



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:59 PM UTC

PDB ID : 8AWK / pdb_00008awk
Title : Structure of recombinant human beta-glucocerebrosidase in complex with D-carboxylosyl chloride
Authors : Rowland, R.J.; Davies, G.J.
Deposited on : 2022-08-30
Resolution : 1.58 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 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)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

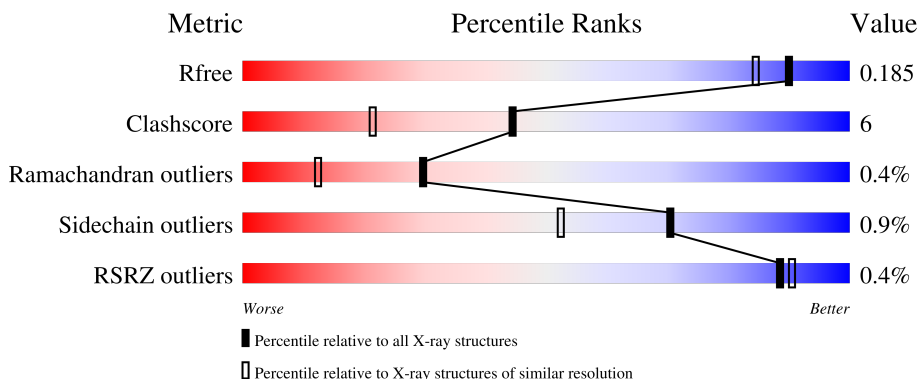
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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	1094 (1.58-1.58)
Clashscore	190562	1105 (1.58-1.58)
Ramachandran outliers	187476	1082 (1.58-1.58)
Sidechain outliers	187428	1081 (1.58-1.58)
RSRZ outliers	180081	1094 (1.58-1.58)

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	AAA	497	
2	AaA	4	

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
4	EDO	AAA	513	-	-	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 9182 atoms, of which 4310 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 Lysosomal acid glucosylceramidase.

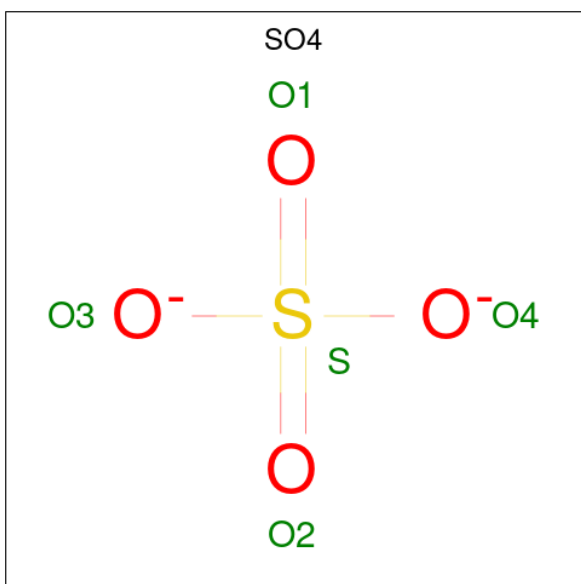
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	AAA	497	8234	2657	4096	718	747	16	222	25	0

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



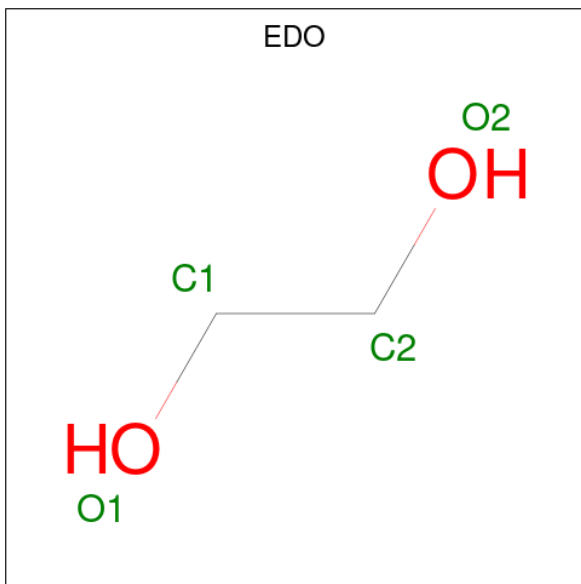
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	AaA	4	100	28	50	2	20	11	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



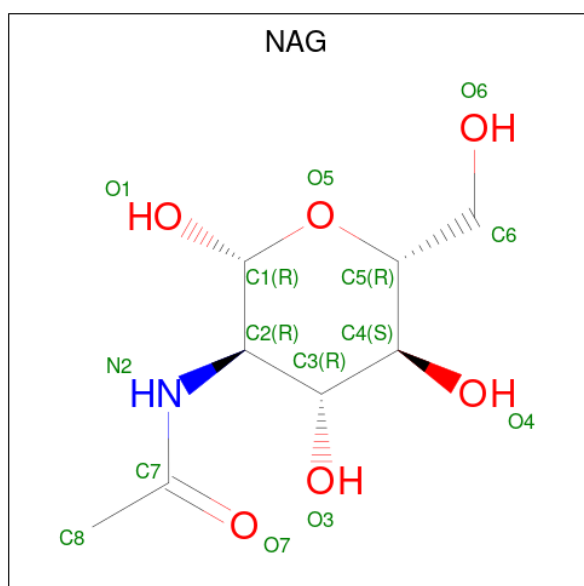
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		

