



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 07:08 AM UTC

PDB ID : 6YTP / pdb_00006ytp
Title : Structure of recombinant human beta-glucocerebrosidase in complex with
azide tagged cyclophellitol epoxide inhibitor
Authors : Rowland, R.J.; Davies, G.J.
Deposited on : 2020-04-24
Resolution : 1.70 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)
Xtriage (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

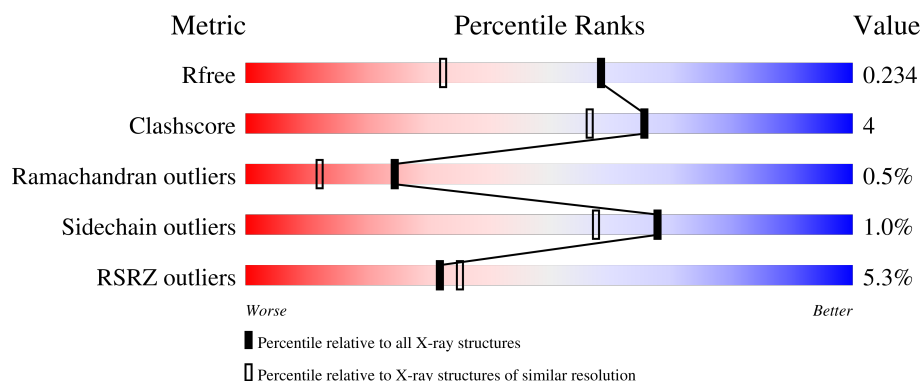
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	5% 94% 6%
1	BBB	497	5% 93% 7%
2	A	2	100%
2	B	2	50% 50%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 16941 atoms, of which 8042 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 Glucosylceramidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	AAA	497	Total	C	H	N	O	S	214	9	0
			7895	2566	3907	682	724	16			
1	BBB	497	Total	C	H	N	O	S	207	8	0
			7871	2560	3898	675	721	17			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	495	HIS	ARG	conflict	UNP P04062
BBB	495	HIS	ARG	conflict	UNP P04062

- 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	A	2	Total	C	H	N	O	5	0	0
			55	16	27	2	10			
2	B	2	Total	C	H	N	O	5	0	0
			56	16	28	2	10			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 4 is SULFATE ION (CCD ID: SO₄) (formula: O₄S).



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

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

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



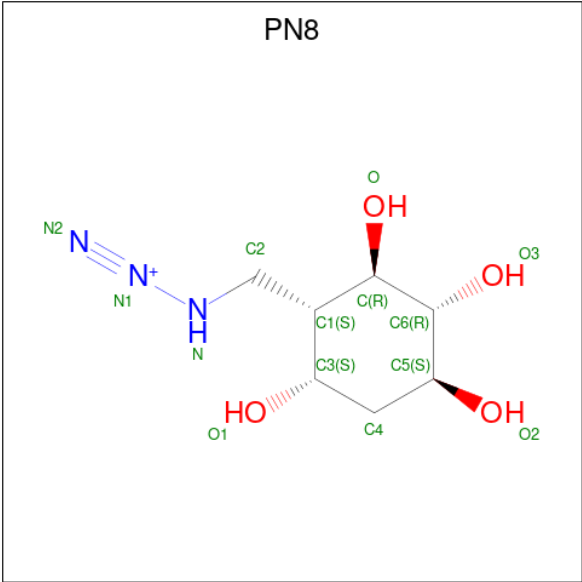
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
5	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
5	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
5	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
5	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
5	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
5	AAA	1	Total	C	H	O	1	0
			10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

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	AAA	1	Total	C	H	O	2	0
			14	3	8	3		
6	AAA	1	Total	C	H	O	2	0
			14	3	8	3		
6	BBB	1	Total	C	H	O	2	0
			14	3	8	3		
6	BBB	1	Total	C	H	O	2	0
			14	3	8	3		
6	BBB	1	Total	C	H	O	2	0
			14	3	8	3		
6	BBB	1	Total	C	H	O	2	0
			14	3	8	3		

- Molecule 7 is (1 {S},2 {R},3 {R},4 {S},5 {S})-4-[[(\$l^{5}\$-azanylidyne-\$l^{5}\$-azanyl)amino]methyl]cyclohexane-1,2,3,5-tetrol (CCD ID: PN8) (formula: C₇H₁₄N₃O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	AAA	1	Total	C	H	N	O	4	0
			27	7	13	3	4		
7	BBB	1	Total	C	H	N	O	4	0
			27	7	13	3	4		

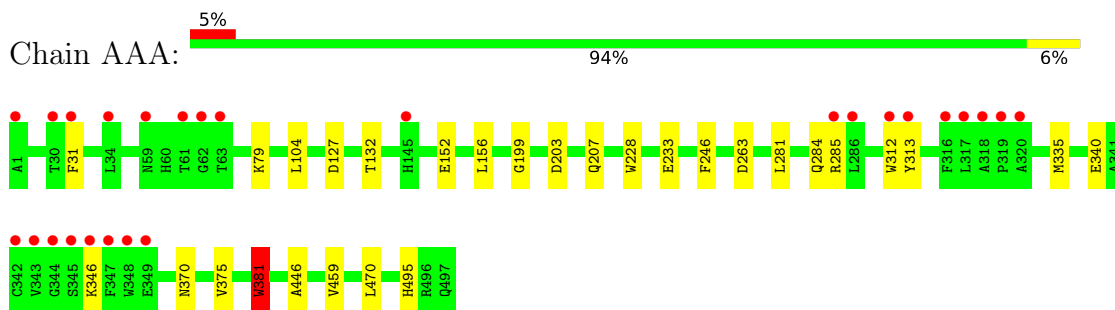
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	AAA	338	Total	O	0	0
			338	338		
8	BBB	323	Total	O	0	0
			323	323		

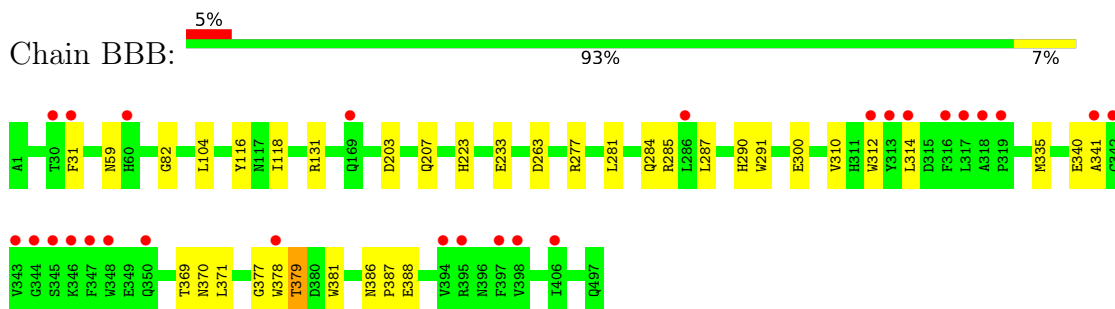
3 Residue-property plots [i](#)

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.

