Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 09:22 PM BST

PDB ID	:	3L4X
Title	:	Crystal complex of N-terminal Human Maltase-Glucoamylase with NR4-8
Authors	:	Sim, L.; Rose, D.R.
Deposited on	:	2009-12-21
Resolution	:	1.90 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

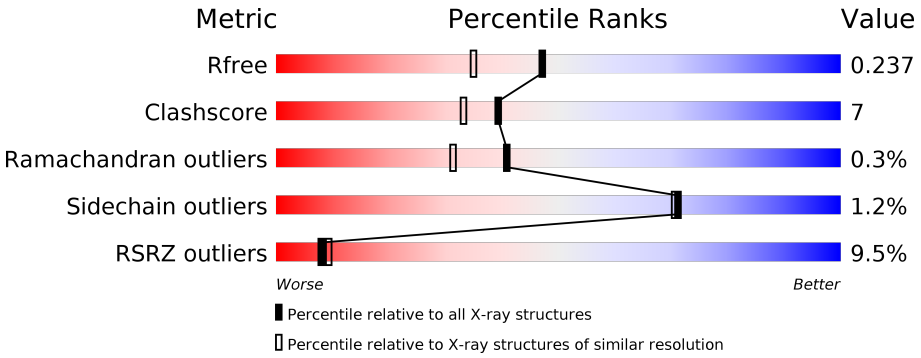
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria 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 <=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	875	9%, 84%, 14%
2	B	2	100%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7641 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 Maltase-glucoamylase, intestinal.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	863	Total	C	N	O	S	0	4	0
			6936	4424	1177	1308	27			

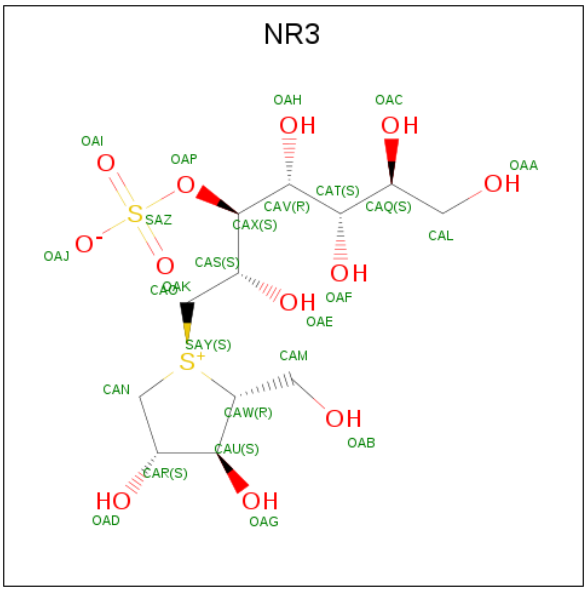
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	772	ASP	ASN	variant	UNP O43451
A	869	ALA	-	expression tag	UNP O43451
A	870	HIS	-	expression tag	UNP O43451
A	871	HIS	-	expression tag	UNP O43451
A	872	HIS	-	expression tag	UNP O43451
A	873	HIS	-	expression tag	UNP O43451
A	874	HIS	-	expression tag	UNP O43451
A	875	HIS	-	expression tag	UNP O43451

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

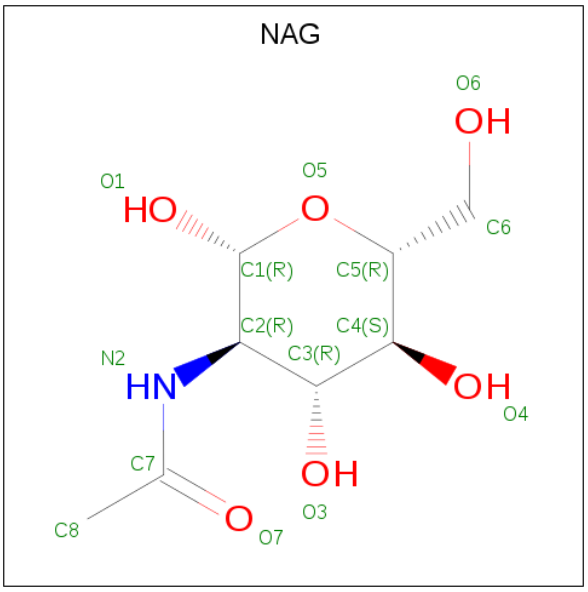
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is (1S,2R,3S,4S)-1-{(1S)-2-[(2R,3S,4S)-3,4-dihydroxy-2-(hydroxymethyl)tetrahydrothiophenium-1-yl]-1-hydroxyethyl}-2,3,4,5-tetrahydroxypentyl sulfate (three-letter code: NR3) (formula: $C_{12}H_{24}O_{12}S_2$).



