



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 07:37 AM UTC

PDB ID : 5ZSB / pdb_00005zsb
Title : Crystal structure of monkey TLR7 in complex with IMDQ and AAUUA
Authors : Zhang, Z.; Ohto, U.; Shimizu, T.
Deposited on : 2018-04-28
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

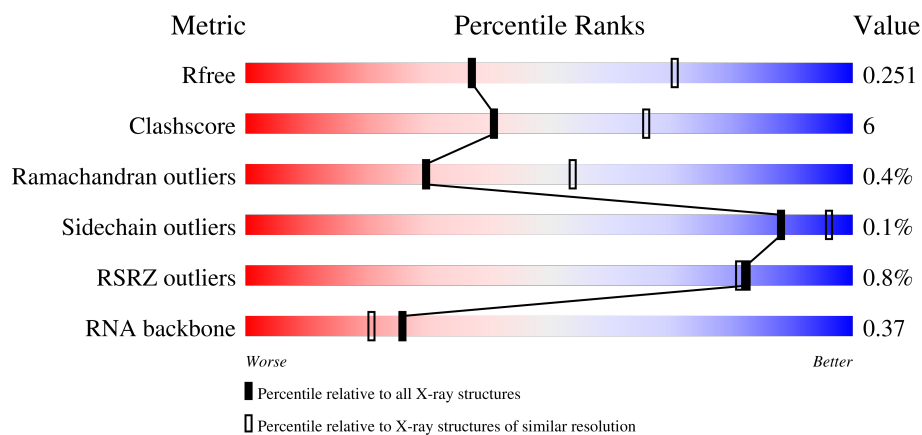
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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.



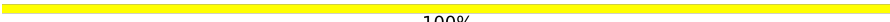
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)
RNA backbone	3983	1044 (2.90-2.50)

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	823	75% 18% 6%
1	B	823	83% 11% 6%
2	C	6	17% 50% 33% 17%
2	D	6	67% 33%

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Mol	Chain	Length	Quality of chain
3	E	2	 100%
3	F	2	 50%50%
3	G	2	 100%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 13229 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 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	774	Total	C	N	O	S	0	0	0
			6272	4021	1069	1152	30			
1	A	773	Total	C	N	O	S	0	0	0
			6261	4012	1068	1151	30			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	23	ARG	-	expression tag	UNP B3Y653
B	24	SER	-	expression tag	UNP B3Y653
B	25	PRO	-	expression tag	UNP B3Y653
B	26	TRP	-	expression tag	UNP B3Y653
B	167	GLN	ASN	engineered mutation	UNP B3Y653
B	389	GLN	ASN	engineered mutation	UNP B3Y653
B	440	LEU	SER	see sequence details	UNP B3Y653
B	441	VAL	GLU	see sequence details	UNP B3Y653
B	442	PRO	VAL	see sequence details	UNP B3Y653
B	443	ARG	GLY	see sequence details	UNP B3Y653
B	444	GLY	PHE	see sequence details	UNP B3Y653
B	445	SER	CYS	see sequence details	UNP B3Y653
B	488	GLN	ASN	engineered mutation	UNP B3Y653
B	799	GLN	ASN	engineered mutation	UNP B3Y653
B	840	GLU	-	expression tag	UNP B3Y653
B	841	PHE	-	expression tag	UNP B3Y653
B	842	LEU	-	expression tag	UNP B3Y653
B	843	VAL	-	expression tag	UNP B3Y653
B	844	PRO	-	expression tag	UNP B3Y653
B	845	ARG	-	expression tag	UNP B3Y653
A	23	ARG	-	expression tag	UNP B3Y653
A	24	SER	-	expression tag	UNP B3Y653
A	25	PRO	-	expression tag	UNP B3Y653
A	26	TRP	-	expression tag	UNP B3Y653
A	167	GLN	ASN	engineered mutation	UNP B3Y653

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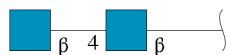
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Chain	Residue	Modelled	Actual	Comment	Reference
A	389	GLN	ASN	engineered mutation	UNP B3Y653
A	440	LEU	SER	see sequence details	UNP B3Y653
A	441	VAL	GLU	see sequence details	UNP B3Y653
A	442	PRO	VAL	see sequence details	UNP B3Y653
A	443	ARG	GLY	see sequence details	UNP B3Y653
A	444	GLY	PHE	see sequence details	UNP B3Y653
A	445	SER	CYS	see sequence details	UNP B3Y653
A	488	GLN	ASN	engineered mutation	UNP B3Y653
A	799	GLN	ASN	engineered mutation	UNP B3Y653
A	840	GLU	-	expression tag	UNP B3Y653
A	841	PHE	-	expression tag	UNP B3Y653
A	842	LEU	-	expression tag	UNP B3Y653
A	843	VAL	-	expression tag	UNP B3Y653
A	844	PRO	-	expression tag	UNP B3Y653
A	845	ARG	-	expression tag	UNP B3Y653

- Molecule 2 is a RNA chain called RNA (5'-R(*AP*UP*UP*AP*A)-3').

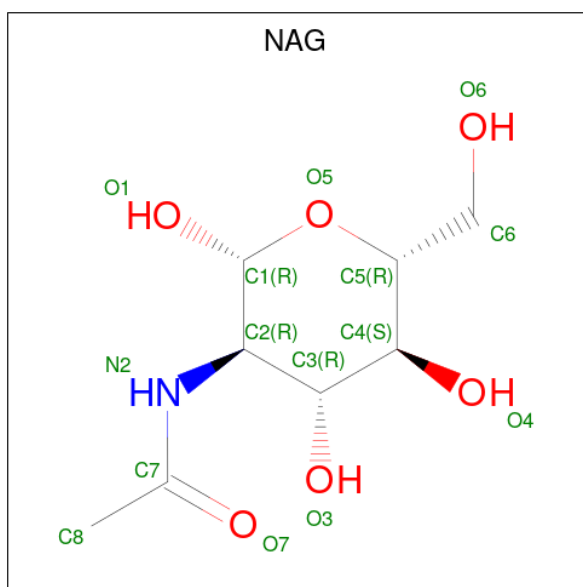
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	5	Total	C	N	O	P	0	0	0
			85	38	14	29	4			
2	D	4	Total	C	N	O	P	0	0	0
			66	28	9	25	4			

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



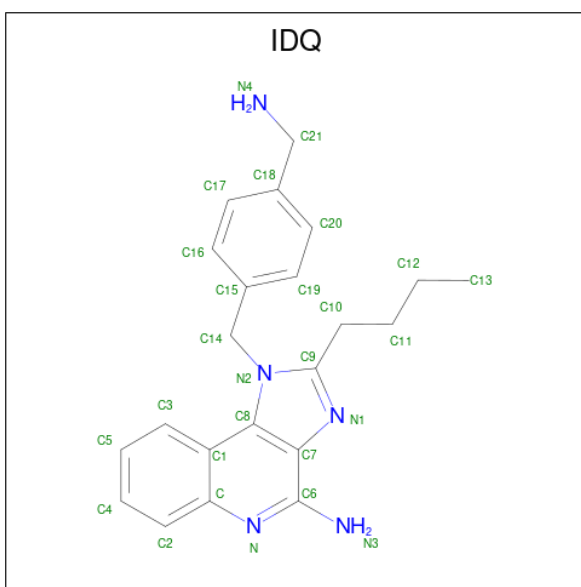
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