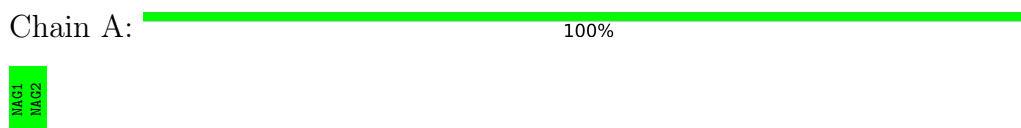
- Molecule 1: Glucosylceramidase



- Molecule 1: Glucosylceramidase



- 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



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	108.89Å 285.77Å 91.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	68.20 – 1.70 68.20 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (68.20-1.70) 99.9 (68.20-1.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.186 , 0.212 0.208 , 0.234	Depositor DCC
R_{free} test set	7842 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	21.8	Xtriage
Anisotropy	0.607	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 34.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16941	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% 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: GOL, PN8, SO4, NAG, EDO

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	0.99	1/4110 (0.0%)	1.20	3/5607 (0.1%)
1	BBB	0.99	1/4094 (0.0%)	1.22	2/5584 (0.0%)
All	All	0.99	2/8204 (0.0%)	1.21	5/11191 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BBB	340	GLU	CD-OE2	9.77	1.44	1.25
1	AAA	340	GLU	CD-OE2	8.88	1.42	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BBB	379	THR	CA-CB-OG1	-8.46	96.91	109.60
1	BBB	31	PHE	CB-CA-C	7.81	118.68	109.47
1	AAA	132	THR	CB-CA-C	5.28	118.46	109.75
1	AAA	346	LYS	CA-C-N	5.15	127.18	120.28
1	AAA	346	LYS	C-N-CA	5.15	127.18	120.28

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	3988	3907	3867	26	0
1	BBB	3973	3898	3863	32	0
2	A	28	27	25	0	0
2	B	28	28	25	0	0
3	AAA	14	14	13	0	0
3	BBB	14	14	13	0	0
4	AAA	35	0	0	1	0
4	BBB	40	0	0	0	0
5	AAA	32	48	48	0	0
5	BBB	16	24	24	1	0
6	AAA	12	16	16	1	0
6	BBB	30	40	40	6	0
7	AAA	14	13	0	1	0
7	BBB	14	13	0	0	0
8	AAA	338	0	0	2	0
8	BBB	323	0	0	4	0
All	All	8899	8042	7934	62	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 4.

All (62) 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:BBB:370:ASN:CB	1:BBB:378:TRP:HE1	1.89	0.86
1:AAA:285:ARG:CZ	1:AAA:312:TRP:HZ3	1.91	0.82
1:BBB:370:ASN:HB3	1:BBB:378:TRP:HE1	1.45	0.81
1:BBB:207:GLN:NE2	1:BBB:263:ASP:OD1	2.17	0.78
1:AAA:207:GLN:NE2	1:AAA:263:ASP:OD1	2.18	0.73
1:AAA:285:ARG:CZ	1:AAA:312:TRP:CZ3	2.74	0.69
6:AAA:519:GOL:O2	8:AAA:601:HOH:O	2.12	0.68
1:AAA:370:ASN:HD22	1:AAA:375:VAL:HG11	1.59	0.67
1:BBB:388:GLU:OE1	8:BBB:601:HOH:O	2.14	0.66
1:BBB:310[B]:VAL:HG12	8:BBB:676:HOH:O	1.95	0.65
1:BBB:312:TRP:HE1	1:BBB:370:ASN:HD21	1.46	0.63
1:AAA:152:GLU:HA	1:AAA:156[A]:LEU:HD12	1.82	0.61
1:AAA:285:ARG:NE	1:AAA:312:TRP:HZ3	1.97	0.61
1:BBB:312:TRP:CE3	1:BBB:341:ALA:HB1	2.36	0.61
1:BBB:82:GLY:HA3	1:BBB:118:ILE:O	2.04	0.56
1:BBB:131:ARG:HH22	6:BBB:517:GOL:H11	1.71	0.56
1:BBB:131:ARG:HH22	6:BBB:517:GOL:C1	2.19	0.56
7:AAA:521:PN8:O1	7:AAA:521:PN8:N1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:285:ARG:NE	1:AAA:312:TRP:CZ3	2.75	0.53
1:BBB:312:TRP:CE3	1:BBB:341:ALA:CB	2.92	0.53
1:BBB:203:ASP:OD1	1:BBB:203:ASP:C	2.51	0.52
1:AAA:207:GLN:HE22	1:AAA:263:ASP:HA	1.74	0.52
1:AAA:285:ARG:HD3	1:AAA:312:TRP:CH2	2.45	0.52
1:AAA:284:GLN:OE1	1:AAA:313:TYR:CE1	2.63	0.52
1:BBB:312:TRP:HE1	1:BBB:370:ASN:ND2	2.09	0.50
1:BBB:207:GLN:HE22	1:BBB:263:ASP:HA	1.76	0.50
1:BBB:223:HIS:HE1	8:BBB:873:HOH:O	1.93	0.50
1:BBB:377:GLY:C	1:BBB:378:TRP:CE3	2.89	0.50
1:AAA:284:GLN:NE2	1:AAA:313:TYR:CD1	2.81	0.49
1:BBB:370:ASN:HB2	1:BBB:378:TRP:HE1	1.74	0.46
1:BBB:277:ARG:HH11	6:BBB:520:GOL:H32	1.79	0.46
1:BBB:377:GLY:C	1:BBB:378:TRP:CD2	2.94	0.46
1:AAA:381:TRP:HA	1:AAA:381:TRP:CE3	2.51	0.46
1:AAA:127:ASP:HB3	1:AAA:246:PHE:CG	2.51	0.46
1:AAA:312:TRP:HE1	1:AAA:370:ASN:HD21	1.62	0.46
1:AAA:284:GLN:NE2	1:AAA:313:TYR:CE1	2.84	0.46
1:BBB:277:ARG:HH11	6:BBB:520:GOL:C3	2.29	0.45
1:AAA:312:TRP:NE1	1:AAA:370:ASN:HD21	2.14	0.45
1:BBB:104:LEU:C	1:BBB:104:LEU:HD23	2.42	0.45
1:AAA:31:PHE:CB	1:AAA:495:HIS:CE1	2.99	0.45
1:AAA:79:LYS:HE2	1:AAA:228:TRP:CE2	2.52	0.44
1:AAA:284:GLN:NE2	1:AAA:284:GLN:HA	2.32	0.44
1:BBB:285:ARG:HB3	1:BBB:310[B]:VAL:HG11	2.00	0.44
1:BBB:371:LEU:HD21	1:BBB:378:TRP:CH2	2.51	0.44
1:BBB:371:LEU:CD2	1:BBB:378:TRP:CH2	3.01	0.44
1:AAA:446:ALA:HA	1:AAA:459:VAL:O	2.18	0.43
1:AAA:199:GLY:HA3	1:AAA:203:ASP:OD2	2.19	0.43
6:BBB:520:GOL:H11	8:BBB:800:HOH:O	2.18	0.43
1:BBB:378:TRP:CE3	1:BBB:378:TRP:N	2.88	0.42
1:BBB:82:GLY:HA2	1:BBB:116:TYR:CD2	2.53	0.42
1:BBB:287:LEU:HB3	1:BBB:291:TRP:CD1	2.55	0.42
1:BBB:290:HIS:ND1	6:BBB:519:GOL:H11	2.34	0.42
1:AAA:203:ASP:C	1:AAA:203:ASP:OD1	2.62	0.42
1:AAA:381:TRP:HA	1:AAA:381:TRP:HE3	1.85	0.42
1:AAA:152:GLU:O	1:AAA:156[B]:LEU:HB2	2.20	0.41
4:AAA:508:SO4:O3	8:AAA:603:HOH:O	2.18	0.41
1:BBB:285:ARG:HB3	1:BBB:310[B]:VAL:CG1	2.50	0.41
1:BBB:284:GLN:HG3	1:BBB:314:LEU:HD12	2.01	0.41
1:BBB:369:THR:HG21	5:BBB:514:EDO:C1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BBB:386:ASN:HB2	1:BBB:387:PRO:CD	2.50	0.41
1:AAA:104:LEU:C	1:AAA:104:LEU:HD23	2.46	0.41
1:AAA:207:GLN:NE2	1:AAA:263:ASP:HA	2.34	0.41