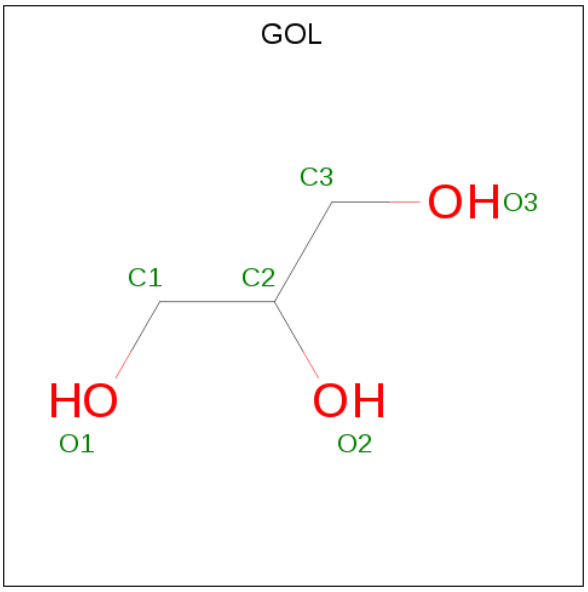
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			26	12	12	2		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 6 is water.

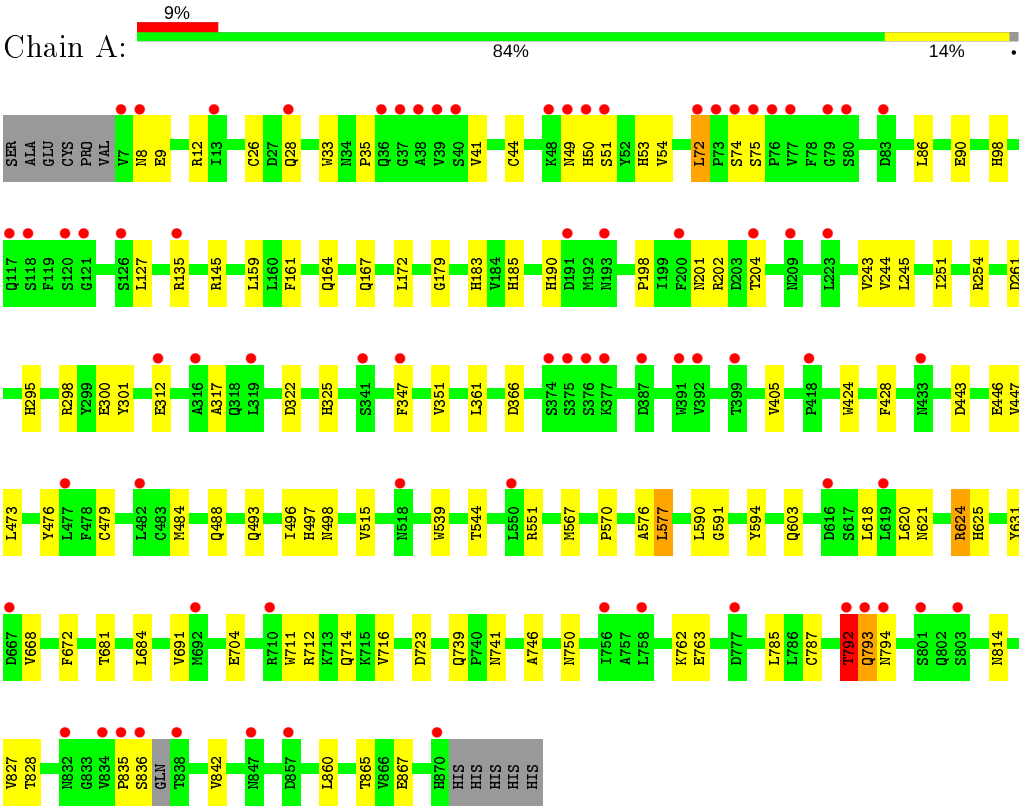
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	613	Total O 613 613	0	0

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.

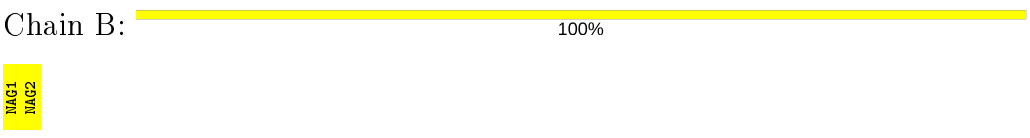
• Molecule 1: Maltase-glucoamylase, intestinal

Chain A:



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

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	87.17Å 109.44Å 109.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	18.88 – 1.90 18.76 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.2 (18.88-1.90) 97.2 (18.76-1.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.64 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.205 , 0.244 0.199 , 0.237	Depositor DCC
R_{free} test set	4032 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	22.9	Xtriage
Anisotropy	0.210	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.57 , 74.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.008 for -h,l,k	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7641	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: NR3, GOL, NAG

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	0.75	1/7147 (0.0%)	0.78	3/9747 (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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	787	CYS	CB-SG	-5.29	1.73	1.81

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	12	ARG	NE-CZ-NH2	-6.06	117.27	120.30
1	A	72	LEU	CA-CB-CG	5.41	127.73	115.30
1	A	624	ARG	NE-CZ-NH2	-5.15	117.73	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	50	HIS	Peptide
1	A	792	THR	Peptide

5.2 Too-close contacts (i)

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	6936	0	6619	100	0
2	B	28	0	25	0	0
3	A	26	0	24	1	0
4	A	14	0	13	1	0
5	A	24	0	32	0	0
6	A	613	0	0	11	0
All	All	7641	0	6713	101	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 7.

