



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 19, 2026 – 04:07 AM UTC

PDB ID : 6R41 / pdb_00006r41
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 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

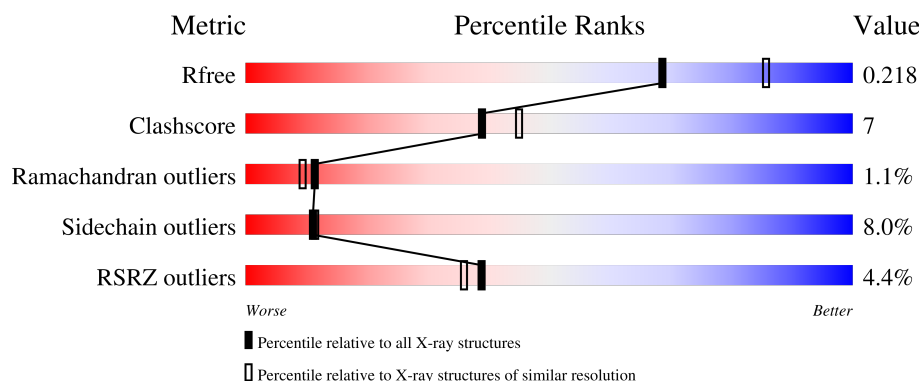
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.21 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}	180053	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (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 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	916	4% 76% 17% • •
2	B	2	100%

2 Entry composition [i](#)

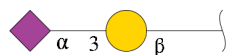
There are 7 unique types of molecules in this entry. The entry contains 7124 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

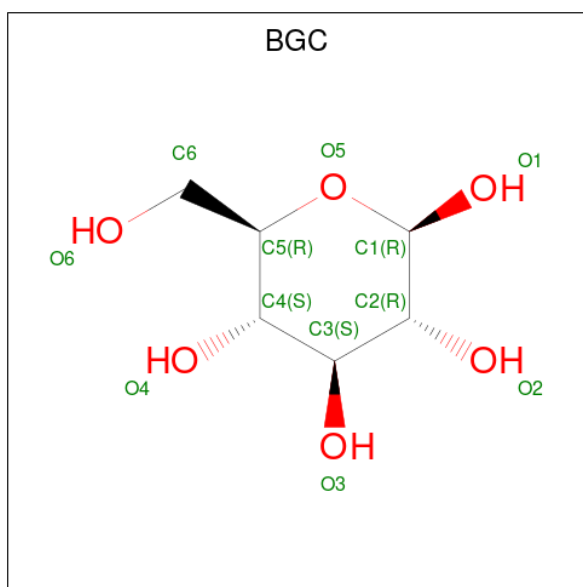


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	N	O	0	0	0
			31	17	1	13			

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

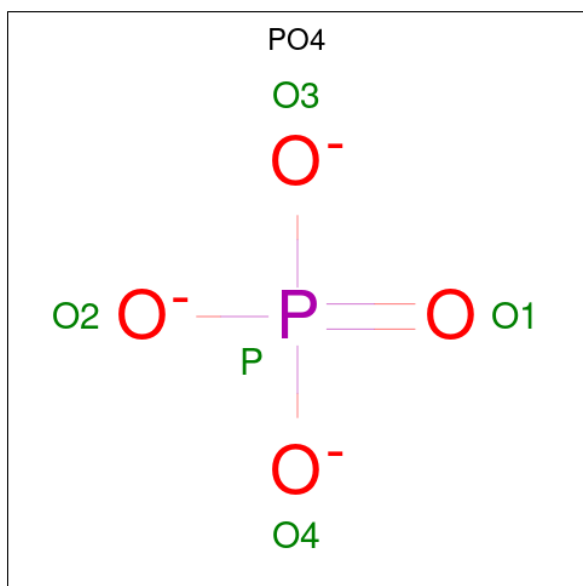
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	K	0	0
			1	1		

- Molecule 4 is beta-D-glucopyranose (CCD ID: 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 (CCD ID: 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 (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

