



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 15, 2024 – 05:32 PM EST

PDB ID : 6WY0
Title : CRYSTAL STRUCTURE OF MYELOPEROXIDASE SUBFORM C (MPO)
COMPLEX WITH Compound-40 A.K.A 7-[(1R)-1-phenyl-3-{[(1r,4r)-4-phenylcyclohexyl]amino}propyl]-3H-[1,2,3]triazolo[4,5-b]pyridin-5-amine
Authors : Khan, J.A.
Deposited on : 2020-05-12
Resolution : 2.80 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

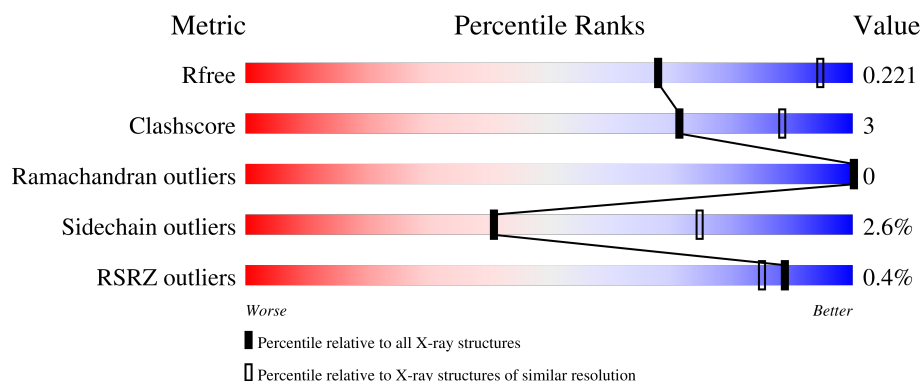
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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.







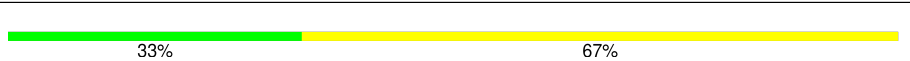
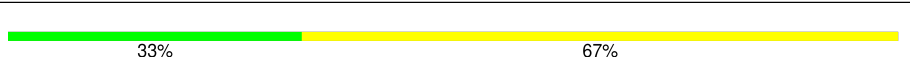
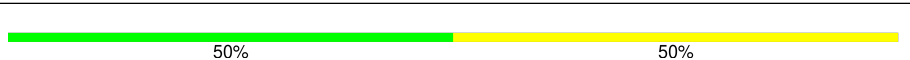
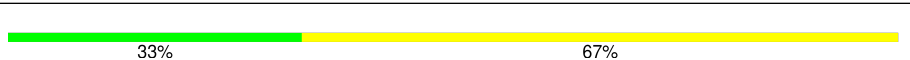
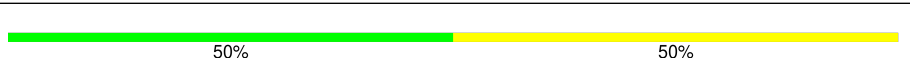
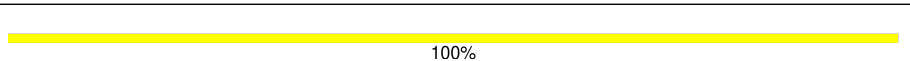
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	3657 (2.80-2.80)
Clashscore	180529	4123 (2.80-2.80)
Ramachandran outliers	177936	4071 (2.80-2.80)
Sidechain outliers	177891	4073 (2.80-2.80)
RSRZ outliers	164620	3659 (2.80-2.80)

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	<div> <div>84%</div> <div>14%</div> <div>.</div> </div>
1	D	105	<div> <div>92%</div> <div>6%</div> <div>..</div> </div>
1	F	105	<div> <div>93%</div> <div>6%</div> <div>.</div> </div>
1	H	105	<div> <div>90%</div> <div>9%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
2	B	467	
2	E	467	
2	G	467	
2	I	467	
3	C	6	
3	K	6	
3	M	6	
3	N	6	
4	J	2	
4	L	2	

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
8	CL	D	202	-	-	X	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 18744 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.

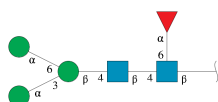
- Molecule 1 is a protein called Myeloperoxidase light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	103	Total	C	N	O	S	3	0	0
			825	522	145	153	5			
1	D	104	Total	C	N	O	S	0	0	0
			823	522	146	150	5			
1	F	104	Total	C	N	O	S	3	0	0
			824	522	145	152	5			
1	H	103	Total	C	N	O	S	0	0	0
			817	518	145	149	5			

- Molecule 2 is a protein called Myeloperoxidase heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	464	Total	C	N	O	S	25	0	0
			3638	2295	658	658	27			
2	E	465	Total	C	N	O	S	31	0	0
			3647	2307	655	658	27			
2	G	464	Total	C	N	O	S	28	0	0
			3650	2312	650	661	27			
2	I	465	Total	C	N	O	S	32	0	0
			3640	2305	652	656	27			

- 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
3	C	6	Total	C	N	O	0	0	0
			71	40	2	29			

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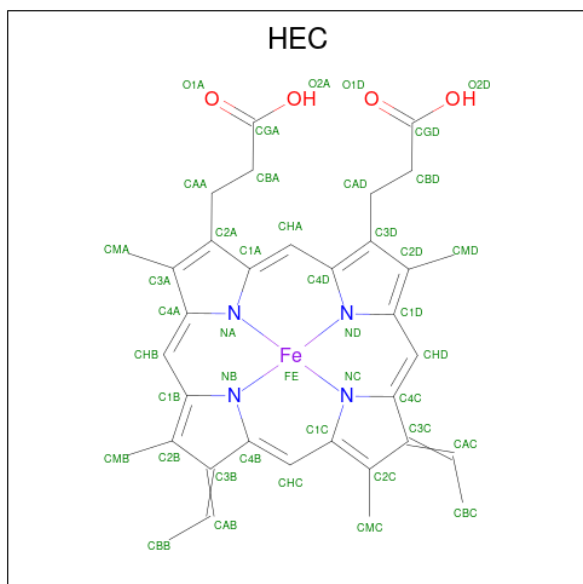
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	K	6	Total	C	N	O	0	0	0
			71	40	2	29			
3	M	6	Total	C	N	O	0	0	0
			71	40	2	29			
3	N	6	Total	C	N	O	0	0	0
			71	40	2	29			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	L	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is HEME C (three-letter code: HEC) (formula: C₃₄H₃₄FeN₄O₄).



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

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	G	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	I	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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



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

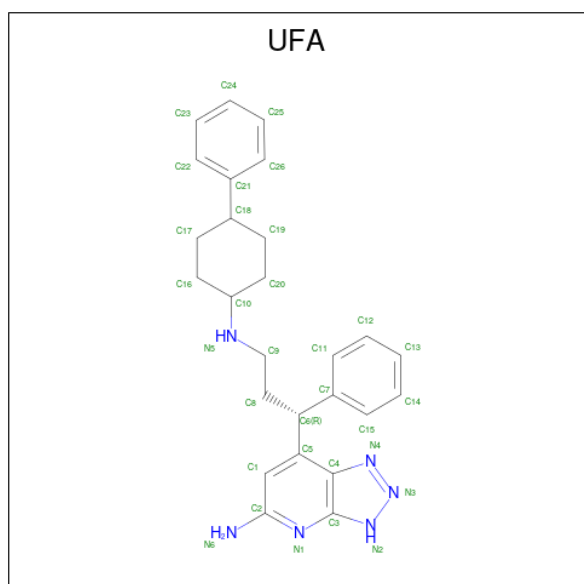
- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total Ca 1 1	0	0
7	E	1	Total Ca 1 1	0	0
7	G	1	Total Ca 1 1	0	0
7	I	1	Total Ca 1 1	0	0

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	2	Total Cl 2 2	0	0
8	D	1	Total Cl 1 1	0	0
8	E	2	Total Cl 2 2	0	0
8	F	1	Total Cl 1 1	0	0
8	G	1	Total Cl 1 1	0	0
8	I	1	Total Cl 1 1	0	0

- Molecule 9 is 7-{(1R)-1-phenyl-3-[(trans-4-phenylcyclohexyl)amino]propyl}-3H-[1,2,3]triazolo[4,5-b]pyridin-5-amine (three-letter code: UFA) (formula: C₂₆H₃₀N₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	N	0	0
			27	21	6		
9	E	1	Total	C	N	0	0
			32	26	6		
9	G	1	Total	C	N	0	0
			32	26	6		
9	I	1	Total	C	N	0	0
			32	26	6		

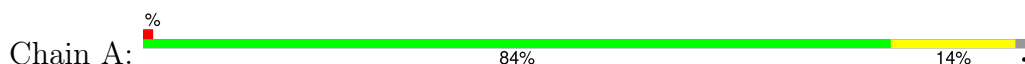
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	3	Total	O	0	0
			3	3		
10	B	28	Total	O	0	0
			28	28		
10	D	12	Total	O	0	0
			12	12		
10	E	31	Total	O	0	0
			31	31		
10	F	8	Total	O	0	0
			8	8		
10	G	28	Total	O	0	0
			28	28		
10	H	8	Total	O	0	0
			8	8		
10	I	31	Total	O	0	0
			31	31		

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 light chain



- Molecule 1: Myeloperoxidase light chain



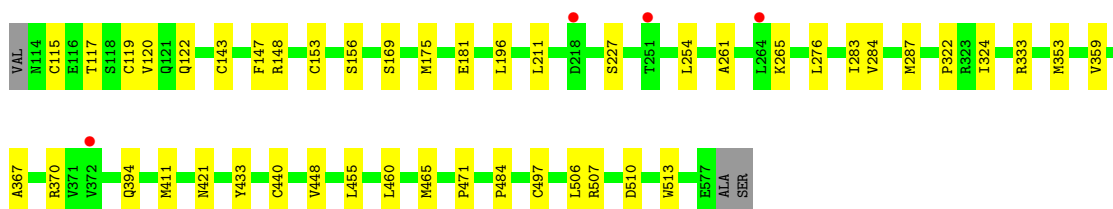
- Molecule 1: Myeloperoxidase light chain



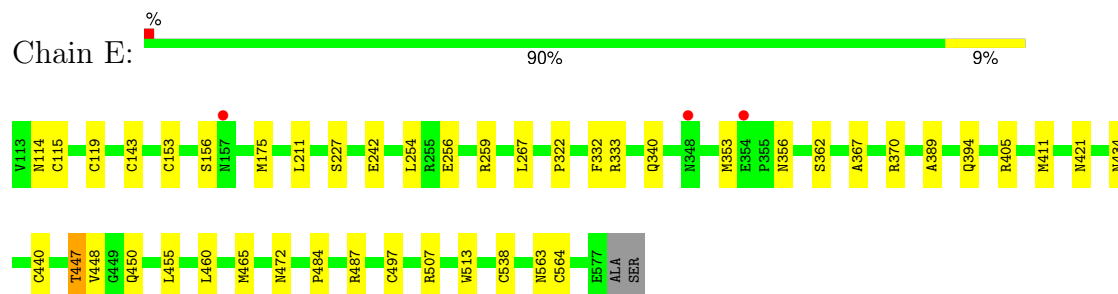
- Molecule 1: Myeloperoxidase light chain



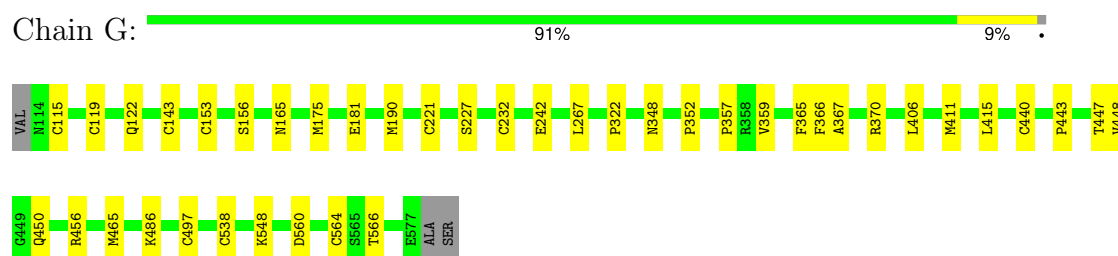
- Molecule 2: Myeloperoxidase heavy chain



