



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:26 AM UTC

PDB ID : 7R53 / pdb_00007r53
Title : Crystal structure of human TLR8 in complex with Compound 15
Authors : Faller, M.; Zink, F.
Deposited on : 2022-02-10
Resolution : 3.12 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

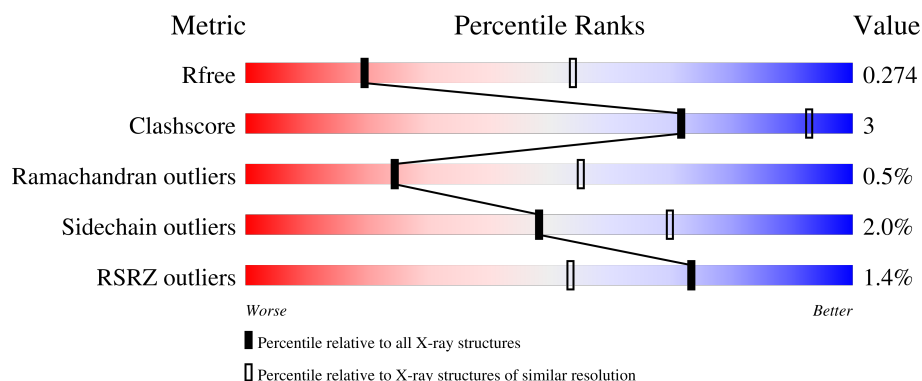
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

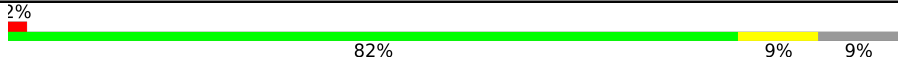
The reported resolution of this entry is 3.12 Å.

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	1816 (3.14-3.10)
Clashscore	190562	1906 (3.14-3.10)
Ramachandran outliers	187476	1802 (3.14-3.10)
Sidechain outliers	187428	1802 (3.14-3.10)
RSRZ outliers	180081	1816 (3.14-3.10)

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	807	
1	B	807	
2	C	5	
2	E	5	
2	F	5	

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Mol	Chain	Length	Quality of chain
2	H	5	 40% 60%
3	D	3	 67% 33%
3	G	3	 67% 33%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 12272 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.

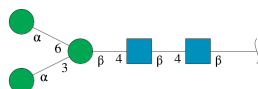
- Molecule 1 is a protein called Toll-like receptor 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	737	Total	C	N	O	S	0	0	0
			5775	3689	982	1087	17			
1	B	736	Total	C	N	O	S	0	0	0
			5812	3716	988	1091	17			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	828	GLU	-	expression tag	UNP Q9NR97
A	829	PHE	-	expression tag	UNP Q9NR97
A	830	LEU	-	expression tag	UNP Q9NR97
A	831	VAL	-	expression tag	UNP Q9NR97
A	832	PRO	-	expression tag	UNP Q9NR97
A	833	ARG	-	expression tag	UNP Q9NR97
B	828	GLU	-	expression tag	UNP Q9NR97
B	829	PHE	-	expression tag	UNP Q9NR97
B	830	LEU	-	expression tag	UNP Q9NR97
B	831	VAL	-	expression tag	UNP Q9NR97
B	832	PRO	-	expression tag	UNP Q9NR97
B	833	ARG	-	expression tag	UNP Q9NR97

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



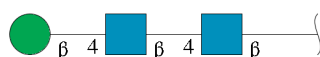
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	5	Total	C	N	O	0	0	0
			61	34	2	25			

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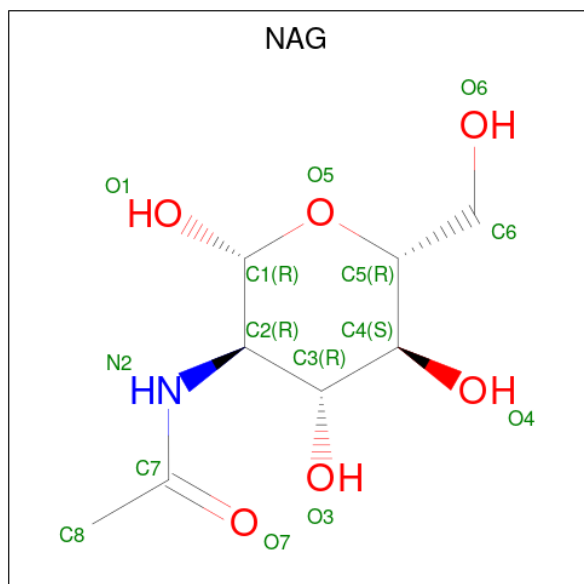
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	5	Total	C	N	O	0	0	0
			61	34	2	25			
2	F	5	Total	C	N	O	0	0	0
			61	34	2	25			
2	H	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 3 is an oligosaccharide called beta-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	D	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	G	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



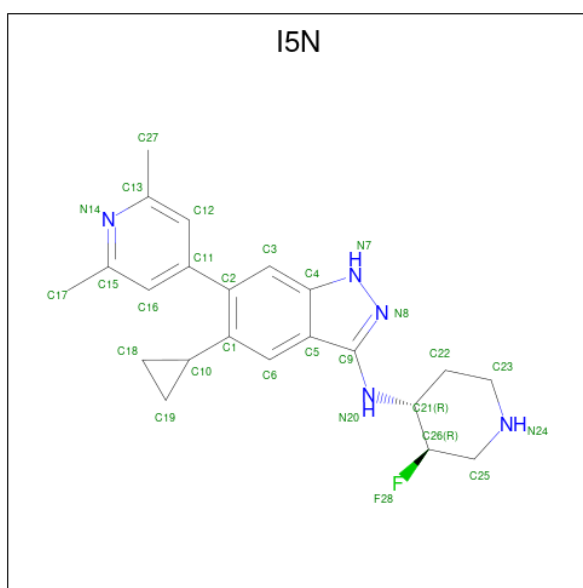
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

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

- Molecule 5 is 5-cyclopropyl-6-(2,6-dimethylpyridin-4-yl)- {N}-[(3 {R},4 {R})-3-fluoranyl piperidin-4-yl]-1 {H}-indazol-3-amine (CCD ID: I5N) (formula: C₂₂H₂₆FN₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	F	N	0	0
			28	22	1	5		
5	A	1	Total	C	F	N	0	0
			28	22	1	5		

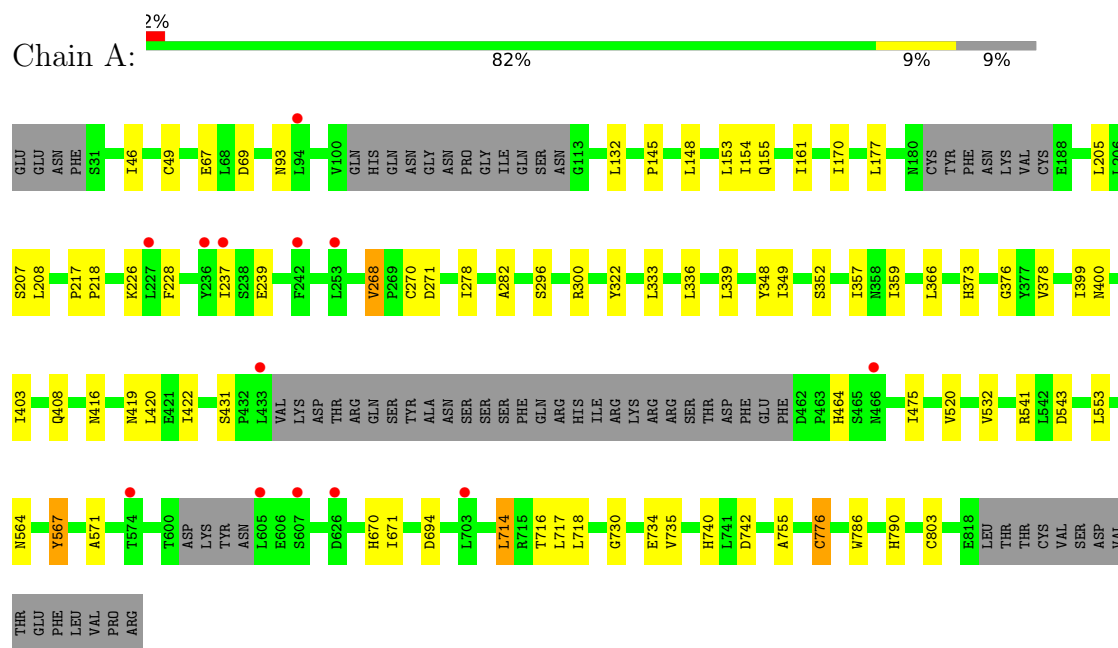
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	55	Total	O	0	0
			55	55		
6	B	84	Total	O	0	0
			84	84		

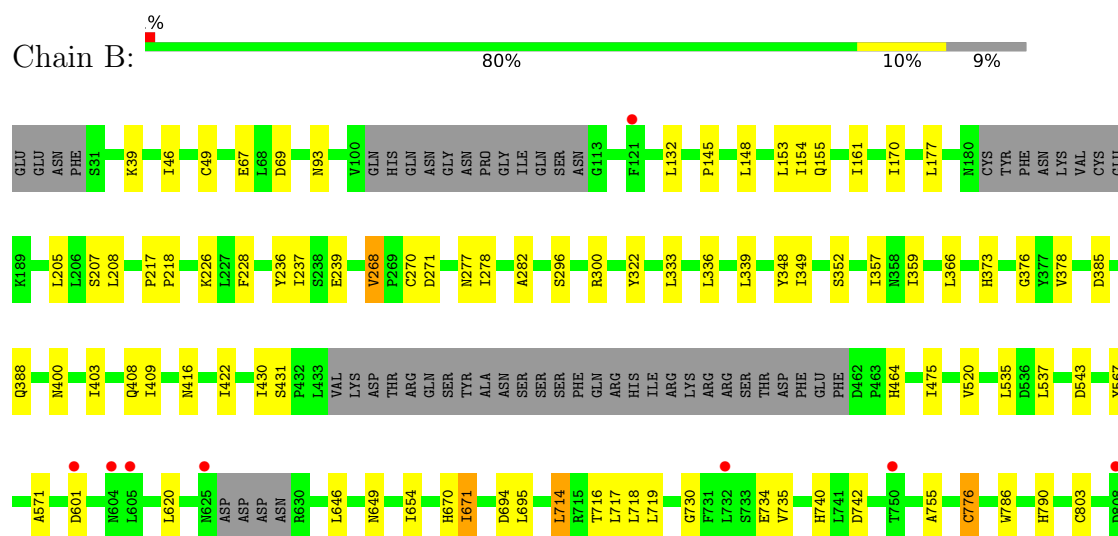
3 Residue-property plots [i](#)

