



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 17, 2020 – 09:40 AM BST

PDB ID : 5HF9  
Title : Crystal structure of human acetylcholinesterase in complex with paraoxon and HI6  
Authors : Franklin, M.F.; Rudolph, M.J.; Ginter, C.; Cassidy, M.S.; Cheung, J.  
Deposited on : 2016-01-06  
Resolution : 2.20 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](mailto: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.

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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

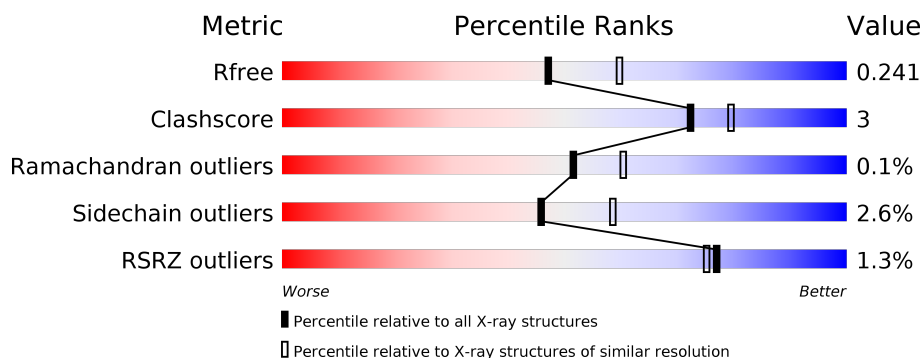
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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  $\geq 3$ , 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>%</div> <div> <div></div> <div>92%</div> <div>6%</div> <div>••</div> </div> </div>
1	B	542	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>9%</div> <div>••</div> </div> </div>
2	C	3	<div> <div>67%</div> <div>33%</div> </div>
2	D	3	<div> <div>33%</div> <div>67%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DEP	A	604[A]	-	-	X	-

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 9133 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.

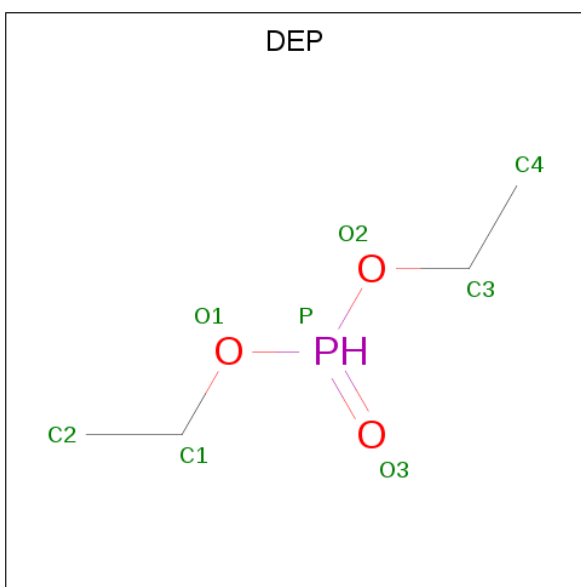
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	530	Total	C	N	O	S	0	5	0
			4174	2680	730	751	13			
1	B	533	Total	C	N	O	S	0	4	0
			4176	2682	730	751	13			

- 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			

- Molecule 3 is DIETHYL PHOSPHONATE (three-letter code: DEP) (formula: C<sub>4</sub>H<sub>11</sub>O<sub>3</sub>P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	1
			8	4	3	1		
3	B	1	Total	C	O	P	0	1
			8	4	3	1		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



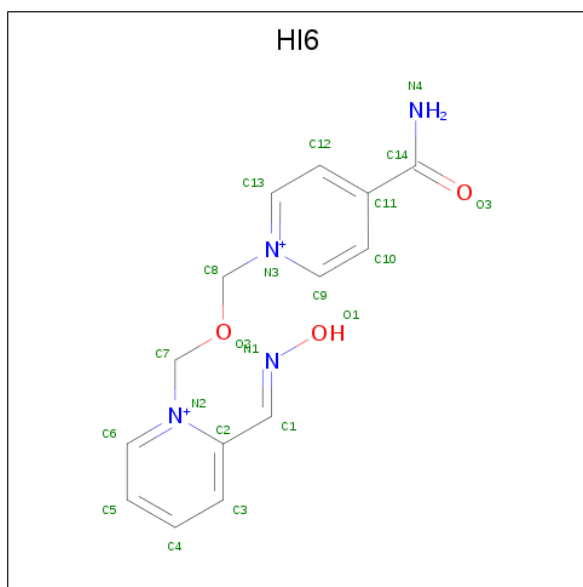
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		

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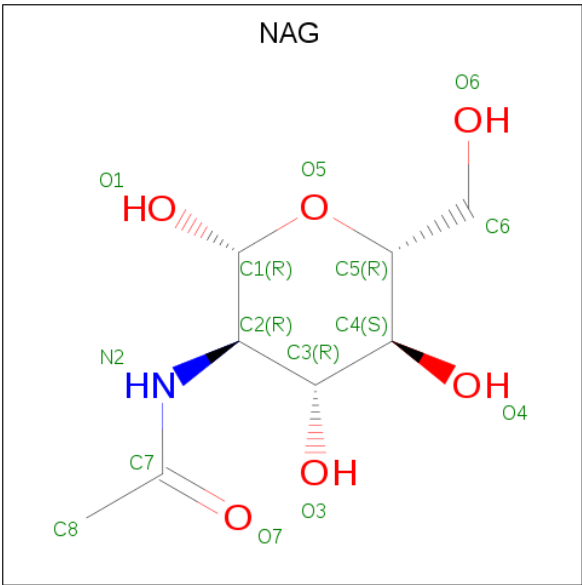
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is 4-(AMINOCARBONYL)-1-[(2-[(E)-(HYDROXYIMINO)METHYL]PYRIDINIUM-1-YL}METHOXY)METHYL]PYRIDINIUM (three-letter code: HI6) (formula:  $C_{14}H_{16}N_4O_3$ ).



