



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 08:43 AM BST

PDB ID : 6NIH
Title : Crystal structure of human TLR1
Authors : Su, L.; Zhang, H.
Deposited on : 2018-12-27
Resolution : 2.30 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 : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

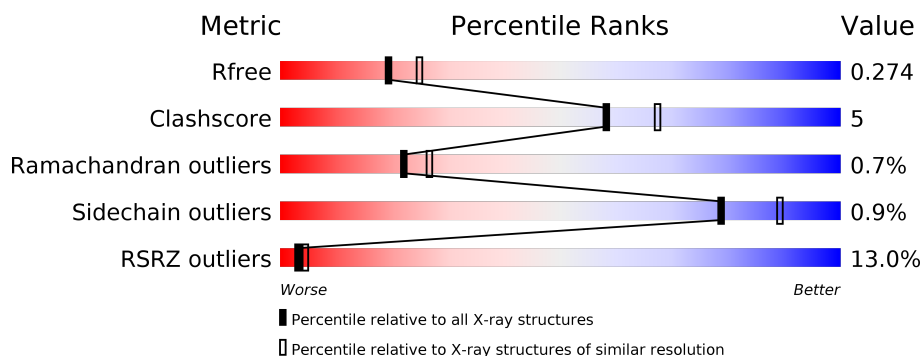
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	545	
1	B	545	
2	C	2	
2	D	2	
2	F	2	
3	E	3	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 17381 atoms, of which 8624 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 Toll-like receptor 1, Variable lymphocyte receptor B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	519	Total	C	H	N	O	S	0	3	0
			8413	2677	4232	700	784	20			
1	B	520	Total	C	H	N	O	S	0	3	0
			8434	2686	4242	701	785	20			

There are 2 discrepancies between the modelled and reference sequences:

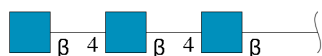
Chain	Residue	Modelled	Actual	Comment	Reference
A	476	ALA	-	linker	UNP Q15399
B	476	ALA	-	linker	UNP Q15399

- 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	C	2	Total	C	H	N	O		0	0	0
			53	16	25	2	10				
2	D	2	Total	C	H	N	O		0	0	0
			53	16	25	2	10				
2	F	2	Total	C	H	N	O		0	0	0
			52	16	24	2	10				

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(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	E	3	Total	C	H	N	O	0	0	0
			79	24	37	3	15			

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
4	B	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
4	B	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

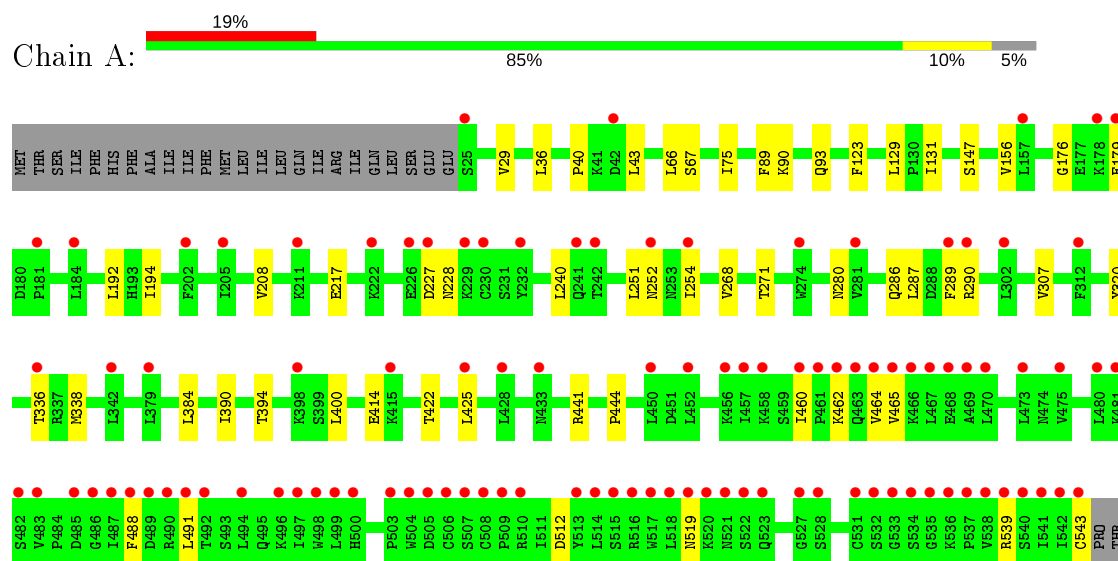
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	77	Total O 77 77	0	0
5	B	139	Total O 139 139	0	0

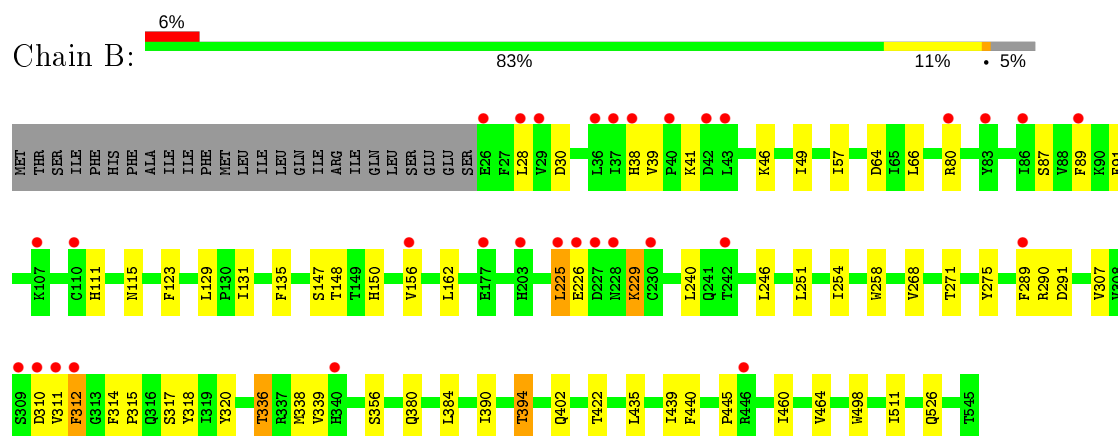
3 Residue-property plots [i](#)

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: Toll-like receptor 1, Variable lymphocyte receptor B



