



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 6, 2026 – 03:29 PM JST

PDB ID : 7Y3U / pdb_00007y3u
Title : Crystal structure of the complex of Lactoperoxidase with Nitric oxide at 2.50Å resolution
Authors : Singh, P.K.; Viswanathan, V.; Ahmad, N.; Rani, C.; Sharma, P.; Sharma, S.; Singh, T.P.
Deposited on : 2022-06-13
Resolution : 2.50 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

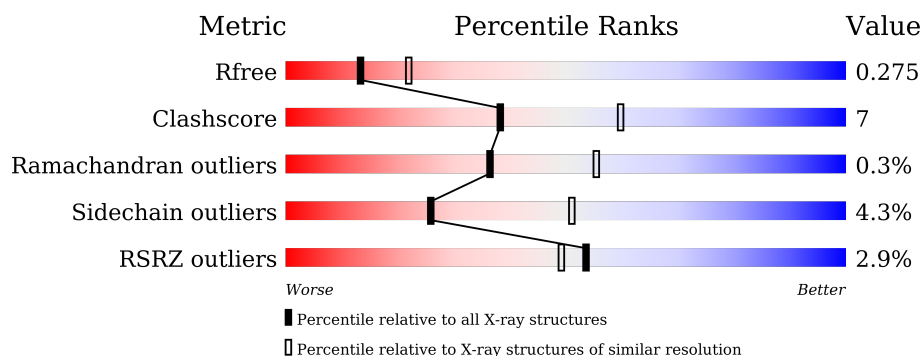
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	595	3% 85% 12% .
1	B	595	3% 86% 13% .
2	C	3	100%
2	D	3	33% 67%

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
3	MH0	A	601	X	-	-	-
3	MH0	B	602	X	-	-	-

2 Entry composition [i](#)

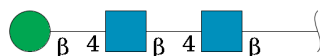
There are 9 unique types of molecules in this entry. The entry contains 9986 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Lactoperoxidase.

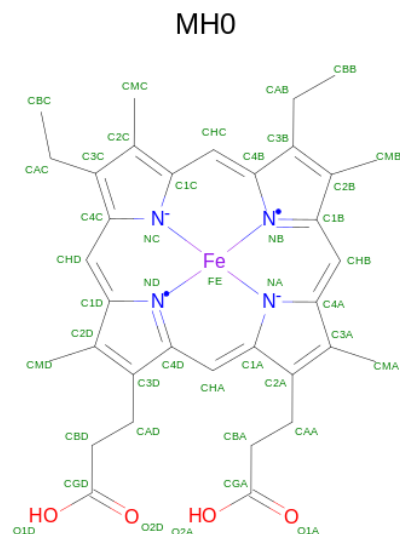
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	S	0	0	0
			4771	3037	847	861	26			
1	B	595	Total	C	N	O	S	0	0	0
			4771	3037	847	861	26			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	D	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 3 is Mesoheme (CCD ID: MH0) (formula: C₃₄H₃₆FeN₄O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

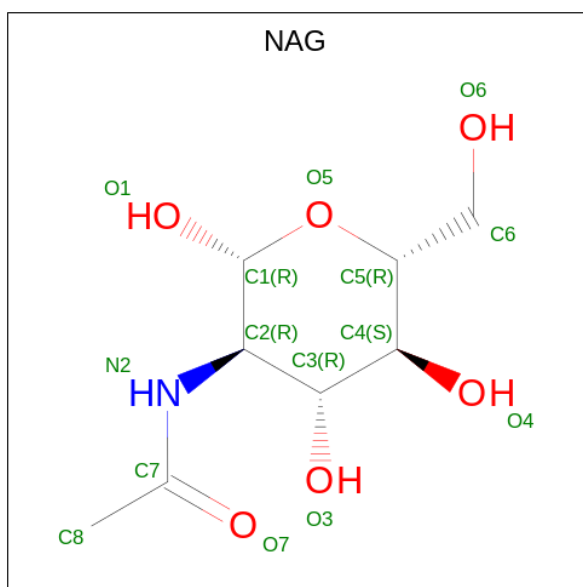
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Ca 1 1	0	0
4	B	1	Total Ca 1 1	0	0

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

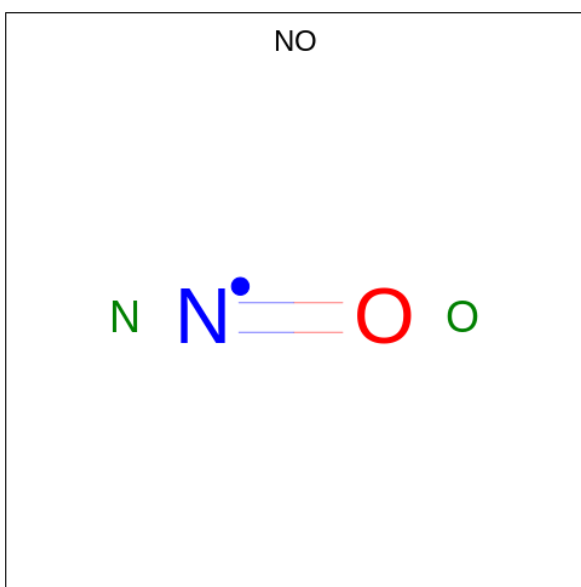
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Cl 1 1	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $\text{C}_8\text{H}_{15}\text{NO}_6$).



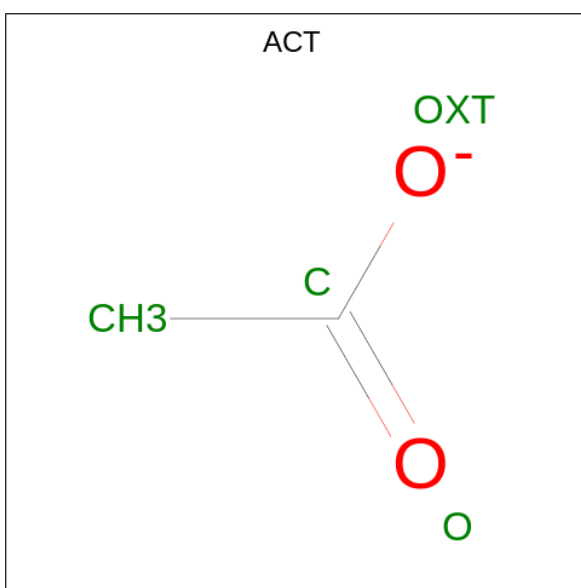
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is NITRIC OXIDE (CCD ID: NO) (formula: NO) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	N	O	0	0
			2	1	1		
7	B	1	Total	N	O	0	0
			2	1	1		

