



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:34 AM UTC

PDB ID : 9L2K / pdb_00009l2k
Title : The crystal structure of SFTSV Gn and SD22 antibody complex
Authors : Shi, W.F.; Quan, C.S.; Qi, J.X.
Deposited on : 2024-12-17
Resolution : 2.78 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
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

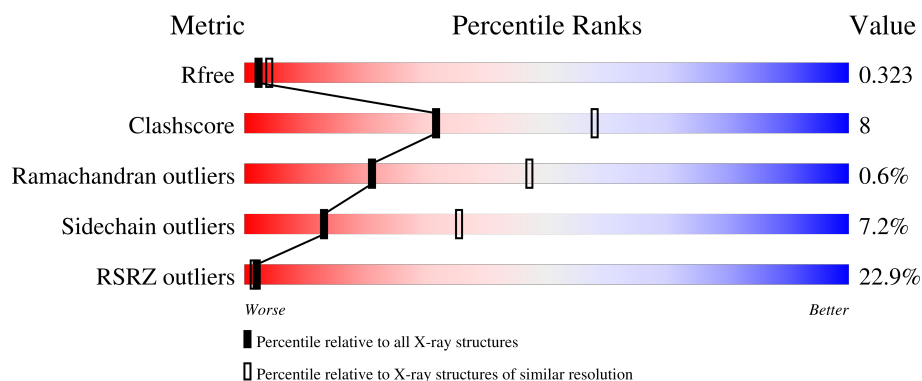
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.78 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	5248 (2.80-2.76)
Clashscore	190562	5693 (2.80-2.76)
Ramachandran outliers	187476	5590 (2.80-2.76)
Sidechain outliers	187428	5592 (2.80-2.76)
RSRZ outliers	180081	5251 (2.80-2.76)

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	344	
2	H	223	
3	L	214	
4	B	3	
5	C	2	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4262 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 Envelopment polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	0	0
			2462	1539	428	469	26			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A1S6K8S9
A	2	GLY	-	expression tag	UNP A0A1S6K8S9
A	3	TRP	-	expression tag	UNP A0A1S6K8S9
A	4	SER	-	expression tag	UNP A0A1S6K8S9
A	5	CYS	-	expression tag	UNP A0A1S6K8S9
A	6	ILE	-	expression tag	UNP A0A1S6K8S9
A	7	ILE	-	expression tag	UNP A0A1S6K8S9
A	8	LEU	-	expression tag	UNP A0A1S6K8S9
A	9	PHE	-	expression tag	UNP A0A1S6K8S9
A	10	LEU	-	expression tag	UNP A0A1S6K8S9
A	11	VAL	-	expression tag	UNP A0A1S6K8S9
A	12	ALA	-	expression tag	UNP A0A1S6K8S9
A	13	THR	-	expression tag	UNP A0A1S6K8S9
A	14	ALA	-	expression tag	UNP A0A1S6K8S9
A	15	THR	-	expression tag	UNP A0A1S6K8S9
A	16	GLY	-	expression tag	UNP A0A1S6K8S9
A	17	VAL	-	expression tag	UNP A0A1S6K8S9
A	18	HIS	-	expression tag	UNP A0A1S6K8S9
A	339	HIS	-	expression tag	UNP A0A1S6K8S9
A	340	HIS	-	expression tag	UNP A0A1S6K8S9
A	341	HIS	-	expression tag	UNP A0A1S6K8S9
A	342	HIS	-	expression tag	UNP A0A1S6K8S9
A	343	HIS	-	expression tag	UNP A0A1S6K8S9
A	344	HIS	-	expression tag	UNP A0A1S6K8S9

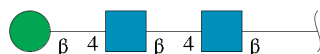
- Molecule 2 is a protein called SD22 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	121	Total	C	N	O	S	0	0	0
			921	582	157	179	3			

- Molecule 3 is a protein called SD22 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	108	Total	C	N	O	S	0	0	0
			812	510	137	162	3			

- 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.