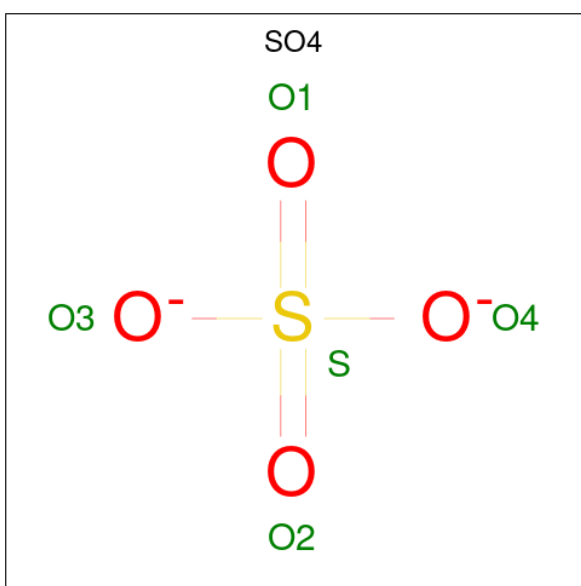
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1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

- Molecule 5 is 1-[[4-(aminomethyl)phenyl]methyl]-2-butyl-imidazo[4,5-c]quinolin-4-amine (CCD ID: IDQ) (formula: C₂₂H₂₅N₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	N	0	0
			27	22	5		
5	A	1	Total	C	N	0	0
			27	22	5		

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		

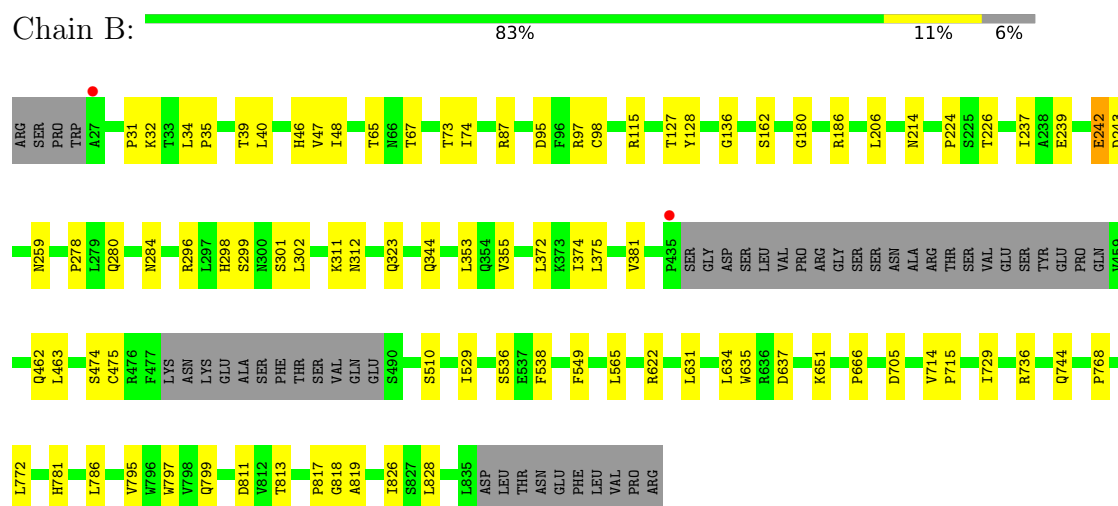
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	118	Total	O	0	0
			118	118		
7	A	68	Total	O	0	0
			68	68		
7	D	2	Total	O	0	0
			2	2		

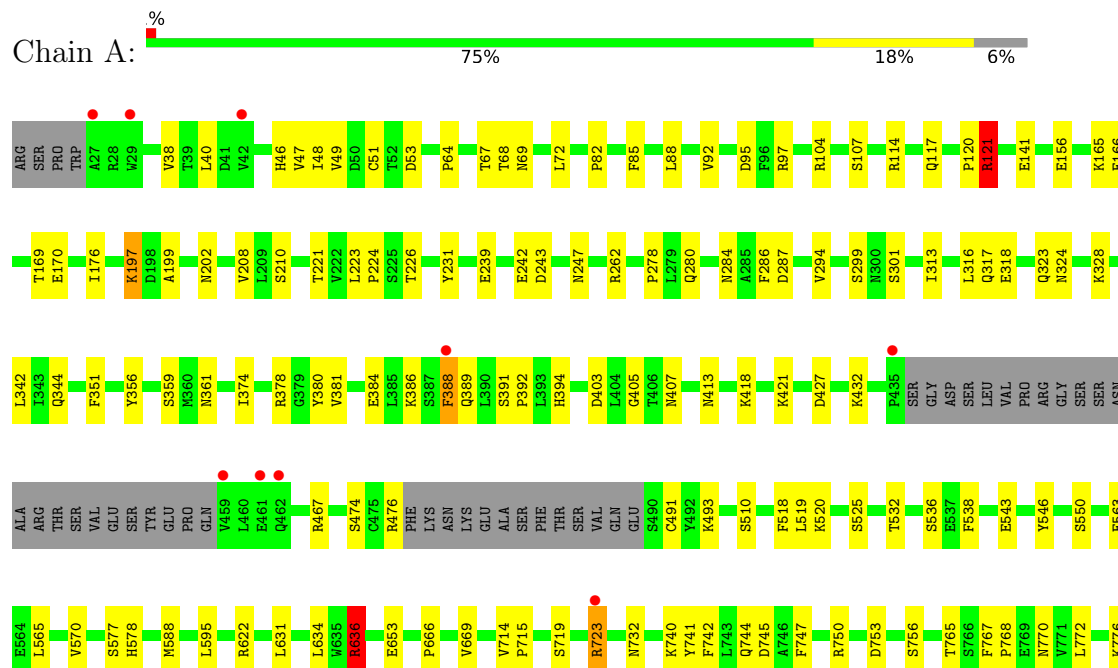
3 Residue-property plots

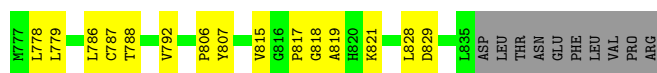
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Toll-like receptor 7

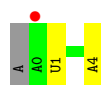


• Molecule 1: Toll-like receptor 7

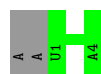




- Molecule 2: RNA (5'-R(*AP*UP*UP*AP*A)-3')



- Molecule 2: RNA (5'-R(*AP*UP*UP*AP*A)-3')



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



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	98.92Å 139.23Å 150.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.46 – 2.70 49.46 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (49.46-2.70) 99.6 (49.46-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.69Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.192 , 0.251 0.192 , 0.251	Depositor DCC
R_{free} test set	2788 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	53.7	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 30.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13229	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.18% 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, SO4, IDQ

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	0.43	2/6392 (0.0%)	0.70	11/8660 (0.1%)
1	B	0.41	0/6404	0.63	0/8676
2	C	0.31	0/94	0.53	0/145
2	D	0.29	0/72	0.51	0/110
All	All	0.42	2/12962 (0.0%)	0.67	11/17591 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	388	PHE	CD2-CE2	5.97	1.56	1.38
1	A	723	ARG	CG-CD	5.42	1.68	1.52

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	723	ARG	CB-CA-C	8.88	125.32	111.02
1	A	723	ARG	CB-CG-CD	-8.77	91.14	111.30
1	A	197	LYS	CB-CG-CD	-8.54	91.67	111.30
1	A	636	ARG	CD-NE-CZ	7.37	134.72	124.40
1	A	121	ARG	CB-CA-C	-7.28	94.89	110.76

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	121	ARG	Sidechain
1	A	636	ARG	Sidechain