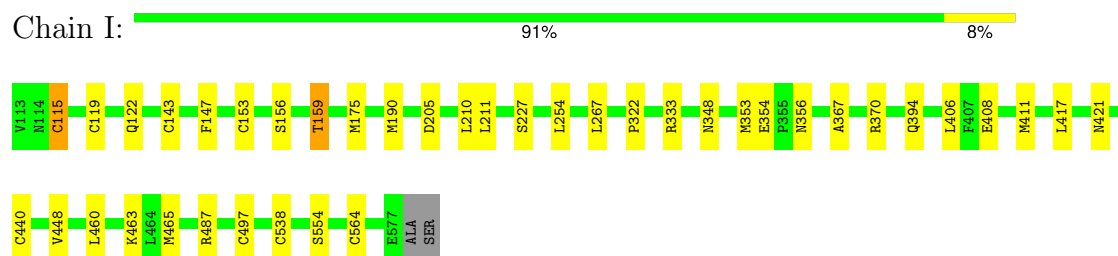
- Molecule 2: Myeloperoxidase heavy chain



- Molecule 2: Myeloperoxidase heavy chain



- Molecule 2: Myeloperoxidase heavy chain



- 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-acetamid o-2-deoxy-beta-D-glucopyranose

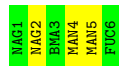


- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamid o-2-deoxy-beta-D-glucopyranose



- Molecule 3: α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-[α -L-fucopyranose-(1-6)]2-acetamido-2-deoxy- β -D-glucopyranose

Chain M:  50% 50%



- Molecule 3: α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-[α -L-fucopyranose-(1-6)]2-acetamido-2-deoxy- β -D-glucopyranose

Chain N:  33% 67%



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

Chain J:  50% 50%



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

Chain L:  100%



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	145.35Å 151.40Å 229.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.69 – 2.80 47.69 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.69-2.80) 99.9 (47.69-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.11.7 (17-DEC-2019)	Depositor
R, R_{free}	0.185 , 0.216 0.191 , 0.221	Depositor DCC
R_{free} test set	3172 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	53.4	Xtriage
Anisotropy	0.218	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.037 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	18744	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.50% 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, BMA, FUC, CL, CSO, NAG, HEC, UFA, MAN

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	0.43	0/850	0.63	0/1159
1	D	0.44	0/848	0.63	0/1157
1	F	0.44	0/849	0.64	0/1159
1	H	0.43	0/842	0.63	0/1149
2	B	0.41	0/3715	0.56	0/5052
2	E	0.43	0/3724	0.57	0/5065
2	G	0.43	0/3727	0.57	0/5065
2	I	0.42	0/3717	0.57	0/5057
All	All	0.43	0/18272	0.58	0/24863

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	825	0	780	9	0
1	D	823	0	779	6	0
1	F	824	0	774	4	0
1	H	817	0	772	6	0
2	B	3638	0	3562	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	3647	0	3589	24	0
2	G	3650	0	3598	20	0
2	I	3640	0	3572	19	0
3	C	71	0	61	0	0
3	K	71	0	61	0	0
3	M	71	0	61	0	0
3	N	71	0	61	0	0
4	J	28	0	25	0	0
4	L	28	0	25	0	0
5	A	43	0	28	1	0
5	D	43	0	28	2	0
5	G	43	0	28	2	0
5	I	43	0	28	2	0
6	B	28	0	26	0	0
6	E	14	0	13	0	0
6	G	14	0	13	0	0
6	I	28	0	26	0	0
7	B	1	0	0	0	0
7	E	1	0	0	0	0
7	G	1	0	0	0	0
7	I	1	0	0	0	0
8	B	2	0	0	0	0
8	D	1	0	0	2	0
8	E	2	0	0	1	0
8	F	1	0	0	0	0
8	G	1	0	0	0	0
8	I	1	0	0	0	0
9	B	27	0	0	0	0
9	E	32	0	0	1	0
9	G	32	0	0	1	0
9	I	32	0	0	0	0
10	A	3	0	0	0	0
10	B	28	0	0	0	0
10	D	12	0	0	0	0
10	E	31	0	0	0	0
10	F	8	0	0	0	0
10	G	28	0	0	0	0
10	H	8	0	0	0	0
10	I	31	0	0	0	0
All	All	18744	0	17910	101	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.

The worst 5 of 101 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:I:119:CYS:HG	2:I:143:CYS:HG	1.00	0.96
2:B:119:CYS:HG	2:B:143:CYS:HG	1.05	0.92
2:E:119:CYS:HG	2:E:143:CYS:HG	0.89	0.84
2:G:221:CYS:HG	2:G:232:CYS:HG	0.85	0.82
2:E:440:CYS:HG	2:E:497:CYS:HG	1.06	0.82

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	101/105 (96%)	98 (97%)	3 (3%)	0	100	100
1	D	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
1	F	102/105 (97%)	99 (97%)	3 (3%)	0	100	100
1	H	101/105 (96%)	97 (96%)	4 (4%)	0	100	100
2	B	461/467 (99%)	447 (97%)	14 (3%)	0	100	100
2	E	462/467 (99%)	448 (97%)	14 (3%)	0	100	100
2	G	461/467 (99%)	447 (97%)	14 (3%)	0	100	100
2	I	462/467 (99%)	448 (97%)	14 (3%)	0	100	100
All	All	2252/2288 (98%)	2184 (97%)	68 (3%)	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	88/90 (98%)	85 (97%)	3 (3%)	32	66
1	D	86/90 (96%)	84 (98%)	2 (2%)	45	78
1	F	86/90 (96%)	85 (99%)	1 (1%)	67	89
1	H	86/90 (96%)	85 (99%)	1 (1%)	67	89
2	B	390/411 (95%)	382 (98%)	8 (2%)	48	80
2	E	392/411 (95%)	382 (97%)	10 (3%)	41	75
2	G	394/411 (96%)	383 (97%)	11 (3%)	38	72
2	I	389/411 (95%)	375 (96%)	14 (4%)	30	64
All	All	1911/2004 (95%)	1861 (97%)	50 (3%)	41	75

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	190	MET
1	H	1	CYS
2	I	487	ARG
2	G	227	SER
2	G	359	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	348	ASN
2	I	421	ASN
2	I	563	ASN
2	E	114	ASN
2	E	122	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	E	150	2	3,6,7	0.79	0	1,6,8	0.09	0
2	CSO	I	150	2	3,6,7	0.73	0	1,6,8	0.41	0
2	CSO	G	150	2	3,6,7	0.86	0	1,6,8	0.21	0
2	CSO	B	150	2	3,6,7	0.89	0	1,6,8	0.71	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	CSO	E	150	2	-	0/1/5/7	-
2	CSO	I	150	2	-	0/1/5/7	-
2	CSO	G	150	2	-	0/1/5/7	-
2	CSO	B	150	2	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

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 ⓘ

28 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	C	1	3,2	14,14,15	0.31	0	17,19,21	0.98	1 (5%)
3	NAG	C	2	3	14,14,15	0.30	0	17,19,21	0.77	1 (5%)
3	BMA	C	3	3	11,11,12	0.27	0	15,15,17	0.72	0
3	MAN	C	4	3	11,11,12	0.31	0	15,15,17	1.14	1 (6%)
3	MAN	C	5	3	11,11,12	0.33	0	15,15,17	0.89	1 (6%)
3	FUC	C	6	3	10,10,11	0.37	0	14,14,16	0.67	0
4	NAG	J	1	4,2	14,14,15	0.28	0	17,19,21	0.52	0
4	NAG	J	2	4	14,14,15	0.31	0	17,19,21	1.56	3 (17%)
3	NAG	K	1	3,2	14,14,15	0.34	0	17,19,21	1.01	1 (5%)
3	NAG	K	2	3	14,14,15	0.36	0	17,19,21	0.94	1 (5%)
3	BMA	K	3	3	11,11,12	0.28	0	15,15,17	0.67	0
3	MAN	K	4	3	11,11,12	0.32	0	15,15,17	1.26	1 (6%)
3	MAN	K	5	3	11,11,12	0.32	0	15,15,17	1.05	1 (6%)
3	FUC	K	6	3	10,10,11	0.37	0	14,14,16	0.61	0
4	NAG	L	1	4,2	14,14,15	0.28	0	17,19,21	0.89	1 (5%)
4	NAG	L	2	4	14,14,15	0.28	0	17,19,21	0.75	1 (5%)
3	NAG	M	1	3,2	14,14,15	0.40	0	17,19,21	1.00	0
3	NAG	M	2	3	14,14,15	0.35	0	17,19,21	0.88	1 (5%)
3	BMA	M	3	3	11,11,12	0.27	0	15,15,17	0.65	0
3	MAN	M	4	3	11,11,12	0.26	0	15,15,17	1.19	1 (6%)
3	MAN	M	5	3	11,11,12	0.36	0	15,15,17	0.92	1 (6%)
3	FUC	M	6	3	10,10,11	0.34	0	14,14,16	0.62	0
3	NAG	N	1	3,2	14,14,15	0.33	0	17,19,21	1.13	2 (11%)
3	NAG	N	2	3	14,14,15	0.33	0	17,19,21	0.95	1 (5%)
3	BMA	N	3	3	11,11,12	0.28	0	15,15,17	0.73	0
3	MAN	N	4	3	11,11,12	0.33	0	15,15,17	1.21	1 (6%)
3	MAN	N	5	3	11,11,12	0.30	0	15,15,17	0.92	1 (6%)
3	FUC	N	6	3	10,10,11	0.42	0	14,14,16	0.56	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	C	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1
3	MAN	C	4	3	-	0/2/19/22	0/1/1/1
3	MAN	C	5	3	-	0/2/19/22	0/1/1/1
3	FUC	C	6	3	-	-	0/1/1/1
4	NAG	J	1	4,2	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	1/6/23/26	0/1/1/1
3	NAG	K	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	K	2	3	-	0/6/23/26	0/1/1/1
3	BMA	K	3	3	-	0/2/19/22	0/1/1/1
3	MAN	K	4	3	-	2/2/19/22	0/1/1/1
3	MAN	K	5	3	-	0/2/19/22	0/1/1/1
3	FUC	K	6	3	-	-	0/1/1/1
4	NAG	L	1	4,2	-	1/6/23/26	0/1/1/1
4	NAG	L	2	4	-	1/6/23/26	0/1/1/1
3	NAG	M	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	M	2	3	-	0/6/23/26	0/1/1/1
3	BMA	M	3	3	-	0/2/19/22	0/1/1/1
3	MAN	M	4	3	-	1/2/19/22	0/1/1/1
3	MAN	M	5	3	-	0/2/19/22	0/1/1/1
3	FUC	M	6	3	-	-	0/1/1/1
3	NAG	N	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	N	2	3	-	0/6/23/26	0/1/1/1
3	BMA	N	3	3	-	0/2/19/22	0/1/1/1
3	MAN	N	4	3	-	1/2/19/22	0/1/1/1
3	MAN	N	5	3	-	0/2/19/22	0/1/1/1
3	FUC	N	6	3	-	-	0/1/1/1

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	4	MAN	C1-O5-C5	4.40	118.09	112.19
3	K	4	MAN	C1-O5-C5	4.32	117.97	112.19
4	J	2	NAG	C1-O5-C5	4.26	117.90	112.19
3	M	4	MAN	C1-O5-C5	4.21	117.83	112.19
3	C	4	MAN	C1-O5-C5	3.95	117.49	112.19

There are no chirality outliers.

