



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 26, 2017 – 08:06 AM EDT

PDB ID : 5NN6  
Title : Crystal structure of human lysosomal acid-alpha-glucosidase, GAA, in complex with N-hydroxyethyl-1-deoxynojirimycin  
Authors : Roig-Zamboni, V.; Cobucci-Ponzano, B.; Iacono, R.; Ferrara, M.C.; Germany, S.; Parenti, G.; Bourne, Y.; Moracci, M.  
Deposited on : unknown  
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
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) : rb-20030345

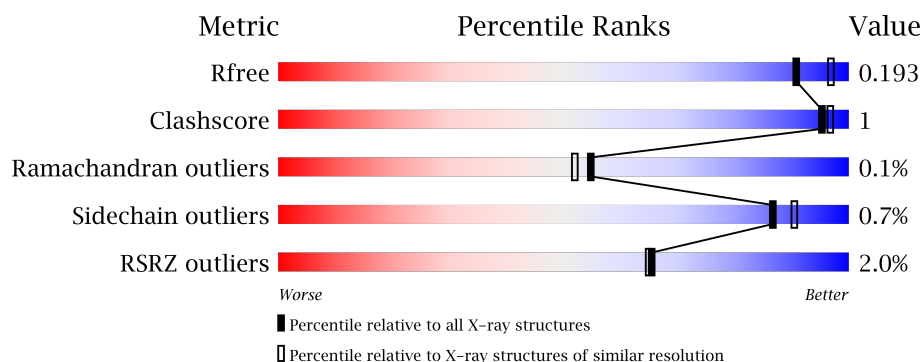
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	872	

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
10	GOL	A	1039	-	-	-	X
10	GOL	A	1040	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	GOL	A	1041	-	-	-	X
2	NAG	A	1004	-	-	-	X
2	NAG	A	1006	-	-	-	X
2	NAG	A	1011	-	-	-	X
6	SO4	A	1018	-	-	-	X
8	EDO	A	1022	-	-	-	X
8	EDO	A	1023	-	-	-	X
8	EDO	A	1024	-	-	-	X
8	EDO	A	1029	-	-	-	X
8	EDO	A	1030	-	-	-	X
8	EDO	A	1033	-	-	-	X
9	PGE	A	1035	-	-	-	X
9	PGE	A	1036	-	-	-	X
9	PGE	A	1037	-	-	-	X

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 7608 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.

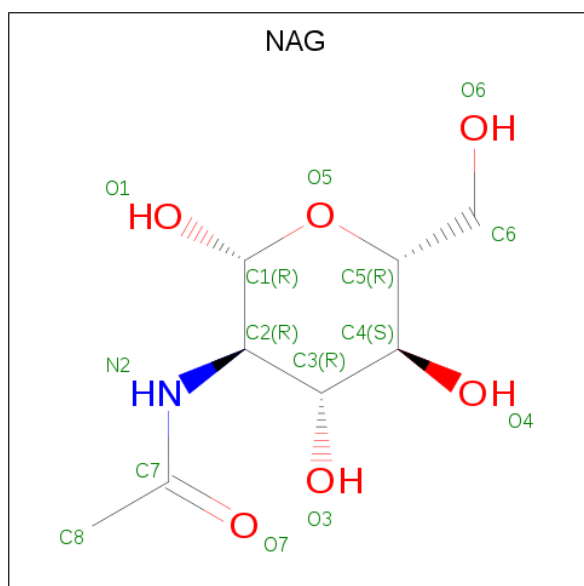
- Molecule 1 is a protein called Lysosomal alpha-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	845	6672	4281	1123	1237	31	0	4	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	199	ARG	HIS	conflict	UNP P10253
A	223	HIS	ARG	conflict	UNP P10253
A	780	ILE	VAL	conflict	UNP P10253

