



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 19, 2026 – 06:43 AM UTC

PDB ID : 7NI3 / pdb_00007ni3
Title : CRYSTAL STRUCTURE OF NATIVE HUMAN MYELOPEROXIDASE IN COMPLEX WITH CPD 3
Authors : Sjogren, T.; Inghardt, T.
Deposited on : 2021-02-11
Resolution : 2.10 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 : 2022.3.0, CSD as543be (2022)
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 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

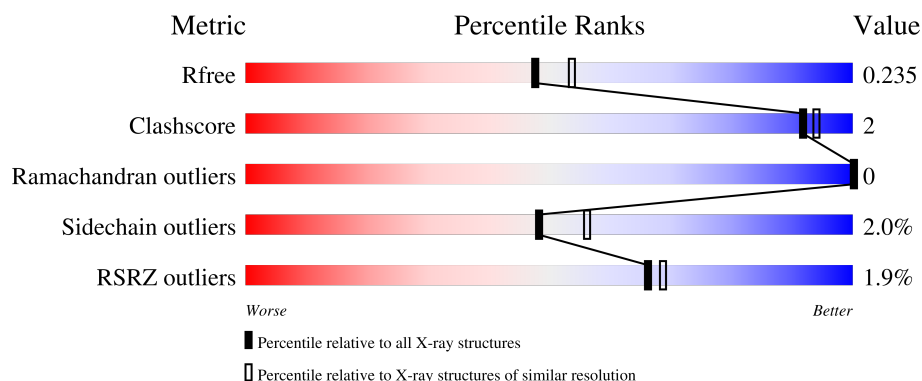
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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.



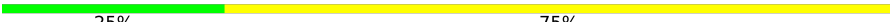
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	105	6% 90% 10%
1	B	105	% 89% 10%
2	C	466	2% 91% 8%
2	D	466	2% 92% 7%
3	E	4	25% 75%

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Mol	Chain	Length	Quality of chain
3	F	4	 A horizontal bar chart showing the quality of chain F. The bar is divided into two segments: a green segment on the left representing 25% and a yellow segment on the right representing 75%. The labels '25%' and '75%' are placed below their respective segments.

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 10213 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.

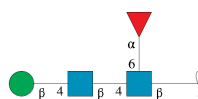
- Molecule 1 is a protein called Myeloperoxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	105	Total	C	N	O	S	0	0	0
			842	532	149	156	5			
1	B	103	Total	C	N	O	S	0	0	0
			832	526	147	154	5			

- Molecule 2 is a protein called Myeloperoxidase.

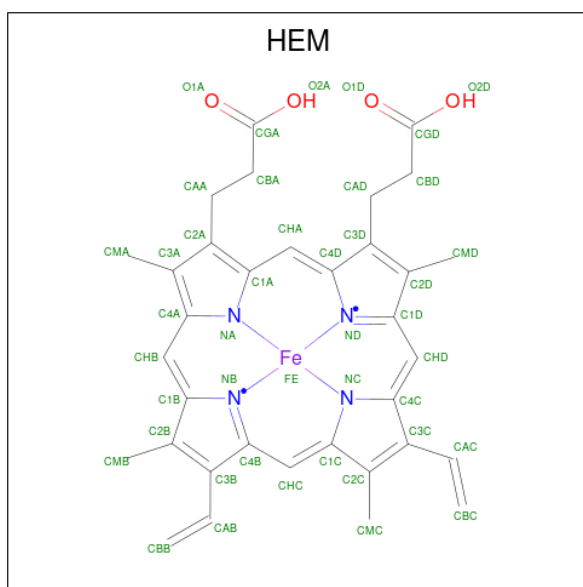
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	464	Total	C	N	O	S	0	0	0
			3720	2343	685	665	27			
2	D	464	Total	C	N	O	S	0	0	0
			3720	2343	685	665	27			

- Molecule 3 is an oligosaccharide called 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
3	E	4	Total	C	N	O	0	0	0
			49	28	2	19			
3	F	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄).

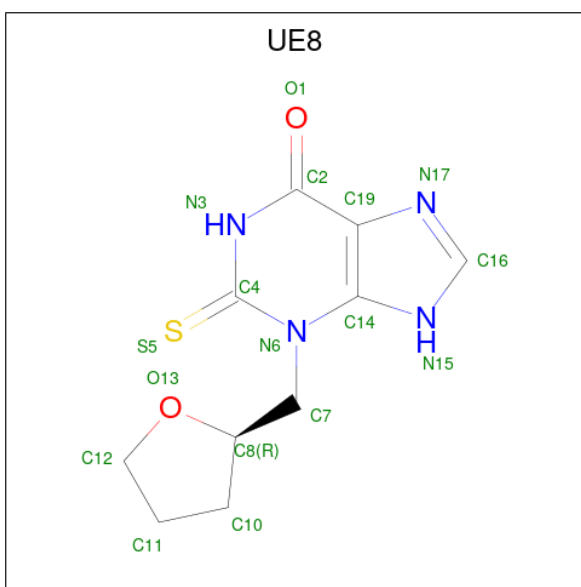


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- 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
5	B	2	Total Cl 2 2	0	0
5	C	2	Total Cl 2 2	0	0

- Molecule 6 is 2-sulfanylidene-3-[(2R)-tetrahydro-2-furanylmethyl]-1,2,3,7-tetrahydro-6H-purin-6-one (CCD ID: UE8) (formula: C₁₀H₁₂N₄O₂S) (labeled as "Ligand of Interest" by depositor).

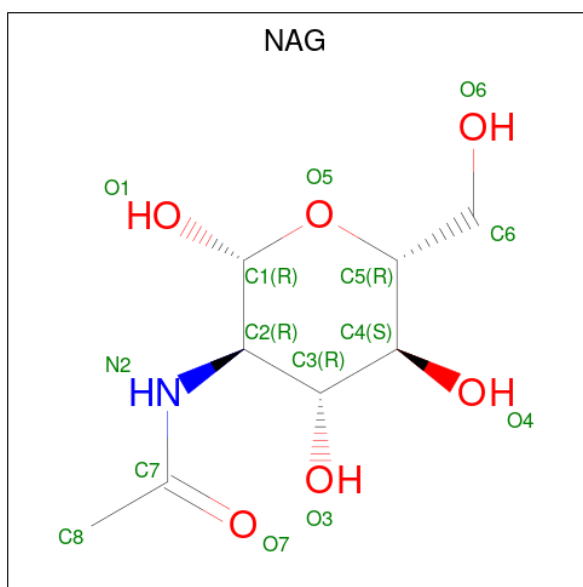


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	N	O	S	0	0
			17	10	4	2	1		
6	D	1	Total	C	N	O	S	0	0
			17	10	4	2	1		

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

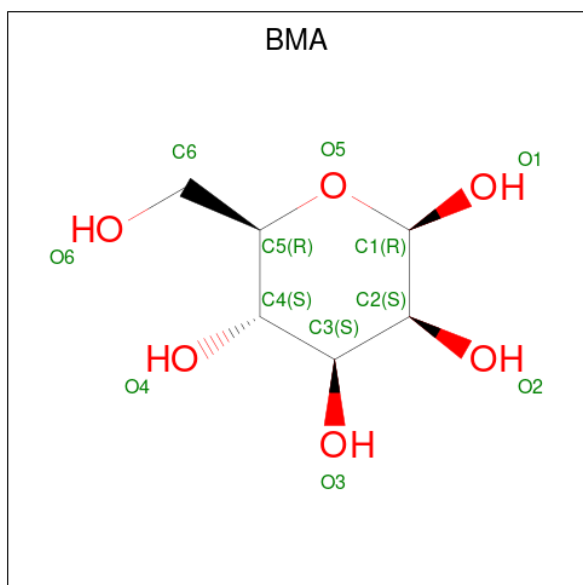
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	1	Total	Ca	0	0
			1	1		
7	D	1	Total	Ca	0	0
			1	1		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 9 is beta-D-mannopyranose (CCD ID: BMA) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	C	1	Total	C	O	0	0
			11	6	5		
9	D	1	Total	C	O	0	0
			11	6	5		

