



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 11:55 PM BST

PDB ID : 1NOU  
Title : Native human lysosomal beta-hexosaminidase isoform B  
Authors : Mark, B.L.; Mahuran, D.J.; Cherney, M.M.; Zhao, D.; Knapp, S.; James, M.N.G.  
Deposited on : 2003-01-16  
Resolution : 2.40 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 : 2.13.1  
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) : 2.13.1

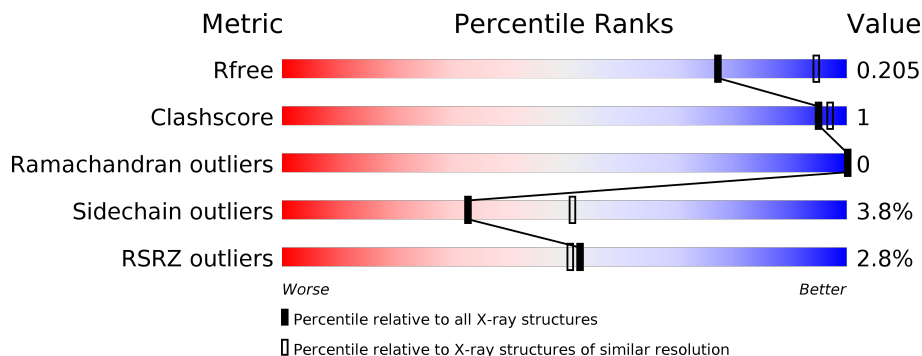
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 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	507	 3% 86% 7% • 5%
1	B	507	 3% 86% 8% • 5%
2	C	2	 50% 50%
2	D	2	 50% 50%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8061 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called beta-hexosaminidase beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	480	3878	2506	643	716	13	0	0	0
1	B	480	3878	2506	643	716	13	0	0	0

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	2	28	16	2	10	0	0	0
2	D	2	28	16	2	10	0	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

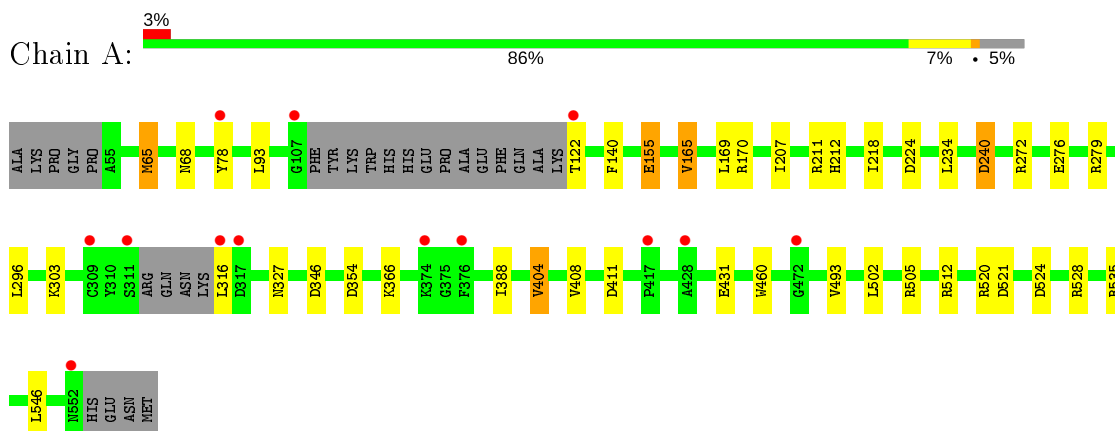
- Molecule 5 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	A	109	Total 109	O 109	0	0
5	B	117	Total 117	O 117	0	0

