



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:36 AM UTC

PDB ID : 5WKV / pdb_00005wkv
Title : Structure of an acid sensing ion channel in a resting state with calcium
Authors : Yoder, N.; Gouaux, E.
Deposited on : 2017-07-25
Resolution : 3.20 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 types of validation reports are described at

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

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

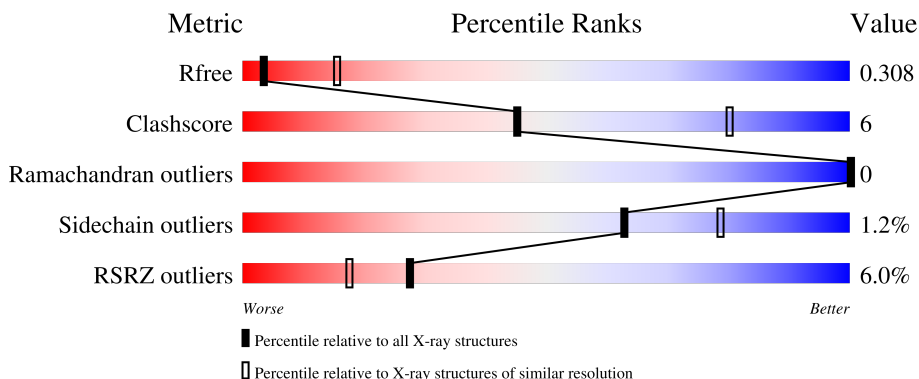
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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 $\leq 5\%$. 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	439	5% 80% 14% 5%
1	B	439	6% 82% 13% 5%
1	C	439	7% 80% 14% 6%
2	D	2	50% 50%
2	E	2	100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9383 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 Acid-sensing ion channel 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	417	Total	C	N	O	S	0	0	0
			3136	2017	515	577	27			
1	C	414	Total	C	N	O	S	0	0	0
			3012	1933	494	559	26			
1	B	418	Total	C	N	O	S	0	0	0
			3115	2000	508	580	27			

- 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
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

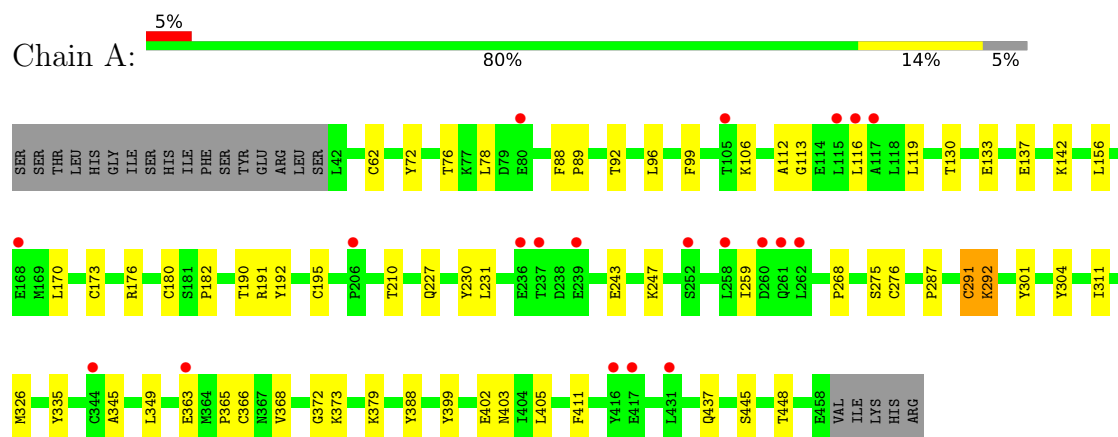
- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Ca	0	0
			2	2		
5	C	2	Total	Ca	0	0
			2	2		
5	B	2	Total	Ca	0	0
			2	2		

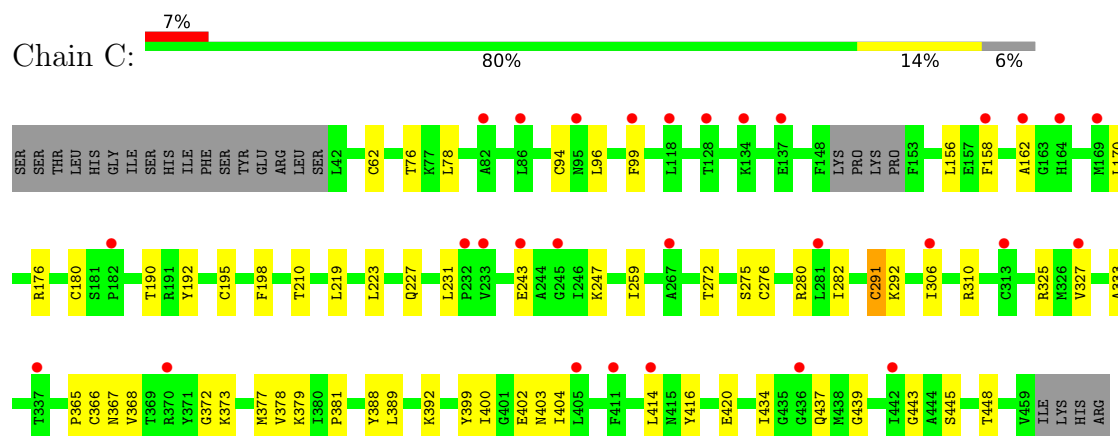
3 Residue-property plots [i](#)

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.