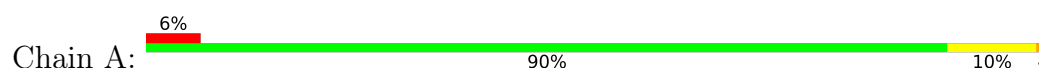
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	84	Total	O	0	0
			84	84		
10	B	75	Total	O	0	0
			75	75		
10	C	342	Total	O	0	0
			342	342		
10	D	295	Total	O	0	0
			295	295		

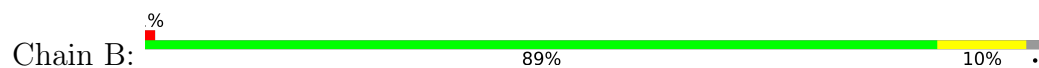
3 Residue-property plots [i](#)

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.

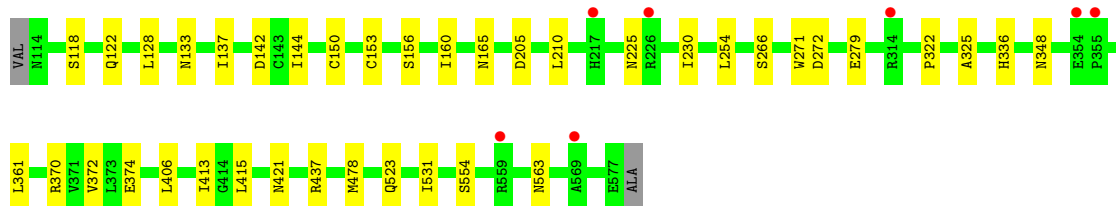
- Molecule 1: Myeloperoxidase



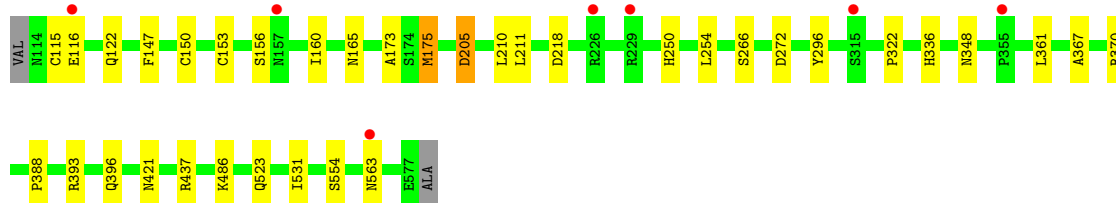
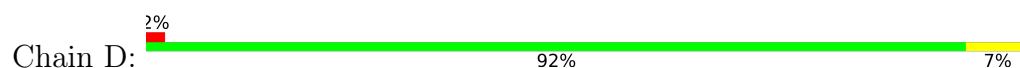
- Molecule 1: Myeloperoxidase



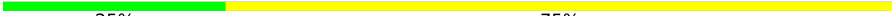
- Molecule 2: Myeloperoxidase



- Molecule 2: Myeloperoxidase



- Molecule 3: 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 E:  25% 75%

MAG1
MAG2
BMA3
FUC4

- Molecule 3: 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 F:  25% 75%

MAG1
MAG2
BMA3
FUC4

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	92.66Å 63.64Å 111.03Å 90.00° 97.15° 90.00°	Depositor
Resolution (Å)	30.61 – 2.10 30.61 – 2.10	Depositor EDS
% Data completeness (in resolution range)	75.0 (30.61-2.10) 75.0 (30.61-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.10Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.175 , 0.224 0.182 , 0.235	Depositor DCC
R_{free} test set	2737 reflections (3.63%)	wwPDB-VP
Wilson B-factor (Å ²)	12.2	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 52.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10213	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.38% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, UE8, CSO, HEM, NAG, CL, FUC, BMA

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	0.84	0/867	1.24	4/1181 (0.3%)
1	B	0.81	0/857	1.20	3/1167 (0.3%)
2	C	0.87	0/3798	1.25	10/5151 (0.2%)
2	D	0.85	0/3798	1.24	14/5151 (0.3%)
All	All	0.85	0/9320	1.24	31/12650 (0.2%)

There are no bond length outliers.

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	133	ASN	CA-CB-CG	7.95	120.55	112.60
1	A	74	ASP	CA-CB-CG	6.82	119.42	112.60
1	B	9	THR	N-CA-C	-6.52	101.74	110.55
2	D	147	PHE	CA-CB-CG	6.36	120.16	113.80
2	D	116	GLU	CB-CG-CD	6.14	123.03	112.60

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	842	0	803	6	0
1	B	832	0	793	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	3720	0	3711	15	0
2	D	3720	0	3711	11	0
3	E	49	0	43	0	0
3	F	49	0	43	0	0
4	A	43	0	30	0	0
4	B	43	0	30	1	0
5	A	1	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
6	C	17	0	0	0	0
6	D	17	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	C	28	0	26	0	0
8	D	28	0	26	0	0
9	C	11	0	10	0	0
9	D	11	0	10	0	0
10	A	84	0	0	0	0
10	B	75	0	0	0	0
10	C	342	0	0	0	0
10	D	295	0	0	0	0
All	All	10213	0	9236	29	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 2.

The worst 5 of 29 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)
2:D:336:HIS:HD1	2:D:421:ASN:HD21	1.22	0.85
2:C:336:HIS:HD1	2:C:421:ASN:HD21	1.21	0.83
2:C:137:ILE:HG12	2:C:413:ILE:HD11	1.90	0.53
1:A:83:SER:HB3	2:C:554:SER:O	2.09	0.52
4:B:202:HEM:HMC2	4:B:202:HEM:HBC2	1.92	0.49

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	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
1	B	101/105 (96%)	99 (98%)	2 (2%)	0	100	100
2	C	461/466 (99%)	450 (98%)	11 (2%)	0	100	100
2	D	461/466 (99%)	450 (98%)	11 (2%)	0	100	100
All	All	1126/1142 (99%)	1099 (98%)	27 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	90/90 (100%)	88 (98%)	2 (2%)	45	53
1	B	90/90 (100%)	89 (99%)	1 (1%)	65	74
2	C	409/410 (100%)	401 (98%)	8 (2%)	48	56
2	D	409/410 (100%)	400 (98%)	9 (2%)	45	53
All	All	998/1000 (100%)	978 (98%)	20 (2%)	48	56

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	348	ASN
2	D	523	GLN
2	D	563	ASN

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Mol	Chain	Res	Type
2	D	531	ILE
2	C	348	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	523	GLN
2	D	571	ASN
2	C	540	ASN
2	C	571	ASN
2	D	204	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	CSO	C	150	2	3,6,7	0.78	0	1,6,8	3.31	1 (100%)
2	CSO	D	150	2	3,6,7	0.86	0	1,6,8	3.41	1 (100%)

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	CSO	C	150	2	-	0/1/5/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CSO	D	150	2	-	0/1/5/7	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	150	CSO	CB-CA-C	-3.41	101.54	110.80
2	C	150	CSO	CB-CA-C	-3.31	101.81	110.80

