



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 09:58 AM BST

PDB ID : 5JCE  
Title : Crystal structure of OsCEBiP complex  
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Deposited on : 2016-04-15  
Resolution : 2.51 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 : 2.13.1  
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) : 2.13.1

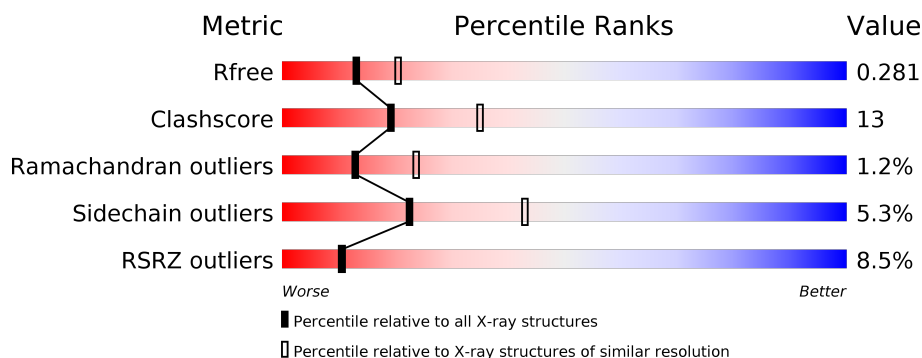
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.51 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 on 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	297	<div> <div>10%</div> <div> <div></div> <div>76%</div> <div>20%</div> <div>...</div> </div> </div>
1	B	297	<div> <div>7%</div> <div> <div></div> <div>74%</div> <div>22%</div> <div>.</div> </div> </div>
2	C	3	<div> <div>33%</div> <div>67%</div> </div>

## 2 Entry composition [i](#)

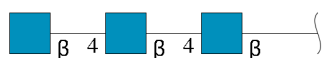
There are 3 unique types of molecules in this entry. The entry contains 4407 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Chitin elicitor-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	0	0
			2137	1317	366	436	18			
1	B	297	Total	C	N	O	S	0	0	0
			2171	1336	372	444	19			

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(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
2	C	3	Total	C	N	O	0	0	0
			43	24	3	16			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).

