Full wwPDB X-ray Structure Validation Report (i)

Jun 26, 2024 – 07:53 AM EDT

PDB ID	:	6YGF
Title	:	NADase from Aspergillus fumigatus with trapped reaction products
Authors	:	Stromland, O.; Ziegler, M.; Kallio, J.P.
Deposited on	:	2020-03-27
Resolution	:	1.70 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 (i) 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 (i)) were used in the production of this report:

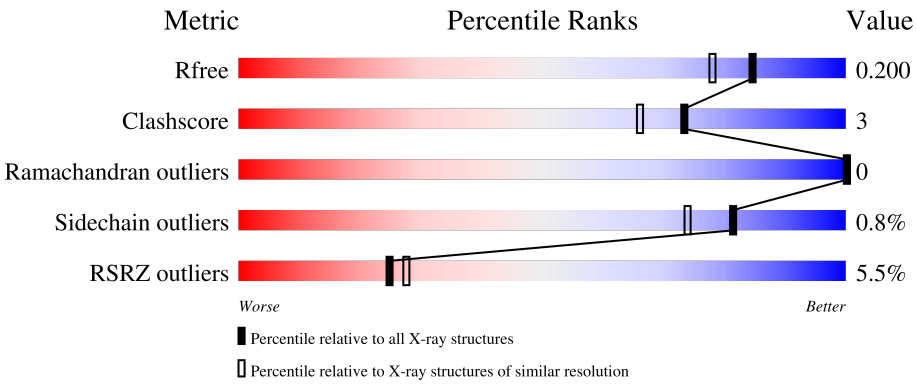
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 <=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	248	4%, 77%, 7%, 16%
1	B	248	5%, 79%, 5%, 16%
2	C	2	100%
2	E	2	50%, 50%
3	D	6	67%, 33%

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Mol	Chain	Length	Quality of chain
4	F	3	67% 33%

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	FUC	C	2	-	-	-	X
3	MAN	D	4	-	-	-	X
4	NAG	F	1	-	-	-	X
4	NAG	F	2	-	-	-	X

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 4173 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 AfNADase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	209	1676	1085	267	317	7	0	3	0
1	A	209	1670	1081	266	316	7	0	2	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	235	ASP	-	expression tag	UNP Q4WL81
B	236	VAL	-	expression tag	UNP Q4WL81
B	237	LEU	-	expression tag	UNP Q4WL81
B	238	PHE	-	expression tag	UNP Q4WL81
B	239	GLN	-	expression tag	UNP Q4WL81
B	240	GLY	-	expression tag	UNP Q4WL81
B	241	PRO	-	expression tag	UNP Q4WL81
B	242	GLY	-	expression tag	UNP Q4WL81
B	243	HIS	-	expression tag	UNP Q4WL81
B	244	HIS	-	expression tag	UNP Q4WL81
B	245	HIS	-	expression tag	UNP Q4WL81
B	246	HIS	-	expression tag	UNP Q4WL81
B	247	HIS	-	expression tag	UNP Q4WL81
B	248	HIS	-	expression tag	UNP Q4WL81
A	235	ASP	-	expression tag	UNP Q4WL81
A	236	VAL	-	expression tag	UNP Q4WL81
A	237	LEU	-	expression tag	UNP Q4WL81
A	238	PHE	-	expression tag	UNP Q4WL81
A	239	GLN	-	expression tag	UNP Q4WL81
A	240	GLY	-	expression tag	UNP Q4WL81
A	241	PRO	-	expression tag	UNP Q4WL81
A	242	GLY	-	expression tag	UNP Q4WL81
A	243	HIS	-	expression tag	UNP Q4WL81
A	244	HIS	-	expression tag	UNP Q4WL81
A	245	HIS	-	expression tag	UNP Q4WL81

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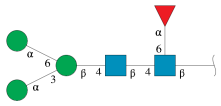
Chain	Residue	Modelled	Actual	Comment	Reference
A	246	HIS	-	expression tag	UNP Q4WL81
A	247	HIS	-	expression tag	UNP Q4WL81
A	248	HIS	-	expression tag	UNP Q4WL81

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

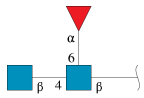
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	2	24	14	1	9	0	0	0
2	E	2	24	14	1	9	0	0	0

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	D	6	71	40	2	29	0	0	0

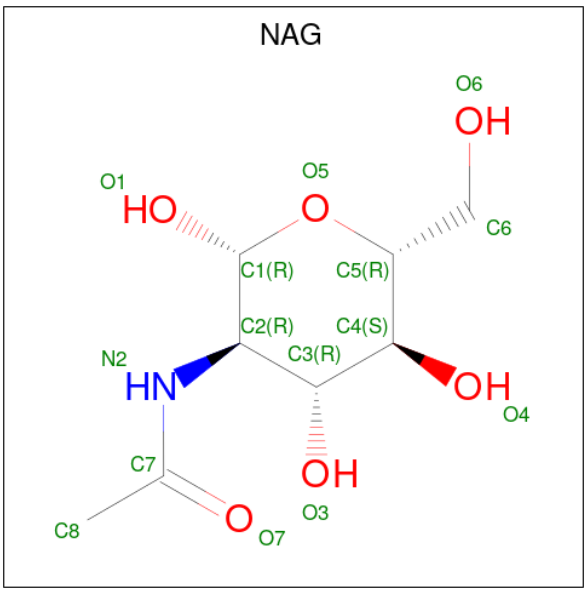
- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



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

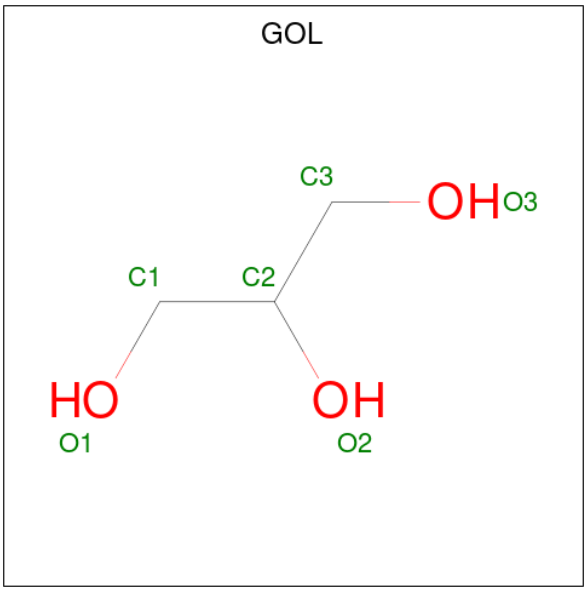
- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:

$C_8H_{15}NO_6$).