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	6261	0	6312	109	0
1	B	6272	0	6317	56	0
2	C	85	0	43	2	0
2	D	66	0	31	0	0
3	E	28	0	25	0	0
3	F	28	0	25	0	0
3	G	28	0	25	0	0
4	A	42	0	39	2	0
4	B	112	0	104	1	0
5	A	27	0	23	2	0
5	B	27	0	25	4	0
6	A	25	0	0	1	0
6	B	40	0	0	0	0
7	A	68	0	0	9	0
7	B	118	0	0	5	0
7	D	2	0	0	0	0
All	All	13229	0	12969	168	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 168 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:LYS:HB2	1:A:388:PHE:CE1	1.85	1.09
1:A:767:PHE:HB3	1:A:772:LEU:HD11	1.47	0.93
1:A:386:LYS:HE3	1:A:388:PHE:HZ	1.41	0.86
1:A:432:LYS:NZ	7:A:1102:HOH:O	2.12	0.82
4:B:1008:NAG:O7	7:B:1101:HOH:O	1.98	0.80

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	767/823 (93%)	712 (93%)	52 (7%)	3 (0%)	30	54
1	B	768/823 (93%)	712 (93%)	53 (7%)	3 (0%)	30	54
All	All	1535/1646 (93%)	1424 (93%)	105 (7%)	6 (0%)	30	54

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	818	GLY
1	A	818	GLY
1	A	742	PHE
1	B	242	GLU
1	B	381	VAL

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	726/774 (94%)	725 (100%)	1 (0%)	88	96
1	B	727/774 (94%)	726 (100%)	1 (0%)	88	96
All	All	1453/1548 (94%)	1451 (100%)	2 (0%)	88	96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	813	THR
1	A	792	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	708	HIS
1	A	599	GLN
1	B	581	GLN
1	A	337	HIS
1	B	558	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	3/6 (50%)	0	0
2	D	2/6 (33%)	0	0
All	All	5/12 (41%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

6 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	E	1	1,3	14,14,15	0.45	0	17,19,21	1.79	3 (17%)
3	NAG	E	2	3	14,14,15	1.15	1 (7%)	17,19,21	0.74	0
3	NAG	F	1	1,3	14,14,15	0.37	0	17,19,21	0.54	0
3	NAG	F	2	3	14,14,15	0.26	0	17,19,21	1.06	1 (5%)
3	NAG	G	1	1,3	14,14,15	0.82	1 (7%)	17,19,21	0.97	1 (5%)
3	NAG	G	2	3	14,14,15	0.43	0	17,19,21	1.02	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	E	1	1,3	-	6/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1
3	NAG	G	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	G	2	3	-	4/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	2	NAG	O5-C1	-4.02	1.36	1.43
3	G	1	NAG	O5-C1	-2.73	1.39	1.43

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	1	NAG	C2-N2-C7	4.88	129.44	122.90
3	F	2	NAG	C1-O5-C5	3.91	117.43	112.19
3	E	1	NAG	C1-C2-N2	3.69	116.25	110.43
3	G	2	NAG	C1-O5-C5	3.36	116.69	112.19
3	G	1	NAG	C1-O5-C5	2.60	115.67	112.19

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	2	NAG	C4-C5-C6-O6

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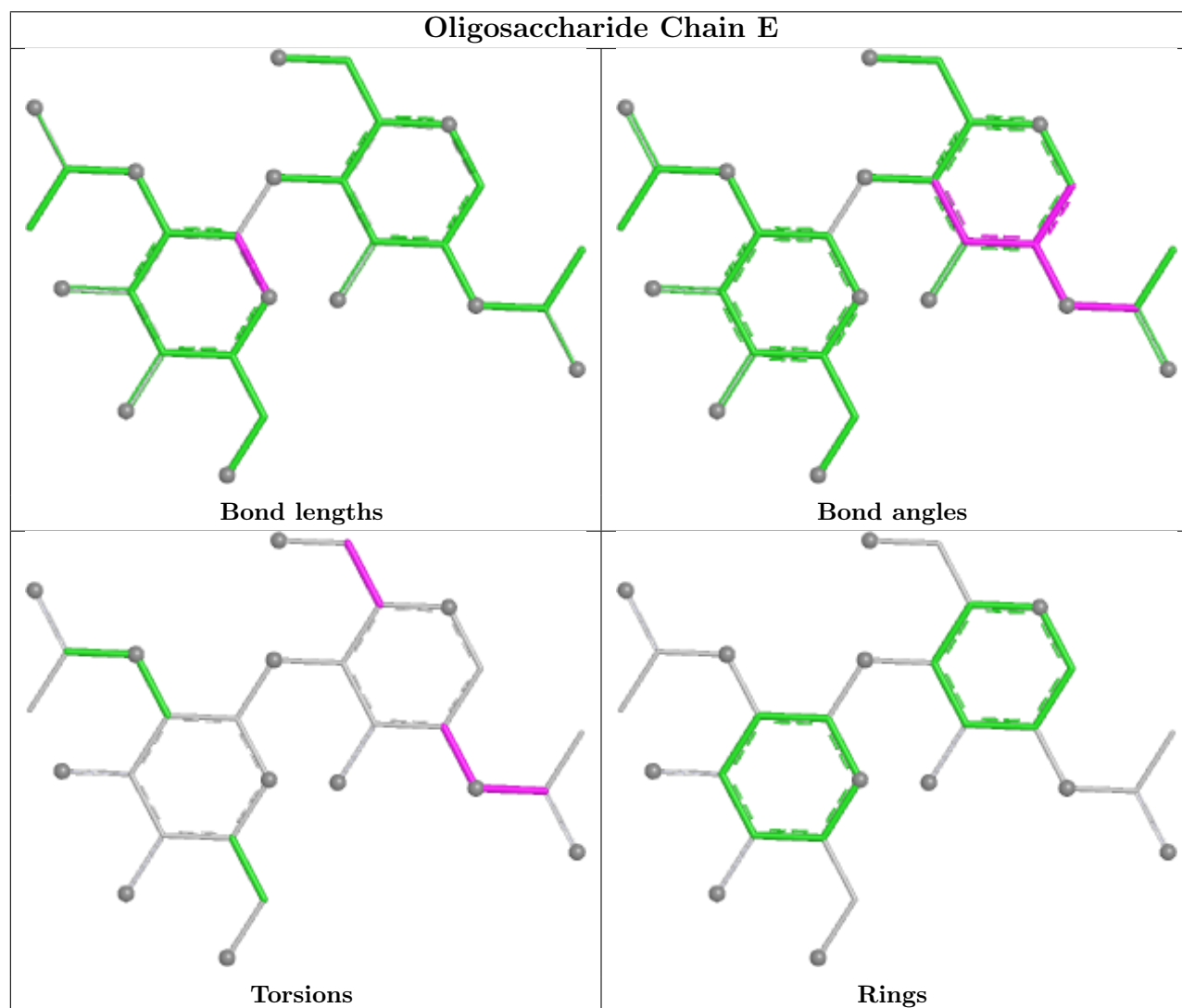
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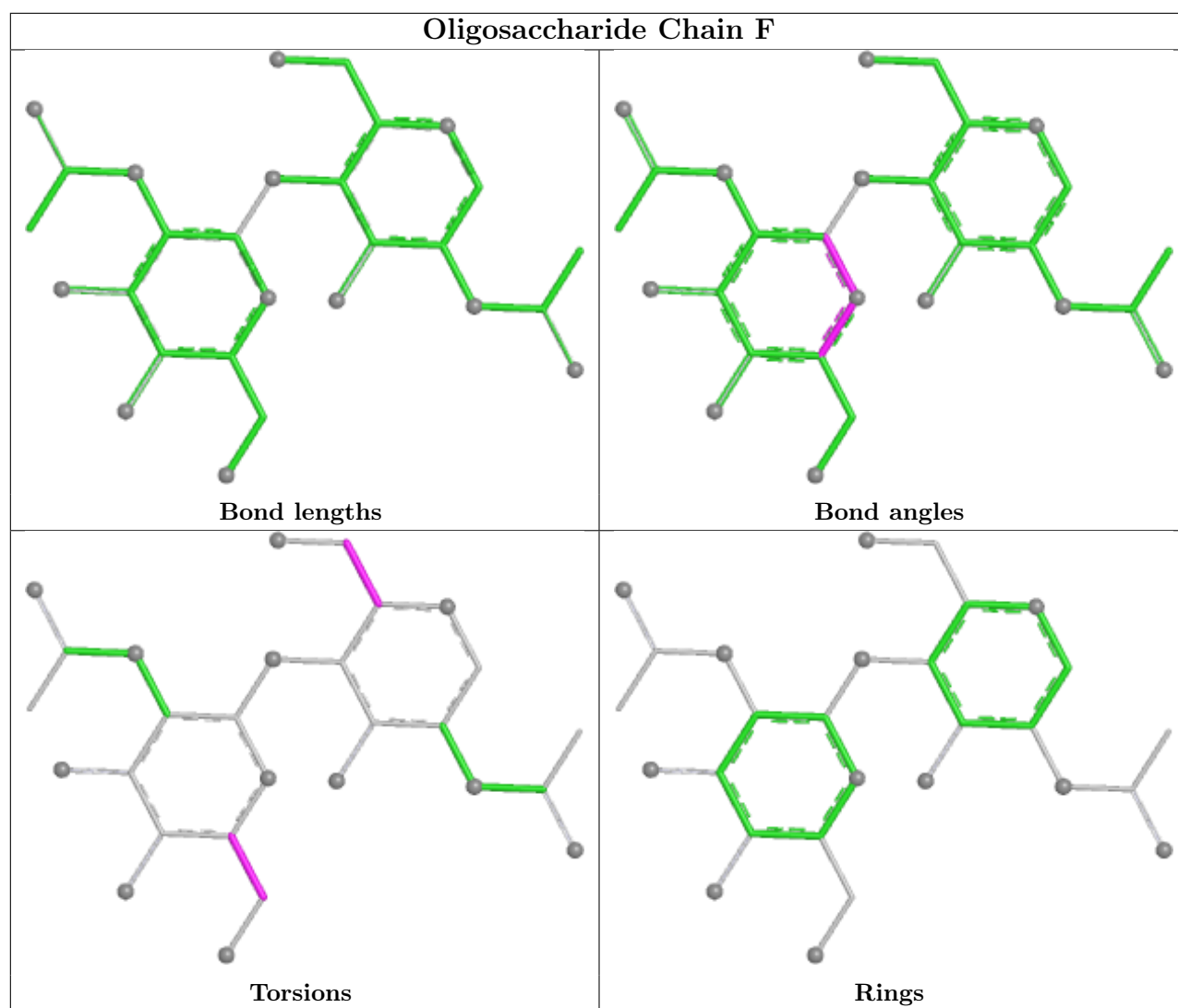
Mol	Chain	Res	Type	Atoms
3	E	1	NAG	O5-C5-C6-O6
3	E	1	NAG	C4-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
3	E	1	NAG	C8-C7-N2-C2

