



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 01:36 PM UTC

PDB ID : 6WEU / pdb_00006weu
Title : Crystal structures of human E-NPP 1: bound to adenosine-5'-thio-monophosphate
Authors : Peat, T.S.; Dennis, M.; Newman, J.
Deposited on : 2020-04-03
Resolution : 2.65 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

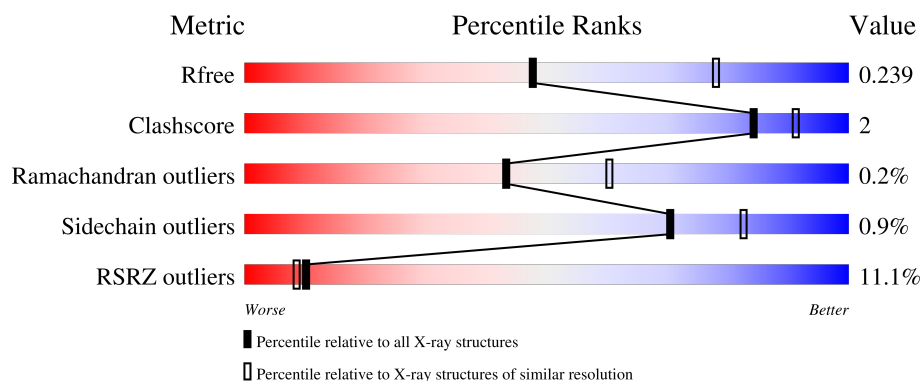
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	AbA	925	4% 82% 6% 12%
1	BbB	925	15% 81% 6% 14%
2	AcA	3	100%
3	AfA	2	50% 50%
3	BfB	2	100%

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Mol	Chain	Length	Quality of chain
4	BcB	3	 67% 33%

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
3	NAG	BfB	2	X	-	-	-
6	NAG	AbA	1005	X	-	-	-

2 Entry composition [i](#)

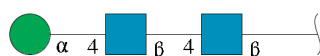
There are 9 unique types of molecules in this entry. The entry contains 13105 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1.

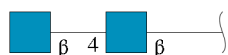
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AbA	816	Total	C	N	O	S	0	3	0
			6564	4188	1111	1216	49			
1	BbB	799	Total	C	N	O	S	0	0	0
			6161	3921	1047	1147	46			

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



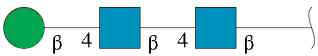
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	AcA	3	Total	C	N	O	0	0	0
			39	22	2	15			

- 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
3	AfA	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	BfB	2	Total	C	N	O	0	0	0
			28	16	2	10			

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

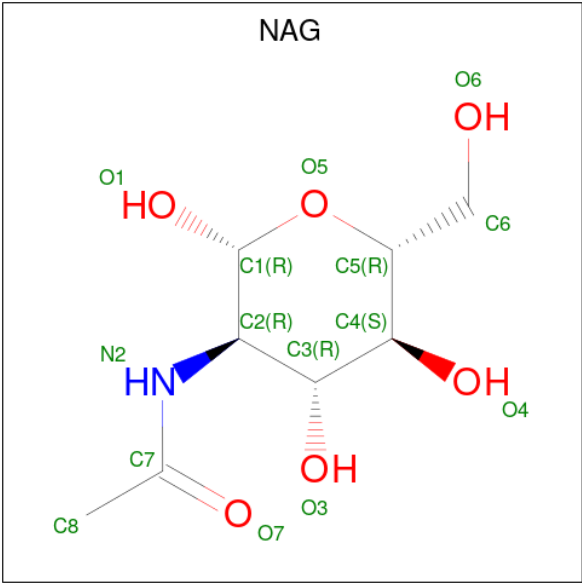


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	BcB	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	AbA	2	Total	Zn	0	0
			2	2		
5	BbB	2	Total	Zn	0	0
			2	2		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



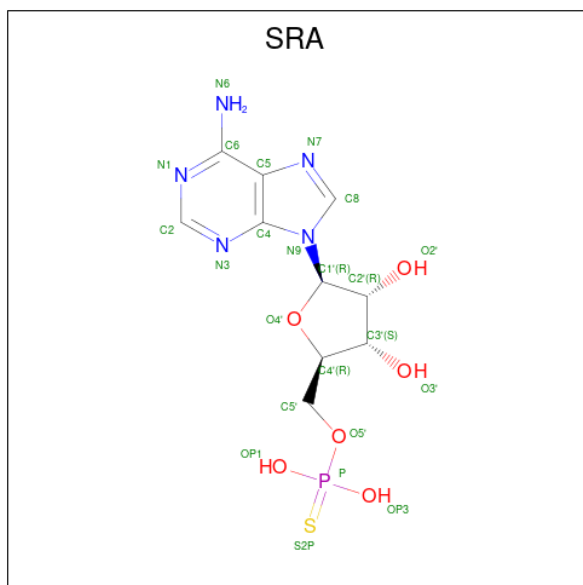
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	AbA	1	Total	C	N	O	0	0
			14	8	1	5		
6	AbA	1	Total	C	N	O	0	0
			14	8	1	5		
6	AbA	1	Total	C	N	O	0	0
			14	8	1	5		
6	BbB	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	BbB	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is ADENOSINE -5'-THIO-MONOPHOSPHATE (CCD ID: SRA) (formula: $C_{10}H_{14}N_5O_6PS$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
7	AbA	1	Total	C	N	O	P	S	0	0
			23	10	5	6	1	1		
7	BbB	1	Total	C	N	O	P	S	0	0
			23	10	5	6	1	1		

- Molecule 8 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	AbA	1	Total	C	O	0	0
			4	2	2		

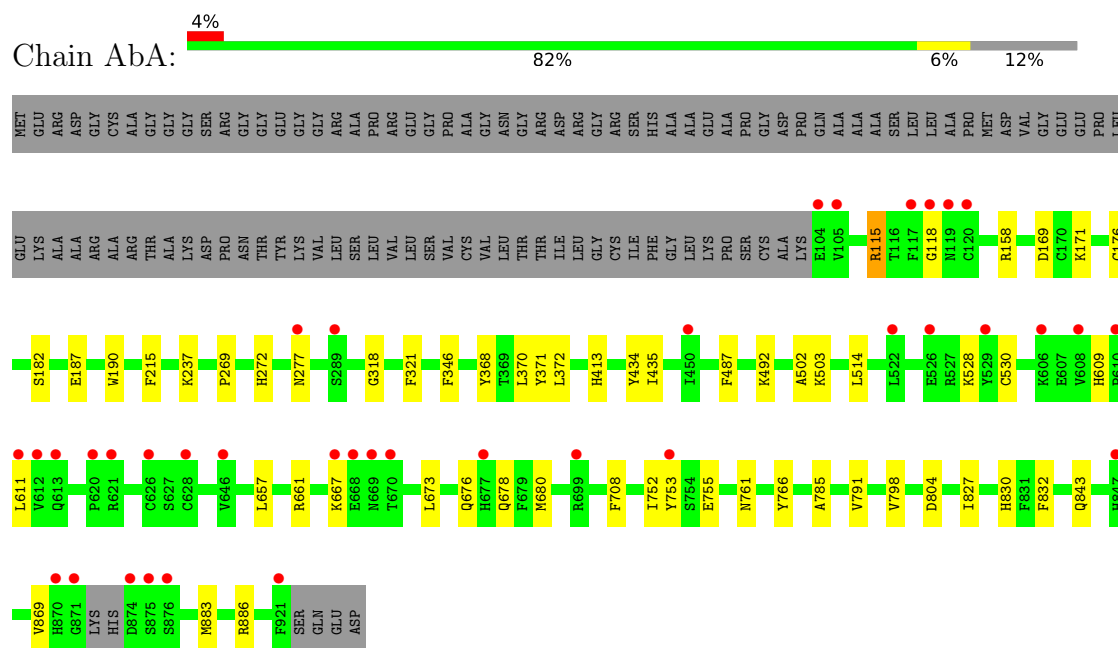
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	AbA	86	Total	O	0	0
			86	86		
9	BbB	36	Total	O	0	0
			36	36		