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	AAA	504/497 (101%)	488 (97%)	13 (3%)	3 (1%)	21	9
1	BBB	503/497 (101%)	482 (96%)	19 (4%)	2 (0%)	30	16
All	All	1007/994 (101%)	970 (96%)	32 (3%)	5 (0%)	24	12

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	233	GLU
1	AAA	381	TRP
1	BBB	233	GLU
1	BBB	281	LEU
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	427/424 (101%)	424 (99%)	3 (1%)	76	69
1	BBB	428/424 (101%)	422 (99%)	6 (1%)	59	46
All	All	855/848 (101%)	846 (99%)	9 (1%)	68	54

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

Mol	Chain	Res	Type
1	AAA	335	MET
1	AAA	381	TRP
1	AAA	470	LEU
1	BBB	59	ASN
1	BBB	300[A]	GLU
1	BBB	300[B]	GLU
1	BBB	335	MET
1	BBB	379	THR
1	BBB	381	TRP

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

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 ⓘ

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	A	1	1,2	14,14,15	0.44	0	17,19,21	0.56	0
2	NAG	A	2	2	14,14,15	0.55	0	17,19,21	0.73	0
2	NAG	B	1	1,2	14,14,15	0.65	0	17,19,21	0.89	0
2	NAG	B	2	2	14,14,15	0.56	0	17,19,21	1.26	3 (17%)

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	A	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	2	2	-	2/6/23/26	0/1/1/1
2	NAG	B	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	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(°)	Ideal(°)
2	B	2	NAG	O4-C4-C5	2.16	114.65	109.32
2	B	2	NAG	C3-C4-C5	-2.14	106.36	110.23
2	B	2	NAG	C1-O5-C5	2.05	114.94	112.19

There are no chirality outliers.

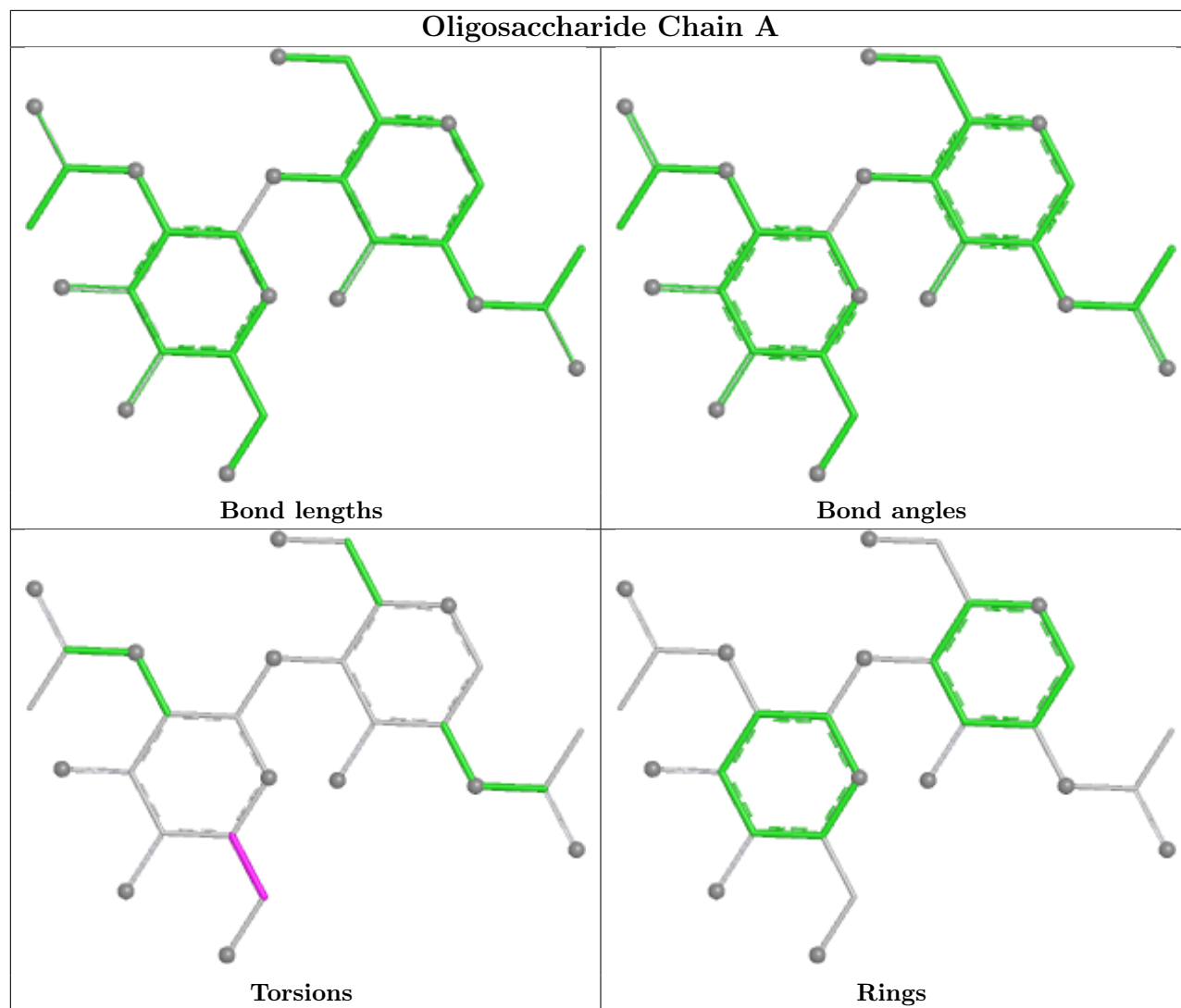
All (2) torsion outliers are listed below:

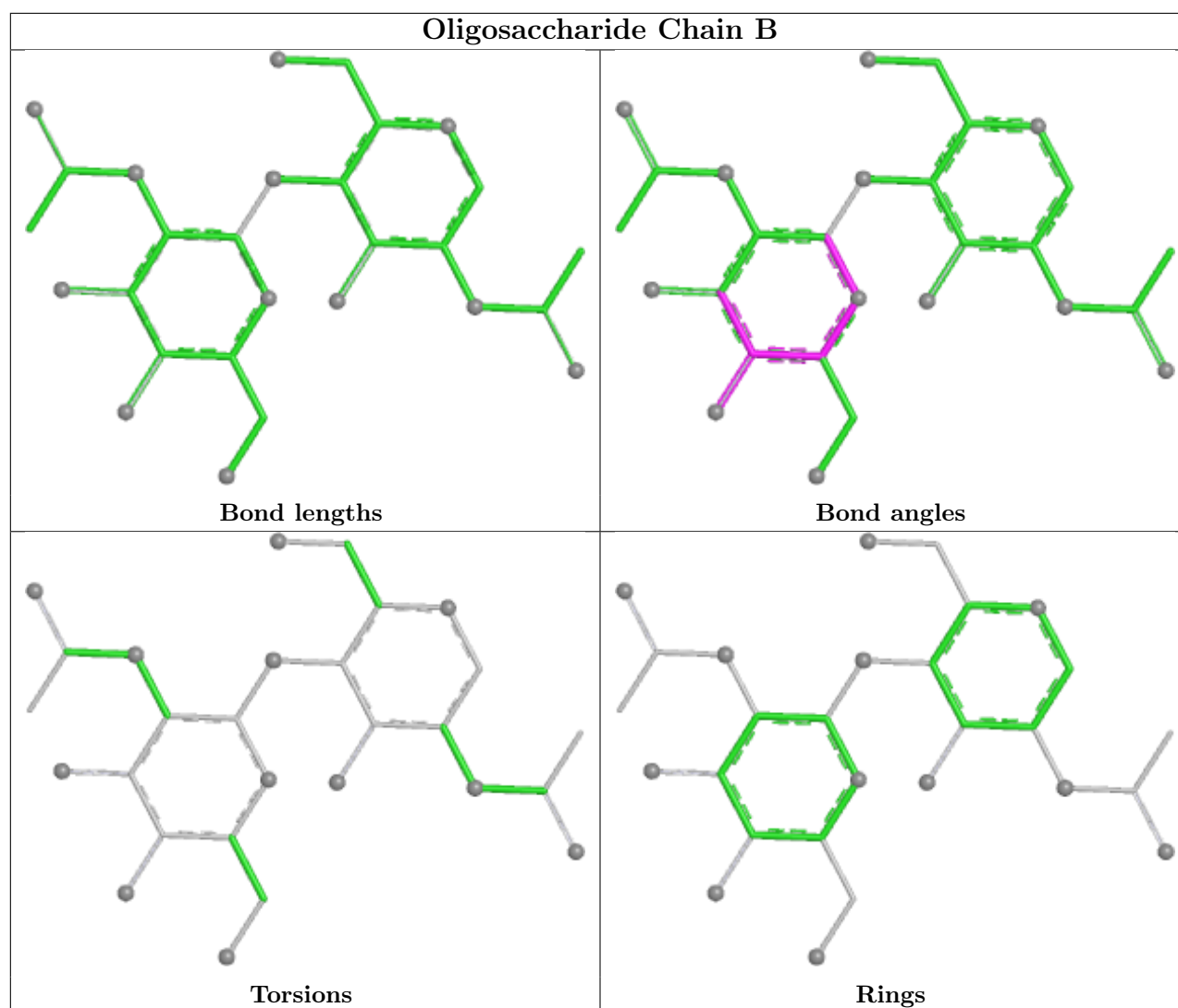
Mol	Chain	Res	Type	Atoms
2	A	2	NAG	C4-C5-C6-O6
2	A	2	NAG	O5-C5-C6-O6

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](#)

38 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	NAG	BBB	503	1	14,14,15	0.52	0	17,19,21	0.89	1 (5%)
5	EDO	AAA	511	-	3,3,3	0.09	0	2,2,2	0.11	0
4	SO4	BBB	511	-	4,4,4	0.32	0	6,6,6	0.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	GOL	BBB	517	-	5,5,5	0.18	0	5,5,5	0.49	0
6	GOL	BBB	516	-	5,5,5	0.13	0	5,5,5	0.32	0
5	EDO	AAA	516	-	3,3,3	0.03	0	2,2,2	0.05	0
5	EDO	AAA	518	-	3,3,3	0.10	0	2,2,2	0.19	0
6	GOL	BBB	518	-	5,5,5	0.10	0	5,5,5	0.31	0
4	SO4	AAA	506	-	4,4,4	0.32	0	6,6,6	0.06	0
4	SO4	AAA	508	-	4,4,4	0.33	0	6,6,6	0.13	0
6	GOL	AAA	520	-	5,5,5	0.10	0	5,5,5	0.27	0
4	SO4	AAA	507	-	4,4,4	0.35	0	6,6,6	0.07	0
6	GOL	BBB	519	-	5,5,5	0.10	0	5,5,5	0.26	0
4	SO4	BBB	507	-	4,4,4	0.38	0	6,6,6	0.12	0
6	GOL	BBB	520	-	5,5,5	0.09	0	5,5,5	0.28	0
4	SO4	AAA	504	-	4,4,4	0.39	0	6,6,6	0.11	0
5	EDO	AAA	513	-	3,3,3	0.11	0	2,2,2	0.27	0
3	NAG	AAA	503	1	14,14,15	0.61	0	17,19,21	1.44	3 (17%)
6	GOL	AAA	519	-	5,5,5	0.12	0	5,5,5	0.49	0
4	SO4	AAA	509	-	4,4,4	0.31	0	6,6,6	0.07	0
4	SO4	BBB	510	-	4,4,4	0.29	0	6,6,6	0.10	0
4	SO4	BBB	504	-	4,4,4	0.36	0	6,6,6	0.24	0
4	SO4	BBB	508	-	4,4,4	0.34	0	6,6,6	0.07	0
4	SO4	BBB	509	-	4,4,4	0.33	0	6,6,6	0.09	0
4	SO4	AAA	505	-	4,4,4	0.32	0	6,6,6	0.24	0
4	SO4	AAA	510	-	4,4,4	0.32	0	6,6,6	0.09	0
4	SO4	BBB	505	-	4,4,4	0.35	0	6,6,6	0.13	0
5	EDO	AAA	515	-	3,3,3	0.07	0	2,2,2	0.16	0
5	EDO	AAA	512	-	3,3,3	0.42	0	2,2,2	0.51	0
4	SO4	BBB	506	-	4,4,4	0.32	0	6,6,6	0.08	0
5	EDO	BBB	513	-	3,3,3	0.08	0	2,2,2	0.10	0
5	EDO	BBB	512	-	3,3,3	0.07	0	2,2,2	0.11	0
5	EDO	BBB	515	-	3,3,3	0.33	0	2,2,2	0.38	0
5	EDO	AAA	514	-	3,3,3	0.16	0	2,2,2	0.10	0
5	EDO	AAA	517	-	3,3,3	0.09	0	2,2,2	0.13	0
7	PN8	AAA	521	1	13,14,14	1.32	1 (7%)	14,19,19	0.85	0
5	EDO	BBB	514	-	3,3,3	0.04	0	2,2,2	0.21	0
7	PN8	BBB	521	1	13,14,14	1.20	1 (7%)	14,19,19	1.00	1 (7%)

