



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 2, 2026 – 04:46 PM UTC

PDB ID : 3WPC / pdb_00003wpc
Title : Crystal structure of horse TLR9 in complex with agonistic DNA1668_12mer
Authors : Ohto, U.; Tanji, H.; Shimizu, T.
Deposited on : 2014-01-11
Resolution : 1.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

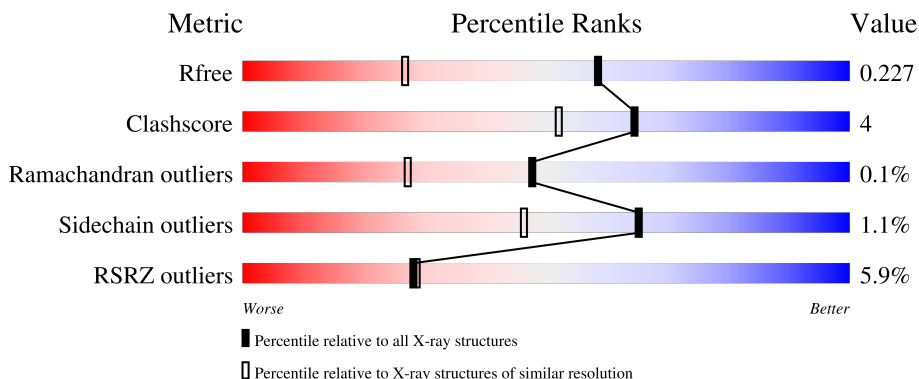
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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.



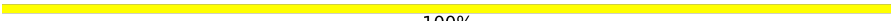
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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 ≥ 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	802	
1	B	802	
2	E	12	
2	F	12	
3	C	2	

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Mol	Chain	Length	Quality of chain
3	D	2	 100%

2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 14350 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 Toll-like receptor 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	747	6013	3834	1058	1093	28	7	19	0
1	B	749	6009	3833	1054	1093	29	12	18	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	ARG	-	expression tag	UNP Q2EEY0
A	23	SER	-	expression tag	UNP Q2EEY0
A	24	PRO	-	expression tag	UNP Q2EEY0
A	25	TRP	-	expression tag	UNP Q2EEY0
A	818	GLU	-	expression tag	UNP Q2EEY0
A	819	PHE	-	expression tag	UNP Q2EEY0
A	820	LEU	-	expression tag	UNP Q2EEY0
A	821	VAL	-	expression tag	UNP Q2EEY0
A	822	PRO	-	expression tag	UNP Q2EEY0
A	823	ARG	-	expression tag	UNP Q2EEY0
B	22	ARG	-	expression tag	UNP Q2EEY0
B	23	SER	-	expression tag	UNP Q2EEY0
B	24	PRO	-	expression tag	UNP Q2EEY0
B	25	TRP	-	expression tag	UNP Q2EEY0
B	818	GLU	-	expression tag	UNP Q2EEY0
B	819	PHE	-	expression tag	UNP Q2EEY0
B	820	LEU	-	expression tag	UNP Q2EEY0
B	821	VAL	-	expression tag	UNP Q2EEY0
B	822	PRO	-	expression tag	UNP Q2EEY0
B	823	ARG	-	expression tag	UNP Q2EEY0

- Molecule 2 is a DNA chain called DNA (5'-D(*CP*AP*TP*GP*AP*CP*GP*TP*TP*CP*CP*T)-3').

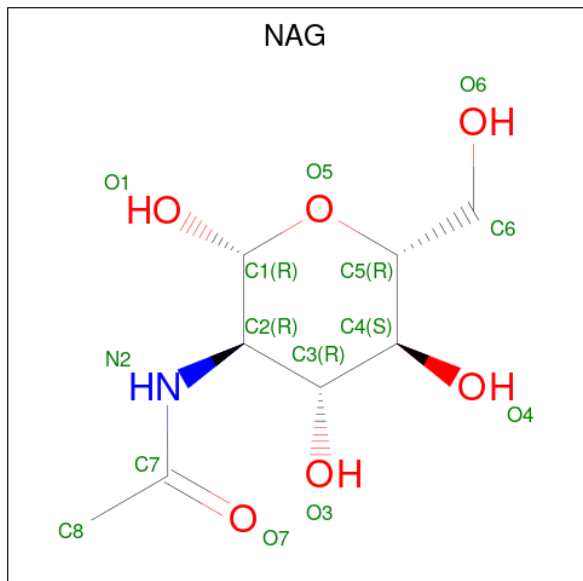
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	F	12	Total 239	C 116	N 40	O 72	P 11	0	0	0
2	E	12	Total 239	C 116	N 40	O 72	P 11	0	0	0