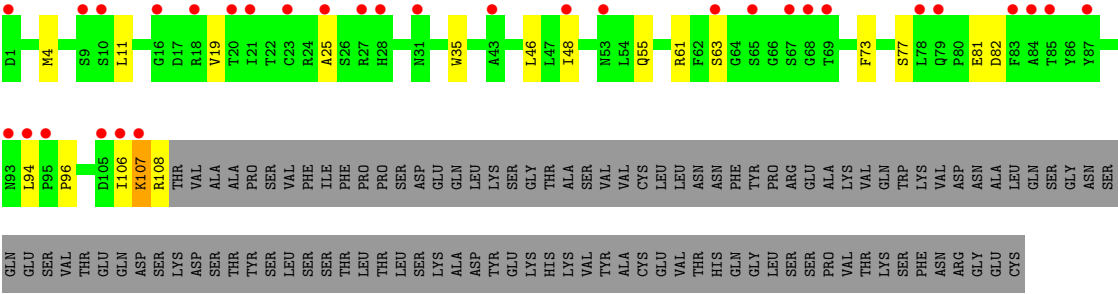


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	B	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 5 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
5	C	2	Total	C	N	O	0	0	0
			28	16	2	10			



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

Chain B:

100%



● Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:

50%

50%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	64.47Å 70.35Å 177.47Å 90.00° 90.18° 90.00°	Depositor
Resolution (Å)	41.94 – 2.78 41.94 – 2.79	Depositor EDS
% Data completeness (in resolution range)	84.3 (41.94-2.78) 84.3 (41.94-2.79)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	44.44 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.304 , 0.312 0.309 , 0.323	Depositor DCC
R_{free} test set	813 reflections (4.05%)	wwPDB-VP
Wilson B-factor (Å ²)	46.6	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 23.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o, F_c correlation	0.79	EDS
Total number of atoms	4262	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, BMA

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	0.18	0/2526	0.43	1/3408 (0.0%)
2	H	0.16	0/944	0.46	1/1279 (0.1%)
3	L	0.20	0/833	0.39	0/1136
All	All	0.18	0/4303	0.43	2/5823 (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	325	ARG	CB-CA-C	-6.45	104.63	110.44
2	H	103	PHE	CA-CB-CG	6.22	120.02	113.80

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	2462	0	2331	33	0
2	H	921	0	858	27	0
3	L	812	0	755	18	0
4	B	39	0	34	0	0
5	C	28	0	25	1	0
All	All	4262	0	4003	67	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 8.