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

8 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	$\# Z > 2$
3	NAG	E	1	3,2	14,14,15	0.29	0	17,19,21	1.09	1 (5%)
3	NAG	E	2	3	14,14,15	0.30	0	17,19,21	1.15	2 (11%)
3	BMA	E	3	3	11,11,12	0.30	0	15,15,17	0.88	1 (6%)
3	FUC	E	4	3	10,10,11	0.47	0	14,14,16	0.56	0
3	NAG	F	1	3,2	14,14,15	0.39	0	17,19,21	0.96	1 (5%)
3	NAG	F	2	3	14,14,15	0.26	0	17,19,21	0.91	1 (5%)
3	BMA	F	3	3	11,11,12	0.37	0	15,15,17	0.73	1 (6%)
3	FUC	F	4	3	10,10,11	0.51	0	14,14,16	0.54	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
3	NAG	E	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	1/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	FUC	E	4	3	-	-	0/1/1/1
3	NAG	F	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	BMA	F	3	3	-	0/2/19/22	0/1/1/1
3	FUC	F	4	3	-	-	0/1/1/1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	2	NAG	C1-O5-C5	3.47	116.84	112.19
3	E	1	NAG	O5-C1-C2	-3.16	106.41	111.29
3	E	3	BMA	C1-O5-C5	3.11	116.35	112.19
3	F	1	NAG	O5-C1-C2	-2.78	106.99	111.29
3	F	2	NAG	C1-O5-C5	2.43	115.44	112.19

There are no chirality outliers.

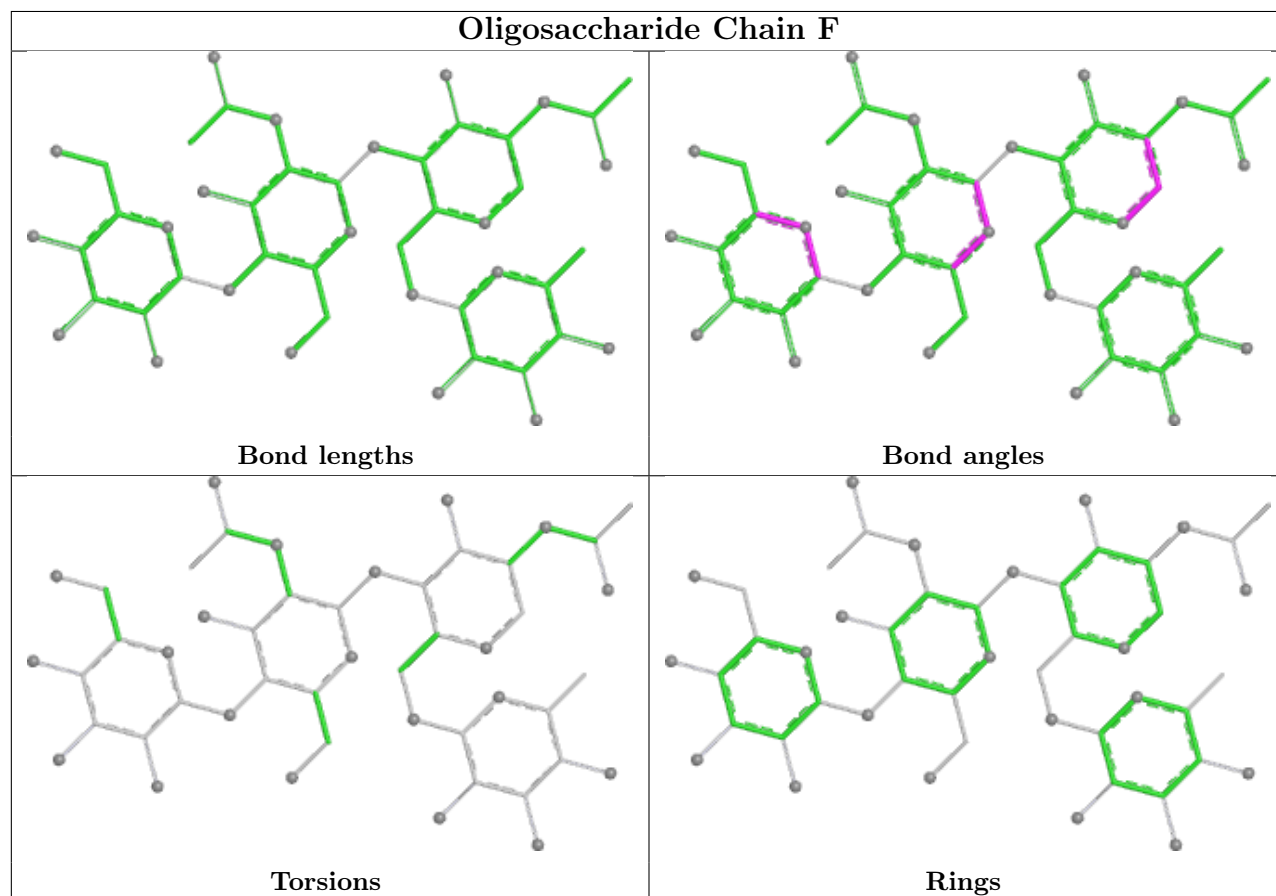
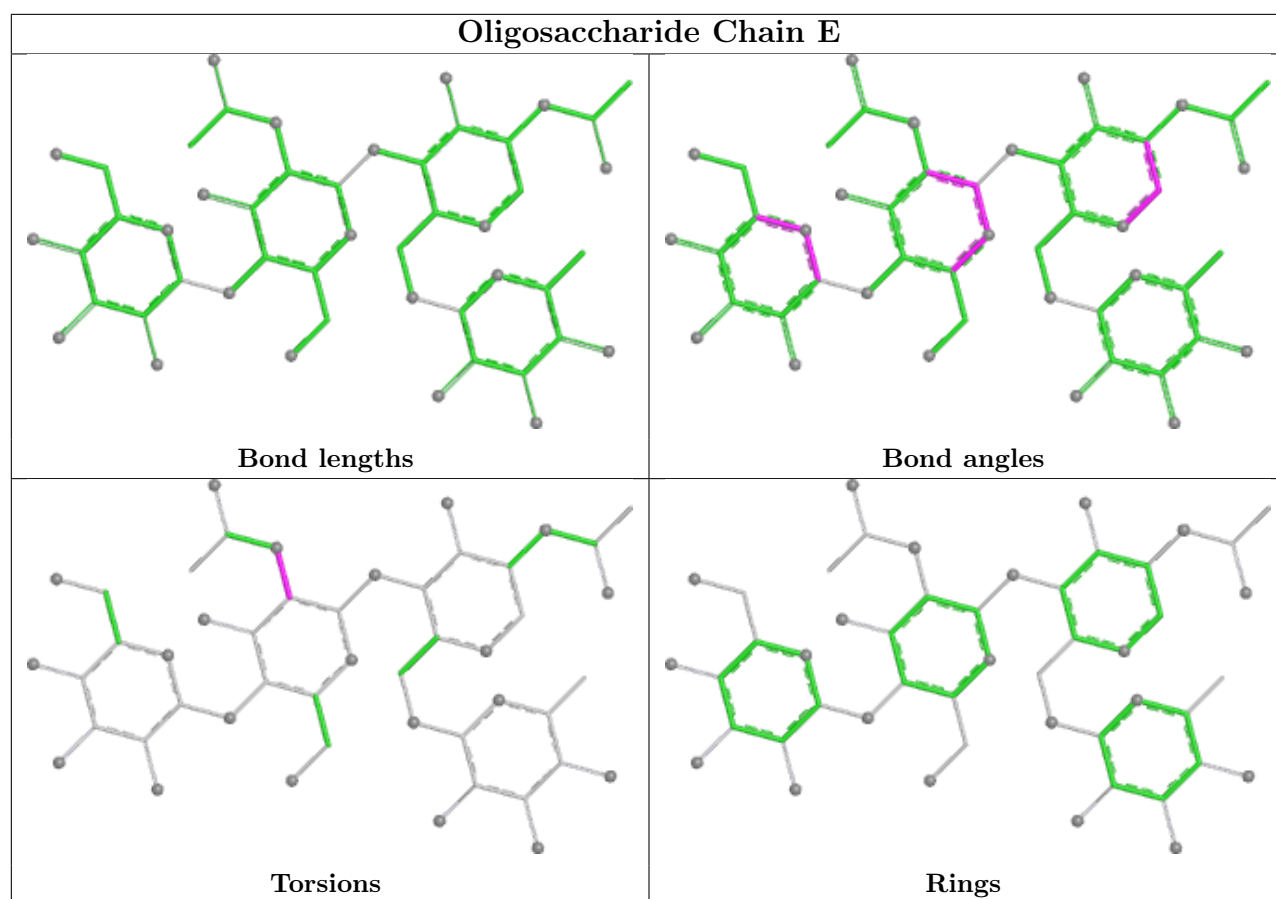
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	2	NAG	C1-C2-N2-C7