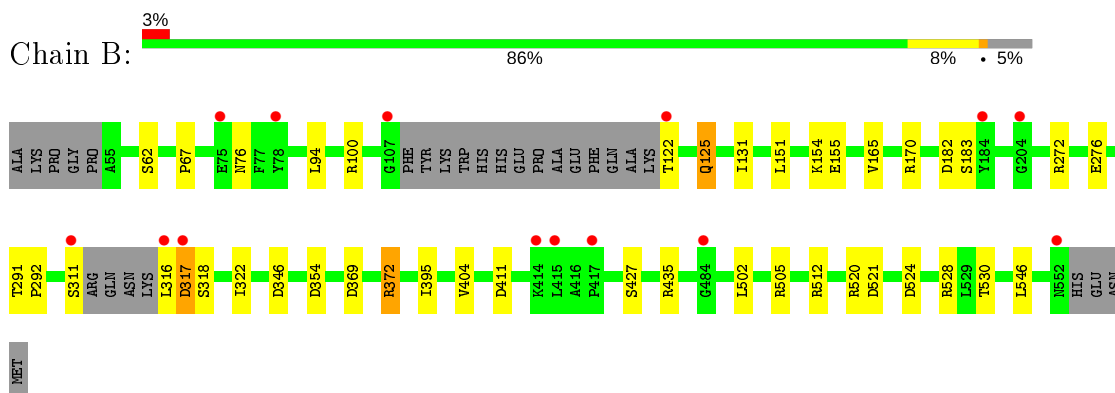
### 3 Residue-property plots [i](#)

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: beta-hexosaminidase beta chain



- Molecule 1: beta-hexosaminidase beta chain



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	112.47Å 112.47Å 397.87Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.71 – 2.40 34.80 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.71-2.40) 99.5 (34.80-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.31 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.0	Depositor
R, $R_{free}$	0.201 , 0.231 0.204 , 0.205	Depositor DCC
$R_{free}$ test set	2951 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.4	Xtrriage
Anisotropy	0.692	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 39.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8061	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.77% 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 i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NAG, 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	0.53	0/3988	0.92	16/5423 (0.3%)
1	B	0.52	0/3988	0.93	18/5423 (0.3%)
All	All	0.52	0/7976	0.93	34/10846 (0.3%)

There are no bond length outliers.

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	505	ARG	NE-CZ-NH2	-8.92	115.84	120.30
1	B	354	ASP	CB-CG-OD2	8.62	126.06	118.30
1	A	505	ARG	NE-CZ-NH2	-8.06	116.27	120.30
1	B	505	ARG	NE-CZ-NH1	7.83	124.22	120.30
1	A	354	ASP	CB-CG-OD2	7.81	125.33	118.30
1	A	346	ASP	CB-CG-OD2	7.70	125.23	118.30
1	A	505	ARG	NE-CZ-NH1	7.36	123.98	120.30
1	A	520	ARG	NE-CZ-NH1	7.02	123.81	120.30
1	B	372	ARG	NE-CZ-NH1	6.73	123.67	120.30
1	A	411	ASP	CB-CG-OD2	6.66	124.29	118.30
1	A	521	ASP	CB-CG-OD2	6.63	124.27	118.30
1	A	240	ASP	CB-CG-OD2	6.57	124.21	118.30
1	B	411	ASP	CB-CG-OD2	6.48	124.14	118.30
1	B	346	ASP	CB-CG-OD2	6.12	123.81	118.30
1	A	224	ASP	CB-CG-OD2	6.08	123.77	118.30
1	B	170	ARG	NE-CZ-NH1	6.01	123.31	120.30
1	A	535	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	A	512	ARG	NE-CZ-NH1	5.91	123.26	120.30
1	A	170	ARG	NE-CZ-NH1	5.86	123.23	120.30
1	B	524	ASP	CB-CG-OD2	5.85	123.56	118.30
1	A	524	ASP	CB-CG-OD2	5.82	123.54	118.30
1	B	520	ARG	NE-CZ-NH1	5.82	123.21	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	272	ARG	NE-CZ-NH1	5.75	123.17	120.30
1	A	272	ARG	NE-CZ-NH1	5.75	123.17	120.30
1	B	100	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	B	512	ARG	NE-CZ-NH1	5.55	123.07	120.30
1	B	528	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	B	317	ASP	CB-CG-OD2	5.42	123.18	118.30
1	A	528	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	B	435	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	B	521	ASP	CB-CG-OD2	5.23	123.01	118.30
1	B	369	ASP	CB-CG-OD2	5.21	122.98	118.30
1	A	520	ARG	NE-CZ-NH2	-5.09	117.76	120.30
1	B	182	ASP	CB-CG-OD1	5.08	122.87	118.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3878	0	3786	9	0
1	B	3878	0	3786	9	0
2	C	28	0	25	1	0
2	D	28	0	25	0	0
3	A	12	0	16	0	0
3	B	6	0	8	0	0
4	B	5	0	0	1	0
5	A	109	0	0	0	0
5	B	117	0	0	0	0
All	All	8061	0	7646	18	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 (18) 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:122:THR:N	1:A:155:GLU:OE1	2.22	0.72
1:B:311:SER:HG	1:B:316:LEU:N	1.99	0.60
1:B:122:THR:N	1:B:155:GLU:OE2	2.39	0.55
1:A:140:PHE:CE1	1:A:279:ARG:HD3	2.45	0.51
1:B:372:ARG:NH2	4:B:557:SO4:O3	2.44	0.50
1:B:94:LEU:HD11	1:B:131:ILE:CD1	2.43	0.49
1:A:207:ILE:HG12	1:A:234:LEU:HD11	1.96	0.47
1:B:311:SER:OG	1:B:316:LEU:N	2.50	0.45
1:A:93:LEU:HD22	1:A:165:VAL:HG13	1.98	0.45
1:B:291:THR:HB	1:B:292:PRO:HA	1.99	0.44
1:B:291:THR:HB	1:B:322:ILE:HD12	2.00	0.44
1:B:76:ASN:ND2	1:B:125:GLN:HE22	2.17	0.43
1:A:404:VAL:HG13	1:A:408:VAL:HB	2.02	0.42
1:A:460:TRP:CD1	1:A:546:LEU:HD22	2.55	0.42
1:A:93:LEU:HD21	1:A:169:LEU:HD11	2.03	0.41
1:B:530:THR:HG22	1:B:546:LEU:HD12	2.02	0.41
1:A:65:MET:HE2	2:C:1:NAG:H82	2.02	0.41
1:A:212:HIS:ND1	1:A:493:VAL:O	2.51	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	474/507 (94%)	463 (98%)	11 (2%)	0	100	100
1	B	474/507 (94%)	466 (98%)	8 (2%)	0	100	100
All	All	948/1014 (94%)	929 (98%)	19 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	426/449 (95%)	408 (96%)	18 (4%)	30	47
1	B	426/449 (95%)	412 (97%)	14 (3%)	38	57
All	All	852/898 (95%)	820 (96%)	32 (4%)	33	51

