



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 07:29 PM EDT

PDB ID : 3R1B / pdb_00003r1b
Title : Open crystal structure of cytochrome P450 2B4 covalently bound to the mechanism-based inactivator tert-butylphenylacetylene
Authors : Gay, S.C.; Zhang, H.; Stout, C.D.; Hollenberg, P.F.; Halpert, J.R.
Deposited on : 2011-03-09
Resolution : 3.00 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 : 9.0.015 (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

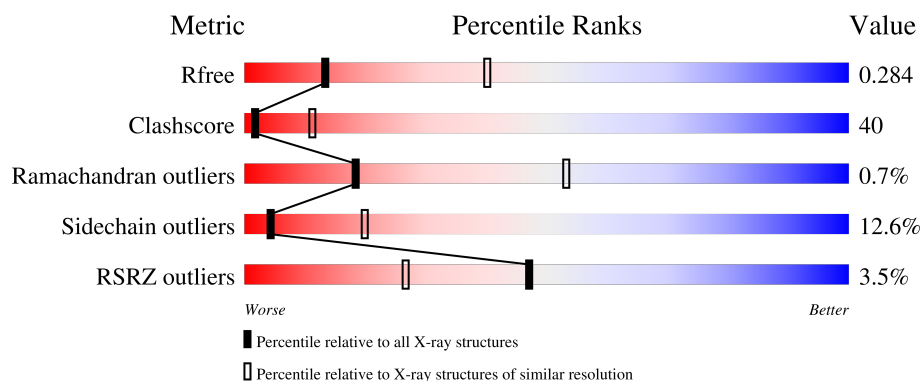
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

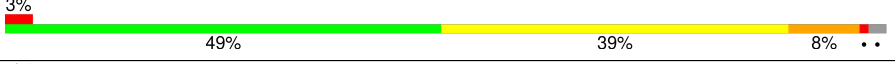
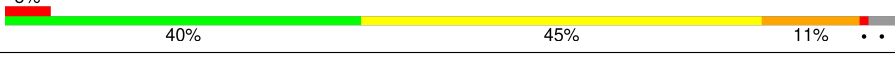
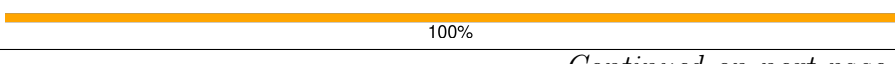
The reported resolution of this entry is 3.00 Å.

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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	476	
1	B	476	
1	C	476	
1	D	476	
2	E	2	

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Mol	Chain	Length	Quality of chain
2	F	2	 100%
2	G	2	 100%
2	H	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GLC	F	1	-	-	X	-
2	FRU	F	2	-	-	X	-
2	GLC	H	1	-	-	X	-
2	FRU	H	2	-	-	X	-
3	HEM	D	500	-	-	X	-
4	TB2	A	501	-	-	X	-
4	TB2	C	501	-	-	X	-
4	TB2	D	501	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14499 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 Cytochrome P450 2B4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	465	Total	C	N	O	S	2	0	0
			3583	2294	619	659	11			
1	B	465	Total	C	N	O	S	2	0	0
			3589	2308	615	656	10			
1	C	456	Total	C	N	O	S	1	0	0
			3406	2171	589	638	8			
1	D	464	Total	C	N	O	S	0	0	0
			3445	2199	598	640	8			

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	ALA	GLU	engineered mutation	UNP P00178
A	?	-	PHE	deletion	UNP P00178
A	?	-	SER	deletion	UNP P00178
A	?	-	LEU	deletion	UNP P00178
A	?	-	LEU	deletion	UNP P00178
A	?	-	LEU	deletion	UNP P00178
A	?	-	LEU	deletion	UNP P00178
A	?	-	LEU	deletion	UNP P00178
A	?	-	ALA	deletion	UNP P00178
A	?	-	PHE	deletion	UNP P00178
A	?	-	LEU	deletion	UNP P00178
A	?	-	ALA	deletion	UNP P00178
A	?	-	GLY	deletion	UNP P00178
A	?	-	LEU	deletion	UNP P00178
A	?	-	LEU	deletion	UNP P00178
A	?	-	LEU	deletion	UNP P00178
A	?	-	LEU	deletion	UNP P00178
A	?	-	LEU	deletion	UNP P00178
A	?	-	PHE	deletion	UNP P00178
A	?	-	ARG	deletion	UNP P00178
A	22	LYS	GLY	engineered mutation	UNP P00178

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Chain	Residue	Modelled	Actual	Comment	Reference
A	23	LYS	HIS	engineered mutation	UNP P00178
A	24	THR	PRO	engineered mutation	UNP P00178
A	25	SER	LYS	engineered mutation	UNP P00178
A	26	SER	ALA	engineered mutation	UNP P00178
A	27	LYS	HIS	engineered mutation	UNP P00178
A	29	LYS	ARG	engineered mutation	UNP P00178
A	221	SER	PRO	conflict	UNP P00178
A	226	TYR	HIS	engineered mutation	UNP P00178
A	492	HIS	-	expression tag	UNP P00178
A	493	HIS	-	expression tag	UNP P00178
A	494	HIS	-	expression tag	UNP P00178
A	495	HIS	-	expression tag	UNP P00178
B	21	ALA	GLU	engineered mutation	UNP P00178
B	?	-	PHE	deletion	UNP P00178
B	?	-	SER	deletion	UNP P00178
B	?	-	LEU	deletion	UNP P00178
B	?	-	LEU	deletion	UNP P00178
B	?	-	LEU	deletion	UNP P00178
B	?	-	LEU	deletion	UNP P00178
B	?	-	LEU	deletion	UNP P00178
B	?	-	ALA	deletion	UNP P00178
B	?	-	PHE	deletion	UNP P00178
B	?	-	LEU	deletion	UNP P00178
B	?	-	ALA	deletion	UNP P00178
B	?	-	GLY	deletion	UNP P00178
B	?	-	LEU	deletion	UNP P00178
B	?	-	LEU	deletion	UNP P00178
B	?	-	LEU	deletion	UNP P00178
B	?	-	LEU	deletion	UNP P00178
B	?	-	LEU	deletion	UNP P00178
B	?	-	PHE	deletion	UNP P00178
B	?	-	ARG	deletion	UNP P00178
B	22	LYS	GLY	engineered mutation	UNP P00178
B	23	LYS	HIS	engineered mutation	UNP P00178
B	24	THR	PRO	engineered mutation	UNP P00178
B	25	SER	LYS	engineered mutation	UNP P00178
B	26	SER	ALA	engineered mutation	UNP P00178
B	27	LYS	HIS	engineered mutation	UNP P00178
B	29	LYS	ARG	engineered mutation	UNP P00178
B	221	SER	PRO	conflict	UNP P00178
B	226	TYR	HIS	engineered mutation	UNP P00178
B	492	HIS	-	expression tag	UNP P00178

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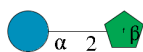
Chain	Residue	Modelled	Actual	Comment	Reference
B	493	HIS	-	expression tag	UNP P00178
B	494	HIS	-	expression tag	UNP P00178
B	495	HIS	-	expression tag	UNP P00178
C	21	ALA	GLU	engineered mutation	UNP P00178
C	?	-	PHE	deletion	UNP P00178
C	?	-	SER	deletion	UNP P00178
C	?	-	LEU	deletion	UNP P00178
C	?	-	LEU	deletion	UNP P00178
C	?	-	LEU	deletion	UNP P00178
C	?	-	LEU	deletion	UNP P00178
C	?	-	LEU	deletion	UNP P00178
C	?	-	ALA	deletion	UNP P00178
C	?	-	PHE	deletion	UNP P00178
C	?	-	LEU	deletion	UNP P00178
C	?	-	ALA	deletion	UNP P00178
C	?	-	GLY	deletion	UNP P00178
C	?	-	LEU	deletion	UNP P00178
C	?	-	LEU	deletion	UNP P00178
C	?	-	LEU	deletion	UNP P00178
C	?	-	LEU	deletion	UNP P00178
C	?	-	LEU	deletion	UNP P00178
C	?	-	PHE	deletion	UNP P00178
C	?	-	ARG	deletion	UNP P00178
C	22	LYS	GLY	engineered mutation	UNP P00178
C	23	LYS	HIS	engineered mutation	UNP P00178
C	24	THR	PRO	engineered mutation	UNP P00178
C	25	SER	LYS	engineered mutation	UNP P00178
C	26	SER	ALA	engineered mutation	UNP P00178
C	27	LYS	HIS	engineered mutation	UNP P00178
C	29	LYS	ARG	engineered mutation	UNP P00178
C	221	SER	PRO	conflict	UNP P00178
C	226	TYR	HIS	engineered mutation	UNP P00178
C	492	HIS	-	expression tag	UNP P00178
C	493	HIS	-	expression tag	UNP P00178
C	494	HIS	-	expression tag	UNP P00178
C	495	HIS	-	expression tag	UNP P00178
D	21	ALA	GLU	engineered mutation	UNP P00178
D	?	-	PHE	deletion	UNP P00178
D	?	-	SER	deletion	UNP P00178
D	?	-	LEU	deletion	UNP P00178
D	?	-	LEU	deletion	UNP P00178
D	?	-	LEU	deletion	UNP P00178

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Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	LEU	deletion	UNP P00178
D	?	-	LEU	deletion	UNP P00178
D	?	-	ALA	deletion	UNP P00178
D	?	-	PHE	deletion	UNP P00178
D	?	-	LEU	deletion	UNP P00178
D	?	-	ALA	deletion	UNP P00178
D	?	-	GLY	deletion	UNP P00178
D	?	-	LEU	deletion	UNP P00178
D	?	-	LEU	deletion	UNP P00178
D	?	-	LEU	deletion	UNP P00178
D	?	-	LEU	deletion	UNP P00178
D	?	-	LEU	deletion	UNP P00178
D	?	-	PHE	deletion	UNP P00178
D	?	-	ARG	deletion	UNP P00178
D	22	LYS	GLY	engineered mutation	UNP P00178
D	23	LYS	HIS	engineered mutation	UNP P00178
D	24	THR	PRO	engineered mutation	UNP P00178
D	25	SER	LYS	engineered mutation	UNP P00178
D	26	SER	ALA	engineered mutation	UNP P00178
D	27	LYS	HIS	engineered mutation	UNP P00178
D	29	LYS	ARG	engineered mutation	UNP P00178
D	221	SER	PRO	conflict	UNP P00178
D	226	TYR	HIS	engineered mutation	UNP P00178
D	492	HIS	-	expression tag	UNP P00178
D	493	HIS	-	expression tag	UNP P00178
D	494	HIS	-	expression tag	UNP P00178
D	495	HIS	-	expression tag	UNP P00178

- Molecule 2 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	0	0	0
			23	12	11			
2	F	2	Total	C	O	0	0	0
			23	12	11			
2	G	2	Total	C	O	0	0	0
			23	12	11			

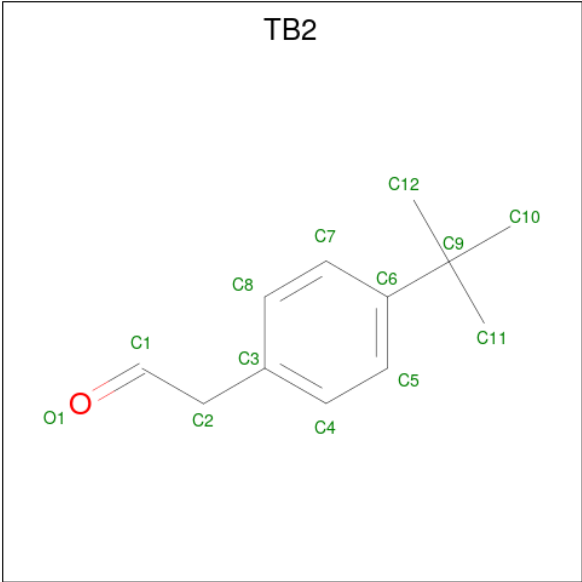
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	H	2	Total C O 23 12 11	0	0	0

- # HEM

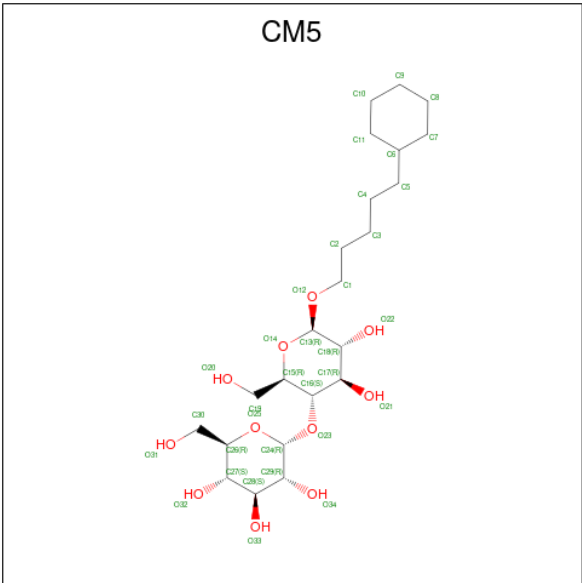
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- 



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	12	1		
4	B	1	Total	C	O	0	0
			13	12	1		
4	C	1	Total	C	O	0	0
			13	12	1		
4	D	1	Total	C	O	0	0
			13	12	1		

- Molecule 5 is 5-CYCLOHEXYL-1-PENTYL-BETA-D-MALTOSIDE (CCD ID: CM5) (formula: C₂₃H₄₂O₁₁).