All (101) 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:312:GLU:HG3	6:A:4628:HOH:O	1.45	1.16
1:A:204:THR:HG21	1:A:473:LEU:CD2	1.76	1.14
1:A:204:THR:CG2	1:A:473:LEU:HD23	1.81	1.11
1:A:204:THR:HG21	1:A:473:LEU:HD23	1.11	1.10
1:A:98:HIS:HE1	1:A:261:ASP:OD1	1.47	0.97
1:A:835:PRO:CA	1:A:836:SER:HB2	1.94	0.97
1:A:835:PRO:HA	1:A:836:SER:HB2	1.49	0.93
1:A:204:THR:CG2	1:A:473:LEU:CD2	2.47	0.88
1:A:26:CYS:HG	1:A:44:CYS:HG	1.23	0.87
1:A:763:GLU:OE2	1:A:792:THR:HG23	1.80	0.80
1:A:835:PRO:CB	1:A:836:SER:HB2	2.11	0.80
1:A:54:VAL:HB	1:A:135:ARG:HB3	1.63	0.80
1:A:835:PRO:HB3	1:A:836:SER:CB	2.12	0.79
1:A:835:PRO:HB3	1:A:836:SER:HB2	1.65	0.79
1:A:28:GLN:HG3	6:A:4184:HOH:O	1.83	0.78
1:A:814:ASN:HB3	6:A:4250:HOH:O	1.85	0.75
1:A:244:VAL:HG21	1:A:254[A]:ARG:NH2	2.01	0.74
1:A:98:HIS:CE1	1:A:261:ASP:OD1	2.37	0.73
1:A:712:ARG:H	1:A:714:GLN:HE21	1.38	0.71
1:A:488:GLN:HB2	1:A:496:ILE:HD11	1.73	0.70
1:A:493:GLN:HE21	1:A:497:HIS:HD2	1.37	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:493:GLN:NE2	1:A:497:HIS:HD2	1.90	0.67
1:A:183:HIS:HE1	1:A:198:PRO:O	1.82	0.62
1:A:201:ASN:O	1:A:497:HIS:HE1	1.82	0.62
1:A:464:ASN:ND2	1:A:484:MET:H	1.97	0.62
1:A:794:ASN:N	6:A:4622:HOH:O	2.33	0.61
1:A:464:ASN:HD21	1:A:484:MET:H	1.48	0.61
1:A:625:HIS:HE1	1:A:704:GLU:OE2	1.83	0.61
1:A:179:GLY:O	1:A:190:HIS:HE1	1.83	0.60
1:A:167:GLN:HE21	1:A:254[A]:ARG:HG3	1.65	0.60
1:A:835:PRO:HB3	1:A:836:SER:HB3	1.81	0.60
1:A:835:PRO:CA	1:A:836:SER:CB	2.74	0.59
1:A:493:GLN:NE2	1:A:497:HIS:CD2	2.71	0.59
1:A:835:PRO:CB	1:A:836:SER:CB	2.76	0.58
1:A:681:THR:HG22	1:A:691:VAL:HG11	1.85	0.58
1:A:245:LEU:CD2	1:A:251[B]:ILE:HG12	2.34	0.58
1:A:828:THR:HG23	1:A:836:SER:OG	2.04	0.57
1:A:295:HIS:HD2	1:A:325:HIS:NE2	2.02	0.57
1:A:544:THR:CG2	1:A:577:LEU:HD22	2.34	0.57
1:A:90:GLU:OE1	1:A:98:HIS:HD2	1.88	0.57
1:A:591:GLY:HA2	1:A:594:TYR:CD2	2.40	0.57
1:A:204:THR:HG21	1:A:473:LEU:HD22	1.80	0.56
1:A:202:ARG:HG3	1:A:204:THR:HG23	1.87	0.56
1:A:292:LEU:HD23	1:A:567:MET:CE	2.36	0.55
1:A:291:ALA:O	1:A:295:HIS:HE1	1.90	0.54
1:A:576:ALA:O	1:A:577:LEU:HB2	2.08	0.54
1:A:446:GLU:N	1:A:447:VAL:HA	2.24	0.52
1:A:28:GLN:CG	6:A:4184:HOH:O	2.49	0.52
4:A:2003:NAG:H83	6:A:4558:HOH:O	2.10	0.52
1:A:243:VAL:HG11	1:A:251[A]:ILE:HD11	1.93	0.51
1:A:351:VAL:HG22	1:A:361:LEU:HD22	1.93	0.51
1:A:763:GLU:OE2	1:A:792:THR:CG2	2.54	0.50
1:A:621:ASN:OD1	1:A:624:ARG:NH2	2.43	0.50
1:A:53:HIS:HD2	1:A:72:LEU:HD22	1.76	0.50
1:A:127:LEU:O	1:A:145[A]:ARG:HD3	2.11	0.50
1:A:762:LYS:HE3	6:A:4297:HOH:O	2.11	0.50
1:A:201:ASN:H	1:A:498:ASN:ND2	2.10	0.49
1:A:424:TRP:CE2	1:A:428:PHE:HE2	2.30	0.49
1:A:201:ASN:H	1:A:498:ASN:HD21	1.61	0.48
1:A:245:LEU:HD23	1:A:251[B]:ILE:HG12	1.94	0.48
1:A:793:GLN:HA	6:A:4525:HOH:O	2.12	0.48
1:A:183:HIS:HD2	1:A:185:HIS:NE2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:ALA:HB1	1:A:620:LEU:HD21	1.95	0.47
1:A:631:TYR:HA	1:A:634:LEU:HG	1.97	0.47
1:A:865:THR:HG22	1:A:867:GLU:HG3	1.97	0.47
1:A:54:VAL:HB	1:A:135:ARG:CB	2.42	0.46
1:A:243:VAL:CG1	1:A:251[A]:ILE:HD11	2.45	0.46
1:A:366:ASP:HB3	6:A:4131:HOH:O	2.15	0.46
1:A:300:GLU:HG3	1:A:603:GLN:HG3	1.97	0.46
1:A:26:CYS:CB	1:A:44:CYS:HG	2.29	0.46
1:A:618:LEU:HD11	1:A:723:ASP:HB3	1.98	0.46
1:A:785:LEU:CD2	1:A:860:LEU:HG	2.46	0.45
1:A:204:THR:HG22	1:A:473:LEU:CD2	2.41	0.45
1:A:464:ASN:HD21	1:A:484:MET:N	2.14	0.45
1:A:164:GLN:HE22	1:A:462:ASN:HB2	1.81	0.45
1:A:190:HIS:HD2	6:A:4090:HOH:O	1.98	0.45
1:A:428:PHE:HB3	1:A:515:VAL:HG21	1.99	0.44
1:A:86:LEU:HB2	1:A:104:GLN:HG3	1.99	0.44
1:A:655:LEU:HD22	1:A:668:VAL:HG11	2.00	0.44
1:A:167:GLN:NE2	1:A:254[A]:ARG:HH11	2.16	0.43
1:A:476:TYR:HB2	1:A:479[B]:CYS:SG	2.58	0.43
1:A:711:TRP:CG	1:A:716:VAL:HG11	2.53	0.43
1:A:202:ARG:CG	1:A:204:THR:HG23	2.48	0.43
1:A:298:ARG:HG2	1:A:301:TYR:CZ	2.54	0.43
1:A:9:GLU:HB2	1:A:41:VAL:HG11	1.99	0.43
1:A:827:VAL:HG21	1:A:842:VAL:HG21	2.00	0.43
1:A:691:VAL:HG23	6:A:4207:HOH:O	2.19	0.42
1:A:739:GLN:HB3	1:A:750:ASN:HB3	2.01	0.42
1:A:172:LEU:HD11	1:A:251[B]:ILE:HG13	2.00	0.42
1:A:570:PRO:HD2	1:A:594:TYR:CD2	2.55	0.42
1:A:544:THR:HG22	1:A:577:LEU:HD22	2.00	0.42
1:A:244:VAL:HG21	1:A:254[A]:ARG:HH22	1.79	0.42
1:A:741:ASN:ND2	1:A:746:ALA:HB1	2.35	0.42
1:A:51:SER:HB2	1:A:159:LEU:O	2.20	0.41
1:A:33:TRP:CE2	1:A:35:PRO:HG3	2.56	0.41
1:A:443:ASP:OD2	3:A:1001:NR3:HANA	2.21	0.41
1:A:590:LEU:HD11	1:A:672:PHE:HE2	1.86	0.41
1:A:298:ARG:HG2	1:A:301:TYR:CE1	2.56	0.41
1:A:167:GLN:NE2	1:A:254[B]:ARG:HE	2.19	0.41
1:A:551:ARG:HG2	1:A:684:LEU:HB3	2.03	0.40
1:A:201:ASN:O	1:A:497:HIS:CE1	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	863/875 (99%)	818 (95%)	42 (5%)	3 (0%)	41 31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	793	GLN
1	A	8	ASN
1	A	405	VAL

