W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 03:22 PM GMT

PDB ID : 1V84
Title : Crystal structure of human GlcAT-P in complex with N-acetyllactosamine, Udp, and Mn2+
Authors : Kakuda, S.; Shiba, T.; Ishiguro, M.; Tagawa, H.; Oka, S.; Kajihara, Y.; Kawasaki, T.; Wakatsuki, S.; Kato, R.
Deposited on : 2003-12-27
Resolution : 1.82 Å(reported)

1 Overall quality at a glance ⓘ

The reported resolution of this entry is 1.82 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.
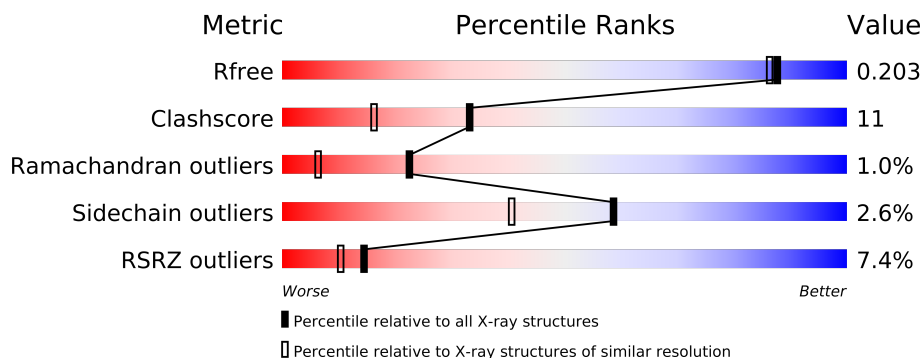
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	4101 (1.84-1.80)
Clashscore	79885	5140 (1.84-1.80)
Ramachandran outliers	78287	5077 (1.84-1.80)
Sidechain outliers	78261	5077 (1.84-1.80)
RSRZ outliers	66119	4103 (1.84-1.80)

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. 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	253	
1	B	253	

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 4418 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 Galactosylgalactosylxylosylprotein3-beta-glucuronosyltransferase1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	245	Total 1984	C 1266	N 365	O 348	S 5	0	0	0
1	B	243	Total 1960	C 1248	N 362	O 345	S 5	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	ALA	-	CLONING ARTIFACT	UNP Q9P2W7
B	82	ALA	-	CLONING ARTIFACT	UNP Q9P2W7

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	2	Total 26	C 14	N 1	O 11	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	ALA	-	CLONING ARTIFACT	UNP Q9P2W7

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	2	Total 26	C 14	N 1	O 11	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	82	ALA	-	CLONING ARTIFACT	UNP Q9P2W7

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Mn 1	0	0
4	A	1	Total 1	Mn 1	0	0

- Molecule 5 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: $C_4H_6O_6$).
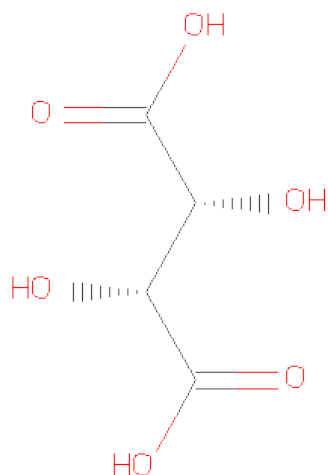
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 10	C 4	O 6	0	0

- Molecule 6 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: $C_9H_{14}N_2O_{12}P_2$).
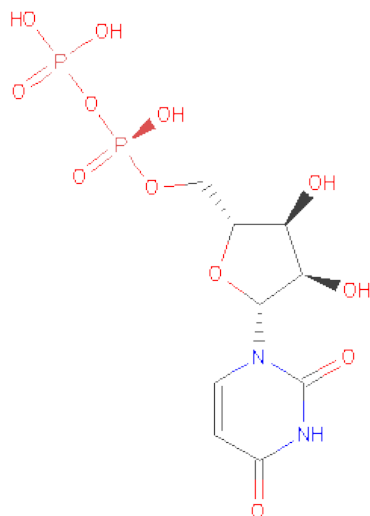
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total 25	C 9	N 2	O 12	P 2	0	0
6	B	1	Total 25	C 9	N 2	O 12	P 2	0	0

• Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	156	Total 156	O 156	0	0
7	B	204	Total 204	O 204	0	0

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 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: Galactosylgalactosylxylosylprotein3-beta-glucuronosyltransferase1