- Molecule 3 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			
3	C	2	Total 28	C 16	N 2	O 10	0	0	0
3	D	2	Total 28	C 16	N 2	O 10	0	0	0

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



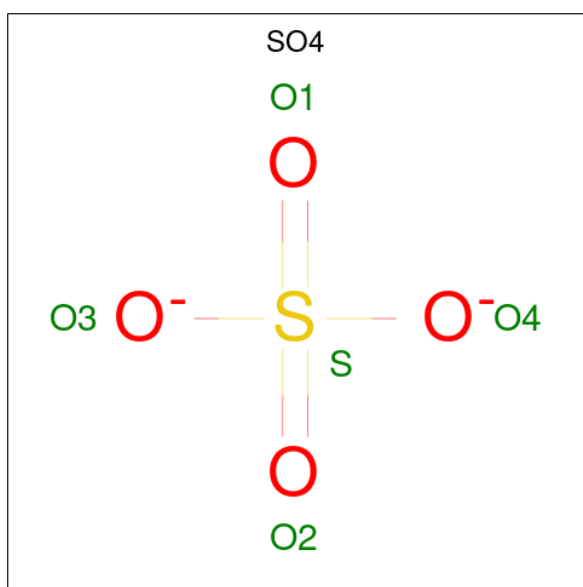
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	Total 14	C 8	N 1	O 5	0	0
4	A	1	Total 14	C 8	N 1	O 5	0	0

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

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

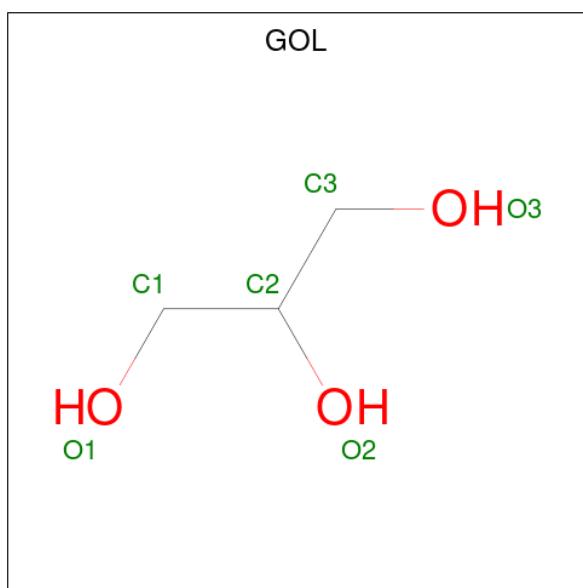


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0

- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total Na 1 1	0	0

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

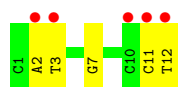
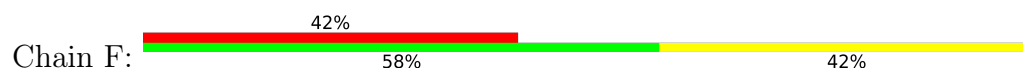
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	766	Total O 766 766	0	0
8	B	788	Total O 788 788	0	0
8	F	21	Total O 21 21	0	0

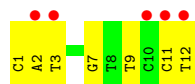
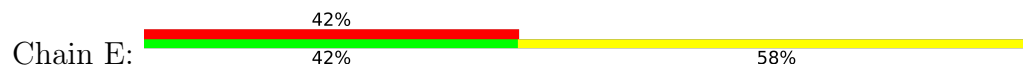
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	E	20	Total	O	0	0
			20	20		



- Molecule 2: DNA (5'-D(*CP*AP*TP*GP*AP*CP*GP*TP*TP*CP*CP*T)-3')