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

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	B	1	6	3	3	0	0

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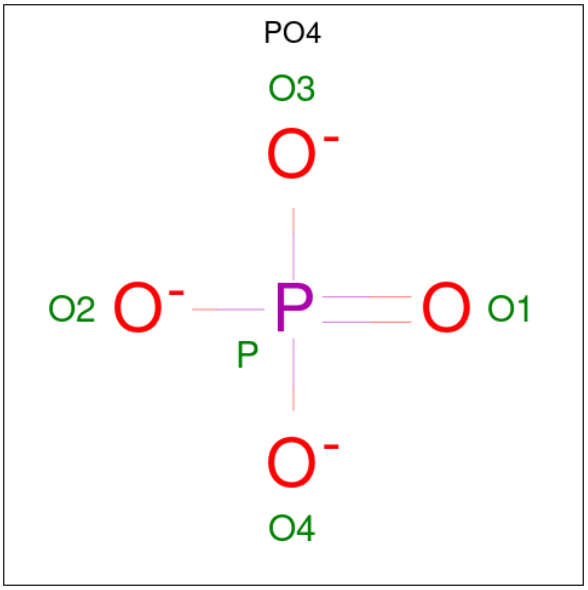
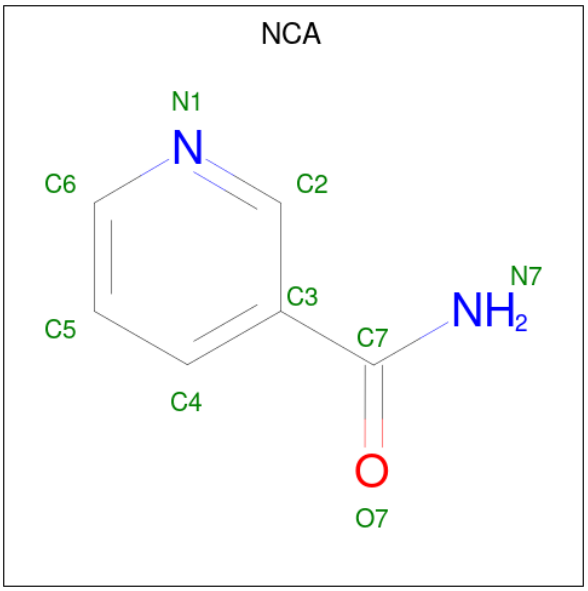
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	B	1	6	3	3	0	0
			Total	C	O		
6	A	1	6	3	3	0	0

- Molecule 7 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



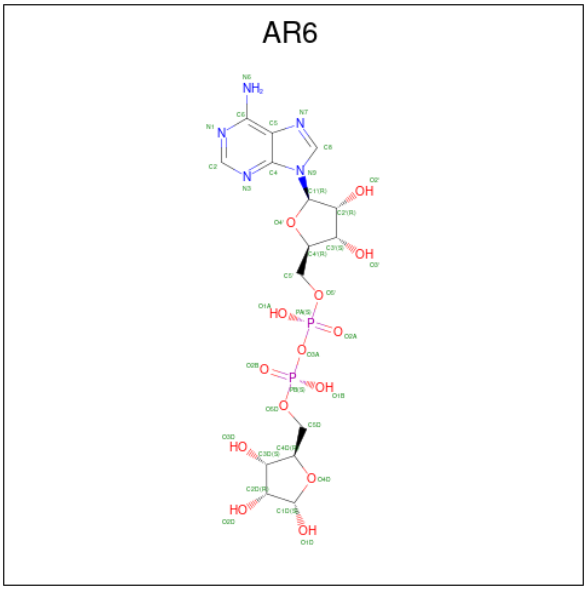
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
7	B	1	5	4	1	0	0
			Total	O	P		
7	A	1	5	4	1	0	0
			Total	O	P		
7	A	1	5	4	1	0	0

- Molecule 8 is NICOTINAMIDE (three-letter code: NCA) (formula: $C_6H_6N_2O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
8	A	1	9	6	2	1	0	0

- Molecule 9 is [(2R,3S,4R,5R)-5-(6-AMINOPURIN-9-YL)-3,4-DIHYDROXY-OXOLAN-2-YL]METHYL [HYDROXY-[[(2R,3S,4R,5S)-3,4,5-TRIHYDROXYOXOLAN-2-YL]METHOXY]PHOSPHORYL] HYDROGEN PHOSPHATE (three-letter code: AR6) (formula: $C_{15}H_{23}N_5O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
9	A	1	36	15	5	14	2	0	0

- Molecule 10 is water.

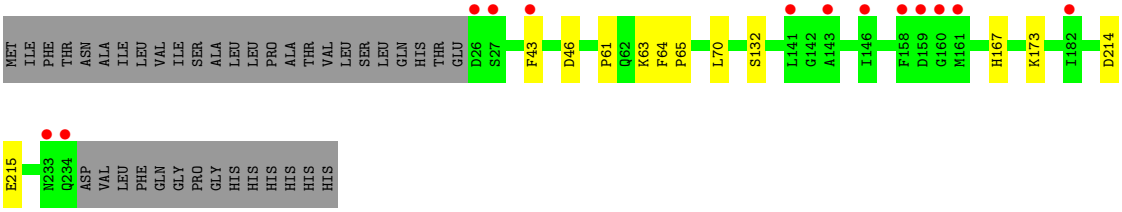
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
10	B	277	280	280	0	3
			Total	O		
10	A	282	284	284	0	2

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.

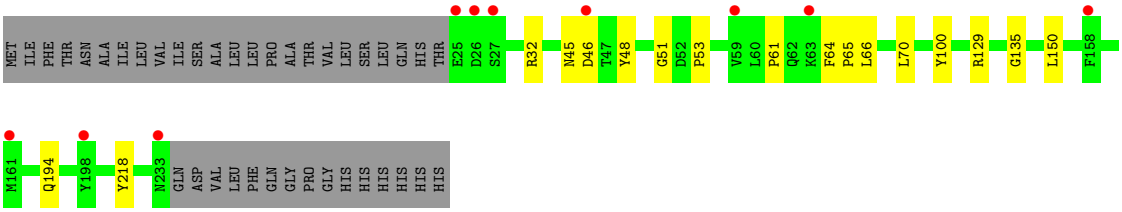
• Molecule 1: AfNADase

Chain B:



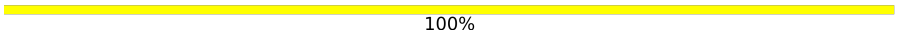
• Molecule 1: AfNADase

Chain A:



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

Chain C:



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

Chain E:

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

Chain D: 67% 33%

NAG1 NAG2 BMA3 MAN4 MAN5 FUC6

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

Chain F: 67% 33%

NAG1 NAG2 FUC3

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	63.81Å 63.81Å 257.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	85.90 – 1.70 42.95 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (85.90-1.70) 99.8 (42.95-1.70)	Depositor EDS
R_{merge}	0.02	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.26 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.169 , 0.201 0.168 , 0.200	Depositor DCC
R_{free} test set	3387 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	27.1	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 49.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	4173	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: NCA, GOL, AR6, FUC, PO4, MAN, BMA, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.37	0/1727	0.55	0/2368
1	B	0.38	0/1733	0.55	0/2376
All	All	0.37	0/3460	0.55	0/4744

