Full wwPDB X-ray Structure Validation Report (i)

Sep 3, 2023 – 10:55 PM EDT

PDB ID	:	3S3W
Title	:	Structure of chicken acid-sensing ion channel 1 at 2.6 a resolution and ph 7.5
Authors	:	Dawson, R.J.P.; Benz, J.; Stohler, P.; Tetaz, T.; Joseph, C.; Huber, S.; Schmid, G.; Huegin, D.; Pflimlin, P.; Trube, G.; Rudolph, M.G.; Hennig, M.; Ruf, A.
Deposited on	:	2011-05-18
Resolution	:	2.60 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

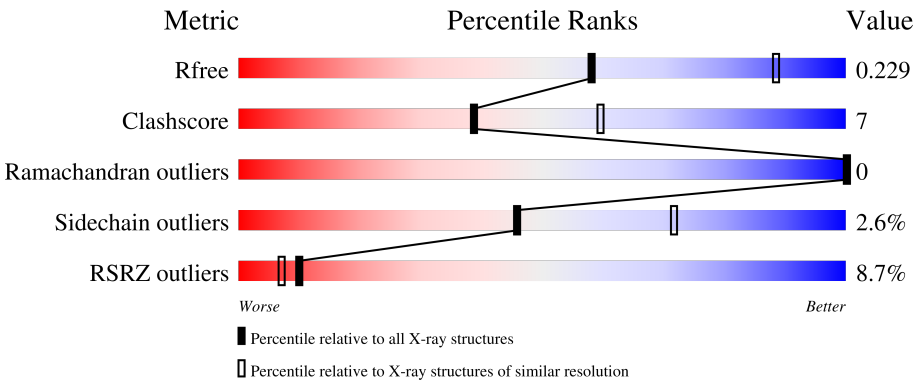
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=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	459	8%, 70%, 14%, •, 14%
1	B	459	9%, 70%, 15%, •, 14%
1	C	459	6%, 71%, 15%, •, 13%
2	D	2	100%
2	E	2	50%, 50%

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Mol	Chain	Length	Quality of chain
2	F	2	100%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9925 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 Amiloride-sensitive cation channel 2, neuronal.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	396	3162	2022	515	598	27	0	0	0
1	B	397	3177	2032	516	603	26	0	0	0
1	C	401	3209	2058	521	603	27	0	0	0

There are 63 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	MET	-	expression tag	UNP Q1XA76
A	6	SER	-	expression tag	UNP Q1XA76
A	7	TYR	-	expression tag	UNP Q1XA76
A	8	TYR	-	expression tag	UNP Q1XA76
A	9	HIS	-	expression tag	UNP Q1XA76
A	10	HIS	-	expression tag	UNP Q1XA76
A	11	HIS	-	expression tag	UNP Q1XA76
A	12	HIS	-	expression tag	UNP Q1XA76
A	13	HIS	-	expression tag	UNP Q1XA76
A	14	HIS	-	expression tag	UNP Q1XA76
A	15	GLY	-	expression tag	UNP Q1XA76
A	16	ALA	-	expression tag	UNP Q1XA76
A	17	SER	-	expression tag	UNP Q1XA76
A	18	LEU	-	expression tag	UNP Q1XA76
A	19	VAL	-	expression tag	UNP Q1XA76
A	20	PRO	-	expression tag	UNP Q1XA76
A	21	ARG	-	expression tag	UNP Q1XA76
A	22	GLY	-	expression tag	UNP Q1XA76
A	23	SER	-	expression tag	UNP Q1XA76
A	24	HIS	-	expression tag	UNP Q1XA76
A	25	MET	-	expression tag	UNP Q1XA76
B	5	MET	-	expression tag	UNP Q1XA76
B	6	SER	-	expression tag	UNP Q1XA76

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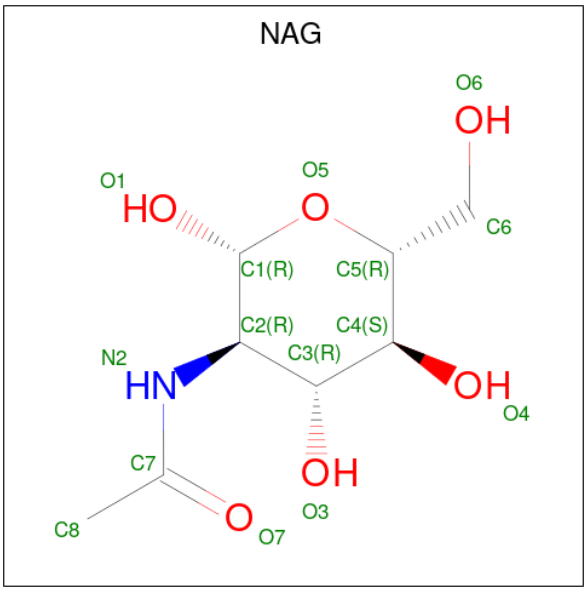
Chain	Residue	Modelled	Actual	Comment	Reference
B	7	TYR	-	expression tag	UNP Q1XA76
B	8	TYR	-	expression tag	UNP Q1XA76
B	9	HIS	-	expression tag	UNP Q1XA76
B	10	HIS	-	expression tag	UNP Q1XA76
B	11	HIS	-	expression tag	UNP Q1XA76
B	12	HIS	-	expression tag	UNP Q1XA76
B	13	HIS	-	expression tag	UNP Q1XA76
B	14	HIS	-	expression tag	UNP Q1XA76
B	15	GLY	-	expression tag	UNP Q1XA76
B	16	ALA	-	expression tag	UNP Q1XA76
B	17	SER	-	expression tag	UNP Q1XA76
B	18	LEU	-	expression tag	UNP Q1XA76
B	19	VAL	-	expression tag	UNP Q1XA76
B	20	PRO	-	expression tag	UNP Q1XA76
B	21	ARG	-	expression tag	UNP Q1XA76
B	22	GLY	-	expression tag	UNP Q1XA76
B	23	SER	-	expression tag	UNP Q1XA76
B	24	HIS	-	expression tag	UNP Q1XA76
B	25	MET	-	expression tag	UNP Q1XA76
C	5	MET	-	expression tag	UNP Q1XA76
C	6	SER	-	expression tag	UNP Q1XA76
C	7	TYR	-	expression tag	UNP Q1XA76
C	8	TYR	-	expression tag	UNP Q1XA76
C	9	HIS	-	expression tag	UNP Q1XA76
C	10	HIS	-	expression tag	UNP Q1XA76
C	11	HIS	-	expression tag	UNP Q1XA76
C	12	HIS	-	expression tag	UNP Q1XA76
C	13	HIS	-	expression tag	UNP Q1XA76
C	14	HIS	-	expression tag	UNP Q1XA76
C	15	GLY	-	expression tag	UNP Q1XA76
C	16	ALA	-	expression tag	UNP Q1XA76
C	17	SER	-	expression tag	UNP Q1XA76
C	18	LEU	-	expression tag	UNP Q1XA76
C	19	VAL	-	expression tag	UNP Q1XA76
C	20	PRO	-	expression tag	UNP Q1XA76
C	21	ARG	-	expression tag	UNP Q1XA76
C	22	GLY	-	expression tag	UNP Q1XA76
C	23	SER	-	expression tag	UNP Q1XA76
C	24	HIS	-	expression tag	UNP Q1XA76
C	25	MET	-	expression tag	UNP Q1XA76

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	D	2	28	16	2	10	0	0	0
			Total	C	N	O			
2	E	2	28	16	2	10	0	0	0
			Total	C	N	O			
2	F	2	28	16	2	10	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
4	A	1	1	1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
4	B	1	1	1	0	0
			Total	Cl		
4	C	1	1	1	0	0

- Molecule 5 is water.

