



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 11:57 AM BST

PDB ID : 6R41
Title : Structure of P110 from Mycoplasma genitalium complexed with 3'SL
Authors : Aparicio, D.; Fita, I.
Deposited on : 2019-03-21
Resolution : 2.21 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 : 2.13.1
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) : 2.13.1

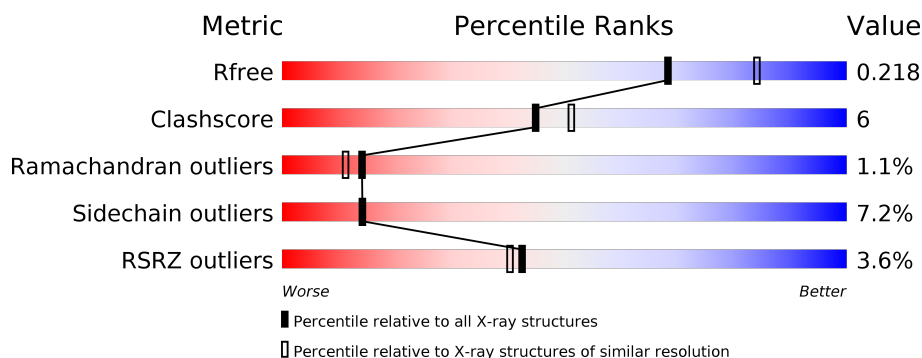
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.21 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	5912 (2.24-2.20)
Clashscore	141614	6646 (2.24-2.20)
Ramachandran outliers	138981	6543 (2.24-2.20)
Sidechain outliers	138945	6544 (2.24-2.20)
RSRZ outliers	127900	5797 (2.24-2.20)

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 on 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	916	<div> <div>3%</div> <div> <div></div> <div>79%</div> <div>14%</div> <div>• •</div> </div> </div>
2	B	2	<div> <div>100%</div> </div>

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	BGC	A	1004	-	-	-	X

2 Entry composition [i](#)

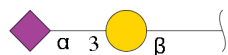
There are 7 unique types of molecules in this entry. The entry contains 7124 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Mgp-operon protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	886	Total	C	N	O	S	0	1	0
			6829	4283	1139	1401	6			

- Molecule 2 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	N	O	0	0	0
			31	17	1	13			

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	K	0	0
			1	1		

- Molecule 4 is beta-D-glucopyranose (three-letter code: BGC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	6	6		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		

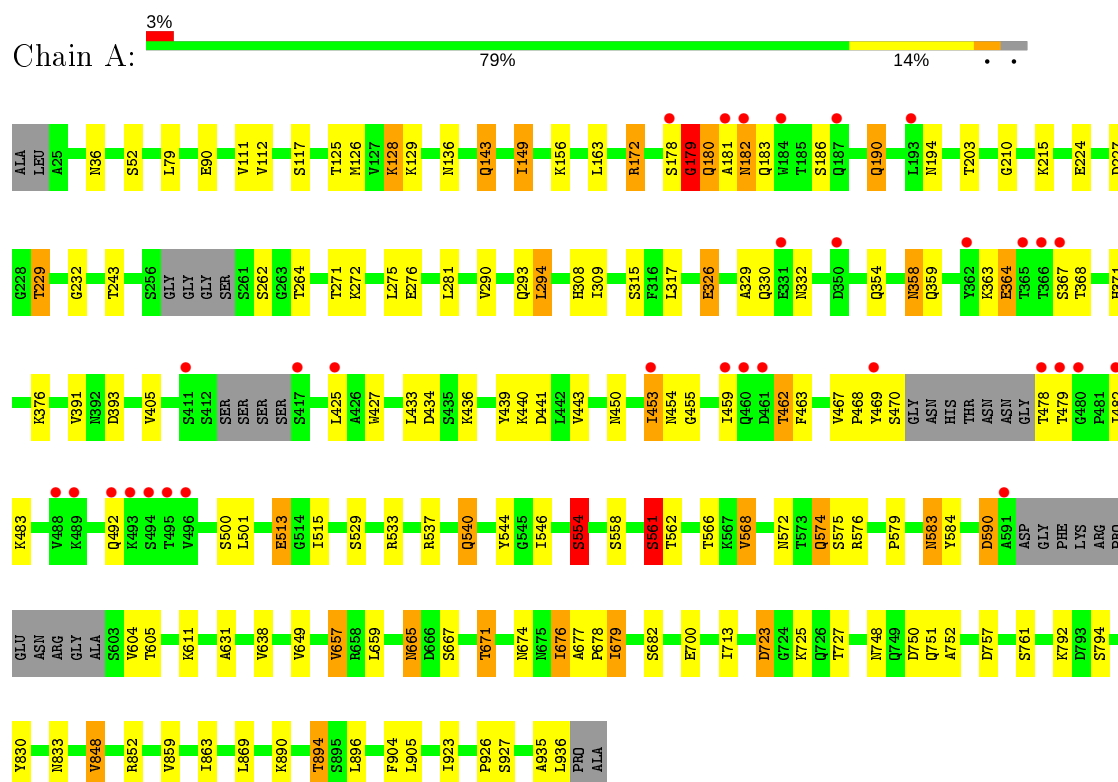
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	240	Total	O	0	0
			240	240		