Chain A:
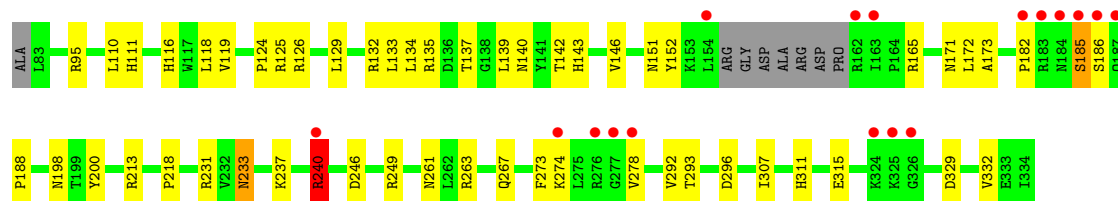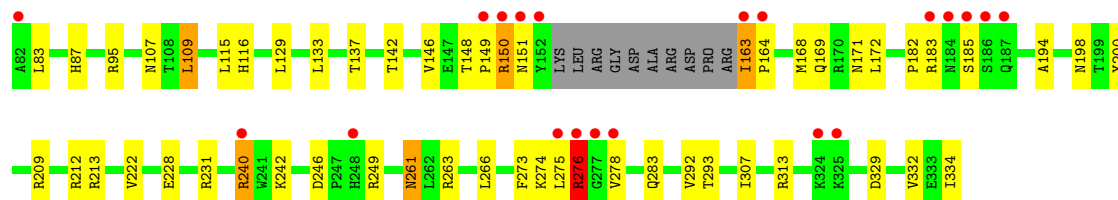

• Molecule 1: Galactosylgalactosylxylosylprotein3-beta-glucuronosyltransferase1

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	61.31Å 85.78Å 122.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.82 42.89 – 1.82	Depositor EDS
% Data completeness (in resolution range)	97.1 (40.00-1.82) 97.1 (42.89-1.82)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.15 (at 1.82Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.205 , 0.244 0.205 , 0.203	Depositor DCC
R_{free} test set	2892 reflections (5.34%)	DCC
Wilson B-factor (Å^2)	19.2	Xtriage
Anisotropy	0.864	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 36.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Outliers	0 of 57094 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4418	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities 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: UDP, NAG, MN, NDG, TLA, GAL

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	0.32	0/2033	0.57	0/2764
1	B	0.31	0/2008	0.56	0/2731
All	All	0.32	0/4041	0.57	0/5495

There are no bond length outliers.

There are no bond angle outliers.

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	1984	0	2012	51	0
1	B	1960	0	1984	42	0
2	A	26	0	24	0	0
3	B	26	0	24	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	10	0	4	0	0
6	A	25	0	11	2	0
6	B	25	0	11	0	0
7	A	156	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	204	0	0	3	0
All	All	4418	0	4070	90	0

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 11.

