Full wwPDB X-ray Structure Validation Report (i)

Jan 2, 2024 – 02:26 pm GMT

PDB ID	:	5HZW
Title	:	Crystal structure of the orphan region of human endoglin/CD105 in complex with BMP9
Authors	:	Bokhove, M.; Saito, T.; Jovine, L.
Deposited on	:	2016-02-03
Resolution	:	4.45 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

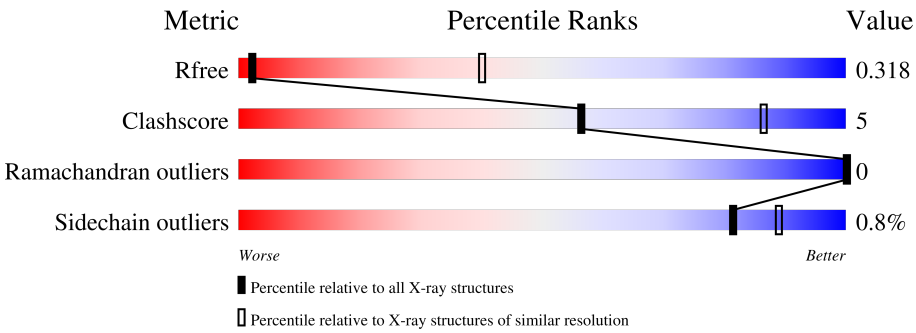
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 4.45 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	1051 (5.12-3.80)
Clashscore	141614	1119 (5.12-3.80)
Ramachandran outliers	138981	1065 (5.12-3.80)
Sidechain outliers	138945	1047 (5.12-3.80)

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%

Mol	Chain	Length	Quality of chain
1	A	691	88% 9% •
2	B	110	79% 15% • 5%
3	C	2	100%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11917 atoms, of which 5932 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 Maltose-binding periplasmic protein,Endoglin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	668	10189	3277	5077	855	964	16	0	0	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	GLU	-	expression tag	UNP P0AEX9
A	48	THR	-	expression tag	UNP P0AEX9
A	49	GLY	-	expression tag	UNP P0AEX9
A	50	HIS	-	expression tag	UNP P0AEX9
A	51	HIS	-	expression tag	UNP P0AEX9
A	52	HIS	-	expression tag	UNP P0AEX9
A	53	HIS	-	expression tag	UNP P0AEX9
A	54	HIS	-	expression tag	UNP P0AEX9
A	55	HIS	-	expression tag	UNP P0AEX9
A	57	THR	ILE	engineered mutation	UNP P0AEX9
A	137	ALA	ASP	engineered mutation	UNP P0AEX9
A	138	ALA	LYS	engineered mutation	UNP P0AEX9
A	227	ALA	GLU	engineered mutation	UNP P0AEX9
A	228	ALA	ASN	engineered mutation	UNP P0AEX9
A	270	HIS	ALA	engineered mutation	UNP P0AEX9
A	274	HIS	LYS	engineered mutation	UNP P0AEX9
A	294	ALA	LYS	engineered mutation	UNP P0AEX9
A	367	VAL	ALA	engineered mutation	UNP P0AEX9
A	372	VAL	ILE	engineered mutation	UNP P0AEX9
A	414	ALA	GLU	engineered mutation	UNP P0AEX9
A	417	ALA	LYS	engineered mutation	UNP P0AEX9
A	418	ALA	ASP	engineered mutation	UNP P0AEX9
A	422	ASN	ARG	engineered mutation	UNP P0AEX9
A	423	ALA	-	linker	UNP P0AEX9
A	424	ALA	-	linker	UNP P0AEX9
A	425	ALA	-	linker	UNP P0AEX9

