



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:47 PM GMT

PDB ID : 3S5Y  
Title : Pharmacological Chaperoning in Human alpha-Galactosidase  
Authors : Guce, A.I.; Clark, N.E.; Garman, S.C.  
Deposited on : 2011-05-23  
Resolution : 2.10 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 (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

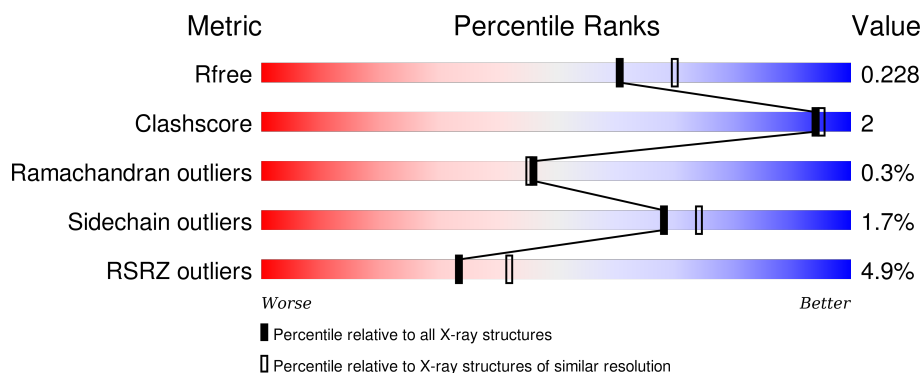
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	398	<div> <div>5%</div> <div>93%</div> <div>5%</div> </div>
1	B	398	<div> <div>5%</div> <div>90%</div> <div>8%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	ACY	B	842	-	-	-	X
2	NAG	A	639	-	-	-	X
2	XYP	A	645	X	-	-	X
3	XYP	A	698	X	-	-	-
6	2PE	B	810	-	-	-	X
6	2PE	B	811	-	-	-	X
6	2PE	B	812	-	-	-	X
6	2PE	B	815	-	-	-	X
7	NAG	B	639	-	-	-	X
8	XYP	B	698	X	-	-	-

## 2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 7134 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 Alpha-galactosidase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	4	0
			3141	1999	538	575	29			
1	B	391	Total	C	N	O	S	0	4	0
			3150	2004	540	577	29			

- Molecule 2 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	7	Total	C	N	O	0	0
			80	45	2	33		

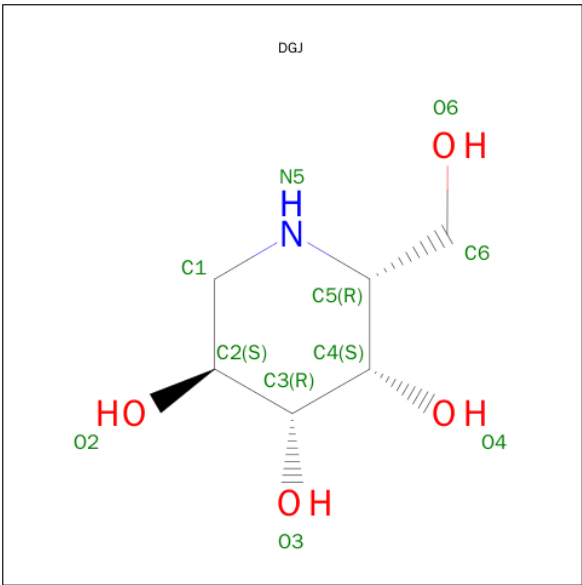
- Molecule 3 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	5	Total	C	N	O	0	0
			58	33	2	23		

- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

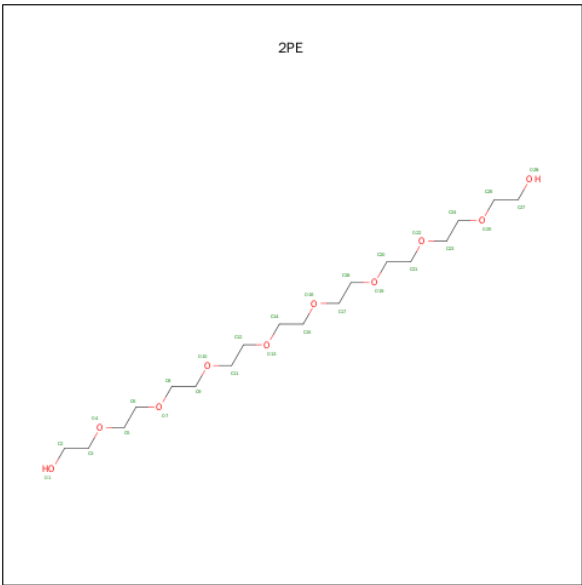
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 5 is (2R,3S,4R,5S)-2-(HYDROXYMETHYL)PIPERIDINE-3,4,5-TRIOL (three-letter code: DGJ) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>).