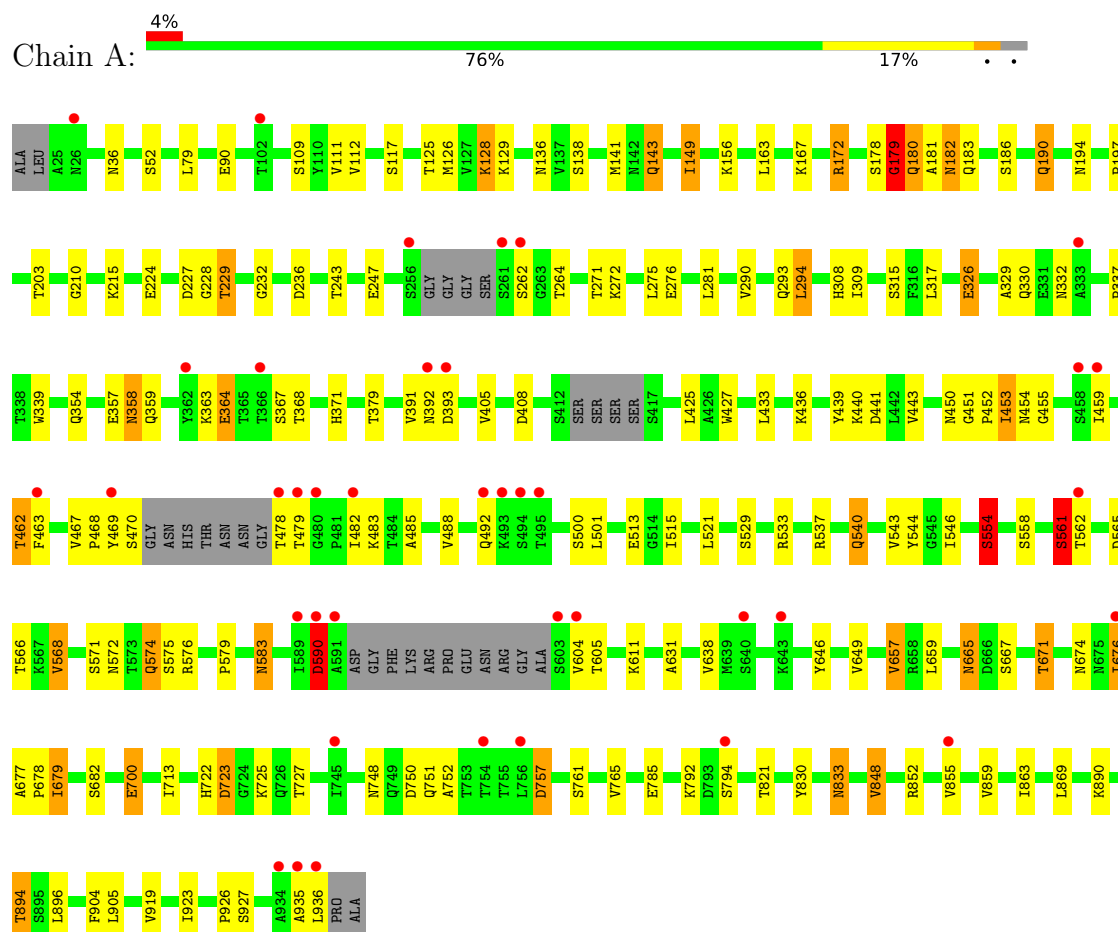
- Molecule 7 is water.

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

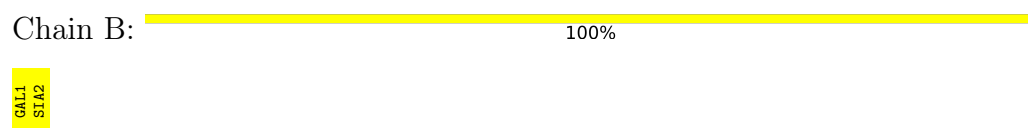
3 Residue-property plots

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 (5.01%)	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)	0.33 , 48.5	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: GAL, GOL, PO4, K, BGC, SIA

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	1.18	15/6968 (0.2%)	1.45	21/9478 (0.2%)

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 (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	354	GLN	C-O	12.18	1.38	1.24
1	A	562	THR	C-O	10.67	1.36	1.23
1	A	358	ASN	CB-CG	9.93	1.76	1.52
1	A	136	ASN	CB-CG	8.23	1.72	1.52
1	A	923	ILE	C-O	7.51	1.32	1.24
1	A	561	SER	CB-OG	7.20	1.56	1.42
1	A	485	ALA	C-O	6.63	1.31	1.23
1	A	197	PRO	C-O	6.59	1.31	1.23
1	A	450	ASN	CG-OD1	6.41	1.35	1.23
1	A	646	TYR	C-O	5.95	1.31	1.23
1	A	337	PRO	C-O	-5.85	1.16	1.23
1	A	451	GLY	C-N	5.53	1.41	1.33
1	A	919	VAL	N-CA	5.38	1.50	1.46
1	A	821	THR	C-O	5.18	1.30	1.23
1	A	452	PRO	N-CD	5.01	1.54	1.47

