



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 5, 2023 – 02:10 PM EST

PDB ID : 6BJR
Title : Crystal structure of prothrombin mutant S101C/A470C
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Deposited on : 2017-11-06
Resolution : 6.00 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 : 1.8.5 (274361), 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

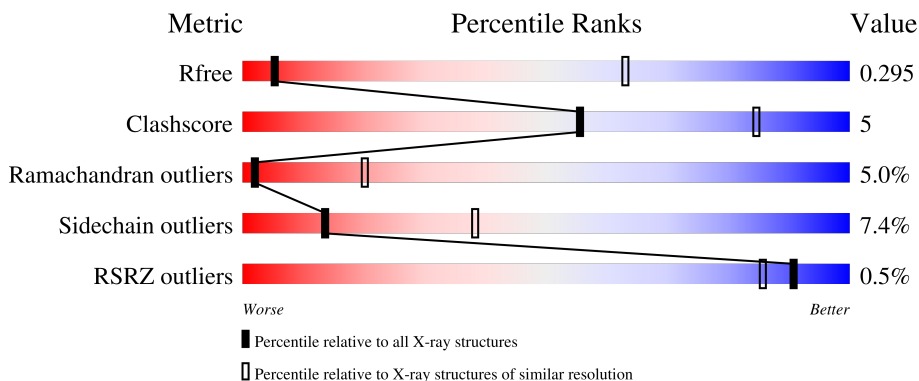
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


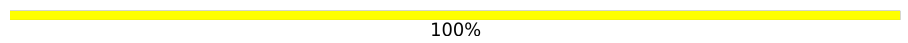
The reported resolution of this entry is 6.00 Å.

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	1000 (8.00-3.88)
Clashscore	141614	1049 (8.00-3.90)
Ramachandran outliers	138981	1016 (8.00-3.86)
Sidechain outliers	138945	1017 (8.00-3.82)
RSRZ outliers	127900	1015 (8.20-3.78)

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	582	 76% 21% ..
2	B	2	 100%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4639 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 Prothrombin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	575	4594	2861	801	897	35	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	101	CYS	SER	engineered mutation	UNP P00734
A	122	MET	THR	conflict	UNP P00734
A	470	CYS	ALA	engineered mutation	UNP P00734
A	580	TYR	-	expression tag	UNP P00734
A	581	LEU	-	expression tag	UNP P00734
A	582	GLU	-	expression tag	UNP P00734

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

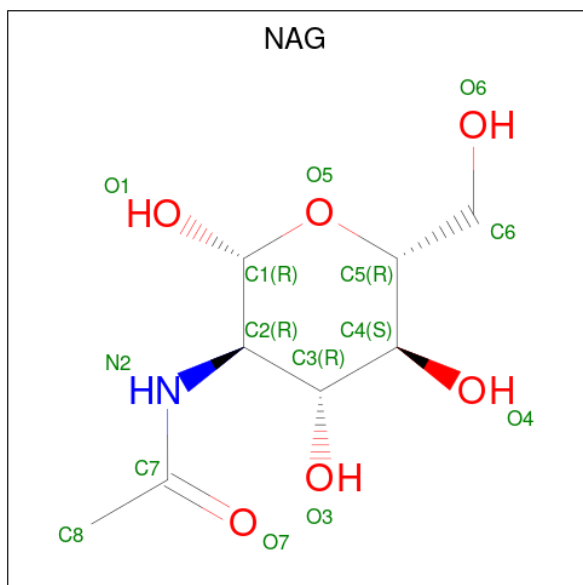


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	2	25	14	1	10	0	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	6	6	6	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).

