Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 10:22 AM BST

PDB ID	:	4RWF
Title	:	Crystal structure of the CLR:RAMP2 extracellular domain heterodimer with bound adrenomedullin
Authors	:	Booe, J.; Pioszak, A.
Deposited on	:	2014-12-03
Resolution	:	1.76 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ①) were used in the production of this report:

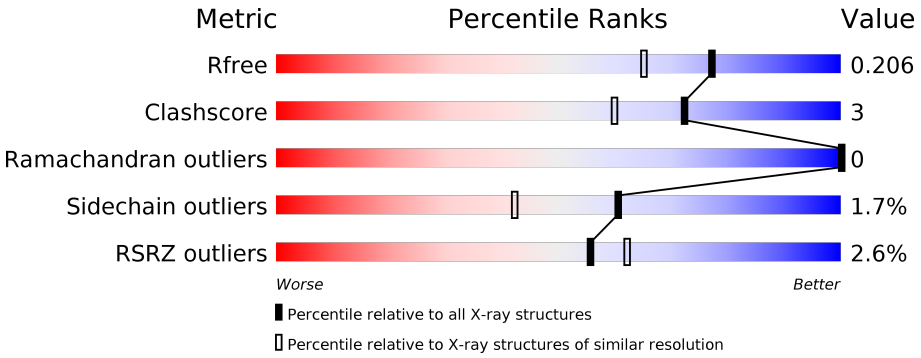
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 >=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 <=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	591	2% 87% 6% • 6%
2	B	29	10% 59% 7% 34%
3	C	2	100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5009 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 Maltose transporter subunit, Receptor activity-modifying protein 2, Calcitonin gene-related peptide type 1 receptor fusion protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	555	4424	2832	731	840	21	0	4	0

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP P0AEX9
A	1106	ARG	LEU	conflict	UNP O60895
A	1139	SER	-	linker	UNP O60895
A	2019	ASP	-	expression tag	UNP Q16602
A	2020	GLY	-	expression tag	UNP Q16602
A	2021	SER	-	expression tag	UNP Q16602
A	2022	ALA	-	expression tag	UNP Q16602
A	2023	GLY	-	expression tag	UNP Q16602
A	2024	SER	-	expression tag	UNP Q16602
A	2025	ALA	-	expression tag	UNP Q16602
A	2026	GLY	-	expression tag	UNP Q16602
A	2027	SER	-	expression tag	UNP Q16602
A	2028	ALA	-	expression tag	UNP Q16602
A	2029	GLU	-	expression tag	UNP Q16602
A	2030	ASP	-	expression tag	UNP Q16602

- Molecule 2 is a protein called Adrenomedullin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	19	148	90	28	30	0	1	1

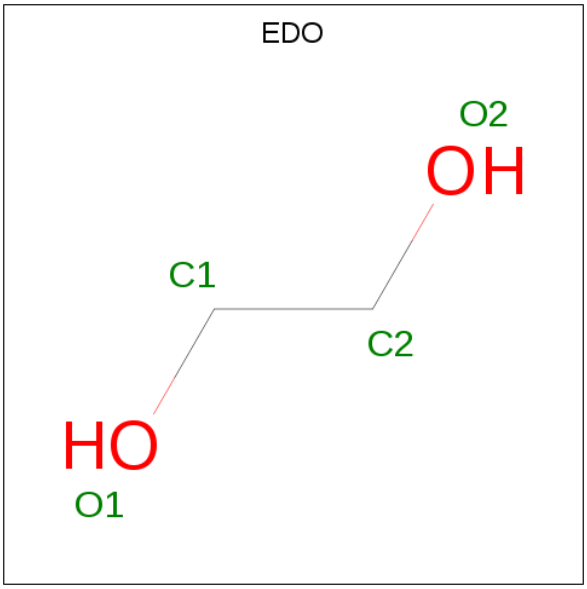
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	53	NH2	-	amidation	UNP P35318

- Molecule 3 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	C	2	Total C O 23 12 11	0	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0

