



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2021 – 11:37 AM JST

PDB ID : 7BRK
Title : Atrial Natriuretic Peptide Receptor complexed with deletion mutant of human Atrial Natriuretic Peptide[5-27]
Authors : Ogawa, H.
Deposited on : 2020-03-29
Resolution : 2.85 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 ⓘ](#)) 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 : 2.18
buster-report : 1.1.7 (2018)
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) : 2.18

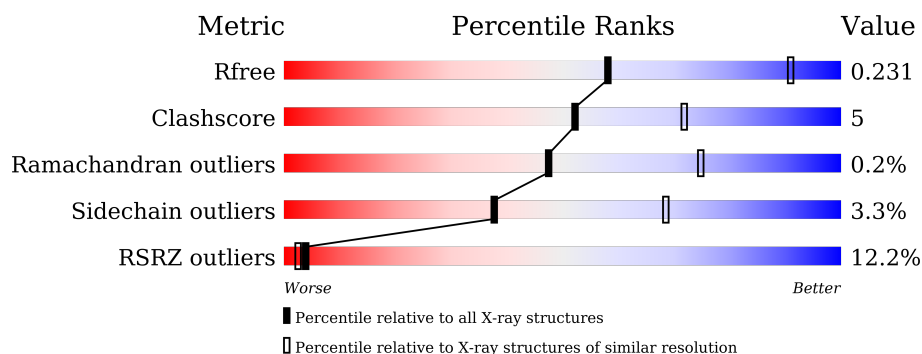
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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	435	<div> <div>11%</div> <div> <div></div> <div>82%</div> <div>15%</div> <div></div> </div> </div>
1	B	435	<div> <div>11%</div> <div> <div></div> <div>82%</div> <div>15%</div> <div></div> </div> </div>
2	L	23	<div> <div>57%</div> <div> <div></div> <div>57%</div> <div>39%</div> <div></div> </div> </div>
3	C	3	<div> <div></div> <div> <div>67%</div> <div>33%</div> </div> </div>
3	E	3	<div> <div></div> <div> <div>67%</div> <div>33%</div> </div> </div>
4	D	4	<div> <div></div> <div> <div>25%</div> <div>75%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
4	F	4	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7388 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 Atrial natriuretic peptide receptor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	426	Total	C	N	O	S	0	3	0
			3383	2167	590	615	11			
1	B	426	Total	C	N	O	S	0	3	0
			3383	2167	590	615	11			

- Molecule 2 is a protein called Natriuretic peptides A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	23	Total	C	N	O	S	0	23	0
			332	194	68	64	6			

There are 5 discrepancies between the modelled and reference sequences:

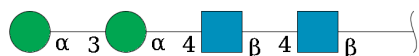
Chain	Residue	Modelled	Actual	Comment	Reference
L	?	-	SER	deletion	UNP P01160
L	?	-	LEU	deletion	UNP P01160
L	?	-	ARG	deletion	UNP P01160
L	?	-	ARG	deletion	UNP P01160
L	?	-	TYR	deletion	UNP P01160

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-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	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	E	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	4	Total	C	N	O	0	0	0
			50	28	2	20			
4	F	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

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

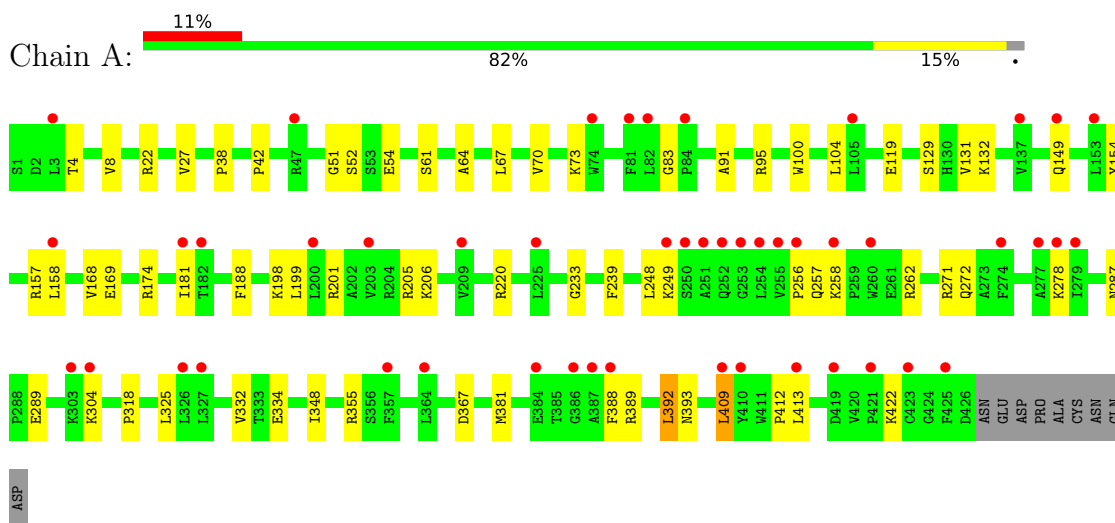
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	48	Total	O	0	0
			48	48		
6	B	48	Total	O	0	0
			48	48		
6	L	14	Total	O	0	0
			14	14		