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	760/767 (99%)	751 (99%)	9 (1%)	71 70

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	74	SER
1	A	75	SER
1	A	161	PHE
1	A	322	ASP
1	A	347	PHE
1	A	539	TRP
1	A	577	LEU

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Mol	Chain	Res	Type
1	A	792	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	53	HIS
1	A	62	ASN
1	A	98	HIS
1	A	107	ASN
1	A	148	ASN
1	A	164	GLN
1	A	167	GLN
1	A	183	HIS
1	A	190	HIS
1	A	239	ASN
1	A	295	HIS
1	A	464	ASN
1	A	493	GLN
1	A	497	HIS
1	A	498	ASN
1	A	625	HIS
1	A	628	ASN
1	A	669	HIS
1	A	670	GLN
1	A	714	GLN
1	A	781	ASN
1	A	802	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

2 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	B	1	1,2	14,14,15	0.55	0	17,19,21	1.18	2 (11%)
2	NAG	B	2	2	14,14,15	0.49	0	17,19,21	1.45	1 (5%)

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	B	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	2	NAG	C1-O5-C5	4.84	118.75	112.19
2	B	1	NAG	O5-C1-C2	-2.41	107.49	111.29
2	B	1	NAG	O7-C7-C8	-2.12	118.11	122.06

There are no chirality outliers.

