



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 01:44 PM BST

PDB ID : 6CQU
Title : Crystal Structure of Recombinant Human Acetylcholinesterase with Reactiva-
tor HI-6
Authors : Bester, S.M.; Guelta, M.A.; Pegan, S.D.; Height, J.J.
Deposited on : 2018-03-16
Resolution : 2.31 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
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

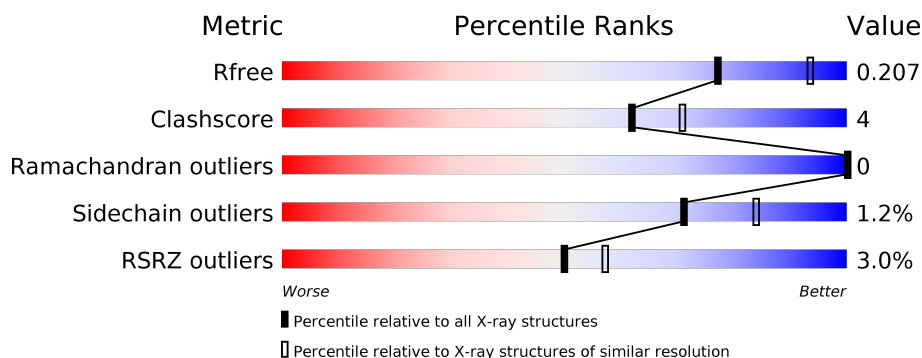
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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	542	<div> <div>3%</div> <div> <div></div> <div>91%</div> <div>7%</div> <div></div> </div> </div>
1	B	542	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>9%</div> <div></div> </div> </div>
2	C	3	<div> <div></div> <div>100%</div> </div>
2	D	3	<div> <div></div> <div> <div>33%</div> <div>67%</div> </div> </div>
2	E	3	<div> <div></div> <div> <div>33%</div> <div>67%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	C	1	X	-	-	-
2	NAG	C	2	-	-	-	X
2	NAG	D	1	-	-	X	-
2	NAG	D	2	-	-	-	X
2	FUC	D	3	-	-	X	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9294 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 Acetylcholinesterase.

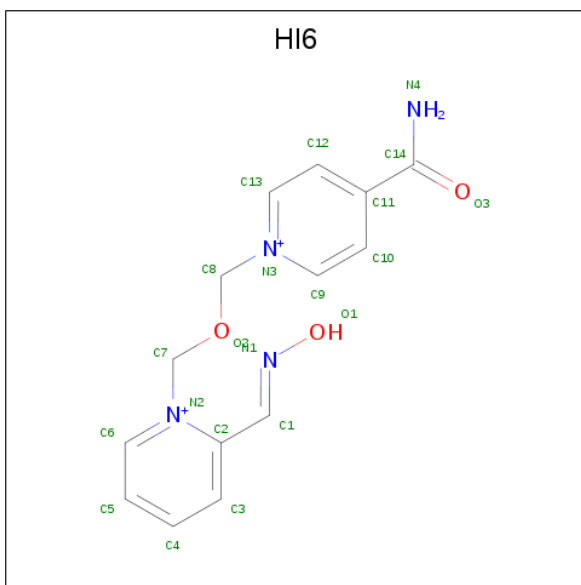
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	532	Total	C	N	O	S	0	2	0
			4153	2665	729	746	13			
1	B	530	Total	C	N	O	S	0	2	0
			4143	2660	727	743	13			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			38	22	2	14			
2	D	3	Total	C	N	O	0	0	0
			38	22	2	14			
2	E	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 3 is 4-(AMINOCARBONYL)-1-[(2-[(E)-(HYDROXYIMINO)METHYL]PYRIDINIUM-1-YL}METHOXY)METHYL]PYRIDINIUM (three-letter code: HI6) (formula: C₁₄H₁₆N₄O₃).



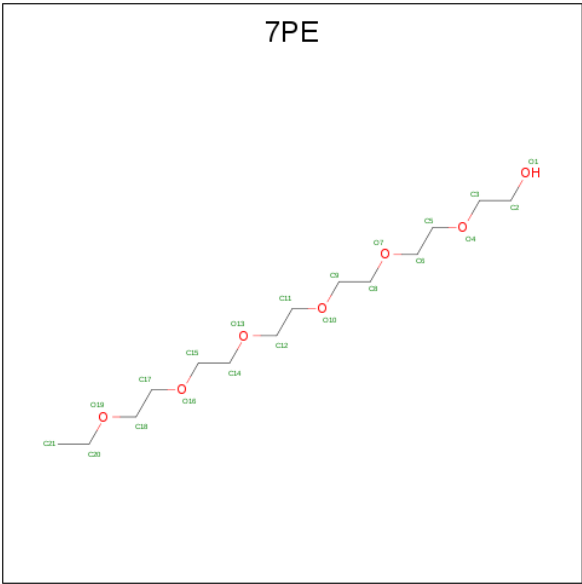
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			21	14	4	3		
3	B	1	Total	C	N	O	0	0
			21	14	4	3		

- 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	N	O	0	0
			14	8	1	5		

- Molecule 5 is 2-(2-(2-(2-(2-ETHOXYETHOXY)ETHOXY)ETHOXY)ETHOXY)ETHOXY)ETHANOL (three-letter code: 7PE) (formula: C₁₄H₃₀O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			21	14	7		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	373	Total	O	0	0
			373	373		
6	B	434	Total	O	0	0
			434	434		



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	105.14Å 105.14Å 324.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.75 – 2.31 34.75 – 2.31	Depositor EDS
% Data completeness (in resolution range)	97.6 (34.75-2.31) 97.6 (34.75-2.31)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.44 (at 2.31Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.170 , 0.207 0.170 , 0.207	Depositor DCC
R_{free} test set	4524 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	40.9	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9294	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% 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: 7PE, NAG, HI6, FUC

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	0.26	0/4284	0.46	0/5851
1	B	0.27	0/4274	0.45	0/5839
All	All	0.27	0/8558	0.45	0/11690

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	4153	0	4040	25	0
1	B	4143	0	4034	32	0
2	C	38	0	34	8	0
2	D	38	0	34	9	0
2	E	38	0	34	2	0
3	A	21	0	16	1	0
3	B	21	0	16	2	0
4	A	14	0	13	0	0
5	A	21	0	30	1	0
6	A	373	0	0	5	0
6	B	434	0	0	6	0
All	All	9294	0	8251	74	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 4.