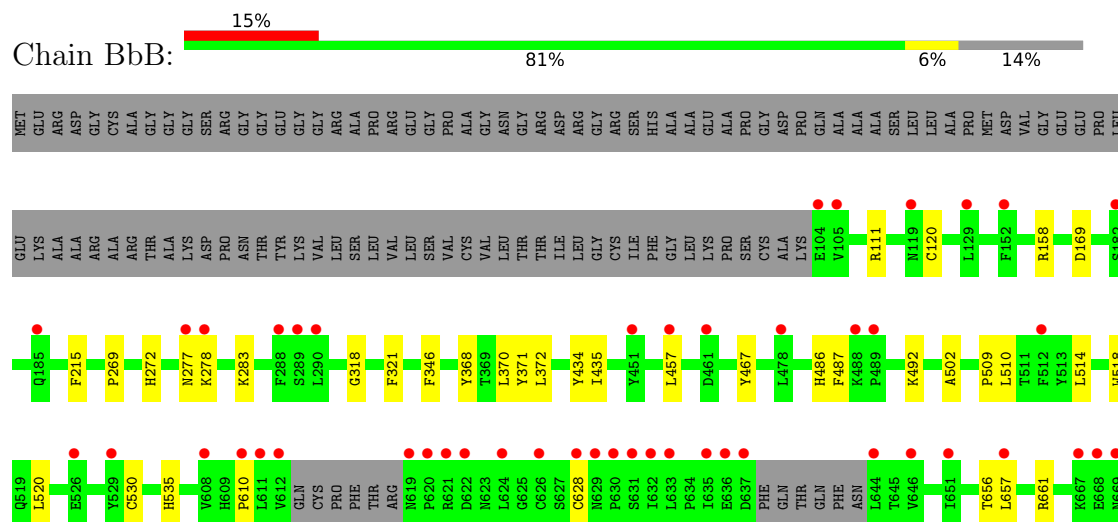
3 Residue-property plots

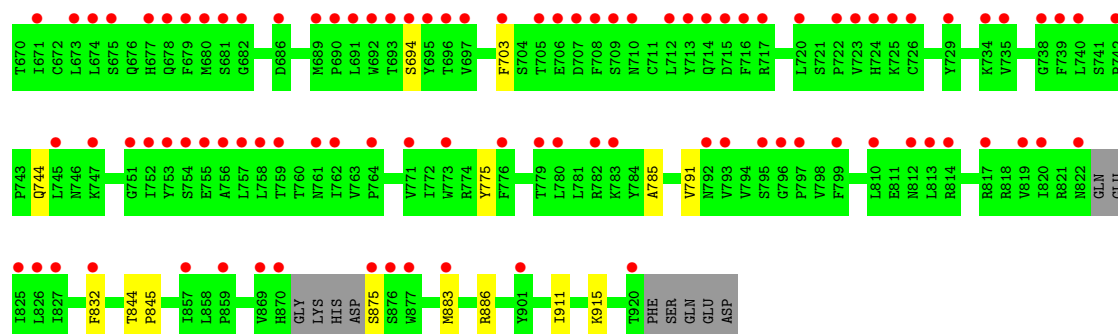
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Ectonucleotide pyrophosphatase/phosphodiesterase family member 1

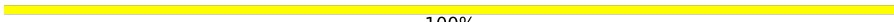


- Molecule 1: Ectonucleotide pyrophosphatase/phosphodiesterase family member 1





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

Chain AcA:  100%

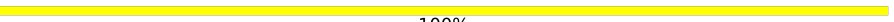
MAG1
MAG2
MAN3

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

Chain AfA:  50%

MAG1
MAG2

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

Chain BfB:  100%

MAG1
MAG2

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

Chain BcB:  67%

MAG1
MAG2
BXA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.01Å 160.14Å 209.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.57 – 2.65 47.57 – 2.65	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.57-2.65) 100.0 (47.57-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.207 , 0.239 0.211 , 0.239	Depositor DCC
R_{free} test set	4208 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	53.9	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 49.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13105	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, BMA, SRA, MAN, ZN, 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	AbA	0.96	1/6749 (0.0%)	1.31	0/9163
1	BbB	0.99	0/6332	1.32	0/8619
All	All	0.98	1/13081 (0.0%)	1.31	0/17782

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AbA	528	LYS	N-CA	5.71	1.49	1.46

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AbA	6564	0	6297	29	0
1	BbB	6161	0	5673	26	0
2	AcA	39	0	34	0	0
3	AfA	28	0	25	0	0
3	BfB	28	0	25	0	0
4	BcB	39	0	34	0	0
5	AbA	2	0	0	0	0
5	BbB	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	AbA	42	0	39	0	0
6	BbB	28	0	26	0	0
7	AbA	23	0	11	4	0
7	BbB	23	0	11	3	0
8	AbA	4	0	6	0	0
9	AbA	86	0	0	0	0
9	BbB	36	0	0	0	0
All	All	13105	0	12181	57	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 2.

All (57) 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)
7:AbA:1006:SRA:O4'	7:AbA:1006:SRA:C1'	1.64	1.17
7:BbB:1005:SRA:O4'	7:BbB:1005:SRA:C1'	1.64	1.14
1:BbB:492:LYS:HE3	1:BbB:502:ALA:O	1.95	0.67
1:AbA:171:LYS:HD2	1:AbA:176:CYS:SG	2.35	0.66
1:AbA:883:MET:O	1:AbA:886:ARG:HD3	1.97	0.64
1:BbB:883:MET:O	1:BbB:886:ARG:HD3	1.98	0.64
1:BbB:492:LYS:HD3	1:BbB:509:PRO:HA	1.81	0.62
1:AbA:869:VAL:O	1:AbA:869:VAL:HG23	2.00	0.61
1:AbA:611:LEU:HD21	1:AbA:673:LEU:HG	1.85	0.57
1:AbA:708:PHE:HB3	1:AbA:752:ILE:HD13	1.85	0.56
1:BbB:283:LYS:HE2	1:BbB:467:TYR:OH	2.04	0.56
1:BbB:277:ASN:OD1	1:BbB:278:LYS:HG3	2.06	0.56
1:AbA:371:TYR:OH	7:AbA:1006:SRA:H8	2.06	0.55
1:AbA:673:LEU:HD22	1:AbA:680:MET:HE3	1.89	0.54
1:AbA:798:VAL:HB	1:AbA:830:HIS:HB2	1.89	0.53
1:AbA:277:ASN:ND2	7:AbA:1006:SRA:S2P	2.82	0.52
1:AbA:678:GLN:HB2	1:AbA:753:TYR:CE2	2.46	0.51
1:BbB:514:LEU:HD21	1:BbB:520:LEU:HB2	1.93	0.50
1:BbB:703:PHE:HA	1:BbB:744:GLN:O	2.12	0.50
1:AbA:158:ARG:NH2	1:AbA:169:ASP:OD1	2.45	0.50
1:BbB:457:LEU:HD21	1:BbB:510:LEU:HD23	1.93	0.50
1:BbB:158:ARG:NH2	1:BbB:169:ASP:OD1	2.44	0.49
1:AbA:371:TYR:CZ	7:AbA:1006:SRA:H8	2.47	0.49
1:BbB:371:TYR:OH	7:BbB:1005:SRA:H8	2.13	0.49
1:AbA:115:ARG:HA	1:AbA:115:ARG:HD2	1.71	0.48
1:BbB:844:THR:OG1	1:BbB:845:PRO:HD2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AbA:657:LEU:HD13	1:AbA:661:ARG:HB3	1.95	0.47
1:BbB:318:GLY:O	1:BbB:368:TYR:HA	2.14	0.47
1:AbA:318:GLY:O	1:AbA:368:TYR:HA	2.15	0.46
1:AbA:753:TYR:CZ	1:AbA:755:GLU:HB2	2.49	0.46
1:BbB:657:LEU:HD13	1:BbB:661:ARG:HB3	1.97	0.46
1:BbB:775:TYR:CE2	1:BbB:875:SER:HB2	2.50	0.46
1:BbB:785:ALA:HA	1:BbB:791:VAL:HG23	1.97	0.46
1:AbA:346:PHE:CD1	1:AbA:372:LEU:HD22	2.50	0.46
1:AbA:190:TRP:CH2	1:AbA:237[B]:LYS:HG2	2.51	0.46
1:AbA:766:TYR:CZ	1:AbA:827:ILE:HG21	2.51	0.46
1:AbA:785:ALA:HA	1:AbA:791:VAL:HG23	1.98	0.46
1:BbB:346:PHE:CD1	1:BbB:372:LEU:HD22	2.50	0.46
1:BbB:457:LEU:C	1:BbB:457:LEU:HD12	2.40	0.46
1:AbA:269:PRO:HA	1:AbA:272:HIS:CE1	2.52	0.45
1:BbB:911:ILE:HG22	1:BbB:915:LYS:HE2	2.00	0.44
1:AbA:832:PHE:CD1	1:AbA:832:PHE:C	2.96	0.43
1:AbA:182:SER:HA	1:AbA:187:GLU:O	2.18	0.43
1:AbA:503:LYS:HE2	1:AbA:804:ASP:HB2	1.99	0.43
1:BbB:457:LEU:HD11	1:BbB:510:LEU:HD23	2.00	0.43
1:BbB:269:PRO:HA	1:BbB:272:HIS:CE1	2.53	0.43
1:BbB:111:ARG:NH2	1:BbB:120:CYS:O	2.51	0.43
1:BbB:435:ILE:HD13	1:BbB:487:PHE:CD1	2.53	0.42
1:BbB:486:HIS:ND1	1:BbB:518:TRP:CZ2	2.87	0.42
1:AbA:435:ILE:HD13	1:AbA:487:PHE:CD1	2.54	0.42
1:BbB:656:THR:CG2	1:BbB:694:SER:O	2.68	0.42
1:BbB:832:PHE:CD1	1:BbB:832:PHE:C	2.98	0.42
1:AbA:761:ASN:O	1:AbA:761:ASN:CG	2.64	0.41
1:AbA:492:LYS:CE	1:AbA:502:ALA:O	2.68	0.41
1:BbB:535:HIS:HE1	7:BbB:1005:SRA:OP3	2.04	0.41
1:AbA:413:HIS:H	1:AbA:413:HIS:CD2	2.39	0.40
1:AbA:609:HIS:CE1	1:AbA:667:LYS:O	2.75	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	AbA	815/925 (88%)	774 (95%)	39 (5%)	2 (0%)	43	60
1	BbB	789/925 (85%)	746 (95%)	41 (5%)	2 (0%)	36	52
All	All	1604/1850 (87%)	1520 (95%)	80 (5%)	4 (0%)	43	60

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AbA	118	GLY
1	AbA	321	PHE
1	BbB	321	PHE
1	BbB	610	PRO

