



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 3, 2022 – 12:04 PM EST

PDB ID : 7SLX
Title : Vanin-1 complexed with Compound 11
Authors : Vajdos, F.F.
Deposited on : 2021-10-25
Resolution : 2.35 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.25
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.25

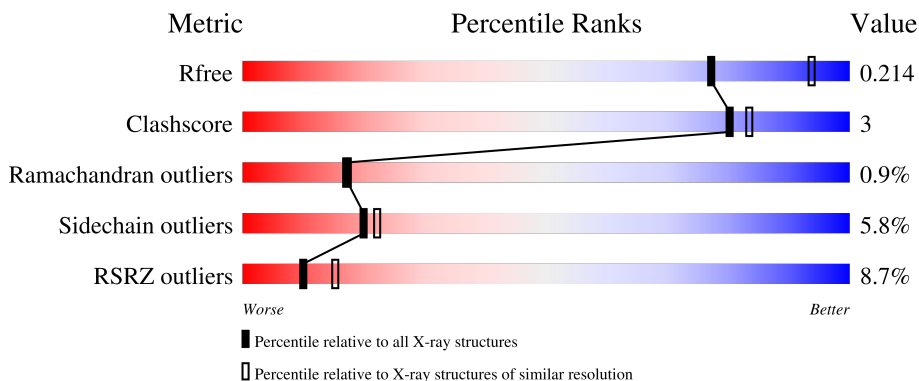
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

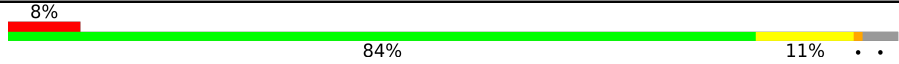
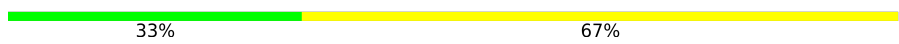

The reported resolution of this entry is 2.35 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	482	
2	B	3	
3	D	6	

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	NAG	A	503	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4023 atoms, of which 19 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.

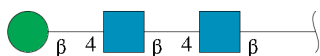
- Molecule 1 is a protein called Pantetheinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	461	3620	2307	597	697	19	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

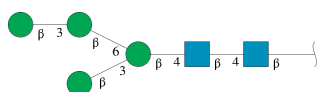
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	GLY	-	expression tag	UNP O95497
A	-18	SER	-	expression tag	UNP O95497
A	-17	GLY	-	expression tag	UNP O95497
A	-16	HIS	-	expression tag	UNP O95497
A	-15	HIS	-	expression tag	UNP O95497
A	-14	HIS	-	expression tag	UNP O95497
A	-13	HIS	-	expression tag	UNP O95497
A	-12	HIS	-	expression tag	UNP O95497
A	-11	HIS	-	expression tag	UNP O95497
A	-10	GLY	-	expression tag	UNP O95497
A	-9	SER	-	expression tag	UNP O95497
A	-8	GLY	-	expression tag	UNP O95497
A	-7	ASP	-	expression tag	UNP O95497
A	-6	TYR	-	expression tag	UNP O95497
A	-5	LYS	-	expression tag	UNP O95497
A	-4	ASP	-	expression tag	UNP O95497
A	-3	ASP	-	expression tag	UNP O95497
A	-2	ASP	-	expression tag	UNP O95497
A	-1	ASP	-	expression tag	UNP O95497
A	0	LYS	-	expression tag	UNP O95497

- Molecule 2 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.



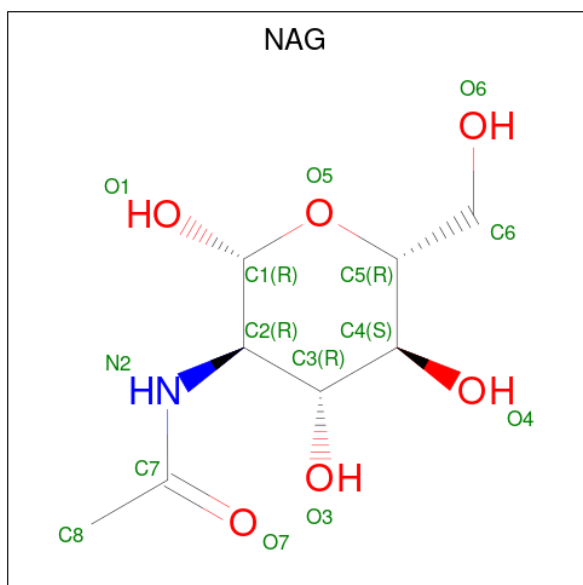
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	3	39	22	2	15	0	0	0

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-6)-[beta-D-mannopyranose-(1-3)]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	N	O			
3	D	6	72	40	2	30	0	0	0