All (90) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:274:LYS:HD2	1:A:278:VAL:HG13	1.38	0.99
1:A:171:ASN:HD21	1:A:273:PHE:H	1.28	0.79
1:B:171:ASN:HD21	1:B:273:PHE:H	1.33	0.76
1:B:212:ARG:HD2	7:B:610:HOH:O	1.85	0.75
1:A:261:ASN:ND2	1:A:263:ARG:HB3	2.02	0.73
1:B:261:ASN:HD22	1:B:263:ARG:H	1.34	0.73
1:B:150:ARG:H	1:B:150:ARG:HD3	1.54	0.72
1:A:133:LEU:O	1:A:137:THR:HG23	1.95	0.67
1:B:149:PRO:HD3	1:B:168:MET:SD	2.37	0.65
1:A:231:ARG:NH2	1:A:240:ARG:CB	2.61	0.64
1:A:118:LEU:HD23	1:A:173:ALA:HB1	1.80	0.64
1:B:150:ARG:N	1:B:150:ARG:HD3	2.11	0.64
1:A:274:LYS:HD2	1:A:278:VAL:CG1	2.22	0.62
1:A:218:PRO:HB2	1:A:307:ILE:HD13	1.81	0.62
1:A:261:ASN:HD21	1:A:263:ARG:HB3	1.63	0.62
1:B:275:LEU:H	1:B:275:LEU:HD23	1.66	0.60
1:A:233:ASN:C	1:A:233:ASN:HD22	2.05	0.60
1:A:292:VAL:HG22	1:A:296:ASP:HB2	1.85	0.59
1:B:261:ASN:ND2	1:B:263:ARG:H	2.00	0.59
1:A:111:HIS:HE1	1:B:107:ASN:O	1.85	0.59
1:A:315:GLU:HB2	1:B:313:ARG:HB2	1.84	0.58
1:A:146:VAL:HB	1:A:172:LEU:HD22	1.85	0.58
1:A:292:VAL:HG22	1:A:293:THR:H	1.70	0.57
1:A:118:LEU:HD12	1:A:142:THR:HB	1.87	0.56
1:A:274:LYS:CD	1:A:278:VAL:HG13	2.26	0.55
1:B:246:ASP:O	1:B:249:ARG:HG2	2.05	0.55
1:A:307:ILE:HG13	1:B:334:ILE:HG22	1.88	0.54
1:A:274:LYS:HB2	7:A:602:HOH:O	2.07	0.54
1:A:132:ARG:HD2	7:A:634:HOH:O	2.06	0.54
1:A:263:ARG:O	1:A:267:GLN:HG3	2.10	0.52
1:B:148:THR:HG23	1:B:149:PRO:HD2	1.93	0.51
1:A:116:HIS:HE1	1:A:142:THR:OG1	1.94	0.50
1:A:182:PRO:HG2	1:A:185:SER:HB2	1.93	0.49
1:A:198:ASN:ND2	1:A:311:HIS:HA	2.28	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:213:ARG:HD2	7:B:611:HOH:O	2.12	0.49
1:B:169:GLN:NE2	1:B:169:GLN:H	2.09	0.49
1:B:146:VAL:HB	1:B:172:LEU:HD22	1.95	0.48
1:B:87:HIS:ND1	1:B:116:HIS:HD2	2.11	0.48
1:B:292:VAL:HG22	1:B:293:THR:N	2.29	0.48
1:B:275:LEU:N	1:B:275:LEU:HD23	2.28	0.48
1:B:116:HIS:HE1	1:B:142:THR:OG1	1.97	0.48
1:B:133:LEU:O	1:B:137:THR:HG23	2.14	0.47
1:A:292:VAL:CG2	1:A:296:ASP:HB2	2.44	0.47
1:A:231:ARG:NH2	1:A:240:ARG:HB3	2.30	0.47
1:A:110:LEU:HA	1:A:139:LEU:HD21	1.96	0.47
1:B:240:ARG:HH11	1:B:240:ARG:HG2	1.80	0.47
1:B:182:PRO:HG2	1:B:185:SER:HB3	1.97	0.46
1:A:292:VAL:HG23	7:A:606:HOH:O	2.15	0.46
1:A:292:VAL:HG22	1:A:293:THR:N	2.29	0.46
1:A:171:ASN:HD21	1:A:273:PHE:N	2.07	0.46
1:A:233:ASN:ND2	1:A:237:LYS:H	2.13	0.46
1:A:165:ARG:HB2	6:A:503:UDP:H5'2	1.98	0.46
1:A:274:LYS:HE3	7:A:602:HOH:O	2.17	0.45
1:A:233:ASN:C	1:A:233:ASN:ND2	2.70	0.45
1:A:129:LEU:C	1:A:129:LEU:HD23	2.36	0.45
1:A:116:HIS:CE1	1:A:142:THR:OG1	2.70	0.45
1:A:329:ASP:HB3	1:A:332:VAL:HG23	1.99	0.45
1:B:329:ASP:HB3	1:B:332:VAL:HG23	1.98	0.44
1:B:129:LEU:C	1:B:129:LEU:HD23	2.37	0.44
1:A:119:VAL:HG21	1:A:134:LEU:HD21	2.00	0.44
1:A:240:ARG:HH21	1:A:240:ARG:HG2	1.83	0.44
1:B:274:LYS:C	1:B:278:VAL:HG21	2.39	0.44
1:A:231:ARG:NH2	1:A:240:ARG:HB2	2.32	0.43
1:B:198:ASN:HB2	1:B:200:TYR:CZ	2.52	0.43
1:A:151:ASN:HD22	1:A:152:TYR:HD2	1.66	0.43
1:B:249:ARG:H	1:B:249:ARG:HG2	1.61	0.43
1:A:132:ARG:HG3	1:A:135:ARG:NH1	2.34	0.43
1:A:240:ARG:NH2	1:A:240:ARG:HG2	2.33	0.43
1:B:275:LEU:HG	1:B:276:ARG:HE	1.84	0.43
1:A:126:ARG:HB3	1:A:143:HIS:CE1	2.54	0.43
1:B:148:THR:CG2	1:B:149:PRO:HD2	2.49	0.42
1:A:198:ASN:HB2	1:A:200:TYR:CZ	2.55	0.42
1:B:283:GLN:NE2	7:B:525:HOH:O	2.52	0.42
1:B:183:ARG:HA	1:B:266:LEU:HB3	2.02	0.42
1:B:109:LEU:HG	1:B:115:LEU:HD11	2.02	0.42
1:A:124:PRO:O	1:A:125:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:231:ARG:HA	1:B:242:LYS:NZ	2.34	0.41
1:B:307:ILE:HD12	1:B:307:ILE:N	2.36	0.41
1:A:246:ASP:O	1:A:249:ARG:HG2	2.20	0.41
1:B:133:LEU:HD23	1:B:133:LEU:C	2.41	0.41
1:B:116:HIS:CE1	1:B:142:THR:OG1	2.73	0.41
1:A:165:ARG:HE	6:A:503:UDP:H5	1.69	0.41
1:B:274:LYS:O	1:B:278:VAL:HG21	2.20	0.41
1:B:163:ILE:HD13	1:B:163:ILE:HG21	1.91	0.41
1:B:194:ALA:HB1	1:B:200:TYR:CZ	2.57	0.40
1:A:186:SER:O	1:A:188:PRO:HD3	2.21	0.40
1:A:133:LEU:HD23	1:A:133:LEU:C	2.42	0.40
1:A:213:ARG:HD2	1:A:296:ASP:HB3	2.03	0.40
1:B:222:VAL:HG23	1:B:228:GLU:HG3	2.02	0.40
1:B:83:LEU:HG	1:B:209:ARG:HD3	2.04	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	241/253 (95%)	234 (97%)	5 (2%)	2 (1%)	27	9
1	B	239/253 (94%)	224 (94%)	12 (5%)	3 (1%)	18	4
All	All	480/506 (95%)	458 (95%)	17 (4%)	5 (1%)	22	6