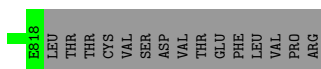
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 8



• Molecule 1: Toll-like receptor 8





• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



• Molecule 3: beta-D-mannopyranose-(1-4)-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	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	164.88Å 89.06Å 152.27Å 90.00° 120.26° 90.00°	Depositor
Resolution (Å)	68.48 – 3.12 68.48 – 3.12	Depositor EDS
% Data completeness (in resolution range)	95.6 (68.48-3.12) 95.6 (68.48-3.12)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 3.13Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
R, R_{free}	0.238 , 0.269 0.232 , 0.274	Depositor DCC
R_{free} test set	1552 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	83.7	Xtriage
Anisotropy	0.779	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 48.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12272	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, NAG, BMA, I5N

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	0.53	0/5891	0.87	0/8011
1	B	0.53	0/5929	0.88	0/8054
All	All	0.53	0/11820	0.87	0/16065

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

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	5775	0	5638	38	0
1	B	5812	0	5719	44	0
2	C	61	0	52	0	0
2	E	61	0	52	0	0
2	F	61	0	52	0	0
2	H	61	0	52	0	0
3	D	39	0	34	0	0
3	G	39	0	34	0	0
4	A	84	0	78	0	0
4	B	84	0	78	0	0
5	A	56	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	55	0	0	0	0
6	B	84	0	0	0	0
All	All	12272	0	11789	80	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (80) 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:730:GLY:H	1:B:755:ALA:HA	1.51	0.74
1:A:730:GLY:H	1:A:755:ALA:HA	1.51	0.74
1:A:373:HIS:HA	1:A:400:ASN:HB3	1.74	0.70
1:B:373:HIS:HA	1:B:400:ASN:HB3	1.74	0.70
1:A:268:VAL:HG13	1:B:571:ALA:HB3	1.75	0.68
1:B:408:GLN:HE22	1:B:431:SER:H	1.43	0.65
1:A:154:ILE:HG22	1:A:155:GLN:HG3	1.83	0.61
1:A:520:VAL:HA	1:A:543:ASP:HB3	1.81	0.61
1:A:571:ALA:HB3	1:B:268:VAL:HG13	1.83	0.60
1:B:154:ILE:HG22	1:B:155:GLN:HG3	1.83	0.60
1:A:333:LEU:HD22	1:A:366:LEU:HD11	1.87	0.57
1:B:207:SER:HA	1:B:228:PHE:HB2	1.87	0.56
1:B:333:LEU:HD22	1:B:366:LEU:HD11	1.87	0.56
1:A:207:SER:HA	1:A:228:PHE:HB2	1.88	0.56
1:B:46:ILE:HG22	1:B:67:GLU:HB2	1.88	0.56
1:B:336:LEU:HD13	1:B:339:LEU:HD22	1.89	0.55
1:A:336:LEU:HD13	1:A:339:LEU:HD22	1.89	0.55
1:A:46:ILE:HG22	1:A:67:GLU:HB2	1.88	0.54
1:B:422:ILE:HG23	1:B:475:ILE:HD12	1.89	0.54
1:A:399:ILE:HD12	1:A:420:LEU:HD11	1.89	0.54
1:A:714:LEU:HD21	1:A:717:LEU:HD13	1.90	0.54
1:B:714:LEU:HD21	1:B:717:LEU:HD13	1.90	0.53
1:B:520:VAL:HA	1:B:543:ASP:HB3	1.90	0.52
1:B:154:ILE:HD12	1:B:464:HIS:CE1	2.45	0.51
1:A:154:ILE:HD12	1:A:464:HIS:CE1	2.45	0.51
1:A:239:GLU:HA	1:A:282:ALA:HA	1.93	0.50
1:B:239:GLU:HA	1:B:282:ALA:HA	1.93	0.50
1:A:670:HIS:HA	1:A:694:ASP:HB3	1.94	0.50
1:B:535:LEU:HG	1:B:537:LEU:HG	1.94	0.50
1:B:670:HIS:HA	1:B:694:ASP:HB3	1.94	0.49
1:A:776:CYS:HB2	1:A:803:CYS:HB3	1.66	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:422:ILE:HG23	1:A:475:ILE:HD12	1.95	0.48
1:B:161:ILE:HD12	1:B:177:LEU:HD13	1.94	0.48
1:A:541:ARG:NH1	1:A:567:TYR:CD1	2.82	0.48
1:A:161:ILE:HD12	1:A:177:LEU:HD13	1.94	0.48
1:A:730:GLY:O	1:A:734:GLU:HG2	2.15	0.47
1:B:349:ILE:HB	1:B:352:SER:HB3	1.97	0.47
1:B:730:GLY:O	1:B:734:GLU:HG2	2.15	0.46
1:B:408:GLN:NE2	1:B:431:SER:H	2.09	0.46
1:B:237:ILE:HB	1:B:278:ILE:HA	1.98	0.46
1:A:237:ILE:HB	1:A:278:ILE:HA	1.98	0.46
1:B:300:ARG:HG2	1:B:322:TYR:HB2	1.98	0.46
1:A:718:LEU:HA	1:A:742:ASP:HB3	1.98	0.45
1:B:718:LEU:HA	1:B:742:ASP:HB3	1.98	0.45
1:A:349:ILE:HB	1:A:352:SER:HB3	1.98	0.45
1:B:776:CYS:HB2	1:B:803:CYS:HB3	1.66	0.45
1:B:786:TRP:CD1	1:B:790:HIS:CD2	3.05	0.44
1:B:620:LEU:HD11	1:B:646:LEU:HD22	1.99	0.44
1:A:786:TRP:CD1	1:A:790:HIS:CD2	3.05	0.44
1:A:177:LEU:HB2	1:A:208:LEU:HD23	2.00	0.44
1:A:300:ARG:HG2	1:A:322:TYR:HB2	1.98	0.44
1:A:217:PRO:HA	1:A:218:PRO:HD3	1.92	0.43
1:B:39:LYS:HE2	1:B:46:ILE:HD11	1.99	0.43
1:A:357:ILE:HG12	1:A:359:ILE:HG12	2.00	0.43
1:A:132:LEU:HB2	1:A:153:LEU:HD23	2.01	0.43
1:A:408:GLN:HE22	1:A:431:SER:H	1.66	0.43
1:B:348:TYR:HB3	1:B:376:GLY:O	2.19	0.43
1:B:654:ILE:HD11	1:B:671:ILE:HG21	2.01	0.42
1:B:69:ASP:HA	1:B:93:ASN:HB3	2.02	0.42
1:A:205:LEU:HG	1:A:226:LYS:HB2	2.02	0.42
1:B:217:PRO:HA	1:B:218:PRO:HD3	1.91	0.42
1:A:69:ASP:HA	1:A:93:ASN:HB3	2.02	0.42
1:A:145:PRO:HG2	1:A:148:LEU:HG	2.01	0.42
1:B:132:LEU:HB2	1:B:153:LEU:HD23	2.01	0.42
1:B:177:LEU:HB2	1:B:208:LEU:HD23	2.00	0.42
1:B:357:ILE:HG12	1:B:359:ILE:HG12	2.01	0.42
1:B:145:PRO:HG2	1:B:148:LEU:HG	2.01	0.42
1:B:409:ILE:HD12	1:B:430:ILE:HD11	2.02	0.41
1:B:695:LEU:HB2	1:B:719:LEU:HD23	2.02	0.41
1:A:348:TYR:HB3	1:A:376:GLY:O	2.19	0.41
1:B:205:LEU:HG	1:B:226:LYS:HB2	2.01	0.41
1:B:786:TRP:NE1	1:B:790:HIS:CD2	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:154:ILE:HD12	1:B:464:HIS:HE1	1.86	0.41
1:A:716:THR:HG23	1:A:740:HIS:ND1	2.36	0.41
1:A:786:TRP:NE1	1:A:790:HIS:CD2	2.89	0.41
1:B:716:THR:HG23	1:B:740:HIS:ND1	2.36	0.41
1:A:532:VAL:HB	1:A:553:LEU:HD22	2.03	0.41
1:B:236:TYR:HD1	1:B:277:ASN:HB3	1.86	0.41
1:B:620:LEU:HB2	1:B:649:ASN:HB3	2.02	0.41
1:A:154:ILE:HD12	1:A:464:HIS:HE1	1.85	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	727/807 (90%)	672 (92%)	52 (7%)	3 (0%)	30	60
1	B	726/807 (90%)	671 (92%)	51 (7%)	4 (1%)	21	50
All	All	1453/1614 (90%)	1343 (92%)	103 (7%)	7 (0%)	24	55

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	271	ASP
1	B	271	ASP
1	B	601	ASP
1	A	714	LEU
1	B	714	LEU
1	A	378	VAL
1	B	378	VAL

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	645/751 (86%)	632 (98%)	13 (2%)	48	70
1	B	654/751 (87%)	641 (98%)	13 (2%)	48	70
All	All	1299/1502 (86%)	1273 (98%)	26 (2%)	48	70