- Molecule 1: Toll-like receptor 1, Variable lymphocyte receptor B



- 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

Chain D:  50% 50%



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

Chain F:  100%



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

Chain E:  67% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.03Å 74.38Å 106.08Å 90.00° 96.97° 90.00°	Depositor
Resolution (Å)	46.40 – 2.30 46.40 – 2.30	Depositor EDS
% Data completeness (in resolution range)	74.7 (46.40-2.30) 74.7 (46.40-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.243 , 0.274 0.244 , 0.274	Depositor DCC
R_{free} test set	1958 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	27.0	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	17381	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% 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: 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	0.25	0/4275	0.49	0/5791
1	B	0.26	0/4288	0.49	0/5810
All	All	0.26	0/8563	0.49	0/11601

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	4181	4232	4232	31	0
1	B	4192	4242	4241	51	0
2	C	28	25	25	0	0
2	D	28	25	25	0	0
2	F	28	24	25	0	0
3	E	42	37	37	1	0
4	A	14	13	13	1	0
4	B	28	26	26	0	0
5	A	77	0	0	0	0
5	B	139	0	0	2	0
All	All	8757	8624	8624	82	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 (82) 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:225:LEU:HD22	1:B:229:LYS:HG3	1.58	0.83
1:B:251:LEU:HB3	1:B:254:ILE:HD11	1.68	0.75
1:A:251:LEU:HB3	1:A:254:ILE:HD11	1.70	0.73
1:B:225:LEU:CD2	1:B:229:LYS:HG3	2.27	0.63
1:B:440:PHE:CD1	1:B:464:VAL:HG22	2.34	0.62
1:A:384:LEU:HB3	1:A:390:ILE:HD11	1.82	0.62
1:A:394:THR:HG23	1:A:400:LEU:HD23	1.81	0.62
1:B:148:THR:HG22	1:B:150[B]:HIS:H	1.65	0.61
1:B:148:THR:HG22	1:B:150[A]:HIS:H	1.65	0.61
1:B:275:TYR:HE1	3:E:1:NAG:H81	1.66	0.60
1:A:208:VAL:HG23	1:A:240:LEU:HD21	1.82	0.60
1:B:38:HIS:O	1:B:57:ILE:HG23	2.02	0.59
1:A:460:ILE:HG23	1:A:464:VAL:HG21	1.84	0.58
1:B:66:LEU:HD21	1:B:91:PHE:CD2	2.38	0.58
1:B:460:ILE:HG23	1:B:464:VAL:HG21	1.86	0.57
1:B:28:LEU:HD11	1:B:30:ASP:HB2	1.86	0.57
1:B:123:PHE:N	1:B:147:SER:OG	2.39	0.55
1:A:192:LEU:HD21	1:A:194:ILE:HD11	1.89	0.54
1:B:226:GLU:HA	1:B:226:GLU:OE1	2.09	0.53
1:B:225:LEU:CD2	1:B:229:LYS:HA	2.38	0.53
1:B:320:TYR:HE1	1:B:338:MET:HG3	1.75	0.52
1:B:384:LEU:HB3	1:B:390:ILE:HD11	1.91	0.52
1:A:286:GLN:OE1	1:A:287:LEU:N	2.44	0.51
1:A:307:VAL:HB	1:A:336:THR:HG22	1.92	0.51
1:A:66:LEU:HD12	1:A:67:SER:N	2.26	0.51
1:B:336:THR:HG22	1:B:338:MET:H	1.75	0.51
1:A:29:VAL:HG11	1:A:43:LEU:HD22	1.93	0.50
1:B:240:LEU:HD22	1:B:246:LEU:HD22	1.94	0.50
1:B:336:THR:CG2	1:B:338:MET:HB2	2.42	0.49
1:A:123:PHE:N	1:A:147:SER:OG	2.45	0.49
1:B:251:LEU:CB	1:B:254:ILE:HD11	2.41	0.49
1:A:217:GLU:OE1	1:A:252:ASN:ND2	2.40	0.49
1:B:28:LEU:CD1	1:B:30:ASP:HB2	2.44	0.47
1:B:394:THR:CG2	1:B:422:THR:H	2.27	0.47
1:B:156:VAL:O	1:B:156:VAL:HG12	2.15	0.47
1:B:320:TYR:OH	1:B:339:VAL:HG22	2.15	0.47
1:A:320:TYR:HE1	1:A:338:MET:HG3	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:425:LEU:HD23	1:A:444:PRO:HG3	1.96	0.46
1:A:462:LYS:O	1:A:465:VAL:HG22	2.15	0.46
1:B:511:ILE:O	1:B:511:ILE:HG13	2.15	0.46
1:B:402:GLN:NE2	5:B:824:HOH:O	2.47	0.46
1:A:176:GLY:O	1:A:179:GLU:HG3	2.16	0.46
1:A:75:ILE:CD1	4:A:601:NAG:H82	2.46	0.46
1:B:307:VAL:HB	1:B:336:THR:OG1	2.16	0.46
1:B:435:LEU:HD22	1:B:439:ILE:HD13	1.99	0.45
1:A:156:VAL:HG12	1:A:156:VAL:O	2.17	0.44
1:B:225:LEU:HD23	1:B:229:LYS:HA	1.99	0.44
1:B:310:ASP:OD1	1:B:311:VAL:N	2.51	0.44
1:B:87:SER:HB3	1:B:111:HIS:HB2	2.00	0.44
1:B:38:HIS:CG	1:B:39:VAL:H	2.35	0.44
1:A:394:THR:CG2	1:A:422:THR:HG22	2.48	0.43
1:A:251:LEU:CB	1:A:254:ILE:HD11	2.45	0.43
1:B:129:LEU:HD23	1:B:131:ILE:HD12	2.00	0.43
1:B:129:LEU:HD12	1:B:148:THR:OG1	2.19	0.43
1:B:38:HIS:O	1:B:57:ILE:HG12	2.19	0.43
1:A:414:GLU:OE2	1:A:441:ARG:NH1	2.51	0.43
1:A:488:PHE:HD1	1:A:491:LEU:HD12	1.84	0.43
1:B:258:TRP:CZ2	1:B:315:PRO:HD3	2.54	0.43
1:B:39:VAL:HG11	1:B:64:ASP:HB3	2.00	0.42
1:B:289:PHE:CE1	1:B:291:ASP:OD1	2.72	0.42
1:B:498:TRP:CD1	1:B:526:GLN:HB2	2.54	0.42
1:A:90:LYS:O	1:A:93:GLN:NE2	2.52	0.42
1:B:135:PHE:O	1:B:162:LEU:HD11	2.20	0.42
1:B:147:SER:O	1:B:148:THR:OG1	2.37	0.42
1:A:460:ILE:CG2	1:A:464:VAL:HG21	2.48	0.42
1:B:336:THR:CG2	1:B:338:MET:H	2.32	0.42
1:A:129:LEU:HD23	1:A:131:ILE:HD12	2.01	0.42
1:A:36:LEU:HD13	1:A:40:PRO:HD3	2.01	0.41
1:B:28:LEU:HD23	1:B:49:ILE:HB	2.03	0.41
1:B:310:ASP:O	1:B:312:PHE:N	2.53	0.41
1:A:512:ASP:OD1	1:A:543:CYS:HB2	2.20	0.41
1:B:268:VAL:HA	1:B:271:THR:HG23	2.01	0.41
1:B:356:SER:HA	1:B:380:GLN:O	2.21	0.41
1:B:80:ARG:NH2	5:B:832:HOH:O	2.52	0.41
1:A:290:ARG:HD2	1:A:290:ARG:HA	1.91	0.41
1:B:290:ARG:HD2	1:B:318:TYR:CE1	2.56	0.41
1:B:41:LYS:HD3	1:B:41:LYS:HA	1.95	0.41
1:A:268:VAL:HA	1:A:271:THR:HG23	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:THR:HG22	1:A:422:THR:HG22	2.03	0.40
1:A:519:ASN:HA	1:A:539:ARG:NE	2.37	0.40
1:B:394:THR:HG22	1:B:422:THR:H	1.87	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	520/545 (95%)	474 (91%)	43 (8%)	3 (1%)	25	31
1	B	521/545 (96%)	476 (91%)	40 (8%)	5 (1%)	15	17
All	All	1041/1090 (96%)	950 (91%)	83 (8%)	8 (1%)	22	23

