



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2021 – 11:31 PM EDT

PDB ID : 1QWU  
Title : Golgi alpha-mannosidase II D341N mutant complex with 5-F-guloside  
Authors : Numao, S.; Kuntz, D.A.; Withers, S.G.; Rose, D.R.  
Deposited on : 2003-09-03  
Resolution : 2.03 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.2

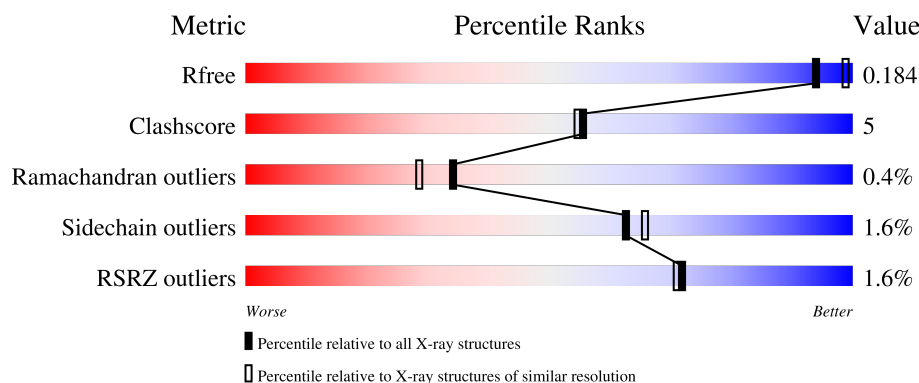
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


The reported resolution of this entry is 2.03 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))
$R_{free}$	130704	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	1045	

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
2	NAG	A	2001	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	MPD	A	2002	X	-	-	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9241 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-mannosidase II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1014	Total	C	N	O	S	0	0	0
			8181	5202	1435	1505	39			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ARG	-	cloning artifact	UNP Q24451
A	2	SER	-	cloning artifact	UNP Q24451
A	3	SER	-	cloning artifact	UNP Q24451
A	4	HIS	-	expression tag	UNP Q24451
A	5	HIS	-	expression tag	UNP Q24451
A	6	HIS	-	expression tag	UNP Q24451
A	7	HIS	-	expression tag	UNP Q24451
A	8	HIS	-	expression tag	UNP Q24451
A	9	HIS	-	expression tag	UNP Q24451
A	10	GLY	-	cloning artifact	UNP Q24451
A	11	GLU	-	cloning artifact	UNP Q24451
A	12	PHE	-	cloning artifact	UNP Q24451
A	341	ASN	ASP	engineered mutation	UNP Q24451
A	907	LYS	GLU	SEE REMARK 999	UNP Q24451

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).