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	CYS
1	A	170	ILE
1	A	268	VAL
1	A	270	CYS
1	A	296	SER
1	A	403	ILE
1	A	416	ASN
1	A	419	ASN
1	A	564	ASN
1	A	567	TYR
1	A	671	ILE
1	A	735	VAL
1	A	776	CYS
1	B	49	CYS
1	B	170	ILE
1	B	268	VAL
1	B	270	CYS
1	B	296	SER
1	B	385	ASP
1	B	388	GLN
1	B	403	ILE
1	B	416	ASN
1	B	567	TYR
1	B	671	ILE
1	B	735	VAL
1	B	776	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	215	HIS
1	A	277	ASN
1	A	285	ASN
1	A	312	HIS
1	A	400	ASN
1	A	469	HIS
1	A	576	HIS
1	A	582	ASN
1	A	585	ASN
1	A	593	HIS
1	B	215	HIS
1	B	277	ASN
1	B	285	ASN
1	B	312	HIS
1	B	400	ASN
1	B	469	HIS
1	B	564	ASN
1	B	576	HIS
1	B	582	ASN
1	B	585	ASN
1	B	593	HIS
1	B	790	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 ⓘ

26 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	2,1	14,14,15	0.30	0	17,19,21	0.59	0
2	NAG	C	2	2	14,14,15	0.28	0	17,19,21	0.63	0
2	BMA	C	3	2	11,11,12	0.25	0	15,15,17	0.51	0
2	MAN	C	4	2	11,11,12	0.30	0	15,15,17	0.81	1 (6%)
2	MAN	C	5	2	11,11,12	0.35	0	15,15,17	0.82	1 (6%)
3	NAG	D	1	3,1	14,14,15	0.27	0	17,19,21	0.73	1 (5%)
3	NAG	D	2	3	14,14,15	0.30	0	17,19,21	0.51	0
3	BMA	D	3	3	11,11,12	0.28	0	15,15,17	0.50	0
2	NAG	E	1	2,1	14,14,15	0.30	0	17,19,21	0.51	0
2	NAG	E	2	2	14,14,15	0.29	0	17,19,21	0.50	0
2	BMA	E	3	2	11,11,12	0.27	0	15,15,17	0.48	0
2	MAN	E	4	2	11,11,12	0.29	0	15,15,17	0.66	1 (6%)
2	MAN	E	5	2	11,11,12	0.29	0	15,15,17	0.86	1 (6%)
2	NAG	F	1	2,1	14,14,15	0.30	0	17,19,21	0.58	0
2	NAG	F	2	2	14,14,15	0.29	0	17,19,21	0.62	0
2	BMA	F	3	2	11,11,12	0.26	0	15,15,17	0.52	0
2	MAN	F	4	2	11,11,12	0.30	0	15,15,17	0.79	1 (6%)
2	MAN	F	5	2	11,11,12	0.32	0	15,15,17	0.78	1 (6%)
3	NAG	G	1	3,1	14,14,15	0.30	0	17,19,21	0.60	0
3	NAG	G	2	3	14,14,15	0.29	0	17,19,21	0.65	1 (5%)
3	BMA	G	3	3	11,11,12	0.28	0	15,15,17	0.41	0
2	NAG	H	1	2,1	14,14,15	0.30	0	17,19,21	0.58	1 (5%)
2	NAG	H	2	2	14,14,15	0.28	0	17,19,21	0.49	0
2	BMA	H	3	2	11,11,12	0.27	0	15,15,17	0.58	0
2	MAN	H	4	2	11,11,12	0.32	0	15,15,17	0.76	1 (6%)
2	MAN	H	5	2	11,11,12	0.31	0	15,15,17	0.92	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
2	NAG	C	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	MAN	C	4	2	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	C	5	2	-	0/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1
2	NAG	E	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	BMA	E	3	2	-	0/2/19/22	0/1/1/1
2	MAN	E	4	2	-	0/2/19/22	0/1/1/1
2	MAN	E	5	2	-	0/2/19/22	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
2	BMA	F	3	2	-	0/2/19/22	0/1/1/1
2	MAN	F	4	2	-	0/2/19/22	0/1/1/1
2	MAN	F	5	2	-	0/2/19/22	0/1/1/1
3	NAG	G	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	BMA	G	3	3	-	0/2/19/22	0/1/1/1
2	NAG	H	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	0/6/23/26	0/1/1/1
2	BMA	H	3	2	-	0/2/19/22	0/1/1/1
2	MAN	H	4	2	-	0/2/19/22	0/1/1/1
2	MAN	H	5	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	5	MAN	C1-O5-C5	3.38	116.72	112.19
2	E	5	MAN	C1-O5-C5	3.13	116.38	112.19
2	C	5	MAN	C1-O5-C5	3.05	116.28	112.19
2	F	5	MAN	C1-O5-C5	2.91	116.08	112.19
2	C	4	MAN	C1-O5-C5	2.89	116.06	112.19
2	F	4	MAN	C1-O5-C5	2.84	115.99	112.19
2	H	4	MAN	C1-O5-C5	2.80	115.94	112.19
3	D	1	NAG	C1-C2-N2	-2.74	106.12	110.43
2	E	4	MAN	C1-O5-C5	2.34	115.32	112.19
3	G	2	NAG	C1-O5-C5	2.25	115.20	112.19
2	H	1	NAG	C1-O5-C5	2.03	114.90	112.19

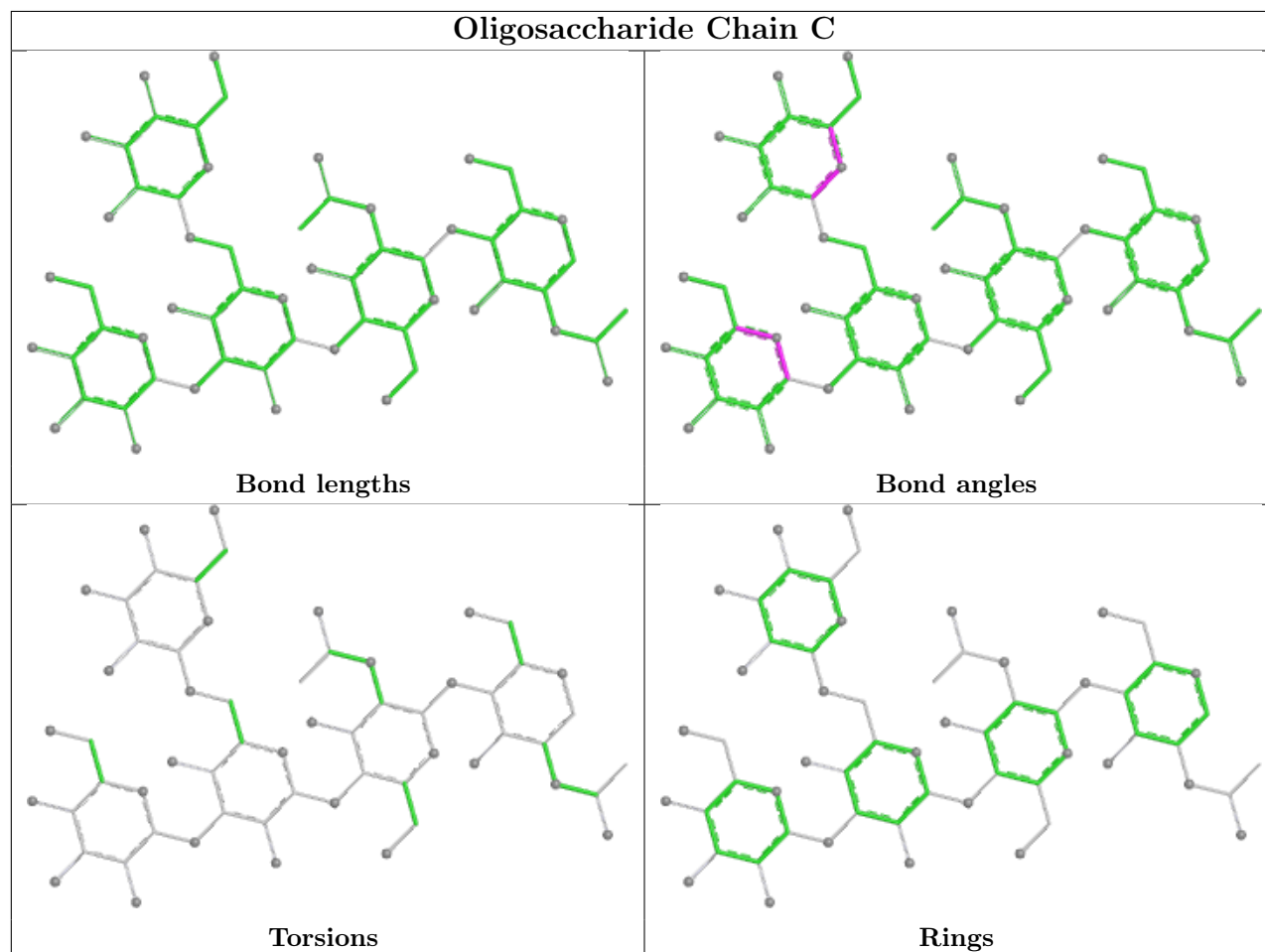
There are no chirality outliers.

