A	931	ALA	5.4
1	A	523	SER	4.9
1	A	543	SER	4.0
1	A	522	GLY	3.8
1	A	811	TRP	3.7
1	A	524	SER	3.6
1	A	888	SER	3.5
1	A	886	PRO	3.5
1	A	889	SER	3.2
1	A	678	THR	3.0
1	A	368	ILE	2.9
1	A	885	GLY	2.9
1	A	527	ALA	2.8
1	A	38	ALA	2.7
1	A	39	LYS	2.7
1	A	616	LYS	2.7
1	A	673	GLN	2.7
1	A	345	PHE	2.6
1	A	672	VAL	2.5
1	A	341	ILE	2.5
1	A	72	LEU	2.5
1	A	275	ASN	2.5
1	A	85	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	350	TRP	2.4
1	A	545	LEU	2.4
1	A	143	VAL	2.4
1	A	67	VAL	2.3
1	A	382	LEU	2.3
1	A	362	TYR	2.3
1	A	206	GLU	2.2
1	A	890	SER	2.2
1	A	70	PHE	2.1
1	A	422	LYS	2.1
1	A	88	LEU	2.1
1	A	521	PHE	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](#)

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
4	MAN	A	1038	11/12	0.94	0.14	3.02	17,22,26,27	0
3	MAN	A	1031	11/12	0.95	0.08	1.08	24,26,28,30	0
6	NAG	A	1043	14/15	0.93	0.14	0.69	32,37,44,46	0
4	NAG	A	1032	14/15	0.93	0.11	0.07	13,18,24,30	0
3	NAG	A	1025	14/15	0.97	0.08	-0.48	13,15,25,27	0
3	MAN	A	1029	11/12	0.97	0.07	-0.70	15,16,28,35	0
3	NAG	A	1026	14/15	0.97	0.06	-1.27	13,15,21,22	0
4	MAN	A	1039	11/12	0.92	0.12	-	24,30,35,38	0
4	MAN	A	1036	11/12	0.68	0.38	-	55,62,64,65	0
6	NAG	A	1044	14/15	0.76	0.33	-	46,56,63,63	0
3	BMA	A	1027	11/12	0.97	0.07	-	13,16,19,19	0
4	MAN	A	1037	11/12	0.93	0.12	-	22,25,31,34	0
4	GLC	A	1040	11/12	0.80	0.16	-	41,47,48,49	0
3	MAN	A	1028	11/12	0.95	0.08	-	13,15,18,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	MAN	A	1030	11/12	0.89	0.29	-	30,35,41,47	0
4	BMA	A	1034	11/12	0.97	0.10	-	19,21,25,29	0
4	NAG	A	1033	14/15	0.96	0.13	-	16,23,37,39	0
4	MAN	A	1035	11/12	0.89	0.21	-	34,40,45,48	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(\AA^2)	Q<0.9
5	NAG	A	1042	14/15	0.93	0.24	6.15	33,39,48,52	0
5	NAG	A	1041	14/15	0.77	0.22	3.18	39,48,56,59	0
2	IPT	A	1024	15/15	0.97	0.11	-0.06	9,12,26,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.