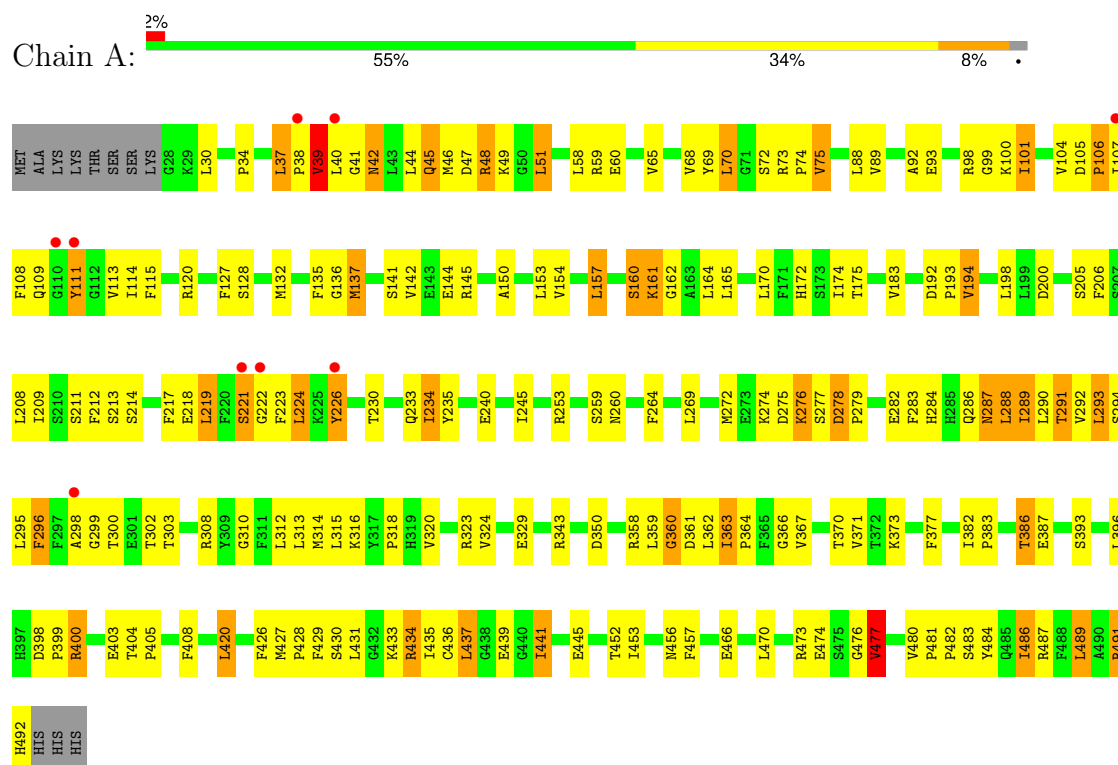


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 24	C 18	O 6	0	0
5	A	1	Total 34	C 23	O 11	0	0
5	B	1	Total 34	C 23	O 11	0	0
5	B	1	Total 34	C 23	O 11	0	0
5	D	1	Total 34	C 23	O 11	0	0

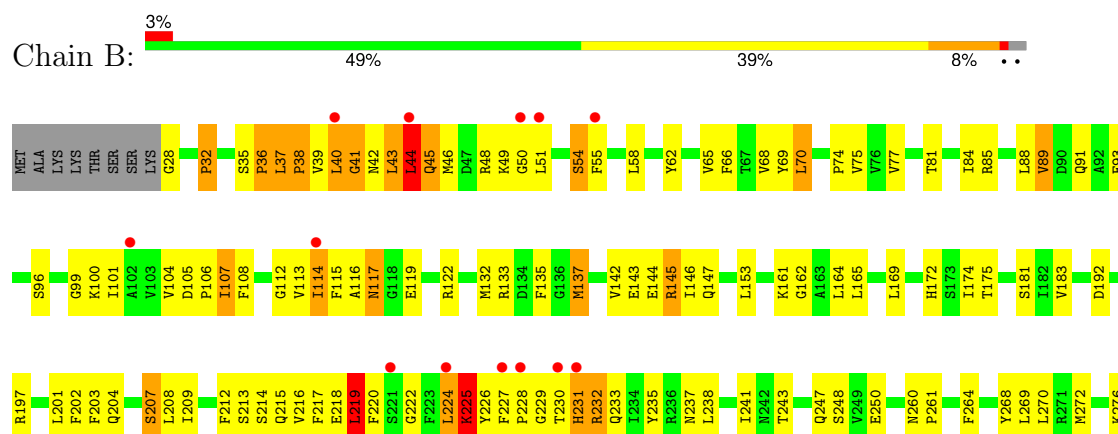
3 Residue-property plots [i](#)

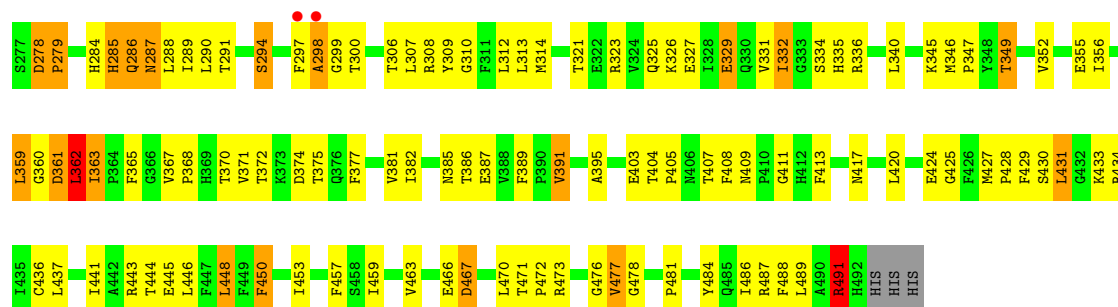
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: Cytochrome P450 2B4

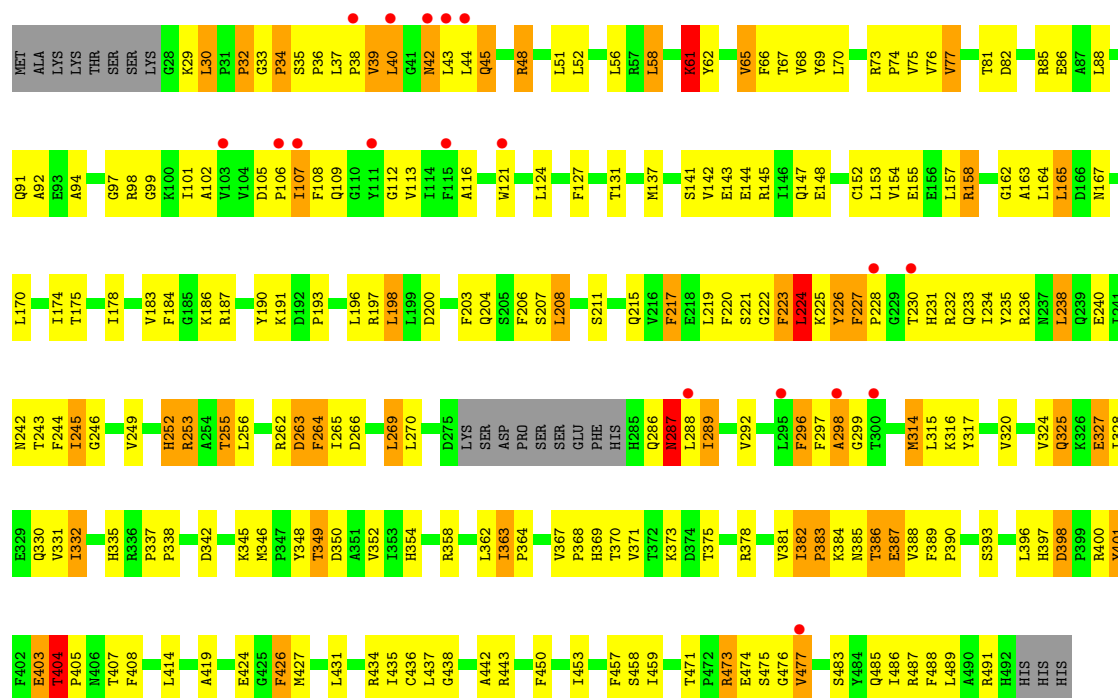


• Molecule 1: Cytochrome P450 2B4

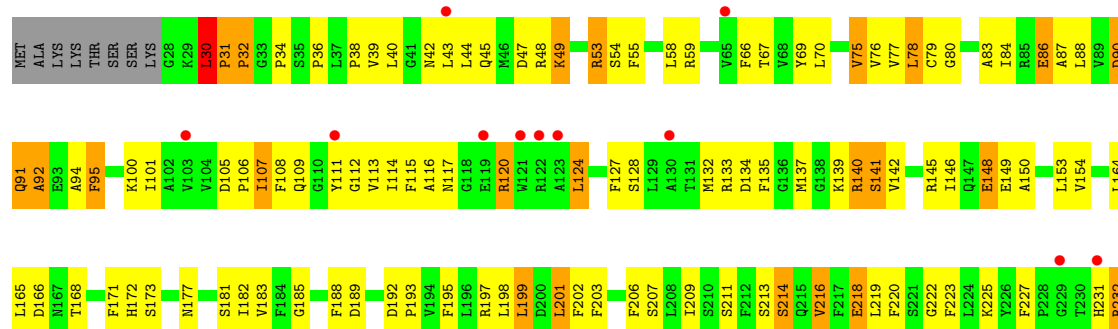


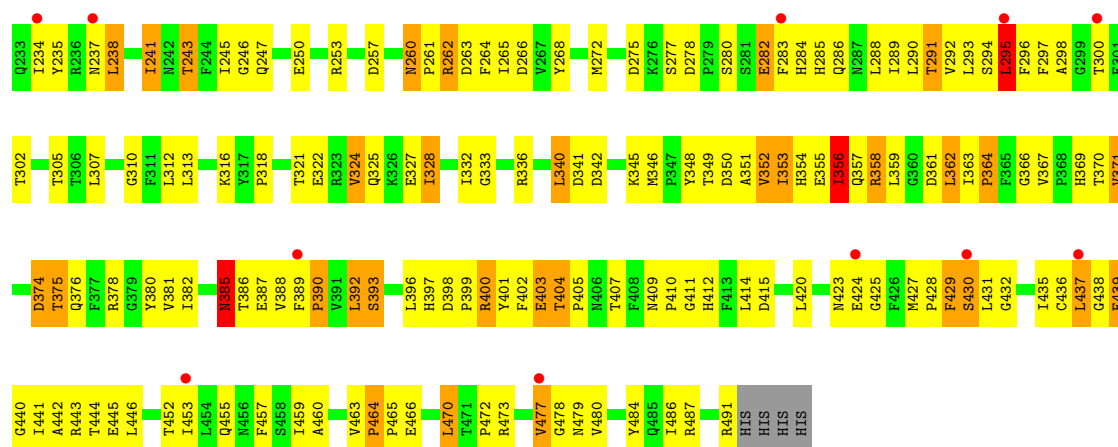


• Molecule 1: Cytochrome P450 2B4



• Molecule 1: Cytochrome P450 2B4





- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain E: 100%



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain F: 100%



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain G: 100%



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain H: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	193.92Å 153.69Å 129.66Å 90.00° 122.22° 90.00°	Depositor
Resolution (Å)	53.43 – 3.00 53.43 – 3.00	Depositor EDS
% Data completeness (in resolution range)	94.8 (53.43-3.00) 99.3 (53.43-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.6.4_486	Depositor
R, R_{free}	0.242 , 0.288 0.244 , 0.284	Depositor DCC
R_{free} test set	3237 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	92.5	Xtriage
Anisotropy	0.236	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 95.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14499	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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: FRU, GLC, TB2, CM5, HEM

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	3/3672 (0.1%)	0.94	22/4995 (0.4%)
1	B	0.47	2/3679 (0.1%)	1.15	49/5003 (1.0%)
1	C	0.38	0/3484	1.11	37/4749 (0.8%)
1	D	0.44	0/3527	1.15	47/4814 (1.0%)
All	All	0.43	5/14362 (0.0%)	1.09	155/19561 (0.8%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	278	ASP	C-N	-9.04	1.25	1.33
1	A	161	LYS	CA-CB	-8.48	1.41	1.53
1	B	37	LEU	CA-CB	6.91	1.63	1.53
1	B	278	ASP	C-N	-5.94	1.28	1.33
1	A	221	SER	C-N	-5.07	1.27	1.33

The worst 5 of 155 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	107	ILE	N-CA-C	15.05	126.16	110.36
1	B	231	HIS	N-CA-C	-13.48	95.24	113.30
1	D	378	ARG	N-CA-C	11.74	127.12	113.38
1	B	37	LEU	N-CA-C	-10.66	94.85	110.20
1	B	335	HIS	N-CA-C	10.63	127.07	112.93

There are no chirality outliers.

There are no planarity outliers.

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	3583	0	3434	235	0
1	B	3589	0	3460	221	0
1	C	3406	0	3187	305	0
1	D	3445	0	3216	386	0
2	E	23	0	21	5	0
2	F	23	0	21	9	0
2	G	23	0	21	4	0
2	H	23	0	21	10	0
3	A	43	0	30	17	0
3	B	43	0	30	14	0
3	C	43	0	30	12	0
3	D	43	0	30	25	0
4	A	13	0	15	8	0
4	B	13	0	15	5	0
4	C	13	0	15	6	0
4	D	13	0	15	14	0
5	A	58	0	73	5	0
5	B	68	0	84	5	0
5	D	34	0	42	3	0
All	All	14499	0	13760	1143	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 40.