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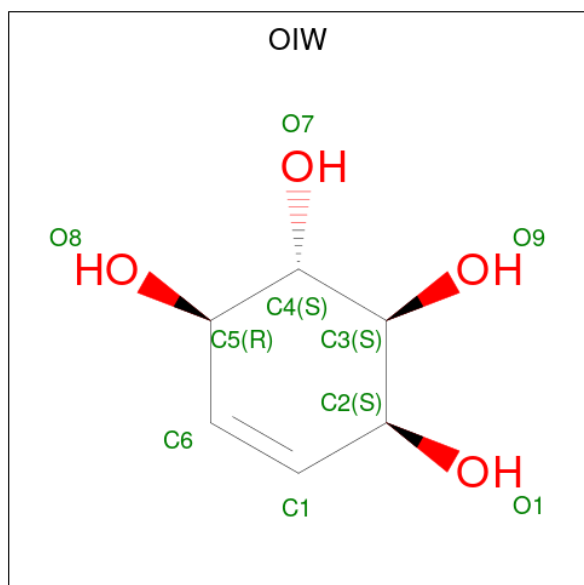
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
5	AAA	1	Total	C	H	N	O	3	0
			28	8	14	1	5		
5	AAA	1	Total	C	H	N	O	3	0
			28	8	14	1	5		

- Molecule 6 is (2 {S},3 {S},4 {R})-cyclohex-5-ene-1,2,3,4-tetrol (CCD ID: OIW) (formula: C₆H₁₀O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	AAA	1	Total	C	H	O	2	0
			19	6	10	3		

- Molecule 7 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	AAA	1	Total	Na	0	0
			1	1		

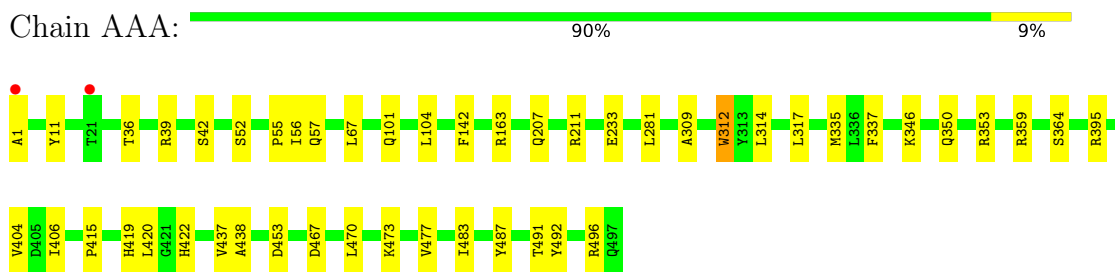
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	AAA	547	Total	O	0	0
			547	547		

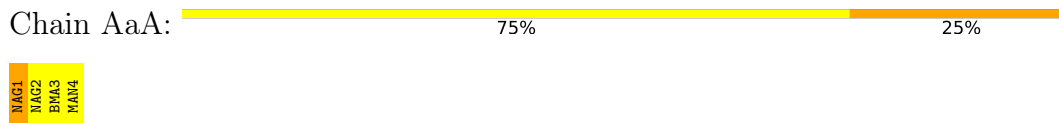
3 Residue-property plots [i](#)

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: Lysosomal acid glucosylceramidase



- Molecule 2: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.28Å 76.47Å 68.47Å 90.00° 102.05° 90.00°	Depositor
Resolution (Å)	52.16 – 1.58 52.16 – 1.58	Depositor EDS
% Data completeness (in resolution range)	99.9 (52.16-1.58) 99.9 (52.16-1.58)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 1.58Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.151 , 0.185 0.152 , 0.185	Depositor DCC
R_{free} test set	3644 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	17.3	Xtrriage
Anisotropy	0.070	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	9182	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% 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: MAN, SO4, OIW, EDO, BMA, NAG, 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	AAA	0.97	1/4257 (0.0%)	1.10	1/5797 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	487	TYR	C-O	6.01	1.31	1.23

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	453	ASP	CA-CB-CG	5.91	118.51	112.60

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	AAA	4138	4096	4054	50	1
2	AaA	50	50	43	1	1
3	AAA	15	0	0	1	0
4	AAA	84	126	126	9	0
5	AAA	28	28	26	1	0
6	AAA	9	10	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	AAA	1	0	0	0	0
8	AAA	547	0	0	10	0
All	All	4872	4310	4249	52	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 6.