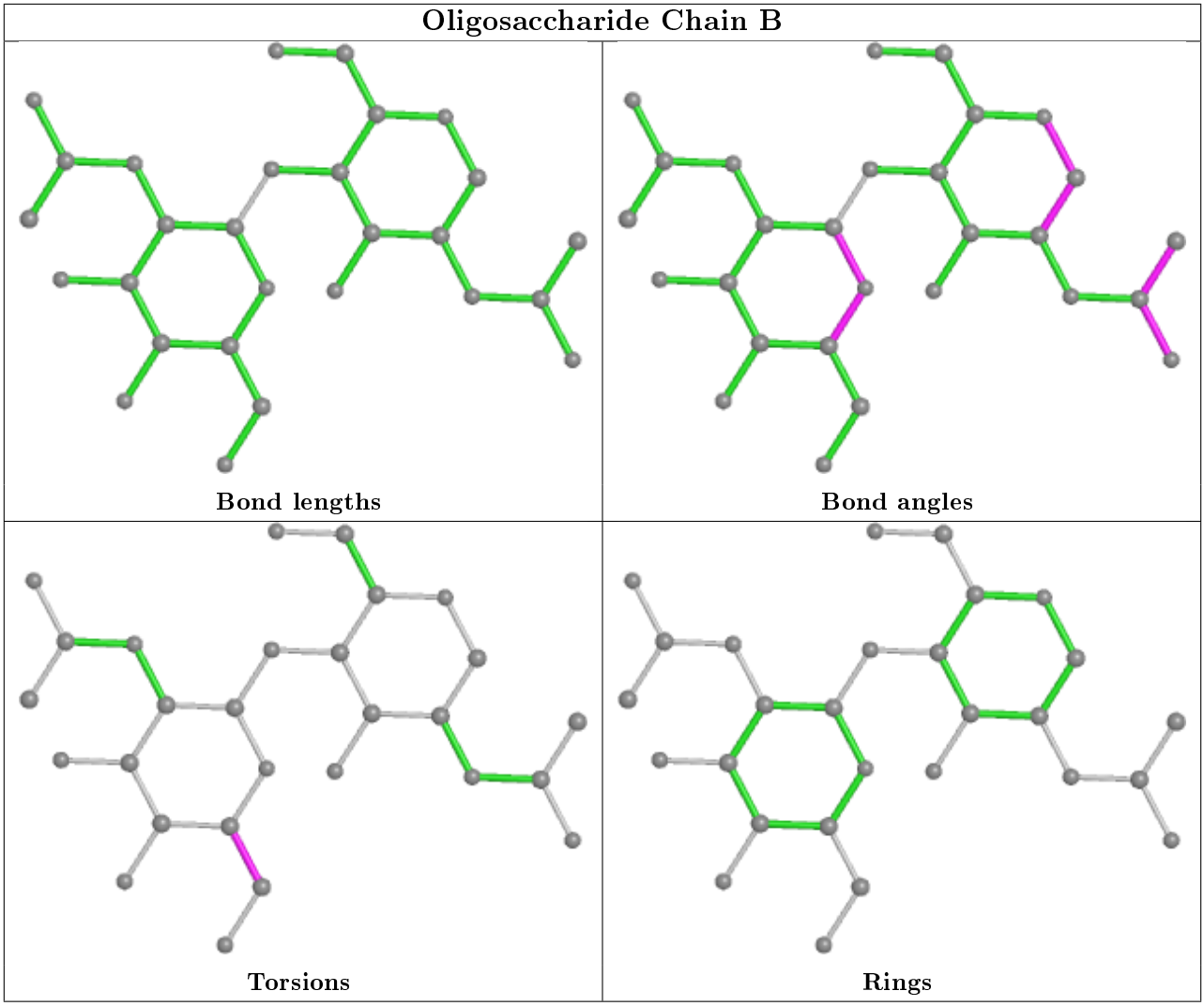
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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

6 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	GOL	A	3001	-	5,5,5	0.84	0	5,5,5	0.73	0
5	GOL	A	3004	-	5,5,5	0.33	0	5,5,5	0.52	0
3	NR3	A	1001	-	21,26,26	1.38	3 (14%)	25,38,38	1.61	5 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	NAG	A	2003	1	14,14,15	0.59	0	17,19,21	1.77	2 (11%)
5	GOL	A	3003	-	5,5,5	0.42	0	5,5,5	0.42	0
5	GOL	A	3002	-	5,5,5	0.28	0	5,5,5	0.73	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
5	GOL	A	3001	-	-	1/4/4/4	-
5	GOL	A	3004	-	-	0/4/4/4	-
3	NR3	A	1001	-	-	4/28/45/45	0/1/1/1
4	NAG	A	2003	1	-	2/6/23/26	0/1/1/1
5	GOL	A	3003	-	-	0/4/4/4	-
5	GOL	A	3002	-	-	0/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	NR3	OAP-SAZ	-3.90	1.45	1.57
3	A	1001	NR3	CAV-CAX	2.78	1.56	1.53
3	A	1001	NR3	OAD-CAR	2.17	1.47	1.43

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	2003	NAG	C1-O5-C5	5.06	119.05	112.19
3	A	1001	NR3	CAT-CAV-CAX	4.72	119.14	112.36
4	A	2003	NAG	O5-C1-C2	-3.58	105.63	111.29
3	A	1001	NR3	CAS-CAX-CAV	-3.42	106.20	113.60
3	A	1001	NR3	OAD-CAR-CAN	3.21	115.36	109.42
3	A	1001	NR3	CAR-CAU-CAW	-2.21	103.87	106.71
3	A	1001	NR3	CAQ-CAT-CAV	2.15	115.82	112.47