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	229	LYS
1	B	312	PHE
1	A	227	ASP
1	A	280[A]	ASN
1	A	280[B]	ASN
1	B	225	LEU
1	B	317	SER
1	B	445	PRO

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	496/518 (96%)	493 (99%)	3 (1%)	86	94
1	B	497/518 (96%)	491 (99%)	6 (1%)	71	84
All	All	993/1036 (96%)	984 (99%)	9 (1%)	78	89

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89	PHE
1	A	228	ASN
1	A	289	PHE
1	B	46	LYS
1	B	89	PHE
1	B	115	ASN
1	B	314	PHE
1	B	336	THR
1	B	394	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	270	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

9 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	C	1	1,2	14,14,15	0.28	0	17,19,21	0.35	0
2	NAG	C	2	2	14,14,15	0.22	0	17,19,21	0.43	0
2	NAG	D	1	1,2	14,14,15	0.37	0	17,19,21	0.50	0
2	NAG	D	2	2	14,14,15	1.20	1 (7%)	17,19,21	1.21	2 (11%)
3	NAG	E	1	1,3	14,14,15	0.22	0	17,19,21	0.54	0
3	NAG	E	2	3	14,14,15	0.26	0	17,19,21	0.37	0
3	NAG	E	3	3	14,14,15	0.19	0	17,19,21	0.41	0
2	NAG	F	1	1,2	14,14,15	0.52	0	17,19,21	0.65	0
2	NAG	F	2	2	14,14,15	0.29	0	17,19,21	0.37	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	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	1/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
3	NAG	E	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	NAG	E	3	3	-	0/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	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	O5-C1	-2.82	1.39	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	C1-O5-C5	3.75	117.27	112.19
2	D	2	NAG	C6-C5-C4	-2.00	108.31	113.00

There are no chirality outliers.

All (7) torsion outliers are listed below:

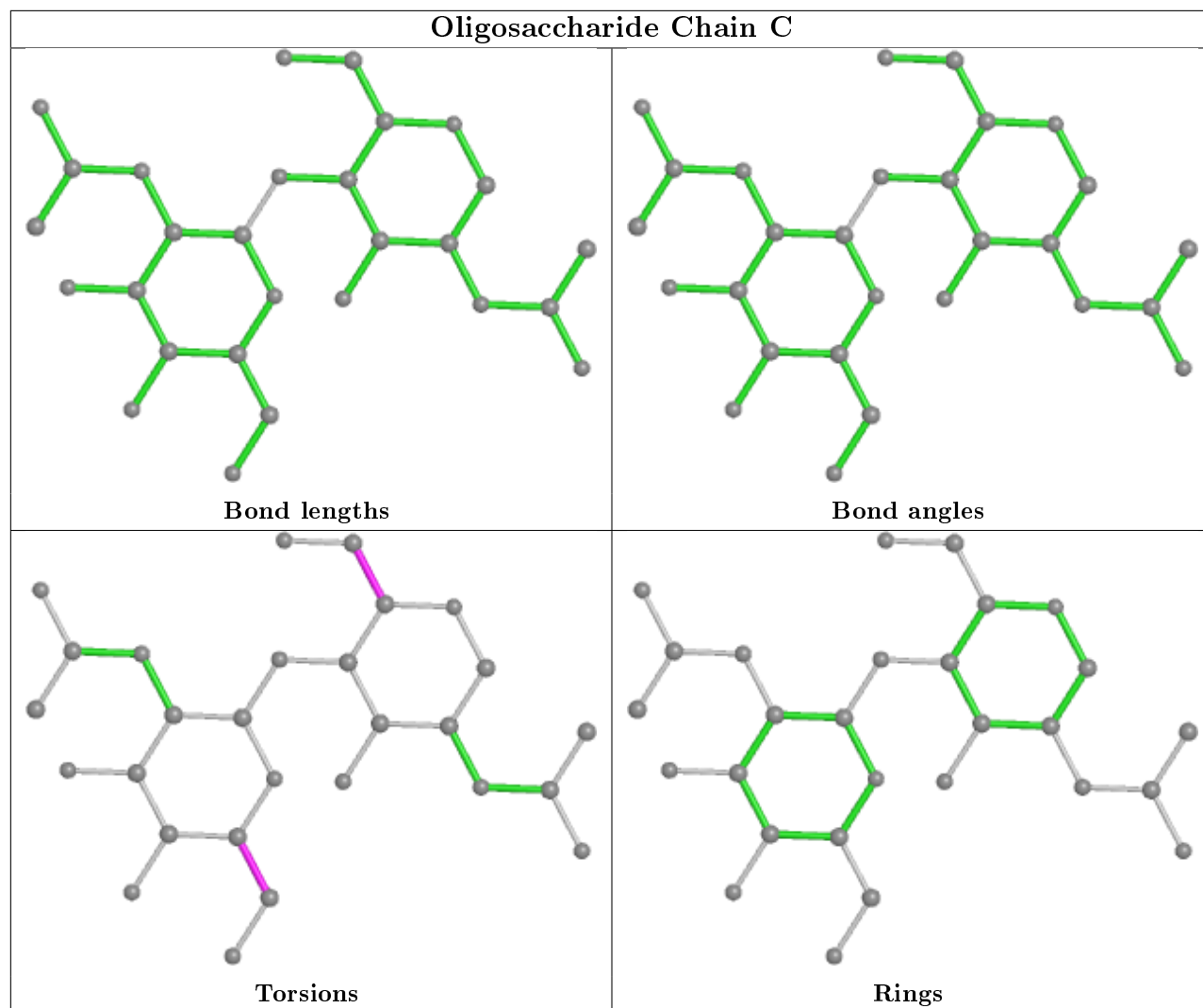
Mol	Chain	Res	Type	Atoms
3	E	1	NAG	C4-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
2	F	1	NAG	C4-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
2	F	1	NAG	O5-C5-C6-O6