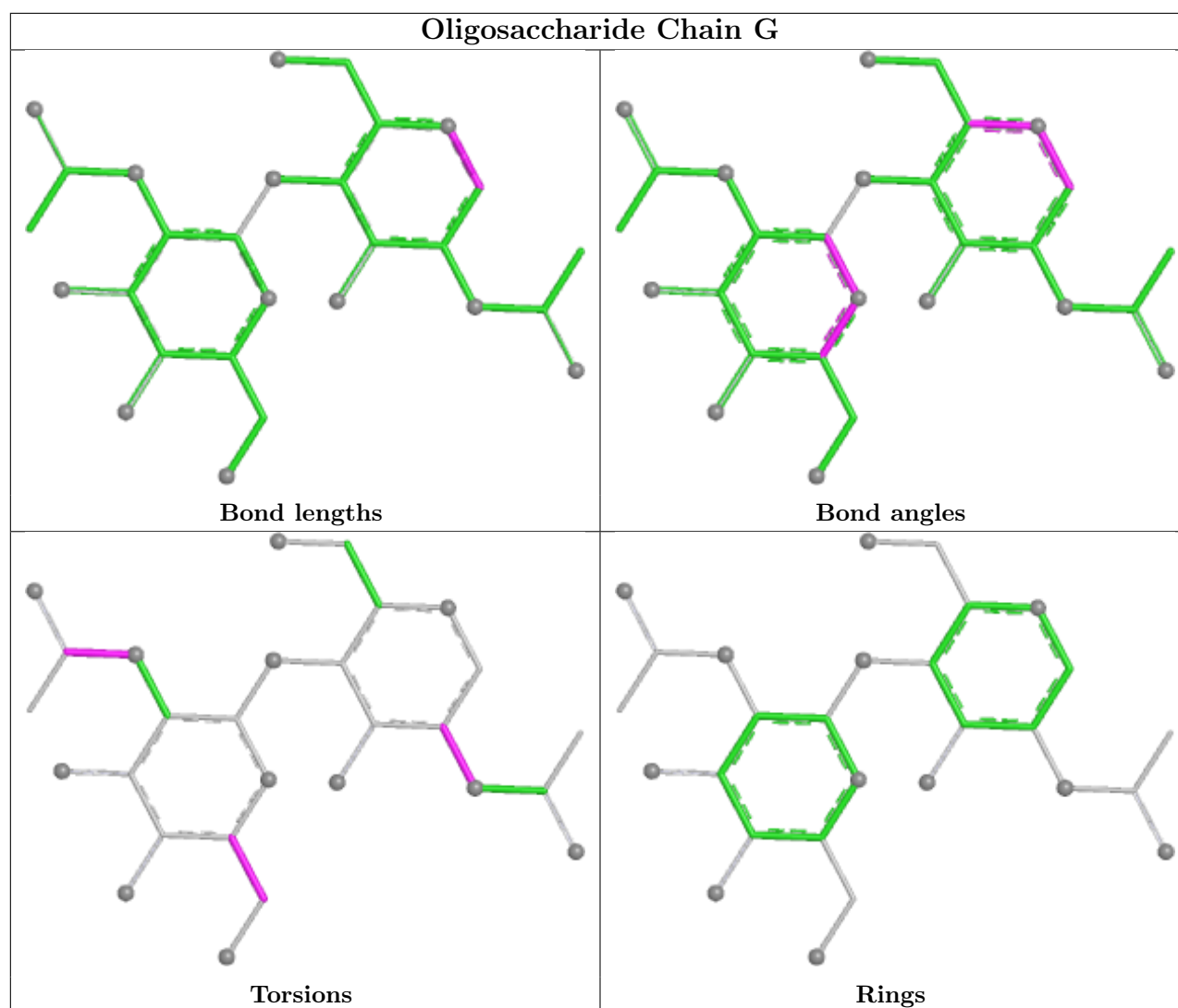
There are no ring outliers.