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1670	0	1572	13	0
1	B	1676	0	1579	7	0
2	C	24	0	22	0	0
2	E	24	0	22	0	0
3	D	71	0	61	0	0
4	F	38	0	34	0	0
5	A	14	0	13	0	0
5	B	14	0	13	0	0
6	A	6	0	8	0	0
6	B	12	0	16	2	0
7	A	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	5	0	0	1	0
8	A	9	0	6	3	0
9	A	36	0	19	3	0
10	A	284	0	0	3	0
10	B	280	0	0	1	0
All	All	4173	0	3365	23	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 (23) 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)
9:A:408:AR6:O4'	9:A:408:AR6:C1'	1.65	1.10
1:B:167:HIS:HD2	10:B:523:HOH:O	1.85	0.59
1:B:214:ASP:HA	6:B:411:GOL:H32	1.85	0.59
1:A:150:LEU:HD21	8:A:407:NCA:H4	1.87	0.55
8:A:407:NCA:H5	10:A:593:HOH:O	2.08	0.54
1:A:100:TYR:CD1	9:A:408:AR6:H1D	2.44	0.52
1:A:64:PHE:CD1	1:A:65:PRO:HA	2.46	0.50
1:A:64:PHE:CG	1:A:65:PRO:HA	2.48	0.49
1:B:215:GLU:H	6:B:411:GOL:C3	2.27	0.48
1:A:45:ASN:O	1:A:51:GLY:HA2	2.14	0.48
1:A:48:TYR:CG	1:A:53:PRO:HA	2.49	0.47
1:B:63:LYS:HD3	7:B:412:PO4:O2	2.17	0.45
1:A:66:LEU:HD23	1:A:66:LEU:HA	1.80	0.44
1:A:65:PRO:HG3	1:A:218:TYR:HD2	1.83	0.43
1:B:61:PRO:HD2	1:B:70[B]:LEU:HD22	2.01	0.43
1:A:32[A]:ARG:HD3	10:A:517:HOH:O	2.18	0.42
1:B:43:PHE:HZ	1:B:46:ASP:HB3	1.85	0.42
1:B:64:PHE:CD1	1:B:65:PRO:HA	2.54	0.41
1:A:129:ARG:NH2	1:A:135:GLY:HA3	2.34	0.41
1:A:61:PRO:HD2	1:A:70[A]:LEU:HD22	2.03	0.41
1:A:194:GLN:HB3	8:A:407:NCA:H6	2.03	0.41
7:A:411:PO4:O3	10:A:501:HOH:O	2.22	0.41
1:A:100:TYR:CE1	9:A:408:AR6:H1D	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	209/248 (84%)	206 (99%)	3 (1%)	0	100	100
1	B	210/248 (85%)	208 (99%)	2 (1%)	0	100	100
All	All	419/496 (84%)	414 (99%)	5 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	179/211 (85%)	178 (99%)	1 (1%)	86	80
1	B	180/211 (85%)	178 (99%)	2 (1%)	73	63
All	All	359/422 (85%)	356 (99%)	3 (1%)	81	74

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	132	SER
1	B	173	LYS
1	A	46	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

13 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	C	1	2,1	14,14,15	0.31	0	17,19,21	0.81	1 (5%)
2	FUC	C	2	2	10,10,11	0.73	0	14,14,16	0.94	1 (7%)
3	NAG	D	1	3,1	14,14,15	0.39	0	17,19,21	0.53	0
3	NAG	D	2	3	14,14,15	0.59	0	17,19,21	0.43	0
3	BMA	D	3	3	11,11,12	0.63	0	15,15,17	0.77	0
3	MAN	D	4	3	11,11,12	0.78	0	15,15,17	1.01	2 (13%)
3	MAN	D	5	3	11,11,12	0.92	1 (9%)	15,15,17	0.85	1 (6%)
3	FUC	D	6	3	10,10,11	0.82	0	14,14,16	0.86	0
2	NAG	E	1	2,1	14,14,15	0.25	0	17,19,21	0.55	0
2	FUC	E	2	2	10,10,11	0.75	0	14,14,16	0.94	1 (7%)
4	NAG	F	1	4,1	14,14,15	0.41	0	17,19,21	0.59	1 (5%)
4	NAG	F	2	4	14,14,15	0.46	0	17,19,21	0.42	0
4	FUC	F	3	4	10,10,11	0.79	0	14,14,16	0.92	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	2,1	-	1/6/23/26	0/1/1/1

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	5	MAN	O5-C1	-2.28	1.40	1.43

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	4	MAN	C1-O5-C5	2.68	115.82	112.19
2	C	1	NAG	C1-O5-C5	2.46	115.52	112.19
3	D	5	MAN	O2-C2-C3	-2.16	105.81	110.14
3	D	4	MAN	O2-C2-C3	-2.15	105.83	110.14
2	E	2	FUC	C1-O5-C5	2.12	117.58	112.78
2	C	2	FUC	C1-O5-C5	2.08	117.49	112.78
4	F	1	NAG	C1-O5-C5	2.03	114.95	112.19

There are no chirality outliers.

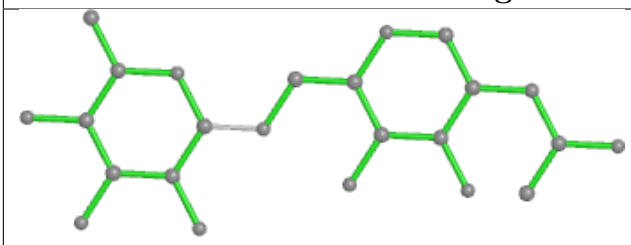
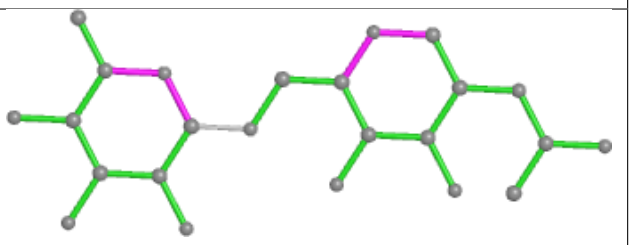
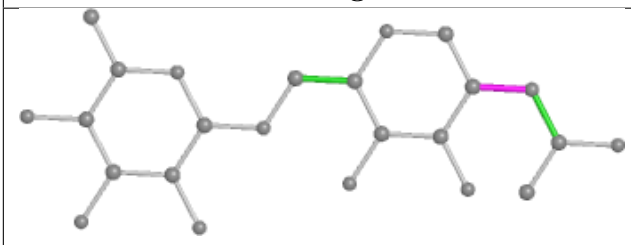
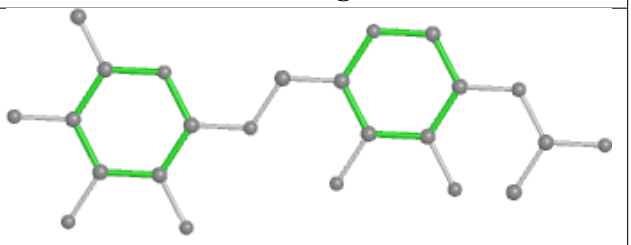
All (8) torsion outliers are listed below:

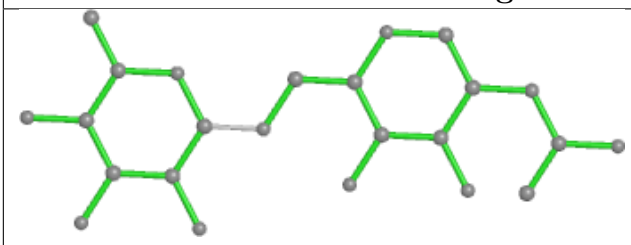
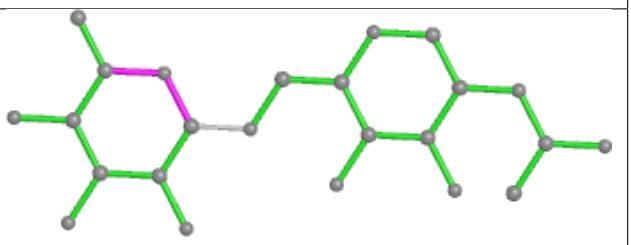
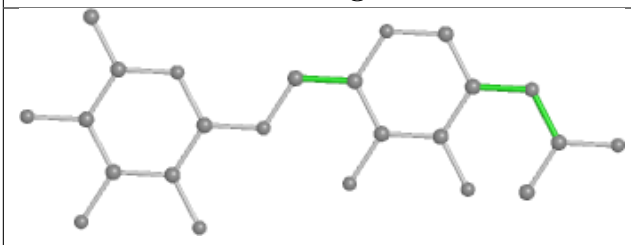
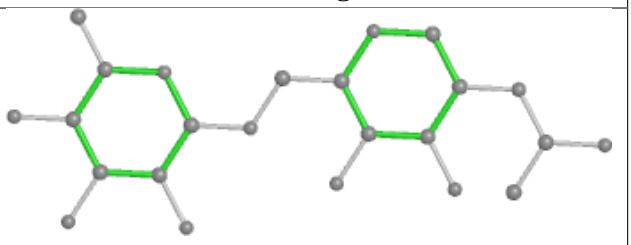
Mol	Chain	Res	Type	Atoms
3	D	5	MAN	O5-C5-C6-O6
4	F	2	NAG	C4-C5-C6-O6
3	D	5	MAN	C4-C5-C6-O6
3	D	4	MAN	O5-C5-C6-O6
4	F	2	NAG	O5-C5-C6-O6
2	C	1	NAG	C3-C2-N2-C7
3	D	4	MAN	C4-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6

There are no ring outliers.

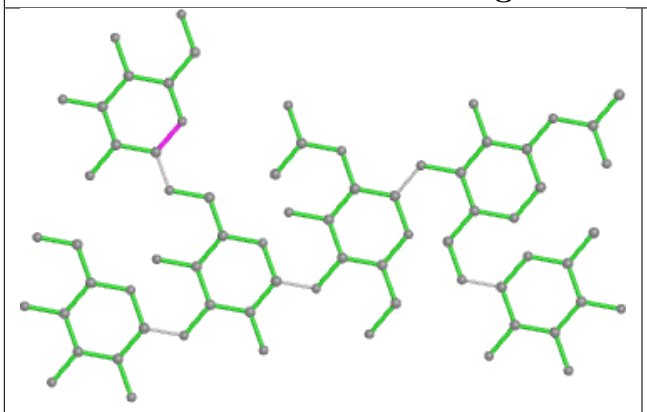
No monomer is involved in short contacts.

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

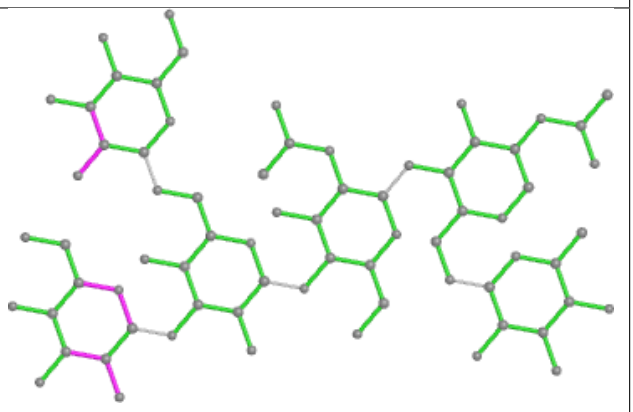
Oligosaccharide Chain C	
 Bond lengths	 Bond angles
 Torsions	 Rings