- Molecule 8 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

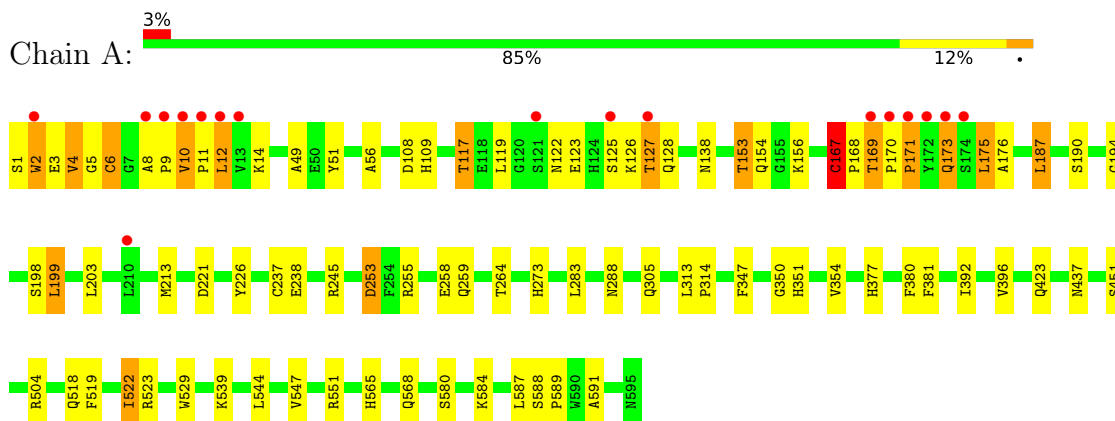
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	101	Total 101	O 101	0	0
9	B	84	Total 84	O 84	0	0

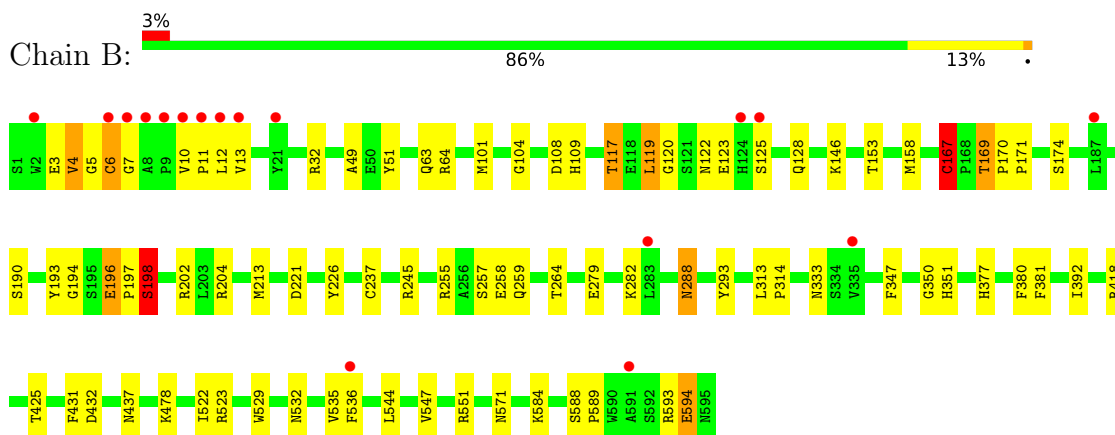
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

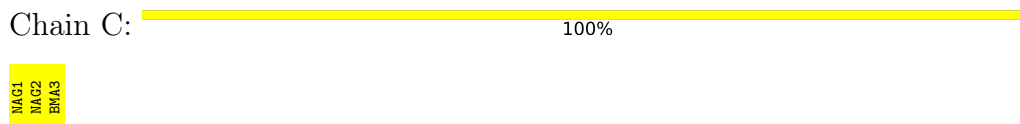
- Molecule 1: Lactoperoxidase



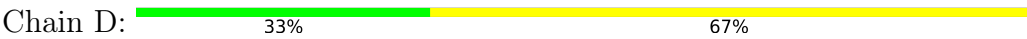
- Molecule 1: Lactoperoxidase



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.73Å 93.17Å 82.32Å 90.00° 91.20° 90.00°	Depositor
Resolution (Å)	48.86 – 2.50 48.86 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.9 (48.86-2.50) 98.9 (48.86-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.219 , 0.277 0.219 , 0.275	Depositor DCC
R_{free} test set	2105 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	48.7	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.035 for h,-k,-l 0.021 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9986	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, CA, NO, MH0, BMA, ACT, CL

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	1.00	0/4899	1.39	8/6645 (0.1%)
1	B	1.00	0/4899	1.40	6/6645 (0.1%)
All	All	1.00	0/9798	1.40	14/13290 (0.1%)

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

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

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	170	PRO	N-CA-C	8.46	121.03	110.70
1	B	194	GLY	CA-C-O	-5.53	118.41	122.23
1	A	194	GLY	CA-C-O	-5.46	118.46	122.23
1	A	253	ASP	CA-C-N	5.43	128.32	120.38
1	A	253	ASP	C-N-CA	5.43	128.32	120.38

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	119	LEU	Peptide
1	B	167	CYS	Peptide

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	4771	0	4687	73	0
1	B	4771	0	4688	69	0
2	C	39	0	33	0	0
2	D	39	0	34	0	0
3	A	43	0	34	14	0
3	B	43	0	34	13	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	1	0	0	0	0
6	A	42	0	38	0	0
6	B	42	0	39	0	0
7	A	2	0	0	0	0
7	B	2	0	0	0	0
8	B	4	0	3	0	0
9	A	101	0	0	3	0
9	B	84	0	0	2	0
All	All	9986	0	9590	134	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 7.

The worst 5 of 134 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:258:GLU:OE2	3:A:601:MH0:H15	1.20	1.32
1:B:258:GLU:OE2	3:B:602:MH0:H15	1.25	1.29
1:B:5:GLY:O	1:B:167:CYS:HA	1.35	1.22
1:B:108:ASP:OD2	3:B:602:MH0:H31	1.03	1.19
1:A:108:ASP:OD2	3:A:601:MH0:CMD	1.93	1.17

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	593/595 (100%)	558 (94%)	33 (6%)	2 (0%)	36	55
1	B	593/595 (100%)	565 (95%)	27 (5%)	1 (0%)	43	63
All	All	1186/1190 (100%)	1123 (95%)	60 (5%)	3 (0%)	36	55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	VAL
1	A	167	CYS
1	B	4	VAL

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	518/518 (100%)	494 (95%)	24 (5%)	24	48
1	B	518/518 (100%)	497 (96%)	21 (4%)	27	53
All	All	1036/1036 (100%)	991 (96%)	45 (4%)	26	51

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	119	LEU
1	B	196	GLU
1	B	146	LYS

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Mol	Chain	Res	Type
1	B	169	THR
1	B	245	ARG

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	B	521	GLN
1	B	273	HIS
1	B	63	GLN
1	A	571	ASN
1	B	138	ASN

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	2,1	14,14,15	0.48	0	17,19,21	1.79	2 (11%)
2	NAG	C	2	2	14,14,15	0.67	0	17,19,21	1.63	5 (29%)
2	BMA	C	3	2	11,11,12	0.60	0	15,15,17	1.16	1 (6%)
2	NAG	D	1	2,1	14,14,15	0.43	0	17,19,21	0.98	0
2	NAG	D	2	2	14,14,15	0.78	0	17,19,21	1.54	4 (23%)
2	BMA	D	3	2	11,11,12	1.01	0	15,15,17	1.74	3 (20%)

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	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	BMA	C	3	2	-	2/2/19/22	0/1/1/1
2	NAG	D	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	NAG	C3-C4-C5	4.87	118.94	110.24
2	D	2	NAG	C4-C3-C2	4.41	117.48	111.02
2	C	1	NAG	C1-O5-C5	4.28	117.98	112.19
2	D	3	BMA	C1-C2-C3	3.68	114.19	109.67
2	C	3	BMA	C3-C4-C5	3.32	116.16	110.24

There are no chirality outliers.