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1001	NR3	OAA-CAL-CAQ-OAC

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Mol	Chain	Res	Type	Atoms
3	A	1001	NR3	OAA-CAL-CAQ-CAT
4	A	2003	NAG	C8-C7-N2-C2
4	A	2003	NAG	O7-C7-N2-C2
5	A	3001	GOL	C1-C2-C3-O3
3	A	1001	NR3	OAC-CAQ-CAT-CAV
3	A	1001	NR3	CAQ-CAT-CAV-CAX

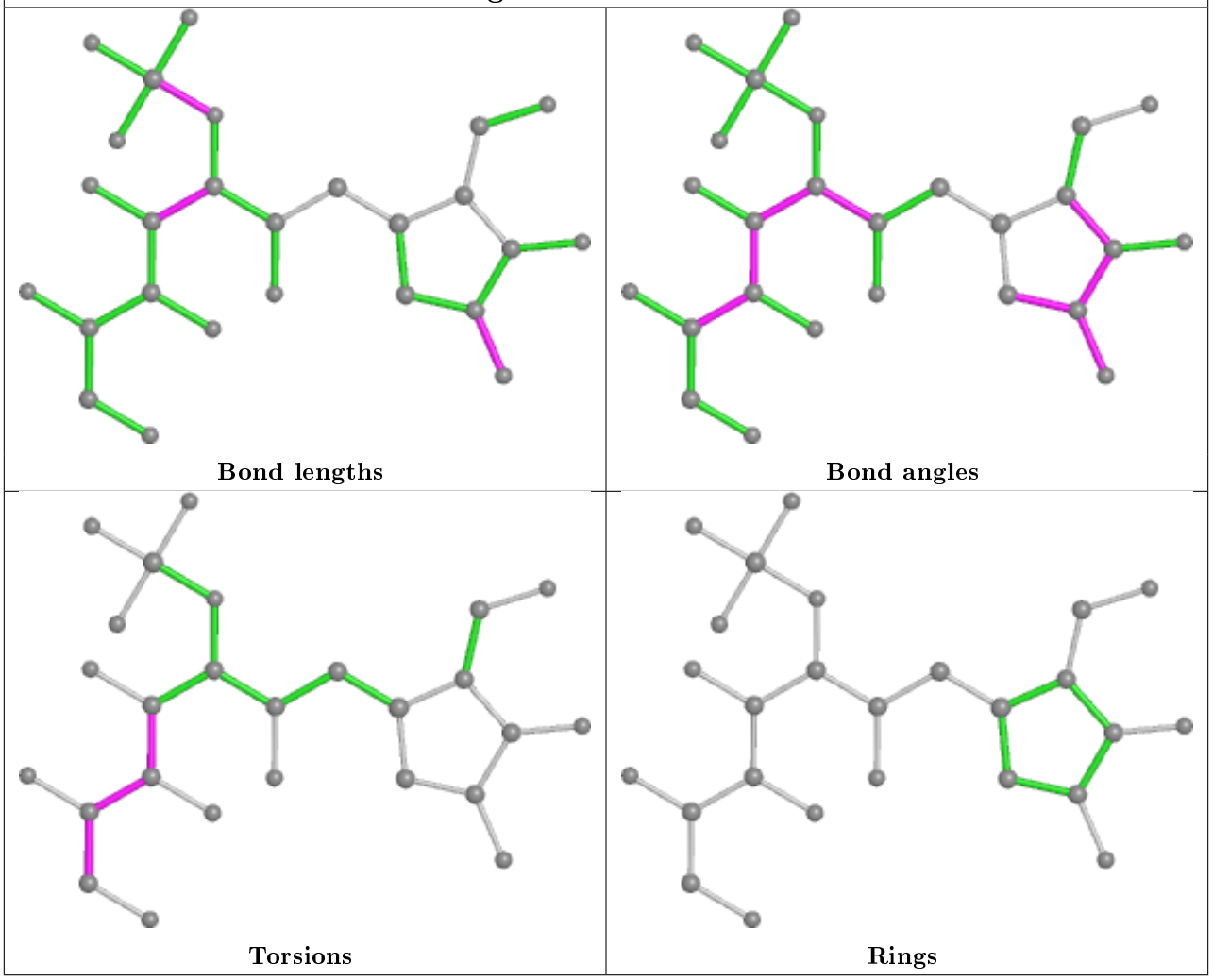
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1001	NR3	1	0
4	A	2003	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand NR3 A 1001



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^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	863/875 (98%)	0.54	82 (9%) 8 9	10, 19, 33, 51	0