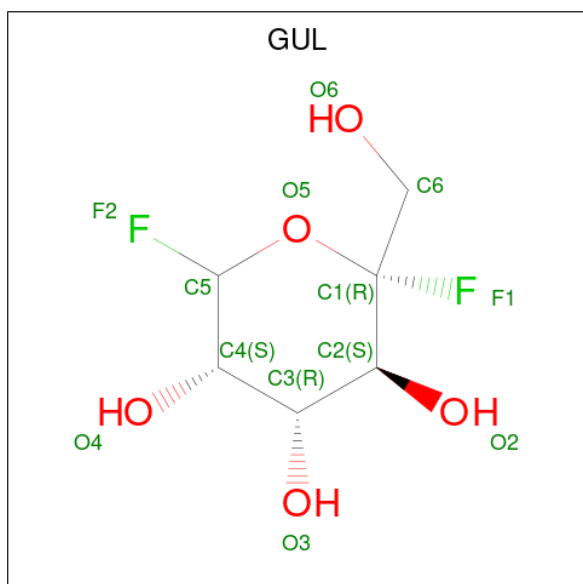


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

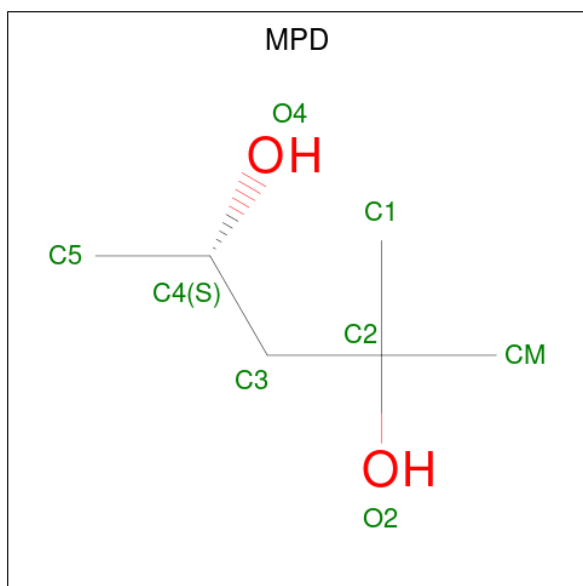
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is (2R,3S,4R,5S)-2,6-difluoro-2-(hydroxymethyl)oxane-3,4,5-triol (three-letter code: GUL) (formula: C<sub>6</sub>H<sub>10</sub>F<sub>2</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	F	O	0	0
			12	6	1	5		

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula:  $C_6H_{14}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			8	6	2		

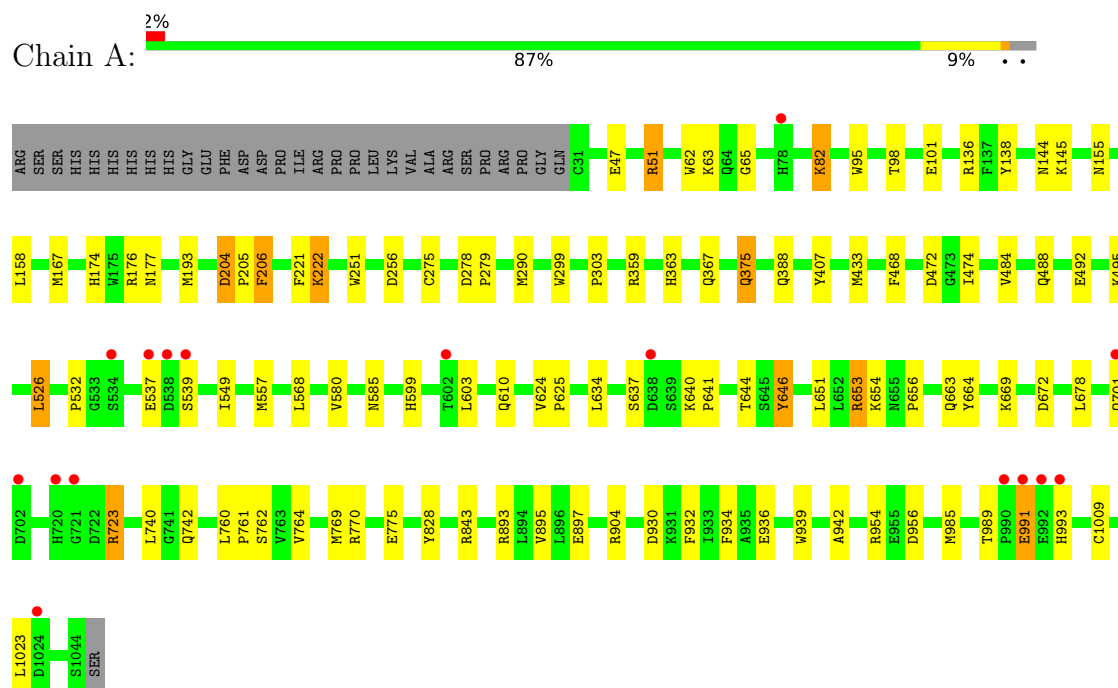
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1025	Total	O	0	0
			1025	1025		

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

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Alpha-mannosidase II



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.85Å 109.80Å 138.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.84 – 2.03 19.84 – 2.03	Depositor EDS
% Data completeness (in resolution range)	96.6 (19.84-2.03) 96.7 (19.84-2.03)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.61 (at 2.02Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.151 , 0.189 0.146 , 0.184	Depositor DCC
$R_{free}$ test set	2385 reflections (3.48%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.5	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 57.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	9241	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% 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: ZN, NAG, MPD, GUL