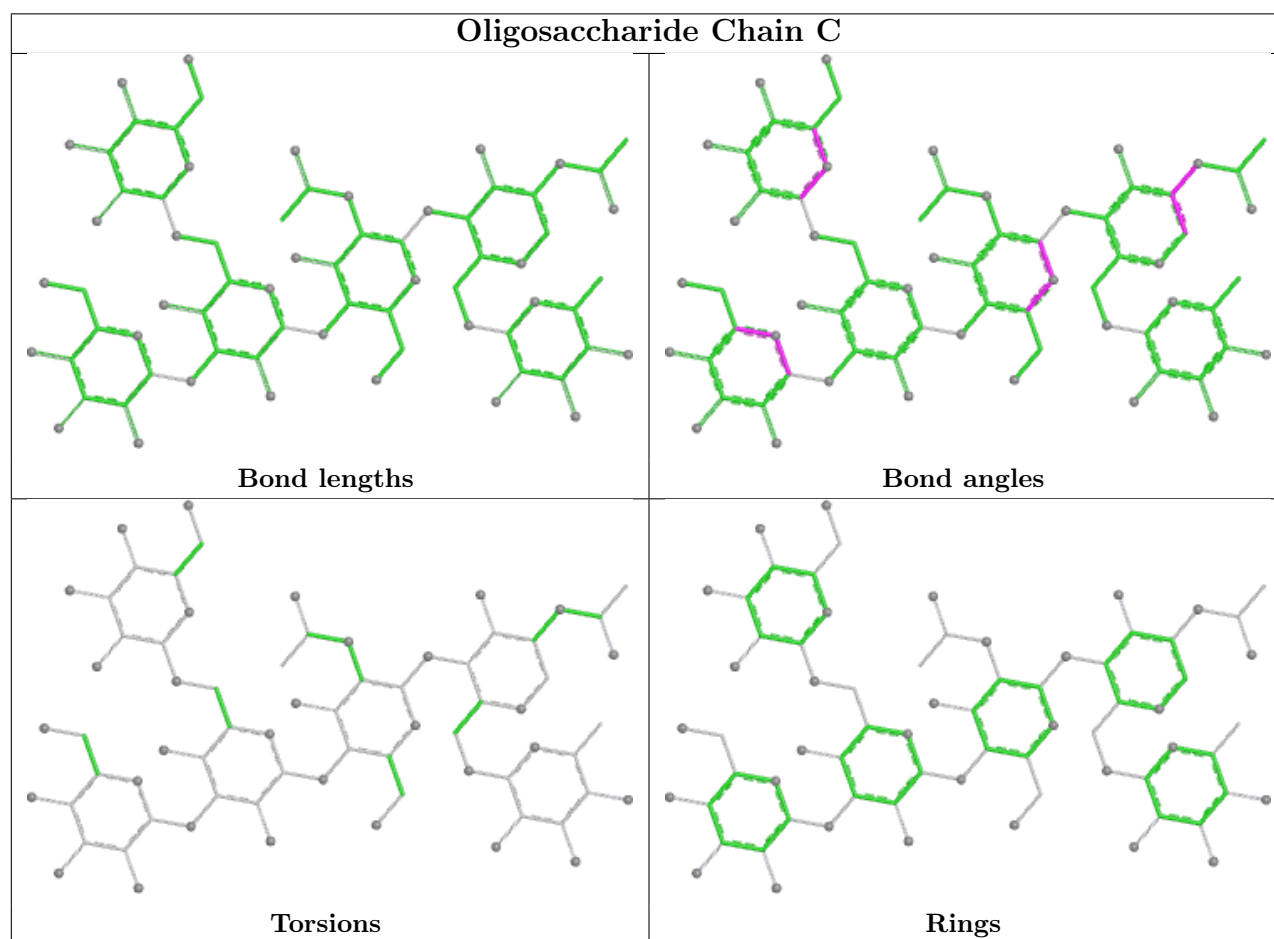
5 of 7 torsion outliers are listed below:

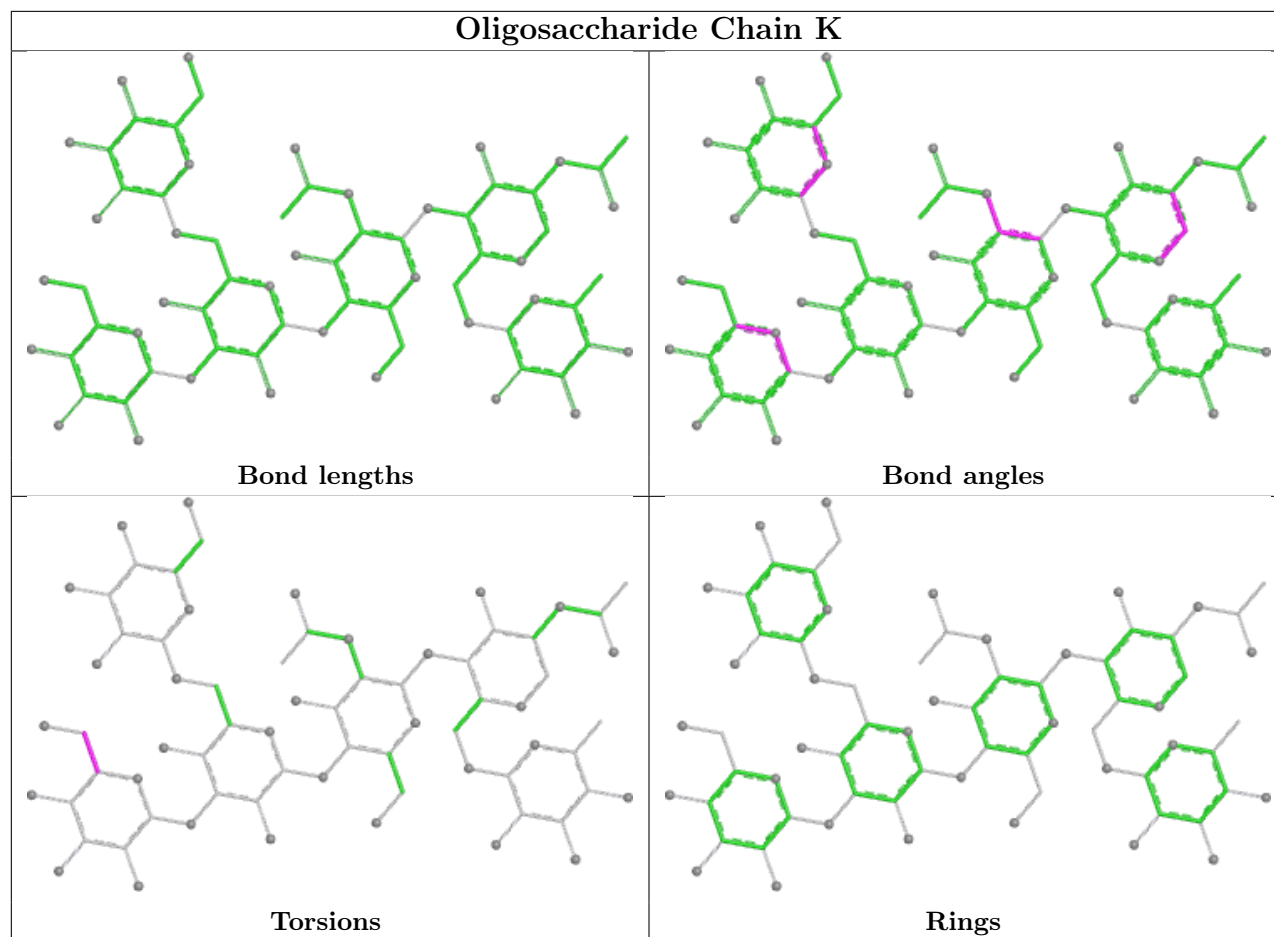
Mol	Chain	Res	Type	Atoms
3	K	4	MAN	O5-C5-C6-O6
3	N	4	MAN	O5-C5-C6-O6
4	L	2	NAG	O5-C5-C6-O6
3	M	4	MAN	O5-C5-C6-O6
4	L	1	NAG	C4-C5-C6-O6

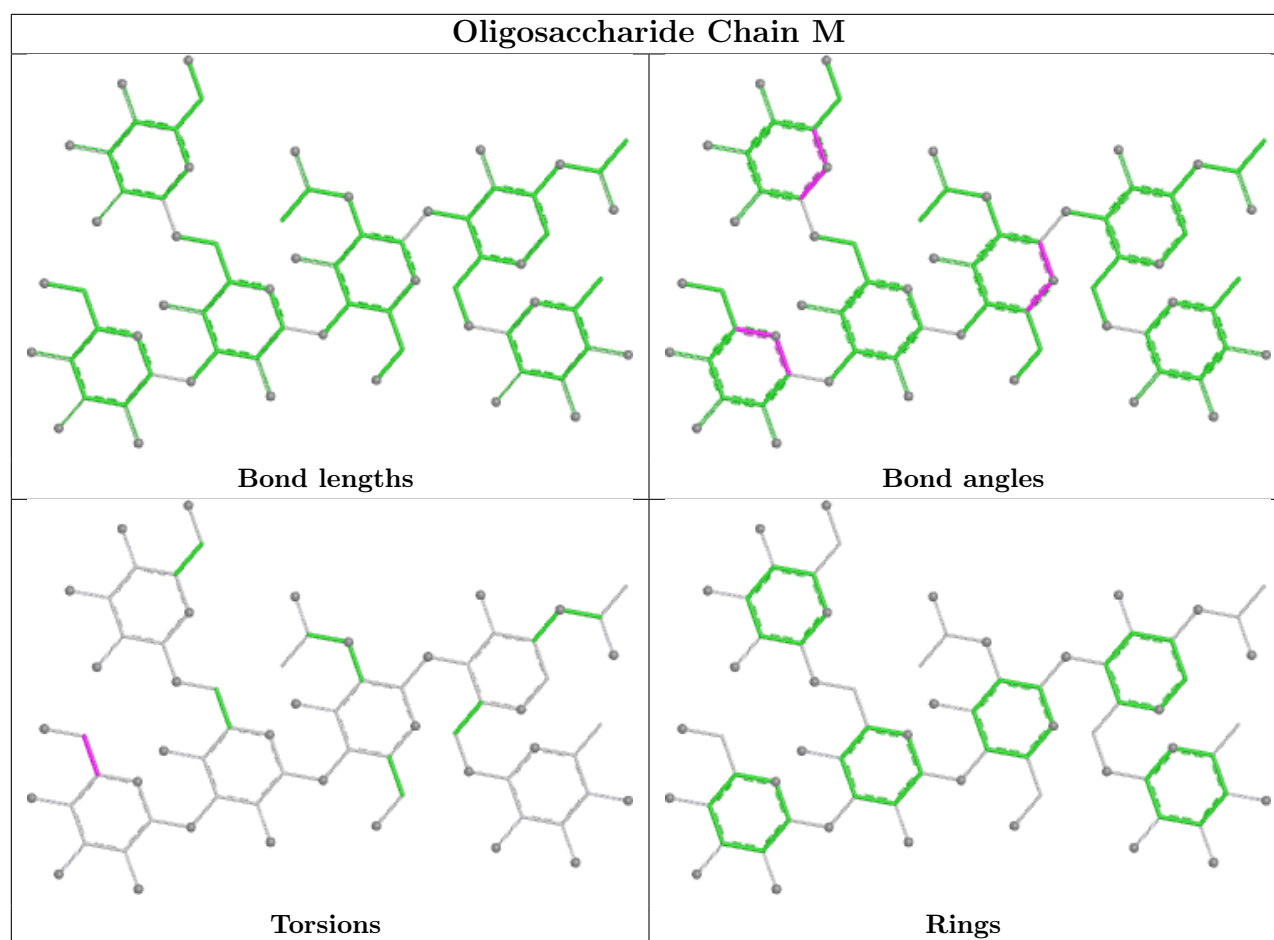
There are no ring outliers.