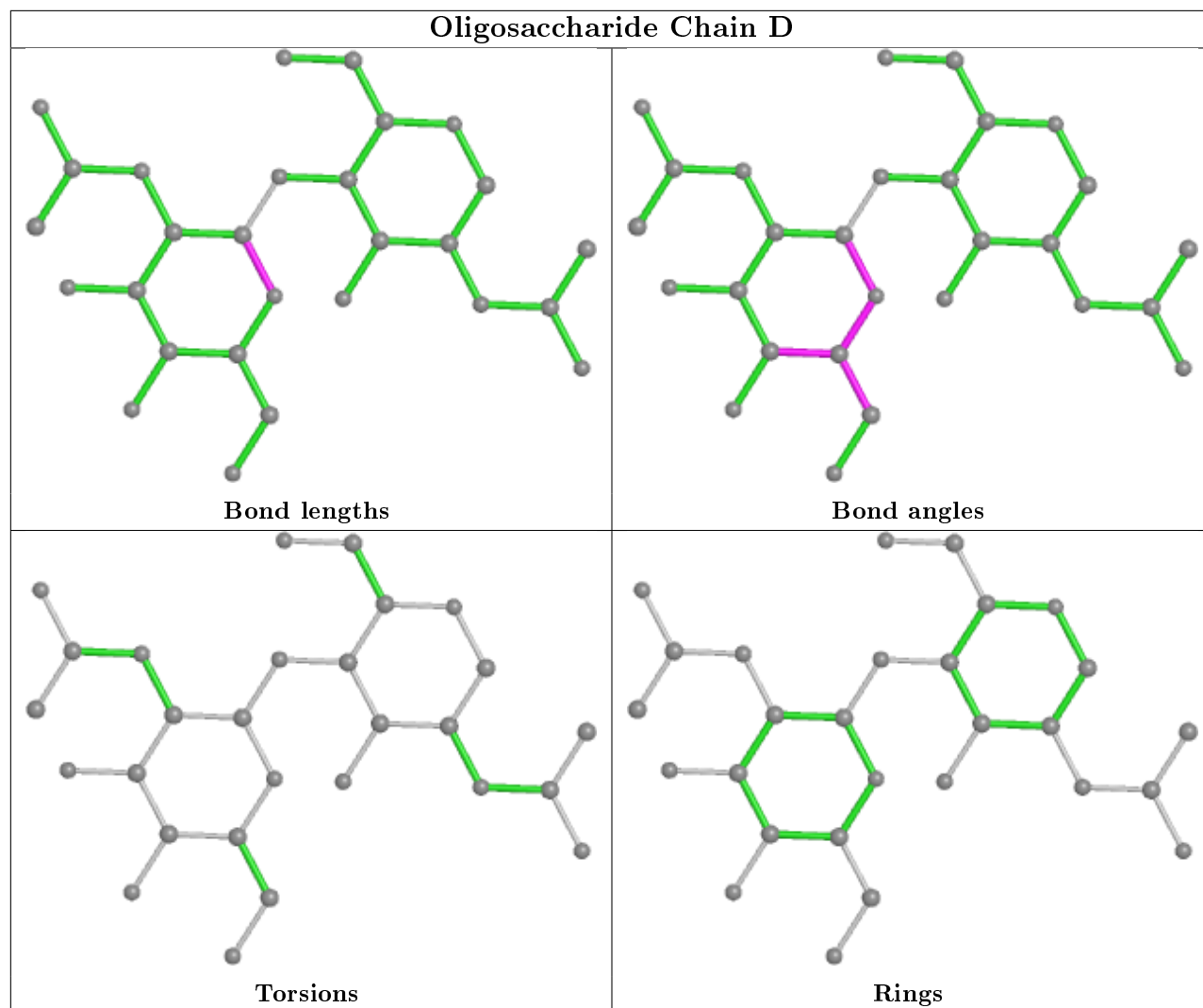
There are no ring outliers.