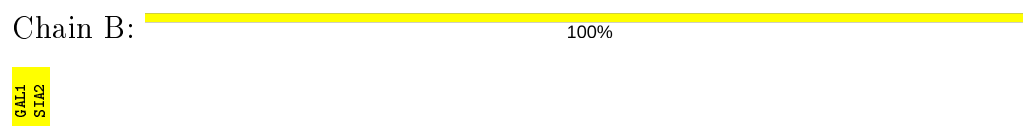
3 Residue-property plots [i](#)

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: Mgp-operon protein 3



• Molecule 2: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	110.03Å 151.57Å 176.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	115.00 – 2.21 115.00 – 2.21	Depositor EDS
% Data completeness (in resolution range)	99.7 (115.00-2.21) 99.7 (115.00-2.21)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.190 , 0.216 0.194 , 0.218	Depositor DCC
R_{free} test set	3707 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	54.6	Xtriage
Anisotropy	0.191	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 46.8	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	0.96	EDS
Total number of atoms	7124	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% 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: GOL, BGC, K, SIA, GAL, PO4

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	0.84	8/6968 (0.1%)	0.96	2/9478 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	358	ASN	CB-CG	11.23	1.76	1.51
1	A	561	SER	CB-OG	11.01	1.56	1.42
1	A	136	ASN	CB-CG	9.38	1.72	1.51
1	A	354	GLN	C-O	7.76	1.38	1.23
1	A	562	THR	C-O	7.12	1.36	1.23
1	A	450	ASN	CG-OD1	5.35	1.35	1.24
1	A	513	GLU	CD-OE1	5.32	1.31	1.25
1	A	923	ILE	C-O	5.05	1.32	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	723	ASP	CB-CA-C	-6.84	96.72	110.40
1	A	554	SER	N-CA-CB	5.07	118.11	110.50

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	179	GLY	Peptide
1	A	243	THR	Peptide
1	A	330	GLN	Peptide
1	A	935	ALA	Peptide

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	6829	0	6608	88	0
2	B	31	0	26	0	0
3	A	1	0	0	0	0
4	A	12	0	11	0	0
5	A	5	0	0	0	0
6	A	6	0	8	0	0
7	A	240	0	0	2	0
All	All	7124	0	6653	88	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 6.