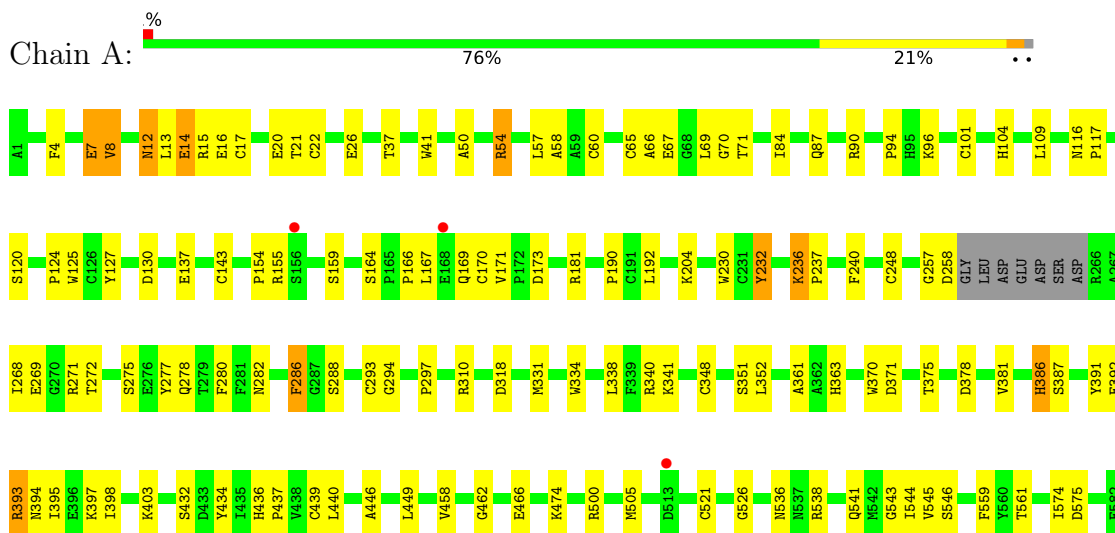


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	14	8	1	5	0	0

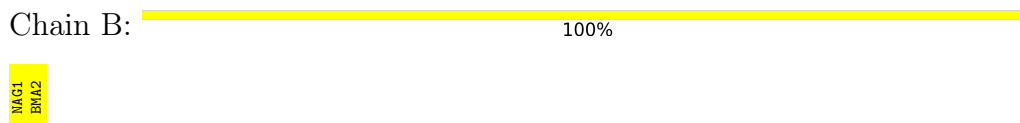
3 Residue-property plots [i](#)

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 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: Prothrombin



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



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	114.13Å 124.17Å 157.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 6.00 40.59 – 5.91	Depositor EDS
% Data completeness (in resolution range)	84.3 (40.00-6.00) 84.7 (40.59-5.91)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 5.72Å)	Xtrriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.237 , 0.293 0.247 , 0.295	Depositor DCC
R_{free} test set	137 reflections (5.22%)	wwPDB-VP
Wilson B-factor (Å ²)	219.3	Xtrriage
Anisotropy	0.056	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.18 , 160.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.34$, $\langle L^2 \rangle = 0.16$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4639	wwPDB-VP
Average B, all atoms (Å ²)	232.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, MG, CGU

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	0.49	0/4576	0.72	0/6190

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	4594	0	4330	46	0
2	B	25	0	22	0	0
3	A	6	0	0	0	0
4	A	14	0	13	0	0
All	All	4639	0	4365	46	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 5.