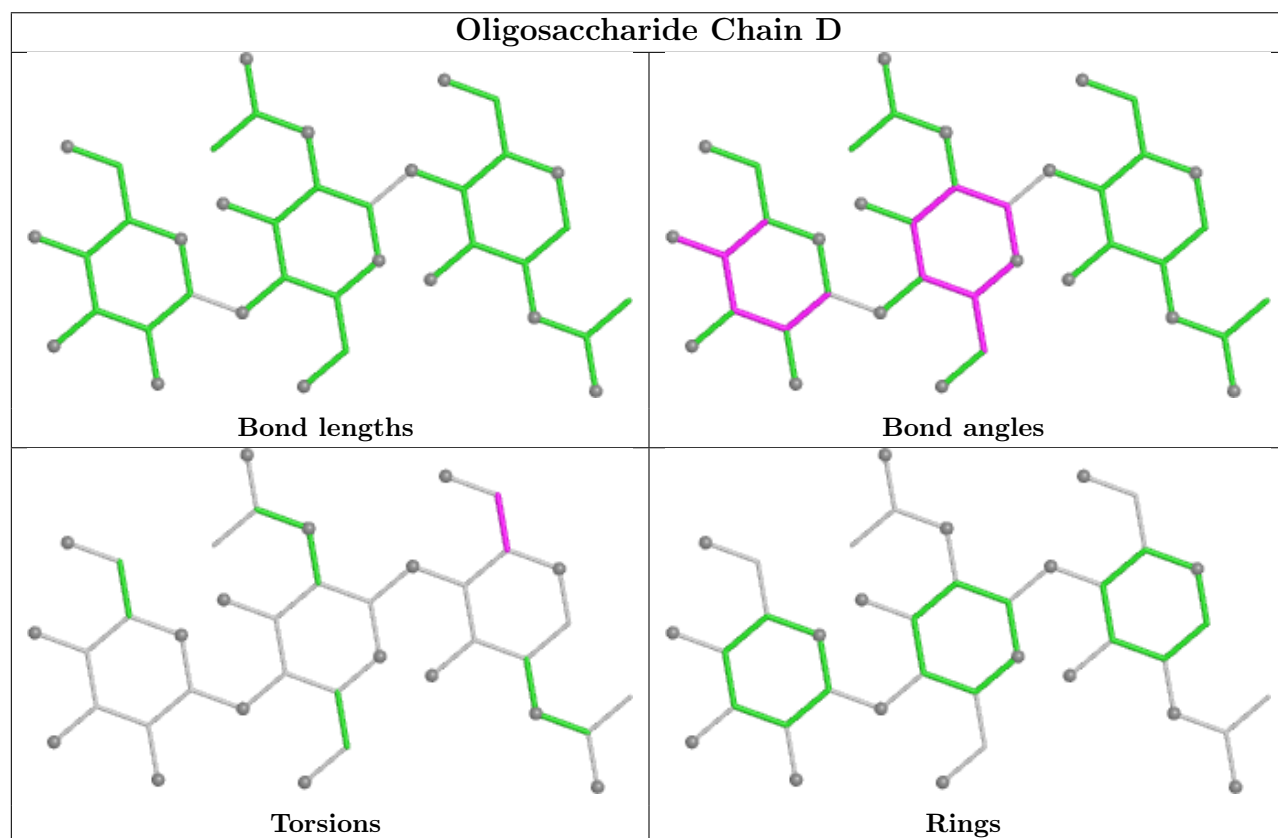
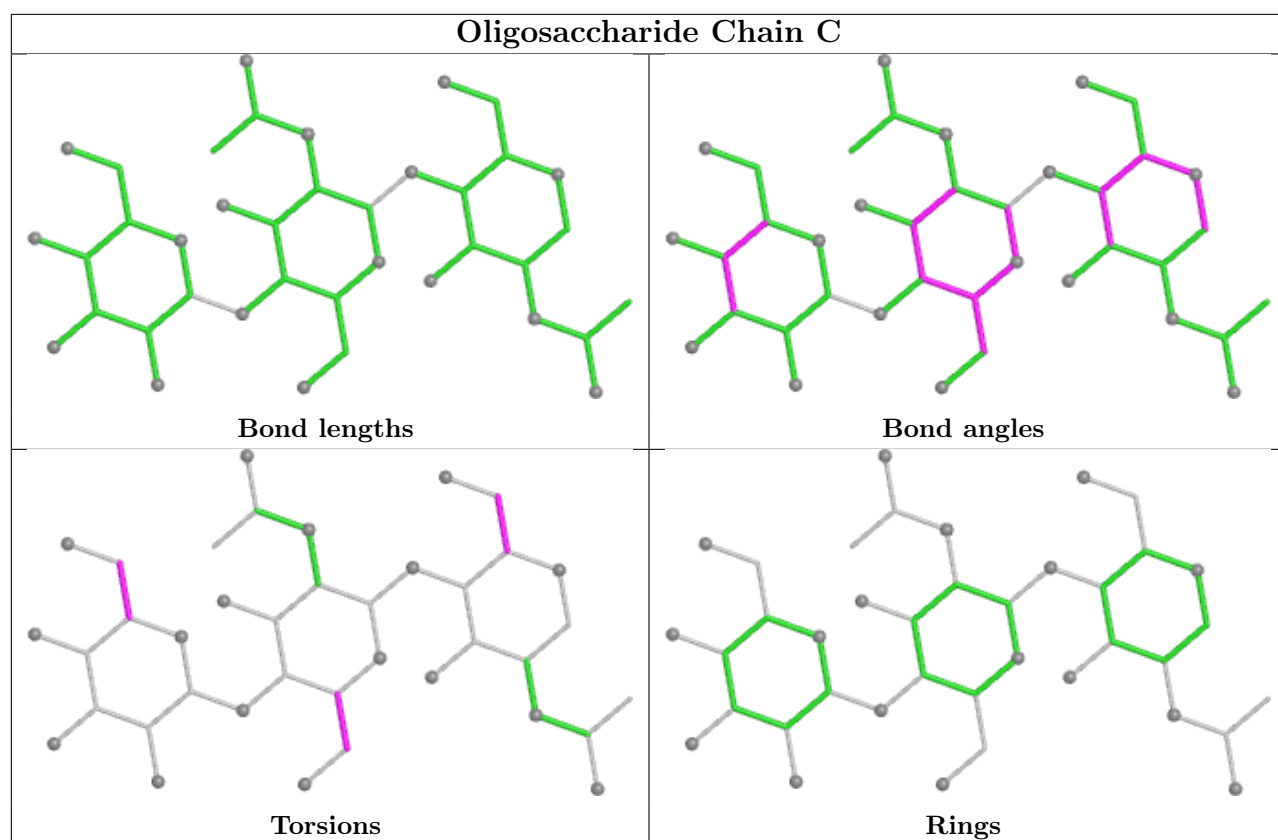
5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	2	NAG	O5-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
2	C	3	BMA	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.