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	AbA	736/824 (89%)	728 (99%)	8 (1%)	65	80
1	BbB	648/824 (79%)	643 (99%)	5 (1%)	73	85
All	All	1384/1648 (84%)	1371 (99%)	13 (1%)	70	82

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AbA	115	ARG
1	AbA	215	PHE
1	AbA	370	LEU
1	AbA	434	TYR
1	AbA	514	LEU
1	AbA	530	CYS
1	AbA	676	GLN
1	AbA	843	GLN
1	BbB	215	PHE

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Mol	Chain	Res	Type
1	BbB	370	LEU
1	BbB	434	TYR
1	BbB	530	CYS
1	BbB	628	CYS

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 ⓘ

10 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	AcA	1	2,1	14,14,15	0.78	1 (7%)	17,19,21	1.29	2 (11%)
2	NAG	AcA	2	2	14,14,15	0.66	0	17,19,21	1.35	2 (11%)
2	MAN	AcA	3	2	11,11,12	0.29	0	15,15,17	1.11	1 (6%)
3	NAG	AfA	1	3,1	14,14,15	0.85	1 (7%)	17,19,21	2.07	4 (23%)
3	NAG	AfA	2	3	14,14,15	0.43	0	17,19,21	0.80	0
4	NAG	BcB	1	1,4	14,14,15	0.51	0	17,19,21	1.33	2 (11%)
4	NAG	BcB	2	4	14,14,15	0.44	0	17,19,21	0.73	0
4	BMA	BcB	3	4	11,11,12	0.38	0	15,15,17	0.87	0
3	NAG	BfB	1	3,1	14,14,15	0.66	0	17,19,21	1.76	5 (29%)
3	NAG	BfB	2	3	14,14,15	0.39	0	17,19,21	1.64	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
2	NAG	AcA	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	AcA	2	2	-	0/6/23/26	0/1/1/1
2	MAN	AcA	3	2	-	2/2/19/22	1/1/1/1
3	NAG	AfA	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	AfA	2	3	-	2/6/23/26	0/1/1/1
4	NAG	BcB	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	BcB	2	4	-	2/6/23/26	0/1/1/1
4	BMA	BcB	3	4	-	2/2/19/22	0/1/1/1
3	NAG	BfB	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	BfB	2	3	1/1/5/7	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	AfA	1	NAG	C1-C2	2.45	1.55	1.52
2	AcA	1	NAG	O5-C5	-2.20	1.39	1.43

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	AfA	1	NAG	O7-C7-N2	-4.82	113.46	121.98
3	AfA	1	NAG	C8-C7-N2	4.46	123.51	116.12
3	BfB	1	NAG	O7-C7-N2	-3.82	115.23	121.98
3	BfB	2	NAG	C8-C7-N2	-3.50	110.32	116.12
3	BfB	2	NAG	C1-C2-N2	3.48	115.91	110.43
2	AcA	2	NAG	C3-C4-C5	3.37	116.35	110.23
4	BcB	1	NAG	O5-C1-C2	-3.23	106.30	111.29
3	BfB	1	NAG	C8-C7-N2	3.17	121.38	116.12
3	BfB	1	NAG	C1-O5-C5	-3.17	107.93	112.19
3	BfB	2	NAG	C2-N2-C7	-3.16	118.67	122.90
2	AcA	1	NAG	O5-C1-C2	-3.08	106.52	111.29
3	AfA	1	NAG	C2-N2-C7	-2.97	118.93	122.90
3	AfA	1	NAG	O5-C1-C2	-2.72	107.08	111.29
2	AcA	3	MAN	C1-C2-C3	-2.58	105.89	109.64
4	BcB	1	NAG	C3-C4-C5	2.45	114.67	110.23
3	BfB	1	NAG	C4-C3-C2	-2.44	107.44	111.02
3	BfB	2	NAG	O5-C1-C2	-2.23	107.83	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AcA	1	NAG	C1-O5-C5	-2.19	109.25	112.19
3	BfB	1	NAG	O5-C5-C4	-2.15	105.58	110.83
2	AcA	2	NAG	O7-C7-N2	2.01	125.54	121.98

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	BfB	2	NAG	C1

All (20) torsion outliers are listed below:

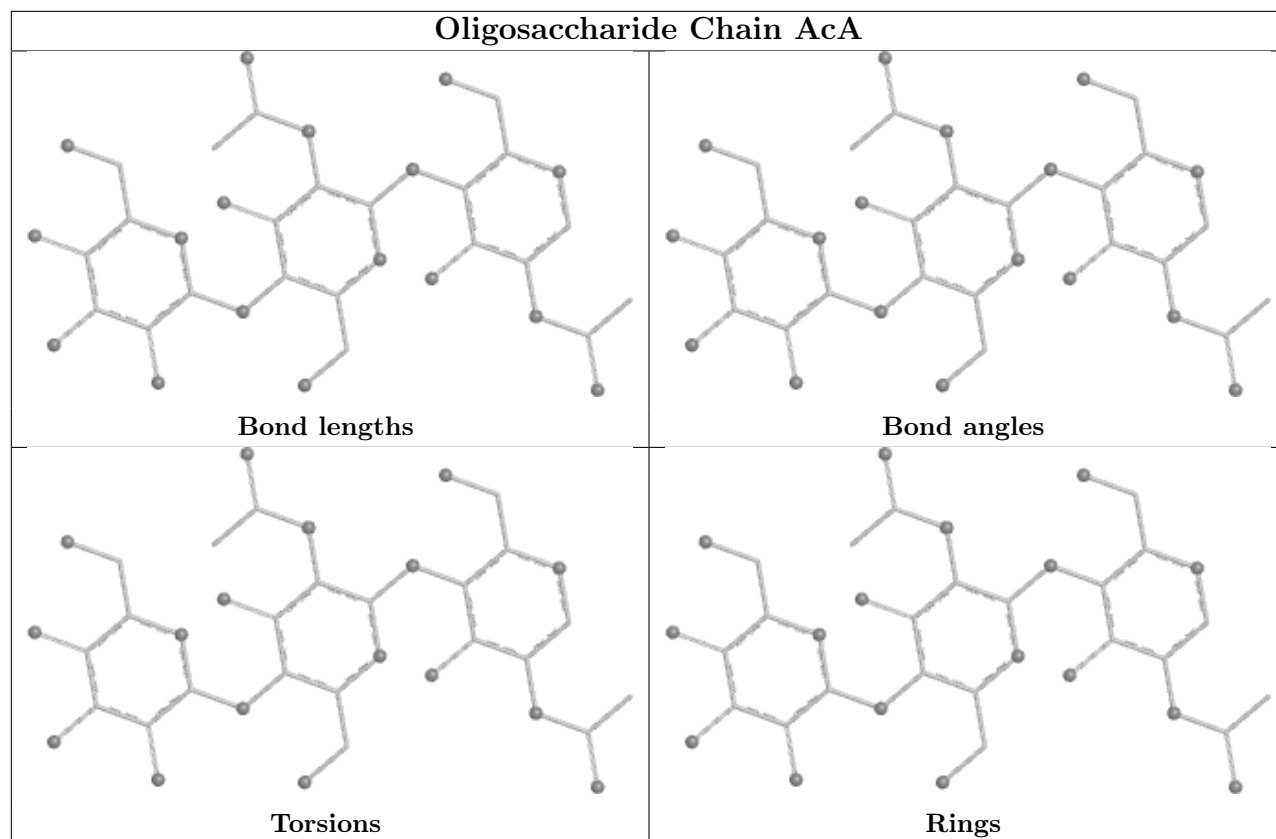
Mol	Chain	Res	Type	Atoms
3	AfA	1	NAG	C8-C7-N2-C2
3	AfA	1	NAG	O7-C7-N2-C2
3	BfB	1	NAG	C8-C7-N2-C2
3	BfB	1	NAG	O7-C7-N2-C2
3	BfB	2	NAG	C8-C7-N2-C2
3	BfB	2	NAG	O7-C7-N2-C2
2	AcA	3	MAN	O5-C5-C6-O6
3	BfB	1	NAG	O5-C5-C6-O6
3	AfA	2	NAG	O5-C5-C6-O6
3	AfA	2	NAG	C4-C5-C6-O6
3	BfB	1	NAG	C4-C5-C6-O6
2	AcA	3	MAN	C4-C5-C6-O6
4	BcB	3	BMA	O5-C5-C6-O6
4	BcB	3	BMA	C4-C5-C6-O6
3	AfA	1	NAG	O5-C5-C6-O6
4	BcB	1	NAG	O5-C5-C6-O6
3	AfA	1	NAG	C4-C5-C6-O6
4	BcB	1	NAG	C4-C5-C6-O6
4	BcB	2	NAG	O5-C5-C6-O6
4	BcB	2	NAG	C4-C5-C6-O6