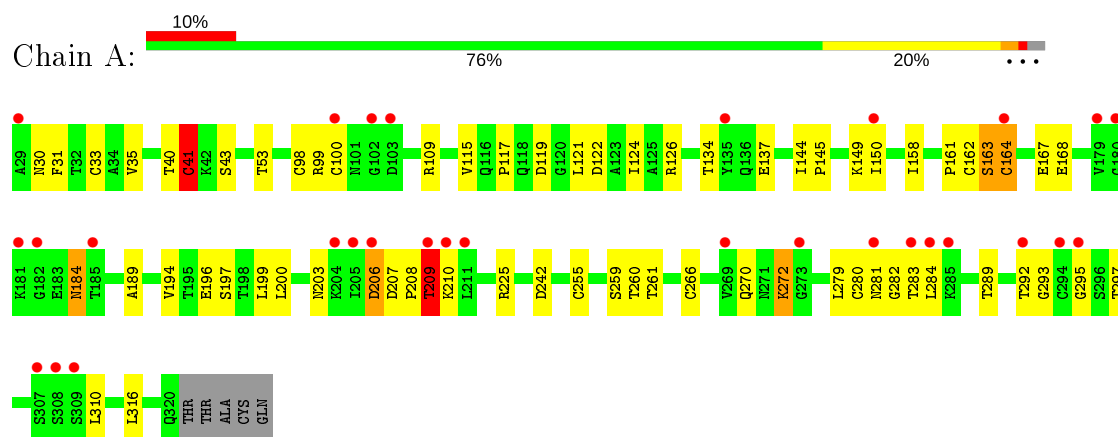


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

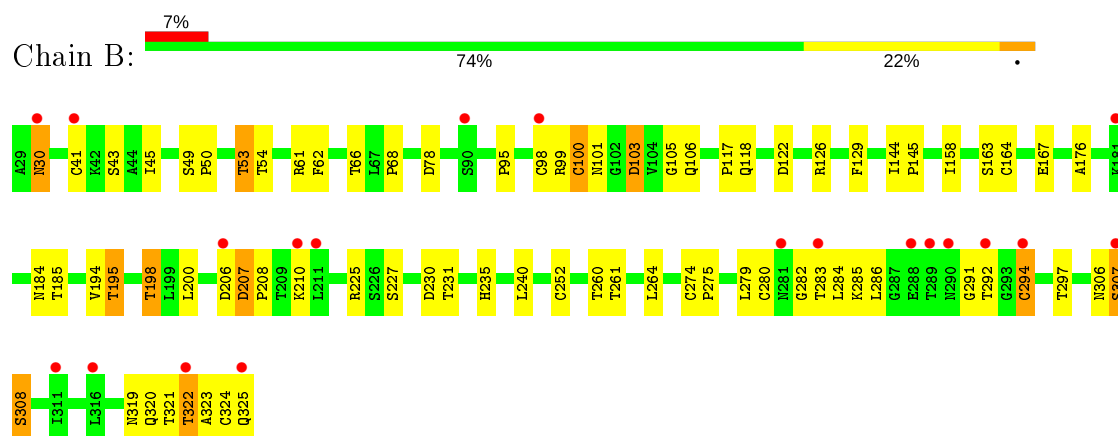
### 3 Residue-property plots [i](#)

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: Chitin elicitor-binding protein



#### • Molecule 1: Chitin elicitor-binding protein



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.45Å 99.77Å 87.65Å 90.00° 103.73° 90.00°	Depositor
Resolution (Å)	39.16 – 2.51 39.16 – 2.51	Depositor EDS
% Data completeness (in resolution range)	97.5 (39.16-2.51) 92.9 (39.16-2.51)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.65 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.220 , 0.256 0.264 , 0.281	Depositor DCC
$R_{free}$ test set	2000 reflections (5.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.5	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 36.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4407	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.14% 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: 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	0.64	2/2173 (0.1%)	0.74	3/2969 (0.1%)
1	B	0.64	1/2207 (0.0%)	0.68	0/3016
All	All	0.64	3/4380 (0.1%)	0.71	3/5985 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	41	CYS	CB-SG	-5.80	1.72	1.81
1	B	163	SER	C-O	-5.64	1.12	1.23
1	A	99	ARG	CZ-NH2	-5.42	1.26	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	163	SER	N-CA-C	-6.37	93.81	111.00
1	A	163	SER	CA-C-N	5.46	129.22	117.20
1	A	158	ILE	C-N-CD	5.31	139.55	128.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	270	GLN	Peptide
1	B	103	ASP	Peptide

## 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	2137	0	2095	50	1
1	B	2171	0	2126	58	1
2	C	43	0	39	1	0
3	A	14	0	13	1	0
3	B	42	0	39	6	0
All	All	4407	0	4312	109	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 13.