5.6 Ligand geometry

Of 14 ligands modelled in this entry, 3 are monoatomic - leaving 11 for Mogul analysis.

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
6	NAG	A	604	1	14,14,15	0.70	0	17,19,21	1.93	3 (17%)
6	NAG	B	605	1	14,14,15	0.72	0	17,19,21	1.28	1 (5%)
8	ACT	B	601	-	3,3,3	1.01	0	3,3,3	0.73	0
7	NO	B	607	3	0,1,1	-	-	-		
7	NO	A	607	3	0,1,1	-	-	-		
3	MH0	B	602	1,7	50,50,50	1.84	9 (18%)	68,82,82	1.72	16 (23%)
6	NAG	A	606	1	14,14,15	1.52	1 (7%)	17,19,21	1.58	3 (17%)
6	NAG	A	605	1	14,14,15	0.71	0	17,19,21	2.06	3 (17%)
6	NAG	B	606	1	14,14,15	0.34	0	17,19,21	0.93	0
6	NAG	B	604	1	14,14,15	0.44	0	17,19,21	0.70	0
3	MH0	A	601	1,7	50,50,50	1.83	10 (20%)	68,82,82	1.77	18 (26%)

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
6	NAG	A	604	1	-	1/6/23/26	0/1/1/1
6	NAG	B	605	1	-	2/6/23/26	0/1/1/1
3	MH0	B	602	1,7	1/1/3/7	8/14/54/54	-
6	NAG	A	606	1	-	2/6/23/26	0/1/1/1
6	NAG	A	605	1	-	0/6/23/26	0/1/1/1
6	NAG	B	606	1	-	0/6/23/26	0/1/1/1
6	NAG	B	604	1	-	2/6/23/26	0/1/1/1
3	MH0	A	601	1,7	1/1/3/7	8/14/54/54	-

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	602	MH0	FE-NB	5.62	2.12	1.94
6	A	606	NAG	C1-C2	-5.04	1.44	1.52
3	A	601	MH0	FE-NB	4.96	2.10	1.94
3	A	601	MH0	CBC-CAC	-4.31	1.32	1.51
3	A	601	MH0	CBB-CAB	-4.10	1.33	1.51

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	604	NAG	C1-O5-C5	5.97	120.27	112.19
6	A	605	NAG	C1-O5-C5	5.93	120.23	112.19
3	B	602	MH0	CBB-CAB-C3B	4.52	124.89	112.43
3	A	601	MH0	CBB-CAB-C3B	4.36	124.45	112.43
3	B	602	MH0	CBC-CAC-C3C	4.25	124.15	112.43

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	601	MH0	NA
3	B	602	MH0	NA

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	MH0	C4C-C3C-CAC-CBC
3	B	602	MH0	C4C-C3C-CAC-CBC
3	A	601	MH0	C2B-C3B-CAB-CBB
3	B	602	MH0	C2B-C3B-CAB-CBB
6	B	604	NAG	O5-C5-C6-O6

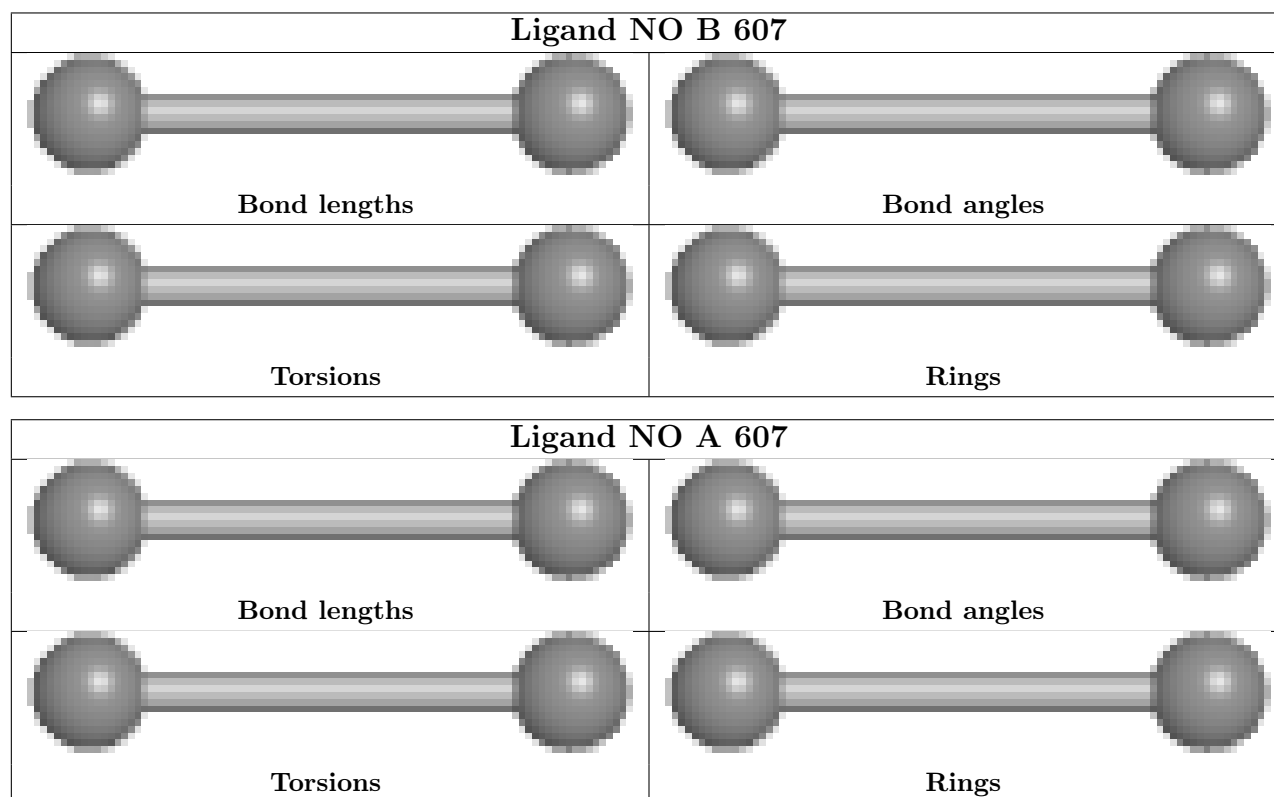
There are no ring outliers.