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

- Molecule 6 is NONAETHYLENE GLYCOL (three-letter code: 2PE) (formula: C<sub>18</sub>H<sub>38</sub>O<sub>10</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			10	6	4		
6	B	1	Total	C	O	0	0
			16	10	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			28	18	10		
6	B	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 7 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 8 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	5	Total	C	N	O	0	0
			59	33	2	24		

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

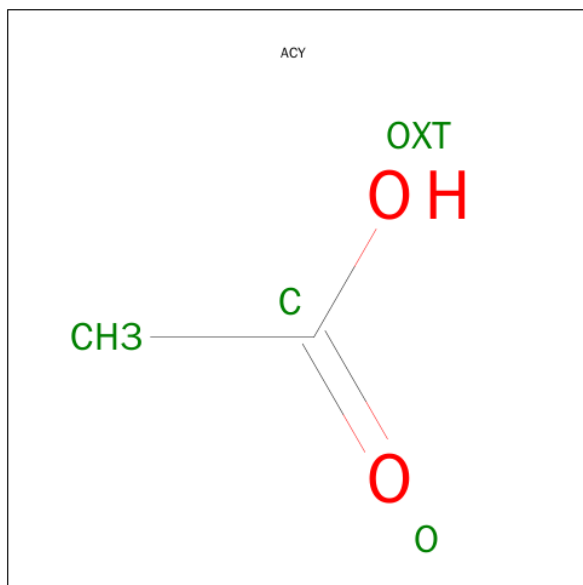
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	4	Total	C	N	O	0	0
			49	28	2	19		

- Molecule 10 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 11 is ACETIC ACID (three-letter code: ACY) (formula:  $C_2H_4O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	B	1	Total	C	O	0	0
			4	2	2		
11	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 12 is water.

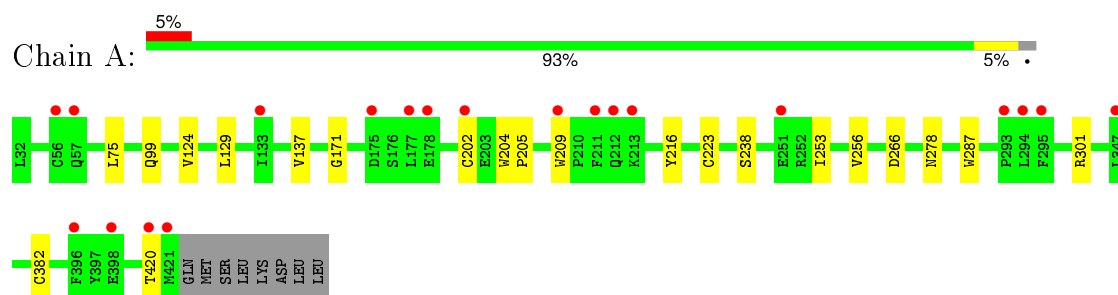
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	235	Total 235	O 235	0	0
12	B	205	Total 205	O 205	0	0



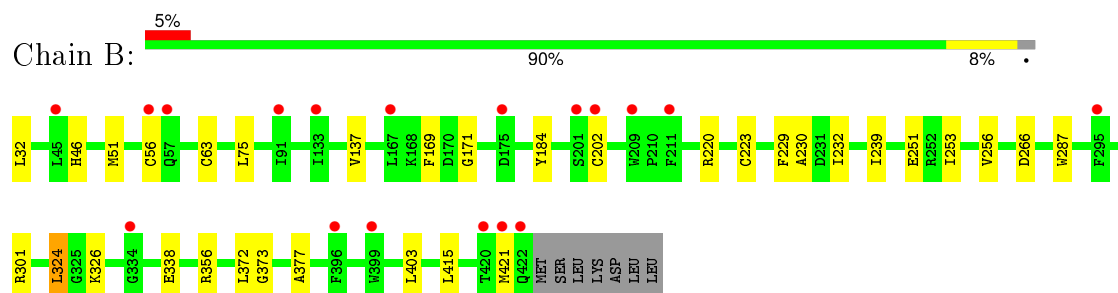
### 3 Residue-property plots [i](#)