All (74) 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:24:THR:HG22	1:B:27:GLY:O	1.31	1.25
1:B:498:PRO:HB3	6:B:1056:HOH:O	1.57	1.03
2:D:1:NAG:H61	2:D:3:FUC:H5	1.40	1.03
6:A:894:HOH:O	2:C:2:NAG:H81	1.56	1.03
2:C:2:NAG:O7	2:C:2:NAG:O4	1.93	0.87
2:C:1:NAG:H61	2:C:2:NAG:C1	2.04	0.87
2:C:1:NAG:C6	2:C:2:NAG:H83	2.06	0.85
2:D:1:NAG:H61	2:D:3:FUC:C5	2.07	0.85
2:C:1:NAG:H62	2:C:2:NAG:H83	1.67	0.75
2:D:1:NAG:H61	2:D:3:FUC:H3	1.70	0.74
1:A:313:GLU:N	1:A:313:GLU:OE1	2.18	0.73
1:A:460:ASP:HB3	1:A:463:ARG:HG3	1.71	0.72
2:C:1:NAG:H61	2:C:2:NAG:H83	1.71	0.72
1:B:527:GLN:NE2	6:B:707:HOH:O	2.25	0.69
2:D:1:NAG:C6	2:D:3:FUC:H5	2.21	0.69
2:D:1:NAG:H61	2:D:3:FUC:C3	2.24	0.68
1:A:113:PRO:HG3	1:A:485:ARG:HG2	1.75	0.68
2:C:1:NAG:O5	2:C:3:FUC:H5	1.95	0.66
2:D:1:NAG:C6	2:D:3:FUC:H3	2.26	0.65
6:B:702:HOH:O	2:E:1:NAG:O7	2.14	0.65
1:A:51:GLU:OE1	1:A:51:GLU:N	2.30	0.64
1:B:345:GLY:N	2:E:2:NAG:O7	2.26	0.64
1:B:521:ARG:NH1	6:B:709:HOH:O	2.32	0.61
1:B:24:THR:CG2	1:B:27:GLY:O	2.27	0.60
1:A:45:ARG:HH21	1:A:51:GLU:HG2	1.66	0.59
1:B:417:ARG:NH1	1:B:421:GLN:OE1	2.35	0.59
1:B:5:ASP:OD1	1:B:105:TYR:OH	2.15	0.58
1:B:313:GLU:N	1:B:313:GLU:OE2	2.30	0.58
1:A:200:PHE:HB2	1:A:226:VAL:HB	1.85	0.57
1:A:285:GLU:OE1	6:A:701:HOH:O	2.18	0.57
1:B:404:ASP:OD1	1:B:525[B]:ARG:NH1	2.39	0.54
1:A:265:ASN:ND2	2:D:1:NAG:C7	2.70	0.54
3:B:601:HI6:H9	6:B:994:HOH:O	2.09	0.53
1:A:433:ARG:NH2	1:A:439:TRP:O	2.41	0.53
1:B:286:TRP:HH2	1:B:297:PHE:HD1	1.57	0.52
2:D:1:NAG:C6	2:D:3:FUC:C3	2.86	0.52
1:B:68:VAL:HG23	1:B:90:ARG:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:SER:OG	6:B:703:HOH:O	2.18	0.52
1:A:165:ARG:NH1	6:A:717:HOH:O	2.43	0.51
1:A:525[B]:ARG:NH1	6:A:718:HOH:O	2.44	0.50
1:A:45:ARG:HA	1:A:48:LEU:HD12	1.93	0.50
1:B:103:THR:HG21	1:B:190:PHE:HB3	1.94	0.49
1:A:200:PHE:CB	1:A:226:VAL:HB	2.41	0.49
1:B:509:GLN:HA	1:B:521:ARG:O	2.13	0.49
1:A:124:TYR:CE1	3:A:601:HI6:H13	2.48	0.48
1:B:180:LEU:HD21	1:B:199:LEU:HD21	1.94	0.48
1:B:24:THR:HG21	1:B:140:GLN:HG3	1.96	0.48
1:B:46:ARG:HH21	1:B:94:GLU:CD	2.17	0.48
2:C:1:NAG:O3	2:C:1:NAG:H82	2.14	0.48
1:A:68:VAL:HG23	1:A:90:ARG:HB2	1.96	0.47
1:A:510:TYR:CZ	1:A:521:ARG:HB2	2.49	0.47
1:B:116:VAL:HB	1:B:199:LEU:HD23	1.96	0.46
1:B:433:ARG:NH2	1:B:439:TRP:O	2.47	0.46
1:B:200:PHE:CB	1:B:226:VAL:HB	2.46	0.46
1:B:91:GLU:CD	1:B:91:GLU:H	2.20	0.45
1:A:203:SER:OG	6:A:702:HOH:O	2.21	0.44
1:A:113:PRO:HG2	1:A:144:THR:HG22	2.00	0.44
1:A:392:ALA:O	1:A:396:GLU:OE1	2.35	0.43
1:B:17:LEU:HD23	1:B:60:VAL:HB	1.99	0.43
1:B:165:ARG:O	1:B:165:ARG:HG2	2.18	0.43
1:A:304:ASP:O	5:A:606:7PE:H91	2.18	0.43
1:B:219[B]:ARG:HD2	1:B:219[B]:ARG:HA	1.85	0.43
1:A:265:ASN:ND2	2:D:1:NAG:O7	2.52	0.42
1:B:337:TYR:CE2	3:B:601:HI6:H1	2.55	0.42
1:B:25:PRO:HG3	1:B:461:PRO:HD3	2.02	0.42
1:A:20:ILE:HG23	1:A:63:THR:HG22	2.01	0.42
1:A:177:ARG:CZ	1:A:217:PRO:HB2	2.49	0.42
1:A:329:GLY:HA3	1:A:428:TYR:CE2	2.56	0.41
1:B:458:PRO:HA	1:B:465:TYR:CD1	2.56	0.41
1:B:113:PRO:HG3	1:B:485:ARG:HG2	2.02	0.41
1:B:328:VAL:O	1:B:427:ALA:HA	2.21	0.41
1:B:102:TRP:CE3	1:B:146:LEU:HD12	2.57	0.40
1:A:458:PRO:HA	1:A:465:TYR:CD1	2.56	0.40
1:B:166:GLU:OE2	1:B:274:ARG:NH2	2.53	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	528/542 (97%)	513 (97%)	15 (3%)	0	100	100
1	B	526/542 (97%)	511 (97%)	15 (3%)	0	100	100
All	All	1054/1084 (97%)	1024 (97%)	30 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	433/437 (99%)	429 (99%)	4 (1%)	78	89
1	B	432/437 (99%)	426 (99%)	6 (1%)	67	81
All	All	865/874 (99%)	855 (99%)	10 (1%)	71	84