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



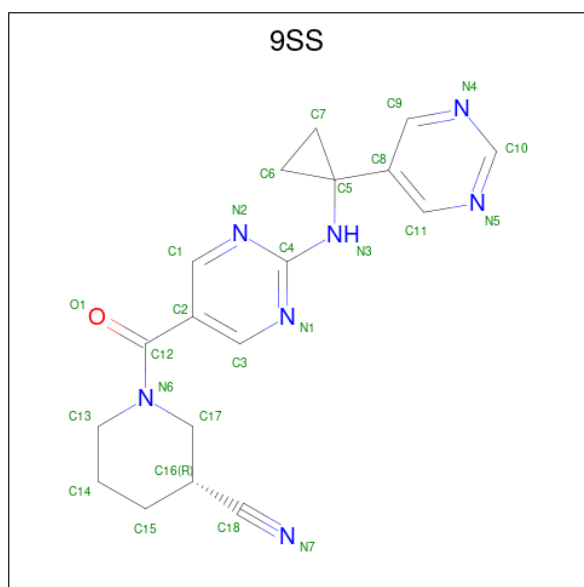
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	14	8	1	5	0	0

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

- Molecule 5 is (3R)-1-(2-{[1-(pyrimidin-5-yl)cyclopropyl]amino}pyrimidine-5-carbonyl)pipe-ridine-3-carbonitrile (three-letter code: 9SS) (formula: C₁₈H₁₉N₇O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
5	A	1	45	18	19	7	1	19	0

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

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

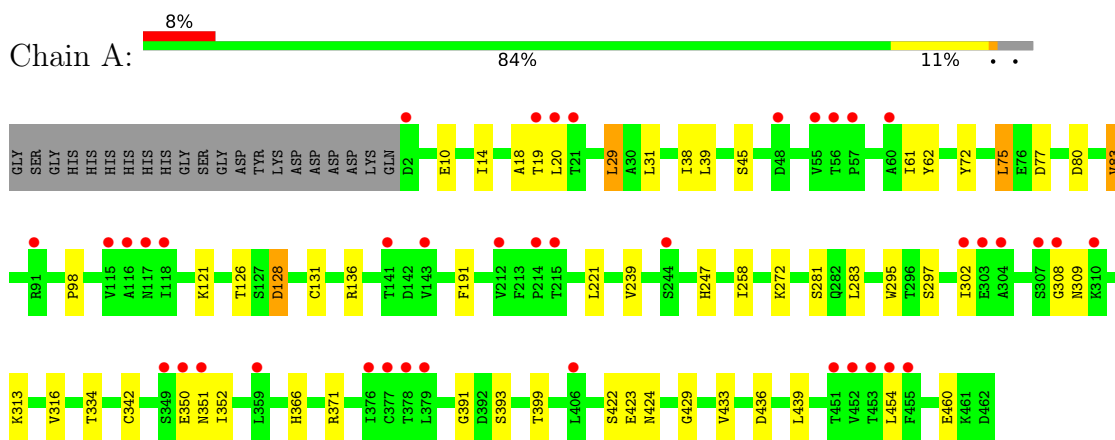
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	218	218	218	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Pantetheinase



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



- Molecule 3: beta-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-6)-[beta-D-mannopyranose-(1-3)]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	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	64.55Å 111.83Å 147.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.63 – 2.35 25.28 – 2.35	Depositor EDS
% Data completeness (in resolution range)	98.3 (25.63-2.35) 98.3 (25.28-2.35)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.36Å)	Xtrriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.174 , 0.217 0.172 , 0.214	Depositor DCC
R_{free} test set	1112 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	53.5	Xtrriage
Anisotropy	0.482	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 57.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4023	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.70% 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: BMA, NAG, CSO, 9SS, NA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.53	0/3708	0.77	2/5048 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	422	SER	C-N-CA	5.20	134.70	121.70
1	A	429	GLY	N-CA-C	-5.12	100.29	113.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3620	0	3457	19	0
2	B	39	0	34	0	0
3	D	72	0	61	1	0
4	A	28	0	26	0	0
5	A	26	19	0	0	0
6	A	1	0	0	0	0
7	A	218	0	0	0	0
All	All	4004	19	3578	20	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 3.

All (20) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295:TRP:CH2	1:A:433:VAL:HG11	2.36	0.60
1:A:39:LEU:HD12	1:A:61:ILE:HD11	1.85	0.57
1:A:80:ASP:O	1:A:83:VAL:HB	2.05	0.56
1:A:221:LEU:HB2	1:A:393:SER:HB2	1.90	0.54
1:A:10:GLU:HG2	1:A:247:HIS:HB2	1.92	0.51
1:A:334:THR:HA	1:A:342:CYS:O	2.14	0.46
1:A:352:ILE:HD13	1:A:399:THR:HA	1.97	0.46
1:A:316:VAL:HG22	1:A:391:GLY:HA3	1.97	0.46
1:A:439:LEU:HB2	1:A:454:LEU:HD21	1.98	0.46
1:A:128:ASP:OD1	1:A:131:CYS:HB2	2.16	0.46
1:A:72:TYR:CE1	1:A:121:LYS:HD2	2.50	0.46
3:D:2:NAG:O3	3:D:4:BMA:H3	2.16	0.45
1:A:221:LEU:HD11	1:A:424:ASN:HD21	1.81	0.45
1:A:72:TYR:CZ	1:A:121:LYS:HD2	2.53	0.44
1:A:39:LEU:CD1	1:A:61:ILE:HD11	2.48	0.43
1:A:258:ILE:HG23	1:A:283:LEU:HD11	2.01	0.42
1:A:14:ILE:HD11	1:A:38:ILE:HD11	2.02	0.42
1:A:366:HIS:O	1:A:371:ARG:HA	2.20	0.42
1:A:29:LEU:HD11	1:A:98:PRO:HG3	2.02	0.42
1:A:75:LEU:HB3	1:A:121:LYS:HB2	2.03	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	A	458/482 (95%)	427 (93%)	27 (6%)	4 (1%)	17 17

