



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 11:53 pm BST

PDB ID : 5WBG  
Title : Crystal Structure of human Cytochrome P450 2B6 (Y226H/K262R) in complex with an analog of a drug Efavirenz  
Authors : Shah, M.B.; Halpert, J.R.  
Deposited on : 2017-06-29  
Resolution : 2.99 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

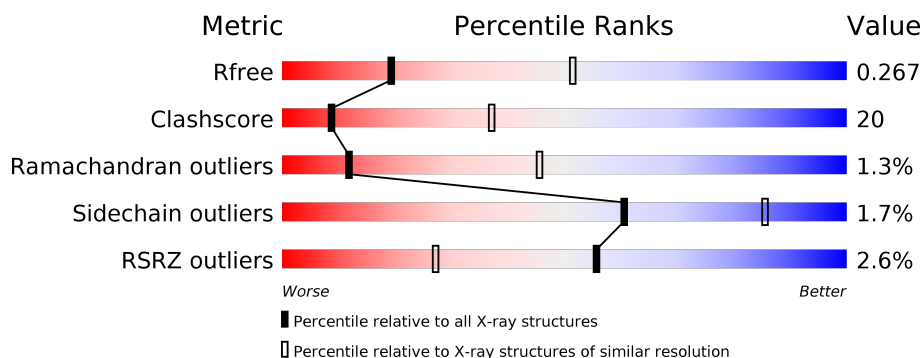
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.99 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	<div> <div>2%</div> <div> <div></div> <div>72%</div> <div>23%</div> <div>• •</div> </div> </div>
1	B	476	<div> <div>%</div> <div> <div></div> <div>69%</div> <div>26%</div> <div>• •</div> </div> </div>
1	C	476	<div> <div>2%</div> <div> <div></div> <div>71%</div> <div>23%</div> <div>• •</div> </div> </div>
1	D	476	<div> <div>3%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>• •</div> </div> </div>
1	E	476	<div> <div>3%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div>• •</div> </div> </div>
1	F	476	<div> <div>4%</div> <div> <div></div> <div>71%</div> <div>23%</div> <div>• •</div> </div> </div>

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	HEM	D	501	-	-	X	-
3	9ZJ	A	502	-	-	X	-
3	9ZJ	B	502	-	-	X	-
3	9ZJ	C	502	-	-	X	X
3	9ZJ	D	502	-	-	-	X
3	9ZJ	E	502	-	-	X	-
3	9ZJ	F	503	-	-	X	-
4	ZAZ	A	503	-	-	-	X
5	CM5	B	503	-	-	-	X
5	CM5	C	503	-	-	-	X
5	CM5	F	502	-	-	X	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 22570 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 2B6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	463	Total	C	N	O	S	0	0	0
			3637	2362	614	645	16			
1	B	464	Total	C	N	O	S	0	0	0
			3650	2370	614	650	16			
1	C	464	Total	C	N	O	S	0	0	0
			3655	2373	616	650	16			
1	D	464	Total	C	N	O	S	0	0	0
			3631	2360	612	643	16			
1	E	463	Total	C	N	O	S	0	0	0
			3643	2366	614	647	16			
1	F	464	Total	C	N	O	S	0	0	0
			3633	2362	613	642	16			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	MET	-	initiating methionine	UNP P20813
A	21	ALA	GLN	engineered mutation	UNP P20813
A	22	LYS	ARG	engineered mutation	UNP P20813
A	23	LYS	HIS	engineered mutation	UNP P20813
A	24	THR	PRO	engineered mutation	UNP P20813
A	25	SER	ASN	engineered mutation	UNP P20813
A	26	SER	THR	engineered mutation	UNP P20813
A	27	LYS	HIS	engineered mutation	UNP P20813
A	28	GLY	ASP	engineered mutation	UNP P20813
A	29	LYS	ARG	engineered mutation	UNP P20813
A	226	HIS	TYR	engineered mutation	UNP P20813
A	262	ARG	LYS	engineered mutation	UNP P20813
A	492	HIS	-	expression tag	UNP P20813
A	493	HIS	-	expression tag	UNP P20813
A	494	HIS	-	expression tag	UNP P20813
A	495	HIS	-	expression tag	UNP P20813
B	20	MET	-	initiating methionine	UNP P20813

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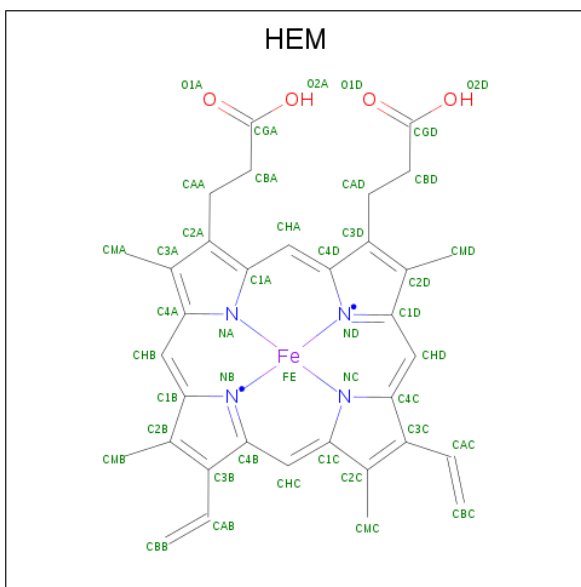
Chain	Residue	Modelled	Actual	Comment	Reference
B	21	ALA	GLN	engineered mutation	UNP P20813
B	22	LYS	ARG	engineered mutation	UNP P20813
B	23	LYS	HIS	engineered mutation	UNP P20813
B	24	THR	PRO	engineered mutation	UNP P20813
B	25	SER	ASN	engineered mutation	UNP P20813
B	26	SER	THR	engineered mutation	UNP P20813
B	27	LYS	HIS	engineered mutation	UNP P20813
B	28	GLY	ASP	engineered mutation	UNP P20813
B	29	LYS	ARG	engineered mutation	UNP P20813
B	226	HIS	TYR	engineered mutation	UNP P20813
B	262	ARG	LYS	engineered mutation	UNP P20813
B	492	HIS	-	expression tag	UNP P20813
B	493	HIS	-	expression tag	UNP P20813
B	494	HIS	-	expression tag	UNP P20813
B	495	HIS	-	expression tag	UNP P20813
C	20	MET	-	initiating methionine	UNP P20813
C	21	ALA	GLN	engineered mutation	UNP P20813
C	22	LYS	ARG	engineered mutation	UNP P20813
C	23	LYS	HIS	engineered mutation	UNP P20813
C	24	THR	PRO	engineered mutation	UNP P20813
C	25	SER	ASN	engineered mutation	UNP P20813
C	26	SER	THR	engineered mutation	UNP P20813
C	27	LYS	HIS	engineered mutation	UNP P20813
C	28	GLY	ASP	engineered mutation	UNP P20813
C	29	LYS	ARG	engineered mutation	UNP P20813
C	226	HIS	TYR	engineered mutation	UNP P20813
C	262	ARG	LYS	engineered mutation	UNP P20813
C	492	HIS	-	expression tag	UNP P20813
C	493	HIS	-	expression tag	UNP P20813
C	494	HIS	-	expression tag	UNP P20813
C	495	HIS	-	expression tag	UNP P20813
D	20	MET	-	initiating methionine	UNP P20813
D	21	ALA	GLN	engineered mutation	UNP P20813
D	22	LYS	ARG	engineered mutation	UNP P20813
D	23	LYS	HIS	engineered mutation	UNP P20813
D	24	THR	PRO	engineered mutation	UNP P20813
D	25	SER	ASN	engineered mutation	UNP P20813
D	26	SER	THR	engineered mutation	UNP P20813
D	27	LYS	HIS	engineered mutation	UNP P20813
D	28	GLY	ASP	engineered mutation	UNP P20813
D	29	LYS	ARG	engineered mutation	UNP P20813
D	226	HIS	TYR	engineered mutation	UNP P20813

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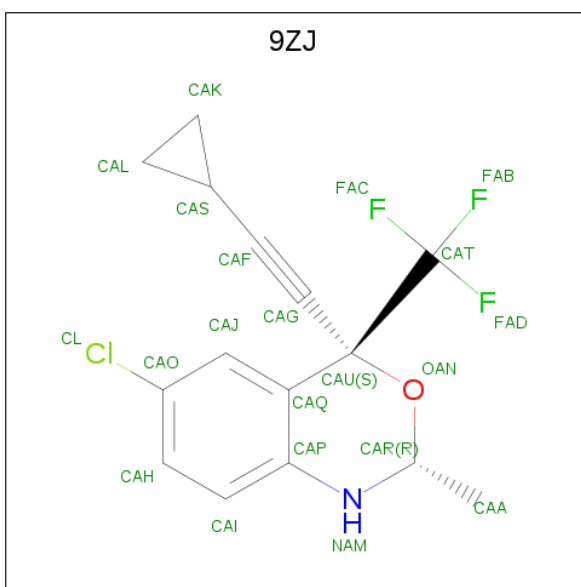
Chain	Residue	Modelled	Actual	Comment	Reference
D	262	ARG	LYS	engineered mutation	UNP P20813
D	492	HIS	-	expression tag	UNP P20813
D	493	HIS	-	expression tag	UNP P20813
D	494	HIS	-	expression tag	UNP P20813
D	495	HIS	-	expression tag	UNP P20813
E	20	MET	-	initiating methionine	UNP P20813
E	21	ALA	GLN	engineered mutation	UNP P20813
E	22	LYS	ARG	engineered mutation	UNP P20813
E	23	LYS	HIS	engineered mutation	UNP P20813
E	24	THR	PRO	engineered mutation	UNP P20813
E	25	SER	ASN	engineered mutation	UNP P20813
E	26	SER	THR	engineered mutation	UNP P20813
E	27	LYS	HIS	engineered mutation	UNP P20813
E	28	GLY	ASP	engineered mutation	UNP P20813
E	29	LYS	ARG	engineered mutation	UNP P20813
E	226	HIS	TYR	engineered mutation	UNP P20813
E	262	ARG	LYS	engineered mutation	UNP P20813
E	492	HIS	-	expression tag	UNP P20813
E	493	HIS	-	expression tag	UNP P20813
E	494	HIS	-	expression tag	UNP P20813
E	495	HIS	-	expression tag	UNP P20813
F	20	MET	-	initiating methionine	UNP P20813
F	21	ALA	GLN	engineered mutation	UNP P20813
F	22	LYS	ARG	engineered mutation	UNP P20813
F	23	LYS	HIS	engineered mutation	UNP P20813
F	24	THR	PRO	engineered mutation	UNP P20813
F	25	SER	ASN	engineered mutation	UNP P20813
F	26	SER	THR	engineered mutation	UNP P20813
F	27	LYS	HIS	engineered mutation	UNP P20813
F	28	GLY	ASP	engineered mutation	UNP P20813
F	29	LYS	ARG	engineered mutation	UNP P20813
F	226	HIS	TYR	engineered mutation	UNP P20813
F	262	ARG	LYS	engineered mutation	UNP P20813
F	492	HIS	-	expression tag	UNP P20813
F	493	HIS	-	expression tag	UNP P20813
F	494	HIS	-	expression tag	UNP P20813
F	495	HIS	-	expression tag	UNP P20813

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



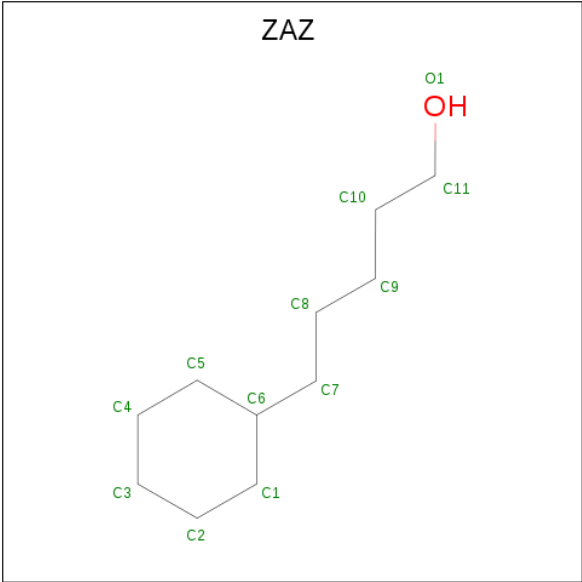
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is (2R,4S)-6-chloro-4-(cyclopropylethynyl)-2-methyl-4-(trifluoromethyl)-1,4-dihydro-2H-3,1-benzoxazine (three-letter code: 9ZJ) (formula: C<sub>15</sub>H<sub>13</sub>ClF<sub>3</sub>NO).



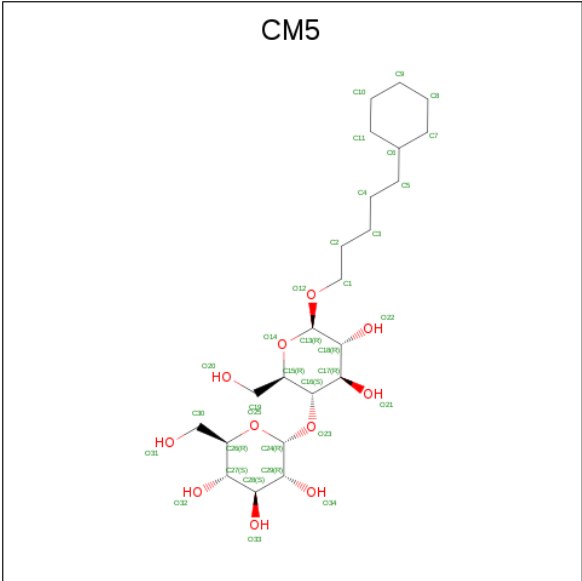
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total 21	C 15	Cl 1	F 3	N 1	O 1	0	0
3	B	1	Total 21	C 15	Cl 1	F 3	N 1	O 1	0	0
3	C	1	Total 21	C 15	Cl 1	F 3	N 1	O 1	0	0
3	D	1	Total 21	C 15	Cl 1	F 3	N 1	O 1	0	0
3	E	1	Total 21	C 15	Cl 1	F 3	N 1	O 1	0	0
3	F	1	Total 21	C 15	Cl 1	F 3	N 1	O 1	0	0

- Molecule 4 is 5-cyclohexylpentan-1-ol (three-letter code: ZAZ) (formula:  $C_{11}H_{22}O$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	11	1		

- Molecule 5 is 5-CYCLOHEXYL-1-PENTYL-BETA-D-MALTOSE (three-letter code: CM5) (formula: C<sub>23</sub>H<sub>42</sub>O<sub>11</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			34	23	11		
5	C	1	Total	C	O	0	0
			34	23	11		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			34	23	11		
5	E	1	Total	C	O	0	0
			34	23	11		
5	F	1	Total	C	O	0	0
			34	23	11		

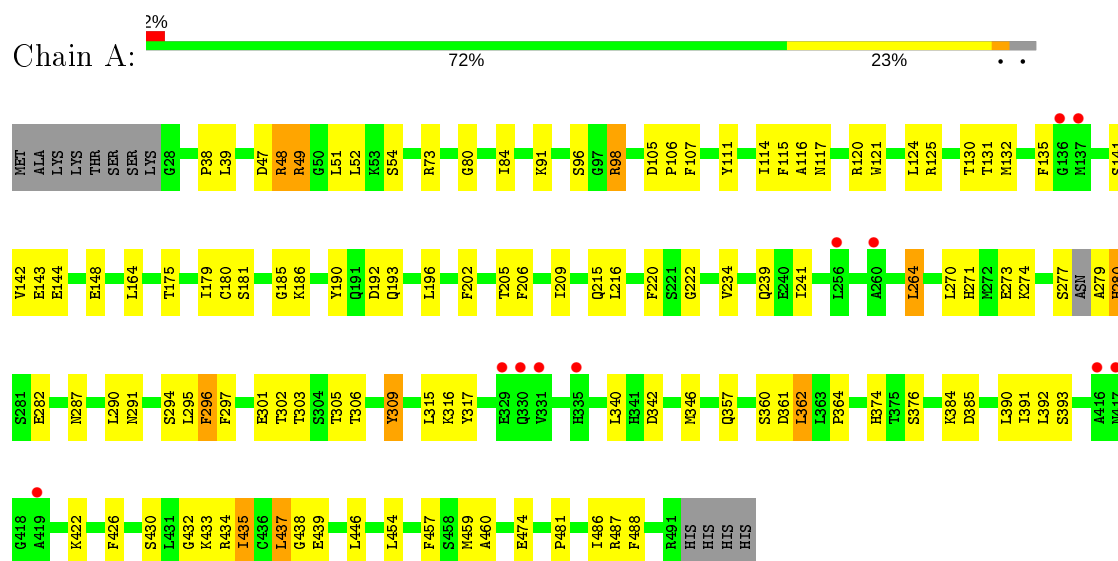
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	36	Total	O	0	0
			36	36		
6	B	39	Total	O	0	0
			39	39		
6	C	25	Total	O	0	0
			25	25		
6	D	26	Total	O	0	0
			26	26		
6	E	17	Total	O	0	0
			17	17		
6	F	12	Total	O	0	0
			12	12		

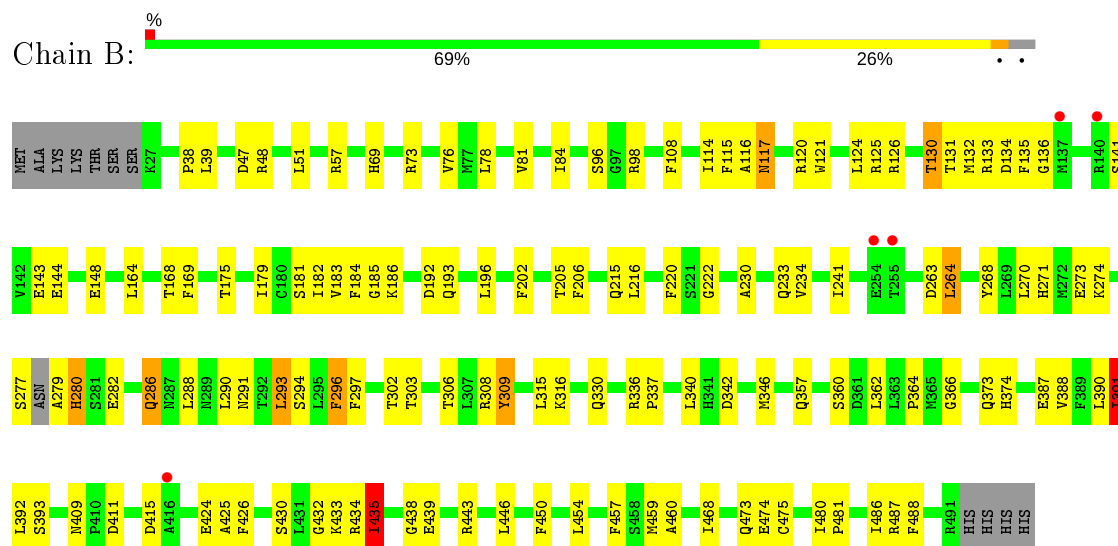
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 2B6

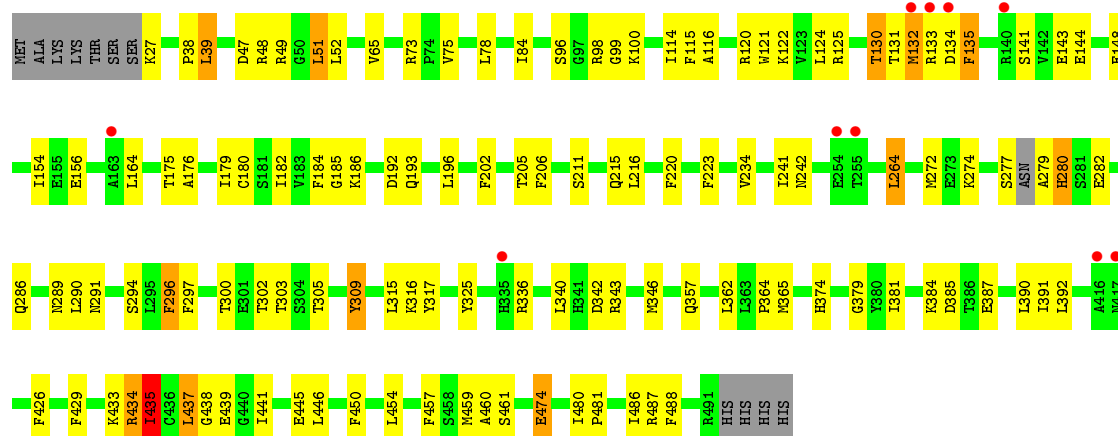


#### • Molecule 1: Cytochrome P450 2B6

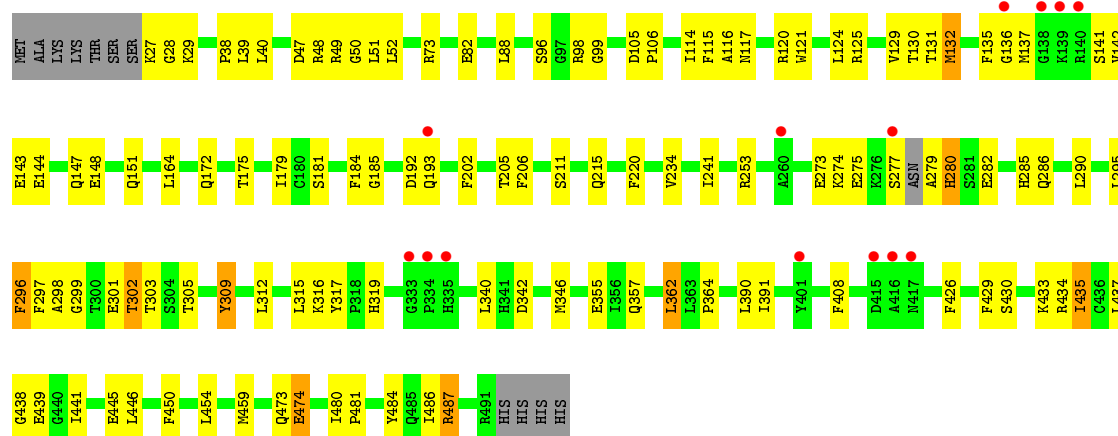
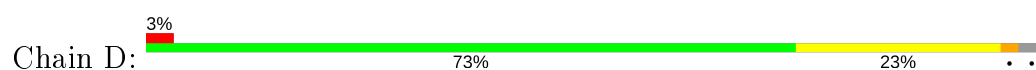


