



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 9, 2026 – 09:55 PM UTC

PDB ID : 9RCU / pdb\_00009rcu  
Title : Cardioderma bat coronavirus 2B receptor binding domain in complex with human CEACAM6  
Authors : Gallo, G.; Bailey, D.; Graham, S.C.  
Deposited on : 2025-05-29  
Resolution : 2.99 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

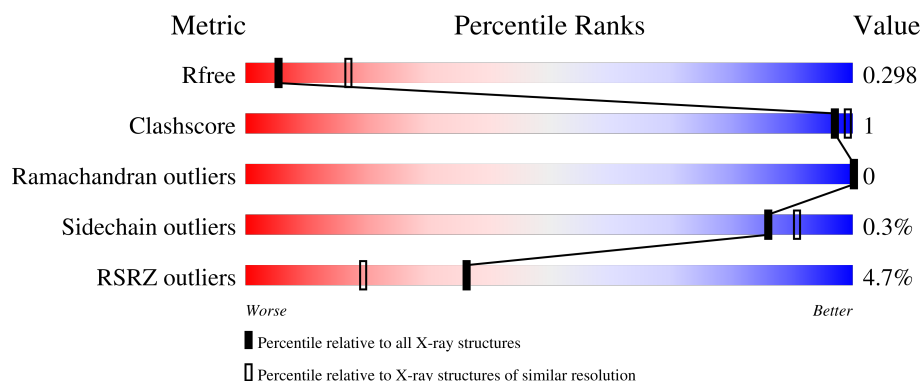
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.99 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))
$R_{free}$	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	299	<div> <div>5%</div> <div> <div></div> <div>89%</div> <div>•</div> <div>8%</div> </div> </div>
2	B	150	<div> <div>3%</div> <div> <div></div> <div>83%</div> <div>•</div> <div>16%</div> </div> </div>
3	C	2	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>
3	D	2	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3275 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 Cell adhesion molecule CEACAM6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	0	0
			2120	1330	359	424	7			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	327	LYS	-	expression tag	UNP P40199
A	328	LEU	-	expression tag	UNP P40199
A	329	GLU	-	expression tag	UNP P40199
A	330	VAL	-	expression tag	UNP P40199
A	331	LEU	-	expression tag	UNP P40199
A	332	PHE	-	expression tag	UNP P40199
A	333	GLN	-	expression tag	UNP P40199

- Molecule 2 is a protein called Spike protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	126	Total	C	N	O	S	0	0	0
			987	640	158	184	5			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	626	ASN	-	expression tag	UNP A0AB38ZDI6
B	627	ASP	-	expression tag	UNP A0AB38ZDI6
B	628	ILE	-	expression tag	UNP A0AB38ZDI6
B	629	PHE	-	expression tag	UNP A0AB38ZDI6
B	630	GLU	-	expression tag	UNP A0AB38ZDI6
B	631	ALA	-	expression tag	UNP A0AB38ZDI6
B	632	GLN	-	expression tag	UNP A0AB38ZDI6
B	633	LYS	-	expression tag	UNP A0AB38ZDI6
B	634	ILE	-	expression tag	UNP A0AB38ZDI6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	635	GLU	-	expression tag	UNP A0AB38ZDI6
B	636	TRP	-	expression tag	UNP A0AB38ZDI6
B	637	HIS	-	expression tag	UNP A0AB38ZDI6
B	638	GLU	-	expression tag	UNP A0AB38ZDI6
B	639	LYS	-	expression tag	UNP A0AB38ZDI6
B	640	HIS	-	expression tag	UNP A0AB38ZDI6
B	641	HIS	-	expression tag	UNP A0AB38ZDI6
B	642	HIS	-	expression tag	UNP A0AB38ZDI6
B	643	HIS	-	expression tag	UNP A0AB38ZDI6
B	644	HIS	-	expression tag	UNP A0AB38ZDI6
B	645	HIS	-	expression tag	UNP A0AB38ZDI6

- Molecule 3 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
3	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).

