



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 6, 2021 – 08:07 PM JST

PDB ID : 7E3G  
Title : Crystal structure of Trypanosoma brucei cathepsin B R91C/T223C mutant in the living cell  
Authors : Abe, S.; Pham, T.T.; Negishi, H.; Yamashita, K.; Hirata, K.; Ueno, T.  
Deposited on : 2021-02-08  
Resolution : 3.86 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](mailto: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.

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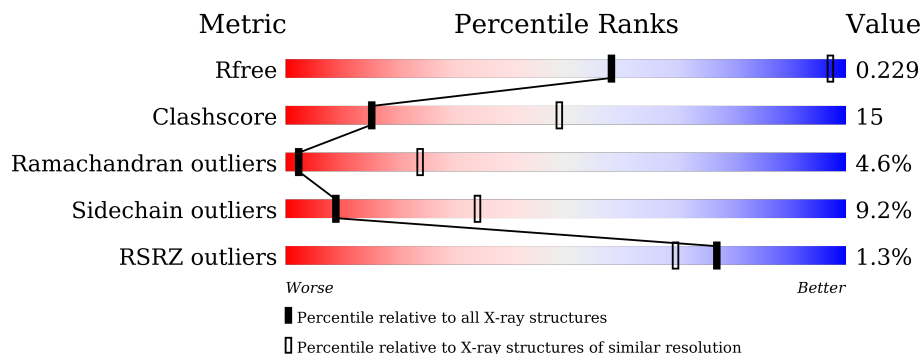
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.24  
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) : 2.24

i

## X-RAY DIFFRACTION

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.



<b>Metric</b>	<b>Whole archive (#Entries)</b>	<b>Similar resolution (#Entries, resolution range(Å))</b>
R <sub>free</sub>	130704	1048 (4.10-3.62)
Clashscore	141614	1015 (4.08-3.64)
Ramachandran outliers	138981	1069 (4.10-3.62)
Sidechain outliers	138945	1062 (4.10-3.62)
RSRZ outliers	127900	1206 (4.12-3.60)

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  $\geq 3$ , 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	340	<div> <div></div> <div>56%</div> <div>31%</div> <div>9%</div> </div>
2	B	2	<div> <div></div> <div>100%</div> </div>
3	C	3	<div> <div></div> <div>100%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	B	2	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2447 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 Cysteine peptidase C (CPC).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	308	Total	C	N	O	S	0	0	0
			2377	1496	409	453	19			

There are 2 discrepancies between the modelled and reference sequences:

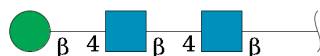
Chain	Residue	Modelled	Actual	Comment	Reference
A	91	CYS	ARG	engineered mutation	UNP D6XHE1
A	223	CYS	THR	engineered mutation	UNP D6XHE1

- Molecule 2 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
2	B	2	Total	C	N	O		0	0	0
			28	16	2	10				

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



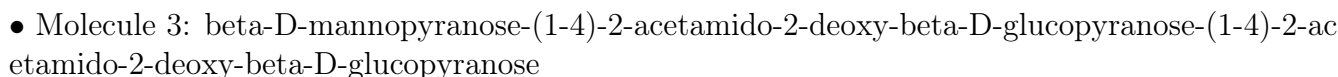
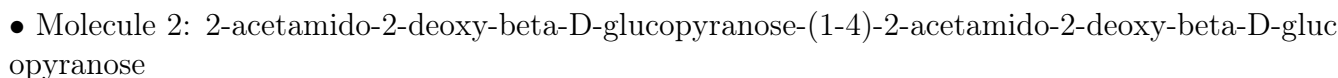
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	3	Total	C	N	O		0	0	0
			39	22	2	15				

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total 3	O 3	0	0



- Molecule 1: Cysteine peptidase C (CPC)



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	124.08Å 124.08Å 52.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.76 – 3.86 48.71 – 3.86	Depositor EDS
% Data completeness (in resolution range)	96.8 (48.76-3.86) 96.8 (48.71-3.86)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.65 (at 3.88Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.177 , 0.214 0.186 , 0.229	Depositor DCC
$R_{free}$ test set	204 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	76.5	Xtriage
Anisotropy	0.006	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 77.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	2447	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: BMA, 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	0.67	0/2449	0.86	0/3333

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	A	2377	0	2185	70	0
2	B	28	0	25	0	0
3	C	39	0	34	0	0
4	A	3	0	0	0	0
All	All	2447	0	2244	70	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 15.

