Full wwPDB X-ray Structure Validation Report ⓘ

Feb 2, 2025 – 01:56 am GMT

PDB ID	:	8RWB
Title	:	Crystal structure of ULBP6 in complex with a blocking antibody
Authors	:	Bharill, S.; Chen, I.; Ivic, N.; Bahrami Dizicheh, Z.; Wu, Y.; Doamekpor, S.; Koenig, P.; Fuh, G.
Deposited on	:	2024-02-02
Resolution	:	2.31 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:

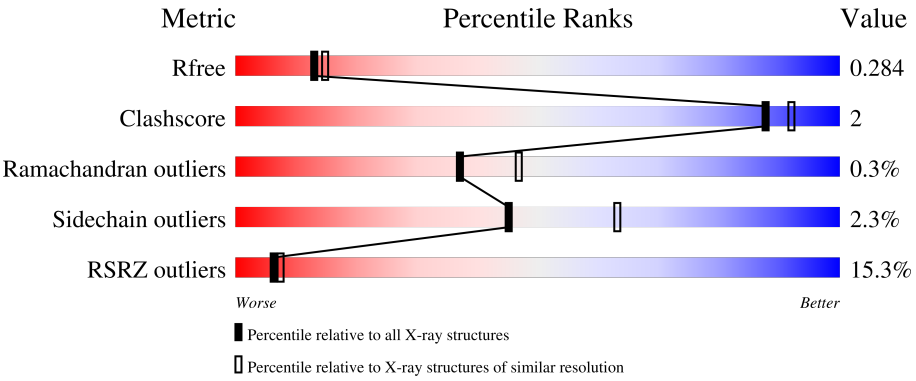
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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 <=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	P	172	13% 94% 6%
2	H	217	15% 93% 7%
3	L	212	17% 92% 8%
4	A	2	100%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 4857 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 UL16-binding protein 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	172	Total	C	N	O	S	14	3	0
			1402	891	236	264	11			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	85	THR	MET	variant	UNP Q5VY80

- Molecule 2 is a protein called Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	217	Total	C	N	O	S	9	2	0
			1623	1021	275	322	5			

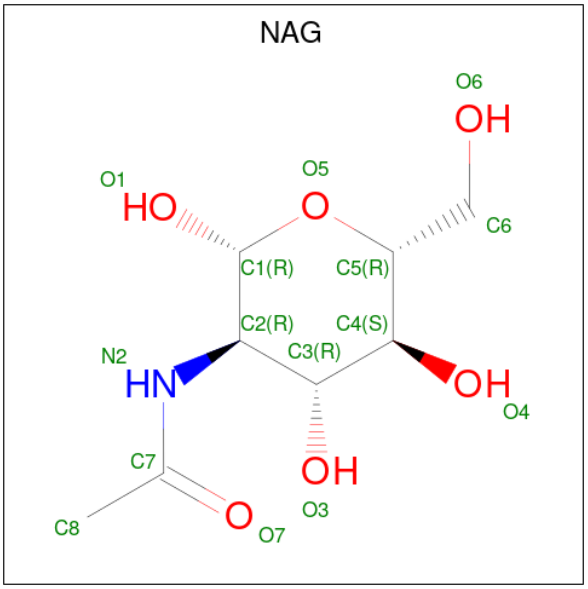
- Molecule 3 is a protein called Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	212	Total	C	N	O	S	12	2	0
			1638	1021	278	334	5			