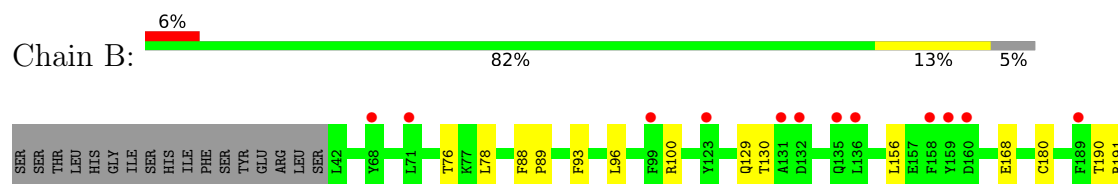
• Molecule 1: Acid-sensing ion channel 1

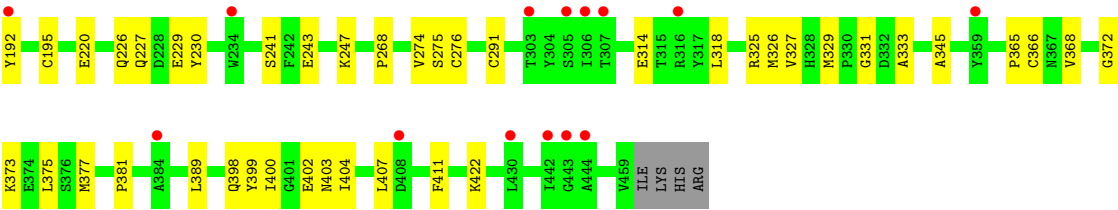


• Molecule 1: Acid-sensing ion channel 1

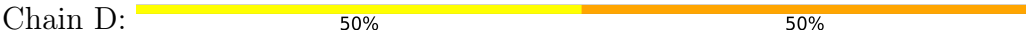


• Molecule 1: Acid-sensing ion channel 1

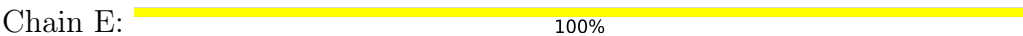




● Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



● Molecule 2: 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, α , β , γ	109.18Å 133.70Å 157.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.95 – 3.20 24.95 – 3.20	Depositor EDS
% Data completeness (in resolution range)	94.0 (24.95-3.20) 97.2 (24.95-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 3.17Å)	Xtriage
Refinement program	PHENIX (dev_2597: ???)	Depositor
R, R_{free}	0.287 , 0.297 0.294 , 0.308	Depositor DCC
R_{free} test set	1877 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	95.1	Xtriage
Anisotropy	0.328	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 37.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	9383	wwPDB-VP
Average B, all atoms (Å ²)	157.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, NAG, CL

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	0.16	0/3211	0.41	0/4371
1	B	0.15	0/3189	0.40	0/4349
1	C	0.13	0/3081	0.39	0/4206
All	All	0.15	0/9481	0.40	0/12926

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 [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	3136	0	2890	39	0
1	B	3115	0	2836	36	0
1	C	3012	0	2680	38	0
2	D	28	0	25	1	0
2	E	28	0	25	0	0
3	A	28	0	26	0	0
3	B	14	0	13	0	0
3	C	14	0	13	0	0
4	A	1	0	0	0	0
4	B	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
All	All	9383	0	8508	106	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 6.