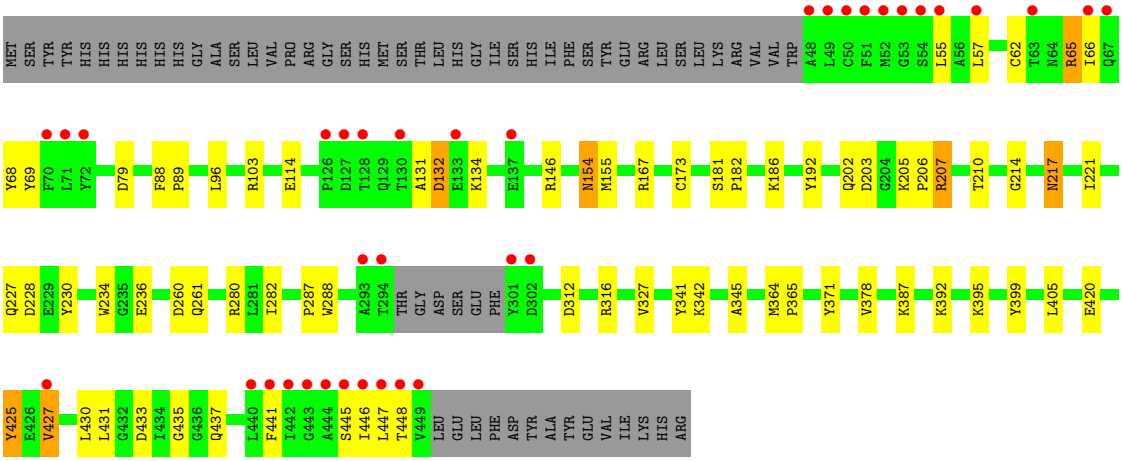
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	85	85	85	0	0
			Total	O		
5	B	87	87	87	0	0
			Total	O		
5	C	76	76	76	0	0

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.

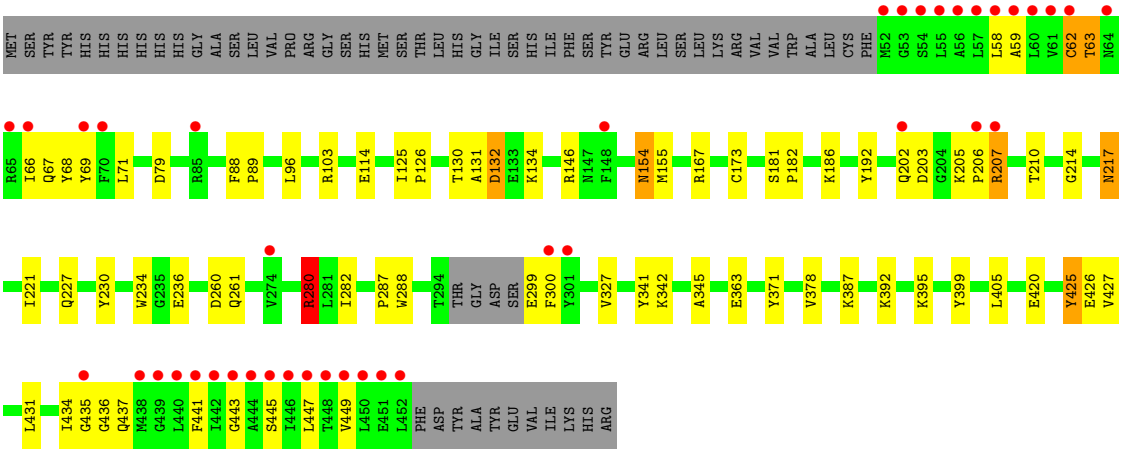
• Molecule 1: Amiloride-sensitive cation channel 2, neuronal

Chain A:



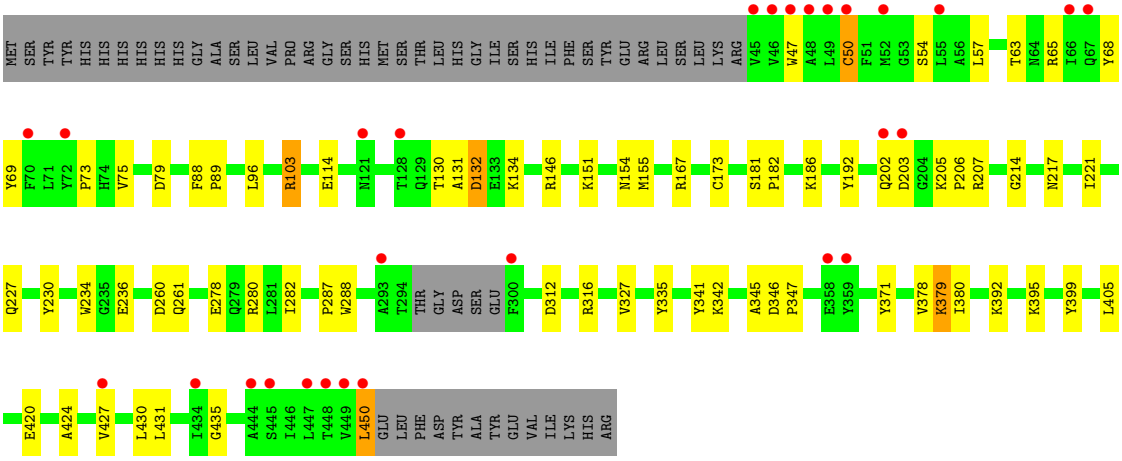
• Molecule 1: Amiloride-sensitive cation channel 2, neuronal

Chain B:



• Molecule 1: Amiloride-sensitive cation channel 2, neuronal

Chain C:



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

Chain D: 100%

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

Chain E: 50% 50%

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

Chain F: 100%

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	110.47Å 142.69Å 159.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.94 – 2.60 47.94 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.94-2.60) 95.7 (47.94-2.60)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	0.16	Depositor
$< I/\sigma(I) >$ [1]	1.32 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.212 , 0.236 0.205 , 0.229	Depositor DCC
R_{free} test set	3924 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	49.3	Xtriage
Anisotropy	0.180	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 48.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	9925	wwPDB-VP
Average B, all atoms (Å^2)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.58% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, 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	0.23	0/3234	0.55	10/4377 (0.2%)
1	B	0.24	0/3249	0.76	13/4397 (0.3%)
1	C	0.24	0/3284	0.81	12/4447 (0.3%)
All	All	0.24	0/9767	0.72	35/13221 (0.3%)