All (46) 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:170:CYS:SG	1:A:171:VAL:N	2.67	0.67
1:A:458:VAL:HG13	1:A:545:VAL:HG21	1.82	0.62
1:A:170:CYS:SG	1:A:248:CYS:N	2.73	0.61
1:A:116:ASN:HD21	1:A:120:SER:HB3	1.73	0.52
1:A:361:ALA:HB2	1:A:544:ILE:HG21	1.92	0.52
1:A:361:ALA:HB3	1:A:363:HIS:CE1	2.45	0.52
1:A:87:GLN:N	1:A:127:TYR:O	2.43	0.51
1:A:439:CYS:SG	1:A:538:ARG:NH1	2.77	0.51
1:A:391:TYR:CE2	1:A:393:ARG:HA	2.46	0.50
1:A:395:ILE:HG22	1:A:434:TYR:CE2	2.47	0.50
1:A:60:CYS:HA	1:A:65:CYS:SG	2.53	0.48
1:A:338:LEU:HD12	1:A:381:VAL:HG12	1.95	0.47
1:A:386:HIS:CG	1:A:387:SER:N	2.83	0.47
1:A:125:TRP:HA	1:A:137:GLU:HA	1.97	0.47
1:A:334:TRP:HB2	1:A:352:LEU:HB3	1.97	0.46
1:A:124:PRO:O	1:A:137:GLU:HA	2.15	0.46
1:A:230:TRP:CE3	1:A:240:PHE:CD2	3.03	0.46
1:A:54:ARG:HA	1:A:57:LEU:HB3	1.97	0.46
1:A:96:LYS:HB2	1:A:370:TRP:CE2	2.51	0.46
1:A:125:TRP:CD1	1:A:125:TRP:N	2.84	0.45
1:A:505:MET:SD	1:A:561:THR:HG23	2.57	0.45
1:A:334:TRP:HA	1:A:352:LEU:HD23	1.99	0.44
1:A:338:LEU:HD23	1:A:348:CYS:HB2	1.99	0.44
1:A:395:ILE:HG22	1:A:434:TYR:CZ	2.52	0.44
1:A:446:ALA:HA	1:A:449:LEU:HD12	2.00	0.43
1:A:541:GLN:NE2	1:A:543:GLY:O	2.51	0.43
1:A:286:PHE:HB2	1:A:574:ILE:HG21	2.00	0.43
1:A:392:GLU:O	1:A:394:ASN:N	2.52	0.43
1:A:67:GLU:N	1:A:143:CYS:SG	2.92	0.42
1:A:282:ASN:O	1:A:286:PHE:HB3	2.20	0.42
1:A:297:PRO:HD3	1:A:436:HIS:CG	2.54	0.41
1:A:391:TYR:CZ	1:A:393:ARG:HA	2.55	0.41
1:A:397:LYS:O	1:A:398:ILE:HD13	2.20	0.41
1:A:84:ILE:HD13	1:A:130:ASP:HB2	2.03	0.41
1:A:66:ALA:HB1	1:A:69:LEU:O	2.20	0.41
1:A:334:TRP:HB3	1:A:437:PRO:HA	2.03	0.41
1:A:4:PHE:O	1:A:8:VAL:HG23	2.19	0.41
1:A:7:CGU:O	1:A:8:VAL:C	2.59	0.41
1:A:293:CYS:SG	1:A:538:ARG:NH1	2.94	0.41
1:A:462:GLY:O	1:A:466:GLU:N	2.52	0.41
1:A:526:GLY:N	1:A:545:VAL:O	2.50	0.41
1:A:192:LEU:HD12	1:A:232:TYR:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:LEU:C	1:A:15:ARG:N	2.72	0.40
1:A:14:CGU:CD1	1:A:14:CGU:O	2.70	0.40
1:A:109:LEU:HD11	1:A:117:PRO:HG3	2.03	0.40
1:A:278:GLN:HG3	1:A:280:PHE:HB2	2.03	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	561/582 (96%)	435 (78%)	98 (18%)	28 (5%)	2 20

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	164	SER
1	A	237	PRO
1	A	272	THR
1	A	474	LYS
1	A	521	CYS
1	A	37	THR
1	A	50	ALA
1	A	318	ASP
1	A	393	ARG
1	A	12	ASN
1	A	58	ALA
1	A	90	ARG
1	A	371	ASP
1	A	94	PRO
1	A	155	ARG
1	A	166	PRO
1	A	169	GLN