All (88) 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:358:ASN:CG	1:A:358:ASN:CB	1.76	1.51
1:A:554:SER:HB2	1:A:568:VAL:HG13	1.59	0.82
1:A:583:ASN:HD22	1:A:583:ASN:C	1.84	0.81
1:A:453:ILE:HG12	1:A:467:VAL:HG21	1.64	0.80
1:A:272:LYS:NZ	1:A:276:GLU:OE1	2.17	0.78
1:A:194:ASN:HD22	1:A:483:LYS:HD2	1.51	0.74
1:A:574:GLN:HE21	1:A:575:SER:H	1.35	0.73
1:A:859:VAL:HG11	1:A:890:LYS:HG3	1.70	0.73
1:A:454:ASN:OD1	1:A:467:VAL:HG23	1.89	0.72
1:A:540:GLN:HG2	1:A:579:PRO:HA	1.71	0.71
1:A:281:LEU:H	1:A:293:GLN:HE22	1.38	0.70
1:A:126:MET:HE1	1:A:129:LYS:HD2	1.74	0.69
1:A:126:MET:HE1	1:A:129:LYS:HB2	1.75	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:894:THR:CG2	7:A:1293:HOH:O	2.42	0.67
1:A:723:ASP:HB3	1:A:725:LYS:H	1.59	0.67
1:A:894:THR:HG23	7:A:1293:HOH:O	1.95	0.66
1:A:665:ASN:H	1:A:665:ASN:HD22	1.43	0.66
1:A:190:GLN:HE21	1:A:190:GLN:CA	2.10	0.64
1:A:126:MET:HE1	1:A:129:LYS:CG	2.28	0.62
1:A:561:SER:HB2	1:A:566:THR:OG1	2.00	0.60
1:A:848:VAL:HG22	1:A:852:ARG:HD3	1.81	0.60
1:A:210:GLY:O	1:A:232:GLY:HA3	2.01	0.60
1:A:440:LYS:HB2	1:A:674:ASN:HB3	1.83	0.60
1:A:391:VAL:CG2	1:A:631:ALA:HB1	2.34	0.58
1:A:638:VAL:HG23	1:A:748:ASN:O	2.04	0.58
1:A:190:GLN:HE21	1:A:190:GLN:N	2.02	0.58
1:A:665:ASN:N	1:A:665:ASN:HD22	2.02	0.57
1:A:126:MET:HE1	1:A:129:LYS:CD	2.35	0.56
1:A:359:GLN:HG3	1:A:427:TRP:CH2	2.40	0.56
1:A:126:MET:CE	1:A:129:LYS:HB2	2.35	0.56
1:A:682:SER:OG	1:A:761:SER:HB3	2.05	0.55
1:A:558:SER:HA	1:A:566:THR:HB	1.89	0.55
1:A:358:ASN:CG	1:A:358:ASN:CA	2.67	0.55
1:A:671:THR:HG21	1:A:676:ILE:HD11	1.89	0.55
1:A:501:LEU:C	1:A:501:LEU:HD12	2.27	0.54
1:A:126:MET:HE1	1:A:129:LYS:CB	2.36	0.54
1:A:679:ILE:HD11	1:A:757:ASP:C	2.27	0.54
1:A:117:SER:HB3	1:A:125:THR:HG21	1.90	0.54
1:A:583:ASN:C	1:A:583:ASN:ND2	2.57	0.53
1:A:665:ASN:ND2	1:A:667:SER:OG	2.39	0.53
1:A:433:LEU:HD12	1:A:468:PRO:HA	1.91	0.53
1:A:149:ILE:HD12	1:A:215:LYS:HG2	1.92	0.52
1:A:210:GLY:N	1:A:232:GLY:HA3	2.25	0.51