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



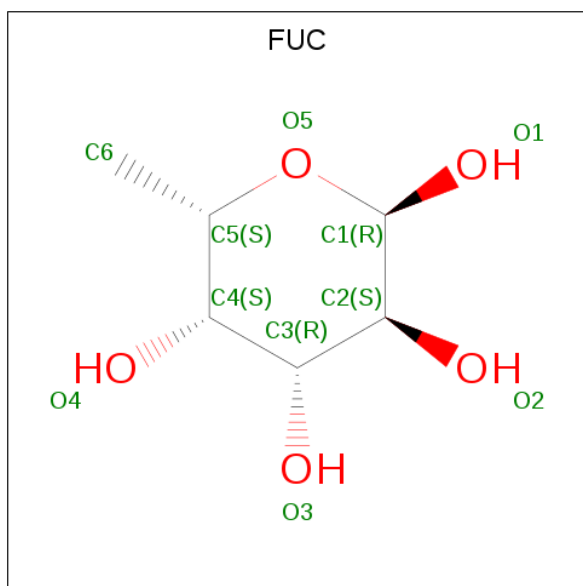
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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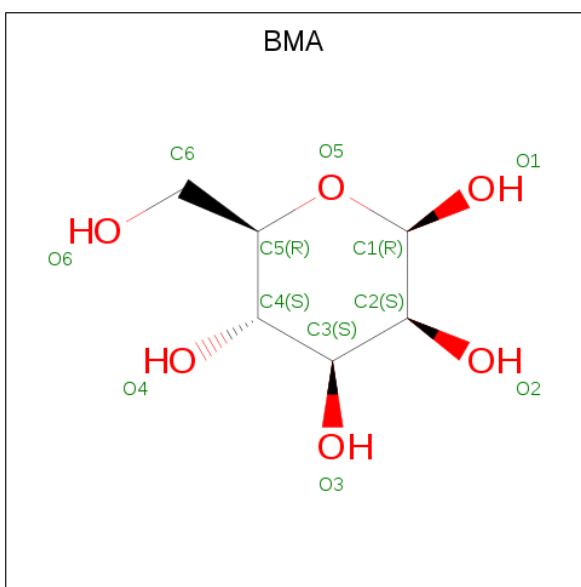
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>5</sub>).



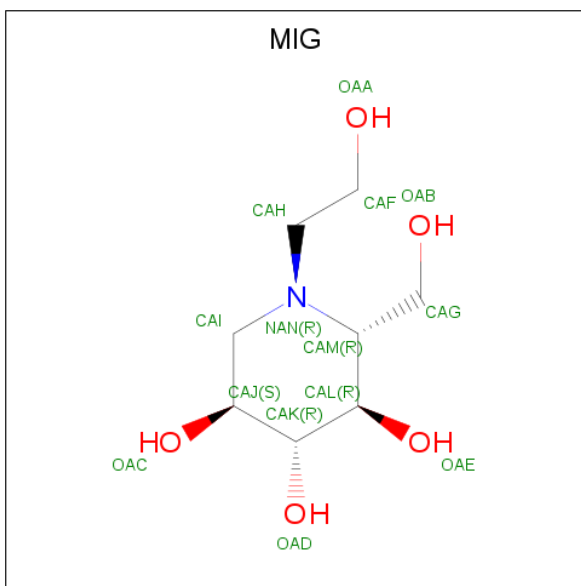
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	6	4		
3	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 4 is BETA-D-MANNOSE (three-letter code: BMA) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



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

- Molecule 5 is (2R,3R,4R,5S)-1-(2-hydroxyethyl)-2-(hydroxymethyl)piperidine-3,4,5-triol (three-letter code: MIG) (formula:  $C_8H_{17}NO_5$ ).



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

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).