All (106) 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:192:TYR:HE2	1:A:247:LYS:HD3	1.50	0.76
1:A:365:PRO:HG2	1:A:368:VAL:HG22	1.73	0.70
1:A:78:LEU:HD12	1:B:76:THR:HG21	1.73	0.69
1:C:96:LEU:HD13	1:C:243:GLU:HG3	1.75	0.69
1:B:192:TYR:HE2	1:B:247:LYS:HD3	1.59	0.68
1:C:275:SER:O	1:C:373:LYS:HA	1.97	0.64
1:C:76:THR:HG21	1:B:78:LEU:HD12	1.80	0.63
2:D:1:NAG:O4	2:D:2:NAG:O7	2.19	0.60
1:C:227:GLN:NE2	1:C:402:GLU:O	2.34	0.60
1:A:304:TYR:OH	1:A:363:GLU:O	2.16	0.60
1:A:191:ARG:HH22	1:A:349:LEU:HD13	1.68	0.59
1:B:130:THR:O	1:B:130:THR:HG22	2.02	0.59
1:A:96:LEU:HD13	1:A:243:GLU:HG3	1.86	0.58
1:A:192:TYR:CE2	1:A:247:LYS:HD3	2.36	0.57
1:B:192:TYR:CE2	1:B:247:LYS:HD3	2.39	0.57
1:A:76:THR:HG21	1:C:78:LEU:HD12	1.86	0.56
1:C:192:TYR:HE2	1:C:247:LYS:HD3	1.70	0.56
1:A:113:GLY:HA3	1:A:119:LEU:HD12	1.87	0.56
1:A:133:GLU:O	1:A:137:GLU:HG2	2.06	0.56
1:A:268:PRO:HA	1:A:405:LEU:HB3	1.88	0.55
1:A:190:THR:OG1	1:A:195:CYS:SG	2.63	0.55
1:A:379:LYS:HB2	1:B:268:PRO:HD2	1.88	0.55
1:A:326:MET:HE3	1:A:345:ALA:HB1	1.89	0.55
1:C:381:PRO:HB3	1:C:389:LEU:HD12	1.89	0.55
1:A:291:CYS:SG	1:A:292:LYS:N	2.81	0.54
1:B:191:ARG:NH2	1:B:314:GLU:OE1	2.42	0.53
1:B:276:CYS:HA	1:B:372:GLY:O	2.09	0.53
1:A:176:ARG:HD2	1:A:210:THR:HA	1.90	0.53
1:C:247:LYS:O	1:C:259:ILE:HD11	2.09	0.53
1:B:325:ARG:HH22	1:B:331:GLY:C	2.16	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:190:THR:OG1	1:C:195:CYS:SG	2.68	0.52
1:B:365:PRO:HG2	1:B:368:VAL:HG22	1.92	0.52
1:C:99:PHE:CZ	1:C:231:LEU:HD21	2.45	0.52
1:C:276:CYS:HA	1:C:372:GLY:O	2.10	0.52
1:B:275:SER:O	1:B:373:LYS:HA	2.10	0.51
1:A:445:SER:H	1:A:448:THR:HB	1.74	0.51
1:B:326:MET:HE3	1:B:345:ALA:HB1	1.92	0.51
1:A:275:SER:O	1:A:373:LYS:HA	2.12	0.49
1:C:434:ILE:HA	1:C:437:GLN:NE2	2.26	0.49
1:A:156:LEU:HD13	1:A:335:TYR:CZ	2.48	0.49
1:C:280:ARG:HD2	1:C:416:TYR:CE2	2.47	0.49
1:A:276:CYS:HA	1:A:372:GLY:O	2.12	0.49
1:C:62:CYS:HA	1:C:437:GLN:NE2	2.27	0.49
1:C:94:CYS:SG	1:C:259:ILE:HG21	2.53	0.49
1:C:156:LEU:HD11	1:C:327:VAL:HA	1.94	0.49
1:C:365:PRO:HG2	1:C:368:VAL:HG22	1.95	0.48
1:C:388:TYR:CZ	1:C:392:LYS:HD2	2.49	0.48
1:B:318:LEU:HD12	1:B:329:MET:HE1	1.95	0.48
1:A:96:LEU:HD11	1:C:378:VAL:HG11	1.94	0.48
1:C:192:TYR:CE2	1:C:247:LYS:HD3	2.49	0.48
1:B:381:PRO:HB3	1:B:389:LEU:HD12	1.96	0.48
1:A:112:ALA:O	1:A:116:LEU:HG	2.14	0.48
1:A:99:PHE:CE2	1:A:231:LEU:HD21	2.49	0.47
1:A:268:PRO:HD2	1:C:379:LYS:HB2	1.95	0.47
1:C:325:ARG:HD3	1:C:333:ALA:HB3	1.96	0.47
1:C:170:LEU:HA	1:C:223:LEU:HD23	1.96	0.47
1:A:170:LEU:HD11	1:A:173:CYS:HB2	1.97	0.47
1:B:168:GLU:HB3	1:B:226:GLN:NE2	2.30	0.47
1:B:398:GLN:O	1:B:402:GLU:HG2	2.14	0.47
1:B:220:GLU:HA	1:B:407:LEU:O	2.15	0.46
1:B:89:PRO:HD3	1:B:411:PHE:CZ	2.50	0.46
1:C:282:ILE:HG22	1:C:367:ASN:OD1	2.15	0.46
1:B:325:ARG:NH2	1:B:333:ALA:H	2.14	0.46
1:B:227:GLN:HA	1:B:230:TYR:CD1	2.51	0.46
1:A:227:GLN:NE2	1:A:402:GLU:O	2.48	0.46
1:C:282:ILE:HD11	1:C:420:GLU:HB3	1.98	0.46
1:C:94:CYS:SG	1:C:259:ILE:HD13	2.56	0.45
1:C:158:PHE:O	1:C:162:ALA:HB3	2.16	0.45
1:A:106:LYS:HG3	1:A:142:LYS:O	2.16	0.45
1:B:93:PHE:HA	1:B:247:LYS:O	2.16	0.45
1:C:198:PHE:CD2	1:C:219:LEU:HD22	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:PHE:CG	1:A:89:PRO:HD2	2.53	0.44
1:A:210:THR:HG21	1:A:411:PHE:HD2	1.81	0.44
1:A:99:PHE:CE1	1:A:116:LEU:HD22	2.52	0.44
1:B:325:ARG:CG	1:B:329:MET:HB2	2.48	0.44
1:B:422:LYS:NZ	4:B:504:CL:CL	2.70	0.43
1:C:176:ARG:HD2	1:C:210:THR:HA	2.00	0.43
1:C:439:GLY:HA2	1:C:443:GLY:HA2	1.99	0.43
1:A:301:TYR:CE2	1:A:311:ILE:HD11	2.53	0.43
1:C:400:ILE:HA	1:C:404:ILE:HG12	2.01	0.43
1:B:190:THR:OG1	1:B:195:CYS:SG	2.77	0.42
1:A:62:CYS:HA	1:A:437:GLN:NE2	2.35	0.42
1:C:272:THR:HG22	1:C:377:MET:HG2	2.00	0.42
1:B:400:ILE:HA	1:B:404:ILE:HG12	2.02	0.42
1:A:92:THR:CG2	1:A:259:ILE:HD11	2.50	0.42
1:A:227:GLN:HA	1:A:230:TYR:CD1	2.55	0.42
1:A:170:LEU:HD23	1:A:182:PRO:HG3	2.01	0.42
1:A:399:TYR:O	1:A:403:ASN:HB2	2.20	0.42
1:C:306:ILE:O	1:C:310:ARG:HG2	2.20	0.42
1:C:377:MET:HE1	1:B:377:MET:HB2	2.02	0.42
1:C:291:CYS:SG	1:C:292:LYS:N	2.89	0.41
1:A:72:TYR:CD1	1:A:287:PRO:HG2	2.54	0.41
1:B:88:PHE:CG	1:B:89:PRO:HD2	2.54	0.41
1:B:227:GLN:HE21	1:B:227:GLN:HB2	1.67	0.41
1:B:399:TYR:O	1:B:403:ASN:HB2	2.20	0.41
1:C:414:LEU:HD23	1:C:414:LEU:HA	1.89	0.41
1:A:388:TYR:N	1:B:130:THR:HG21	2.35	0.41
1:B:129:GLN:H	1:B:129:GLN:HG3	1.72	0.41
1:A:227:GLN:HE21	1:A:227:GLN:HB2	1.65	0.41
1:B:274:VAL:HG22	1:B:375:LEU:CD2	2.51	0.41
1:C:399:TYR:O	1:C:403:ASN:HB2	2.20	0.40
1:C:445:SER:H	1:C:448:THR:HB	1.86	0.40
1:B:100:ARG:HB3	1:B:229:GLU:OE2	2.20	0.40
1:B:241:SER:HB2	1:B:243:GLU:CD	2.47	0.40
1:B:156:LEU:HD12	1:B:327:VAL:HG12	2.03	0.40
1:B:96:LEU:HD13	1:B:243:GLU:HG3	2.04	0.40