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

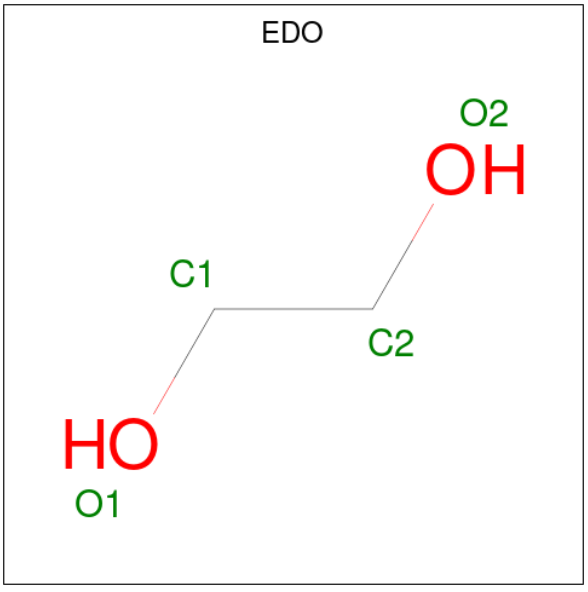
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	A	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	H	1	Total	C	O	0	0
			4	2	2		

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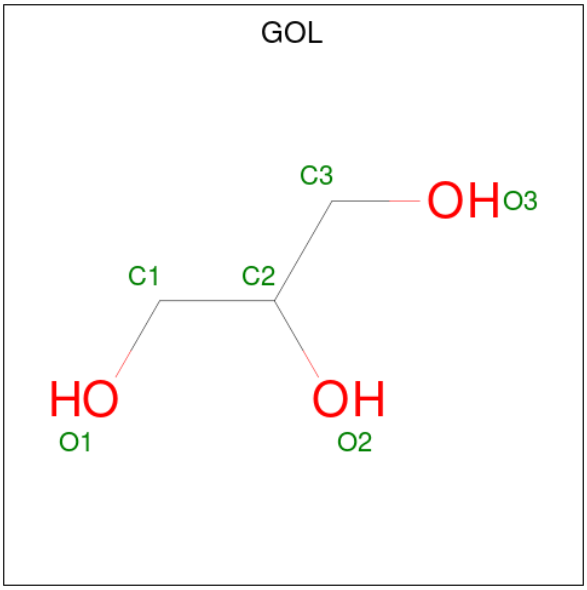
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	L	1	Total C O 4 2 2	0	0
6	L	1	Total C O 4 2 2	0	0

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

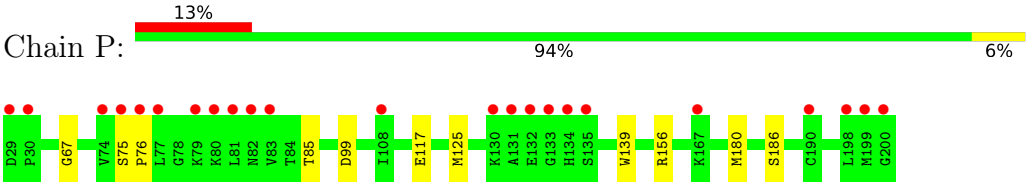
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	P	27	Total O 27 27	0	0
8	H	52	Total O 52 52	0	0
8	L	55	Total O 55 55	0	0

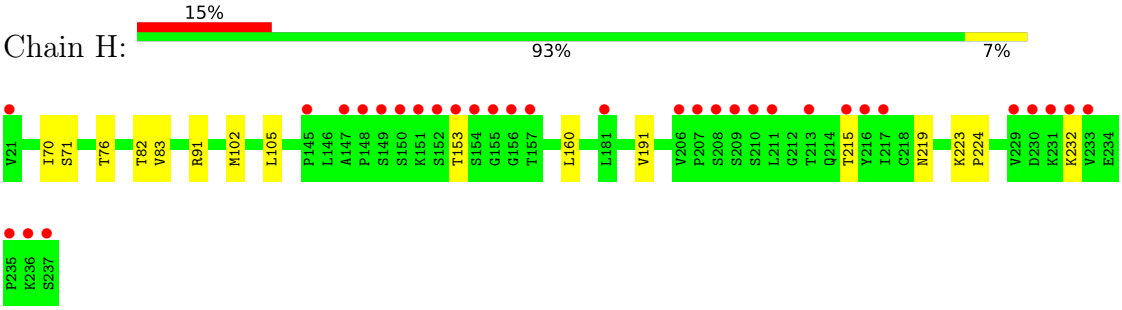
3 Residue-property plots (i)

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.