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Mol	Chain	Res	Type
1	A	8	VAL
1	A	159	SER
1	A	236	LYS
1	A	294	GLY
1	A	341	LYS
1	A	375	THR
1	A	275	SER
1	A	154	PRO
1	A	70	GLY
1	A	190	PRO
1	A	257	GLY

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	484/490 (99%)	448 (93%)	36 (7%)	13 38

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ASN
1	A	17	CYS
1	A	21	THR
1	A	22	CYS
1	A	41	TRP
1	A	54	ARG
1	A	71	THR
1	A	101	CYS
1	A	104	HIS
1	A	167	LEU
1	A	173	ASP
1	A	181	ARG
1	A	204	LYS
1	A	232	TYR
1	A	236	LYS

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Mol	Chain	Res	Type
1	A	258	ASP
1	A	268	ILE
1	A	269	GLU
1	A	271	ARG
1	A	277	TYR
1	A	286	PHE
1	A	288	SER
1	A	310	ARG
1	A	331	MET
1	A	340	ARG
1	A	351	SER
1	A	378	ASP
1	A	386	HIS
1	A	403	LYS
1	A	432	SER
1	A	440	LEU
1	A	500	ARG
1	A	536	ASN
1	A	546	SER
1	A	559	PHE
1	A	575	ASP

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](#)

10 non-standard protein/DNA/RNA residues 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
1	CGU	A	14	1,3	9,11,12	1.55	1 (11%)	9,14,16	0.99	1 (11%)
1	CGU	A	32	1,3	9,11,12	1.08	0	9,14,16	1.10	0
1	CGU	A	19	1,3	9,11,12	1.18	0	9,14,16	0.87	0
1	CGU	A	20	1,3	9,11,12	1.05	0	9,14,16	1.51	1 (11%)
1	CGU	A	16	1,3	9,11,12	1.27	1 (11%)	9,14,16	1.93	3 (33%)
1	CGU	A	29	1,3	9,11,12	1.14	0	9,14,16	0.88	0
1	CGU	A	6	1	9,11,12	1.00	0	9,14,16	0.61	0
1	CGU	A	26	1,3	9,11,12	1.18	0	9,14,16	1.26	1 (11%)
1	CGU	A	25	1,3	9,11,12	1.08	0	9,14,16	0.46	0
1	CGU	A	7	1	9,11,12	1.08	0	9,14,16	1.06	1 (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
1	CGU	A	14	1,3	-	0/13/14/16	-
1	CGU	A	32	1,3	-	2/13/14/16	-
1	CGU	A	19	1,3	-	1/13/14/16	-
1	CGU	A	20	1,3	-	4/13/14/16	-
1	CGU	A	16	1,3	-	4/13/14/16	-
1	CGU	A	29	1,3	-	4/13/14/16	-
1	CGU	A	6	1	-	0/13/14/16	-
1	CGU	A	26	1,3	-	4/13/14/16	-
1	CGU	A	25	1,3	-	0/13/14/16	-
1	CGU	A	7	1	-	3/13/14/16	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	14	CGU	CG-CD1	-2.46	1.49	1.52
1	A	16	CGU	CA-N	2.01	1.54	1.48

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	16	CGU	CB-CG-CD2	4.11	121.47	113.11
1	A	20	CGU	CB-CG-CD1	-3.89	105.21	113.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	16	CGU	CB-CG-CD1	2.78	118.76	113.11
1	A	7	CGU	CB-CG-CD2	-2.71	107.60	113.11
1	A	26	CGU	CB-CA-N	2.38	115.61	110.32
1	A	16	CGU	CB-CA-N	2.37	115.60	110.32
1	A	14	CGU	CB-CA-N	2.18	115.19	110.32

