Full wwPDB X-ray Structure Validation Report (i)

Sep 18, 2021 – 08:06 AM BST

PDB ID	:	6XUN
Title	:	Ab 5b1 bound to CA19-9
Authors	:	Diskin, R.; Borenstein-Katz, A.
Deposited on	:	2020-01-20
Resolution	:	2.41 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 (i) symbol.

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

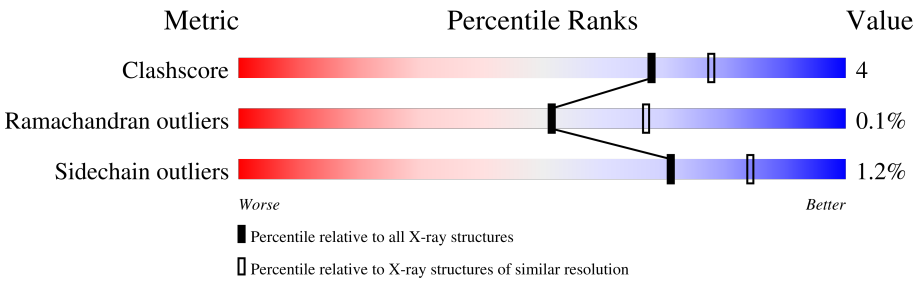
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.1

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 2.41 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))
Clashscore	141614	5161 (2.44-2.40)
Ramachandran outliers	138981	5073 (2.44-2.40)
Sidechain outliers	138945	5074 (2.44-2.40)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	230	86% 9% 5%
1	C	230	83% 13% .
1	H	230	91% 5% .
2	B	218	89% 10%
2	D	218	88% 11%
2	L	218	92% 7%
3	E	4	25% 50% 25%
3	F	4	25% 25% 50%

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Mol	Chain	Length	Quality of chain
3	G	4	25% 75%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 10655 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.

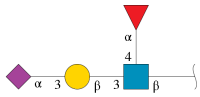
- Molecule 1 is a protein called Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	H	220	1674	1055	290	322	7	0	0	0
1	A	218	1665	1051	288	319	7	0	1	0
1	C	221	1686	1063	292	324	7	0	1	0

- Molecule 2 is a protein called Light chain.

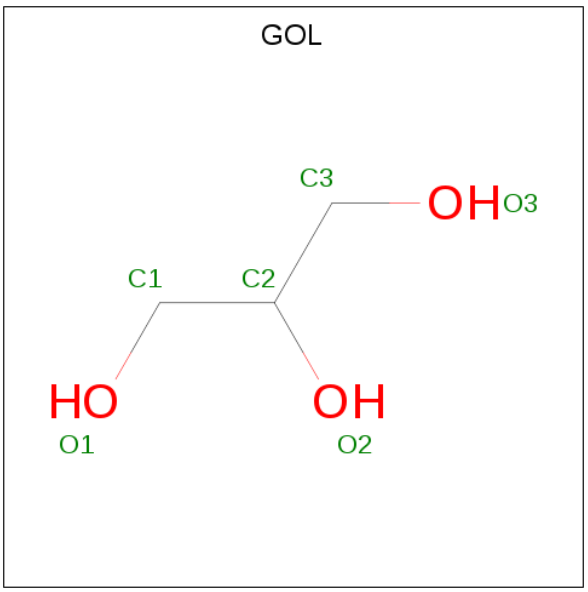
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	217	1651	1026	284	336	5	0	1	0
2	D	217	1651	1026	284	336	5	0	1	0
2	L	217	1651	1026	284	336	5	0	1	0

- Molecule 3 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galacto pyranose-(1-3)-[alpha-L-fucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	E	4	56	31	2	23	0	0	0
3	F	4	56	31	2	23	0	0	0
3	G	4	56	31	2	23	0	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	B	1	6	3	3	0	0
			Total	C	O		
4	B	1	6	3	3	0	0
			Total	C	O		
4	D	1	6	3	3	0	0
			Total	C	O		
4	C	1	6	3	3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	H	84	84	84	0	0
			Total	O		
5	B	76	76	76	0	0
			Total	O		
5	D	62	62	62	0	0
			Total	O		
5	L	52	52	52	0	0
			Total	O		
5	A	112	112	112	0	0
			Total	O		
5	C	99	99	99	0	0