All (67) 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)
2:H:103:PHE:CE1	3:L:94:LEU:HD11	2.02	0.93
2:H:103:PHE:CZ	3:L:94:LEU:HD11	2.05	0.92
1:A:22:SER:OG	1:A:79:SER:HB2	1.93	0.69
2:H:103:PHE:HE1	3:L:94:LEU:HD11	1.56	0.66
1:A:74:GLN:HG3	1:A:75:ARG:HG3	1.78	0.66
1:A:184:MET:HE2	1:A:186:PRO:HA	1.79	0.65
2:H:51:ILE:HD12	2:H:58:THR:HG22	1.80	0.64
2:H:103:PHE:HZ	3:L:94:LEU:HD11	1.64	0.63
2:H:103:PHE:CE1	3:L:94:LEU:CD1	2.78	0.62
2:H:35:HIS:HB2	2:H:97:VAL:HB	1.84	0.60
2:H:91:THR:HG23	2:H:118:THR:HA	1.83	0.59
1:A:283:GLY:HA2	1:A:305:ARG:HG3	1.84	0.58
2:H:113:GLN:NE2	2:H:114:GLY:O	2.34	0.58
3:L:61:ARG:NE	3:L:82:ASP:OD2	2.38	0.56
2:H:103:PHE:HE1	3:L:94:LEU:CD1	2.20	0.54
2:H:103:PHE:CZ	3:L:94:LEU:CD1	2.87	0.53
1:A:131:PHE:HB3	1:A:174:LEU:HB3	1.91	0.53
2:H:67:ARG:NH2	2:H:90:ASP:OD2	2.41	0.53
1:A:26:ILE:HD11	1:A:49:ILE:HB	1.91	0.51
2:H:47:TRP:CE3	3:L:96:PRO:HD2	2.46	0.51
3:L:35:TRP:CE2	3:L:73:PHE:HB2	2.45	0.51
1:A:33:SER:O	2:H:100:ARG:NH1	2.39	0.51
1:A:195:LEU:HB3	1:A:239:ILE:HD12	1.93	0.50
2:H:99:ASP:OD1	2:H:100:ARG:N	2.29	0.50
2:H:51:ILE:HD11	2:H:55:GLY:HA2	1.94	0.50
1:A:62:LEU:HD11	1:A:130:PHE:HB2	1.94	0.49
1:A:22:SER:OG	1:A:79:SER:CB	2.61	0.48
1:A:316:VAL:HG22	1:A:325:ARG:HG2	1.95	0.48
1:A:42:LEU:HD13	1:A:47:GLU:HB3	1.96	0.48
1:A:228:VAL:HG21	1:A:240:ILE:HB	1.96	0.48
2:H:6:GLU:OE2	2:H:95:TYR:HA	2.14	0.47
1:A:21:ASP:C	1:A:22:SER:HG	2.23	0.47
1:A:39:ILE:HD13	1:A:60:SER:HB2	1.96	0.47
1:A:82:SER:OG	1:A:173:VAL:O	2.33	0.47
3:L:4:MET:HE1	3:L:25:ALA:HB2	1.96	0.47
2:H:19:ARG:HH11	2:H:21:SER:HB3	1.79	0.47
3:L:11:LEU:HD23	3:L:19:VAL:HG13	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:102:TYR:CE1	2:H:103:PHE:HB2	2.50	0.47
1:A:195:LEU:HB3	1:A:239:ILE:CD1	2.46	0.46
3:L:55:GLN:HE22	5:C:1:NAG:H81	1.79	0.46
1:A:102:ALA:HB1	1:A:107:MET:HB2	1.96	0.46
1:A:184:MET:HE1	1:A:234:GLY:HA3	1.97	0.46
1:A:231:MET:HE3	1:A:239:ILE:HD13	1.97	0.46
3:L:94:LEU:O	3:L:96:PRO:HD3	2.16	0.46
1:A:84:TYR:CD2	1:A:123:PRO:HG3	2.51	0.45
2:H:102:TYR:CG	2:H:103:PHE:N	2.85	0.45
2:H:36:TRP:HD1	2:H:70:ILE:HD12	1.83	0.44
1:A:88:ASN:HD21	1:A:178:ASP:HA	1.82	0.44
1:A:51:GLN:HB3	1:A:56:ILE:HB	2.00	0.43
1:A:208:LYS:HG2	1:A:213:VAL:HA	2.00	0.43
1:A:281:CYS:O	1:A:293:CYS:HA	2.18	0.43
2:H:47:TRP:CD2	3:L:96:PRO:HD2	2.53	0.43
1:A:274:ALA:O	1:A:278:SER:HB3	2.18	0.43
2:H:13:GLN:H	2:H:13:GLN:HG2	1.67	0.42
1:A:57:HIS:HB3	1:A:104:TRP:CD2	2.54	0.42
1:A:57:HIS:HB3	1:A:104:TRP:CG	2.55	0.42
1:A:190:GLU:O	1:A:194:GLU:HG2	2.20	0.42
3:L:107:LYS:HE2	3:L:107:LYS:HB2	1.56	0.41
1:A:121:PRO:HD3	1:A:335:MET:HE1	2.02	0.41
3:L:46:LEU:HG	3:L:55:GLN:HG3	2.02	0.41
2:H:19:ARG:NH1	2:H:21:SER:HB3	2.35	0.41
1:A:78:ARG:NH2	1:A:96:LEU:O	2.54	0.41
1:A:25:ILE:HG23	1:A:309:VAL:HG13	2.03	0.41
1:A:239:ILE:HD11	1:A:319:TYR:CE2	2.56	0.41
2:H:87:ARG:HB3	2:H:88:PRO:HD2	2.03	0.41
2:H:103:PHE:HZ	3:L:94:LEU:HD21	1.86	0.40
2:H:12:VAL:O	2:H:119:VAL:HA	2.21	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	A	319/344 (93%)	301 (94%)	15 (5%)	3 (1%)	14	37
2	H	119/223 (53%)	114 (96%)	5 (4%)	0	100	100
3	L	106/214 (50%)	102 (96%)	4 (4%)	0	100	100
All	All	544/781 (70%)	517 (95%)	24 (4%)	3 (1%)	21	47