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucofuranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucofuranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	68.76Å 81.62Å 81.52Å 87.50° 83.50° 85.98°	Depositor
Resolution (Å)	47.49 – 1.60 47.49 – 1.60	Depositor EDS
% Data completeness (in resolution range)	95.6 (47.49-1.60) 95.6 (47.49-1.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 1.60Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.184 , 0.220 0.193 , 0.227	Depositor DCC
R_{free} test set	11134 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	17.9	Xtrriage
Anisotropy	0.223	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.086 for -h,-l,-k	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14350	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.14% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: NAG, SO4, GOL, NA

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	0.92	1/6152 (0.0%)	0.94	1/8370 (0.0%)
1	B	0.92	0/6149	0.95	4/8366 (0.0%)
2	E	0.62	1/266 (0.4%)	1.16	2/408 (0.5%)
2	F	0.53	0/266	1.04	0/408
All	All	0.91	2/12833 (0.0%)	0.95	7/17552 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	178	CYS	CA-C	-6.41	1.47	1.53
2	E	7	DG	O3'-P	-5.56	1.52	1.61

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	9	DT	C2'-C3'-O3'	-6.63	101.56	111.50
1	B	349	VAL	N-CA-C	6.61	118.45	108.80
1	B	432	GLU	CB-CA-C	-6.59	97.57	110.10
2	E	1	DC	C5'-C4'-O4'	5.51	117.67	109.40
1	A	349	VAL	N-CA-C	5.45	117.94	108.95

There are no chirality outliers.

There are no planarity outliers.

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	6013	0	6008	41	0
1	B	6009	0	6005	42	0
2	E	239	0	138	9	0
2	F	239	0	138	10	0
3	C	28	0	25	0	0
3	D	28	0	25	0	0
4	A	84	0	78	0	0
4	B	98	0	91	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
6	B	1	0	0	0	0
7	B	6	0	8	1	0
8	A	766	0	0	13	1
8	B	788	0	0	10	2
8	E	20	0	0	0	0
8	F	21	0	0	0	0
All	All	14350	0	12516	99	2

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 4.

The worst 5 of 99 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:642[B]:THR:OG1	2:F:7:DG:H5''	1.57	1.01
2:F:11:DC:OP1	2:F:12:DT:H73	1.82	0.79
1:B:277[A]:SER:OG	1:B:302:ARG:NH1	2.17	0.78
1:B:653:LYS:HA	1:B:653:LYS:HE2	1.69	0.72
2:E:11:DC:OP1	2:E:12:DT:H73	1.92	0.69

All (2) 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)
8:A:1286:HOH:O	8:B:1285:HOH:O[1_655]	1.71	0.49
8:B:1218:HOH:O	8:B:1753:HOH:O[1_556]	2.13	0.07

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	760/802 (95%)	729 (96%)	30 (4%)	1 (0%)	48	27
1	B	763/802 (95%)	723 (95%)	39 (5%)	1 (0%)	48	27
All	All	1523/1604 (95%)	1452 (95%)	69 (4%)	2 (0%)	48	27

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	375	PHE
1	A	375	PHE

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	683/712 (96%)	674 (99%)	9 (1%)	61	40
1	B	683/712 (96%)	676 (99%)	7 (1%)	68	50
All	All	1366/1424 (96%)	1350 (99%)	16 (1%)	65	43

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	381	GLN
1	B	362[B]	SER
1	A	799	ARG
1	B	362[A]	SER

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Mol	Chain	Res	Type
1	A	653	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	260	HIS
1	B	494	GLN
1	A	309	ASN
1	A	637	GLN
1	A	650	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	$\# Z > 2$
3	NAG	C	1	3,1	14,14,15	0.82	0	17,19,21	1.14	2 (11%)
3	NAG	C	2	3	14,14,15	0.48	0	17,19,21	1.55	3 (17%)
3	NAG	D	1	3,1	14,14,15	0.74	0	17,19,21	1.04	1 (5%)
3	NAG	D	2	3	14,14,15	0.56	0	17,19,21	1.43	4 (23%)

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	NAG	C	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	NAG	D	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	2	NAG	O5-C1-C2	-3.77	105.45	111.29
3	C	2	NAG	O5-C1-C2	-3.45	105.95	111.29
3	C	2	NAG	C1-O5-C5	3.10	116.34	112.19
3	C	2	NAG	C1-C2-N2	2.74	114.75	110.43
3	D	1	NAG	C3-C4-C5	-2.34	105.99	110.23

There are no chirality outliers.