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: Alpha-galactosidase A



#### • Molecule 1: Alpha-galactosidase A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	136.81Å 182.63Å 47.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.44 – 2.10 30.44 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.5 (30.44-2.10) 94.5 (30.44-2.10)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.98 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.194 , 0.230 0.191 , 0.228	Depositor DCC
$R_{free}$ test set	3360 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.8	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 46.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	3 of 66564 reflections (0.005%)	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7134	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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, 0.375 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: XYP, BMA, NAG, DGJ, EDO, 2PE, FUC, ACY, 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	0.36	0/3238	0.54	0/4396
1	B	0.37	0/3247	0.55	0/4408
All	All	0.36	0/6485	0.54	0/8804

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A	3	0
3	A	3	0
8	B	3	0
All	All	9	0

There are no bond length outliers.

There are no bond angle outliers.

All (9) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	645	XYP	C4B,C2B,C3B
3	A	698	XYP	C4B,C2B,C3B
8	B	698	XYP	C4B,C2B,C3B

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	3141	0	3004	9	0
1	B	3150	0	3012	15	0
2	A	80	0	67	0	0
3	A	58	0	49	0	0
4	A	38	0	34	0	0
5	A	11	0	13	0	0
5	B	11	0	13	0	0
6	A	10	0	13	0	0
6	B	61	0	81	2	0
7	B	14	0	13	0	0
8	B	59	0	49	0	0
9	B	49	0	43	0	0
10	B	4	0	6	0	0
11	B	8	0	6	0	0
12	A	235	0	0	2	0
12	B	205	0	0	0	0
All	All	7134	0	6403	24	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 (24) 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:B:403:LEU:HD21	1:B:415:LEU:CD1	2.31	0.61
1:B:75:LEU:HD11	1:B:301:ARG:HG2	1.83	0.61
1:B:338:GLU:OE2	1:B:356:ARG:NH1	2.39	0.56
1:B:137:VAL:HG12	1:B:171:GLY:HA2	1.93	0.51
1:A:278:ASN:ND2	12:A:1183:HOH:O	2.37	0.50
1:B:202[B]:CYS:SG	1:B:223:CYS:SG	3.03	0.48
1:A:253:ILE:O	1:A:256:VAL:HG12	2.13	0.48
1:A:216:TYR:HB3	1:A:256:VAL:HG21	1.96	0.47
1:B:229:PHE:HB3	6:B:812:2PE:H52	1.96	0.46
1:B:56[B]:CYS:HB3	1:B:63:CYS:SG	2.56	0.46
1:A:202[B]:CYS:SG	1:A:223:CYS:SG	3.08	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:TRP:HB3	1:A:205:PRO:HD3	1.98	0.45
1:B:184:TYR:CE1	1:B:202[B]:CYS:HB2	2.53	0.44
1:A:137:VAL:HG12	1:A:171:GLY:HA2	1.99	0.44
1:B:324:LEU:HD22	1:B:326:LYS:HG3	1.99	0.43
1:A:382:CYS:HA	1:A:420:THR:HG22	2.00	0.43
12:A:1414:HOH:O	1:B:51:MET:HE2	2.19	0.43
1:A:124:VAL:HG13	1:A:129:LEU:HB2	2.01	0.43
1:B:373:GLY:HA3	1:B:377:ALA:HB2	2.01	0.43
1:B:232:ILE:HD11	1:B:239:ILE:HD13	2.00	0.42
1:A:75:LEU:HD11	1:A:301:ARG:HG2	2.02	0.41
1:B:230:ALA:HB3	6:B:812:2PE:H32	2.04	0.40
1:B:253:ILE:O	1:B:256:VAL:HG22	2.20	0.40
1:B:32:LEU:N	1:B:220:ARG:O	2.55	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	392/398 (98%)	383 (98%)	8 (2%)	1 (0%)	46	45
1	B	393/398 (99%)	381 (97%)	11 (3%)	1 (0%)	46	45
All	All	785/796 (99%)	764 (97%)	19 (2%)	2 (0%)	46	45

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	ASP
1	B	266	ASP

### 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	335/339 (99%)	331 (99%)	4 (1%)	78	84
1	B	336/339 (99%)	329 (98%)	7 (2%)	61	66
All	All	671/678 (99%)	660 (98%)	11 (2%)	68	76