All (52) 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:AAA:404[A]:VAL:HG11	1:AAA:406[A]:ILE:HD11	1.56	0.87
1:AAA:317[B]:LEU:C	1:AAA:317[B]:LEU:HD23	2.01	0.83
1:AAA:142:PHE:O	1:AAA:211[B]:ARG:NH1	2.15	0.78
1:AAA:404[A]:VAL:CG1	1:AAA:406[A]:ILE:CD1	2.62	0.77
1:AAA:395[B]:ARG:NH1	8:AAA:601:HOH:O	2.18	0.76
1:AAA:359:ARG:HH21	4:AAA:513:EDO:C2	2.01	0.73
1:AAA:55:PRO:HG2	1:AAA:57[B]:GLN:HE22	1.54	0.72
1:AAA:404[A]:VAL:CG1	1:AAA:406[A]:ILE:HD11	2.21	0.69
1:AAA:101:GLN:HE21	1:AAA:163:ARG:HH22	1.40	0.68
1:AAA:346[B]:LYS:HE3	8:AAA:971:HOH:O	1.94	0.67
1:AAA:404[A]:VAL:CG1	1:AAA:406[A]:ILE:HD13	2.25	0.65
1:AAA:207[A]:GLN:O	1:AAA:211[A]:ARG:HG3	1.97	0.65
1:AAA:359:ARG:HH21	4:AAA:513:EDO:H22	1.62	0.63
1:AAA:496:ARG:HH22	4:AAA:523:EDO:H21	1.63	0.63
1:AAA:317[B]:LEU:C	1:AAA:317[B]:LEU:CD2	2.72	0.61
1:AAA:353[A]:ARG:HD3	3:AAA:501:SO4:O1	2.02	0.60
1:AAA:364:SER:OG	1:AAA:419:HIS:HD2	1.84	0.60
1:AAA:42:SER:OG	1:AAA:422:HIS:HE1	1.85	0.59
1:AAA:346[A]:LYS:NZ	8:AAA:604:HOH:O	2.29	0.58
5:AAA:505:NAG:H83	5:AAA:505:NAG:H3	1.86	0.57
1:AAA:346[B]:LYS:CE	8:AAA:971:HOH:O	2.53	0.55
1:AAA:56:ILE:HG21	1:AAA:477:VAL:HG12	1.89	0.54
1:AAA:346[B]:LYS:NZ	8:AAA:604:HOH:O	2.41	0.54
1:AAA:359:ARG:HE	4:AAA:513:EDO:C2	2.21	0.53
1:AAA:39[B]:ARG:CZ	1:AAA:52:SER:OG	2.57	0.53
1:AAA:67:LEU:HG	1:AAA:470[A]:LEU:HD11	1.90	0.53
1:AAA:39[B]:ARG:HG3	1:AAA:492:TYR:CE1	2.43	0.53
1:AAA:317[B]:LEU:HD23	1:AAA:317[B]:LEU:O	2.08	0.52
1:AAA:359:ARG:HH21	4:AAA:513:EDO:H21	1.75	0.51
1:AAA:314:LEU:O	1:AAA:317[B]:LEU:HD22	2.12	0.50
1:AAA:438:ALA:HB2	4:AAA:526:EDO:H11	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:39[B]:ARG:HE	1:AAA:39[B]:ARG:C	2.20	0.49
1:AAA:404[A]:VAL:HG12	1:AAA:406[A]:ILE:CD1	2.42	0.49
1:AAA:11:TYR:CE1	1:AAA:353[A]:ARG:HG3	2.49	0.47
1:AAA:438:ALA:HB2	4:AAA:526:EDO:C1	2.43	0.47
1:AAA:406[B]:ILE:HD12	8:AAA:1083:HOH:O	2.14	0.46
1:AAA:404[B]:VAL:HG23	1:AAA:404[B]:VAL:O	2.15	0.46
1:AAA:101:GLN:NE2	1:AAA:163:ARG:HH12	2.16	0.43
1:AAA:404[A]:VAL:HG12	1:AAA:406[A]:ILE:HD13	1.99	0.43
1:AAA:437[A]:VAL:HG12	8:AAA:988:HOH:O	2.17	0.43
1:AAA:1:ALA:HB3	8:AAA:654:HOH:O	2.19	0.43
1:AAA:11:TYR:CD1	1:AAA:353[A]:ARG:HG3	2.54	0.43
1:AAA:36[B]:THR:HG21	8:AAA:862:HOH:O	2.19	0.43
1:AAA:350:GLN:CD	1:AAA:353[B]:ARG:HG3	2.44	0.42
1:AAA:467:ASP:HB3	1:AAA:483[A]:ILE:HD11	2.00	0.42
1:AAA:39[A]:ARG:NE	4:AAA:520:EDO:O2	2.54	0.41
1:AAA:104:LEU:HD23	1:AAA:104:LEU:C	2.46	0.41
1:AAA:309:ALA:HA	1:AAA:337:PHE:O	2.21	0.41
1:AAA:422:HIS:HD2	1:AAA:491:THR:OG1	2.04	0.40
1:AAA:359:ARG:NH2	4:AAA:513:EDO:H21	2.35	0.40
8:AAA:608:HOH:O	2:AaA:1:NAG:H82	2.21	0.40
1:AAA:312:TRP:CD1	1:AAA:312:TRP:C	2.99	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)
1:AAA:473:LYS:HZ3	2:AaA:1:NAG:HO3[1_455]	0.98	0.62

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	AAA	519/497 (104%)	506 (98%)	11 (2%)	2 (0%)	30 12

