wwPDB X-ray Structure Validation Summary Report (i)

Jun 11, 2024 – 09:19 PM EDT

PDB ID	:	1F73
Title	:	CRYSTAL STRUCTURE ANALYSIS OF N-ACETYLNEURAMINATE LYASE FROM HAEMOPHILUS INFLUENZAE: CRYSTAL FORM III IN COMPLEX WITH SIALIC ACID ALDITOL
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Deposited on	:	2000-06-25
Resolution	:	1.95 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (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:

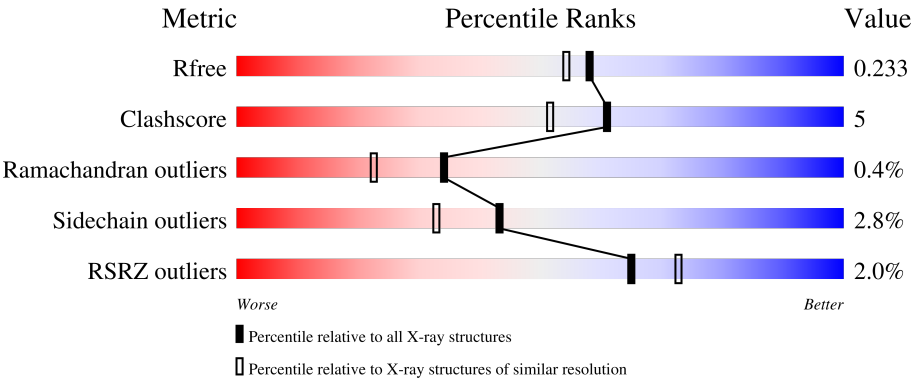
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	293	81% 16%
1	B	293	82% 14%
1	C	293	81% 15%
1	D	293	80% 15%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9738 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.

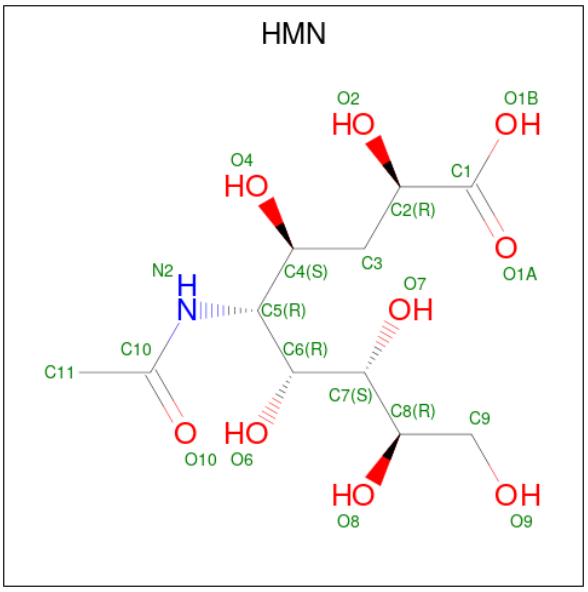
- Molecule 1 is a protein called N-ACETYL NEURAMINATE LYASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	1	0
			2258	1453	369	426	10			
1	B	288	Total	C	N	O	S	0	0	0
			2253	1450	368	425	10			
1	C	288	Total	C	N	O	S	0	1	0
			2257	1453	369	425	10			
1	D	288	Total	C	N	O	S	0	2	0
			2261	1455	369	427	10			

There are 16 discrepancies between the modelled and reference sequences:

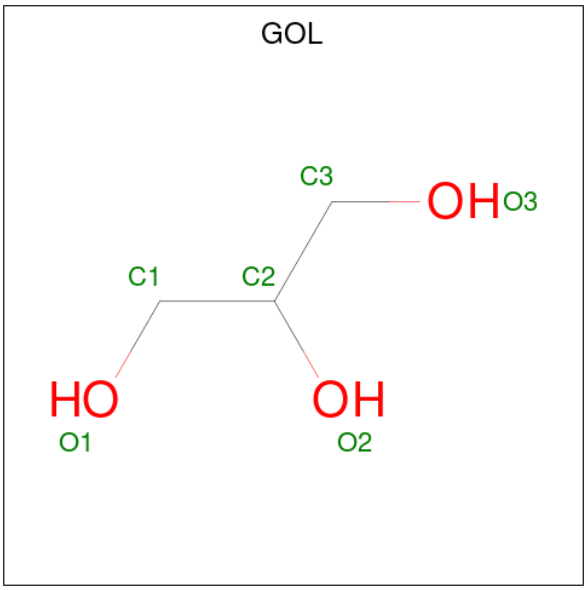
Chain	Residue	Modelled	Actual	Comment	Reference
A	131	SER	ASN	SEE REMARK 999	UNP P44539
A	229	LYS	ALA	SEE REMARK 999	UNP P44539
A	278	ALA	GLU	SEE REMARK 999	UNP P44539
A	281	VAL	LEU	SEE REMARK 999	UNP P44539
B	131	SER	ASN	SEE REMARK 999	UNP P44539
B	229	LYS	ALA	SEE REMARK 999	UNP P44539
B	278	ALA	GLU	SEE REMARK 999	UNP P44539
B	281	VAL	LEU	SEE REMARK 999	UNP P44539
C	131	SER	ASN	SEE REMARK 999	UNP P44539
C	229	LYS	ALA	SEE REMARK 999	UNP P44539
C	278	ALA	GLU	SEE REMARK 999	UNP P44539
C	281	VAL	LEU	SEE REMARK 999	UNP P44539
D	131	SER	ASN	SEE REMARK 999	UNP P44539
D	229	LYS	ALA	SEE REMARK 999	UNP P44539
D	278	ALA	GLU	SEE REMARK 999	UNP P44539
D	281	VAL	LEU	SEE REMARK 999	UNP P44539

- Molecule 2 is 2,4,6,7,8,9-HEXAHYDROXY-5-METHYLCARBOXAMIDO NONANOIC ACID (three-letter code: HMN) (formula: $C_{11}H_{21}NO_9$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 21 11 1 9	0	0
2	B	1	Total C N O 21 11 1 9	0	0
2	C	1	Total C N O 21 11 1 9	0	0
2	D	1	Total C N O 21 11 1 9	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is water.