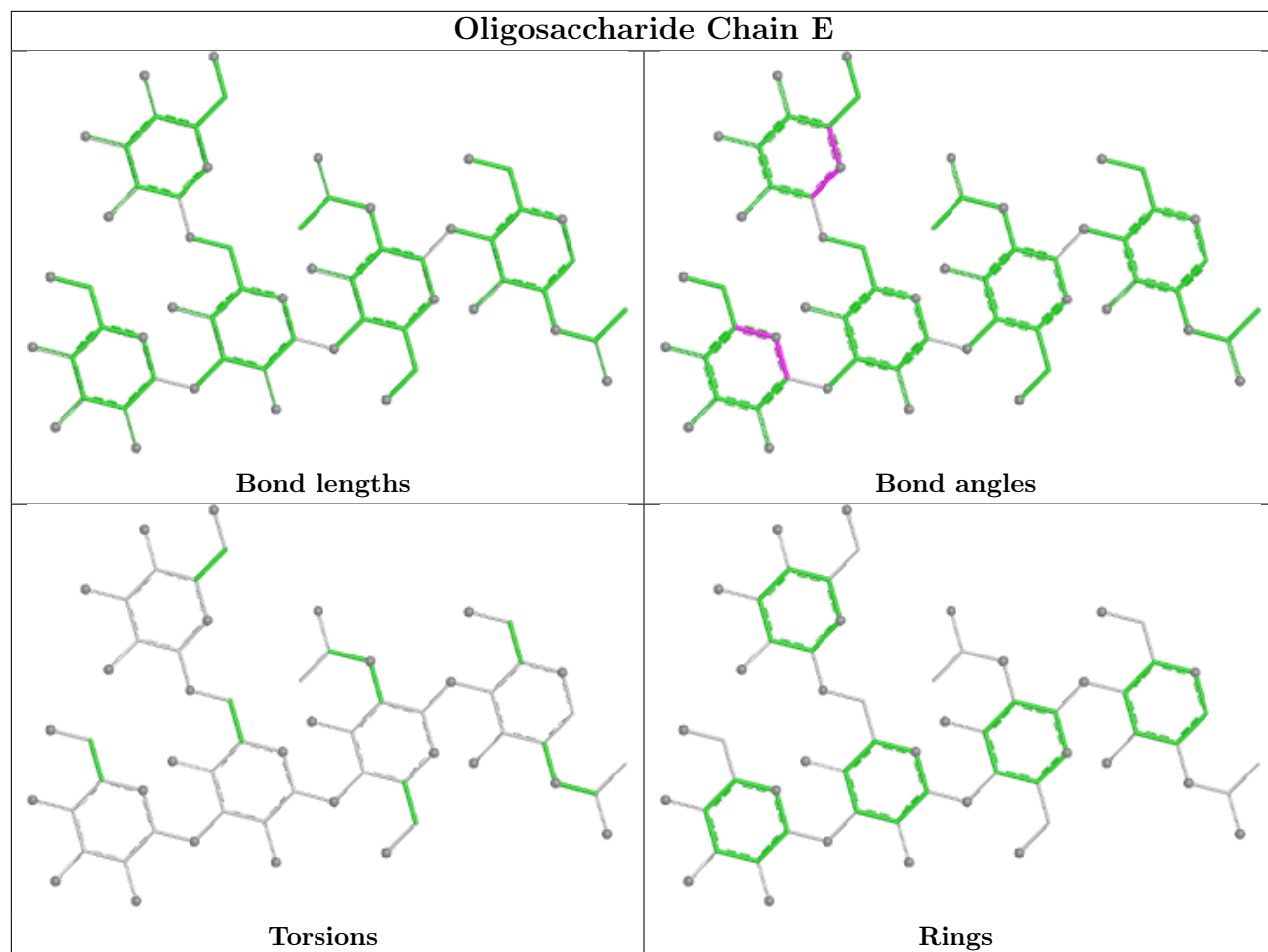
There are no torsion outliers.

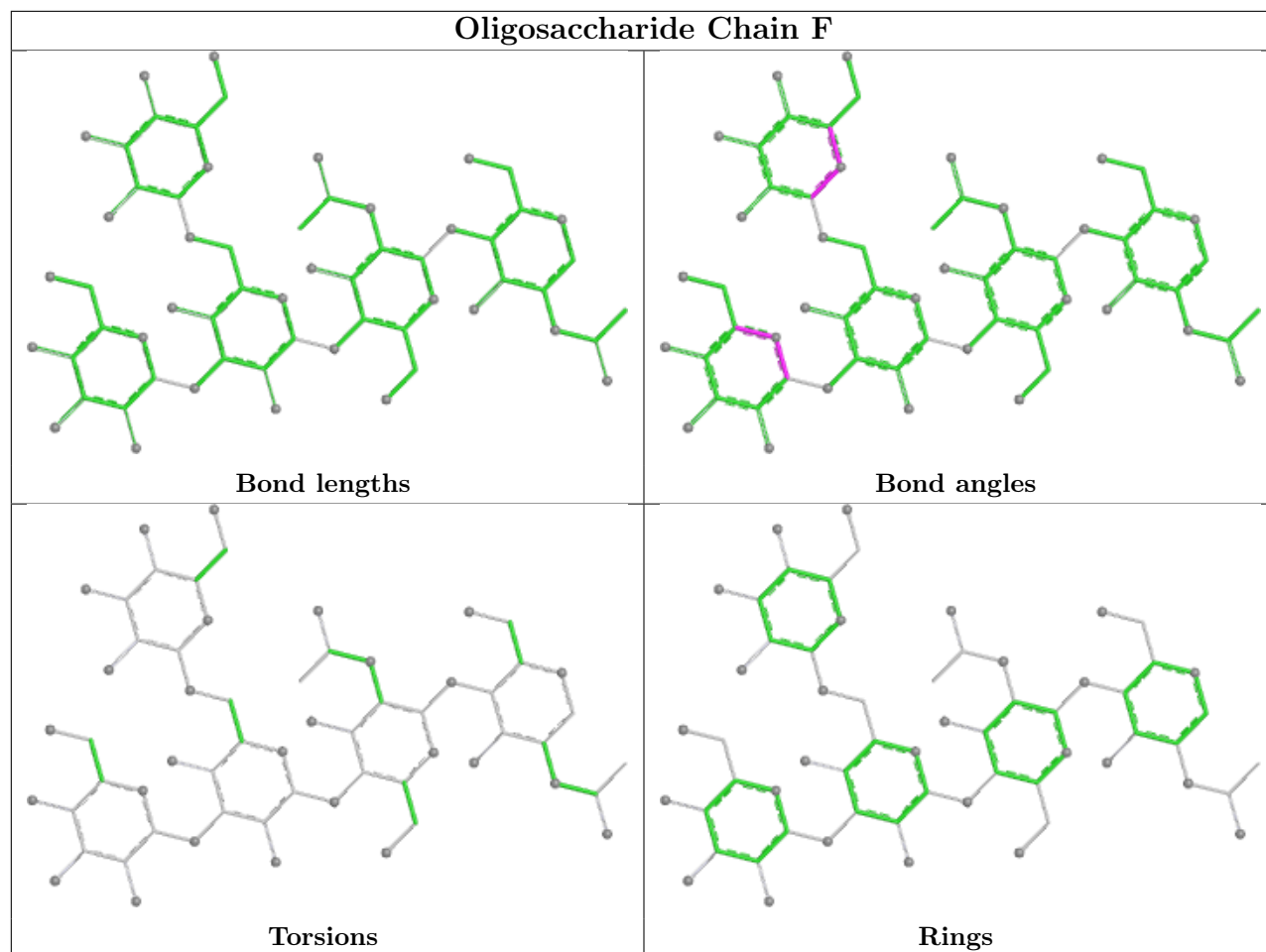
There are no ring outliers.