Oligosaccharide Chain E	
 Bond lengths	 Bond angles
 Torsions	 Rings

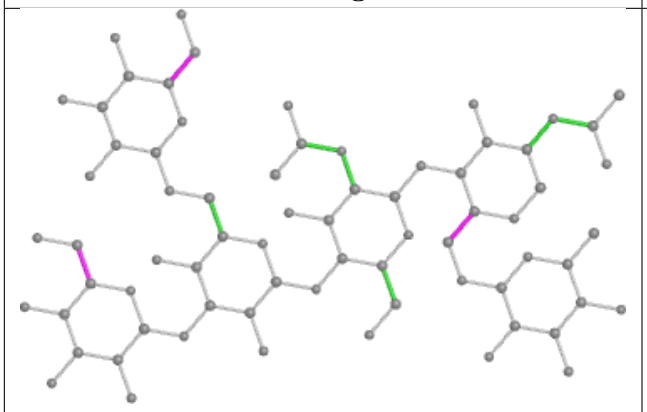
Oligosaccharide Chain D



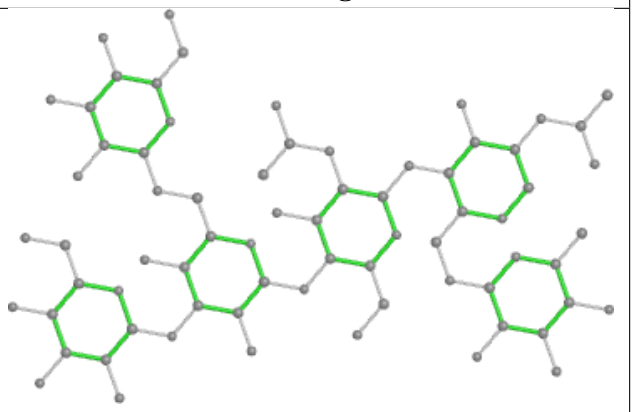
Bond lengths



Bond angles

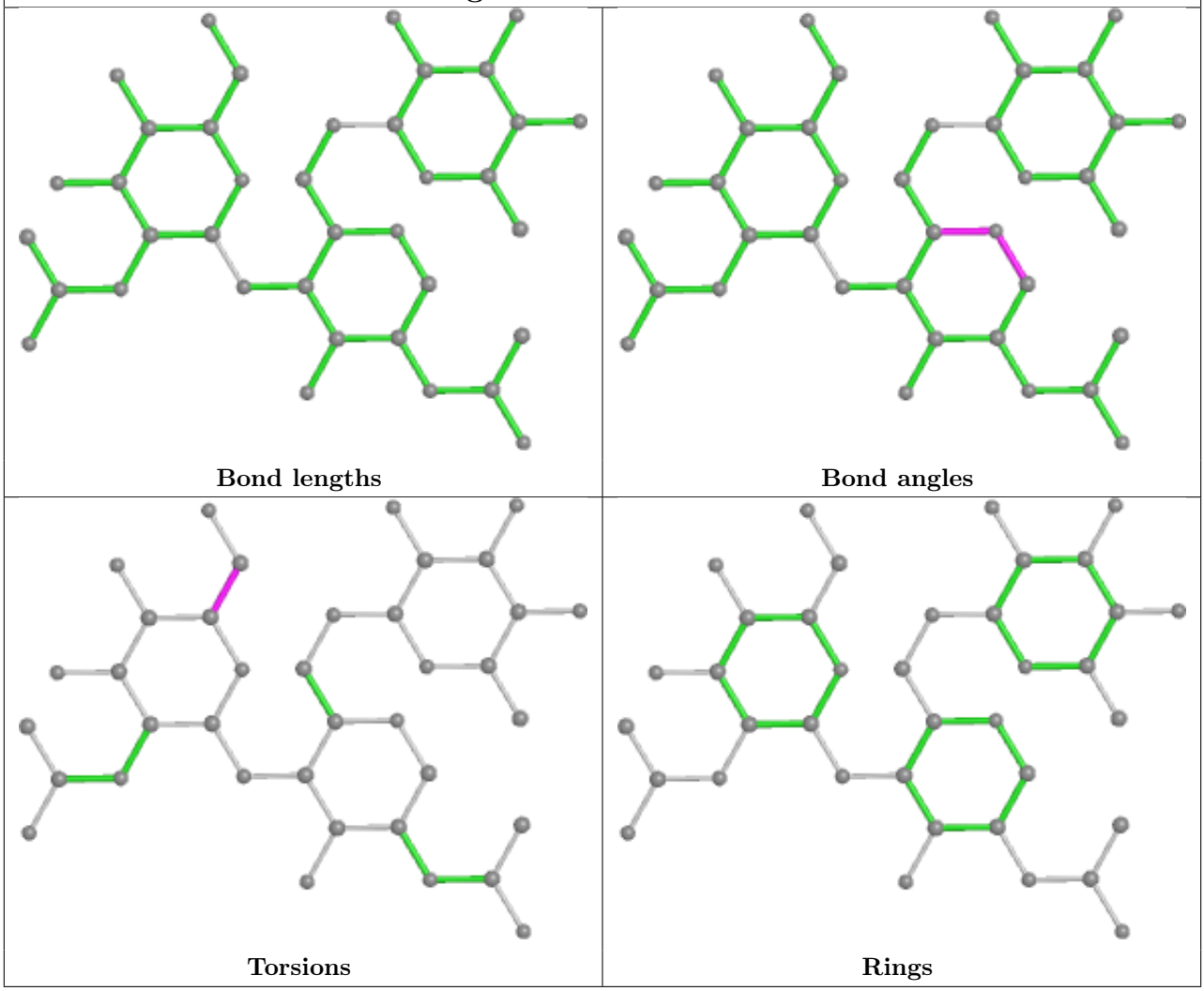


Torsions



Rings

Oligosaccharide Chain F



5.6 Ligand geometry (i)

10 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	NAG	B	409	1	14,14,15	0.17	0	17,19,21	0.41	0
5	NAG	A	406	1	14,14,15	0.30	0	17,19,21	0.46	0
7	PO4	B	412	-	4,4,4	0.92	0	6,6,6	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	GOL	B	411	-	5,5,5	0.86	0	5,5,5	1.03	1 (20%)
7	PO4	A	410	-	4,4,4	0.78	0	6,6,6	0.41	0
8	NCA	A	407	-	9,9,9	2.50	2 (22%)	11,11,11	1.56	2 (18%)
6	GOL	A	409	-	5,5,5	0.90	0	5,5,5	0.87	0
6	GOL	B	410	-	5,5,5	0.94	0	5,5,5	1.03	0
7	PO4	A	411	-	4,4,4	0.86	0	6,6,6	0.47	0
9	AR6	A	408	-	34,39,39	5.45	15 (44%)	40,60,60	1.58	5 (12%)

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	NAG	B	409	1	-	2/6/23/26	0/1/1/1
5	NAG	A	406	1	-	0/6/23/26	0/1/1/1
6	GOL	B	411	-	-	2/4/4/4	-
8	NCA	A	407	-	-	0/4/4/4	0/1/1/1
6	GOL	A	409	-	-	2/4/4/4	-
6	GOL	B	410	-	-	2/4/4/4	-
9	AR6	A	408	-	-	8/18/54/54	0/4/4/4

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	408	AR6	O4'-C1'	17.70	1.65	1.41
9	A	408	AR6	O4D-C1D	15.37	1.61	1.43
9	A	408	AR6	C2'-C1'	-14.01	1.32	1.53
9	A	408	AR6	O4D-C4D	-7.12	1.29	1.45
9	A	408	AR6	C3D-C2D	-6.93	1.34	1.53
8	A	407	NCA	C7-N7	6.34	1.45	1.33
9	A	408	AR6	O4'-C4'	-6.03	1.31	1.45
9	A	408	AR6	C3D-C4D	5.25	1.66	1.53
9	A	408	AR6	O1D-C1D	-4.57	1.25	1.39
9	A	408	AR6	O3'-C3'	-4.52	1.32	1.43
9	A	408	AR6	C6-N6	3.42	1.46	1.34
8	A	407	NCA	O7-C7	-2.71	1.19	1.24
9	A	408	AR6	C2-N1	2.48	1.38	1.33
9	A	408	AR6	O2D-C2D	2.46	1.48	1.43
9	A	408	AR6	PA-O5'	2.36	1.68	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	408	AR6	PB-O5D	2.28	1.68	1.59
9	A	408	AR6	O2'-C2'	2.18	1.48	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	A	408	AR6	N3-C2-N1	-5.63	119.88	128.68
9	A	408	AR6	C5-C6-N6	5.16	128.19	120.35
8	A	407	NCA	C3-C2-N1	-3.23	118.72	123.49
9	A	408	AR6	N6-C6-N1	-3.20	111.94	118.57
9	A	408	AR6	PB-O3A-PA	-2.87	122.99	132.83
8	A	407	NCA	C6-N1-C2	2.80	121.70	116.85
9	A	408	AR6	C3'-C2'-C1'	2.56	104.83	100.98
6	B	411	GOL	C3-C2-C1	-2.10	103.55	111.70

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	410	GOL	O1-C1-C2-C3
9	A	408	AR6	C5D-O5D-PB-O1B
9	A	408	AR6	C5D-O5D-PB-O2B
9	A	408	AR6	C3D-C4D-C5D-O5D
9	A	408	AR6	O4D-C4D-C5D-O5D
6	B	410	GOL	O1-C1-C2-O2
9	A	408	AR6	C3'-C4'-C5'-O5'
5	B	409	NAG	C4-C5-C6-O6
5	B	409	NAG	O5-C5-C6-O6
6	A	409	GOL	O2-C2-C3-O3
9	A	408	AR6	O4'-C4'-C5'-O5'
9	A	408	AR6	PA-O3A-PB-O5D
6	B	411	GOL	O1-C1-C2-C3
6	B	411	GOL	C1-C2-C3-O3
9	A	408	AR6	C5D-O5D-PB-O3A
6	A	409	GOL	C1-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	412	PO4	1	0