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	MET
1	A	68	ASN
1	A	78	TYR
1	A	155	GLU
1	A	165	VAL
1	A	211	ARG
1	A	218	ILE
1	A	240	ASP
1	A	276	GLU
1	A	296	LEU
1	A	303	LYS
1	A	316	LEU
1	A	327	ASN
1	A	366	LYS
1	A	388	ILE
1	A	404	VAL
1	A	431	GLU
1	A	502	LEU
1	B	62	SER
1	B	67	PRO
1	B	125	GLN
1	B	151	LEU
1	B	154	LYS
1	B	165	VAL
1	B	183	SER
1	B	276	GLU
1	B	317	ASP

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Mol	Chain	Res	Type
1	B	318	SER
1	B	395	ILE
1	B	404	VAL
1	B	427	SER
1	B	502	LEU

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

Mol	Chain	Res	Type
1	A	123	GLN
1	A	327	ASN
1	B	123	GLN
1	B	125	GLN
1	B	327	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

4 monosaccharides 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	C	1	1,2	14,14,15	0.76	0	17,19,21	1.26	3 (17%)
2	NAG	C	2	2	14,14,15	0.99	1 (7%)	17,19,21	0.66	0
2	NAG	D	1	1,2	14,14,15	0.55	0	17,19,21	1.05	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	D	2	2	14,14,15	0.95	1 (7%)	17,19,21	0.66	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	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	5/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	1/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	NAG	O5-C1	-2.22	1.40	1.43
2	D	2	NAG	C2-N2	2.04	1.49	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	NAG	C4-C3-C2	-2.30	107.64	111.02
2	C	1	NAG	O5-C1-C2	-2.20	107.81	111.29
2	C	1	NAG	O7-C7-C8	-2.18	118.00	122.06

There are no chirality outliers.