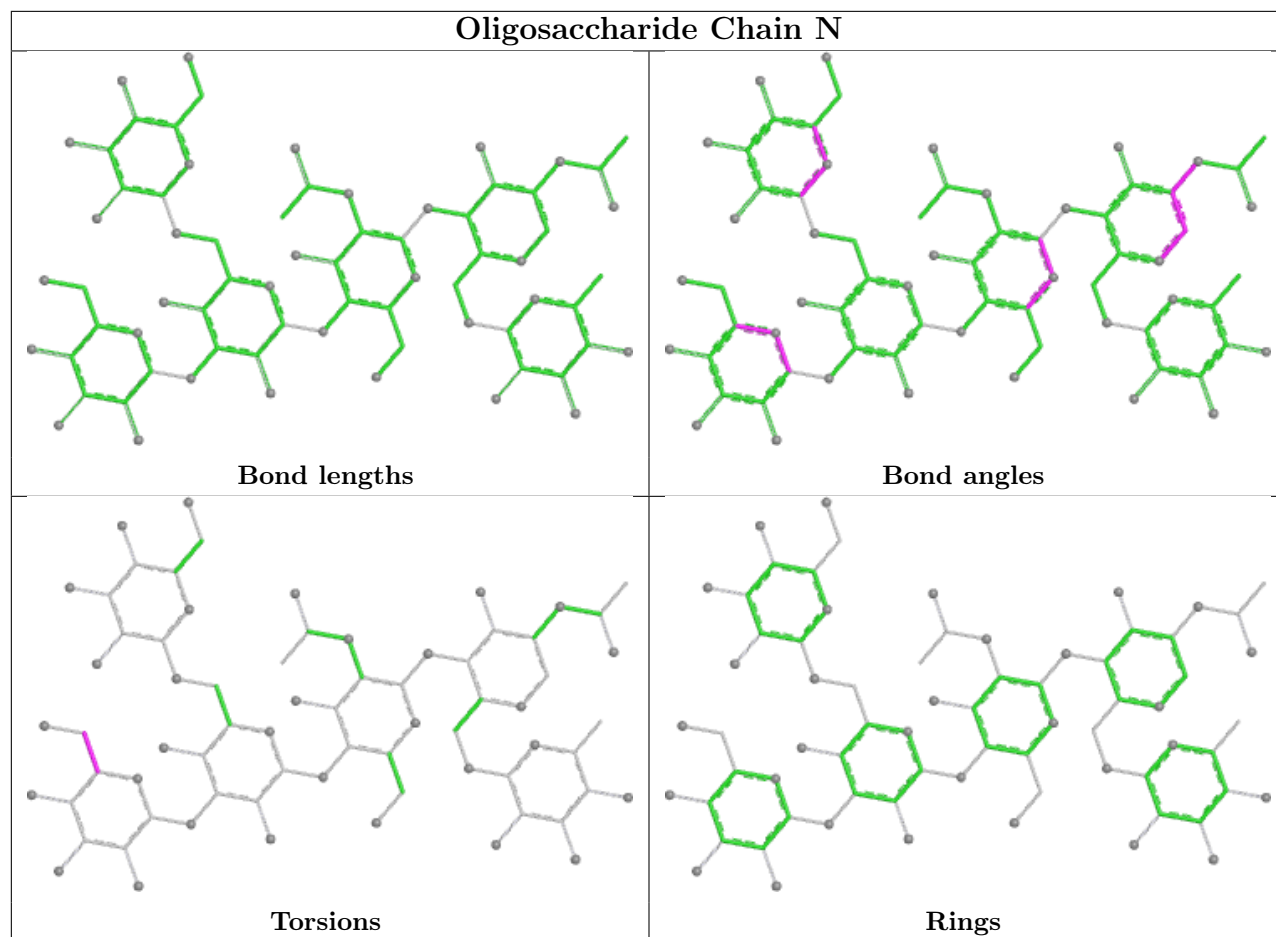
No monomer is involved in short contacts.

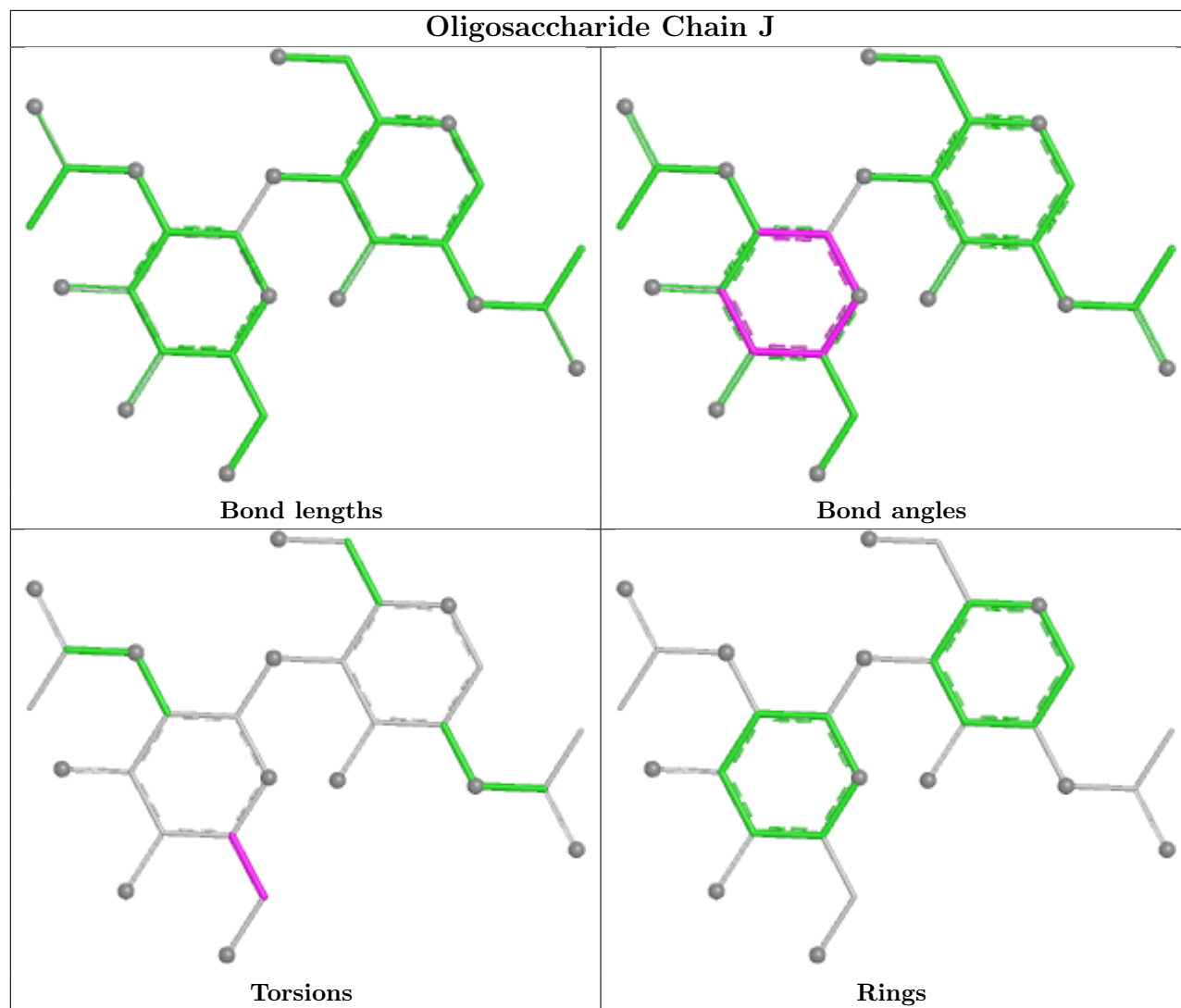
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

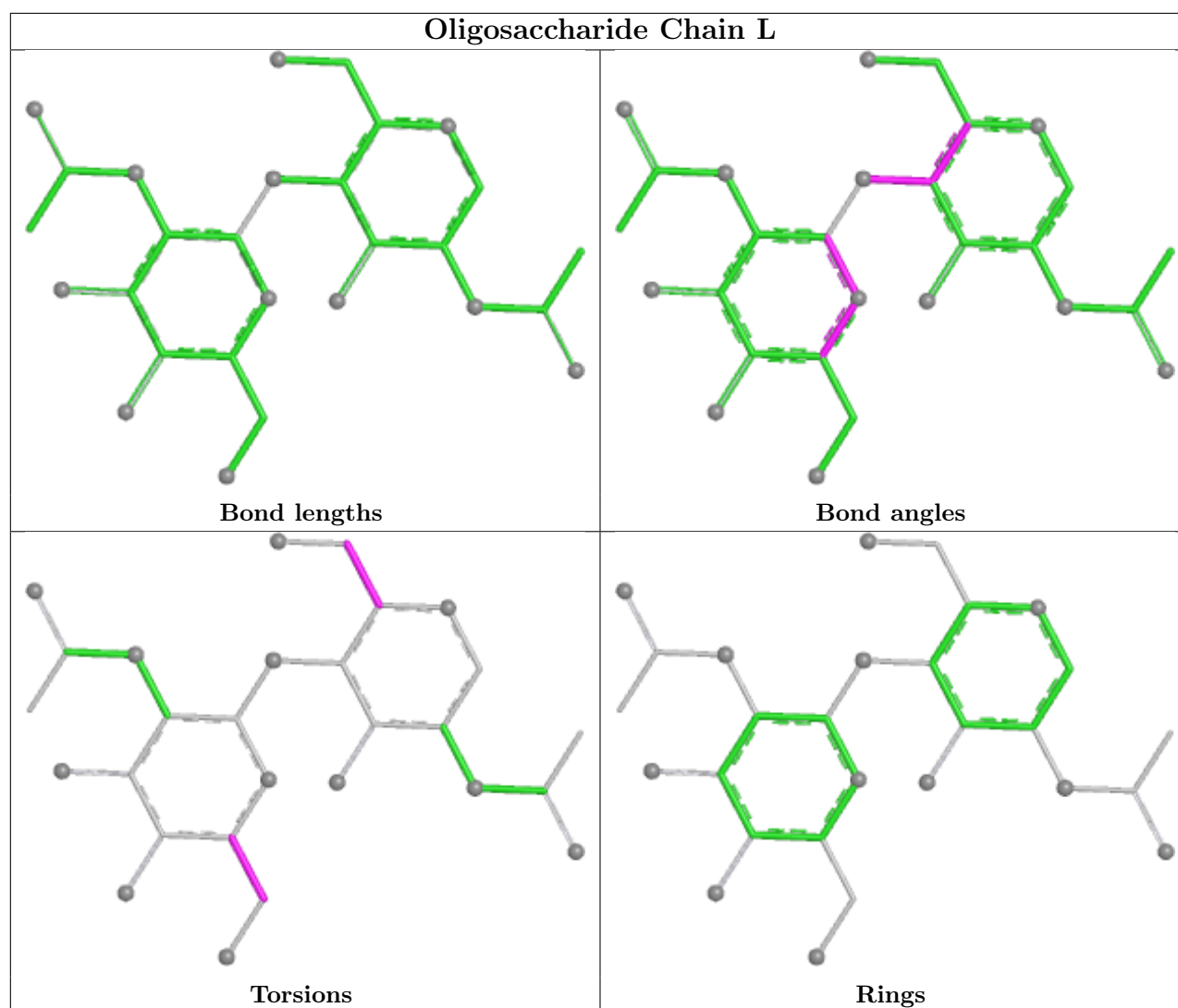












5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 12 are monoatomic - leaving 14 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	$\# Z > 2$
9	UFA	E	605	-	33,36,36	1.60	5 (15%)	39,49,49	1.40	3 (7%)
5	HEC	G	601	2	32,50,50	1.82	5 (15%)	30,82,82	1.61	7 (23%)
6	NAG	E	601	2	14,14,15	0.33	0	17,19,21	0.99	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	G	602	2	14,14,15	0.32	0	17,19,21	0.89	1 (5%)
6	NAG	I	603	2	14,14,15	0.29	0	17,19,21	0.59	0
9	UFA	B	606	-	27,30,36	1.78	4 (14%)	31,41,49	1.58	5 (16%)
9	UFA	I	606	-	33,36,36	1.35	6 (18%)	39,49,49	1.82	6 (15%)
5	HEC	A	201	2	32,50,50	1.86	5 (15%)	30,82,82	1.86	9 (30%)
6	NAG	B	601	2	14,14,15	0.29	0	17,19,21	1.11	1 (5%)
6	NAG	B	602	2	14,14,15	0.28	0	17,19,21	0.67	1 (5%)
5	HEC	D	201	2	32,50,50	1.70	4 (12%)	30,82,82	1.98	10 (33%)
5	HEC	I	601	2	32,50,50	1.77	5 (15%)	30,82,82	1.78	8 (26%)
9	UFA	G	605	-	33,36,36	1.63	9 (27%)	39,49,49	1.32	4 (10%)
6	NAG	I	602	2	14,14,15	0.31	0	17,19,21	1.22	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
9	UFA	E	605	-	-	2/18/28/28	0/5/5/5
5	HEC	G	601	2	-	4/10/54/54	-
6	NAG	E	601	2	-	0/6/23/26	0/1/1/1
6	NAG	G	602	2	-	0/6/23/26	0/1/1/1
6	NAG	I	603	2	-	0/6/23/26	0/1/1/1
9	UFA	B	606	-	-	2/14/24/28	0/4/4/5
9	UFA	I	606	-	-	2/18/28/28	0/5/5/5
5	HEC	A	201	2	-	4/10/54/54	-
6	NAG	B	601	2	-	0/6/23/26	0/1/1/1
6	NAG	B	602	2	-	0/6/23/26	0/1/1/1
5	HEC	D	201	2	-	4/10/54/54	-
5	HEC	I	601	2	-	4/10/54/54	-
9	UFA	G	605	-	-	1/18/28/28	0/5/5/5
6	NAG	I	602	2	-	0/6/23/26	0/1/1/1