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](#)

26 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	1006	1	14,14,15	1.29	2 (14%)	17,19,21	0.61	0
4	NAG	B	1008	1	14,14,15	0.53	0	17,19,21	0.70	1 (5%)
4	NAG	A	1006	1	14,14,15	1.03	1 (7%)	17,19,21	0.83	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	1001	1	14,14,15	0.35	0	17,19,21	0.58	0
6	SO4	B	1015	-	4,4,4	0.30	0	6,6,6	0.29	0
4	NAG	B	1005	1	14,14,15	0.37	0	17,19,21	0.54	0
6	SO4	B	1014	-	4,4,4	0.58	0	6,6,6	0.49	0
6	SO4	B	1013	-	4,4,4	0.30	0	6,6,6	0.41	0
6	SO4	B	1019	-	4,4,4	0.41	0	6,6,6	0.45	0
4	NAG	B	1009	1	14,14,15	0.32	0	17,19,21	0.61	0
4	NAG	A	1007	1	14,14,15	0.29	0	17,19,21	0.86	1 (5%)
6	SO4	A	1013	-	4,4,4	0.43	0	6,6,6	0.98	1 (16%)
4	NAG	B	1002	1	14,14,15	0.19	0	17,19,21	0.92	1 (5%)
6	SO4	A	1012	-	4,4,4	0.61	0	6,6,6	0.49	0
6	SO4	B	1017	-	4,4,4	0.44	0	6,6,6	0.24	0
6	SO4	B	1016	-	4,4,4	0.31	0	6,6,6	0.31	0
4	NAG	B	1001	1	14,14,15	0.39	0	17,19,21	0.70	0
6	SO4	A	1009	-	4,4,4	0.24	0	6,6,6	0.29	0
6	SO4	B	1012	-	4,4,4	0.36	0	6,6,6	0.42	0
6	SO4	A	1010	-	4,4,4	0.37	0	6,6,6	0.36	0
4	NAG	B	1007	1	14,14,15	0.43	0	17,19,21	0.57	0
5	IDQ	B	1011	-	30,30,30	2.18	7 (23%)	41,42,42	1.76	7 (17%)
6	SO4	B	1018	-	4,4,4	0.32	0	6,6,6	0.24	0
4	NAG	B	1010	1	14,14,15	0.38	0	17,19,21	0.51	0
5	IDQ	A	1008	-	30,30,30	2.34	6 (20%)	41,42,42	1.73	8 (19%)
6	SO4	A	1011	-	4,4,4	0.39	0	6,6,6	0.16	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	1001	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1007	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1006	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1008	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1009	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1006	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1001	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1007	1	-	2/6/23/26	0/1/1/1
5	IDQ	B	1011	-	-	1/10/10/10	0/4/4/4
4	NAG	B	1010	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	1002	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1005	1	-	0/6/23/26	0/1/1/1
5	IDQ	A	1008	-	-	0/10/10/10	0/4/4/4

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1008	IDQ	C8-C7	9.95	1.47	1.39
5	B	1011	IDQ	C8-C7	8.14	1.46	1.39
5	B	1011	IDQ	C1-C	4.71	1.49	1.42
4	B	1006	NAG	O5-C1	4.16	1.50	1.43
5	B	1011	IDQ	C8-N2	-3.80	1.34	1.39

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1008	IDQ	C11-C10-C9	-5.39	103.48	113.38
5	B	1011	IDQ	C15-C14-N2	-4.91	105.48	113.46
5	B	1011	IDQ	C8-C7-N1	-4.86	105.68	111.51
5	A	1008	IDQ	C8-C7-N1	-4.51	106.09	111.51
5	A	1008	IDQ	C15-C14-N2	-4.12	106.77	113.46

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1007	NAG	O5-C5-C6-O6
4	B	1006	NAG	C4-C5-C6-O6
4	A	1007	NAG	C4-C5-C6-O6
4	B	1001	NAG	O5-C5-C6-O6
4	B	1001	NAG	C4-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 10 short contacts:

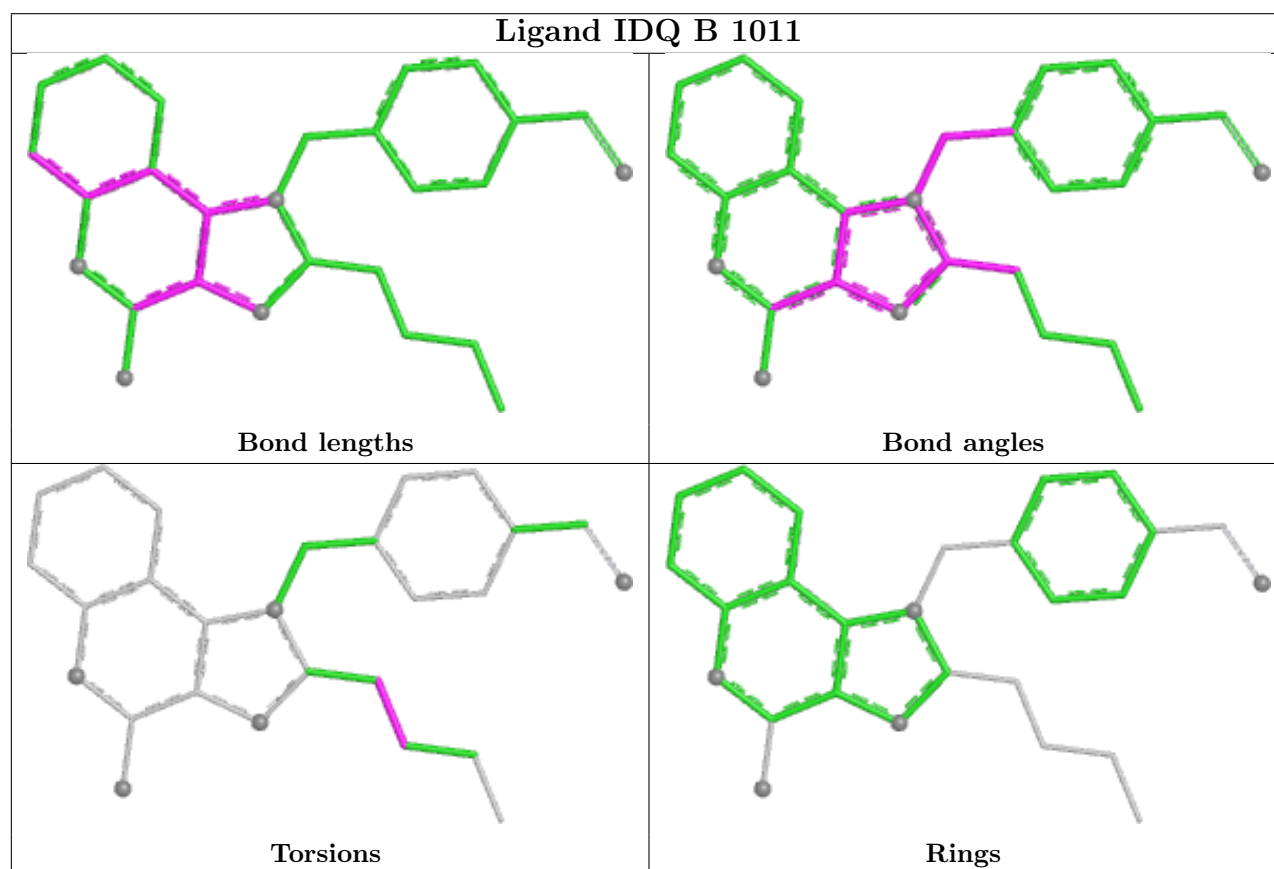
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1008	NAG	1	0
4	A	1001	NAG	1	0
4	A	1007	NAG	1	0
6	A	1010	SO4	1	0
5	B	1011	IDQ	4	0