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	233	GLU
1	AAA	281	LEU

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	AAA	448/424 (106%)	444 (99%)	4 (1%)	70 52

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	312	TRP
1	AAA	335	MET
1	AAA	415	PRO
1	AAA	420	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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	AaA	1	1,2	14,14,15	0.86	0	17,19,21	1.19	3 (17%)
2	NAG	AaA	2	2	14,14,15	0.46	0	17,19,21	1.64	2 (11%)
2	BMA	AaA	3	2	11,11,12	0.45	0	15,15,17	1.25	1 (6%)
2	MAN	AaA	4	2	11,11,12	0.69	0	15,15,17	1.16	2 (13%)

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	AaA	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	AaA	2	2	-	0/6/23/26	0/1/1/1
2	BMA	AaA	3	2	-	0/2/19/22	0/1/1/1
2	MAN	AaA	4	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AaA	2	NAG	C1-O5-C5	5.26	119.24	112.19
2	AaA	3	BMA	C1-O5-C5	3.36	116.68	112.19
2	AaA	4	MAN	C1-C2-C3	3.28	114.42	109.64
2	AaA	2	NAG	C3-C4-C5	2.51	114.78	110.23
2	AaA	4	MAN	C2-C3-C4	2.25	114.82	110.86
2	AaA	1	NAG	O7-C7-N2	2.22	125.90	121.98
2	AaA	1	NAG	O7-C7-C8	-2.05	118.40	122.05
2	AaA	1	NAG	C4-C3-C2	-2.02	108.06	111.02

There are no chirality outliers.

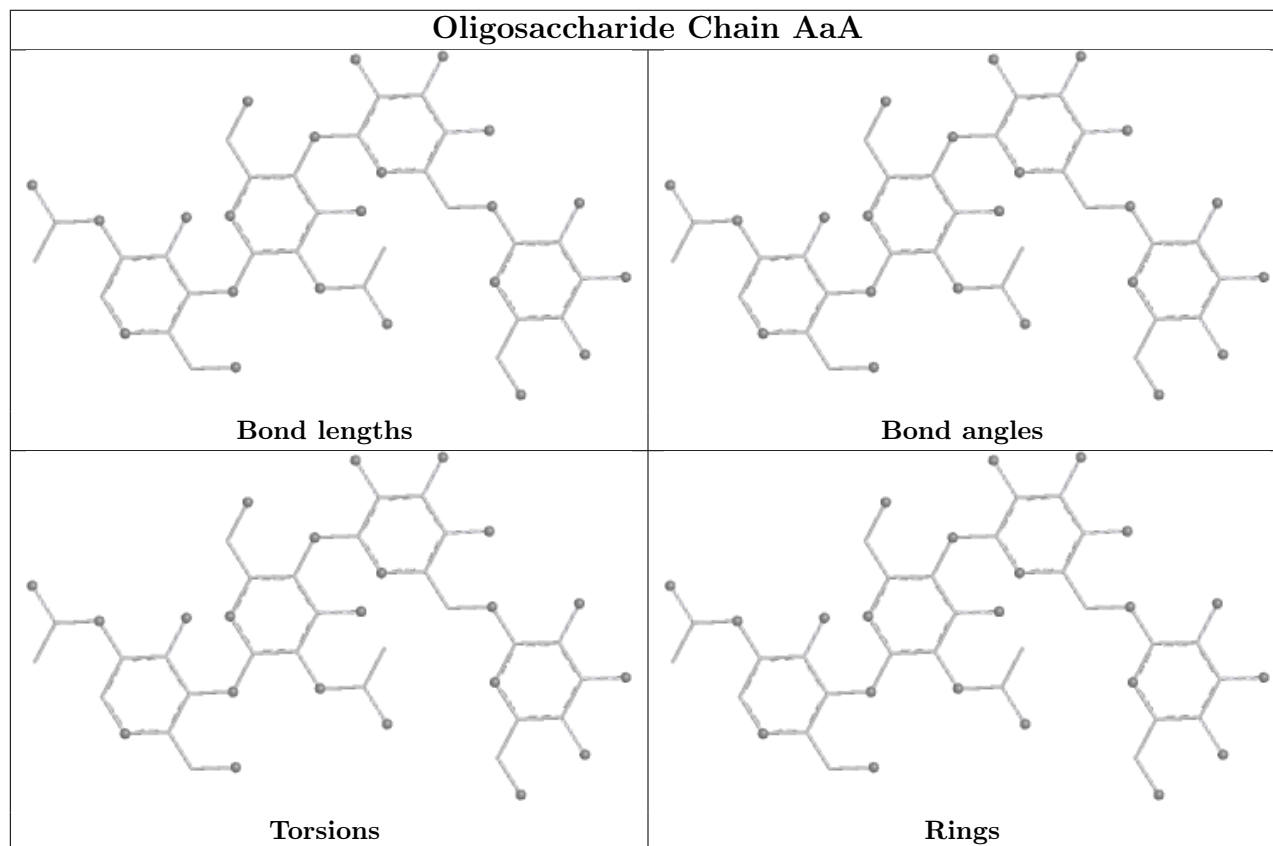
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AaA	1	NAG	1	1