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	BBB	503	1	-	0/6/23/26	0/1/1/1
5	EDO	AAA	511	-	-	1/1/1/1	-
6	GOL	BBB	517	-	-	4/4/4/4	-
6	GOL	BBB	516	-	-	2/4/4/4	-
5	EDO	AAA	518	-	-	0/1/1/1	-
6	GOL	BBB	518	-	-	0/4/4/4	-
5	EDO	AAA	516	-	-	1/1/1/1	-
6	GOL	AAA	520	-	-	2/4/4/4	-
6	GOL	BBB	519	-	-	0/4/4/4	-
6	GOL	BBB	520	-	-	3/4/4/4	-
5	EDO	AAA	513	-	-	1/1/1/1	-
3	NAG	AAA	503	1	-	0/6/23/26	0/1/1/1
6	GOL	AAA	519	-	-	2/4/4/4	-
5	EDO	AAA	515	-	-	0/1/1/1	-
5	EDO	BBB	513	-	-	1/1/1/1	-
5	EDO	AAA	512	-	-	1/1/1/1	-
5	EDO	BBB	512	-	-	1/1/1/1	-
5	EDO	BBB	515	-	-	1/1/1/1	-
5	EDO	AAA	514	-	-	1/1/1/1	-
5	EDO	AAA	517	-	-	1/1/1/1	-
7	PN8	AAA	521	1	-	1/2/24/24	0/1/1/1
5	EDO	BBB	514	-	-	1/1/1/1	-
7	PN8	BBB	521	1	-	2/2/24/24	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	AAA	521	PN8	N-N1	3.63	1.40	1.32
7	BBB	521	PN8	N-N1	3.29	1.40	1.32

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	BBB	521	PN8	C5-C4-C3	-3.17	107.81	111.50
3	AAA	503	NAG	C1-O5-C5	2.86	116.02	112.19
3	AAA	503	NAG	O5-C1-C2	-2.57	107.32	111.29
3	AAA	503	NAG	O4-C4-C5	2.56	115.63	109.32
3	BBB	503	NAG	C1-O5-C5	2.17	115.10	112.19

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	AAA	520	GOL	C1-C2-C3-O3
6	BBB	517	GOL	O1-C1-C2-C3
7	BBB	521	PN8	C3-C1-C2-N
6	AAA	519	GOL	C1-C2-C3-O3
6	BBB	516	GOL	O1-C1-C2-C3
6	BBB	517	GOL	C1-C2-C3-O3
6	BBB	520	GOL	O1-C1-C2-C3
6	BBB	520	GOL	C1-C2-C3-O3
6	AAA	519	GOL	O2-C2-C3-O3
6	AAA	520	GOL	O2-C2-C3-O3
6	BBB	517	GOL	O1-C1-C2-O2
5	AAA	511	EDO	O1-C1-C2-O2
5	BBB	513	EDO	O1-C1-C2-O2
5	BBB	514	EDO	O1-C1-C2-O2
6	BBB	517	GOL	O2-C2-C3-O3
5	BBB	515	EDO	O1-C1-C2-O2
7	AAA	521	PN8	C3-C1-C2-N
7	BBB	521	PN8	C-C1-C2-N
5	AAA	512	EDO	O1-C1-C2-O2
5	AAA	514	EDO	O1-C1-C2-O2
5	BBB	512	EDO	O1-C1-C2-O2
6	BBB	516	GOL	O1-C1-C2-O2
6	BBB	520	GOL	O1-C1-C2-O2
5	AAA	516	EDO	O1-C1-C2-O2
5	AAA	517	EDO	O1-C1-C2-O2
5	AAA	513	EDO	O1-C1-C2-O2

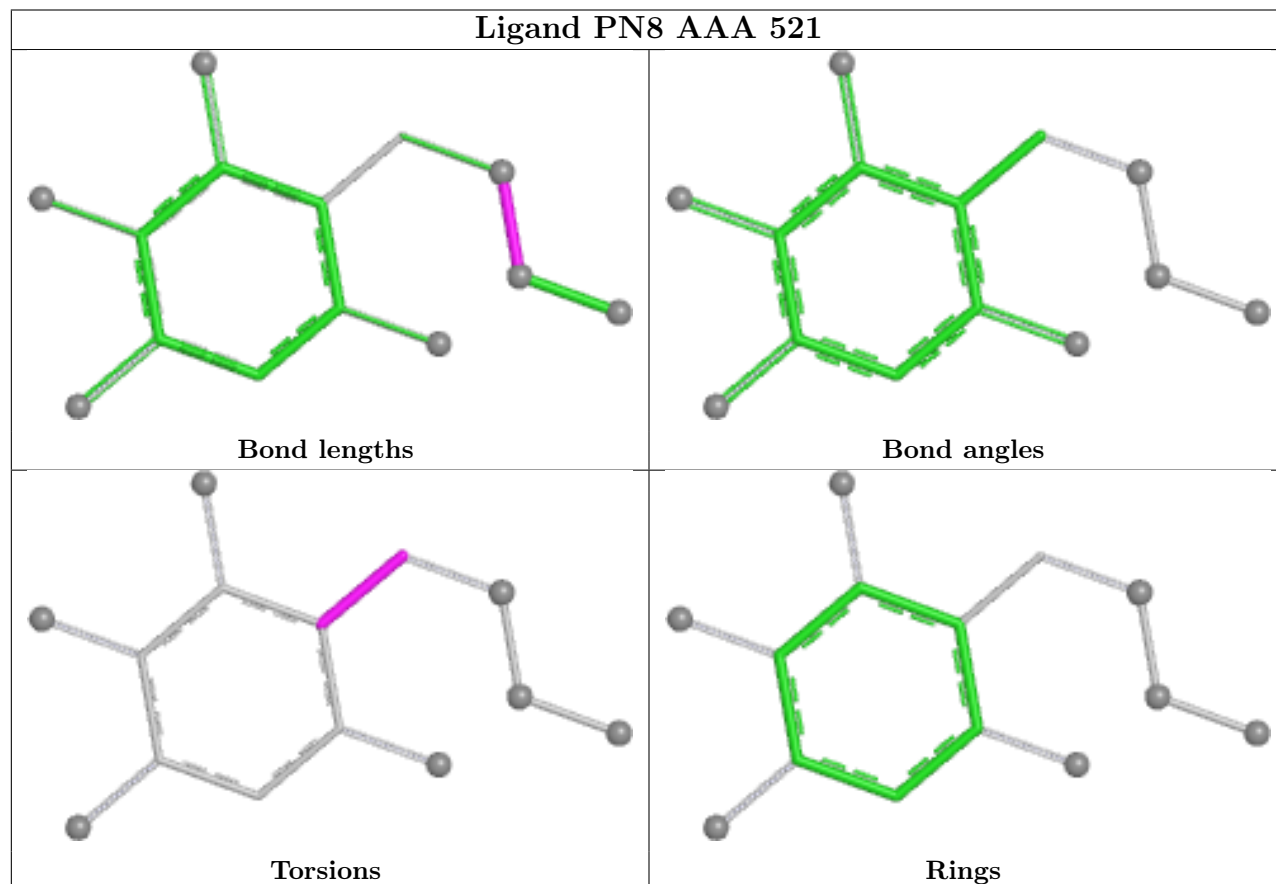
There are no ring outliers.