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 17 ligands modelled in this entry, 7 are monoatomic - leaving 10 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	$\# Z > 2$
4	HEM	B	202	2,1	50,50,50	1.22	7 (14%)	67,82,82	1.54	17 (25%)
6	UE8	D	2201	-	19,19,19	1.59	3 (15%)	18,27,27	1.27	3 (16%)
8	NAG	D	2204	2	14,14,15	0.29	0	17,19,21	0.71	1 (5%)
8	NAG	C	605	2	14,14,15	0.33	0	17,19,21	0.74	1 (5%)
9	BMA	C	607	-	11,11,12	0.36	0	15,15,17	0.89	1 (6%)
6	UE8	C	602	-	19,19,19	1.53	2 (10%)	18,27,27	1.25	3 (16%)
8	NAG	D	2203	2	14,14,15	0.32	0	17,19,21	0.79	1 (5%)
9	BMA	D	2202	-	11,11,12	0.35	0	15,15,17	0.82	1 (6%)
4	HEM	A	201	2,1,10	50,50,50	1.30	7 (14%)	67,82,82	1.54	13 (19%)
8	NAG	C	606	2	14,14,15	0.37	0	17,19,21	0.66	1 (5%)

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	HEM	B	202	2,1	-	4/14/54/54	-
6	UE8	D	2201	-	-	0/4/11/11	0/3/3/3
8	NAG	D	2204	2	-	0/6/23/26	0/1/1/1
8	NAG	C	605	2	-	0/6/23/26	0/1/1/1
9	BMA	C	607	-	-	2/2/19/22	0/1/1/1
6	UE8	C	602	-	-	0/4/11/11	0/3/3/3
8	NAG	D	2203	2	-	0/6/23/26	0/1/1/1
9	BMA	D	2202	-	-	2/2/19/22	0/1/1/1
4	HEM	A	201	2,1,10	-	4/14/54/54	-
8	NAG	C	606	2	-	0/6/23/26	0/1/1/1

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	2201	UE8	C4-N6	5.15	1.44	1.38
6	C	602	UE8	C4-N6	5.12	1.44	1.38
4	A	201	HEM	CMB-C2B	3.22	1.57	1.50
4	A	201	HEM	C2A-C3A	-3.10	1.30	1.38
4	B	202	HEM	C4D-C3D	2.68	1.49	1.45

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	201	HEM	C2B-C1B-NB	4.11	114.57	109.84
4	A	201	HEM	CBA-CAA-C2A	-3.54	102.74	112.53
4	B	202	HEM	CBD-CAD-C3D	-3.35	103.26	112.53
6	D	2201	UE8	C14-C19-N17	-3.30	104.98	109.26
6	C	602	UE8	C14-C19-N17	-3.27	105.02	109.26

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	C	607	BMA	C4-C5-C6-O6
9	D	2202	BMA	C4-C5-C6-O6
4	B	202	HEM	CAD-CBD-CGD-O1D
4	A	201	HEM	CAD-CBD-CGD-O2D
4	A	201	HEM	CAD-CBD-CGD-O1D

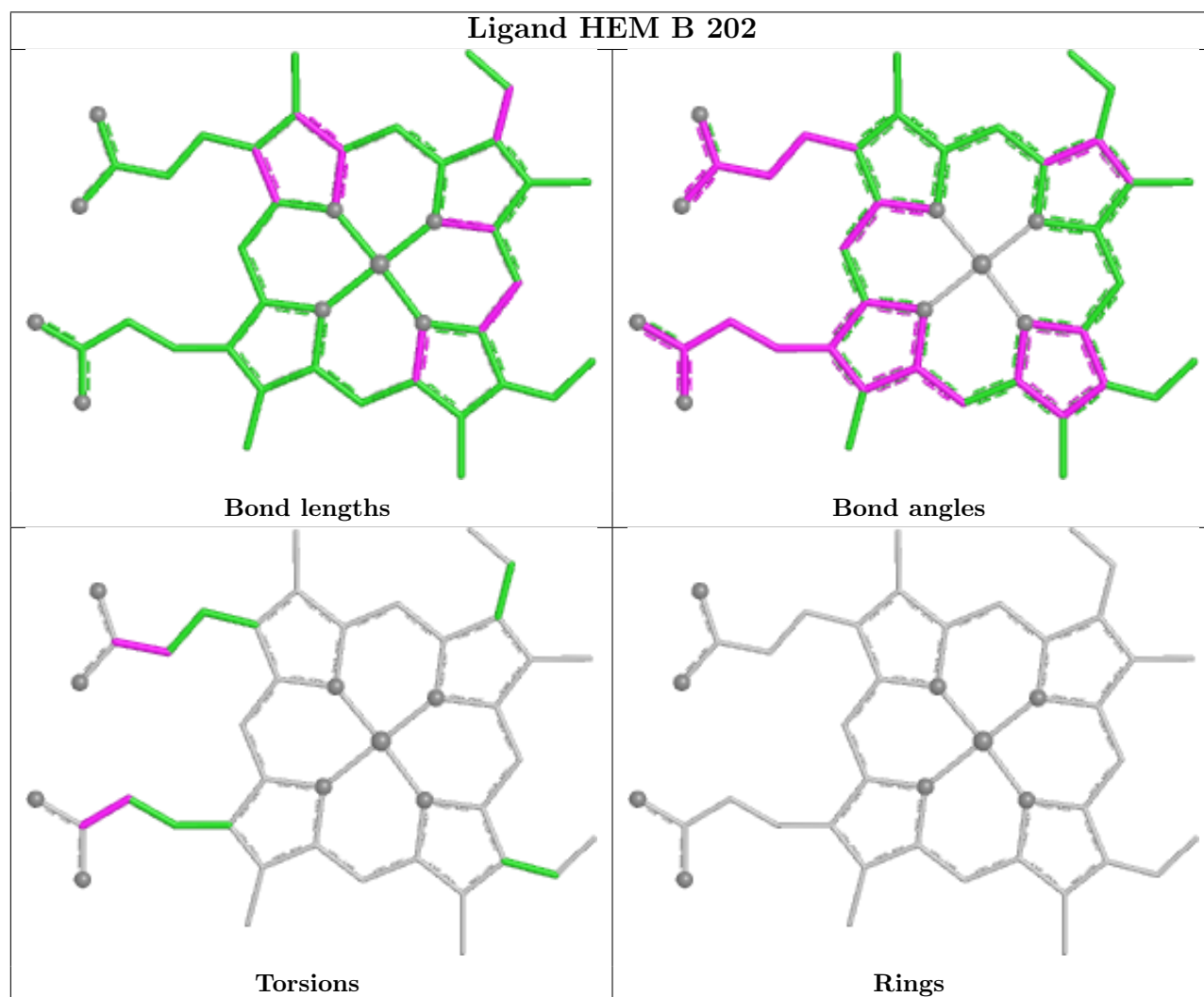
There are no ring outliers.