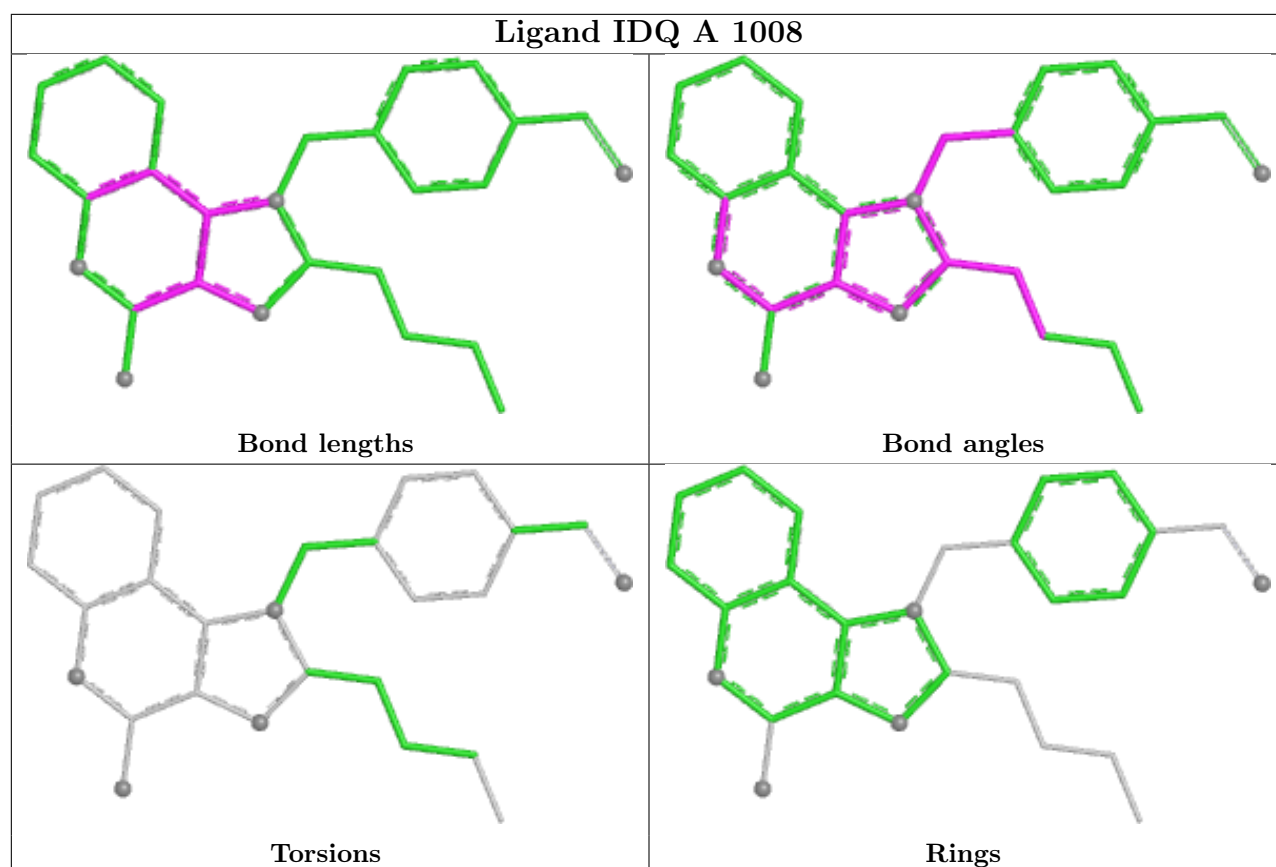
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1008	IDQ	2	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	773/823 (93%)	-0.10	9 (1%) 76 75	35, 54, 77, 93	0
1	B	774/823 (94%)	-0.39	2 (0%) 90 89	29, 45, 64, 87	0
2	C	5/6 (83%)	0.41	1 (20%) 3 2	55, 61, 73, 94	0
2	D	4/6 (66%)	-0.63	0 100 100	53, 56, 64, 68	0
All	All	1556/1658 (93%)	-0.25	12 (0%) 82 81	29, 49, 71, 94	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	0	A	4.0
1	A	27	ALA	3.7
1	A	388	PHE	3.5
1	A	461	GLU	2.8
1	A	459	VAL	2.8

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

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

6.3 Carbohydrates [i](#)

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

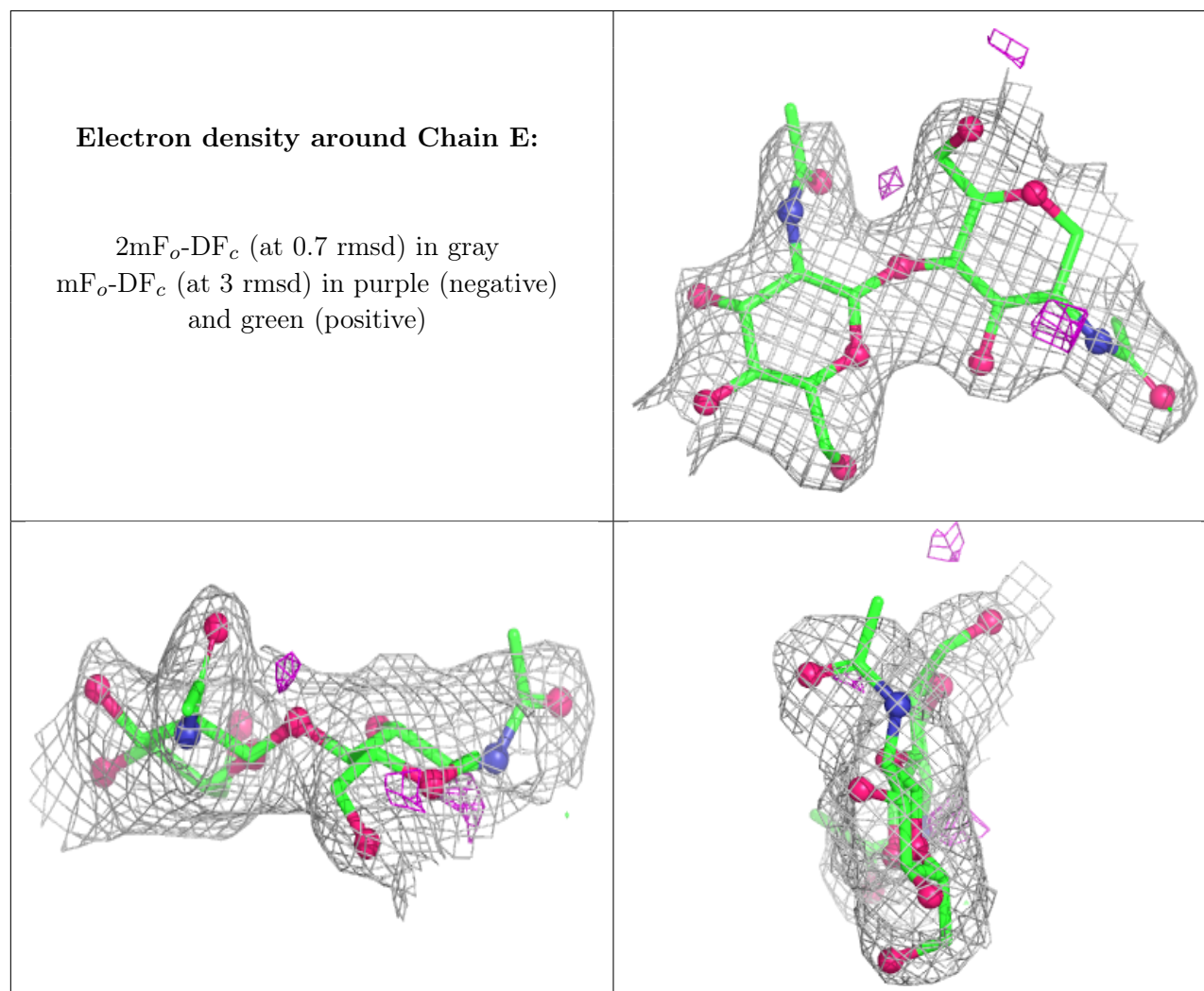
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	G	2	14/15	0.55	0.17	79,86,95,98	0
3	NAG	F	2	14/15	0.88	0.09	59,62,68,68	0