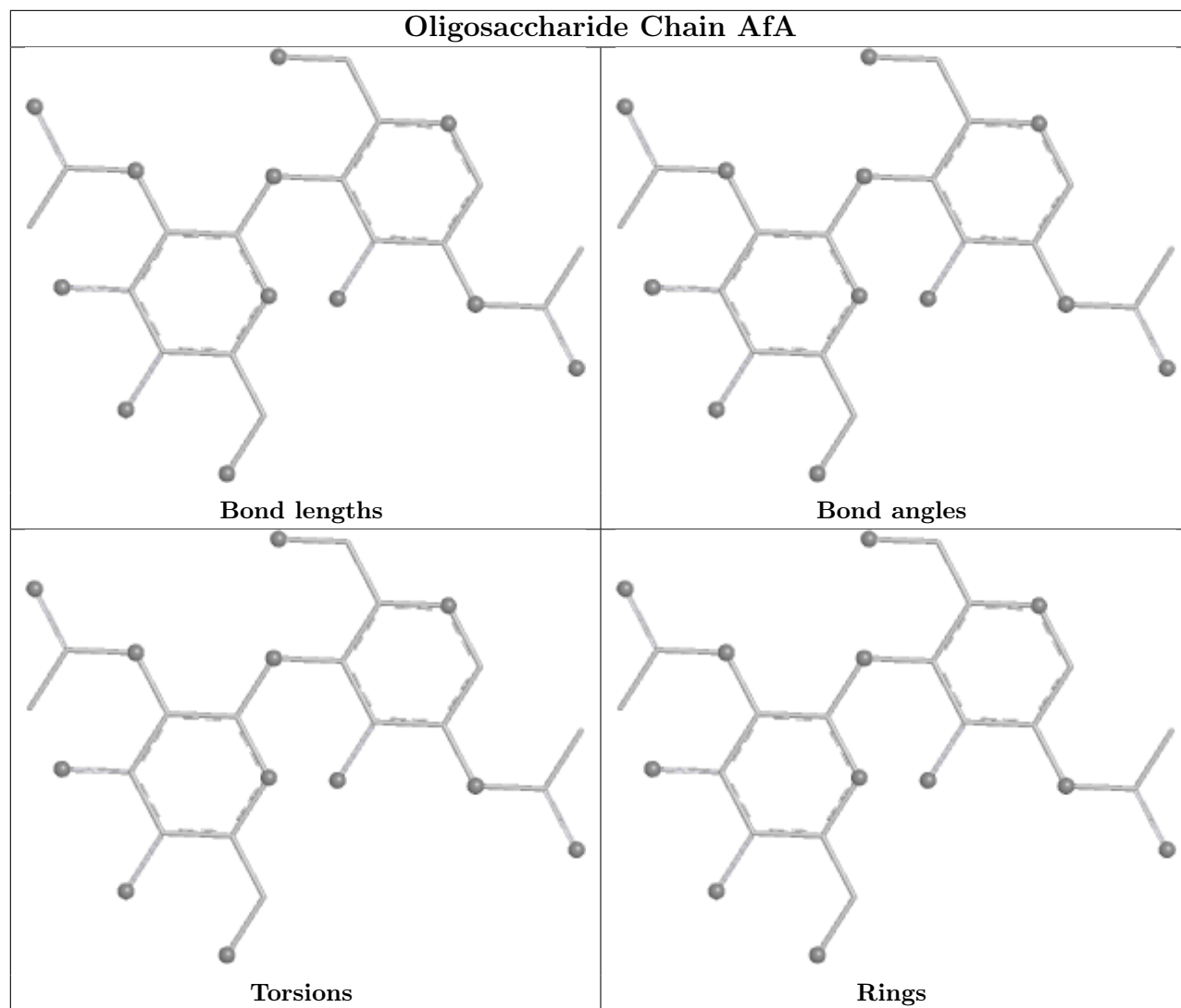
All (1) ring outliers are listed below:

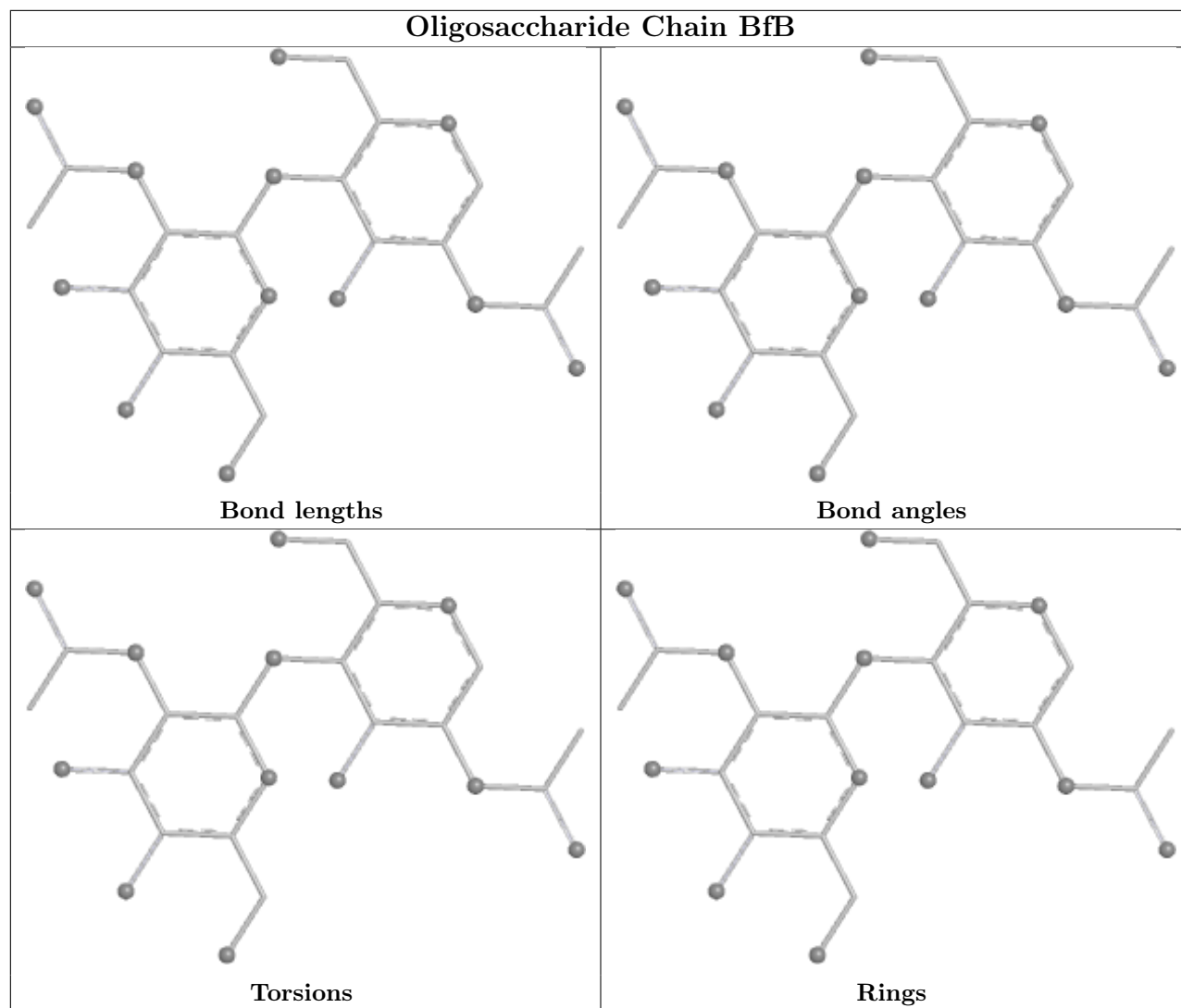
Mol	Chain	Res	Type	Atoms
2	AcA	3	MAN	C1-C2-C3-C4-C5-O5

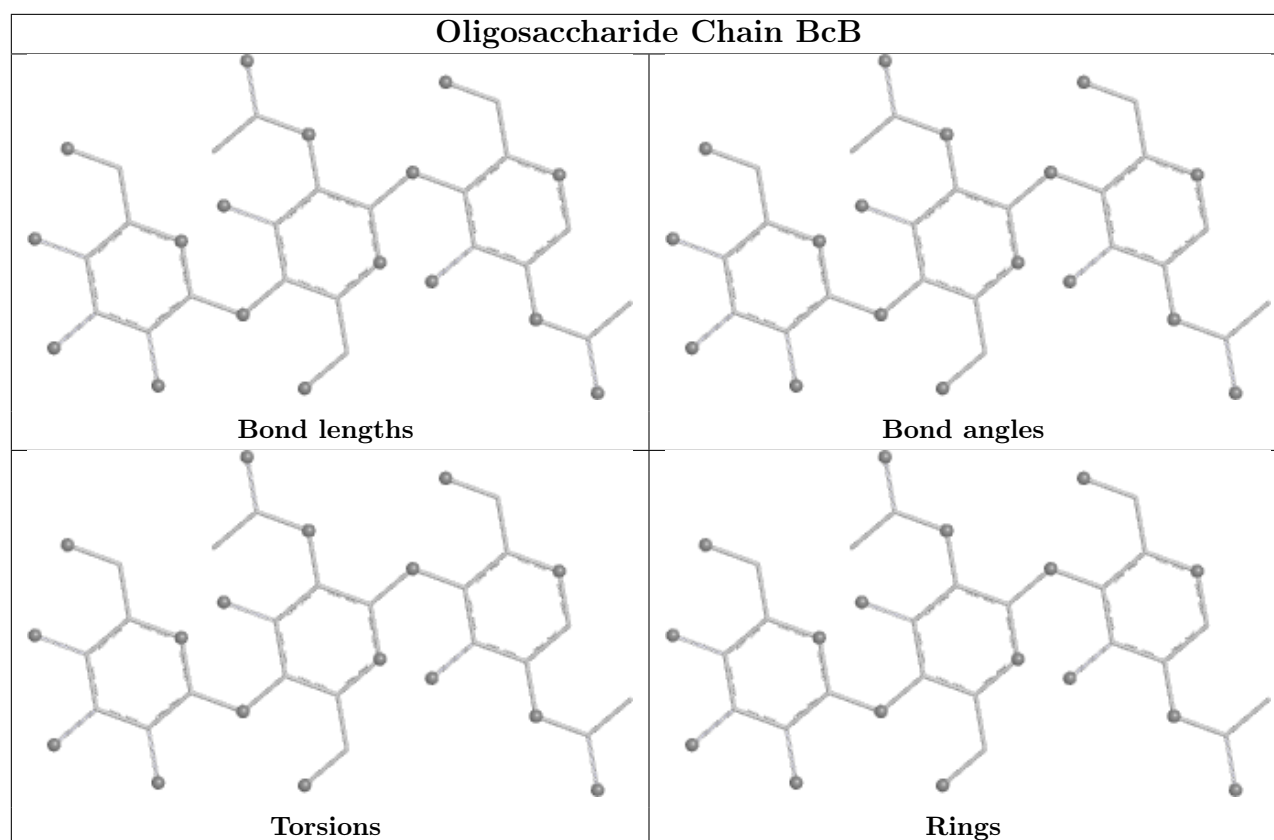
No monomer is involved in short contacts.