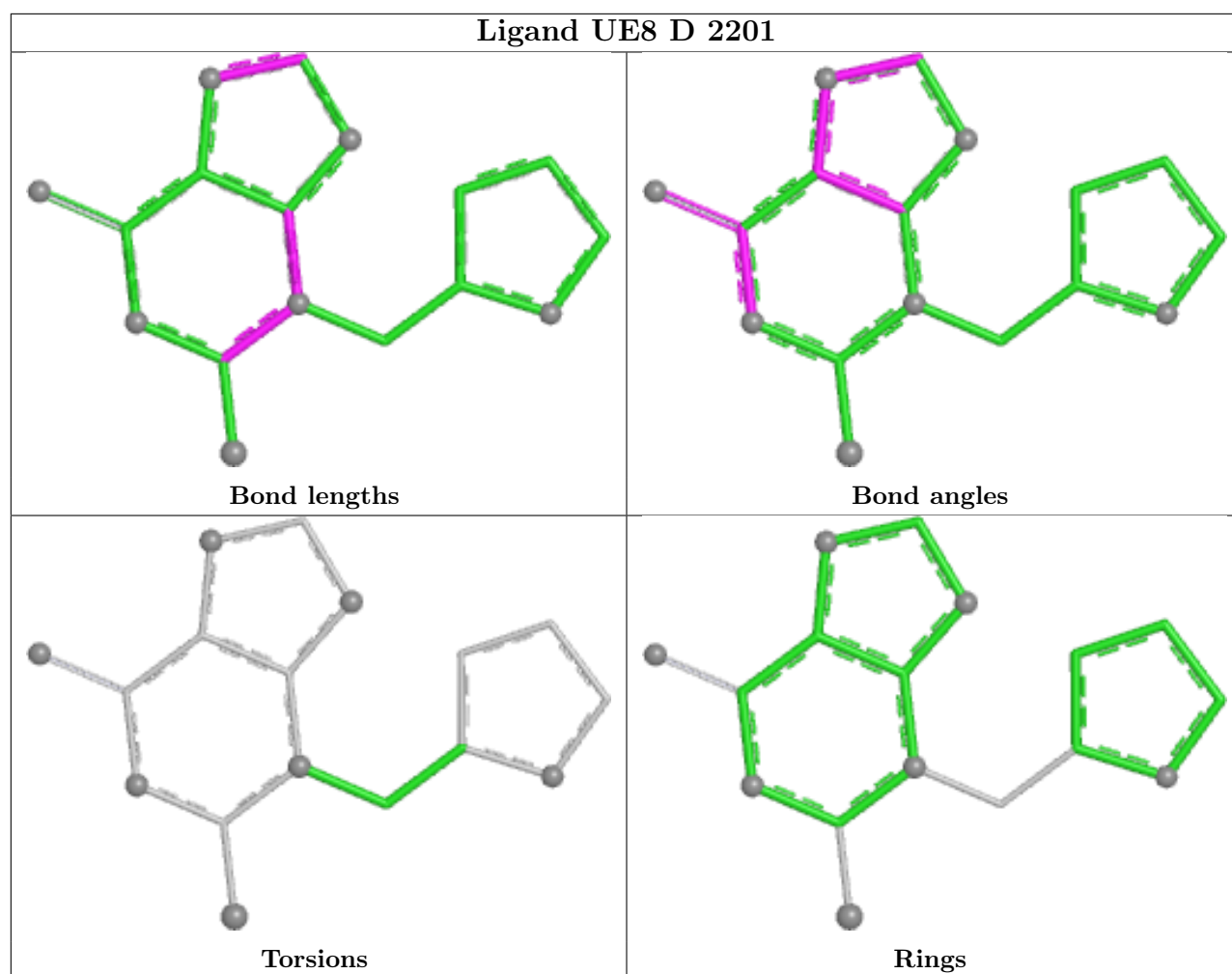
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	202	HEM	1	0

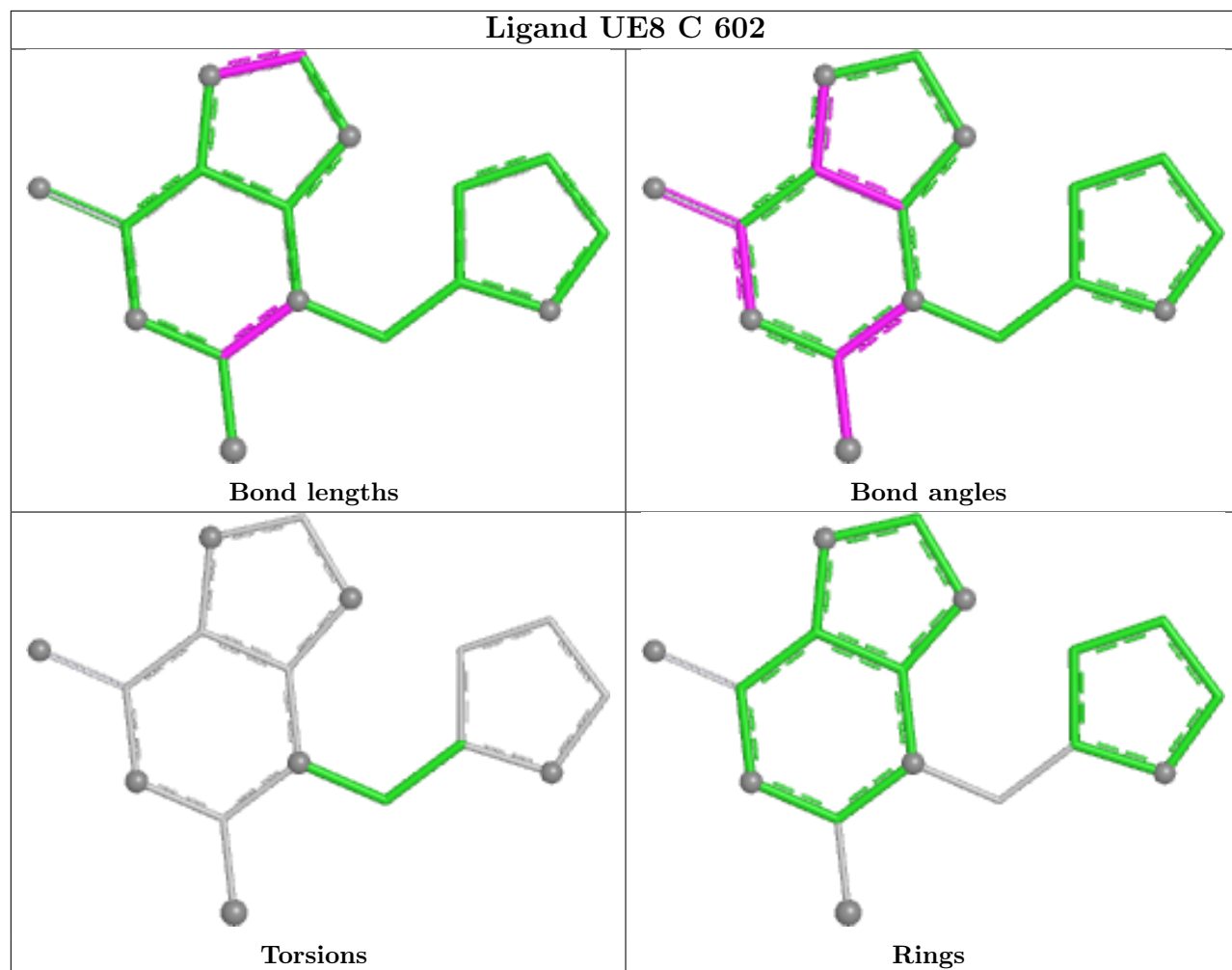
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