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	103	ARG	NE-CZ-NH2	22.90	131.75	120.30
1	C	103	ARG	NE-CZ-NH1	-22.42	109.09	120.30
1	B	280	ARG	NE-CZ-NH1	-17.44	111.58	120.30
1	C	207	ARG	NE-CZ-NH2	-17.29	111.65	120.30
1	C	207	ARG	NE-CZ-NH1	16.23	128.41	120.30
1	B	280	ARG	NE-CZ-NH2	15.73	128.17	120.30
1	B	146	ARG	NE-CZ-NH2	-15.56	112.52	120.30
1	B	146	ARG	NE-CZ-NH1	15.08	127.84	120.30
1	B	167	ARG	NE-CZ-NH1	-15.04	112.78	120.30
1	B	167	ARG	NE-CZ-NH2	14.57	127.59	120.30
1	C	103	ARG	CD-NE-CZ	10.81	138.73	123.60
1	C	280	ARG	NE-CZ-NH2	-8.93	115.83	120.30
1	A	280	ARG	NE-CZ-NH2	-8.91	115.84	120.30
1	A	280	ARG	NE-CZ-NH1	8.23	124.41	120.30
1	C	280	ARG	NE-CZ-NH1	8.21	124.40	120.30
1	B	280	ARG	CD-NE-CZ	7.89	134.65	123.60
1	A	146	ARG	NE-CZ-NH1	-7.83	116.39	120.30
1	C	146	ARG	NE-CZ-NH1	-7.81	116.39	120.30
1	A	207	ARG	NE-CZ-NH1	-7.70	116.45	120.30
1	B	146	ARG	CD-NE-CZ	7.59	134.23	123.60
1	C	167	ARG	NE-CZ-NH2	-7.58	116.51	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	146	ARG	NE-CZ-NH2	7.51	124.06	120.30
1	A	146	ARG	NE-CZ-NH2	7.49	124.05	120.30
1	A	167	ARG	NE-CZ-NH2	-7.42	116.59	120.30
1	C	207	ARG	CD-NE-CZ	7.26	133.76	123.60
1	C	167	ARG	NE-CZ-NH1	7.19	123.89	120.30
1	A	207	ARG	NE-CZ-NH2	7.13	123.87	120.30
1	A	167	ARG	NE-CZ-NH1	7.12	123.86	120.30
1	B	167	ARG	CD-NE-CZ	7.10	133.54	123.60
1	B	207	ARG	NE-CZ-NH1	-6.90	116.85	120.30
1	B	103	ARG	NE-CZ-NH2	-6.81	116.90	120.30
1	A	103	ARG	NE-CZ-NH2	-6.66	116.97	120.30
1	B	207	ARG	NE-CZ-NH2	6.36	123.48	120.30
1	A	103	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	B	103	ARG	NE-CZ-NH1	5.31	122.96	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	3162	0	3068	55	0
1	B	3177	0	3081	55	1
1	C	3209	0	3116	48	1
2	D	28	0	25	0	0
2	E	28	0	25	1	0
2	F	28	0	25	0	0
3	A	14	0	13	0	0
3	C	28	0	26	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	A	85	0	0	1	0
5	B	87	0	0	0	0
5	C	76	0	0	2	0
All	All	9925	0	9379	142	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 7.