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	723	ASP	CB-CA-C	-6.89	96.72	110.42
1	A	785	GLU	CB-CG-CD	6.67	123.94	112.60
1	A	451	GLY	CA-C-N	6.51	126.53	119.89
1	A	451	GLY	C-N-CA	6.51	126.53	119.89
1	A	236	ASP	CA-C-N	6.17	128.88	120.54
1	A	236	ASP	C-N-CA	6.17	128.88	120.54
1	A	408	ASP	CA-CB-CG	6.09	118.69	112.60
1	A	723	ASP	CA-CB-CG	5.98	118.58	112.60
1	A	722	HIS	CA-C-N	5.95	132.90	121.54
1	A	722	HIS	C-N-CA	5.95	132.90	121.54
1	A	919	VAL	CA-C-O	5.84	122.59	119.15
1	A	392	ASN	CA-C-N	-5.42	115.10	123.17
1	A	392	ASN	C-N-CA	-5.42	115.10	123.17
1	A	833	ASN	N-CA-C	-5.35	106.34	112.92
1	A	757	ASP	CA-CB-CG	5.31	117.91	112.60
1	A	228	GLY	CA-C-N	5.14	129.31	120.72
1	A	228	GLY	C-N-CA	5.14	129.31	120.72
1	A	109	SER	CB-CA-C	5.11	118.86	109.46
1	A	590	ASP	CA-CB-CG	5.06	117.66	112.60
1	A	554	SER	N-CA-CB	5.05	118.11	110.28
1	A	700	GLU	CB-CA-C	5.04	118.90	110.43

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

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	92	0
2	B	31	0	26	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	92	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 7.

All (92) 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:CB	1:A:358:ASN:CG	1.76	1.56
1:A:583:ASN:C	1:A:583:ASN:HD22	1.84	0.86
1:A:554:SER:HB2	1:A:568:VAL:HG13	1.59	0.82
1:A:126:MET:HE2	1:A:129:LYS:HB2	1.63	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:894:THR:CG2	7:A:1293:HOH:O	2.42	0.67
1:A:126:MET:HE1	1:A:129:LYS:HD2	1.76	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:HD22	1:A:665:ASN:H	1.43	0.66
1:A:358:ASN:CG	1:A:358:ASN:CA	2.67	0.64
1:A:190:GLN:CA	1:A:190:GLN:HE21	2.10	0.64
1:A:112:VAL:CG1	1:A:126:MET:HE3	2.30	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:501:LEU:C	1:A:501:LEU:HD12	2.27	0.59
1:A:679:ILE:HD11	1:A:757:ASP:C	2.27	0.58
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:665:ASN:HD22	1:A:665:ASN:N	2.02	0.57
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:896:LEU:HD12	1:A:896:LEU:C	2.31	0.55
1:A:558:SER:HA	1:A:566:THR:HB	1.89	0.55
1:A:869:LEU:C	1:A:869:LEU:HD12	2.31	0.55
1:A:671:THR:HG21	1:A:676:ILE:HD11	1.89	0.55
1:A:112:VAL:HG13	1:A:126:MET:HE3	1.89	0.54
1:A:677:ALA:O	1:A:678:PRO:C	2.50	0.54
1:A:117:SER:HB3	1:A:125:THR:HG21	1.90	0.54
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:750:ASP:O	1:A:751:GLN:C	2.53	0.52
1:A:210:GLY:N	1:A:232:GLY:HA3	2.25	0.51
1:A:179:GLY:C	1:A:180:GLN:HG2	2.36	0.51
1:A:583:ASN:C	1:A:583:ASN:ND2	2.57	0.51
1:A:638:VAL:CG2	1:A:748:ASN:HB3	2.41	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:CB	1:A:358:ASN:ND2	2.63	0.49
1:A:126:MET:HE1	1:A:129:LYS:CD	2.43	0.49
1:A:439:TYR:CZ	1:A:443:VAL:HG11	2.48	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
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:141:MET:HE3	1:A:339:TRP:CD2	2.50	0.46
1:A:436:LYS:HB2	1:A:441:ASP:HB3	1.97	0.46
1:A:190:GLN:HE21	1:A:190:GLN:HA	1.78	0.46
1:A:182:ASN:HD22	1:A:182:ASN:N	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:126:MET:HE1	1:A:129:LYS:CG	2.46	0.45
1:A:357:GLU:OE1	1:A:379:THR:OG1	2.27	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:112:VAL:HG11	1:A:126:MET:HE3	1.99	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: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:128:LYS:NZ	1:A:329:ALA:O	2.41	0.42
1:A:149:ILE:HG22	1:A:501:LEU:HB3	2.01	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:364:GLU:CD	1:A:364:GLU:O	2.64	0.41
1:A:904:PHE:CG	1:A:905:LEU:N	2.89	0.41
1:A:138:SER:OG	1:A:565:ASP:OD1	2.36	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%)	11 9