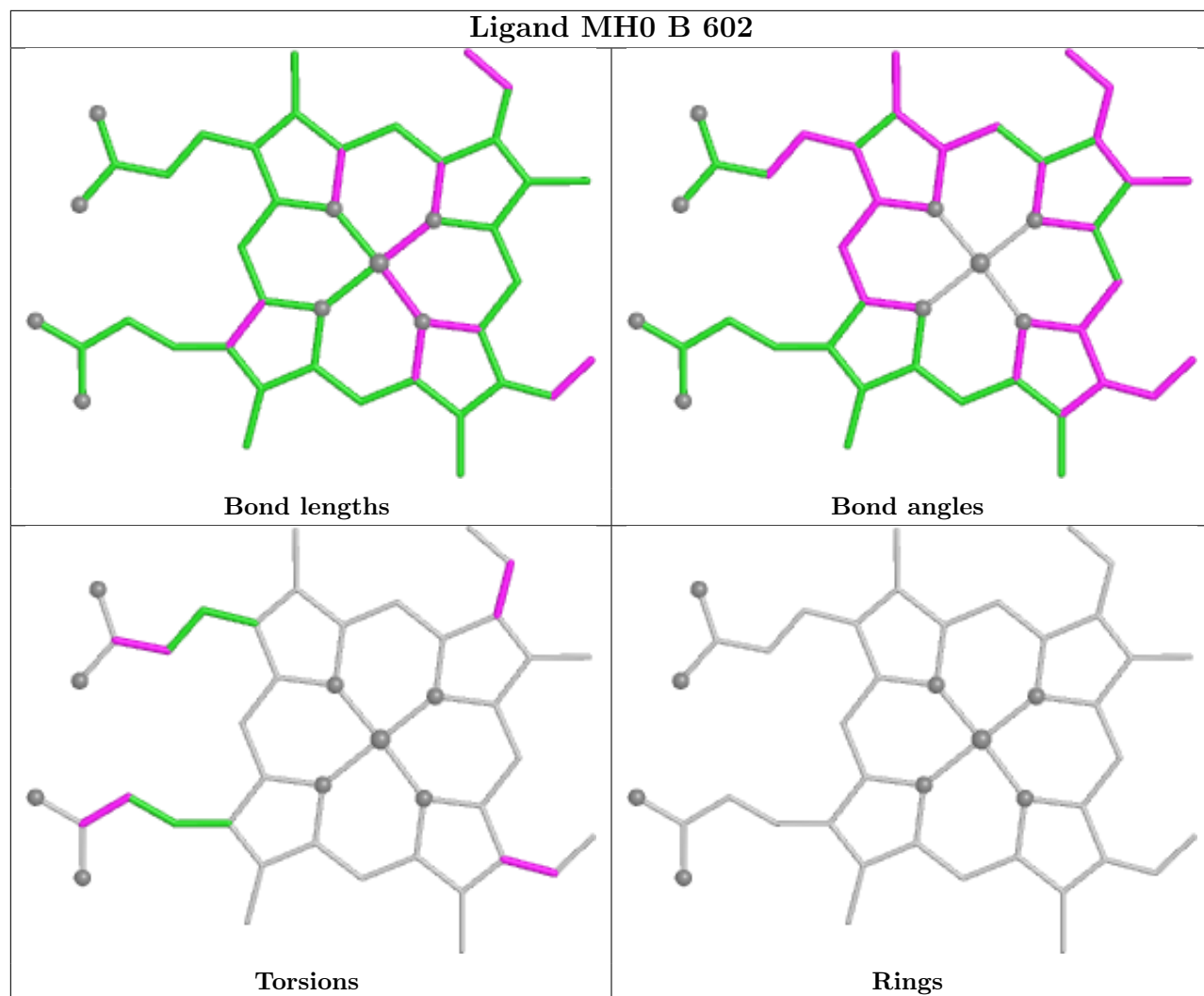
2 monomers are involved in 27 short contacts:

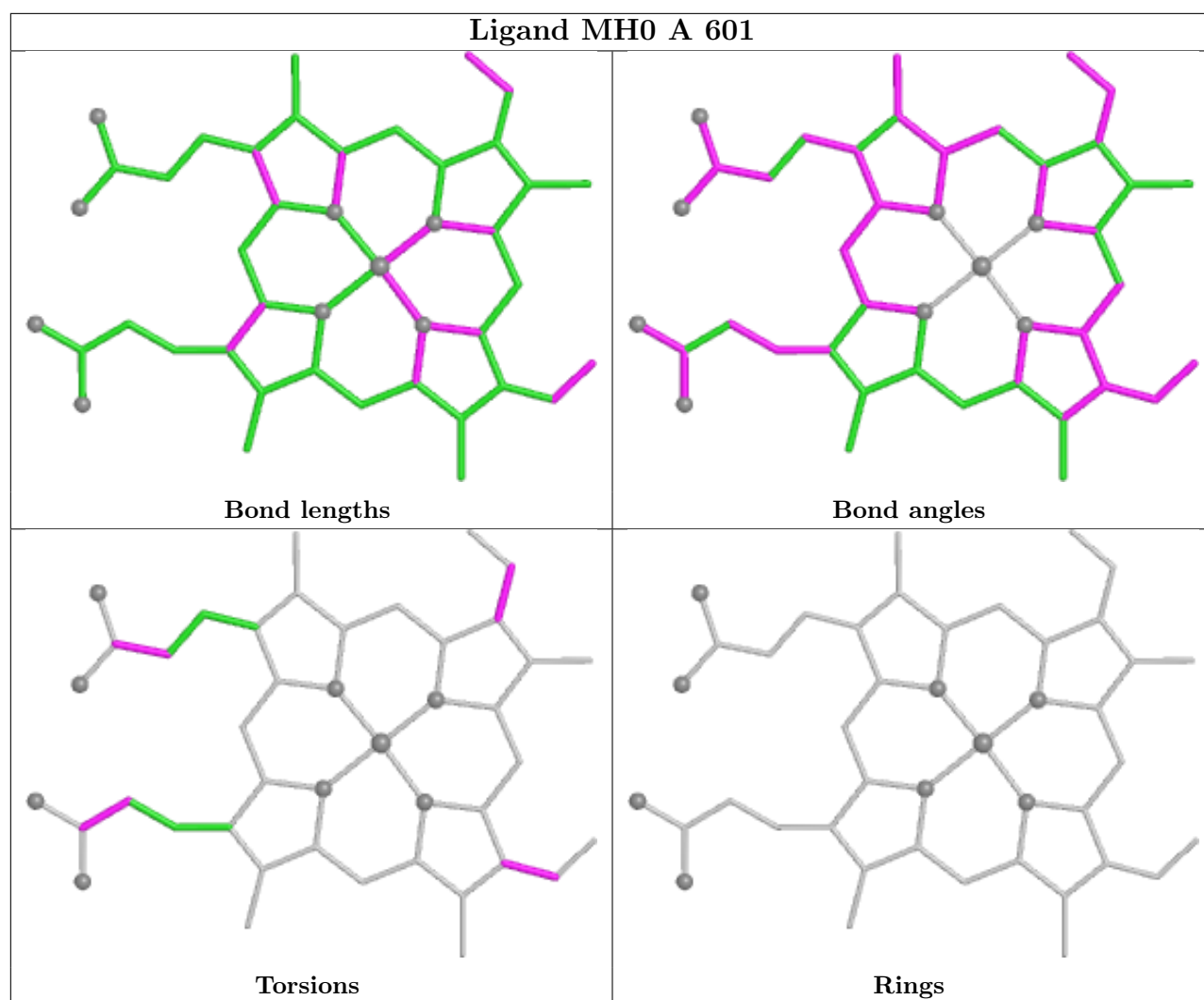
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	MH0	13	0
3	A	601	MH0	14	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	595/595 (100%)	0.13	17 (2%) 53 49	32, 56, 117, 190	0
1	B	595/595 (100%)	0.24	17 (2%) 53 49	33, 57, 107, 199	0
All	All	1190/1190 (100%)	0.19	34 (2%) 53 49	32, 56, 115, 199	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	10	VAL	5.7
1	A	13	VAL	4.8
1	A	12	LEU	4.5
1	B	11	PRO	4.1
1	B	8	ALA	4.0