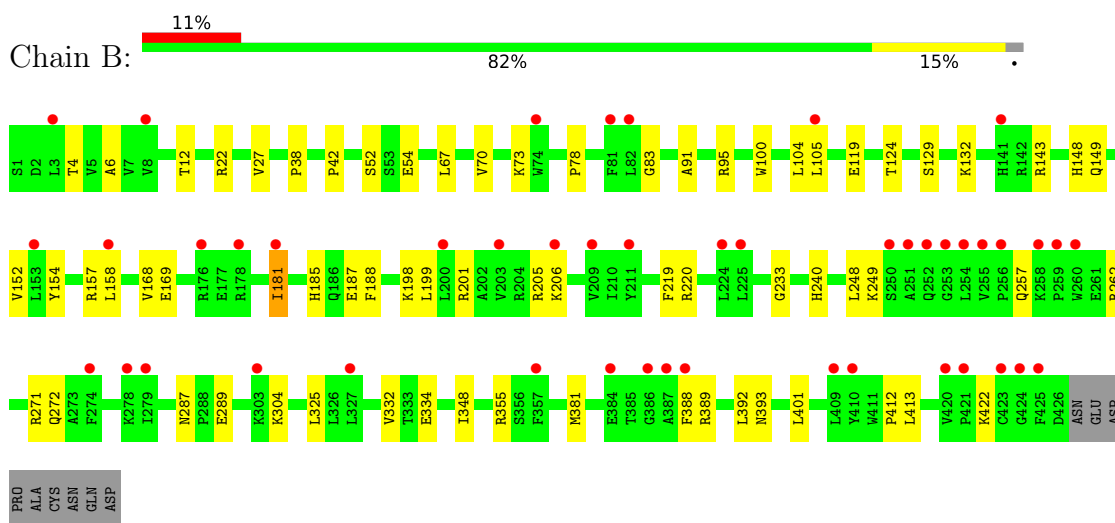
3 Residue-property plots

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: Atrial natriuretic peptide receptor 1

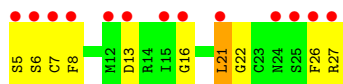


- Molecule 1: Atrial natriuretic peptide receptor 1



- Molecule 2: Natriuretic peptides A





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

Chain C: 67% 33%



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

Chain E: 67% 33%



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

Chain D: 25% 75%



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

Chain F: 50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	99.42Å 99.42Å 259.67Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.11 – 2.85 43.11 – 2.85	Depositor EDS
% Data completeness (in resolution range)	90.4 (43.11-2.85) 90.4 (43.11-2.85)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.09 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.176 , 0.231 0.176 , 0.231	Depositor DCC
R_{free} test set	906 reflections (2.96%)	wwPDB-VP
Wilson B-factor (Å ²)	72.1	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 78.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.488 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7388	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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: MAN, 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	0.34	0/3475	0.51	0/4734
1	B	0.34	0/3475	0.51	0/4734
2	L	0.37	0/334	0.69	0/434
All	All	0.34	0/7284	0.52	0/9902

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	3383	0	3325	37	0
1	B	3383	0	3325	36	0
2	L	332	0	306	17	0
3	C	39	0	34	0	0
3	E	39	0	34	0	0
4	D	50	0	43	0	0
4	F	50	0	43	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	48	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	48	0	0	3	0
6	L	14	0	0	2	0
All	All	7388	0	7110	79	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 5.