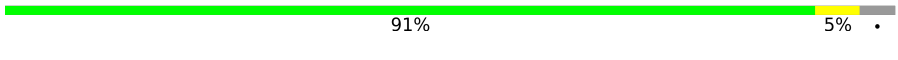
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

• Molecule 1: Heavy chain

Chain H:

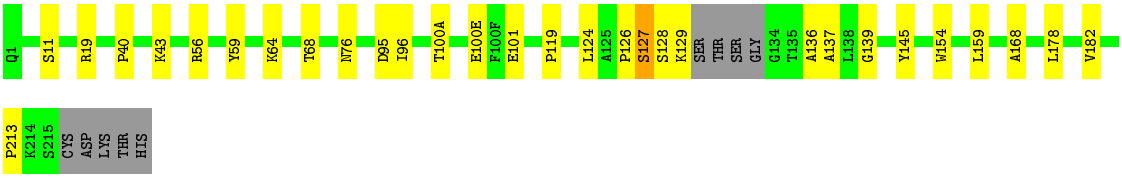


• Molecule 1: Heavy chain

Chain A:

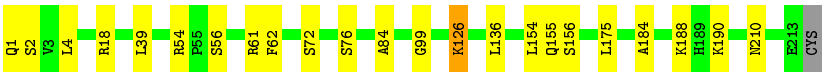
• Molecule 1: Heavy chain

Chain C:



• Molecule 2: Light chain

Chain B:

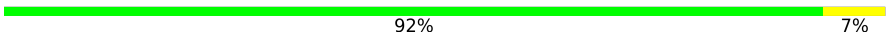


• Molecule 2: Light chain

Chain D:

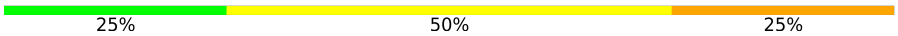
• Molecule 2: Light chain

Chain L:



• Molecule 3: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-[alpha-L-fucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:

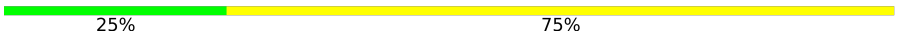


• Molecule 3: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-[alpha-L-fucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:

• Molecule 3: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-[alpha-L-fucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	152.54Å 152.54Å 60.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.58 – 2.41	Depositor
% Data completeness (in resolution range)	99.8 (47.58-2.41)	Depositor
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.169 , 0.215	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10655	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

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: GAL, SIA, GOL, FUC, NAG

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	0.37	0/1709	0.58	0/2323
1	C	0.36	0/1730	0.55	0/2350
1	H	0.35	0/1715	0.53	0/2331
2	B	0.37	0/1691	0.59	2/2300 (0.1%)
2	D	0.32	0/1691	0.52	0/2300
2	L	0.32	0/1691	0.54	0/2300
All	All	0.35	0/10227	0.55	2/13904 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	126	LYS	CB-CG-CD	-7.87	91.14	111.60
2	B	126	LYS	CD-CE-NZ	-5.99	97.91	111.70

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	1665	0	1624	13	0
1	C	1686	0	1647	21	0
1	H	1674	0	1630	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1651	0	1588	13	0
2	D	1651	0	1588	14	0
2	L	1651	0	1588	9	0
3	E	56	0	49	1	0
3	F	56	0	49	1	0
3	G	56	0	49	0	0
4	B	12	0	16	0	0
4	C	6	0	8	0	0
4	D	6	0	8	1	0
5	A	112	0	0	4	0
5	B	76	0	0	3	0
5	C	99	0	0	4	1
5	D	62	0	0	3	0
5	H	84	0	0	2	0
5	L	52	0	0	3	0
All	All	10655	0	9844	76	1

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 4.