#### • Molecule 1: Cytochrome P450 2B6

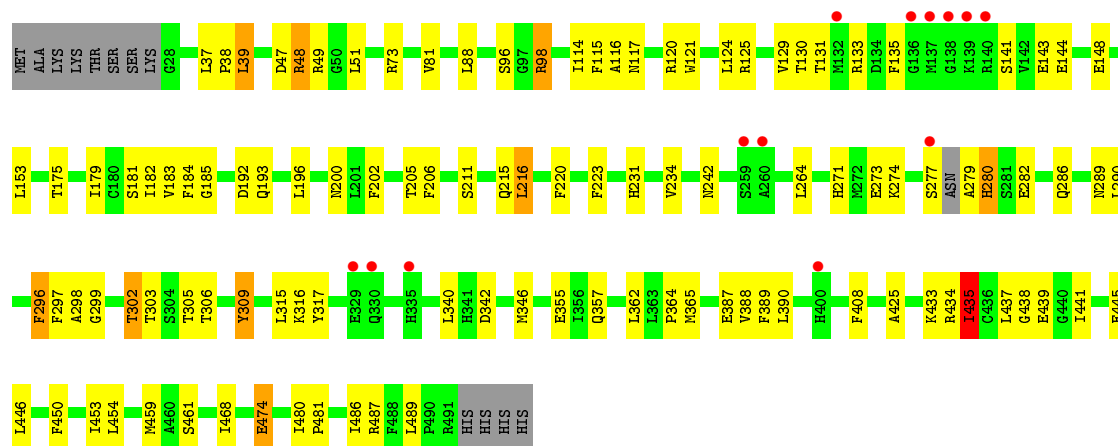




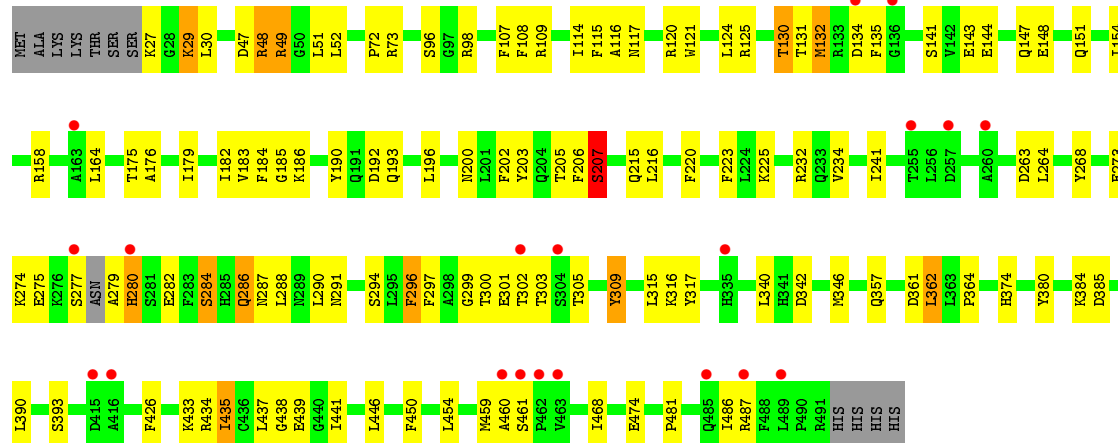
• Molecule 1: Cytochrome P450 2B6



• Molecule 1: Cytochrome P450 2B6



• Molecule 1: Cytochrome P450 2B6



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.29 Å   197.79 Å   119.22 Å 90.00°   98.51°   90.00°	Depositor
Resolution (Å)	50.00 – 2.99 39.65 – 2.99	Depositor EDS
% Data completeness (in resolution range)	99.2 (50.00-2.99) 99.2 (39.65-2.99)	Depositor EDS
$R_{merge}$	0.19	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.94 (at 3.01 Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.227   ,   0.262 0.236   ,   0.267	Depositor DCC
$R_{free}$ test set	4745 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	64.6	Xtriage
Anisotropy	0.156	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 60.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	22570	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, 9ZJ, ZAZ, CM5

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	0.64	0/3737	0.74	4/5074 (0.1%)
1	B	0.67	0/3749	0.75	3/5088 (0.1%)
1	C	0.63	0/3755	0.75	6/5096 (0.1%)
1	D	0.62	0/3731	0.71	3/5066 (0.1%)
1	E	0.61	0/3743	0.72	3/5081 (0.1%)
1	F	0.59	0/3733	0.71	4/5069 (0.1%)
All	All	0.63	0/22448	0.73	23/30474 (0.1%)

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	437	LEU	CB-CG-CD1	-8.87	95.93	111.00
1	C	435	ILE	CB-CA-C	-8.08	95.45	111.60
1	F	435	ILE	CB-CA-C	-8.05	95.50	111.60
1	B	435	ILE	CB-CA-C	-7.66	96.28	111.60
1	A	132	MET	N-CA-C	-6.98	92.15	111.00
1	F	29	LYS	N-CA-CB	-6.94	98.11	110.60
1	F	207	SER	CA-CB-OG	6.64	129.13	111.20
1	C	132	MET	N-CA-C	-6.57	93.27	111.00
1	C	48	ARG	CB-CA-C	-6.42	97.55	110.40
1	B	475	CYS	N-CA-CB	-6.20	99.44	110.60
1	A	98	ARG	NE-CZ-NH2	-5.90	117.35	120.30
1	C	437	LEU	CA-CB-CG	5.85	128.76	115.30
1	F	132	MET	N-CA-C	-5.70	95.62	111.00
1	A	98	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	D	40	LEU	N-CA-CB	5.51	121.43	110.40
1	B	391	ILE	N-CA-C	-5.48	96.21	111.00
1	E	435	ILE	CB-CA-C	-5.42	100.76	111.60
1	D	487	ARG	NE-CZ-NH1	5.41	123.00	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	39	LEU	CB-CA-C	-5.22	100.27	110.20
1	E	98	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	D	50	GLY	N-CA-C	5.19	126.06	113.10
1	C	39	LEU	CB-CA-C	-5.17	100.39	110.20
1	C	434	ARG	NE-CZ-NH1	5.08	122.84	120.30

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	3637	0	3515	125	0
1	B	3650	0	3533	153	0
1	C	3655	0	3538	164	0
1	D	3631	0	3502	138	0
1	E	3643	0	3524	156	0
1	F	3633	0	3511	141	0
2	A	43	0	30	5	0
2	B	43	0	30	4	0
2	C	43	0	30	11	0
2	D	43	0	30	22	0
2	E	43	0	30	15	0
2	F	43	0	30	1	0
3	A	21	0	0	10	0
3	B	21	0	0	8	0
3	C	21	0	0	7	0
3	D	21	0	0	6	0
3	E	21	0	0	7	0
3	F	21	0	0	10	0
4	A	12	0	0	0	0
5	B	34	0	42	7	0
5	C	34	0	42	20	0
5	D	34	0	42	13	0
5	E	34	0	42	18	0
5	F	34	0	42	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	36	0	0	8	0
6	B	39	0	0	10	0
6	C	25	0	0	8	0
6	D	26	0	0	5	0
6	E	17	0	0	5	0
6	F	12	0	0	3	0
All	All	22570	0	21513	900	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 20.