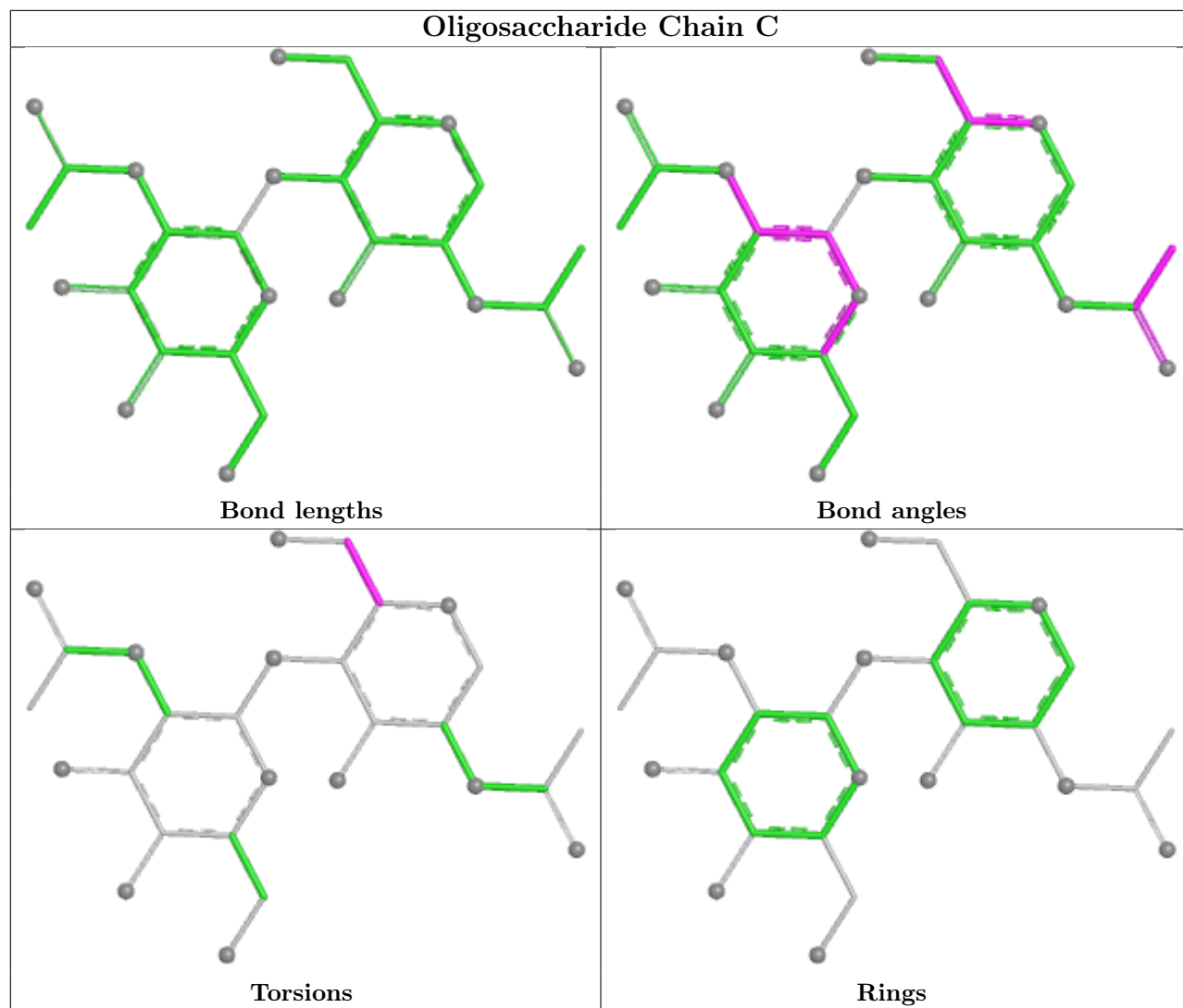
5 of 6 torsion outliers are listed below:

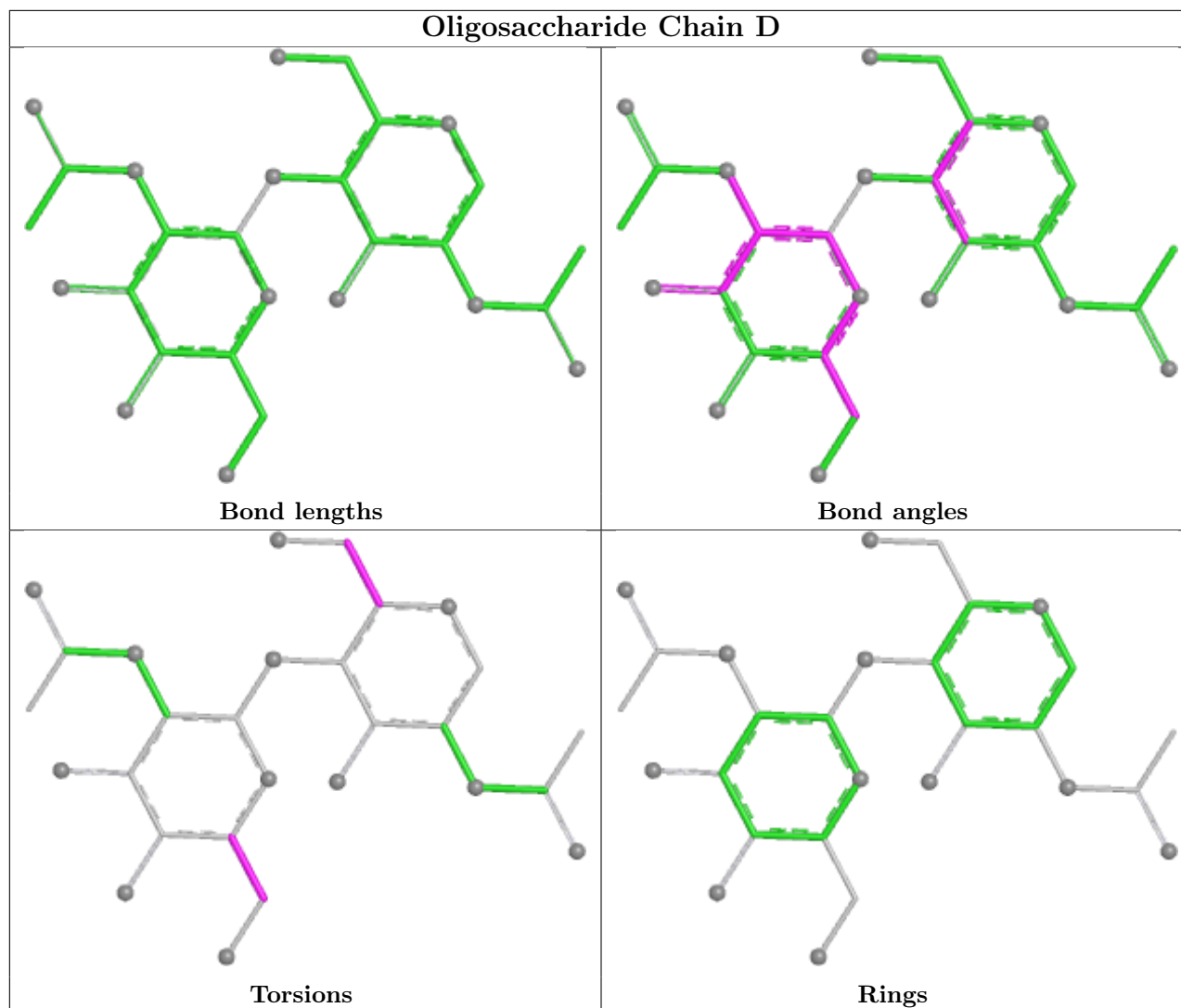
Mol	Chain	Res	Type	Atoms
3	C	1	NAG	C4-C5-C6-O6
3	D	1	NAG	C4-C5-C6-O6
3	C	1	NAG	O5-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6
3	D	2	NAG	O5-C5-C6-O6

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 [i](#)