All (70) 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:228:ASN:HD22	1:A:230:ARG:HH21	1.33	0.75
1:A:44:ASN:ND2	1:A:48:TRP:O	2.22	0.72
1:A:185:GLN:NE2	1:A:216:ASN:HB2	2.10	0.66
1:A:30:PRO:HA	1:A:59:ILE:O	1.96	0.65
1:A:63:GLU:O	1:A:66:ARG:HB3	1.96	0.65
1:A:28:ASP:HA	1:A:60:THR:CG2	2.28	0.63
1:A:109:THR:HA	1:A:112:GLN:HE21	1.63	0.62
1:A:183:TYR:CZ	1:A:224:ILE:HD11	2.36	0.61
1:A:109:THR:HA	1:A:112:GLN:NE2	2.16	0.60
1:A:325:ILE:HG23	1:A:326:GLU:HG3	1.84	0.60
1:A:282:HIS:HE1	1:A:302:ASN:OD1	1.85	0.59
1:A:66:ARG:NH1	1:A:210:PHE:O	2.36	0.58
1:A:183:TYR:CE2	1:A:224:ILE:HD13	2.39	0.57
1:A:45:ARG:HH11	1:A:45:ARG:HB3	1.70	0.57
1:A:183:TYR:CE2	1:A:224:ILE:CD1	2.88	0.56
1:A:237:LEU:HD21	1:A:246:GLU:HB2	1.87	0.55
1:A:28:ASP:HA	1:A:60:THR:HG23	1.89	0.55
1:A:166:ASP:HB3	1:A:169:ARG:HG3	1.90	0.54
1:A:115:ASP:O	1:A:117:SER:N	2.40	0.53
1:A:232:TRP:CD2	1:A:233:THR:HG22	2.44	0.53
1:A:85:PHE:CE1	1:A:245:ARG:HB3	2.45	0.52
1:A:110:ILE:HB	1:A:111:PRO:HD3	1.92	0.52
1:A:37:VAL:HG21	1:A:52:TYR:HA	1.90	0.52
1:A:71:ILE:O	1:A:71:ILE:HG13	2.10	0.52
1:A:261:GLU:HB2	1:A:276:GLY:HA3	1.92	0.51
1:A:45:ARG:O	1:A:47:ILE:N	2.43	0.51
1:A:79:ILE:HD13	1:A:169:ARG:HD3	1.92	0.51
1:A:237:LEU:HD13	1:A:253:PHE:CE2	2.46	0.51
1:A:298:TRP:CD2	1:A:318:ARG:HD3	2.46	0.50
1:A:228:ASN:ND2	1:A:230:ARG:HH21	2.06	0.50
1:A:53:ASP:HA	1:A:57:GLN:OE1	2.12	0.49
1:A:243:TYR:CE2	1:A:326:GLU:HA	2.47	0.49
1:A:228:ASN:HD22	1:A:230:ARG:NH2	2.07	0.48
1:A:123:TRP:O	1:A:254:GLU:OE1	2.31	0.48
1:A:176:SER:OG	1:A:177:THR:N	2.46	0.48
1:A:241:ASP:O	1:A:244:MET:N	2.45	0.47
1:A:34:LYS:HG3	1:A:52:TYR:CD2	2.50	0.46
1:A:62:ARG:HB3	1:A:62:ARG:CZ	2.44	0.46
1:A:132:SER:OG	1:A:145:HIS:HA	2.15	0.46
1:A:237:LEU:CD2	1:A:246:GLU:HB2	2.45	0.46
1:A:79:ILE:CD1	1:A:169:ARG:HD3	2.45	0.46
1:A:266:TYR:CD2	1:A:271:TYR:HB2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:TYR:CE2	1:A:224:ILE:HD11	2.51	0.46
1:A:48:TRP:CZ3	1:A:50:ALA:HB2	2.52	0.45
1:A:59:ILE:HG21	1:A:264:ILE:HG21	1.98	0.45
1:A:31:VAL:CG2	1:A:61:LEU:HA	2.47	0.44
1:A:79:ILE:HD11	1:A:169:ARG:HA	1.99	0.43
1:A:155:CYS:HB2	1:A:173:TYR:CD2	2.53	0.43
1:A:126:ALA:HB3	1:A:254:GLU:OE1	2.19	0.43
1:A:187:TYR:HA	1:A:188:PRO:HD3	1.87	0.43
1:A:110:ILE:HD13	1:A:133:ASP:HB3	2.00	0.43
1:A:153:ALA:HB2	1:A:213:PRO:HG2	2.00	0.43
1:A:266:TYR:OH	1:A:310:MET:CE	2.67	0.43
1:A:144:VAL:O	1:A:144:VAL:HG13	2.18	0.43
1:A:219:CYS:SG	1:A:224:ILE:HG22	2.59	0.42
1:A:194:HIS:NE2	1:A:205:CYS:HB2	2.35	0.42
1:A:167:PRO:O	1:A:168:ASP:C	2.58	0.42
1:A:166:ASP:HB3	1:A:169:ARG:CG	2.48	0.41
1:A:95:PRO:HB2	1:A:97:SER:O	2.21	0.41
1:A:44:ASN:OD1	1:A:46:GLY:N	2.54	0.41
1:A:297:TYR:CD1	1:A:315:LEU:HG	2.55	0.41
1:A:44:ASN:OD1	1:A:44:ASN:C	2.60	0.41
1:A:185:GLN:HE21	1:A:216:ASN:HB2	1.85	0.41
1:A:56:MET:O	1:A:57:GLN:C	2.59	0.40
1:A:57:GLN:HG2	1:A:58:ASN:OD1	2.21	0.40
1:A:251:GLY:O	1:A:252:PRO:C	2.58	0.40
1:A:260:TYR:O	1:A:261:GLU:C	2.58	0.40
1:A:89:GLU:O	1:A:245:ARG:NH1	2.54	0.40
1:A:194:HIS:CD2	1:A:205:CYS:HB2	2.57	0.40
1:A:232:TRP:CE3	1:A:233:THR:HG22	2.56	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	304/340 (89%)	257 (84%)	33 (11%)	14 (5%)	2	24