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	LEU
1	A	200	PHE
1	A	286	TRP
1	A	295	PHE
1	B	70	TYR
1	B	200	PHE
1	B	286	TRP
1	B	295	PHE

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Mol	Chain	Res	Type
1	B	396	GLU
1	B	414	LEU

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	413	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

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	0.29	0	17,19,21	0.61	0
2	NAG	C	2	2	14,14,15	0.38	0	17,19,21	0.74	0
2	FUC	C	3	2	10,10,11	0.26	0	14,14,16	0.62	0
2	NAG	D	1	1,2	14,14,15	0.28	0	17,19,21	0.60	0
2	NAG	D	2	2	14,14,15	0.28	0	17,19,21	0.60	0
2	FUC	D	3	2	10,10,11	0.27	0	14,14,16	0.83	0
2	NAG	E	1	2	14,14,15	0.28	0	17,19,21	0.60	0
2	NAG	E	2	2	14,14,15	0.28	0	17,19,21	0.59	0
2	FUC	E	3	2	10,10,11	0.27	0	14,14,16	0.62	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	1/1/5/7	4/6/23/26	0/1/1/1
2	NAG	C	2	2	-	4/6/23/26	0/1/1/1
2	FUC	C	3	2	-	-	0/1/1/1
2	NAG	D	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	FUC	D	3	2	-	-	0/1/1/1
2	NAG	E	1	2	-	2/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	FUC	E	3	2	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	1	NAG	C1

All (14) torsion outliers are listed below:

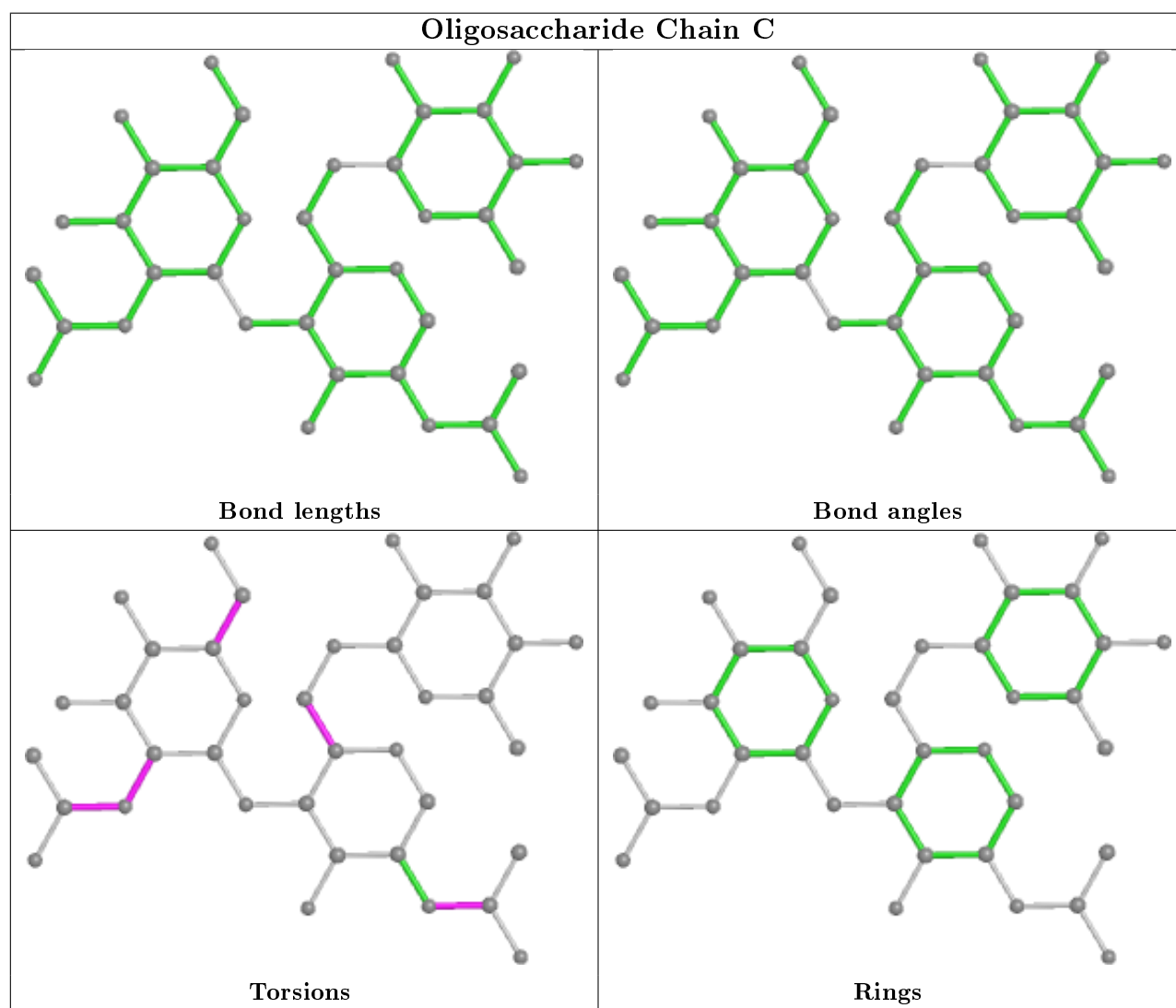
Mol	Chain	Res	Type	Atoms
2	E	1	NAG	C8-C7-N2-C2
2	E	1	NAG	O7-C7-N2-C2
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2
2	D	2	NAG	C8-C7-N2-C2
2	D	2	NAG	O7-C7-N2-C2
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
2	C	1	NAG	O5-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
2	C	2	NAG	C1-C2-N2-C7
2	C	2	NAG	O5-C5-C6-O6