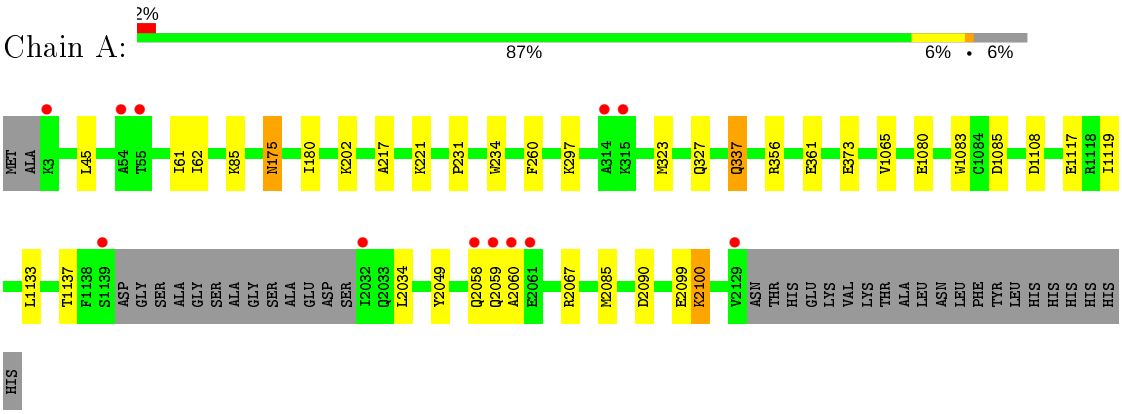
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	383	Total O 383 383	0	0
5	B	11	Total O 11 11	0	0

3 Residue-property plots (i)

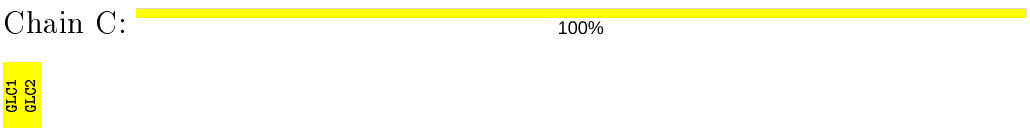
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Maltose transporter subunit, Receptor activity-modifying protein 2, Calcitonin gene-related peptide type 1 receptor fusion protein



• Molecule 2: Adrenomedullin

• Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	71.45Å 84.28Å 115.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.76 39.68 – 1.76	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-1.76) 99.9 (39.68-1.76)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 1.76Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.157 , 0.200 0.169 , 0.206	Depositor DCC
R_{free} test set	3470 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	28.4	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 41.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	5009	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: GLC, EDO, NH2

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	1.01	4/4554 (0.1%)	0.97	5/6188 (0.1%)
2	B	0.98	0/152	0.91	0/203
All	All	1.01	4/4706 (0.1%)	0.97	5/6391 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2099	GLU	CD-OE2	-9.62	1.15	1.25
1	A	2099	GLU	CD-OE1	5.88	1.32	1.25
1	A	361	GLU	CD-OE1	5.30	1.31	1.25
1	A	2049	TYR	CD1-CE1	5.12	1.47	1.39

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	2090	ASP	CB-CG-OD1	7.76	125.29	118.30
1	A	1085	ASP	CB-CG-OD2	7.76	125.28	118.30
1	A	2067	ARG	NE-CZ-NH2	-6.43	117.09	120.30
1	A	373	GLU	OE1-CD-OE2	-6.20	115.87	123.30
1	A	2034	LEU	CB-CG-CD2	-5.01	102.49	111.00

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	4424	0	4263	30	0
2	B	148	0	146	1	0
3	C	23	0	20	0	0
4	A	20	0	30	1	0
5	A	383	0	0	7	0
5	B	11	0	0	2	0
All	All	5009	0	4459	31	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 3.