1:A:896:LEU:HD12	1:A:896:LEU:C	2.31	0.51
1:A:638:VAL:CG2	1:A:748:ASN:HB3	2.41	0.50
1:A:869:LEU:HD12	1:A:869:LEU:C	2.31	0.50
1:A:36:ASN:HA	1:A:52:SER:O	2.11	0.50
1:A:574:GLN:HE21	1:A:575:SER:N	2.05	0.50
1:A:358:ASN:ND2	1:A:358:ASN:CB	2.63	0.49
1:A:439:TYR:CZ	1:A:443:VAL:HG11	2.48	0.49
1:A:677:ALA:O	1:A:678:PRO:C	2.50	0.49
1:A:359:GLN:O	1:A:405:VAL:HA	2.12	0.49
1:A:546:ILE:O	1:A:572:ASN:HB2	2.13	0.49
1:A:224:GLU:OE1	1:A:271:THR:HG21	2.13	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:544:TYR:CD2	1:A:659:LEU:HD22	2.49	0.47
1:A:308:HIS:NE2	1:A:326:GLU:OE2	2.45	0.47
1:A:172:ARG:HH11	1:A:181:ALA:HB2	1.79	0.47
1:A:513:GLU:HG3	1:A:515:ILE:HG22	1.96	0.47
1:A:750:ASP:O	1:A:751:GLN:C	2.53	0.47
1:A:179:GLY:C	1:A:180:GLN:HG2	2.36	0.47
1:A:436:LYS:HB2	1:A:441:ASP:HB3	1.97	0.46
1:A:190:GLN:HA	1:A:190:GLN:HE21	1.78	0.46
1:A:182:ASN:N	1:A:182:ASN:HD22	2.14	0.46
1:A:203:THR:O	1:A:425:LEU:HA	2.16	0.45
1:A:462:THR:OG1	1:A:463:PHE:N	2.50	0.45
1:A:830:TYR:CE1	1:A:926:PRO:HD3	2.51	0.45
1:A:723:ASP:HB2	1:A:727:THR:H	1.81	0.44
1:A:111:VAL:HG11	1:A:309:ILE:HG21	1.98	0.44
1:A:172:ARG:NH1	1:A:181:ALA:HB2	2.33	0.43
1:A:143:GLN:NE2	1:A:371:HIS:CD2	2.86	0.43
1:A:227:ASP:OD1	1:A:229:THR:HB	2.19	0.43
1:A:210:GLY:H	1:A:232:GLY:HA3	1.83	0.43
1:A:470:SER:HA	1:A:482:ILE:HD13	1.99	0.43
1:A:750:ASP:O	1:A:752:ALA:N	2.52	0.43
1:A:180:GLN:HG3	1:A:183:GLN:HG2	2.01	0.42
1:A:583:ASN:HD22	1:A:584:TYR:N	2.17	0.42
1:A:364:GLU:HG2	1:A:367:SER:HB2	2.02	0.42
1:A:649:VAL:HA	1:A:657:VAL:O	2.19	0.42
1:A:149:ILE:HG22	1:A:501:LEU:HB3	2.01	0.42
1:A:128:LYS:NZ	1:A:329:ALA:O	2.41	0.42
1:A:364:GLU:HG2	1:A:367:SER:CB	2.50	0.42
1:A:391:VAL:HG21	1:A:631:ALA:HB1	2.01	0.42
1:A:859:VAL:O	1:A:863:ILE:HG13	2.21	0.41
1:A:904:PHE:CG	1:A:905:LEU:N	2.89	0.41
1:A:112:VAL:HG13	1:A:126:MET:HE2	2.03	0.40
1:A:290:VAL:HG12	1:A:294:LEU:HD22	2.03	0.40
1:A:713:ILE:HD13	1:A:713:ILE:N	2.36	0.40
1:A:180:GLN:HG2	1:A:183:GLN:HE21	1.86	0.40