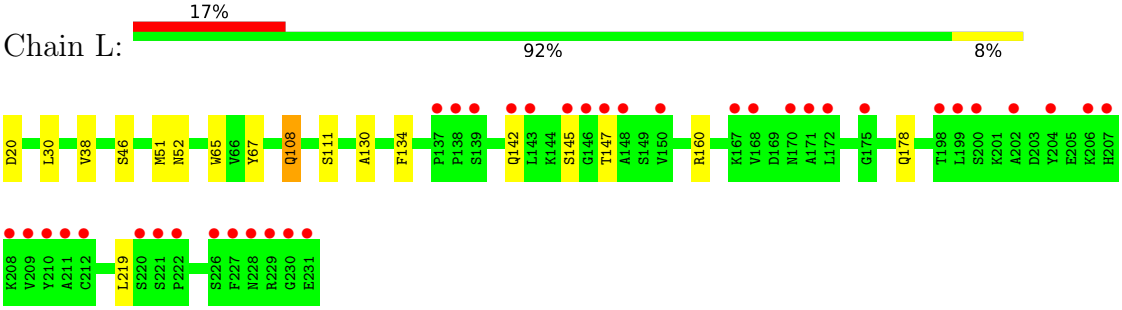
• Molecule 1: UL16-binding protein 6



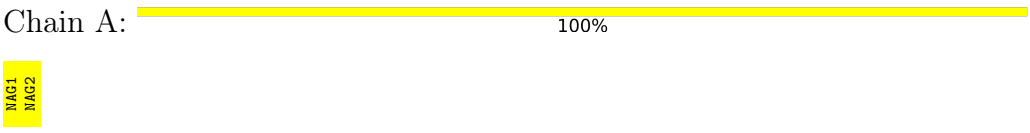
• Molecule 2: Heavy chain



• Molecule 3: Light chain



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



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	106.55Å 95.80Å 97.20Å 90.00° 117.74° 90.00°	Depositor
Resolution (Å)	86.03 – 2.31 86.03 – 2.31	Depositor EDS
% Data completeness (in resolution range)	52.4 (86.03-2.31) 52.4 (86.03-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.85 (at 2.32Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.216 , 0.286 0.218 , 0.284	Depositor DCC
R_{free} test set	1891 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	40.3	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 39.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	4857	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.34% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	P	0.65	0/1442	0.80	0/1955
2	H	0.68	0/1665	0.81	0/2268
3	L	0.68	0/1674	0.81	0/2272
All	All	0.67	0/4781	0.81	0/6495

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	P	1402	0	1357	3	0
2	H	1623	0	1577	8	0
3	L	1638	0	1583	8	0
4	A	28	0	25	0	0
5	P	14	0	13	0	0
6	H	4	0	6	0	0
6	L	8	0	12	0	0
7	L	6	0	8	0	0
8	H	52	0	0	0	0
8	L	55	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	P	27	0	0	0	0
All	All	4857	0	4581	17	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (17) 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:82:THR:HG23	2:H:83:VAL:HG13	1.89	0.52
2:H:71:SER:HB2	2:H:76:THR:HB	1.96	0.48
1:P:75:SER:HB2	1:P:76:PRO:HA	1.96	0.47
2:H:153:THR:HG23	3:L:134:PHE:HB3	1.98	0.46
3:L:108:GLN:OE1	3:L:111[A]:SER:N	2.48	0.46
2:H:70:ILE:HD13	2:H:91:ARG:HG3	1.99	0.45
1:P:156:ARG:HD2	1:P:180:MET:HE1	1.97	0.45
3:L:30:LEU:HD11	3:L:38:VAL:HG13	1.97	0.45
2:H:102:MET:HB3	2:H:105:LEU:HD21	1.99	0.45
3:L:142[A]:GLN:HG2	3:L:147:THR:HG23	1.99	0.45
2:H:215:THR:HG23	2:H:232:LYS:HE3	1.98	0.44
3:L:130:ALA:HB1	3:L:219:LEU:CD1	2.48	0.44
2:H:191:VAL:HG21	3:L:178:GLN:HB3	2.01	0.43
1:P:125:MET:HG3	1:P:139:TRP:CZ2	2.54	0.41
2:H:223:LYS:N	2:H:224:PRO:CD	2.83	0.41
3:L:108:GLN:OE1	3:L:111[B]:SER:N	2.51	0.40
3:L:52:ASN:OD1	3:L:67:TYR:HA	2.21	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	P	173/172 (101%)	164 (95%)	7 (4%)	2 (1%)	11 12
2	H	217/217 (100%)	207 (95%)	10 (5%)	0	100 100
3	L	212/212 (100%)	204 (96%)	8 (4%)	0	100 100
All	All	602/601 (100%)	575 (96%)	25 (4%)	2 (0%)	37 47