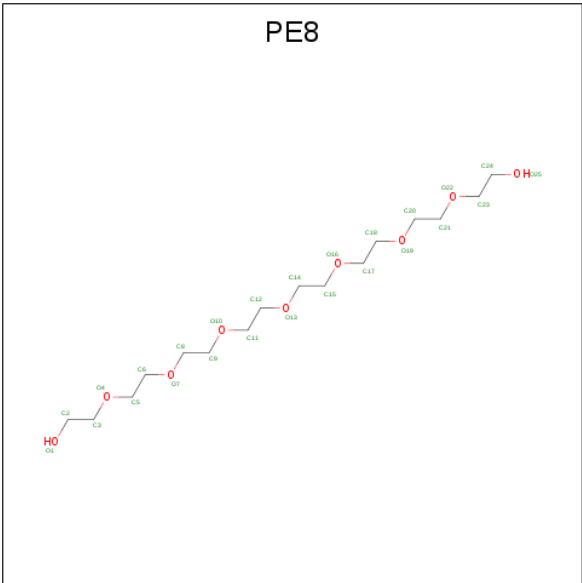
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			21	14	4	3		
5	B	1	Total	C	N	O	0	0
			21	14	4	3		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



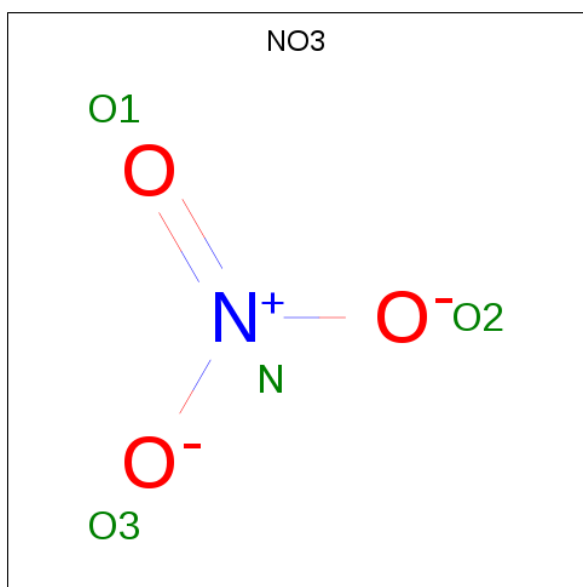
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is 3,6,9,12,15,18,21-HEPTAOXATRICOSANE-1,23-DIOL (three-letter code: PE8) (formula: C<sub>16</sub>H<sub>34</sub>O<sub>9</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			25	16	9		

- Molecule 8 is NITRATE ION (three-letter code: NO3) (formula: NO<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	N	O	0	0
			4	1	3		

- Molecule 9 is water.

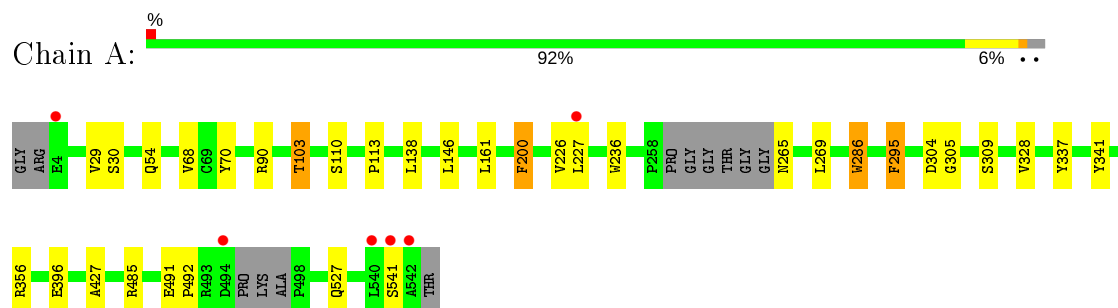
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	332	Total	O	0	0
			332	332		
9	B	258	Total	O	0	0
			258	258		



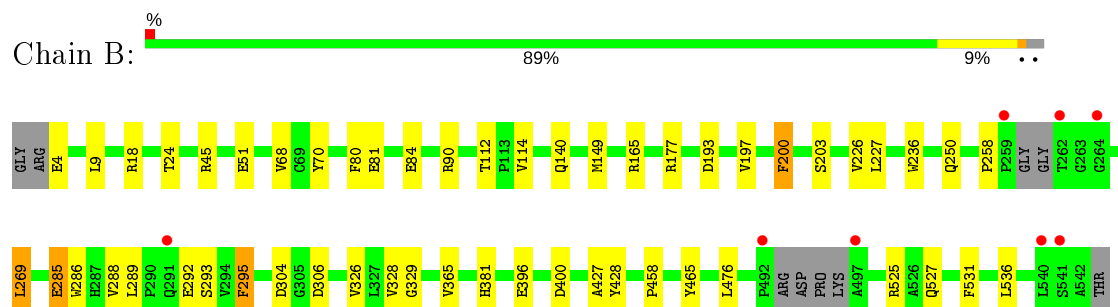
### 3 Residue-property plots [i](#)

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.

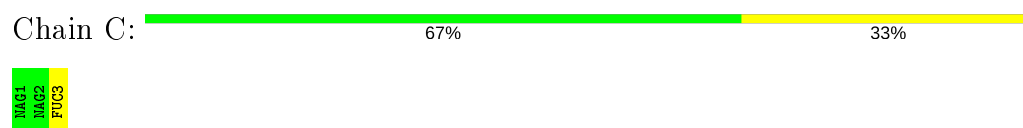
- Molecule 1: Acetylcholinesterase



- Molecule 1: Acetylcholinesterase



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



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.93Å 105.93Å 324.42Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.42 – 2.20 46.58 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.2 (45.42-2.20) 99.0 (46.58-2.20)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.26 (at 2.20Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.201 , 0.240 0.204 , 0.241	Depositor DCC
$R_{free}$ test set	5399 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.1	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 34.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	9133	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PE8, NAG, HI6, DEP, EDO, FUC, NO3

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	0.51	0/4307	0.60	0/5883
1	B	0.50	0/4307	0.58	0/5886
All	All	0.50	0/8614	0.59	0/11769