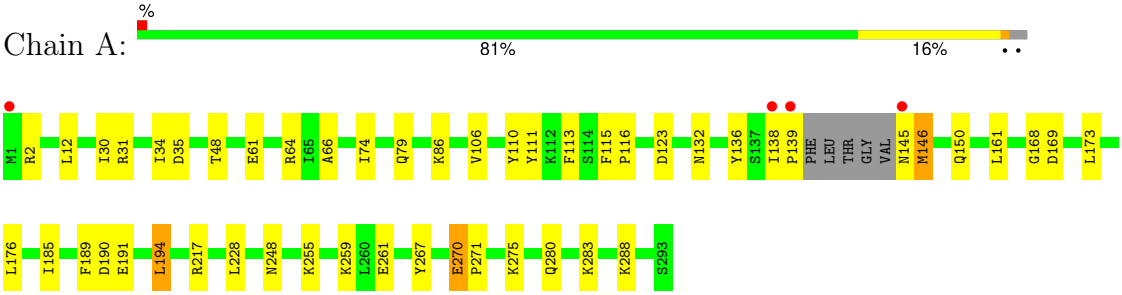
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	112	Total O 112 112	0	0
4	B	171	Total O 171 171	0	0
4	C	164	Total O 164 164	0	0
4	D	172	Total O 172 172	0	0

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.

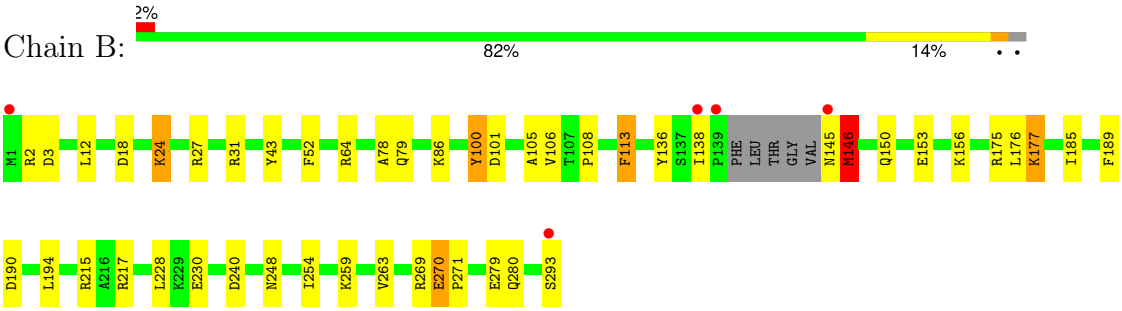
• Molecule 1: N-ACETYL NEURAMINATE LYASE

Chain A:



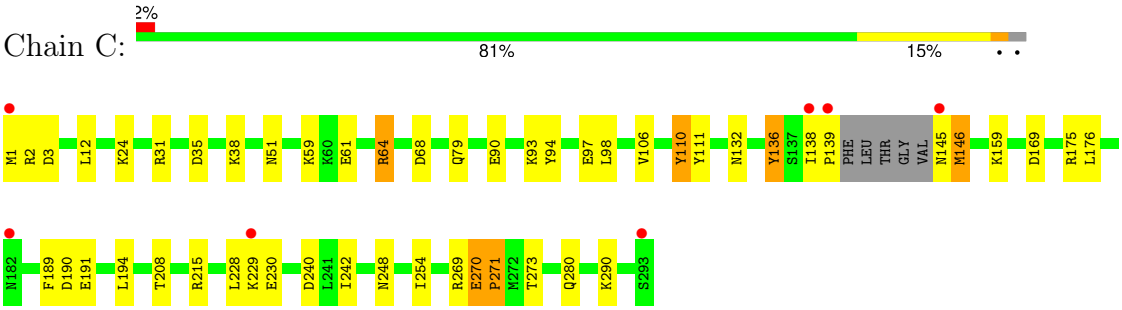
• Molecule 1: N-ACETYL NEURAMINATE LYASE

Chain B:



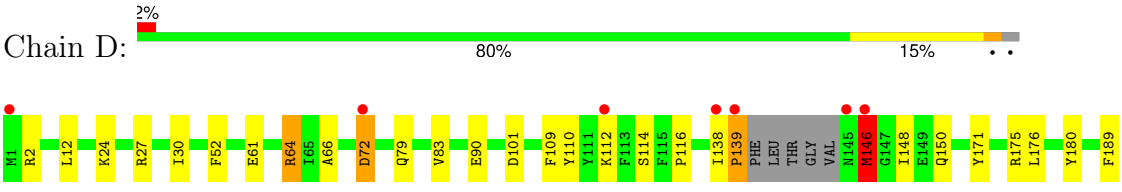
• Molecule 1: N-ACETYL NEURAMINATE LYASE

Chain C:



• Molecule 1: N-ACETYL NEURAMINATE LYASE

Chain D:




D190
T208
R215
A216
R217
L228
D240
L241
I242
N248
I254
E261
Y267
C268
R269
E270
P271
K275
A276
T277
A278
E279
Q280
V281
A282
K283
D286
L287
K288
A289
K290
F291
L292
S293

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	81.55Å 116.73Å 129.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.95 19.91 – 1.95	Depositor EDS
% Data completeness (in resolution range)	97.1 (20.00-1.95) 95.7 (19.91-1.95)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.79 (at 1.94Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.201 , 0.256 0.187 , 0.233	Depositor DCC
R_{free} test set	8772 reflections (9.98%)	wwPDB-VP
Wilson B-factor (Å^2)	21.2	Xtriage
Anisotropy	0.170	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 54.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	9738	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.10 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.1037e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HMN, GOL

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	0.59	0/2300	1.31	13/3092 (0.4%)
1	B	0.63	0/2291	1.39	23/3080 (0.7%)
1	C	0.63	0/2300	1.40	28/3091 (0.9%)
1	D	0.61	0/2309	1.39	25/3103 (0.8%)
All	All	0.62	0/9200	1.37	89/12366 (0.7%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	8

There are no bond length outliers.

The worst 5 of 89 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	269	ARG	NE-CZ-NH2	-14.53	113.04	120.30
1	D	269	ARG	NE-CZ-NH1	12.82	126.71	120.30
1	C	110	TYR	CB-CG-CD2	11.43	127.86	121.00
1	B	269	ARG	NE-CZ-NH1	11.39	126.00	120.30
1	D	271	PRO	N-CA-CB	11.00	116.50	103.30

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	270	GLU	Peptide,Mainchain
1	B	270	GLU	Peptide,Mainchain
1	C	270	GLU	Peptide,Mainchain
1	D	270	GLU	Peptide,Mainchain

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	2258	0	2296	24	0
1	B	2253	0	2292	15	0
1	C	2257	0	2301	25	0
1	D	2261	0	2303	28	0
2	A	21	0	20	0	0
2	B	21	0	20	0	0
2	C	21	0	20	0	0
2	D	21	0	20	0	0
3	B	6	0	8	2	0
4	A	112	0	0	0	0
4	B	171	0	0	2	0
4	C	164	0	0	3	0
4	D	172	0	0	1	0
All	All	9738	0	9280	83	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 5.

The worst 5 of 83 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:228:LEU:HD11	1:D:228:LEU:HD21	1.53	0.91
1:A:248:ASN:HB2	1:A:283:LYS:HE2	1.59	0.84
1:C:138:ILE:HB	1:C:139:PRO:HD2	1.62	0.81
1:D:290[A]:LYS:HG2	1:D:291:PHE:CZ	2.18	0.79
1:B:248:ASN:HD21	1:B:280:GLN:HA	1.55	0.70

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	285/293 (97%)	277 (97%)	5 (2%)	3 (1%)	14 5
1	B	284/293 (97%)	276 (97%)	7 (2%)	1 (0%)	34 22
1	C	285/293 (97%)	276 (97%)	8 (3%)	1 (0%)	34 22
1	D	286/293 (98%)	278 (97%)	8 (3%)	0	100 100
All	All	1140/1172 (97%)	1107 (97%)	28 (2%)	5 (0%)	34 22

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	146	MET
1	B	146	MET
1	C	146	MET
1	A	110	TYR
1	A	168	GLY

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	239/242 (99%)	234 (98%)	5 (2%)	53 46
1	B	238/242 (98%)	229 (96%)	9 (4%)	33 21
1	C	239/242 (99%)	235 (98%)	4 (2%)	60 55
1	D	240/242 (99%)	231 (96%)	9 (4%)	33 21
All	All	956/968 (99%)	929 (97%)	27 (3%)	43 33

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	24	LYS
1	C	189	PHE
1	D	176	LEU
1	C	176	LEU
1	D	24	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	248	ASN
1	C	248	ASN
1	C	51	ASN
1	B	248	ASN
1	C	120	HIS

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)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

5 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	$\#\|Z\|>2$
2	HMN	C	702	-	20,20,20	0.75	0	21,27,27	1.75	4 (19%)
2	HMN	A	700	-	20,20,20	0.78	0	21,27,27	1.34	4 (19%)
3	GOL	B	704	-	5,5,5	0.28	0	5,5,5	0.63	0
2	HMN	B	701	-	20,20,20	0.82	1 (5%)	21,27,27	1.51	4 (19%)
2	HMN	D	703	-	20,20,20	0.86	0	21,27,27	1.38	4 (19%)

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	HMN	C	702	-	-	3/30/30/30	-
2	HMN	A	700	-	-	3/30/30/30	-
3	GOL	B	704	-	-	3/4/4/4	-
2	HMN	B	701	-	-	3/30/30/30	-
2	HMN	D	703	-	-	3/30/30/30	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	HMN	O1B-C1	-2.13	1.23	1.30

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	702	HMN	C9-C8-C7	-4.22	103.57	112.17
2	B	701	HMN	O1B-C1-C2	3.89	120.97	112.74
2	C	702	HMN	O1B-C1-C2	3.58	120.32	112.74
2	C	702	HMN	O10-C10-C11	-2.94	116.82	122.05
2	A	700	HMN	C9-C8-C7	-2.78	106.51	112.17

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	704	GOL	C1-C2-C3-O3
3	B	704	GOL	O2-C2-C3-O3
2	C	702	HMN	O8-C8-C9-O9

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Mol	Chain	Res	Type	Atoms
2	D	703	HMN	O1B-C1-C2-O2
3	B	704	GOL	O1-C1-C2-O2