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	201	HEC	C2B-C3B	-5.87	1.34	1.40
9	B	606	UFA	C2-N1	5.84	1.40	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	601	HEC	C2B-C3B	-5.21	1.34	1.40
9	E	605	UFA	C2-N1	5.13	1.39	1.33
5	D	201	HEC	C2B-C3B	-5.12	1.35	1.40

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	606	UFA	C2-N1-C3	-5.66	110.53	119.22
9	I	606	UFA	C8-C9-N5	5.49	121.04	111.89
9	B	606	UFA	C2-N1-C3	-5.40	110.93	119.22
9	E	605	UFA	C2-N1-C3	-4.72	111.98	119.22
9	I	606	UFA	N6-C2-N1	-4.31	114.67	118.24

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	B	606	UFA	C6-C8-C9-N5
9	E	605	UFA	C6-C8-C9-N5
9	G	605	UFA	C6-C8-C9-N5
9	I	606	UFA	C16-C10-N5-C9
9	E	605	UFA	C7-C6-C8-C9

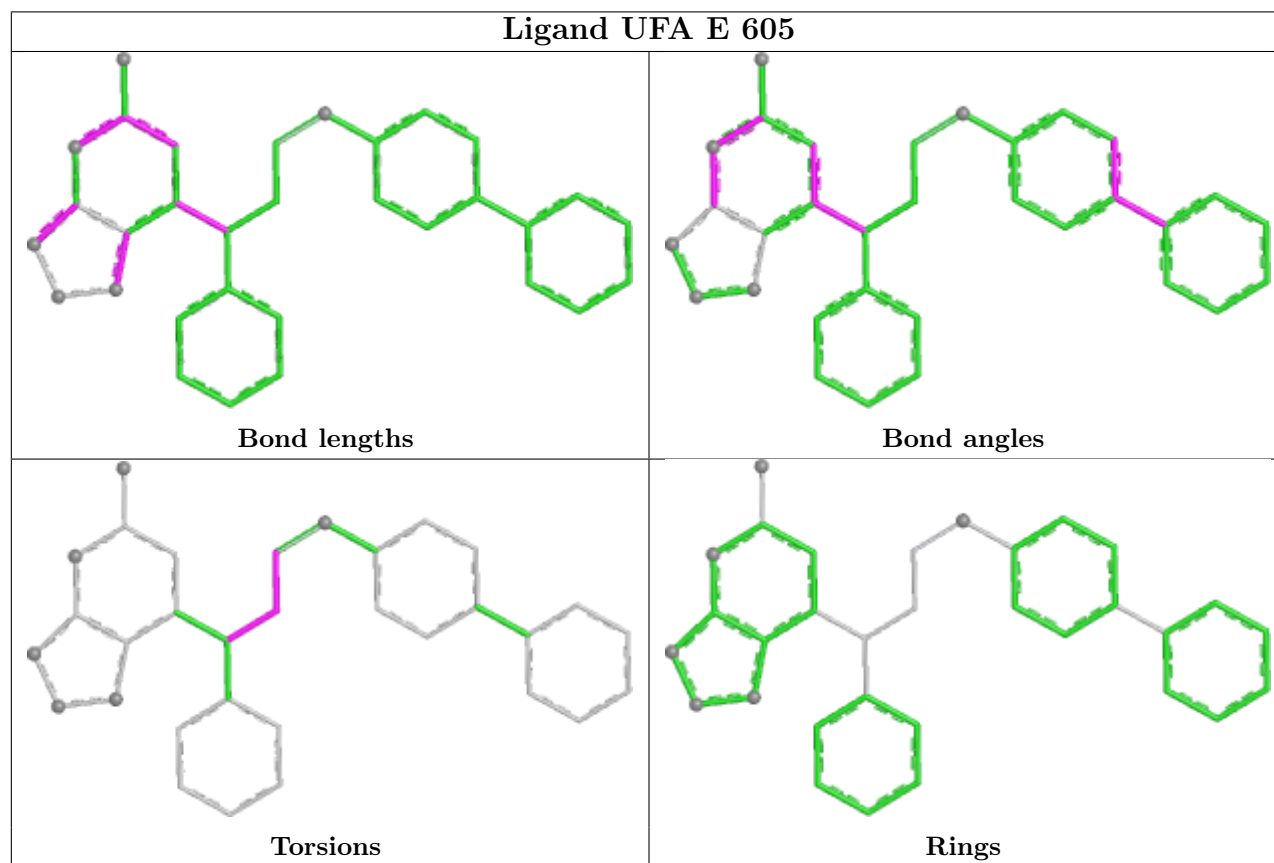
There are no ring outliers.

6 monomers are involved in 8 short contacts:

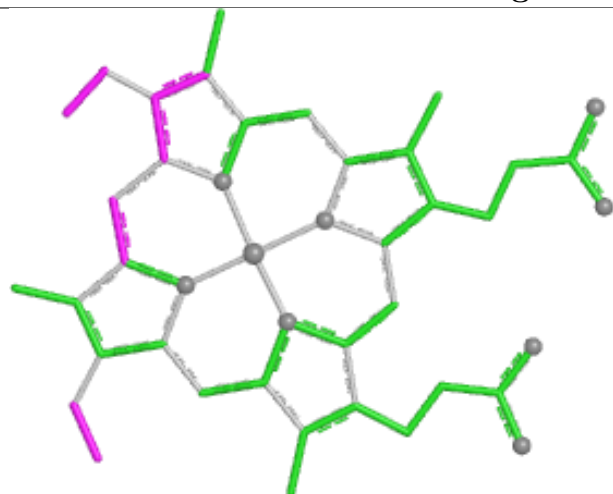
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	E	605	UFA	1	0
5	G	601	HEC	2	0
5	A	201	HEC	1	0
5	D	201	HEC	2	0
5	I	601	HEC	2	0
9	G	605	UFA	1	0

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

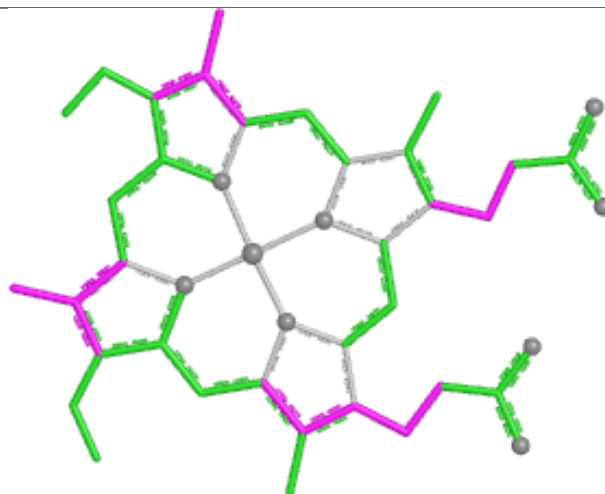
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