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 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	$\# Z > 2$
7	SRA	BbB	1005	-	25,25,25	3.30	11 (44%)	35,38,38	2.10	9 (25%)
6	NAG	AbA	1004	1	14,14,15	0.53	0	17,19,21	1.25	4 (23%)
8	EDO	AbA	1007	-	3,3,3	0.06	0	2,2,2	0.10	0
6	NAG	AbA	1003	1	14,14,15	0.47	0	17,19,21	1.26	1 (5%)
6	NAG	BbB	1003	1	14,14,15	0.67	1 (7%)	17,19,21	1.83	6 (35%)
7	SRA	AbA	1006	-	25,25,25	3.30	11 (44%)	35,38,38	2.09	9 (25%)
6	NAG	AbA	1005	1	14,14,15	0.35	0	17,19,21	0.53	0
6	NAG	BbB	1004	1	14,14,15	0.60	1 (7%)	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
7	SRA	BbB	1005	-	-	4/10/26/26	0/3/3/3
6	NAG	AbA	1004	1	-	5/6/23/26	0/1/1/1
8	EDO	AbA	1007	-	-	1/1/1/1	-
6	NAG	AbA	1003	1	-	4/6/23/26	0/1/1/1
6	NAG	BbB	1003	1	-	4/6/23/26	0/1/1/1
7	SRA	AbA	1006	-	-	5/10/26/26	0/3/3/3
6	NAG	AbA	1005	1	1/1/5/7	2/6/23/26	0/1/1/1
6	NAG	BbB	1004	1	-	4/6/23/26	0/1/1/1

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	BbB	1005	SRA	O4'-C1'	9.82	1.64	1.42
7	AbA	1006	SRA	O4'-C1'	9.62	1.64	1.42
7	AbA	1006	SRA	O4'-C4'	-7.92	1.27	1.45
7	BbB	1005	SRA	O4'-C4'	-7.66	1.28	1.45
7	AbA	1006	SRA	C2'-C1'	-5.92	1.34	1.53
7	BbB	1005	SRA	C2'-C1'	-5.88	1.35	1.53
7	AbA	1006	SRA	O2'-C2'	4.93	1.55	1.43
7	BbB	1005	SRA	O2'-C2'	4.83	1.54	1.43
7	AbA	1006	SRA	O3'-C3'	-2.84	1.35	1.43
7	BbB	1005	SRA	O3'-C3'	-2.75	1.36	1.43
7	AbA	1006	SRA	C3'-C4'	2.75	1.60	1.53
7	BbB	1005	SRA	P-S2P	2.66	1.96	1.90
7	AbA	1006	SRA	P-O5'	2.64	1.65	1.58
7	AbA	1006	SRA	C8-N9	-2.64	1.33	1.37
7	BbB	1005	SRA	P-O5'	2.62	1.65	1.58
7	BbB	1005	SRA	C5'-C4'	2.60	1.59	1.51
7	BbB	1005	SRA	C8-N9	-2.57	1.33	1.37
7	BbB	1005	SRA	C3'-C4'	2.54	1.59	1.53
7	AbA	1006	SRA	C5'-C4'	2.52	1.59	1.51
7	AbA	1006	SRA	P-S2P	2.24	1.95	1.90
7	AbA	1006	SRA	P-OP1	-2.20	1.47	1.54
7	BbB	1005	SRA	P-OP1	-2.18	1.47	1.54
6	BbB	1004	NAG	C1-C2	2.07	1.55	1.52
6	BbB	1003	NAG	C1-C2	2.04	1.55	1.52

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	BbB	1005	SRA	C5-C4-N3	-5.88	118.61	126.72
7	AbA	1006	SRA	C5-C4-N3	-5.70	118.86	126.72
7	AbA	1006	SRA	N3-C2-N1	-5.06	120.93	128.58
7	BbB	1005	SRA	N3-C2-N1	-5.02	120.98	128.58
7	BbB	1005	SRA	C2-N3-C4	3.93	121.43	111.83
7	AbA	1006	SRA	C2-N3-C4	3.88	121.31	111.83
6	BbB	1003	NAG	O5-C1-C2	-3.87	105.31	111.29
7	BbB	1005	SRA	C4-C5-N7	-3.64	106.42	110.58
7	BbB	1005	SRA	N3-C4-N9	3.60	133.29	127.17
7	AbA	1006	SRA	C4-C5-N7	-3.60	106.47	110.58
7	AbA	1006	SRA	N3-C4-N9	3.54	133.19	127.17
7	BbB	1005	SRA	C5-N7-C8	3.15	108.40	103.45
7	AbA	1006	SRA	C5-N7-C8	3.05	108.25	103.45
6	BbB	1003	NAG	O7-C7-N2	2.96	127.21	121.98
6	BbB	1004	NAG	O7-C7-N2	2.87	127.05	121.98
7	BbB	1005	SRA	N9-C8-N7	-2.74	110.05	113.94
7	AbA	1006	SRA	C3'-C2'-C1'	2.68	106.53	101.46
6	BbB	1003	NAG	C3-C4-C5	2.66	115.05	110.23
6	AbA	1003	NAG	C1-O5-C5	-2.66	108.62	112.19
6	BbB	1003	NAG	C4-C3-C2	2.64	114.89	111.02
7	AbA	1006	SRA	N9-C8-N7	-2.61	110.23	113.94
7	BbB	1005	SRA	C3'-C2'-C1'	2.59	106.37	101.46
6	BbB	1003	NAG	C2-N2-C7	2.57	126.34	122.90
6	BbB	1003	NAG	C8-C7-N2	-2.56	111.87	116.12
6	AbA	1004	NAG	O7-C7-N2	2.56	126.50	121.98
6	BbB	1004	NAG	C8-C7-N2	-2.47	112.03	116.12
6	AbA	1004	NAG	O5-C1-C2	-2.41	107.56	111.29
6	BbB	1004	NAG	C2-N2-C7	2.23	125.89	122.90
7	BbB	1005	SRA	C5-C4-N9	2.10	108.10	105.81
6	AbA	1004	NAG	C8-C7-N2	-2.09	112.65	116.12
6	AbA	1004	NAG	C2-N2-C7	2.04	125.63	122.90
7	AbA	1006	SRA	O5'-P-S2P	-2.02	108.44	115.86

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	AbA	1005	NAG	C1

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	AbA	1003	NAG	C8-C7-N2-C2
6	AbA	1003	NAG	O7-C7-N2-C2
6	BbB	1003	NAG	C1-C2-N2-C7
7	BbB	1005	SRA	O4'-C4'-C5'-O5'
7	BbB	1005	SRA	C3'-C4'-C5'-O5'
6	AbA	1004	NAG	C8-C7-N2-C2
6	BbB	1004	NAG	C8-C7-N2-C2
6	BbB	1003	NAG	C8-C7-N2-C2
6	AbA	1005	NAG	O5-C5-C6-O6
7	AbA	1006	SRA	O4'-C4'-C5'-O5'
6	BbB	1003	NAG	O5-C5-C6-O6
7	AbA	1006	SRA	C3'-C4'-C5'-O5'
6	AbA	1003	NAG	C4-C5-C6-O6
6	AbA	1004	NAG	O7-C7-N2-C2
7	BbB	1005	SRA	C5'-O5'-P-S2P
6	BbB	1004	NAG	O7-C7-N2-C2
6	AbA	1004	NAG	C4-C5-C6-O6
8	AbA	1007	EDO	O1-C1-C2-O2
6	AbA	1003	NAG	O5-C5-C6-O6
6	AbA	1004	NAG	C1-C2-N2-C7
6	BbB	1004	NAG	C1-C2-N2-C7
6	BbB	1003	NAG	O7-C7-N2-C2
6	AbA	1004	NAG	O5-C5-C6-O6
7	AbA	1006	SRA	C2'-C1'-N9-C8
6	AbA	1005	NAG	C4-C5-C6-O6
7	AbA	1006	SRA	C2'-C1'-N9-C4
7	BbB	1005	SRA	C5'-O5'-P-OP3
6	BbB	1004	NAG	C3-C2-N2-C7
7	AbA	1006	SRA	O4'-C1'-N9-C8