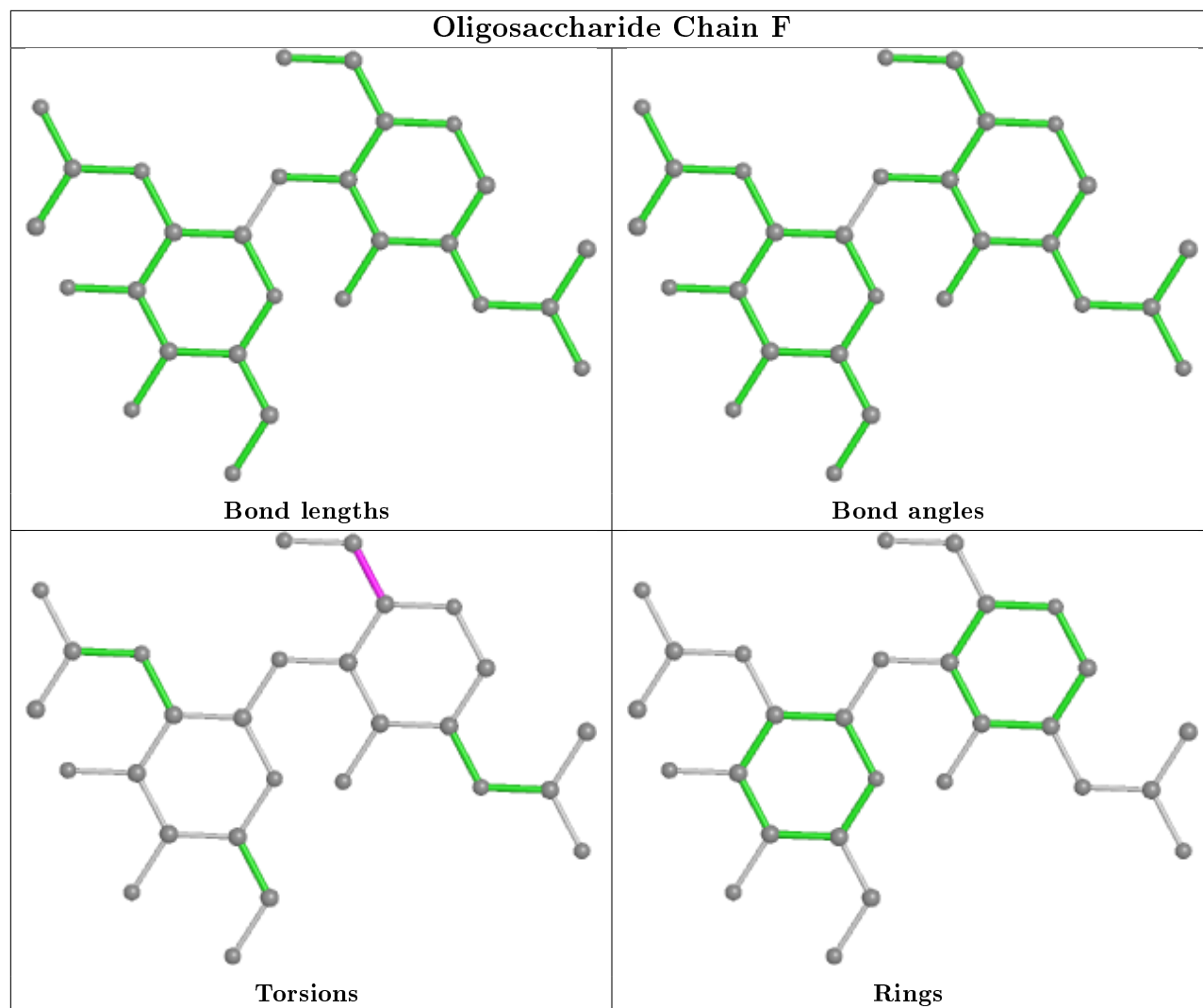
1 monomer is involved in 1 short contact:

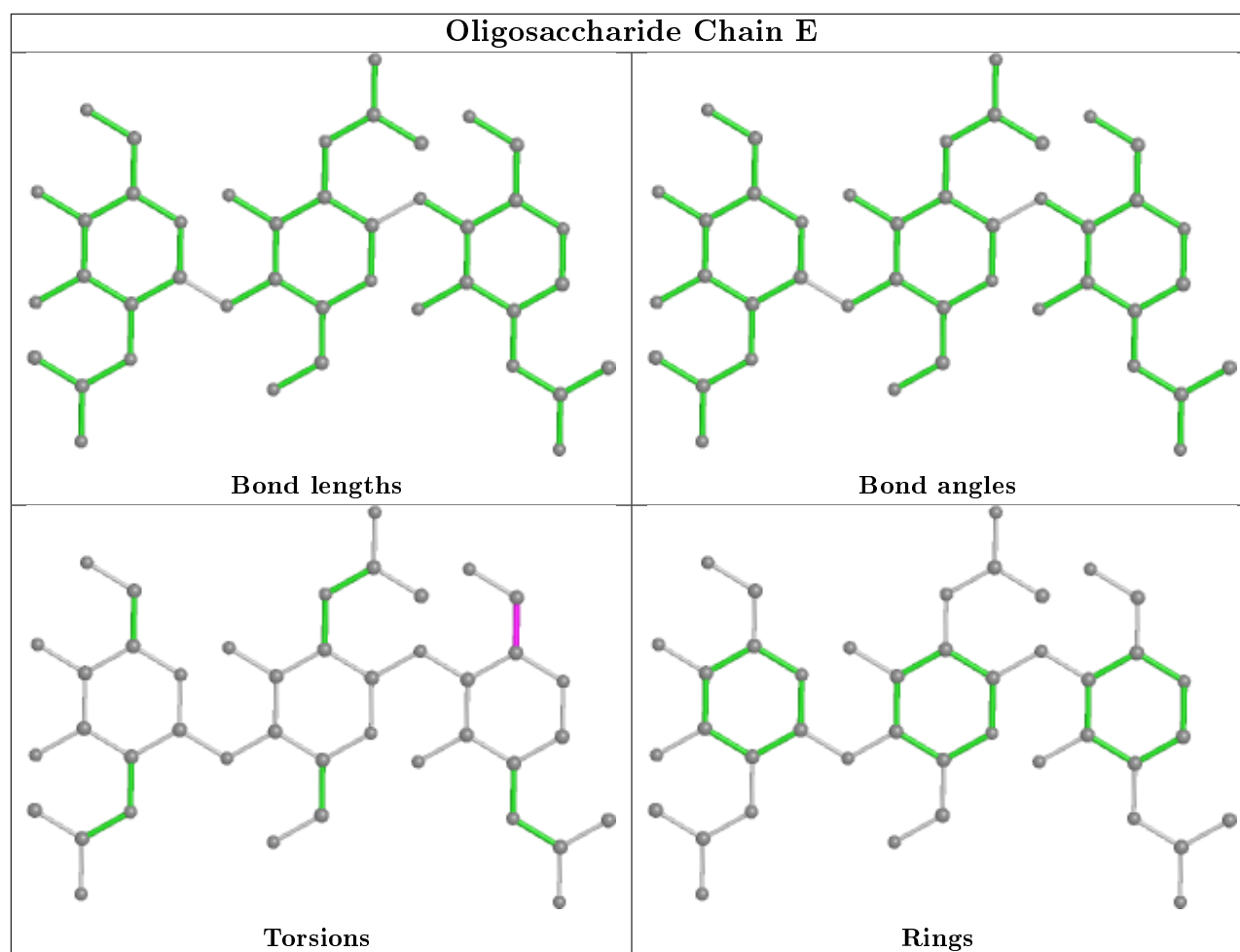
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	1	NAG	1	0