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	877/916 (96%)	817 (93%)	50 (6%)	10 (1%)	14 11

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	332	ASN
1	A	529	SER
1	A	178	SER
1	A	179	GLY
1	A	262	SER
1	A	453	ILE
1	A	590	ASP
1	A	180	GLN
1	A	794	SER
1	A	455	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	776/795 (98%)	720 (93%)	56 (7%)	14 14

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	90	GLU
1	A	128	LYS
1	A	143	GLN
1	A	149	ILE
1	A	156	LYS
1	A	163	LEU
1	A	172	ARG
1	A	182	ASN
1	A	186	SER
1	A	190	GLN
1	A	229	THR
1	A	264	THR
1	A	275	LEU
1	A	294	LEU
1	A	315	SER
1	A	317	LEU
1	A	326	GLU
1	A	363	LYS
1	A	364	GLU
1	A	368	THR
1	A	376	LYS
1	A	393	ASP
1	A	434	ASP
1	A	459	ILE
1	A	462	THR
1	A	469	TYR
1	A	478	THR
1	A	479	THR
1	A	492	GLN
1	A	500	SER
1	A	533	ARG
1	A	537	ARG
1	A	540	GLN
1	A	554	SER
1	A	561	SER
1	A	568	VAL
1	A	574	GLN
1	A	576	ARG
1	A	583	ASN
1	A	590	ASP
1	A	604	VAL
1	A	605	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	611	LYS
1	A	657	VAL
1	A	665	ASN
1	A	671	THR
1	A	676	ILE
1	A	679	ILE
1	A	700	GLU
1	A	792	LYS
1	A	833	ASN
1	A	848	VAL
1	A	894	THR
1	A	927	SER
1	A	936	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	ASN
1	A	119	ASN
1	A	143	GLN
1	A	180	GLN
1	A	182	ASN
1	A	183	GLN
1	A	187	GLN
1	A	189	ASN
1	A	190	GLN
1	A	194	ASN
1	A	231	GLN
1	A	250	ASN
1	A	293	GLN
1	A	307	ASN
1	A	330	GLN
1	A	369	ASN
1	A	371	HIS
1	A	574	GLN
1	A	583	ASN
1	A	665	ASN
1	A	674	ASN
1	A	748	ASN
1	A	749	GLN
1	A	770	GLN
1	A	864	ASN

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 ⓘ

2 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	GAL	B	1	2	11,11,12	0.87	0	15,15,17	2.12	4 (26%)
2	SIA	B	2	2	17,20,21	0.48	0	21,28,31	0.93	1 (4%)

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	GAL	B	1	2	-	0/2/19/22	0/1/1/1
2	SIA	B	2	2	-	2/14/34/38	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	GAL	C2-C3-C4	-3.65	104.57	110.89
2	B	1	GAL	O5-C5-C6	3.64	112.90	107.20
2	B	1	GAL	C1-C2-C3	-3.51	105.36	109.67
2	B	1	GAL	O3-C3-C2	3.45	116.61	109.99
2	B	2	SIA	C4-C3-C2	2.25	113.85	109.81

There are no chirality outliers.

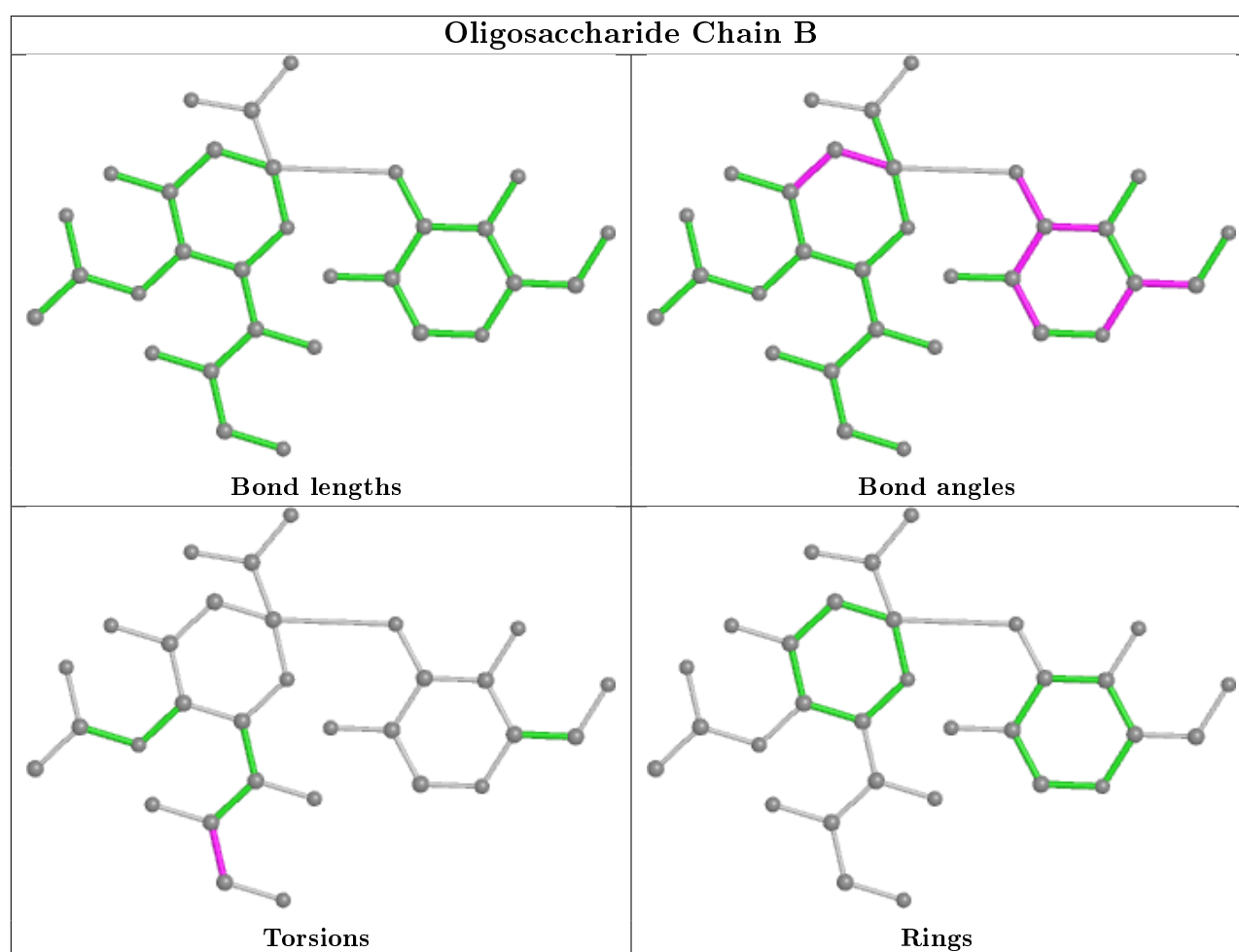
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	SIA	O8-C8-C9-O9
2	B	2	SIA	C7-C8-C9-O9