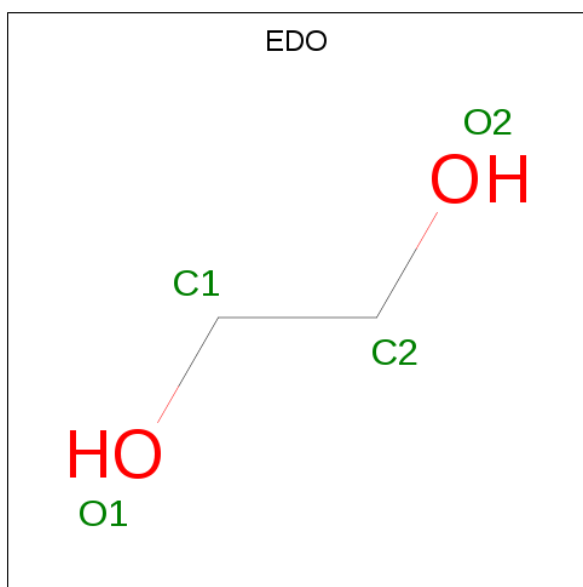


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

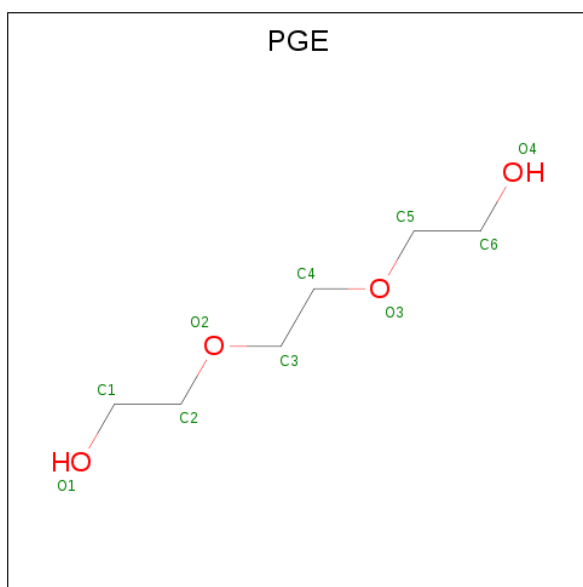
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	3	Total	Cl	0	0
			3	3		

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



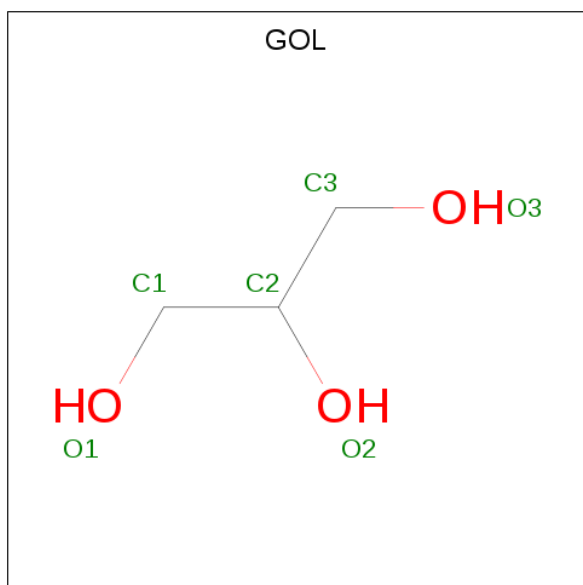
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total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

- Molecule 9 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			7	4	3		
9	A	1	Total	C	O	0	0
			10	6	4		
9	A	1	Total	C	O	0	0
			7	4	3		
9	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 10 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

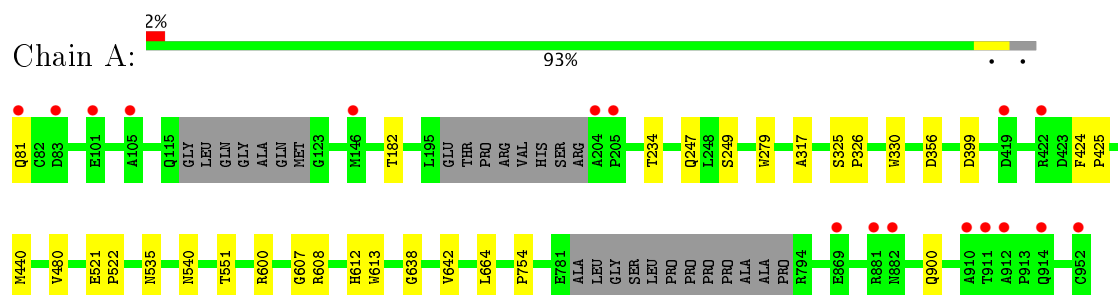
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	633	Total	O	0	0
			633	633		

### 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 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: Lysosomal alpha-glucosidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	96.63Å 102.19Å 128.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.52 – 2.00 47.47 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.3 (47.52-2.00) 99.4 (47.47-2.00)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.34 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.153 , 0.184 0.164 , 0.193	Depositor DCC
$R_{free}$ test set	4283 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	19.8	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 50.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7608	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 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: GOL, CSO, PGE, NAG, CL, EDO, MIG, BMA, FUC, 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	0.42	0/6875	0.62	0/9393

There are no bond length outliers.

There are no bond angle outliers.

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	6672	0	6451	16	0
2	A	126	0	110	0	0
3	A	20	0	20	0	0
4	A	11	0	10	0	0
5	A	14	0	17	0	0
6	A	25	0	0	0	0
7	A	3	0	0	0	0
8	A	52	0	78	1	0
9	A	34	0	46	6	0
10	A	18	0	24	0	0
11	A	633	0	0	4	0
All	All	7608	0	6756	19	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 1.