All (142) 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:68:TYR:HD2	1:A:425:TYR:HD2	1.03	0.95
1:A:68:TYR:CD2	1:A:425:TYR:HD2	1.85	0.94
1:A:68:TYR:HD2	1:A:425:TYR:CD2	1.86	0.93
1:B:436:GLY:HA2	1:C:57:LEU:HD22	1.59	0.83
1:A:447:LEU:HD12	1:C:450:LEU:HD23	1.63	0.79
1:B:59:ALA:O	1:B:63:THR:OG1	2.07	0.72
1:A:392:LYS:NZ	1:B:236:GLU:OE2	2.23	0.71
1:B:392:LYS:NZ	1:C:236:GLU:OE2	2.23	0.70
1:B:299:GLU:HG2	1:B:300:PHE:H	1.57	0.70
1:B:299:GLU:HG2	1:B:300:PHE:N	2.08	0.68
1:C:395:LYS:HG2	1:C:399:TYR:CD1	2.31	0.66
1:A:395:LYS:HG2	1:A:399:TYR:CD1	2.31	0.65
1:B:58:LEU:O	1:B:62:CYS:HB2	1.97	0.65
1:B:395:LYS:HG2	1:B:399:TYR:CD1	2.31	0.65
1:B:443:GLY:HA3	1:C:50:CYS:SG	2.38	0.64
1:A:68:TYR:CD2	1:A:425:TYR:CD2	2.74	0.61
1:C:75:VAL:HG13	1:C:424:ALA:HB2	1.84	0.59
1:A:228:ASP:HB3	5:A:492:HOH:O	2.02	0.59
1:B:68:TYR:HA	1:B:71:LEU:HD12	1.82	0.59
1:C:54:SER:O	1:C:57:LEU:HG	2.02	0.58
1:A:62:CYS:O	1:A:66:ILE:HG12	2.04	0.58
1:A:441:PHE:O	1:A:445:SER:OG	2.11	0.58
1:B:447:LEU:HD21	1:C:47:TRP:CZ2	2.39	0.57
1:B:186:LYS:HE2	1:B:202:GLN:OE1	2.05	0.57
1:A:186:LYS:HE2	1:A:202:GLN:OE1	2.05	0.57
1:C:186:LYS:HE2	1:C:202:GLN:OE1	2.04	0.57
1:C:131:ALA:HB2	1:C:234:TRP:HE1	1.70	0.56
1:B:62:CYS:O	1:B:434:ILE:HD11	2.06	0.56
1:B:447:LEU:HD11	1:C:47:TRP:NE1	2.21	0.56
1:A:131:ALA:HB2	1:A:234:TRP:HE1	1.70	0.55
1:A:425:TYR:HE1	1:A:430:LEU:N	2.04	0.55
1:A:425:TYR:CE1	1:A:430:LEU:HA	2.42	0.55
1:C:312:ASP:OD2	1:C:316:ARG:NH1	2.40	0.55
1:C:181:SER:HB2	1:C:182:PRO:HD2	1.90	0.54
1:B:181:SER:HB2	1:B:182:PRO:HD2	1.90	0.54
1:B:131:ALA:HB2	1:B:234:TRP:HE1	1.71	0.54
1:C:203:ASP:HB3	1:C:205:LYS:HG3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:ASP:HB3	1:B:205:LYS:HG3	1.91	0.53
1:A:387:LYS:HG2	1:B:130:THR:HB	1.91	0.53
1:A:181:SER:HB2	1:A:182:PRO:HD2	1.90	0.52
1:A:203:ASP:HB3	1:A:205:LYS:HG3	1.91	0.52
1:A:236:GLU:OE2	1:C:392:LYS:NZ	2.43	0.52
1:A:425:TYR:OH	1:A:430:LEU:HA	2.10	0.52
1:A:65:ARG:HD3	1:A:433:ASP:HB3	1.93	0.51
1:A:69:TYR:CE2	1:A:427:VAL:HG23	2.46	0.51
1:C:395:LYS:HG2	1:C:399:TYR:CE1	2.46	0.51
1:A:341:TYR:HA	1:A:345:ALA:HB3	1.94	0.50
1:A:155:MET:HB2	1:A:327:VAL:HG11	1.94	0.50
1:A:395:LYS:HG2	1:A:399:TYR:CE1	2.46	0.50
1:A:154:ASN:C	1:A:154:ASN:OD1	2.50	0.50
1:A:173:CYS:SG	1:A:221:ILE:HG22	2.52	0.50
1:B:395:LYS:HG2	1:B:399:TYR:CE1	2.46	0.50
1:B:173:CYS:SG	1:B:221:ILE:HG22	2.51	0.50
1:C:173:CYS:SG	1:C:221:ILE:HG22	2.52	0.50
1:B:437:GLN:N	1:B:437:GLN:OE1	2.45	0.50
1:C:427:VAL:HG23	5:C:524:HOH:O	2.11	0.49
1:B:341:TYR:HA	1:B:345:ALA:HB3	1.94	0.49
1:C:341:TYR:HA	1:C:345:ALA:HB3	1.94	0.49
1:B:155:MET:HB2	1:B:327:VAL:HG11	1.95	0.48
1:B:405:LEU:HD12	1:B:405:LEU:C	2.33	0.48
1:C:68:TYR:CE1	1:C:73:PRO:HG3	2.48	0.48
1:B:88:PHE:CG	1:B:89:PRO:HD2	2.49	0.48
1:A:57:LEU:HB3	1:A:437:GLN:OE1	2.14	0.48
1:A:88:PHE:CG	1:A:89:PRO:HD2	2.48	0.48
1:C:278:GLU:OE1	5:C:507:HOH:O	2.20	0.48
1:B:431:LEU:O	1:B:435:GLY:N	2.44	0.48
1:A:55:LEU:HD13	1:A:441:PHE:CE1	2.49	0.48
1:C:88:PHE:CG	1:C:89:PRO:HD2	2.48	0.47
1:B:68:TYR:HD2	1:B:425:TYR:CD2	2.32	0.47
1:A:405:LEU:C	1:A:405:LEU:HD12	2.33	0.47
1:C:155:MET:HB2	1:C:327:VAL:HG11	1.96	0.47
1:C:131:ALA:HB2	1:C:234:TRP:NE1	2.30	0.47
1:C:405:LEU:C	1:C:405:LEU:HD12	2.34	0.47
1:C:287:PRO:HD2	1:C:288:TRP:CZ3	2.50	0.47
1:A:227:GLN:HA	1:A:230:TYR:CD1	2.49	0.47
1:B:69:TYR:CE2	1:B:427:VAL:HG22	2.50	0.47
1:A:287:PRO:HD2	1:A:288:TRP:CZ3	2.50	0.47
1:B:67:GLN:O	1:B:71:LEU:HG	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:89:PRO:HB3	1:C:371:TYR:CZ	2.51	0.47
1:C:132:ASP:OD1	1:C:134:LYS:N	2.48	0.47
1:C:227:GLN:HA	1:C:230:TYR:CD1	2.50	0.46
1:B:89:PRO:HB3	1:B:371:TYR:CZ	2.51	0.46
1:B:443:GLY:O	1:B:447:LEU:HB2	2.15	0.46
1:B:227:GLN:HA	1:B:230:TYR:CD1	2.50	0.46
1:A:131:ALA:HB2	1:A:234:TRP:NE1	2.30	0.46
1:A:431:LEU:O	1:A:435:GLY:N	2.23	0.46
1:B:287:PRO:HD2	1:B:288:TRP:CZ3	2.50	0.46
1:A:132:ASP:OD1	1:A:134:LYS:N	2.48	0.46
1:B:132:ASP:OD1	1:B:134:LYS:N	2.48	0.46
1:A:89:PRO:HB3	1:A:371:TYR:CZ	2.51	0.46
1:B:154:ASN:OD1	1:B:154:ASN:C	2.55	0.46
1:B:387:LYS:HG2	1:C:130:THR:HB	1.97	0.46
1:B:131:ALA:HB2	1:B:234:TRP:NE1	2.30	0.45
1:B:445:SER:O	1:B:449:VAL:HG23	2.17	0.45
1:C:431:LEU:O	1:C:435:GLY:N	2.46	0.45
1:C:192:TYR:CE2	1:C:260:ASP:HA	2.52	0.45
1:A:425:TYR:HE1	1:A:430:LEU:CA	2.30	0.45
1:C:132:ASP:OD1	1:C:132:ASP:C	2.55	0.45
1:A:214:GLY:HA2	1:B:261:GLN:O	2.17	0.45
1:B:181:SER:HB2	1:B:182:PRO:CD	2.47	0.45
1:C:54:SER:HA	1:C:57:LEU:HD23	1.99	0.45
1:A:192:TYR:CE2	1:A:260:ASP:HA	2.52	0.44
1:A:261:GLN:O	1:C:214:GLY:HA2	2.17	0.44
1:B:58:LEU:HD13	1:B:441:PHE:HB2	1.99	0.44
1:B:132:ASP:OD1	1:B:132:ASP:C	2.55	0.44
1:C:181:SER:HB2	1:C:182:PRO:CD	2.47	0.44
1:B:114:GLU:HG2	1:B:342:LYS:HE3	1.99	0.44
1:C:379:LYS:HG3	1:C:380:ILE:N	2.32	0.44
1:A:205:LYS:HB3	1:A:206:PRO:HD2	2.00	0.44
1:A:114:GLU:HG2	1:A:342:LYS:HE3	1.99	0.43
1:B:192:TYR:CE2	1:B:260:ASP:HA	2.52	0.43
1:A:425:TYR:CE1	1:A:430:LEU:CA	3.01	0.43
1:A:446:ILE:HG22	1:A:446:ILE:O	2.19	0.43
1:B:214:GLY:HA2	1:C:261:GLN:O	2.18	0.43
1:C:114:GLU:HG2	1:C:342:LYS:HE3	1.99	0.43
1:A:132:ASP:OD1	1:A:132:ASP:C	2.56	0.43
1:A:57:LEU:HD23	1:A:57:LEU:HA	1.86	0.43
1:A:364:MET:HA	1:A:365:PRO:HD3	1.90	0.43
1:C:450:LEU:HD12	1:C:450:LEU:HA	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:378:VAL:HG11	1:C:96:LEU:HD11	2.01	0.43
1:A:181:SER:HB2	1:A:182:PRO:CD	2.48	0.42
1:B:205:LYS:HB3	1:B:206:PRO:HD2	2.01	0.42
1:C:205:LYS:HB3	1:C:206:PRO:HD2	2.01	0.42
1:A:378:VAL:HG11	1:B:96:LEU:HD11	2.00	0.42
1:B:280:ARG:HH11	2:E:1:NAG:H3	1.84	0.42
1:C:282:ILE:HB	1:C:420:GLU:HG3	2.02	0.42
1:A:282:ILE:HB	1:A:420:GLU:HG3	2.02	0.41
1:B:282:ILE:HB	1:B:420:GLU:HG3	2.02	0.41
1:B:427:VAL:O	1:B:431:LEU:HG	2.20	0.41
1:B:62:CYS:O	1:B:66:ILE:HG13	2.20	0.41
1:C:154:ASN:HD21	1:C:335:TYR:HD2	1.66	0.41
1:A:312:ASP:OD2	1:A:316:ARG:NH2	2.53	0.41
1:A:210:THR:HG23	1:A:217:ASN:HB3	2.03	0.41
1:C:65:ARG:HB3	1:C:430:LEU:CD1	2.51	0.41
1:A:65:ARG:HB3	1:A:430:LEU:HD11	2.02	0.41
1:B:280:ARG:HA	1:B:280:ARG:HD3	1.79	0.41
1:A:425:TYR:CZ	1:A:430:LEU:HA	2.56	0.40
1:C:346:ASP:HB2	1:C:347:PRO:HD3	2.03	0.40
1:A:96:LEU:HD11	1:C:378:VAL:HG11	2.02	0.40
1:B:210:THR:HG23	1:B:217:ASN:HB3	2.04	0.40
1:B:125:ILE:HA	1:B:126:PRO:HD3	1.89	0.40
1:C:69:TYR:OH	1:C:427:VAL:HG22	2.21	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:B:363:GLU:OE1	1:C:151:LYS:NZ[3_555]	2.09	0.11