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](#)

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	BGC	A	1004	-	12,12,12	0.57	0	17,17,17	1.51	2 (11%)
5	PO4	A	1005	-	4,4,4	0.92	0	6,6,6	0.34	0
6	GOL	A	1006	-	5,5,5	0.12	0	5,5,5	0.39	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BGC	A	1004	-	-	0/2/22/22	0/1/1/1
6	GOL	A	1006	-	-	2/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1004	BGC	C1-C2-C3	3.45	117.48	110.31
4	A	1004	BGC	O5-C5-C4	-2.32	105.48	109.69

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1006	GOL	O1-C1-C2-C3
6	A	1006	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	886/916 (96%)	0.34	32 (3%) 42 40	38, 74, 132, 193	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	417	SER	7.2
1	A	460	GLN	6.2
1	A	492	GLN	5.5
1	A	493	LYS	5.5
1	A	411	SER	5.3
1	A	461	ASP	4.2
1	A	178	SER	3.6
1	A	365	THR	3.3
1	A	182	ASN	3.3
1	A	494	SER	3.2
1	A	366	THR	2.9
1	A	184	TRP	2.9
1	A	187	GLN	2.8
1	A	181	ALA	2.6
1	A	367	SER	2.6
1	A	362	TYR	2.6
1	A	425	LEU	2.5
1	A	489	LYS	2.4
1	A	496	VAL	2.4
1	A	488	VAL	2.4
1	A	453	ILE	2.3
1	A	478	THR	2.3
1	A	469	TYR	2.2
1	A	350	ASP	2.2
1	A	495	THR	2.2
1	A	482	ILE	2.2
1	A	479	THR	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	480	GLY	2.1
1	A	331	GLU	2.1
1	A	591	ALA	2.1
1	A	459	ILE	2.1
1	A	193	LEU	2.1