All (31) 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)
2:B:46:LYS:NZ	5:B:110:HOH:O	1.91	0.99
1:A:1117:GLU:OE2	5:A:2580:HOH:O	1.97	0.82
1:A:1108:ASP:HB2	5:A:2459:HOH:O	1.85	0.77
1:A:45:LEU:CD1	1:A:62:ILE:HD11	2.18	0.72
1:A:1108:ASP:OD1	5:A:2680:HOH:O	2.12	0.66
1:A:217:ALA:O	1:A:221:LYS:HG3	1.96	0.64
1:A:337:GLN:H	1:A:337:GLN:HE21	1.47	0.61
1:A:1117:GLU:CD	5:A:2580:HOH:O	2.36	0.61
1:A:202:LYS:CE	5:A:2567:HOH:O	2.50	0.60
1:A:202:LYS:HE2	5:A:2567:HOH:O	2.03	0.58
1:A:323:MET:O	1:A:327:GLN:HG2	2.04	0.58
1:A:337:GLN:H	1:A:337:GLN:NE2	2.02	0.57
1:A:337:GLN:HA	4:A:2204:EDO:H22	1.90	0.52
1:A:2058:GLN:OE1	1:A:2058:GLN:HA	2.09	0.52
1:A:356[B]:ARG:HG2	5:B:109:HOH:O	2.10	0.50
1:A:1108:ASP:CB	5:A:2459:HOH:O	2.52	0.50
1:A:2085:MET:SD	1:A:2100:LYS:HG2	2.52	0.49
1:A:1133:LEU:CD2	1:A:1137:THR:HG21	2.42	0.49
1:A:1133:LEU:HD22	1:A:1137:THR:HG21	1.93	0.49
1:A:45:LEU:HD11	1:A:62:ILE:HD11	1.95	0.47
1:A:45:LEU:HD13	1:A:62:ILE:HD11	1.97	0.46
1:A:2058:GLN:HE21	1:A:2060:ALA:HB3	1.80	0.46
1:A:1080:GLU:HA	1:A:1083:TRP:CE2	2.51	0.45
1:A:45:LEU:HD13	1:A:62:ILE:CD1	2.47	0.44
1:A:45:LEU:HD12	1:A:45:LEU:C	2.38	0.43
1:A:1065:VAL:CG1	1:A:1119:ILE:HG13	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:PRO:HA	1:A:234:TRP:CE2	2.54	0.42
1:A:175:ASN:HA	1:A:175:ASN:HD22	1.54	0.41
1:A:61:ILE:HG21	1:A:61:ILE:HD13	1.91	0.41
1:A:1065:VAL:HG13	1:A:1119:ILE:HG13	2.02	0.41
1:A:2059:GLN:N	1:A:2059:GLN:OE1	2.50	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	555/591 (94%)	550 (99%)	5 (1%)	0	100	100
2	B	18/29 (62%)	18 (100%)	0	0	100	100
All	All	573/620 (92%)	568 (99%)	5 (1%)	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	465/489 (95%)	458 (98%)	7 (2%)	65	49
2	B	17/25 (68%)	16 (94%)	1 (6%)	19	4
All	All	482/514 (94%)	474 (98%)	8 (2%)	60	42

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	LYS
1	A	175	ASN
1	A	180	ILE
1	A	260	PHE
1	A	297	LYS
1	A	337	GLN
1	A	2100	LYS
2	B	36	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	51	GLN
1	A	102	ASN
1	A	175	ASN
1	A	220	ASN
1	A	337	GLN
1	A	1130	ASN
1	A	2050	GLN
1	A	2086	GLN

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)

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	GLC	C	1	3	12,12,12	0.89	0	17,17,17	1.37	2 (11%)
3	GLC	C	2	3	11,11,12	0.87	0	15,15,17	1.14	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GLC	C	1	3	-	0/2/22/22	0/1/1/1
3	GLC	C	2	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	1	GLC	O5-C1-C2	3.41	116.36	110.28
3	C	1	GLC	O2-C2-C3	-2.59	104.36	110.35
3	C	2	GLC	O2-C2-C3	-2.14	105.85	110.14
3	C	2	GLC	C1-O5-C5	2.09	115.03	112.19