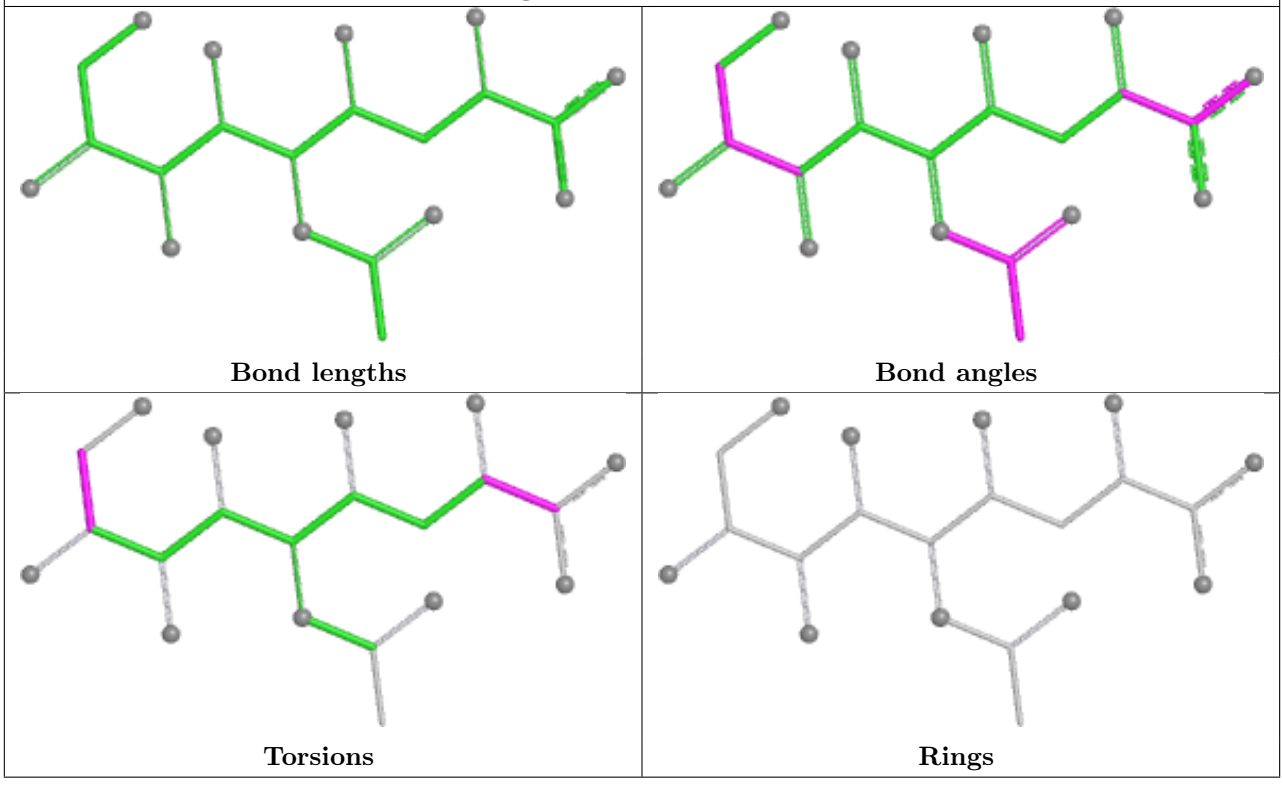
There are no ring outliers.

1 monomer is involved in 2 short contacts:

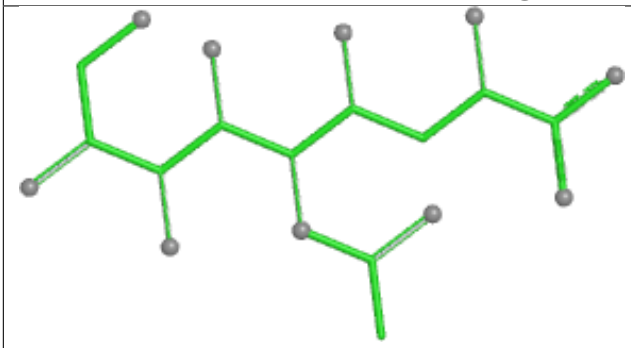
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	704	GOL	2	0

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 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.