All (900) 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:E:131:THR:HG21	1:E:264:LEU:CD2	1.17	1.59
1:A:135:PHE:CE2	1:A:142:VAL:CG2	2.05	1.39
1:A:135:PHE:CE2	1:A:142:VAL:HG22	1.57	1.38
1:A:135:PHE:HE2	1:A:142:VAL:CG2	1.41	1.31
1:E:220:PHE:CD2	5:E:503:CM5:H101	1.67	1.30
1:E:131:THR:CG2	1:E:264:LEU:CD2	2.14	1.26
1:E:131:THR:CG2	1:E:264:LEU:HD23	1.70	1.21
1:E:114:ILE:HD13	3:E:502:9ZJ:CAI	1.71	1.20
1:A:114:ILE:HD13	3:A:502:9ZJ:CAI	1.73	1.19
1:C:211:SER:HA	1:C:474:GLU:OE2	1.43	1.17
1:C:216:LEU:HD21	5:C:503:CM5:H92	1.18	1.17
1:B:206:PHE:CD1	3:B:502:9ZJ:CAK	2.28	1.16
1:A:206:PHE:CD1	3:A:502:9ZJ:CAK	2.28	1.16
1:F:223:PHE:CG	5:F:502:CM5:H31A	1.81	1.15
1:E:223:PHE:HB3	6:E:601:HOH:O	1.46	1.14
1:D:135:PHE:CE2	1:D:142:VAL:CG2	2.29	1.14
1:F:223:PHE:CD2	5:F:502:CM5:H31A	1.82	1.14
1:C:114:ILE:HD13	3:C:502:9ZJ:CAI	1.78	1.14
1:D:135:PHE:HE2	1:D:142:VAL:CG2	1.60	1.13
1:F:114:ILE:CD1	3:F:503:9ZJ:CAI	2.27	1.12
1:F:232:ARG:NH2	6:F:601:HOH:O	1.83	1.12
1:E:206:PHE:CD1	3:E:502:9ZJ:CAK	2.34	1.10
1:F:435:ILE:O	1:F:435:ILE:HG23	1.48	1.10
1:C:216:LEU:HD11	5:C:503:CM5:H101	1.25	1.10
1:E:302:THR:HG21	2:E:501:HEM:CHC	1.80	1.10
1:A:206:PHE:CE1	3:A:502:9ZJ:CAK	2.34	1.09
1:D:114:ILE:HD13	3:D:502:9ZJ:CAI	1.81	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:336:ARG:HD2	6:C:601:HOH:O	1.51	1.09
1:D:135:PHE:HE2	1:D:142:VAL:HG23	1.14	1.08
1:D:132:MET:HA	1:D:135:PHE:CE1	1.88	1.08
1:D:27:LYS:O	1:D:29:LYS:N	1.86	1.08
1:C:206:PHE:CD1	3:C:502:9ZJ:CAK	2.37	1.08
1:E:220:PHE:CD2	5:E:503:CM5:C10	2.37	1.07
1:A:220:PHE:O	6:A:601:HOH:O	1.73	1.07
1:F:114:ILE:HD13	3:F:503:9ZJ:CAI	1.83	1.07
1:D:206:PHE:CD1	3:D:502:9ZJ:CAK	2.36	1.07
1:C:302:THR:HG21	2:C:501:HEM:C3B	1.90	1.06
1:F:192:ASP:O	1:F:196:LEU:HD23	1.53	1.06
1:A:437:LEU:HD23	1:A:437:LEU:H	1.22	1.05
1:A:84:ILE:HG12	1:A:390:LEU:HD12	1.30	1.04
1:E:131:THR:HG21	1:E:264:LEU:HD22	1.12	1.04
1:E:114:ILE:CD1	3:E:502:9ZJ:CAI	2.36	1.04
1:D:302:THR:HG21	2:D:501:HEM:CHC	1.87	1.03
1:C:84:ILE:HG12	1:C:390:LEU:HD12	1.40	1.03
1:D:211:SER:HA	1:D:474:GLU:OE2	1.58	1.03
1:E:220:PHE:CE2	5:E:503:CM5:H101	1.92	1.02
1:D:302:THR:CG2	2:D:501:HEM:HAB	1.88	1.02
1:E:220:PHE:CG	5:E:503:CM5:H112	1.94	1.01
1:E:179:ILE:HD11	1:E:299:GLY:HA3	1.35	1.01
1:C:114:ILE:CD1	3:C:502:9ZJ:CAI	2.39	1.00
1:B:84:ILE:HG12	1:B:390:LEU:HD12	1.44	1.00
1:D:302:THR:HG21	2:D:501:HEM:C4B	1.97	1.00
1:A:220:PHE:C	6:A:601:HOH:O	1.99	0.99
1:E:125:ARG:NH1	1:E:437:LEU:HD11	1.78	0.98
1:B:374:HIS:H	1:C:286:GLN:HE22	0.99	0.98
1:A:135:PHE:CZ	1:A:142:VAL:HG22	1.99	0.96
1:B:362:LEU:HD12	1:B:362:LEU:N	1.79	0.96
1:A:114:ILE:CD1	3:A:502:9ZJ:CAI	2.43	0.96
1:E:131:THR:HG21	1:E:264:LEU:HD23	0.96	0.95
1:B:293:LEU:C	1:B:293:LEU:HD13	1.86	0.94
1:F:435:ILE:O	1:F:435:ILE:CG2	2.15	0.94
1:B:114:ILE:HD12	1:B:294:SER:OG	1.67	0.94
1:A:202:PHE:HB3	1:A:301:GLU:OE1	1.66	0.93
1:B:114:ILE:HD12	1:B:294:SER:CB	1.99	0.93
1:F:220:PHE:CE2	5:F:502:CM5:H101	2.04	0.93
1:A:135:PHE:CE2	1:A:142:VAL:HG23	2.01	0.93
1:C:302:THR:CG2	2:C:501:HEM:CAB	2.46	0.93
1:D:135:PHE:CE2	1:D:142:VAL:HG22	2.02	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:220:PHE:CD1	5:E:503:CM5:H112	2.04	0.92
1:C:220:PHE:CG	5:C:503:CM5:H112	2.03	0.92
1:B:443:ARG:HD2	6:B:612:HOH:O	1.69	0.91
1:B:114:ILE:CD1	1:B:294:SER:HB3	2.01	0.91
1:D:220:PHE:CG	5:D:503:CM5:H112	2.05	0.91
1:C:216:LEU:HD21	5:C:503:CM5:C9	2.00	0.91
1:D:302:THR:CG2	2:D:501:HEM:CAB	2.48	0.91
1:F:220:PHE:CD2	5:F:502:CM5:H102	2.05	0.90
1:B:206:PHE:CE1	3:B:502:9ZJ:CAK	2.55	0.89
1:E:305:THR:CG2	1:E:362:LEU:HD11	2.03	0.89
1:D:132:MET:HA	1:D:135:PHE:HE1	1.30	0.89
1:D:114:ILE:CD1	3:D:502:9ZJ:CAI	2.51	0.89
1:E:390:LEU:N	1:E:390:LEU:HD12	1.86	0.89
1:B:141:SER:HB3	1:B:144:GLU:HG3	1.55	0.88
1:C:216:LEU:CD1	5:C:503:CM5:H101	2.04	0.88
1:D:116:ALA:O	1:D:434:ARG:NH2	2.07	0.88
1:B:132:MET:O	1:B:135:PHE:CD2	2.28	0.87
1:D:302:THR:HG22	2:D:501:HEM:HAB	1.54	0.86
1:B:120:ARG:O	1:B:124:LEU:HD23	1.75	0.86
1:B:362:LEU:CD1	1:B:362:LEU:N	2.38	0.86
1:B:374:HIS:H	1:C:286:GLN:NE2	1.73	0.86
1:C:220:PHE:CD2	5:C:503:CM5:C11	2.59	0.86
1:E:302:THR:HG21	2:E:501:HEM:HHC	1.58	0.86
1:F:179:ILE:HD11	1:F:299:GLY:HA3	1.58	0.85
1:E:125:ARG:NH1	1:E:437:LEU:CD1	2.40	0.85
1:D:220:PHE:CD2	5:D:503:CM5:H101	2.12	0.85
1:B:315:LEU:HD11	1:B:486:ILE:HG13	1.58	0.84
1:E:206:PHE:CE1	3:E:502:9ZJ:CAK	2.61	0.84
1:C:141:SER:HB3	1:C:144:GLU:HG3	1.57	0.84
1:C:179:ILE:H	1:C:179:ILE:HD12	1.42	0.84
1:C:437:LEU:CD1	2:C:501:HEM:HBD2	2.07	0.84
1:A:135:PHE:HE2	1:A:142:VAL:HG21	1.42	0.84
1:D:220:PHE:CD1	5:D:503:CM5:H112	2.13	0.83
1:C:302:THR:HG21	2:C:501:HEM:C4B	2.14	0.83
1:E:487:ARG:NH1	1:E:489:LEU:HD21	1.93	0.82
1:E:302:THR:HG21	2:E:501:HEM:C4B	2.14	0.82
1:D:27:LYS:C	1:D:29:LYS:H	1.83	0.82
1:E:302:THR:HG22	1:E:303:THR:N	1.92	0.82
1:C:216:LEU:HD11	5:C:503:CM5:C10	2.08	0.82
1:A:202:PHE:CB	1:A:301:GLU:OE1	2.27	0.81
1:D:253:ARG:NE	6:D:601:HOH:O	2.14	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:SER:HB3	1:A:144:GLU:HG3	1.62	0.81
1:B:114:ILE:CD1	1:B:294:SER:CB	2.57	0.81
1:E:302:THR:CG2	2:E:501:HEM:CAB	2.59	0.81
1:F:141:SER:HB3	1:F:144:GLU:HG3	1.61	0.81
1:B:132:MET:O	1:B:135:PHE:HD2	1.65	0.80
1:D:141:SER:HB3	1:D:144:GLU:HG3	1.64	0.80
1:D:206:PHE:CE1	3:D:502:9ZJ:CAK	2.64	0.80
1:F:223:PHE:CB	5:F:502:CM5:H31A	2.11	0.80
1:B:132:MET:HA	1:B:135:PHE:CE2	2.17	0.80
1:D:135:PHE:CE2	1:D:142:VAL:HG23	2.03	0.79
1:E:141:SER:HB3	1:E:144:GLU:HG3	1.63	0.79
1:E:390:LEU:N	1:E:390:LEU:CD1	2.45	0.79
1:B:293:LEU:HD13	1:B:293:LEU:O	1.81	0.79
1:C:279:ALA:O	1:C:280:HIS:HB2	1.82	0.79
1:F:48:ARG:O	1:F:49:ARG:CB	2.29	0.79
5:D:503:CM5:H24	5:D:503:CM5:O21	1.83	0.79
5:B:503:CM5:O21	5:B:503:CM5:H24	1.83	0.79
1:C:435:ILE:HG23	1:C:435:ILE:O	1.80	0.78
1:C:184:PHE:CE2	1:C:296:PHE:HE2	2.00	0.78
1:B:114:ILE:HD11	1:B:294:SER:HB3	1.64	0.78
1:D:211:SER:CA	1:D:474:GLU:OE2	2.31	0.78
1:F:48:ARG:HG2	1:F:48:ARG:O	1.83	0.78
1:F:184:PHE:HE2	1:F:296:PHE:CE2	2.01	0.78
1:C:302:THR:CG2	2:C:501:HEM:C3B	2.66	0.78
5:C:503:CM5:H24	5:C:503:CM5:O21	1.83	0.78
1:F:220:PHE:CE2	5:F:502:CM5:C10	2.67	0.78
5:F:502:CM5:H24	5:F:502:CM5:O21	1.83	0.78
1:C:206:PHE:CE1	3:C:502:9ZJ:CAK	2.66	0.77
1:D:302:THR:CG2	2:D:501:HEM:C3B	2.67	0.77
1:E:302:THR:HG23	2:E:501:HEM:CAB	2.13	0.77
5:E:503:CM5:O21	5:E:503:CM5:H24	1.83	0.77
1:B:435:ILE:HG23	1:B:435:ILE:O	1.84	0.77
1:F:286:GLN:HA	1:F:286:GLN:HE21	1.50	0.77
1:E:305:THR:HG21	1:E:362:LEU:HD11	1.66	0.77
1:E:120:ARG:O	1:E:124:LEU:HD23	1.84	0.76
1:C:220:PHE:CD2	5:C:503:CM5:H112	2.19	0.76
1:C:73:ARG:NE	1:C:387:GLU:OE2	2.19	0.76
1:D:434:ARG:O	1:D:435:ILE:O	2.02	0.76
1:F:232:ARG:CZ	6:F:601:HOH:O	2.23	0.76
1:E:315:LEU:HD11	1:E:486:ILE:HG13	1.66	0.76
1:B:415:ASP:HB2	6:B:626:HOH:O	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:437:LEU:HD11	2:C:501:HEM:HBD2	1.65	0.76
1:E:131:THR:CG2	1:E:264:LEU:HD22	1.93	0.76
1:C:120:ARG:O	1:C:124:LEU:HD23	1.85	0.76
1:B:454:LEU:HD21	1:B:459:MET:HE2	1.66	0.75
1:E:51:LEU:HD22	1:E:215:GLN:HG2	1.67	0.75
1:B:78:LEU:HB2	1:B:390:LEU:HD13	1.69	0.75
1:F:220:PHE:CD1	5:F:502:CM5:H112	2.20	0.74
1:F:220:PHE:CZ	5:F:502:CM5:H101	2.23	0.74
1:F:120:ARG:O	1:F:124:LEU:HD23	1.86	0.74
1:A:120:ARG:HA	1:A:282:GLU:HG2	1.68	0.74
1:D:315:LEU:HD11	1:D:486:ILE:HG13	1.68	0.74
1:B:362:LEU:H	1:B:362:LEU:CD1	2.00	0.73
1:D:279:ALA:O	1:D:280:HIS:HB2	1.87	0.73
1:C:192:ASP:O	1:C:196:LEU:CD1	2.37	0.73
1:C:302:THR:HG21	2:C:501:HEM:CAB	2.14	0.73
1:D:302:THR:HG21	2:D:501:HEM:C3B	2.23	0.73
1:A:279:ALA:O	1:A:280:HIS:HB2	1.89	0.73
1:D:120:ARG:HA	1:D:282:GLU:HG2	1.71	0.73
1:E:435:ILE:HG23	1:E:435:ILE:O	1.88	0.73
1:B:293:LEU:C	1:B:293:LEU:CD1	2.57	0.72
1:C:179:ILE:N	1:C:179:ILE:HD12	2.03	0.72
1:F:190:TYR:O	1:F:196:LEU:HD21	1.89	0.72
1:A:84:ILE:HG12	1:A:390:LEU:CD1	2.16	0.72
1:B:73:ARG:HD2	1:B:387:GLU:OE2	1.89	0.72
1:F:220:PHE:CD2	5:F:502:CM5:C10	2.72	0.72
1:B:169:PHE:CD2	6:B:614:HOH:O	2.41	0.71
1:C:47:ASP:OD1	1:C:49:ARG:HB2	1.91	0.71
1:C:73:ARG:CD	1:C:387:GLU:OE2	2.39	0.71
1:E:220:PHE:CG	5:E:503:CM5:C11	2.71	0.71
1:F:179:ILE:HD11	1:F:299:GLY:CA	2.21	0.71
1:C:175:THR:O	1:C:179:ILE:CD1	2.39	0.71
1:E:196:LEU:HD13	1:E:196:LEU:O	1.90	0.71
1:B:114:ILE:HD13	3:B:502:9ZJ:CAI	2.21	0.71
1:A:120:ARG:O	1:A:124:LEU:HD23	1.91	0.70
1:B:84:ILE:CG1	1:B:390:LEU:HD12	2.19	0.70
1:D:302:THR:HG23	2:D:501:HEM:HAB	1.72	0.70
1:E:120:ARG:HA	1:E:282:GLU:HG2	1.73	0.70
1:E:389:PHE:C	1:E:390:LEU:HD12	2.11	0.70
1:E:299:GLY:HA3	2:E:501:HEM:HBC2	1.71	0.70
1:B:454:LEU:HD21	1:B:459:MET:CE	2.20	0.70
1:C:135:PHE:HZ	1:C:182:ILE:HG12	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:223:PHE:HB2	5:F:502:CM5:H31A	1.72	0.70
1:D:298:ALA:O	1:D:302:THR:HB	1.91	0.70
1:D:302:THR:HG23	2:D:501:HEM:CAB	2.21	0.70
1:A:179:ILE:H	1:A:179:ILE:HD12	1.57	0.70
1:A:432:GLY:O	1:A:435:ILE:HG22	1.91	0.70
1:C:216:LEU:CD2	5:C:503:CM5:H92	2.12	0.70
1:A:279:ALA:O	1:A:280:HIS:CB	2.39	0.70
1:B:374:HIS:N	1:C:286:GLN:HE22	1.84	0.70
1:D:120:ARG:O	1:D:124:LEU:HD23	1.92	0.70
1:D:184:PHE:HE2	1:D:296:PHE:CE2	2.09	0.70
1:E:279:ALA:O	1:E:280:HIS:HB2	1.91	0.70
1:B:279:ALA:O	1:B:280:HIS:CB	2.40	0.69
1:F:220:PHE:CE1	5:F:502:CM5:H112	2.27	0.69
1:D:129:VAL:HG22	1:D:437:LEU:HD23	1.73	0.69
1:B:279:ALA:O	1:B:280:HIS:HB2	1.91	0.69
1:C:184:PHE:HE2	1:C:296:PHE:HE2	1.41	0.69
1:C:120:ARG:HA	1:C:282:GLU:HG2	1.75	0.69
1:F:130:THR:O	1:F:134:ASP:HB2	1.91	0.69
1:B:432:GLY:O	1:B:435:ILE:HG22	1.92	0.69
1:C:302:THR:HG22	2:C:501:HEM:HAB	1.74	0.69
1:F:279:ALA:O	1:F:280:HIS:HB2	1.92	0.69
1:D:135:PHE:CZ	1:D:142:VAL:CG2	2.76	0.69
1:E:279:ALA:O	1:E:280:HIS:CB	2.41	0.69
1:E:357:GLN:OE1	1:E:446:LEU:CD1	2.40	0.69
1:A:175:THR:O	1:A:179:ILE:CD1	2.40	0.69
1:C:192:ASP:O	1:C:196:LEU:HD13	1.92	0.69
1:B:120:ARG:HA	1:B:282:GLU:HG2	1.74	0.69
1:A:315:LEU:HD11	1:A:486:ILE:HG13	1.75	0.68
1:C:302:THR:HG22	2:C:501:HEM:CAB	2.22	0.68
1:E:220:PHE:CD2	5:E:503:CM5:C11	2.77	0.68
1:A:309:TYR:CD2	1:A:481:PRO:HB3	2.28	0.68
1:F:132:MET:O	1:F:135:PHE:HD2	1.75	0.68
1:F:206:PHE:CD1	3:F:503:9ZJ:CAK	2.77	0.68
1:F:184:PHE:CE2	1:F:296:PHE:HE2	2.11	0.68
1:B:342:ASP:O	1:B:346:MET:HG2	1.94	0.68
1:F:225:LYS:O	6:F:601:HOH:O	2.12	0.68
1:D:279:ALA:O	1:D:280:HIS:CB	2.42	0.68
1:A:205:THR:HG23	1:A:234:VAL:HG13	1.74	0.68
1:D:135:PHE:CZ	1:D:142:VAL:HG22	2.28	0.68
1:E:73:ARG:NE	1:E:387:GLU:OE2	2.25	0.68
1:C:184:PHE:HE2	1:C:296:PHE:CE2	2.11	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:184:PHE:CE2	1:F:296:PHE:CE2	2.82	0.67
1:C:286:GLN:OE1	1:C:290:LEU:HD11	1.95	0.67
1:F:47:ASP:O	1:F:48:ARG:C	2.30	0.67
1:A:202:PHE:HB3	1:A:301:GLU:CD	2.14	0.67
1:E:125:ARG:CZ	1:E:437:LEU:HD11	2.24	0.67
1:B:366:GLY:HA3	6:B:611:HOH:O	1.93	0.67
1:D:179:ILE:H	1:D:179:ILE:HD12	1.60	0.67
1:D:285:HIS:HD2	6:D:608:HOH:O	1.77	0.67
1:F:131:THR:HG21	1:F:264:LEU:HD22	1.76	0.67
1:F:223:PHE:CD2	5:F:502:CM5:C3	2.72	0.67
1:B:130:THR:HG22	1:B:133:ARG:NH2	2.10	0.67
1:B:360:SER:CB	1:B:362:LEU:HD11	2.25	0.67
1:D:131:THR:O	1:D:132:MET:HG2	1.96	0.66
1:A:111:TYR:HD1	1:A:287:ASN:OD1	1.78	0.66
1:D:220:PHE:CD2	5:D:503:CM5:C10	2.79	0.66
1:B:286:GLN:HE21	1:B:286:GLN:HA	1.59	0.66
1:B:309:TYR:CD2	1:B:481:PRO:HB3	2.30	0.66
1:C:279:ALA:O	1:C:280:HIS:CB	2.44	0.66
1:F:114:ILE:HD12	3:F:503:9ZJ:CAI	2.25	0.66
1:C:130:THR:O	1:C:134:ASP:HB2	1.96	0.66
1:E:184:PHE:HE2	1:E:296:PHE:CE2	2.14	0.66
1:B:179:ILE:HD12	1:B:179:ILE:H	1.61	0.66
1:E:125:ARG:CZ	1:E:437:LEU:CD1	2.74	0.65
1:F:223:PHE:HB2	5:F:502:CM5:C3	2.26	0.65
1:D:47:ASP:O	1:D:49:ARG:N	2.29	0.65
1:F:132:MET:O	1:F:135:PHE:CD2	2.49	0.65
1:E:47:ASP:O	1:E:49:ARG:N	2.29	0.65
1:B:308:ARG:HD2	6:B:610:HOH:O	1.94	0.65
1:B:454:LEU:CD2	1:B:459:MET:HE2	2.26	0.65
1:F:132:MET:HE1	1:F:437:LEU:HD12	1.78	0.65
1:F:286:GLN:O	1:F:290:LEU:HD23	1.96	0.65
1:E:133:ARG:HH11	1:E:133:ARG:CB	2.09	0.65
3:E:502:9ZJ:FAC	3:E:502:9ZJ:CAJ	2.31	0.65
1:F:223:PHE:CG	5:F:502:CM5:C3	2.72	0.65
1:A:271:HIS:C	1:A:273:GLU:H	2.00	0.65
3:A:502:9ZJ:CAJ	3:A:502:9ZJ:FAC	2.31	0.65
1:D:286:GLN:O	1:D:290:LEU:HD23	1.95	0.65
1:D:302:THR:HG21	2:D:501:HEM:HHC	1.79	0.65
1:E:302:THR:CG2	1:E:303:THR:N	2.60	0.65
1:A:179:ILE:N	1:A:179:ILE:HD12	2.12	0.64
1:A:116:ALA:O	1:A:434:ARG:NH2	2.26	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:98:ARG:HB3	1:D:117:ASN:OD1	1.96	0.64
1:D:273:GLU:C	1:D:275:GLU:H	2.01	0.64
1:B:220:PHE:CG	5:B:503:CM5:H112	2.32	0.64
1:B:184:PHE:HE2	1:B:296:PHE:CE2	2.15	0.64
1:E:98:ARG:HB3	1:E:117:ASN:OD1	1.98	0.64
3:F:503:9ZJ:CAJ	3:F:503:9ZJ:FAC	2.31	0.64
1:E:47:ASP:OD1	1:E:49:ARG:HB3	1.97	0.64
1:F:120:ARG:HA	1:F:282:GLU:HG2	1.78	0.64
1:D:129:VAL:CG2	1:D:437:LEU:HD23	2.27	0.63
1:F:315:LEU:HD11	1:F:486:ILE:HG13	1.79	0.63
1:C:51:LEU:HD22	1:C:215:GLN:HG2	1.80	0.63
3:D:502:9ZJ:FAC	3:D:502:9ZJ:CAJ	2.31	0.63
1:D:131:THR:O	1:D:132:MET:CG	2.47	0.63
1:B:179:ILE:HD12	1:B:179:ILE:N	2.14	0.63
1:E:298:ALA:O	1:E:302:THR:HB	1.98	0.63
1:B:168:THR:HB	6:B:614:HOH:O	1.98	0.62
1:B:360:SER:HB2	1:B:362:LEU:HD11	1.80	0.62
1:C:179:ILE:H	1:C:179:ILE:CD1	2.11	0.62
3:C:502:9ZJ:FAC	3:C:502:9ZJ:CAJ	2.31	0.62
1:A:116:ALA:HA	6:A:602:HOH:O	1.98	0.62
1:B:216:LEU:HD11	1:B:220:PHE:HD2	1.64	0.62
1:F:279:ALA:O	1:F:280:HIS:CB	2.46	0.62
1:A:84:ILE:CG1	1:A:390:LEU:HD12	2.19	0.62
1:A:47:ASP:O	1:A:49:ARG:N	2.33	0.62
1:B:306:THR:OG1	1:B:362:LEU:HD21	2.00	0.62
1:C:302:THR:CG2	2:C:501:HEM:HAB	2.27	0.62
1:E:365:MET:N	6:E:602:HOH:O	2.25	0.62
1:F:192:ASP:O	1:F:196:LEU:CD2	2.39	0.62
1:C:302:THR:HG22	1:C:303:THR:N	2.13	0.62
1:D:184:PHE:CE2	1:D:296:PHE:CE2	2.88	0.62
1:D:434:ARG:HD2	2:D:501:HEM:O2D	1.99	0.62
1:B:373:GLN:HA	1:C:286:GLN:HE21	1.65	0.62
1:A:271:HIS:C	1:A:273:GLU:N	2.54	0.61
1:A:360:SER:HB3	6:A:615:HOH:O	1.99	0.61
1:B:216:LEU:HD11	1:B:220:PHE:CD2	2.35	0.61
1:E:179:ILE:HD11	1:E:299:GLY:CA	2.20	0.61
1:C:206:PHE:HB2	1:C:297:PHE:HZ	1.63	0.61
1:D:357:GLN:OE1	1:D:446:LEU:CD1	2.49	0.61
1:A:357:GLN:OE1	1:A:446:LEU:CD1	2.48	0.61
1:E:220:PHE:CE2	5:E:503:CM5:C10	2.75	0.61
1:C:202:PHE:CD1	1:C:297:PHE:HD1	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:503:CM5:O20	5:E:503:CM5:H26	2.01	0.61
1:A:342:ASP:O	1:A:346:MET:HG2	2.00	0.61
5:B:503:CM5:O20	5:B:503:CM5:H26	2.01	0.61
1:C:286:GLN:OE1	1:C:290:LEU:CD1	2.49	0.61
5:C:503:CM5:H26	5:C:503:CM5:O20	2.01	0.61
1:F:274:LYS:HG3	1:F:277:SER:HB2	1.83	0.61
1:A:460:ALA:HB3	1:A:487:ARG:CG	2.31	0.61
1:D:184:PHE:CE2	1:D:296:PHE:HE2	2.18	0.61
1:F:273:GLU:C	1:F:275:GLU:H	2.03	0.60
5:F:502:CM5:O20	5:F:502:CM5:H26	2.01	0.60
3:B:502:9ZJ:CAJ	3:B:502:9ZJ:FAC	2.31	0.60
1:C:374:HIS:HB2	6:C:604:HOH:O	2.02	0.60
1:E:135:PHE:HZ	1:E:182:ILE:HG12	1.65	0.60
1:F:179:ILE:HG21	1:F:296:PHE:HA	1.83	0.60
1:A:437:LEU:HD23	1:A:437:LEU:N	2.03	0.60
1:E:133:ARG:HB2	1:E:133:ARG:NH1	2.17	0.60
1:E:299:GLY:CA	2:E:501:HEM:HBC2	2.31	0.60
1:D:132:MET:CA	1:D:135:PHE:CE1	2.76	0.60
1:E:220:PHE:HB3	6:E:601:HOH:O	2.00	0.60
1:C:342:ASP:O	1:C:346:MET:HG2	2.01	0.60
1:D:342:ASP:O	1:D:346:MET:HG2	2.01	0.60
1:F:284:SER:OG	1:F:287:ASN:ND2	2.34	0.60
1:E:437:LEU:CD1	2:E:501:HEM:HBD2	2.32	0.60
1:B:454:LEU:CD2	1:B:459:MET:CE	2.79	0.60
1:E:184:PHE:CE2	1:E:296:PHE:HE2	2.20	0.60
1:E:143:GLU:HG3	1:E:340:LEU:HG	1.84	0.60
1:E:184:PHE:CE2	1:E:296:PHE:CE2	2.89	0.59
1:F:114:ILE:HD13	3:F:503:9ZJ:CAP	2.29	0.59
1:A:192:ASP:OD1	1:A:193:GLN:N	2.35	0.59
1:C:435:ILE:CG2	1:C:435:ILE:O	2.49	0.59
5:D:503:CM5:O20	5:D:503:CM5:H26	2.01	0.59
1:C:454:LEU:HD21	1:C:459:MET:HE2	1.84	0.59
1:B:144:GLU:O	1:B:148:GLU:HG3	2.03	0.59
1:C:433:LYS:N	6:C:602:HOH:O	2.34	0.59
1:E:437:LEU:HD13	2:E:501:HEM:HBD2	1.83	0.59
1:A:437:LEU:H	1:A:437:LEU:CD2	2.04	0.59
1:A:131:THR:HG21	1:A:264:LEU:HD22	1.83	0.59
1:B:216:LEU:CD1	1:B:220:PHE:HD2	2.16	0.59
1:B:51:LEU:HD13	1:B:215:GLN:HB3	1.83	0.59
1:F:342:ASP:O	1:F:346:MET:HG2	2.02	0.59
1:A:180:CYS:SG	1:A:296:PHE:CZ	2.96	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:220:PHE:CG	5:F:502:CM5:H102	2.37	0.59
1:B:184:PHE:CE2	1:B:296:PHE:CE2	2.90	0.59
1:C:454:LEU:CD2	1:C:459:MET:HE2	2.33	0.58
1:E:342:ASP:O	1:E:346:MET:HG2	2.02	0.58
1:D:309:TYR:CD2	1:D:481:PRO:HB3	2.38	0.58
1:F:357:GLN:OE1	1:F:446:LEU:CD1	2.52	0.58
1:A:437:LEU:HD21	2:A:501:HEM:CMD	2.33	0.58
1:E:196:LEU:HD13	1:E:196:LEU:C	2.23	0.58
1:D:430:SER:HB3	2:D:501:HEM:HBA1	1.85	0.58
1:D:206:PHE:CG	3:D:502:9ZJ:CAK	2.87	0.58
1:E:305:THR:CG2	1:E:362:LEU:CD1	2.80	0.58
1:A:143:GLU:HG3	1:A:340:LEU:HG	1.85	0.58
1:B:175:THR:O	1:B:179:ILE:CD1	2.52	0.58
1:F:205:THR:HG23	1:F:234:VAL:HG13	1.85	0.58
1:F:143:GLU:HG3	1:F:340:LEU:HG	1.86	0.58
1:D:302:THR:HG23	2:D:501:HEM:C3B	2.38	0.58
1:C:357:GLN:HE21	1:C:426:PHE:HZ	1.51	0.58
1:C:98:ARG:HB2	1:C:434:ARG:NH2	2.19	0.58
2:B:501:HEM:HBB2	2:B:501:HEM:HMB1	1.86	0.57
1:D:430:SER:CB	2:D:501:HEM:HBA1	2.34	0.57
1:D:437:LEU:CD1	2:D:501:HEM:HBD2	2.34	0.57
1:E:223:PHE:CD1	5:E:503:CM5:H42	2.40	0.57
1:E:454:LEU:HD21	1:E:459:MET:HE2	1.86	0.57
1:B:309:TYR:CE2	1:B:481:PRO:HB3	2.40	0.57
1:F:223:PHE:CB	5:F:502:CM5:C3	2.83	0.57
1:B:126:ARG:HD3	6:B:635:HOH:O	2.05	0.57
1:C:132:MET:O	1:C:135:PHE:HD2	1.87	0.57
1:D:51:LEU:HD22	1:D:215:GLN:HG2	1.87	0.57
1:F:116:ALA:O	1:F:434:ARG:NH2	2.32	0.57
1:B:184:PHE:CE2	1:B:296:PHE:HE2	2.22	0.57
1:C:131:THR:HG21	1:C:264:LEU:HD22	1.85	0.57
1:D:454:LEU:CD2	1:D:459:MET:HE2	2.33	0.57
1:E:133:ARG:HH11	1:E:133:ARG:HB2	1.69	0.57
1:E:96:SER:OG	1:E:433:LYS:HD3	2.05	0.57
1:C:179:ILE:O	1:C:182:ILE:N	2.38	0.57
1:D:220:PHE:CE2	5:D:503:CM5:H101	2.39	0.57
1:E:302:THR:CG2	2:E:501:HEM:C3B	2.88	0.57
1:B:130:THR:O	1:B:134:ASP:HB2	2.04	0.57
1:B:206:PHE:CE2	1:B:480:ILE:HG12	2.40	0.57
1:B:308:ARG:CD	6:B:610:HOH:O	2.53	0.57
1:E:116:ALA:O	1:E:434:ARG:NH2	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:51:LEU:HD22	1:F:215:GLN:HG2	1.87	0.57
1:E:305:THR:HG22	1:E:362:LEU:HD11	1.84	0.56
1:E:47:ASP:C	1:E:49:ARG:N	2.55	0.56
1:A:47:ASP:O	1:A:48:ARG:C	2.43	0.56
1:C:206:PHE:CE2	1:C:480:ILE:HG12	2.39	0.56
1:F:309:TYR:CD2	1:F:481:PRO:HB3	2.40	0.56
1:A:305:THR:HG21	1:A:362:LEU:HD13	1.87	0.56
1:C:116:ALA:O	1:C:434:ARG:NH2	2.37	0.56
1:C:220:PHE:CD2	5:C:503:CM5:H111	2.40	0.56
1:D:179:ILE:HD12	1:D:179:ILE:N	2.20	0.56
1:D:175:THR:O	1:D:179:ILE:CD1	2.54	0.56
1:E:309:TYR:CD2	1:E:481:PRO:HB3	2.41	0.56
1:A:274:LYS:HG3	1:A:277:SER:HB2	1.87	0.56
1:E:223:PHE:HB2	5:E:503:CM5:H12	1.86	0.56
1:E:306:THR:HG21	1:E:357:GLN:HG2	1.87	0.56
1:E:47:ASP:C	1:E:49:ARG:H	2.09	0.56
1:A:422:LYS:HA	6:A:618:HOH:O	2.05	0.56
1:B:98:ARG:HG2	1:B:115:PHE:HA	1.89	0.55
1:C:144:GLU:O	1:C:148:GLU:HG3	2.07	0.55
1:D:143:GLU:HG3	1:D:340:LEU:HG	1.88	0.55
1:F:454:LEU:CD2	1:F:459:MET:HE2	2.36	0.55
1:C:315:LEU:HD11	1:C:486:ILE:HG13	1.87	0.55
1:D:164:LEU:HD23	1:D:487:ARG:HB3	1.88	0.55
1:B:143:GLU:HG3	1:B:340:LEU:HG	1.88	0.55
1:B:274:LYS:HG3	1:B:277:SER:HB2	1.89	0.55
2:B:501:HEM:HBC2	2:B:501:HEM:HHD	1.87	0.55
1:C:211:SER:HA	1:C:474:GLU:CD	2.23	0.55
1:B:164:LEU:HD23	1:B:487:ARG:HB3	1.89	0.55
1:C:202:PHE:CD1	1:C:297:PHE:CD1	2.94	0.55
1:B:116:ALA:O	1:B:434:ARG:NH2	2.38	0.55
1:C:305:THR:HG21	1:C:362:LEU:HD13	1.88	0.54
1:F:286:GLN:NE2	1:F:286:GLN:HA	2.21	0.54
1:F:131:THR:CG2	1:F:264:LEU:HD22	2.38	0.54
1:F:135:PHE:HZ	1:F:182:ILE:HG12	1.71	0.54
1:E:274:LYS:HG3	1:E:277:SER:HB2	1.88	0.54
1:C:274:LYS:HG3	1:C:277:SER:HB2	1.89	0.54
1:C:325:TYR:CD1	6:C:615:HOH:O	2.54	0.54
1:C:220:PHE:CD2	5:C:503:CM5:H101	2.42	0.54
1:A:309:TYR:CE2	1:A:481:PRO:HB3	2.42	0.54
1:B:316:LYS:NZ	1:B:468:ILE:O	2.39	0.54
1:F:384:LYS:O	1:F:385:ASP:HB2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:SER:HB2	2:A:501:HEM:HBA1	1.89	0.54
1:D:437:LEU:HD13	2:D:501:HEM:HMD1	1.90	0.54
1:A:454:LEU:CD2	1:A:459:MET:HE2	2.38	0.53
1:F:27:LYS:HB2	1:F:380:TYR:HE1	1.73	0.53
1:C:143:GLU:HG3	1:C:340:LEU:HG	1.90	0.53
1:D:175:THR:O	1:D:179:ILE:HD12	2.08	0.53
1:D:437:LEU:HD12	2:D:501:HEM:HBD2	1.90	0.53
1:A:192:ASP:C	1:A:192:ASP:OD1	2.47	0.53
1:C:192:ASP:O	1:C:196:LEU:HD12	2.08	0.53