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.

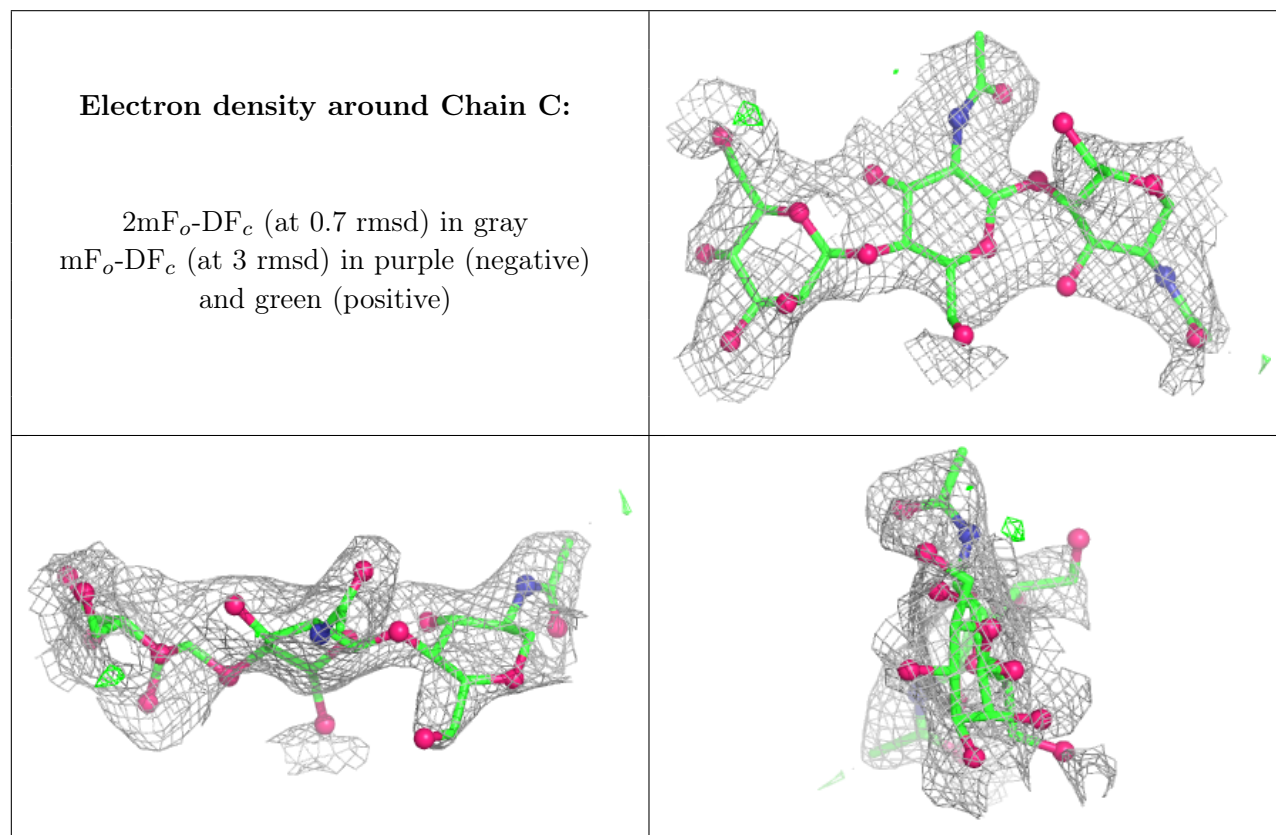
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BMA	C	3	11/12	0.40	0.12	96,113,123,124	0
2	BMA	D	3	11/12	0.66	0.11	76,85,87,88	0
2	NAG	C	1	14/15	0.70	0.12	90,104,116,119	0
2	NAG	D	2	14/15	0.78	0.10	81,92,99,102	0
2	NAG	C	2	14/15	0.81	0.11	82,109,121,129	0