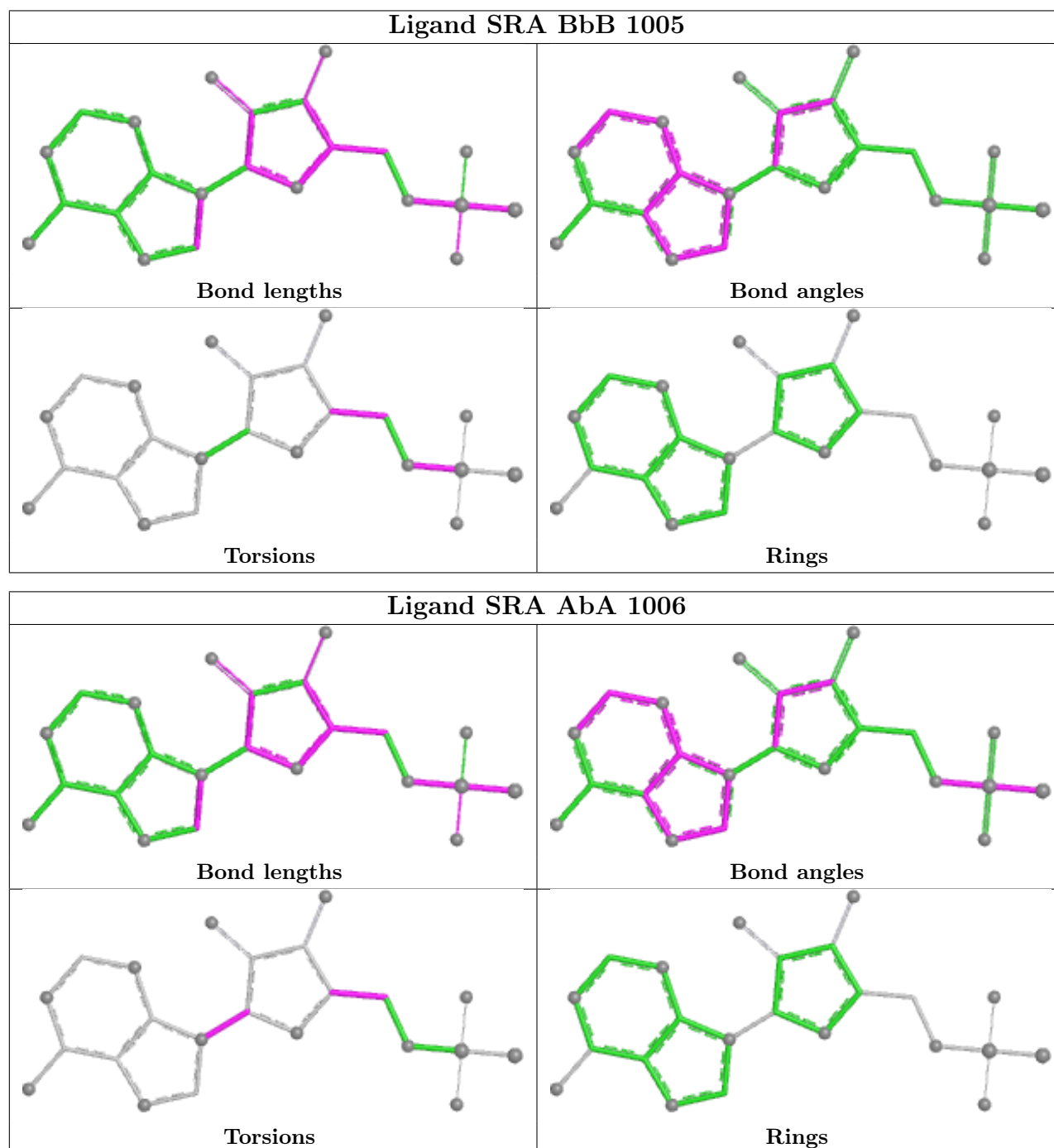
There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	BbB	1005	SRA	3	0
7	AbA	1006	SRA	4	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	AbA	816/925 (88%)	0.13	37 (4%) 38 31	18, 51, 100, 141	3 (0%)
1	BbB	799/925 (86%)	0.85	142 (17%) 4 2	35, 73, 137, 166	0
All	All	1615/1850 (87%)	0.48	179 (11%) 10 8	18, 59, 128, 166	3 (0%)

All (179) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BbB	678	GLN	7.5
1	BbB	753	TYR	6.0
1	AbA	874	ASP	5.3
1	BbB	637	ASP	5.2
1	BbB	612	VAL	5.2
1	BbB	819	VAL	5.0
1	AbA	612	VAL	4.9
1	AbA	921	PHE	4.8
1	BbB	870	HIS	4.8
1	BbB	461	ASP	4.7
1	BbB	619	ASN	4.7
1	BbB	739	PHE	4.7
1	BbB	724	HIS	4.6
1	AbA	871	GLY	4.4
1	BbB	620	PRO	4.3
1	AbA	526	GLU	4.3
1	BbB	710	ASN	4.2
1	BbB	669	ASN	4.1
1	BbB	920	THR	4.1
1	BbB	629	ASN	4.1
1	BbB	729	TYR	4.0
1	BbB	822	ASN	4.0
1	BbB	693	THR	3.9
1	AbA	104	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
1	AbA	119	ASN	3.9
1	BbB	709	SER	3.9
1	BbB	827	ILE	3.9
1	BbB	820	ILE	3.9
1	BbB	799	PHE	3.9
1	AbA	105	VAL	3.8
1	AbA	529[A]	TYR	3.8
1	AbA	669	ASN	3.8
1	BbB	883	MET	3.8
1	BbB	694	SER	3.7
1	BbB	723	VAL	3.6
1	BbB	712	LEU	3.6
1	BbB	622	ASP	3.6
1	BbB	692	TRP	3.6
1	BbB	810	LEU	3.6
1	BbB	826	LEU	3.6
1	AbA	277	ASN	3.5
1	BbB	277	ASN	3.5
1	BbB	621	ARG	3.5
1	AbA	608	VAL	3.5
1	BbB	104	GLU	3.5
1	BbB	680	MET	3.4
1	BbB	624	LEU	3.4
1	BbB	674	LEU	3.4
1	BbB	756	ALA	3.4
1	BbB	668	GLU	3.4
1	BbB	679	PHE	3.4
1	BbB	825	ILE	3.3
1	BbB	752	ILE	3.3
1	AbA	677	HIS	3.3
1	BbB	773	TRP	3.3
1	BbB	757	LEU	3.3
1	BbB	708	PHE	3.3
1	BbB	814	ARG	3.3
1	BbB	795	SER	3.3
1	BbB	695	TYR	3.3
1	BbB	722	PRO	3.2
1	BbB	677	HIS	3.2
1	BbB	716	PHE	3.2
1	BbB	751	GLY	3.2
1	BbB	611	LEU	3.1
1	BbB	740	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	BbB	761	ASN	3.1
1	BbB	707	ASP	3.1
1	BbB	691	LEU	3.0
1	BbB	630	PRO	3.0
1	AbA	626[A]	CYS	3.0
1	BbB	734	LYS	3.0
1	BbB	759	THR	3.0
1	BbB	813	LEU	3.0
1	BbB	875	SER	3.0
1	BbB	735	VAL	2.9
1	AbA	610	PRO	2.9
1	BbB	745	LEU	2.9
1	BbB	651	ILE	2.9
1	AbA	611	LEU	2.9
1	BbB	105	VAL	2.9
1	BbB	697	VAL	2.9
1	BbB	703	PHE	2.9
1	BbB	764	PRO	2.9
1	BbB	797	PRO	2.9
1	BbB	713	TYR	2.8
1	BbB	633	LEU	2.8
1	BbB	714	GLN	2.8
1	BbB	812	ASN	2.8
1	BbB	682	GLY	2.8
1	BbB	776	PHE	2.8
1	AbA	670	THR	2.8
1	BbB	636	GLU	2.8
1	AbA	668	GLU	2.7
1	BbB	686	ASP	2.7
1	BbB	631	SER	2.7
1	BbB	696	THR	2.7
1	BbB	779	THR	2.7
1	BbB	754	SER	2.7
1	BbB	689	MET	2.6
1	BbB	817	ARG	2.6
1	BbB	793	VAL	2.6
1	BbB	783	LYS	2.6
1	BbB	742	PRO	2.6
1	BbB	717	ARG	2.6
1	BbB	288	PHE	2.5
1	BbB	671	ILE	2.5
1	BbB	869	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	BbB	832	PHE	2.5
1	BbB	478	LEU	2.5
1	AbA	876	SER	2.5
1	BbB	738	GLY	2.5
1	BbB	747	LYS	2.4
1	AbA	522	LEU	2.4
1	BbB	877	TRP	2.4
1	BbB	755	GLU	2.4
1	BbB	119	ASN	2.4
1	AbA	120	CYS	2.4
1	BbB	715	ASP	2.4
1	BbB	488	LYS	2.4
1	BbB	529	TYR	2.4
1	BbB	771	VAL	2.4
1	AbA	628	CYS	2.4
1	BbB	725	LYS	2.4
1	BbB	635	ILE	2.4
1	BbB	758	LEU	2.3
1	BbB	667	LYS	2.3
1	BbB	681	SER	2.3
1	BbB	876	SER	2.3
1	BbB	859	PRO	2.3
1	BbB	152	PHE	2.3
1	BbB	673	LEU	2.3
1	BbB	720	LEU	2.3
1	BbB	901	TYR	2.3
1	BbB	182	SER	2.3
1	BbB	610	PRO	2.3
1	BbB	690	PRO	2.3
1	AbA	646	VAL	2.3
1	BbB	762	ILE	2.3
1	BbB	278	LYS	2.3
1	AbA	289	SER	2.3
1	BbB	608	VAL	2.3
1	AbA	117	PHE	2.3
1	BbB	792	ASN	2.2
1	AbA	620	PRO	2.2
1	BbB	632	ILE	2.2
1	AbA	699	ARG	2.2
1	BbB	289	SER	2.2
1	BbB	644	LEU	2.2
1	BbB	451	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	BbB	796	GLY	2.2
1	BbB	628	CYS	2.2
1	BbB	657	LEU	2.2
1	AbA	870	HIS	2.2
1	BbB	512	PHE	2.2
1	AbA	606	LYS	2.1
1	BbB	185	GLN	2.1
1	BbB	129	LEU	2.1
1	BbB	290	LEU	2.1
1	AbA	875	SER	2.1
1	BbB	626	CYS	2.1
1	AbA	118	GLY	2.1
1	BbB	706	GLU	2.1
1	AbA	621	ARG	2.1
1	BbB	726	CYS	2.1
1	AbA	753	TYR	2.1
1	BbB	675	SER	2.1
1	BbB	782	ARG	2.1
1	AbA	613	GLN	2.1
1	BbB	857	ILE	2.1
1	BbB	526	GLU	2.0
1	BbB	705	THR	2.0
1	BbB	489	PRO	2.0
1	BbB	780	LEU	2.0
1	AbA	450	ILE	2.0
1	BbB	646	VAL	2.0
1	AbA	667	LYS	2.0
1	BbB	457	LEU	2.0
1	AbA	847	HIS	2.0