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	7	CGU	C-CA-CB-CG
1	A	16	CGU	C-CA-CB-CG
1	A	16	CGU	CA-CB-CG-CD2
1	A	19	CGU	N-CA-CB-CG
1	A	29	CGU	C-CA-CB-CG
1	A	32	CGU	N-CA-CB-CG
1	A	32	CGU	C-CA-CB-CG
1	A	7	CGU	OE21-CD2-CG-CB
1	A	7	CGU	OE22-CD2-CG-CB
1	A	16	CGU	N-CA-CB-CG
1	A	20	CGU	OE21-CD2-CG-CB
1	A	20	CGU	OE22-CD2-CG-CB
1	A	26	CGU	OE21-CD2-CG-CB
1	A	26	CGU	OE22-CD2-CG-CB
1	A	29	CGU	OE11-CD1-CG-CB
1	A	26	CGU	CA-CB-CG-CD1
1	A	29	CGU	N-CA-CB-CG
1	A	29	CGU	OE12-CD1-CG-CB
1	A	16	CGU	OE11-CD1-CG-CD2
1	A	20	CGU	OE11-CD1-CG-CD2
1	A	20	CGU	OE12-CD1-CG-CD2
1	A	26	CGU	OE11-CD1-CG-CD2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	14	CGU	1	0
1	A	7	CGU	1	0

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
2	NAG	B	1	2,1	14,14,15	0.50	0	17,19,21	1.60	2 (11%)
2	BMA	B	2	2	11,11,12	0.39	0	15,15,17	1.17	2 (13%)

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	NAG	B	1	2,1	-	2/6/23/26	0/1/1/1
2	BMA	B	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	NAG	C4-C3-C2	4.71	117.93	111.02
2	B	2	BMA	C1-C2-C3	2.93	113.26	109.67
2	B	2	BMA	C1-O5-C5	2.93	116.16	112.19
2	B	1	NAG	C1-C2-N2	-2.32	106.52	110.49

There are no chirality outliers.

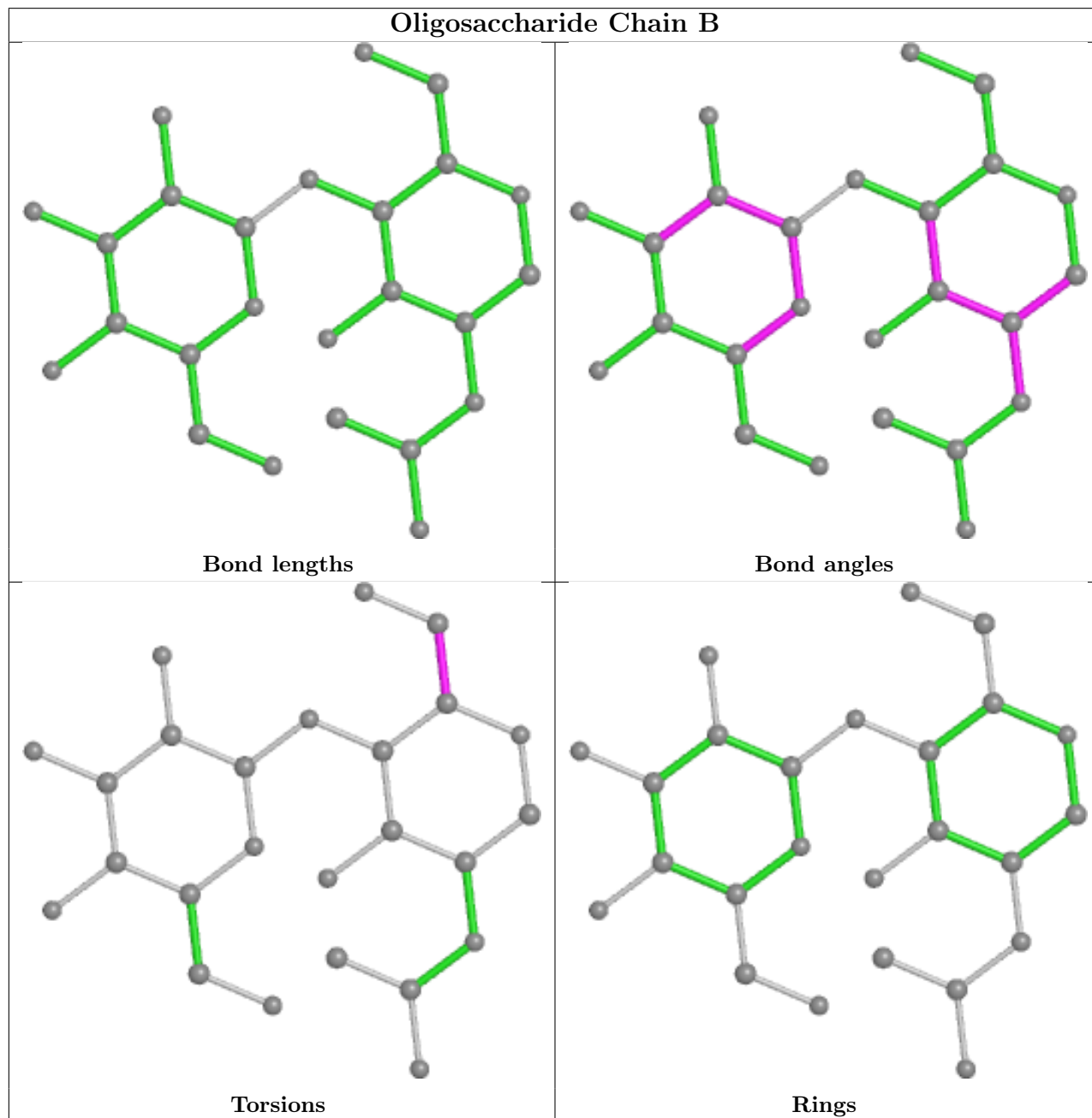
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1	NAG	O5-C5-C6-O6
2	B	1	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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