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 ⓘ

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%)	714 (92%)	62 (8%)	11	11

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	LEU
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	167	LYS
1	A	172	ARG
1	A	182	ASN
1	A	186	SER
1	A	190	GLN
1	A	229	THR
1	A	247	GLU
1	A	264	THR
1	A	275	LEU
1	A	294	LEU

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Mol	Chain	Res	Type
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	393	ASP
1	A	459	ILE
1	A	462	THR
1	A	469	TYR
1	A	478	THR
1	A	479	THR
1	A	488	VAL
1	A	492	GLN
1	A	500	SER
1	A	521	LEU
1	A	533	ARG
1	A	537	ARG
1	A	540	GLN
1	A	543	VAL
1	A	554	SER
1	A	561	SER
1	A	568	VAL
1	A	571	SER
1	A	574	GLN
1	A	576	ARG
1	A	583	ASN
1	A	590	ASP
1	A	604	VAL
1	A	605	THR
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	765	VAL
1	A	792	LYS
1	A	833	ASN
1	A	848	VAL
1	A	855	VAL

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Mol	Chain	Res	Type
1	A	894	THR
1	A	927	SER
1	A	936	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	A	69	GLN
1	A	73	ASN
1	A	96	ASN
1	A	119	ASN
1	A	143	GLN
1	A	171	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	293	GLN
1	A	307	ASN
1	A	330	GLN
1	A	344	ASN
1	A	352	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	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	0.85	0	15,15,17	1.88	4 (26%)
2	SIA	B	2	2	20,20,21	0.92	1 (5%)	21,28,31	1.03	2 (9%)

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	-	3/18/34/38	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	SIA	O1B-C1	-3.51	1.19	1.30

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	GAL	C2-C3-C4	-3.58	104.57	110.86
2	B	1	GAL	O3-C3-C2	3.21	116.61	110.05
2	B	1	GAL	C1-C2-C3	-2.95	105.36	109.64
2	B	1	GAL	O5-C5-C6	2.69	112.90	107.66
2	B	2	SIA	O1B-C1-C2	2.57	119.40	112.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	SIA	C6-C5-N5	-2.02	107.69	110.91

There are no chirality outliers.