All (8) torsion outliers are listed below:

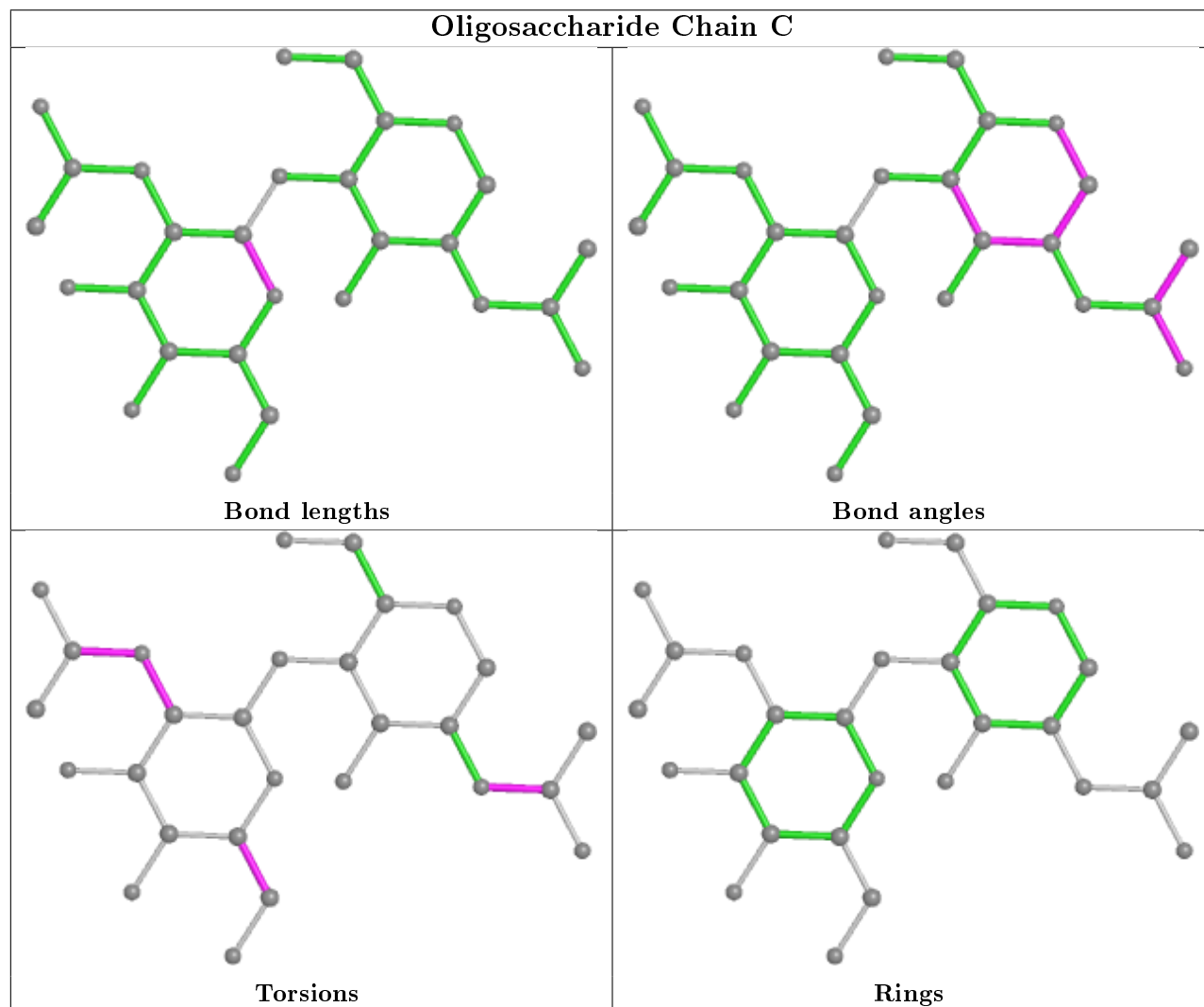
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C8-C7-N2-C2
2	C	2	NAG	O5-C5-C6-O6
2	C	1	NAG	O7-C7-N2-C2
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
2	C	2	NAG	C4-C5-C6-O6
2	C	2	NAG	C3-C2-N2-C7
2	D	2	NAG	C3-C2-N2-C7