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

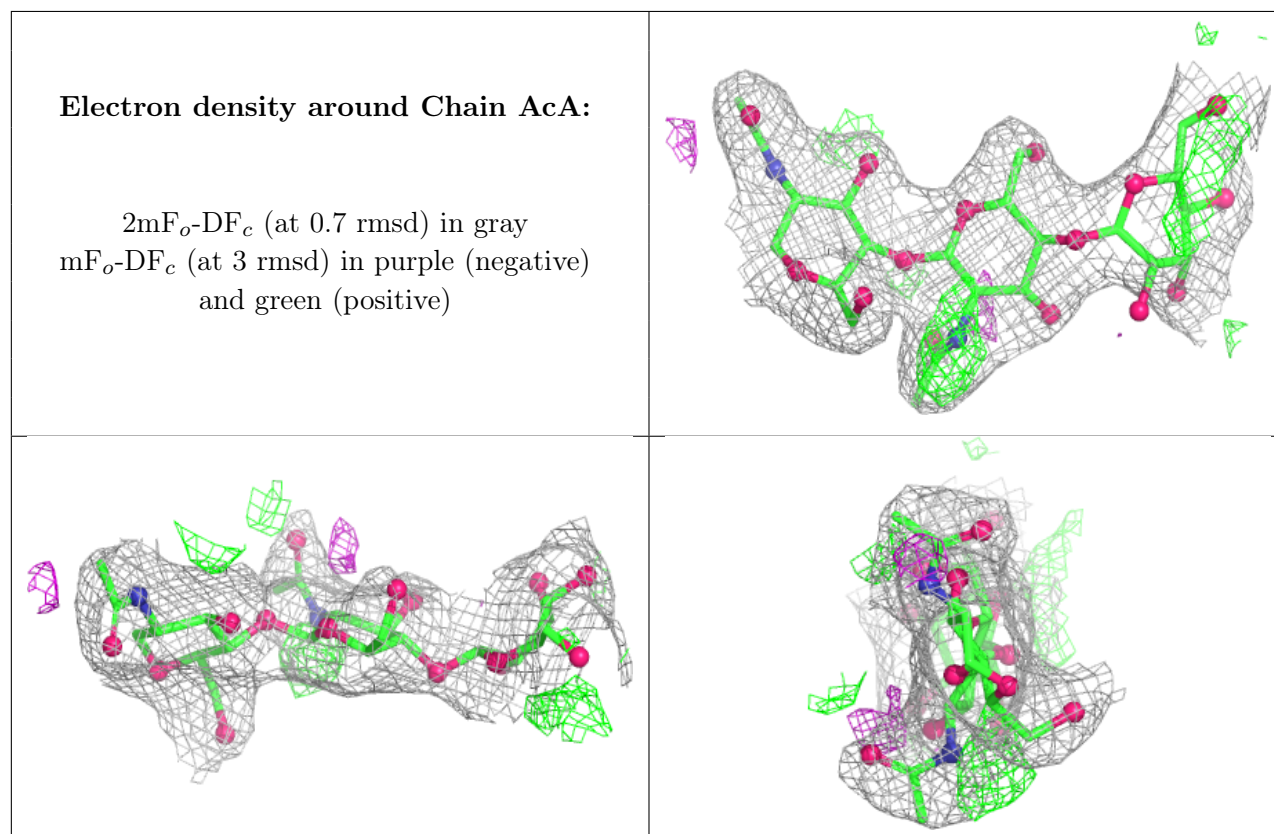
There are no non-standard protein/DNA/RNA residues in this entry.

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.

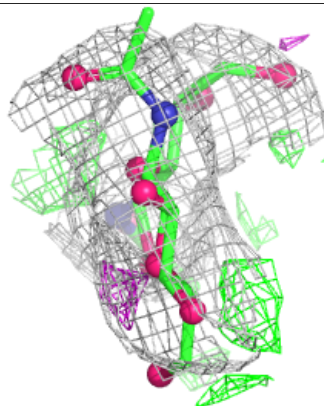
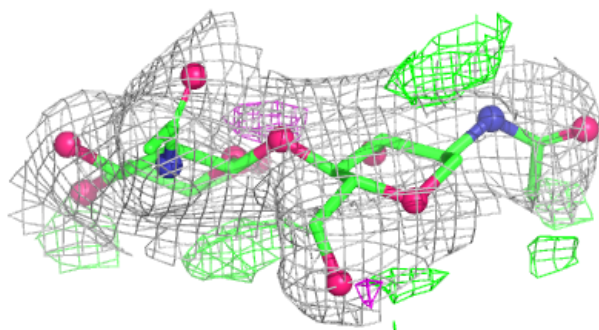
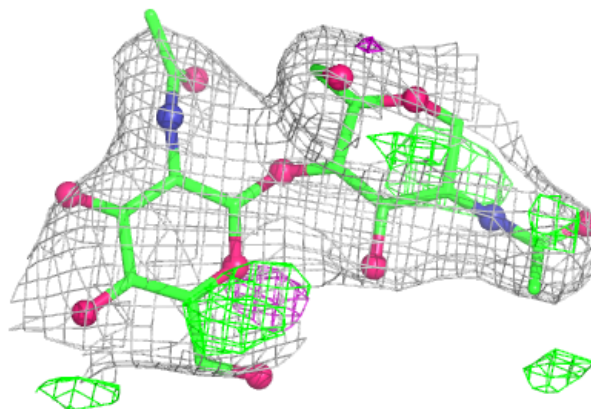
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	AcA	1	14/15	-	-	44,47,51,61	0
2	NAG	AcA	2	14/15	-	-	62,72,80,93	0
2	MAN	AcA	3	11/12	-	-	93,103,106,114	0
3	NAG	AfA	1	14/15	-	-	68,76,83,83	0
3	NAG	AfA	2	14/15	-	-	89,98,109,119	0
3	NAG	BfB	1	14/15	-	-	80,92,100,100	0
3	NAG	BfB	2	14/15	-	-	96,107,115,116	0
4	NAG	BcB	1	14/15	-	-	60,64,74,84	0
4	NAG	BcB	2	14/15	-	-	82,98,111,116	0
4	BMA	BcB	3	11/12	-	-	105,114,120,123	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.

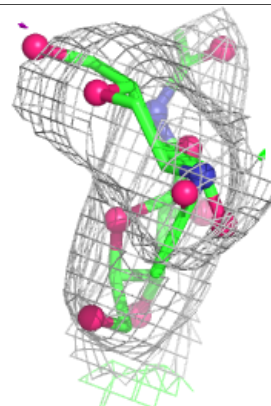
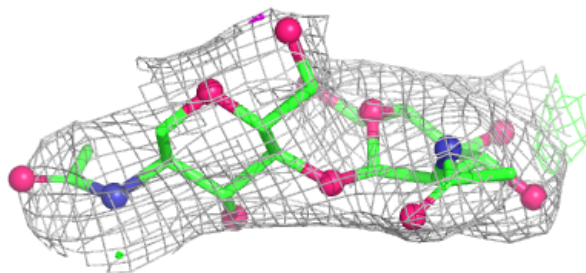
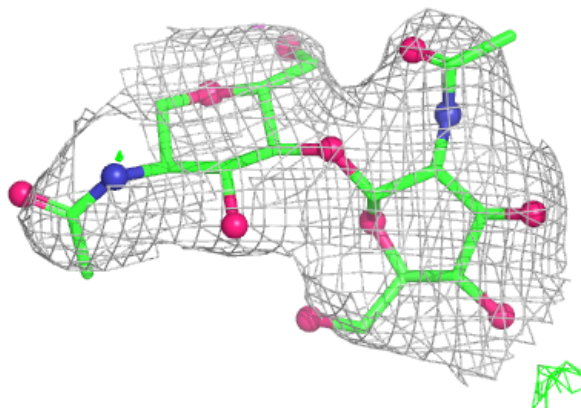