All (76) 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:117:LYS:NZ	5:A:404:HOH:O	2.15	0.80
1:A:100:SER:OG	5:A:401:HOH:O	2.00	0.80
2:D:69:THR:OG1	5:D:401:HOH:O	2.04	0.75
1:C:43:LYS:O	5:C:401:HOH:O	2.04	0.75
2:B:72:SER:OG	5:B:401:HOH:O	2.03	0.75
2:L:177:SER:OG	5:L:301:HOH:O	2.05	0.74
1:A:46:GLU:OE1	5:A:402:HOH:O	2.05	0.74
2:B:190:LYS:HE3	2:B:210:ASN:HB3	1.71	0.71
1:C:68:THR:OG1	5:C:402:HOH:O	2.12	0.68
5:H:401:HOH:O	3:E:4:FUC:O4	2.11	0.67
1:C:127:SER:OG	1:C:128:SER:N	2.20	0.67
1:C:56:ARG:HG3	1:C:100(A):THR:HG23	1.76	0.66
2:D:40:PRO:O	5:D:402:HOH:O	2.12	0.66
2:B:1:GLN:HG3	2:B:2:SER:H	1.61	0.65
1:A:165:THR:O	5:A:403:HOH:O	2.15	0.65
1:C:40:PRO:HG2	1:C:43:LYS:HB2	1.83	0.61
1:H:126:PRO:HG3	1:H:138:LEU:HB3	1.82	0.60
1:C:76:ASN:OD1	5:C:403:HOH:O	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:126:PRO:HD2	1:C:213:PRO:HA	1.84	0.60
2:D:80:SER:HA	2:D:106:VAL:HG21	1.83	0.59
2:L:161:GLU:OE1	5:L:303:HOH:O	2.17	0.58
1:H:126:PRO:HD2	1:H:213:PRO:HA	1.85	0.58
1:H:82:MET:HB3	1:H:82(C):LEU:HD21	1.85	0.58
2:B:39:LEU:HD23	2:B:84:ALA:HB2	1.85	0.57
1:C:129:LYS:HD2	1:C:136:ALA:HA	1.86	0.57
2:L:69:THR:OG1	5:L:302:HOH:O	2.17	0.57
2:D:61:ARG:NH1	2:D:82:ASP:OD2	2.28	0.56
3:F:2:GAL:H62	3:F:4:FUC:H3	1.87	0.56
2:B:18:ARG:NH1	5:B:403:HOH:O	2.26	0.55
2:L:49:TYR:HD2	2:L:50:ARG:HG3	1.70	0.54
1:A:95:ASP:HA	1:A:100(E):GLU:O	2.08	0.54
1:C:127:SER:HB3	1:C:129:LYS:HE3	1.91	0.53
1:C:19:ARG:NH2	5:C:408:HOH:O	2.41	0.53
2:L:40:PRO:HB3	2:L:165:GLU:HG3	1.92	0.52
2:D:116:PHE:CD2	1:C:129:LYS:HE2	2.45	0.51
1:A:39:GLN:HB2	1:A:45:LEU:HD23	1.92	0.51
2:L:167:ASP:OD1	2:L:169:LYS:HG3	2.11	0.50
1:A:126:PRO:HG3	1:A:138:LEU:HB3	1.93	0.50
2:D:132:VAL:HG13	2:D:179:LEU:HB3	1.92	0.50
1:C:159:LEU:HD21	1:C:182:VAL:HG21	1.93	0.50
2:D:199:GLN:NE2	5:D:403:HOH:O	2.21	0.49
1:A:159:LEU:HD21	1:A:182:VAL:HG21	1.93	0.49
2:B:4:LEU:HB2	2:B:99:GLY:HA2	1.95	0.49
2:D:14:THR:HG22	2:D:15:PRO:HD2	1.95	0.49
2:B:61:ARG:HB3	2:B:76:SER:O	2.12	0.48
2:L:44:PRO:O	2:L:45:LYS:HE2	2.14	0.48
1:C:59:TYR:HB2	1:C:64:LYS:HD3	1.96	0.47
1:H:1:GLN:N	5:H:406:HOH:O	2.41	0.47
1:C:96:ILE:HG12	1:C:101:GLU:HB2	1.97	0.46
1:H:11:SER:HB2	1:H:147:PRO:HG3	1.97	0.46
1:A:11:SER:HB3	1:A:147:PRO:HG3	1.98	0.46
1:A:214:LYS:HG2	1:A:215:SER:N	2.31	0.45
2:D:92:ASP:O	2:D:95(B):GLY:HA2	2.17	0.45
2:B:126:LYS:NZ	5:B:407:HOH:O	2.49	0.44
2:D:16:GLY:O	2:D:77:GLY:HA2	2.17	0.44
1:C:129:LYS:HD2	1:C:137:ALA:H	1.82	0.44
2:B:54:ARG:HD3	2:B:62:PHE:O	2.17	0.43
2:B:126:LYS:O	2:B:126:LYS:HD3	2.17	0.43
2:D:166:GLN:HG3	2:D:173:TYR:CZ	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:168:ALA:HB2	1:C:178:LEU:HD23	2.01	0.43
1:C:95:ASP:HA	1:C:100(E):GLU:O	2.19	0.43
4:D:301:GOL:H32	1:C:101:GLU:HG3	2.01	0.43
2:D:35:TRP:HB2	2:D:48:ILE:HB	2.02	0.42
1:C:119:PRO:HB3	1:C:145:TYR:HB3	2.00	0.42
2:B:154:LEU:HG	2:B:155:GLN:N	2.35	0.42
2:B:136:LEU:HB2	2:B:175:LEU:HB3	2.00	0.42
1:A:56:ARG:HA	1:A:56:ARG:HD3	1.91	0.42
2:D:118:PHE:CD2	1:C:124:LEU:HB3	2.55	0.41
1:C:139:GLY:HA2	1:C:154:TRP:CH2	2.56	0.41
1:H:214:LYS:HA	1:H:214:LYS:HD2	1.77	0.41
1:A:13:GLN:HB2	1:A:16:ARG:HG2	2.02	0.41
2:D:40:PRO:CG	2:D:165:GLU:HG2	2.52	0.40
2:L:49:TYR:CD2	2:L:50:ARG:HG3	2.53	0.40
2:B:184:ALA:O	2:B:188:LYS:HG3	2.22	0.40
2:L:163:VAL:HG22	2:L:175:LEU:HD12	2.03	0.40
1:A:82:MET:HB3	1:A:82(C):LEU:HD21	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:406:HOH:O	5:C:490:HOH:O[2_555]	2.11	0.09