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	117	SER
1	A	196	SER
1	A	46	GLY
1	A	116	GLN
1	A	142	GLN
1	A	161	GLY
1	A	323	CYS
1	A	54	GLY
1	A	176	SER
1	A	240	GLU
1	A	93	PRO
1	A	95	PRO
1	A	261	GLU

### 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	250/276 (91%)	227 (91%)	23 (9%)	9	34

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	SER
1	A	39	ARG
1	A	43	LEU
1	A	45	ARG
1	A	55	VAL
1	A	68	ASN
1	A	72	LYS

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Mol	Chain	Res	Type
1	A	78	SER
1	A	109	THR
1	A	135	PHE
1	A	156	SER
1	A	179	LEU
1	A	182	ASP
1	A	193	SER
1	A	195	HIS
1	A	197	LYS
1	A	233	THR
1	A	238	GLN
1	A	277	GLN
1	A	292	SER
1	A	303	SER
1	A	315	LEU
1	A	338	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	112	GLN
1	A	207	GLN
1	A	228	ASN
1	A	277	GLN
1	A	282	HIS
1	A	293	ASN

### 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](#)

5 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	0.70	0	17,19,21	2.96	3 (17%)
2	NAG	B	2	2	14,14,15	0.68	0	17,19,21	2.45	6 (35%)
3	NAG	C	1	3,1	14,14,15	0.61	0	17,19,21	2.16	5 (29%)
3	NAG	C	2	3	14,14,15	0.52	0	17,19,21	1.23	2 (11%)
3	BMA	C	3	3	11,11,12	0.50	0	15,15,17	1.48	3 (20%)

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	NAG	B	2	2	-	5/6/23/26	0/1/1/1
3	NAG	C	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	NAG	C1-O5-C5	11.24	127.42	112.19
3	C	1	NAG	O5-C5-C6	-5.08	99.24	107.20
2	B	2	NAG	C2-N2-C7	4.81	129.75	122.90
2	B	2	NAG	C8-C7-N2	4.60	123.89	116.10
3	C	1	NAG	C3-C4-C5	4.35	117.99	110.24
2	B	2	NAG	O5-C5-C6	4.31	113.96	107.20
3	C	1	NAG	C1-O5-C5	3.58	117.05	112.19
3	C	3	BMA	C3-C4-C5	3.23	116.00	110.24
2	B	2	NAG	C1-O5-C5	3.12	116.42	112.19
2	B	1	NAG	O5-C5-C4	2.83	117.70	110.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	O7-C7-C8	-2.78	116.90	122.06
3	C	1	NAG	O4-C4-C3	-2.73	104.05	110.35
2	B	2	NAG	C6-C5-C4	-2.66	106.76	113.00
2	B	1	NAG	O5-C1-C2	-2.57	107.23	111.29
3	C	2	NAG	O5-C5-C4	-2.53	104.67	110.83
3	C	2	NAG	C1-O5-C5	-2.28	109.11	112.19
3	C	3	BMA	C1-C2-C3	-2.26	106.89	109.67
3	C	3	BMA	O2-C2-C1	2.11	113.46	109.15
3	C	1	NAG	O5-C5-C4	2.05	115.80	110.83