All (109) 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:B:41:CYS:SG	1:B:164:CYS:HB3	1.45	1.56
1:B:306:ASN:ND2	3:B:400:NAG:C1	1.70	1.52
1:B:294:CYS:SG	1:B:324:CYS:SG	1.24	1.24
1:B:294:CYS:SG	1:B:324:CYS:CB	2.26	1.23
1:B:41:CYS:SG	1:B:164:CYS:CB	2.41	1.07
1:B:306:ASN:ND2	3:B:400:NAG:O5	1.99	0.95
1:B:225:ARG:NH1	1:B:320:GLN:O	2.02	0.92
1:A:41:CYS:HB2	1:A:164:CYS:SG	2.13	0.88
1:A:100:CYS:SG	1:A:164:CYS:CB	2.64	0.85
1:A:293:GLY:O	1:A:295:GLY:N	2.08	0.84
1:B:306:ASN:ND2	3:B:400:NAG:C2	2.40	0.83
1:A:282:GLY:O	1:A:283:THR:OG1	1.96	0.82
1:A:209:THR:OG1	1:A:210:LYS:N	2.13	0.81
1:B:307:SER:O	1:B:308:SER:OG	1.99	0.80
1:B:322:THR:HA	1:B:325:GLN:HG3	1.64	0.78
1:B:319:ASN:OD1	1:B:321:THR:HG23	1.84	0.77
1:A:279:LEU:HD13	1:A:283:THR:H	1.52	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:ARG:HG3	1:A:109:ARG:HH11	1.51	0.73
1:A:33:CYS:SG	1:A:164:CYS:HB3	2.29	0.73
1:B:306:ASN:CG	3:B:400:NAG:C1	2.57	0.71
1:A:292:THR:OG1	1:A:293:GLY:N	2.24	0.71
1:B:321:THR:O	1:B:323:ALA:N	2.20	0.70
1:B:322:THR:HA	1:B:325:GLN:CG	2.22	0.69
1:A:100:CYS:SG	1:A:164:CYS:HB2	2.32	0.69
1:A:109:ARG:HG3	1:A:109:ARG:NH1	2.08	0.68
1:A:98:CYS:CB	1:A:162:CYS:SG	2.83	0.66
1:B:282:GLY:O	1:B:283:THR:OG1	2.13	0.66
1:B:294:CYS:SG	1:B:324:CYS:HB3	2.31	0.66
1:B:122:ASP:OD1	1:B:126:ARG:NH1	2.28	0.66
1:A:33:CYS:SG	1:A:164:CYS:CB	2.85	0.65
1:B:321:THR:O	1:B:322:THR:HG23	1.98	0.63
1:A:209:THR:HG1	1:A:210:LYS:H	1.45	0.63
1:B:30:ASN:OD1	1:B:30:ASN:N	2.31	0.63
1:B:291:GLY:C	1:B:292:THR:HG23	2.19	0.62
1:B:184:ASN:HD21	3:B:402:NAG:C1	2.13	0.61
1:B:240:LEU:HD12	1:B:264:LEU:HD11	1.81	0.61
1:B:291:GLY:O	1:B:292:THR:HG23	2.01	0.61
1:B:195:THR:OG1	1:B:198:THR:OG1	2.20	0.60
1:A:30:ASN:OD1	1:A:31:PHE:N	2.33	0.59
1:B:206:ASP:HB2	1:B:210:LYS:NZ	2.19	0.57
1:B:206:ASP:HB2	1:B:210:LYS:HZ3	1.68	0.57
1:A:242:ASP:OD1	1:A:259:SER:N	2.32	0.56
2:C:2:NAG:H61	2:C:3:NAG:C1	2.35	0.56
1:A:293:GLY:C	1:A:295:GLY:H	2.06	0.56
1:B:194:VAL:HG12	1:B:195:THR:N	2.22	0.55
1:B:252:CYS:SG	1:B:275:PRO:HD2	2.46	0.55
1:A:184:ASN:HD21	3:A:403:NAG:C1	2.20	0.54
1:A:30:ASN:HB2	1:A:161:PRO:HB3	1.90	0.54
1:A:260:THR:HG22	1:A:261:THR:HG23	1.88	0.54
1:A:98:CYS:HB2	1:A:162:CYS:SG	2.47	0.54
1:A:207:ASP:CG	1:A:209:THR:CG2	2.77	0.53
1:B:45:ILE:HG22	1:B:176:ALA:HB3	1.90	0.53
1:B:194:VAL:CG1	1:B:195:THR:N	2.73	0.52
1:B:207:ASP:H	1:B:210:LYS:HE2	1.75	0.52
1:B:279:LEU:HD13	1:B:283:THR:HA	1.90	0.51