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	215/230 (94%)	211 (98%)	4 (2%)	0	100 100
1	C	218/230 (95%)	213 (98%)	4 (2%)	1 (0%)	29 40
1	H	216/230 (94%)	211 (98%)	5 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	216/218 (99%)	210 (97%)	6 (3%)	0	100	100
2	D	216/218 (99%)	210 (97%)	6 (3%)	0	100	100
2	L	216/218 (99%)	211 (98%)	5 (2%)	0	100	100
All	All	1297/1344 (96%)	1266 (98%)	30 (2%)	1 (0%)	51	67

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	127	SER

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	184/194 (95%)	184 (100%)	0	100	100
1	C	187/194 (96%)	186 (100%)	1 (0%)	88	95
1	H	185/194 (95%)	183 (99%)	2 (1%)	73	86
2	B	187/187 (100%)	185 (99%)	2 (1%)	73	86
2	D	187/187 (100%)	184 (98%)	3 (2%)	62	78
2	L	187/187 (100%)	182 (97%)	5 (3%)	44	63
All	All	1117/1143 (98%)	1104 (99%)	13 (1%)	71	84

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	71	ARG
1	H	98	ARG
2	B	56	SER
2	B	156	SER
2	D	79	ARG
2	D	127	SER
2	D	195	GLU

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Mol	Chain	Res	Type
2	L	70	SER
2	L	72	SER
2	L	156	SER
2	L	168	SER
2	L	169	LYS
1	C	11	SER

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

Mol	Chain	Res	Type
2	B	138	ASN
1	A	164	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)