There are no chirality outliers.

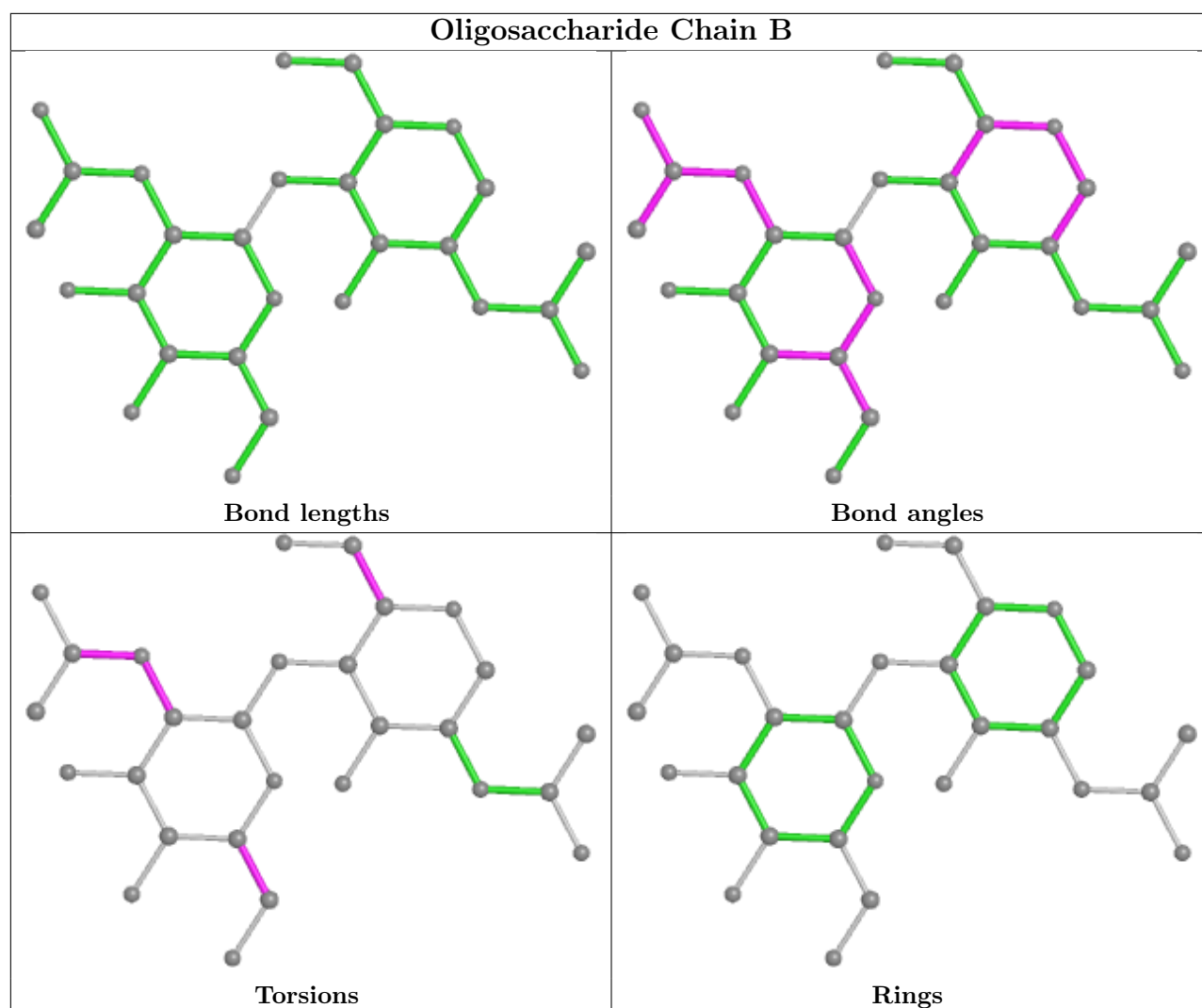
All (10) torsion outliers are listed below:

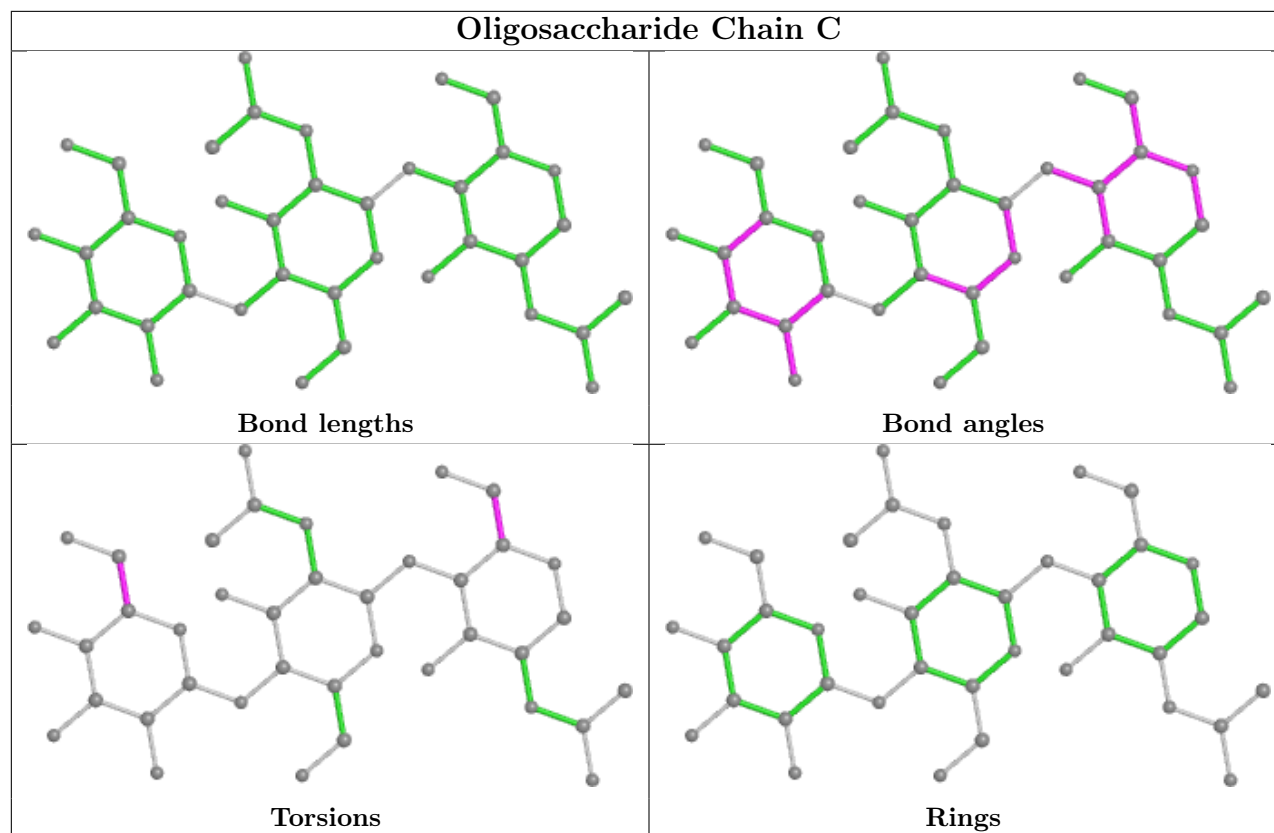
Mol	Chain	Res	Type	Atoms
2	B	1	NAG	O5-C5-C6-O6
3	C	3	BMA	C4-C5-C6-O6
2	B	1	NAG	C4-C5-C6-O6
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
2	B	2	NAG	O5-C5-C6-O6
3	C	3	BMA	O5-C5-C6-O6
2	B	2	NAG	C4-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
2	B	2	NAG	C3-C2-N2-C7

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](#)

There are no ligands in this entry.