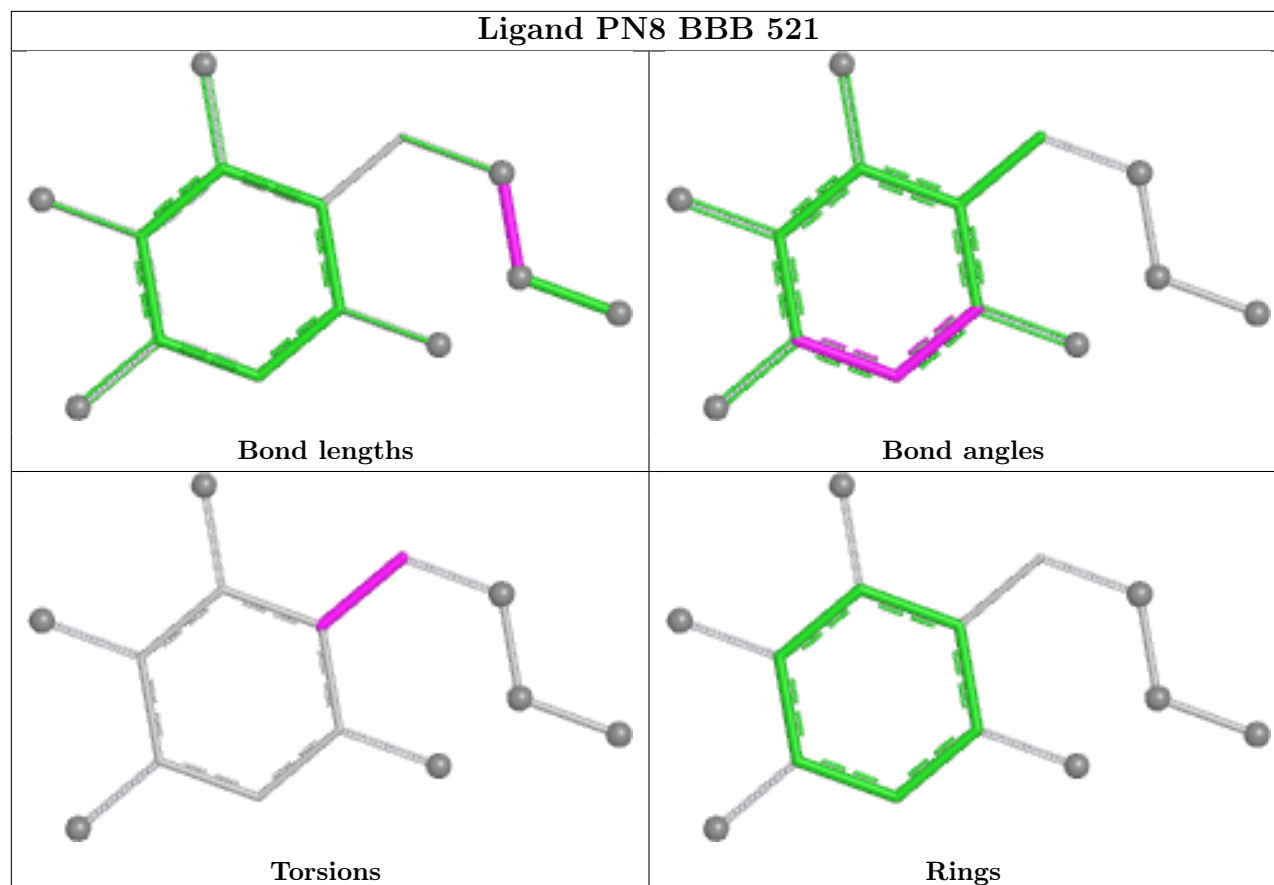
7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	BBB	517	GOL	2	0
4	AAA	508	SO4	1	0
6	BBB	519	GOL	1	0
6	BBB	520	GOL	3	0
6	AAA	519	GOL	1	0
7	AAA	521	PN8	1	0
5	BBB	514	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

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, 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%)	0.15	26 (5%) 33 36	13, 28, 47, 92	18 (3%)
1	BBB	497/497 (100%)	0.23	27 (5%) 31 34	12, 30, 50, 79	15 (3%)
All	All	994/994 (100%)	0.19	53 (5%) 32 35	12, 29, 49, 92	33 (3%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	316[A]	PHE	36.3
1	AAA	347	PHE	16.4
1	AAA	317	LEU	7.6
1	BBB	313	TYR	7.0
1	BBB	318	ALA	6.7
1	AAA	312	TRP	5.8
1	AAA	318	ALA	5.7
1	BBB	378	TRP	5.5
1	AAA	345	SER	5.3
1	BBB	314	LEU	5.0
1	BBB	347	PHE	5.0
1	BBB	345	SER	4.4
1	BBB	317	LEU	4.4
1	AAA	348	TRP	4.4
1	BBB	312	TRP	4.3
1	BBB	31	PHE	4.3
1	BBB	344	GLY	4.2
1	AAA	316	PHE	4.2
1	AAA	145[A]	HIS	4.1
1	AAA	63	THR	4.0
1	BBB	397	PHE	3.8
1	AAA	343	VAL	3.6
1	AAA	319	PRO	3.5
1	BBB	342	CYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	BBB	406	ILE	3.4
1	AAA	349[A]	GLU	3.2
1	BBB	346	LYS	3.2
1	AAA	342	CYS	3.2
1	AAA	61	THR	3.2
1	AAA	313	TYR	3.1
1	AAA	286	LEU	3.1
1	AAA	1	ALA	2.8
1	BBB	398[A]	VAL	2.8
1	BBB	343	VAL	2.8
1	BBB	286	LEU	2.8
1	AAA	344	GLY	2.8
1	BBB	319	PRO	2.6
1	AAA	30[A]	THR	2.6
1	BBB	348	TRP	2.6
1	AAA	31	PHE	2.5
1	AAA	285	ARG	2.4
1	AAA	59	ASN	2.4
1	BBB	169	GLN	2.4
1	BBB	394[A]	VAL	2.3
1	BBB	30	THR	2.3
1	BBB	341	ALA	2.3
1	AAA	62	GLY	2.3
1	BBB	395	ARG	2.2
1	AAA	320	ALA	2.2
1	BBB	350	GLN	2.2
1	BBB	60	HIS	2.1
1	AAA	34	LEU	2.1
1	AAA	346	LYS	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