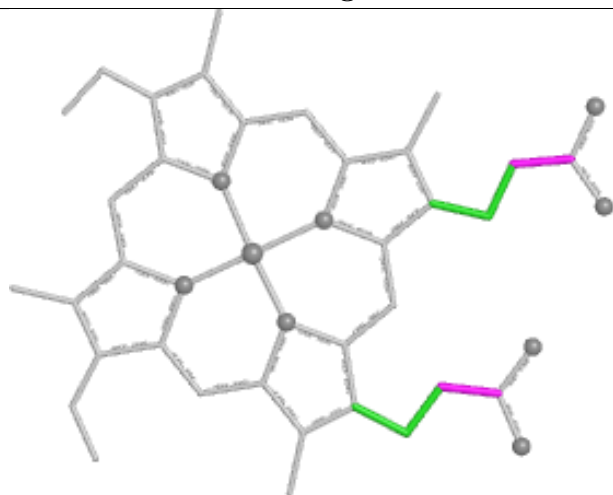
Ligand HEC G 601



Bond lengths



Bond angles

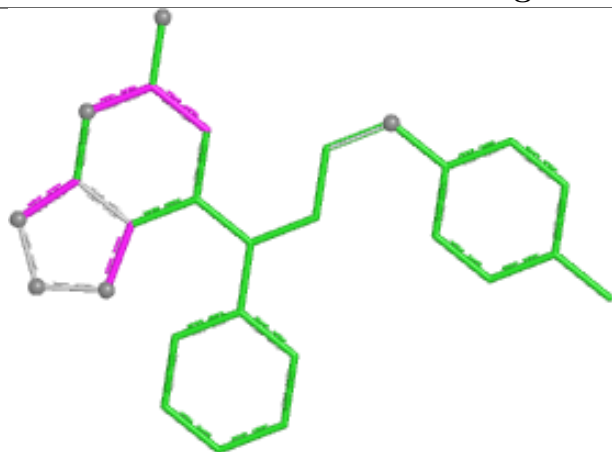


Torsions

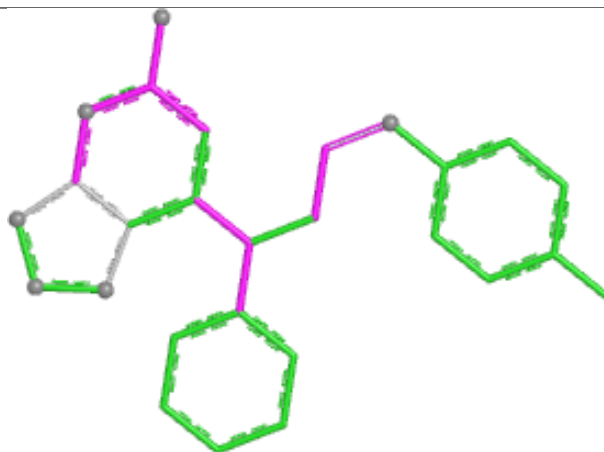


Rings

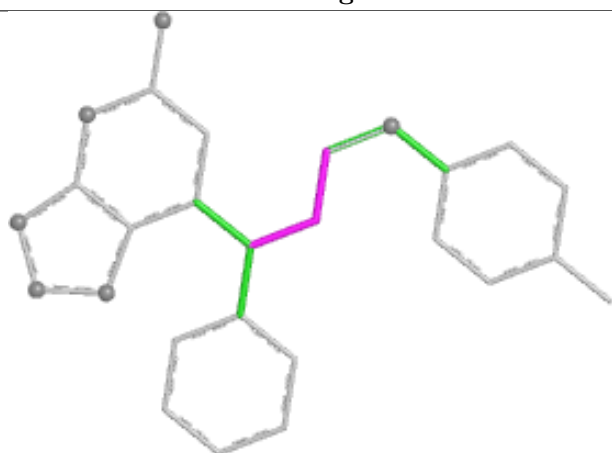
Ligand UFA B 606



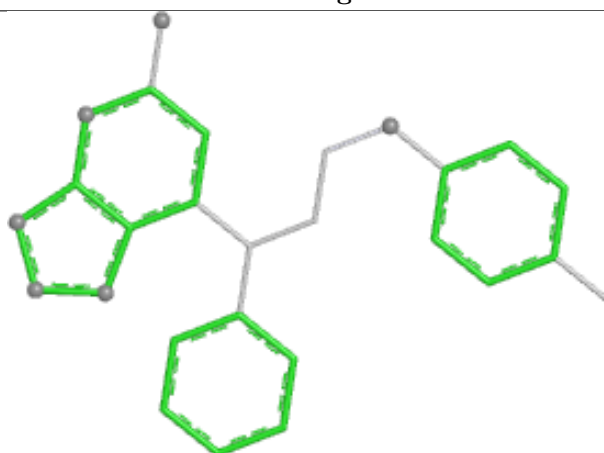
Bond lengths



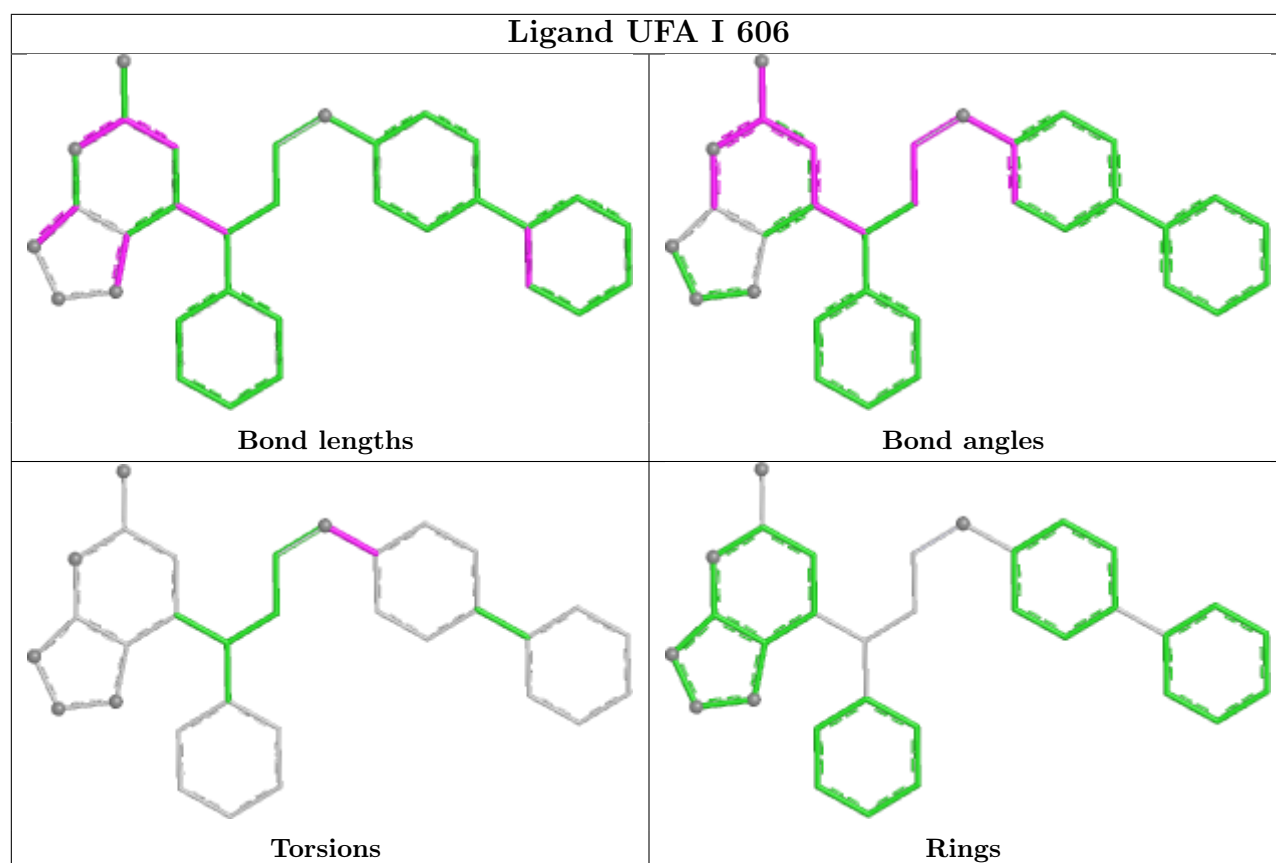
Bond angles



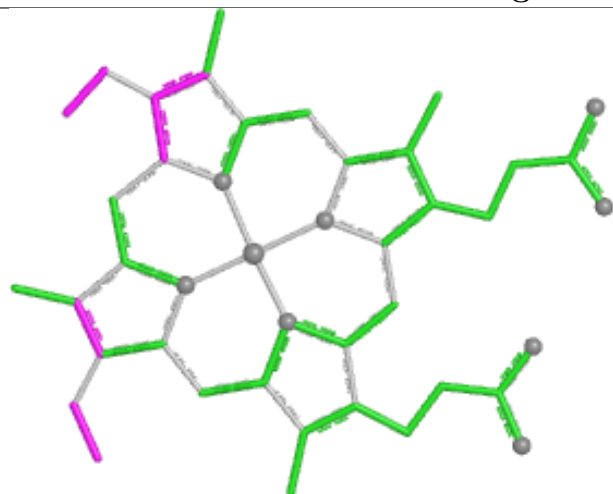
Torsions



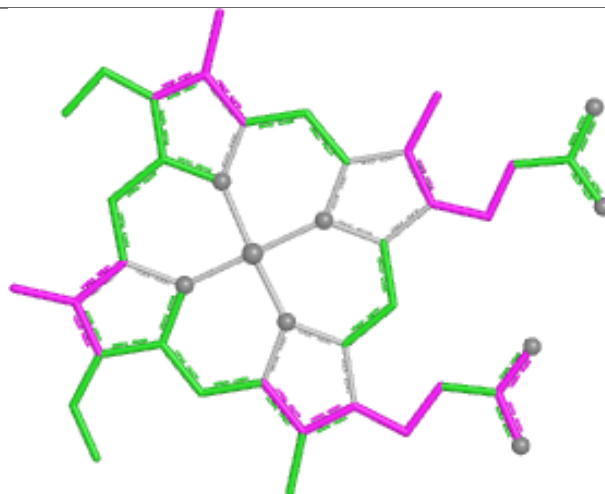
Rings



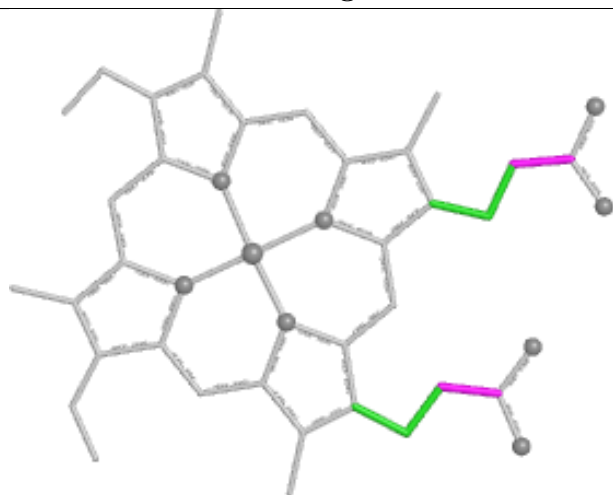
Ligand HEC A 201



Bond lengths



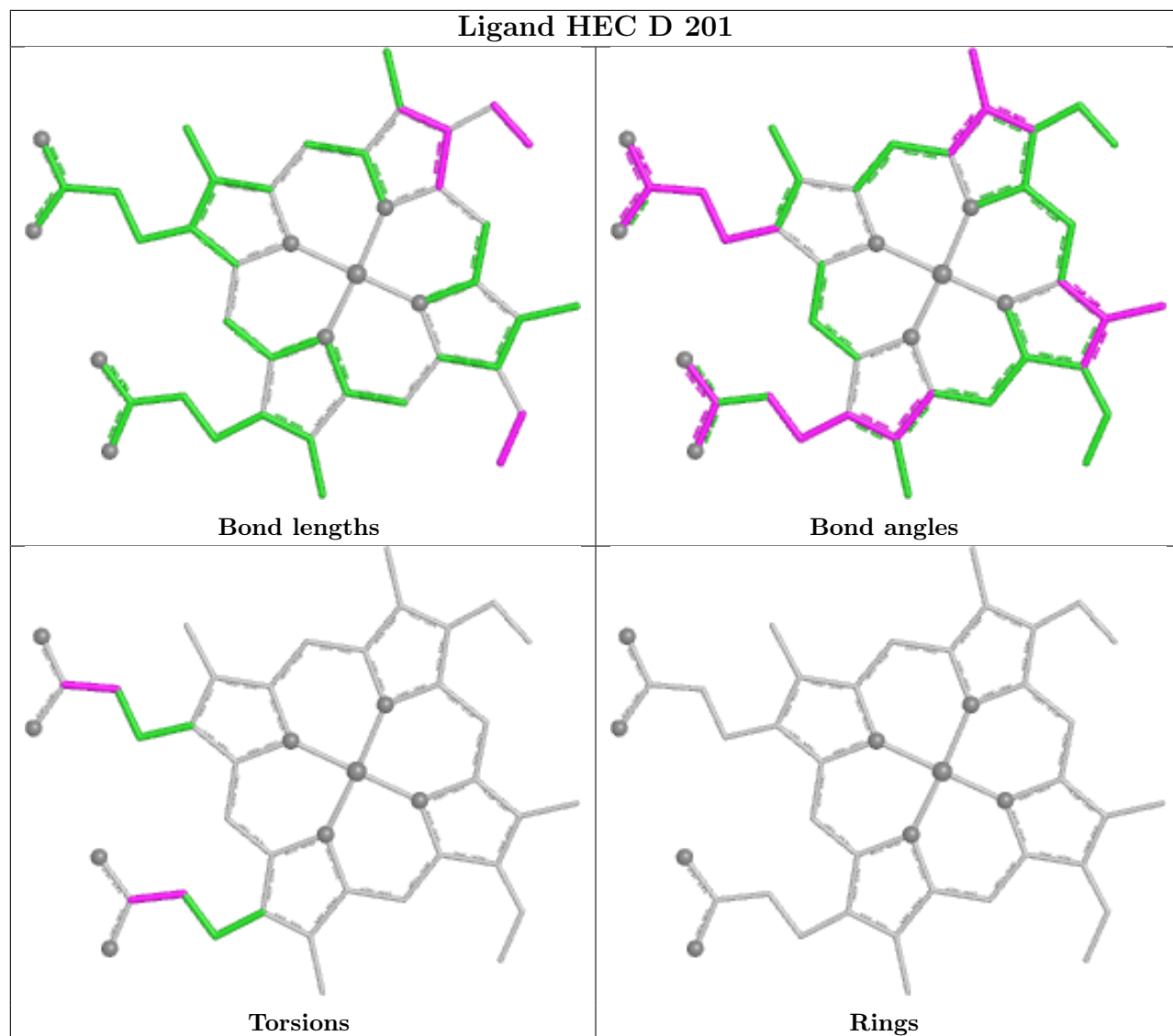
Bond angles



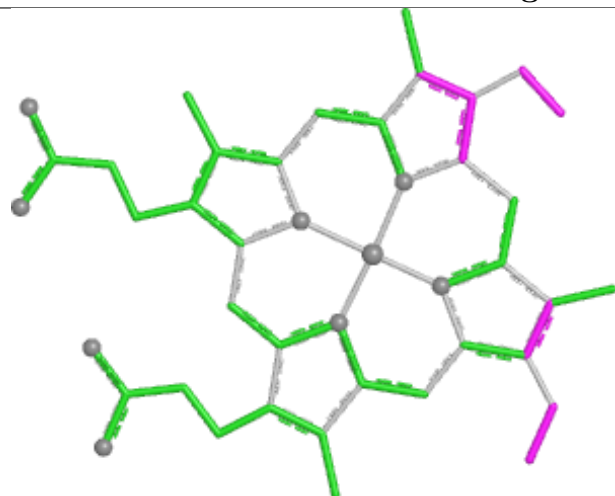
Torsions



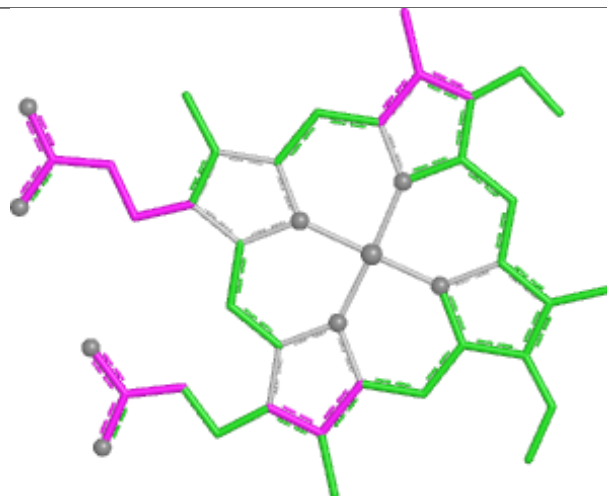
Rings



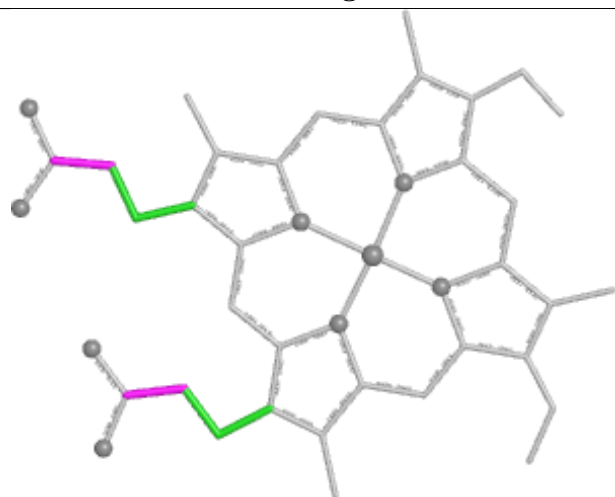
Ligand HEC I 601



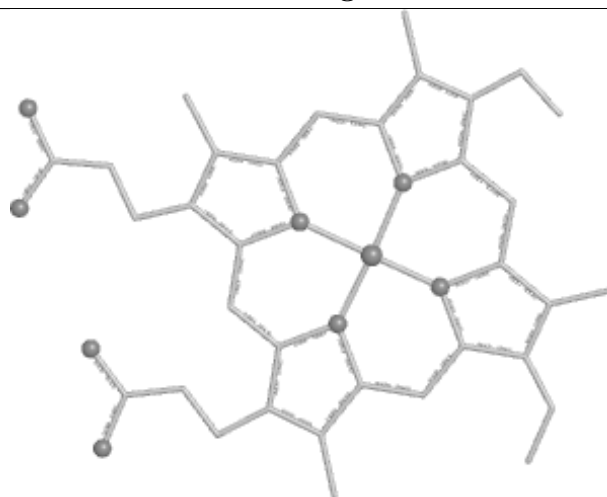
Bond lengths



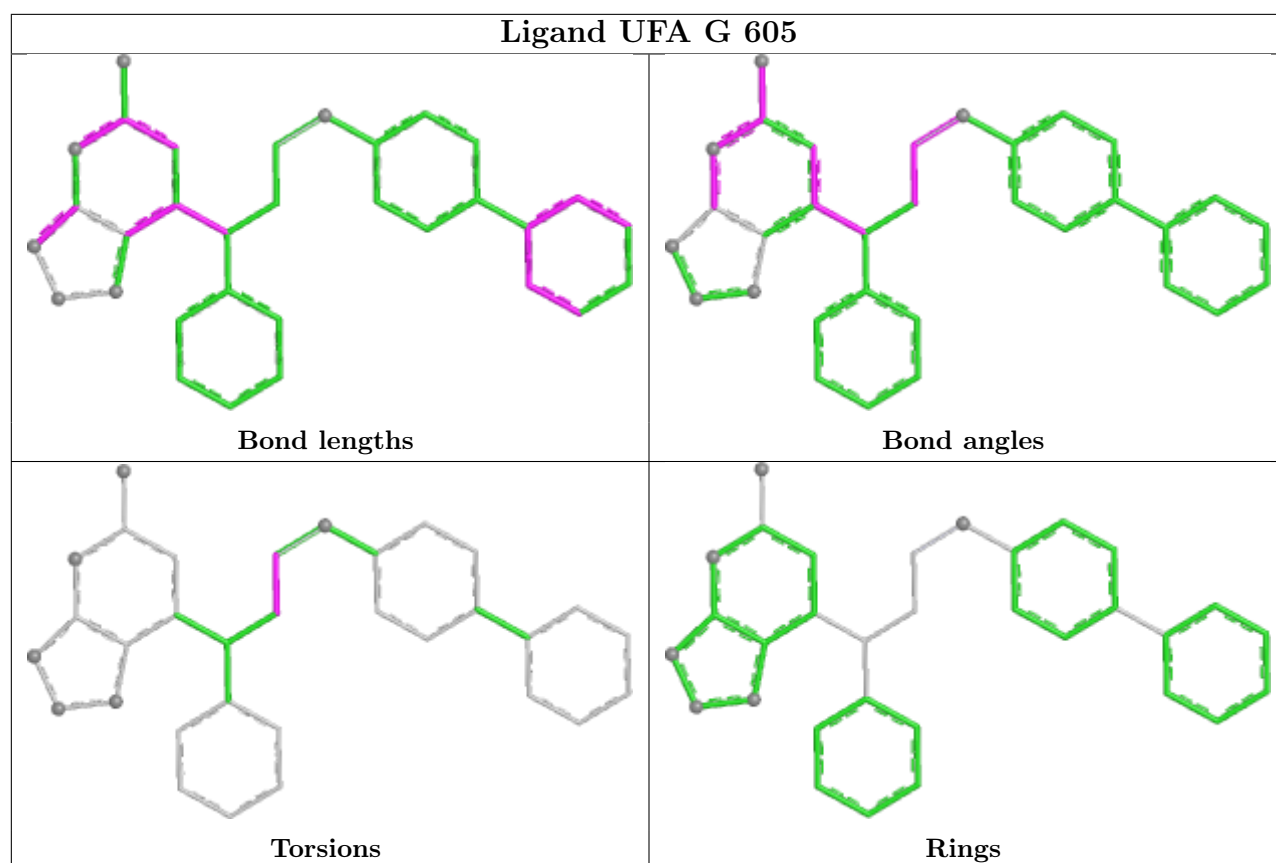
Bond angles



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, 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	103/105 (98%)	-0.31	1 (0%) 79 73	33, 54, 72, 87	1 (0%)
1	D	104/105 (99%)	-0.32	0 100 100	31, 47, 68, 88	0
1	F	104/105 (99%)	-0.32	0 100 100	30, 46, 64, 77	1 (0%)
1	H	103/105 (98%)	-0.46	0 100 100	33, 46, 68, 78	0
2	B	463/467 (99%)	-0.11	4 (0%) 81 75	31, 61, 94, 100	7 (1%)
2	E	464/467 (99%)	-0.29	3 (0%) 85 81	24, 52, 80, 92	10 (2%)
2	G	463/467 (99%)	-0.37	0 100 100	26, 51, 69, 79	8 (1%)
2	I	464/467 (99%)	-0.27	0 100 100	26, 55, 81, 89	10 (2%)
All	All	2268/2288 (99%)	-0.28	8 (0%) 89 85	24, 52, 83, 100	37 (1%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	4	GLN	2.9
2	E	348	ASN	2.8
2	B	372	VAL	2.8
2	B	264	LEU	2.5
2	E	157	ASN	2.4

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