5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	609	1	14,14,15	0.65	0	17,19,21	1.19	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	609	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	609	NAG	O5-C5-C6	2.65	111.36	107.20
4	A	609	NAG	C1-O5-C5	2.03	114.94	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	609	NAG	O5-C5-C6-O6
4	A	609	NAG	C4-C5-C6-O6
4	A	609	NAG	C1-C2-N2-C7
4	A	609	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	565/582 (97%)	-0.49	3 (0%) 91 86	156, 240, 240, 240	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	513	ASP	3.3
1	A	168	GLU	2.4
1	A	156	SER	2.3

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

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

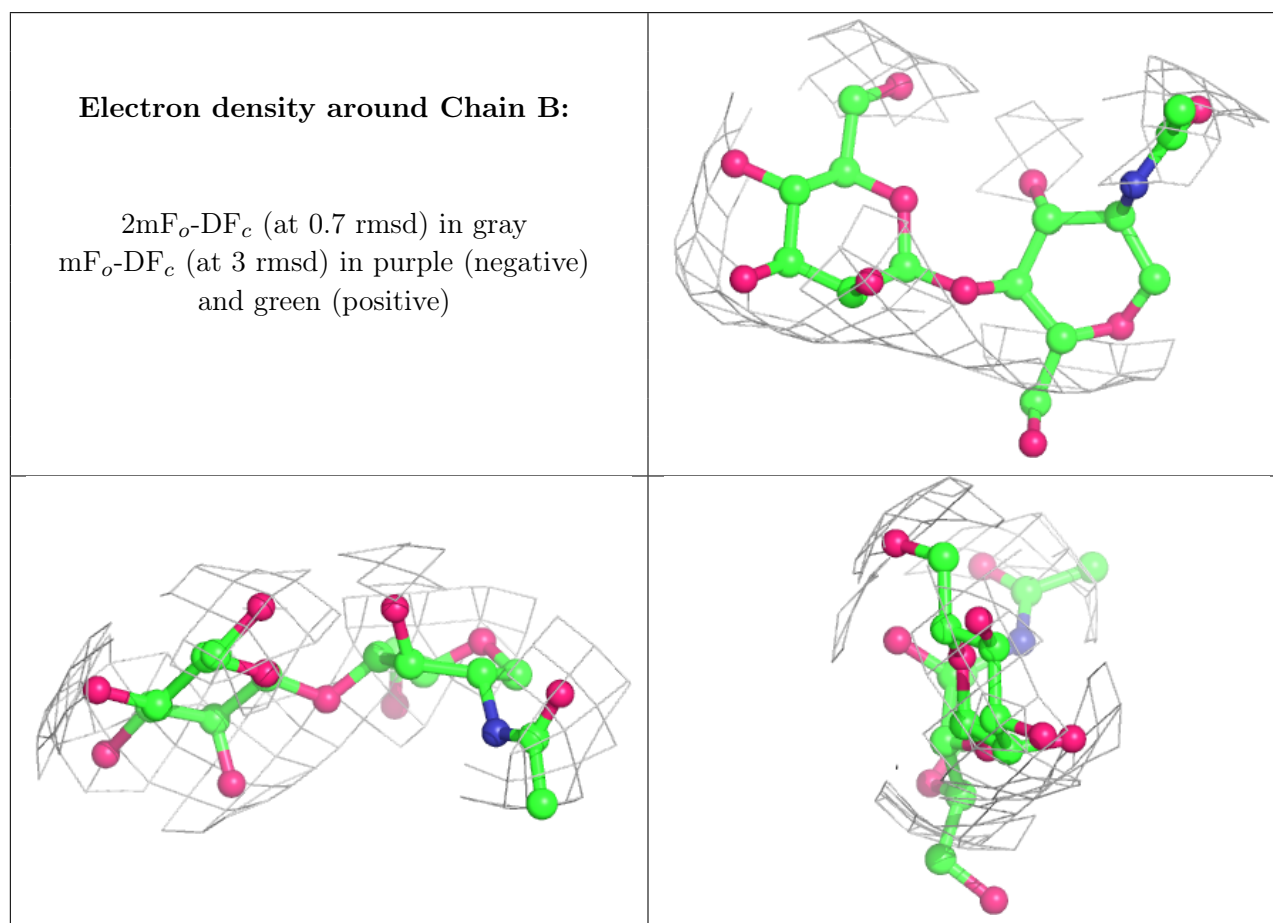
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	CGU	A	32	12/13	0.92	0.33	240,240,240,240	0
1	CGU	A	29	12/13	0.94	0.12	221,233,240,240	0