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

Mol	Chain	Res	Type
1	A	99	GLN
1	A	209	TRP
1	A	238	SER
1	A	287	TRP
1	B	46	HIS
1	B	169	PHE
1	B	251	GLU
1	B	287	TRP
1	B	324	LEU
1	B	372	LEU
1	B	421	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	228	ASN
1	A	330	GLN
1	A	379	ASN
1	B	179	ASN
1	B	221	GLN
1	B	228	ASN

### 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 ⓘ

24 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	NAG	A	639	1,2	14,14,15	0.58	0	15,19,21	0.73	0
2	NAG	A	640	2	14,14,15	0.55	0	15,19,21	1.08	1 (6%)
2	BMA	A	641	2	11,11,12	0.49	0	14,15,17	0.79	0
2	MAN	A	642	2	11,11,12	0.56	0	14,15,17	0.98	2 (14%)
2	MAN	A	643	2	11,11,12	0.53	0	14,15,17	1.43	2 (14%)
2	FUC	A	644	2	10,10,11	0.51	0	14,14,16	1.02	2 (14%)
2	XYP	A	645	2	9,9,10	1.25	1 (11%)	12,12,14	0.79	0
3	NAG	A	692	1,3	14,14,15	0.46	0	15,19,21	1.14	1 (6%)
3	NAG	A	693	3	14,14,15	0.48	0	15,19,21	0.79	0
3	BMA	A	694	3	11,11,12	0.40	0	14,15,17	1.20	2 (14%)
3	FUC	A	697	3	10,10,11	0.56	0	14,14,16	1.82	3 (21%)
3	XYP	A	698	3	9,9,10	1.34	1 (11%)	12,12,14	1.13	1 (8%)
4	NAG	A	715	1,4	14,14,15	0.55	0	15,19,21	0.66	0
4	NAG	A	716	4	14,14,15	0.49	0	15,19,21	0.75	0
4	FUC	A	720	4	10,10,11	0.55	0	14,14,16	0.86	1 (7%)
8	NAG	B	692	1,8	14,14,15	0.58	0	15,19,21	1.18	1 (6%)
8	NAG	B	693	8	14,14,15	0.50	0	15,19,21	1.10	1 (6%)
8	BMA	B	694	8	11,11,12	0.32	0	14,15,17	0.90	0
8	MAN	B	695	8	11,11,12	0.55	0	14,15,17	0.72	0
8	XYP	B	698	8	9,9,10	1.34	1 (11%)	12,12,14	0.80	0
9	NAG	B	715	9,1	14,14,15	0.51	0	15,19,21	0.63	0
9	NAG	B	716	9	14,14,15	0.50	0	15,19,21	0.76	0
9	BMA	B	717	9	11,11,12	0.30	0	14,15,17	0.63	0
9	FUC	B	720	9	10,10,11	0.53	0	14,14,16	0.95	1 (7%)

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	639	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	640	2	-	0/6/23/26	0/1/1/1
2	BMA	A	641	2	-	0/2/19/22	0/1/1/1
2	MAN	A	642	2	-	0/2/19/22	0/1/1/1
2	MAN	A	643	2	-	0/2/19/22	0/1/1/1
2	FUC	A	644	2	-	0/0/17/20	0/1/1/1
2	XYP	A	645	2	3/3/3/4	0/0/14/17	0/1/1/1
3	NAG	A	692	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	693	3	-	0/6/23/26	0/1/1/1
3	BMA	A	694	3	-	0/2/19/22	0/1/1/1
3	FUC	A	697	3	-	0/0/17/20	0/1/1/1
3	XYP	A	698	3	3/3/3/4	0/0/14/17	0/1/1/1
4	NAG	A	715	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	716	4	-	0/6/23/26	0/1/1/1
4	FUC	A	720	4	-	0/0/17/20	0/1/1/1
8	NAG	B	692	1,8	-	0/6/23/26	0/1/1/1
8	NAG	B	693	8	-	0/6/23/26	0/1/1/1
8	BMA	B	694	8	-	0/2/19/22	0/1/1/1
8	MAN	B	695	8	-	0/2/19/22	0/1/1/1
8	XYP	B	698	8	3/3/3/4	0/0/14/17	0/1/1/1
9	NAG	B	715	9,1	-	0/6/23/26	0/1/1/1
9	NAG	B	716	9	-	0/6/23/26	0/1/1/1
9	BMA	B	717	9	-	0/2/19/22	0/1/1/1
9	FUC	B	720	9	-	0/0/17/20	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	698	XYP	O5B-C5B	-3.65	1.35	1.42
3	A	698	XYP	O5B-C5B	-3.62	1.35	1.42
2	A	645	XYP	O5B-C5B	-3.36	1.36	1.42