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 28 ligands modelled in this entry, 1 is monoatomic - leaving 27 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	EDO	AAA	511	-	3,3,3	0.22	0	2,2,2	0.21	0
3	SO4	AAA	506	-	4,4,4	0.34	0	6,6,6	0.12	0
4	EDO	AAA	520	-	3,3,3	0.23	0	2,2,2	0.09	0
4	EDO	AAA	522	-	3,3,3	0.23	0	2,2,2	0.29	0
5	NAG	AAA	505	1	14,14,15	0.78	0	17,19,21	1.83	5 (29%)
5	NAG	AAA	517	1	14,14,15	1.05	1 (7%)	17,19,21	0.91	0
4	EDO	AAA	507	-	3,3,3	0.05	0	2,2,2	0.06	0
4	EDO	AAA	504	-	3,3,3	0.10	0	2,2,2	0.20	0
4	EDO	AAA	519	-	3,3,3	0.35	0	2,2,2	0.20	0
4	EDO	AAA	508	-	3,3,3	0.22	0	2,2,2	0.24	0
4	EDO	AAA	526	-	3,3,3	0.12	0	2,2,2	0.38	0
4	EDO	AAA	512	-	3,3,3	0.21	0	2,2,2	0.14	0
4	EDO	AAA	514	-	3,3,3	0.44	0	2,2,2	0.14	0
4	EDO	AAA	525	-	3,3,3	0.20	0	2,2,2	0.27	0
4	EDO	AAA	509	-	3,3,3	0.06	0	2,2,2	0.04	0
4	EDO	AAA	516	-	3,3,3	0.05	0	2,2,2	0.01	0
4	EDO	AAA	515	-	3,3,3	0.05	0	2,2,2	0.23	0
4	EDO	AAA	503	-	3,3,3	0.19	0	2,2,2	0.04	0
3	SO4	AAA	501	-	4,4,4	0.50	0	6,6,6	0.25	0
4	EDO	AAA	518	-	3,3,3	0.20	0	2,2,2	0.07	0
6	OIW	AAA	527	1	9,9,10	1.06	0	9,12,14	1.70	1 (11%)
4	EDO	AAA	513	-	3,3,3	0.41	0	2,2,2	0.54	0
4	EDO	AAA	523	-	3,3,3	0.44	0	2,2,2	0.50	0
4	EDO	AAA	510	-	3,3,3	0.25	0	2,2,2	0.08	0
3	SO4	AAA	502	-	4,4,4	0.37	0	6,6,6	0.17	0
4	EDO	AAA	521	-	3,3,3	0.08	0	2,2,2	0.21	0
4	EDO	AAA	524	-	3,3,3	0.06	0	2,2,2	0.09	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	EDO	AAA	511	-	-	0/1/1/1	-
4	EDO	AAA	520	-	-	0/1/1/1	-
4	EDO	AAA	522	-	-	1/1/1/1	-
5	NAG	AAA	505	1	-	3/6/23/26	0/1/1/1
5	NAG	AAA	517	1	-	0/6/23/26	0/1/1/1
4	EDO	AAA	507	-	-	0/1/1/1	-
4	EDO	AAA	504	-	-	1/1/1/1	-
4	EDO	AAA	519	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	AAA	508	-	-	1/1/1/1	-
4	EDO	AAA	526	-	-	1/1/1/1	-
4	EDO	AAA	512	-	-	1/1/1/1	-
4	EDO	AAA	514	-	-	0/1/1/1	-
4	EDO	AAA	525	-	-	1/1/1/1	-
4	EDO	AAA	509	-	-	0/1/1/1	-
4	EDO	AAA	516	-	-	1/1/1/1	-
4	EDO	AAA	515	-	-	0/1/1/1	-
4	EDO	AAA	503	-	-	1/1/1/1	-
4	EDO	AAA	518	-	-	0/1/1/1	-
6	OIW	AAA	527	1	-	-	0/1/1/1
4	EDO	AAA	513	-	-	1/1/1/1	-
4	EDO	AAA	523	-	-	1/1/1/1	-
4	EDO	AAA	510	-	-	0/1/1/1	-
4	EDO	AAA	521	-	-	1/1/1/1	-
4	EDO	AAA	524	-	-	1/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	AAA	517	NAG	C1-C2	2.26	1.55	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	AAA	527	OIW	C3-C2-C1	-4.47	106.95	112.42
5	AAA	505	NAG	C8-C7-N2	4.44	123.49	116.12
5	AAA	505	NAG	C2-N2-C7	3.30	127.33	122.90
5	AAA	505	NAG	C1-O5-C5	2.56	115.61	112.19
5	AAA	505	NAG	O7-C7-C8	-2.16	118.21	122.05
5	AAA	505	NAG	O7-C7-N2	-2.08	118.30	121.98

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	AAA	505	NAG	C8-C7-N2-C2
5	AAA	505	NAG	O7-C7-N2-C2
4	AAA	503	EDO	O1-C1-C2-O2
4	AAA	525	EDO	O1-C1-C2-O2
4	AAA	513	EDO	O1-C1-C2-O2