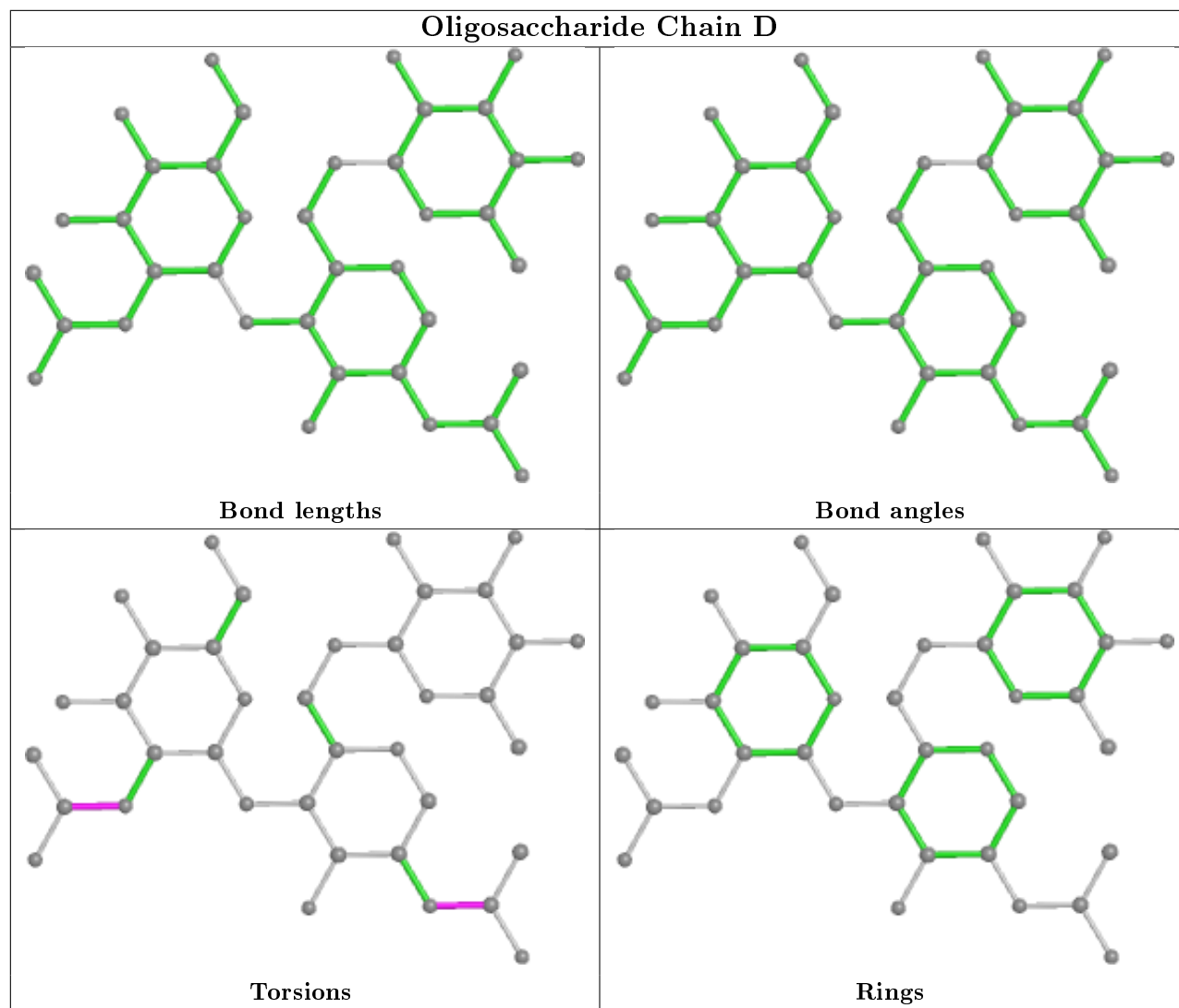
There are no ring outliers.

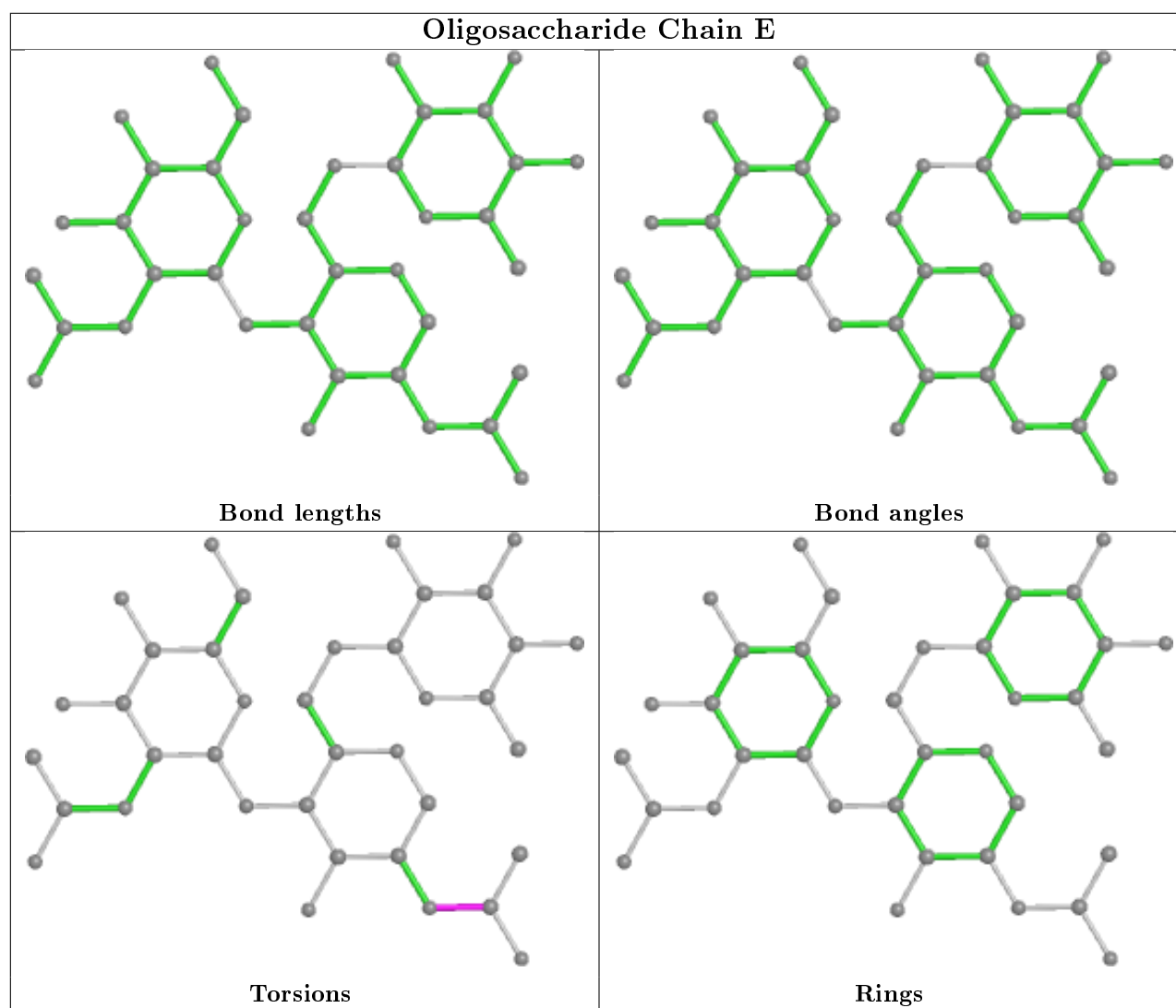
7 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	NAG	1	0
2	D	3	FUC	7	0
2	C	1	NAG	6	0
2	C	3	FUC	1	0
2	D	1	NAG	9	0
2	C	2	NAG	6	0
2	E	2	NAG	1	0