All (19) 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:664:LEU:HD13	1:A:754:PRO:HG3	1.88	0.55
1:A:182:THR:HG21	9:A:1035:PGE:H22	1.90	0.54
1:A:81:GLN:NE2	9:A:1036:PGE:O3	2.41	0.54
9:A:1037:PGE:H4	11:A:1524:HOH:O	2.12	0.49
1:A:521:GLU:N	1:A:522:PRO:HA	2.29	0.47
8:A:1024:EDO:H11	11:A:1326:HOH:O	2.15	0.46
1:A:608:ARG:NH1	11:A:1108:HOH:O	2.49	0.46
1:A:234:THR:HA	1:A:249:SER:O	2.16	0.45
1:A:325:SER:N	1:A:326:PRO:HA	2.32	0.45
1:A:247:GLN:HA	1:A:330:TRP:O	2.17	0.45
1:A:900:GLN:HE22	9:A:1038:PGE:H2	1.81	0.44
1:A:600:ARG:O	1:A:612:HIS:CE1	2.71	0.44
9:A:1037:PGE:H22	11:A:1292:HOH:O	2.16	0.44
1:A:182:THR:HG21	9:A:1035:PGE:C2	2.48	0.42
1:A:424:PHE:HB3	1:A:425:PRO:HD3	2.01	0.42
1:A:607:GLY:HA3	1:A:638:GLY:O	2.20	0.42
1:A:279:TRP:CE3	1:A:317:ALA:HB2	2.54	0.42
1:A:535:ASN:OD1	1:A:540:ASN:ND2	2.52	0.42
1:A:612:HIS:O	1:A:642:VAL:HA	2.20	0.41

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	840/872 (96%)	817 (97%)	22 (3%)	1 (0%)	55 52

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	480	VAL

### 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	725/741 (98%)	720 (99%)	5 (1%)	87 90

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	356	ASP
1	A	399	ASP
1	A	440	MET
1	A	551	THR
1	A	613	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