12 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	$\#\|Z\| > 2$
3	NAG	E	1	3	15,15,15	0.22	0	21,21,21	0.42	0
3	GAL	E	2	3	11,11,12	0.62	0	15,15,17	1.16	1 (6%)
3	SIA	E	3	3	17,20,21	0.84	1 (5%)	21,28,31	1.08	2 (9%)
3	FUC	E	4	3	10,10,11	0.99	1 (10%)	14,14,16	0.97	0
3	NAG	F	1	3	15,15,15	0.24	0	21,21,21	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	GAL	F	2	3	11,11,12	1.07	1 (9%)	15,15,17	0.90	0
3	SIA	F	3	3	17,20,21	0.82	0	21,28,31	1.12	2 (9%)
3	FUC	F	4	3	10,10,11	1.02	1 (10%)	14,14,16	0.90	0
3	NAG	G	1	3	15,15,15	0.16	0	21,21,21	0.41	0
3	GAL	G	2	3	11,11,12	0.76	0	15,15,17	1.09	1 (6%)
3	SIA	G	3	3	17,20,21	0.90	1 (5%)	21,28,31	1.14	1 (4%)
3	FUC	G	4	3	10,10,11	1.15	1 (10%)	14,14,16	0.76	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
3	NAG	E	1	3	-	1/6/26/26	0/1/1/1
3	GAL	E	2	3	-	0/2/19/22	0/1/1/1
3	SIA	E	3	3	-	2/14/34/38	0/1/1/1
3	FUC	E	4	3	-	-	0/1/1/1
3	NAG	F	1	3	-	0/6/26/26	0/1/1/1
3	GAL	F	2	3	-	2/2/19/22	0/1/1/1
3	SIA	F	3	3	-	1/14/34/38	0/1/1/1
3	FUC	F	4	3	-	-	0/1/1/1
3	NAG	G	1	3	-	0/6/26/26	0/1/1/1
3	GAL	G	2	3	-	0/2/19/22	0/1/1/1
3	SIA	G	3	3	-	4/14/34/38	0/1/1/1
3	FUC	G	4	3	-	-	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	4	FUC	O5-C1	-3.18	1.38	1.43
3	F	2	GAL	O5-C1	-2.86	1.39	1.43
3	E	4	FUC	O5-C1	-2.60	1.39	1.43
3	F	4	FUC	O5-C1	-2.46	1.39	1.43
3	G	3	SIA	C7-C6	2.38	1.56	1.53
3	E	3	SIA	C7-C6	2.00	1.55	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	G	3	SIA	C6-O6-C2	3.30	118.40	111.34
3	E	2	GAL	C1-O5-C5	3.24	116.58	112.19
3	F	3	SIA	C6-O6-C2	2.82	117.38	111.34
3	E	3	SIA	C6-O6-C2	2.56	116.82	111.34
3	G	2	GAL	O2-C2-C3	-2.55	105.03	110.14
3	F	3	SIA	C3-C4-C5	-2.08	108.95	111.46
3	E	3	SIA	C4-C3-C2	2.04	113.47	109.81

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	3	SIA	O8-C8-C9-O9
3	G	3	SIA	C7-C8-C9-O9
3	F	2	GAL	O5-C5-C6-O6
3	F	2	GAL	C4-C5-C6-O6
3	G	3	SIA	C6-C7-C8-O8
3	E	3	SIA	C7-C8-C9-O9
3	F	3	SIA	C6-C7-C8-O8
3	E	1	NAG	C4-C5-C6-O6
3	G	3	SIA	O7-C7-C8-O8
3	E	3	SIA	O8-C8-C9-O9

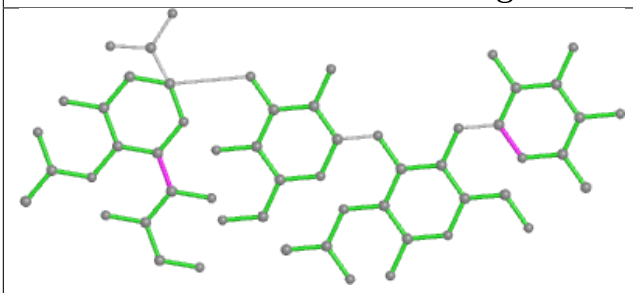
There are no ring outliers.