The worst 5 of 1143 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:D:30:LEU:HD12	1:D:31:PRO:CD	1.18	1.61
1:A:298:ALA:HB1	4:A:501:TB2:C8	1.39	1.52
1:D:30:LEU:CD1	1:D:31:PRO:HD2	1.39	1.51
1:D:298:ALA:HB2	4:D:501:TB2:C7	1.52	1.37
1:C:233:GLN:NE2	1:C:236:ARG:HD3	1.43	1.34

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	463/476 (97%)	440 (95%)	18 (4%)	5 (1%)	11	43
1	B	463/476 (97%)	426 (92%)	36 (8%)	1 (0%)	43	76
1	C	452/476 (95%)	423 (94%)	27 (6%)	2 (0%)	30	65
1	D	462/476 (97%)	415 (90%)	43 (9%)	4 (1%)	14	48
All	All	1840/1904 (97%)	1704 (93%)	124 (7%)	12 (1%)	18	53

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	39	VAL
1	A	45	GLN
1	D	430	SER
1	A	136	GLY
1	B	36	PRO

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	375/421 (89%)	333 (89%)	42 (11%)	6	24
1	B	377/421 (90%)	329 (87%)	48 (13%)	4	20
1	C	343/421 (82%)	296 (86%)	47 (14%)	3	17
1	D	345/421 (82%)	301 (87%)	44 (13%)	4	19
All	All	1440/1684 (86%)	1259 (87%)	181 (13%)	4	20

5 of 181 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	269	LEU
1	D	90	ASP
1	C	314	MET
1	C	443	ARG
1	D	198	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	45	GLN
1	D	237	ASN
1	D	233	GLN
1	D	242	ASN
1	B	409	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 ⓘ

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	$\# Z > 2$
2	GLC	E	1	2	11,11,12	1.21	1 (9%)	15,15,17	2.29	8 (53%)
2	FRU	E	2	2	11,12,12	1.38	2 (18%)	10,18,18	1.78	4 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLC	F	1	2	11,11,12	1.19	1 (9%)	15,15,17	2.28	7 (46%)
2	FRU	F	2	2	11,12,12	1.28	1 (9%)	10,18,18	1.70	3 (30%)
2	GLC	G	1	2	11,11,12	1.23	1 (9%)	15,15,17	2.52	7 (46%)
2	FRU	G	2	2	11,12,12	1.30	1 (9%)	10,18,18	1.73	3 (30%)
2	GLC	H	1	2	11,11,12	1.20	1 (9%)	15,15,17	2.19	7 (46%)
2	FRU	H	2	2	11,12,12	1.29	1 (9%)	10,18,18	1.73	3 (30%)

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	GLC	E	1	2	-	0/2/19/22	0/1/1/1
2	FRU	E	2	2	-	1/5/24/24	0/1/1/1
2	GLC	F	1	2	-	0/2/19/22	0/1/1/1
2	FRU	F	2	2	-	1/5/24/24	0/1/1/1
2	GLC	G	1	2	-	2/2/19/22	0/1/1/1
2	FRU	G	2	2	-	4/5/24/24	0/1/1/1
2	GLC	H	1	2	-	0/2/19/22	0/1/1/1
2	FRU	H	2	2	-	2/5/24/24	0/1/1/1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	2	FRU	O3-C3	-2.34	1.38	1.42
2	E	2	FRU	O3-C3	-2.30	1.38	1.42
2	H	2	FRU	O3-C3	-2.22	1.38	1.42
2	E	1	GLC	O2-C2	-2.18	1.38	1.43
2	F	2	FRU	O3-C3	-2.15	1.38	1.42

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1	GLC	O5-C5-C6	4.70	116.81	107.66
2	F	1	GLC	O5-C5-C6	4.43	116.28	107.66
2	H	1	GLC	O5-C5-C6	4.25	115.94	107.66
2	E	1	GLC	O5-C5-C6	4.03	115.52	107.66
2	G	1	GLC	O3-C3-C2	3.76	117.72	110.05

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

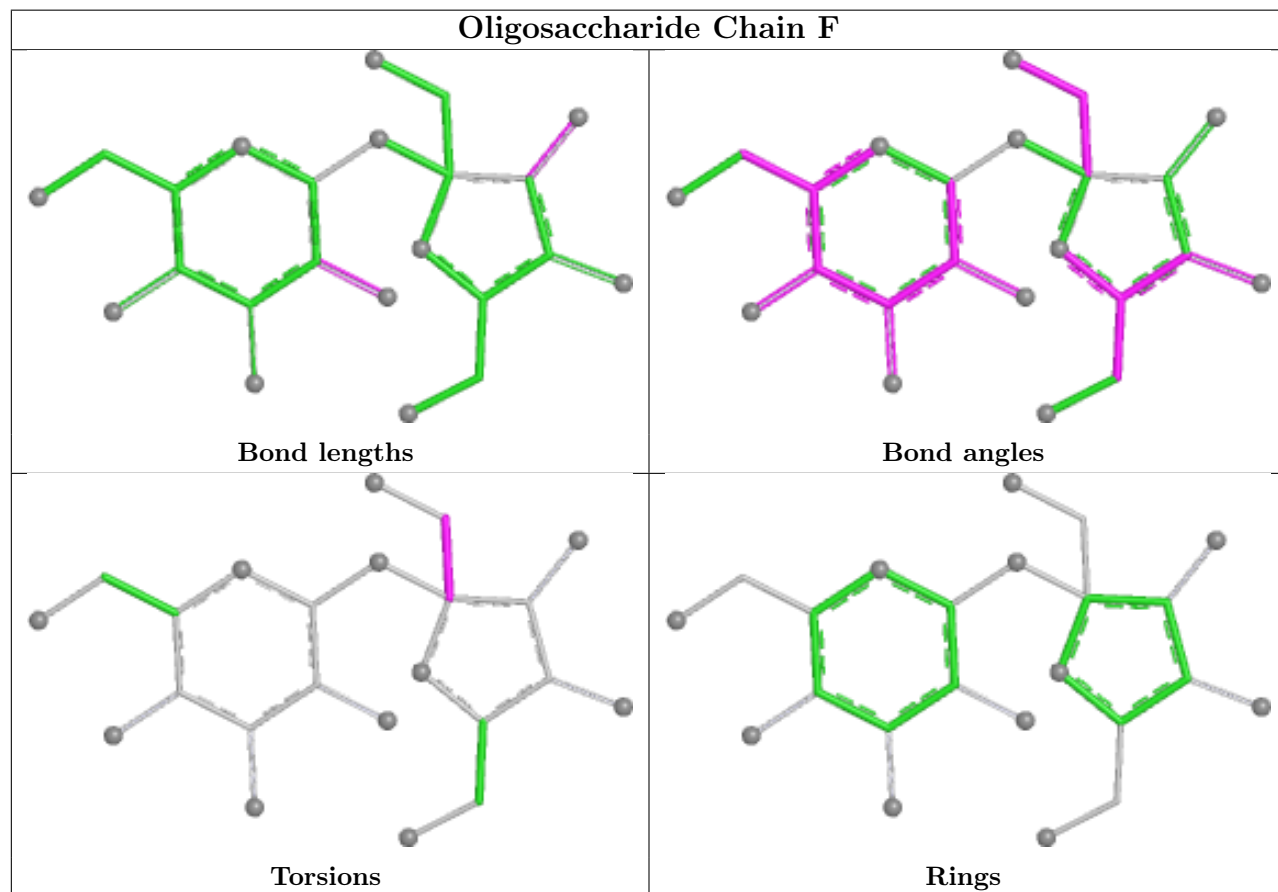
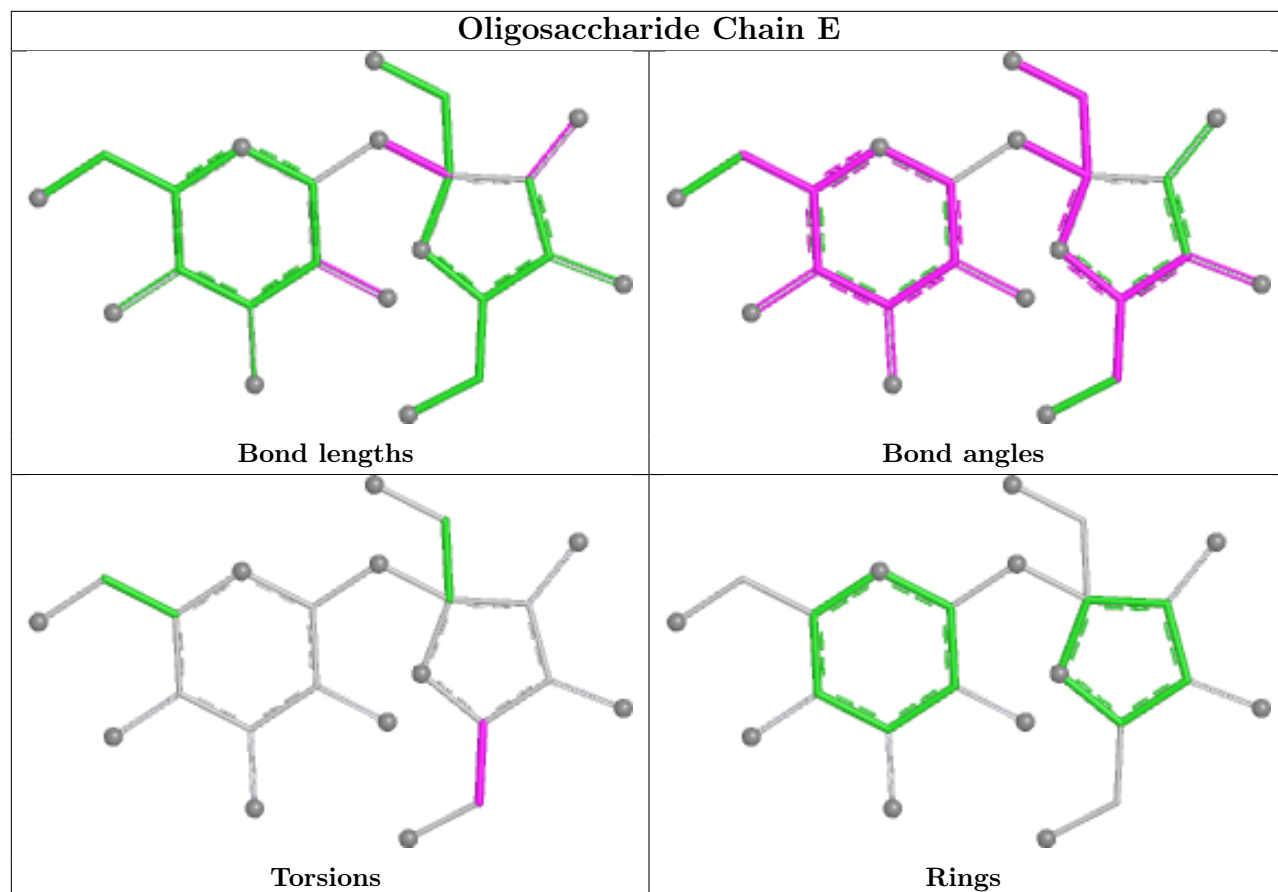
Mol	Chain	Res	Type	Atoms
2	G	2	FRU	O1-C1-C2-O2
2	G	2	FRU	C4-C5-C6-O6
2	G	2	FRU	O5-C5-C6-O6
2	G	1	GLC	O5-C5-C6-O6
2	G	1	GLC	C4-C5-C6-O6

There are no ring outliers.

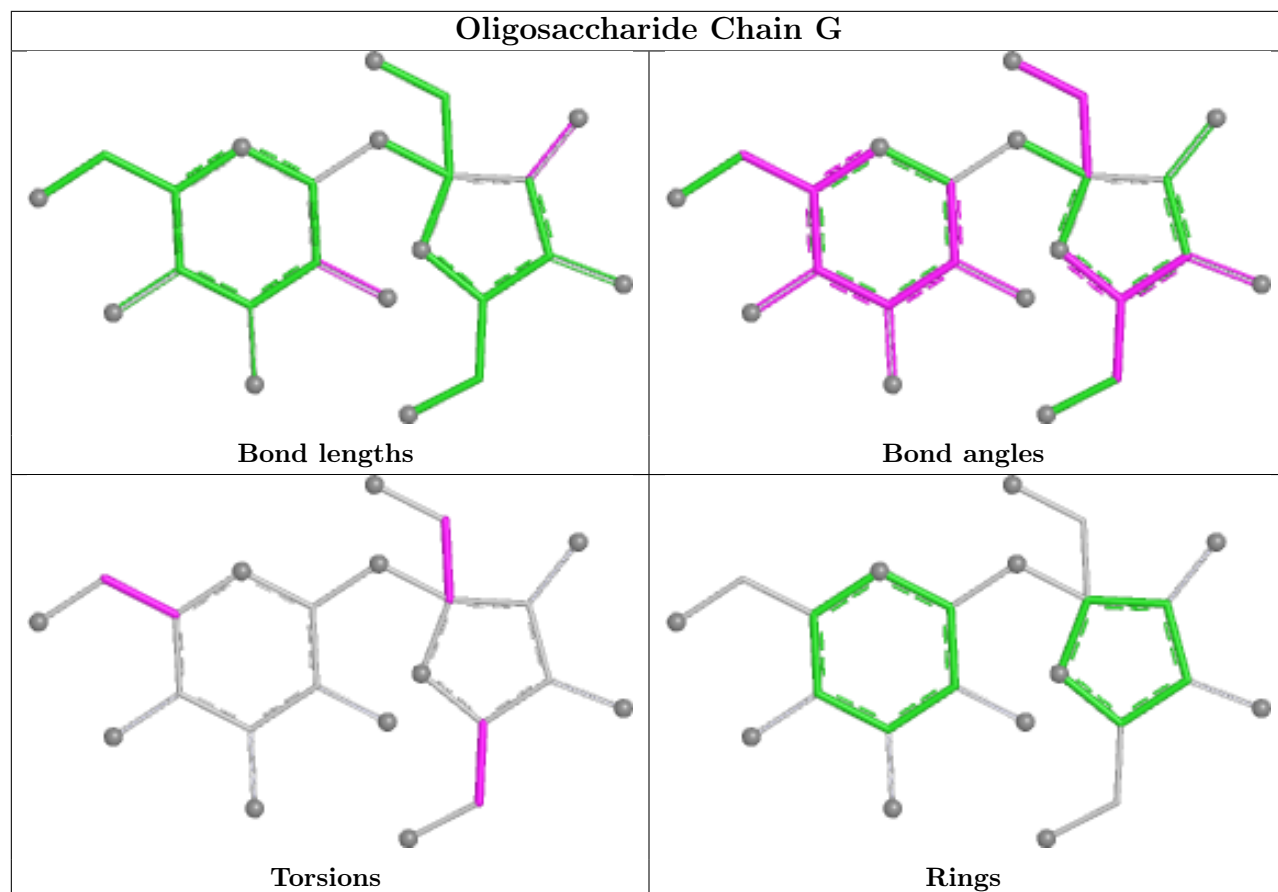
8 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1	GLC	3	0
2	H	1	GLC	10	0
2	E	2	FRU	5	0
2	G	2	FRU	2	0
2	H	2	FRU	7	0
2	F	2	FRU	9	0
2	F	1	GLC	8	0
2	E	1	GLC	5	0