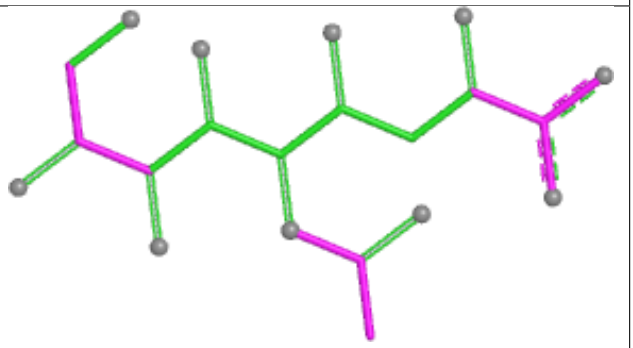
Ligand HMN C 702



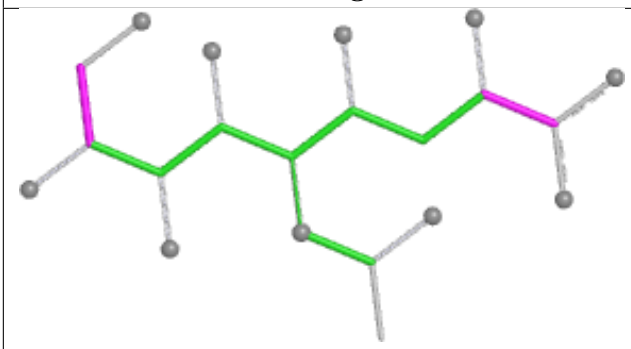
Ligand HMN A 700



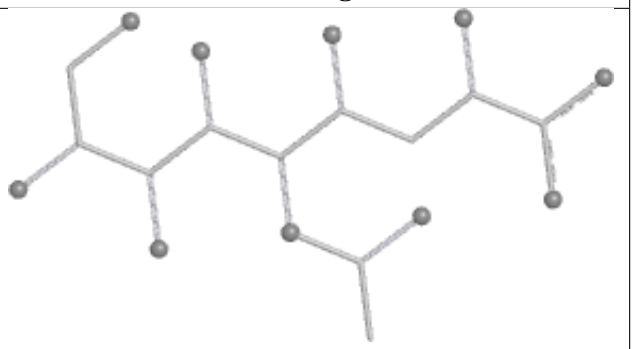
Bond lengths



Bond angles

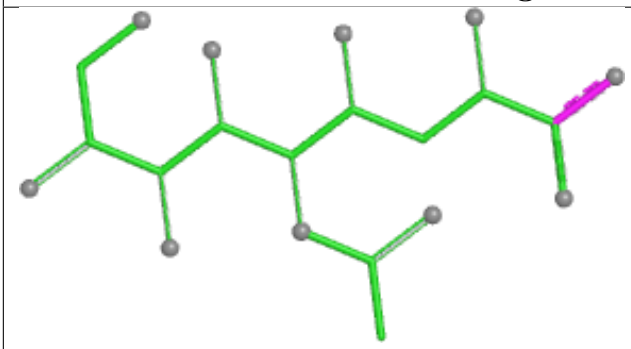


Torsions

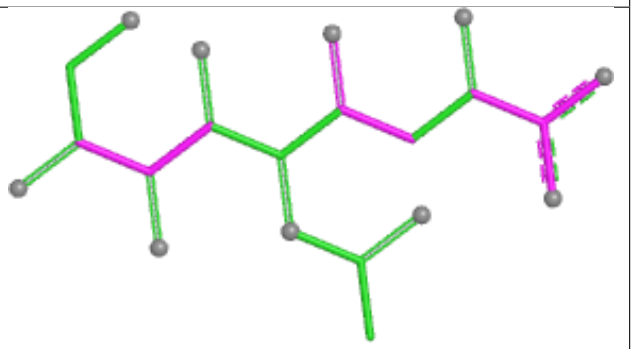


Rings

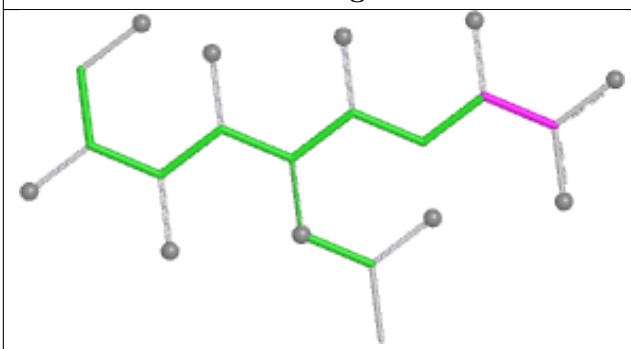
Ligand HMN B 701



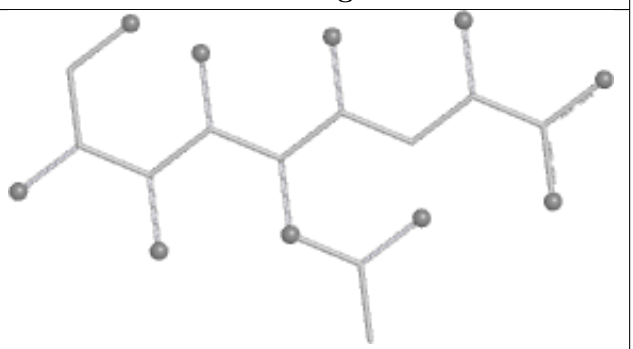
Bond lengths



Bond angles

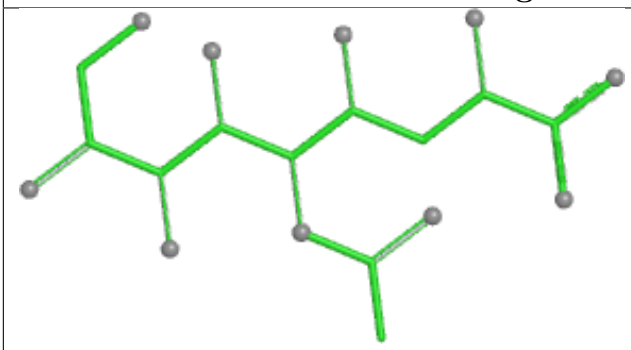


Torsions

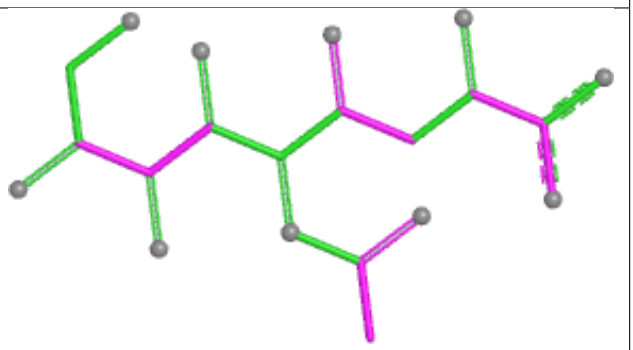


Rings

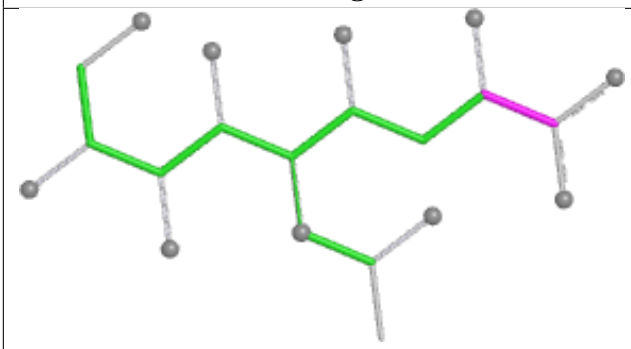
Ligand HMN D 703



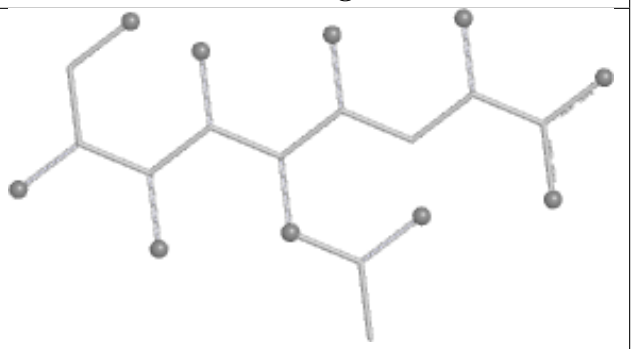
Bond lengths



Bond angles



Torsions



Rings

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, 95^{th} 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	288/293 (98%)	0.12	4 (1%)	75	82	17, 25, 40, 55	0