1:E:290:LEU:HD12	1:E:290:LEU:N	2.24	0.53
1:E:454:LEU:HD21	1:E:459:MET:CE	2.39	0.53
1:F:192:ASP:OD1	1:F:193:GLN:N	2.41	0.53
1:B:98:ARG:HB2	1:B:434:ARG:NH2	2.22	0.53
1:C:309:TYR:CD2	1:C:481:PRO:HB3	2.43	0.53
1:D:434:ARG:O	1:D:435:ILE:C	2.47	0.53
1:E:121:TRP:CZ2	1:E:125:ARG:HD3	2.43	0.53
1:B:357:GLN:HE21	1:B:426:PHE:HZ	1.56	0.53
1:C:384:LYS:O	1:C:385:ASP:HB2	2.08	0.53
1:F:454:LEU:HD21	1:F:459:MET:HE2	1.90	0.53
1:D:82:GLU:HA	1:D:82:GLU:OE2	2.09	0.53
1:E:305:THR:HG22	1:E:362:LEU:CD1	2.39	0.53
1:B:130:THR:HG21	6:B:615:HOH:O	2.08	0.53
1:D:454:LEU:HD21	1:D:459:MET:HE2	1.90	0.53
1:A:270:LEU:O	1:A:273:GLU:CB	2.57	0.53
1:A:98:ARG:HG2	1:A:115:PHE:HA	1.91	0.52
1:B:286:GLN:NE2	1:B:286:GLN:HA	2.24	0.52
1:C:184:PHE:CE2	1:C:296:PHE:CE2	2.86	0.52
1:E:88:LEU:HD21	1:E:390:LEU:HD21	1.91	0.52
1:A:430:SER:CB	2:A:501:HEM:HBA1	2.39	0.52
1:B:114:ILE:HD12	1:B:294:SER:HB3	1.71	0.52
1:B:360:SER:HB3	1:B:362:LEU:HD11	1.90	0.52
1:B:114:ILE:HD13	3:B:502:9ZJ:CAH	2.39	0.52
1:D:285:HIS:CD2	6:D:608:HOH:O	2.59	0.52
1:F:206:PHE:CE1	3:F:503:9ZJ:CAK	2.93	0.52
1:B:390:LEU:O	1:B:392:LEU:N	2.42	0.52
1:E:98:ARG:HG2	1:E:115:PHE:HA	1.91	0.52
1:B:271:HIS:C	1:B:273:GLU:H	2.12	0.52
1:B:271:HIS:C	1:B:273:GLU:N	2.63	0.52
2:B:501:HEM:HBB2	2:B:501:HEM:CMB	2.40	0.52
1:B:96:SER:OG	1:B:433:LYS:HD3	2.10	0.52
1:F:206:PHE:O	1:F:206:PHE:CD1	2.63	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:446:LEU:O	1:F:450:PHE:HB2	2.10	0.52
1:A:144:GLU:O	1:A:148:GLU:HG3	2.09	0.52
1:C:206:PHE:HB2	1:C:297:PHE:CZ	2.45	0.52
1:D:96:SER:OG	1:D:433:LYS:HD3	2.10	0.52
1:E:47:ASP:OD1	1:E:49:ARG:CB	2.58	0.52
1:C:454:LEU:HD21	1:C:459:MET:CE	2.40	0.52
1:D:357:GLN:OE1	1:D:446:LEU:HD13	2.08	0.52
1:F:132:MET:HA	1:F:135:PHE:CE2	2.44	0.52
1:F:96:SER:OG	1:F:433:LYS:HD3	2.10	0.52
1:B:192:ASP:OD1	1:B:193:GLN:N	2.43	0.52
1:C:211:SER:CA	1:C:474:GLU:OE2	2.37	0.52
1:C:206:PHE:CG	3:C:502:9ZJ:CAK	2.92	0.52
1:E:435:ILE:CG2	1:E:435:ILE:O	2.57	0.52
1:E:446:LEU:O	1:E:450:PHE:HB2	2.08	0.52
1:F:390:LEU:HD22	1:F:390:LEU:N	2.25	0.52
1:B:362:LEU:H	1:B:362:LEU:HD13	1.74	0.51
1:E:454:LEU:CD2	1:E:459:MET:HE2	2.40	0.51
1:F:357:GLN:HE21	1:F:426:PHE:HZ	1.57	0.51
1:A:437:LEU:HD21	2:A:501:HEM:C2D	2.45	0.51
1:C:336:ARG:NH1	6:C:601:HOH:O	1.88	0.51
1:D:302:THR:HG22	1:D:303:THR:N	2.25	0.51
1:C:460:ALA:HB3	1:C:487:ARG:CG	2.40	0.51
1:C:486:ILE:HG12	1:C:487:ARG:H	1.74	0.51
1:D:192:ASP:OD1	1:D:193:GLN:N	2.43	0.51
1:E:302:THR:HG23	2:E:501:HEM:C3B	2.45	0.51
1:A:38:PRO:O	1:A:39:LEU:CB	2.58	0.51
1:C:437:LEU:CD1	1:C:437:LEU:H	2.24	0.51
1:C:164:LEU:HD23	1:C:487:ARG:HB3	1.92	0.51
1:E:487:ARG:HH12	1:E:489:LEU:HD21	1.71	0.51
1:B:175:THR:HG21	1:B:303:THR:HB	1.93	0.51
1:F:309:TYR:CE2	1:F:481:PRO:HB3	2.46	0.51
1:A:175:THR:O	1:A:179:ILE:HD12	2.11	0.51
1:E:144:GLU:O	1:E:148:GLU:HG3	2.11	0.51
1:E:125:ARG:NH1	1:E:437:LEU:HD12	2.24	0.51
1:E:220:PHE:CG	5:E:503:CM5:C10	2.92	0.51
1:B:206:PHE:HE2	1:B:480:ILE:HG12	1.73	0.51
1:B:357:GLN:OE1	1:B:446:LEU:CD1	2.59	0.50
1:B:364:PRO:HA	1:B:393:SER:HB2	1.91	0.50
1:F:121:TRP:CZ2	1:F:125:ARG:HD3	2.45	0.50
1:F:460:ALA:HB3	1:F:487:ARG:CG	2.41	0.50
1:D:132:MET:O	1:D:135:PHE:CZ	2.64	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:98:ARG:NH2	2:E:501:HEM:O2D	2.44	0.50
1:C:175:THR:HG21	1:C:303:THR:HB	1.93	0.50
1:D:299:GLY:HA3	2:D:501:HEM:HBC2	1.93	0.50
1:A:107:PHE:CE2	1:A:290:LEU:CD1	2.94	0.50
1:B:130:THR:CG2	1:B:133:ARG:NH2	2.75	0.50
1:D:357:GLN:HE21	1:D:426:PHE:HZ	1.59	0.50
1:F:206:PHE:CD2	1:F:301:GLU:HG3	2.47	0.50
1:B:460:ALA:HB3	1:B:487:ARG:CG	2.42	0.50
1:D:446:LEU:O	1:D:450:PHE:HB2	2.11	0.50
1:A:222:GLY:N	6:A:601:HOH:O	2.44	0.50
1:C:220:PHE:CE2	5:C:503:CM5:H111	2.47	0.50
1:C:220:PHE:CD2	5:C:503:CM5:C10	2.94	0.50
1:E:206:PHE:CG	3:E:502:9ZJ:CAK	2.91	0.50
1:A:357:GLN:HE21	1:A:426:PHE:HZ	1.59	0.49
1:C:84:ILE:CG1	1:C:390:LEU:HD12	2.29	0.49
1:F:47:ASP:OD1	1:F:48:ARG:O	2.30	0.49
1:A:432:GLY:O	1:A:435:ILE:CG2	2.60	0.49
1:A:460:ALA:HB3	1:A:487:ARG:HD2	1.94	0.49
1:D:47:ASP:C	1:D:49:ARG:H	2.16	0.49
1:E:302:THR:HG21	2:E:501:HEM:C3B	2.47	0.49
1:F:27:LYS:HB3	1:F:380:TYR:CD1	2.47	0.49
1:A:179:ILE:H	1:A:179:ILE:CD1	2.25	0.49
1:B:202:PHE:CD1	1:B:297:PHE:CD1	3.00	0.49
1:E:179:ILE:HG22	1:E:183:VAL:HG23	1.93	0.49
1:F:164:LEU:HD23	1:F:487:ARG:HB3	1.95	0.49
1:A:51:LEU:HD22	1:A:215:GLN:HG2	1.93	0.49
1:B:131:THR:OG1	1:B:264:LEU:CD2	2.60	0.49
1:C:390:LEU:O	1:C:392:LEU:N	2.45	0.49
1:C:96:SER:OG	1:C:433:LYS:HD3	2.13	0.49
1:D:312:LEU:HB2	1:D:484:TYR:CE2	2.48	0.49
1:E:88:LEU:HD21	1:E:390:LEU:CD2	2.42	0.49
1:B:205:THR:HG23	1:B:234:VAL:HG13	1.94	0.49
1:B:435:ILE:CG2	1:B:435:ILE:O	2.56	0.49
1:C:130:THR:HG22	1:C:133:ARG:NH2	2.27	0.49
1:C:192:ASP:OD1	1:C:193:GLN:N	2.45	0.49
1:D:98:ARG:HG2	1:D:115:PHE:HA	1.94	0.49
1:F:48:ARG:N	1:F:48:ARG:HD2	2.28	0.49
1:A:192:ASP:O	1:A:196:LEU:HD23	2.12	0.49
1:C:446:LEU:O	1:C:450:PHE:HB2	2.12	0.49
1:E:302:THR:CG2	2:E:501:HEM:HHC	2.36	0.49
1:A:131:THR:CG2	1:A:264:LEU:HD22	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:THR:HG21	1:A:303:THR:HB	1.95	0.49
1:C:73:ARG:HD2	1:C:387:GLU:OE2	2.10	0.49
1:C:47:ASP:OD1	1:C:49:ARG:HD3	2.13	0.49
1:E:290:LEU:CD1	1:E:290:LEU:N	2.76	0.49
1:A:357:GLN:OE1	1:A:446:LEU:HD13	2.12	0.49
1:C:100:LYS:HB2	6:C:613:HOH:O	2.12	0.49
1:A:302:THR:CG2	3:A:502:9ZJ:CAL	2.90	0.48
1:A:438:GLY:O	1:A:439:GLU:C	2.51	0.48
1:B:192:ASP:C	1:B:192:ASP:OD1	2.51	0.48
1:C:290:LEU:N	1:C:290:LEU:HD12	2.27	0.48
1:D:205:THR:HG23	1:D:234:VAL:HG13	1.94	0.48
1:D:316:LYS:HD3	1:D:317:TYR:CE1	2.48	0.48
1:D:121:TRP:CZ2	1:D:125:ARG:HD3	2.48	0.48
1:C:309:TYR:CE2	1:C:481:PRO:HB3	2.49	0.48
1:E:441:ILE:O	1:E:445:GLU:HG3	2.13	0.48
1:C:220:PHE:HD2	5:C:503:CM5:H101	1.78	0.48
1:A:202:PHE:CD1	1:A:297:PHE:CD1	3.02	0.48
1:D:429:PHE:HB2	6:D:605:HOH:O	2.13	0.48
1:F:316:LYS:HD3	1:F:317:TYR:CE1	2.49	0.48
1:B:114:ILE:HD12	1:B:294:SER:HG	1.72	0.48
1:B:222:GLY:HA3	5:B:503:CM5:O21	2.14	0.48
1:D:305:THR:HG21	1:D:362:LEU:HD13	1.96	0.48
1:E:216:LEU:HD11	5:E:503:CM5:H92	1.96	0.48
1:A:202:PHE:CE1	1:A:241:ILE:HD13	2.49	0.48
1:A:202:PHE:HB2	1:A:301:GLU:OE1	2.14	0.48
1:B:47:ASP:OD1	1:B:57:ARG:HD2	2.13	0.48
1:C:121:TRP:CZ2	1:C:125:ARG:HD3	2.49	0.48
1:D:220:PHE:CG	5:D:503:CM5:C11	2.88	0.48
1:D:220:PHE:CD2	5:D:503:CM5:C11	2.97	0.48
1:E:205:THR:HG23	1:E:234:VAL:HG13	1.96	0.48
1:B:169:PHE:CE2	6:B:614:HOH:O	2.62	0.48
1:B:374:HIS:N	1:C:286:GLN:NE2	2.52	0.48
1:E:192:ASP:OD1	1:E:193:GLN:N	2.46	0.48
1:C:206:PHE:HE2	1:C:480:ILE:HG12	1.77	0.48
1:C:486:ILE:HG12	1:C:487:ARG:N	2.28	0.48
1:C:84:ILE:HG12	1:C:390:LEU:CD1	2.29	0.48
1:F:132:MET:SD	1:F:441:ILE:HD12	2.54	0.48
1:C:297:PHE:C	1:C:297:PHE:CD2	2.87	0.47
1:F:202:PHE:CD1	1:F:297:PHE:CD1	3.02	0.47
1:F:132:MET:CE	1:F:437:LEU:HD12	2.44	0.47
1:F:460:ALA:O	1:F:487:ARG:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:PHE:HB3	6:A:626:HOH:O	2.13	0.47
1:B:473:GLN:O	1:B:473:GLN:HG3	2.12	0.47
1:B:206:PHE:CE2	1:B:480:ILE:CG1	2.97	0.47
1:C:52:LEU:HD22	1:C:364:PRO:HB3	1.95	0.47
1:F:203:TYR:O	1:F:207:SER:HB2	2.14	0.47
1:A:454:LEU:HD23	1:A:459:MET:HE2	1.95	0.47
1:B:220:PHE:CG	5:B:503:CM5:C11	2.96	0.47
1:C:357:GLN:NE2	1:C:426:PHE:HZ	2.12	0.47
1:E:175:THR:HG21	1:E:303:THR:HB	1.96	0.47
1:E:357:GLN:OE1	1:E:446:LEU:HD13	2.13	0.47
1:A:302:THR:HG23	3:A:502:9ZJ:CAL	2.44	0.47
1:F:72:PRO:HB3	5:F:502:CM5:O21	2.14	0.47
1:A:190:TYR:O	1:A:196:LEU:HD21	2.14	0.47
1:B:108:PHE:CD1	1:B:290:LEU:HD12	2.49	0.47
1:D:315:LEU:HD11	1:D:486:ILE:CG1	2.42	0.47
1:F:132:MET:SD	1:F:441:ILE:CD1	3.02	0.47
1:C:357:GLN:OE1	1:C:446:LEU:CD1	2.62	0.47
1:D:38:PRO:O	1:D:39:LEU:CB	2.61	0.47
1:E:47:ASP:O	1:E:48:ARG:C	2.52	0.47
1:C:179:ILE:O	1:C:180:CYS:C	2.53	0.47
1:D:309:TYR:CE2	1:D:481:PRO:HB3	2.50	0.47
1:F:176:ALA:HB2	1:F:300:THR:HG23	1.96	0.47
1:A:216:LEU:CD1	1:A:220:PHE:HD2	2.28	0.47
1:A:460:ALA:HB3	1:A:487:ARG:CD	2.45	0.47
1:A:98:ARG:H	1:A:117:ASN:HD21	1.62	0.47
1:B:114:ILE:HD11	1:B:294:SER:CB	2.34	0.47
1:B:98:ARG:H	1:B:117:ASN:HD21	1.62	0.47
1:C:131:THR:CG2	1:C:264:LEU:HD22	2.45	0.47
1:F:305:THR:HG21	1:F:362:LEU:HD13	1.97	0.47
1:C:316:LYS:HD3	1:C:317:TYR:CE1	2.49	0.47
1:F:114:ILE:HD12	3:F:503:9ZJ:CAH	2.44	0.47
1:A:270:LEU:O	1:A:273:GLU:HB2	2.15	0.47
1:A:96:SER:OG	1:A:433:LYS:HD3	2.15	0.47
1:B:120:ARG:HG3	1:B:282:GLU:HG3	1.97	0.47
1:B:446:LEU:O	1:B:450:PHE:HB2	2.15	0.47
1:D:274:LYS:HG3	1:D:277:SER:HB2	1.96	0.47
1:E:223:PHE:CB	6:E:601:HOH:O	2.28	0.47
1:F:179:ILE:HD11	1:F:299:GLY:C	2.35	0.47
1:A:114:ILE:HD13	3:A:502:9ZJ:CAP	2.40	0.46
1:D:144:GLU:O	1:D:148:GLU:HG3	2.15	0.46
1:E:114:ILE:HD13	3:E:502:9ZJ:CAP	2.35	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:LEU:HD23	1:A:487:ARG:HB3	1.98	0.46
1:A:180:CYS:SG	1:A:296:PHE:HZ	2.38	0.46
1:B:84:ILE:HD11	1:B:391:ILE:O	2.15	0.46
1:D:437:LEU:HD13	2:D:501:HEM:CMD	2.43	0.46
1:E:206:PHE:CE2	1:E:480:ILE:HG12	2.51	0.46
1:B:185:GLY:O	1:B:186:LYS:HB3	2.15	0.46
1:B:291:ASN:O	1:B:294:SER:HB2	2.16	0.46
1:C:272:MET:C	1:C:274:LYS:H	2.17	0.46
1:C:291:ASN:O	1:C:294:SER:HB2	2.15	0.46
1:C:437:LEU:HD12	1:C:437:LEU:H	1.80	0.46
5:D:503:CM5:H24	5:D:503:CM5:H21	1.77	0.46
1:F:144:GLU:O	1:F:148:GLU:HG3	2.16	0.46
1:F:302:THR:CG2	3:F:503:9ZJ:CAL	2.93	0.46
1:A:460:ALA:HB3	1:A:487:ARG:HG2	1.96	0.46
1:C:185:GLY:O	1:C:186:LYS:HB3	2.15	0.46
1:B:81:VAL:HG21	1:B:425:ALA:HA	1.97	0.46
1:B:206:PHE:CG	3:B:502:9ZJ:CAK	2.94	0.46
1:C:454:LEU:CD2	1:C:459:MET:CE	2.94	0.46
1:D:319:HIS:HB2	6:D:615:HOH:O	2.15	0.46
1:D:438:GLY:O	1:D:439:GLU:C	2.54	0.46
1:E:355:GLU:HG3	1:E:408:PHE:CD1	2.51	0.46
1:F:27:LYS:HG2	1:F:29:LYS:H	1.81	0.46
1:A:206:PHE:CG	3:A:502:9ZJ:CAK	2.95	0.46
1:D:434:ARG:CD	2:D:501:HEM:O2D	2.63	0.46
1:D:98:ARG:NH2	2:D:501:HEM:O2D	2.46	0.46
1:B:302:THR:HG23	3:B:502:9ZJ:CAL	2.46	0.46
1:D:88:LEU:HD11	1:D:390:LEU:HD13	1.97	0.46
1:E:88:LEU:HG	1:E:390:LEU:HD23	1.98	0.46
1:F:192:ASP:C	1:F:192:ASP:OD1	2.53	0.46
1:A:107:PHE:CE2	1:A:290:LEU:HD11	2.50	0.46
1:A:316:LYS:HD3	1:A:317:TYR:CE1	2.51	0.46
1:B:76:VAL:HB	1:B:388:VAL:HG22	1.98	0.46
1:C:175:THR:O	1:C:179:ILE:HD12	2.16	0.46
5:C:503:CM5:C24	5:C:503:CM5:O21	2.60	0.46
1:F:154:ILE:CD1	1:F:158:ARG:HE	2.29	0.46
1:B:302:THR:CG2	3:B:502:9ZJ:CAL	2.94	0.46
1:A:206:PHE:CE1	3:A:502:9ZJ:CAS	2.98	0.46
1:B:454:LEU:HA	1:B:454:LEU:HD23	1.48	0.46
1:E:133:ARG:CB	1:E:133:ARG:NH1	2.76	0.46
5:E:503:CM5:O21	5:E:503:CM5:C24	2.60	0.46
1:E:88:LEU:HG	1:E:390:LEU:CD2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:223:PHE:CB	5:F:502:CM5:H42	2.45	0.46
1:A:239:GLN:HA	1:A:239:GLN:OE1	2.16	0.45
1:B:179:ILE:CD1	1:B:179:ILE:H	2.28	0.45
1:D:441:ILE:O	1:D:445:GLU:HG3	2.16	0.45
5:D:503:CM5:H41	5:D:503:CM5:H11	1.59	0.45
1:E:202:PHE:CD1	1:E:297:PHE:CD1	3.03	0.45
1:B:121:TRP:CZ2	1:B:125:ARG:HD3	2.51	0.45
1:E:98:ARG:HB2	1:E:434:ARG:NH2	2.31	0.45
1:D:38:PRO:O	1:D:39:LEU:HB2	2.16	0.45
5:D:503:CM5:C24	5:D:503:CM5:O21	2.60	0.45
1:E:271:HIS:C	1:E:273:GLU:N	2.69	0.45
1:F:98:ARG:HB2	1:F:434:ARG:NH2	2.31	0.45
1:A:361:ASP:OD1	1:A:393:SER:HB3	2.17	0.45
1:A:390:LEU:O	1:A:392:LEU:N	2.49	0.45
1:B:181:SER:O	1:B:185:GLY:HA2	2.16	0.45
1:C:114:ILE:HD13	3:C:502:9ZJ:CAP	2.39	0.45
1:D:192:ASP:C	1:D:192:ASP:OD1	2.54	0.45
1:F:302:THR:HG23	3:F:503:9ZJ:CAL	2.47	0.45
1:A:121:TRP:CZ2	1:A:125:ARG:HD3	2.52	0.45
1:C:202:PHE:CE1	1:C:241:ILE:HD13	2.52	0.45
1:F:98:ARG:H	1:F:117:ASN:HD21	1.64	0.45
1:F:438:GLY:O	1:F:439:GLU:C	2.52	0.45
1:A:131:THR:O	1:A:131:THR:HG22	2.16	0.45
1:A:135:PHE:CD2	1:A:142:VAL:HG23	2.46	0.45
1:A:98:ARG:HB2	1:A:434:ARG:NH2	2.32	0.45
1:B:216:LEU:CD1	1:B:220:PHE:CD2	2.96	0.45
1:C:176:ALA:HB2	1:C:300:THR:HG23	1.98	0.45
1:E:316:LYS:HD3	1:E:317:TYR:CE1	2.51	0.45
1:E:88:LEU:HD11	1:E:390:LEU:HD22	1.98	0.45
1:C:286:GLN:O	1:C:290:LEU:HD13	2.16	0.45
1:C:437:LEU:HD12	1:C:437:LEU:N	2.31	0.45
1:C:98:ARG:HG3	1:C:99:GLY:O	2.17	0.45
1:D:175:THR:HG21	1:D:303:THR:HB	1.99	0.45
1:E:73:ARG:CD	1:E:387:GLU:OE2	2.65	0.45
1:C:242:ASN:OD1	1:C:289:ASN:HB3	2.16	0.45
1:A:291:ASN:O	1:A:294:SER:HB2	2.17	0.45
1:C:38:PRO:O	1:C:39:LEU:CB	2.65	0.45
1:D:47:ASP:C	1:D:49:ARG:N	2.68	0.45
1:F:175:THR:HG21	1:F:303:THR:HB	1.99	0.45
1:B:202:PHE:CE1	1:B:241:ILE:HD13	2.52	0.44
1:C:141:SER:HB3	1:C:144:GLU:CG	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:211:SER:HA	1:E:474:GLU:OE2	2.17	0.44
1:D:273:GLU:C	1:D:275:GLU:N	2.70	0.44
1:F:47:ASP:OD1	1:F:47:ASP:C	2.56	0.44
1:C:290:LEU:CD1	1:C:290:LEU:N	2.81	0.44
1:C:365:MET:N	6:C:603:HOH:O	2.38	0.44
1:C:438:GLY:O	1:C:439:GLU:C	2.55	0.44
1:E:179:ILE:HG22	1:E:183:VAL:CG2	2.47	0.44
1:F:48:ARG:H	1:F:48:ARG:HD2	1.82	0.44
1:B:132:MET:CA	1:B:135:PHE:CE2	2.95	0.44
1:E:305:THR:HG21	1:E:362:LEU:CD1	2.43	0.44
1:B:120:ARG:HG3	1:B:282:GLU:CG	2.47	0.44
1:F:154:ILE:O	1:F:158:ARG:HG3	2.18	0.44
5:F:502:CM5:C24	5:F:502:CM5:O21	2.60	0.44
1:A:270:LEU:O	1:A:273:GLU:HB3	2.18	0.44
5:C:503:CM5:H11	5:C:503:CM5:H41	1.59	0.44
1:D:131:THR:C	1:D:132:MET:CG	2.85	0.44
1:E:129:VAL:C	1:E:131:THR:H	2.20	0.44
1:F:202:PHE:CE1	1:F:241:ILE:HD13	2.52	0.44
1:B:120:ARG:O	1:B:124:LEU:CD2	2.57	0.44
1:F:27:LYS:HB2	1:F:380:TYR:CE1	2.52	0.44
1:A:185:GLY:O	1:A:186:LYS:HB3	2.18	0.44
1:A:454:LEU:HD23	1:A:454:LEU:HA	1.62	0.44
1:A:47:ASP:C	1:A:49:ARG:N	2.71	0.44
1:B:73:ARG:CD	1:B:387:GLU:OE2	2.62	0.44
1:C:206:PHE:CE2	1:C:480:ILE:CG1	3.01	0.44
1:C:454:LEU:HD23	1:C:454:LEU:HA	1.54	0.44
1:F:185:GLY:O	1:F:186:LYS:HB3	2.17	0.44
1:F:220:PHE:CZ	5:F:502:CM5:C10	2.95	0.44
1:F:291:ASN:O	1:F:294:SER:HB2	2.18	0.44
1:E:271:HIS:C	1:E:273:GLU:H	2.20	0.44
1:E:290:LEU:H	1:E:290:LEU:CD1	2.31	0.44
1:F:27:LYS:CB	1:F:380:TYR:CE1	3.00	0.44
1:F:454:LEU:HD21	1:F:459:MET:CE	2.47	0.44
1:A:47:ASP:N	1:A:54:SER:OG	2.51	0.43
1:C:205:THR:HG23	1:C:234:VAL:HG13	1.99	0.43
1:D:172:GLN:OE1	1:D:301:GLU:OE1	2.36	0.43
1:D:274:LYS:O	1:D:274:LYS:CG	2.66	0.43
2:A:501:HEM:HBC2	2:A:501:HEM:HHD	2.00	0.43
1:B:430:SER:HB3	2:B:501:HEM:HBA1	2.01	0.43
1:C:132:MET:O	1:C:135:PHE:CD2	2.68	0.43
1:C:202:PHE:HD1	1:C:297:PHE:HD1	1.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:147:GLN:O	1:D:151:GLN:HG2	2.18	0.43
1:E:315:LEU:HD22	1:E:461:SER:HB2	2.00	0.43
1:D:286:GLN:HE22	1:F:374:HIS:CD2	2.35	0.43
1:B:132:MET:O	1:B:135:PHE:CE2	2.70	0.43
1:B:196:LEU:O	1:B:196:LEU:HD12	2.18	0.43
1:C:192:ASP:C	1:C:192:ASP:OD1	2.57	0.43
1:C:78:LEU:HB2	1:C:390:LEU:HD13	2.01	0.43
1:D:316:LYS:HB3	1:D:317:TYR:CD1	2.53	0.43
1:E:135:PHE:CZ	1:E:182:ILE:HG12	2.49	0.43
1:E:38:PRO:O	1:E:39:LEU:CB	2.66	0.43
1:E:220:PHE:CE2	5:E:503:CM5:C11	3.01	0.43
5:F:502:CM5:H41	5:F:502:CM5:H11	1.59	0.43
1:B:432:GLY:O	1:B:435:ILE:CG2	2.63	0.43
1:F:316:LYS:NZ	1:F:468:ILE:O	2.44	0.43
1:E:192:ASP:OD1	1:E:192:ASP:C	2.56	0.43
1:F:141:SER:HB3	1:F:144:GLU:CG	2.41	0.43
1:F:183:VAL:O	1:F:263:ASP:HB2	2.18	0.43
1:B:132:MET:HA	1:B:135:PHE:HE2	1.74	0.43
1:B:69:HIS:HA	1:B:73:ARG:O	2.18	0.43
1:D:136:GLY:O	1:D:137:MET:C	2.56	0.43
1:D:202:PHE:CD1	1:D:297:PHE:CD1	3.07	0.43
1:E:388:VAL:HG12	1:E:390:LEU:CD1	2.49	0.43
1:F:223:PHE:HB3	5:F:502:CM5:H42	2.00	0.43
1:F:460:ALA:HB3	1:F:487:ARG:HD2	2.00	0.43
1:A:486:ILE:HG12	1:A:487:ARG:H	1.84	0.43
1:C:343:ARG:HD2	6:C:622:HOH:O	2.17	0.43
1:E:438:GLY:O	1:E:439:GLU:C	2.57	0.43
1:A:374:HIS:H	1:B:286:GLN:HE22	1.67	0.43
1:A:486:ILE:HG12	1:A:487:ARG:N	2.33	0.43
1:B:270:LEU:O	1:B:273:GLU:CB	2.66	0.43
1:C:216:LEU:O	1:C:216:LEU:HD12	2.18	0.43
1:D:454:LEU:HD23	1:D:459:MET:HE2	1.99	0.43
1:D:206:PHE:CE2	1:D:480:ILE:HG12	2.53	0.43
1:D:220:PHE:CD2	5:D:503:CM5:H112	2.50	0.43
1:F:147:GLN:O	1:F:151:GLN:HG2	2.17	0.43
1:A:91:LYS:HE3	1:A:376:SER:O	2.18	0.43
1:D:202:PHE:CE1	1:D:241:ILE:HD13	2.54	0.43
1:E:121:TRP:CD1	1:E:434:ARG:NH1	2.87	0.43
1:F:108:PHE:O	1:F:109:ARG:C	2.56	0.43
1:A:454:LEU:HD21	1:A:459:MET:HE2	2.01	0.43
5:B:503:CM5:C24	5:B:503:CM5:O21	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:120:ARG:HG3	1:C:282:GLU:CG	2.49	0.43
1:C:120:ARG:HG3	1:C:282:GLU:HG3	2.00	0.43
1:C:429:PHE:O	1:C:435:ILE:HG13	2.19	0.43
1:E:302:THR:CG2	2:E:501:HEM:HAB	2.44	0.43
1:E:88:LEU:CG	1:E:390:LEU:CD2	2.97	0.43
1:B:230:ALA:O	1:B:233:GLN:N	2.52	0.42
1:C:441:ILE:O	1:C:445:GLU:HG3	2.19	0.42
1:D:52:LEU:HD22	1:D:364:PRO:HB3	2.01	0.42
1:E:231:HIS:CD2	1:E:231:HIS:N	2.87	0.42
1:E:454:LEU:CD2	1:E:459:MET:CE	2.97	0.42
1:F:184:PHE:HE2	1:F:296:PHE:CZ	2.36	0.42
1:F:361:ASP:OD1	1:F:393:SER:HB2	2.19	0.42
1:A:306:THR:HG21	1:A:357:GLN:HG2	2.00	0.42
1:F:274:LYS:O	1:F:274:LYS:CG	2.66	0.42
1:E:81:VAL:HG21	1:E:425:ALA:HA	2.01	0.42
1:A:202:PHE:CZ	1:A:296:PHE:HD2	2.37	0.42
1:E:181:SER:O	1:E:185:GLY:HA2	2.20	0.42
1:E:437:LEU:N	1:E:437:LEU:HD12	2.34	0.42
5:E:503:CM5:H41	5:E:503:CM5:H11	1.59	0.42
1:A:364:PRO:HA	1:A:393:SER:HB3	2.01	0.42
1:B:183:VAL:O	1:B:263:ASP:HB2	2.18	0.42
1:D:181:SER:O	1:D:185:GLY:HA2	2.19	0.42
1:E:388:VAL:HG12	1:E:390:LEU:HD11	2.01	0.42
1:A:181:SER:O	1:A:185:GLY:HA2	2.19	0.42
1:A:205:THR:O	1:A:209:ILE:HG13	2.18	0.42
1:A:457:PHE:CD1	1:A:488:PHE:HB3	2.54	0.42
1:B:38:PRO:O	1:B:39:LEU:CB	2.67	0.42
1:E:362:LEU:O	1:E:364:PRO:HD3	2.20	0.42
1:F:107:PHE:CE2	1:F:290:LEU:CD1	3.03	0.42
1:C:27:LYS:O	1:C:379:GLY:O	2.38	0.42
1:C:220:PHE:CB	5:C:503:CM5:H112	2.46	0.42
1:E:220:PHE:CD1	5:E:503:CM5:C11	2.89	0.42
1:F:131:THR:HG22	1:F:131:THR:O	2.19	0.42
1:F:454:LEU:HD23	1:F:454:LEU:HA	1.57	0.42
1:B:220:PHE:CD2	5:B:503:CM5:C11	3.03	0.42
1:A:105:ASP:N	1:A:106:PRO:CD	2.83	0.41
1:D:437:LEU:HD11	2:D:501:HEM:HBD2	2.01	0.41
1:F:52:LEU:HD22	1:F:364:PRO:HB3	2.02	0.41
1:A:52:LEU:HD22	1:A:364:PRO:HB3	2.02	0.41
1:B:409:ASN:ND2	1:B:411:ASP:HB2	2.34	0.41
1:C:121:TRP:O	1:C:122:LYS:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:315:LEU:HD22	1:C:461:SER:HB2	2.03	0.41
1:B:268:TYR:CE1	1:B:288:LEU:HB2	2.55	0.41
1:B:438:GLY:O	1:B:439:GLU:C	2.57	0.41
1:C:154:ILE:C	1:C:156:GLU:H	2.23	0.41
1:D:132:MET:CE	1:D:295:LEU:HD21	2.50	0.41
1:D:355:GLU:HG3	1:D:408:PHE:CD1	2.55	0.41
1:B:179:ILE:CD1	1:B:179:ILE:N	2.83	0.41
1:F:268:TYR:CD1	1:F:288:LEU:HD13	2.56	0.41
1:F:315:LEU:HD22	1:F:461:SER:HB2	2.01	0.41
1:F:268:TYR:CG	1:F:288:LEU:HD13	2.56	0.41
1:C:65:VAL:HG22	1:C:78:LEU:HD23	2.03	0.41
1:D:105:ASP:N	1:D:106:PRO:CD	2.83	0.41
1:E:242:ASN:OD1	1:E:289:ASN:HB3	2.20	0.41
1:E:286:GLN:O	1:E:290:LEU:HD13	2.21	0.41
1:F:486:ILE:HG12	1:F:487:ARG:N	2.35	0.41
1:A:295:LEU:O	1:A:296:PHE:C	2.58	0.41
1:C:131:THR:O	1:C:131:THR:HG22	2.21	0.41
1:C:132:MET:CE	2:C:501:HEM:HBC1	2.51	0.41
1:C:98:ARG:HG2	1:C:115:PHE:HA	2.03	0.41
1:D:98:ARG:HG3	1:D:99:GLY:O	2.20	0.41
1:E:37:LEU:HD13	6:E:609:HOH:O	2.20	0.41
1:E:153:LEU:HD21	1:E:453:ILE:HD11	2.02	0.41
1:F:51:LEU:HA	1:F:51:LEU:HD12	1.85	0.41
1:F:98:ARG:HG2	1:F:115:PHE:HA	2.03	0.41
1:F:98:ARG:NH2	2:F:501:HEM:O2D	2.49	0.41
1:B:184:PHE:HE2	1:B:296:PHE:CZ	2.38	0.41
1:B:306:THR:OG1	1:B:362:LEU:CD2	2.67	0.41
1:D:434:ARG:C	1:D:435:ILE:O	2.59	0.41
1:A:80:GLY:HA3	6:A:623:HOH:O	2.20	0.41
1:B:336:ARG:HA	1:B:337:PRO:HD3	1.95	0.41
1:D:486:ILE:HG12	1:D:487:ARG:N	2.36	0.41
1:A:384:LYS:O	1:A:385:ASP:HB2	2.20	0.41
1:B:457:PHE:CD1	1:B:488:PHE:HB3	2.56	0.41
1:B:216:LEU:O	1:B:216:LEU:HD12	2.21	0.40
1:C:302:THR:HG23	1:C:362:LEU:HD23	2.03	0.40
1:C:73:ARG:HG3	1:C:75:VAL:HG23	2.03	0.40
1:E:231:HIS:H	1:E:231:HIS:CD2	2.39	0.40
1:D:131:THR:C	1:D:132:MET:HG3	2.41	0.40
1:D:473:GLN:O	1:D:474:GLU:O	2.39	0.40
1:B:390:LEU:O	1:B:391:ILE:C	2.59	0.40
1:C:457:PHE:CD1	1:C:488:PHE:HB3	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:362:LEU:HD12	1:D:362:LEU:O	2.22	0.40
1:D:435:ILE:O	1:D:435:ILE:HG23	2.21	0.40
1:B:141:SER:HB3	1:B:144:GLU:CG	2.37	0.40
1:B:179:ILE:O	1:B:182:ILE:N	2.55	0.40
1:B:270:LEU:O	1:B:273:GLU:HB3	2.22	0.40
1:E:88:LEU:CD2	1:E:390:LEU:HD21	2.51	0.40
1:F:454:LEU:CD2	1:F:459:MET:CE	2.99	0.40
1:C:316:LYS:HB3	1:C:317:TYR:CD1	2.57	0.40
1:C:223:PHE:CD1	5:C:503:CM5:H42	2.57	0.40
1:E:316:LYS:NZ	1:E:468:ILE:O	2.48	0.40
1:E:309:TYR:CE2	1:E:481:PRO:HB3	2.56	0.40
1:F:216:LEU:O	1:F:216:LEU:HD12	2.22	0.40