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	694	BMA	O5-C1-C2	-2.39	106.98	110.86
2	A	642	MAN	C1-O5-C5	2.06	114.86	112.25
2	A	644	FUC	O5-C5-C6	2.08	109.56	106.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	697	FUC	O5-C5-C6	2.12	109.63	106.13
4	A	720	FUC	O5-C5-C6	2.23	109.81	106.13
9	B	720	FUC	C1-C2-C3	2.32	112.29	109.54
2	A	644	FUC	C1-O5-C5	2.35	116.00	112.38
3	A	694	BMA	C3-C4-C5	2.57	114.68	110.20
2	A	642	MAN	C1-C2-C3	2.68	112.71	109.54
8	B	693	NAG	C1-O5-C5	2.74	115.72	112.25
2	A	640	NAG	C4-C3-C2	2.75	115.50	111.23
3	A	698	XYP	C1B-C2B-C3B	3.18	113.30	109.54
2	A	643	MAN	C1-O5-C5	3.18	116.29	112.25
3	A	697	FUC	C1-O5-C5	3.28	117.44	112.38
3	A	692	NAG	C1-O5-C5	3.35	116.49	112.25
2	A	643	MAN	C1-C2-C3	3.57	113.76	109.54
8	B	692	NAG	C1-O5-C5	3.90	117.20	112.25
3	A	697	FUC	C1-C2-C3	5.20	115.70	109.54

All (9) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	645	XYP	C4B
2	A	645	XYP	C2B
2	A	645	XYP	C3B
3	A	698	XYP	C4B
3	A	698	XYP	C2B
3	A	698	XYP	C3B
8	B	698	XYP	C4B
8	B	698	XYP	C2B
8	B	698	XYP	C3B

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.6 Ligand geometry

11 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$
5	DGJ	A	801	-	11,11,11	0.84	1 (9%)	11,15,15	0.94	0
6	2PE	A	813	-	9,9,27	0.47	0	8,8,26	0.17	0
7	NAG	B	639	1	14,14,15	0.51	0	15,19,21	0.60	0
5	DGJ	B	802	-	11,11,11	0.73	0	11,15,15	0.65	0
6	2PE	B	810	-	15,15,27	0.48	0	14,14,26	0.24	0
6	2PE	B	811	-	27,27,27	0.50	0	26,26,26	0.18	0
6	2PE	B	812	-	6,6,27	0.55	0	5,5,26	0.22	0
10	EDO	B	814	-	3,3,3	0.45	0	2,2,2	0.35	0
6	2PE	B	815	-	9,9,27	0.49	0	8,8,26	0.25	0
11	ACY	B	842	-	1,3,3	1.53	0	0,3,3	0.00	-
11	ACY	B	843	-	1,3,3	1.44	0	0,3,3	0.00	-

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	DGJ	A	801	-	-	0/2/19/19	0/1/1/1
6	2PE	A	813	-	-	0/7/7/25	0/0/0/0
7	NAG	B	639	1	-	0/6/23/26	0/1/1/1
5	DGJ	B	802	-	-	0/2/19/19	0/1/1/1
6	2PE	B	810	-	-	0/13/13/25	0/0/0/0
6	2PE	B	811	-	-	0/25/25/25	0/0/0/0
6	2PE	B	812	-	-	0/4/4/25	0/0/0/0
10	EDO	B	814	-	-	0/1/1/1	0/0/0/0
6	2PE	B	815	-	-	0/7/7/25	0/0/0/0
11	ACY	B	842	-	-	0/0/0/0	0/0/0/0
11	ACY	B	843	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	801	DGJ	C5-N5	-2.19	1.45	1.47

There are no bond angle outliers.