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	4174	0	4047	21	0
1	B	4176	0	4047	35	0
2	C	38	0	34	0	0
2	D	38	0	34	0	0
3	A	8	0	10	4	0
3	B	8	0	10	2	0
4	A	8	0	12	0	0
4	B	8	0	12	0	0
5	A	21	0	15	3	0
5	B	21	0	15	1	0
6	B	14	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	25	0	34	2	0
8	B	4	0	0	0	0
9	A	332	0	0	4	0
9	B	258	0	0	9	0
All	All	9133	0	8283	58	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 (58) 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:527:GLN:NE2	9:A:702:HOH:O	2.17	0.76
1:B:527:GLN:NE2	9:B:702:HOH:O	2.18	0.76
1:A:304:ASP:OD1	9:A:701:HOH:O	2.07	0.73
1:A:491:GLU:HG3	1:A:492:PRO:HD2	1.72	0.72
1:A:295[A]:PHE:CE1	3:A:604[A]:DEP:H21	2.29	0.68
1:B:304:ASP:OD1	9:B:701:HOH:O	2.12	0.67
1:A:295[A]:PHE:HE1	3:A:604[A]:DEP:H21	1.58	0.67
1:A:341:TYR:CD1	5:A:607:HI6:H72	2.35	0.62
1:A:30:SER:HB2	1:A:103:THR:HG22	1.82	0.61
1:B:4:GLU:N	9:B:706:HOH:O	2.34	0.60
1:A:161:LEU:HD11	1:A:269:LEU:HD22	1.84	0.60
1:A:265:ASN:N	9:A:706:HOH:O	2.34	0.59
1:B:381[B]:HIS:NE2	9:B:705:HOH:O	2.27	0.58
1:B:250[A]:GLN:HG2	1:B:288:VAL:HG12	1.84	0.57
1:A:68:VAL:HG23	1:A:90:ARG:HB2	1.88	0.56
1:B:4:GLU:HG2	1:B:9:LEU:HD11	1.87	0.56
1:B:400:ASP:OD1	1:B:525[B]:ARG:NH1	2.40	0.54
1:A:286:TRP:HB2	5:A:607:HI6:C14	2.38	0.53
1:A:113:PRO:HG3	1:A:485:ARG:HG2	1.91	0.53
1:A:236:TRP:CZ2	3:A:604[A]:DEP:H23	2.46	0.50
1:B:285:GLU:OE1	9:B:703:HOH:O	2.20	0.50
1:A:200:PHE:CB	1:A:226:VAL:HB	2.42	0.49
1:B:306:ASP:HB2	7:B:606:PE8:H111	1.95	0.49
1:A:337:TYR:HE2	5:A:607:HI6:C4	2.27	0.48
1:B:200:PHE:HB3	1:B:226:VAL:HB	1.96	0.47
1:B:68:VAL:HG23	1:B:90:ARG:HB2	1.97	0.47
1:B:328:VAL:O	1:B:427:ALA:HA	2.14	0.46
1:B:45:ARG:HH12	1:B:51:GLU:CD	2.19	0.46
1:B:24:THR:OG1	1:B:140:GLN:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:606:PE8:H181	7:B:606:PE8:H211	1.73	0.45
1:B:114:VAL:HB	1:B:197:VAL:HG22	1.98	0.45
1:B:306:ASP:HB3	9:B:768:HOH:O	2.17	0.45
1:A:200:PHE:HB3	1:A:226:VAL:HB	1.99	0.44
1:A:328:VAL:O	1:A:427:ALA:HA	2.17	0.44
1:B:200:PHE:CB	1:B:226:VAL:HB	2.47	0.44
1:B:177:ARG:NH1	9:B:708:HOH:O	2.38	0.44
1:B:476:LEU:HD23	1:B:476:LEU:HA	1.78	0.44
1:B:258:PRO:HD3	1:B:269:LEU:HD12	1.99	0.44
5:B:610:HI6:N1	5:B:610:HI6:H72	2.33	0.44
1:B:80:PHE:O	1:B:84:GLU:HG2	2.17	0.44
1:A:54:GLN:HG3	9:A:1004:HOH:O	2.17	0.43
1:B:326:VAL:HG12	1:B:328:VAL:HG13	2.01	0.43
1:A:295[A]:PHE:HE1	3:A:604[A]:DEP:C2	2.30	0.43
1:A:227:LEU:HB2	1:A:328:VAL:HG12	2.00	0.43
1:B:112:THR:O	1:B:193:ASP:N	2.46	0.43
1:B:227:LEU:HB2	1:B:328:VAL:HG12	2.00	0.43
1:B:531:PHE:CZ	1:B:536:LEU:HD13	2.54	0.43
1:B:165:ARG:NH1	9:B:719:HOH:O	2.52	0.42
1:B:295[A]:PHE:CE1	3:B:605[A]:DEP:H21	2.55	0.41
1:B:458:PRO:HA	1:B:465:TYR:CD1	2.55	0.41
1:B:525[B]:ARG:NH1	9:B:724:HOH:O	2.54	0.41
1:B:329:GLY:HA3	1:B:428:TYR:CZ	2.56	0.41
1:B:329:GLY:HA3	1:B:428:TYR:CE2	2.56	0.41
1:B:293:SER:HA	1:B:365:VAL:HG13	2.02	0.40
1:B:4:GLU:OE1	1:B:18:ARG:NE	2.49	0.40
1:A:305:GLY:HA2	1:A:309:SER:HA	2.03	0.40
1:B:236:TRP:CZ2	3:B:605[A]:DEP:H23	2.57	0.40
1:B:289:LEU:HD23	1:B:289:LEU:HA	1.91	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	529/542 (98%)	508 (96%)	20 (4%)	1 (0%)	47	55
1	B	531/542 (98%)	513 (97%)	18 (3%)	0	100	100
All	All	1060/1084 (98%)	1021 (96%)	38 (4%)	1 (0%)	51	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	541	SER

### 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	436/437 (100%)	424 (97%)	12 (3%)	43	56
1	B	435/437 (100%)	423 (97%)	12 (3%)	43	56
All	All	871/874 (100%)	847 (97%)	24 (3%)	46	56

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	VAL
1	A	70	TYR
1	A	103	THR
1	A	110	SER
1	A	138	LEU
1	A	146	LEU
1	A	200	PHE
1	A	286	TRP
1	A	295[A]	PHE
1	A	295[B]	PHE
1	A	356	ARG
1	A	396	GLU
1	B	70	TYR
1	B	81	GLU
1	B	149	MET

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Mol	Chain	Res	Type
1	B	200	PHE
1	B	203	SER
1	B	269	LEU
1	B	285	GLU
1	B	286	TRP
1	B	292	GLU
1	B	295[A]	PHE
1	B	295[B]	PHE
1	B	396	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	284	HIS
1	B	369	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

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	$\# Z  > 2$
2	NAG	C	1	1,2	14,14,15	0.37	0	17,19,21	0.50	0
2	NAG	C	2	2	14,14,15	0.34	0	17,19,21	0.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FUC	C	3	2	10,10,11	1.29	2 (20%)	14,14,16	0.91	0
2	NAG	D	1	1,2	14,14,15	0.34	0	17,19,21	0.77	1 (5%)
2	NAG	D	2	2	14,14,15	0.37	0	17,19,21	0.53	0
2	FUC	D	3	2	10,10,11	1.32	2 (20%)	14,14,16	1.06	1 (7%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	1/6/23/26	0/1/1/1
2	FUC	C	3	2	-	-	0/1/1/1
2	NAG	D	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	FUC	D	3	2	-	-	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	3	FUC	C1-C2	2.92	1.58	1.52
2	C	3	FUC	C2-C3	2.51	1.56	1.52
2	D	3	FUC	C2-C3	2.28	1.55	1.52
2	C	3	FUC	O5-C5	2.11	1.48	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	NAG	C1-O5-C5	2.30	115.31	112.19
2	D	3	FUC	C1-O5-C5	2.10	117.55	112.78