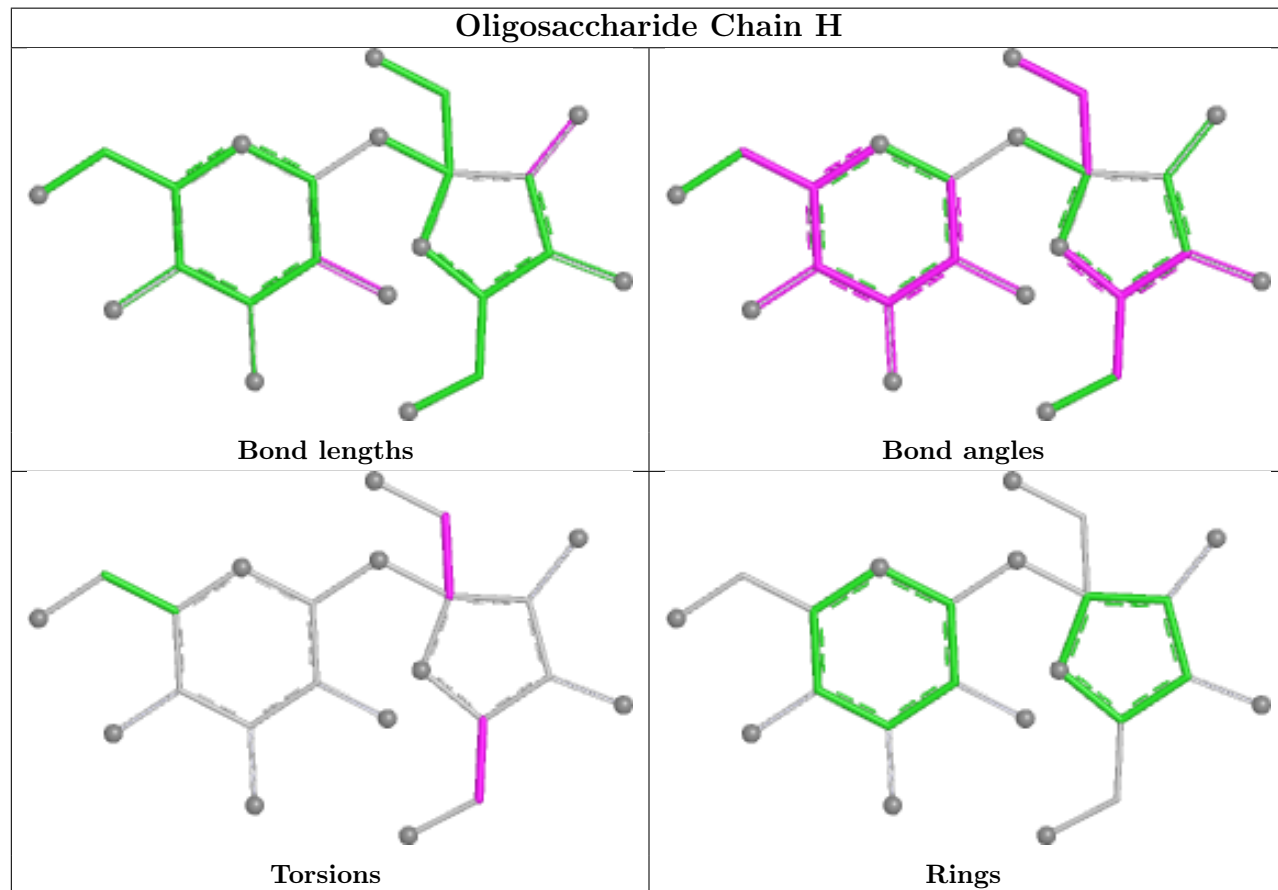
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



Oligosaccharide Chain G



Oligosaccharide Chain H



5.6 Ligand geometry

13 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	CM5	B	606	-	36,36,36	0.41	0	49,49,49	0.99	3 (6%)
3	HEM	C	500	1	50,50,50	1.89	8 (16%)	67,82,82	1.35	4 (5%)
5	CM5	B	607	-	36,36,36	0.41	0	49,49,49	0.78	1 (2%)
5	CM5	A	605	-	25,25,36	0.44	0	32,32,49	0.79	1 (3%)
4	TB2	A	501	1	12,13,13	0.60	0	18,18,18	0.89	0
5	CM5	D	610	-	36,36,36	0.40	0	49,49,49	0.75	1 (2%)
4	TB2	C	501	1	12,13,13	0.60	0	18,18,18	0.92	0
3	HEM	D	500	1	50,50,50	1.87	9 (18%)	67,82,82	1.25	3 (4%)
4	TB2	D	501	1	12,13,13	0.69	0	18,18,18	1.81	1 (5%)
3	HEM	B	500	1	50,50,50	1.85	10 (20%)	67,82,82	1.36	7 (10%)
4	TB2	B	501	1	12,13,13	0.59	0	18,18,18	0.82	0
5	CM5	A	608	-	36,36,36	0.44	0	49,49,49	1.18	4 (8%)
3	HEM	A	500	1	50,50,50	1.90	8 (16%)	67,82,82	1.42	7 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	CM5	B	606	-	-	9/17/65/65	0/3/3/3
3	HEM	C	500	1	-	2/14/54/54	-
5	CM5	B	607	-	-	9/17/65/65	0/3/3/3
5	CM5	A	605	-	-	8/13/41/65	0/2/2/3
4	TB2	A	501	1	-	0/9/9/9	0/1/1/1
5	CM5	D	610	-	-	8/17/65/65	0/3/3/3
4	TB2	C	501	1	-	6/9/9/9	0/1/1/1
3	HEM	D	500	1	-	3/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	TB2	D	501	1	-	0/9/9/9	0/1/1/1
3	HEM	B	500	1	-	6/14/54/54	-
4	TB2	B	501	1	-	6/9/9/9	0/1/1/1
5	CM5	A	608	-	-	9/17/65/65	0/3/3/3
3	HEM	A	500	1	-	8/14/54/54	-

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	500	HEM	C3D-C2D	8.01	1.54	1.36
3	D	500	HEM	C3D-C2D	7.90	1.53	1.36
3	B	500	HEM	C3D-C2D	7.80	1.53	1.36
3	A	500	HEM	C3D-C2D	7.77	1.53	1.36
3	A	500	HEM	FE-ND	4.77	2.09	1.94

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	501	TB2	O1-C1-C2	-6.92	104.91	126.34
3	A	500	HEM	C4D-ND-C1D	5.42	111.63	105.21
3	C	500	HEM	C4D-ND-C1D	5.41	111.61	105.21
3	B	500	HEM	C4D-ND-C1D	5.27	111.45	105.21
3	D	500	HEM	C4D-ND-C1D	5.15	111.30	105.21

There are no chirality outliers.

5 of 74 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	605	CM5	O14-C13-O12-C1
5	B	606	CM5	C18-C13-O12-C1
5	B	606	CM5	O14-C13-O12-C1
5	D	610	CM5	O14-C13-O12-C1
3	A	500	HEM	C2D-C3D-CAD-CBD

There are no ring outliers.

12 monomers are involved in 114 short contacts:

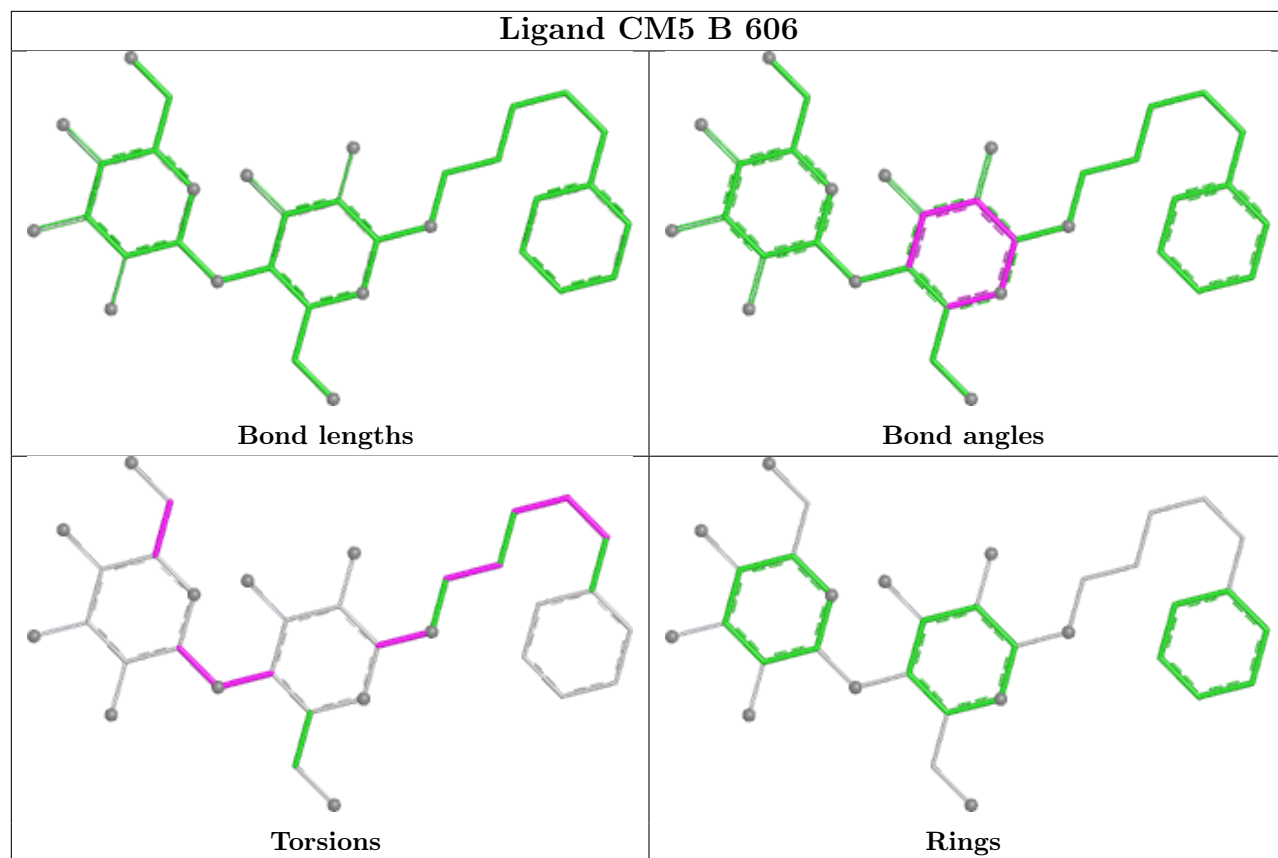
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	606	CM5	2	0
3	C	500	HEM	12	0