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









5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	B	701	1	14,14,15	0.28	0	17,19,21	0.40	0
4	NAG	A	601	1	14,14,15	0.21	0	17,19,21	0.55	0
4	NAG	B	702	1	14,14,15	0.35	0	17,19,21	0.70	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	701	1	-	1/6/23/26	0/1/1/1
4	NAG	A	601	1	-	0/6/23/26	0/1/1/1
4	NAG	B	702	1	-	1/6/23/26	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
4	B	702	NAG	C3-C2-N2-C7
4	B	701	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	601	NAG	1	0

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	519/545 (95%)	1.24	104 (20%) 1 1	16, 51, 117, 149	0
1	B	520/545 (95%)	0.47	31 (5%) 21 28	9, 32, 74, 111	0
All	All	1039/1090 (95%)	0.86	135 (12%) 3 4	9, 41, 101, 149	0

All (135) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	533	GLY	14.3
1	A	486	GLY	10.6
1	A	483	VAL	9.2
1	A	242	THR	7.7
1	A	532	SER	7.4
1	A	517	TRP	7.1
1	A	509	PRO	7.1
1	A	542	ILE	6.5
1	A	490	ARG	6.5
1	A	485	ASP	6.2
1	A	522	SER	6.2
1	B	289	PHE	6.2
1	A	468	GLU	5.9
1	B	227	ASP	5.9
1	A	232	TYR	5.7
1	A	464	VAL	5.7
1	B	312	PHE	5.6
1	A	539	ARG	5.5
1	A	540	SER	5.2
1	A	489	ASP	5.2
1	A	462	LYS	5.1
1	A	507	SER	5.1
1	A	506	CYS	5.0
1	A	515	SER	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	460	ILE	4.9
1	B	38	HIS	4.9
1	A	492	THR	4.8
1	A	467	LEU	4.7
1	A	494	LEU	4.7
1	A	488	PHE	4.7
1	A	518	LEU	4.6
1	A	537	PRO	4.5
1	A	227	ASP	4.5
1	A	290	ARG	4.4
1	B	28	LEU	4.4
1	B	242	THR	4.4
1	A	510	ARG	4.4
1	A	491	LEU	4.4
1	A	541	ILE	4.3
1	A	205	ILE	4.2
1	A	473	LEU	4.1
1	B	310	ASP	4.1
1	A	543	CYS	4.1
1	A	181	PRO	4.0
1	A	538	VAL	4.0
1	A	505	ASP	3.9
1	B	26	GLU	3.9
1	B	225	LEU	3.9
1	A	289	PHE	3.7
1	B	37	ILE	3.7
1	A	415	LYS	3.7
1	B	228	ASN	3.7
1	A	503	PRO	3.6
1	A	531	CYS	3.5
1	A	520	LYS	3.5
1	A	527	GLY	3.5
1	A	504	TRP	3.5
1	A	519	ASN	3.5
1	A	523	GLN	3.5
1	B	340[A]	HIS	3.4
1	A	516	ARG	3.4
1	B	80	ARG	3.4
1	A	302	LEU	3.3
1	B	42	ASP	3.2
1	B	446	ARG	3.2
1	A	428	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	450	LEU	3.2
1	A	470	LEU	3.2
1	A	535	GLY	3.2
1	B	83	TYR	3.2
1	A	513	TYR	3.1
1	B	89	PHE	3.1
1	A	461	PRO	3.0
1	A	508	CYS	3.0
1	A	514	LEU	3.0
1	B	311	VAL	2.9
1	A	481	LYS	2.9
1	A	222	LYS	2.9
1	A	497	ILE	2.9
1	A	202	PHE	2.9
1	B	43	LEU	2.8
1	A	452	LEU	2.8
1	A	475	VAL	2.7
1	B	226	GLU	2.7
1	A	42	ASP	2.6
1	A	466	LYS	2.6
1	A	398	LYS	2.6
1	A	433	ASN	2.6
1	A	465	VAL	2.6
1	A	487	ILE	2.6
1	A	336	THR	2.6
1	A	498	TRP	2.6
1	A	281	VAL	2.6
1	B	40	PRO	2.5
1	A	230	CYS	2.5
1	B	36	LEU	2.5
1	A	469	ALA	2.5
1	B	203	HIS	2.5
1	A	521	ASN	2.5
1	A	463	GLN	2.5
1	A	536	LYS	2.5
1	A	425	LEU	2.5
1	B	29	VAL	2.4
1	A	179	GLU	2.4
1	A	241	GLN	2.4
1	A	528	SER	2.4
1	B	177	GLU	2.4
1	A	482	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	184	LEU	2.4
1	A	480	LEU	2.4
1	A	500	HIS	2.3
1	A	229	LYS	2.3
1	A	496	LYS	2.3
1	A	457	ILE	2.3
1	A	25	SER	2.3
1	A	456	LYS	2.3
1	B	86	ILE	2.3
1	A	534	SER	2.2
1	A	499	LEU	2.2
1	B	230	CYS	2.2
1	B	309	SER	2.2
1	A	178	LYS	2.2
1	A	254	ILE	2.2
1	A	342	LEU	2.2
1	A	312	PHE	2.2
1	A	274	TRP	2.2
1	A	226	GLU	2.1
1	A	211	LYS	2.1
1	A	252	ASN	2.1
1	B	110	CYS	2.1
1	B	107	LYS	2.1
1	A	157	LEU	2.1
1	B	156	VAL	2.0
1	A	379	LEU	2.0
1	A	458	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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.