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	ALA
1	A	20	LEU
1	A	297	SER
1	A	308	GLY

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	399/417 (96%)	376 (94%)	23 (6%)	20 22

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	THR
1	A	29	LEU
1	A	31	LEU
1	A	45	SER
1	A	62	TYR
1	A	75	LEU
1	A	77	ASP
1	A	83	VAL
1	A	126	THR
1	A	128	ASP
1	A	136	ARG
1	A	191	PHE
1	A	239	VAL
1	A	272	LYS
1	A	281	SER
1	A	302	ILE
1	A	309	ASN
1	A	313	LYS
1	A	350	GLU
1	A	351	ASN
1	A	423	GLU

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Mol	Chain	Res	Type
1	A	436	ASP
1	A	460	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	386	ASN
1	A	388	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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
1	CSO	A	190	1	3,6,7	0.51	0	0,6,8	-	-

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
1	CSO	A	190	1	-	1/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	190	CSO	N-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

9 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	B	1	2,1	14,14,15	0.30	0	17,19,21	1.03	1 (5%)
2	NAG	B	2	2	14,14,15	0.28	0	17,19,21	0.68	1 (5%)
2	BMA	B	3	2	11,11,12	0.33	0	15,15,17	0.61	0
3	NAG	D	1	1,3	14,14,15	0.33	0	17,19,21	0.63	0
3	NAG	D	2	3	14,14,15	0.33	0	17,19,21	0.75	0
3	BMA	D	3	3	11,11,12	0.43	0	15,15,17	1.48	2 (13%)
3	BMA	D	4	3	11,11,12	0.44	0	15,15,17	1.89	4 (26%)
3	BMA	D	5	3	11,11,12	0.36	0	15,15,17	0.78	0
3	BMA	D	6	3	11,11,12	0.60	0	15,15,17	1.66	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	B	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	1/6/23/26	0/1/1/1
2	BMA	B	3	2	-	0/2/19/22	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1
3	BMA	D	4	3	-	0/2/19/22	0/1/1/1
3	BMA	D	5	3	-	0/2/19/22	0/1/1/1
3	BMA	D	6	3	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	4	BMA	C1-C2-C3	-4.85	103.71	109.67
3	D	6	BMA	C1-C2-C3	-4.06	104.68	109.67
3	D	3	BMA	O3-C3-C2	3.87	117.40	109.99
3	D	6	BMA	C1-O5-C5	-3.58	107.35	112.19
2	B	1	NAG	C1-C2-N2	3.36	116.23	110.49
3	D	4	BMA	O3-C3-C4	3.01	117.32	110.35
3	D	3	BMA	C1-O5-C5	2.99	116.24	112.19
3	D	4	BMA	C1-O5-C5	-2.52	108.78	112.19
3	D	4	BMA	O3-C3-C2	2.51	114.80	109.99
2	B	2	NAG	O5-C1-C2	-2.33	107.61	111.29

There are no chirality outliers.

All (2) torsion outliers are listed below:

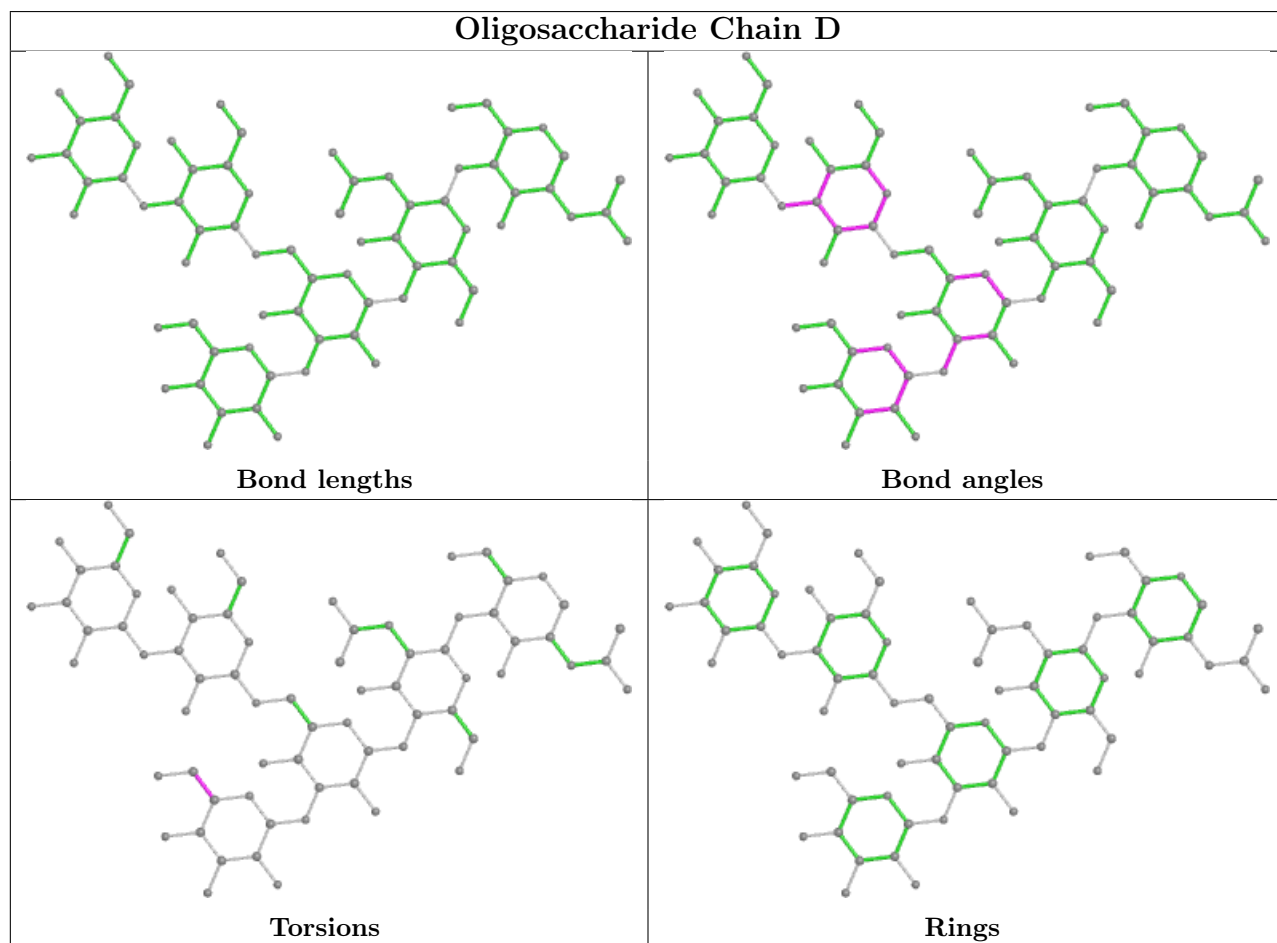
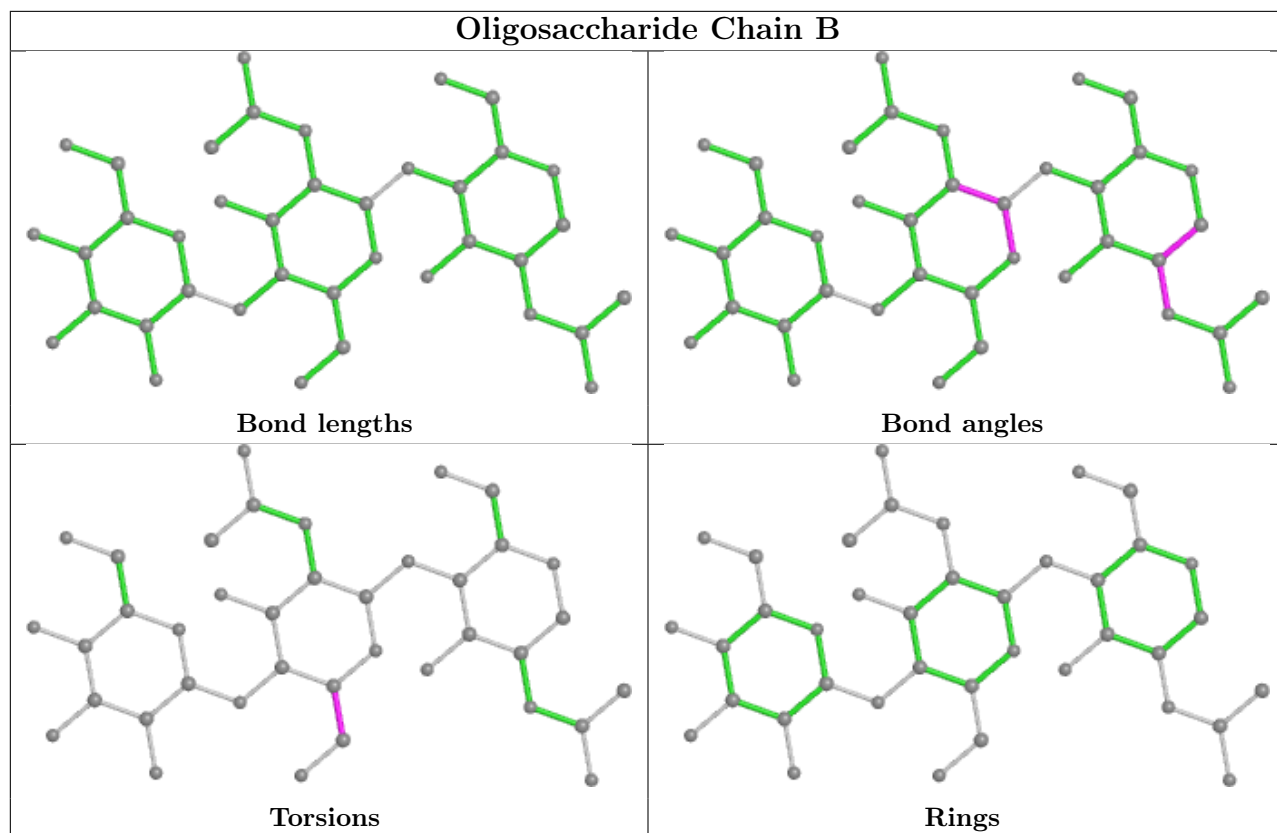
Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C4-C5-C6-O6
3	D	6	BMA	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	2	NAG	1	0
3	D	4	BMA	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 oligosaccharide.