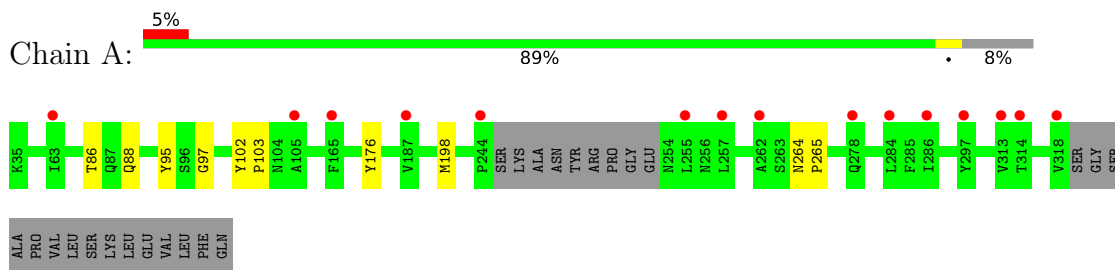


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1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

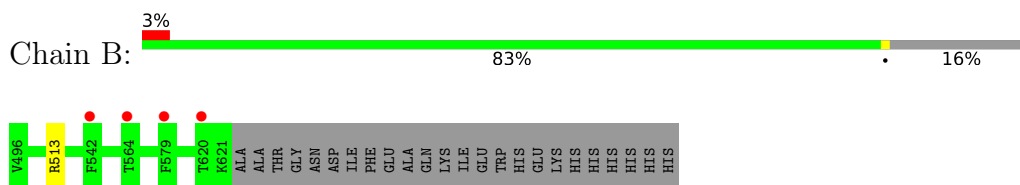
### 3 Residue-property plots [i](#)

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: Cell adhesion molecule CEACAM6



- Molecule 2: Spike protein



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 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 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	47.55Å 76.86Å 204.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	61.49 – 2.99 61.49 – 2.99	Depositor EDS
% Data completeness (in resolution range)	59.1 (61.49-2.99) 53.5 (61.49-2.99)	Depositor EDS
$R_{merge}$	0.23	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.50 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, $R_{free}$	0.253 , 0.297 0.253 , 0.298	Depositor DCC
$R_{free}$ test set	810 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	79.6	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 83.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	3275	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.93% 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	0.20	0/2169	0.49	0/2972
2	B	0.21	0/1018	0.55	0/1390
All	All	0.20	0/3187	0.51	0/4362

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	2120	0	2038	6	0
2	B	987	0	931	0	0
3	C	28	0	25	0	0
3	D	28	0	25	0	0
4	A	70	0	65	0	0
4	B	42	0	39	0	0
All	All	3275	0	3123	6	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 1.

All (6) 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:86:THR:HG22	1:A:88:GLN:H	1.70	0.55
1:A:95:TYR:CZ	1:A:97:GLY:HA2	2.47	0.50
1:A:264:ASN:HA	1:A:265:PRO:C	2.39	0.47
1:A:102:TYR:HB3	1:A:103:PRO:HD2	1.99	0.45
1:A:95:TYR:OH	1:A:97:GLY:HA2	2.18	0.44
1:A:176:TYR:CE2	1:A:198:MET:HG2	2.55	0.41

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	271/299 (91%)	260 (96%)	11 (4%)	0	100	100
2	B	124/150 (83%)	119 (96%)	5 (4%)	0	100	100
All	All	395/449 (88%)	379 (96%)	16 (4%)	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	242/262 (92%)	242 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	110/130 (85%)	109 (99%)	1 (1%)	70	85
All	All	352/392 (90%)	351 (100%)	1 (0%)	86	91

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	513	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	ASN
1	A	123	GLN
1	A	139	HIS
1	A	155	ASN
1	A	232	ASN
2	B	593	GLN
2	B	612	HIS

### 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 ⓘ

4 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	C	1	1,3	14,14,15	0.70	0	17,19,21	0.86	0
3	NAG	C	2	3	14,14,15	0.74	0	17,19,21	1.29	1 (5%)
3	NAG	D	1	1,3	14,14,15	0.71	0	17,19,21	1.56	2 (11%)
3	NAG	D	2	3	14,14,15	0.75	0	17,19,21	0.97	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	C	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	1/6/23/26	0/1/1/1
3	NAG	D	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1	NAG	C1-O5-C5	5.54	119.61	112.19
3	C	2	NAG	C1-O5-C5	4.12	117.70	112.19
3	D	1	NAG	O4-C4-C3	-2.33	104.89	110.38

There are no chirality outliers.