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	392/459 (85%)	383 (98%)	9 (2%)	0	100	100
1	B	393/459 (86%)	384 (98%)	9 (2%)	0	100	100
1	C	397/459 (86%)	390 (98%)	7 (2%)	0	100	100
All	All	1182/1377 (86%)	1157 (98%)	25 (2%)	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	344/401 (86%)	335 (97%)	9 (3%)	46	72
1	B	346/401 (86%)	336 (97%)	10 (3%)	42	68
1	C	349/401 (87%)	341 (98%)	8 (2%)	50	75
All	All	1039/1203 (86%)	1012 (97%)	27 (3%)	46	72

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	ARG
1	A	79	ASP
1	A	132	ASP
1	A	154	ASN
1	A	207	ARG
1	A	217	ASN
1	A	425	TYR
1	A	427	VAL
1	A	448	THR
1	B	62	CYS
1	B	63	THR
1	B	79	ASP
1	B	132	ASP
1	B	154	ASN
1	B	207	ARG

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Mol	Chain	Res	Type
1	B	217	ASN
1	B	280	ARG
1	B	425	TYR
1	B	426	GLU
1	C	50	CYS
1	C	63	THR
1	C	79	ASP
1	C	103	ARG
1	C	132	ASP
1	C	217	ASN
1	C	379	LYS
1	C	450	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

6 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	D	1	2,1	14,14,15	0.57	0	17,19,21	0.78	0
2	NAG	D	2	2	14,14,15	0.50	0	17,19,21	0.78	0
2	NAG	E	1	2,1	14,14,15	0.52	0	17,19,21	0.80	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	E	2	2	14,14,15	0.51	0	17,19,21	0.78	0
2	NAG	F	1	2,1	14,14,15	0.54	0	17,19,21	0.62	0
2	NAG	F	2	2	14,14,15	0.54	0	17,19,21	0.62	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
2	NAG	D	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	NAG	E	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	NAG	F	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	D	2	NAG	C8-C7-N2-C2
2	D	2	NAG	O7-C7-N2-C2
2	E	1	NAG	C8-C7-N2-C2
2	E	1	NAG	O7-C7-N2-C2
2	E	2	NAG	C8-C7-N2-C2
2	E	2	NAG	O7-C7-N2-C2

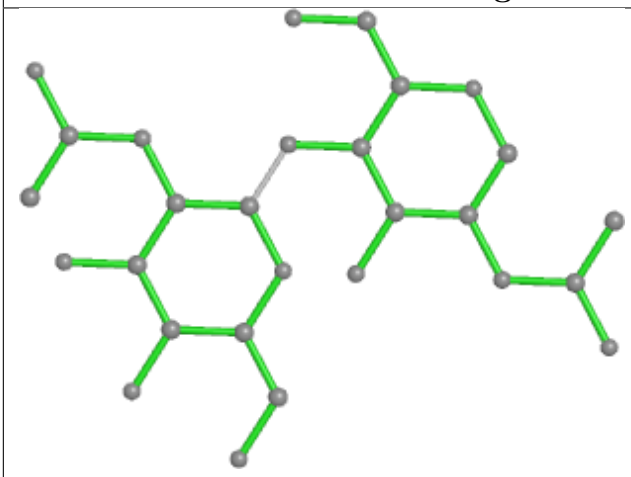
There are no ring outliers.

1 monomer is involved in 1 short contact:

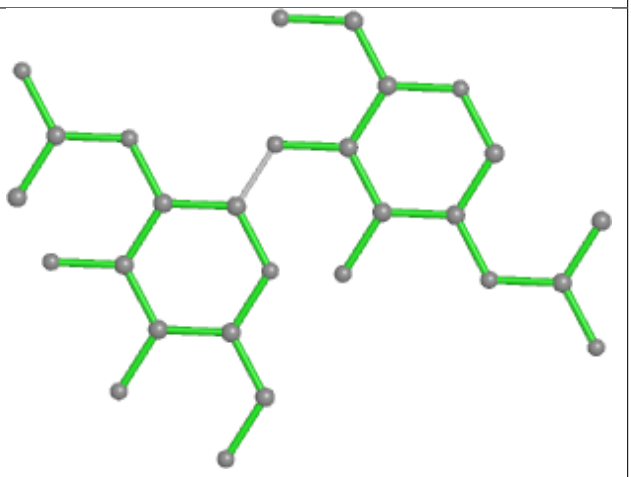
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