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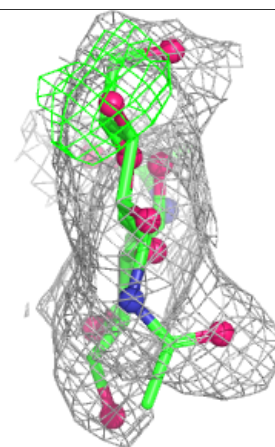
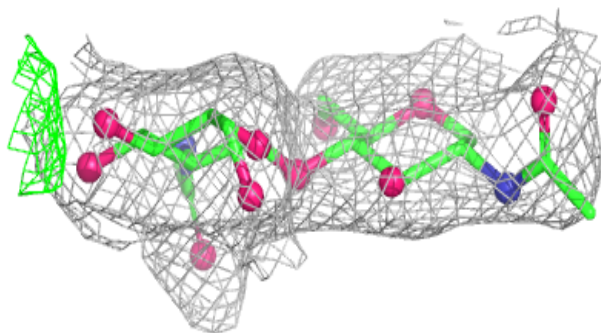
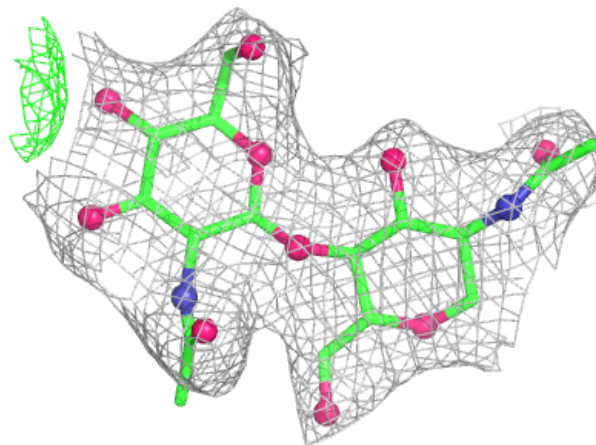
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	E	2	14/15	0.88	0.10	53,62,66,69	0
3	NAG	E	1	14/15	0.89	0.11	48,53,58,59	0
3	NAG	G	1	14/15	0.92	0.09	65,69,78,79	0
3	NAG	F	1	14/15	0.95	0.09	50,52,56,57	0

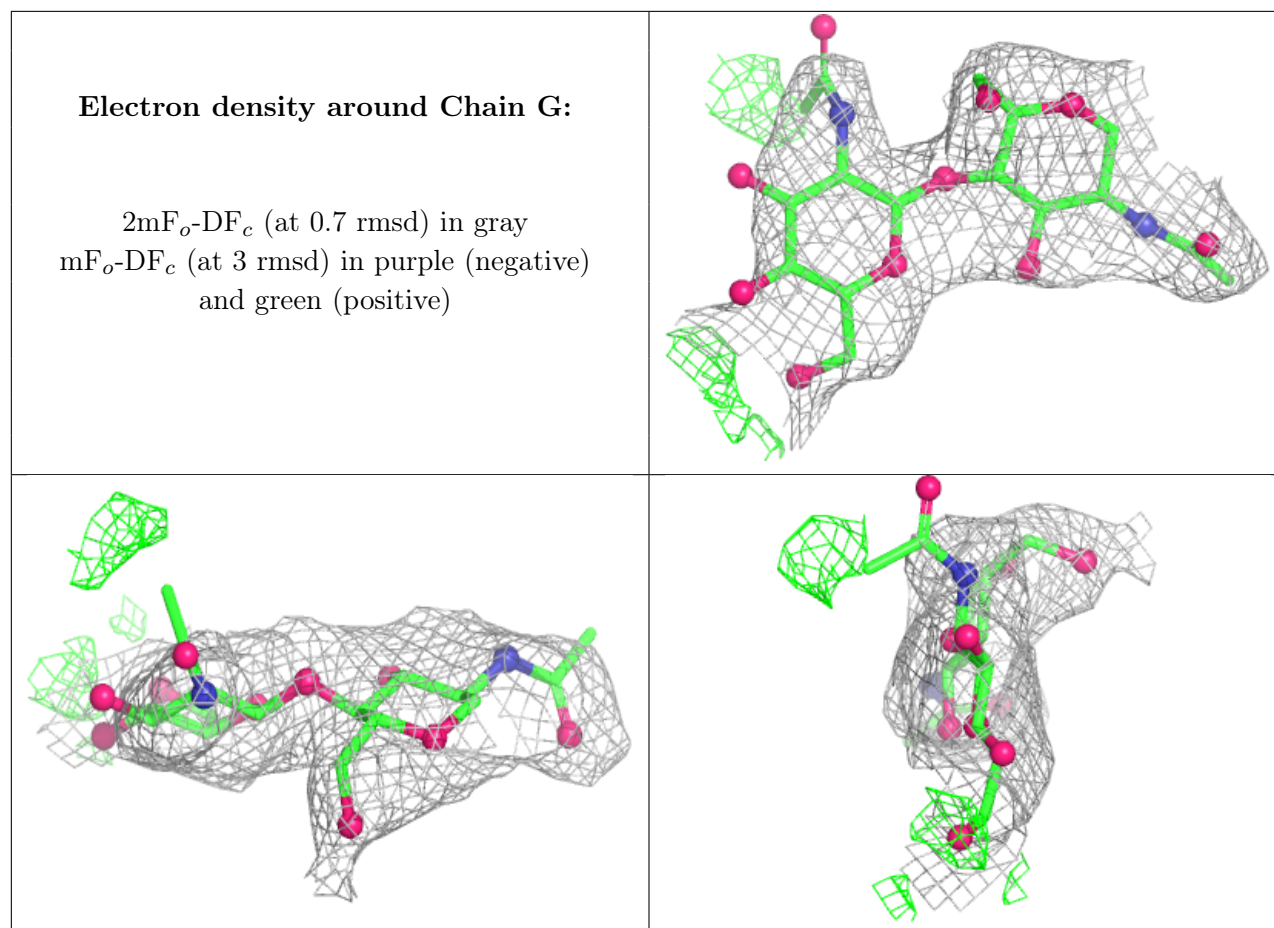
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around Chain 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 ⓘ