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
6	B	812	2PE	2	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 ⓘ

### 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, 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	390/398 (97%)	0.17	20 (5%) 32 40	18, 33, 59, 101	0
1	B	391/398 (98%)	0.20	18 (4%) 36 45	18, 30, 59, 120	0
All	All	781/796 (98%)	0.19	38 (4%) 33 42	18, 31, 59, 120	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	421	MET	8.7
1	A	420	THR	7.2
1	B	422	GLN	7.0
1	A	421	MET	6.3
1	B	175	ASP	5.6
1	B	420	THR	4.5
1	A	56[A]	CYS	4.3
1	B	396	PHE	4.1
1	B	57	GLN	3.9
1	B	399	TRP	3.5
1	A	177	LEU	3.4
1	A	209	TRP	3.3
1	A	175	ASP	3.2
1	A	57	GLN	2.9
1	B	202[A]	CYS	2.8
1	A	211	PHE	2.7
1	B	45	LEU	2.7
1	B	209	TRP	2.7
1	A	251	GLU	2.7
1	A	293	PRO	2.6
1	A	178	GLU	2.6
1	B	211	PHE	2.5
1	A	212	GLN	2.5
1	A	347	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	133	ILE	2.4
1	B	295	PHE	2.4
1	A	398	GLU	2.4
1	A	294	LEU	2.3
1	A	295	PHE	2.3
1	B	201	SER	2.3
1	B	167	LEU	2.3
1	A	133	ILE	2.1
1	A	396	PHE	2.1
1	A	202[A]	CYS	2.1
1	B	91	ILE	2.1
1	A	213	LYS	2.1
1	B	334	GLY	2.1
1	B	56[A]	CYS	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, 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(Å <sup>2</sup> )	Q<0.9
2	XYP	A	645	9/10	0.46	0.40	16.29	97,105,109,111	0
2	NAG	A	639	14/15	0.82	0.35	2.25	72,80,91,93	0
8	NAG	B	692	14/15	0.94	0.14	1.12	32,43,49,56	0
3	NAG	A	692	14/15	0.94	0.12	0.38	31,41,57,65	0
9	NAG	B	715	14/15	0.92	0.12	0.23	37,44,52,60	0
3	BMA	A	694	11/12	0.72	0.32	-	83,88,96,98	0
4	NAG	A	716	14/15	0.90	0.36	-	95,99,104,106	0
3	NAG	A	693	14/15	0.90	0.23	-	46,64,71,72	0
9	BMA	B	717	11/12	0.76	0.34	-	104,110,112,112	0
9	NAG	B	716	14/15	0.91	0.26	-	44,68,85,95	0
8	NAG	B	693	14/15	0.92	0.20	-	54,64,74,77	0
4	FUC	A	720	10/11	0.89	0.42	-	91,93,94,95	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
8	MAN	B	695	11/12	0.88	0.20	-	70,78,80,81	0
3	XYP	A	698	9/10	0.81	0.29	-	79,84,85,88	0
2	MAN	A	642	11/12	0.50	0.41	-	112,116,118,119	0
4	NAG	A	715	14/15	0.90	0.29	-	69,80,88,93	0
3	FUC	A	697	10/11	0.72	0.44	-	80,87,92,92	0
9	FUC	B	720	10/11	0.92	0.24	-	51,60,65,70	0
8	XYP	B	698	9/10	0.86	0.26	-	79,82,84,85	0
2	FUC	A	644	10/11	0.83	0.50	-	94,96,98,99	0
8	BMA	B	694	11/12	0.86	0.23	-	75,81,86,91	0
2	BMA	A	641	11/12	0.70	0.33	-	99,105,108,111	0
2	MAN	A	643	11/12	0.71	0.32	-	89,96,98,101	0
2	NAG	A	640	14/15	0.64	0.47	-	97,103,105,106	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, 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
11	ACY	B	842	4/4	0.56	0.45	14.61	67,72,73,73	0
6	2PE	B	815	10/28	0.59	0.36	11.04	77,87,96,97	0
6	2PE	B	810	16/28	0.79	0.30	9.22	59,78,97,97	0
6	2PE	B	811	28/28	0.81	0.27	9.06	58,72,95,95	0
6	2PE	B	812	7/28	0.64	0.21	3.24	50,53,57,59	0
7	NAG	B	639	14/15	0.60	0.49	2.38	85,96,101,101	0
5	DGJ	A	801	11/11	0.97	0.14	0.38	24,27,30,31	0
6	2PE	A	813	10/28	0.83	0.17	0.17	65,75,76,77	0
5	DGJ	B	802	11/11	0.96	0.14	0.06	18,21,23,24	0
11	ACY	B	843	4/4	0.75	0.32	-	71,72,73,74	0
10	EDO	B	814	4/4	0.83	0.20	-	60,64,68,72	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.