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2

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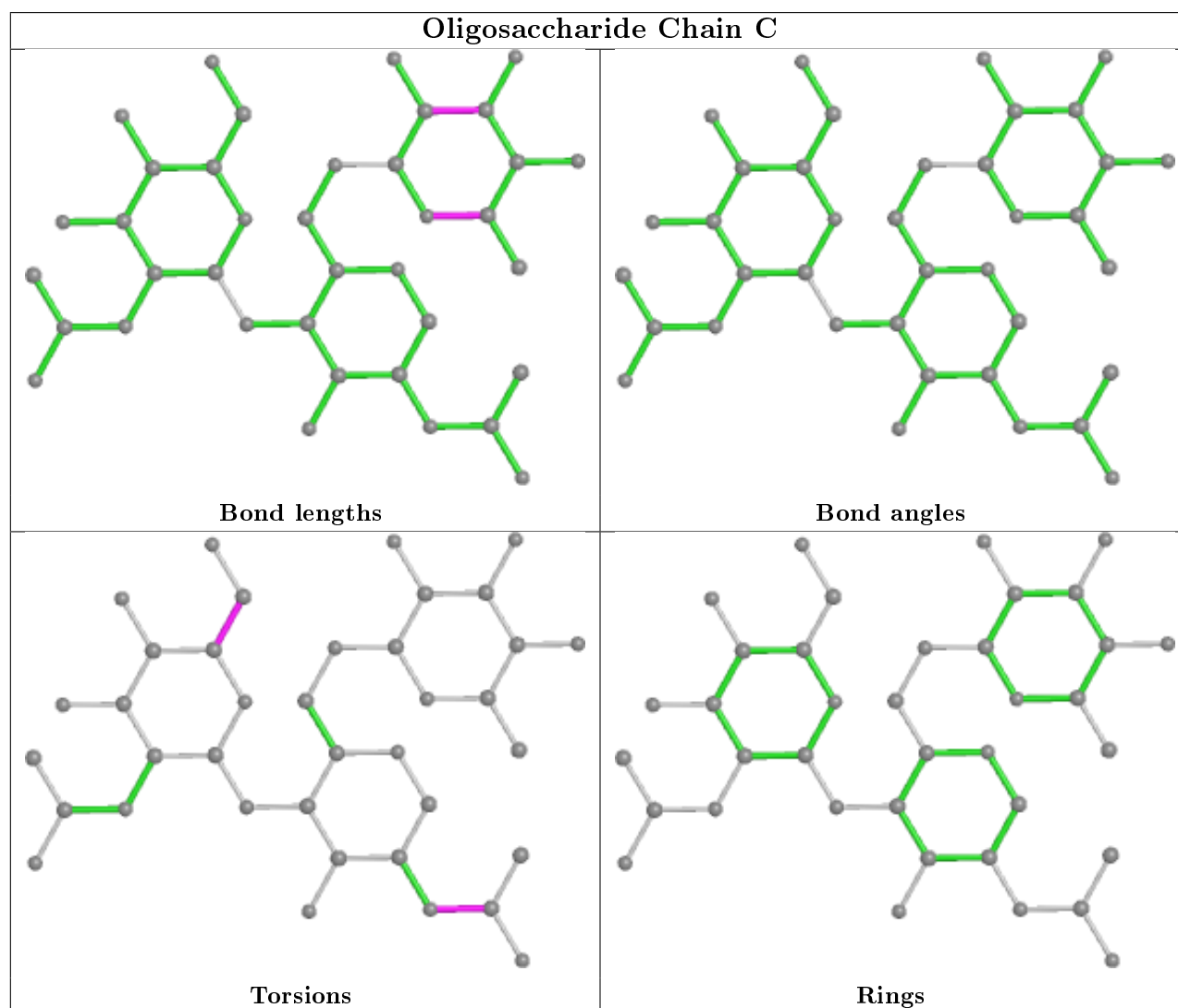
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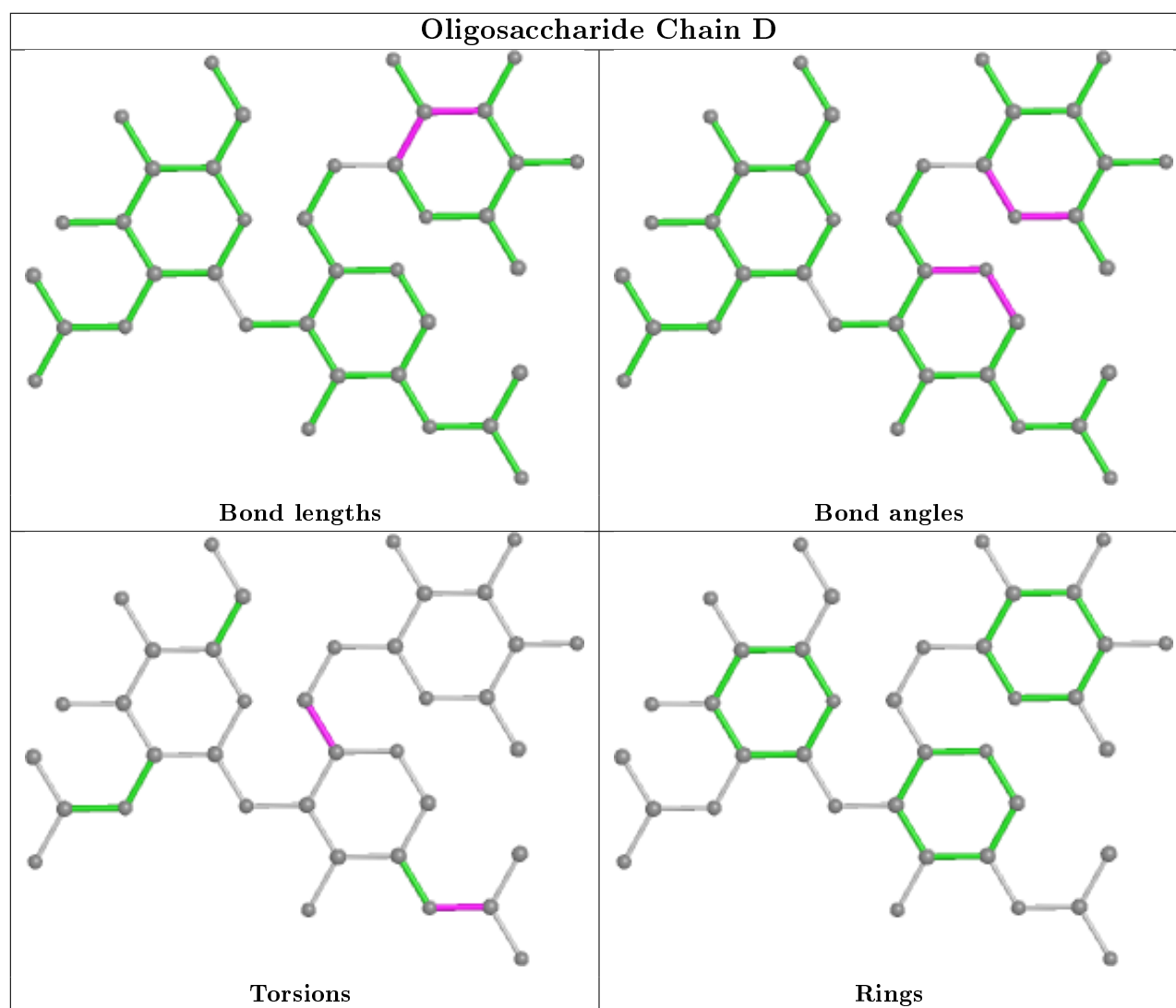
Mol	Chain	Res	Type	Atoms
2	C	2	NAG	O5-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6

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](#)