1:B:66:THR:HB	1:B:68:PRO:HD2	1.91	0.51
1:A:33:CYS:SG	1:A:164:CYS:HB2	2.52	0.50
1:B:100:CYS:SG	1:B:101:ASN:O	2.53	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:261:THR:O	1:B:322:THR:HG22	2.11	0.49
1:A:189:ALA:HB1	1:A:194:VAL:O	2.12	0.49
1:A:255:CYS:HG	1:A:266:CYS:HG	1.59	0.49
1:B:306:ASN:ND2	3:B:400:NAG:H2	2.25	0.49
1:B:185:THR:HG21	1:B:200:LEU:HD21	1.96	0.48
1:B:167:GLU:OE1	1:B:198:THR:HG22	2.13	0.48
1:B:98:CYS:SG	1:B:106:GLN:N	2.87	0.47
1:B:284:LEU:HA	1:B:284:LEU:HD12	1.71	0.47
1:B:61:ARG:HG2	1:B:62:PHE:CD1	2.49	0.47
1:A:134:THR:HG23	1:A:137:GLU:H	1.80	0.47
1:A:280:CYS:O	1:A:281:ASN:HB2	2.13	0.47
1:A:41:CYS:CB	1:A:164:CYS:SG	2.98	0.47
1:B:200:LEU:HD11	1:B:208:PRO:HG3	1.97	0.46
1:A:121:LEU:HD13	1:A:150:ILE:HG21	1.96	0.46
1:A:119:ASP:HB3	1:A:124:ILE:HD11	1.98	0.46
1:B:98:CYS:SG	1:B:105:GLY:C	2.94	0.46
1:B:129:PHE:CE2	1:B:158:ILE:HG13	2.51	0.46
1:A:43:SER:OG	1:A:163:SER:O	2.35	0.45
1:B:260:THR:HG22	1:B:261:THR:HG23	1.97	0.45
1:B:53:THR:HB	1:B:54:THR:H	1.55	0.45
1:B:321:THR:C	1:B:322:THR:CG2	2.85	0.45
1:A:207:ASP:OD1	1:A:209:THR:HG22	2.17	0.44
1:A:33:CYS:SG	1:A:35:VAL:HG22	2.57	0.44
1:B:117:PRO:O	1:B:118:GLN:HB2	2.17	0.44
1:A:293:GLY:C	1:A:295:GLY:N	2.65	0.44
1:B:235:HIS:CD2	1:B:235:HIS:C	2.91	0.43
1:A:282:GLY:C	1:A:283:THR:HG23	2.38	0.43
1:A:199:LEU:O	1:A:203:ASN:HB2	2.19	0.43
1:B:43:SER:O	1:B:95:PRO:HA	2.18	0.43
1:A:163:SER:HA	1:A:164:CYS:HB2	2.01	0.43
1:A:272:LYS:HE3	1:A:272:LYS:HB2	1.43	0.43
1:A:167:GLU:O	1:A:168:GLU:HB2	2.17	0.43
1:B:230:ASP:OD1	1:B:235:HIS:NE2	2.52	0.43
1:B:279:LEU:HD13	1:B:283:THR:H	1.84	0.42
1:A:144:ILE:HA	1:A:145:PRO:HD3	1.75	0.42
1:B:285:LYS:O	1:B:286:LEU:C	2.54	0.42
1:B:49:SER:HA	1:B:50:PRO:HD2	1.93	0.42
1:A:196:GLU:O	1:A:200:LEU:HG	2.19	0.42
1:A:289:THR:HG23	1:A:297:THR:O	2.20	0.42
1:A:121:LEU:HD12	1:A:121:LEU:HA	1.83	0.41
1:A:282:GLY:C	1:A:283:THR:HG1	2.07	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:ILE:HA	1:B:145:PRO:HD3	1.71	0.41
1:A:40:THR:HA	1:A:98:CYS:O	2.21	0.41
1:B:98:CYS:SG	1:B:105:GLY:CA	3.08	0.41
1:A:115:VAL:HG13	1:A:119:ASP:HB2	2.03	0.41
1:A:316:LEU:HA	1:A:316:LEU:HD12	1.93	0.41
1:B:321:THR:C	1:B:323:ALA:N	2.74	0.41
1:A:207:ASP:C	1:A:209:THR:HG23	2.41	0.41
1:B:194:VAL:HG12	1:B:195:THR:O	2.21	0.41
1:A:122:ASP:O	1:A:126:ARG:HG3	2.21	0.41
1:A:255:CYS:SG	1:A:266:CYS:SG	3.17	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)
1:A:281:ASN:OD1	1:B:227:SER:OG[2_545]	1.99	0.21