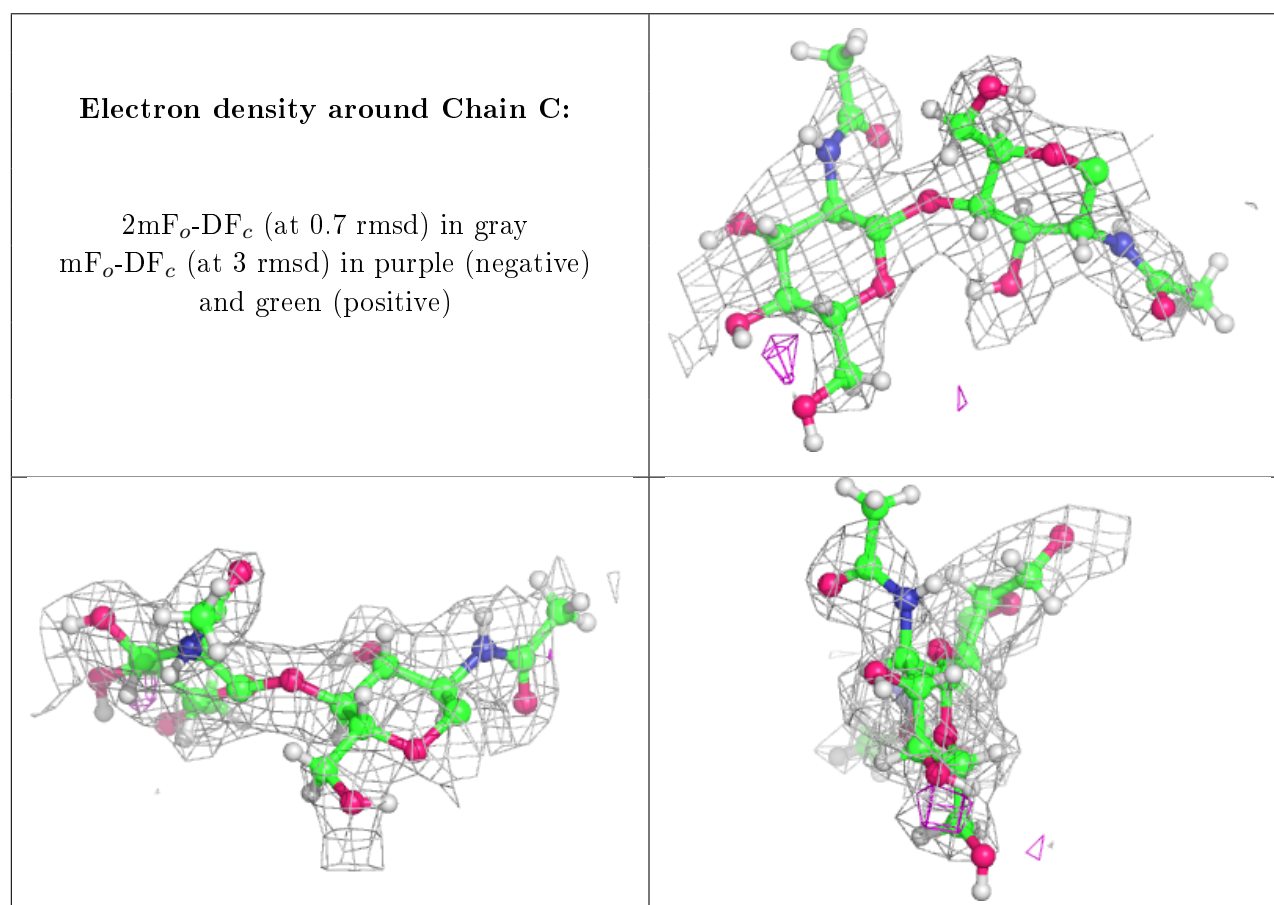
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	E	3	14/15	0.66	0.32	66,80,96,99	0

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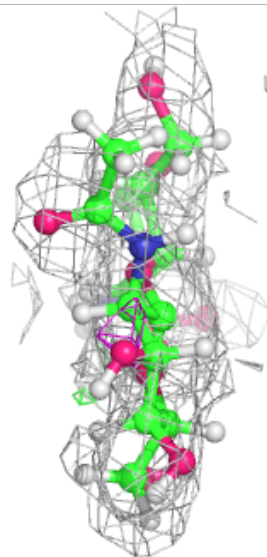
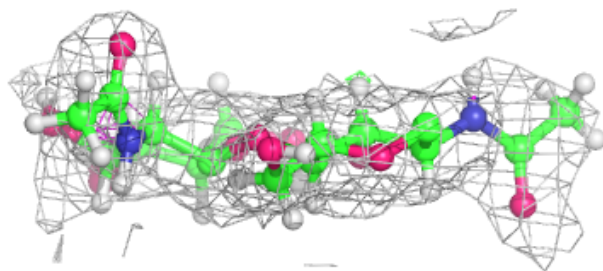
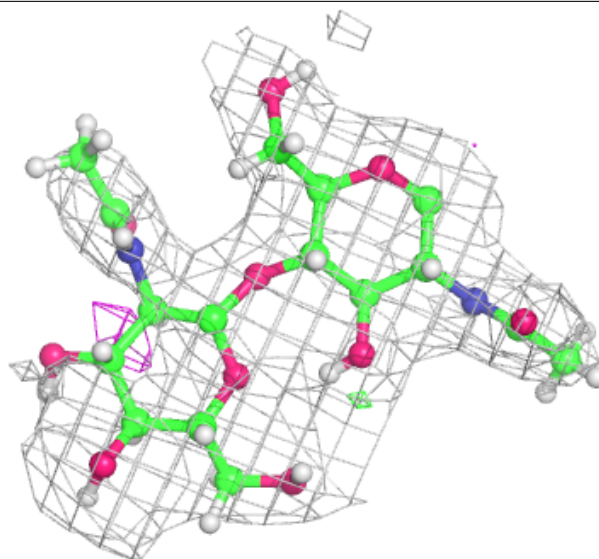
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	D	2	14/15	0.76	0.22	44,62,79,93	0
2	NAG	C	2	14/15	0.82	0.31	59,71,83,87	0
2	NAG	C	1	14/15	0.83	0.20	39,51,60,65	0
3	NAG	E	2	14/15	0.87	0.23	28,47,60,67	0
2	NAG	F	2	14/15	0.91	0.16	15,36,61,73	0
2	NAG	D	1	14/15	0.92	0.14	30,36,40,43	0
3	NAG	E	1	14/15	0.95	0.12	15,34,43,51	0
2	NAG	F	1	14/15	0.97	0.10	6,9,19,23	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.