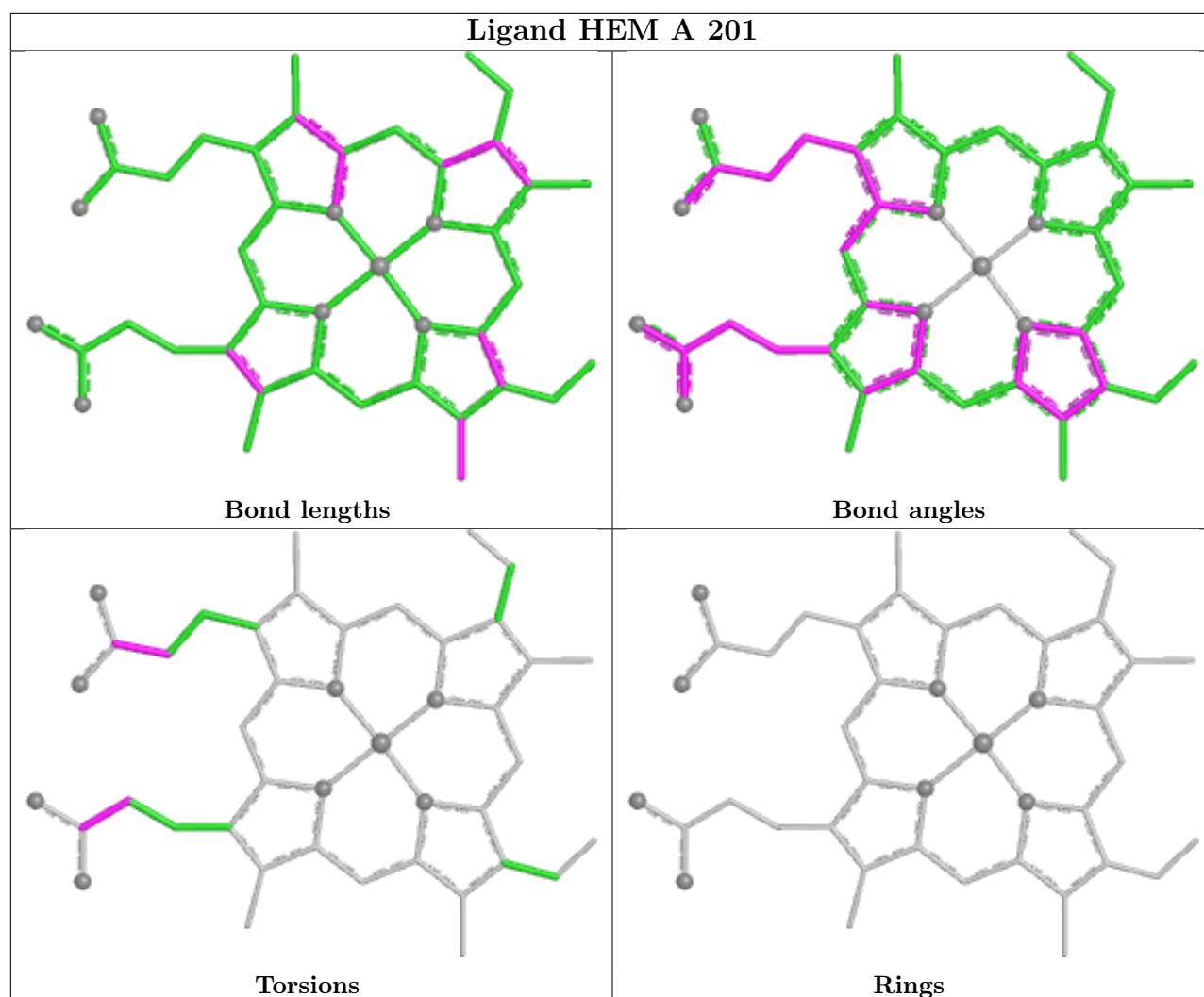
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





Ligand UE8 C 602





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	105/105 (100%)	-0.10	6 (5%) 29 31	4, 10, 36, 57	0
1	B	103/105 (98%)	-0.23	1 (0%) 79 81	6, 13, 28, 44	0
2	C	463/466 (99%)	-0.17	7 (1%) 72 74	4, 13, 33, 52	0
2	D	463/466 (99%)	-0.07	7 (1%) 72 74	5, 16, 35, 56	0
All	All	1134/1142 (99%)	-0.13	21 (1%) 66 69	4, 14, 35, 57	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	4	GLN	4.7
2	D	355	PRO	4.1
1	A	4	GLN	3.8
1	A	3	GLU	3.6
2	C	559	ARG	3.1

6.2 Non-standard residues in protein, DNA, RNA chains [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	CSO	D	150	7/8	0.95	0.08	13,15,25,26	0
2	CSO	C	150	7/8	0.98	0.05	6,12,15,15	0

6.3 Carbohydrates

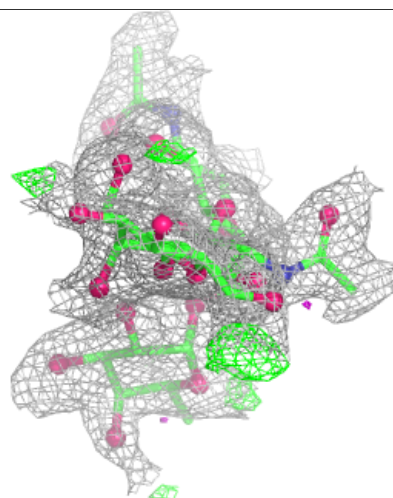
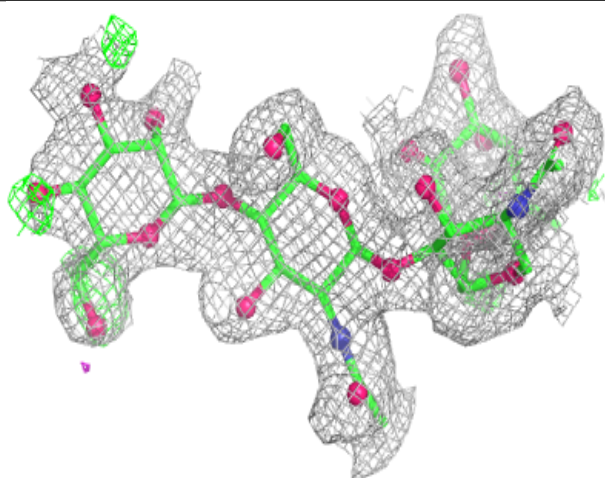
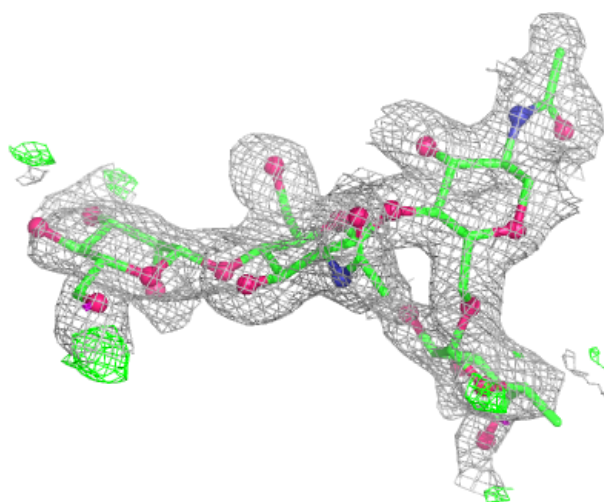
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