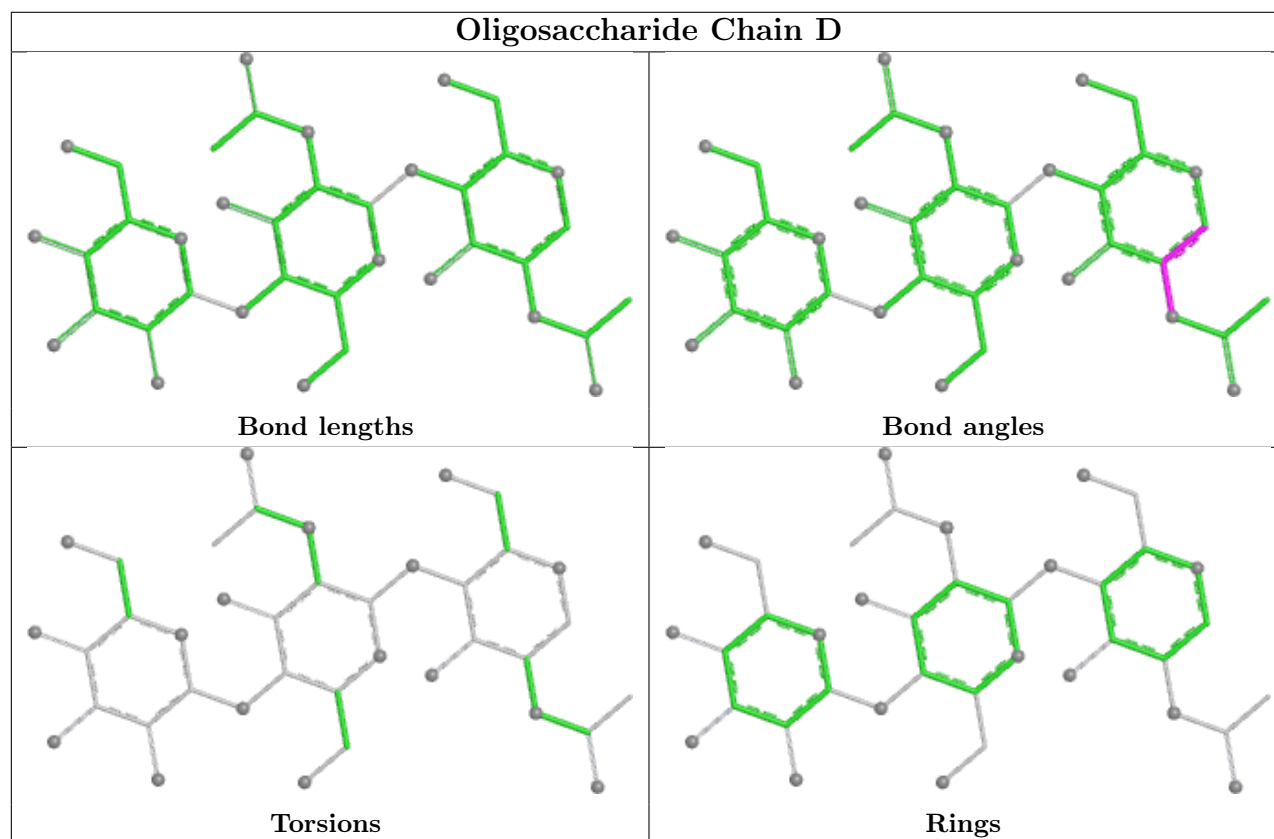
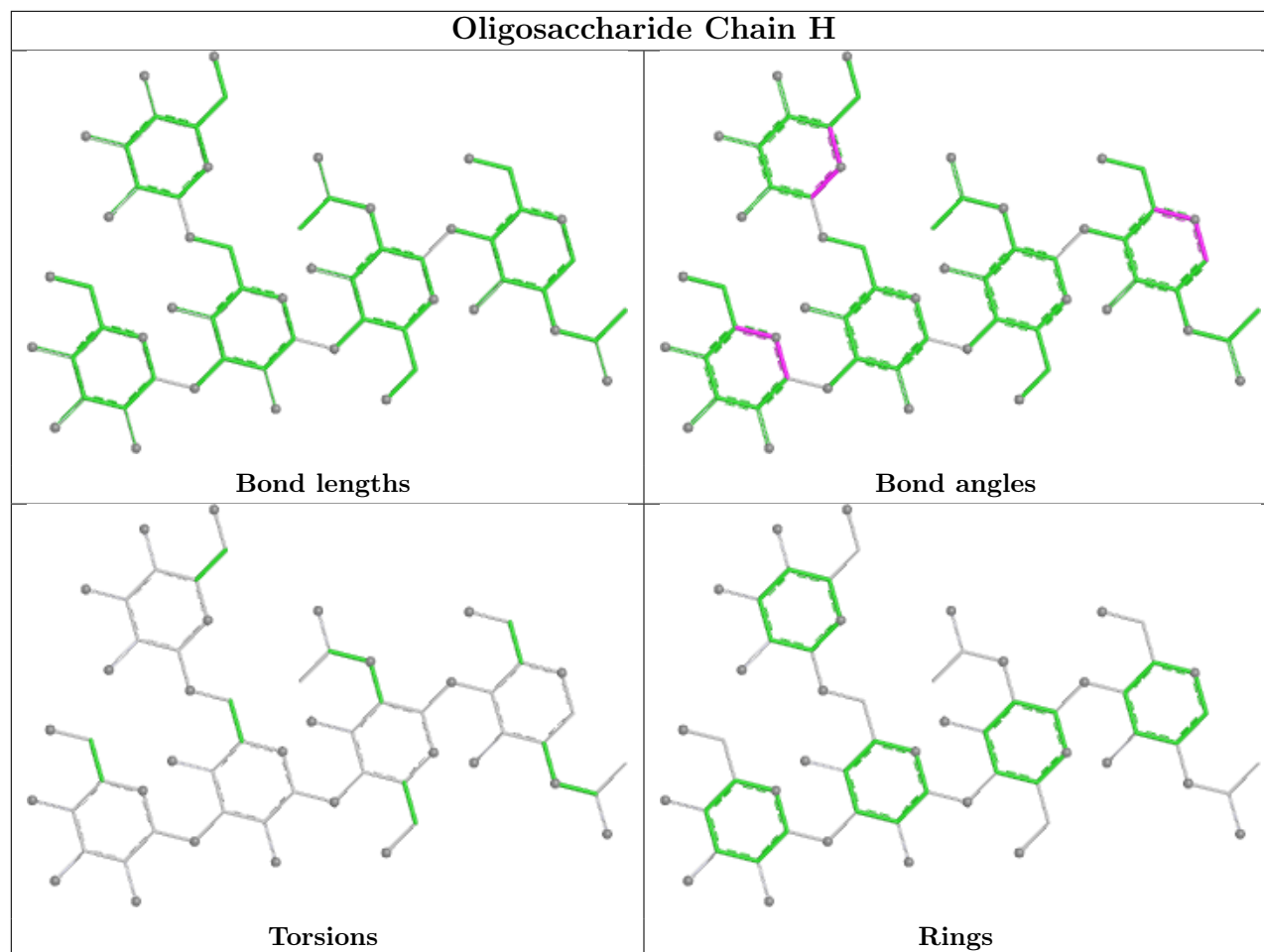
No monomer is involved in short contacts.

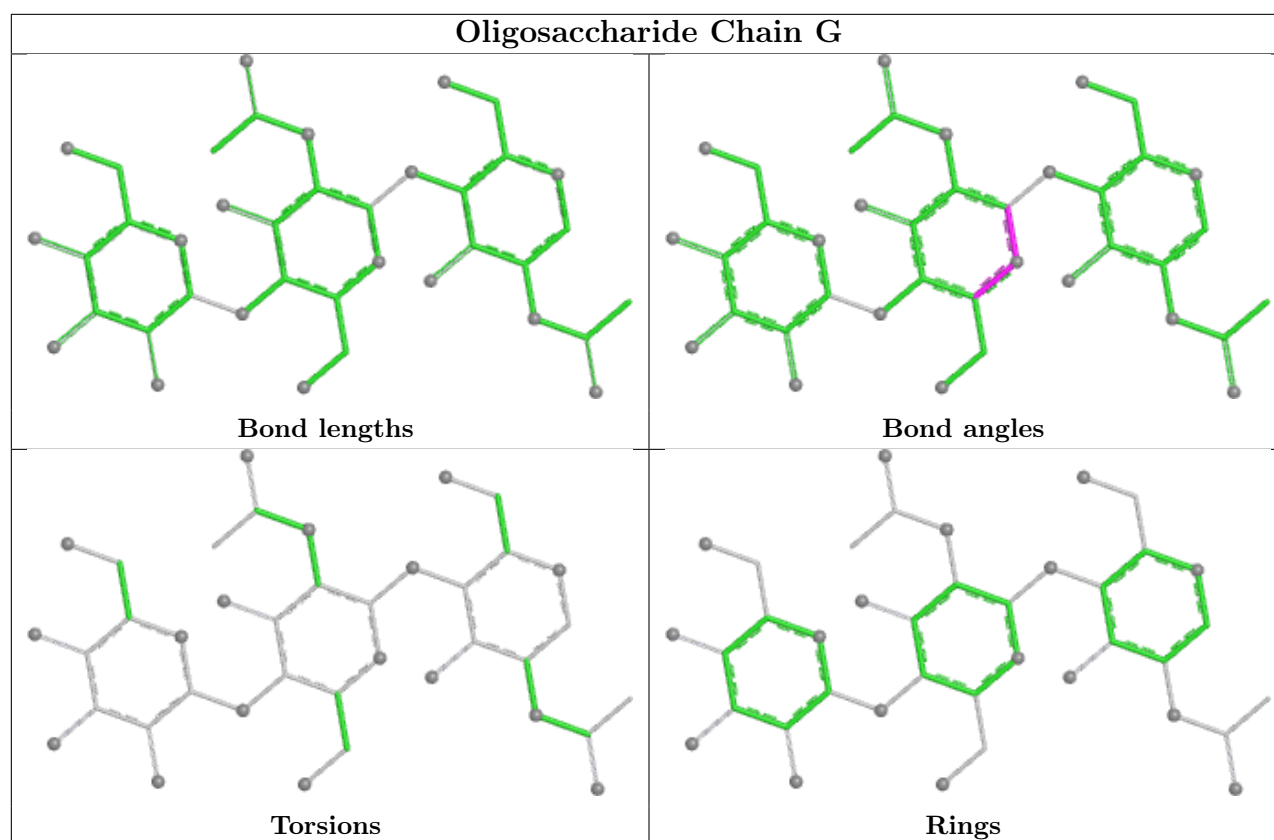
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

14 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	A	904	1	14,14,15	0.33	0	17,19,21	0.63	0
4	NAG	A	902	1	14,14,15	0.29	0	17,19,21	0.76	1 (5%)
4	NAG	A	905	1	14,14,15	0.31	0	17,19,21	0.80	1 (5%)
4	NAG	B	901	1	14,14,15	0.30	0	17,19,21	0.70	1 (5%)
5	I5N	A	907	-	30,32,32	1.29	3 (10%)	38,47,47	2.29	10 (26%)
5	I5N	A	908	-	30,32,32	1.34	4 (13%)	38,47,47	2.24	10 (26%)
4	NAG	A	903	1	14,14,15	0.33	0	17,19,21	0.66	1 (5%)
4	NAG	B	905	1	14,14,15	0.31	0	17,19,21	0.78	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	906	1	14,14,15	0.29	0	17,19,21	0.51	0
4	NAG	B	904	1	14,14,15	0.32	0	17,19,21	0.53	0
4	NAG	B	902	1	14,14,15	0.27	0	17,19,21	0.76	1 (5%)
4	NAG	A	901	1	14,14,15	0.31	0	17,19,21	0.67	1 (5%)
4	NAG	B	906	1	14,14,15	0.29	0	17,19,21	0.45	0
4	NAG	B	903	1	14,14,15	0.33	0	17,19,21	0.57	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	A	904	1	-	0/6/23/26	0/1/1/1
4	NAG	A	902	1	-	0/6/23/26	0/1/1/1
4	NAG	A	905	1	-	0/6/23/26	0/1/1/1
4	NAG	B	901	1	-	0/6/23/26	0/1/1/1
5	I5N	A	907	-	-	3/12/25/25	0/5/5/5
5	I5N	A	908	-	-	0/12/25/25	0/5/5/5
4	NAG	A	903	1	-	0/6/23/26	0/1/1/1
4	NAG	B	905	1	-	0/6/23/26	0/1/1/1
4	NAG	A	906	1	-	0/6/23/26	0/1/1/1
4	NAG	B	904	1	-	0/6/23/26	0/1/1/1
4	NAG	B	902	1	-	0/6/23/26	0/1/1/1
4	NAG	A	901	1	-	0/6/23/26	0/1/1/1
4	NAG	B	906	1	-	0/6/23/26	0/1/1/1
4	NAG	B	903	1	-	0/6/23/26	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	908	I5N	C9-N8	-4.07	1.28	1.32
5	A	907	I5N	C9-N8	-3.88	1.28	1.32
5	A	907	I5N	C5-C4	-2.32	1.38	1.41
5	A	908	I5N	C5-C4	-2.28	1.38	1.41
5	A	908	I5N	C5-C9	2.16	1.50	1.47
5	A	908	I5N	C9-N20	-2.16	1.30	1.35
5	A	907	I5N	F28-C26	-2.07	1.36	1.40