1	B	288/293 (98%)	-0.10	5 (1%)	70	77	14, 20, 33, 58	0
1	C	288/293 (98%)	-0.07	7 (2%)	59	68	15, 21, 34, 58	0
1	D	288/293 (98%)	-0.07	7 (2%)	59	68	15, 21, 32, 60	0
All	All	1152/1172 (98%)	-0.03	23 (1%)	65	73	14, 22, 36, 60	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	139	PRO	7.0
1	A	139	PRO	6.2
1	A	1	MET	5.9
1	C	139	PRO	5.2
1	D	138	ILE	5.0

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

There are no monosaccharides in this entry.

6.4 Ligands

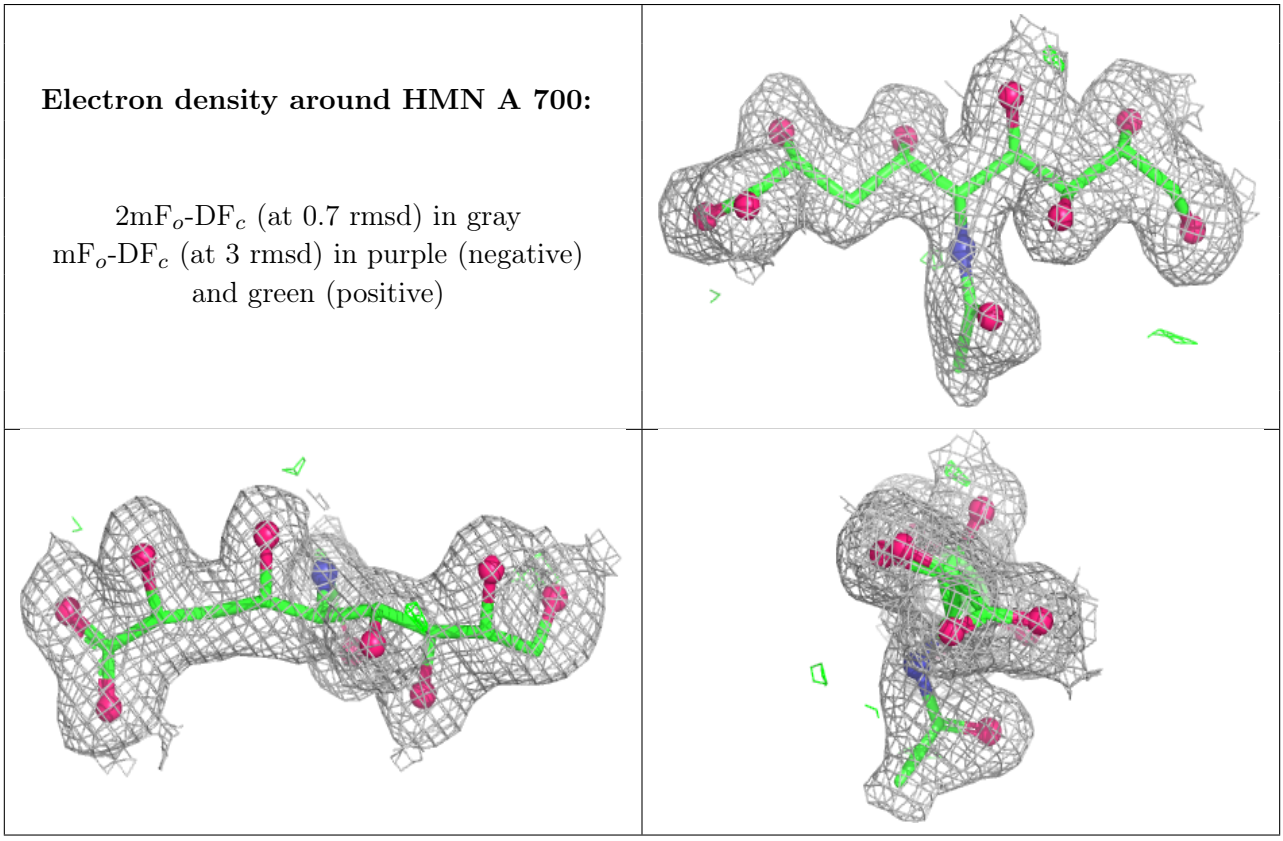
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GOL	B	704	6/6	0.66	0.39	46,49,49,50	0
2	HMN	A	700	21/21	0.94	0.10	19,21,25,29	0
2	HMN	C	702	21/21	0.95	0.10	15,20,27,29	0
2	HMN	D	703	21/21	0.96	0.09	17,20,27,28	0
2	HMN	B	701	21/21	0.96	0.10	17,20,25,26	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.