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	164	PRO
1	B	276	ARG
1	A	185	SER
1	A	240	ARG
1	B	240	ARG

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	216/222 (97%)	212 (98%)	4 (2%)	69	56
1	B	213/222 (96%)	206 (97%)	7 (3%)	50	30
All	All	429/444 (97%)	418 (97%)	11 (3%)	59	40

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	95	ARG
1	A	140	ASN
1	A	233	ASN
1	A	240	ARG
1	B	95	ARG
1	B	109	LEU
1	B	150	ARG
1	B	151	ASN
1	B	163	ILE
1	B	261	ASN
1	B	276	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	107	ASN
1	A	111	HIS
1	A	116	HIS
1	A	140	ASN
1	A	151	ASN
1	A	171	ASN
1	A	187	GLN
1	A	198	ASN
1	A	233	ASN
1	A	261	ASN
1	A	283	GLN
1	B	107	ASN
1	B	114	ASN

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Mol	Chain	Res	Type
1	B	116	HIS
1	B	151	ASN
1	B	169	GLN
1	B	171	ASN
1	B	187	GLN
1	B	198	ASN
1	B	261	ASN
1	B	267	GLN
1	B	283	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 ⓘ

4 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	GAL	A	505	2	10,11,12	0.41	0	11,15,17	0.60	0
2	NDG	A	506	2	15,15,15	0.39	0	21,21,21	0.56	0
3	GAL	B	507	3	10,11,12	0.36	0	11,15,17	0.52	0
3	NAG	B	508	3	15,15,15	0.44	0	21,21,21	0.59	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	GAL	A	505	2	-	0/2/19/22	0/1/1/1
2	NDG	A	506	2	-	0/6/26/26	0/1/1/1
3	GAL	B	507	3	-	0/2/19/22	0/1/1/1
3	NAG	B	508	3	-	0/6/26/26	0/1/1/1

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.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
5	TLA	A	500	-	9,9,9	0.91	0	12,12,12	0.88	0
6	UDP	A	503	4	26,26,26	2.86	6 (23%)	36,40,40	1.83	6 (16%)
6	UDP	B	504	4	26,26,26	2.96	6 (23%)	36,40,40	1.82	5 (13%)