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

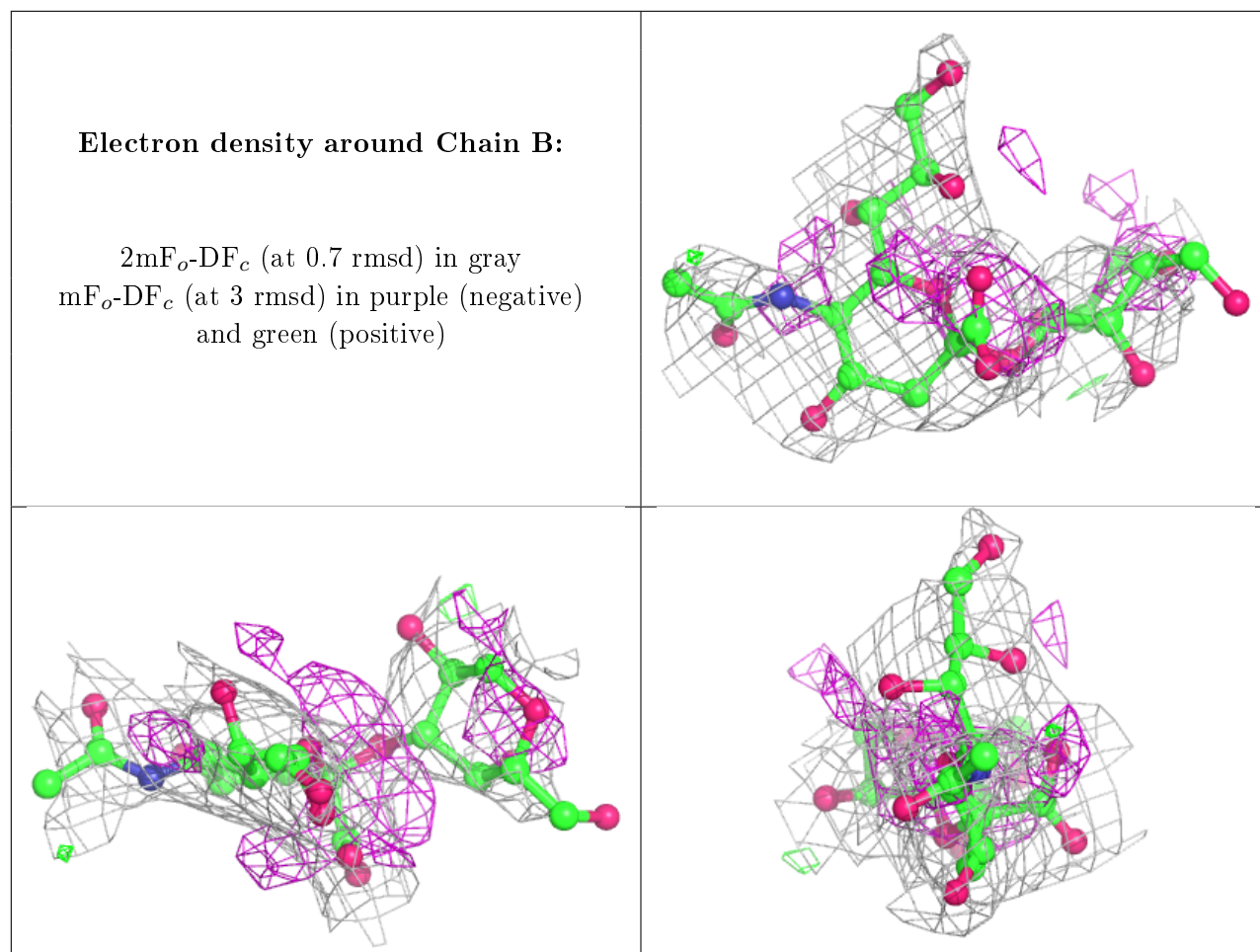
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GAL	B	1	11/12	0.65	0.35	127,146,163,163	0
2	SIA	B	2	20/21	0.89	0.21	87,96,105,106	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	BGC	A	1004	12/12	0.58	0.45	126,152,163,169	0
6	GOL	A	1006	6/6	0.85	0.20	73,80,81,95	0
5	PO4	A	1005	5/5	0.93	0.18	51,52,75,78	5
3	K	A	1001	1/1	0.99	0.19	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.