There are no symmetry-related clashes.

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	415/439 (94%)	409 (99%)	6 (1%)	0	100	100
1	B	416/439 (95%)	408 (98%)	8 (2%)	0	100	100
1	C	410/439 (93%)	403 (98%)	7 (2%)	0	100	100
All	All	1241/1317 (94%)	1220 (98%)	21 (2%)	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	307/384 (80%)	302 (98%)	5 (2%)	55	75
1	B	303/384 (79%)	300 (99%)	3 (1%)	68	80
1	C	278/384 (72%)	275 (99%)	3 (1%)	65	79
All	All	888/1152 (77%)	877 (99%)	11 (1%)	63	79

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	130	THR
1	A	180	CYS
1	A	291	CYS
1	A	292	LYS
1	A	366	CYS

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Mol	Chain	Res	Type
1	C	180	CYS
1	C	291	CYS
1	C	366	CYS
1	B	180	CYS
1	B	291	CYS
1	B	366	CYS

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	217	ASN
1	A	279	GLN
1	C	321	ASN
1	B	226	GLN
1	B	279	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](#)

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	$\# Z > 2$
2	NAG	D	1	2,1	14,14,15	0.39	0	17,19,21	0.68	0
2	NAG	D	2	2	14,14,15	0.61	1 (7%)	17,19,21	1.17	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	E	1	2,1	14,14,15	0.22	0	17,19,21	0.94	1 (5%)
2	NAG	E	2	2	14,14,15	0.21	0	17,19,21	0.68	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
2	NAG	D	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	D	2	2	-	3/6/23/26	0/1/1/1
2	NAG	E	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	NAG	C1-C2	2.17	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	C2-N2-C7	3.83	128.03	122.90
2	E	1	NAG	C1-O5-C5	2.89	116.06	112.19
2	E	2	NAG	C1-O5-C5	2.30	115.27	112.19
2	D	2	NAG	C1-C2-N2	2.17	113.86	110.43

There are no chirality outliers.