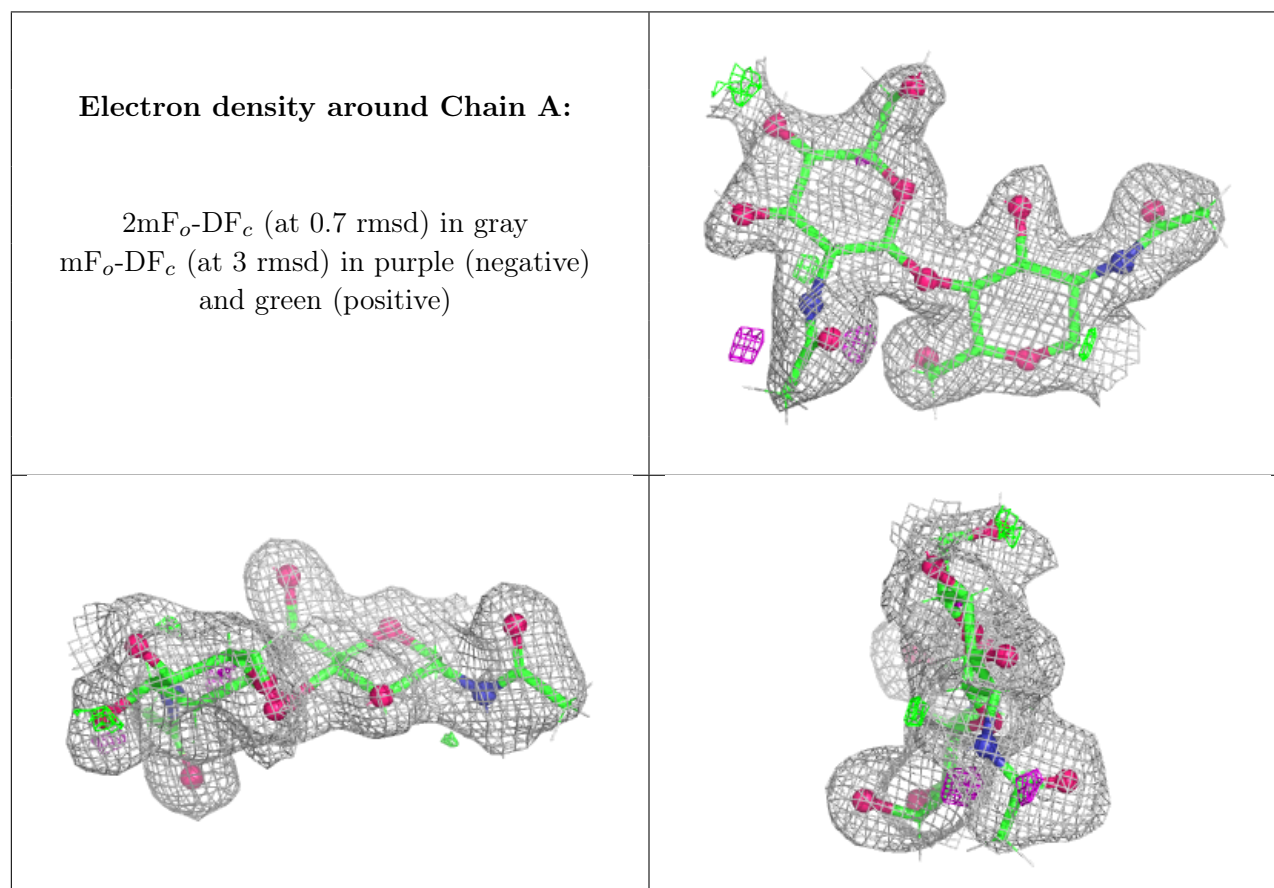
There are no non-standard protein/DNA/RNA residues in this entry.

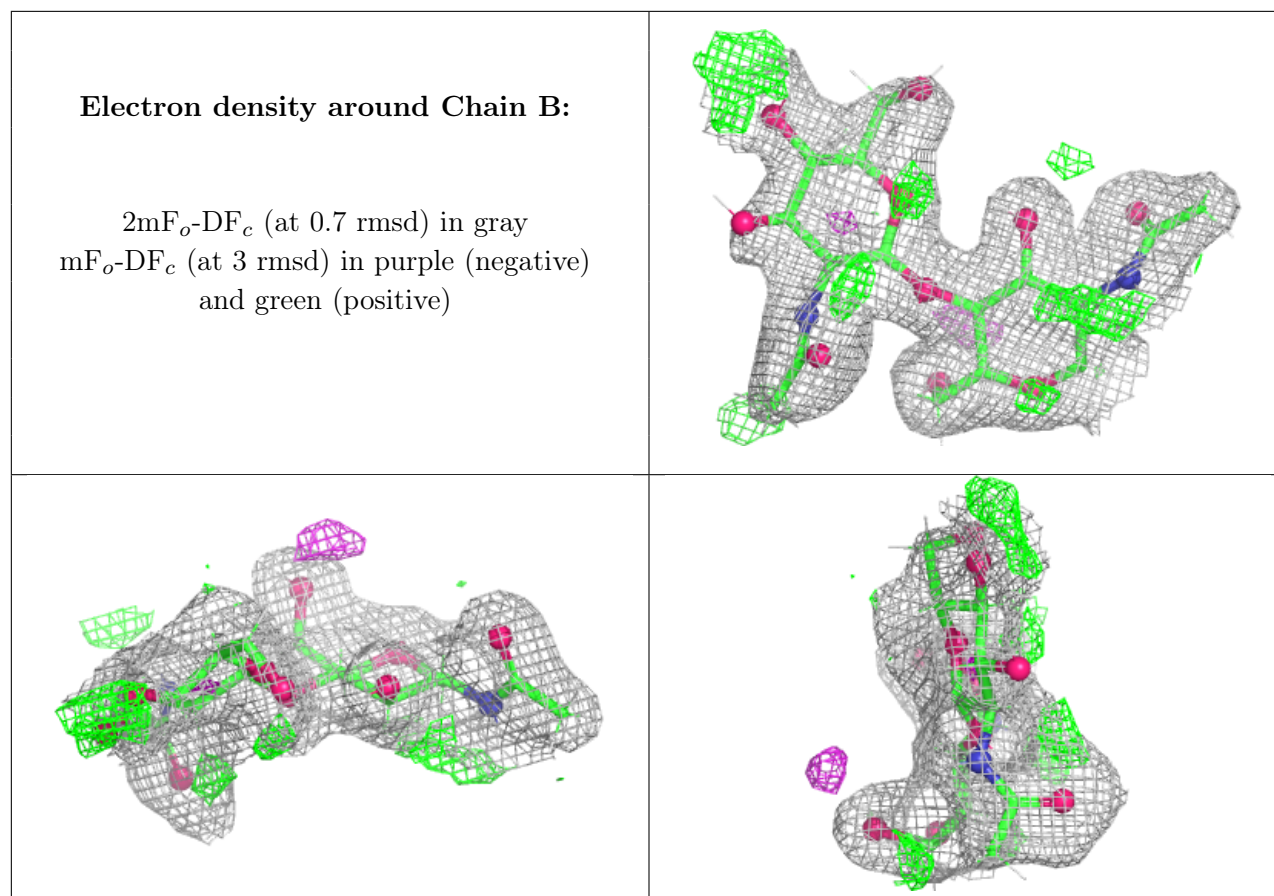
6.3 Carbohydrates ⓘ

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($\text{\AA}^2$)	Q<0.9
2	NAG	A	1	14/15	-	-	33,40,44,47	2
2	NAG	A	2	14/15	-	-	42,55,66,67	3
2	NAG	B	1	14/15	-	-	34,41,43,48	2
2	NAG	B	2	14/15	-	-	51,72,76,81	3

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($\text{\AA}^2$)	Q<0.9
3	NAG	BBB	503	14/15	0.57	0.20	90,110,122,122	3
4	SO4	AAA	510	5/5	0.68	0.11	98,100,107,114	0
4	SO4	BBB	508	5/5	0.73	0.15	89,92,95,104	0
5	EDO	BBB	515	4/4	0.73	0.32	61,64,66,68	1
4	SO4	AAA	509	5/5	0.76	0.11	81,84,90,96	0
3	NAG	AAA	503	14/15	0.76	0.14	56,62,69,69	3
6	GOL	BBB	518	6/6	0.76	0.19	70,72,73,74	2
6	GOL	BBB	517	6/6	0.78	0.17	49,57,64,64	2
6	GOL	BBB	520	6/6	0.80	0.19	74,78,84,85	2
5	EDO	AAA	516	4/4	0.82	0.19	64,68,70,71	1
5	EDO	AAA	512	4/4	0.84	0.21	55,58,58,60	1
4	SO4	BBB	507	5/5	0.84	0.12	60,61,67,68	0
5	EDO	AAA	515	4/4	0.85	0.17	54,61,66,67	1

