



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 9, 2026 – 10:16 PM UTC

PDB ID : 9RCS / pdb\_00009rcs  
Title : Cardioderma bat coronavirus KY43 receptor binding domain in complex with human CEACAM6  
Authors : Gallo, G.; Bailey, D.; Graham, S.C.  
Deposited on : 2025-05-29  
Resolution : 3.01 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

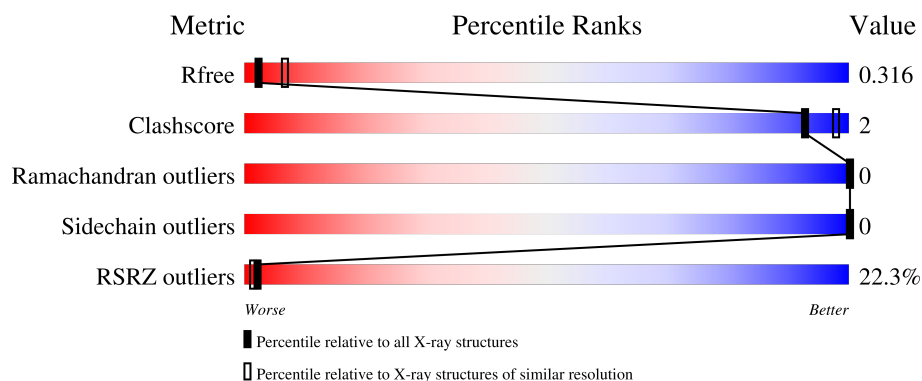
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.01 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	3131 (3.04-3.00)
Clashscore	190562	3444 (3.04-3.00)
Ramachandran outliers	187476	3319 (3.04-3.00)
Sidechain outliers	187428	3322 (3.04-3.00)
RSRZ outliers	180081	3130 (3.04-3.00)

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>17%</div> <div> <div>93%</div> <div>6%</div> </div> </div>
2	B	151	<div> <div>28%</div> <div> <div>75%</div> <div>22%</div> </div> </div>
3	C	2	<div> <div>100%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3343 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	295	Total	C	N	O	S	0	0	0
			2266	1420	385	454	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	118	Total	C	N	O	S	0	0	0
			937	604	149	177	7			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	631	ASN	-	expression tag	UNP F1DAX6
B	632	ASP	-	expression tag	UNP F1DAX6
B	633	ILE	-	expression tag	UNP F1DAX6
B	634	PHE	-	expression tag	UNP F1DAX6
B	635	GLU	-	expression tag	UNP F1DAX6
B	636	ALA	-	expression tag	UNP F1DAX6
B	637	GLN	-	expression tag	UNP F1DAX6
B	638	LYS	-	expression tag	UNP F1DAX6
B	639	ILE	-	expression tag	UNP F1DAX6

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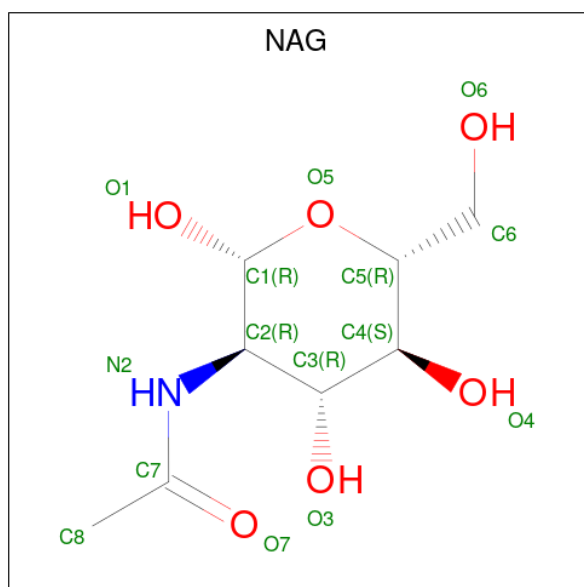
Chain	Residue	Modelled	Actual	Comment	Reference
B	640	GLU	-	expression tag	UNP F1DAX6
B	641	TRP	-	expression tag	UNP F1DAX6
B	642	HIS	-	expression tag	UNP F1DAX6
B	643	GLU	-	expression tag	UNP F1DAX6
B	644	LYS	-	expression tag	UNP F1DAX6
B	645	HIS	-	expression tag	UNP F1DAX6
B	646	HIS	-	expression tag	UNP F1DAX6
B	647	HIS	-	expression tag	UNP F1DAX6
B	648	HIS	-	expression tag	UNP F1DAX6
B	649	HIS	-	expression tag	UNP F1DAX6
B	650	HIS	-	expression tag	UNP F1DAX6