Of 17 ligands modelled in this entry, 1 is monoatomic - leaving 16 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	NAG	B	905	1	14,14,15	0.76	0	17,19,21	0.98	0
4	NAG	B	906	1	14,14,15	0.74	0	17,19,21	1.63	5 (29%)
5	SO4	B	911	-	4,4,4	0.66	0	6,6,6	0.33	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	B	904	1	14,14,15	0.78	0	17,19,21	1.46	3 (17%)
5	SO4	A	909	-	4,4,4	0.68	0	6,6,6	0.22	0
4	NAG	B	902	1	14,14,15	0.71	1 (7%)	17,19,21	1.30	2 (11%)
4	NAG	A	905	1	14,14,15	0.81	1 (7%)	17,19,21	1.06	0
4	NAG	A	903	1	14,14,15	0.41	0	17,19,21	1.34	2 (11%)
4	NAG	B	901	1	14,14,15	0.69	0	17,19,21	1.31	1 (5%)
4	NAG	B	903	1	14,14,15	0.48	0	17,19,21	1.04	1 (5%)
4	NAG	B	907	1	14,14,15	0.62	0	17,19,21	1.30	2 (11%)
7	GOL	B	912	-	5,5,5	0.27	0	5,5,5	0.59	0
4	NAG	A	901	1	14,14,15	0.44	0	17,19,21	1.23	3 (17%)
4	NAG	A	902	1	14,14,15	0.79	1 (7%)	17,19,21	1.12	1 (5%)
4	NAG	A	904	1	14,14,15	0.57	0	17,19,21	1.04	1 (5%)
4	NAG	A	906	1	14,14,15	0.58	0	17,19,21	0.92	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	NAG	B	905	1	-	2/6/23/26	0/1/1/1
4	NAG	B	906	1	-	2/6/23/26	0/1/1/1
4	NAG	B	904	1	-	0/6/23/26	0/1/1/1
4	NAG	B	902	1	-	1/6/23/26	0/1/1/1
4	NAG	A	905	1	-	0/6/23/26	0/1/1/1
4	NAG	A	903	1	-	1/6/23/26	0/1/1/1
4	NAG	B	901	1	-	0/6/23/26	0/1/1/1
4	NAG	B	903	1	-	2/6/23/26	0/1/1/1
4	NAG	B	907	1	-	1/6/23/26	0/1/1/1
7	GOL	B	912	-	-	4/4/4/4	-
4	NAG	A	901	1	-	0/6/23/26	0/1/1/1
4	NAG	A	902	1	-	1/6/23/26	0/1/1/1
4	NAG	A	904	1	-	0/6/23/26	0/1/1/1
4	NAG	A	906	1	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	905	NAG	O5-C1	-2.32	1.39	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	902	NAG	C1-C2	2.18	1.55	1.52
4	A	902	NAG	O5-C1	-2.07	1.40	1.43

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	901	NAG	C1-O5-C5	3.80	117.28	112.19
4	B	906	NAG	C1-O5-C5	3.77	117.25	112.19
4	A	903	NAG	C1-O5-C5	3.67	117.11	112.19
4	B	904	NAG	C2-N2-C7	-3.46	118.26	122.90
4	B	902	NAG	O7-C7-C8	-3.19	116.38	122.05

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	912	GOL	O1-C1-C2-C3
7	B	912	GOL	C1-C2-C3-O3
4	B	905	NAG	O5-C5-C6-O6
4	B	906	NAG	O5-C5-C6-O6
4	B	905	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	912	GOL	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, 95th 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	747/802 (93%)	0.36	38 (5%) 33 34	5, 19, 35, 64	20 (2%)
1	B	749/802 (93%)	0.34	42 (5%) 30 31	6, 18, 37, 58	20 (2%)
2	E	12/12 (100%)	1.61	5 (41%) 0 0	27, 32, 65, 82	0
2	F	12/12 (100%)	1.41	5 (41%) 0 0	23, 32, 62, 102	0
All	All	1520/1628 (93%)	0.37	90 (5%) 28 29	5, 18, 37, 102	40 (2%)

The worst 5 of 90 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	647	THR	6.2
1	B	644	LEU	5.9
1	B	647	THR	5.9
1	A	644	LEU	5.6
1	A	646	CYS	5.4

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, 95th 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.