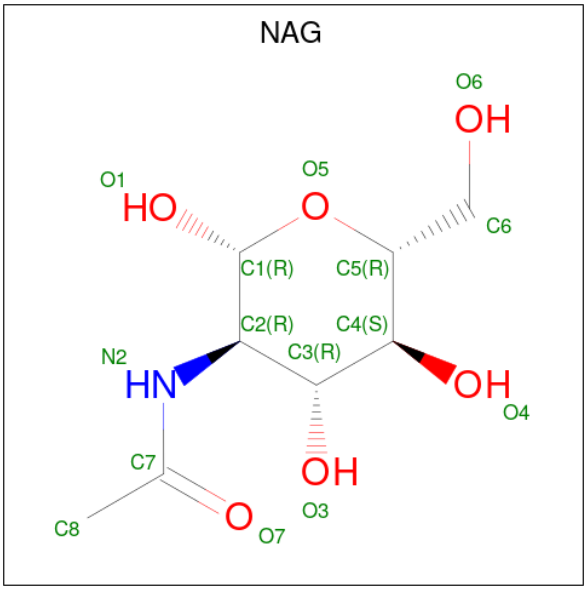
- Molecule 2 is a protein called Growth/differentiation factor 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	B	105	1627	528	805	134	151	9	0	0	0

- Molecule 3 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	H	O			
3	C	2	45	12	22	11	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



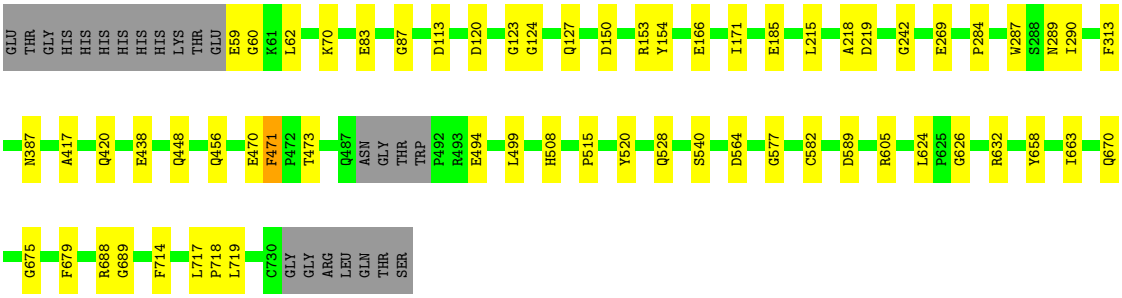
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
4	A	1	28	8	14	1	5	0	0
4	A	1	28	8	14	1	5	0	0

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.

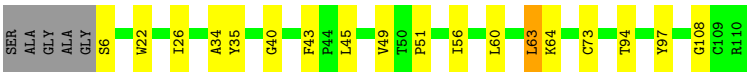
• Molecule 1: Maltose-binding periplasmic protein,Endoglin

Chain A:



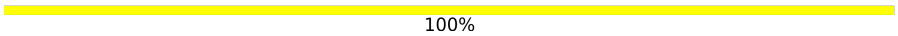
• Molecule 2: Growth/differentiation factor 2

Chain B:



• Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α, β, γ	211.25Å 211.25Å 53.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	52.81 – 4.45 52.81 – 4.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (52.81-4.45) 80.9 (52.81-4.30)	Depositor EDS
R_{merge}	0.40	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.49 (at 4.29Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.285 , 0.318 0.286 , 0.318	Depositor DCC
R_{free} test set	942 reflections (9.86%)	wwPDB-VP
Wilson B-factor (Å^2)	163.2	Xtriage
Anisotropy	0.178	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 152.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.058 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.85	EDS
Total number of atoms	11917	wwPDB-VP
Average B, all atoms (Å^2)	255.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, 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	0.27	0/5238	0.43	0/7139
2	B	0.31	0/845	0.52	0/1145
All	All	0.27	0/6083	0.44	0/8284

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 (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	5112	5077	5078	39	0
2	B	822	805	805	20	1
3	C	23	22	21	2	0
4	A	28	28	26	3	0
All	All	5985	5932	5930	59	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 5.