11 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	EDO	A	606	-	3,3,3	0.48	0	2,2,2	0.08	0
8	NO3	B	609	-	1,3,3	0.78	0	0,3,3	0.00	-
5	HI6	A	607	-	18,22,22	3.94	9 (50%)	19,28,28	2.77	7 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	EDO	B	608	-	3,3,3	0.55	0	2,2,2	0.26	0
3	DEP	A	604[A]	1	4,7,7	1.22	1 (25%)	2,7,7	0.61	0
7	PE8	B	606	-	24,24,24	0.91	0	23,23,23	0.33	0
5	HI6	B	610	-	18,22,22	4.08	9 (50%)	19,28,28	2.84	5 (26%)
6	NAG	B	604	1	14,14,15	0.80	1 (7%)	17,19,21	0.57	0
3	DEP	B	605[A]	1	4,7,7	1.57	1 (25%)	2,7,7	0.49	0
4	EDO	B	607	-	3,3,3	0.50	0	2,2,2	0.38	0
4	EDO	A	605	-	3,3,3	0.44	0	2,2,2	0.40	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	EDO	A	606	-	-	0/1/1/1	-
5	HI6	A	607	-	-	5/12/13/13	0/2/2/2
4	EDO	B	608	-	-	0/1/1/1	-
3	DEP	A	604[A]	1	-	1/2/6/6	-
7	PE8	B	606	-	-	10/22/22/22	-
5	HI6	B	610	-	-	4/12/13/13	0/2/2/2
6	NAG	B	604	1	-	2/6/23/26	0/1/1/1
3	DEP	B	605[A]	1	-	1/2/6/6	-
4	EDO	B	607	-	-	0/1/1/1	-
4	EDO	A	605	-	-	0/1/1/1	-

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	607	HI6	O1-N1	-10.65	1.17	1.40
5	B	610	HI6	O1-N1	-10.53	1.17	1.40
5	B	610	HI6	C1-N1	9.46	1.45	1.27
5	A	607	HI6	C1-N1	8.17	1.43	1.27
5	B	610	HI6	C2-N2	6.02	1.43	1.37
5	A	607	HI6	C2-N2	5.17	1.42	1.37
5	A	607	HI6	C11-C14	4.29	1.57	1.50
5	B	610	HI6	C6-N2	4.18	1.43	1.35
5	A	607	HI6	C14-N4	4.10	1.40	1.33
5	B	610	HI6	C11-C14	3.36	1.55	1.50
5	B	610	HI6	C14-N4	3.34	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	607	HI6	C6-N2	3.00	1.41	1.35
5	A	607	HI6	C3-C2	2.64	1.45	1.39
3	B	605[A]	DEP	O1-C1	-2.52	1.38	1.44
5	B	610	HI6	C3-C2	2.51	1.44	1.39
6	B	604	NAG	O5-C1	2.26	1.47	1.43
5	A	607	HI6	C2-C1	-2.22	1.40	1.46
5	B	610	HI6	C2-C1	-2.18	1.41	1.46
5	B	610	HI6	C5-C4	2.14	1.43	1.38
5	A	607	HI6	C9-N3	2.14	1.39	1.34
3	A	604[A]	DEP	O1-C1	-2.14	1.39	1.44

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	610	HI6	O1-N1-C1	10.19	129.85	111.86
5	A	607	HI6	O1-N1-C1	8.60	127.05	111.86
5	A	607	HI6	C2-C1-N1	5.27	127.93	117.75
5	B	610	HI6	C2-C1-N1	3.76	125.02	117.75
5	A	607	HI6	C12-C11-C10	-3.02	114.28	118.59
5	B	610	HI6	C12-C11-C10	-2.77	114.64	118.59
5	A	607	HI6	C13-C12-C11	2.70	123.29	119.44
5	B	610	HI6	C4-C3-C2	2.67	122.93	118.91
5	A	607	HI6	C4-C3-C2	2.56	122.76	118.91
5	B	610	HI6	C9-C10-C11	2.47	122.97	119.44
5	A	607	HI6	C5-C6-N2	2.37	123.77	120.91
5	A	607	HI6	C11-C14-N4	2.03	120.18	117.75

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	607	HI6	O2-C8-N3-C9
5	A	607	HI6	O2-C7-N2-C6
5	A	607	HI6	N1-C1-C2-N2
5	A	607	HI6	N1-C1-C2-C3
3	A	604[A]	DEP	C2-C1-O1-P
5	B	610	HI6	N1-C1-C2-N2
5	B	610	HI6	N1-C1-C2-C3
5	B	610	HI6	C2-C1-N1-O1
3	B	605[A]	DEP	C2-C1-O1-P
7	B	606	PE8	C21-C20-O19-C18
6	B	604	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
7	B	606	PE8	O4-C5-C6-O7
7	B	606	PE8	O19-C20-C21-O22
7	B	606	PE8	O22-C23-C24-O25
6	B	604	NAG	O5-C5-C6-O6
5	A	607	HI6	N3-C8-O2-C7
5	B	610	HI6	N3-C8-O2-C7
7	B	606	PE8	O10-C11-C12-O13
7	B	606	PE8	O16-C17-C18-O19
7	B	606	PE8	C2-C3-O4-C5
7	B	606	PE8	C14-C15-O16-C17
7	B	606	PE8	C5-C6-O7-C8
7	B	606	PE8	C11-C12-O13-C14

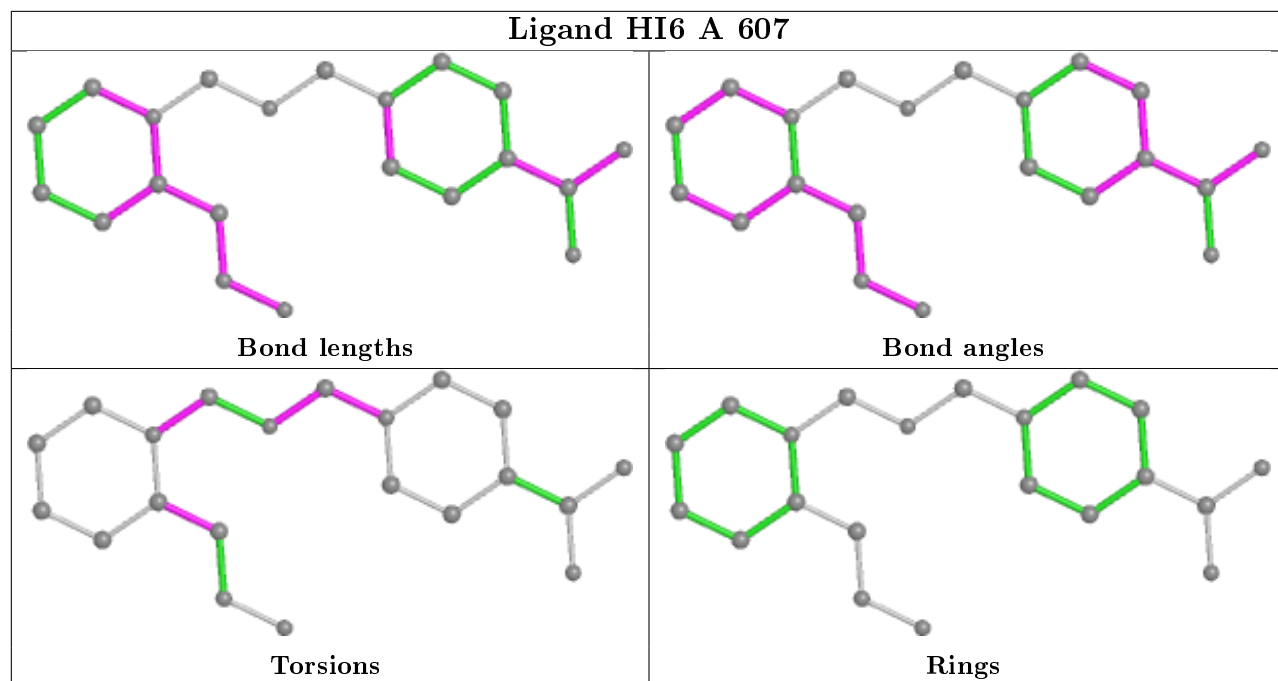
There are no ring outliers.