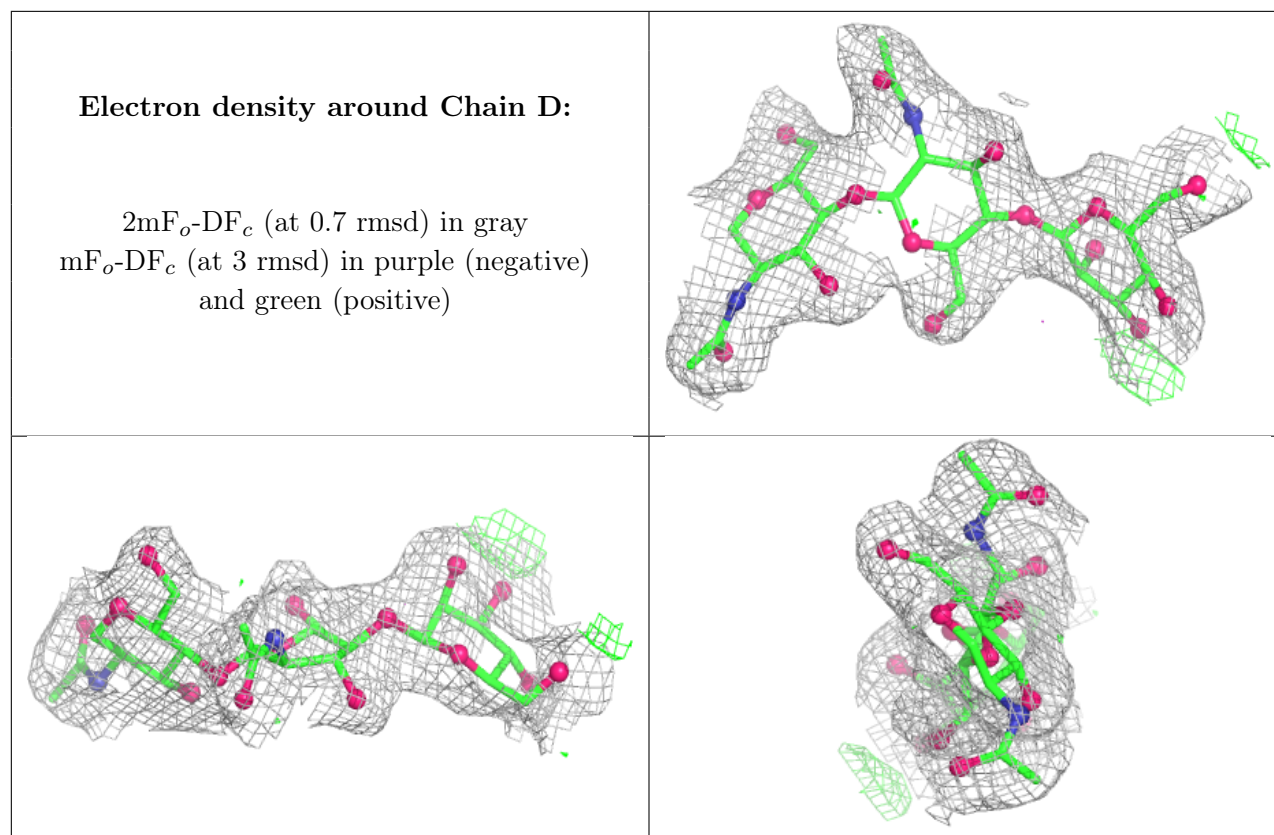
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	D	1	14/15	0.92	0.07	67,78,82,88	0

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 [i](#)

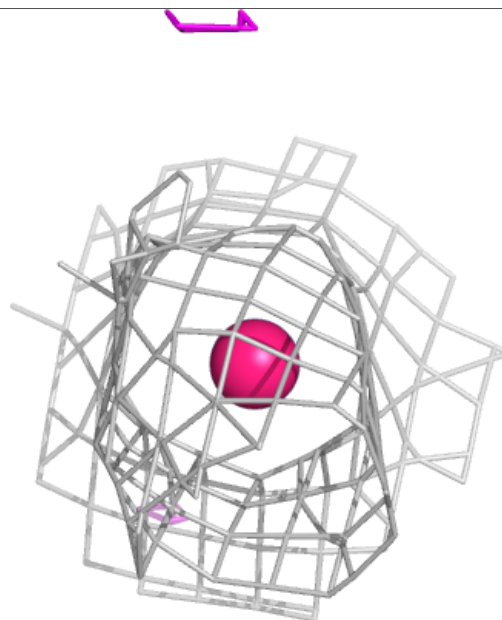
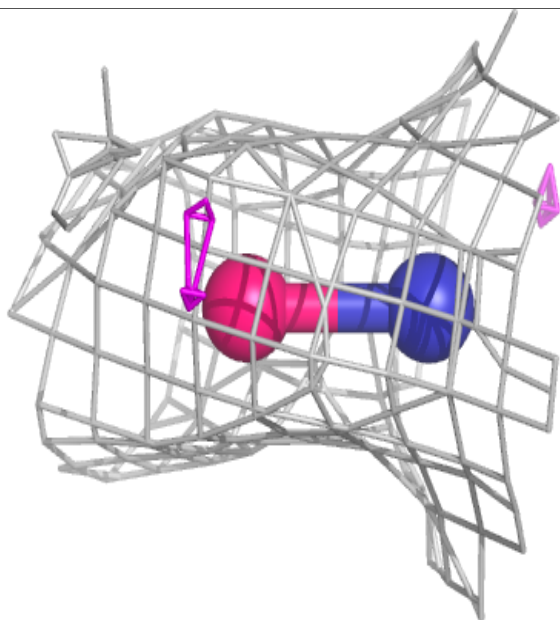
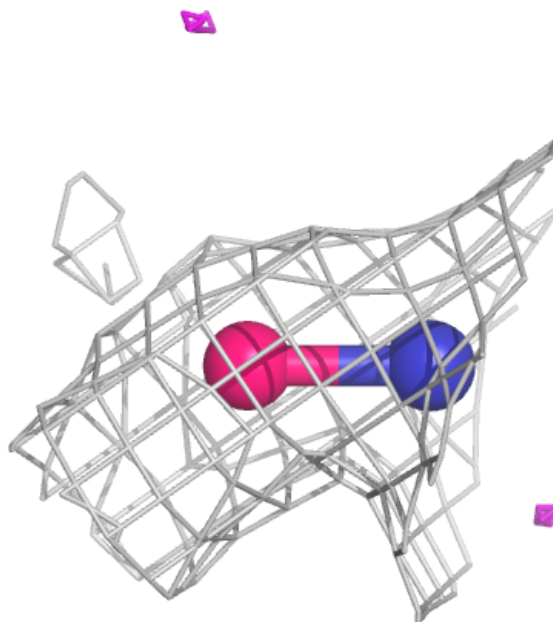
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	NAG	B	606	14/15	0.66	0.11	94,111,119,122	0
6	NAG	A	604	14/15	0.73	0.12	76,87,95,97	0
6	NAG	A	606	14/15	0.74	0.15	73,95,104,105	0
6	NAG	B	604	14/15	0.83	0.10	92,101,106,108	0
6	NAG	B	605	14/15	0.85	0.09	60,65,74,80	0
8	ACT	B	601	4/4	0.90	0.15	58,63,64,66	0
6	NAG	A	605	14/15	0.91	0.08	45,49,55,56	0
7	NO	B	607	2/2	0.95	0.13	55,55,55,60	0
7	NO	A	607	2/2	0.95	0.11	53,53,53,54	0
5	CL	A	603	1/1	0.97	0.08	48,48,48,48	0
3	MH0	B	602	43/43	0.97	0.06	32,38,42,44	0
3	MH0	A	601	43/43	0.98	0.06	27,37,41,43	0
4	CA	A	602	1/1	0.99	0.05	43,43,43,43	0
4	CA	B	603	1/1	0.99	0.06	45,45,45,45	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.