All (79) 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:B:169:GLU:HG3	2:L:8[A]:PHE:HB3	1.70	0.74
1:A:169:GLU:HG3	2:L:8[B]:PHE:HB3	1.70	0.73
1:A:22:ARG:NH1	6:A:602:HOH:O	2.13	0.72
1:A:168:VAL:HG12	2:L:21[A]:LEU:HD11	1.71	0.71
1:B:22:ARG:NH1	6:B:602:HOH:O	2.14	0.71
1:B:168:VAL:HG12	2:L:21[B]:LEU:HD11	1.71	0.71
1:A:119[B]:GLU:OE2	6:A:601:HOH:O	2.10	0.70
1:A:70:VAL:HG11	1:B:70:VAL:HG11	1.74	0.68
1:B:119[B]:GLU:OE2	6:B:601:HOH:O	2.12	0.67
1:A:149:GLN:NE2	1:A:206:LYS:O	2.26	0.67
2:L:7[B]:CYS:O	6:L:101:HOH:O	2.11	0.67
1:B:149:GLN:NE2	1:B:206:LYS:O	2.28	0.65
2:L:7[A]:CYS:O	6:L:102:HOH:O	2.14	0.65
1:A:154:TYR:HB3	1:A:168:VAL:HG21	1.80	0.64
1:A:220:ARG:HD2	1:A:262:ARG:HH21	1.62	0.63
1:B:154:TYR:HB3	1:B:168:VAL:HG21	1.83	0.60
1:A:52:SER:OG	1:A:54:GLU:HG2	2.02	0.59
1:A:158:LEU:HB2	2:L:27[B]:ARG:HH22	1.69	0.58
1:B:158:LEU:HB2	2:L:27[A]:ARG:HH22	1.69	0.58
1:B:381:MET:HB3	1:B:388:PHE:CE1	2.39	0.57
1:B:95[B]:ARG:NH2	2:L:13[B]:ASP:OD1	2.35	0.57
1:A:381:MET:HB3	1:A:388:PHE:CE1	2.40	0.56
1:B:52:SER:OG	1:B:54:GLU:HG2	2.08	0.54
1:B:129:SER:HB2	1:B:132:LYS:HG2	1.89	0.54
1:A:332:VAL:HG22	1:A:348:ILE:HD13	1.89	0.53
1:A:83:GLY:O	1:A:104:LEU:HD11	2.10	0.52
1:B:220:ARG:HD2	1:B:262:ARG:HH21	1.74	0.51
1:A:91:ALA:O	1:A:95[B]:ARG:HG3	2.11	0.50
1:A:287:ASN:HD22	1:A:289:GLU:HB2	1.77	0.50
1:B:233:GLY:HA3	1:B:412:PRO:HG2	1.93	0.50
1:B:143:ARG:HD3	1:B:401:LEU:HD12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:287:ASN:HD22	1:B:289:GLU:HB2	1.77	0.50
2:L:5[B]:SER:HB3	2:L:8[B]:PHE:O	2.11	0.49
1:A:233:GLY:HA3	1:A:412:PRO:HG2	1.94	0.49
1:B:83:GLY:O	1:B:104:LEU:HD11	2.12	0.49
1:B:188:PHE:CG	1:B:199:LEU:HD11	2.48	0.48
1:A:198:LYS:HB3	2:L:26[B]:PHE:CZ	2.49	0.48
6:B:607:HOH:O	2:L:16[B]:GLY:HA3	2.13	0.48
1:B:249:LYS:HB2	1:B:257:GLN:HE22	1.79	0.48
1:A:188:PHE:CG	1:A:199:LEU:HD11	2.49	0.47
1:A:201:ARG:HE	1:A:205:ARG:NH1	2.12	0.47
1:B:198:LYS:HB3	2:L:26[A]:PHE:CZ	2.50	0.47
1:B:334:GLU:OE1	1:B:355:ARG:NH2	2.47	0.47
1:B:38:PRO:O	1:B:42:PRO:HG3	2.14	0.47
2:L:5[A]:SER:HB3	2:L:8[A]:PHE:O	2.14	0.47
1:B:201:ARG:HE	1:B:205:ARG:NH1	2.12	0.47
1:A:129:SER:HB2	1:A:132:LYS:HG2	1.97	0.46
1:B:91:ALA:O	1:B:95[B]:ARG:HG3	2.15	0.46
1:B:27:VAL:HG13	1:B:325:LEU:HD22	1.97	0.46
1:A:38:PRO:O	1:A:42:PRO:HG3	2.16	0.46
1:B:332:VAL:HG22	1:B:348:ILE:HD13	1.97	0.45
1:A:248:LEU:HD22	1:A:257:GLN:HG3	1.98	0.45
1:B:73:LYS:HG3	1:B:100:TRP:CE3	2.51	0.45
1:B:12:THR:HB	1:B:54:GLU:OE2	2.16	0.45
6:A:604:HOH:O	2:L:16[A]:GLY:HA3	2.17	0.43
1:A:334:GLU:OE1	1:A:355:ARG:NH2	2.52	0.43
1:A:27:VAL:HG13	1:A:325:LEU:CD2	2.49	0.43
1:A:61:SER:HB3	1:A:64:ALA:HB3	2.01	0.43
1:B:154:TYR:CZ	1:B:187:GLU:HB2	2.54	0.43
1:A:73:LYS:HG3	1:A:100:TRP:CE3	2.54	0.42
1:B:248:LEU:HD22	1:B:257:GLN:HG3	2.00	0.42
1:A:392:LEU:HD23	1:A:392:LEU:HA	1.87	0.42
1:A:8:VAL:HA	1:A:51:GLY:O	2.19	0.42
1:A:249:LYS:HB2	1:A:257:GLN:HE22	1.84	0.42
1:B:152:VAL:O	1:B:185:HIS:HA	2.20	0.42
1:A:27:VAL:HG13	1:A:325:LEU:HD22	2.02	0.41
1:B:148:HIS:O	1:B:181:ILE:HB	2.20	0.41
1:B:73:LYS:HE2	1:B:100:TRP:CG	2.56	0.41
1:B:105:LEU:HD23	1:B:124:THR:HB	2.02	0.41
1:A:22:ARG:HG2	1:A:318:PRO:HG3	2.02	0.40
1:A:131:VAL:HB	1:A:174:ARG:CZ	2.51	0.40
1:A:239:PHE:CD1	1:A:278:LYS:HB2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:PRO:HG2	1:A:258:LYS:HE3	2.02	0.40
1:A:409:LEU:H	1:A:409:LEU:HD12	1.86	0.40
1:A:95[A]:ARG:NH2	2:L:13[A]:ASP:OD2	2.54	0.40
1:B:6:ALA:HB2	1:B:78:PRO:HG3	2.04	0.40
1:A:367:ASP:HB2	6:A:639:HOH:O	2.21	0.40
1:B:219:PHE:CZ	1:B:240:HIS:HB2	2.57	0.40
2:L:6[A]:SER:O	2:L:22[A]:GLY:HA3	2.21	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	427/435 (98%)	409 (96%)	17 (4%)	1 (0%)	47	75
1	B	427/435 (98%)	408 (96%)	18 (4%)	1 (0%)	47	75
2	L	42/23 (183%)	30 (71%)	12 (29%)	0	100	100
All	All	896/893 (100%)	847 (94%)	47 (5%)	2 (0%)	47	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	422	LYS
1	A	422	LYS

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	356/361 (99%)	344 (97%)	12 (3%)	37	67
1	B	356/361 (99%)	345 (97%)	11 (3%)	40	71
2	L	34/17 (200%)	32 (94%)	2 (6%)	19	45
All	All	746/739 (101%)	721 (97%)	25 (3%)	38	67

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	THR
1	A	67	LEU
1	A	157	ARG
1	A	181	ILE
1	A	271	ARG
1	A	272	GLN
1	A	304	LYS
1	A	389	ARG
1	A	392	LEU
1	A	393	ASN
1	A	409	LEU
1	A	413	LEU
1	B	4	THR
1	B	67	LEU
1	B	157	ARG
1	B	181	ILE
1	B	271	ARG
1	B	272	GLN
1	B	304	LYS
1	B	389	ARG
1	B	392	LEU
1	B	393	ASN
1	B	413	LEU
2	L	21[A]	LEU
2	L	21[B]	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	HIS
1	A	246	GLN

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Mol	Chain	Res	Type
1	A	252	GLN
1	A	266	GLN
1	A	322	HIS
1	A	358	GLN
1	A	393	ASN
1	A	399	GLN
1	B	246	GLN
1	B	252	GLN
1	B	266	GLN
1	B	322	HIS
1	B	358	GLN
1	B	393	ASN
1	B	399	GLN