All (59) 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:417:ALA:O	1:A:420:GLN:HG2	1.74	0.87
2:B:60:LEU:O	2:B:63:LEU:HG	1.77	0.83
1:A:688:ARG:NH1	1:A:689:GLY:O	2.16	0.79
1:A:540:SER:HB3	4:A:802:NAG:H61	1.68	0.74
2:B:6:SER:O	2:B:40:GLY:N	2.21	0.73
1:A:456:GLN:NE2	1:A:577:GLY:O	2.23	0.72
1:A:473:THR:HG23	1:A:473:THR:O	1.88	0.71
2:B:45:LEU:HD12	2:B:56:ILE:HG12	1.75	0.69
2:B:45:LEU:HD13	2:B:51:PRO:CB	2.23	0.68
2:B:45:LEU:CB	2:B:51:PRO:HG3	2.24	0.68
1:A:626:GLY:HA3	1:A:719:LEU:HD11	1.78	0.66
1:A:589:ASP:OD2	1:A:632:ARG:NH2	2.32	0.62
2:B:63:LEU:HD12	2:B:64:LYS:N	2.16	0.60
2:B:43:PHE:CE2	2:B:63:LEU:HD23	2.38	0.59
2:B:49:VAL:HG13	2:B:108:GLY:HA2	1.83	0.59
1:A:150:ASP:OD1	1:A:153:ARG:NH2	2.37	0.57
1:A:83:GLU:O	1:A:87:GLY:N	2.36	0.57
2:B:45:LEU:HB3	2:B:51:PRO:HG3	1.87	0.57
2:B:45:LEU:HB2	2:B:51:PRO:HG3	1.85	0.56
1:A:499:LEU:HD11	1:A:520:TYR:HB2	1.88	0.56
2:B:22:TRP:HB3	2:B:26:ILE:HD12	1.89	0.55
1:A:171:ILE:HG21	1:A:290:ILE:CD1	2.37	0.55
2:B:45:LEU:HD12	2:B:56:ILE:CG1	2.37	0.54
1:A:166:GLU:OE1	3:C:1:GLC:O2	2.22	0.54
1:A:508:HIS:ND1	1:A:528:GLN:OE1	2.38	0.53
1:A:624:LEU:N	1:A:717:LEU:O	2.41	0.51
1:A:540:SER:CB	4:A:802:NAG:H61	2.41	0.51
1:A:448:GLN:HG3	1:A:718:PRO:HB2	1.93	0.50
1:A:123:GLY:HA3	1:A:387:ASN:O	2.12	0.50
1:A:269:GLU:OE2	1:A:289:ASN:ND2	2.27	0.50
1:A:215:LEU:O	1:A:218:ALA:N	2.45	0.49
1:A:626:GLY:HA3	1:A:719:LEU:CD1	2.42	0.48
2:B:45:LEU:HD13	2:B:51:PRO:HB3	1.94	0.47
1:A:470:GLU:O	1:A:564:ASP:N	2.40	0.47
4:A:802:NAG:O7	4:A:802:NAG:O3	2.29	0.47
1:A:215:LEU:O	1:A:218:ALA:HB3	2.14	0.47
2:B:45:LEU:HD13	2:B:51:PRO:HB2	1.96	0.47
1:A:675:GLY:O	1:A:689:GLY:N	2.42	0.46
1:A:605:ARG:O	1:A:714:PHE:N	2.51	0.44
2:B:34:ALA:O	2:B:35:TYR:C	2.56	0.44
2:B:22:TRP:CE3	2:B:26:ILE:CD1	3.01	0.44
2:B:43:PHE:CZ	2:B:63:LEU:HD22	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:LEU:HD23	1:A:113:ASP:OD2	2.18	0.43
1:A:70:LYS:NZ	1:A:166:GLU:OE2	2.51	0.42
2:B:43:PHE:CZ	2:B:63:LEU:CD2	3.02	0.42
1:A:494:GLU:HA	1:A:515:PRO:HG2	2.01	0.42
1:A:626:GLY:HA3	1:A:658:TYR:OH	2.18	0.42
1:A:219:ASP:O	1:A:242:GLY:HA3	2.19	0.42
2:B:63:LEU:HD12	2:B:64:LYS:HG2	2.01	0.42
1:A:124:GLY:O	1:A:127:GLN:HB3	2.20	0.42
1:A:471:PHE:CD1	1:A:471:PHE:N	2.88	0.41
1:A:284:PRO:HA	1:A:287:TRP:CE2	2.56	0.41
1:A:120:ASP:OD2	3:C:2:GLC:O3	2.33	0.41
1:A:670:GLN:OE1	2:B:94:THR:HG23	2.20	0.41
1:A:127:GLN:OE1	1:A:154:TYR:OH	2.31	0.40
1:A:59:GLU:HG2	1:A:60:GLY:N	2.37	0.40
1:A:438:GLU:OE1	1:A:438:GLU:N	2.48	0.40
1:A:663:ILE:HB	1:A:679:PHE:CD2	2.55	0.40
1:A:185:GLU:OE1	1:A:185:GLU:N	2.50	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)
2:B:73:CYS:SG	2:B:73:CYS:SG[4_545]	2.03	0.17