5 monomers are involved in 12 short contacts:

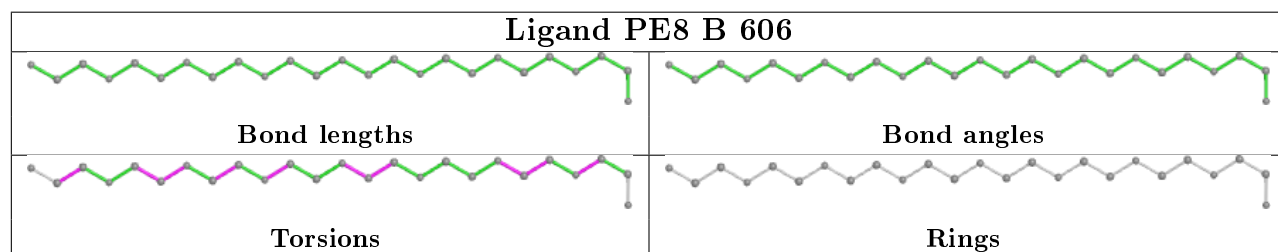
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	607	HI6	3	0
3	A	604[A]	DEP	4	0
7	B	606	PE8	2	0
5	B	610	HI6	1	0
3	B	605[A]	DEP	2	0

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.

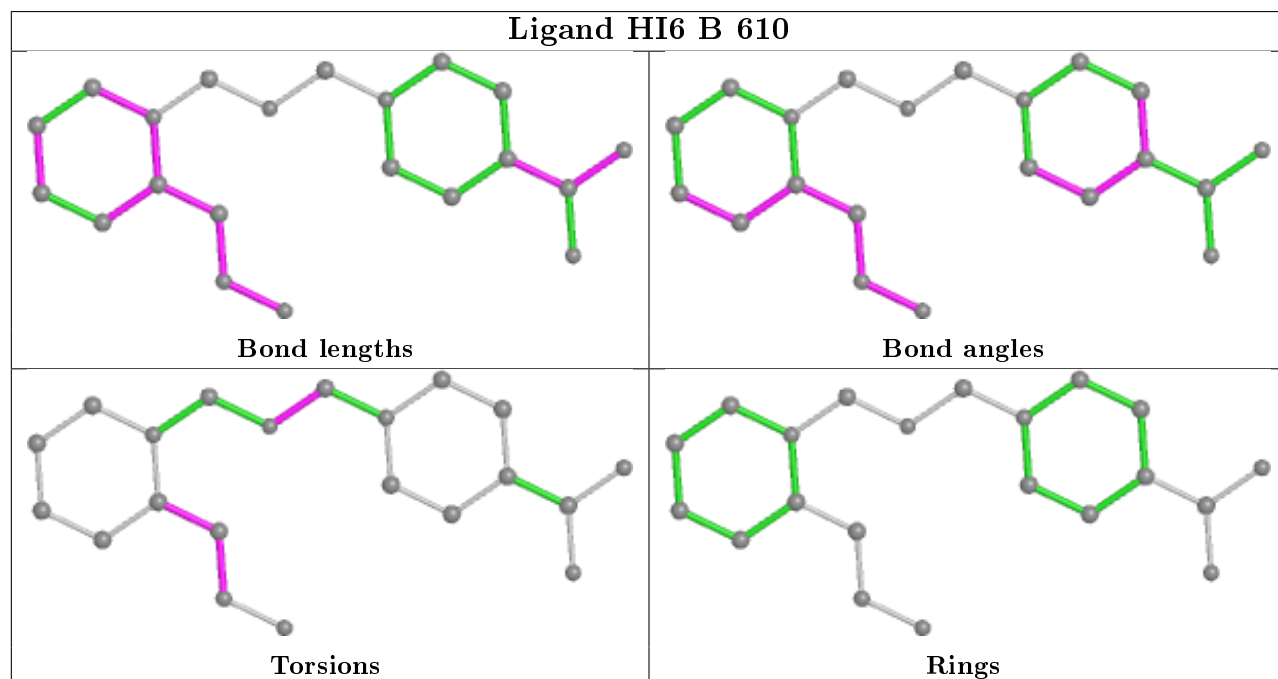
## Ligand HI6 A 607



## Ligand PE8 B 606



## Ligand HI6 B 610



## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	530/542 (97%)	-0.38	6 (1%) 80 79	31, 45, 65, 93	0
1	B	533/542 (98%)	-0.30	8 (1%) 73 72	33, 47, 67, 83	0
All	All	1063/1084 (98%)	-0.34	14 (1%) 77 75	31, 46, 65, 93	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	262	THR	5.4
1	B	497	ALA	3.5
1	B	540	LEU	3.4
1	B	259	PRO	3.4
1	A	540	LEU	3.1
1	B	492	PRO	3.1
1	A	542	ALA	2.9
1	B	264	GLY	2.6
1	A	4	GLU	2.4
1	B	541	SER	2.4
1	B	291	GLN	2.3
1	A	494	ASP	2.1
1	A	541	SER	2.1
1	A	227	LEU	2.0