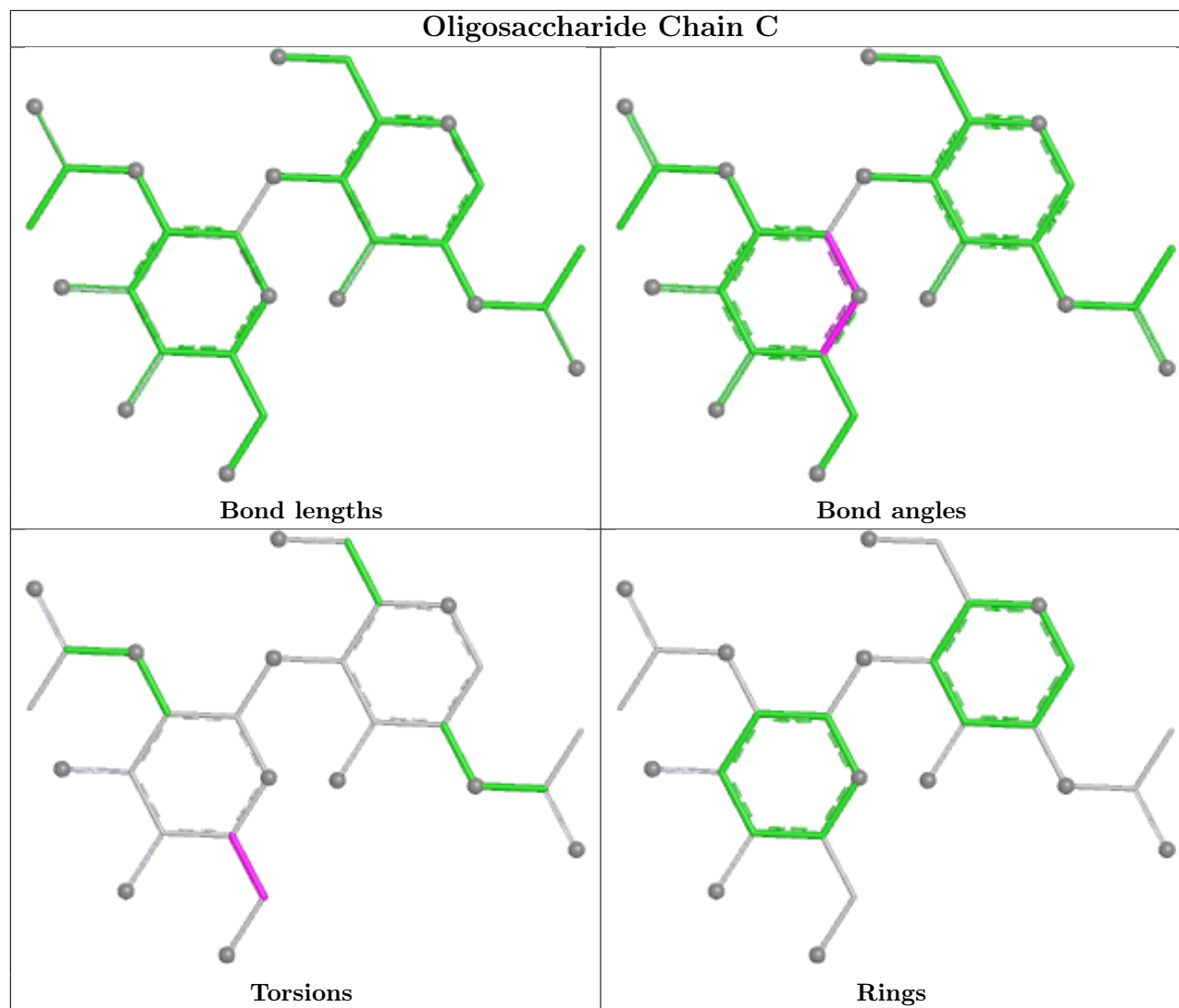
All (2) torsion outliers are listed below:

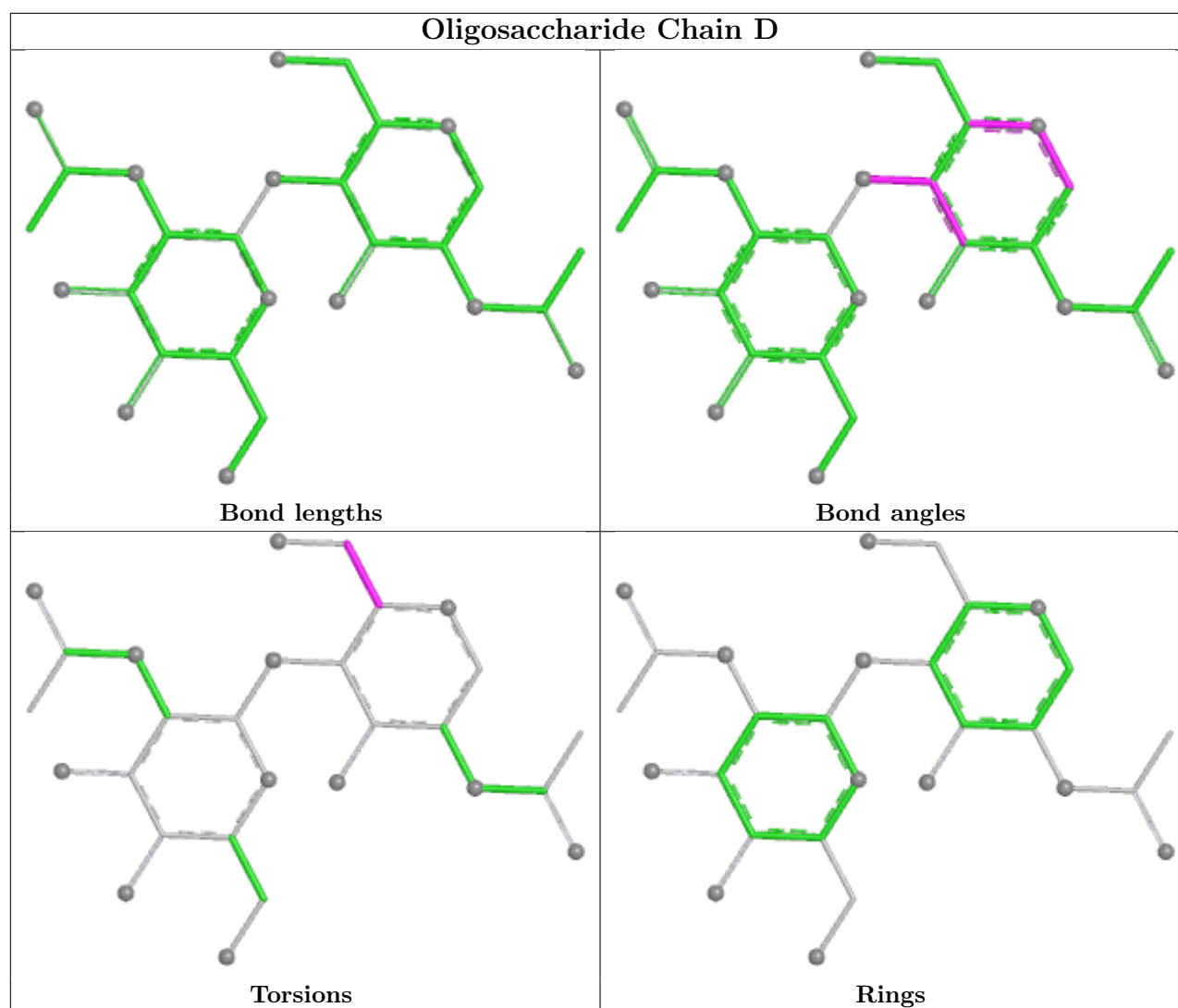
Mol	Chain	Res	Type	Atoms
3	D	1	NAG	O5-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6

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](#)

8 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	901	1	14,14,15	0.76	0	17,19,21	0.86	0
4	NAG	B	901	2	14,14,15	0.67	0	17,19,21	1.54	3 (17%)
4	NAG	A	902	1	14,14,15	0.75	0	17,19,21	1.32	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	A	904	1	14,14,15	0.73	0	17,19,21	1.35	2 (11%)
4	NAG	B	902	2	14,14,15	0.81	0	17,19,21	1.62	3 (17%)
4	NAG	B	903	2	14,14,15	0.79	0	17,19,21	1.68	3 (17%)
4	NAG	A	903	1	14,14,15	0.81	0	17,19,21	0.95	0
4	NAG	A	905	1	14,14,15	0.71	0	17,19,21	1.22	1 (5%)