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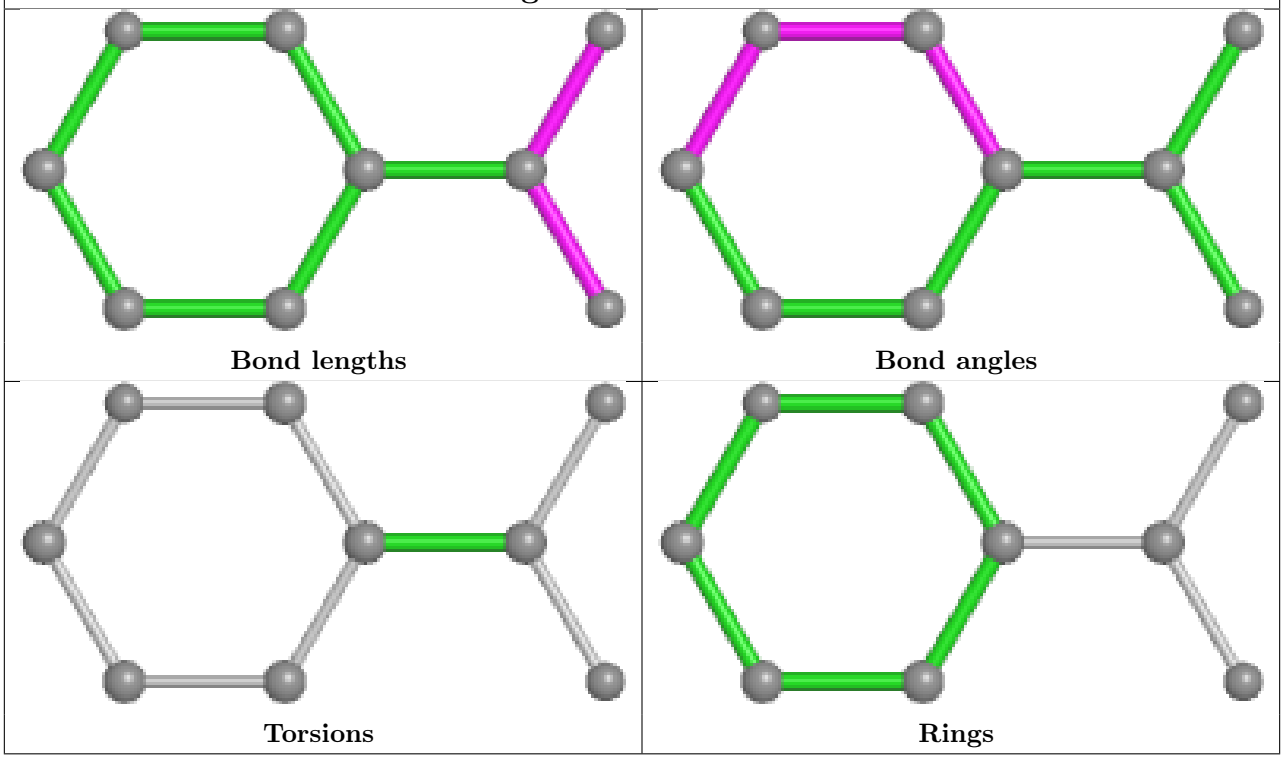
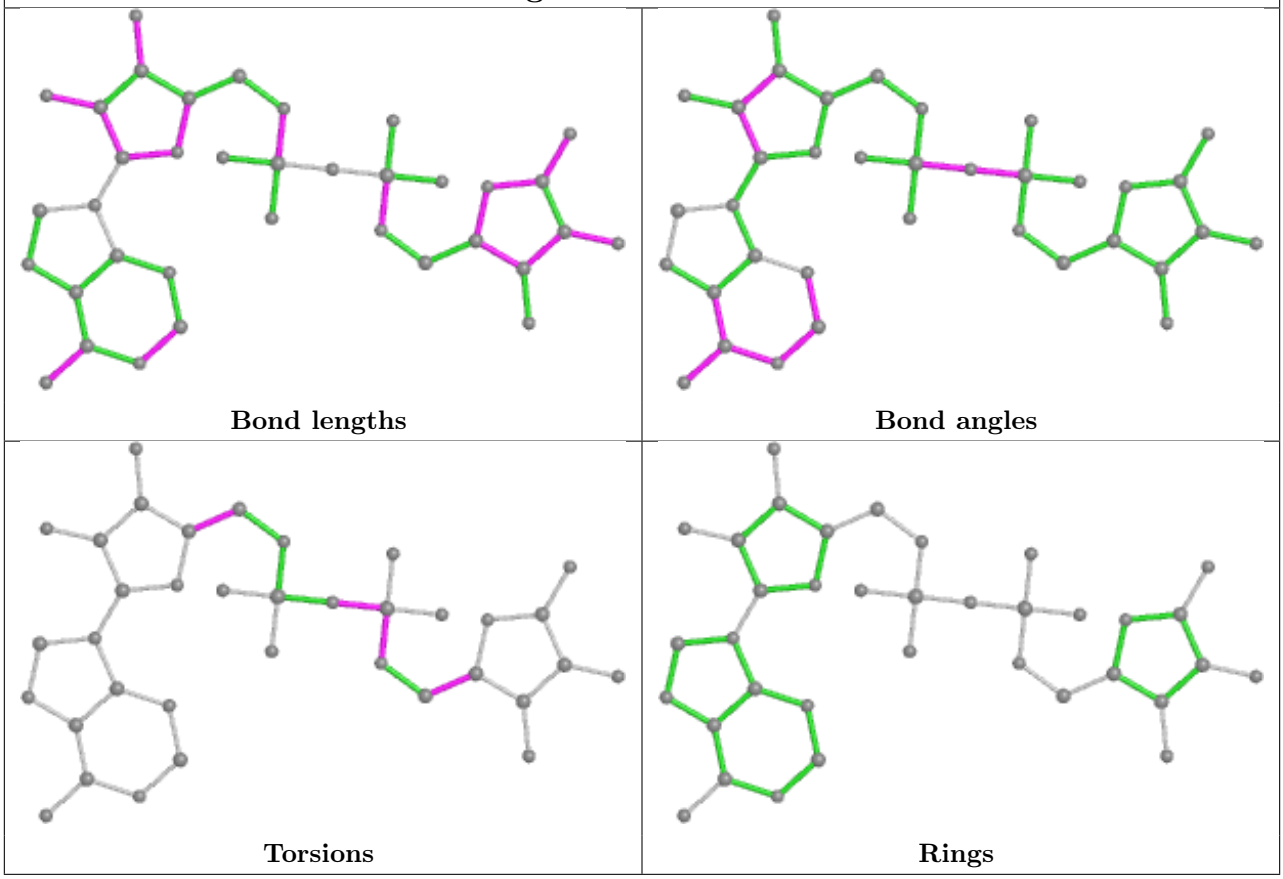
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	411	GOL	2	0
8	A	407	NCA	3	0
7	A	411	PO4	1	0
9	A	408	AR6	3	0

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 then 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 NCA A 407