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P	117	GLU
1	P	67	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	P	157/154 (102%)	154 (98%)	3 (2%)	52 69
2	H	181/179 (101%)	179 (99%)	2 (1%)	70 83
3	L	189/187 (101%)	182 (96%)	7 (4%)	29 43
All	All	527/520 (101%)	515 (98%)	12 (2%)	45 63

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	85	THR
1	P	99	ASP
1	P	186	SER
2	H	160	LEU
2	H	219	ASN
3	L	20	ASP
3	L	46	SER
3	L	51	MET
3	L	65	TRP
3	L	108	GLN
3	L	145	SER

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Mol	Chain	Res	Type
3	L	160	ARG

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

Mol	Chain	Res	Type
3	L	165	GLN
3	L	207	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

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	$\#\|Z\| > 2$
4	NAG	A	1	4,1	14,14,15	0.41	0	17,19,21	0.77	1 (5%)
4	NAG	A	2	4	14,14,15	0.40	0	17,19,21	1.65	2 (11%)

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	1	4,1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	2	4	-	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(^{o})	Ideal(^{o})
4	A	2	NAG	C1-O5-C5	5.35	119.44	112.19
4	A	2	NAG	C4-C3-C2	-2.84	106.86	111.02
4	A	1	NAG	C1-O5-C5	2.56	115.67	112.19