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	901	1	-	1/6/23/26	0/1/1/1
4	NAG	B	901	2	-	0/6/23/26	0/1/1/1
4	NAG	A	902	1	-	0/6/23/26	0/1/1/1
4	NAG	A	904	1	-	0/6/23/26	0/1/1/1
4	NAG	B	902	2	-	1/6/23/26	0/1/1/1
4	NAG	B	903	2	-	2/6/23/26	0/1/1/1
4	NAG	A	903	1	-	1/6/23/26	0/1/1/1
4	NAG	A	905	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	903	NAG	C1-O5-C5	4.42	118.11	112.19
4	B	902	NAG	C1-O5-C5	4.40	118.08	112.19
4	A	904	NAG	C1-O5-C5	4.27	117.91	112.19
4	B	901	NAG	C1-O5-C5	4.05	117.62	112.19
4	A	902	NAG	C1-O5-C5	3.85	117.35	112.19
4	A	905	NAG	C1-O5-C5	3.68	117.12	112.19
4	B	903	NAG	C2-N2-C7	3.52	127.62	122.90
4	B	902	NAG	C2-N2-C7	2.90	126.79	122.90
4	A	904	NAG	C2-N2-C7	2.54	126.31	122.90
4	B	902	NAG	C1-C2-N2	-2.41	106.63	110.43
4	B	901	NAG	O5-C1-C2	-2.26	107.79	111.29
4	B	903	NAG	C1-C2-N2	2.26	114.00	110.43
4	B	901	NAG	C2-N2-C7	2.16	125.80	122.90
4	A	902	NAG	C4-C3-C2	-2.04	108.03	111.02

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	901	NAG	O5-C5-C6-O6
4	B	903	NAG	C1-C2-N2-C7
4	B	902	NAG	C3-C2-N2-C7
4	B	903	NAG	C3-C2-N2-C7
4	A	903	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 [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	275/299 (91%)	0.41	15 (5%)	30 15	48, 84, 123, 142	0
2	B	126/150 (84%)	0.37	4 (3%)	50 29	46, 83, 113, 167	0
All	All	401/449 (89%)	0.40	19 (4%)	36 19	46, 84, 121, 167	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	255	LEU	5.8
1	A	257	LEU	5.7
1	A	286	ILE	5.1
1	A	318	VAL	3.3
1	A	313	VAL	3.3
1	A	284	LEU	3.1
1	A	314	THR	3.0
1	A	187	VAL	2.9
1	A	297	TYR	2.7
2	B	579	PHE	2.5
1	A	105	ALA	2.5
1	A	278	GLN	2.5
1	A	165	PHE	2.4
2	B	564	THR	2.4
2	B	620	THR	2.4
1	A	244	PRO	2.4
1	A	262	ALA	2.3
1	A	63	ILE	2.2
2	B	542	PHE	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](#)

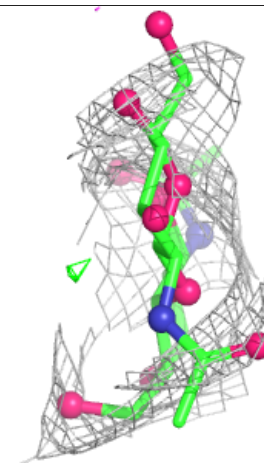
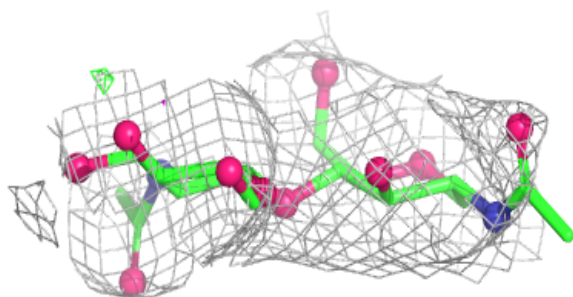
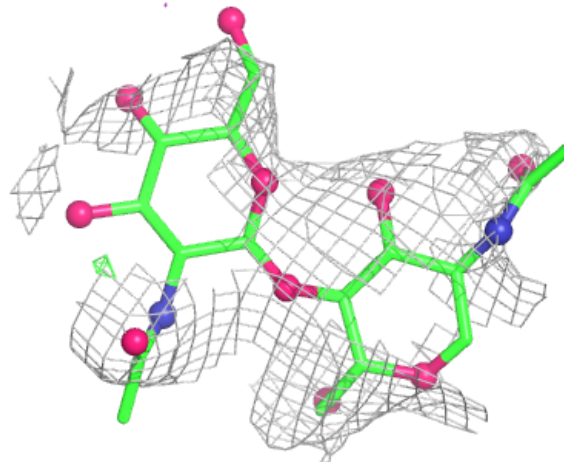
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