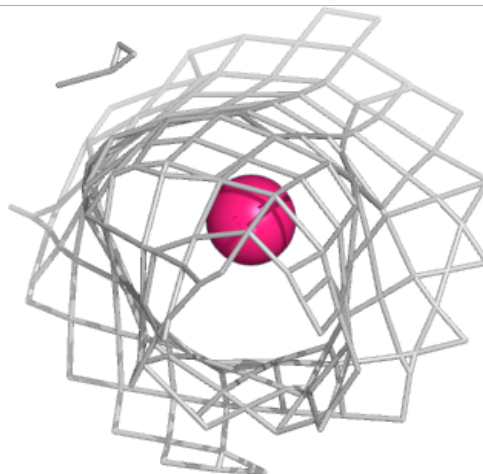
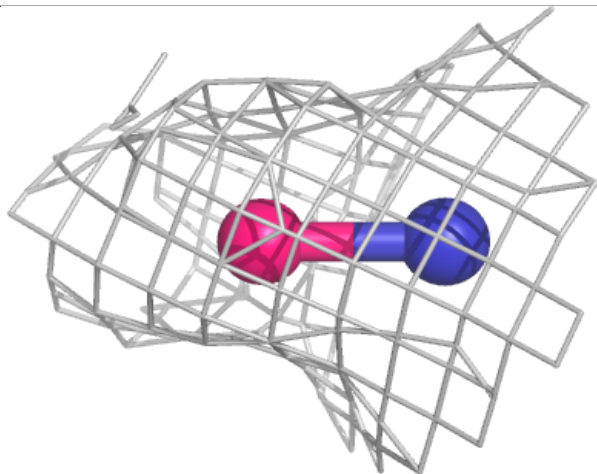
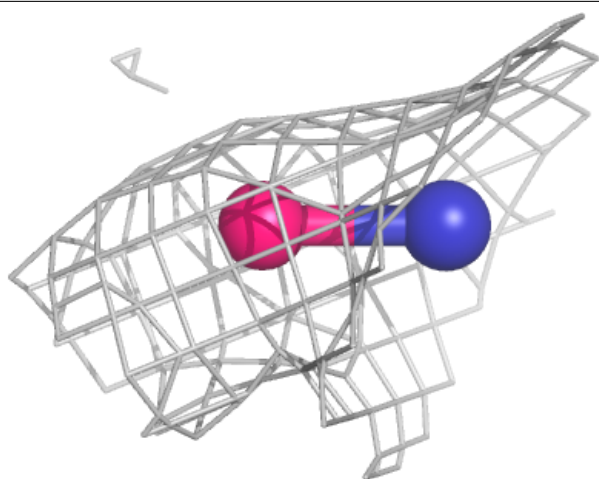
Electron density around NO B 607:

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



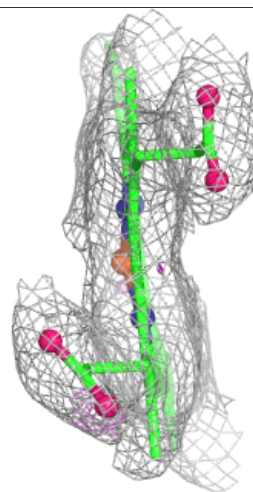
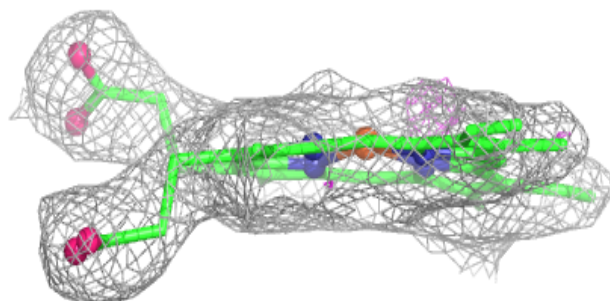
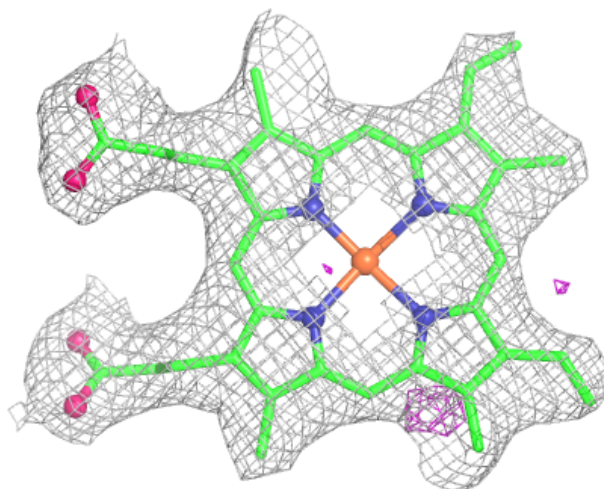
Electron density around NO A 607:

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



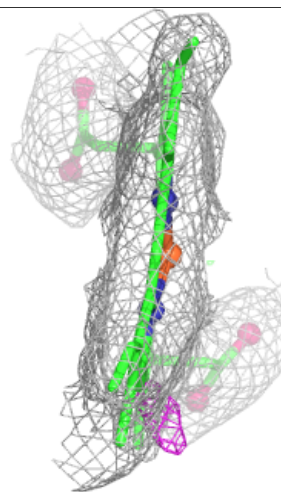
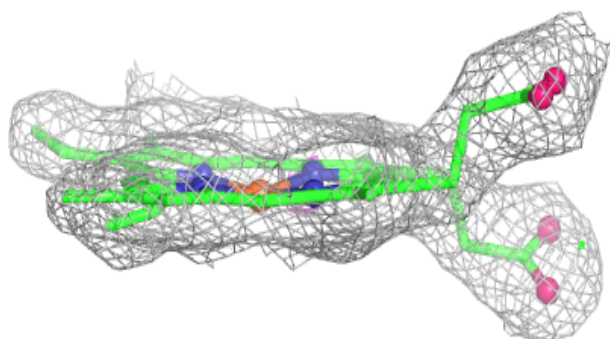
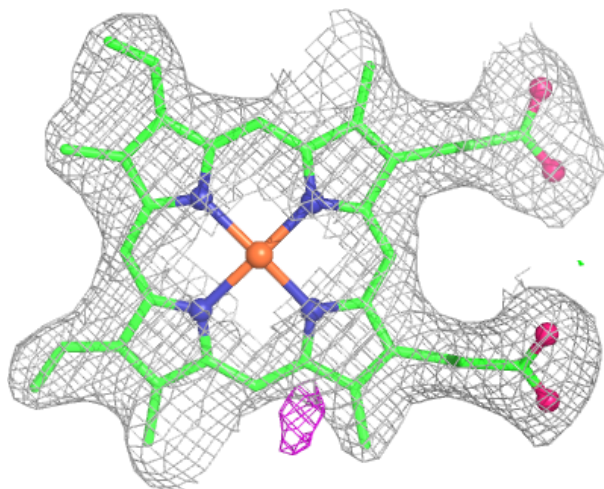
Electron density around MH0 B 602:

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



Electron density around MH0 A 601:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.