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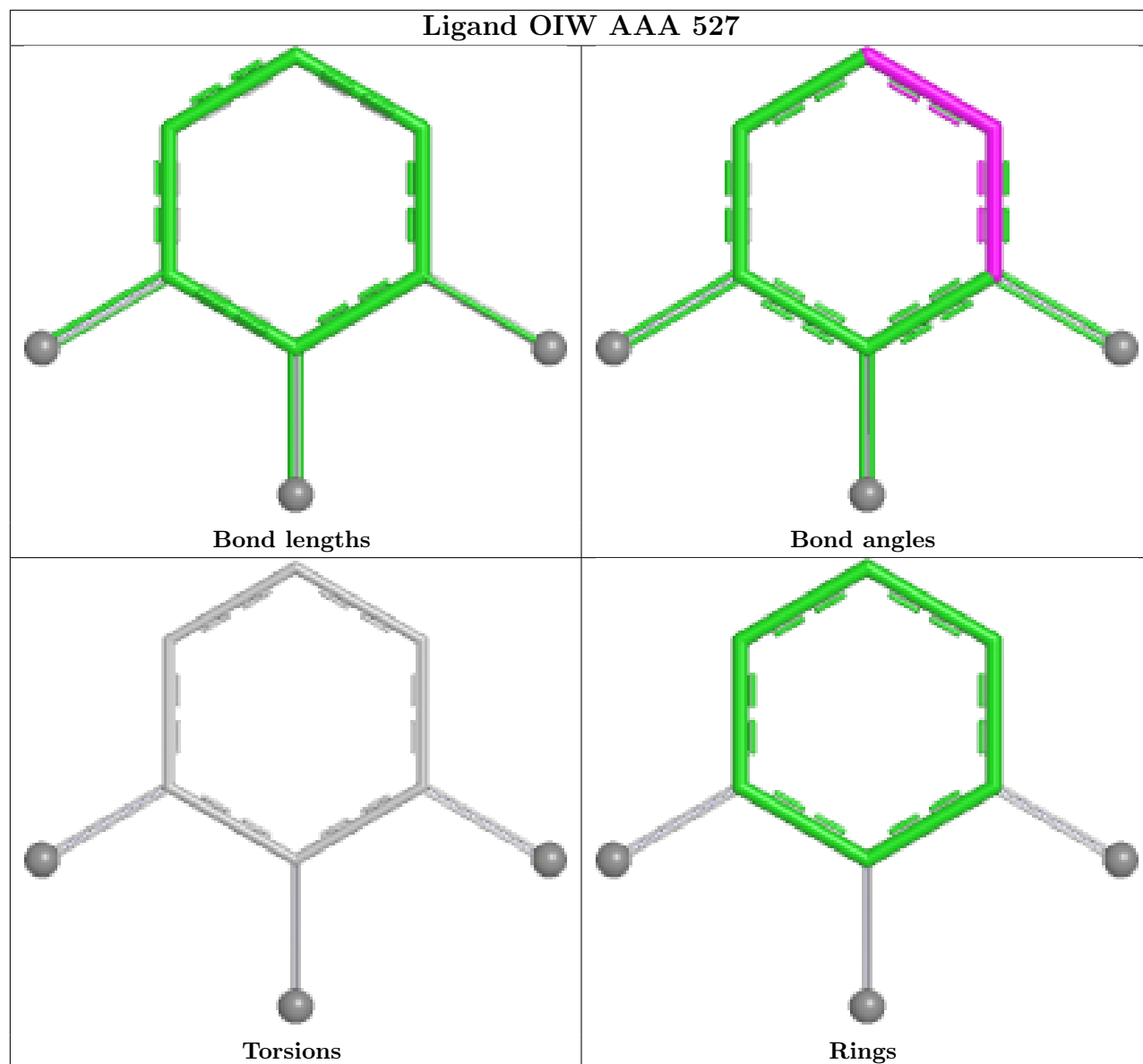
Mol	Chain	Res	Type	Atoms
4	AAA	522	EDO	O1-C1-C2-O2
4	AAA	523	EDO	O1-C1-C2-O2
4	AAA	521	EDO	O1-C1-C2-O2
4	AAA	524	EDO	O1-C1-C2-O2
4	AAA	508	EDO	O1-C1-C2-O2
5	AAA	505	NAG	C3-C2-N2-C7
4	AAA	526	EDO	O1-C1-C2-O2
4	AAA	504	EDO	O1-C1-C2-O2
4	AAA	512	EDO	O1-C1-C2-O2
4	AAA	516	EDO	O1-C1-C2-O2

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	AAA	520	EDO	1	0
5	AAA	505	NAG	1	0
4	AAA	526	EDO	2	0
3	AAA	501	SO4	1	0
4	AAA	513	EDO	5	0
4	AAA	523	EDO	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 than 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.