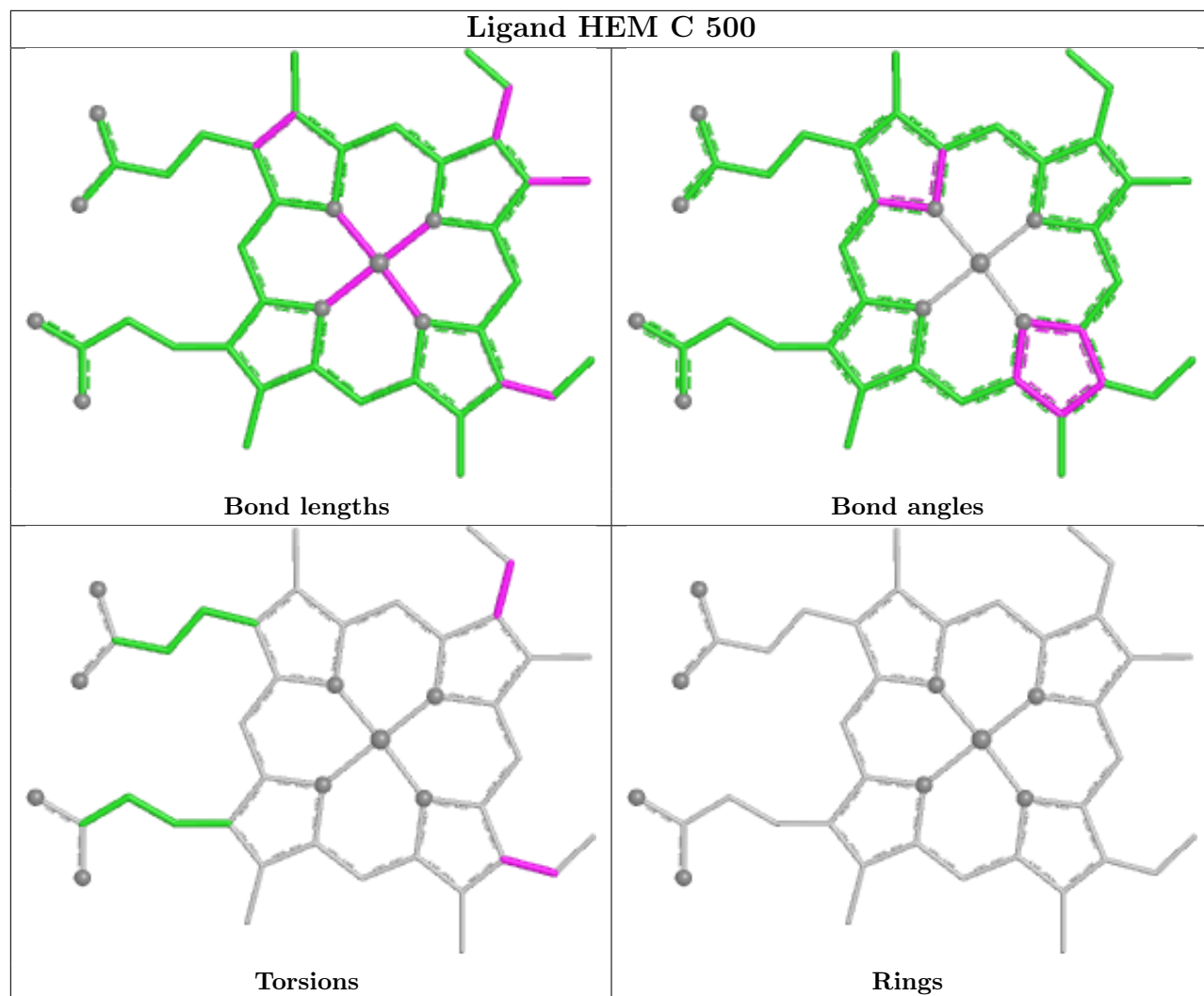
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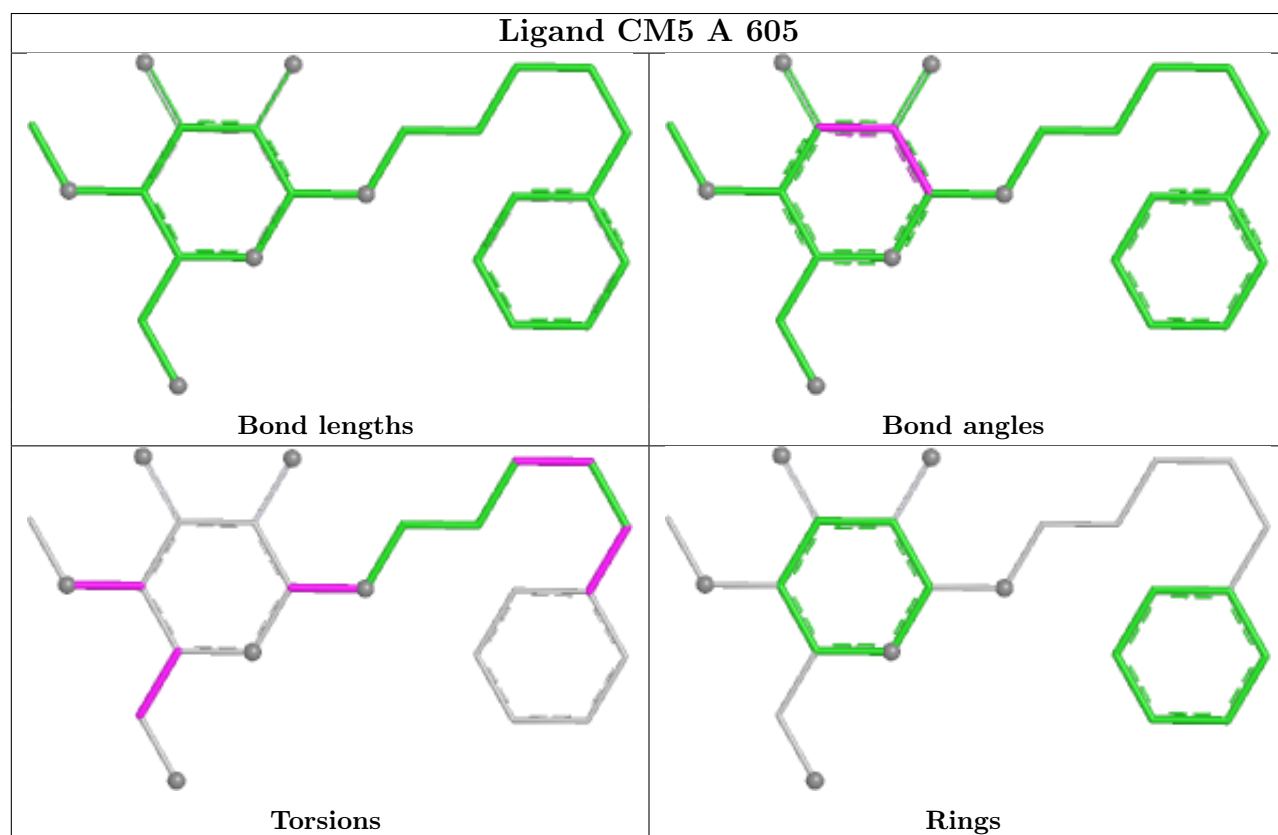
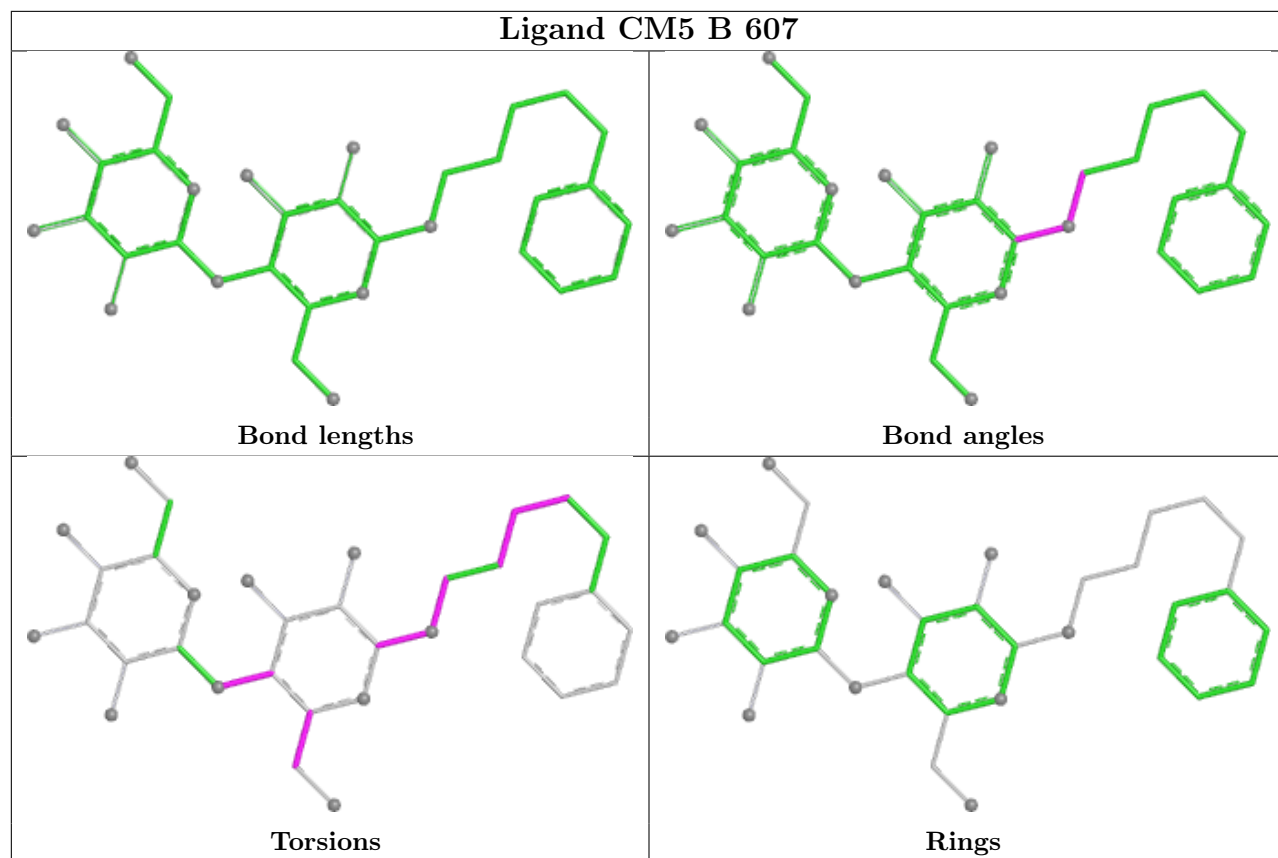
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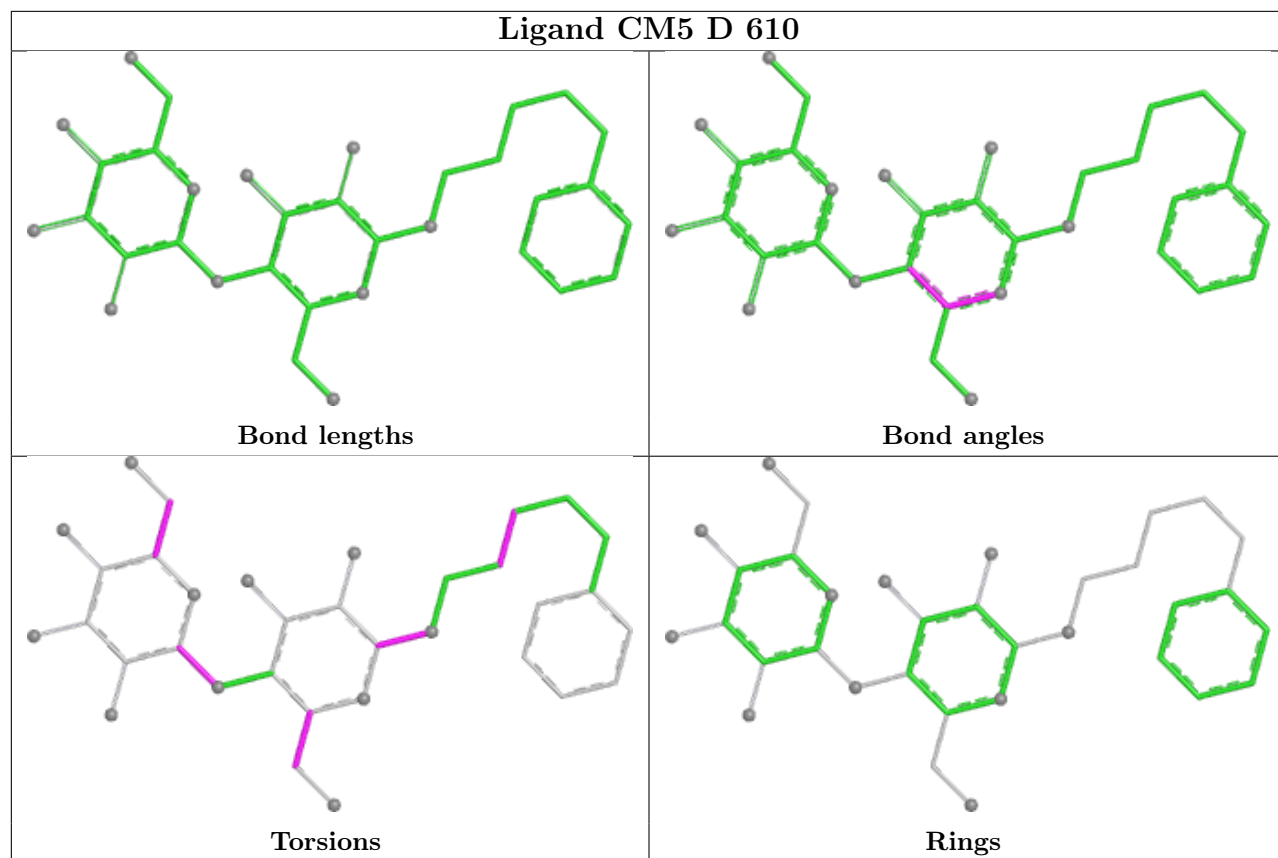
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	607	CM5	3	0
5	A	605	CM5	5	0
4	A	501	TB2	8	0
5	D	610	CM5	3	0
4	C	501	TB2	6	0
3	D	500	HEM	25	0
4	D	501	TB2	14	0
3	B	500	HEM	14	0
4	B	501	TB2	5	0
3	A	500	HEM	17	0

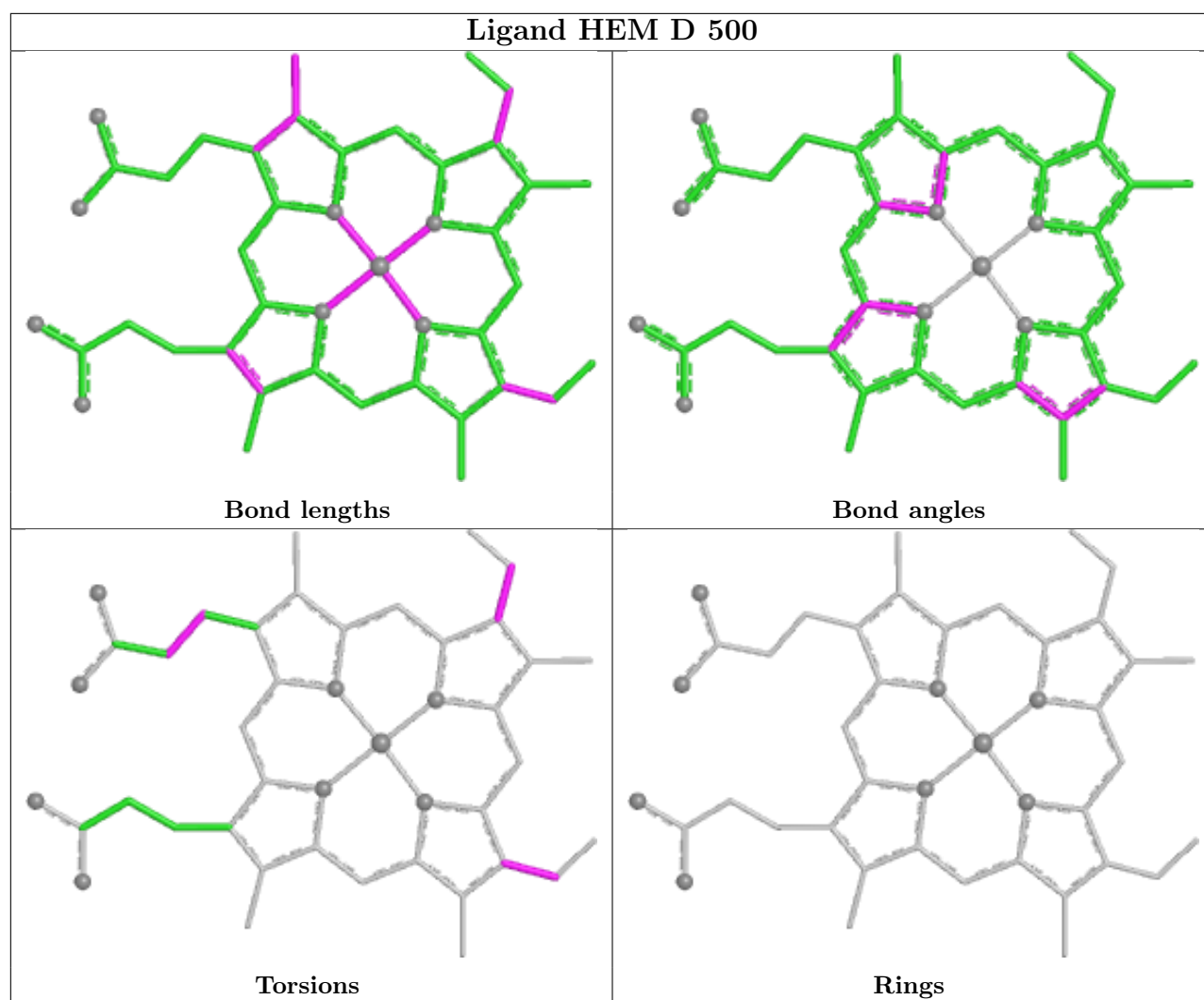
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