Ligand AR6 A 408



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	209/248 (84%)	0.17	10 (4%)	30	34	20, 30, 48, 72	0
1	B	209/248 (84%)	0.27	13 (6%)	20	23	20, 28, 47, 74	0
All	All	418/496 (84%)	0.22	23 (5%)	25	27	20, 29, 48, 74	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	26	ASP	6.7
1	B	158	PHE	5.3
1	B	233	ASN	4.3
1	A	158	PHE	3.8
1	B	27	SER	3.6
1	A	46	ASP	3.2
1	B	234	GLN	3.2
1	A	25	GLU	3.0
1	B	146	ILE	3.0
1	A	27	SER	2.7
1	B	43	PHE	2.6
1	B	182	ILE	2.5
1	B	159	ASP	2.5
1	A	59	VAL	2.5
1	A	63	LYS	2.4
1	A	198	TYR	2.4
1	A	26	ASP	2.4
1	A	233	ASN	2.2
1	A	161	MET	2.1
1	B	141	LEU	2.1
1	B	143	ALA	2.1
1	B	160	GLY	2.0
1	B	161	MET	2.0

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

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

6.3 Carbohydrates (i)

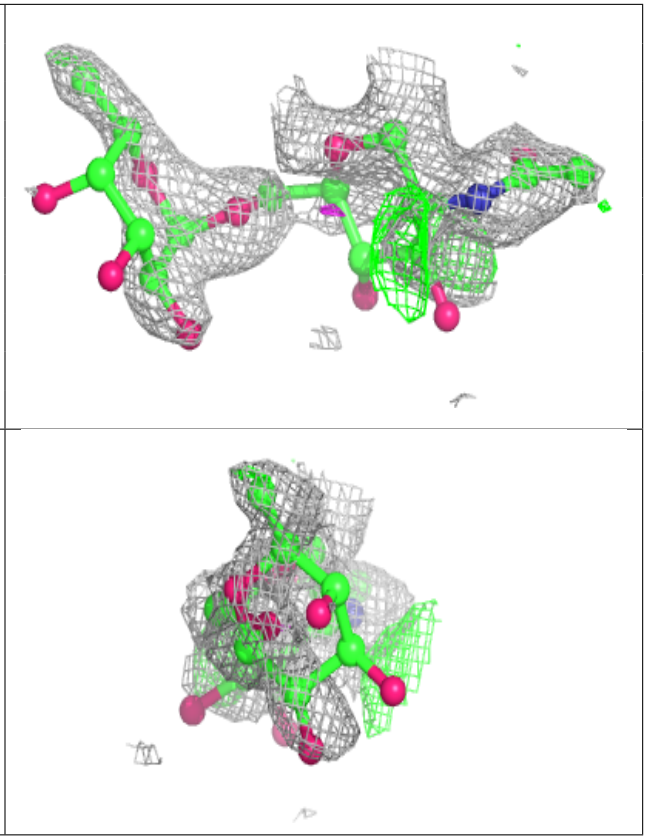
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NAG	F	2	14/15	0.30	0.64	100,110,116,117	0
2	FUC	C	2	10/11	0.39	0.51	86,94,102,104	0
2	NAG	C	1	14/15	0.51	0.37	70,88,100,103	0
3	MAN	D	4	11/12	0.56	0.57	78,92,105,109	0
4	NAG	F	1	14/15	0.61	0.41	51,64,80,96	0
2	FUC	E	2	10/11	0.72	0.37	57,66,75,76	0
3	BMA	D	3	11/12	0.78	0.25	50,53,57,63	0
3	MAN	D	5	11/12	0.80	0.32	66,76,84,87	0
4	FUC	F	3	10/11	0.80	0.33	80,83,89,90	0
3	FUC	D	6	10/11	0.87	0.19	38,45,47,47	0
2	NAG	E	1	14/15	0.89	0.15	28,44,63,68	0
3	NAG	D	2	14/15	0.92	0.27	31,47,57,67	0
3	NAG	D	1	14/15	0.93	0.15	30,36,42,42	0

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

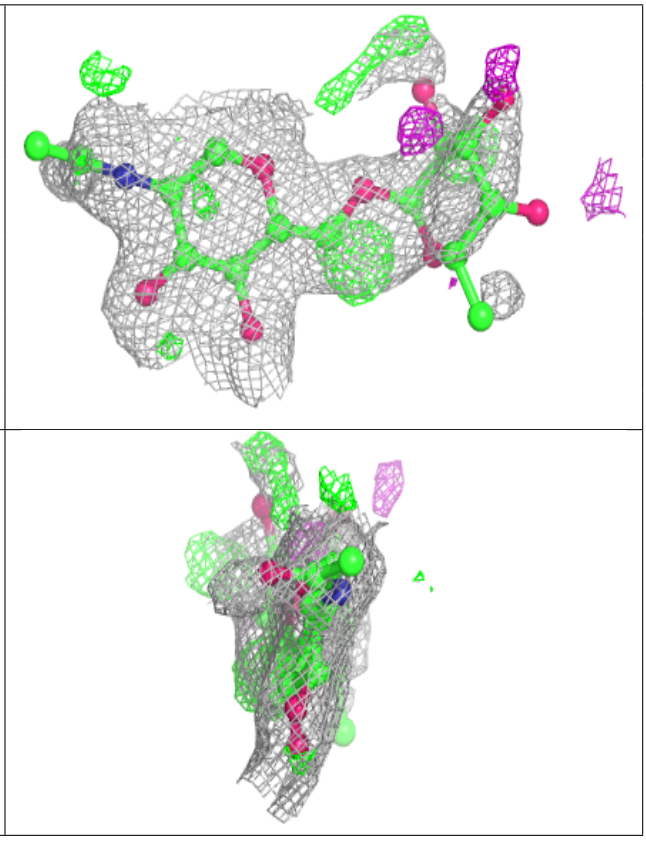
Electron density around Chain C:

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



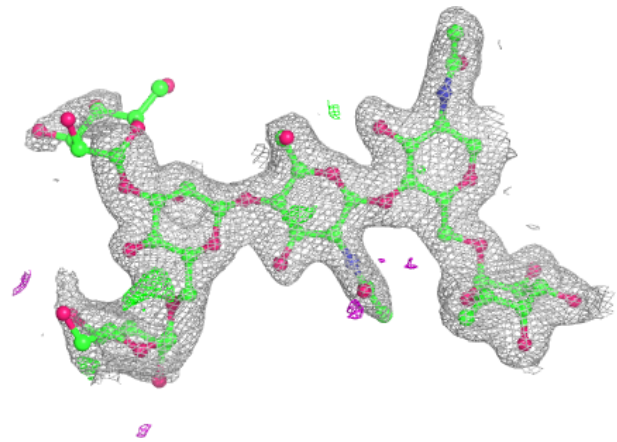
Electron density around Chain E:

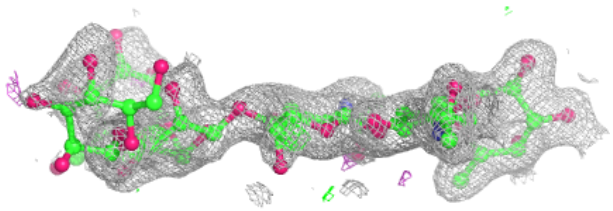
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