- 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			

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

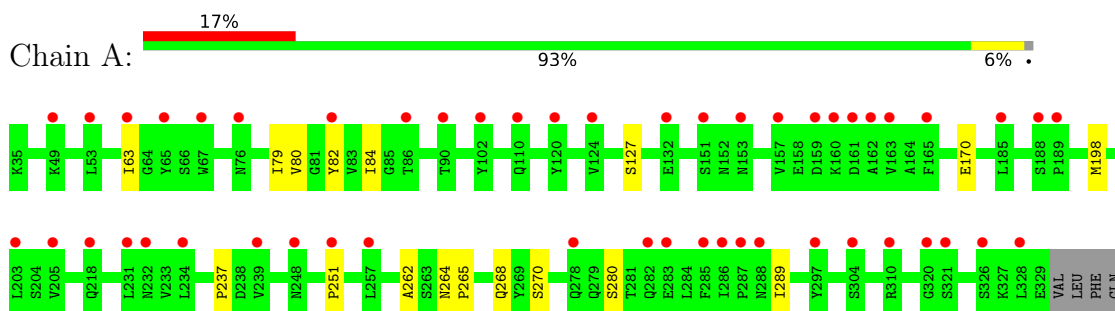


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

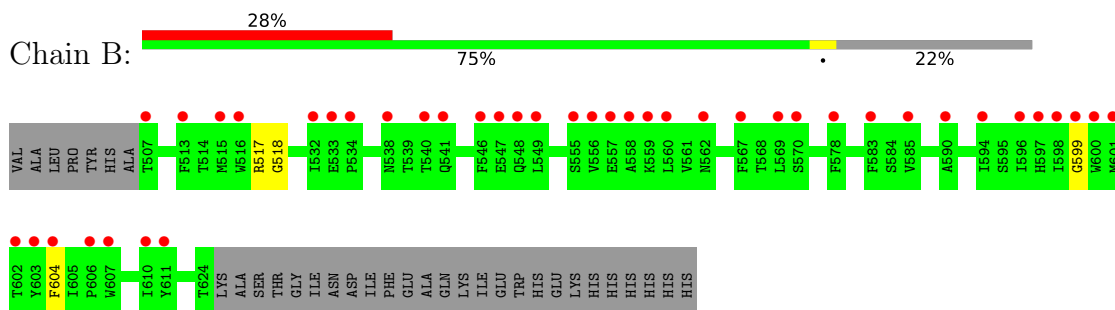
### 3 Residue-property plots

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.

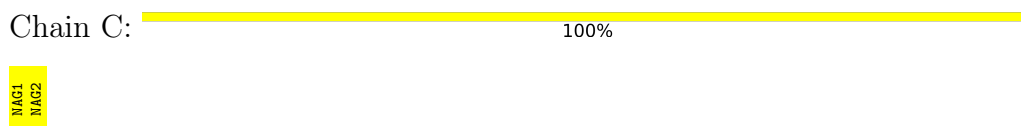
- Molecule 1: Cell adhesion molecule CEACAM6



- Molecule 2: Spike protein



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.01Å 78.80Å 82.34Å 90.00° 88.64° 90.00°	Depositor
Resolution (Å)	82.32 – 3.01 82.32 – 3.01	Depositor EDS
% Data completeness (in resolution range)	48.6 (82.32-3.01) 43.8 (82.32-3.01)	Depositor EDS
$R_{merge}$	0.20	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.06 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, $R_{free}$	0.256 , 0.317 0.256 , 0.316	Depositor DCC
$R_{free}$ test set	396 reflections (2.22%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.1	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 72.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k 0.002 for -h,-l,-k 0.044 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.79	EDS
Total number of atoms	3343	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.70% 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	0.26	0/2319	0.59	0/3176
2	B	0.25	0/965	0.59	0/1317
All	All	0.25	0/3284	0.59	0/4493

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	2266	0	2185	8	1
2	B	937	0	882	2	1
3	C	28	0	25	0	0
4	A	98	0	91	0	0
4	B	14	0	13	0	0
All	All	3343	0	3196	10	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 2.