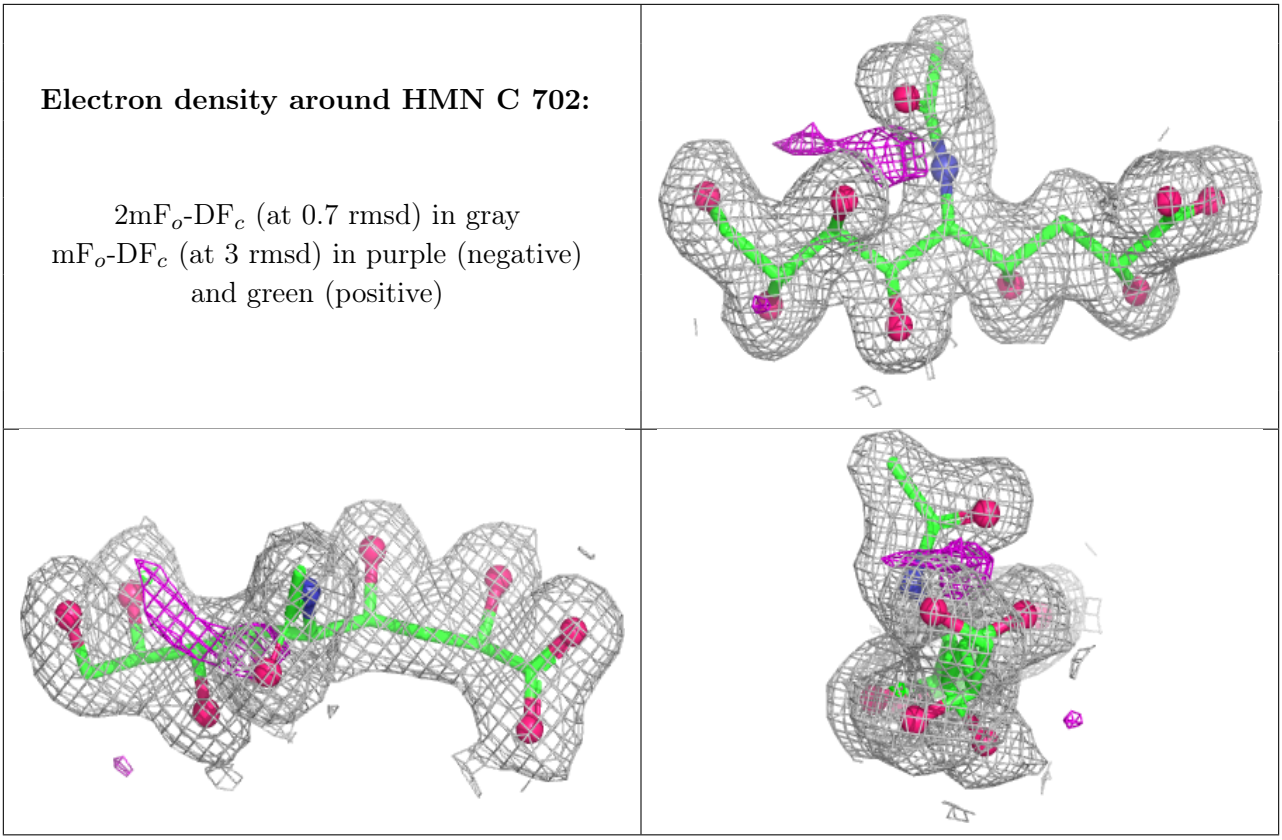
Electron density around HMN A 700:

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



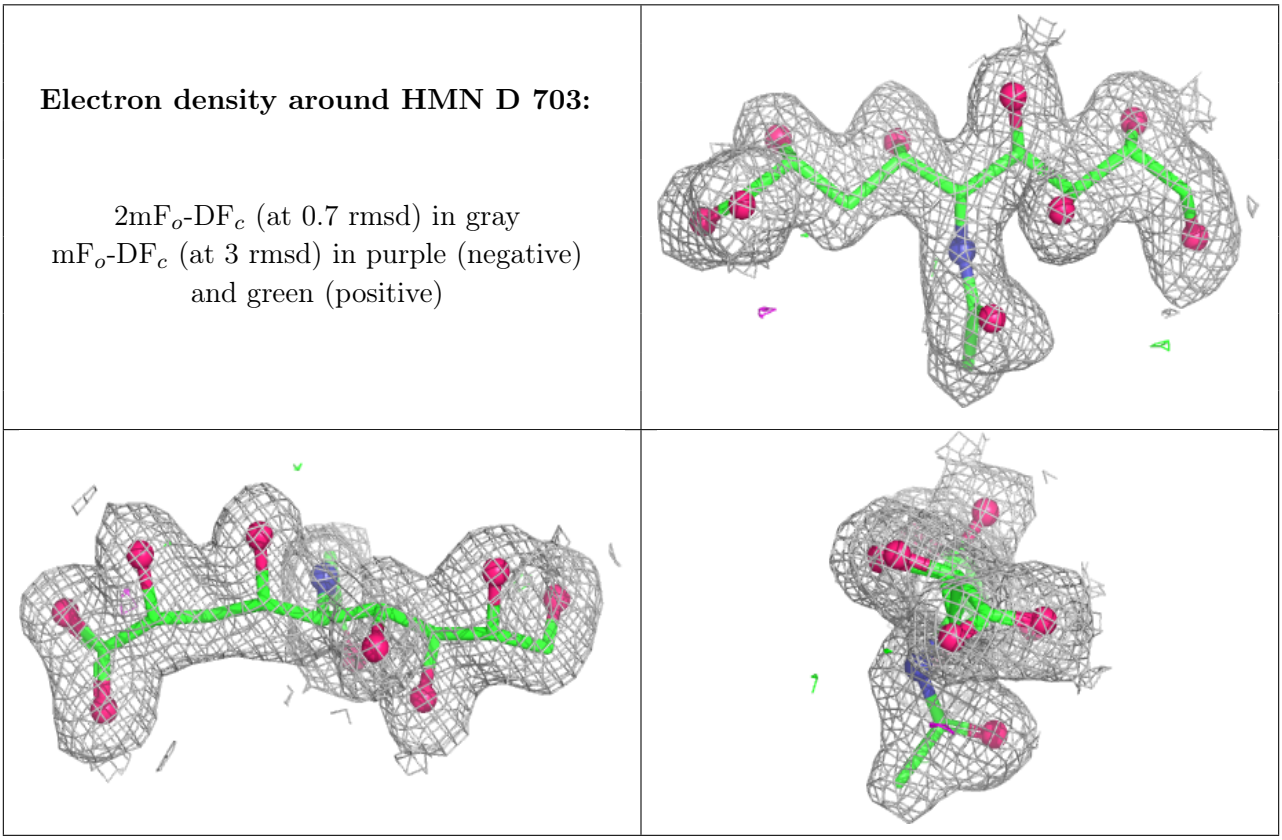
Electron density around HMN C 702:

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



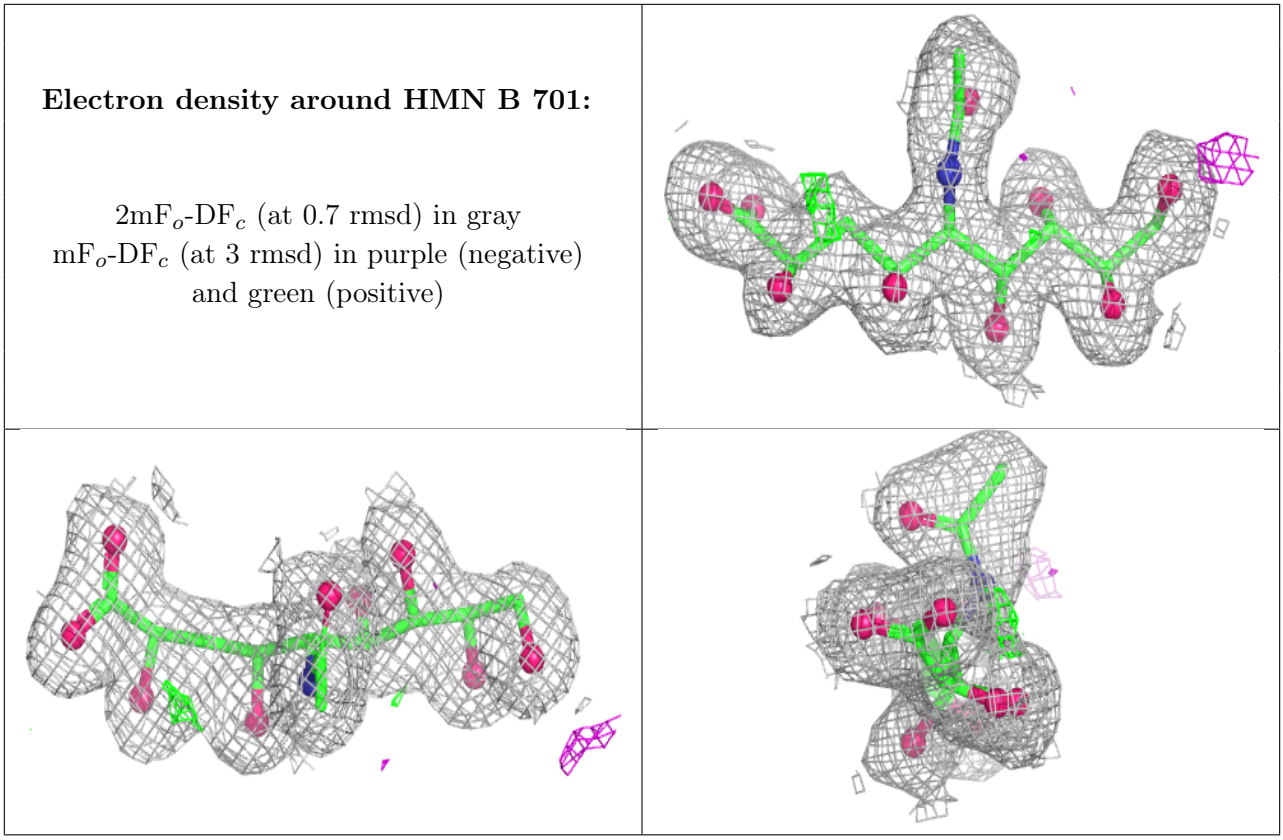
Electron density around HMN D 703:

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



Electron density around HMN B 701:

$2mF_o$-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.