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	0.67	0/8406	0.77	2/11416 (0.0%)

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
1	A	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	167	MET	N-CA-C	-5.73	95.52	111.00
1	A	764	VAL	N-CA-C	-5.01	97.48	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	407	TYR	Sidechain
1	A	646	TYR	Sidechain

### 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	8181	0	7973	80	0
2	A	14	0	13	0	0
3	A	1	0	0	0	0
4	A	12	0	4	1	0
5	A	8	0	14	4	0
6	A	1025	0	0	20	1
All	All	9241	0	8004	82	1

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 5.

All (82) 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:897:GLU:HB2	6:A:3023:HOH:O	1.57	1.02
1:A:47:GLU:OE2	1:A:51:ARG:HD3	1.79	0.82
1:A:256:ASP:HB2	6:A:3012:HOH:O	1.79	0.81
1:A:989:THR:HG22	1:A:991:GLU:HG3	1.63	0.81
1:A:678:LEU:HD12	1:A:769:MET:HE1	1.69	0.74
1:A:568:LEU:HD12	1:A:770:ARG:HD3	1.69	0.74
1:A:82:LYS:HE3	1:A:375:GLN:CD	2.10	0.71
1:A:82:LYS:HE3	1:A:375:GLN:OE1	1.90	0.71
5:A:2002:MPD:H11	6:A:2843:HOH:O	1.89	0.71
1:A:82:LYS:HE3	1:A:375:GLN:NE2	2.10	0.67
1:A:222:LYS:HE3	6:A:2821:HOH:O	1.97	0.63
1:A:897:GLU:CB	6:A:3023:HOH:O	2.29	0.63
1:A:742:GLN:HG3	6:A:2683:HOH:O	2.00	0.62
1:A:144:ASN:HB3	6:A:2554:HOH:O	1.99	0.62
1:A:723:ARG:HG2	1:A:723:ARG:HH11	1.64	0.61
1:A:989:THR:CG2	1:A:991:GLU:HG3	2.31	0.61
1:A:484:VAL:O	1:A:488:GLN:HG3	2.03	0.59
1:A:155:ASN:HB3	6:A:2364:HOH:O	2.04	0.57
1:A:641:PRO:HG2	1:A:644:THR:HB	1.87	0.57
1:A:290:MET:CG	1:A:303:PRO:HG2	2.35	0.57
1:A:637:SER:HB2	6:A:2526:HOH:O	2.03	0.57
1:A:599:HIS:HD2	1:A:610:GLN:CG	2.18	0.57
1:A:580:VAL:HG22	1:A:634:LEU:HD22	1.88	0.56
1:A:954:ARG:NH1	1:A:956:ASP:OD2	2.39	0.56
1:A:537:GLU:HG2	1:A:539:SER:HB3	1.87	0.55
1:A:603:LEU:N	1:A:603:LEU:HD22	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1009:CYS:SG	1:A:1023:LEU:HD12	2.47	0.55
1:A:599:HIS:HD2	1:A:610:GLN:HG3	1.72	0.54
1:A:654:LYS:HE3	1:A:672:ASP:OD1	2.09	0.53
1:A:678:LEU:HD12	1:A:769:MET:CE	2.38	0.53
5:A:2002:MPD:H13	6:A:2695:HOH:O	2.07	0.53
1:A:177:ASN:HD21	1:A:433:MET:HB2	1.74	0.52
1:A:468:PHE:CZ	1:A:474:ILE:HA	2.44	0.52
1:A:895:VAL:HG12	1:A:897:GLU:CG	2.38	0.52