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

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

### 6.3 Carbohydrates [i](#)

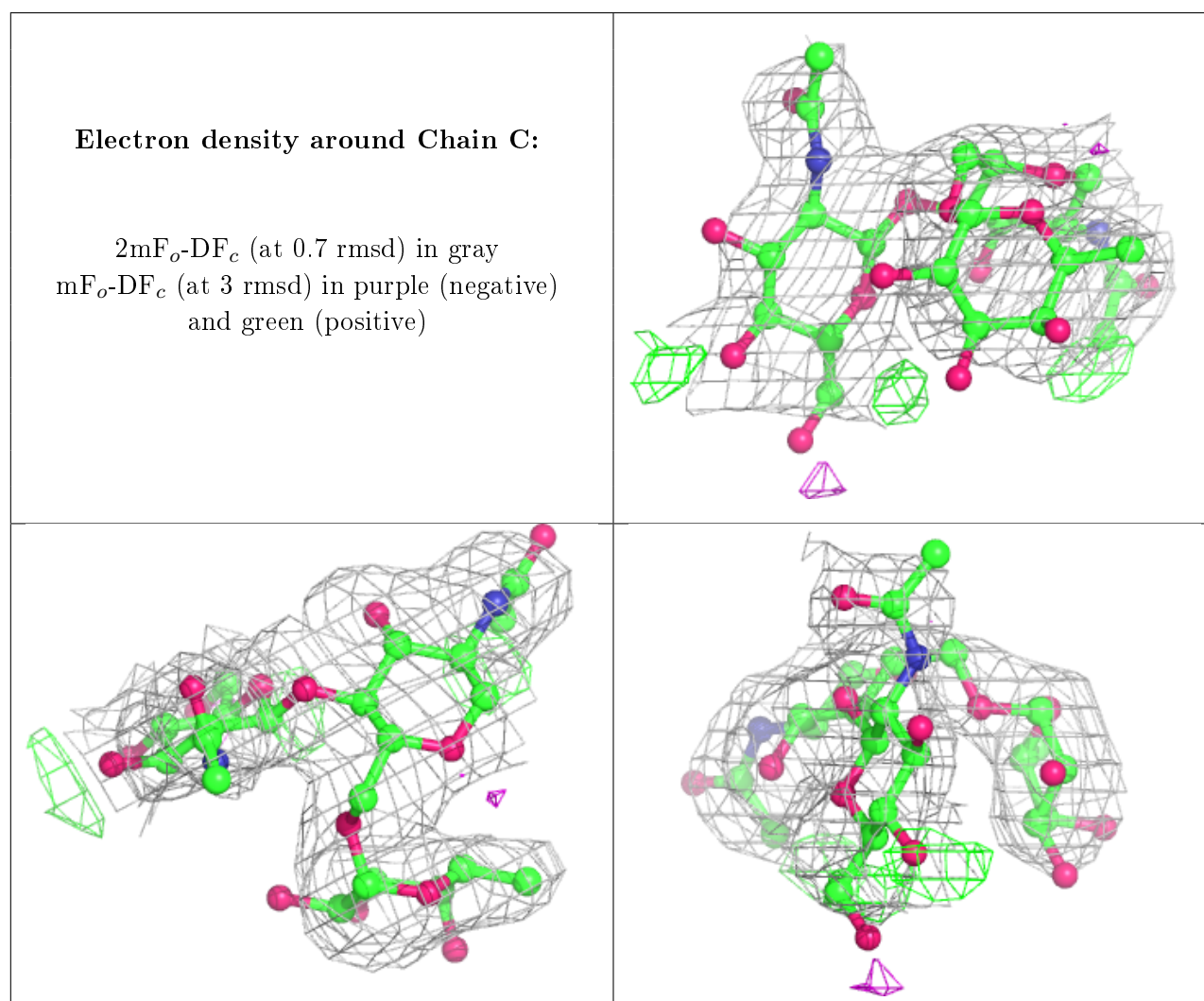
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

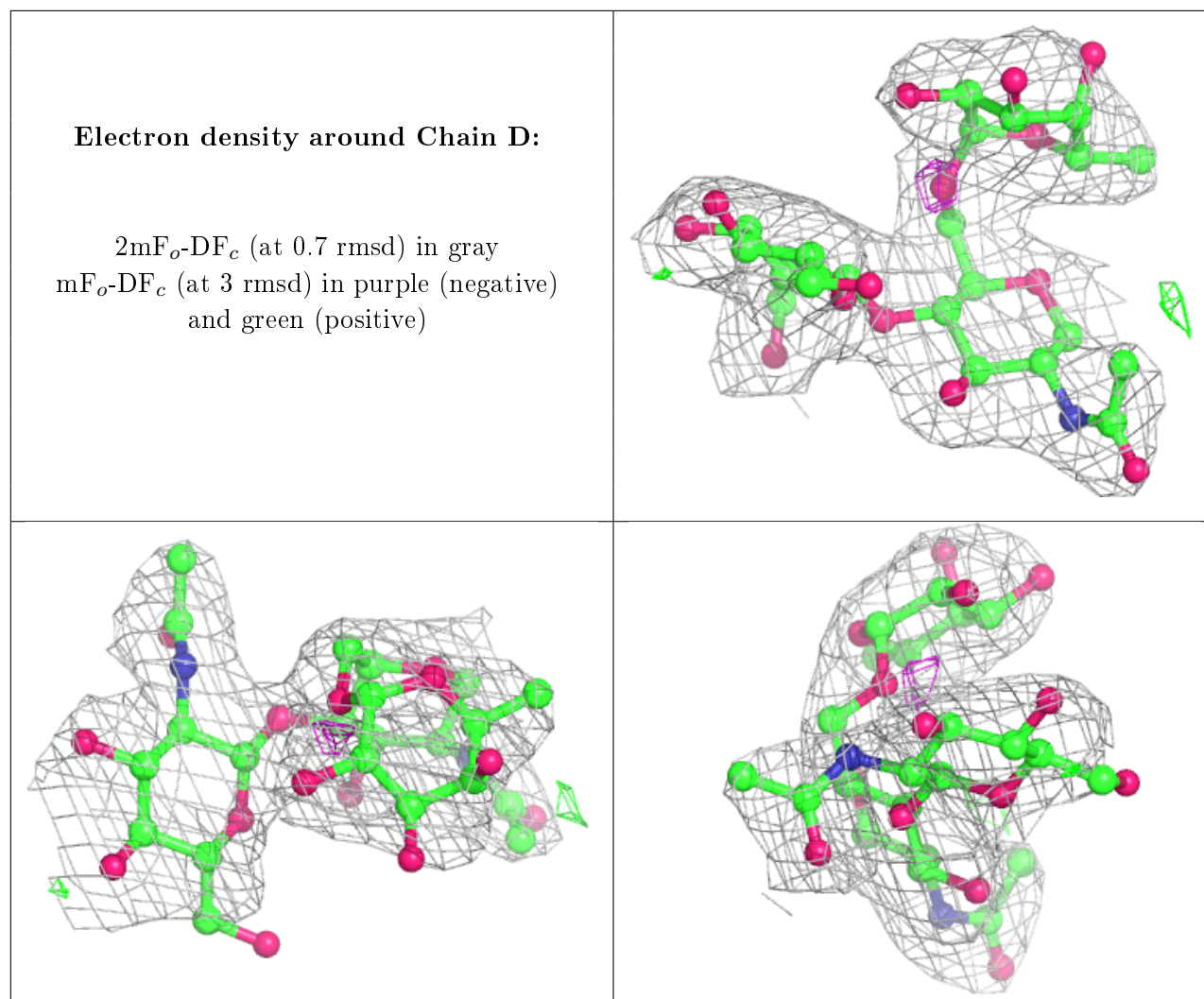


median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	D	2	14/15	0.86	0.33	63,84,95,96	0
2	FUC	C	3	10/11	0.87	0.41	67,87,95,99	0
2	NAG	C	2	14/15	0.87	0.40	66,96,102,103	0
2	NAG	D	1	14/15	0.90	0.23	63,70,84,84	0
2	NAG	C	1	14/15	0.90	0.24	65,74,83,92	0
2	FUC	D	3	10/11	0.91	0.32	66,80,92,94	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.