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	459/476 (96%)	420 (92%)	32 (7%)	7 (2%)	10	42
1	B	460/476 (97%)	419 (91%)	34 (7%)	7 (2%)	10	42
1	C	460/476 (97%)	414 (90%)	41 (9%)	5 (1%)	14	50
1	D	460/476 (97%)	414 (90%)	38 (8%)	8 (2%)	9	39
1	E	459/476 (96%)	417 (91%)	37 (8%)	5 (1%)	14	50
1	F	460/476 (97%)	416 (90%)	40 (9%)	4 (1%)	17	55
All	All	2758/2856 (97%)	2500 (91%)	222 (8%)	36 (1%)	12	45

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	280	HIS

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Mol	Chain	Res	Type
1	B	280	HIS
1	C	280	HIS
1	D	28	GLY
1	D	280	HIS
1	D	435	ILE
1	D	474	GLU
1	E	280	HIS
1	E	474	GLU
1	F	280	HIS
1	F	474	GLU
1	A	474	GLU
1	B	136	GLY
1	C	474	GLU
1	D	48	ARG
1	D	132	MET
1	E	48	ARG
1	F	49	ARG
1	A	48	ARG
1	B	48	ARG
1	B	130	THR
1	B	474	GLU
1	C	130	THR
1	A	391	ILE
1	F	130	THR
1	A	49	ARG
1	A	130	THR
1	D	130	THR
1	E	130	THR
1	A	435	ILE
1	B	435	ILE
1	C	391	ILE
1	C	435	ILE
1	D	391	ILE
1	E	435	ILE
1	B	391	ILE