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	AAA	497/497 (100%)	-0.62	2 (0%) 88 90	7, 17, 26, 37	30 (6%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	1	ALA	2.6
1	AAA	21	THR	2.1

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

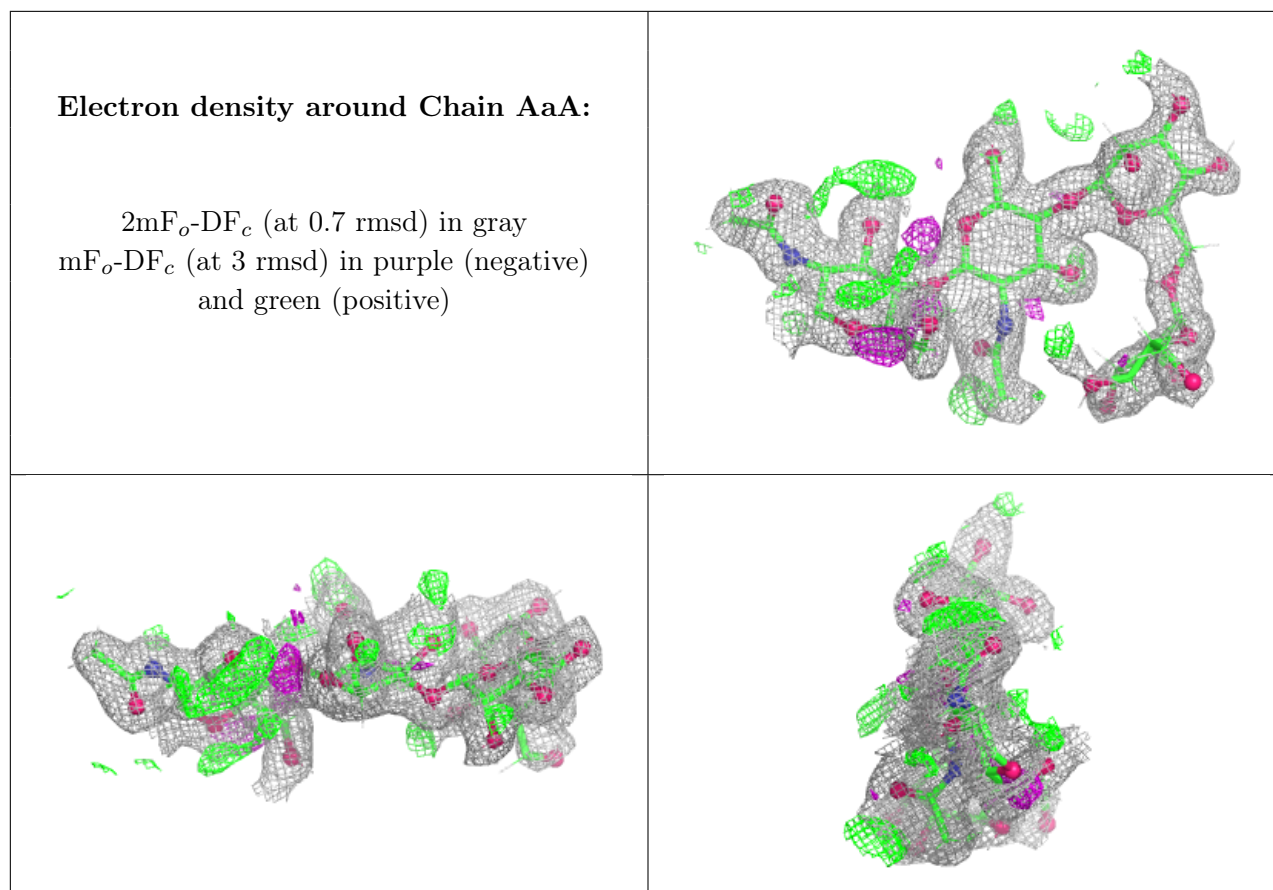
There are no non-standard protein/DNA/RNA residues in this entry.

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
2	NAG	AaA	1	14/15	-	-	24,30,33,36	4
2	NAG	AaA	2	14/15	-	-	29,37,42,47	2
2	BMA	AaA	3	11/12	-	-	57,62,67,68	3
2	MAN	AaA	4	11/12	-	-	71,76,79,80	4

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.