All (9) torsion outliers are listed below:

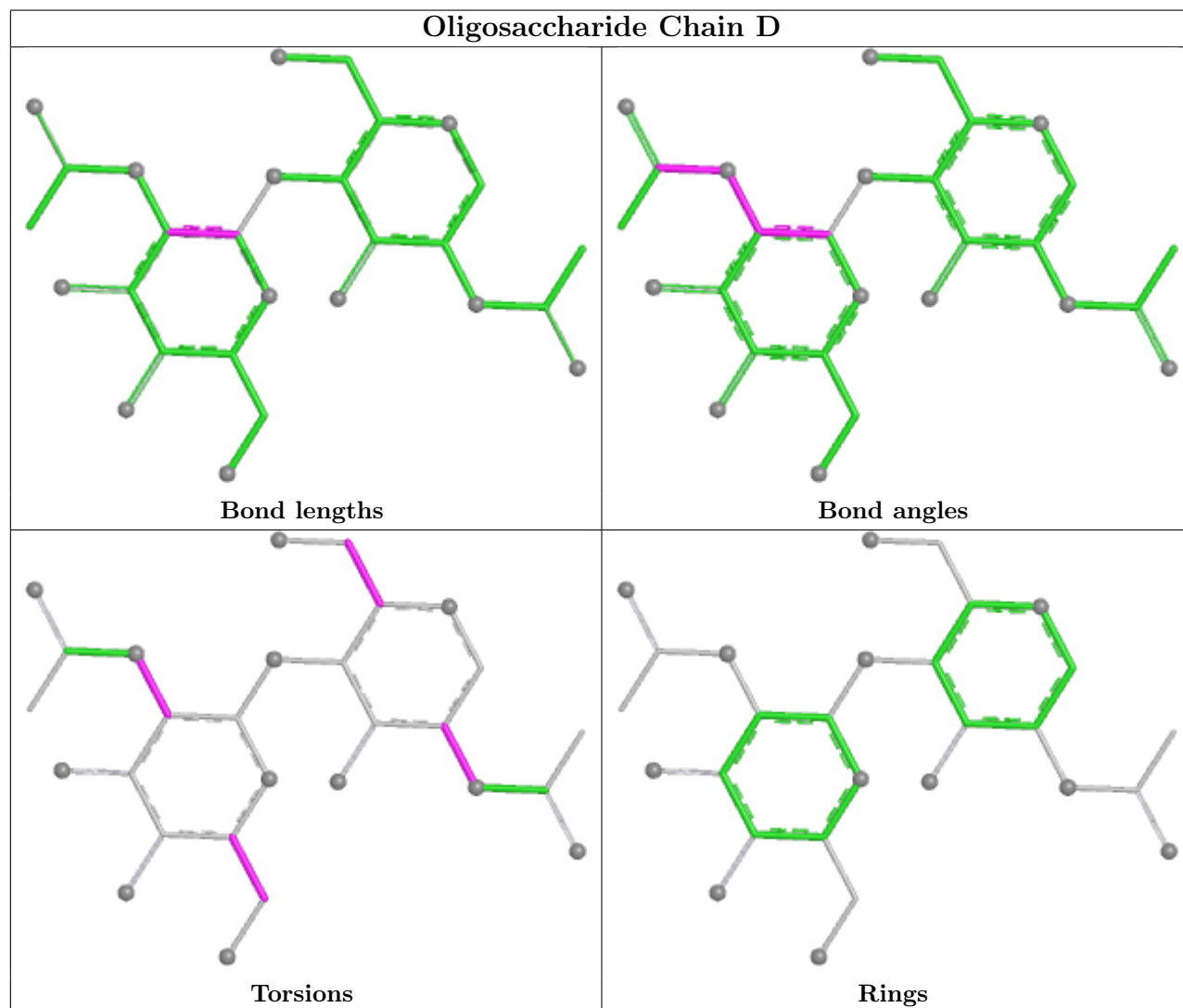
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	C1-C2-N2-C7
2	E	2	NAG	O5-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
2	D	1	NAG	C1-C2-N2-C7
2	D	1	NAG	C4-C5-C6-O6
2	D	1	NAG	C3-C2-N2-C7
2	D	1	NAG	O5-C5-C6-O6