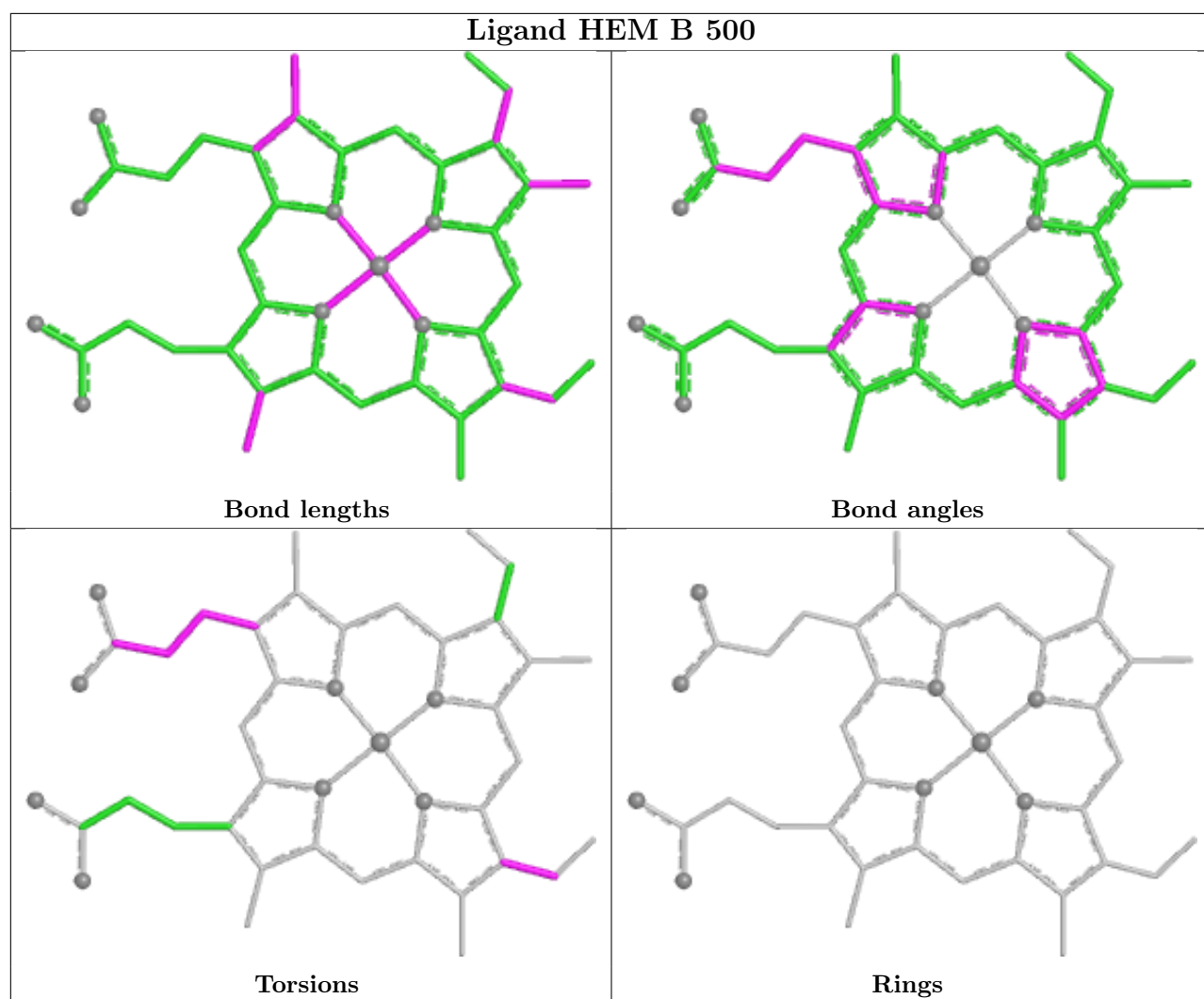


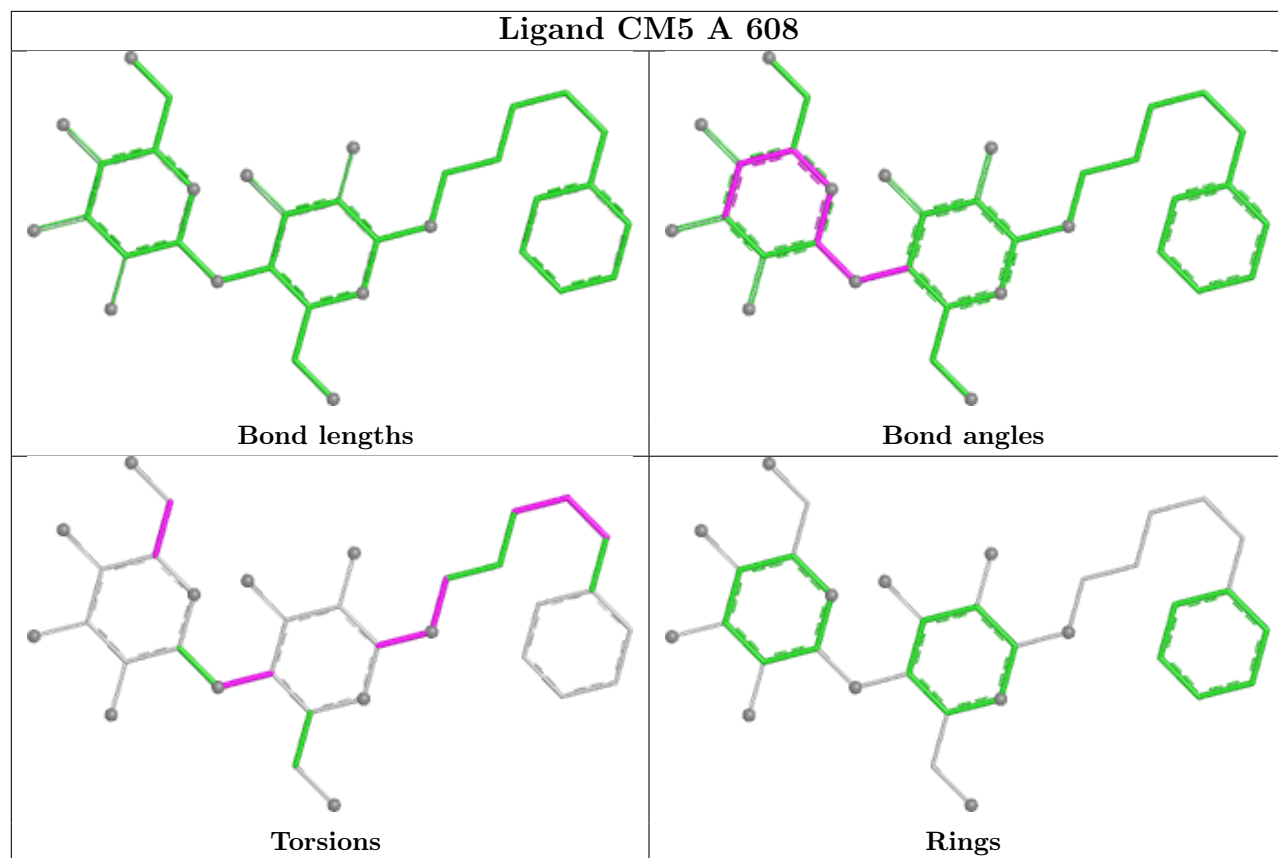


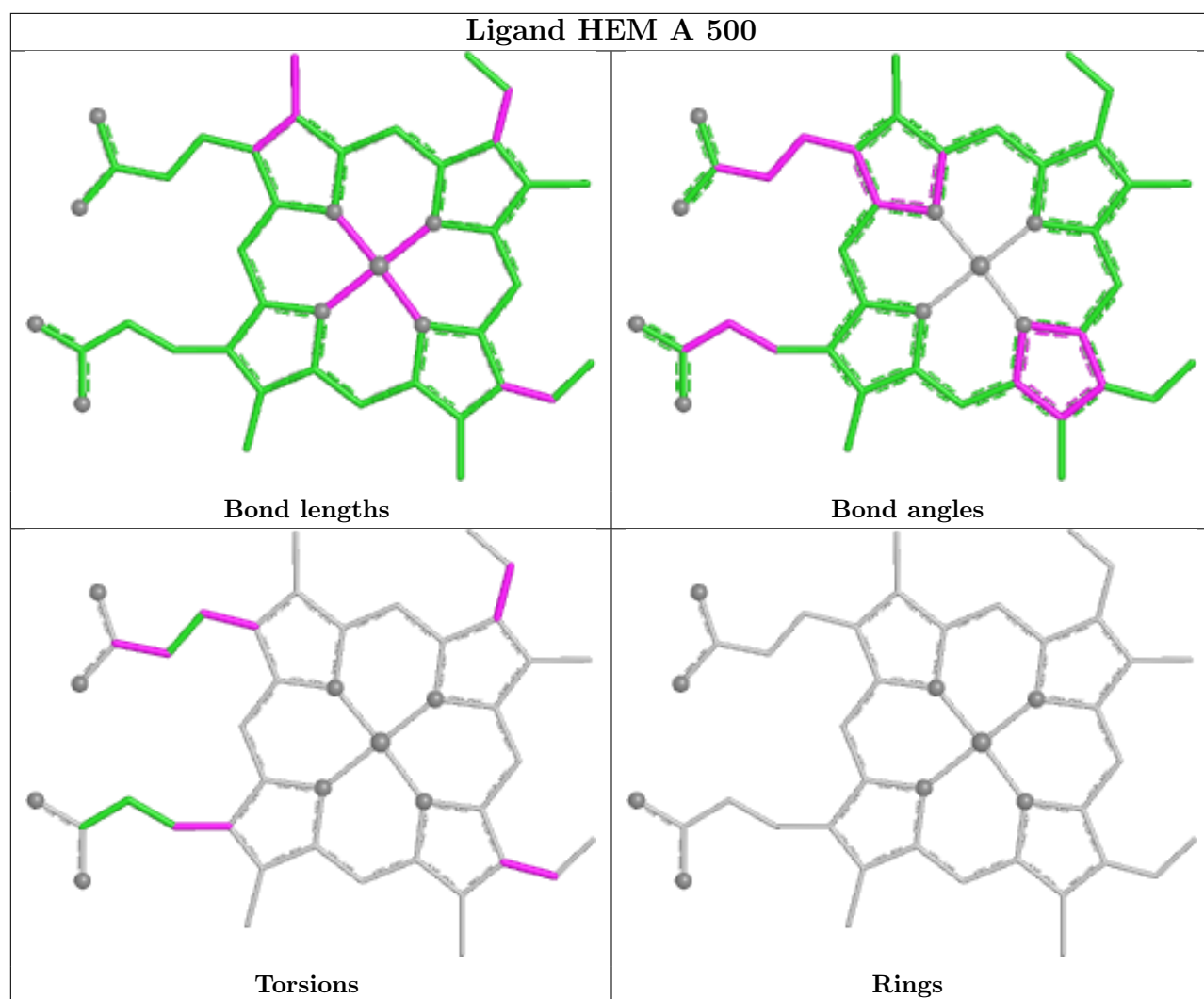












5.7 Other polymers [i](#)

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	465/476 (97%)	-0.12	9 (1%) 66 43	49, 78, 130, 196	1 (0%)
1	B	465/476 (97%)	0.09	15 (3%) 50 29	54, 88, 160, 184	2 (0%)
1	C	456/476 (95%)	0.22	18 (3%) 43 24	56, 97, 181, 211	1 (0%)
1	D	464/476 (97%)	0.46	22 (4%) 36 19	60, 127, 166, 206	0
All	All	1850/1904 (97%)	0.16	64 (3%) 47 27	49, 95, 166, 211	4 (0%)

The worst 5 of 64 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	221	SER	6.1
1	B	50	GLY	5.3
1	A	221	SER	5.3
1	B	55	PHE	5.2
1	C	115	PHE	4.6

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.

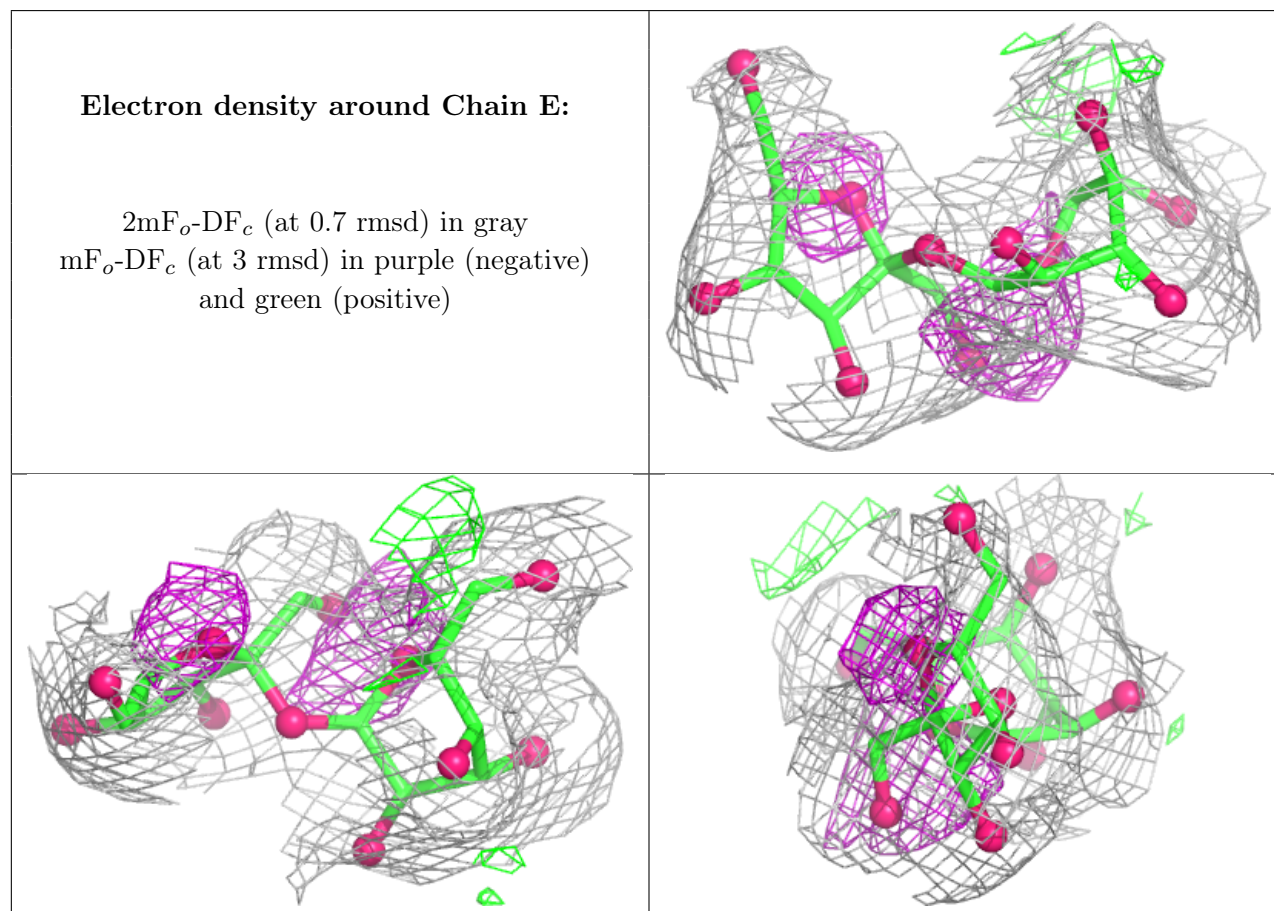
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FRU	G	2	12/12	0.68	0.11	91,108,111,120	0
2	FRU	H	2	12/12	0.73	0.08	141,148,151,154	0