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	22	SER
1	A	46	SER
1	A	301	GLU

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	A	272/294 (92%)	252 (93%)	20 (7%)	13	34
2	H	97/188 (52%)	91 (94%)	6 (6%)	16	42
3	L	87/187 (46%)	80 (92%)	7 (8%)	11	31
All	All	456/669 (68%)	423 (93%)	33 (7%)	13	35

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	ILE
1	A	41	HIS
1	A	62	LEU
1	A	82	SER
1	A	91	SER
1	A	110	VAL
1	A	159	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	196	LYS
1	A	197	SER
1	A	205	ASP
1	A	209	ILE
1	A	239	ILE
1	A	245	LYS
1	A	255	LYS
1	A	290	VAL
1	A	294	GLU
1	A	298	GLU
1	A	325	ARG
1	A	335	MET
1	A	339	HIS
2	H	11	VAL
2	H	12	VAL
2	H	75	SER
2	H	78	THR
2	H	79	LEU
2	H	105	SER
3	L	48	ILE
3	L	63	SER
3	L	77	SER
3	L	81	GLU
3	L	106	ILE
3	L	107	LYS
3	L	108	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	HIS
2	H	39	GLN
3	L	38	HIS
3	L	55	GLN

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 ⓘ

5 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	$\# Z > 2$
4	NAG	B	1	1,4	14,14,15	0.43	0	17,19,21	0.49	0
4	NAG	B	2	4	14,14,15	0.23	0	17,19,21	0.38	0
4	BMA	B	3	4	11,11,12	0.51	0	15,15,17	0.65	0
5	NAG	C	1	1,5	14,14,15	0.36	0	17,19,21	1.00	2 (11%)
5	NAG	C	2	5	14,14,15	0.39	0	17,19,21	0.71	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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	2	4	-	0/6/23/26	0/1/1/1
4	BMA	B	3	4	-	0/2/19/22	0/1/1/1
5	NAG	C	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	C	2	5	-	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(°)
5	C	1	NAG	C1-O5-C5	2.72	115.83	112.19
5	C	1	NAG	C2-N2-C7	2.21	125.86	122.90
5	C	2	NAG	C1-O5-C5	2.12	115.02	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