All (10) 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:82:TYR:CE2	1:A:84:ILE:HA	2.39	0.57
1:A:63:ILE:HD11	1:A:127:SER:HA	1.88	0.55
1:A:79:ILE:HG22	1:A:80:VAL:HG23	1.90	0.53
1:A:264:ASN:HA	1:A:265:PRO:C	2.35	0.51
1:A:237:PRO:HA	1:A:262:ALA:O	2.15	0.46
1:A:270:SER:HA	1:A:280:SER:HA	1.98	0.45
2:B:517:ARG:NH1	2:B:518:GLY:O	2.47	0.45
2:B:599:GLY:HA3	2:B:604:PHE:HA	2.01	0.43
1:A:251:PRO:HA	1:A:289:ILE:HG23	2.01	0.42
1:A:170:GLU:HG3	1:A:198:MET:SD	2.61	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:268:GLN:NE2	2:B:604:PHE:O[2_556]	1.94	0.26

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	293/299 (98%)	278 (95%)	15 (5%)	0	100	100
2	B	116/151 (77%)	112 (97%)	4 (3%)	0	100	100
All	All	409/450 (91%)	390 (95%)	19 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	258/262 (98%)	258 (100%)	0	100	100
2	B	107/135 (79%)	107 (100%)	0	100	100
All	All	365/397 (92%)	365 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	ASN
1	A	300	GLN
2	B	527	HIS
2	B	541	GLN
2	B	597	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 ⓘ

2 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	NAG	C	1	1,3	14,14,15	0.65	0	17,19,21	2.12	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	C	2	3	14,14,15	0.65	0	17,19,21	1.07	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
3	NAG	C	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	NAG	C1-O5-C5	6.69	121.15	112.19
3	C	2	NAG	C1-O5-C5	3.23	116.52	112.19
3	C	1	NAG	C4-C3-C2	-3.07	106.52	111.02
3	C	1	NAG	O5-C5-C6	-2.90	102.03	107.66
3	C	1	NAG	O4-C4-C3	-2.53	104.41	110.38

There are no chirality outliers.