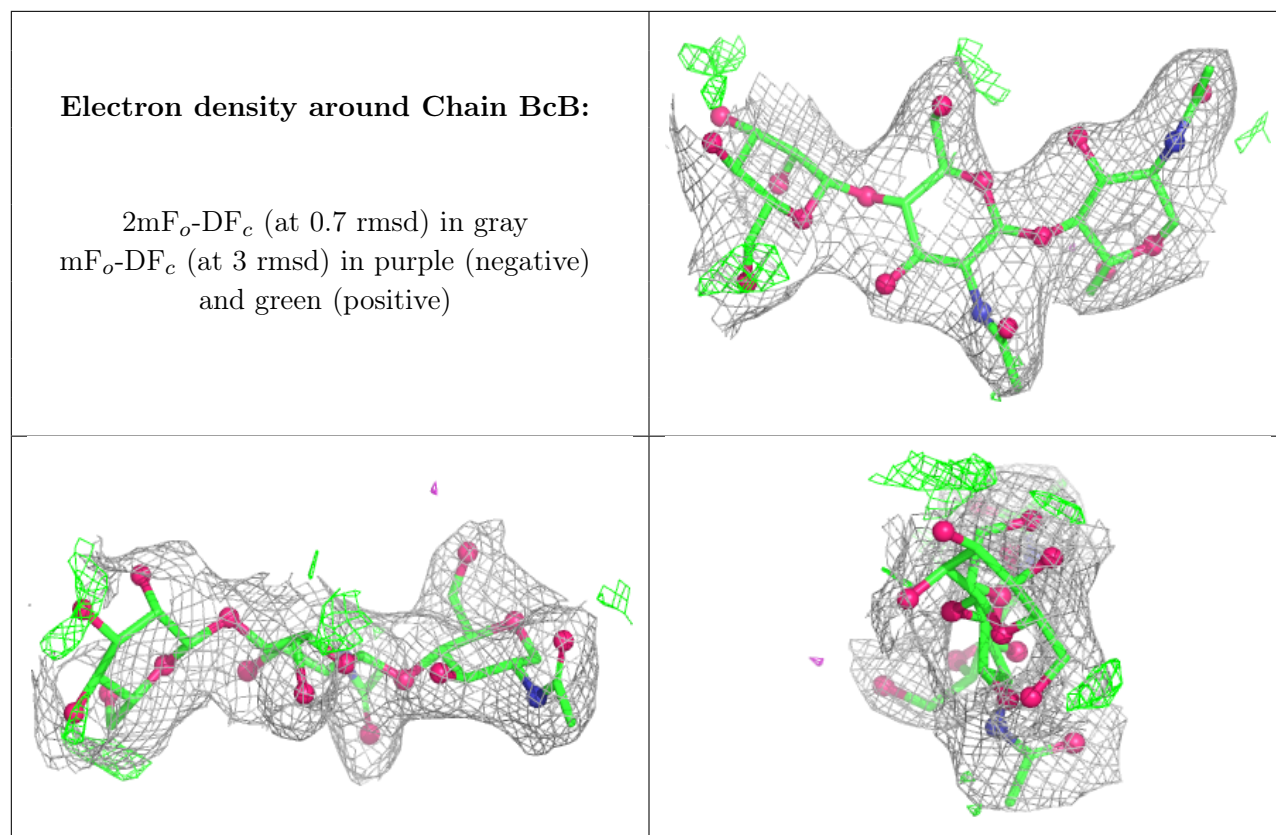
Electron density around Chain AfA:

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

**Electron density around Chain BfB:**

$2mF_o-DF_c$ (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, 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.

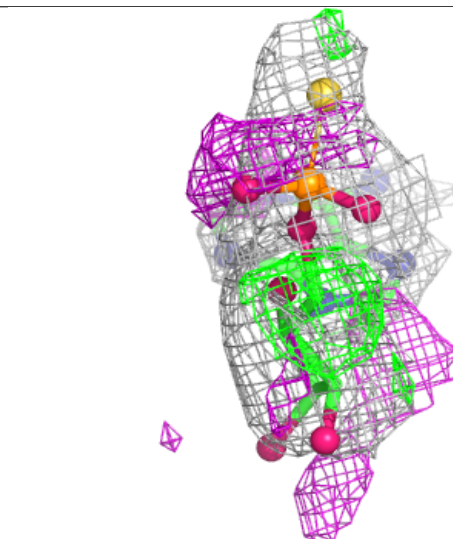
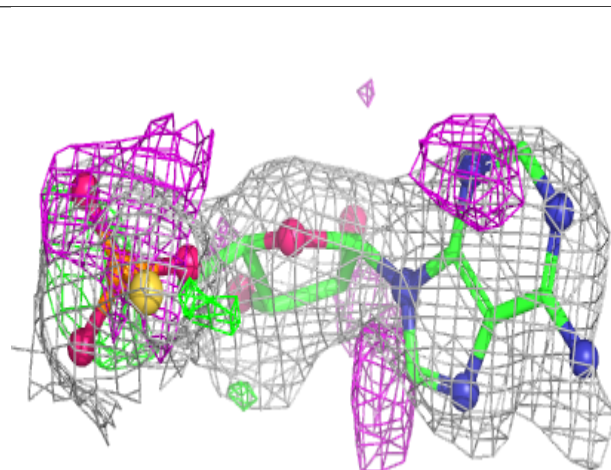
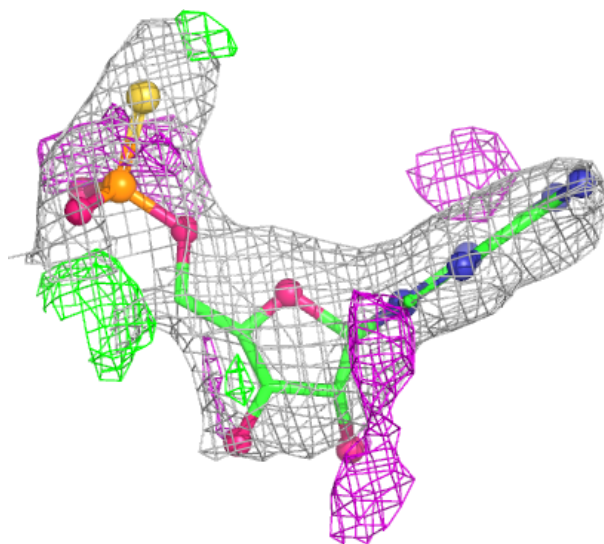
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	NAG	AbA	1005	14/15	0.42	0.21	113,122,129,130	0
6	NAG	BbB	1003	14/15	0.42	0.19	106,143,154,155	0
6	NAG	BbB	1004	14/15	0.47	0.18	98,121,130,130	0
6	NAG	AbA	1004	14/15	0.74	0.15	82,105,117,118	0
6	NAG	AbA	1003	14/15	0.77	0.16	98,106,111,122	0
7	SRA	BbB	1005	23/23	0.80	0.16	71,82,91,99	0
7	SRA	AbA	1006	23/23	0.83	0.16	67,87,103,107	0
8	EDO	AbA	1007	4/4	0.90	0.23	67,69,70,73	0
5	ZN	AbA	1002	1/1	0.92	0.21	93,93,93,93	1
5	ZN	BbB	1002	1/1	0.94	0.23	66,66,66,66	1
5	ZN	BbB	1001	1/1	0.99	0.02	53,53,53,53	0
5	ZN	AbA	1001	1/1	1.00	0.03	49,49,49,49	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.

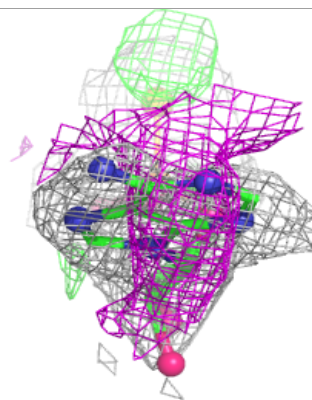
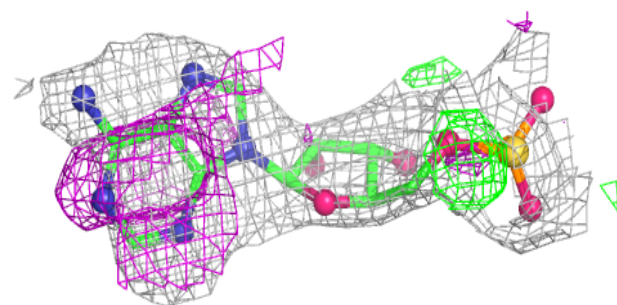
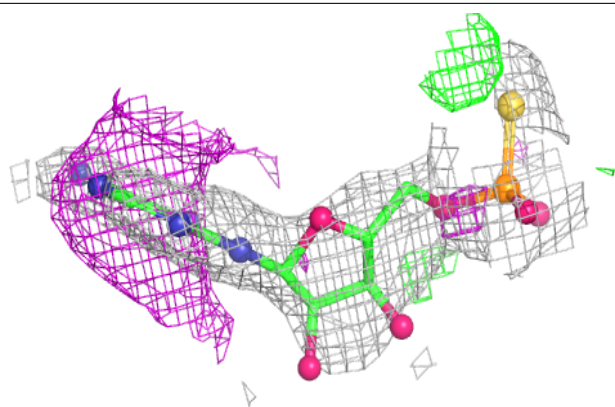
Electron density around SRA BbB 1005:

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



Electron density around SRA AbA 1006:

$2mF_o-DF_c$ (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.