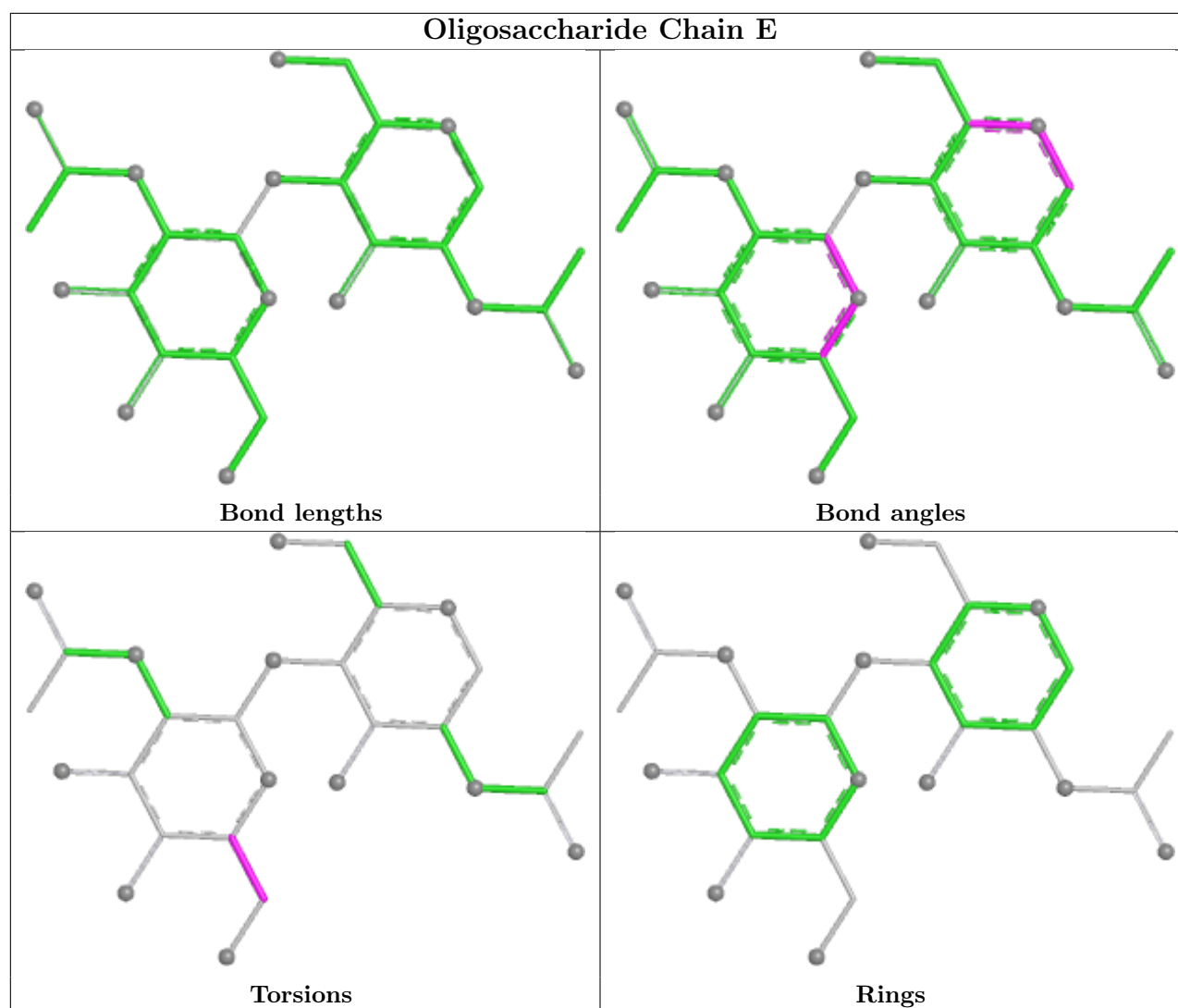
There are no ring outliers.

2 monomers are involved in 1 short contact:

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

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





5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	A	501	1	14,14,15	0.24	0	17,19,21	0.42	0
3	NAG	B	503	1	14,14,15	0.27	0	17,19,21	0.64	1 (5%)
3	NAG	A	502	1	14,14,15	0.30	0	17,19,21	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	C	501	1	14,14,15	0.31	0	17,19,21	0.50	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	A	501	1	-	1/6/23/26	0/1/1/1
3	NAG	B	503	1	-	1/6/23/26	0/1/1/1
3	NAG	A	502	1	-	1/6/23/26	0/1/1/1
3	NAG	C	501	1	-	2/6/23/26	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(°)	Ideal(°)
3	B	503	NAG	C1-O5-C5	2.20	115.14	112.19

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	501	NAG	C8-C7-N2-C2
3	C	501	NAG	O7-C7-N2-C2
3	B	503	NAG	O5-C5-C6-O6
3	A	502	NAG	O5-C5-C6-O6
3	A	501	NAG	O5-C5-C6-O6