1 non-standard protein/DNA/RNA residue 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
1	CSO	A	938	1	4,6,7	0.57	0	1,6,8	1.68	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
1	CSO	A	938	1	-	0/1/5/7	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.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 41 ligands modelled in this entry, 3 are monoatomic - leaving 38 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
2	NAG	A	1001	1,3,2	14,14,15	0.44	0	15,19,21	1.01	1 (6%)
2	NAG	A	1002	2	14,14,15	0.57	0	15,19,21	0.95	2 (13%)
3	FUC	A	1003	2	9,10,11	0.60	0	13,14,16	0.65	0
2	NAG	A	1004	1,2	14,14,15	0.49	0	15,19,21	1.01	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	A	1005	2	14,14,15	0.56	0	15,19,21	0.94	0
2	NAG	A	1006	1,2	14,14,15	0.52	0	15,19,21	0.79	0
2	NAG	A	1007	2	14,14,15	0.62	0	15,19,21	1.04	1 (6%)
2	NAG	A	1008	1,2	14,14,15	0.54	0	15,19,21	1.04	2 (13%)
2	NAG	A	1009	2,4	14,14,15	0.47	0	15,19,21	0.81	0
4	BMA	A	1010	2	11,11,12	0.26	0	13,15,17	0.88	0
2	NAG	A	1011	1,3	14,14,15	0.62	0	15,19,21	1.03	0
3	FUC	A	1012	2	9,10,11	0.65	0	13,14,16	1.05	1 (7%)
5	MIG	A	1013	-	14,14,14	0.42	0	15,19,19	0.71	0
6	SO4	A	1014	-	4,4,4	0.42	0	6,6,6	0.31	0
6	SO4	A	1015	-	4,4,4	0.43	0	6,6,6	0.51	0
6	SO4	A	1016	-	4,4,4	0.40	0	6,6,6	0.18	0
6	SO4	A	1017	-	4,4,4	0.49	0	6,6,6	0.27	0
6	SO4	A	1018	-	4,4,4	0.44	0	6,6,6	0.16	0
8	EDO	A	1022	-	3,3,3	0.46	0	2,2,2	0.39	0
8	EDO	A	1023	-	3,3,3	0.53	0	2,2,2	0.21	0
8	EDO	A	1024	-	3,3,3	0.40	0	2,2,2	0.22	0
8	EDO	A	1025	-	3,3,3	0.57	0	2,2,2	0.10	0
8	EDO	A	1026	-	3,3,3	0.41	0	2,2,2	0.26	0
8	EDO	A	1027	-	3,3,3	0.44	0	2,2,2	0.42	0
8	EDO	A	1028	-	3,3,3	0.56	0	2,2,2	0.20	0
8	EDO	A	1029	-	3,3,3	0.45	0	2,2,2	0.37	0
8	EDO	A	1030	-	3,3,3	0.41	0	2,2,2	0.54	0
8	EDO	A	1031	-	3,3,3	0.51	0	2,2,2	0.27	0
8	EDO	A	1032	-	3,3,3	0.49	0	2,2,2	0.41	0
8	EDO	A	1033	-	3,3,3	0.42	0	2,2,2	0.49	0
8	EDO	A	1034	-	3,3,3	0.47	0	2,2,2	0.14	0
9	PGE	A	1035	-	6,6,9	0.47	0	5,5,8	0.42	0
9	PGE	A	1036	-	9,9,9	0.43	0	8,8,8	0.32	0
9	PGE	A	1037	-	6,6,9	0.49	0	5,5,8	0.36	0
9	PGE	A	1038	-	9,9,9	0.42	0	8,8,8	0.30	0
10	GOL	A	1039	-	5,5,5	0.29	0	5,5,5	0.31	0
10	GOL	A	1040	-	5,5,5	0.50	0	5,5,5	0.54	0
10	GOL	A	1041	-	5,5,5	0.45	0	5,5,5	0.25	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	NAG	A	1001	1,3,2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1002	2	-	0/6/23/26	0/1/1/1
3	FUC	A	1003	2	-	0/0/17/20	0/1/1/1
2	NAG	A	1004	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1005	2	-	0/6/23/26	0/1/1/1
2	NAG	A	1006	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1007	2	-	0/6/23/26	0/1/1/1
2	NAG	A	1008	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1009	2,4	-	0/6/23/26	0/1/1/1
4	BMA	A	1010	2	-	0/2/19/22	0/1/1/1
2	NAG	A	1011	1,3	-	0/6/23/26	0/1/1/1
3	FUC	A	1012	2	-	0/0/17/20	0/1/1/1
5	MIG	A	1013	-	-	0/5/25/25	0/1/1/1
6	SO4	A	1014	-	-	0/0/0/0	0/0/0/0
6	SO4	A	1015	-	-	0/0/0/0	0/0/0/0
6	SO4	A	1016	-	-	0/0/0/0	0/0/0/0
6	SO4	A	1017	-	-	0/0/0/0	0/0/0/0
6	SO4	A	1018	-	-	0/0/0/0	0/0/0/0
8	EDO	A	1022	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1023	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1024	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1025	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1026	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1027	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1028	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1029	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1030	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1031	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1032	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1033	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1034	-	-	0/1/1/1	0/0/0/0