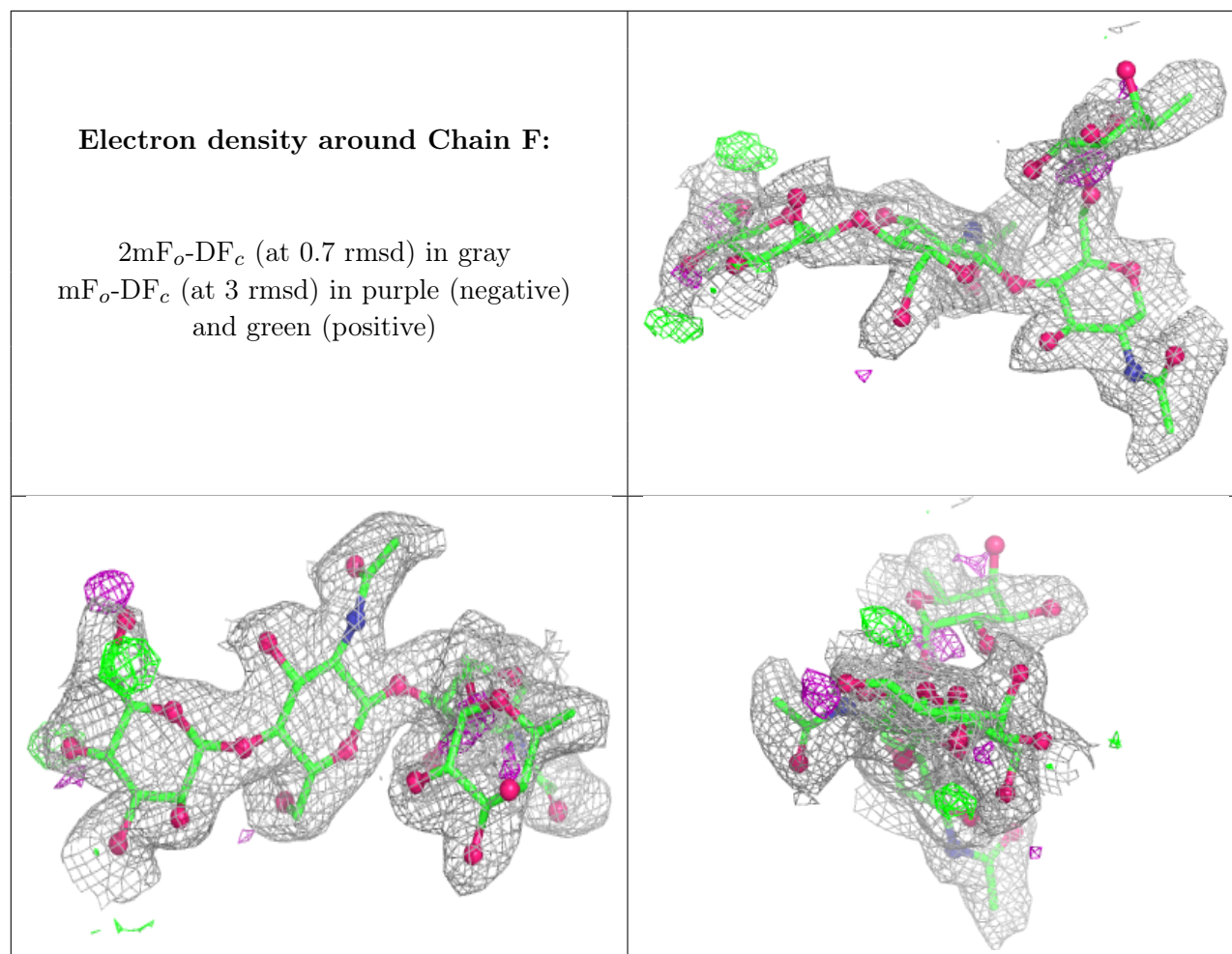
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	BMA	F	3	11/12	0.78	0.15	28,35,36,36	0
3	BMA	E	3	11/12	0.80	0.15	31,35,38,40	0
3	FUC	F	4	10/11	0.83	0.14	35,38,41,45	0
3	FUC	E	4	10/11	0.87	0.12	22,27,28,30	0
3	NAG	F	1	14/15	0.90	0.09	14,18,21,28	0
3	NAG	E	1	14/15	0.96	0.06	6,10,22,24	0
3	NAG	F	2	14/15	0.96	0.06	10,16,19,25	0
3	NAG	E	2	14/15	0.97	0.05	9,10,14,23	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 E:

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





6.4 Ligands [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
9	BMA	D	2202	11/12	0.72	0.24	68,70,72,73	0
8	NAG	D	2204	14/15	0.80	0.14	38,42,47,48	0
9	BMA	C	607	11/12	0.81	0.14	30,36,39,40	0
8	NAG	C	606	14/15	0.88	0.11	31,35,37,38	0
6	UE8	C	602	17/17	0.88	0.12	12,31,43,44	0
8	NAG	D	2203	14/15	0.89	0.10	13,22,27,29	0
6	UE8	D	2201	17/17	0.89	0.13	30,40,50,50	0
8	NAG	C	605	14/15	0.93	0.07	18,23,27,28	0
5	CL	C	604	1/1	0.96	0.05	31,31,31,31	0
4	HEM	B	202	43/43	0.97	0.07	11,12,15,19	0

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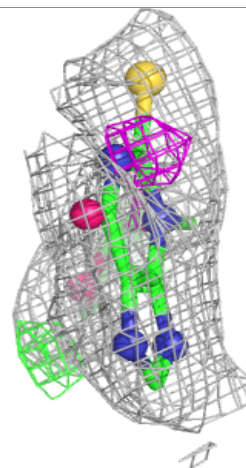
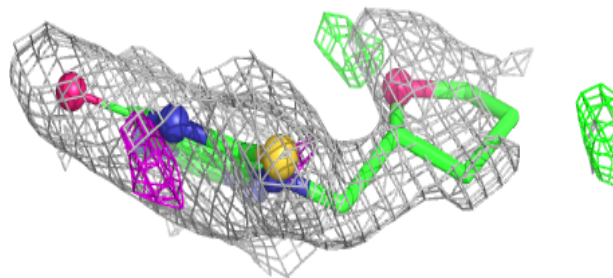
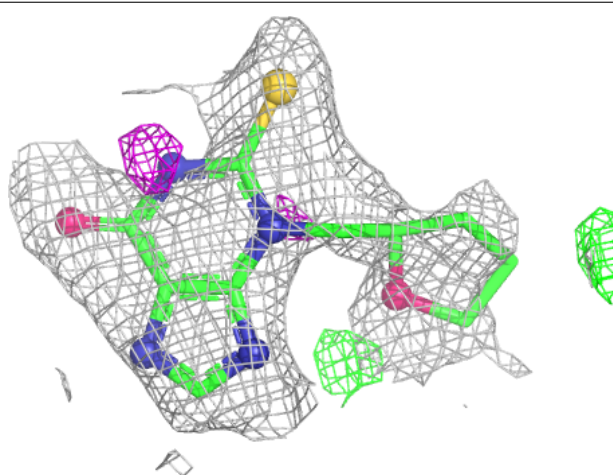
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	CL	B	203	1/1	0.98	0.10	25,25,25,25	0
4	HEM	A	201	43/43	0.98	0.06	7,8,11,17	0
5	CL	A	202	1/1	0.99	0.07	23,23,23,23	0
5	CL	C	601	1/1	0.99	0.02	6,6,6,6	0
7	CA	C	603	1/1	0.99	0.01	3,3,3,3	0
7	CA	D	2205	1/1	0.99	0.05	3,3,3,3	1
5	CL	B	201	1/1	0.99	0.03	11,11,11,11	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.