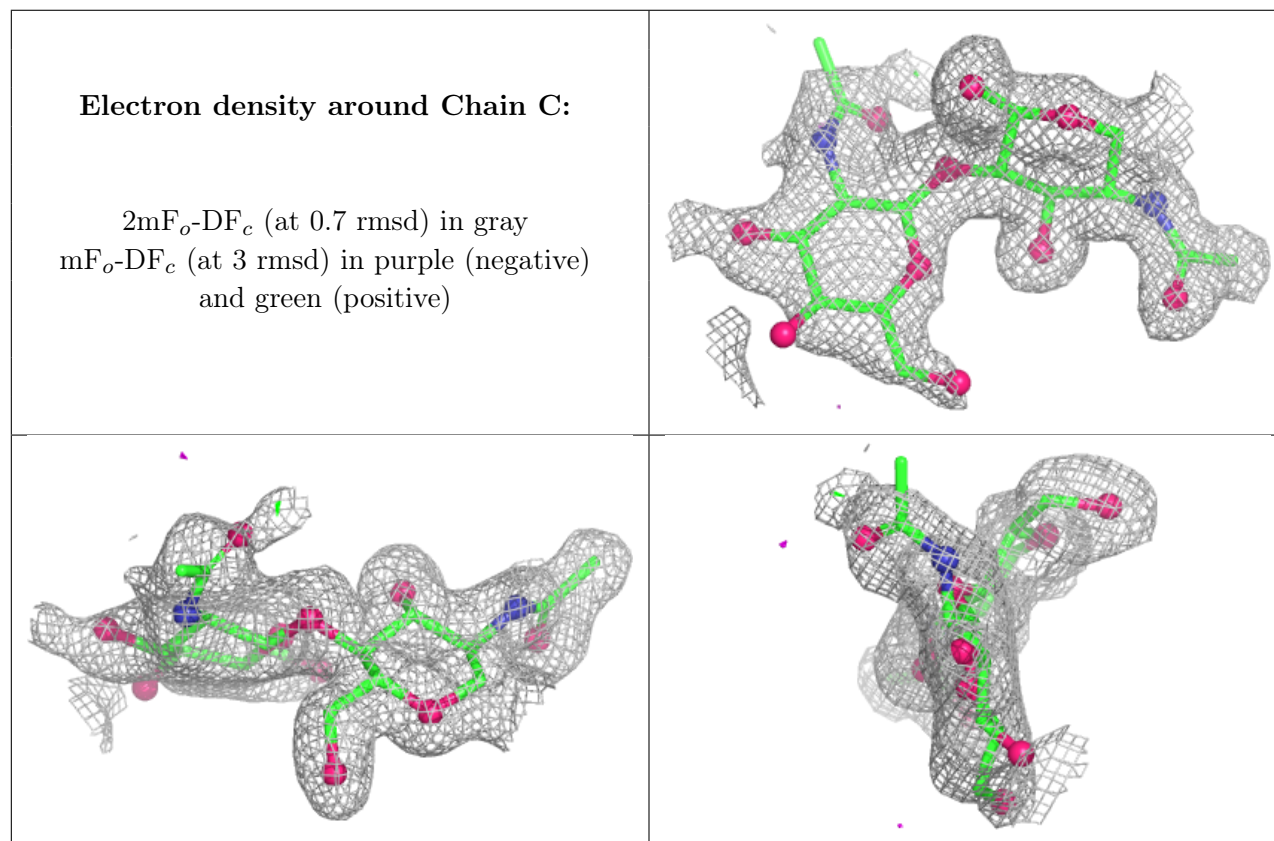
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	C	1	14/15	-	-	16,23,28,32	0
3	NAG	C	2	14/15	-	-	42,56,70,76	0