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







5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
5	7PE	A	606	-	20,20,20	0.55	0	19,19,19	0.19	0
4	NAG	A	605	1	14,14,15	0.28	0	17,19,21	0.60	0
3	HI6	B	601	-	18,22,22	2.03	3 (16%)	19,28,28	1.81	2 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HI6	A	601	-	18,22,22	2.02	3 (16%)	19,28,28	1.46	2 (10%)

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
5	7PE	A	606	-	-	6/18/18/18	-
4	NAG	A	605	1	-	0/6/23/26	0/1/1/1
3	HI6	B	601	-	-	3/12/13/13	0/2/2/2
3	HI6	A	601	-	-	3/12/13/13	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	HI6	C14-N4	6.63	1.45	1.33
3	B	601	HI6	C14-N4	6.60	1.45	1.33
3	B	601	HI6	O3-C14	-2.73	1.18	1.24
3	A	601	HI6	O3-C14	-2.68	1.19	1.24
3	B	601	HI6	C2-C1	2.50	1.53	1.46
3	A	601	HI6	C2-C1	2.48	1.53	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	601	HI6	O1-N1-C1	6.06	122.56	111.86
3	A	601	HI6	O1-N1-C1	4.88	120.48	111.86
3	B	601	HI6	C2-C1-N1	3.39	124.30	117.75
3	A	601	HI6	C3-C2-N2	2.12	120.12	117.52

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	601	HI6	N1-C1-C2-N2
3	A	601	HI6	N1-C1-C2-N2
3	A	601	HI6	N1-C1-C2-C3
5	A	606	7PE	O7-C8-C9-O10
5	A	606	7PE	O10-C11-C12-O13

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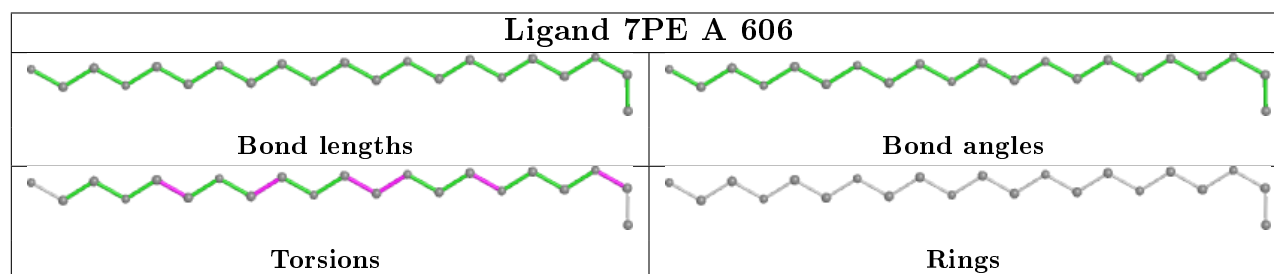
Mol	Chain	Res	Type	Atoms
5	A	606	7PE	O4-C5-C6-O7
3	B	601	HI6	N1-C1-C2-C3
3	A	601	HI6	N3-C8-O2-C7
5	A	606	7PE	C11-C12-O13-C14
3	B	601	HI6	C2-C1-N1-O1
5	A	606	7PE	C14-C15-O16-C17
5	A	606	7PE	C21-C20-O19-C18