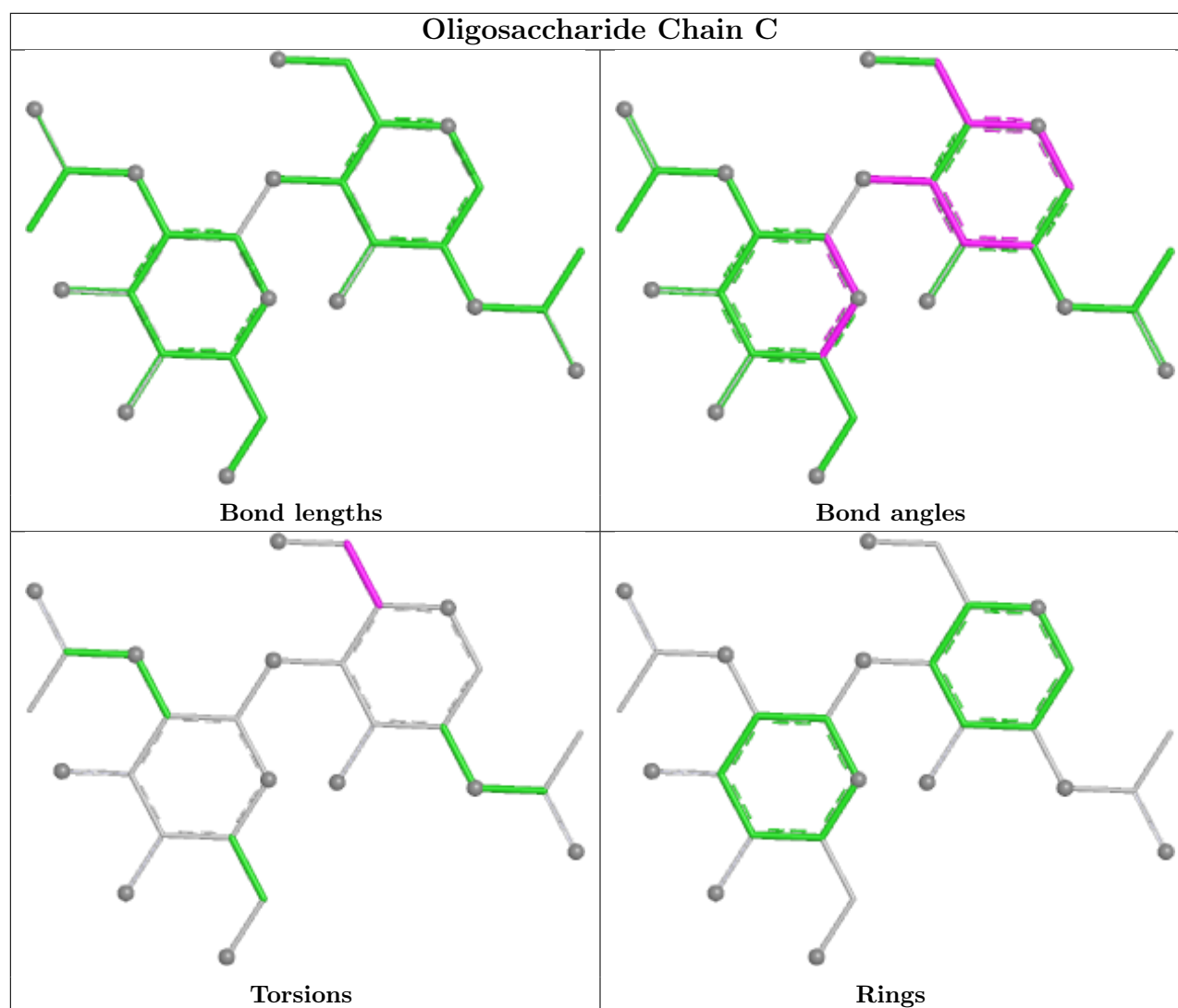
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	1	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	401	1	14,14,15	0.69	0	17,19,21	1.42	2 (11%)
4	NAG	A	404	1	14,14,15	0.70	0	17,19,21	1.08	1 (5%)
4	NAG	A	402	1	14,14,15	0.82	1 (7%)	17,19,21	2.05	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	B	701	2	14,14,15	1.03	1 (7%)	17,19,21	1.18	1 (5%)
4	NAG	A	406	1	14,14,15	0.73	0	17,19,21	1.91	2 (11%)
4	NAG	A	407	1	14,14,15	0.62	0	17,19,21	1.83	5 (29%)
4	NAG	A	405	1	14,14,15	0.81	1 (7%)	17,19,21	1.42	2 (11%)
4	NAG	A	403	1	14,14,15	0.73	0	17,19,21	1.29	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	401	1	-	0/6/23/26	0/1/1/1
4	NAG	A	404	1	-	0/6/23/26	0/1/1/1
4	NAG	A	402	1	-	2/6/23/26	0/1/1/1
4	NAG	B	701	2	-	0/6/23/26	0/1/1/1
4	NAG	A	406	1	-	3/6/23/26	0/1/1/1
4	NAG	A	407	1	-	3/6/23/26	0/1/1/1
4	NAG	A	405	1	-	1/6/23/26	0/1/1/1
4	NAG	A	403	1	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	701	NAG	C1-C2	3.21	1.56	1.52
4	A	402	NAG	C1-C2	2.45	1.55	1.52
4	A	405	NAG	C1-C2	2.22	1.55	1.52

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	406	NAG	C2-N2-C7	5.98	130.91	122.90
4	A	402	NAG	C1-O5-C5	4.82	118.64	112.19
4	A	401	NAG	C1-O5-C5	4.65	118.42	112.19
4	A	402	NAG	C2-N2-C7	4.62	129.09	122.90
4	A	403	NAG	C1-O5-C5	4.17	117.78	112.19
4	A	407	NAG	C1-O5-C5	4.11	117.69	112.19
4	A	405	NAG	C1-O5-C5	4.05	117.61	112.19
4	A	407	NAG	C2-N2-C7	3.11	127.06	122.90
4	A	402	NAG	C4-C3-C2	-3.10	106.48	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	406	NAG	O5-C1-C2	-3.05	106.56	111.29
4	A	407	NAG	C4-C3-C2	-2.97	106.67	111.02
4	B	701	NAG	C1-O5-C5	2.91	116.08	112.19
4	A	407	NAG	C1-C2-N2	2.78	114.81	110.43
4	A	404	NAG	C1-O5-C5	2.78	115.91	112.19
4	A	405	NAG	C2-N2-C7	2.54	126.30	122.90
4	A	407	NAG	O5-C1-C2	-2.43	107.53	111.29
4	A	403	NAG	C2-N2-C7	2.16	125.80	122.90
4	A	401	NAG	C4-C3-C2	-2.12	107.92	111.02