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	664/691 (96%)	641 (96%)	23 (4%)	0	100	100
2	B	103/110 (94%)	100 (97%)	3 (3%)	0	100	100
All	All	767/801 (96%)	741 (97%)	26 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	541/560 (97%)	538 (99%)	3 (1%)	86	92
2	B	92/93 (99%)	90 (98%)	2 (2%)	52	71
All	All	633/653 (97%)	628 (99%)	5 (1%)	81	89

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	313	PHE
1	A	471	PHE
1	A	582	CYS
2	B	63	LEU
2	B	97	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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	$\#\|Z\| > 2$
3	GLC	C	1	3	12,12,12	0.54	0	17,17,17	0.45	0
3	GLC	C	2	3	11,11,12	0.65	0	15,15,17	0.62	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	GLC	C	1	3	-	0/2/22/22	0/1/1/1
3	GLC	C	2	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

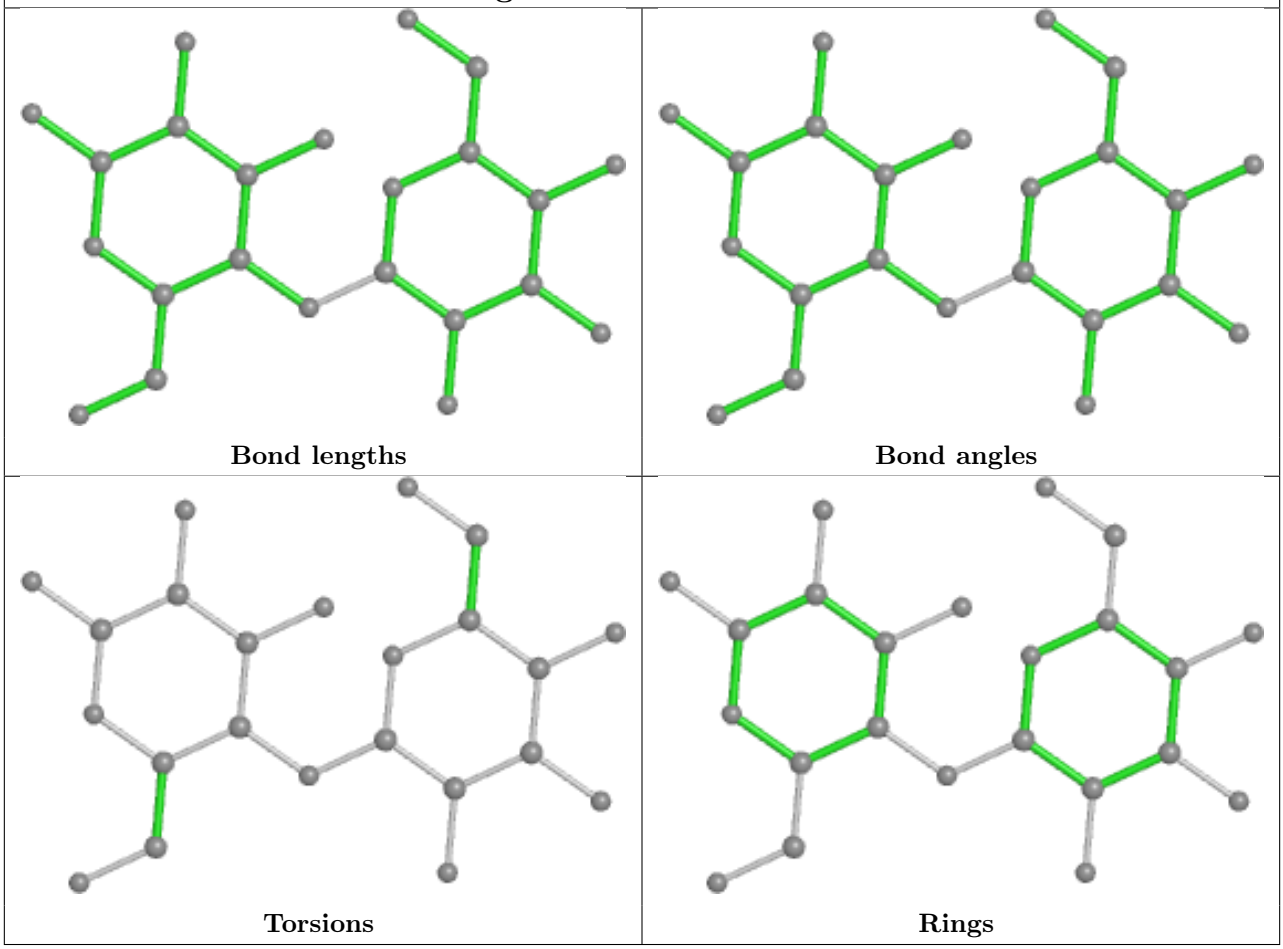
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2	GLC	1	0
3	C	1	GLC	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 C