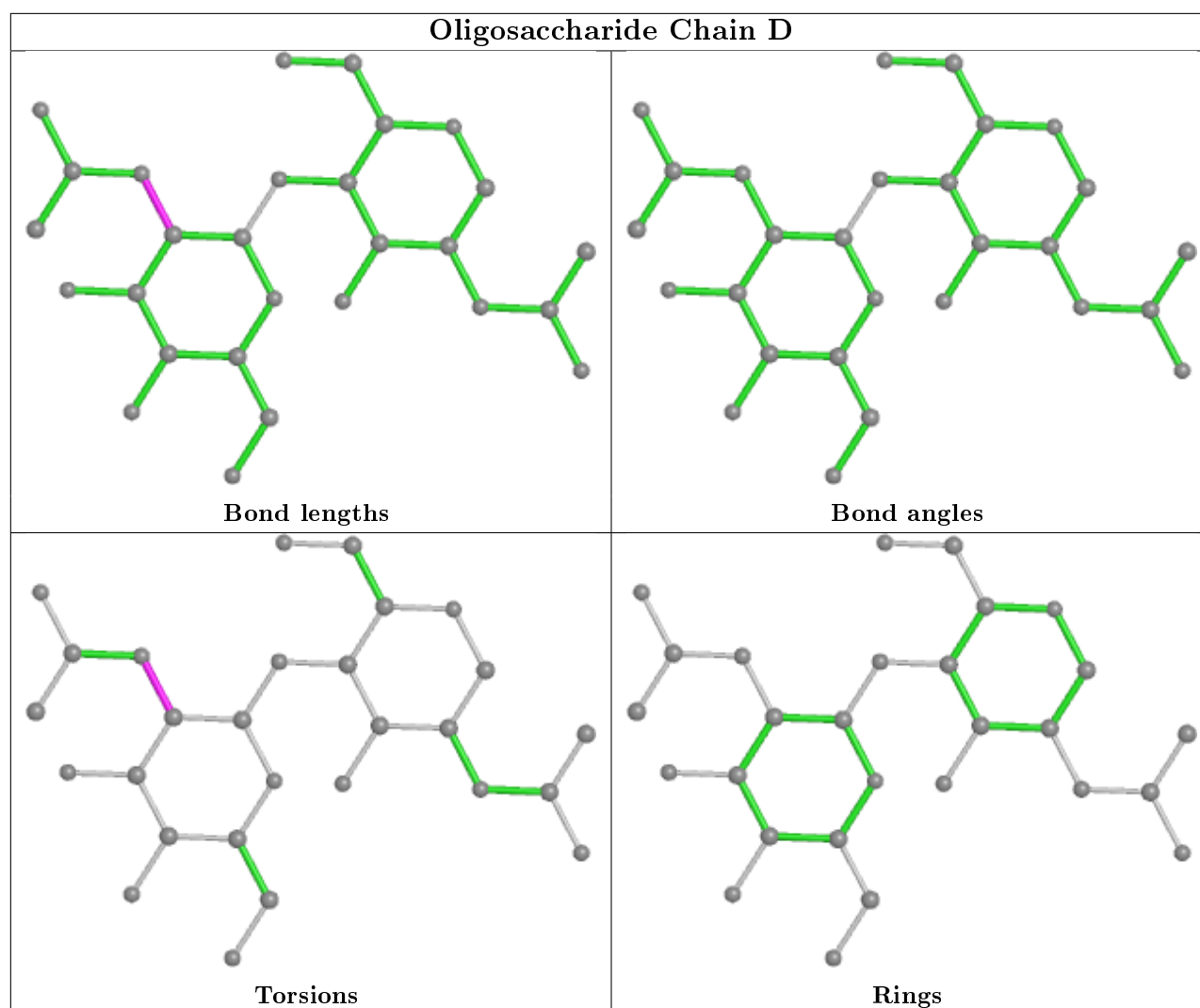
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