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	407	NAG	O5-C5-C6-O6
4	A	406	NAG	O5-C5-C6-O6
4	A	402	NAG	C1-C2-N2-C7
4	A	402	NAG	C3-C2-N2-C7
4	A	406	NAG	C3-C2-N2-C7
4	A	407	NAG	C3-C2-N2-C7
4	A	405	NAG	C1-C2-N2-C7
4	A	406	NAG	C1-C2-N2-C7
4	A	407	NAG	C1-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

### 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	295/299 (98%)	1.04	50 (16%) <b>4</b> <b>2</b>	25, 59, 97, 115	0
2	B	118/151 (78%)	1.99	42 (35%) <b>1</b> <b>1</b>	45, 102, 145, 155	0
All	All	413/450 (91%)	1.31	92 (22%) <b>2</b> <b>1</b>	25, 67, 128, 155	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	558	ALA	7.6
2	B	599	GLY	7.4
2	B	557	GLU	6.7
2	B	600	TRP	6.5
2	B	610	ILE	6.5
1	A	162	ALA	6.2
2	B	596	ILE	5.9
2	B	598	ILE	5.8
1	A	321	SER	5.7
2	B	594	ILE	5.6
2	B	601	MET	5.6
1	A	283	GLU	5.4
2	B	513	PHE	5.1
2	B	546	PHE	5.0
2	B	562	ASN	4.9
2	B	583	PHE	4.8
2	B	585	VAL	4.7
2	B	515	MET	4.7
2	B	560	LEU	4.2
1	A	234	LEU	3.9
1	A	163	VAL	3.9
1	A	153	ASN	3.8
1	A	304	SER	3.8
1	A	161	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	203	LEU	3.7
2	B	556	VAL	3.5
2	B	606	PRO	3.5
1	A	297	TYR	3.5
1	A	288	ASN	3.5
1	A	328	LEU	3.3
1	A	232	ASN	3.2
2	B	533	GLU	3.2
1	A	63	ILE	3.1
2	B	597	HIS	3.1
2	B	555	SER	3.1
1	A	205	VAL	3.1
2	B	541	GLN	3.0
2	B	567	PHE	3.0
2	B	578	PHE	2.9
1	A	257	LEU	2.9
2	B	569	LEU	2.9
1	A	286	ILE	2.8
2	B	570	SER	2.8
1	A	124	VAL	2.8
1	A	165	PHE	2.8
1	A	132	GLU	2.8
1	A	239	VAL	2.7
1	A	185	LEU	2.7
2	B	602	THR	2.7
2	B	516	TRP	2.7
1	A	120	TYR	2.7
1	A	53	LEU	2.7
1	A	76	ASN	2.7
2	B	540	THR	2.6
1	A	110	GLN	2.6
1	A	67	TRP	2.6
2	B	534	PRO	2.5
1	A	231	LEU	2.5
1	A	90	THR	2.4
1	A	65	TYR	2.4
1	A	102	TYR	2.4
1	A	320	GLY	2.4
2	B	611	TYR	2.4
2	B	590	ALA	2.4
1	A	160	LYS	2.4
1	A	282	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	86	THR	2.3
1	A	218	GLN	2.3
1	A	157	VAL	2.3
1	A	159	ASP	2.3
1	A	49	LYS	2.3
2	B	604	PHE	2.3
1	A	310	ARG	2.2
1	A	248	ASN	2.2
2	B	548	GLN	2.2
2	B	507	THR	2.2
2	B	549	LEU	2.2
1	A	82	TYR	2.1
1	A	326	SER	2.1
1	A	285	PHE	2.1
2	B	607	TRP	2.1
1	A	189	PRO	2.1
1	A	251	PRO	2.1
1	A	287	PRO	2.1
2	B	532	ILE	2.1
1	A	151	SER	2.1
2	B	538	ASN	2.1
1	A	278	GLN	2.1
2	B	547	GLU	2.1
1	A	188	SER	2.0
2	B	603	TYR	2.0
2	B	559	LYS	2.0