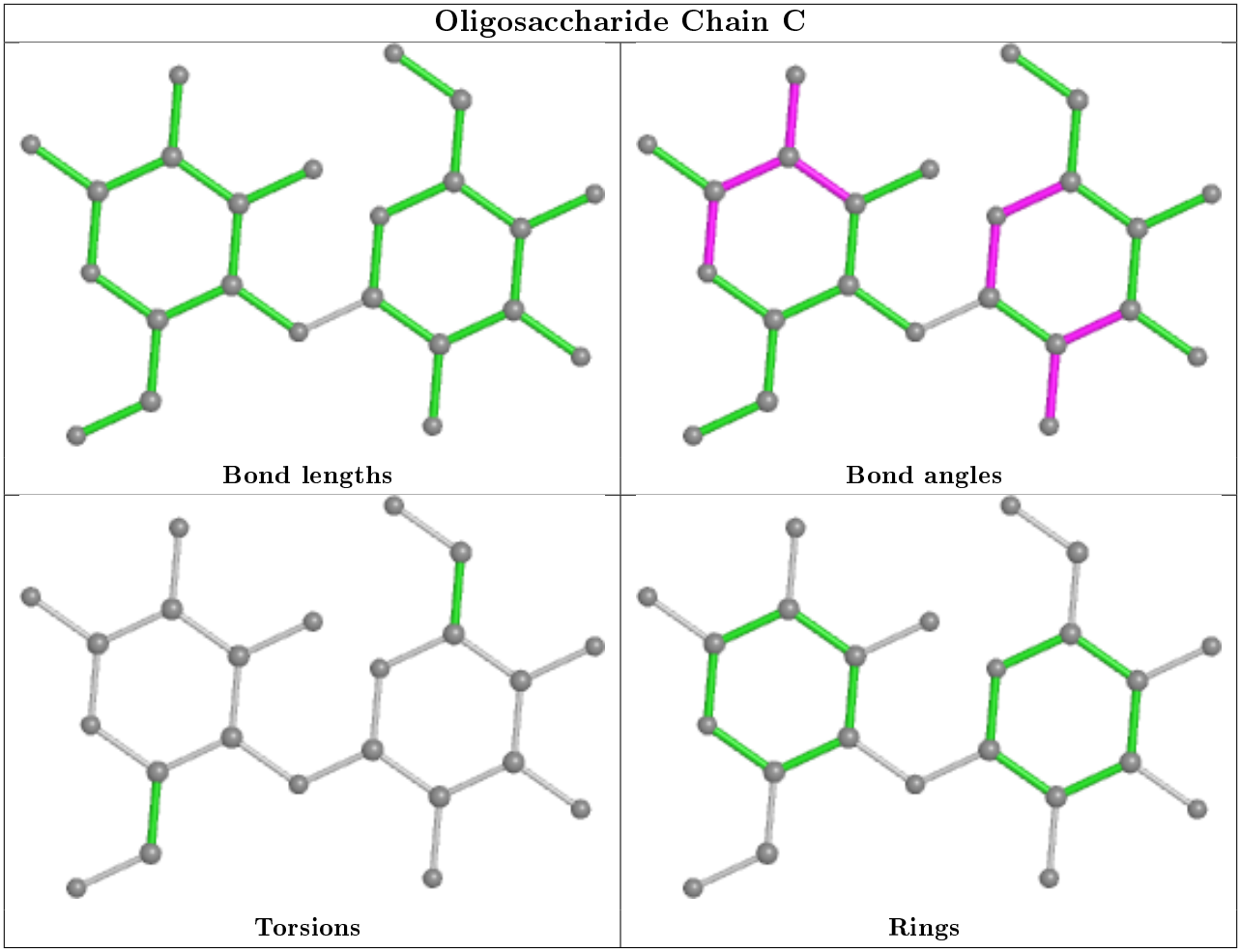
There are no chirality outliers.

There are no torsion outliers.

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)

5 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	EDO	A	2206	-	3,3,3	0.73	0	2,2,2	0.73	0
4	EDO	A	2205	-	3,3,3	0.63	0	2,2,2	0.99	0
4	EDO	A	2202	-	3,3,3	0.55	0	2,2,2	0.51	0
4	EDO	A	2204	-	3,3,3	1.11	0	2,2,2	1.61	1 (50%)
4	EDO	A	2203	-	3,3,3	0.64	0	2,2,2	0.31	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
4	EDO	A	2206	-	-	1/1/1/1	-
4	EDO	A	2205	-	-	1/1/1/1	-
4	EDO	A	2202	-	-	0/1/1/1	-
4	EDO	A	2204	-	-	1/1/1/1	-
4	EDO	A	2203	-	-	0/1/1/1	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	2204	EDO	O2-C2-C1	2.26	128.19	111.91

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	2206	EDO	O1-C1-C2-O2
4	A	2205	EDO	O1-C1-C2-O2
4	A	2204	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2204	EDO	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

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^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	555/591 (93%)	-0.10	12 (2%) 62 69	19, 34, 56, 95	0
2	B	18/29 (62%)	0.44	3 (16%) 1 2	24, 37, 85, 86	0
All	All	573/620 (92%)	-0.08	15 (2%) 56 62	19, 34, 56, 95	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2059	GLN	8.0
1	A	2061	GLU	5.6
1	A	2129	VAL	4.2
2	B	35	ASP	4.2
2	B	36	LYS	4.1
1	A	2060	ALA	4.0
1	A	54	ALA	2.9
2	B	37	ASP	2.9
1	A	55	THR	2.8
1	A	1139	SER	2.6
1	A	2058	GLN	2.2
1	A	2032	ILE	2.2
1	A	3	LYS	2.1
1	A	315	LYS	2.0
1	A	314	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