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 ⓘ

14 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	3,1	14,14,15	0.51	0	17,19,21	0.50	0
3	NAG	C	2	3	14,14,15	0.24	0	17,19,21	0.48	0
3	MAN	C	3	3	11,11,12	0.97	1 (9%)	15,15,17	1.62	2 (13%)
4	NAG	D	1	4,1	14,14,15	0.67	1 (7%)	17,19,21	0.60	0
4	NAG	D	2	4	14,14,15	0.19	0	17,19,21	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MAN	D	3	4	11,11,12	0.96	0	15,15,17	1.36	2 (13%)
4	MAN	D	4	4	11,11,12	0.80	0	15,15,17	0.99	1 (6%)
3	NAG	E	1	3,1	14,14,15	0.48	0	17,19,21	0.51	0
3	NAG	E	2	3	14,14,15	0.22	0	17,19,21	0.49	0
3	MAN	E	3	3	11,11,12	1.11	1 (9%)	15,15,17	1.68	2 (13%)
4	NAG	F	1	4,1	14,14,15	0.52	0	17,19,21	0.65	0
4	NAG	F	2	4	14,14,15	0.17	0	17,19,21	0.46	0
4	MAN	F	3	4	11,11,12	0.91	0	15,15,17	1.33	2 (13%)
4	MAN	F	4	4	11,11,12	0.74	0	15,15,17	1.01	1 (6%)

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	3,1	-	2/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
3	MAN	C	3	3	-	2/2/19/22	1/1/1/1
4	NAG	D	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
4	MAN	D	3	4	-	0/2/19/22	1/1/1/1
4	MAN	D	4	4	-	0/2/19/22	0/1/1/1
3	NAG	E	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	MAN	E	3	3	-	2/2/19/22	1/1/1/1
4	NAG	F	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	MAN	F	3	4	-	0/2/19/22	1/1/1/1
4	MAN	F	4	4	-	0/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	3	MAN	O5-C5	2.48	1.48	1.43
4	D	1	NAG	O5-C1	2.26	1.47	1.43
3	C	3	MAN	O5-C5	2.22	1.47	1.43

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	E	3	MAN	C1-O5-C5	5.10	119.11	112.19
3	C	3	MAN	C1-O5-C5	4.94	118.88	112.19
4	D	3	MAN	C1-O5-C5	3.87	117.43	112.19
4	F	3	MAN	C1-O5-C5	3.85	117.41	112.19
4	F	4	MAN	C1-O5-C5	2.82	116.02	112.19
4	D	4	MAN	C1-O5-C5	2.76	115.94	112.19
4	D	3	MAN	O5-C1-C2	2.66	114.88	110.77
3	E	3	MAN	O5-C1-C2	2.56	114.72	110.77
4	F	3	MAN	O5-C1-C2	2.44	114.53	110.77
3	C	3	MAN	O5-C1-C2	2.37	114.43	110.77

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	1	NAG	O5-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	E	1	NAG	C4-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
4	F	2	NAG	O5-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
3	E	3	MAN	O5-C5-C6-O6
3	E	3	MAN	C4-C5-C6-O6
4	F	2	NAG	C4-C5-C6-O6
3	C	3	MAN	O5-C5-C6-O6
3	C	3	MAN	C4-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6

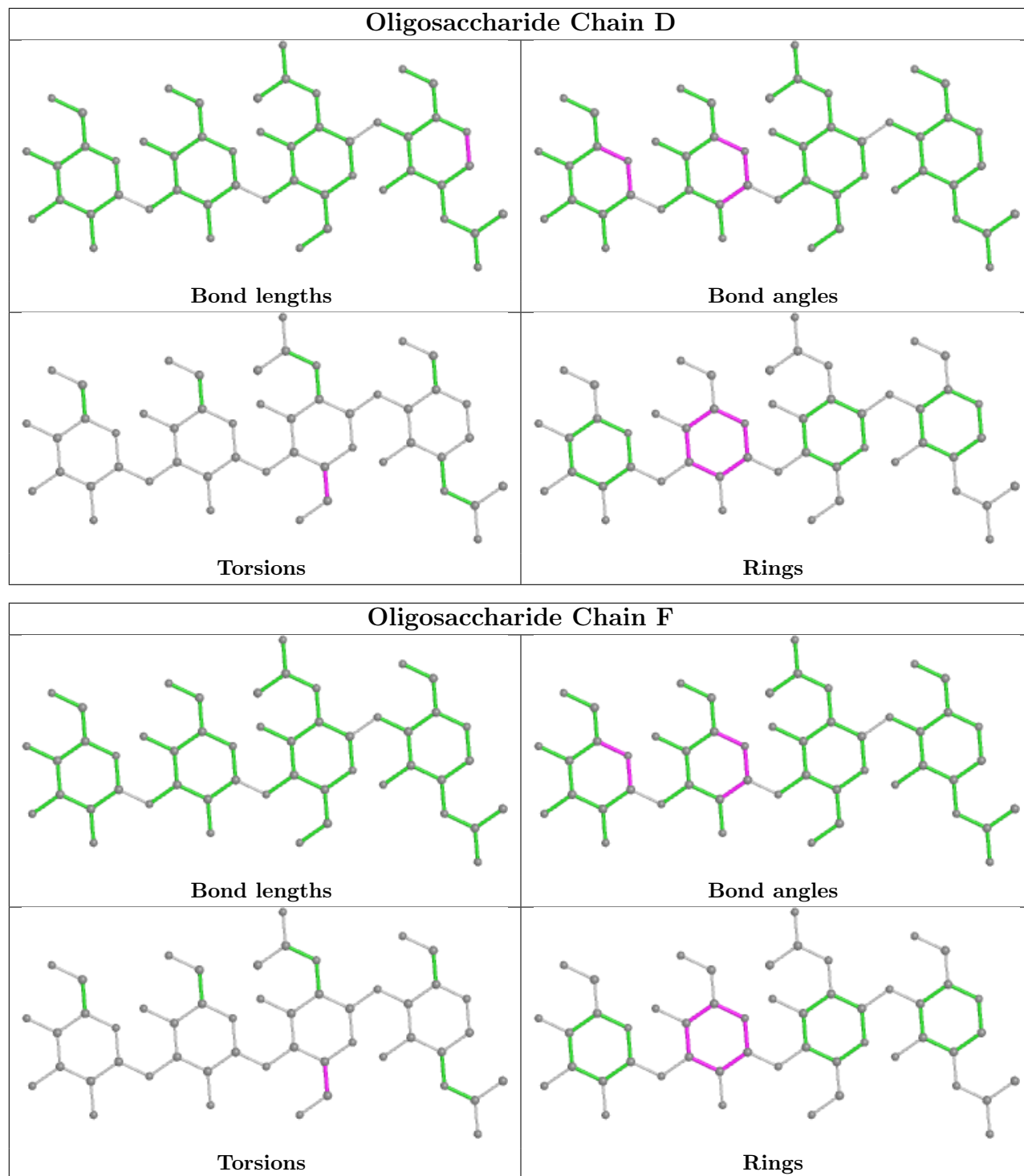
All (4) ring outliers are listed below:

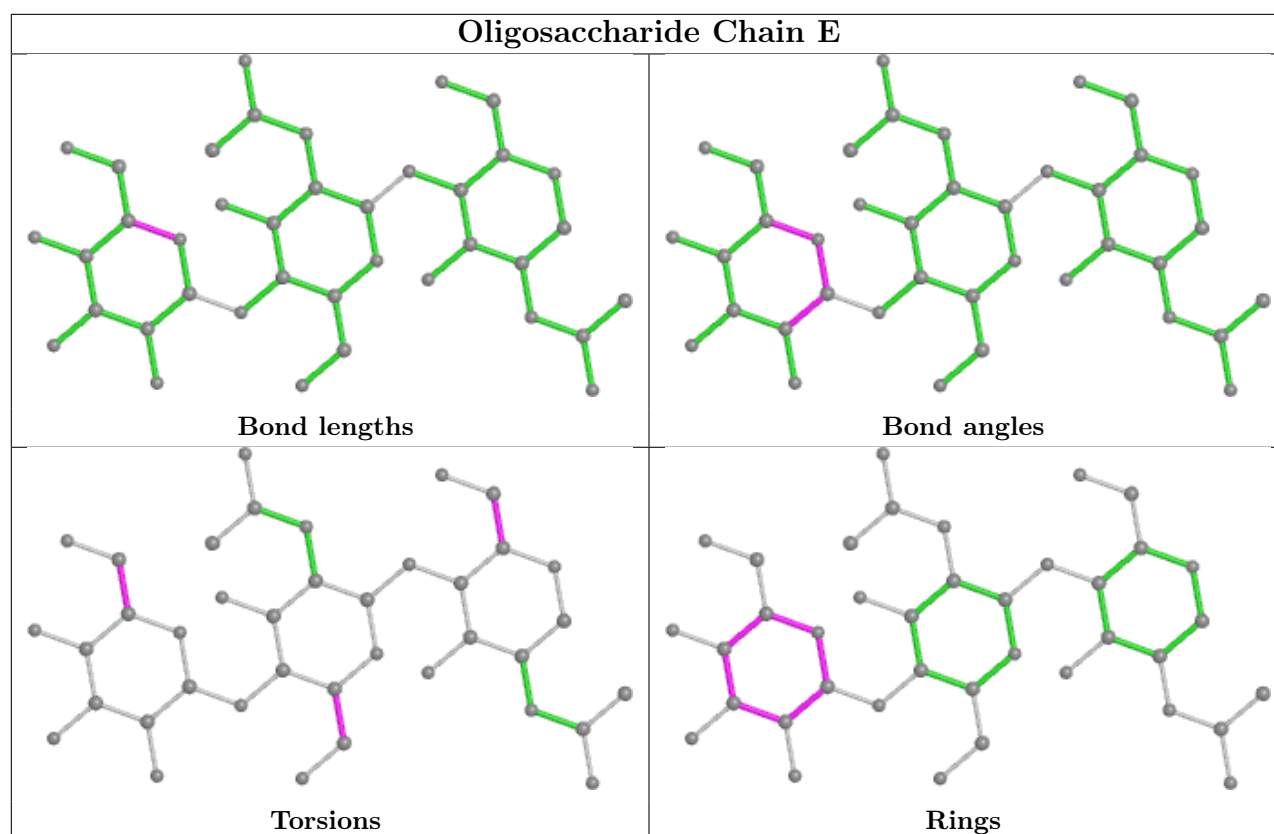
Mol	Chain	Res	Type	Atoms
3	E	3	MAN	C1-C2-C3-C4-C5-O5
3	C	3	MAN	C1-C2-C3-C4-C5-O5
4	F	3	MAN	C1-C2-C3-C4-C5-O5
4	D	3	MAN	C1-C2-C3-C4-C5-O5

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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	426/435 (97%)	0.88	48 (11%) 5 3	48, 83, 147, 245	0
1	B	426/435 (97%)	0.89	46 (10%) 5 4	46, 82, 150, 242	0
2	L	23/23 (100%)	3.82	13 (56%) 0 0	60, 86, 112, 163	0
All	All	875/893 (97%)	0.96	107 (12%) 4 2	46, 83, 150, 245	0

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	27[A]	ARG	16.2
1	B	256	PRO	12.1
1	A	254	LEU	10.6
2	L	26[A]	PHE	9.3
1	A	256	PRO	9.3
1	B	254	LEU	8.5
1	A	250	SER	7.9
1	B	74[A]	TRP	7.8
1	A	74[A]	TRP	7.6
2	L	21[A]	LEU	7.2
2	L	6[A]	SER	7.2
2	L	5[A]	SER	7.2
1	B	158	LEU	5.9
1	A	253	GLY	5.6
2	L	25[A]	SER	5.5
1	A	158	LEU	5.3
1	B	250	SER	5.3
1	B	252	GLN	5.3
1	A	252	GLN	5.2
1	B	421	PRO	5.2
2	L	24[A]	ASN	5.0
1	A	255	VAL	4.9
1	B	253	GLY	4.9