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
5	TLA	A	500	-	-	0/12/12/12	0/0/0/0
6	UDP	A	503	4	-	0/14/32/32	0/2/2/2
6	UDP	B	504	4	-	0/14/32/32	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	504	UDP	C6-C5	10.19	1.52	1.36
6	A	503	UDP	C6-C5	9.90	1.52	1.36
6	B	504	UDP	C5-C4	6.94	1.58	1.40
6	A	503	UDP	C5-C4	6.78	1.57	1.40
6	B	504	UDP	C6-N1	4.96	1.43	1.35
6	A	503	UDP	C6-N1	4.89	1.43	1.35
6	B	504	UDP	C4-N3	3.49	1.43	1.37
6	B	504	UDP	C2-N1	3.34	1.42	1.38
6	A	503	UDP	C4-N3	3.07	1.42	1.37
6	A	503	UDP	C2-N1	2.69	1.41	1.38
6	B	504	UDP	PB-O1B	2.58	1.59	1.51
6	A	503	UDP	PB-O1B	2.43	1.59	1.51

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	504	UDP	O3A-PA-O5'	-5.83	77.32	103.41
6	A	503	UDP	O3A-PA-O5'	-5.67	78.06	103.41
6	A	503	UDP	O3A-PA-O1A	-3.90	83.26	111.28
6	B	504	UDP	O3A-PA-O1A	-3.82	83.88	111.28
6	B	504	UDP	O2A-PA-O3A	-3.47	88.68	105.14
6	A	503	UDP	O2A-PA-O3A	-3.45	88.77	105.14
6	B	504	UDP	O5'-PA-O1A	3.36	122.54	109.37
6	A	503	UDP	O5'-PA-O1A	3.36	122.52	109.37
6	A	503	UDP	O3B-PB-O2B	2.79	118.47	107.61
6	B	504	UDP	O3B-PB-O2B	2.74	118.27	107.61
6	A	503	UDP	C2-N1-C1'	-2.63	116.56	118.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7   Other polymers (i)

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	245/253 (96%)	0.03	17 (6%)	17	12	13, 21, 39, 53	0
1	B	243/253 (96%)	0.33	20 (8%)	12	8	13, 20, 43, 54	0
All	All	488/506 (96%)	0.18	37 (7%)	14	10	13, 21, 41, 54	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	163	ILE	10.8
1	B	152	TYR	9.8
1	A	186	SER	9.2
1	B	151	ASN	6.9
1	B	276	ARG	6.5
1	B	150	ARG	6.4
1	A	185	SER	6.3
1	A	184	ASN	5.9
1	B	82	ALA	5.8
1	B	185	SER	5.5
1	B	186	SER	5.4
1	A	187	GLN	4.7
1	B	277	GLY	4.7
1	B	149	PRO	4.5
1	B	275	LEU	4.4
1	B	278	VAL	4.4
1	A	324	LYS	4.0
1	B	248	HIS	3.9
1	B	240	ARG	3.5
1	A	325	LYS	3.5
1	B	184	ASN	3.0
1	B	164	PRO	2.8
1	A	162	ARG	2.8
1	B	324	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	278	VAL	2.6
1	A	240	ARG	2.6
1	B	183	ARG	2.6
1	B	325	LYS	2.6
1	B	187	GLN	2.6
1	A	326	GLY	2.4
1	A	276	ARG	2.4
1	A	182	PRO	2.4
1	A	274	LYS	2.2
1	A	277	GLY	2.1
1	A	183	ARG	2.1
1	A	163	ILE	2.1
1	A	154	LEU	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 ⓘ

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	NDG	A	506	15/15	0.09	0.74	23,27,29,30	0
3	NAG	B	508	15/15	0.12	0.34	29,33,34,40	0
2	GAL	A	505	11/12	0.06	-0.79	16,18,20,20	0
3	GAL	B	507	11/12	0.07	-1.15	20,22,24,25	0

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
6	UDP	A	503	25/25	0.13	1.82	16,21,31,40	0
6	UDP	B	504	25/25	0.13	0.81	16,22,34,42	0
4	MN	A	501	1/1	0.10	0.16	18,18,18,18	0
5	TLA	A	500	10/10	0.07	-0.69	21,23,24,25	0
4	MN	B	502	1/1	0.10	-1.06	18,18,18,18	0

6.5 Other polymers ⓘ

There are no such residues in this entry.