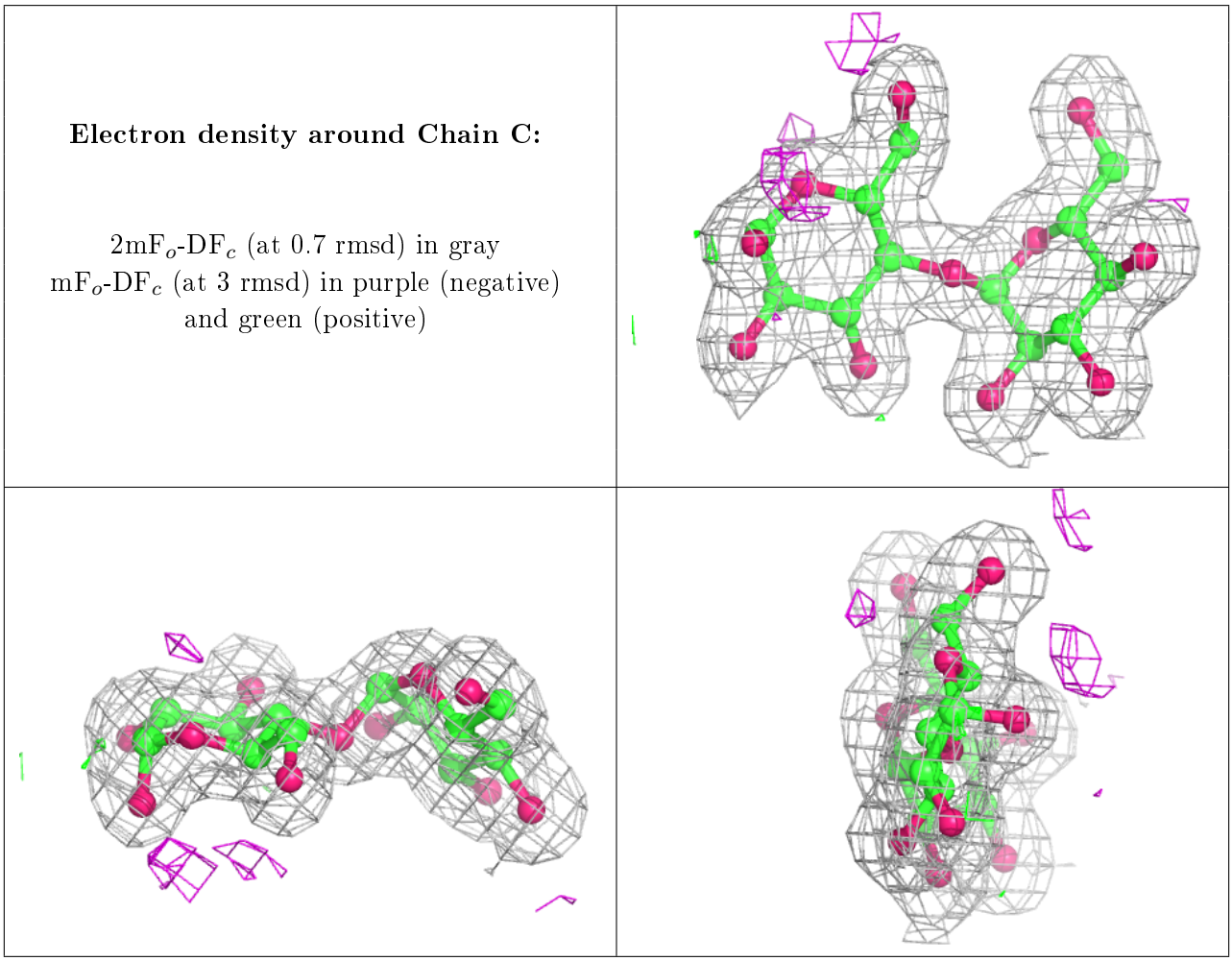
There are no non-standard protein/DNA/RNA residues in this entry.

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^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GLC	C	1	12/12	0.97	0.14	21,24,30,30	0
3	GLC	C	2	11/12	0.98	0.17	20,21,22,22	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^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	EDO	A	2206	4/4	0.84	0.16	44,51,54,59	0
4	EDO	A	2205	4/4	0.85	0.16	40,43,48,54	0
4	EDO	A	2204	4/4	0.88	0.15	28,35,48,51	0
4	EDO	A	2203	4/4	0.96	0.07	34,37,41,42	0
4	EDO	A	2202	4/4	0.97	0.07	23,24,24,25	0

6.5 Other polymers

There are no such residues in this entry.