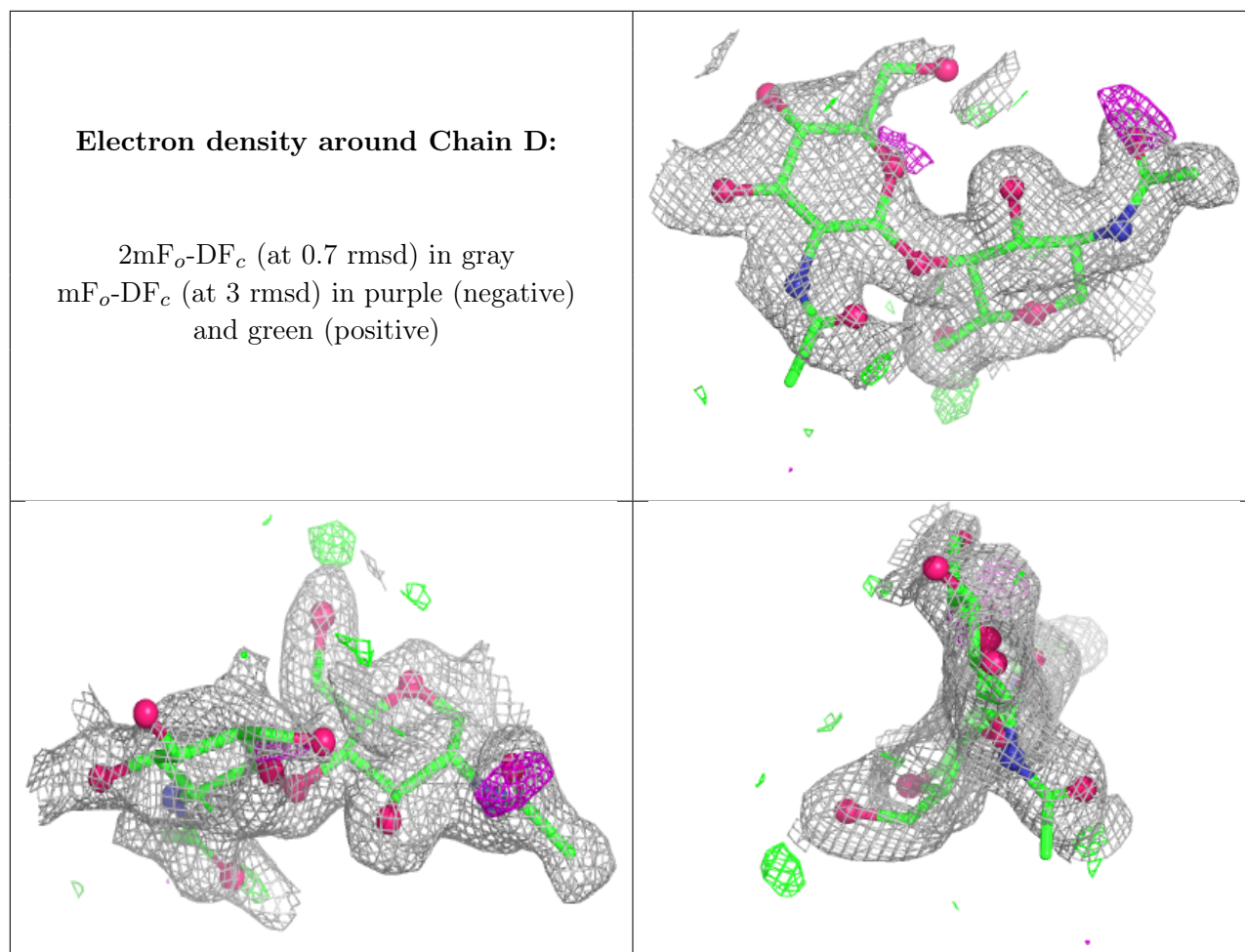
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	D	1	14/15	-	-	17,24,31,33	0
3	NAG	D	2	14/15	-	-	38,53,63,69	0

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.





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, 95th 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	905	14/15	0.76	0.16	35,49,53,58	0
4	NAG	B	906	14/15	0.79	0.18	33,46,58,63	0
4	NAG	A	903	14/15	0.81	0.12	36,42,46,62	0
4	NAG	B	905	14/15	0.82	0.14	31,34,45,47	0
4	NAG	A	901	14/15	0.82	0.12	33,38,46,53	0
7	GOL	B	912	6/6	0.82	0.17	39,46,47,49	0
4	NAG	B	903	14/15	0.83	0.12	29,35,44,57	0
4	NAG	B	901	14/15	0.83	0.12	34,39,50,56	0
4	NAG	A	904	14/15	0.84	0.13	30,40,48,54	0
4	NAG	B	904	14/15	0.86	0.12	22,31,37,45	0
5	SO4	B	911	5/5	0.87	0.12	21,34,45,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	SO4	A	909	5/5	0.87	0.13	21,35,44,46	0
4	NAG	B	907	14/15	0.91	0.10	23,29,35,37	0
4	NAG	A	902	14/15	0.92	0.08	19,23,28,33	0
4	NAG	A	906	14/15	0.93	0.09	22,26,36,38	0
4	NAG	B	902	14/15	0.93	0.08	16,20,30,33	0
6	NA	B	910	1/1	0.97	0.17	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.