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	907	I5N	C5-C4-N7	6.48	111.24	106.59
5	A	908	I5N	C5-C4-N7	6.37	111.17	106.59
5	A	907	I5N	C4-N7-N8	-6.27	107.25	111.90
5	A	908	I5N	C4-N7-N8	-5.62	107.72	111.90
5	A	908	I5N	C6-C5-C9	4.84	136.13	130.55
5	A	907	I5N	C19-C10-C1	-4.58	113.19	121.75
5	A	907	I5N	C6-C5-C9	4.48	135.71	130.55
5	A	908	I5N	C19-C10-C1	-3.64	114.93	121.75
5	A	908	I5N	C18-C10-C1	-3.34	115.50	121.75
5	A	907	I5N	C6-C5-C4	3.27	122.58	119.39
5	A	908	I5N	C6-C5-C4	3.23	122.53	119.39
5	A	907	I5N	C3-C2-C1	2.86	121.07	118.92
5	A	908	I5N	C3-C2-C1	2.84	121.05	118.92
4	B	902	NAG	C1-O5-C5	2.78	115.91	112.19
4	A	902	NAG	C1-O5-C5	2.76	115.88	112.19
4	A	905	NAG	C1-O5-C5	2.74	115.86	112.19
4	B	905	NAG	C1-O5-C5	2.70	115.80	112.19
5	A	907	I5N	C18-C10-C1	-2.55	116.99	121.75
4	A	903	NAG	C1-O5-C5	2.43	115.44	112.19
5	A	908	I5N	C15-N14-C13	2.43	122.05	118.31
5	A	907	I5N	C17-C15-N14	2.41	120.20	116.56
5	A	907	I5N	C15-N14-C13	2.38	121.98	118.31
5	A	907	I5N	C3-C4-C5	-2.36	120.64	122.52
5	A	908	I5N	C17-C15-N14	2.14	119.79	116.56
5	A	908	I5N	C3-C4-N7	-2.09	127.86	131.87
4	B	901	NAG	C1-C2-N2	-2.07	107.18	110.43
4	A	901	NAG	C1-C2-N2	-2.00	107.28	110.43

There are no chirality outliers.

All (3) torsion outliers are listed below:

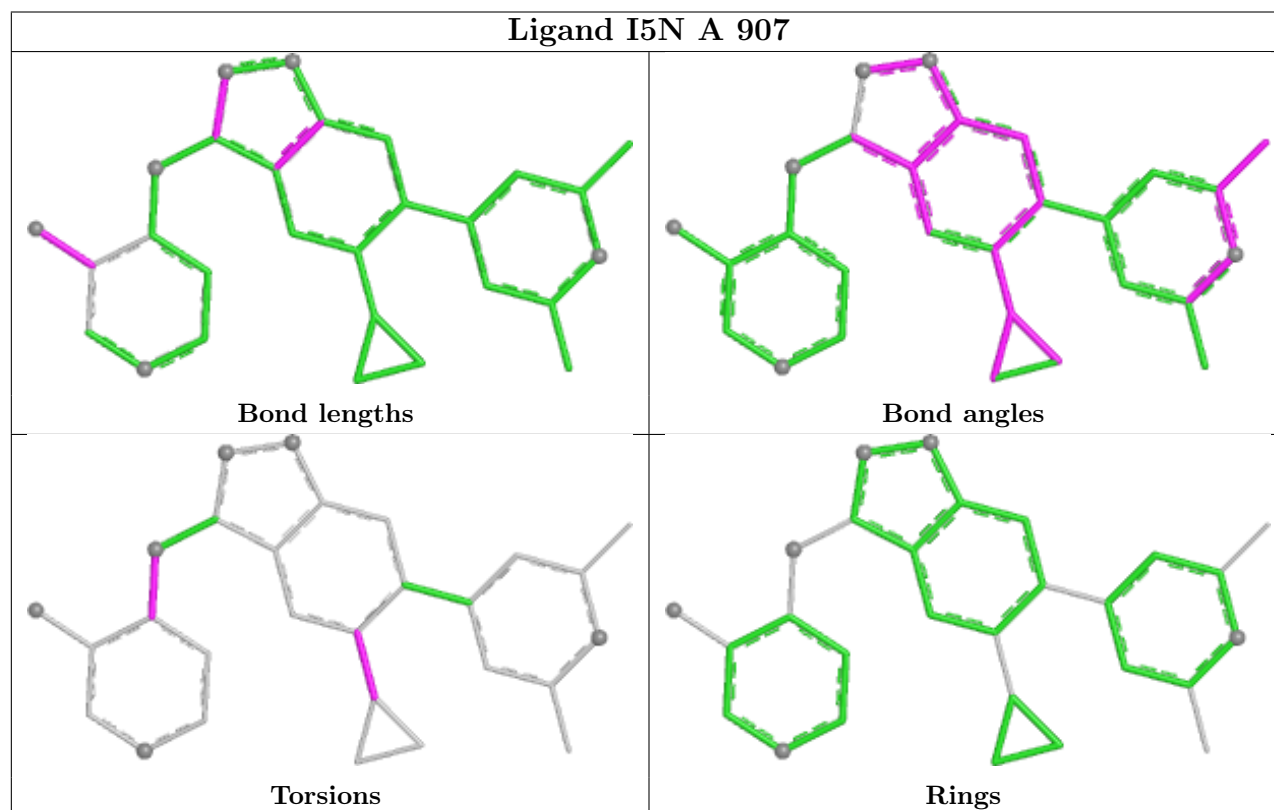
Mol	Chain	Res	Type	Atoms
5	A	907	I5N	C22-C21-N20-C9
5	A	907	I5N	C26-C21-N20-C9
5	A	907	I5N	C6-C1-C10-C19

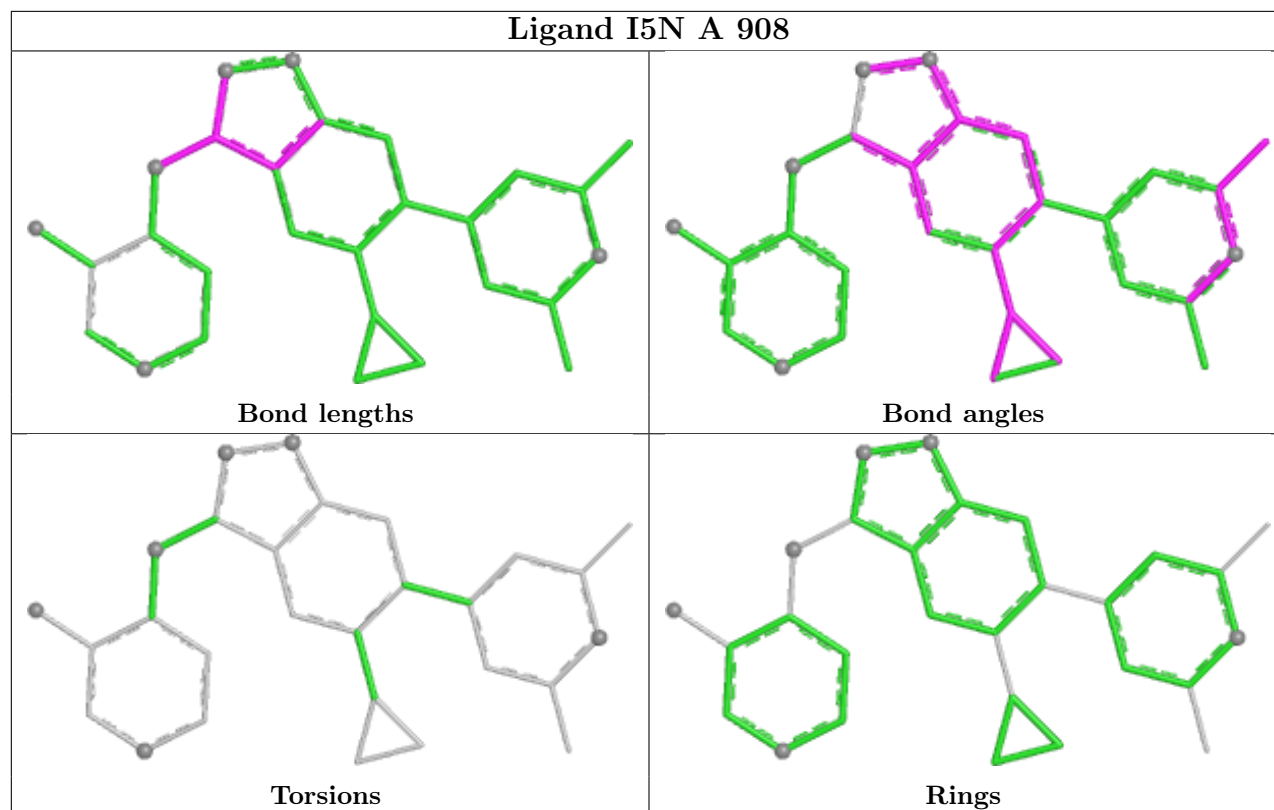
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	737/807 (91%)	0.13	13 (1%) 67 46	58, 102, 126, 145	0
1	B	736/807 (91%)	0.15	8 (1%) 78 59	60, 98, 154, 167	0
All	All	1473/1614 (91%)	0.14	21 (1%) 73 53	58, 101, 146, 167	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	242	PHE	4.8
1	B	121	PHE	4.4
1	B	625	ASN	3.7
1	B	808	ASP	3.3
1	A	703	LEU	3.3
1	B	605	LEU	3.2
1	B	732	LEU	2.8
1	A	626	ASP	2.6
1	A	574	THR	2.6
1	A	237	ILE	2.3
1	B	604	ASN	2.3
1	A	605	LEU	2.3
1	B	601	ASP	2.2
1	A	466	ASN	2.2
1	A	227	LEU	2.2
1	A	433	LEU	2.2
1	A	253	LEU	2.1
1	A	607	SER	2.1
1	B	750	THR	2.1
1	A	94	LEU	2.1
1	A	236	TYR	2.0