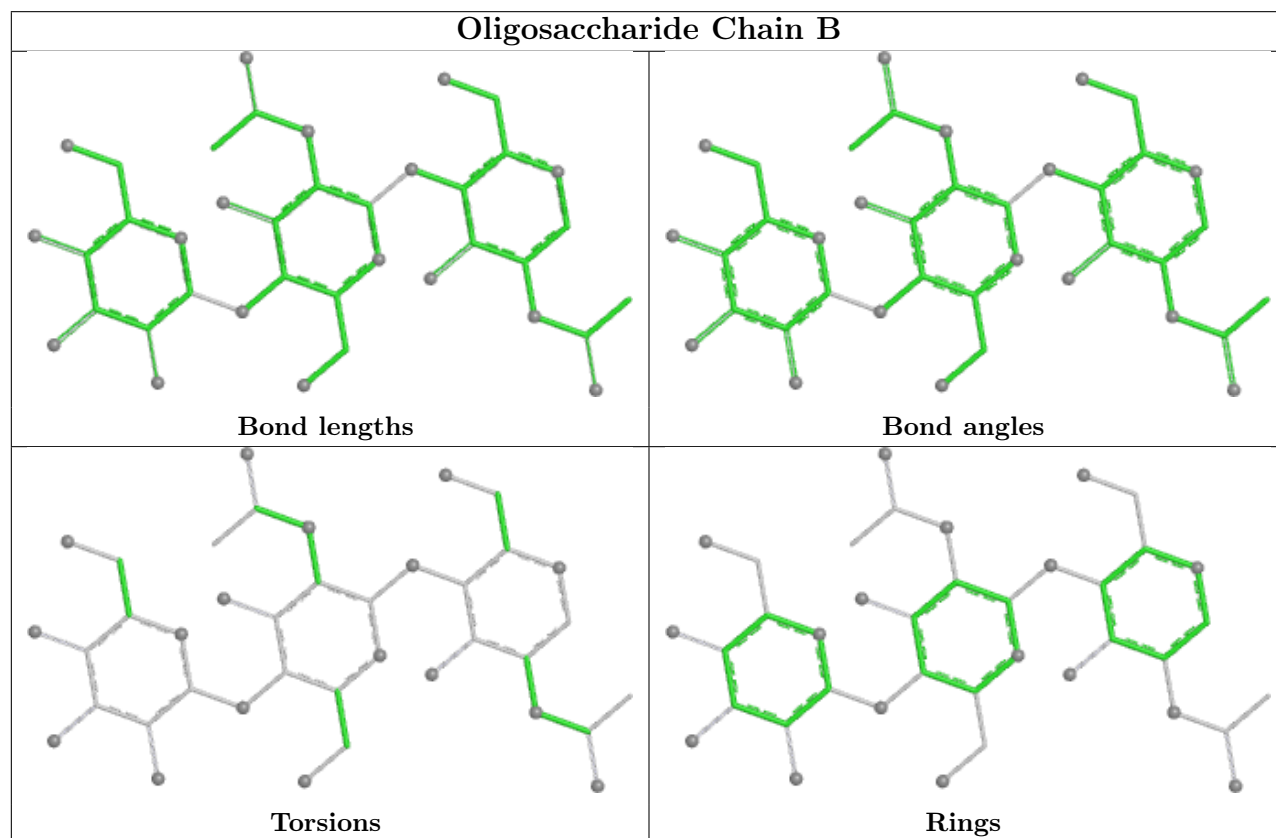
Mol	Chain	Res	Type	Atoms
5	C	1	NAG	O7-C7-N2-C2
5	C	1	NAG	C8-C7-N2-C2