### 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	376/418 (90%)	371 (99%)	5 (1%)	69	89
1	B	378/418 (90%)	370 (98%)	8 (2%)	53	82
1	C	379/418 (91%)	373 (98%)	6 (2%)	62	86
1	D	373/418 (89%)	368 (99%)	5 (1%)	69	89
1	E	377/418 (90%)	372 (99%)	5 (1%)	69	89
1	F	374/418 (90%)	364 (97%)	10 (3%)	44	77
All	All	2257/2508 (90%)	2218 (98%)	39 (2%)	60	85

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	73	ARG
1	A	264	LEU
1	A	296	PHE
1	A	309	TYR
1	A	362	LEU
1	B	117	ASN
1	B	264	LEU
1	B	286	GLN
1	B	293	LEU
1	B	296	PHE
1	B	309	TYR
1	B	330	GLN
1	B	424	GLU
1	C	51	LEU
1	C	135	PHE
1	C	264	LEU
1	C	296	PHE
1	C	309	TYR
1	C	381	ILE
1	D	73	ARG
1	D	296	PHE
1	D	302	THR
1	D	309	TYR
1	D	362	LEU
1	E	200	ASN
1	E	216	LEU
1	E	296	PHE
1	E	302	THR

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Mol	Chain	Res	Type
1	E	309	TYR
1	F	30	LEU
1	F	48	ARG
1	F	73	ARG
1	F	200	ASN
1	F	207	SER
1	F	284	SER
1	F	286	GLN
1	F	296	PHE
1	F	309	TYR
1	F	362	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

18 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
3	9ZJ	B	502	-	22,23,23	2.95	4 (18%)	34,36,36	5.32	6 (17%)
3	9ZJ	C	502	-	22,23,23	2.31	3 (13%)	34,36,36	4.40	7 (20%)
3	9ZJ	D	502	-	22,23,23	2.43	2 (9%)	34,36,36	4.14	7 (20%)
2	HEM	F	501	1	27,50,50	2.32	5 (18%)	17,82,82	2.07	6 (35%)
5	CM5	C	503	-	36,36,36	0.41	0	49,49,49	0.70	1 (2%)
2	HEM	B	501	1	27,50,50	2.08	6 (22%)	17,82,82	1.85	3 (17%)
5	CM5	F	502	-	36,36,36	0.40	0	49,49,49	0.70	1 (2%)
2	HEM	A	501	1	27,50,50	2.07	5 (18%)	17,82,82	1.76	5 (29%)
5	CM5	E	503	-	36,36,36	0.40	0	49,49,49	0.70	1 (2%)
3	9ZJ	F	503	-	22,23,23	2.27	2 (9%)	34,36,36	4.30	7 (20%)
5	CM5	D	503	-	36,36,36	0.40	0	49,49,49	0.70	1 (2%)
5	CM5	B	503	-	36,36,36	0.40	0	49,49,49	0.70	1 (2%)
2	HEM	D	501	1	27,50,50	2.15	6 (22%)	17,82,82	1.82	5 (29%)
4	ZAZ	A	503	-	12,12,12	0.78	0	13,13,13	0.77	0
3	9ZJ	E	502	-	22,23,23	2.40	3 (13%)	34,36,36	4.75	8 (23%)
2	HEM	E	501	1	27,50,50	2.14	7 (25%)	17,82,82	1.95	3 (17%)
3	9ZJ	A	502	-	22,23,23	2.14	1 (4%)	34,36,36	4.38	7 (20%)
2	HEM	C	501	1	27,50,50	2.37	7 (25%)	17,82,82	1.72	3 (17%)

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	9ZJ	B	502	-	-	10/10/32/32	0/3/3/3
3	9ZJ	C	502	-	-	10/10/32/32	0/3/3/3
3	9ZJ	D	502	-	-	10/10/32/32	0/3/3/3
2	HEM	F	501	1	-	0/6/54/54	-
5	CM5	C	503	-	-	14/17/65/65	0/3/3/3
2	HEM	B	501	1	-	0/6/54/54	-
5	CM5	F	502	-	-	14/17/65/65	0/3/3/3
2	HEM	A	501	1	-	0/6/54/54	-
5	CM5	E	503	-	-	14/17/65/65	0/3/3/3
3	9ZJ	F	503	-	-	10/10/32/32	0/3/3/3
5	CM5	D	503	-	-	14/17/65/65	0/3/3/3
5	CM5	B	503	-	-	14/17/65/65	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	D	501	1	-	0/6/54/54	-
4	ZAZ	A	503	-	-	1/6/14/14	0/1/1/1
3	9ZJ	E	502	-	-	10/10/32/32	0/3/3/3
2	HEM	E	501	1	-	0/6/54/54	-
3	9ZJ	A	502	-	-	10/10/32/32	0/3/3/3
2	HEM	C	501	1	-	0/6/54/54	-

All (51) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	9ZJ	CAU-CAQ	-9.57	1.39	1.51
3	C	502	9ZJ	CAU-CAQ	-9.53	1.39	1.51
3	D	502	9ZJ	CAU-CAQ	-9.51	1.39	1.51
3	A	502	9ZJ	CAU-CAQ	-9.51	1.39	1.51
3	F	503	9ZJ	CAU-CAQ	-9.51	1.39	1.51
3	E	502	9ZJ	CAU-CAQ	-9.49	1.39	1.51
3	B	502	9ZJ	OAN-CAR	7.55	1.55	1.43
2	C	501	HEM	C3C-C2C	-6.20	1.31	1.40
3	D	502	9ZJ	CAA-CAR	-5.63	1.42	1.51
2	F	501	HEM	C3B-C2B	-5.60	1.32	1.40
2	E	501	HEM	C3C-C2C	-5.49	1.32	1.40
2	B	501	HEM	C3C-C2C	-5.34	1.33	1.40
2	F	501	HEM	C3C-C2C	-5.27	1.33	1.40
2	F	501	HEM	C3D-C2D	5.20	1.53	1.37
2	C	501	HEM	C3B-C2B	-5.12	1.33	1.40
2	C	501	HEM	C3D-C2D	5.12	1.52	1.37
2	D	501	HEM	C3D-C2D	5.10	1.52	1.37
2	D	501	HEM	C3B-C2B	-4.95	1.33	1.40
3	B	502	9ZJ	CAR-NAM	4.90	1.53	1.45
2	E	501	HEM	C3D-C2D	4.67	1.51	1.37
2	D	501	HEM	C3C-C2C	-4.66	1.33	1.40
2	A	501	HEM	C3D-C2D	4.61	1.51	1.37
2	E	501	HEM	C3B-CAB	4.52	1.57	1.47
2	B	501	HEM	C3D-C2D	4.52	1.51	1.37
2	A	501	HEM	C3B-C2B	-4.41	1.34	1.40
3	E	502	9ZJ	OAN-CAR	4.34	1.50	1.43
2	A	501	HEM	C3C-CAC	4.11	1.56	1.47
2	A	501	HEM	C3C-C2C	-3.95	1.34	1.40
2	A	501	HEM	C3B-CAB	3.92	1.55	1.47
3	F	503	9ZJ	CAA-CAR	-3.91	1.45	1.51
2	C	501	HEM	C3B-CAB	3.77	1.55	1.47
2	F	501	HEM	C3B-CAB	3.67	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	9ZJ	CAA-CAR	-3.64	1.45	1.51
2	B	501	HEM	C3B-C2B	-3.64	1.35	1.40
2	E	501	HEM	C3C-CAC	3.45	1.54	1.47
3	C	502	9ZJ	OAN-CAR	3.41	1.48	1.43
2	F	501	HEM	C3C-CAC	3.26	1.54	1.47
2	B	501	HEM	C3C-CAC	3.22	1.54	1.47
2	C	501	HEM	C3C-CAC	3.20	1.54	1.47
2	D	501	HEM	C3C-CAC	3.20	1.54	1.47
2	B	501	HEM	C3B-CAB	3.15	1.54	1.47
2	D	501	HEM	C3B-CAB	3.10	1.54	1.47
3	E	502	9ZJ	CAA-CAR	-3.07	1.46	1.51
2	D	501	HEM	CAA-C2A	3.02	1.56	1.52
3	C	502	9ZJ	CAR-NAM	2.87	1.50	1.45
2	E	501	HEM	C3B-C2B	-2.83	1.36	1.40
2	B	501	HEM	CAA-C2A	2.71	1.56	1.52
2	C	501	HEM	C4B-CHC	-2.34	1.34	1.41
2	E	501	HEM	C4B-NB	2.06	1.40	1.36
2	C	501	HEM	CAA-C2A	2.02	1.55	1.52
2	E	501	HEM	C1B-C2B	2.02	1.47	1.42

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	9ZJ	OAN-CAU-CAQ	20.31	125.99	111.64
3	C	502	9ZJ	OAN-CAU-CAQ	16.82	123.53	111.64
3	B	502	9ZJ	CAA-CAR-NAM	16.55	127.55	109.64
3	E	502	9ZJ	OAN-CAU-CAG	-13.62	77.13	108.39
3	A	502	9ZJ	OAN-CAU-CAQ	12.33	120.35	111.64
3	E	502	9ZJ	CAA-CAR-NAM	12.15	122.79	109.64
3	B	502	9ZJ	OAN-CAU-CAG	-12.02	80.80	108.39
3	F	503	9ZJ	OAN-CAU-CAG	-11.70	81.55	108.39
3	A	502	9ZJ	OAN-CAR-CAA	11.68	121.55	106.07
3	A	502	9ZJ	OAN-CAU-CAG	-11.53	81.93	108.39
3	E	502	9ZJ	OAN-CAU-CAT	11.27	125.55	104.70
3	E	502	9ZJ	OAN-CAR-CAA	11.09	120.77	106.07
3	F	503	9ZJ	OAN-CAU-CAQ	11.03	119.44	111.64
3	D	502	9ZJ	OAN-CAU-CAG	-10.92	83.33	108.39
3	D	502	9ZJ	CAA-CAR-NAM	10.67	121.19	109.64
3	F	503	9ZJ	OAN-CAR-CAA	10.65	120.19	106.07
3	E	502	9ZJ	OAN-CAU-CAQ	10.54	119.09	111.64
3	C	502	9ZJ	CAA-CAR-NAM	10.48	120.98	109.64
3	F	503	9ZJ	CAA-CAR-NAM	10.02	120.49	109.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	502	9ZJ	OAN-CAU-CAT	9.83	122.88	104.70
3	A	502	9ZJ	CAA-CAR-NAM	9.76	120.21	109.64
3	F	503	9ZJ	OAN-CAU-CAT	9.75	122.74	104.70
3	C	502	9ZJ	OAN-CAR-CAA	9.69	118.92	106.07
3	C	502	9ZJ	OAN-CAU-CAG	-9.69	86.15	108.39
3	D	502	9ZJ	OAN-CAR-CAA	9.62	118.83	106.07
3	D	502	9ZJ	OAN-CAU-CAQ	9.29	118.21	111.64
3	A	502	9ZJ	OAN-CAU-CAT	9.13	121.59	104.70
3	B	502	9ZJ	OAN-CAR-CAA	6.98	115.33	106.07
3	B	502	9ZJ	OAN-CAU-CAT	6.41	116.56	104.70
3	D	502	9ZJ	CAU-OAN-CAR	6.18	125.13	113.97
3	C	502	9ZJ	OAN-CAU-CAT	5.92	115.66	104.70
3	E	502	9ZJ	CAU-OAN-CAR	5.44	123.79	113.97
3	F	503	9ZJ	CAU-OAN-CAR	5.02	123.03	113.97
2	B	501	HEM	CAA-CBA-CGA	-4.84	104.54	112.67
2	D	501	HEM	CMA-C3A-C4A	-4.83	121.04	128.46
2	E	501	HEM	CAA-CBA-CGA	-4.61	104.93	112.67
2	E	501	HEM	CBA-CAA-C2A	4.26	120.34	112.49
2	C	501	HEM	CAA-CBA-CGA	-4.24	105.55	112.67
2	F	501	HEM	CAA-CBA-CGA	-4.20	105.63	112.67
3	A	502	9ZJ	CAU-OAN-CAR	4.08	121.34	113.97
2	A	501	HEM	CBD-CAD-C3D	-4.05	105.01	112.48
2	B	501	HEM	CBD-CAD-C3D	-3.82	105.44	112.48
2	F	501	HEM	C4A-C3A-C2A	3.67	109.55	107.00
2	C	501	HEM	CBD-CAD-C3D	-3.67	105.72	112.48
2	F	501	HEM	CMD-C2D-C1D	-3.37	123.28	128.46
2	E	501	HEM	C4A-C3A-C2A	3.27	109.27	107.00
2	F	501	HEM	CMA-C3A-C4A	-3.23	123.49	128.46
2	A	501	HEM	CAA-CBA-CGA	-2.99	107.65	112.67
2	F	501	HEM	CMD-C2D-C3D	2.85	130.31	124.94
2	D	501	HEM	CMA-C3A-C2A	2.81	130.25	124.94
3	E	502	9ZJ	CAQ-CAP-NAM	-2.79	117.85	121.29
2	B	501	HEM	CBA-CAA-C2A	2.67	117.40	112.49
5	C	503	CM5	C24-O23-C16	-2.51	111.76	117.96
5	E	503	CM5	C24-O23-C16	-2.50	111.77	117.96
2	A	501	HEM	C1D-C2D-C3D	-2.50	105.26	107.00
5	B	503	CM5	C24-O23-C16	-2.50	111.79	117.96
5	F	502	CM5	C24-O23-C16	-2.49	111.81	117.96
5	D	503	CM5	C24-O23-C16	-2.49	111.81	117.96
3	C	502	9ZJ	CAU-OAN-CAR	2.48	118.45	113.97
2	D	501	HEM	C4A-C3A-C2A	2.47	108.72	107.00
2	A	501	HEM	C4A-C3A-C2A	2.39	108.66	107.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	HEM	C4C-C3C-C2C	2.35	108.54	106.90
2	D	501	HEM	CMC-C2C-C3C	2.30	128.97	124.68
2	C	501	HEM	CMB-C2B-C3B	2.26	128.91	124.68
2	A	501	HEM	CMA-C3A-C4A	-2.16	125.14	128.46
3	E	502	9ZJ	CAJ-CAQ-CAU	-2.09	120.28	122.71
2	F	501	HEM	C4C-C3C-C2C	2.09	108.36	106.90
3	D	502	9ZJ	CAJ-CAQ-CAU	-2.09	120.28	122.71
3	A	502	9ZJ	CAJ-CAQ-CAU	-2.08	120.30	122.71
3	C	502	9ZJ	CAJ-CAQ-CAU	-2.07	120.31	122.71
3	F	503	9ZJ	CAJ-CAQ-CAU	-2.06	120.31	122.71
3	B	502	9ZJ	CAJ-CAQ-CAU	-2.05	120.32	122.71

There are no chirality outliers.

All (131) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	502	9ZJ	CAS-CAF-CAG-CAU
3	B	502	9ZJ	FAC-CAT-CAU-CAG
3	B	502	9ZJ	FAD-CAT-CAU-CAG
3	B	502	9ZJ	FAB-CAT-CAU-CAG
3	B	502	9ZJ	FAC-CAT-CAU-OAN
3	B	502	9ZJ	FAD-CAT-CAU-OAN
3	B	502	9ZJ	FAB-CAT-CAU-OAN
3	B	502	9ZJ	FAC-CAT-CAU-CAQ
3	B	502	9ZJ	FAD-CAT-CAU-CAQ
3	B	502	9ZJ	FAB-CAT-CAU-CAQ
5	C	503	CM5	C18-C13-O12-C1
5	C	503	CM5	O14-C13-O12-C1
3	C	502	9ZJ	FAC-CAT-CAU-CAG
3	C	502	9ZJ	FAD-CAT-CAU-CAG
3	C	502	9ZJ	FAB-CAT-CAU-CAG
3	C	502	9ZJ	FAC-CAT-CAU-OAN
3	C	502	9ZJ	FAD-CAT-CAU-OAN
3	C	502	9ZJ	FAB-CAT-CAU-OAN
3	C	502	9ZJ	FAC-CAT-CAU-CAQ
3	C	502	9ZJ	FAD-CAT-CAU-CAQ
3	C	502	9ZJ	FAB-CAT-CAU-CAQ
3	D	502	9ZJ	CAS-CAF-CAG-CAU
3	D	502	9ZJ	FAC-CAT-CAU-CAG
3	D	502	9ZJ	FAD-CAT-CAU-CAG
3	D	502	9ZJ	FAB-CAT-CAU-CAG
3	D	502	9ZJ	FAC-CAT-CAU-OAN