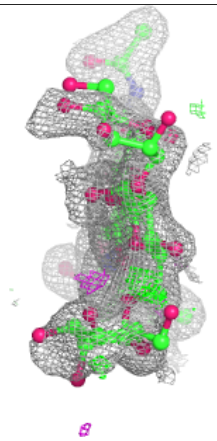


Electron density around Chain D:

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

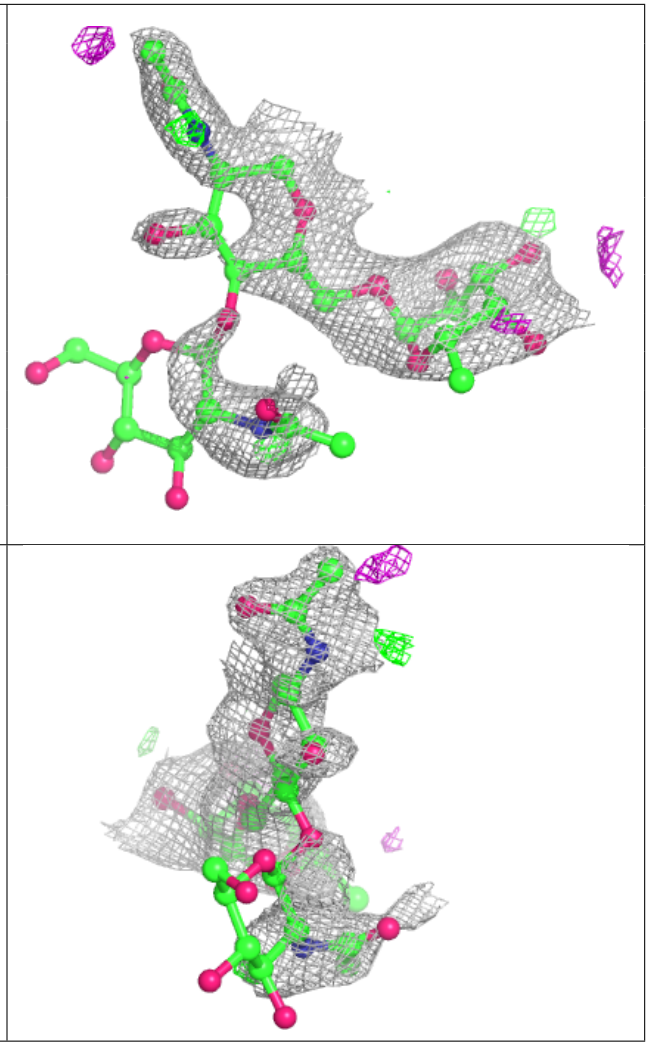






Electron density around Chain F:

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



6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	NAG	A	406	14/15	0.77	0.22	50,63,75,76	0
5	NAG	B	409	14/15	0.80	0.43	66,84,95,96	0
6	GOL	B	411	6/6	0.80	0.19	44,63,67,73	0
6	GOL	B	410	6/6	0.81	0.16	44,57,61,72	0
6	GOL	A	409	6/6	0.81	0.30	47,60,63,68	0
9	AR6	A	408	36/36	0.84	0.20	39,78,88,93	0
7	PO4	A	411	5/5	0.86	0.24	80,81,83,92	0
7	PO4	B	412	5/5	0.88	0.23	93,97,100,100	0
8	NCA	A	407	9/9	0.93	0.10	25,31,37,37	0

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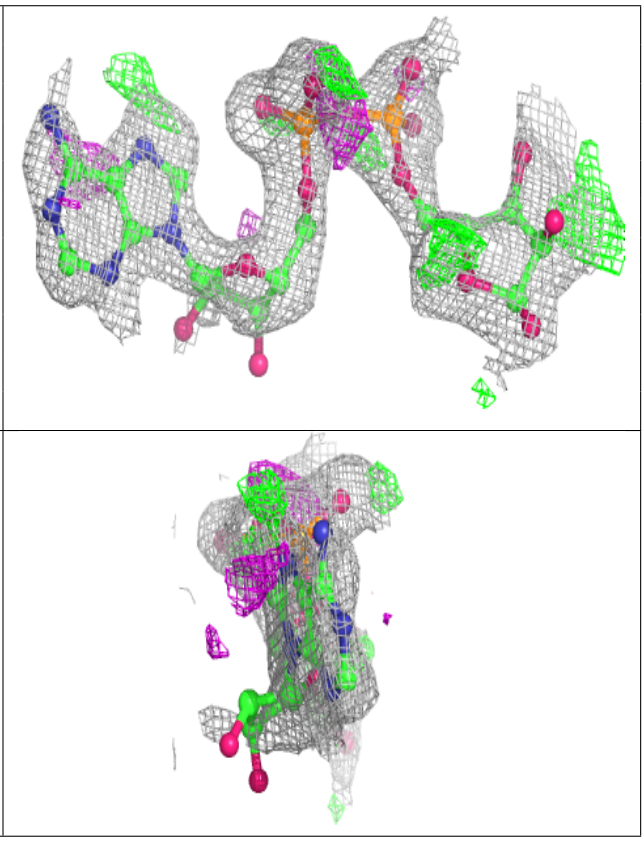
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
7	PO4	A	410	5/5	0.95	0.33	42,48,53,55	0

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.

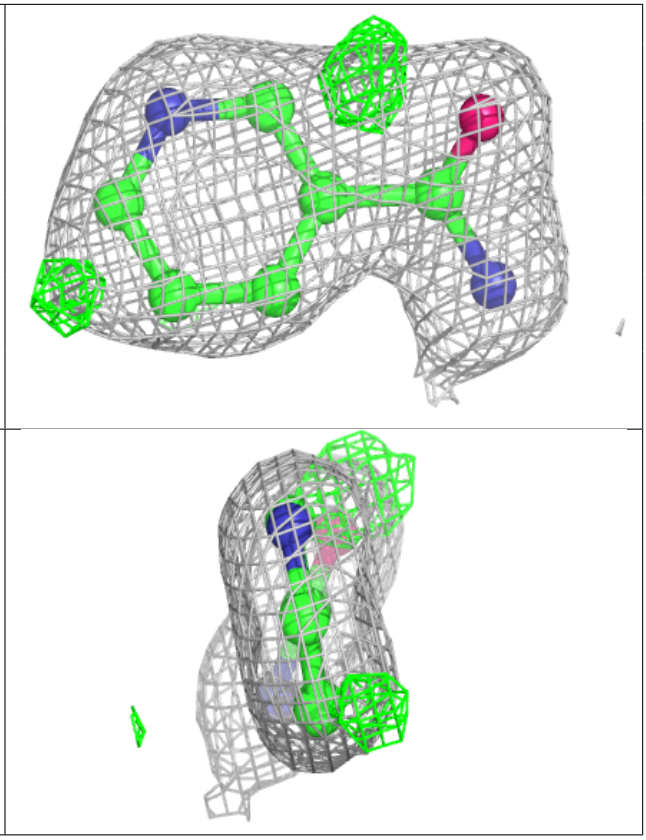
Electron density around AR6 A 408:

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 NCA A 407:

$2mF_o$-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.