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, 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	417/439 (94%)	0.26	20 (4%) 35 22	91, 139, 196, 221	0
1	B	418/439 (95%)	0.36	26 (6%) 26 17	101, 150, 224, 256	0
1	C	414/439 (94%)	0.51	29 (7%) 22 14	107, 166, 241, 259	0
All	All	1249/1317 (94%)	0.38	75 (6%) 27 17	91, 150, 227, 259	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	159	TYR	5.8
1	B	442	ILE	4.7
1	A	117	ALA	4.6
1	A	168	GLU	4.5
1	C	243	GLU	4.5
1	B	408	ASP	4.4
1	C	245	GLY	4.4
1	C	99	PHE	4.3
1	C	158	PHE	4.3
1	A	261	GLN	4.3
1	C	306	ILE	4.1
1	B	136	LEU	4.1
1	B	444	ALA	4.0
1	C	232	PRO	3.7
1	B	131	ALA	3.7
1	B	158	PHE	3.7
1	B	307	THR	3.5
1	B	306	ILE	3.4
1	C	164	HIS	3.3
1	B	132	ASP	3.2
1	A	239	GLU	3.2
1	C	405	LEU	3.2
1	C	162	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	189	PHE	3.2
1	B	303	THR	3.2
1	C	267	ALA	3.1
1	B	316	ARG	3.1
1	C	118	LEU	3.1
1	B	443	GLY	3.1
1	A	115	LEU	3.1
1	A	236	GLU	3.1
1	C	281	LEU	3.0
1	C	169	MET	3.0
1	C	370	ARG	2.9
1	B	234	TRP	2.9
1	C	233	VAL	2.9
1	C	442	ILE	2.9
1	C	327	VAL	2.8
1	B	135	GLN	2.8
1	C	436	GLY	2.8
1	A	416	TYR	2.8
1	A	431	LEU	2.8
1	C	411	PHE	2.7
1	C	414	LEU	2.7
1	C	82	ALA	2.7
1	B	384	ALA	2.6
1	A	262	LEU	2.6
1	B	71	LEU	2.6
1	B	192	TYR	2.6
1	C	182	PRO	2.5
1	B	305	SER	2.5
1	A	206	PRO	2.5
1	B	68	TYR	2.4
1	A	252	SER	2.4
1	C	134	LYS	2.4
1	C	95	ASN	2.4
1	C	128	THR	2.4
1	C	86	LEU	2.3
1	B	160	ASP	2.3
1	A	116	LEU	2.3
1	A	80	GLU	2.2
1	C	337	THR	2.2
1	A	417	GLU	2.2
1	B	430	LEU	2.2
1	A	344	CYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	99	PHE	2.2
1	C	137	GLU	2.1
1	A	260	ASP	2.1
1	B	123	TYR	2.1
1	B	359	TYR	2.1
1	A	105	THR	2.1
1	A	363	GLU	2.1
1	A	237	THR	2.1
1	A	258	LEU	2.0
1	C	313	CYS	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](#)

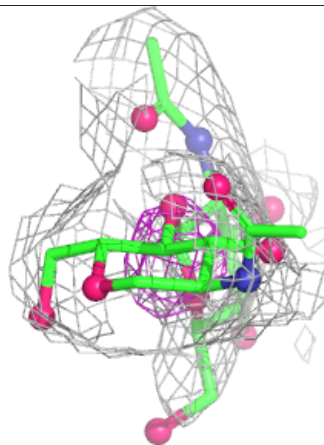
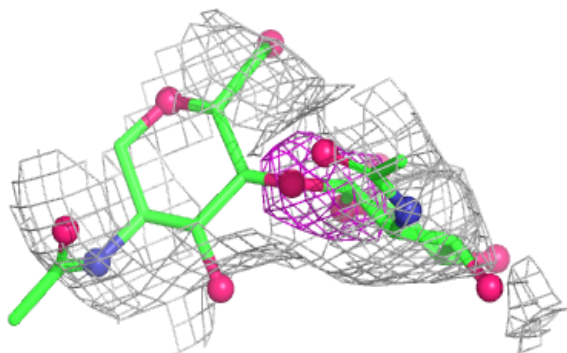
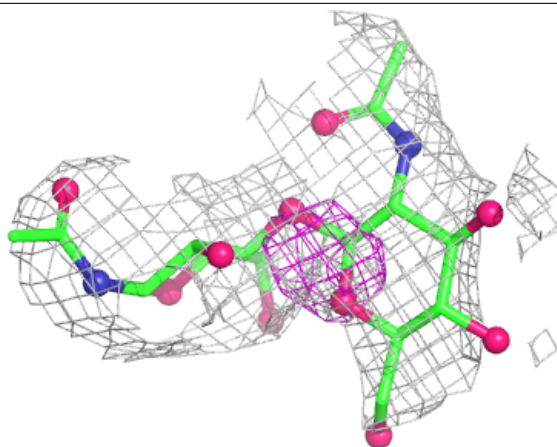
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