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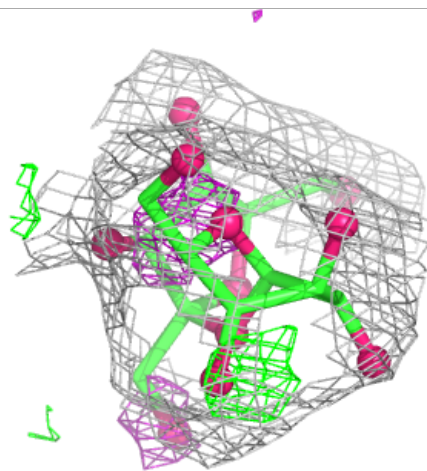
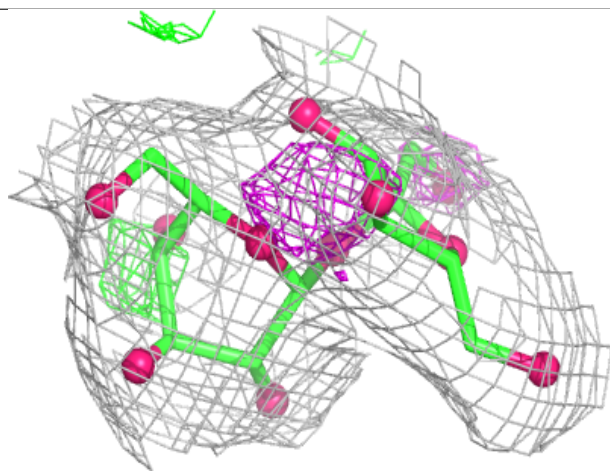
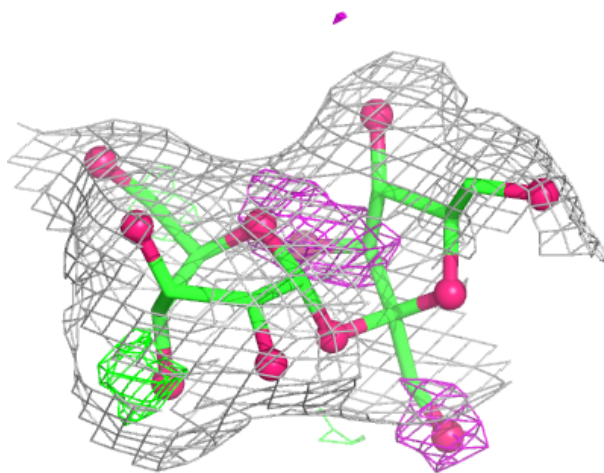
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GLC	H	1	11/12	0.75	0.11	140,144,153,155	0
2	GLC	F	1	11/12	0.75	0.14	78,90,98,100	0
2	GLC	G	1	11/12	0.76	0.14	82,92,101,102	0
2	FRU	F	2	12/12	0.79	0.10	85,89,94,95	0
2	GLC	E	1	11/12	0.80	0.11	54,76,86,98	0
2	FRU	E	2	12/12	0.81	0.12	66,87,93,93	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.



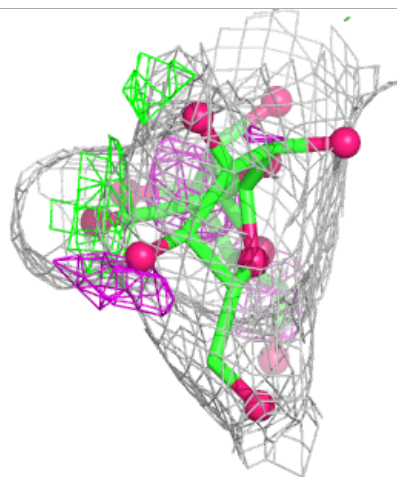
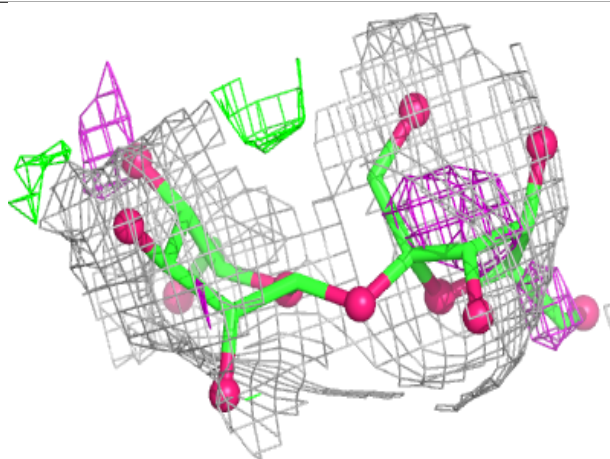
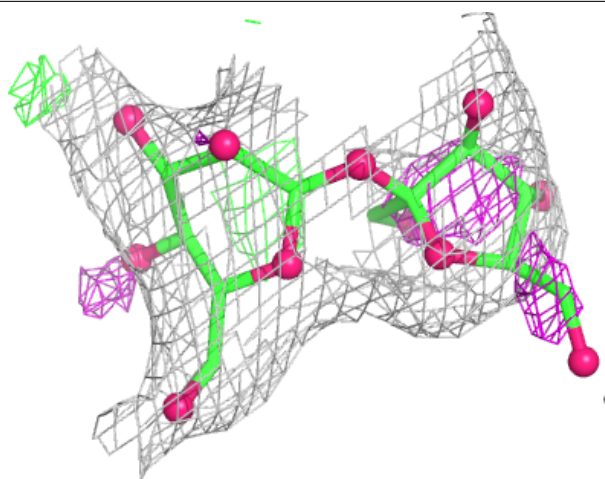
Electron density around Chain F:

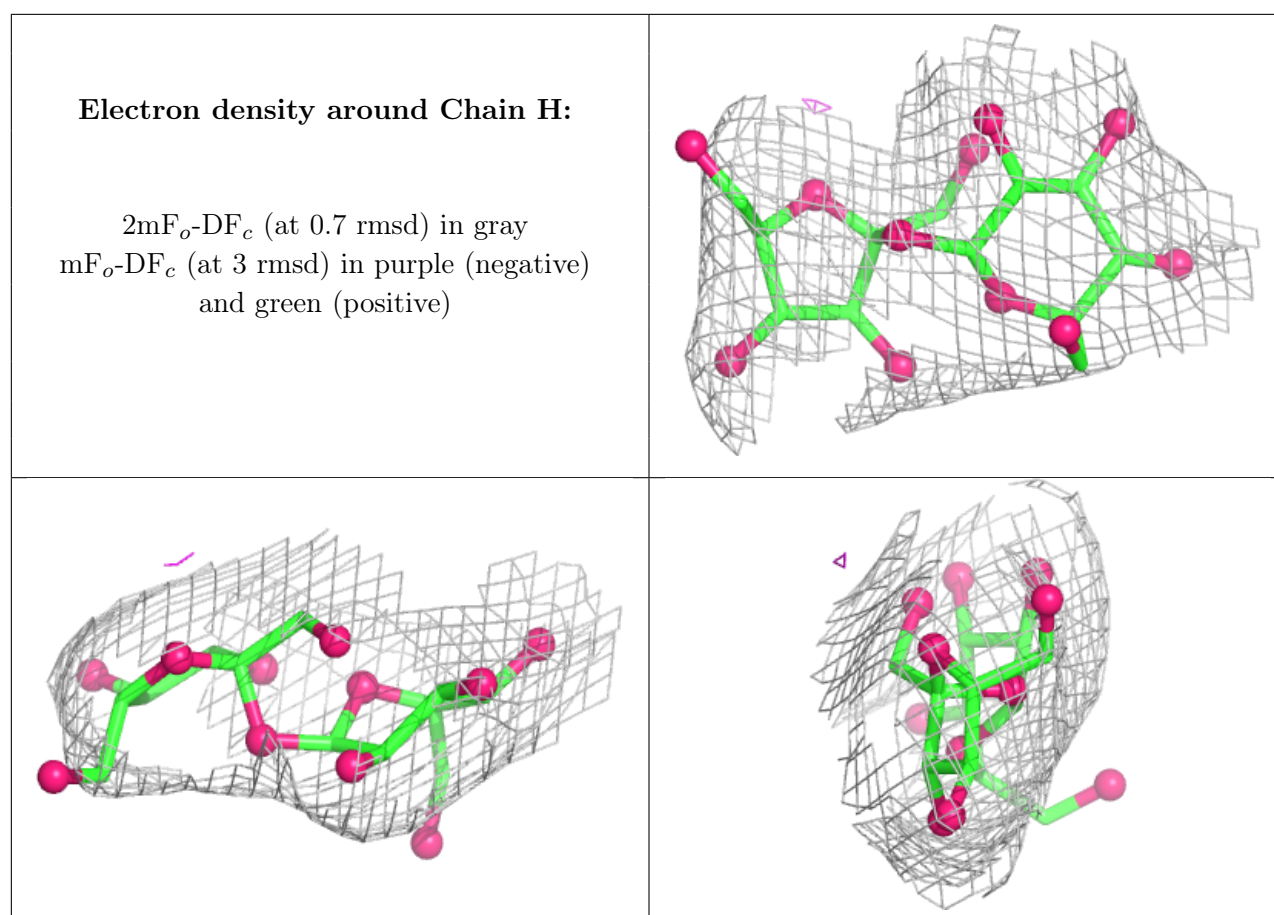
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain G:

$2mF_o-DF_c$ (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.

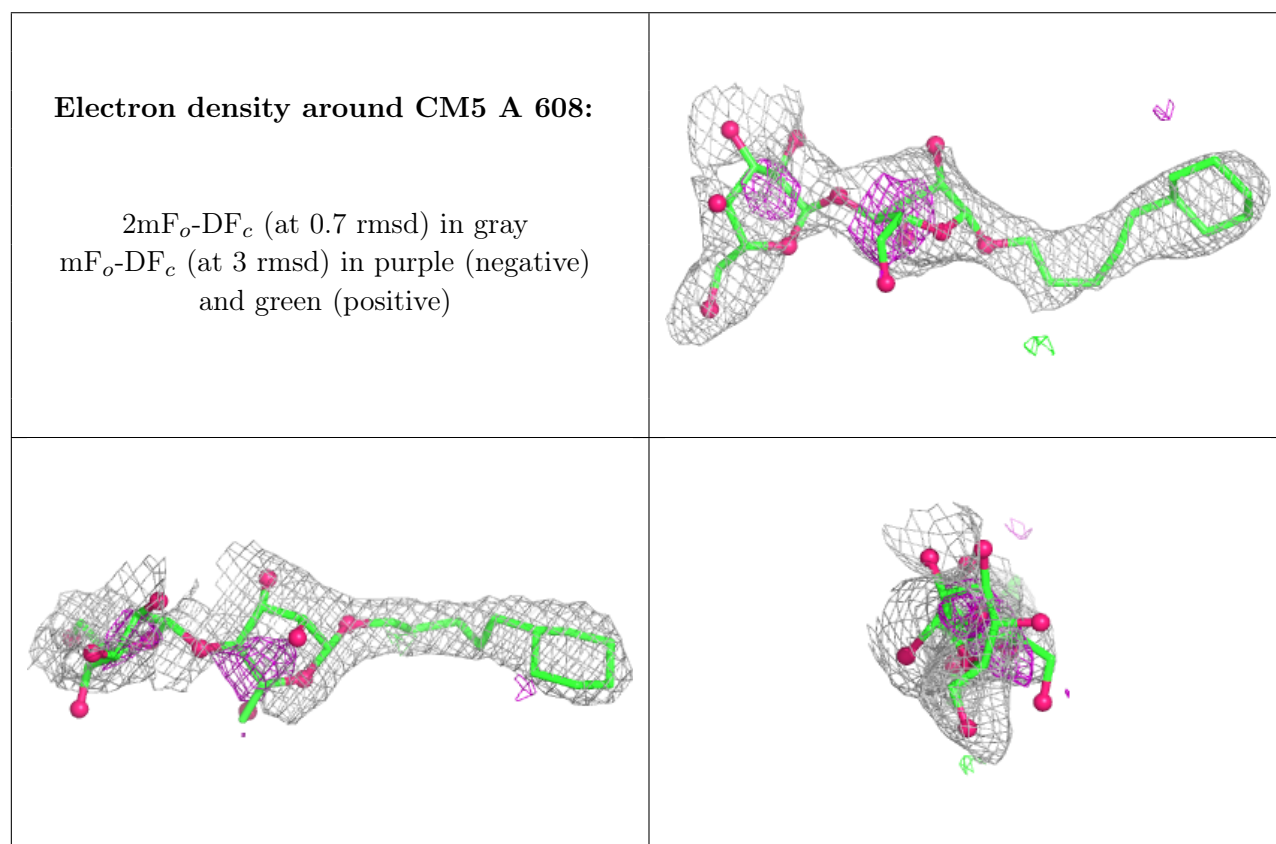
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	CM5	A	608	34/34	0.82	0.15	61,125,148,155	0
5	CM5	B	607	34/34	0.83	0.16	59,122,134,136	0
5	CM5	A	605	24/34	0.86	0.15	65,96,109,115	0
5	CM5	D	610	34/34	0.86	0.14	89,144,167,172	0
4	TB2	D	501	13/13	0.88	0.19	98,106,114,116	0
5	CM5	B	606	34/34	0.90	0.11	68,114,133,137	0
3	HEM	D	500	43/43	0.93	0.15	94,103,118,127	0
4	TB2	B	501	13/13	0.93	0.14	53,65,74,76	0
4	TB2	A	501	13/13	0.95	0.11	50,61,66,68	0
4	TB2	C	501	13/13	0.95	0.12	71,79,85,88	0
3	HEM	C	500	43/43	0.97	0.11	66,83,95,108	0
3	HEM	B	500	43/43	0.98	0.10	46,60,72,85	0

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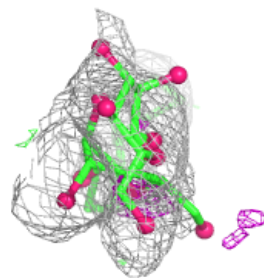
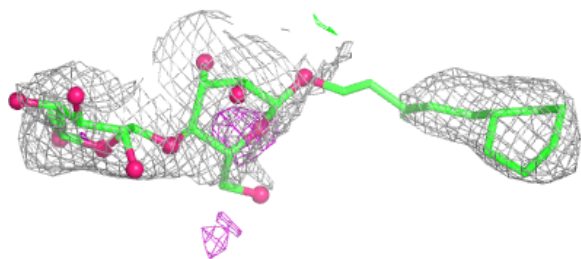
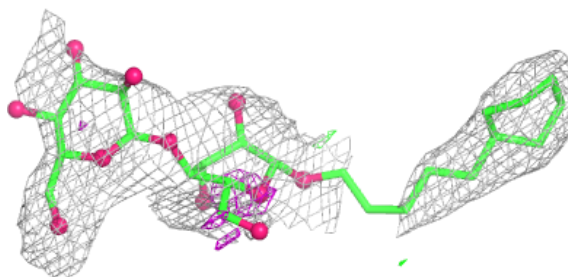
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	HEM	A	500	43/43	0.98	0.09	40,54,64,71	0

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.