9	PGE	A	1035	-	-	0/4/4/7	0/0/0/0
9	PGE	A	1036	-	-	0/7/7/7	0/0/0/0
9	PGE	A	1037	-	-	0/4/4/7	0/0/0/0
9	PGE	A	1038	-	-	0/7/7/7	0/0/0/0
10	GOL	A	1039	-	-	0/4/4/4	0/0/0/0
10	GOL	A	1040	-	-	0/4/4/4	0/0/0/0
10	GOL	A	1041	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	A	1002	NAG	O5-C1-C2	-2.08	108.57	111.47
2	A	1004	NAG	O4-C4-C3	-2.04	105.91	110.36
2	A	1008	NAG	O5-C1-C2	-2.02	108.66	111.47
2	A	1008	NAG	C1-O5-C5	2.02	114.94	112.17
2	A	1007	NAG	C4-C3-C2	2.16	114.19	111.02
3	A	1012	FUC	O5-C5-C4	2.20	113.25	109.62
2	A	1002	NAG	C4-C3-C2	2.31	114.40	111.02
2	A	1001	NAG	C1-O5-C5	2.52	115.64	112.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	1024	EDO	1	0
9	A	1035	PGE	2	0
9	A	1036	PGE	1	0
9	A	1037	PGE	2	0
9	A	1038	PGE	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [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, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	844/872 (96%)	-0.25	17 (2%) 65 65	11, 18, 36, 69	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	914	GLN	3.6
1	A	204	ALA	3.1
1	A	83	ASP	3.0
1	A	422	ARG	2.9
1	A	81	GLN	2.8
1	A	952	CYS	2.8
1	A	101	GLU	2.8
1	A	205	PRO	2.7
1	A	146	MET	2.5
1	A	912	ALA	2.3
1	A	911	THR	2.3
1	A	882	ASN	2.1
1	A	869	GLU	2.1
1	A	881	ARG	2.1
1	A	105	ALA	2.1
1	A	910	ALA	2.1
1	A	419	ASP	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	CSO	A	938	7/8	0.95	0.08	-	24,25,29,31	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
8	EDO	A	1029	4/4	0.85	0.26	15.26	41,41,42,47	0
8	EDO	A	1033	4/4	0.91	0.20	7.07	30,31,36,38	0
8	EDO	A	1030	4/4	0.94	0.30	6.66	31,37,42,43	0
9	PGE	A	1037	7/10	0.78	0.26	6.65	48,50,62,63	0
10	GOL	A	1041	6/6	0.81	0.21	6.38	32,36,39,39	0
2	NAG	A	1004	14/15	0.95	0.12	5.12	20,25,31,41	0
9	PGE	A	1035	7/10	0.81	0.19	5.07	35,40,42,43	0
8	EDO	A	1022	4/4	0.82	0.27	4.17	37,40,41,48	0
2	NAG	A	1011	14/15	0.78	0.24	3.30	36,49,54,63	0
8	EDO	A	1024	4/4	0.95	0.12	3.02	22,32,38,39	0
6	SO4	A	1018	5/5	0.96	0.26	2.84	51,57,64,65	0
10	GOL	A	1039	6/6	0.94	0.13	2.74	25,27,29,30	0
10	GOL	A	1040	6/6	0.92	0.16	2.68	27,33,34,34	0
2	NAG	A	1006	14/15	0.93	0.18	2.41	21,28,38,51	0
8	EDO	A	1023	4/4	0.84	0.14	2.31	38,38,40,41	0
9	PGE	A	1036	10/10	0.81	0.31	2.12	43,52,54,56	0
8	EDO	A	1028	4/4	0.85	0.18	1.95	42,43,44,44	0
8	EDO	A	1034	4/4	0.91	0.21	1.81	42,43,43,44	0
9	PGE	A	1038	10/10	0.93	0.15	1.62	36,40,47,51	0
5	MIG	A	1013	14/14	0.98	0.11	-0.21	11,13,18,22	0
2	NAG	A	1008	14/15	0.97	0.07	-0.89	16,22,26,26	0
6	SO4	A	1014	5/5	0.99	0.10	-	25,25,27,30	0
2	NAG	A	1005	14/15	0.65	0.31	-	51,59,70,72	0
3	FUC	A	1003	10/11	0.87	0.33	-	52,63,70,72	0
7	CL	A	1020	1/1	0.95	0.07	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
8	EDO	A	1026	4/4	0.89	0.11	-	36,38,38,43	0
7	CL	A	1021	1/1	0.99	0.18	-	41,41,41,41	0
2	NAG	A	1002	14/15	0.76	0.37	-	45,65,78,78	0
8	EDO	A	1025	4/4	0.92	0.11	-	30,34,34,40	0
2	NAG	A	1007	14/15	0.84	0.41	-	58,68,76,77	0
8	EDO	A	1027	4/4	0.95	0.29	-	24,33,33,35	0
7	CL	A	1019	1/1	0.88	0.10	-	58,58,58,58	0
4	BMA	A	1010	11/12	0.83	0.28	-	47,57,61,68	0
6	SO4	A	1017	5/5	0.94	0.16	-	43,44,50,52	0
2	NAG	A	1009	14/15	0.96	0.14	-	20,28,34,38	0
6	SO4	A	1015	5/5	0.97	0.14	-	22,25,31,32	0
3	FUC	A	1012	10/11	0.84	0.44	-	61,68,75,76	0
8	EDO	A	1031	4/4	0.85	0.16	-	41,45,48,57	0
6	SO4	A	1016	5/5	0.86	0.26	-	60,63,75,90	0
2	NAG	A	1001	14/15	0.93	0.24	-	27,32,48,55	0
8	EDO	A	1032	4/4	0.77	0.17	-	45,45,46,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.