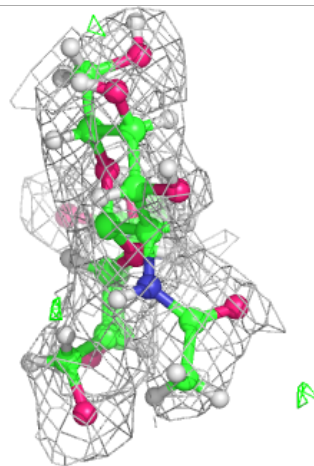
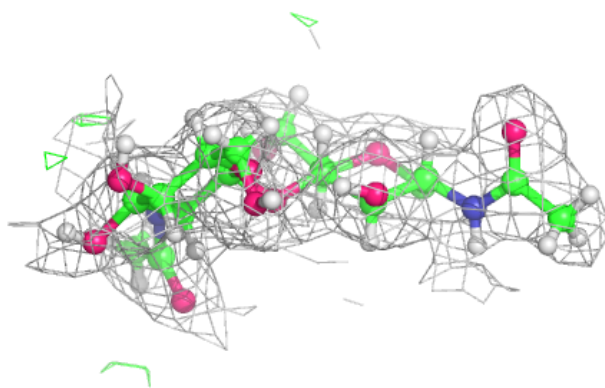
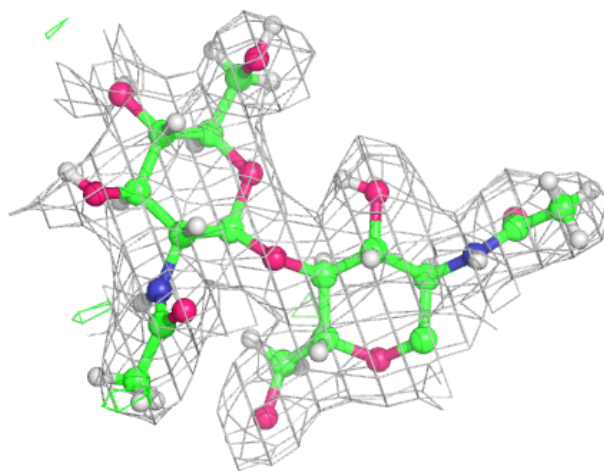
Electron density around Chain D:

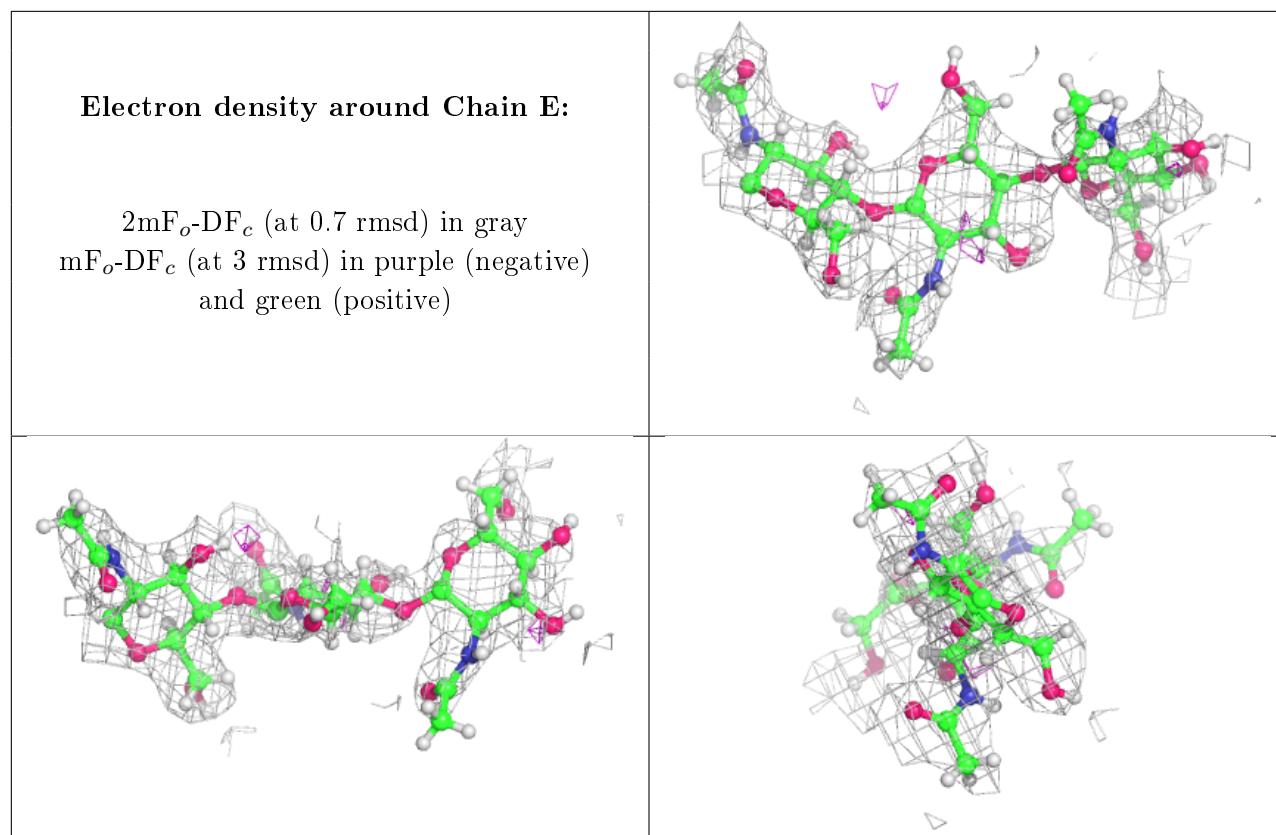
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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(\AA^2)	Q<0.9
4	NAG	B	702	14/15	0.74	0.26	48,64,73,82	0
4	NAG	B	701	14/15	0.81	0.23	48,64,80,89	0
4	NAG	A	601	14/15	0.90	0.15	6,9,19,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.