5.6 Ligand geometry (i)

2 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	NAG	A	802	1	14,14,15	0.88	1 (7%)	17,19,21	0.64	0
4	NAG	A	801	1	14,14,15	0.35	0	17,19,21	0.37	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	NAG	A	802	1	-	2/6/23/26	0/1/1/1
4	NAG	A	801	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	802	NAG	O5-C1	-2.82	1.39	1.43

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	802	NAG	C1-C2-N2-C7
4	A	802	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	802	NAG	3	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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

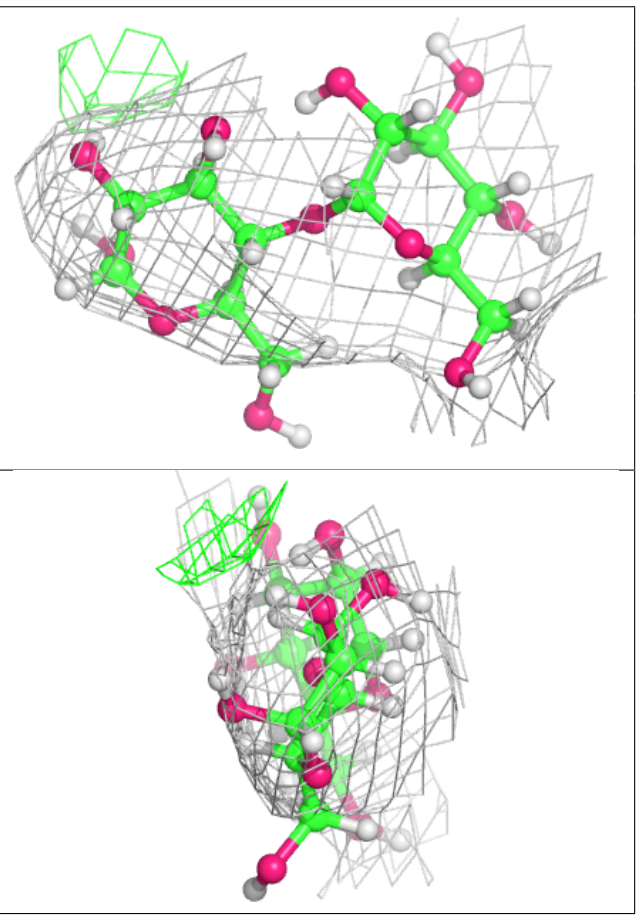
6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Electron density around Chain C:

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



6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.