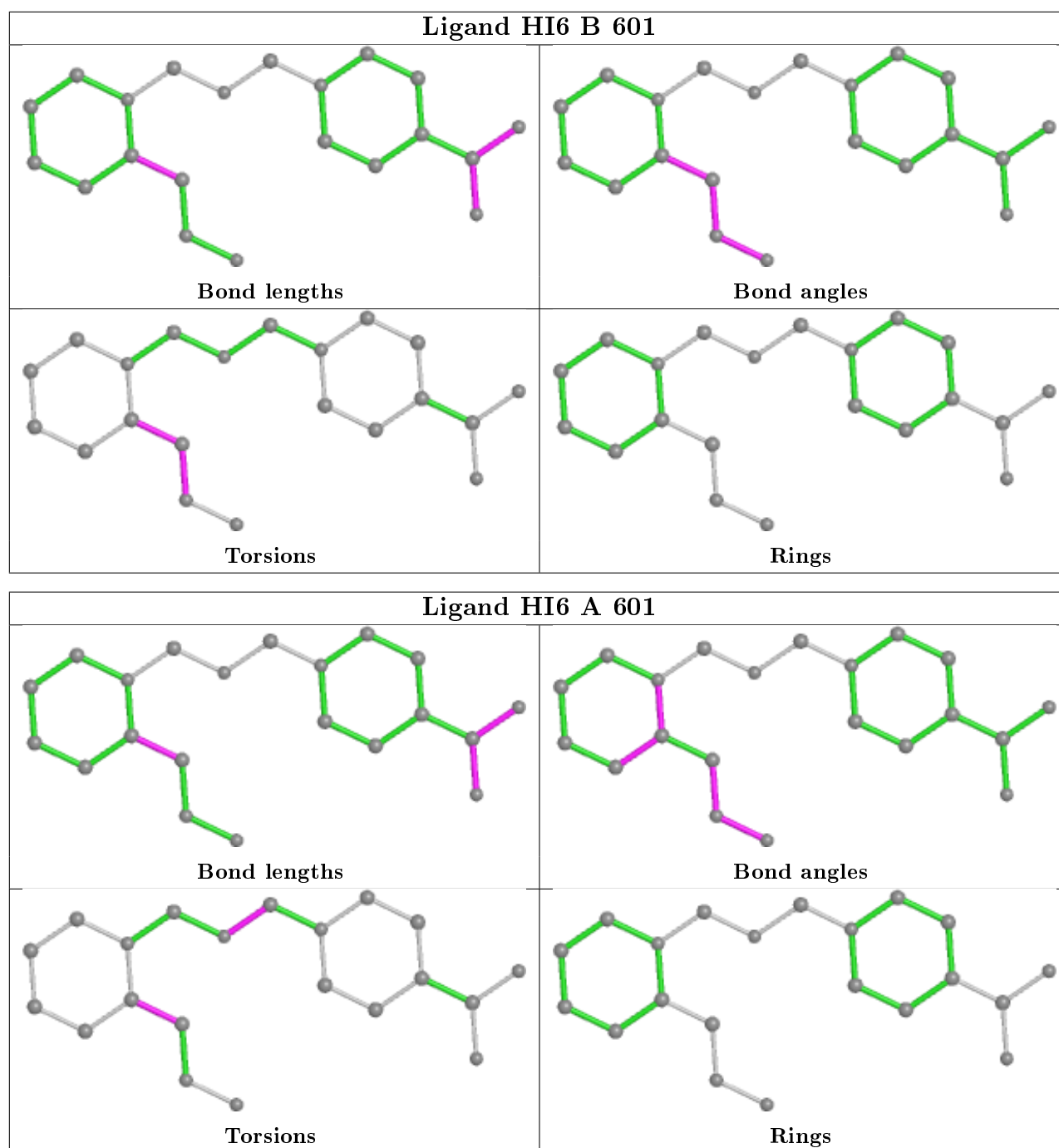
There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	606	7PE	1	0
3	B	601	HI6	2	0
3	A	601	HI6	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 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	532/542 (98%)	-0.14	14 (2%) 56 63	27, 42, 65, 101	0
1	B	530/542 (97%)	-0.17	18 (3%) 45 52	26, 40, 62, 128	0
All	All	1062/1084 (97%)	-0.16	32 (3%) 50 57	26, 41, 64, 128	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	ARG	7.3
1	B	497	ALA	7.2
1	B	259	PRO	5.8
1	A	259	PRO	4.1
1	A	262	THR	3.5
1	A	118	ILE	3.0
1	B	4	GLU	3.0
1	B	231	ALA	2.8
1	B	204	ALA	2.7
1	A	120	GLY	2.7
1	B	201	GLY	2.6
1	B	119	TYR	2.5
1	B	118	ILE	2.5
1	A	264	GLY	2.4
1	A	119	TYR	2.4
1	B	542	ALA	2.4
1	A	204	ALA	2.3
1	A	407	VAL	2.3
1	B	451	ILE	2.3
1	A	3	ARG	2.3
1	A	109	THR	2.3
1	B	203	SER	2.2
1	B	206	ALA	2.2
1	B	541	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	498	PRO	2.2
1	B	163	GLY	2.2
1	B	165	ARG	2.1
1	A	117	TRP	2.1
1	A	230	GLY	2.0
1	B	207	ALA	2.0
1	A	200	PHE	2.0
1	A	318	ALA	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 ⓘ

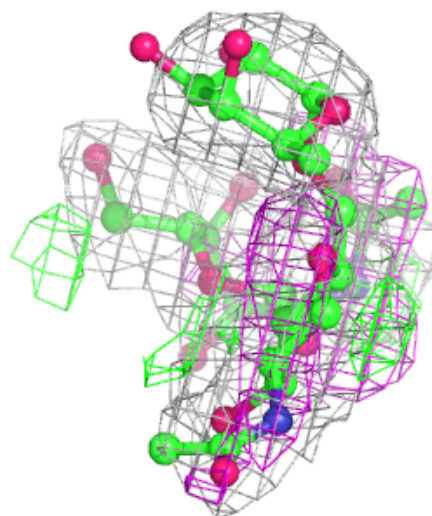
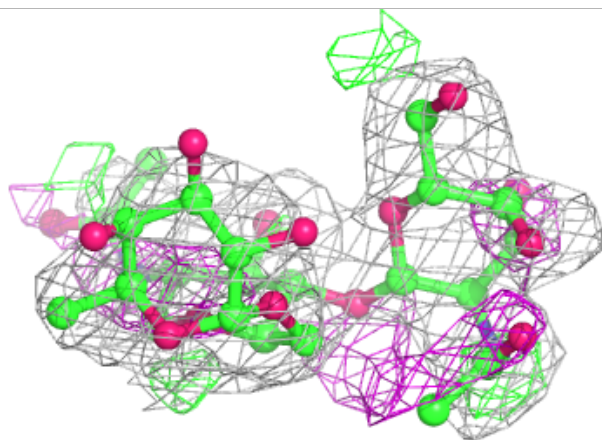
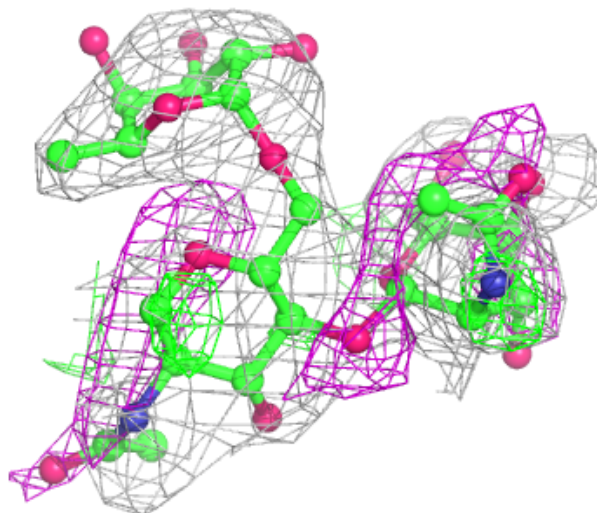
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	D	1	14/15	0.63	0.36	66,103,125,127	0
2	FUC	D	3	10/11	0.70	0.65	113,135,142,150	0
2	NAG	C	2	14/15	0.70	0.48	59,101,110,112	0
2	NAG	D	2	14/15	0.74	0.47	101,125,133,137	0
2	NAG	C	1	14/15	0.79	0.33	47,67,95,104	0
2	NAG	E	2	14/15	0.83	0.43	77,103,110,119	0
2	NAG	E	1	14/15	0.88	0.25	57,74,88,89	0
2	FUC	E	3	10/11	0.88	0.42	63,89,99,103	0
2	FUC	C	3	10/11	0.92	0.37	64,86,112,113	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.