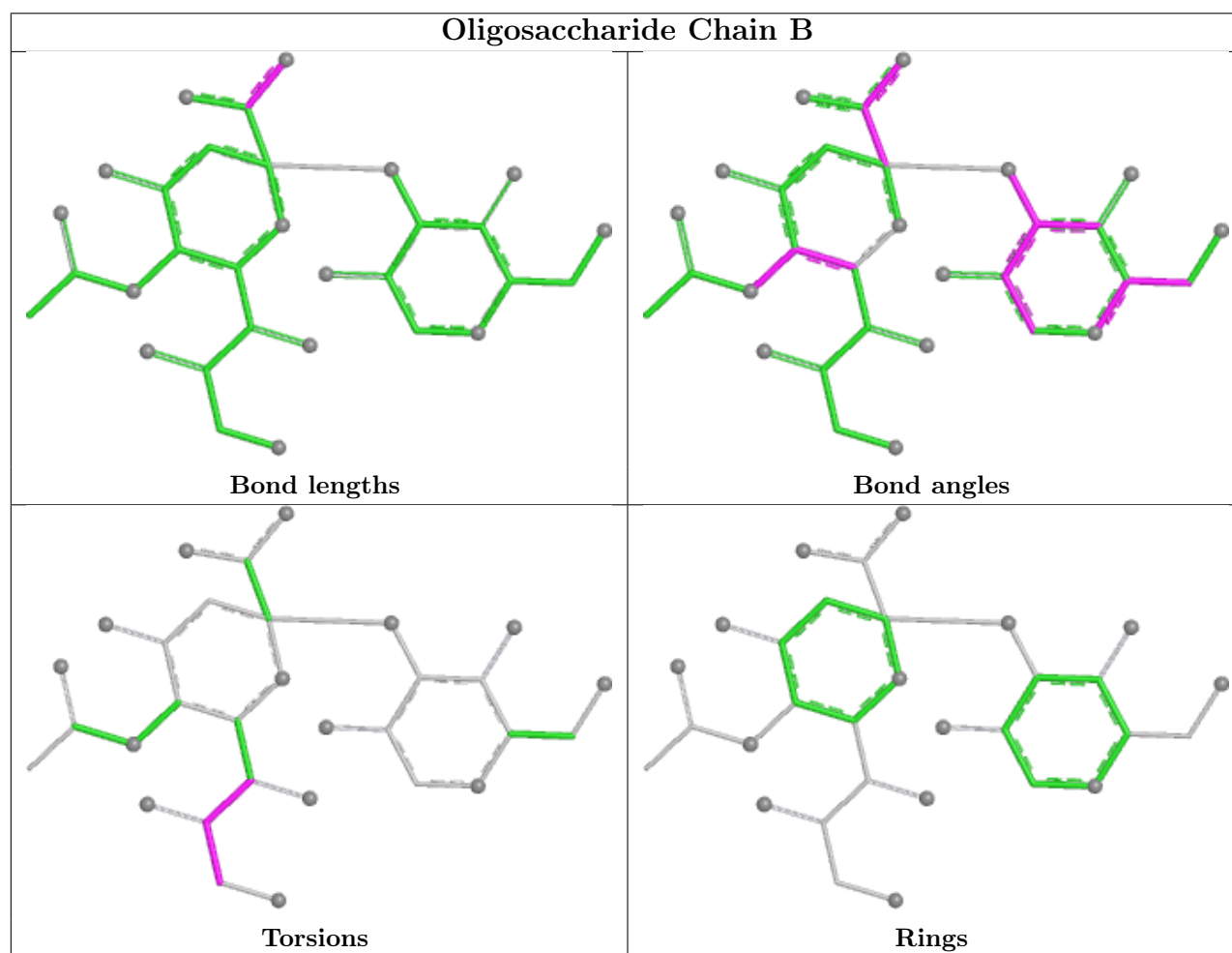
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	SIA	O8-C8-C9-O9
2	B	2	SIA	C7-C8-C9-O9
2	B	2	SIA	C6-C7-C8-O8

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

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
6	GOL	A	1006	-	5,5,5	0.12	0	5,5,5	0.39	0
4	BGC	A	1004	-	12,12,12	0.57	0	17,17,17	1.51	2 (11%)
5	PO4	A	1005	-	4,4,4	0.97	0	6,6,6	0.36	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	3.49	117.48	110.36
4	A	1004	BGC	O5-C5-C4	-2.34	105.48	109.70

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%)	0.26	39 (4%) 39 36	31, 74, 132, 193	1 (0%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	591	ALA	7.2
1	A	589	ILE	5.6
1	A	478	THR	4.6
1	A	256	SER	4.1
1	A	936	LEU	4.0
1	A	590	ASP	4.0
1	A	261	SER	3.9
1	A	492	GLN	3.8
1	A	603	SER	3.5
1	A	479	THR	3.4
1	A	604	VAL	3.4
1	A	562	THR	3.2
1	A	482	ILE	3.2
1	A	495	THR	2.9
1	A	494	SER	2.9
1	A	935	ALA	2.8
1	A	480	GLY	2.7
1	A	469	TYR	2.6
1	A	676	ILE	2.6
1	A	756	LEU	2.5
1	A	333	ALA	2.5
1	A	754	THR	2.5
1	A	463	PHE	2.5
1	A	26[A]	ASN	2.4
1	A	102	THR	2.4
1	A	459	ILE	2.4
1	A	643	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	493	LYS	2.3
1	A	794	SER	2.3
1	A	392	ASN	2.3
1	A	366	THR	2.3
1	A	640	SER	2.3
1	A	855	VAL	2.3
1	A	262	SER	2.3
1	A	393	ASP	2.2
1	A	745	ILE	2.1
1	A	934	ALA	2.1
1	A	458	SER	2.0
1	A	362	TYR	2.0