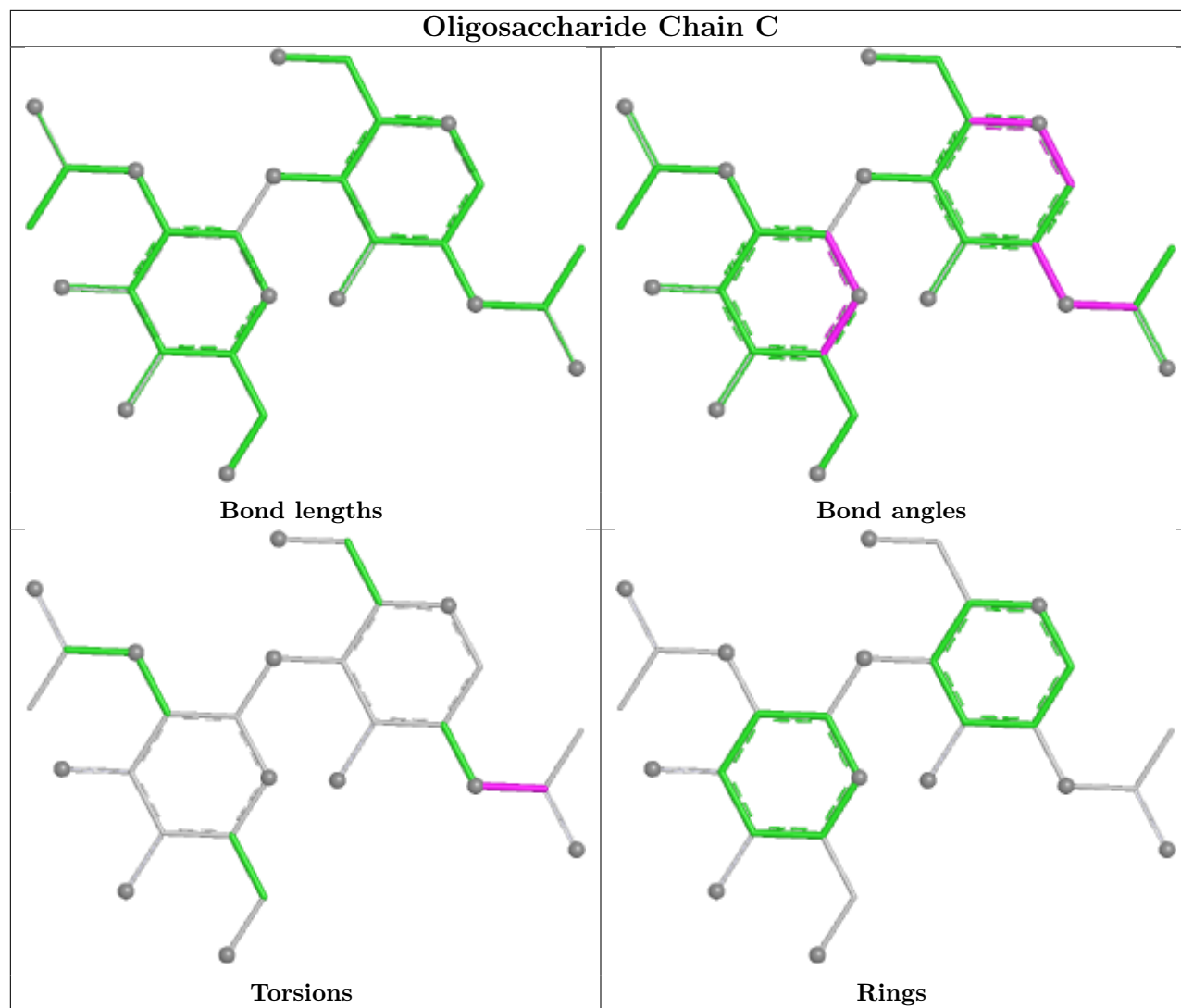
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1	NAG	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](#)

There are no ligands in this entry.

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	321/344 (93%)	1.32	65 (20%) 3 2	22, 38, 76, 144	0
2	H	121/223 (54%)	1.26	29 (23%) 2 1	31, 44, 59, 71	0
3	L	108/214 (50%)	1.60	32 (29%) 1 1	30, 49, 60, 72	0
All	All	550/781 (70%)	1.36	126 (22%) 2 1	22, 41, 66, 144	0