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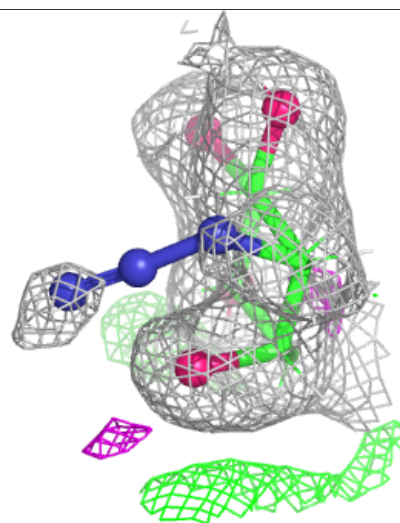
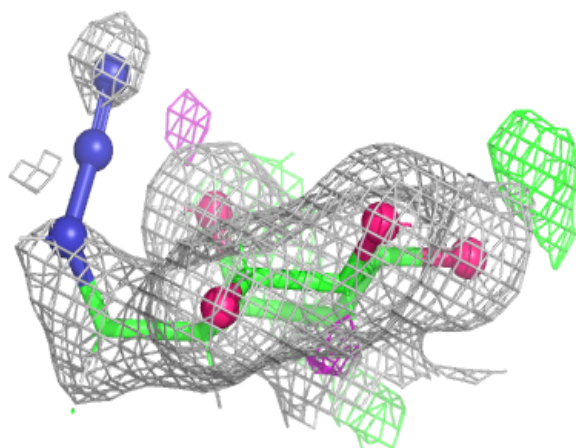
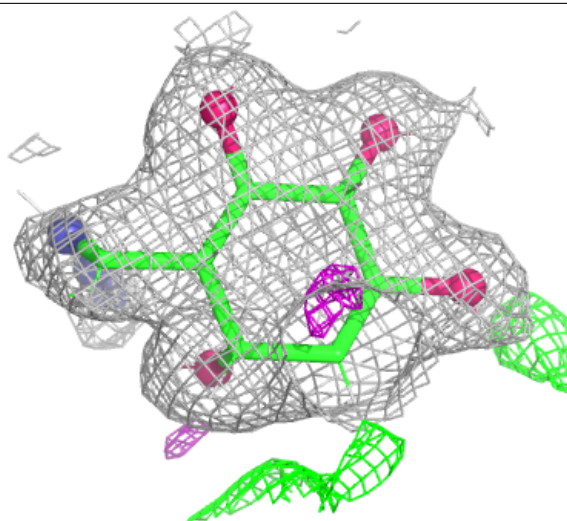
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	GOL	BBB	519	6/6	0.85	0.15	62,65,69,69	2
5	EDO	AAA	513	4/4	0.85	0.18	59,63,64,65	1
4	SO4	BBB	509	5/5	0.86	0.12	60,62,66,72	5
4	SO4	BBB	510	5/5	0.87	0.10	66,67,79,80	0
5	EDO	BBB	512	4/4	0.87	0.22	69,74,78,78	1
5	EDO	BBB	514	4/4	0.87	0.15	65,66,67,67	1
4	SO4	BBB	506	5/5	0.87	0.11	73,75,81,83	0
5	EDO	AAA	518	4/4	0.88	0.19	62,65,66,67	1
4	SO4	BBB	511	5/5	0.88	0.10	76,76,86,88	0
5	EDO	BBB	513	4/4	0.88	0.18	55,60,64,65	1
4	SO4	AAA	506	5/5	0.89	0.08	74,79,80,82	0
6	GOL	AAA	519	6/6	0.89	0.13	36,51,59,60	2
4	SO4	AAA	508	5/5	0.89	0.10	62,67,70,74	0
6	GOL	BBB	516	6/6	0.90	0.16	46,54,62,62	2
5	EDO	AAA	517	4/4	0.91	0.17	51,61,64,64	1
5	EDO	AAA	511	4/4	0.91	0.18	58,63,64,65	1
5	EDO	AAA	514	4/4	0.91	0.14	61,62,62,63	1
6	GOL	AAA	520	6/6	0.92	0.15	41,51,59,62	2
4	SO4	AAA	507	5/5	0.92	0.09	63,64,66,72	0
4	SO4	BBB	504	5/5	0.93	0.09	51,55,58,60	0
7	PN8	BBB	521	14/14	0.94	0.09	30,33,37,39	8
4	SO4	AAA	505	5/5	0.95	0.07	47,50,52,53	0
7	PN8	AAA	521	14/14	0.96	0.07	25,28,37,42	8
4	SO4	BBB	505	5/5	0.98	0.05	35,36,39,42	0
4	SO4	AAA	504	5/5	0.99	0.05	36,38,38,46	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.

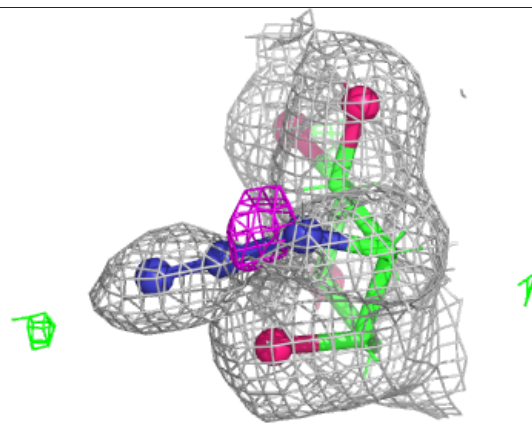
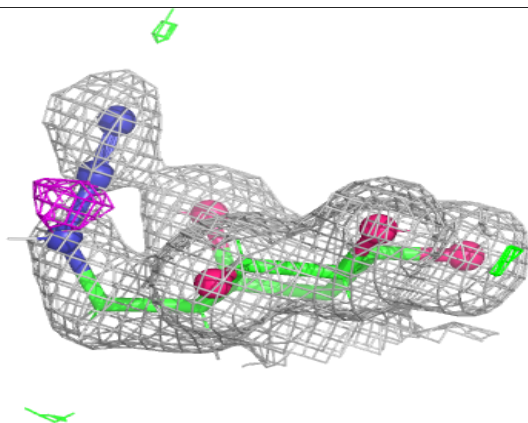
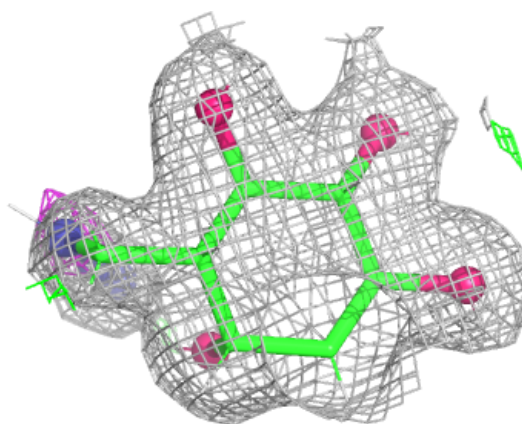
Electron density around PN8 BBB 521:

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



Electron density around PN8 AAA 521:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.