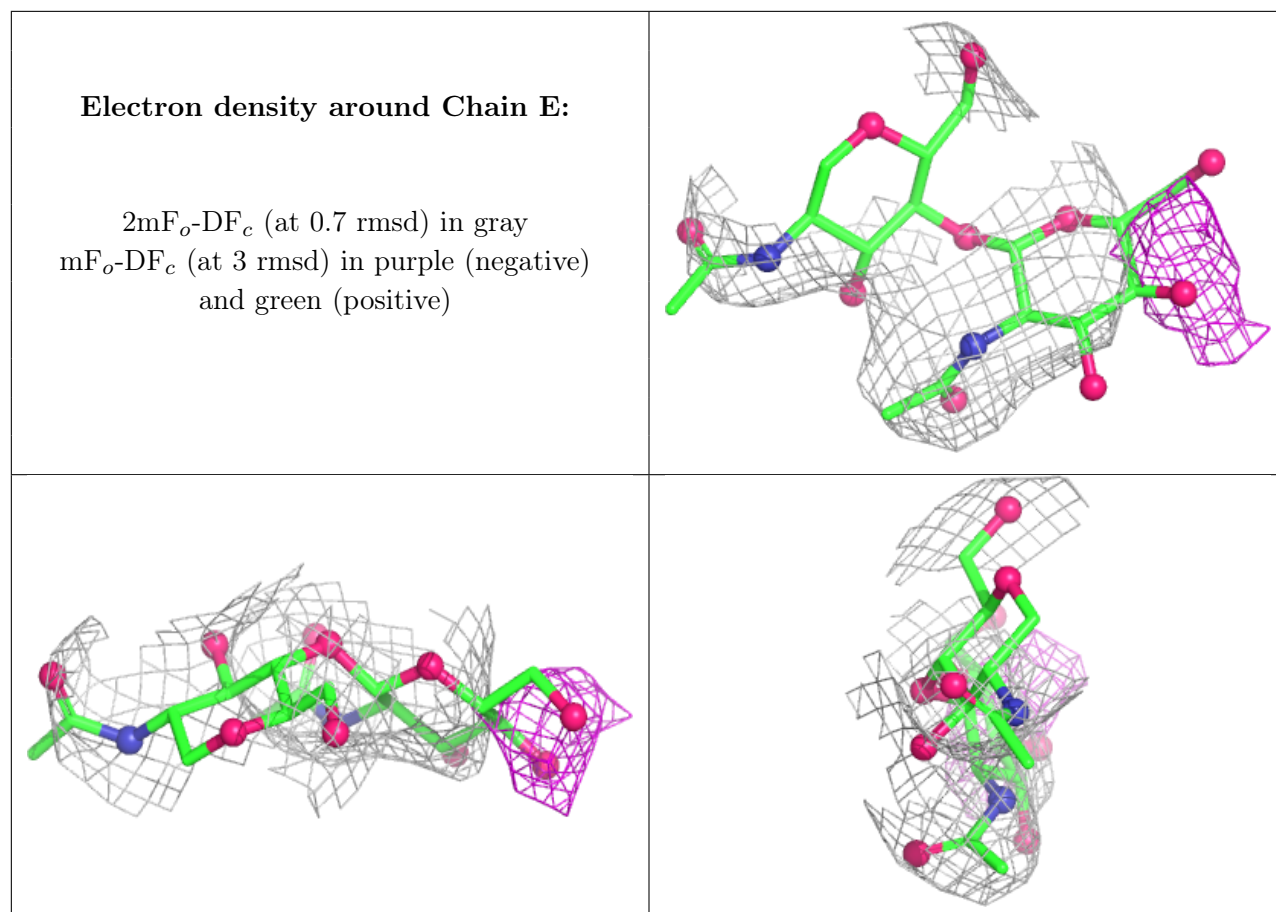
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	D	2	14/15	0.01	0.14	216,216,216,216	0
2	NAG	E	2	14/15	0.31	0.14	170,208,238,239	0
2	NAG	D	1	14/15	0.54	0.10	190,213,231,232	0
2	NAG	E	1	14/15	0.58	0.11	158,187,228,244	0

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)





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	B	503	14/15	0.58	0.10	159,190,201,216	0
3	NAG	A	502	14/15	0.65	0.11	152,152,152,152	0
3	NAG	A	501	14/15	0.68	0.09	142,167,180,184	0
5	CA	B	505	1/1	0.72	0.07	151,151,151,151	0
3	NAG	C	501	14/15	0.77	0.09	163,187,202,203	0
5	CA	C	504	1/1	0.78	0.07	149,149,149,149	0
4	CL	A	503	1/1	0.81	0.19	123,123,123,123	1
5	CA	A	504	1/1	0.90	0.08	136,136,136,136	0
4	CL	B	504	1/1	0.92	0.13	117,117,117,117	1
5	CA	B	506	1/1	0.93	0.06	113,113,113,113	0
5	CA	A	505	1/1	0.96	0.13	123,123,123,123	0
5	CA	C	505	1/1	0.96	0.05	113,113,113,113	0

6.5 Other polymers [i](#)

There are no such residues in this entry.