5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	501	1	14,14,15	0.29	0	17,19,21	0.82	1 (5%)
5	9SS	A	502	-	25,29,29	1.54	4 (16%)	34,41,41	0.86	1 (2%)
4	NAG	A	503	1	14,14,15	0.31	0	17,19,21	0.69	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	501	1	-	2/6/23/26	0/1/1/1
5	9SS	A	502	-	-	0/19/35/35	0/4/4/4
4	NAG	A	503	1	-	0/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	502	9SS	C4-N2	3.95	1.40	1.34
5	A	502	9SS	C4-N1	3.45	1.39	1.34
5	A	502	9SS	C12-N6	2.42	1.40	1.34
5	A	502	9SS	C4-N3	2.34	1.37	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	501	NAG	C1-O5-C5	2.44	115.50	112.19
4	A	503	NAG	C1-O5-C5	2.29	115.29	112.19
5	A	502	9SS	C8-C11-N5	-2.13	122.21	124.09

There are no chirality outliers.

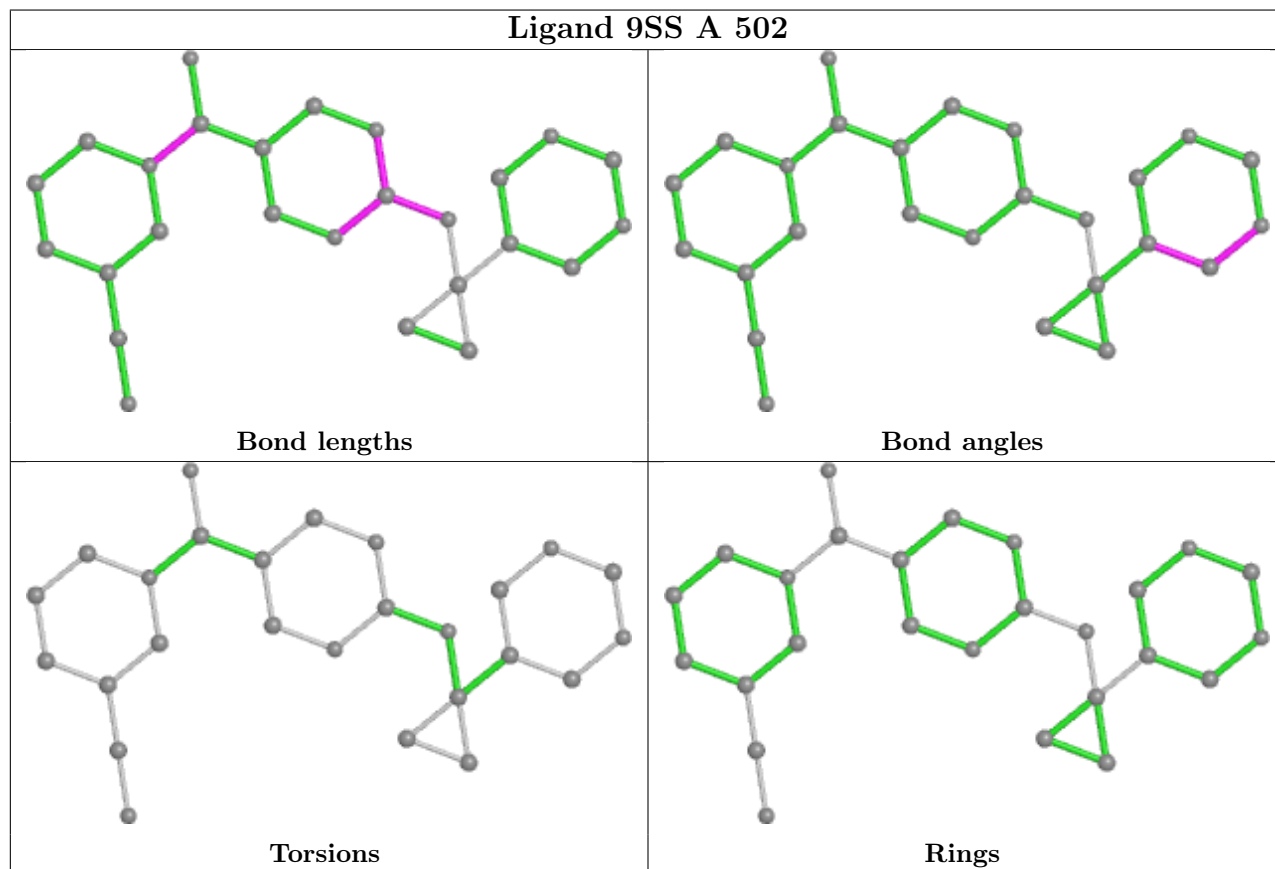
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	NAG	O5-C5-C6-O6
4	A	501	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for 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	A	460/482 (95%)	0.23	40 (8%) 10 15	38, 55, 85, 109	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	20	LEU	9.7