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

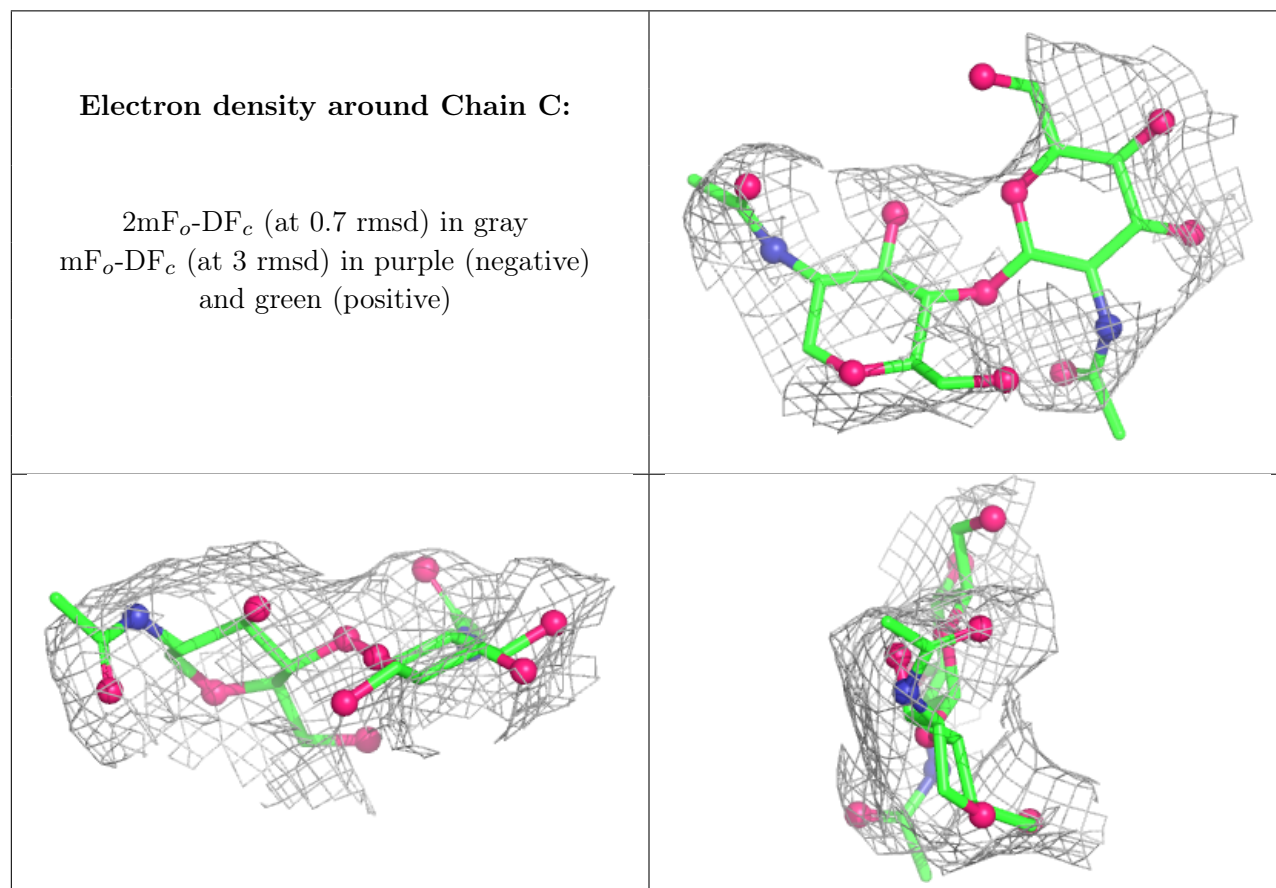
There are no non-standard protein/DNA/RNA residues in this entry.

## 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	0.75	0.14	77,102,131,133	0
3	NAG	C	1	14/15	0.85	0.10	53,69,84,96	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, 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	B	701	14/15	0.65	0.16	60,96,122,134	0
4	NAG	A	406	14/15	0.72	0.13	35,78,88,96	0
4	NAG	A	402	14/15	0.76	0.10	34,76,105,112	0
4	NAG	A	407	14/15	0.81	0.12	58,93,114,117	0
4	NAG	A	403	14/15	0.83	0.17	48,74,107,115	0
4	NAG	A	401	14/15	0.85	0.11	19,53,74,76	0
4	NAG	A	405	14/15	0.89	0.09	52,71,92,94	0
4	NAG	A	404	14/15	0.90	0.12	55,67,83,85	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.