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

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

6.3 Carbohydrates ⓘ

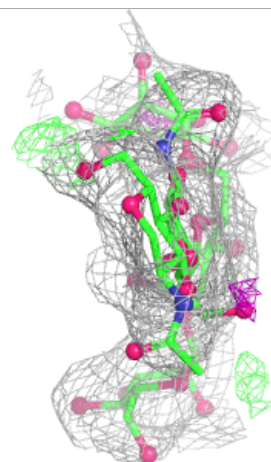
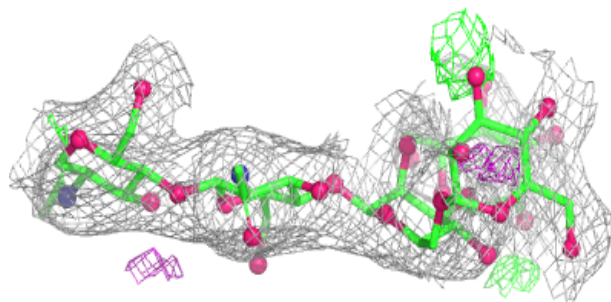
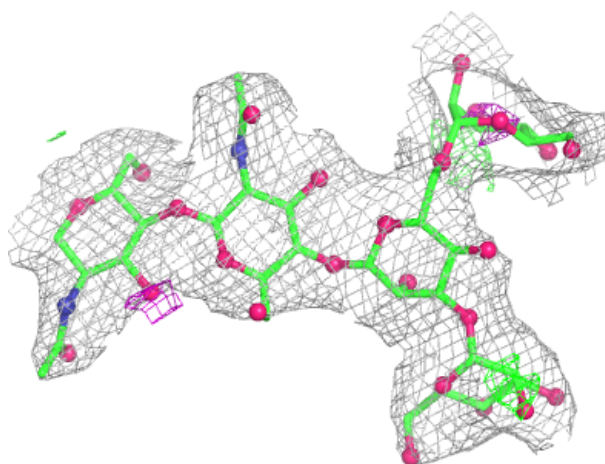
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	MAN	C	5	11/12	0.48	0.14	115,116,116,116	0
2	MAN	F	5	11/12	0.55	0.14	105,105,105,106	0
2	MAN	F	4	11/12	0.59	0.18	104,104,104,104	0
2	MAN	E	4	11/12	0.60	0.12	97,97,98,98	0
2	MAN	H	5	11/12	0.60	0.13	106,107,107,107	0
3	BMA	D	3	11/12	0.62	0.12	90,91,91,91	0
2	MAN	C	4	11/12	0.67	0.13	114,114,114,114	0
3	BMA	G	3	11/12	0.67	0.11	95,95,96,96	0
2	MAN	E	5	11/12	0.68	0.11	99,100,100,100	0
2	MAN	H	4	11/12	0.74	0.11	106,106,107,107	0
2	BMA	C	3	11/12	0.75	0.11	111,113,114,115	0
2	BMA	F	3	11/12	0.76	0.10	100,102,103,104	0
3	NAG	D	2	14/15	0.76	0.13	85,87,87,89	0
2	BMA	E	3	11/12	0.82	0.11	92,94,96,98	0
3	NAG	G	2	14/15	0.83	0.10	90,91,92,93	0
2	BMA	H	3	11/12	0.88	0.10	103,104,105,106	0
2	NAG	C	1	14/15	0.90	0.15	103,104,105,105	0
2	NAG	F	1	14/15	0.90	0.11	90,90,91,92	0
2	NAG	F	2	14/15	0.91	0.12	94,94,96,98	0
2	NAG	H	2	14/15	0.92	0.10	97,97,99,101	0
2	NAG	C	2	14/15	0.92	0.12	106,107,108,110	0
2	NAG	E	2	14/15	0.92	0.10	83,84,86,89	0
2	NAG	H	1	14/15	0.92	0.10	93,93,94,95	0
2	NAG	E	1	14/15	0.94	0.10	76,77,79,81	0
3	NAG	D	1	14/15	0.95	0.10	78,78,80,82	0
3	NAG	G	1	14/15	0.96	0.08	84,85,86,88	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.

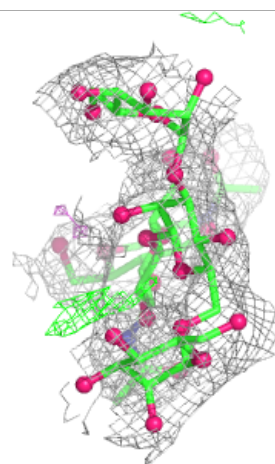
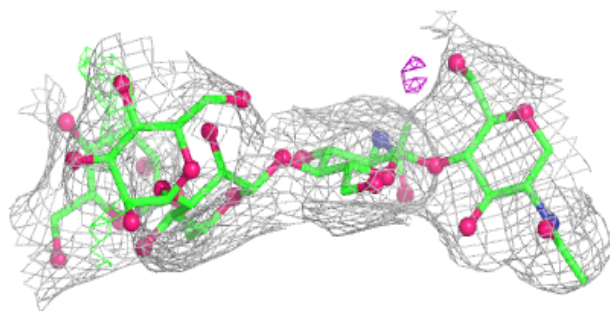
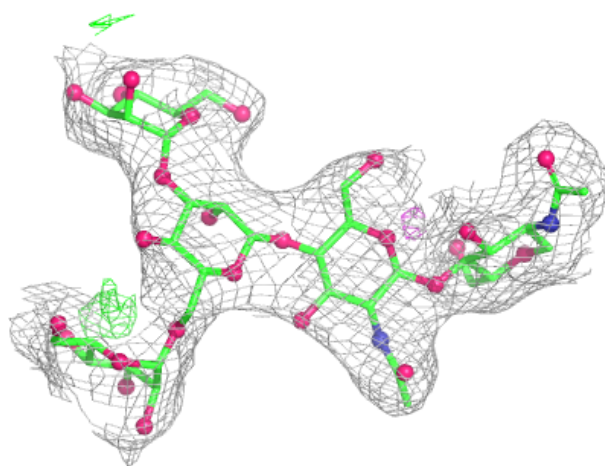
Electron density around Chain C:

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



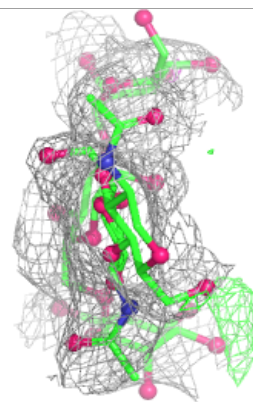
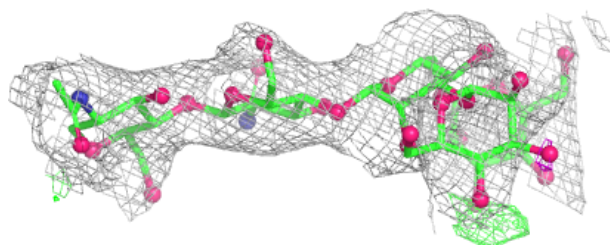
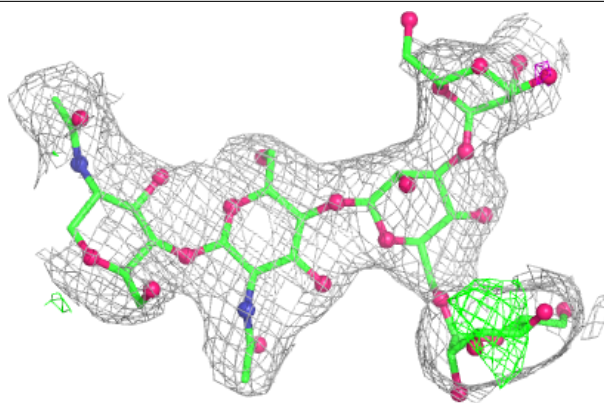
Electron density around Chain E:

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

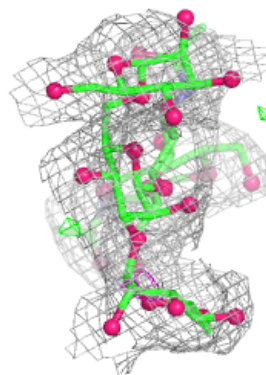
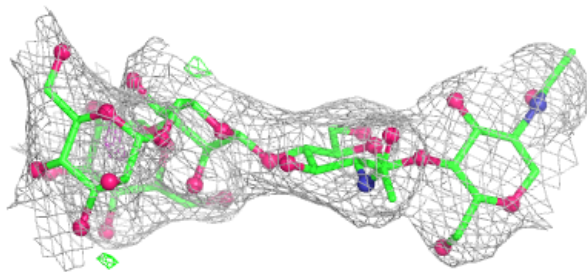
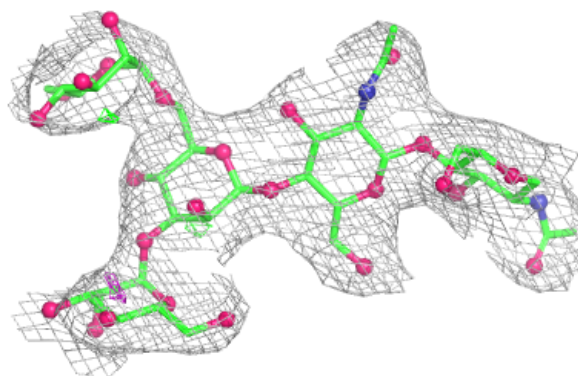