1	A	21	THR	5.7
1	A	116	ALA	5.5
1	A	115	VAL	4.9
1	A	118	ILE	4.4
1	A	302	ILE	4.3
1	A	55	VAL	4.0
1	A	56	THR	4.0
1	A	454	LEU	3.6
1	A	377	CYS	3.5
1	A	351	ASN	3.4
1	A	303	GLU	3.4
1	A	143	VAL	3.4
1	A	117	ASN	3.4
1	A	19	THR	3.3
1	A	453	THR	3.2
1	A	48	ASP	3.2
1	A	57	PRO	3.2
1	A	376	ILE	3.1
1	A	378	THR	3.0
1	A	452	VAL	2.9
1	A	91	ARG	2.8
1	A	455	PHE	2.8
1	A	60	ALA	2.8
1	A	304	ALA	2.7
1	A	212	VAL	2.6
1	A	349	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	379	LEU	2.6
1	A	244	SER	2.5
1	A	359	LEU	2.5
1	A	406	LEU	2.5
1	A	350	GLU	2.5
1	A	308	GLY	2.5
1	A	451	THR	2.4
1	A	141	THR	2.3
1	A	307	SER	2.2
1	A	215	THR	2.2
1	A	310	LYS	2.1
1	A	2	ASP	2.1
1	A	214	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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.

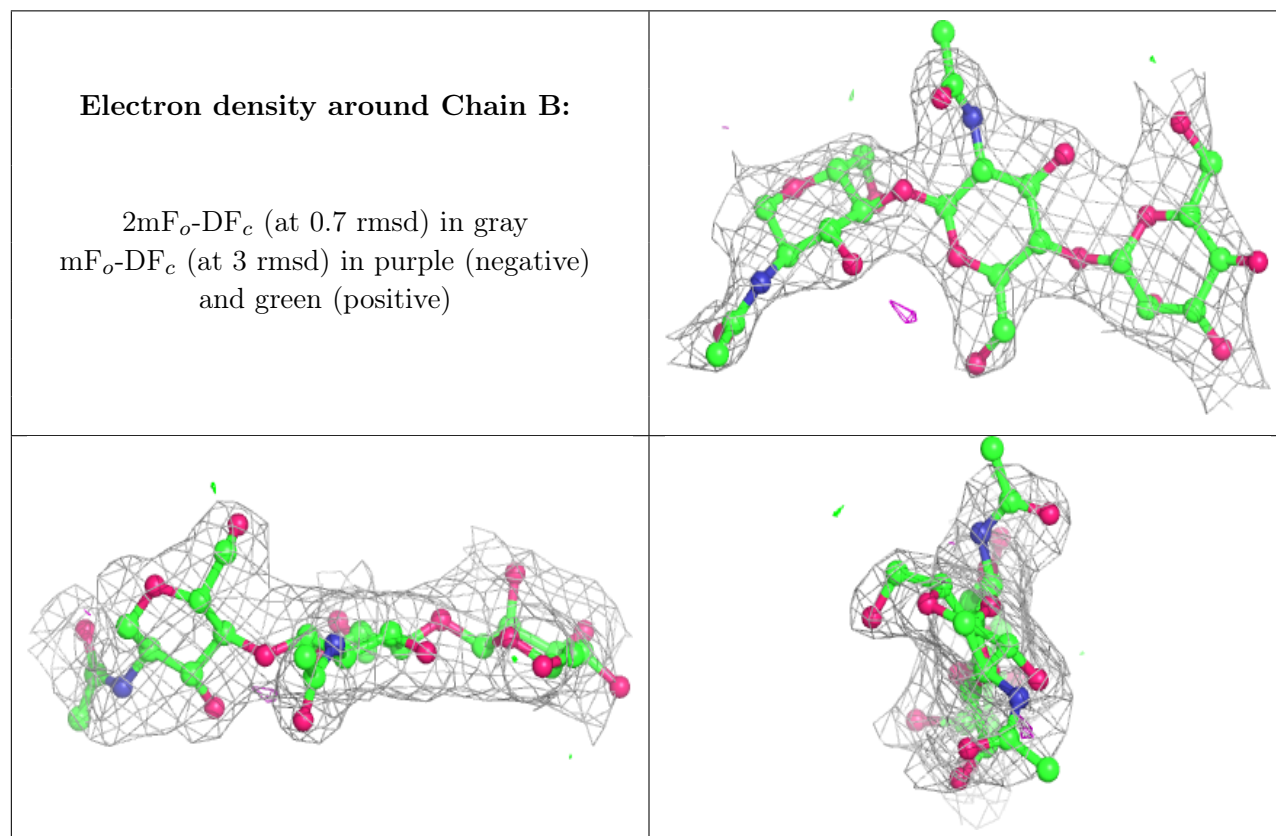
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	CSO	A	190	7/8	0.97	0.12	47,48,54,54	0