## 5.6 Ligand geometry [i](#)

4 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	$\# Z  > 2$
3	GOL	B	558	-	5,5,5	0.44	0	5,5,5	0.32	0
3	GOL	A	558	-	5,5,5	0.41	0	5,5,5	0.81	0
3	GOL	A	557	-	5,5,5	0.34	0	5,5,5	0.35	0
4	SO4	B	557	-	4,4,4	0.31	0	6,6,6	0.68	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
3	GOL	B	558	-	-	0/4/4/4	-
3	GOL	A	558	-	-	2/4/4/4	-
3	GOL	A	557	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	558	GOL	C1-C2-C3-O3
3	A	557	GOL	O1-C1-C2-C3
3	A	558	GOL	O2-C2-C3-O3
3	A	557	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	557	SO4	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	480/507 (94%)	-0.16	13 (2%) 54 52	17, 23, 37, 48	0
1	B	480/507 (94%)	-0.15	14 (2%) 51 50	18, 25, 39, 54	0
All	All	960/1014 (94%)	-0.15	27 (2%) 53 51	17, 25, 38, 54	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	316	LEU	8.6
1	B	317	ASP	6.7
1	A	316	LEU	6.6
1	A	311	SER	6.2
1	B	417	PRO	4.9
1	A	317	ASP	4.4
1	A	374	LYS	4.4
1	B	107	GLY	4.2
1	A	107	GLY	3.8
1	B	122	THR	3.7
1	A	552	ASN	3.4
1	B	414	LYS	3.3
1	A	122	THR	3.3
1	B	311	SER	3.1
1	A	376	PHE	2.7
1	B	78	TYR	2.7
1	B	184	TYR	2.6
1	A	309	CYS	2.6
1	A	78	TYR	2.6
1	B	415	LEU	2.5
1	B	75	GLU	2.5
1	A	417	PRO	2.4
1	A	472	GLY	2.4
1	B	204	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	552	ASN	2.2
1	A	428	ALA	2.2
1	B	484	GLY	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](#)

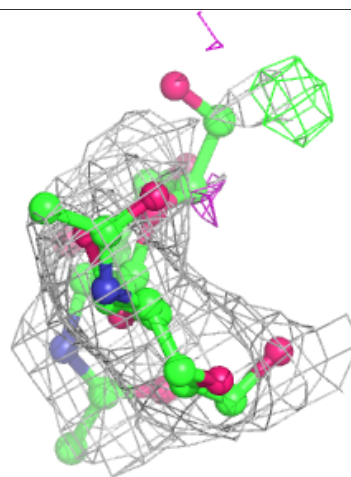
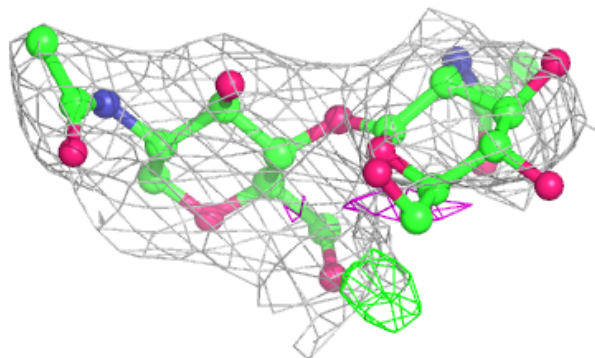
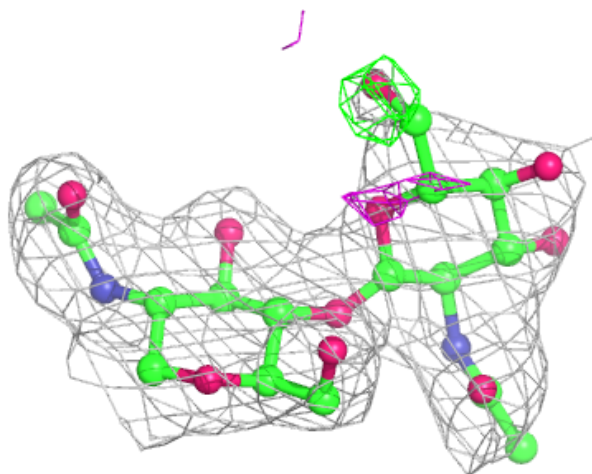
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