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

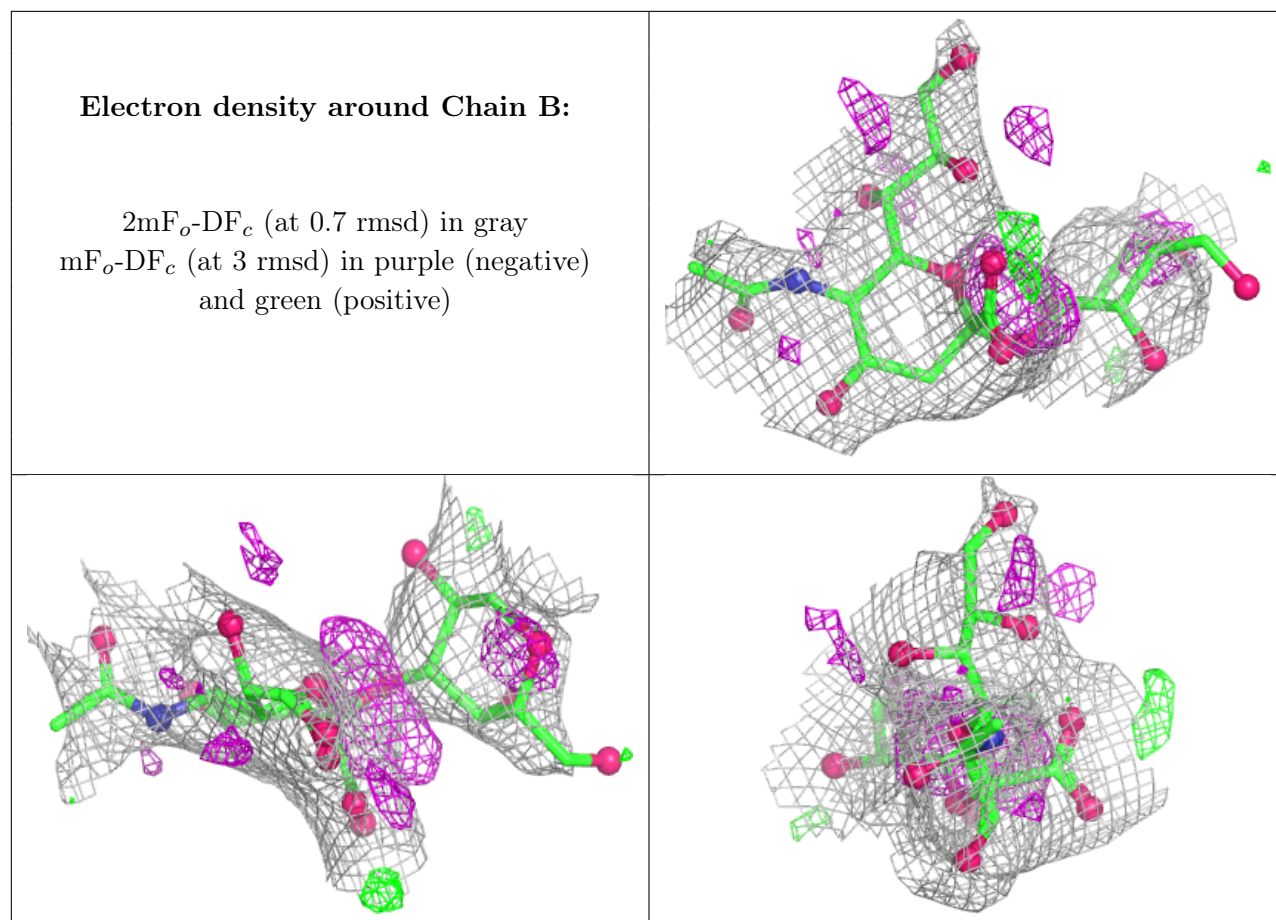
There are no non-standard protein/DNA/RNA residues in this entry.

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
2	GAL	B	1	11/12	0.31	0.16	127,146,163,163	0
2	SIA	B	2	20/21	0.87	0.11	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($\text{\AA}^2$)	Q<0.9
4	BGC	A	1004	12/12	0.60	0.11	126,152,163,169	0
5	PO4	A	1005	5/5	0.87	0.13	51,52,75,78	5
6	GOL	A	1006	6/6	0.88	0.15	73,80,81,95	0
3	K	A	1001	1/1	0.98	0.04	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.