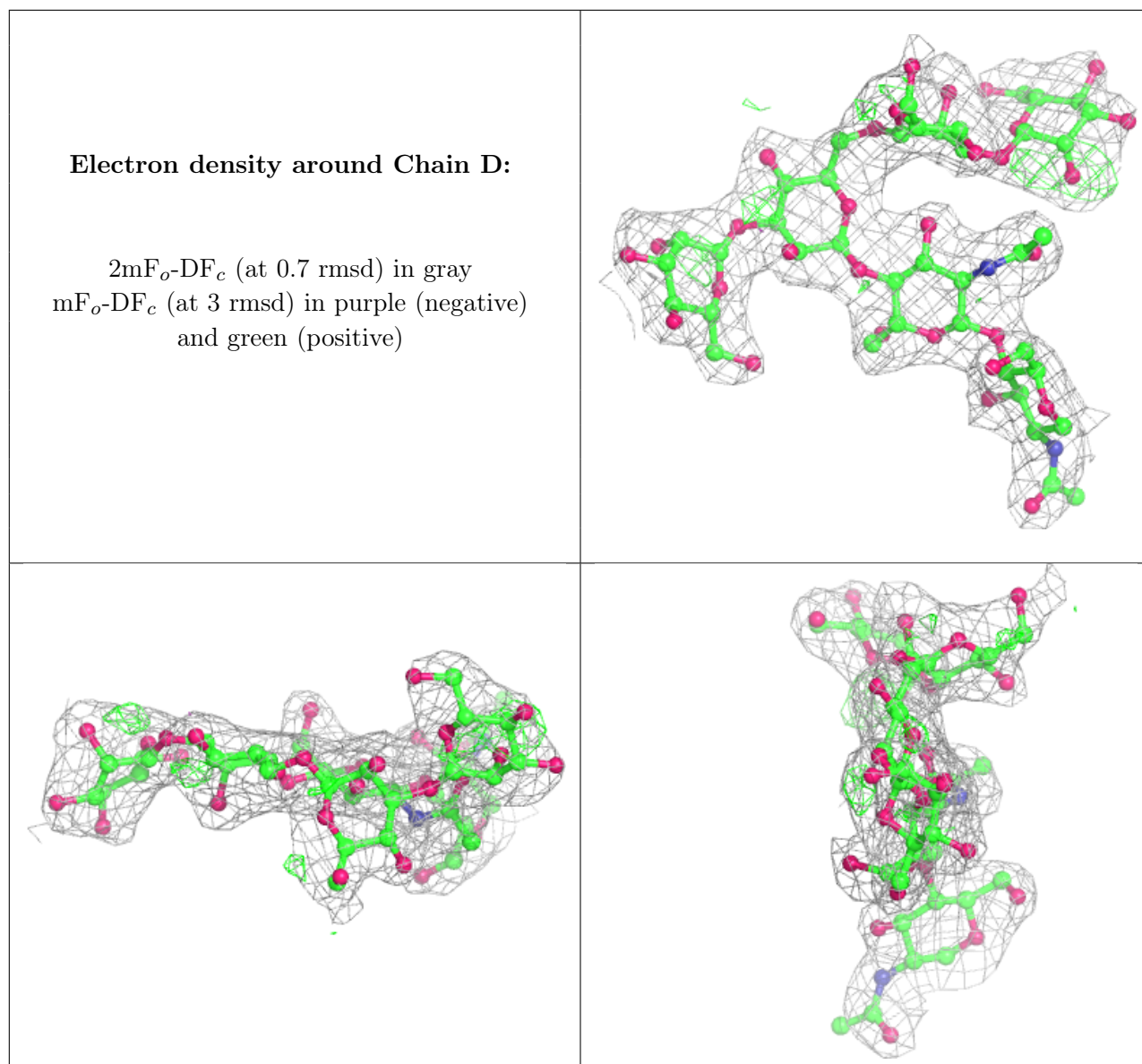
6.3 Carbohydrates [i](#)