All (126) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	299	THR	10.3
1	A	300	SER	8.3
3	L	94	LEU	6.8
1	A	302	ALA	6.5
1	A	338	LEU	5.8
1	A	341	HIS	5.5
1	A	340	HIS	5.5
1	A	264	THR	4.9
1	A	239	ILE	4.8
1	A	296	GLY	4.7
1	A	294	GLU	4.4
1	A	253	SER	4.3
1	A	218	GLU	4.3
1	A	301	GLU	4.2
3	L	93	ASN	4.1
1	A	263	GLY	4.0
3	L	106	ILE	4.0
1	A	129	VAL	4.0
2	H	2	VAL	4.0
1	A	224	GLN	3.8
1	A	303	LYS	3.6
1	A	339	HIS	3.5
3	L	28	HIS	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
3	L	21	ILE	3.4
1	A	154	GLY	3.4
1	A	219	GLY	3.4
1	A	298	GLU	3.3
2	H	95	TYR	3.3
3	L	25	ALA	3.2
3	L	87	TYR	3.2
2	H	29	PHE	3.2
3	L	78	LEU	3.1
1	A	75	ARG	3.1
3	L	9	SER	3.0
1	A	125	TYR	3.0
3	L	53	ASN	3.0
2	H	44	GLY	3.0
1	A	197	SER	3.0
1	A	91	SER	2.9
3	L	85	THR	2.9
2	H	13	GLN	2.9
1	A	205	ASP	2.9
1	A	295	HIS	2.9
1	A	254	SER	2.9
1	A	23	GLY	2.8
3	L	16	GLY	2.8
2	H	20	LEU	2.8
2	H	103	PHE	2.8
2	H	41	PRO	2.8
1	A	22	SER	2.8
1	A	153	SER	2.8
1	A	233	VAL	2.8
3	L	10	SER	2.8
1	A	262	GLU	2.8
2	H	1	GLN	2.7
1	A	261	LYS	2.7
1	A	285	MET	2.7
1	A	41	HIS	2.7
1	A	283	GLY	2.7
2	H	23	ALA	2.7
1	A	217	CYS	2.7
2	H	121	SER	2.7
2	H	27	PHE	2.6
1	A	289	LYS	2.6
2	H	7	SER	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	304	CYS	2.6
3	L	69	THR	2.5
3	L	107	LYS	2.5
3	L	95	PRO	2.5
1	A	222	LEU	2.5
1	A	90	TYR	2.5
1	A	297	GLU	2.5
1	A	260	TYR	2.5
1	A	216	GLN	2.5
1	A	337	THR	2.5
1	A	183	LEU	2.5
3	L	65	SER	2.5
2	H	89	ASP	2.5
1	A	109	VAL	2.5
1	A	336	ALA	2.4
2	H	32	PHE	2.4
2	H	100	ARG	2.4
3	L	48	ILE	2.4
2	H	65	LYS	2.4
3	L	43	ALA	2.4
1	A	310	HIS	2.3
1	A	166	GLY	2.3
3	L	105	ASP	2.3
1	A	272	GLU	2.3
3	L	31	ASN	2.3
3	L	63	SER	2.3
3	L	27	ARG	2.3
2	H	12	VAL	2.3
2	H	54	ASP	2.3
1	A	69	GLN	2.3
3	L	68	GLY	2.3
3	L	84	ALA	2.2
1	A	255	LYS	2.2
2	H	28	THR	2.2
1	A	245	LYS	2.2
2	H	78	THR	2.2
1	A	110	VAL	2.2
2	H	11	VAL	2.2
1	A	214	PHE	2.2
2	H	110	HIS	2.2
1	A	292	GLY	2.2
2	H	25	SER	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	114	ARG	2.2
2	H	3	GLN	2.2
3	L	79	GLN	2.2
1	A	316	VAL	2.2
3	L	67	SER	2.1
2	H	58	THR	2.1
3	L	23	CYS	2.1
1	A	279	GLY	2.1
2	H	104	GLY	2.1
1	A	240	ILE	2.1
3	L	20	THR	2.1
2	H	77	ASN	2.1
3	L	1	ASP	2.1
3	L	18	ARG	2.1
3	L	83	PHE	2.1
1	A	93	TRP	2.0
2	H	31	GLY	2.0
1	A	45	TYR	2.0
1	A	267	CYS	2.0