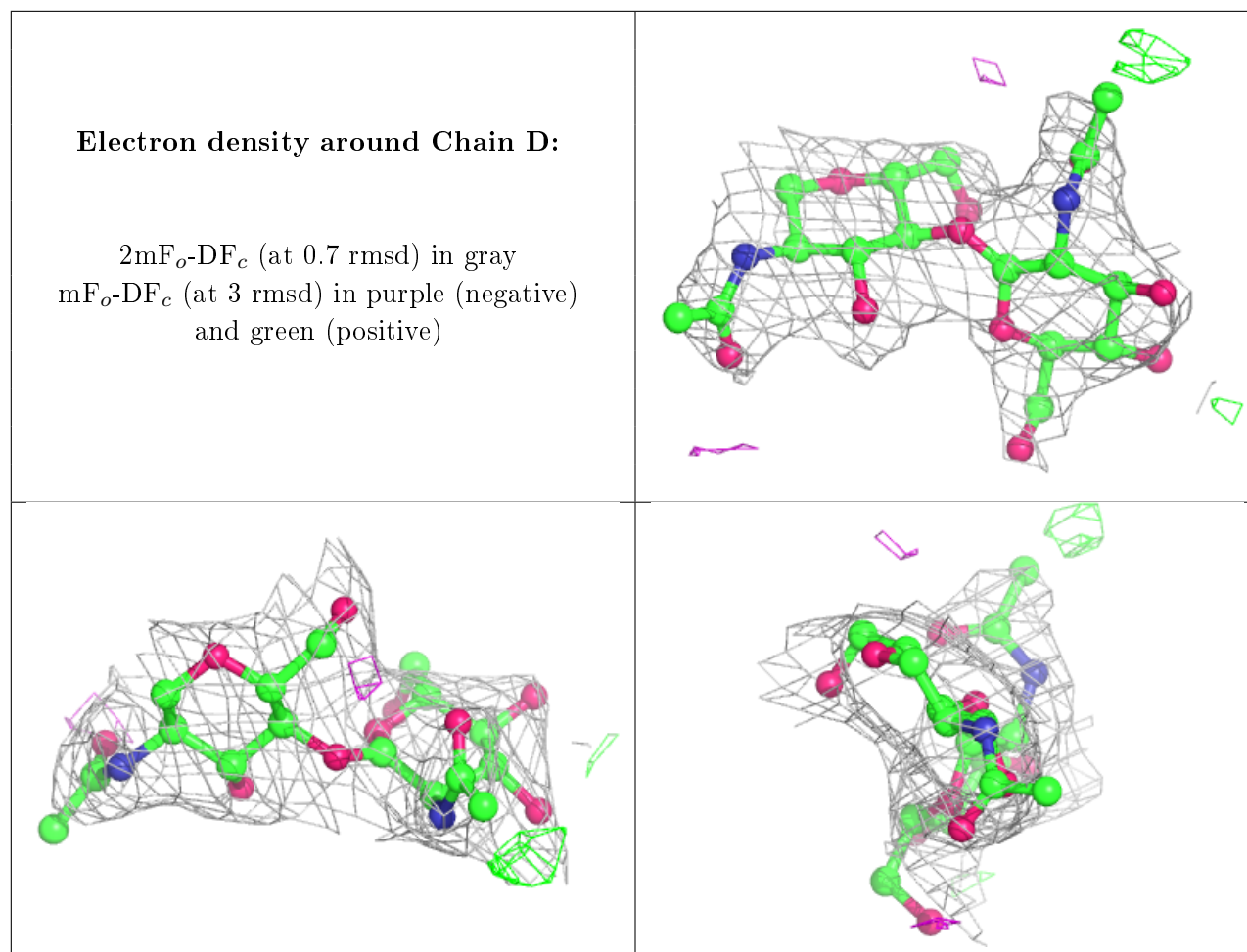
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	C	2	14/15	0.81	0.39	86,92,94,94	0
2	NAG	D	2	14/15	0.86	0.36	106,112,114,114	0
2	NAG	D	1	14/15	0.92	0.21	66,75,77,86	0
2	NAG	C	1	14/15	0.94	0.15	45,50,55,64	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around Chain C:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 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(Å <sup>2</sup> )	Q<0.9
3	GOL	A	557	6/6	0.84	0.24	51,56,56,57	0
3	GOL	B	558	6/6	0.95	0.12	33,34,35,35	0
3	GOL	A	558	6/6	0.97	0.09	35,36,37,38	0
4	SO4	B	557	5/5	0.99	0.12	40,40,42,44	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.