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	BMA	B	3	11/12	0.80	0.27	89,91,94,96	0
3	BMA	D	5	11/12	0.85	0.15	72,76,78,80	0
2	NAG	B	1	14/15	0.89	0.17	74,77,87,88	0
3	BMA	D	4	11/12	0.91	0.15	57,64,68,72	0
3	BMA	D	6	11/12	0.93	0.12	49,53,56,60	0
2	NAG	B	2	14/15	0.94	0.20	80,84,88,88	0
3	BMA	D	3	11/12	0.96	0.12	49,51,57,60	0
3	NAG	D	1	14/15	0.96	0.12	47,52,61,61	0
3	NAG	D	2	14/15	0.98	0.09	46,48,53,55	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.





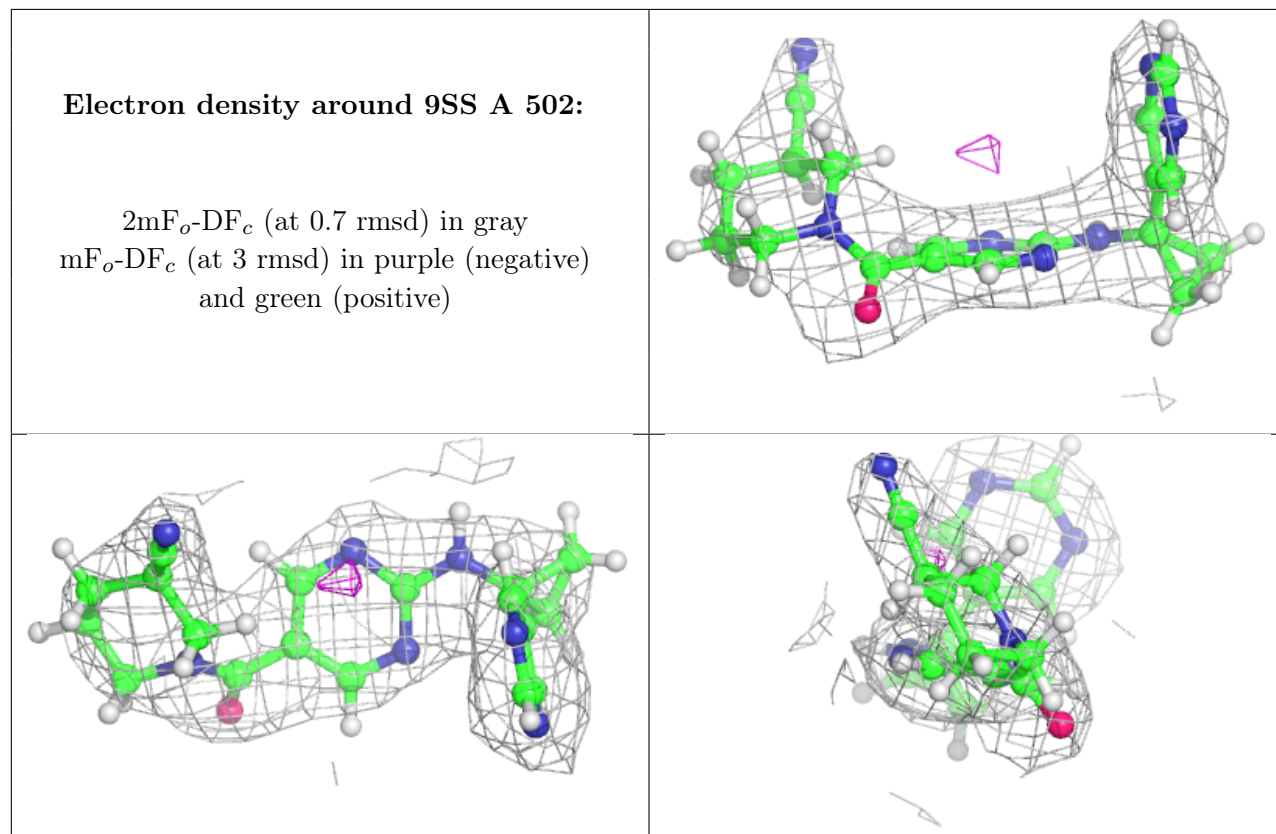
6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	A	503	14/15	0.66	0.42	125,127,128,128	0
4	NAG	A	501	14/15	0.88	0.26	76,84,91,92	0
6	NA	A	504	1/1	0.95	0.35	85,85,85,85	0
5	9SS	A	502	26/26	0.96	0.11	58,63,65,66	19

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.