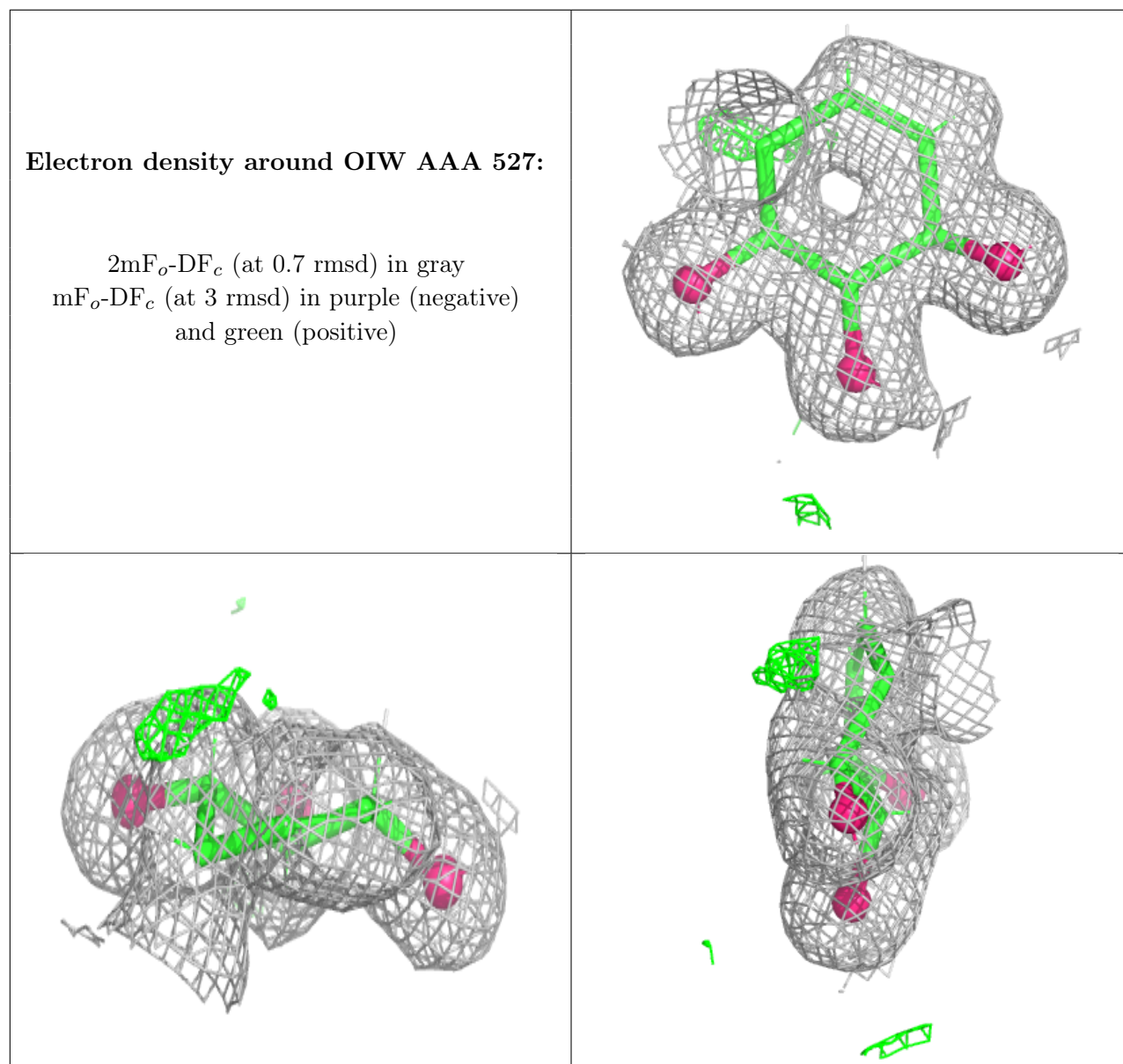
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	AAA	505	14/15	0.61	0.17	67,79,84,93	3
5	NAG	AAA	517	14/15	0.76	0.12	50,54,60,62	3
3	SO4	AAA	506	5/5	0.77	0.14	79,81,88,91	0
4	EDO	AAA	512	4/4	0.81	0.14	47,51,52,53	1
4	EDO	AAA	525	4/4	0.82	0.14	49,53,54,55	1
4	EDO	AAA	522	4/4	0.83	0.16	40,45,46,47	1
4	EDO	AAA	524	4/4	0.84	0.13	51,60,63,63	1
4	EDO	AAA	523	4/4	0.85	0.14	41,44,45,46	1
4	EDO	AAA	526	4/4	0.85	0.16	45,49,50,50	1
4	EDO	AAA	509	4/4	0.86	0.13	51,52,53,54	1
4	EDO	AAA	516	4/4	0.87	0.12	52,53,57,57	1
4	EDO	AAA	518	4/4	0.87	0.15	43,45,49,50	1
4	EDO	AAA	504	4/4	0.87	0.11	48,48,53,53	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	EDO	AAA	503	4/4	0.88	0.11	47,48,48,48	1
4	EDO	AAA	508	4/4	0.88	0.11	44,44,48,49	1
4	EDO	AAA	513	4/4	0.88	0.15	27,29,34,37	10
4	EDO	AAA	521	4/4	0.89	0.13	37,42,52,52	1
4	EDO	AAA	507	4/4	0.89	0.11	35,39,44,45	1
4	EDO	AAA	519	4/4	0.92	0.12	24,28,36,39	1
4	EDO	AAA	515	4/4	0.95	0.08	30,33,37,37	1
3	SO4	AAA	502	5/5	0.96	0.07	36,37,37,39	0
4	EDO	AAA	520	4/4	0.96	0.08	29,33,34,34	1
4	EDO	AAA	511	4/4	0.97	0.06	22,26,27,28	1
6	OIW	AAA	527	9/10	0.97	0.06	17,19,21,22	5
4	EDO	AAA	514	4/4	0.98	0.05	18,20,21,22	1
4	EDO	AAA	510	4/4	0.98	0.04	22,23,24,24	1
3	SO4	AAA	501	5/5	0.98	0.06	22,24,26,31	0
7	NA	AAA	528	1/1	0.99	0.03	17,17,17,17	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.



6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.