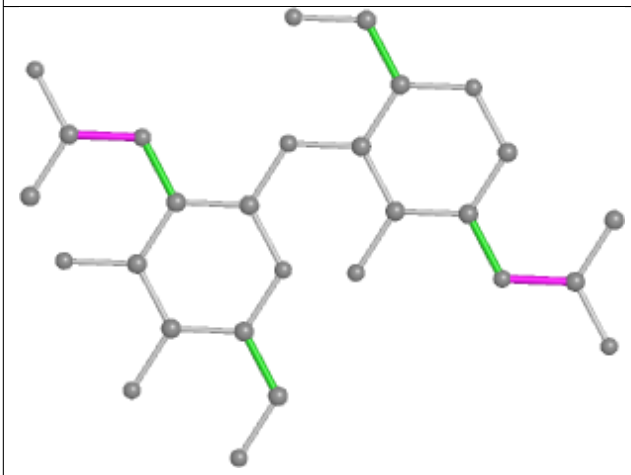
Oligosaccharide Chain D



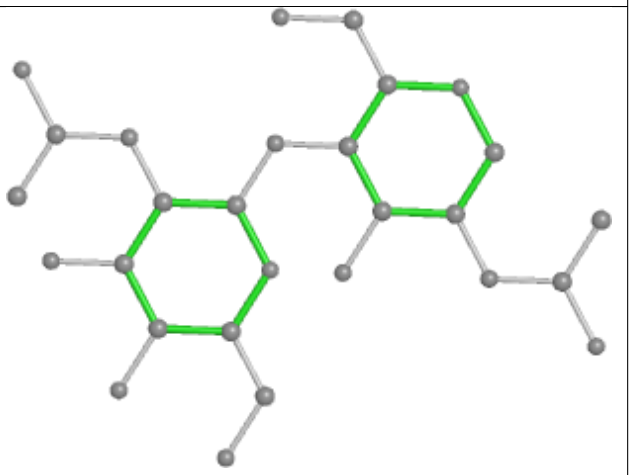
Bond lengths



Bond angles

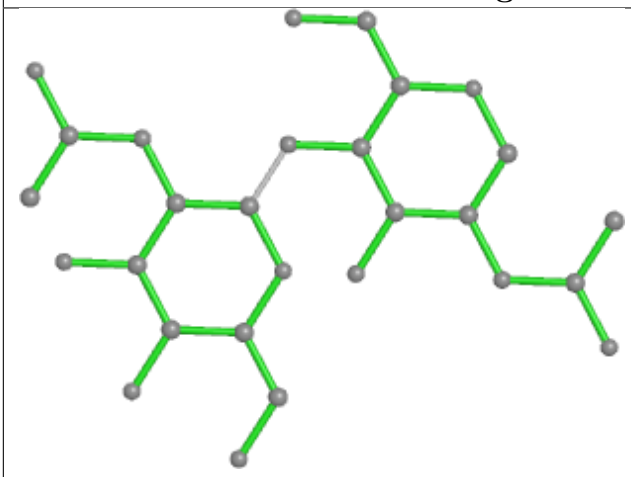


Torsions

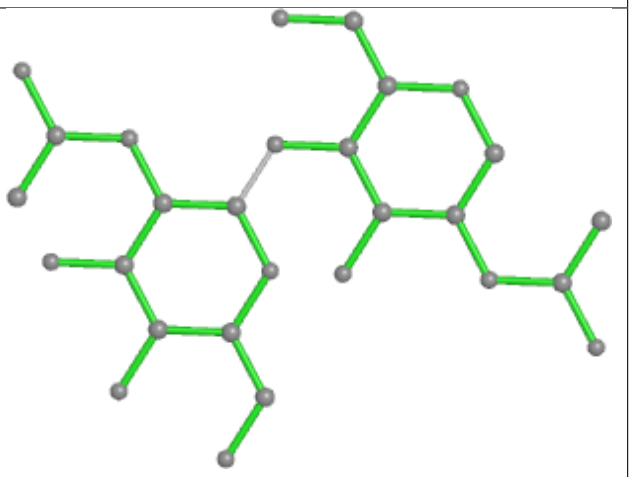


Rings

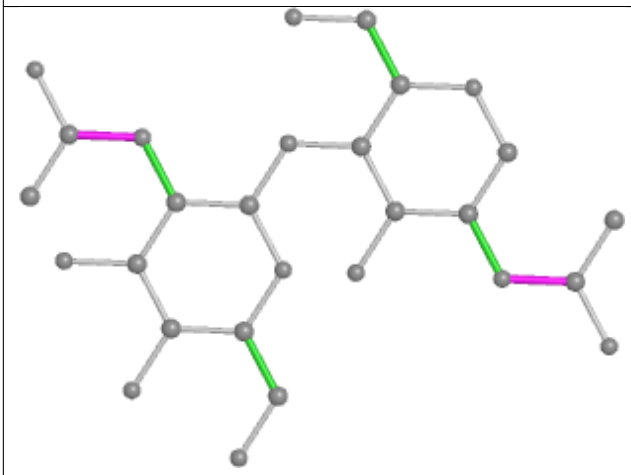
Oligosaccharide Chain E



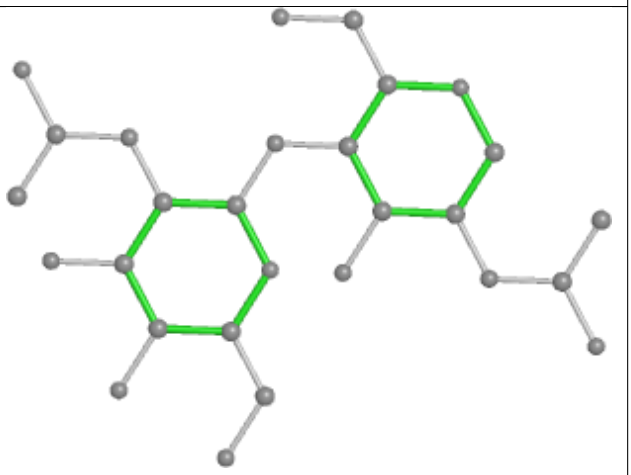
Bond lengths



Bond angles

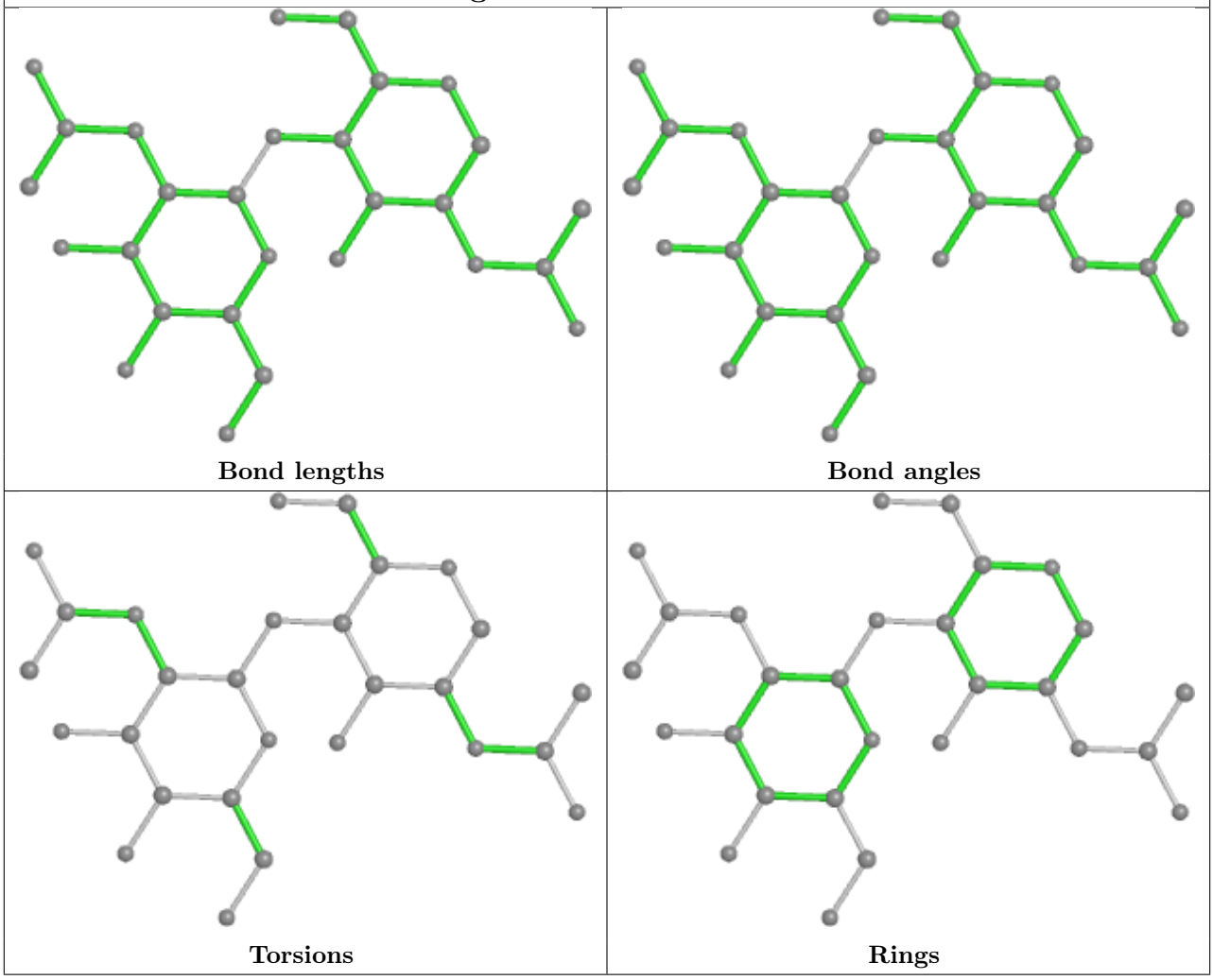


Torsions



Rings

Oligosaccharide Chain F



5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 for Mogul analysis.

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	600	1	14,14,15	0.52	0	17,19,21	0.77	0
3	NAG	A	700	1	14,14,15	0.52	0	17,19,21	0.67	0
3	NAG	C	700	1	14,14,15	0.53	0	17,19,21	0.65	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	600	1	-	2/6/23/26	0/1/1/1
3	NAG	A	700	1	-	0/6/23/26	0/1/1/1
3	NAG	C	700	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	600	NAG	C8-C7-N2-C2
3	C	600	NAG	O7-C7-N2-C2

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, 95th 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	396/459 (86%)	0.26	36 (9%) 9 6	27, 51, 149, 229	0
1	B	397/459 (86%)	0.33	40 (10%) 7 4	26, 50, 177, 233	0
1	C	401/459 (87%)	0.26	28 (6%) 16 12	27, 51, 142, 216	0
All	All	1194/1377 (86%)	0.29	104 (8%) 10 7	26, 51, 156, 233	0

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	45	VAL	12.1
1	B	449	VAL	10.4
1	A	449	VAL	9.7
1	B	446	ILE	9.4
1	C	444	ALA	9.2
1	B	55	LEU	9.2
1	C	447	LEU	8.9
1	B	450	LEU	8.1
1	C	47	TRP	8.1
1	C	448	THR	7.9
1	A	446	ILE	7.7
1	B	452	LEU	7.6
1	A	443	GLY	7.5
1	A	445	SER	7.0