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	838	THR	8.5
1	A	836	SER	6.7
1	A	375	SER	6.3
1	A	793	GLN	6.3
1	A	36	GLN	6.2
1	A	79	GLY	5.9
1	A	374	SER	5.7
1	A	76	PRO	5.5
1	A	7	VAL	5.4
1	A	80	SER	5.4
1	A	48	LYS	5.3
1	A	710	ARG	5.2
1	A	73	PRO	5.2
1	A	37	GLY	5.1
1	A	377	LYS	4.9
1	A	75	SER	4.7
1	A	72	LEU	4.6
1	A	376	SER	4.6
1	A	106	ASN	4.4
1	A	418	PRO	4.3
1	A	74	SER	4.2
1	A	77	VAL	4.0
1	A	826	ASN	3.9
1	A	105	THR	3.9
1	A	477	LEU	3.8
1	A	50	HIS	3.7
1	A	38	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	616	ASP	3.6
1	A	120	SER	3.6
1	A	794	ASN	3.5
1	A	83	ASP	3.2
1	A	49	ASN	3.2
1	A	391	TRP	3.1
1	A	667	ASP	3.1
1	A	193	ASN	3.1
1	A	8	ASN	3.1
1	A	847	ASN	3.0
1	A	399	THR	3.0
1	A	387	ASP	3.0
1	A	792	THR	2.9
1	A	126	SER	2.9
1	A	692	MET	2.8
1	A	51	SER	2.7
1	A	341	SER	2.7
1	A	834	VAL	2.7
1	A	433	ASN	2.7
1	A	118	SER	2.6
1	A	857	ASP	2.6
1	A	870	HIS	2.6
1	A	204	THR	2.6
1	A	482	LEU	2.6
1	A	462	ASN	2.6
1	A	39	VAL	2.6
1	A	777	ASP	2.5
1	A	191	ASP	2.5
1	A	319	LEU	2.5
1	A	200	PHE	2.5
1	A	40	SER	2.5
1	A	818	ILE	2.5
1	A	756	ILE	2.4
1	A	832	ASN	2.4
1	A	13	ILE	2.4
1	A	347	PHE	2.4
1	A	121	GLY	2.4
1	A	107	ASN	2.4
1	A	135	ARG	2.4
1	A	209	ASN	2.4
1	A	518	ASN	2.3
1	A	803	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	835	PRO	2.3
1	A	392	VAL	2.2
1	A	758	LEU	2.2
1	A	316	ALA	2.1
1	A	28	GLN	2.1
1	A	619	LEU	2.1
1	A	266	LEU	2.1
1	A	550	LEU	2.1
1	A	312	GLU	2.1
1	A	824	PRO	2.1
1	A	117	GLN	2.1
1	A	801	SER	2.0
1	A	223	LEU	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)

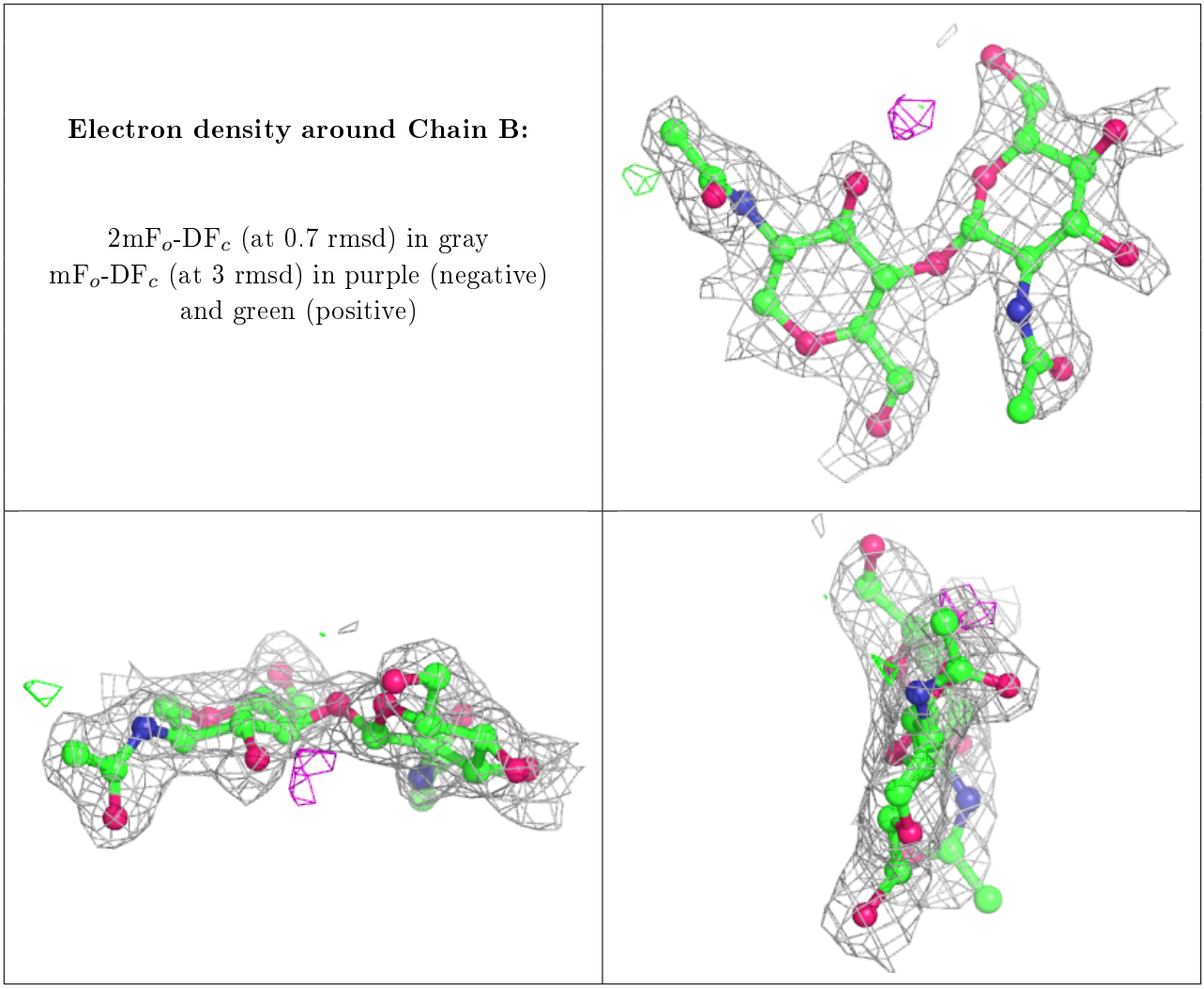
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	B	2	14/15	0.88	0.37	38,41,46,48	0
2	NAG	B	1	14/15	0.90	0.13	24,27,32,34	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 B:

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



6.4 Ligands

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^{th} 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.

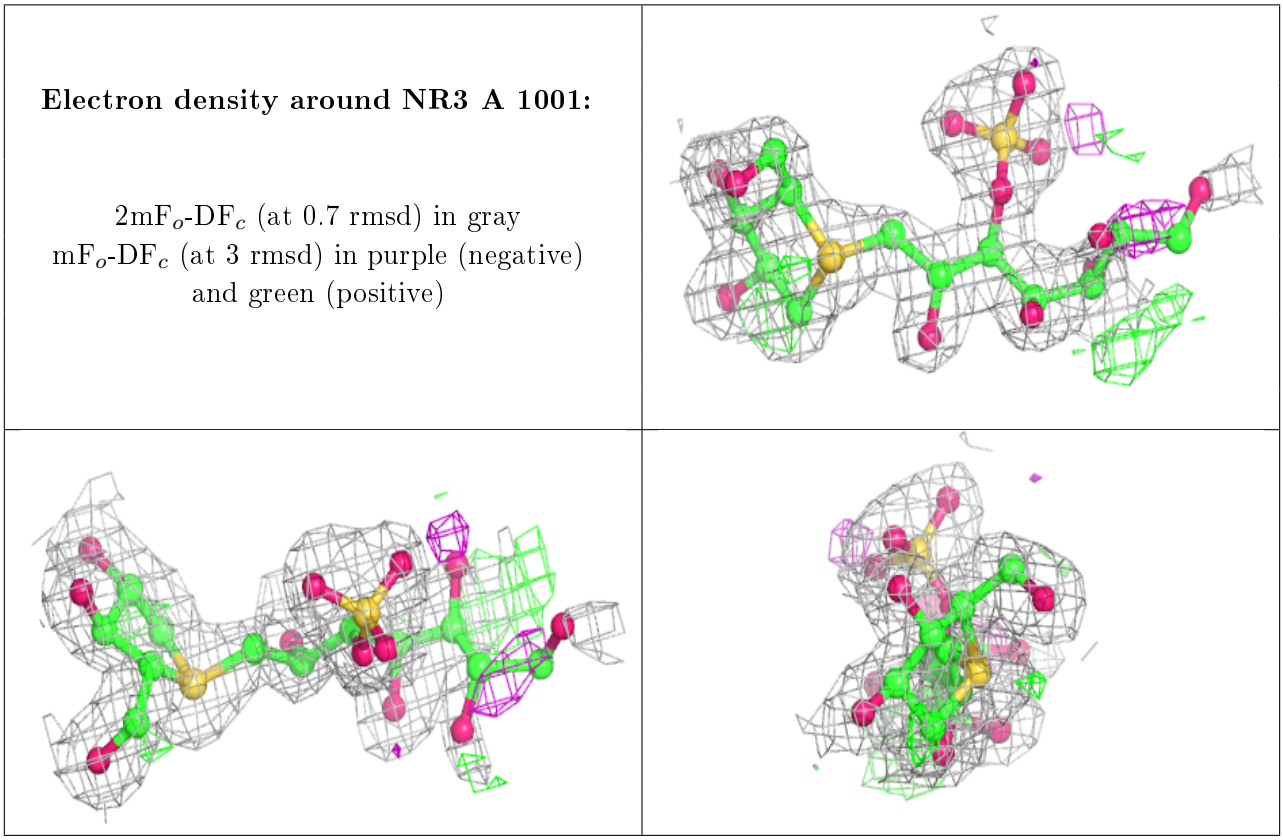
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NAG	A	2003	14/15	0.73	0.32	32,36,41,44	0
5	GOL	A	3002	6/6	0.78	0.17	30,36,39,43	0
3	NR3	A	1001	26/26	0.88	0.18	19,26,44,45	0
5	GOL	A	3004	6/6	0.90	0.14	36,37,38,39	0
5	GOL	A	3001	6/6	0.91	0.15	27,29,29,31	0
5	GOL	A	3003	6/6	0.92	0.10	32,33,34,37	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around NR3 A 1001:

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



6.5 Other polymers (i)

There are no such residues in this entry.