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Mol	Chain	Res	Type	Atoms
3	D	502	9ZJ	FAD-CAT-CAU-OAN
3	D	502	9ZJ	FAB-CAT-CAU-OAN
3	D	502	9ZJ	FAC-CAT-CAU-CAQ
3	D	502	9ZJ	FAD-CAT-CAU-CAQ
3	D	502	9ZJ	FAB-CAT-CAU-CAQ
5	D	503	CM5	C18-C13-O12-C1
5	D	503	CM5	O14-C13-O12-C1
5	F	502	CM5	C18-C13-O12-C1
5	F	502	CM5	O14-C13-O12-C1
3	A	502	9ZJ	FAC-CAT-CAU-CAG
3	A	502	9ZJ	FAD-CAT-CAU-CAG
3	A	502	9ZJ	FAB-CAT-CAU-CAG
3	A	502	9ZJ	FAC-CAT-CAU-OAN
3	A	502	9ZJ	FAD-CAT-CAU-OAN
3	A	502	9ZJ	FAB-CAT-CAU-OAN
3	A	502	9ZJ	FAC-CAT-CAU-CAQ
3	A	502	9ZJ	FAD-CAT-CAU-CAQ
3	A	502	9ZJ	FAB-CAT-CAU-CAQ
5	E	503	CM5	C18-C13-O12-C1
5	E	503	CM5	O14-C13-O12-C1
5	B	503	CM5	C18-C13-O12-C1
5	B	503	CM5	O14-C13-O12-C1
3	F	503	9ZJ	FAC-CAT-CAU-CAG
3	F	503	9ZJ	FAD-CAT-CAU-CAG
3	F	503	9ZJ	FAB-CAT-CAU-CAG
3	F	503	9ZJ	FAC-CAT-CAU-OAN
3	F	503	9ZJ	FAD-CAT-CAU-OAN
3	F	503	9ZJ	FAB-CAT-CAU-OAN
3	F	503	9ZJ	FAC-CAT-CAU-CAQ
3	F	503	9ZJ	FAD-CAT-CAU-CAQ
3	F	503	9ZJ	FAB-CAT-CAU-CAQ
3	E	502	9ZJ	FAC-CAT-CAU-CAG
3	E	502	9ZJ	FAD-CAT-CAU-CAG
3	E	502	9ZJ	FAB-CAT-CAU-CAG
3	E	502	9ZJ	FAC-CAT-CAU-OAN
3	E	502	9ZJ	FAD-CAT-CAU-OAN
3	E	502	9ZJ	FAB-CAT-CAU-OAN
3	E	502	9ZJ	FAC-CAT-CAU-CAQ
3	E	502	9ZJ	FAD-CAT-CAU-CAQ
3	E	502	9ZJ	FAB-CAT-CAU-CAQ
5	C	503	CM5	C1-C2-C3-C4
5	D	503	CM5	C1-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
5	F	502	CM5	C1-C2-C3-C4
5	E	503	CM5	C1-C2-C3-C4
5	B	503	CM5	C1-C2-C3-C4
5	C	503	CM5	O25-C26-C30-O31
5	D	503	CM5	O25-C26-C30-O31
5	F	502	CM5	O25-C26-C30-O31
5	E	503	CM5	O25-C26-C30-O31
5	B	503	CM5	O25-C26-C30-O31
5	C	503	CM5	O14-C15-C19-O20
5	D	503	CM5	O14-C15-C19-O20
5	F	502	CM5	O14-C15-C19-O20
5	E	503	CM5	O14-C15-C19-O20
5	B	503	CM5	O14-C15-C19-O20
5	C	503	CM5	C27-C26-C30-O31
5	D	503	CM5	C27-C26-C30-O31
5	F	502	CM5	C27-C26-C30-O31
5	E	503	CM5	C27-C26-C30-O31
5	B	503	CM5	C27-C26-C30-O31
5	C	503	CM5	C15-C16-O23-C24
5	D	503	CM5	C15-C16-O23-C24
5	F	502	CM5	C15-C16-O23-C24
5	E	503	CM5	C15-C16-O23-C24
5	B	503	CM5	C15-C16-O23-C24
3	F	503	9ZJ	CAS-CAF-CAG-CAU
4	A	503	ZAZ	C6-C7-C8-C9
5	C	503	CM5	C17-C16-O23-C24
5	D	503	CM5	C17-C16-O23-C24
5	F	502	CM5	C17-C16-O23-C24
5	E	503	CM5	C17-C16-O23-C24
5	B	503	CM5	C17-C16-O23-C24
5	C	503	CM5	C2-C3-C4-C5
5	D	503	CM5	C2-C3-C4-C5
5	F	502	CM5	C2-C3-C4-C5
5	E	503	CM5	C2-C3-C4-C5
5	B	503	CM5	C2-C3-C4-C5
5	C	503	CM5	C3-C4-C5-C6
5	D	503	CM5	C3-C4-C5-C6
5	F	502	CM5	C3-C4-C5-C6
5	E	503	CM5	C3-C4-C5-C6
5	B	503	CM5	C3-C4-C5-C6
3	E	502	9ZJ	CAS-CAF-CAG-CAU
5	C	503	CM5	C4-C5-C6-C7

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Mol	Chain	Res	Type	Atoms
5	D	503	CM5	C4-C5-C6-C7
5	F	502	CM5	C4-C5-C6-C7
5	E	503	CM5	C4-C5-C6-C7
5	B	503	CM5	C4-C5-C6-C7
5	C	503	CM5	C4-C5-C6-C11
5	D	503	CM5	C4-C5-C6-C11
5	F	502	CM5	C4-C5-C6-C11
5	E	503	CM5	C4-C5-C6-C11
5	B	503	CM5	C4-C5-C6-C11
5	C	503	CM5	C2-C1-O12-C13
5	D	503	CM5	C2-C1-O12-C13
5	F	502	CM5	C2-C1-O12-C13
5	E	503	CM5	C2-C1-O12-C13
5	B	503	CM5	C2-C1-O12-C13
3	C	502	9ZJ	CAS-CAF-CAG-CAU
3	A	502	9ZJ	CAS-CAF-CAG-CAU
5	C	503	CM5	C16-C15-C19-O20
5	D	503	CM5	C16-C15-C19-O20
5	F	502	CM5	C16-C15-C19-O20
5	E	503	CM5	C16-C15-C19-O20
5	B	503	CM5	C16-C15-C19-O20

There are no ring outliers.

17 monomers are involved in 188 short contacts:

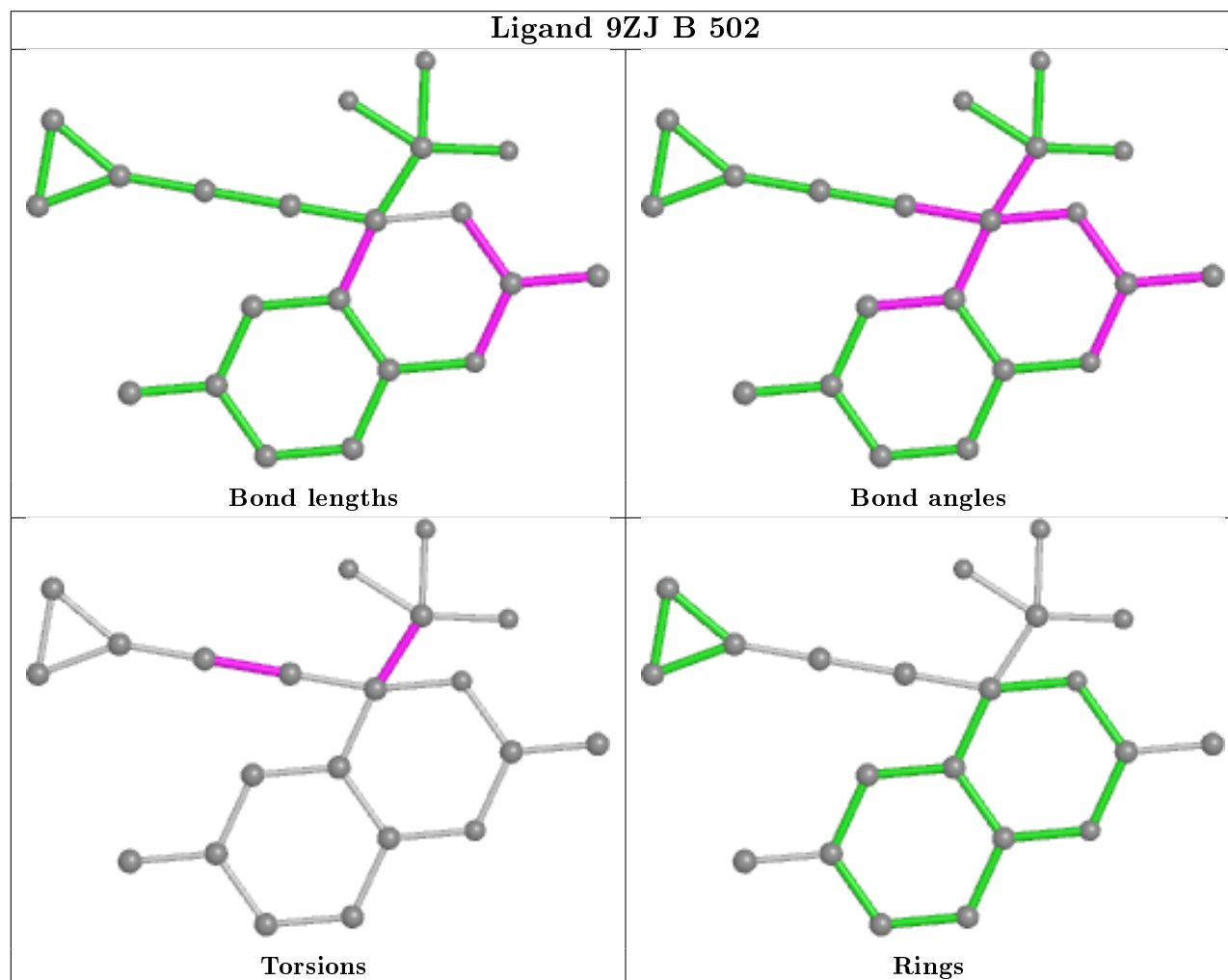
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	502	9ZJ	8	0
3	C	502	9ZJ	7	0
3	D	502	9ZJ	6	0
2	F	501	HEM	1	0
5	C	503	CM5	20	0
2	B	501	HEM	4	0
5	F	502	CM5	24	0
2	A	501	HEM	5	0
5	E	503	CM5	18	0
3	F	503	9ZJ	10	0
5	D	503	CM5	13	0
5	B	503	CM5	7	0
2	D	501	HEM	22	0
3	E	502	9ZJ	7	0
2	E	501	HEM	15	0
3	A	502	9ZJ	10	0

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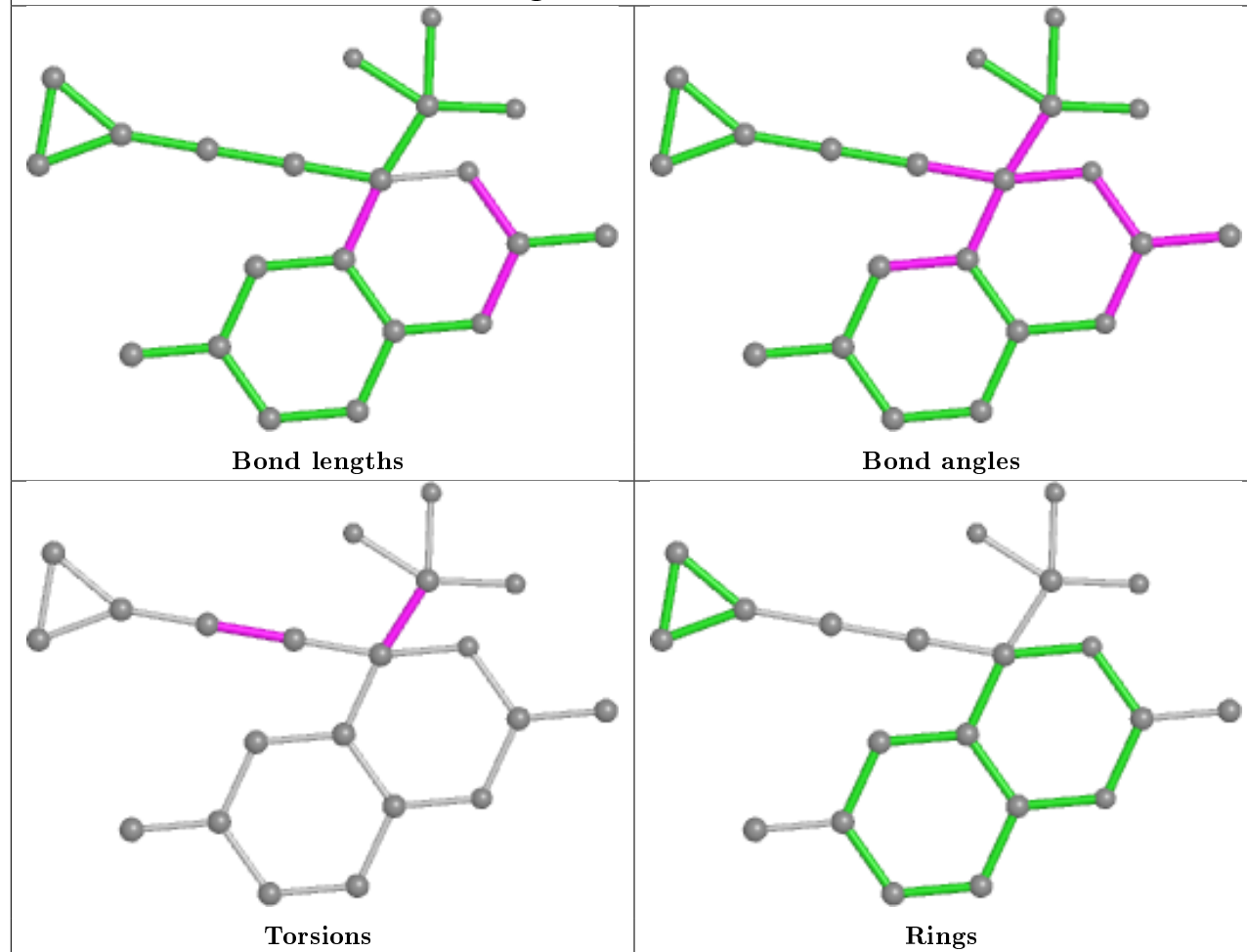
*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	HEM	11	0

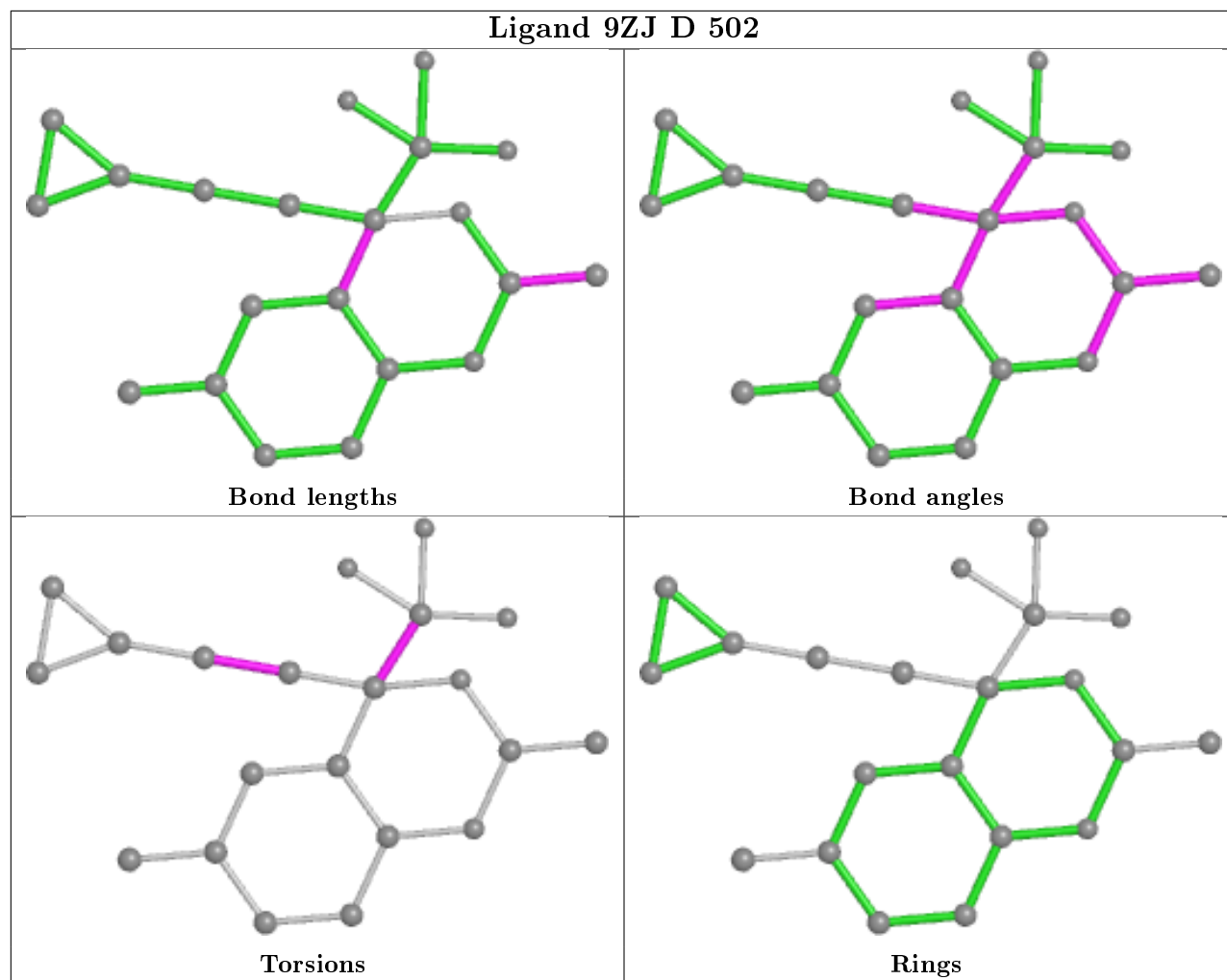
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