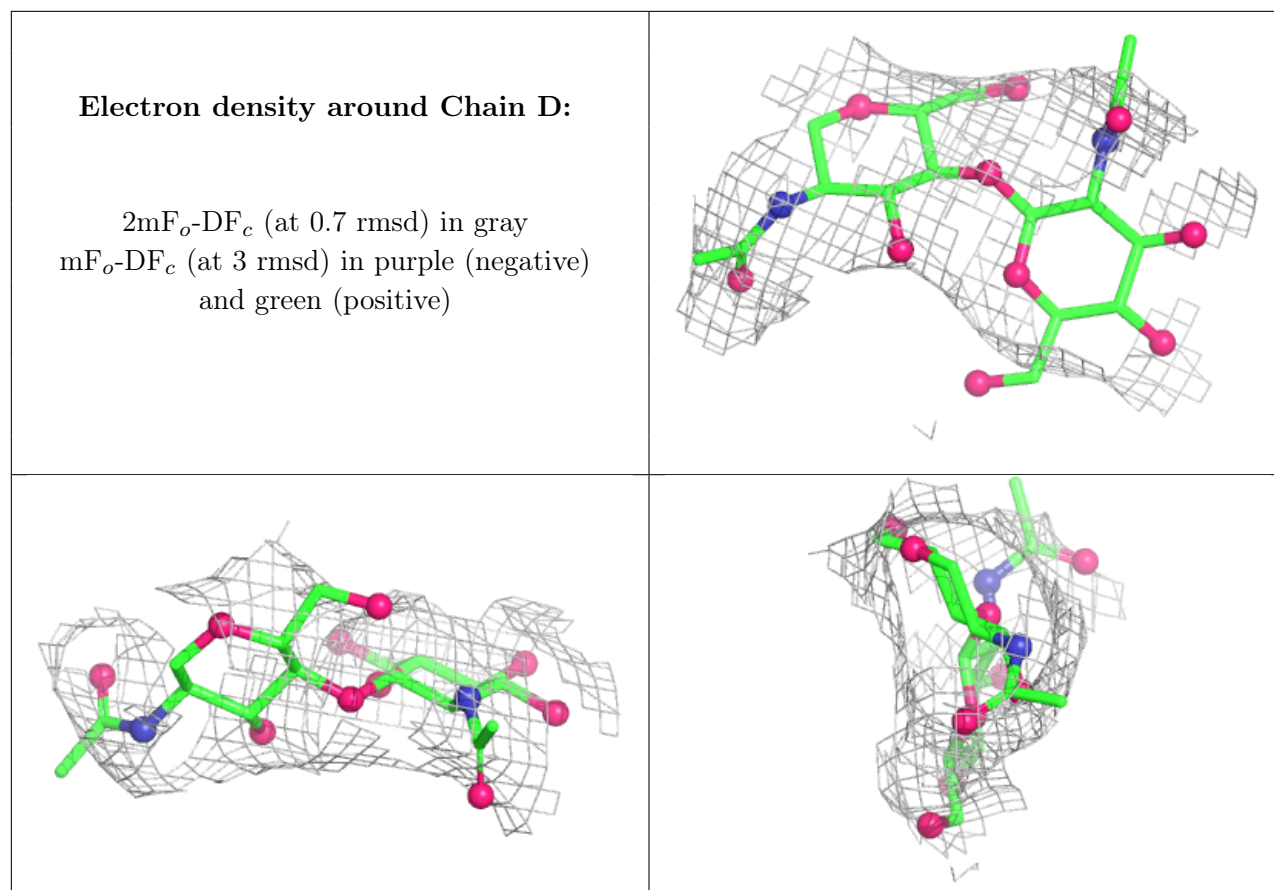
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	C	2	14/15	0.73	0.14	100,119,138,150	0
3	NAG	D	2	14/15	0.83	0.09	93,116,131,133	0
3	NAG	C	1	14/15	0.90	0.11	86,101,114,125	0
3	NAG	D	1	14/15	0.92	0.10	94,105,124,127	0

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 C:

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)





## 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, 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
4	NAG	A	903	14/15	0.54	0.12	105,130,139,143	0
4	NAG	B	903	14/15	0.57	0.11	46,108,117,118	0
4	NAG	A	904	14/15	0.64	0.13	76,100,117,121	0
4	NAG	A	901	14/15	0.69	0.11	90,108,118,119	0
4	NAG	B	902	14/15	0.70	0.14	81,109,129,133	0
4	NAG	A	905	14/15	0.73	0.12	98,130,141,153	0
4	NAG	B	901	14/15	0.75	0.10	68,94,106,112	0
4	NAG	A	902	14/15	0.89	0.12	75,84,97,104	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.