## 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	290/297 (98%)	265 (91%)	20 (7%)	5 (2%)	9	16
1	B	295/297 (99%)	274 (93%)	19 (6%)	2 (1%)	22	39
All	All	585/594 (98%)	539 (92%)	39 (7%)	7 (1%)	13	24

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	164	CYS
1	B	99	ARG
1	A	117	PRO

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Mol	Chain	Res	Type
1	A	206	ASP
1	A	209	THR
1	B	308	SER
1	A	208	PRO

### 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	244/248 (98%)	233 (96%)	11 (4%)	27	51
1	B	248/248 (100%)	233 (94%)	15 (6%)	19	37
All	All	492/496 (99%)	466 (95%)	26 (5%)	22	43

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	CYS
1	A	53	THR
1	A	149	LYS
1	A	184	ASN
1	A	197	SER
1	A	206	ASP
1	A	209	THR
1	A	225	ARG
1	A	272	LYS
1	A	284	LEU
1	A	310	LEU
1	B	30	ASN
1	B	53	THR
1	B	78	ASP
1	B	100	CYS
1	B	103	ASP
1	B	195	THR
1	B	198	THR
1	B	207	ASP

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Mol	Chain	Res	Type
1	B	231	THR
1	B	274	CYS
1	B	280	CYS
1	B	294	CYS
1	B	297	THR
1	B	307	SER
1	B	322	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	184	ASN
1	B	184	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

3 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	C	1	2	15,15,15	0.83	0	21,21,21	1.22	1 (4%)
2	NAG	C	2	2	14,14,15	0.99	0	17,19,21	1.68	4 (23%)
2	NAG	C	3	2	14,14,15	1.33	1 (7%)	17,19,21	1.61	3 (17%)

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	C	1	2	-	2/6/26/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	NAG	C	3	2	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3	NAG	C2-N2	-2.22	1.42	1.46

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	3	NAG	C1-O5-C5	4.31	118.03	112.19
2	C	2	NAG	O5-C5-C6	-3.69	101.42	107.20
2	C	2	NAG	O6-C6-C5	-2.91	101.30	111.29
2	C	2	NAG	C1-O5-C5	2.61	115.72	112.19
2	C	1	NAG	O5-C1-C2	-2.47	107.03	109.52
2	C	2	NAG	O5-C5-C4	-2.42	104.94	110.83
2	C	3	NAG	C1-C2-N2	-2.14	106.83	110.49
2	C	3	NAG	C3-C4-C5	-2.09	106.52	110.24

There are no chirality outliers.

All (6) torsion outliers are listed below:

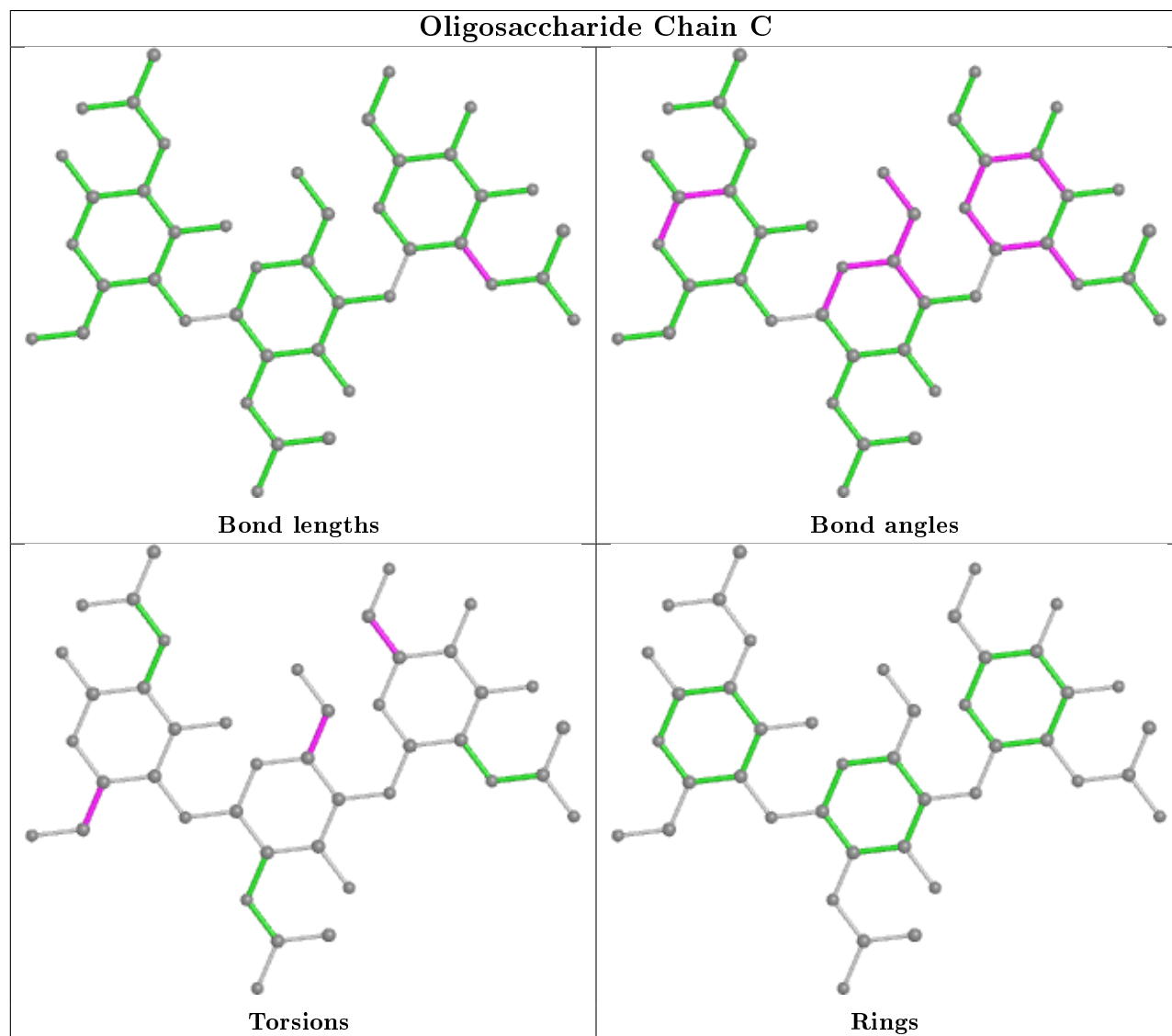
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	O5-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
2	C	3	NAG	O5-C5-C6-O6
2	C	3	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 1 short contact:

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



## 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	$\# Z  > 2$
3	NAG	B	402	-	14,14,15	0.50	0	17,19,21	0.48	0
3	NAG	B	401	-	14,14,15	0.84	1 (7%)	17,19,21	0.80	0
3	NAG	B	400	-	14,14,15	1.60	2 (14%)	17,19,21	1.21	2 (11%)
3	NAG	A	403	-	14,14,15	0.26	0	17,19,21	0.36	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	B	402	-	-	0/6/23/26	0/1/1/1
3	NAG	B	401	-	-	2/6/23/26	0/1/1/1
3	NAG	B	400	-	-	0/6/23/26	0/1/1/1
3	NAG	A	403	-	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	400	NAG	O5-C1	-5.47	1.35	1.43
3	B	400	NAG	C1-C2	-2.31	1.48	1.52
3	B	401	NAG	O5-C1	-2.03	1.40	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	400	NAG	C3-C4-C5	2.94	115.48	110.24
3	B	400	NAG	C1-O5-C5	-2.73	108.50	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	401	NAG	C4-C5-C6-O6
3	B	401	NAG	O5-C5-C6-O6
3	A	403	NAG	O5-C5-C6-O6
3	A	403	NAG	C4-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	402	NAG	1	0
3	B	400	NAG	5	0
3	A	403	NAG	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

### 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<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	292/297 (98%)	0.83	30 (10%) <b>6</b> <b>6</b>	27, 53, 82, 103	0
1	B	297/297 (100%)	0.63	20 (6%) <b>17</b> <b>18</b>	27, 52, 75, 98	0
All	All	589/594 (99%)	0.73	50 (8%) <b>10</b> <b>10</b>	27, 52, 78, 103	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	206	ASP	8.3
1	A	205	ILE	7.9
1	A	307	SER	7.8
1	A	308	SER	6.6
1	A	182	GLY	5.9
1	B	283	THR	5.9
1	A	29	ALA	5.4
1	B	322	THR	5.1
1	A	294	CYS	5.1
1	A	292	THR	5.0
1	B	281	ASN	4.8
1	A	181	LYS	4.6
1	A	209	THR	4.5
1	A	283	THR	4.1
1	B	307	SER	3.9
1	B	294	CYS	3.8
1	A	211	LEU	3.7
1	A	180	GLY	3.6
1	A	284	LEU	3.4
1	B	206	ASP	3.3
1	B	325	GLN	3.3
1	B	98	CYS	3.3
1	A	210	LYS	3.2
1	B	30	ASN	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	269	VAL	3.1
1	A	204	LYS	3.0
1	B	181	LYS	2.9
1	B	316	LEU	2.8
1	A	103	ASP	2.7
1	B	290	ASN	2.6
1	A	309	SER	2.6
1	A	164	CYS	2.6
1	B	210	LYS	2.4
1	A	185	THR	2.4
1	A	100	CYS	2.4
1	A	273	GLY	2.3
1	A	285	LYS	2.3
1	B	211	LEU	2.3
1	A	135	TYR	2.3
1	A	295	GLY	2.3
1	B	288	GLU	2.3
1	B	292	THR	2.2
1	A	102	GLY	2.2
1	A	150	ILE	2.1
1	A	281	ASN	2.1
1	B	311	ILE	2.1
1	B	90	SER	2.0
1	B	41	CYS	2.0
1	A	179	VAL	2.0
1	B	289	THR	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](#)

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.