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

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

6.3 Carbohydrates [i](#)

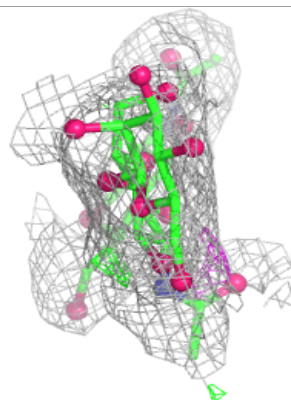
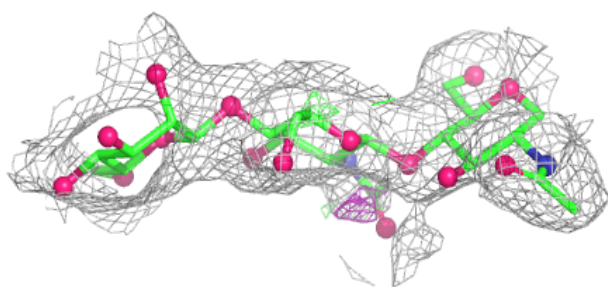
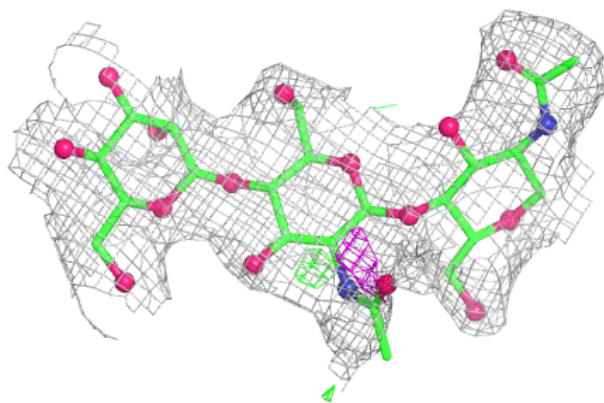
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	B	1	14/15	-	-	27,41,52,54	0
4	NAG	B	2	14/15	-	-	37,44,54,56	0
4	BMA	B	3	11/12	-	-	42,47,53,60	0
5	NAG	C	1	14/15	-	-	60,65,73,79	0
5	NAG	C	2	14/15	-	-	61,69,73,76	0

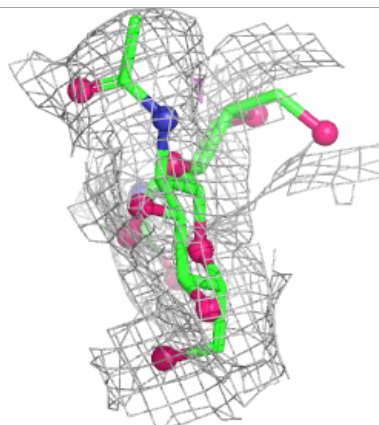
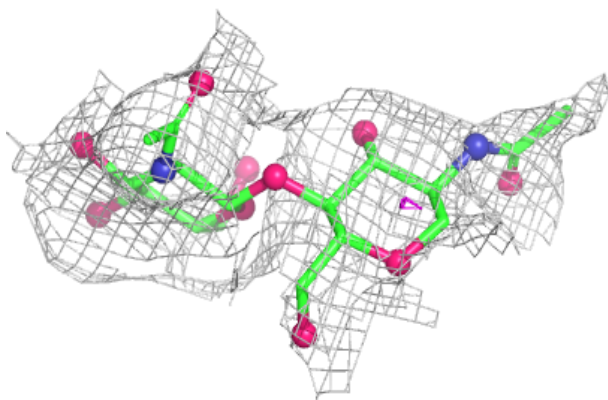
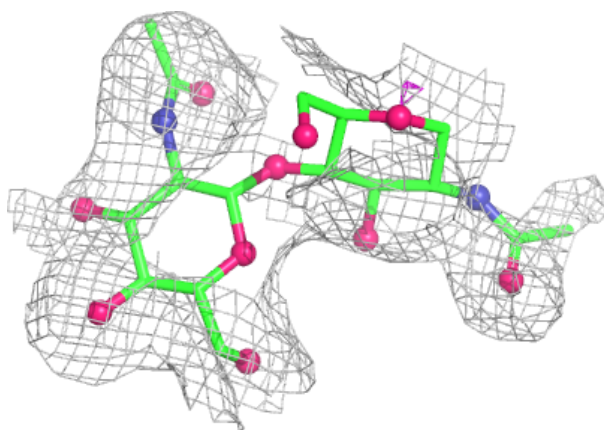
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain B:

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

**Electron density around Chain C:**

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



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.