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	G	150	7/8	0.92	0.08	42,43,44,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CSO	B	150	7/8	0.93	0.09	48,49,51,51	0
2	CSO	I	150	7/8	0.94	0.08	44,45,48,48	0
2	CSO	E	150	7/8	0.96	0.08	47,48,51,51	0

6.3 Carbohydrates [i](#)

SUGAR-RSR INFOmissingINFO

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(\AA^2)	Q<0.9
6	NAG	I	603	14/15	0.75	0.12	84,85,86,86	0
6	NAG	B	601	14/15	0.76	0.12	93,95,96,96	0
6	NAG	B	602	14/15	0.79	0.12	97,98,99,99	0
6	NAG	G	602	14/15	0.80	0.11	65,67,67,68	0
6	NAG	I	602	14/15	0.83	0.10	70,71,72,72	0
6	NAG	E	601	14/15	0.83	0.10	79,79,80,80	0
9	UFA	B	606	27/32	0.83	0.12	54,55,58,58	0
8	CL	B	605	1/1	0.89	0.13	60,60,60,60	0
9	UFA	I	606	32/32	0.93	0.09	50,51,56,56	0
8	CL	D	202	1/1	0.95	0.30	86,86,86,86	0
8	CL	E	603	1/1	0.95	0.16	59,59,59,59	0
9	UFA	G	605	32/32	0.96	0.07	43,44,45,46	0
9	UFA	E	605	32/32	0.96	0.06	35,39,41,41	0
5	HEC	D	201	43/43	0.97	0.07	40,44,49,54	0
8	CL	G	604	1/1	0.97	0.18	56,56,56,56	0
7	CA	I	604	1/1	0.98	0.03	41,41,41,41	0
8	CL	I	605	1/1	0.98	0.16	49,49,49,49	0
5	HEC	A	201	43/43	0.98	0.07	52,56,60,64	0
5	HEC	G	601	43/43	0.98	0.07	37,43,46,49	0
5	HEC	I	601	43/43	0.98	0.07	42,46,51,55	0
8	CL	F	201	1/1	0.98	0.06	41,41,41,41	0
8	CL	E	604	1/1	0.99	0.07	38,38,38,38	0
7	CA	E	602	1/1	0.99	0.03	41,41,41,41	0
7	CA	B	603	1/1	0.99	0.03	50,50,50,50	0
8	CL	B	604	1/1	0.99	0.02	38,38,38,38	0

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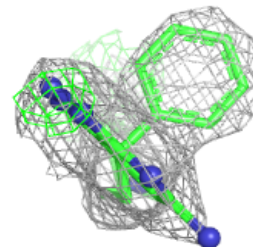
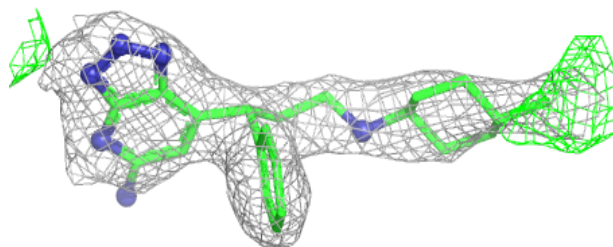
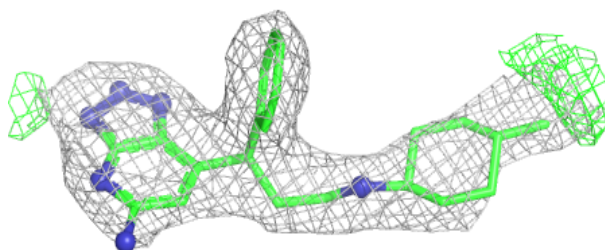
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	CA	G	603	1/1	1.00	0.01	34,34,34,34	0

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.