## 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](#)

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	308/340 (90%)	0.03	4 (1%) 77 69	51, 79, 106, 132	2 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	209	ASN	2.5
1	A	302	ASN	2.4
1	A	26	ALA	2.4
1	A	32	LEU	2.2

### 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](#)

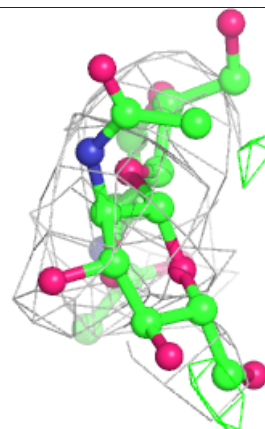
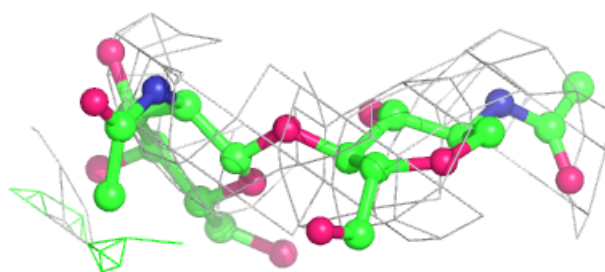
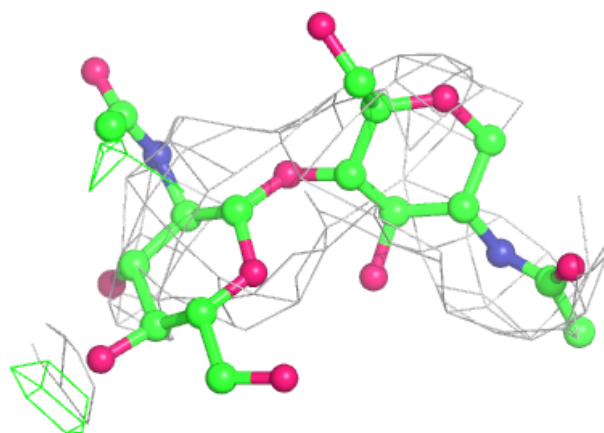
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	B	2	14/15	0.67	0.51	89,113,127,129	9
3	BMA	C	3	11/12	0.85	0.22	99,108,110,111	0
2	NAG	B	1	14/15	0.86	0.35	86,114,125,130	0
3	NAG	C	2	14/15	0.91	0.18	81,94,98,101	0
3	NAG	C	1	14/15	0.93	0.19	66,74,79,83	0

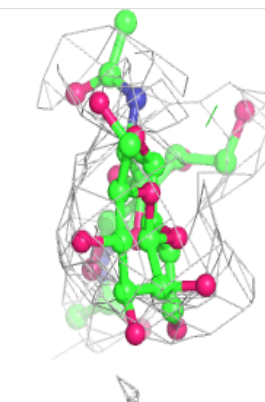
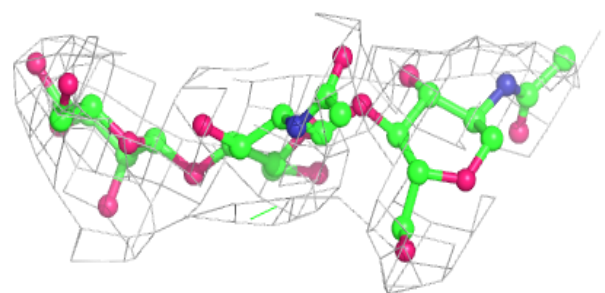
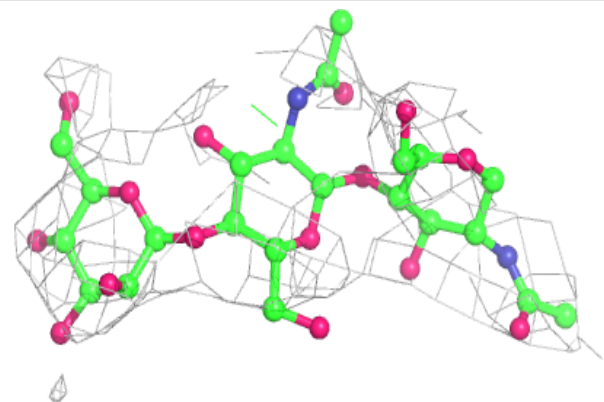
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around Chain B:**

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

**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

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.