1	C	46	VAL	7.0
1	B	66	ILE	6.9
1	B	52	MET	6.8
1	C	52	MET	6.7
1	A	51	PHE	6.5
1	B	448	THR	6.5
1	A	52	MET	6.5
1	C	450	LEU	6.4
1	A	293	ALA	6.4

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Mol	Chain	Res	Type	RSRZ
1	B	442	ILE	6.1
1	B	443	GLY	6.1
1	A	50	CYS	5.9
1	C	449	VAL	5.9
1	B	447	LEU	5.8
1	B	59	ALA	5.7
1	C	445	SER	5.7
1	A	301	TYR	5.7
1	C	434	ILE	5.6
1	B	445	SER	5.6
1	B	439	GLY	5.5
1	A	447	LEU	5.5
1	A	442	ILE	5.5
1	C	70	PHE	5.3
1	C	66	ILE	5.2
1	B	53	GLY	5.2
1	A	444	ALA	5.1
1	C	48	ALA	5.0
1	B	451	GLU	5.0
1	A	127	ASP	4.9
1	B	54	SER	4.8
1	B	444	ALA	4.6
1	A	128	THR	4.6
1	B	70	PHE	4.4
1	B	62	CYS	4.2
1	C	49	LEU	4.2
1	B	441	PHE	4.1
1	B	438	MET	4.0
1	B	301	TYR	4.0
1	A	55	LEU	4.0
1	A	130	THR	4.0
1	A	294	THR	4.0
1	A	71	LEU	3.9
1	B	300	PHE	3.9
1	C	50	CYS	3.6
1	A	48	ALA	3.6
1	B	60	LEU	3.5
1	B	440	LEU	3.5
1	B	207	ARG	3.5
1	A	67	GLN	3.4
1	C	128	THR	3.4
1	B	58	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
1	C	72	TYR	3.4
1	A	70	PHE	3.4
1	A	54	SER	3.3
1	C	427	VAL	3.3
1	C	300	PHE	3.3
1	A	53	GLY	3.2
1	C	202	GLN	3.1
1	B	56	ALA	3.1
1	A	448	THR	3.1
1	A	49	LEU	3.0
1	C	203	ASP	3.0
1	C	293	ALA	3.0
1	B	69	TYR	3.0
1	B	85	ARG	3.0
1	A	133	GLU	2.9
1	A	440	LEU	2.8
1	B	64	ASN	2.8
1	A	441	PHE	2.7
1	A	427	VAL	2.6
1	C	67	GLN	2.6
1	B	435	GLY	2.5
1	C	55	LEU	2.5
1	A	126	PRO	2.4
1	B	57	LEU	2.4
1	A	302	ASP	2.4
1	B	61	VAL	2.4
1	A	72	TYR	2.3
1	A	63	THR	2.3
1	B	65	ARG	2.3
1	B	274	VAL	2.3
1	C	358	GLU	2.3
1	B	206	PRO	2.2
1	B	148	PHE	2.1
1	B	202	GLN	2.1
1	A	57	LEU	2.1
1	C	121	ASN	2.1
1	A	137	GLU	2.1
1	C	359	TYR	2.1
1	A	66	ILE	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)