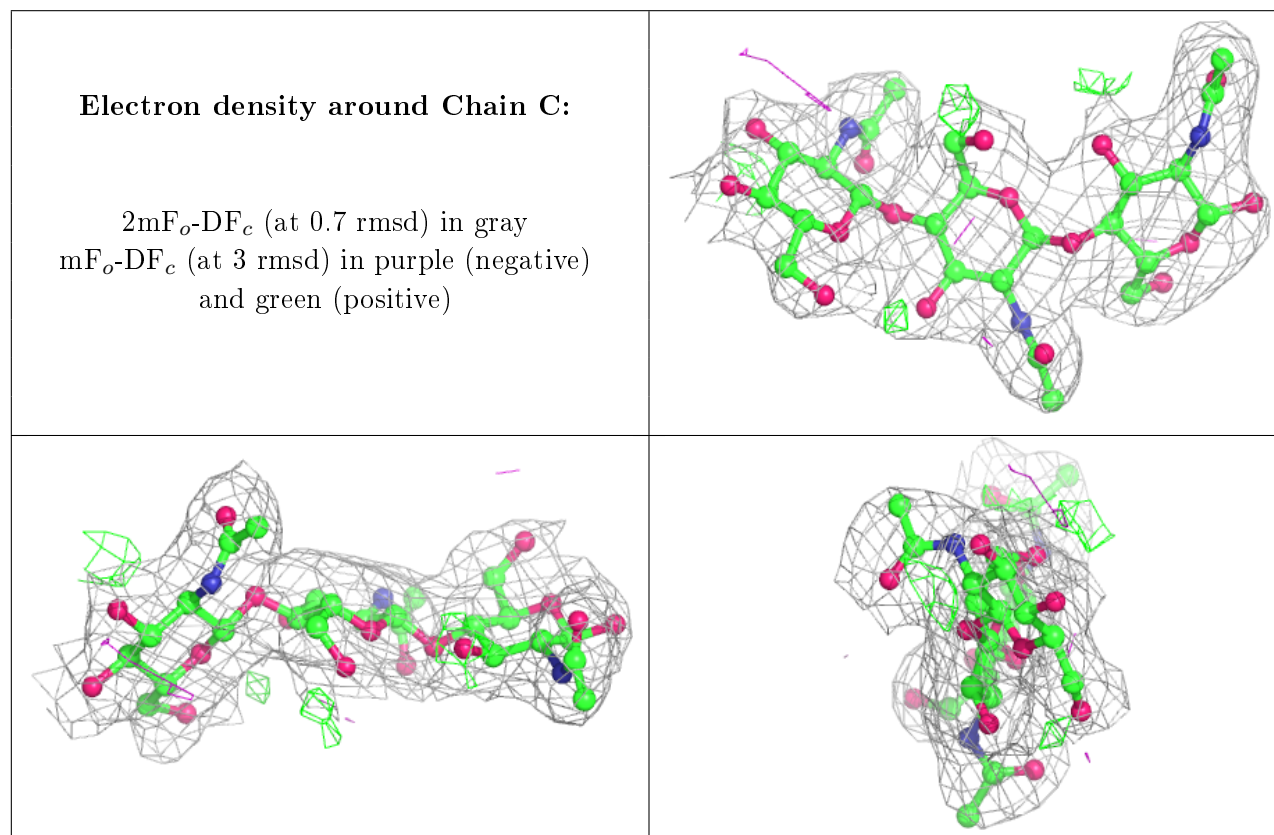
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	C	2	14/15	0.92	0.17	50,60,67,68	0
2	NAG	C	1	15/15	0.95	0.14	49,61,71,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	C	3	14/15	0.95	0.14	46,51,57,59	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 ⓘ

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( $\text{\AA}^2$ )	Q<0.9
3	NAG	A	403	14/15	0.77	0.30	75,82,86,90	0
3	NAG	B	401	14/15	0.79	0.32	54,67,70,74	0
3	NAG	B	402	14/15	0.82	0.19	58,63,70,75	0
3	NAG	B	400	14/15	0.90	0.15	57,61,68,70	0

## 6.5 Other polymers

There are no such residues in this entry.