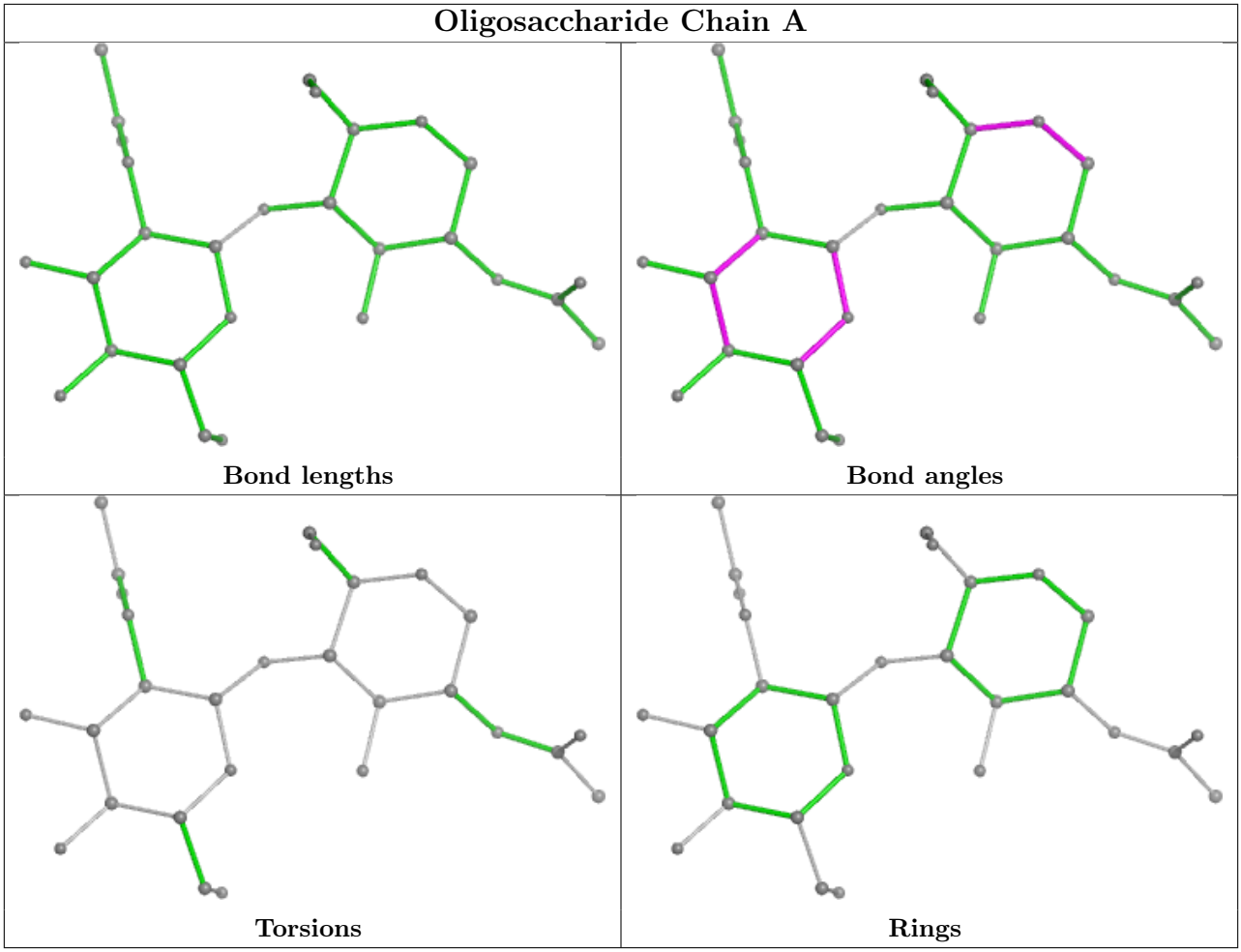
There are no chirality outliers.

There are no torsion outliers.

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)

5 ligands 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	$\#\|Z\| > 2$
7	GOL	L	301	-	5,5,5	0.13	0	5,5,5	0.35	0
6	EDO	H	301	-	3,3,3	0.16	0	2,2,2	0.42	0
5	NAG	P	201	1	14,14,15	0.62	0	17,19,21	1.72	3 (17%)
6	EDO	L	303	-	3,3,3	0.16	0	2,2,2	0.50	0
6	EDO	L	302	-	3,3,3	0.15	0	2,2,2	0.41	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
7	GOL	L	301	-	-	2/4/4/4	-
6	EDO	H	301	-	-	1/1/1/1	-
5	NAG	P	201	1	-	1/6/23/26	0/1/1/1
6	EDO	L	303	-	-	1/1/1/1	-
6	EDO	L	302	-	-	1/1/1/1	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	P	201	NAG	C1-O5-C5	5.45	119.58	112.19
5	P	201	NAG	O5-C5-C6	2.77	111.54	107.20
5	P	201	NAG	C3-C4-C5	-2.12	106.45	110.24

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	L	301	GOL	C1-C2-C3-O3
6	H	301	EDO	O1-C1-C2-O2
6	L	302	EDO	O1-C1-C2-O2
6	L	303	EDO	O1-C1-C2-O2
5	P	201	NAG	O5-C5-C6-O6
7	L	301	GOL	O2-C2-C3-O3

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, 95^{th} 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	P	172/172 (100%)	0.84	23 (13%)	8	9	16, 44, 77, 100	10 (5%)
2	H	217/217 (100%)	0.77	32 (14%)	7	8	18, 39, 83, 111	10 (4%)
3	L	212/212 (100%)	0.76	37 (17%)	5	6	11, 40, 86, 95	8 (3%)
All	All	601/601 (100%)	0.79	92 (15%)	6	7	11, 41, 84, 111	28 (4%)