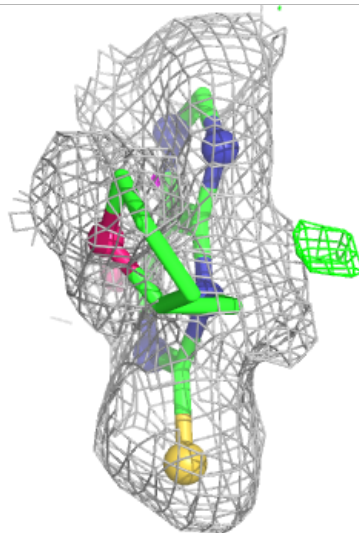
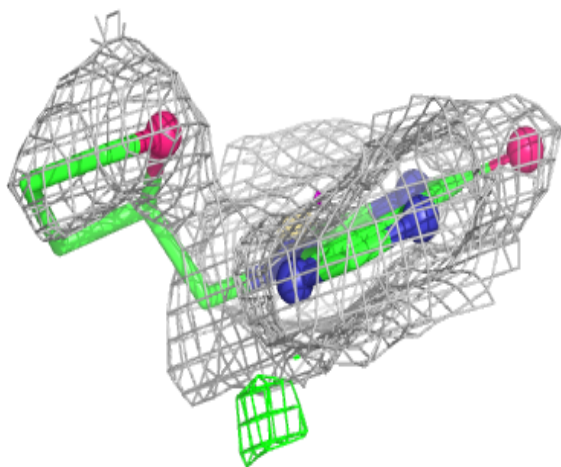
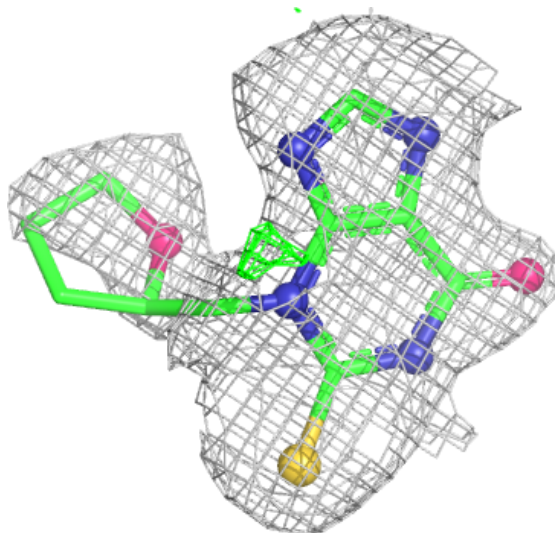
Electron density around UE8 C 602:

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



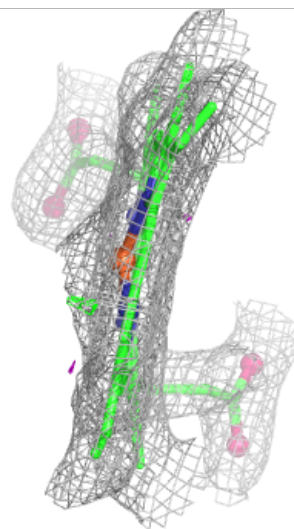
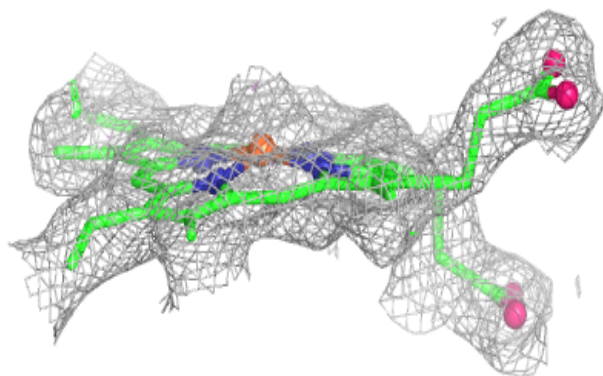
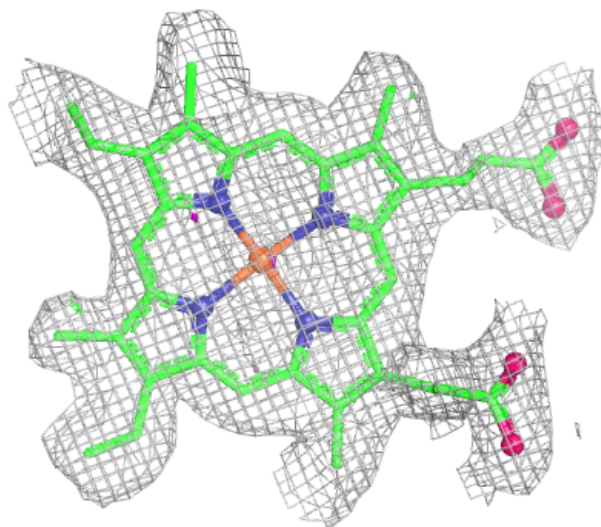
Electron density around UE8 D 2201:

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



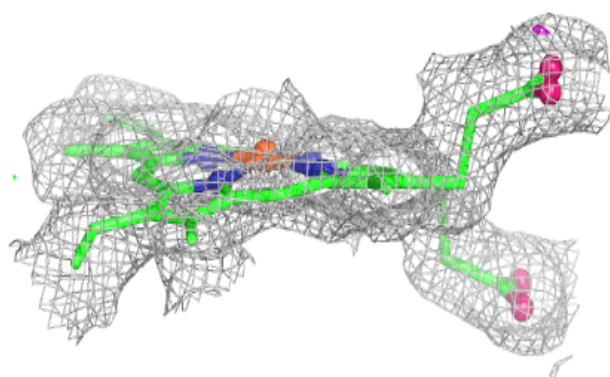
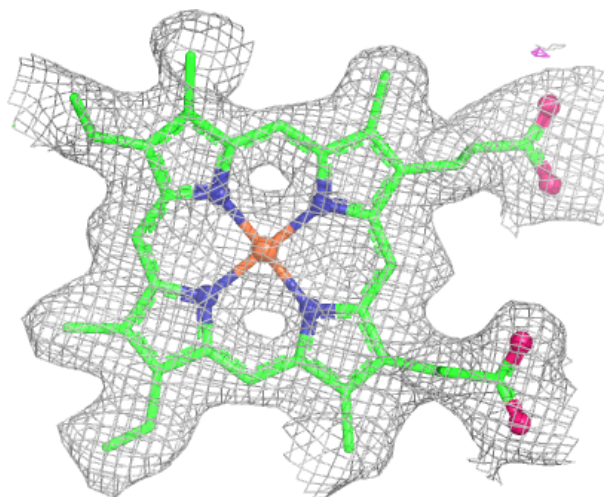
Electron density around HEM B 202:

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



Electron density around HEM A 201:

$2mF_o-DF_c$ (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.