## 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, 95<sup>th</sup> 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
6	NAG	B	604	14/15	0.66	0.34	80,88,93,99	0
7	PE8	B	606	25/25	0.74	0.34	55,61,67,70	25
5	HI6	A	607	21/21	0.82	0.23	51,62,65,71	21
5	HI6	B	610	21/21	0.87	0.17	50,55,60,68	21
3	DEP	A	604[A]	8/8	0.94	0.28	38,43,45,45	8
4	EDO	B	608	4/4	0.94	0.10	43,46,47,48	0
8	NO3	B	609	4/4	0.95	0.17	45,51,52,54	4
4	EDO	A	606	4/4	0.97	0.11	43,46,46,49	4
4	EDO	B	607	4/4	0.97	0.13	39,42,42,44	4

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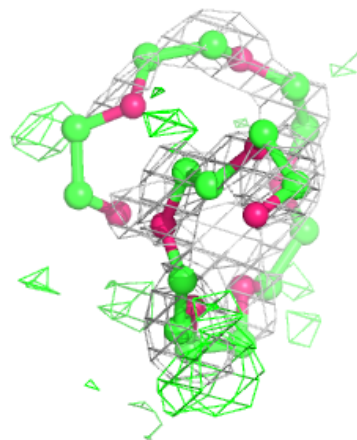
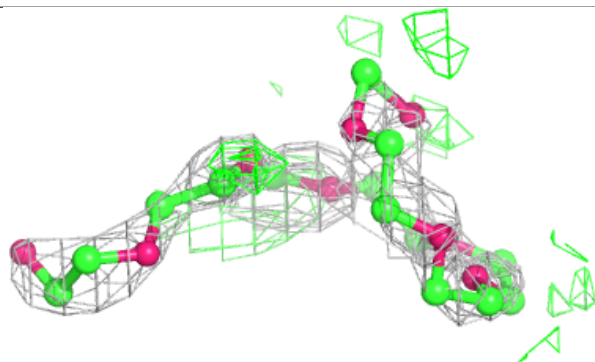
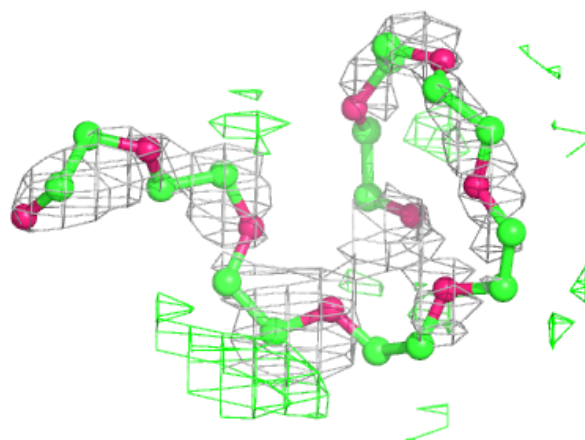
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	DEP	B	605[A]	8/8	0.98	0.27	41,44,47,50	8
4	EDO	A	605	4/4	0.98	0.11	40,43,44,52	0

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.

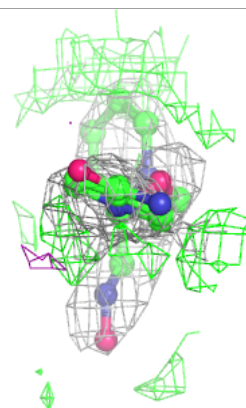
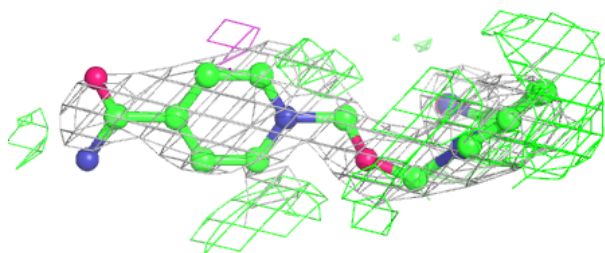
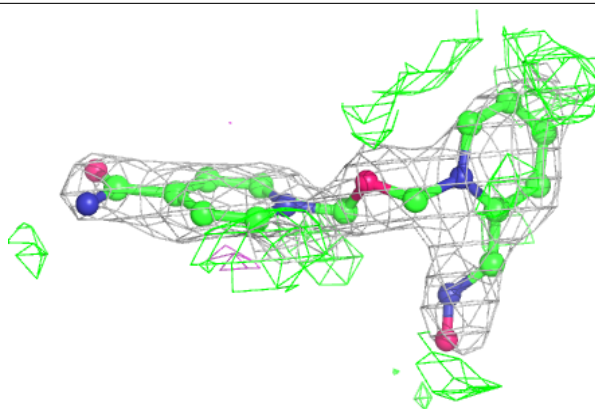
**Electron density around PE8 B 606:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

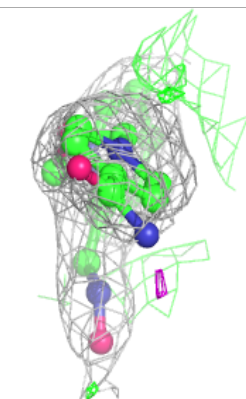
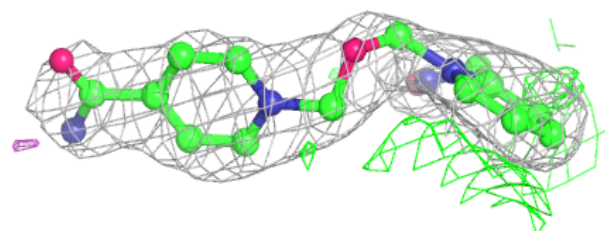
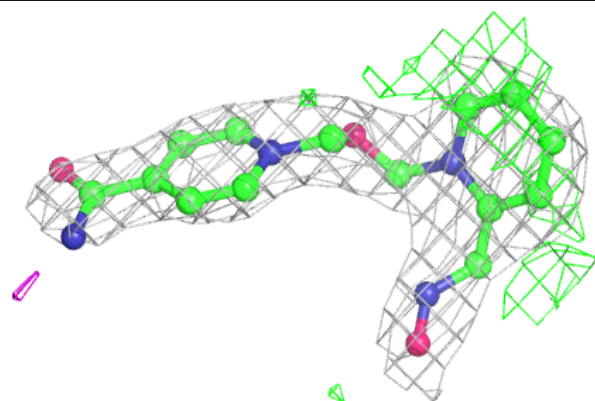


**Electron density around HI6 A 607:**

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

**Electron density around HI6 B 610:**

$2mF_o-DF_c$  (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.