1:A:895:VAL:HG12	1:A:897:GLU:HG3	1.91	0.52
1:A:290:MET:HG2	1:A:303:PRO:HG2	1.92	0.52
1:A:723:ARG:HG2	1:A:723:ARG:NH1	2.23	0.52
1:A:136:ARG:HD3	6:A:2902:HOH:O	2.09	0.52
1:A:761:PRO:O	1:A:762:SER:HB2	2.09	0.51
1:A:204:ASP:H	1:A:205:PRO:HD3	1.76	0.51
1:A:770:ARG:NH1	6:A:2976:HOH:O	2.43	0.50
1:A:843:ARG:HB3	6:A:3023:HOH:O	2.12	0.50
1:A:651:LEU:CD1	1:A:653:ARG:HG2	2.42	0.50
1:A:206:PHE:CD1	1:A:206:PHE:N	2.78	0.49
1:A:651:LEU:HD13	1:A:653:ARG:HG2	1.93	0.49
1:A:98:THR:OG1	1:A:101:GLU:HG3	2.14	0.47
1:A:904:ARG:HG2	1:A:985:MET:SD	2.55	0.47
1:A:290:MET:HG3	1:A:303:PRO:HG2	1.95	0.47
1:A:740:LEU:HD22	1:A:760:LEU:HD22	1.98	0.46
1:A:62:TRP:CD2	1:A:65:GLY:HA3	2.50	0.46
1:A:936:GLU:HA	6:A:3019:HOH:O	2.16	0.46
1:A:363:HIS:O	1:A:367:GLN:HG2	2.15	0.46
1:A:174:HIS:CE1	1:A:176:ARG:HD3	2.51	0.45
1:A:155:ASN:ND2	6:A:3009:HOH:O	2.50	0.45
1:A:557:MET:HA	1:A:930:ASP:O	2.17	0.44
1:A:82:LYS:NZ	6:A:2930:HOH:O	2.51	0.44
1:A:678:LEU:CD1	1:A:769:MET:CE	2.96	0.43
1:A:472:ASP:OD2	4:A:2003:GUL:O3	2.36	0.43
1:A:63:LYS:CB	5:A:2002:MPD:H12	2.48	0.43
1:A:897:GLU:CG	6:A:3023:HOH:O	2.61	0.43
1:A:145:LYS:HE3	6:A:3002:HOH:O	2.18	0.43
1:A:204:ASP:N	1:A:205:PRO:CD	2.81	0.43
1:A:939:TRP:CD2	1:A:942:ALA:HB2	2.54	0.42
1:A:640:LYS:HD2	1:A:646:TYR:CE1	2.55	0.42
1:A:701:GLN:CA	1:A:701:GLN:HE21	2.33	0.42
1:A:279:PRO:HB2	1:A:299:TRP:CZ2	2.54	0.42
1:A:138:TYR:CE1	1:A:193:MET:HE3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:ASP:HA	1:A:279:PRO:HD2	1.95	0.41
1:A:653:ARG:HD2	1:A:656:PRO:HA	2.02	0.41
1:A:388:GLN:HG2	6:A:2548:HOH:O	2.20	0.41
1:A:603:LEU:N	1:A:603:LEU:CD2	2.83	0.41
1:A:663:GLN:O	1:A:664:TYR:C	2.59	0.41
1:A:624:VAL:HA	1:A:625:PRO:HD3	1.93	0.41
1:A:251:TRP:CD1	1:A:251:TRP:C	2.93	0.41
1:A:526:LEU:HD13	1:A:932:PHE:CE2	2.56	0.41
1:A:934:PHE:CE2	1:A:936:GLU:HB2	2.56	0.41
1:A:532:PRO:HB2	1:A:537:GLU:HB3	2.04	0.40
1:A:359:ARG:NE	6:A:2571:HOH:O	2.54	0.40
1:A:221:PHE:O	1:A:222:LYS:HD2	2.22	0.40
1:A:492:GLU:OE1	1:A:495:LYS:NZ	2.44	0.40
1:A:775:GLU:HA	1:A:893:ARG:HD2	2.03	0.40
1:A:63:LYS:HB3	5:A:2002:MPD:H12	2.03	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:2682:HOH:O	6:A:3021:HOH:O[2_565]	2.10	0.10