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Mol	Chain	Res	Type	RSRZ
1	B	255	VAL	4.6
1	B	425	PHE	4.3
1	A	423	CYS	3.7
1	B	386	GLY	3.6
2	L	13[A]	ASP	3.3
1	B	225	LEU	3.2
1	A	425	PHE	3.1
1	A	410	TYR	3.1
1	A	387	ALA	3.1
1	B	424	GLY	3.1
1	B	303	LYS	3.1
1	B	176	ARG	3.1
1	A	200	LEU	3.1
1	B	206	LYS	2.9
2	L	7[A]	CYS	2.9
1	B	410	TYR	2.9
2	L	8[A]	PHE	2.9
1	A	225	LEU	2.8
1	B	387	ALA	2.8
2	L	12[A]	MET	2.8
1	A	47	ARG	2.8
1	A	279	ILE	2.8
1	A	386	GLY	2.7
1	A	260	TRP	2.7
1	B	251	ALA	2.7
1	A	421	PRO	2.7
1	B	211	TYR	2.7
2	L	15[A]	ILE	2.7
1	A	388	PHE	2.6
1	B	3	LEU	2.6
1	A	209	VAL	2.6
1	B	388	PHE	2.6
1	B	8	VAL	2.6
1	A	258	LYS	2.6
1	B	409	LEU	2.5
1	B	81	PHE	2.5
1	B	384	GLU	2.5
1	A	82	LEU	2.5
1	B	200	LEU	2.5
1	A	181	ILE	2.5
1	B	258	LYS	2.5
1	B	153	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	274	PHE	2.4
1	A	251	ALA	2.4
1	B	105	LEU	2.4
1	B	274	PHE	2.4
2	L	16[A]	GLY	2.4
1	B	423	CYS	2.4
1	A	326	LEU	2.4
1	A	278	LYS	2.3
1	B	224	LEU	2.3
1	B	260	TRP	2.3
1	A	384	GLU	2.3
1	A	81	PHE	2.3
1	A	137	VAL	2.3
1	B	279	ILE	2.3
1	A	327	LEU	2.3
1	A	105	LEU	2.3
1	A	149	GLN	2.3
1	A	409	LEU	2.2
1	A	153	LEU	2.2
1	A	3	LEU	2.2
1	A	413	LEU	2.2
1	B	357	PHE	2.2
1	B	141	HIS	2.2
1	B	259	PRO	2.2
1	A	249	LYS	2.2
1	A	303	LYS	2.2
1	A	364	LEU	2.1
1	B	209	VAL	2.1
1	B	82	LEU	2.1
1	B	278	LYS	2.1
1	A	84	PRO	2.1
1	A	203	VAL	2.1
1	B	420	VAL	2.1
1	A	277	ALA	2.1
1	B	181	ILE	2.1
1	A	304	LYS	2.1
1	A	182	THR	2.0
1	B	203	VAL	2.0
1	A	419	ASP	2.0
1	B	178	ARG	2.0
1	B	327	LEU	2.0
1	A	357	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

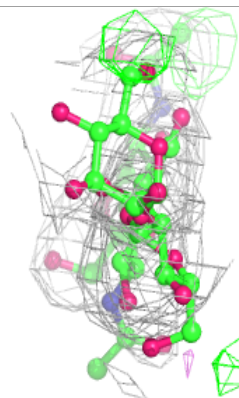
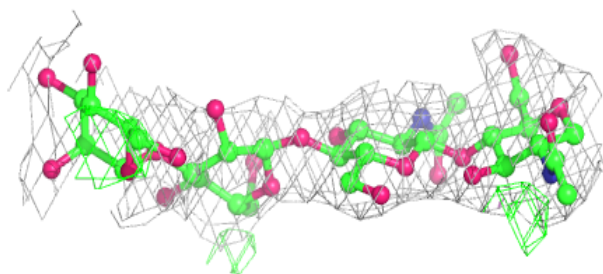
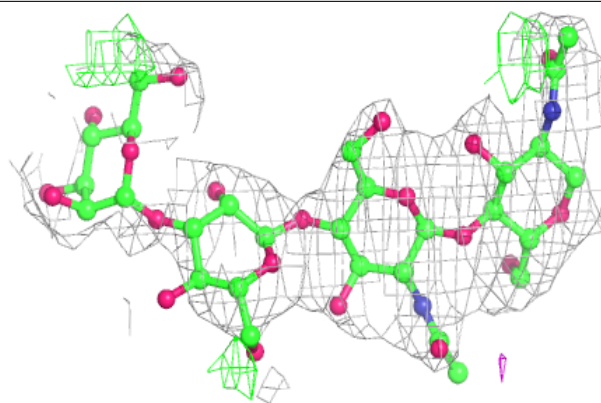
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MAN	C	3	11/12	0.48	0.29	155,162,164,164	0
3	MAN	E	3	11/12	0.49	0.30	156,163,165,166	0
4	MAN	D	3	11/12	0.78	0.17	160,169,174,175	0
4	MAN	D	4	11/12	0.79	0.18	148,159,164,168	0
4	MAN	F	4	11/12	0.83	0.17	153,160,165,168	0
4	MAN	F	3	11/12	0.87	0.13	155,165,172,174	0
3	NAG	C	2	14/15	0.88	0.26	124,130,145,157	0
3	NAG	E	2	14/15	0.89	0.31	126,129,149,154	0
4	NAG	D	2	14/15	0.92	0.18	117,131,141,157	0
4	NAG	F	1	14/15	0.92	0.14	68,84,107,114	0
4	NAG	D	1	14/15	0.93	0.16	67,82,111,113	0
4	NAG	F	2	14/15	0.94	0.19	115,128,139,155	0
3	NAG	C	1	14/15	0.97	0.18	49,82,102,105	0
3	NAG	E	1	14/15	0.97	0.20	54,83,102,102	0