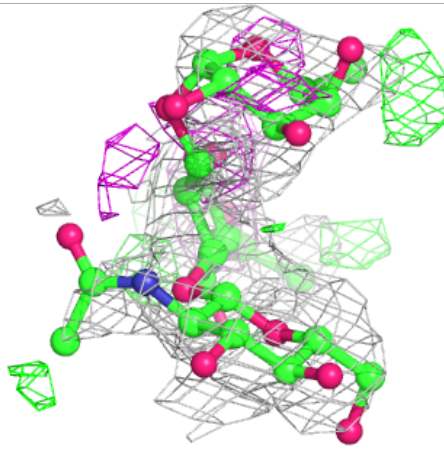
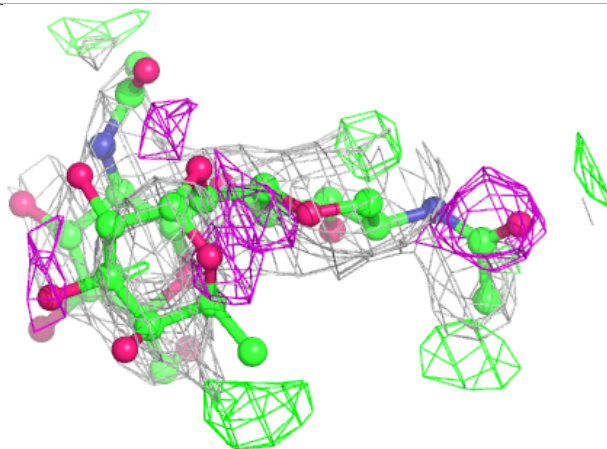
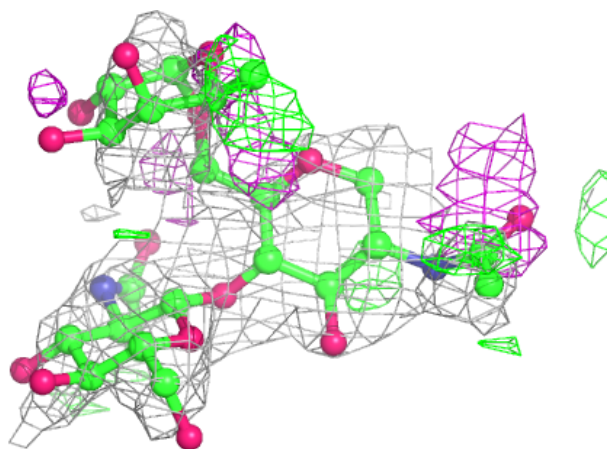
Electron density around Chain C:

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



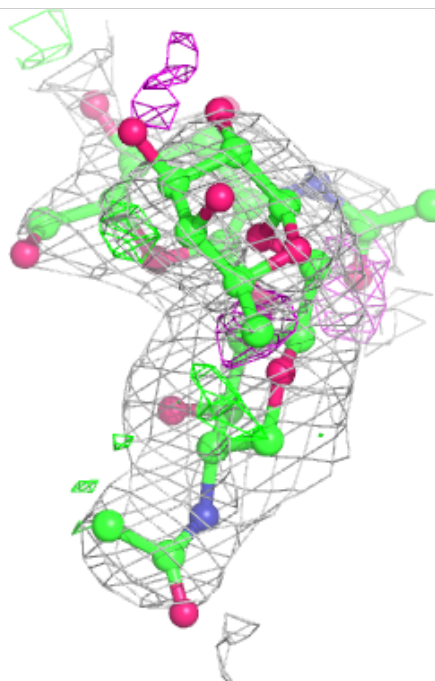
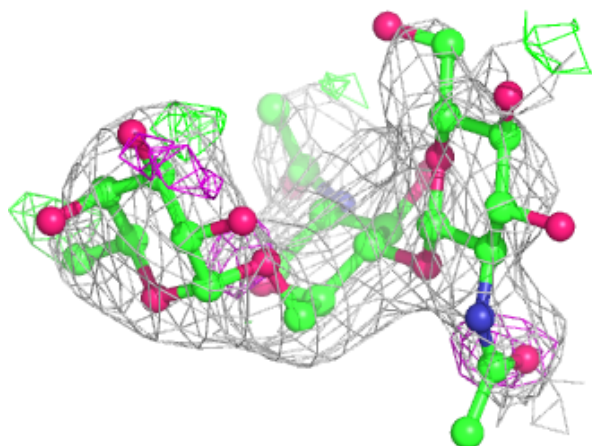
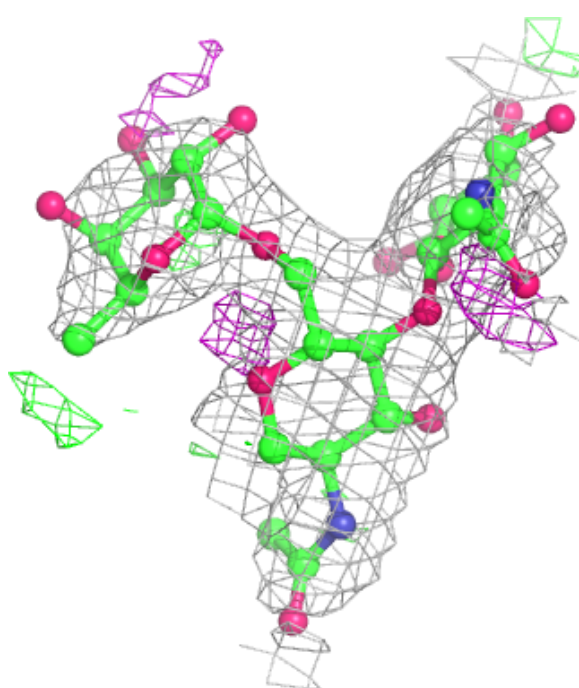
Electron density around Chain D:

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



Electron density around Chain E:

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 ⓘ

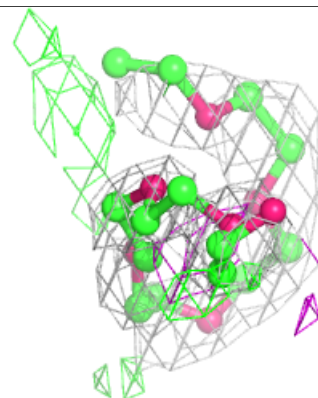
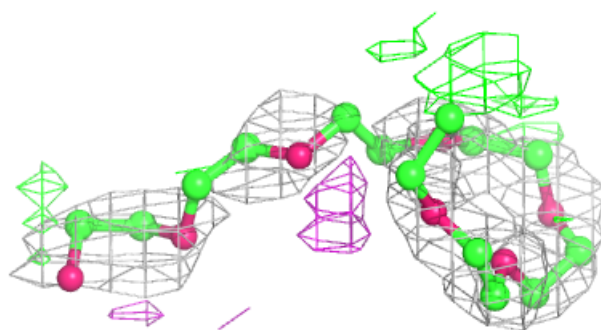
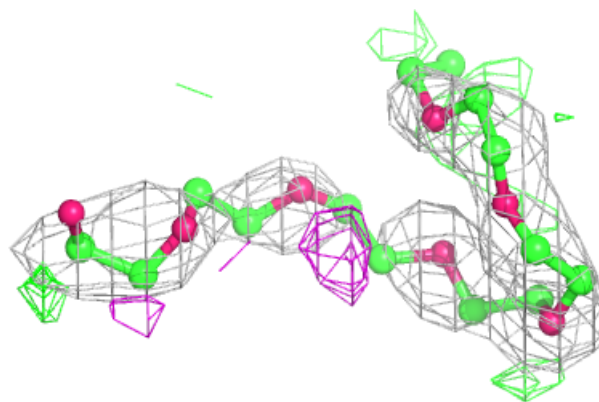
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	7PE	A	606	21/21	0.81	0.32	57,84,95,103	0
4	NAG	A	605	14/15	0.81	0.45	73,100,112,116	0
3	HI6	B	601	21/21	0.87	0.21	52,72,91,95	0
3	HI6	A	601	21/21	0.90	0.17	39,59,72,72	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.

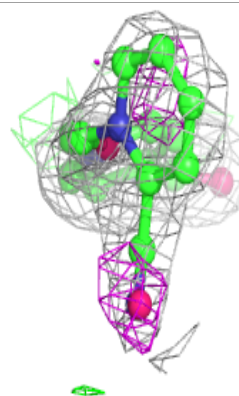
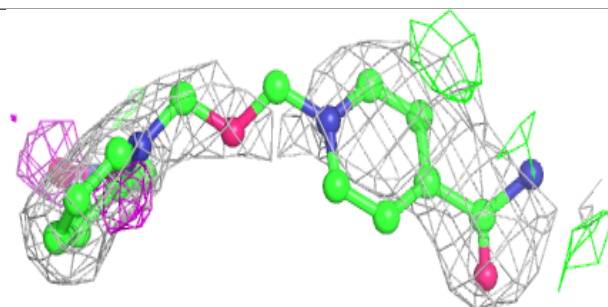
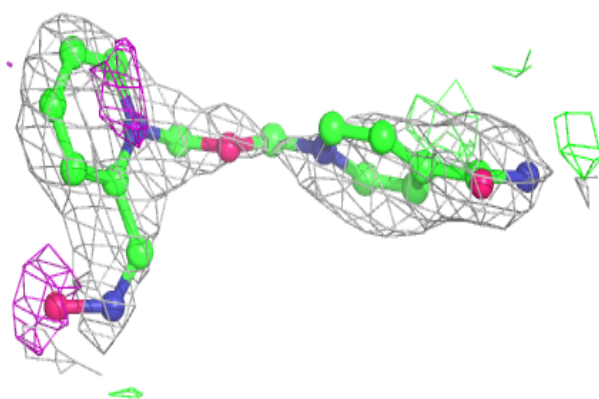
Electron density around 7PE A 606:

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mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

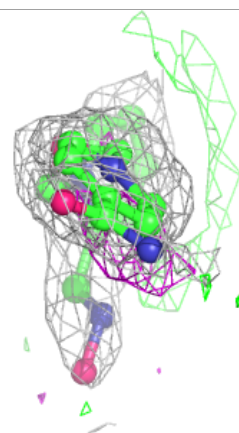
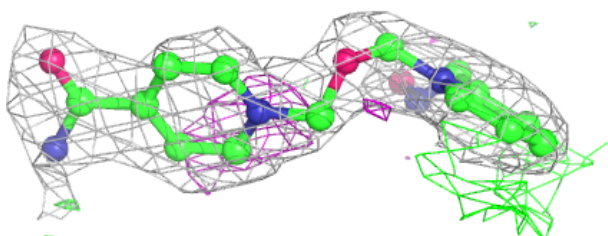
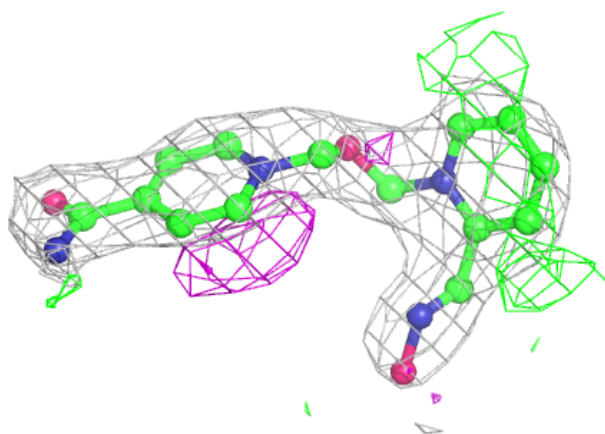


Electron density around HI6 B 601:

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

**Electron density around HI6 A 601:**

$2mF_o-DF_c$ (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.