3 monomers are involved in 2 short contacts:

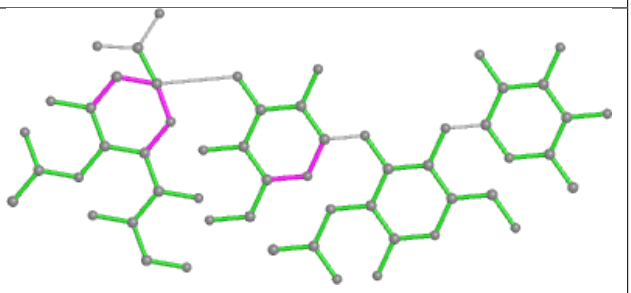
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	4	FUC	1	0
3	F	2	GAL	1	0
3	E	4	FUC	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

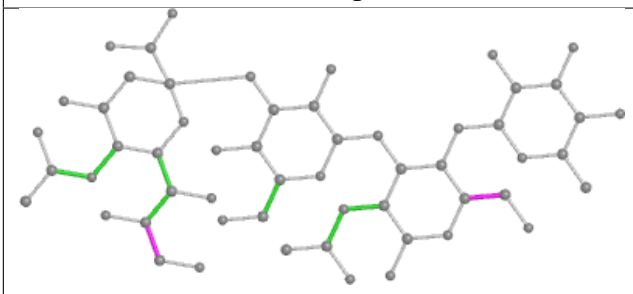
Oligosaccharide Chain E



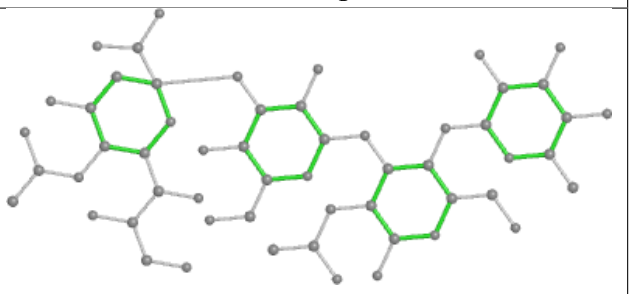
Bond lengths



Bond angles

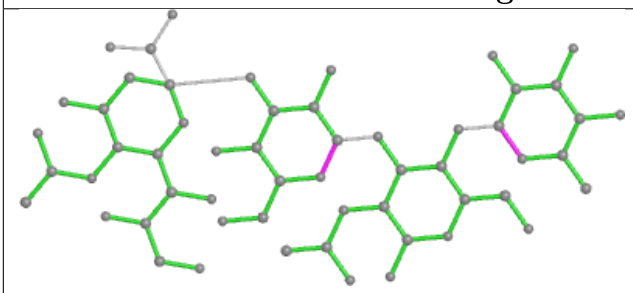


Torsions

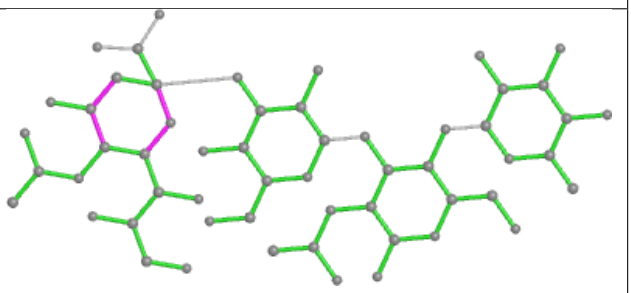


Rings

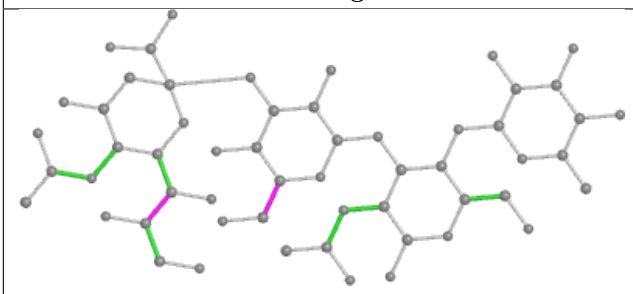
Oligosaccharide Chain F



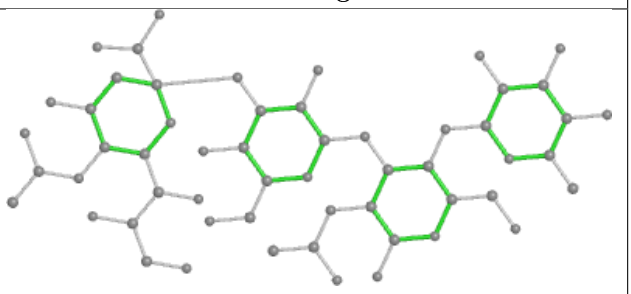
Bond lengths



Bond angles

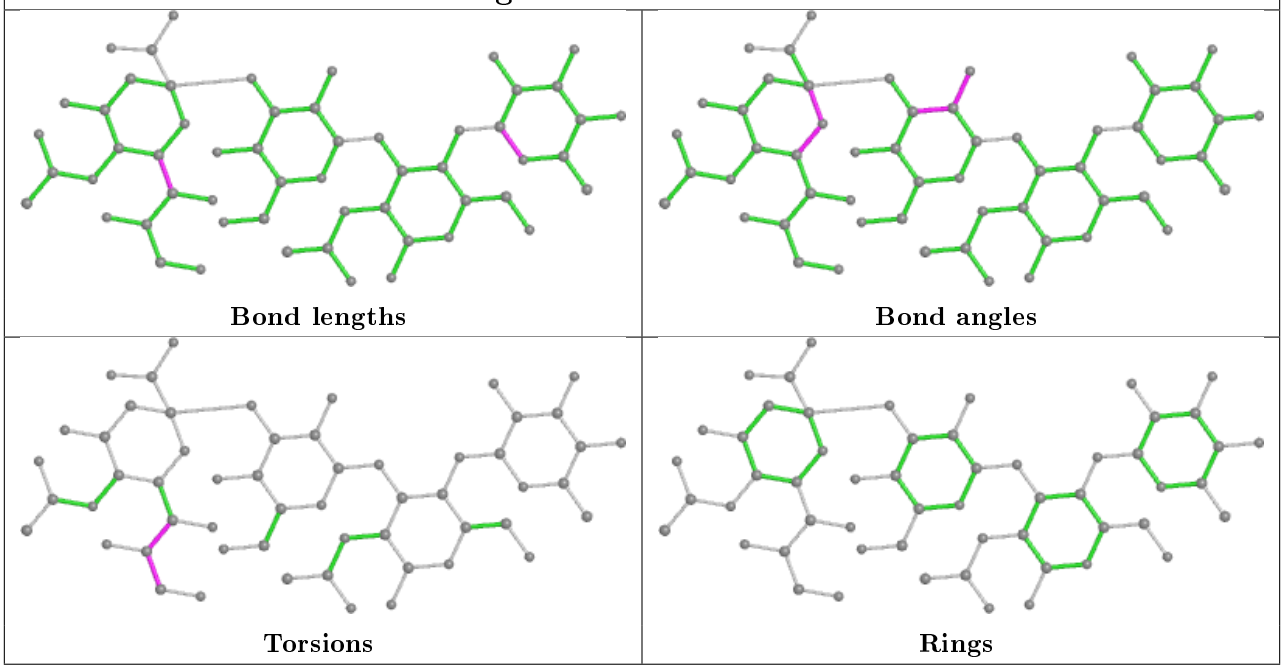


Torsions



Rings

Oligosaccharide Chain G



5.6 Ligand geometry (i)

4 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	$\#\|Z\| > 2$
4	GOL	C	305	-	5,5,5	0.99	0	5,5,5	1.01	0
4	GOL	B	302	-	5,5,5	0.93	0	5,5,5	0.94	0
4	GOL	D	301	-	5,5,5	0.83	0	5,5,5	1.20	0
4	GOL	B	301	-	5,5,5	0.83	0	5,5,5	0.88	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	GOL	C	305	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	B	302	-	-	2/4/4/4	-
4	GOL	D	301	-	-	4/4/4/4	-
4	GOL	B	301	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	301	GOL	O1-C1-C2-C3
4	C	305	GOL	C1-C2-C3-O3
4	B	302	GOL	C1-C2-C3-O3
4	D	301	GOL	C1-C2-C3-O3
4	D	301	GOL	O1-C1-C2-O2
4	C	305	GOL	O2-C2-C3-O3
4	B	302	GOL	O2-C2-C3-O3
4	B	301	GOL	O1-C1-C2-C3
4	D	301	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	301	GOL	1	0

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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.