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

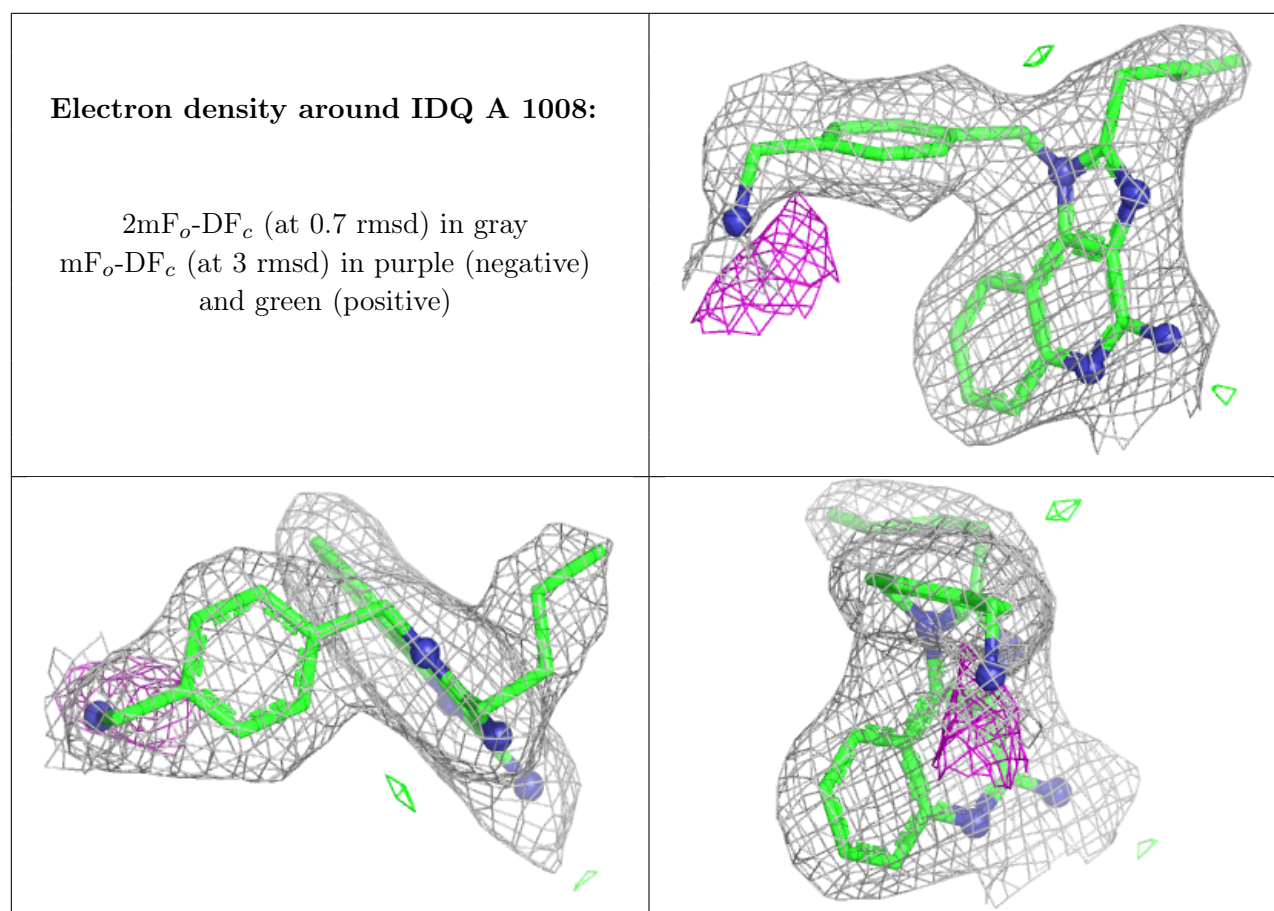
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	A	1006	14/15	0.59	0.15	69,79,86,87	0
6	SO4	A	1011	5/5	0.72	0.15	72,73,93,101	0
6	SO4	B	1013	5/5	0.74	0.13	70,75,85,96	0
6	SO4	B	1016	5/5	0.76	0.21	79,79,104,106	0
4	NAG	B	1010	14/15	0.79	0.12	69,75,77,78	0
4	NAG	B	1007	14/15	0.80	0.12	54,67,72,83	0
6	SO4	A	1013	5/5	0.80	0.24	55,55,66,88	0
6	SO4	A	1012	5/5	0.81	0.21	73,80,85,100	0
6	SO4	B	1015	5/5	0.82	0.14	67,77,89,95	0
6	SO4	B	1014	5/5	0.84	0.20	55,60,62,85	0
4	NAG	B	1008	14/15	0.85	0.09	48,62,65,71	0
4	NAG	B	1006	14/15	0.86	0.10	45,58,64,64	0

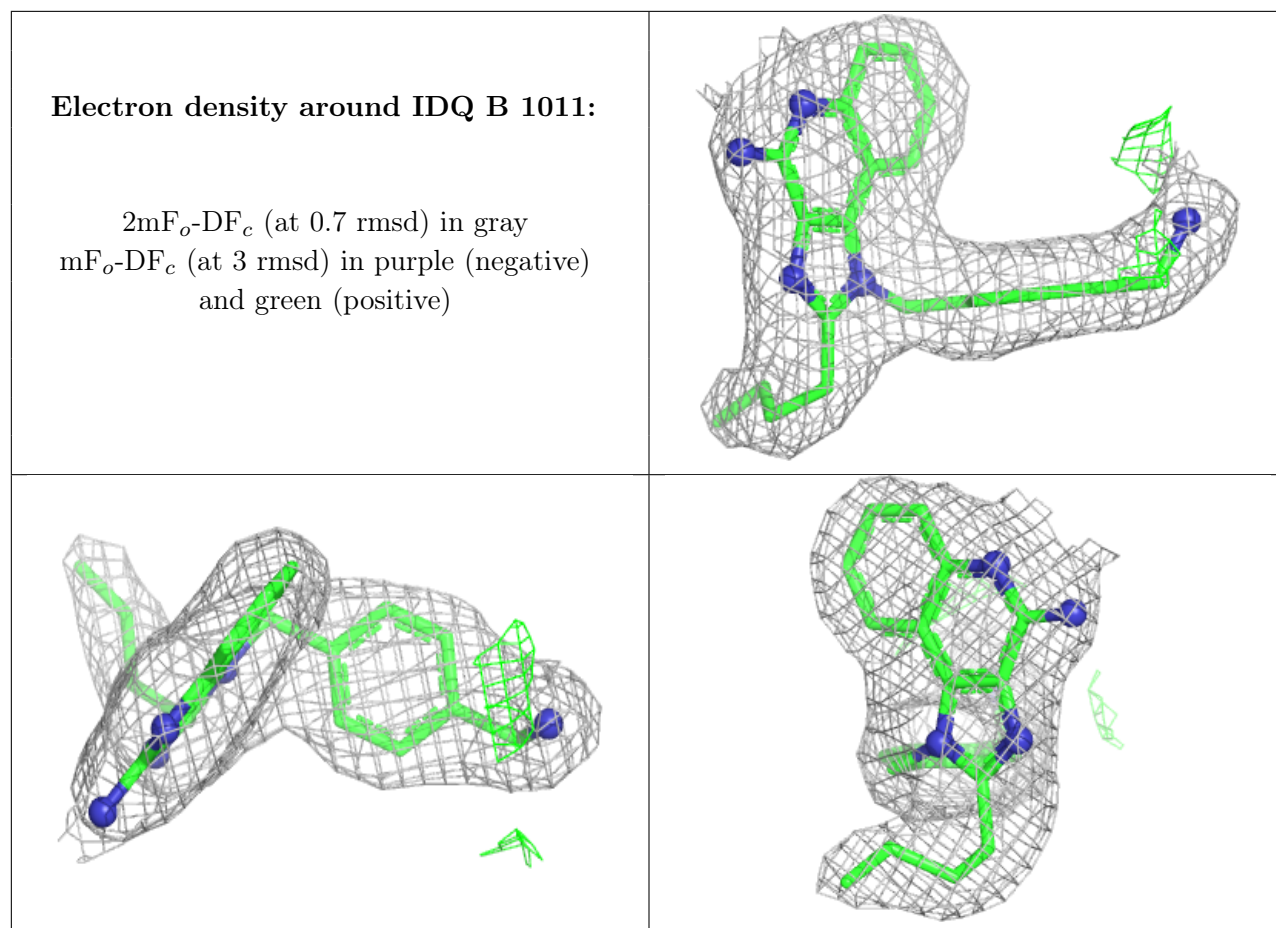
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	B	1002	14/15	0.86	0.11	57,62,71,74	0
6	SO4	B	1019	5/5	0.87	0.23	56,68,74,93	0
6	SO4	A	1010	5/5	0.87	0.14	67,71,78,90	0
4	NAG	A	1007	14/15	0.87	0.10	61,68,75,79	0
6	SO4	B	1012	5/5	0.87	0.11	54,64,74,77	0
6	SO4	B	1017	5/5	0.87	0.16	64,65,83,90	0
6	SO4	B	1018	5/5	0.88	0.13	72,79,83,92	0
4	NAG	B	1009	14/15	0.88	0.10	51,58,65,69	0
4	NAG	B	1005	14/15	0.89	0.09	52,62,67,67	0
4	NAG	A	1001	14/15	0.91	0.08	41,47,56,57	0
5	IDQ	A	1008	27/27	0.94	0.10	37,44,55,73	0
6	SO4	A	1009	5/5	0.94	0.07	61,67,82,82	0
4	NAG	B	1001	14/15	0.94	0.07	35,39,46,56	0
5	IDQ	B	1011	27/27	0.95	0.08	40,46,50,51	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.





6.5 Other polymers ⓘ

There are no such residues in this entry.