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	172	LEU	6.0
1	P	131	ALA	6.0
2	H	147	ALA	5.8
3	L	208	LYS	5.3
2	H	21	VAL	5.2
2	H	150	SER	4.6
3	L	202	ALA	4.6
2	H	152	SER	4.5
2	H	235	PRO	4.4
3	L	206	LYS	4.4
3	L	143	LEU	4.4
2	H	156	GLY	4.3
3	L	210	TYR	4.2
1	P	76	PRO	4.2
1	P	79	LYS	4.1
1	P	81	LEU	4.1
2	H	237	SER	4.0
3	L	209	VAL	4.0
3	L	175	GLY	4.0
2	H	210	SER	4.0
2	H	155	GLY	4.0
2	H	148	PRO	4.0
1	P	80	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
3	L	139	SER	3.9
3	L	171	ALA	3.7
2	H	209	SER	3.7
2	H	151	LYS	3.7
2	H	211	LEU	3.6
1	P	77	LEU	3.5
3	L	227	PHE	3.5
2	H	233	VAL	3.5
2	H	236	LYS	3.5
1	P	83	VAL	3.4
1	P	200	GLY	3.4
1	P	198	LEU	3.4
2	H	149	SER	3.3
1	P	30	PRO	3.2
3	L	212	CYS	3.2
3	L	147	THR	3.2
3	L	142[A]	GLN	3.0
3	L	198	THR	3.0
2	H	232	LYS	3.0
3	L	167	LYS	3.0
1	P	75	SER	2.9
3	L	230	GLY	2.8
2	H	153	THR	2.8
1	P	130	LYS	2.8
2	H	213	THR	2.8
2	H	208[A]	SER	2.8
2	H	231	LYS	2.7
3	L	168	VAL	2.7
1	P	199	MET	2.7
2	H	217	ILE	2.7
3	L	170	ASN	2.6
1	P	29	ASP	2.6
3	L	138	PRO	2.6
3	L	199	LEU	2.6
1	P	167	LYS	2.6
2	H	216	TYR	2.5
1	P	108	ILE	2.5
2	H	207	PRO	2.5
3	L	150	VAL	2.5
3	L	200	SER	2.5
3	L	211	ALA	2.5
2	H	157	THR	2.5

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Mol	Chain	Res	Type	RSRZ
3	L	207	HIS	2.4
1	P	132	GLU	2.4
1	P	133	GLY	2.4
3	L	148	ALA	2.4
2	H	154	SER	2.4
3	L	229	ARG	2.3
2	H	215	THR	2.3
3	L	221	SER	2.3
2	H	230	ASP	2.2
3	L	231	GLU	2.2
3	L	204	TYR	2.2
3	L	146	GLY	2.2
3	L	222	PRO	2.2
1	P	82	ASN	2.2
3	L	137	PRO	2.2
1	P	135	SER	2.1
3	L	220	SER	2.1
1	P	134	HIS	2.1
2	H	145	PRO	2.1
2	H	229	VAL	2.1
3	L	145	SER	2.1
3	L	228	ASN	2.1
3	L	226	SER	2.1
2	H	181	LEU	2.1
2	H	206	VAL	2.0
1	P	190	CYS	2.0
1	P	74	VAL	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)

SUGAR-RSR INFOmissingINFO

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, 95^{th} 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
5	NAG	P	201	14/15	0.76	0.17	74,80,84,86	0
7	GOL	L	301	6/6	0.90	0.13	49,52,54,55	0
6	EDO	L	303	4/4	0.92	0.14	51,52,52,53	0
6	EDO	L	302	4/4	0.93	0.14	46,46,46,46	0
6	EDO	H	301	4/4	0.95	0.10	57,58,58,58	0

6.5 Other polymers (i)

There are no such residues in this entry.