Electron density around Chain F:

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

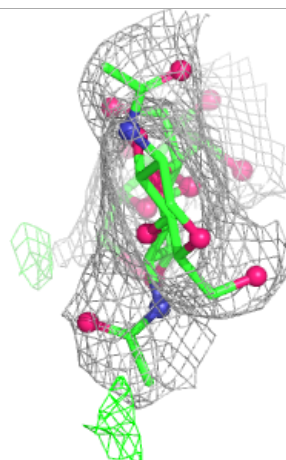
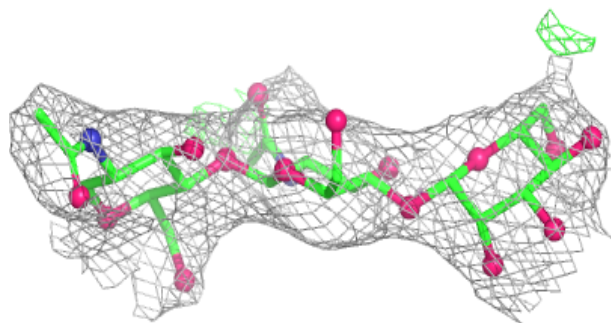
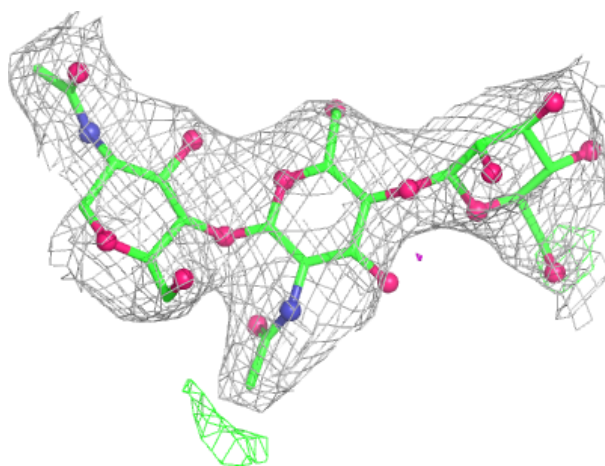
**Electron density around Chain H:**

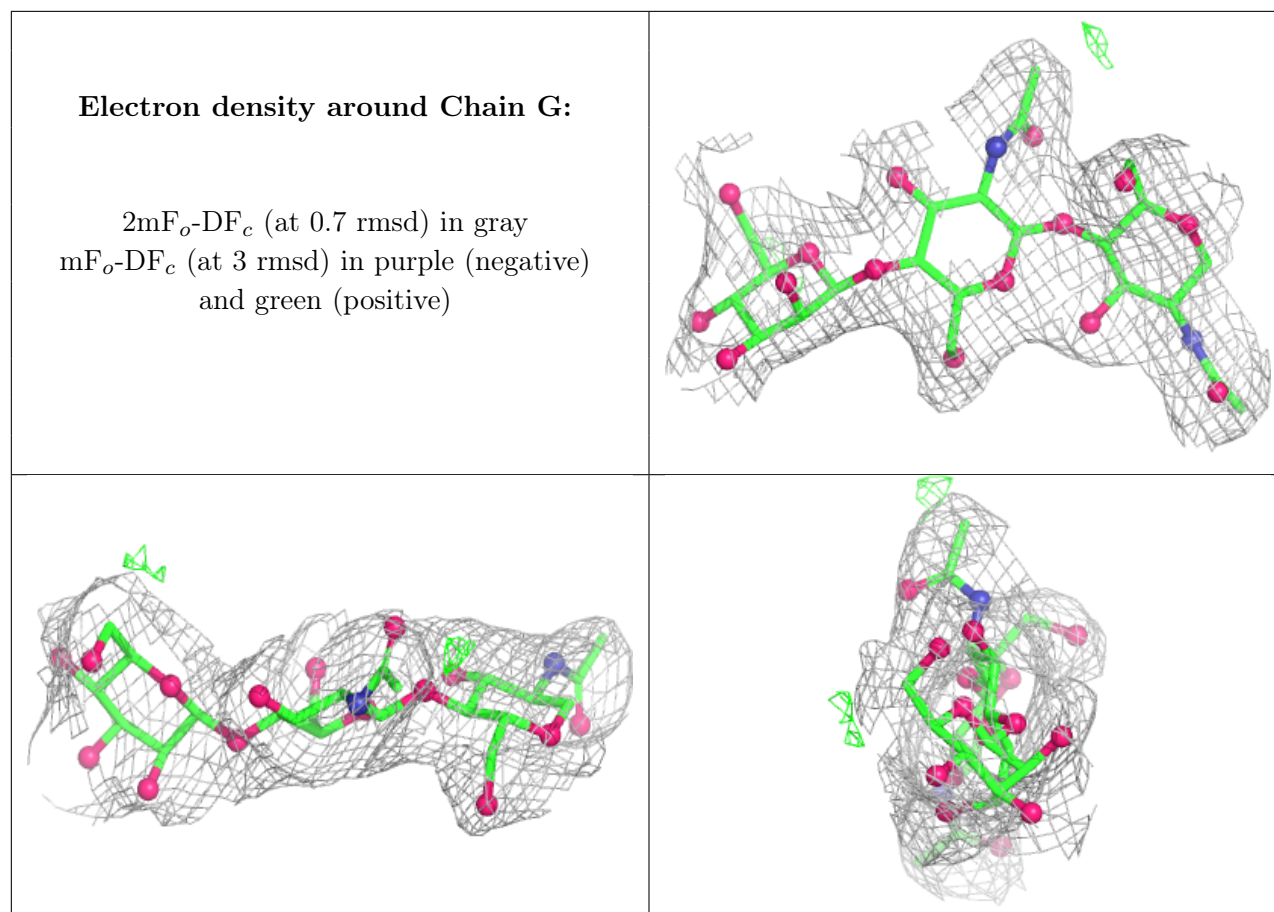
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain 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
4	NAG	B	905	14/15	0.18	0.19	116,116,117,117	0
4	NAG	A	905	14/15	0.35	0.19	105,106,106,106	0
4	NAG	A	906	14/15	0.55	0.11	130,131,131,131	0
4	NAG	B	906	14/15	0.57	0.12	140,140,140,141	0
4	NAG	B	901	14/15	0.63	0.14	95,95,95,95	0
4	NAG	A	903	14/15	0.64	0.11	109,110,110,110	0
4	NAG	B	903	14/15	0.64	0.15	98,99,99,99	0
4	NAG	A	904	14/15	0.69	0.11	112,113,113,113	0
4	NAG	A	901	14/15	0.72	0.15	90,91,92,93	0
4	NAG	B	904	14/15	0.77	0.11	101,102,102,102	0
4	NAG	B	902	14/15	0.80	0.10	112,112,112,112	0
4	NAG	A	902	14/15	0.86	0.10	106,106,107,107	0

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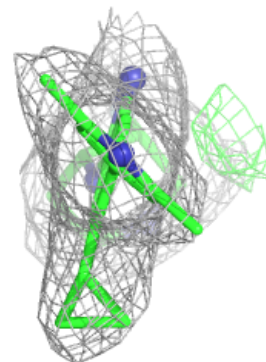
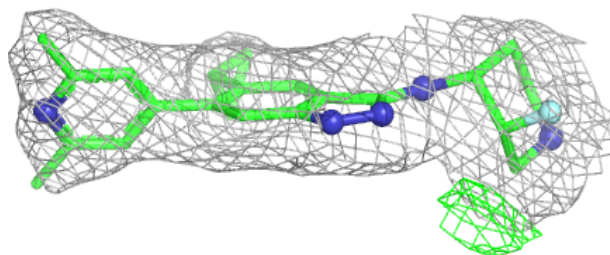
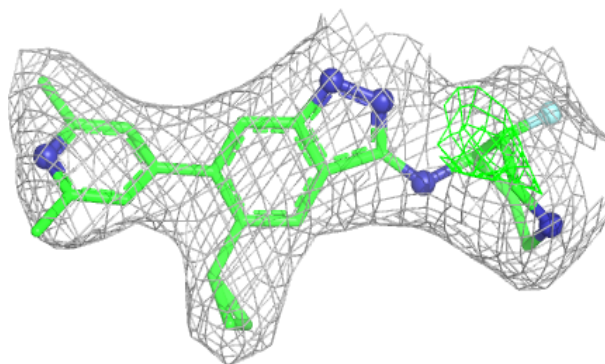
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	I5N	A	907	28/28	0.93	0.10	62,63,64,64	0
5	I5N	A	908	28/28	0.94	0.09	61,62,63,63	0

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.

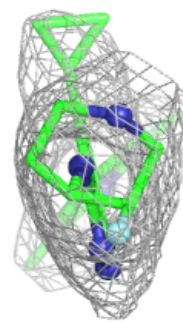
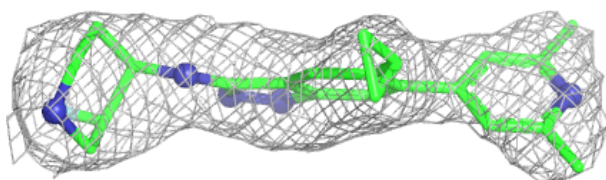
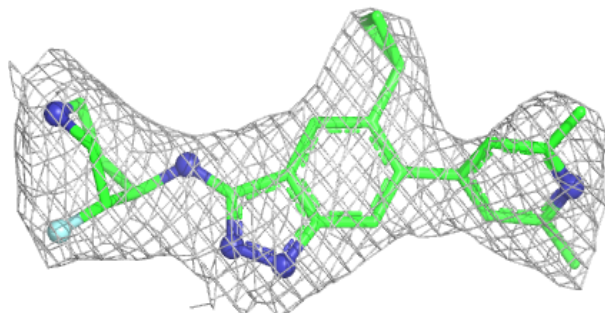
Electron density around I5N A 907:

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 I5N A 908:

$2mF_o-DF_c$ (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.