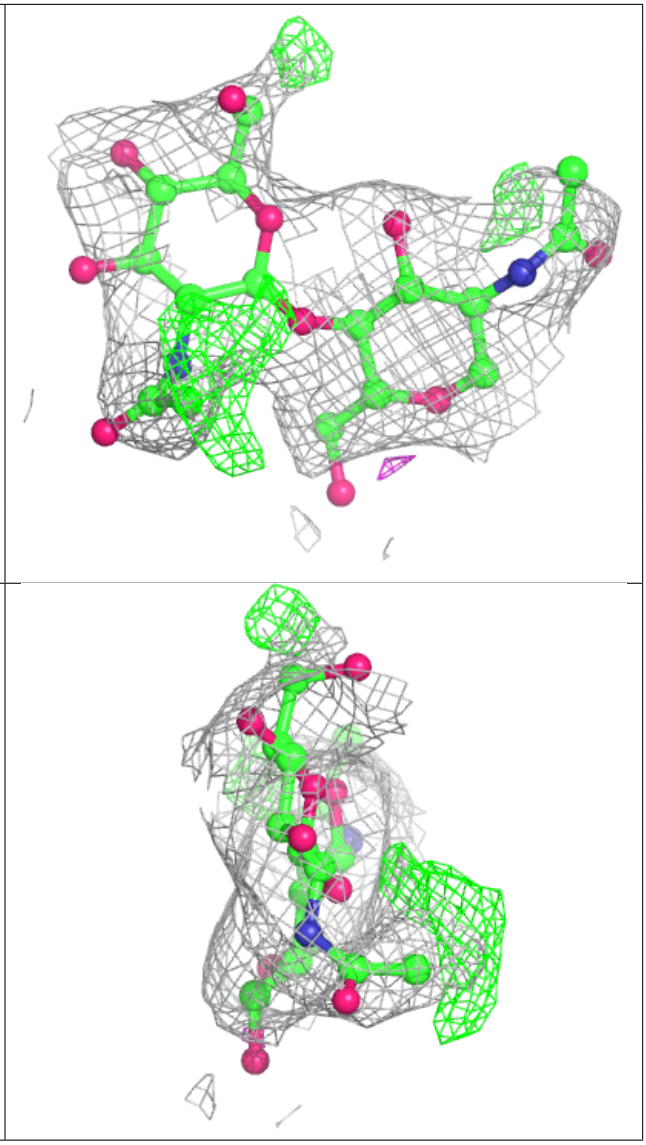
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	D	2	14/15	0.81	0.25	96,136,147,162	0
2	NAG	E	2	14/15	0.85	0.17	93,138,147,164	0
2	NAG	F	2	14/15	0.85	0.38	114,155,167,169	0
2	NAG	F	1	14/15	0.88	0.23	100,121,134,150	0
2	NAG	D	1	14/15	0.93	0.16	58,73,103,106	0
2	NAG	E	1	14/15	0.96	0.11	61,71,101,104	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.

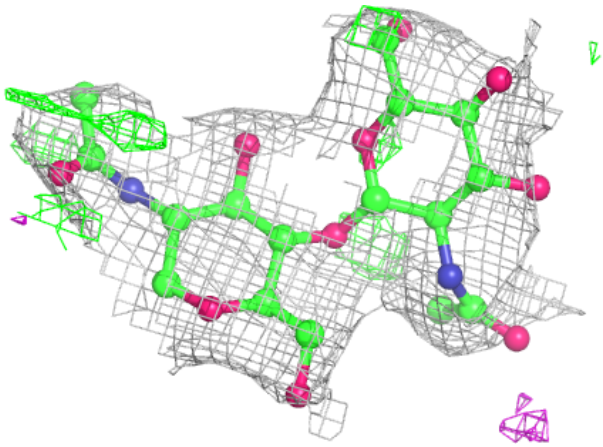
Electron density around Chain D:

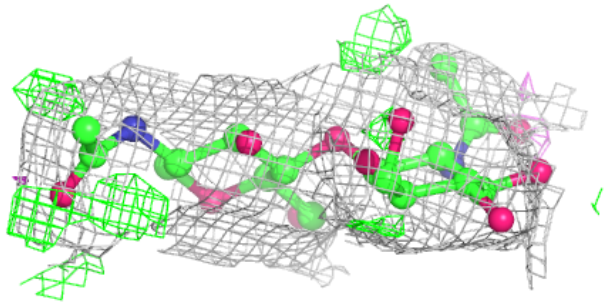
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

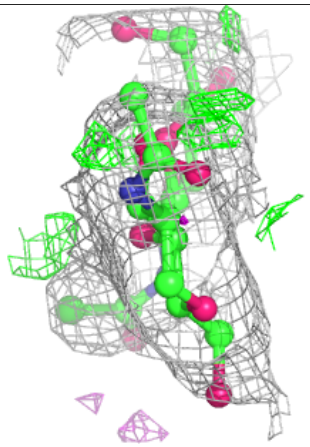


Electron density around Chain E:

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

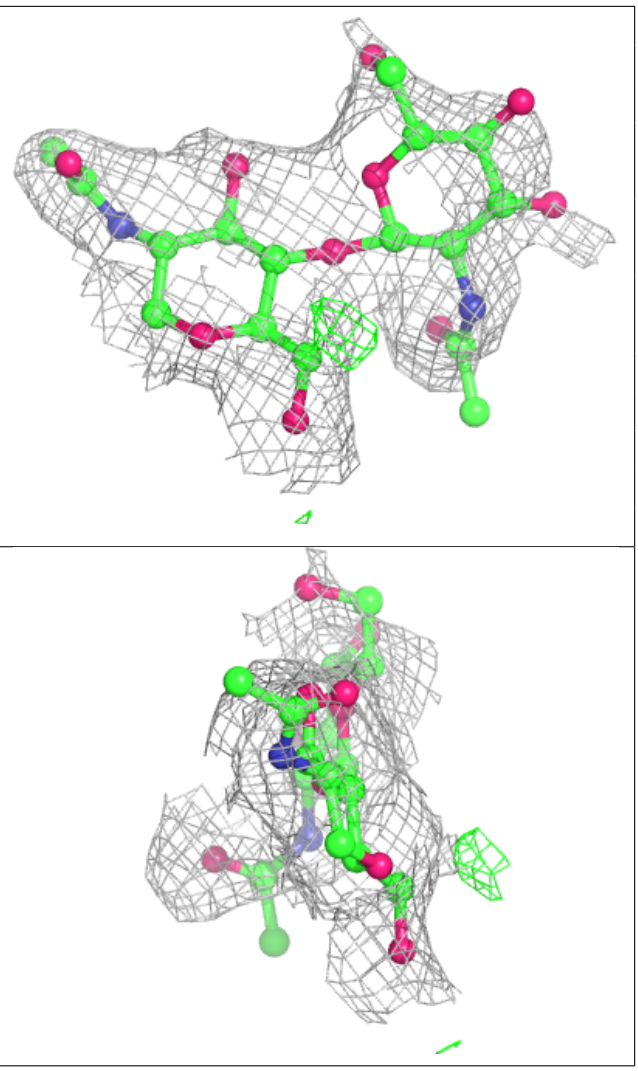






Electron density around Chain F:

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



6.4 Ligands (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, 95th 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	NAG	C	700	14/15	0.74	0.36	102,121,137,154	0
3	NAG	A	700	14/15	0.86	0.20	103,120,135,151	0
3	NAG	C	600	14/15	0.91	0.18	69,77,103,106	0
4	CL	B	464	1/1	0.97	0.08	51,51,51,51	0
4	CL	C	464	1/1	0.97	0.09	55,55,55,55	0
4	CL	A	464	1/1	0.99	0.09	59,59,59,59	0

6.5 Other polymers (i)

There are no such residues in this entry.