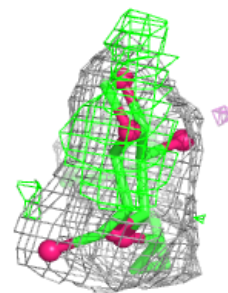
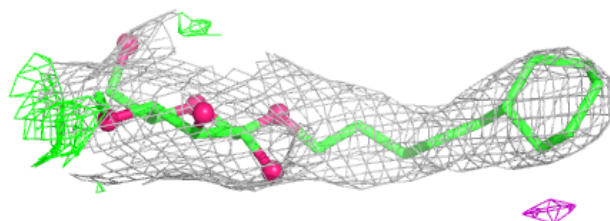
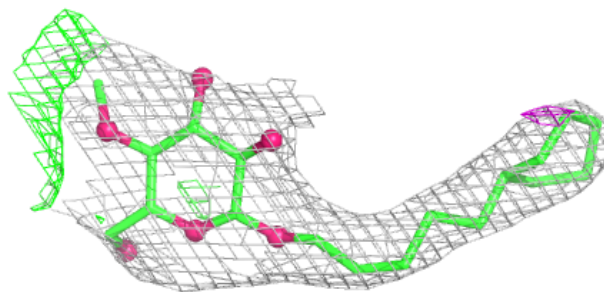


Electron density around CM5 B 607:

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

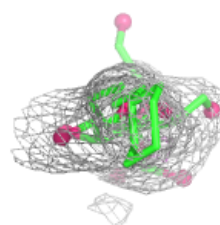
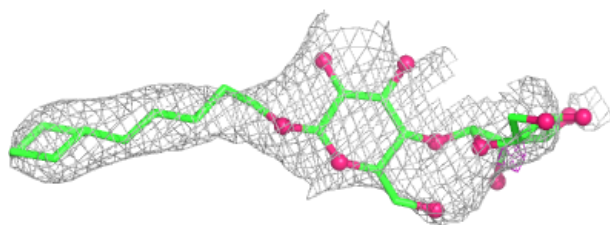
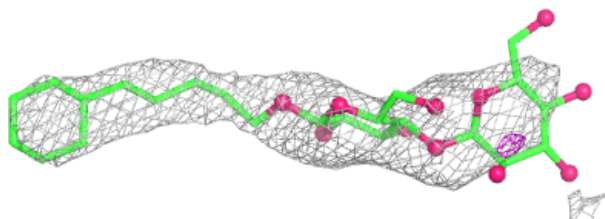
**Electron density around CM5 A 605:**

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

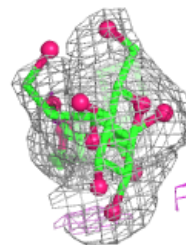
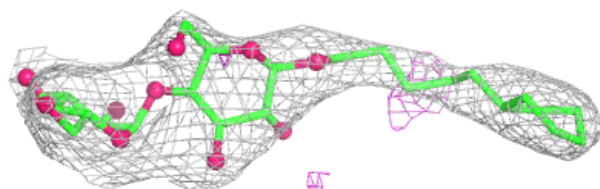
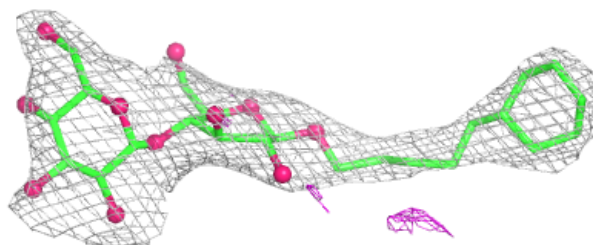


Electron density around CM5 D 610:

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

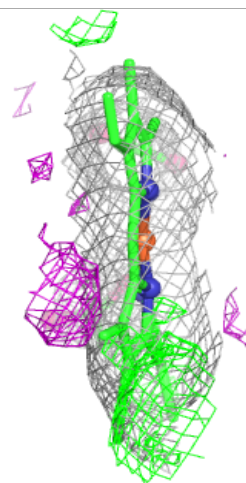
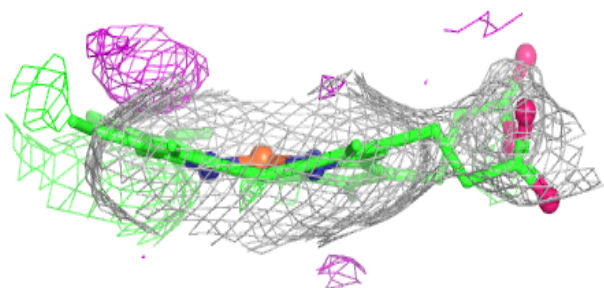
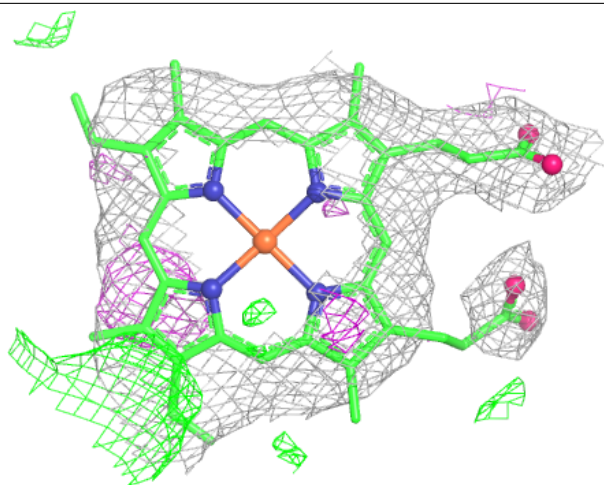
**Electron density around CM5 B 606:**

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



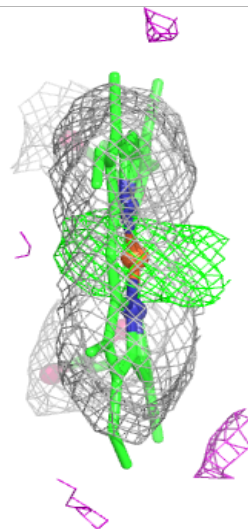
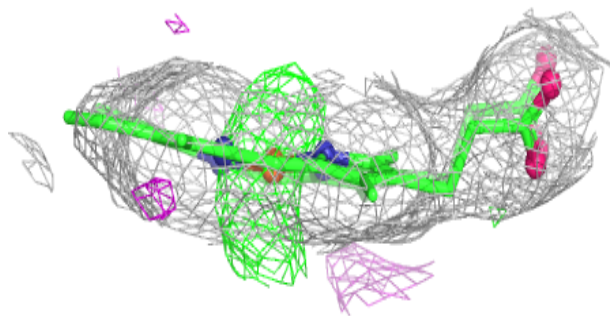
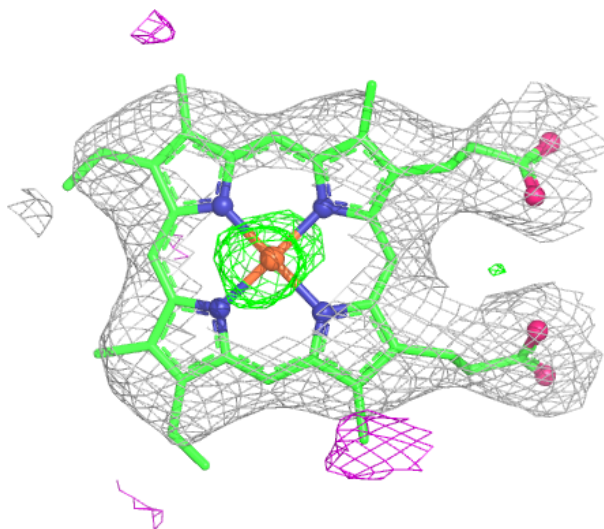
Electron density around HEM D 500:

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



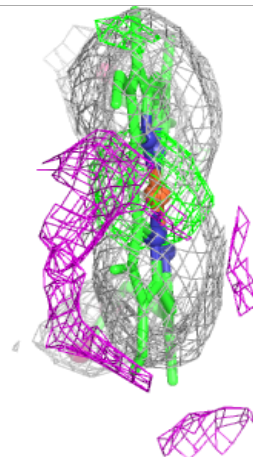
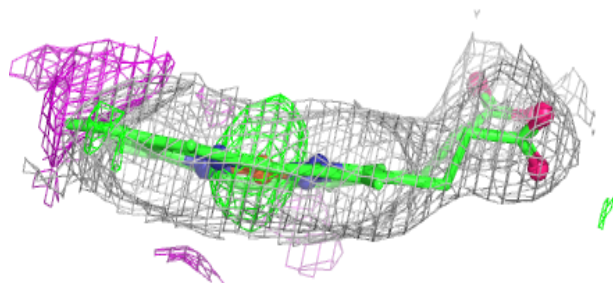
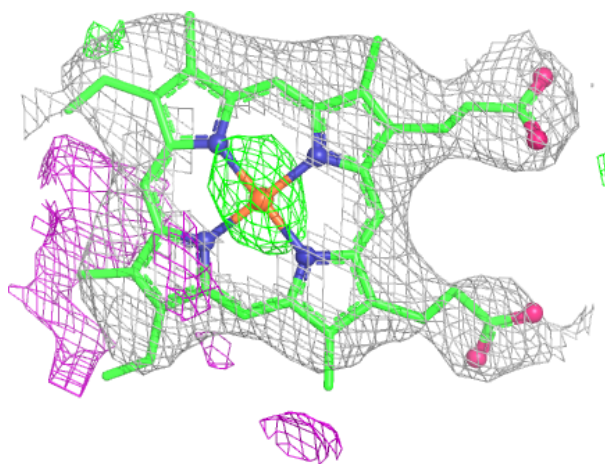
Electron density around HEM C 500:

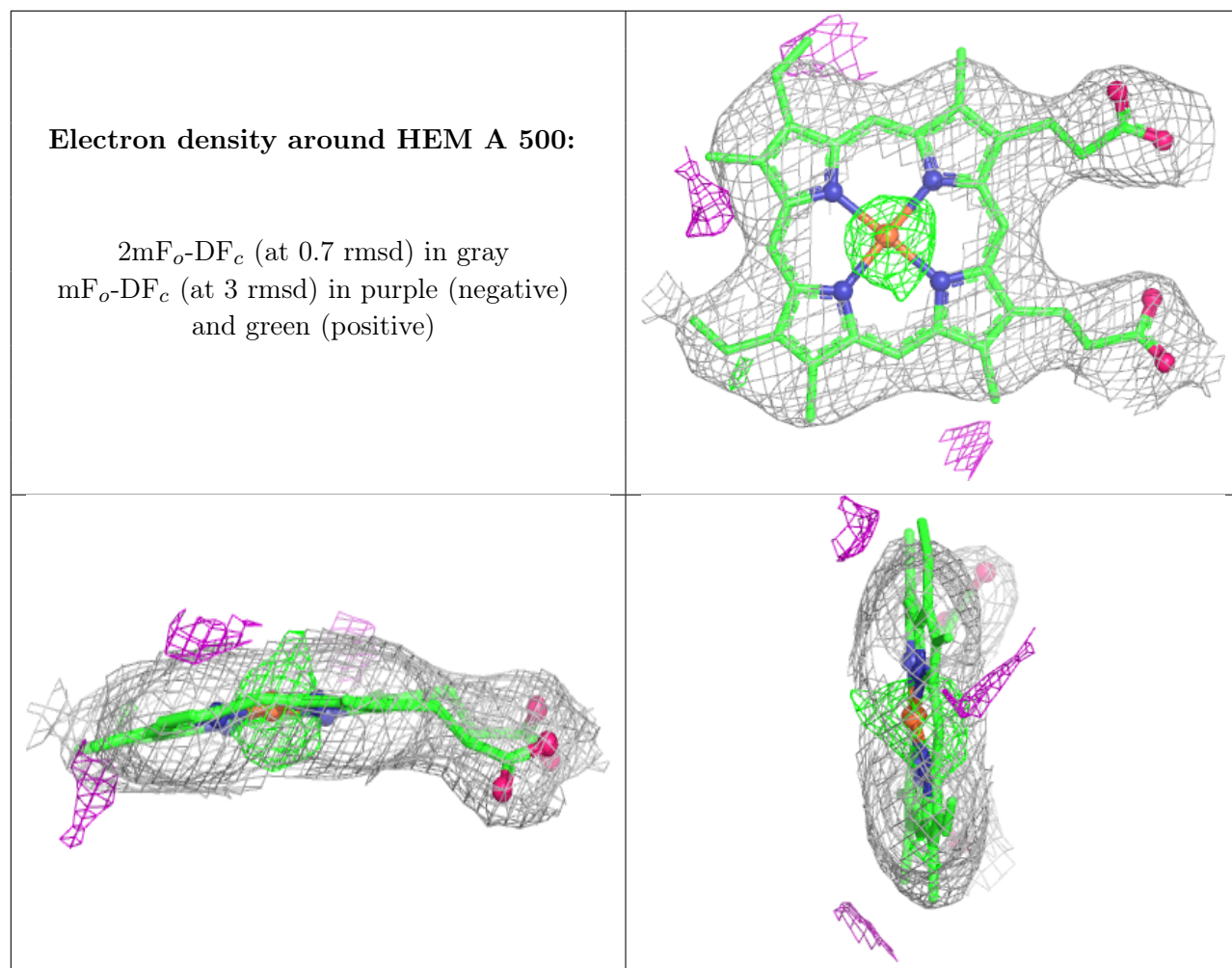
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM B 500:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.