1	CGU	A	6	12/13	0.94	0.16	220,232,240,240	0
1	CGU	A	26	12/13	0.95	0.08	179,188,202,203	0
1	CGU	A	25	12/13	0.96	0.14	204,240,240,240	0
1	CGU	A	7	12/13	0.97	0.09	193,213,224,231	0
1	CGU	A	16	12/13	0.97	0.09	216,240,240,240	0
1	CGU	A	19	12/13	0.98	0.11	174,193,217,220	0
1	CGU	A	20	12/13	0.98	0.08	240,240,240,240	0
1	CGU	A	14	12/13	0.99	0.10	157,162,181,181	0

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BMA	B	2	11/12	0.91	0.23	224,228,234,240	0
2	NAG	B	1	14/15	0.96	0.19	197,202,208,217	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(\AA^2)	Q<0.9
4	NAG	A	609	14/15	0.86	0.28	208,238,240,240	0
3	MG	A	601	1/1	0.94	0.28	100,100,100,100	0
3	MG	A	604	1/1	0.97	0.06	165,165,165,165	0
3	MG	A	602	1/1	0.97	0.27	155,155,155,155	0
3	MG	A	606	1/1	0.98	0.08	118,118,118,118	0
3	MG	A	603	1/1	0.98	0.12	157,157,157,157	0
3	MG	A	605	1/1	0.99	0.03	171,171,171,171	0

6.5 Other polymers [i](#)

There are no such residues in this entry.