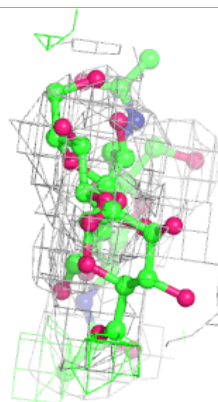
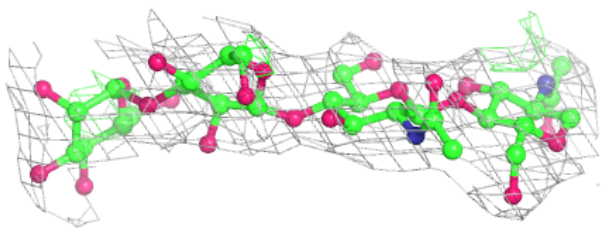
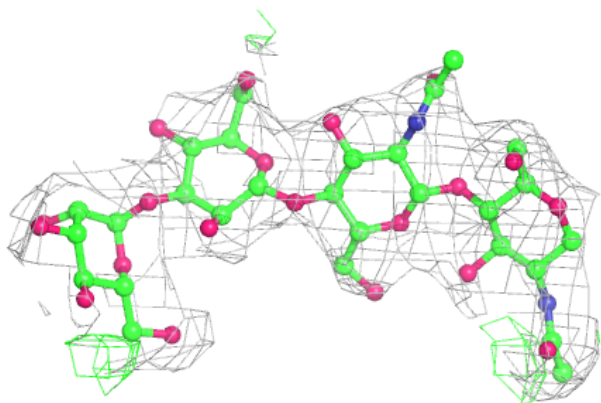
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

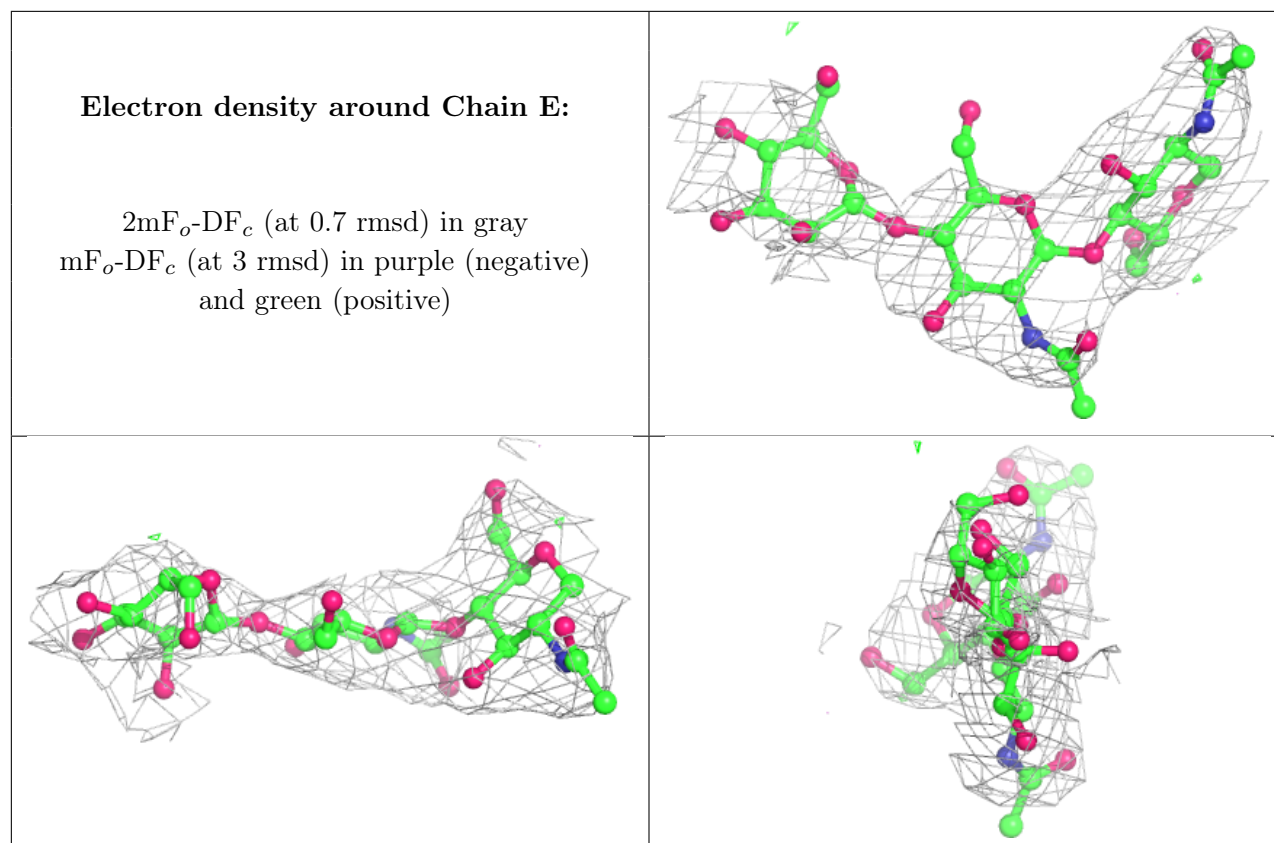
Electron density around Chain D:

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

**Electron density around Chain 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](#)

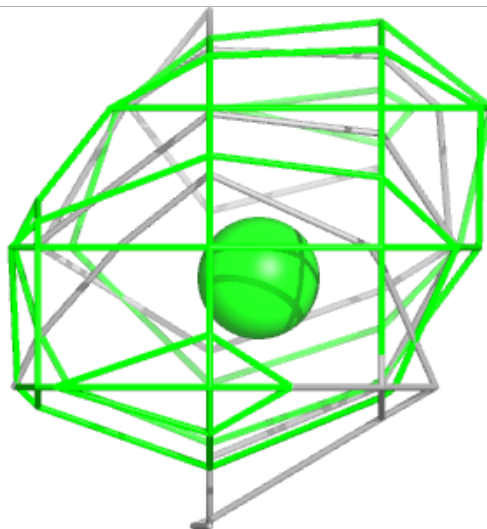
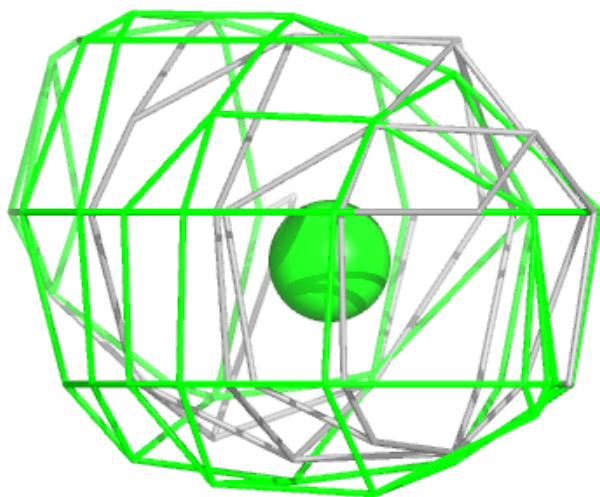
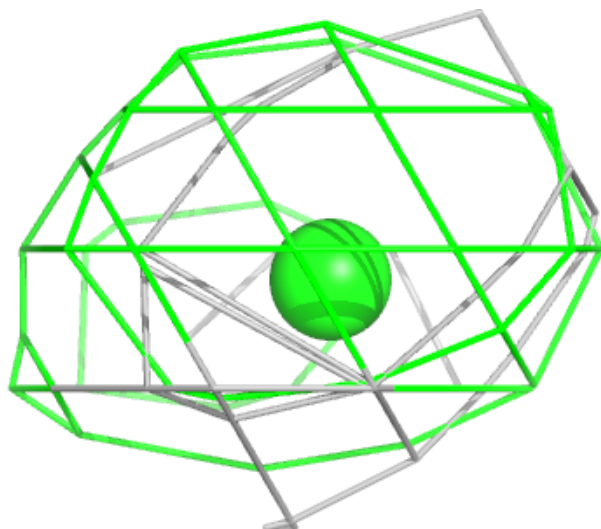
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

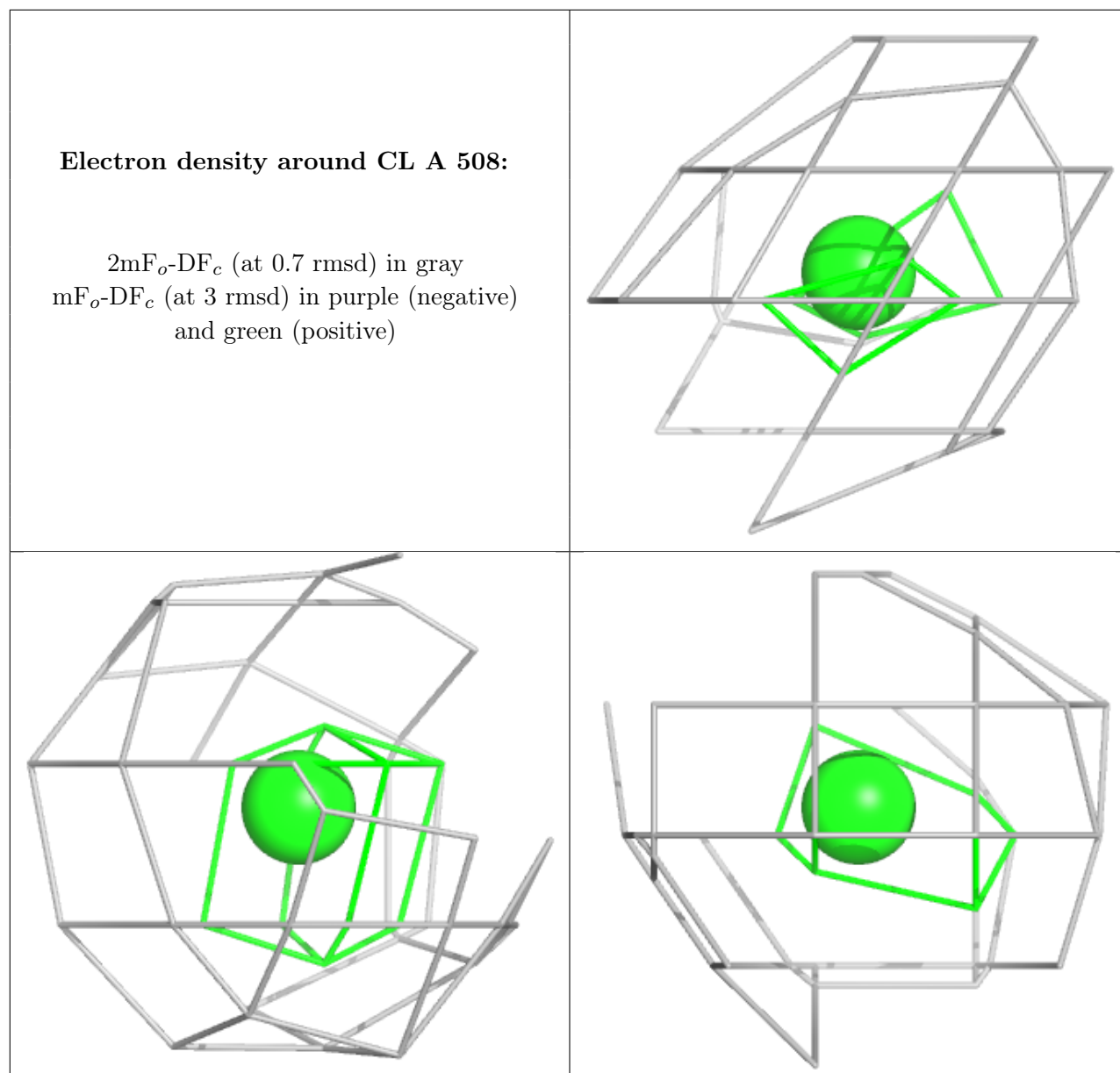
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	CL	B	508	1/1	0.93	0.24	128,128,128,128	0
5	CL	A	508	1/1	0.98	0.19	84,84,84,84	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around CL B 508:

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





6.5 Other polymers [i](#)

There are no such residues in this entry.