## 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	1012/1045 (97%)	980 (97%)	28 (3%)	4 (0%)	34 28

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	991	GLU

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Mol	Chain	Res	Type
1	A	95	TRP
1	A	993	HIS
1	A	204	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	901/929 (97%)	887 (98%)	14 (2%)	62	66

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	ARG
1	A	82	LYS
1	A	158	LEU
1	A	206	PHE
1	A	222	LYS
1	A	275	CYS
1	A	375	GLN
1	A	526	LEU
1	A	549	ILE
1	A	585	ASN
1	A	653	ARG
1	A	669	LYS
1	A	723	ARG
1	A	828	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	HIS
1	A	253	ASN
1	A	373	GLN
1	A	599	HIS

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Mol	Chain	Res	Type
1	A	701	GLN

### 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 ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 1 is 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	$\# Z  > 2$
4	GUL	A	2003	1,3	9,12,13	5.55	7 (77%)	14,18,20	5.06	11 (78%)
5	MPD	A	2002	-	7,7,7	0.68	0	9,10,10	0.30	0
2	NAG	A	2001	1	14,14,15	0.75	0	17,19,21	0.70	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
4	GUL	A	2003	1,3	-	1/2/23/26	0/1/1/1
5	MPD	A	2002	-	1/1/2/2	2/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	2001	1	1/1/5/7	2/6/23/26	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	2003	GUL	O5-C1	8.43	1.54	1.37
4	A	2003	GUL	O6-C6	-8.42	1.14	1.42
4	A	2003	GUL	O2-C2	-6.43	1.29	1.42
4	A	2003	GUL	C3-C2	5.97	1.63	1.53
4	A	2003	GUL	O4-C4	-5.31	1.32	1.43
4	A	2003	GUL	C4-C3	4.03	1.58	1.52
4	A	2003	GUL	C5-C4	3.59	1.60	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2003	GUL	C4-C3-C2	12.97	125.00	110.48
4	A	2003	GUL	O2-C2-C3	8.13	128.06	110.03
4	A	2003	GUL	C5-C4-C3	-5.64	102.73	109.67
4	A	2003	GUL	O5-C1-C2	4.75	115.74	110.17
4	A	2003	GUL	O6-C6-C1	4.02	125.14	111.66
4	A	2003	GUL	C5-O5-C1	3.47	120.31	113.73
4	A	2003	GUL	C6-C1-C2	3.20	117.99	112.02
4	A	2003	GUL	F1-C1-C2	2.86	114.00	108.59
4	A	2003	GUL	O4-C4-C3	2.75	115.64	110.14
4	A	2003	GUL	O2-C2-C1	-2.70	104.77	110.14
4	A	2003	GUL	O4-C4-C5	2.33	113.92	109.15

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	2001	NAG	C1
5	A	2002	MPD	C4

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2001	NAG	C8-C7-N2-C2
2	A	2001	NAG	O7-C7-N2-C2
4	A	2003	GUL	O5-C1-C6-O6
5	A	2002	MPD	C2-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
5	A	2002	MPD	C2-C3-C4-C5

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2003	GUL	1	0
5	A	2002	MPD	4	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	1014/1045 (97%)	-0.41	16 (1%) 72 71	5, 14, 29, 59	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	993	HIS	5.2
1	A	991	GLU	4.1
1	A	702	ASP	4.1
1	A	701	GLN	3.5
1	A	992	GLU	3.5
1	A	78	HIS	3.2
1	A	720	HIS	3.2
1	A	602	THR	3.0
1	A	539	SER	3.0
1	A	721	GLY	2.8
1	A	638	ASP	2.7
1	A	537	GLU	2.7
1	A	538	ASP	2.5
1	A	990	PRO	2.4
1	A	534	SER	2.2
1	A	1024	ASP	2.2

### 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](#)

There are no monosaccharides 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	A	2001	14/15	0.77	0.35	39,43,47,49	0
5	MPD	A	2002	8/8	0.96	0.10	18,21,23,24	0
4	GUL	A	2003	12/13	0.99	0.06	7,10,11,12	0
3	ZN	A	2004	1/1	1.00	0.02	13,13,13,13	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.