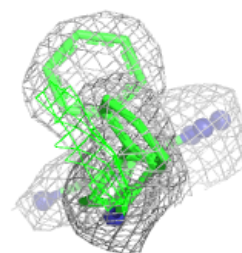
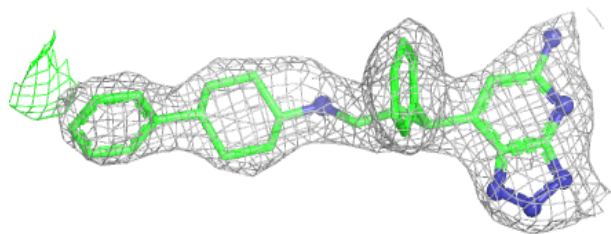
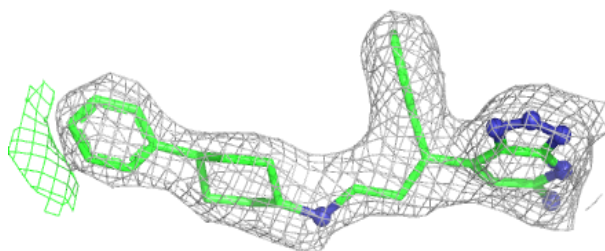
Electron density around UFA B 606:

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

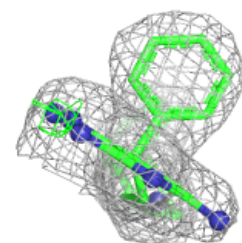
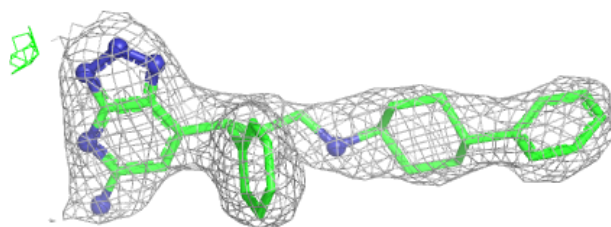
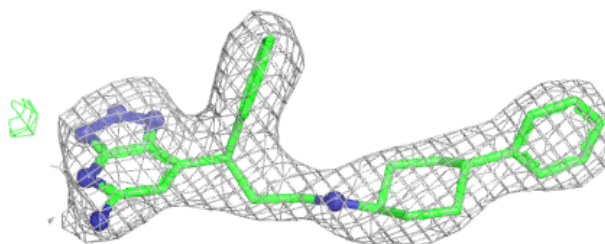


Electron density around UFA I 606:

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

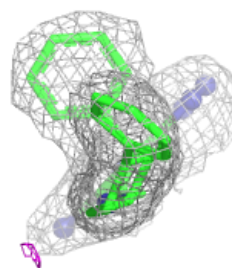
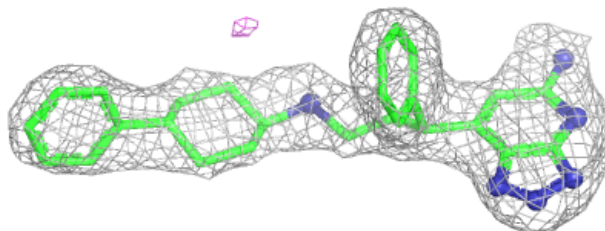
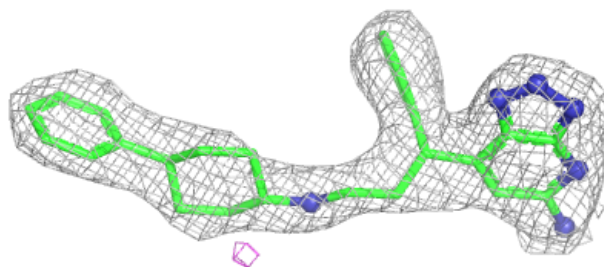
**Electron density around UFA G 605:**

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and green (positive)



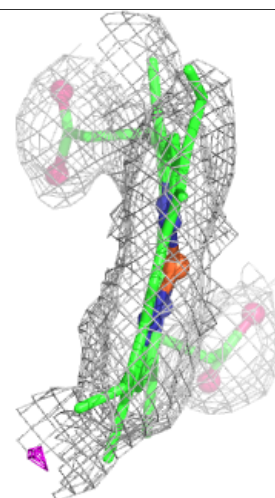
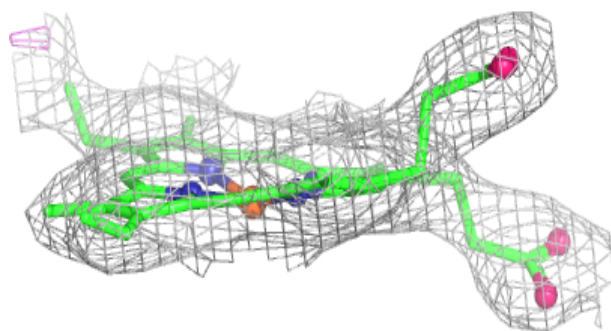
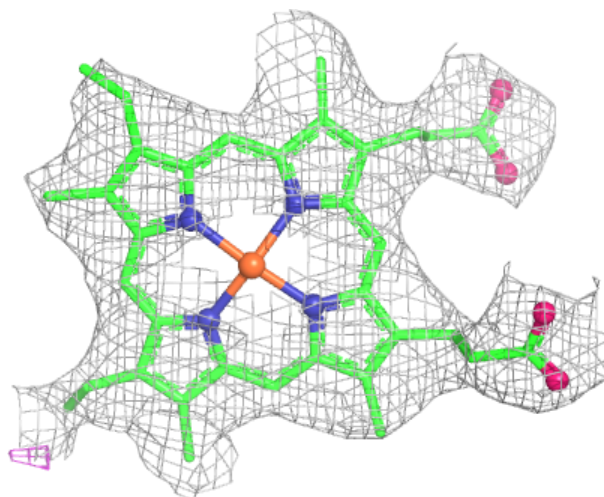
Electron density around UFA E 605:

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and green (positive)



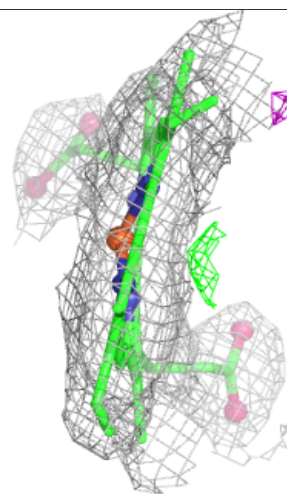
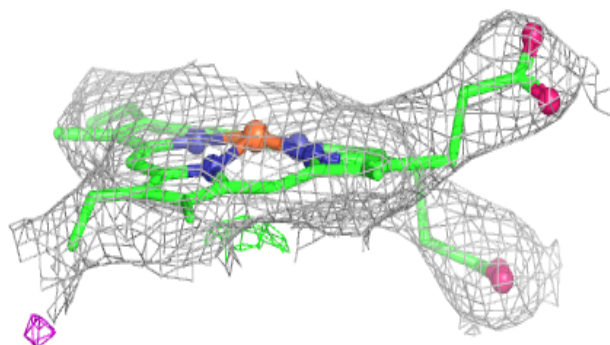
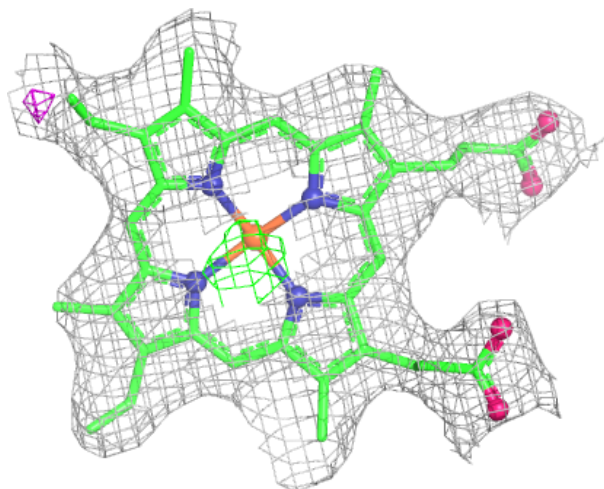
Electron density around HEC D 201:

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



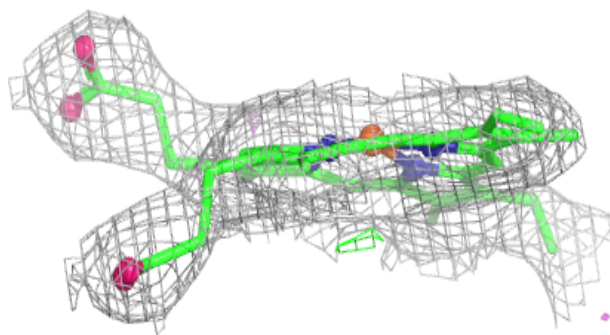
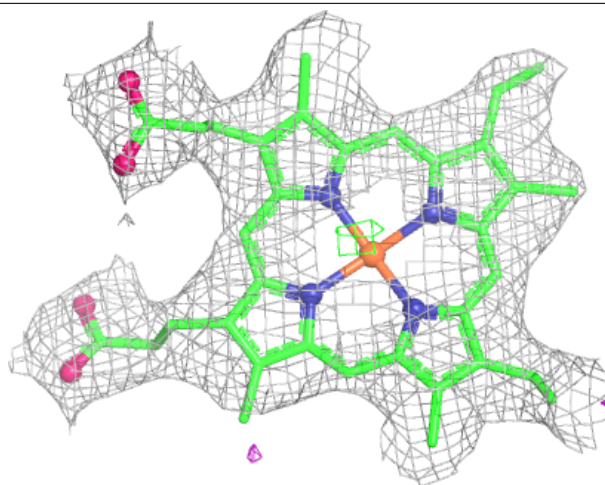
Electron density around HEC A 201:

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and green (positive)



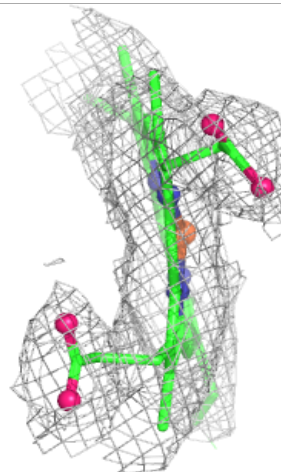
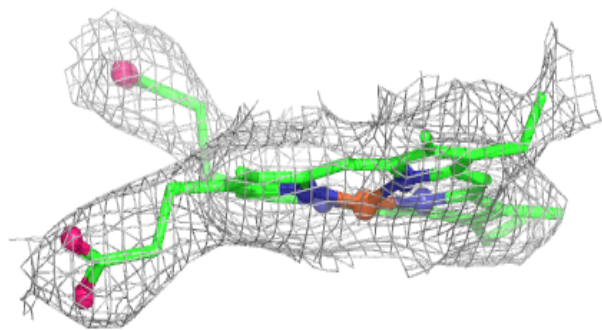
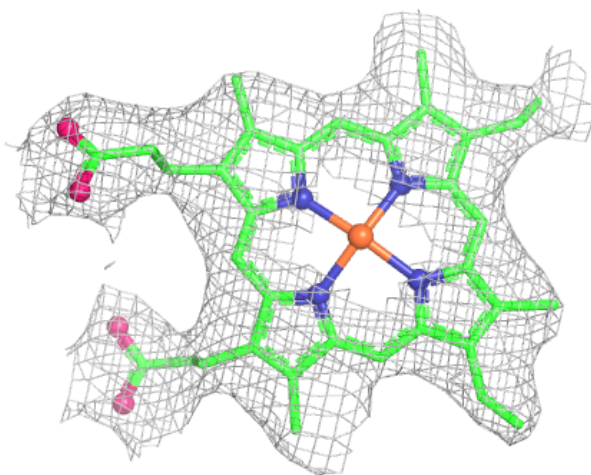
Electron density around HEC G 601:

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



Electron density around HEC I 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.