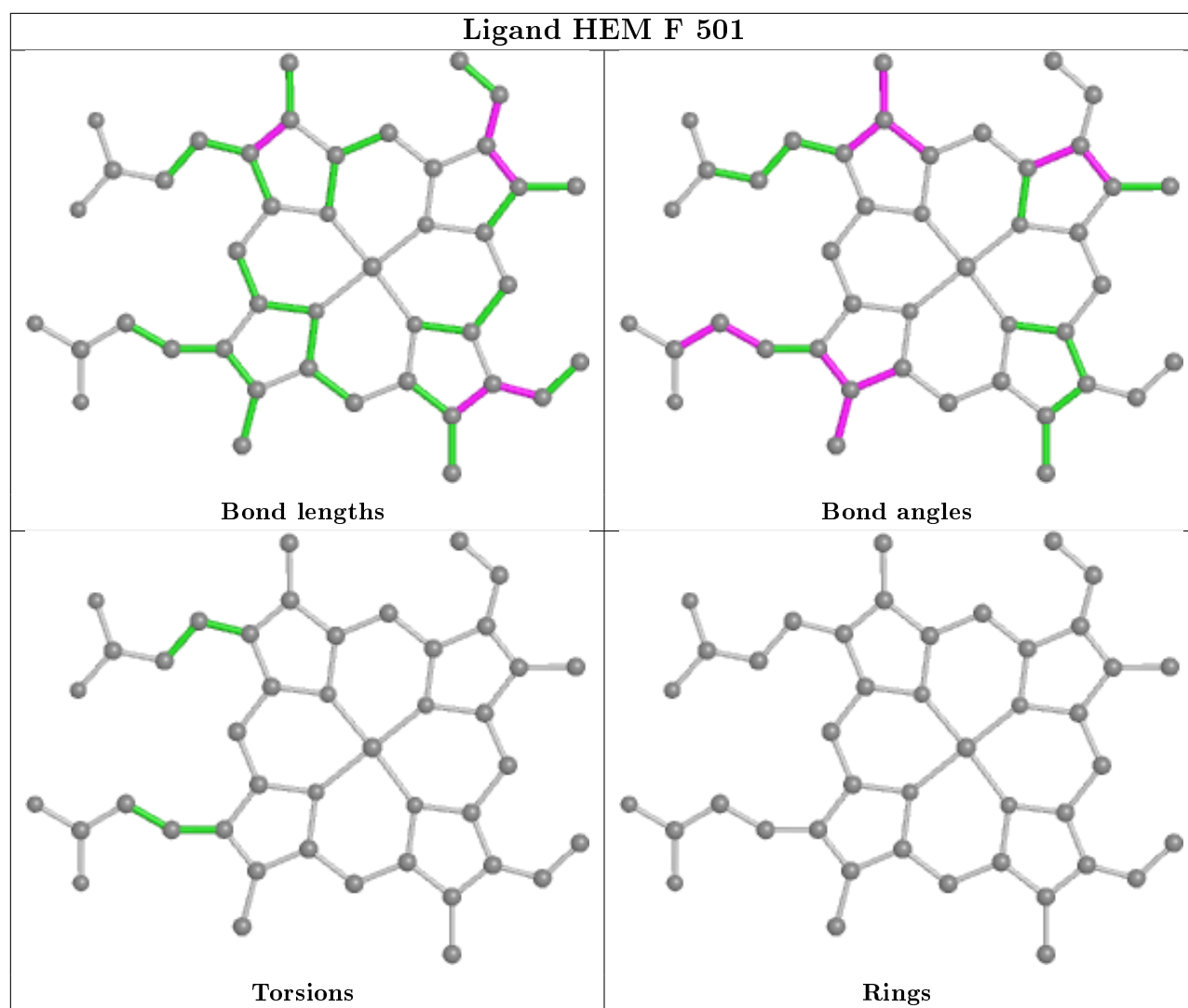


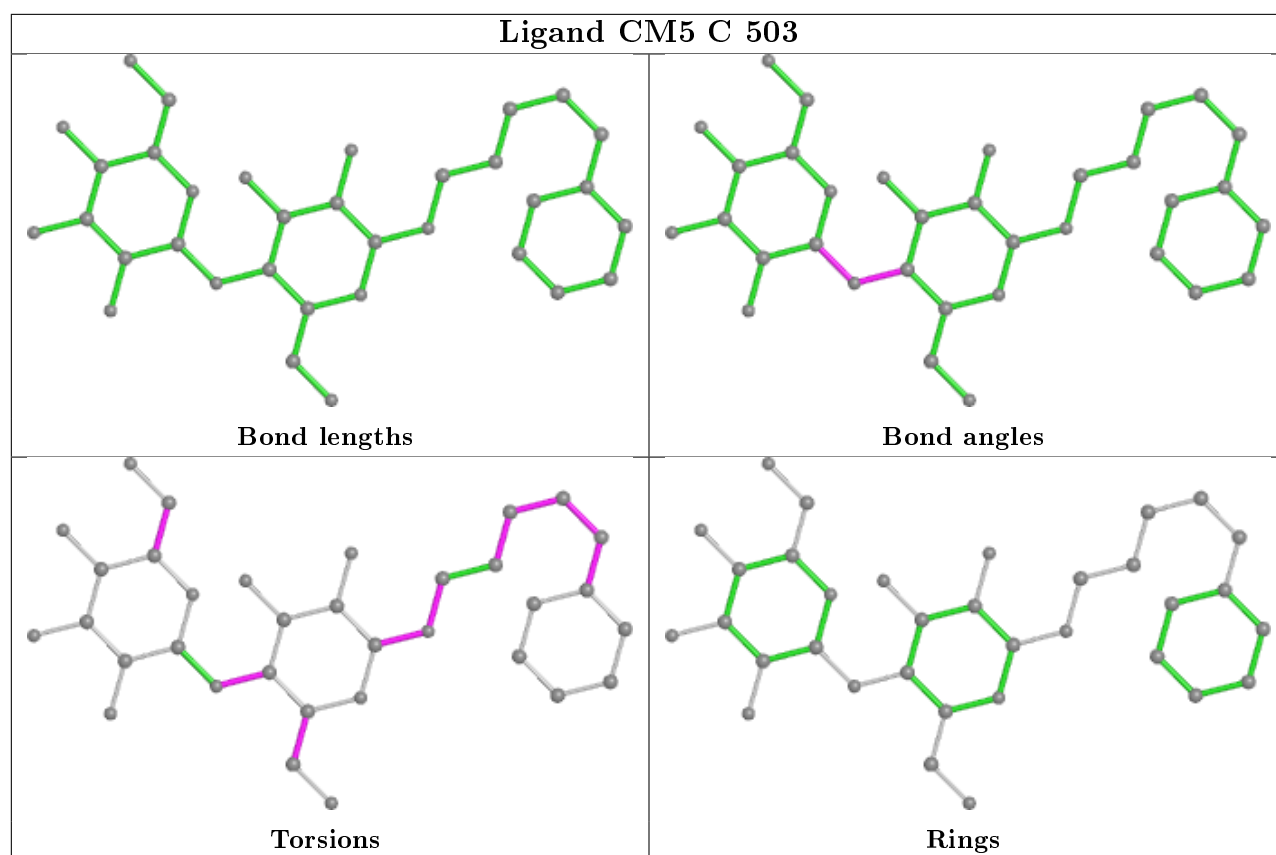
## Ligand 9ZJ C 502

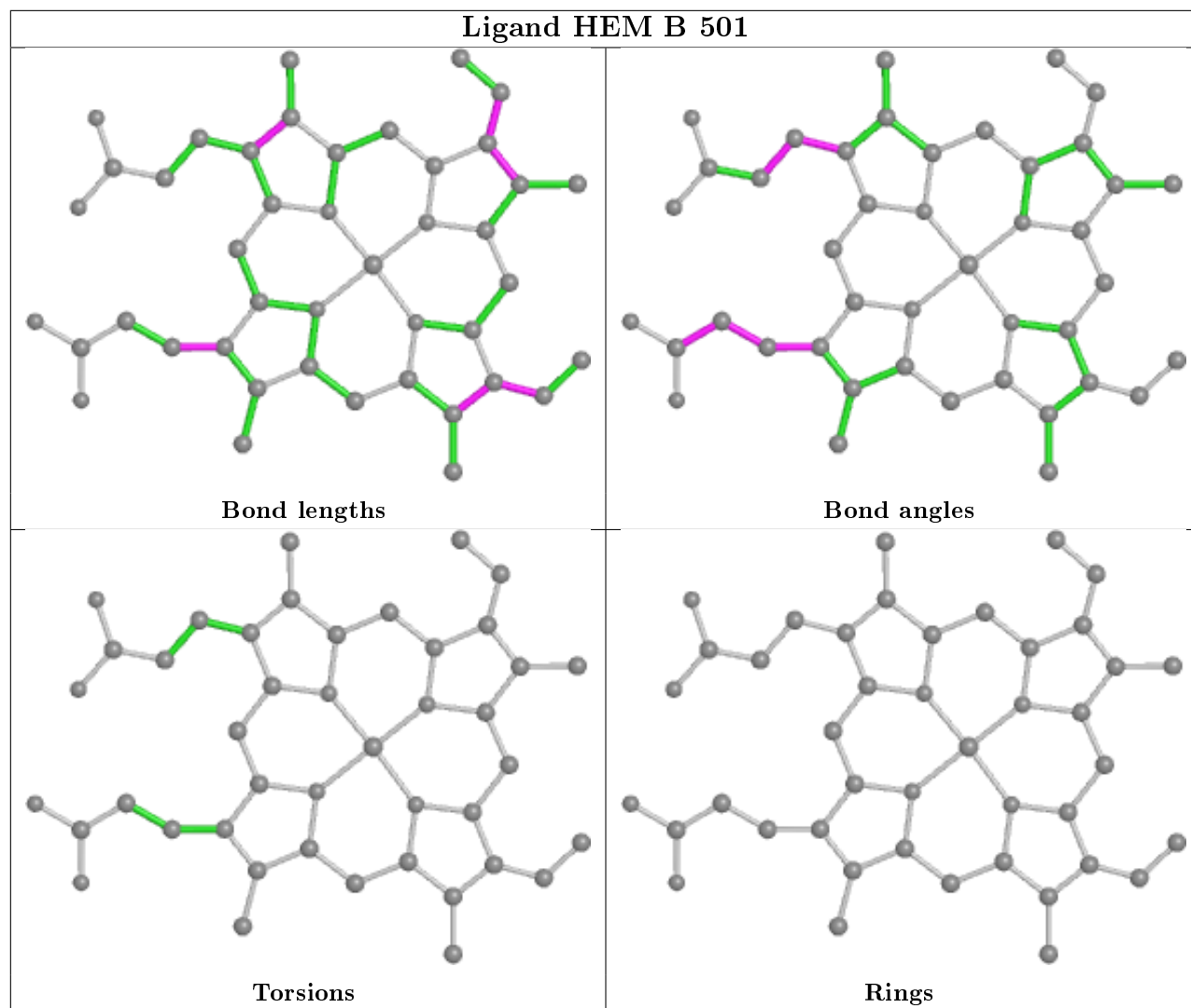


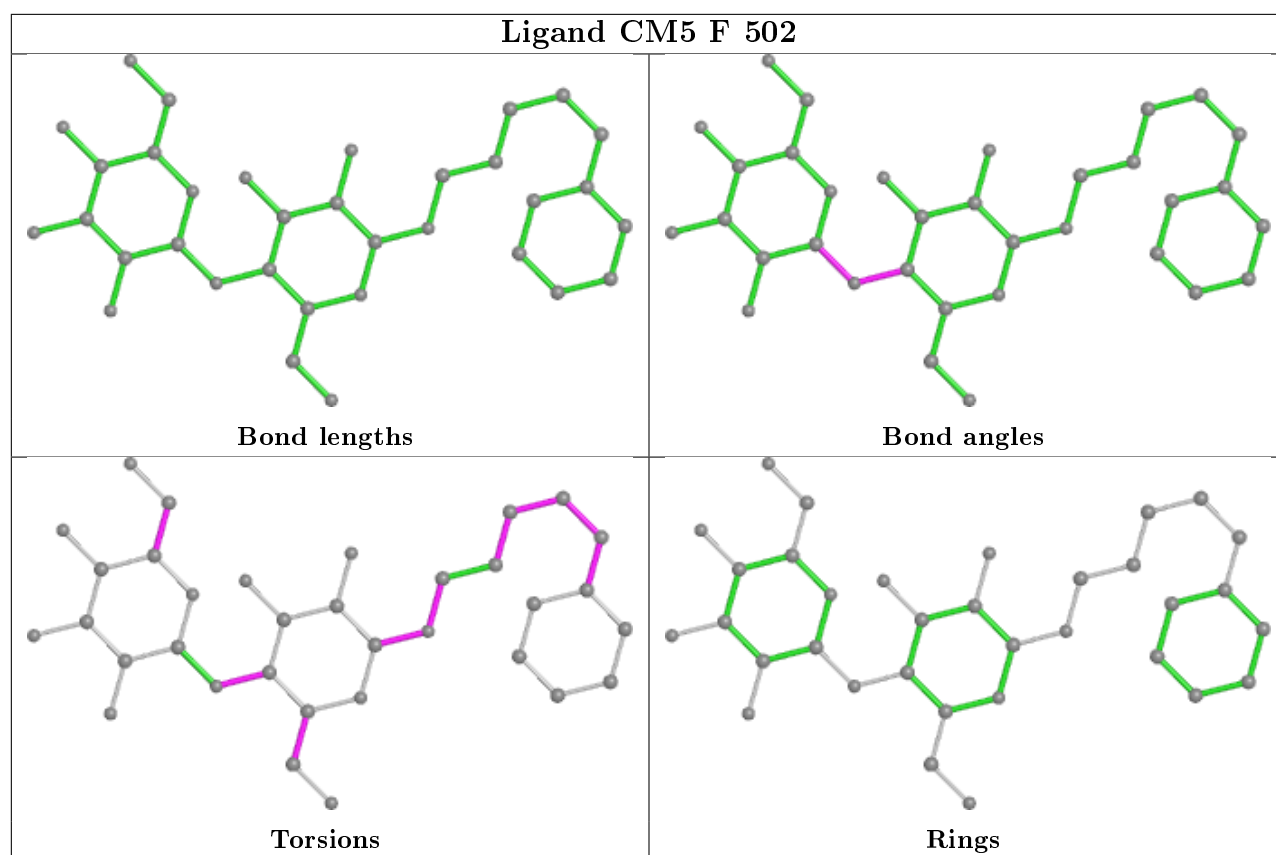
## Ligand 9ZJ D 502

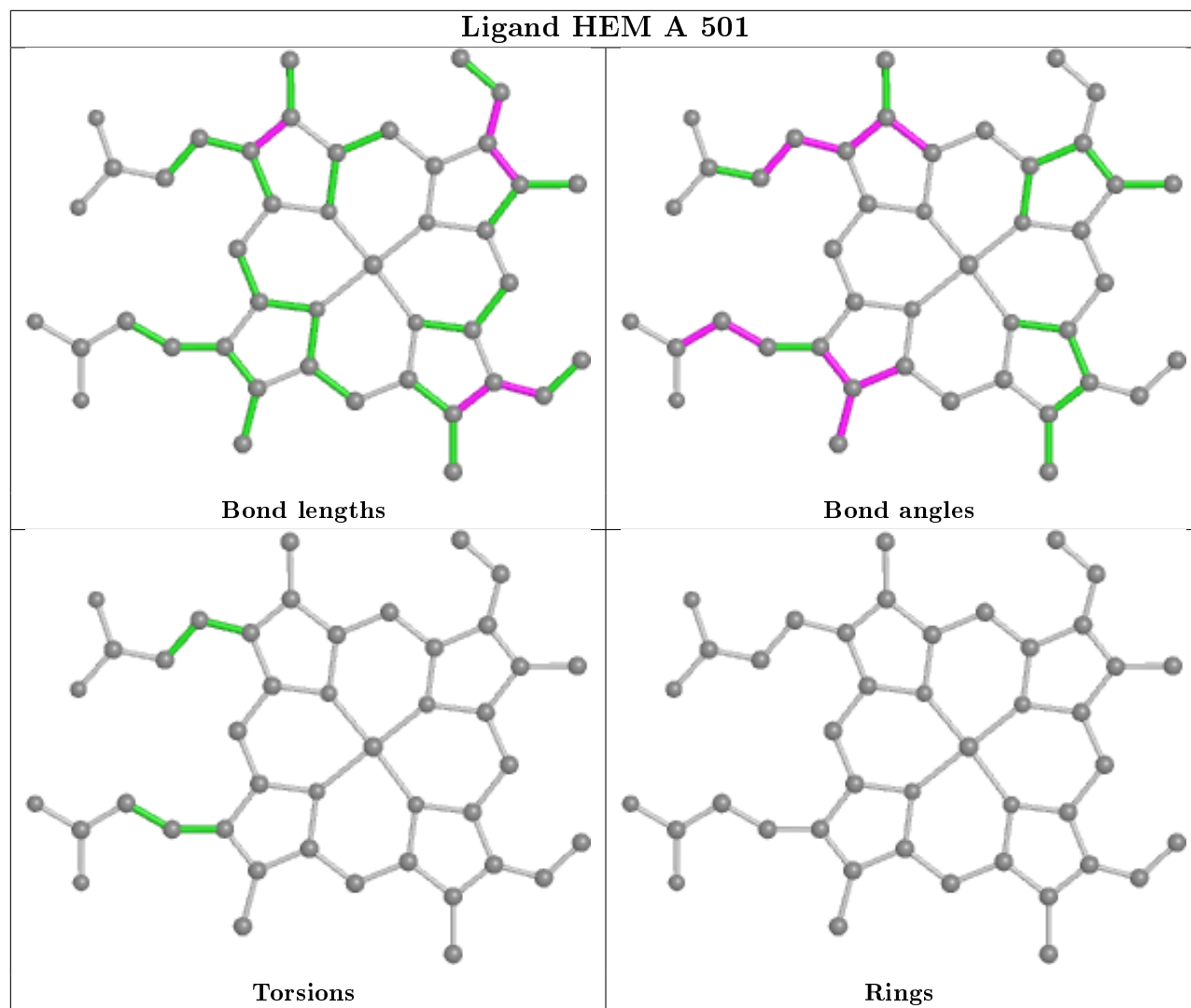


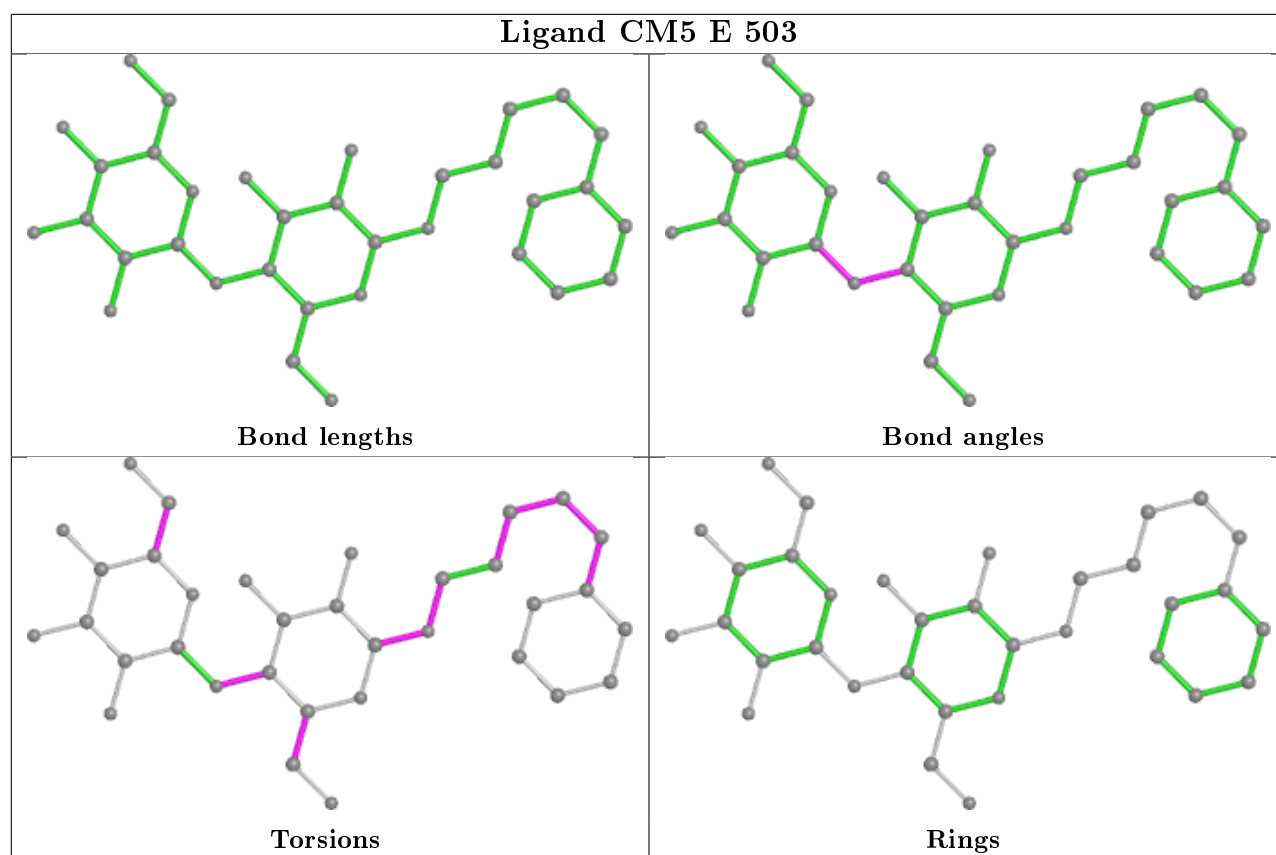




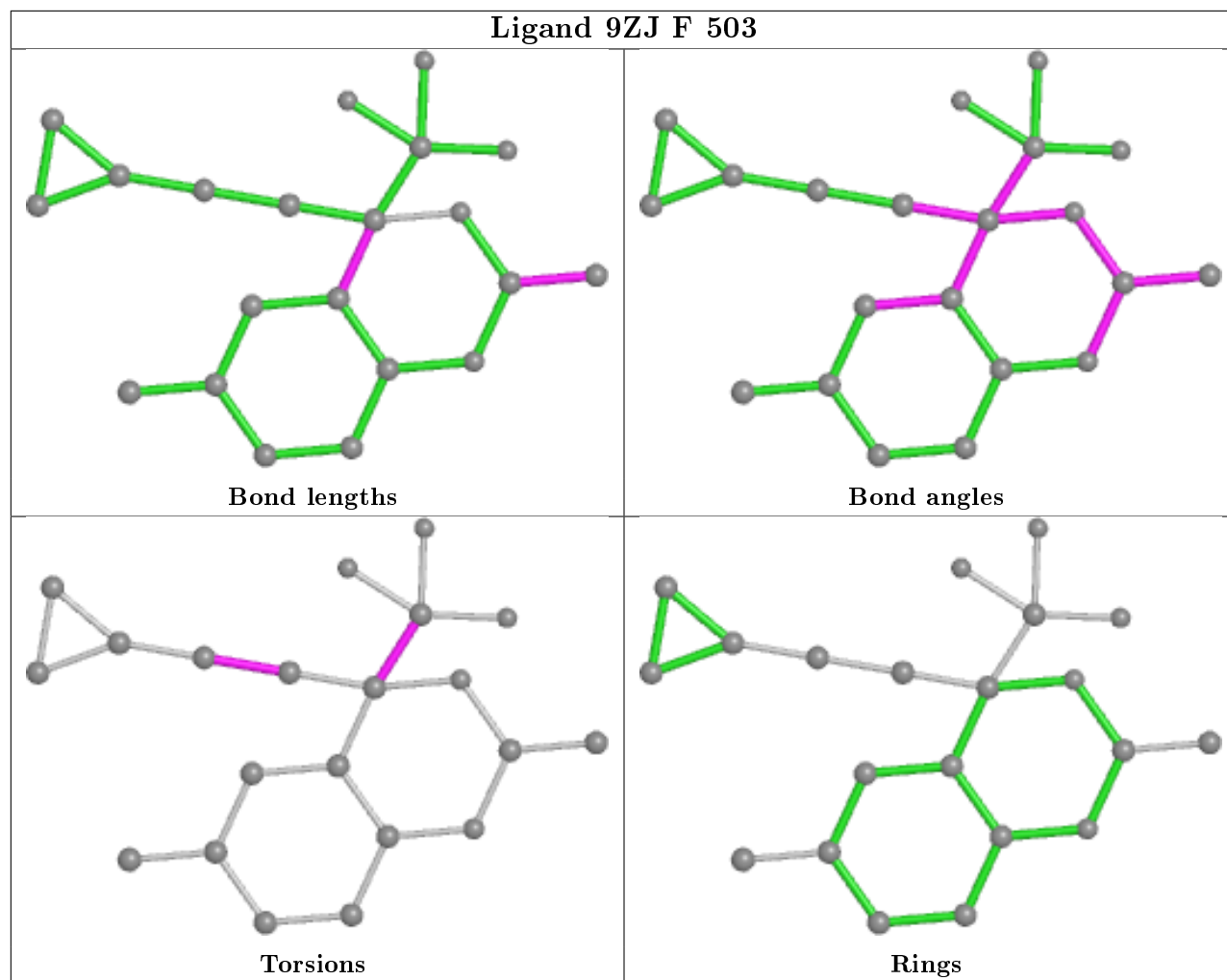


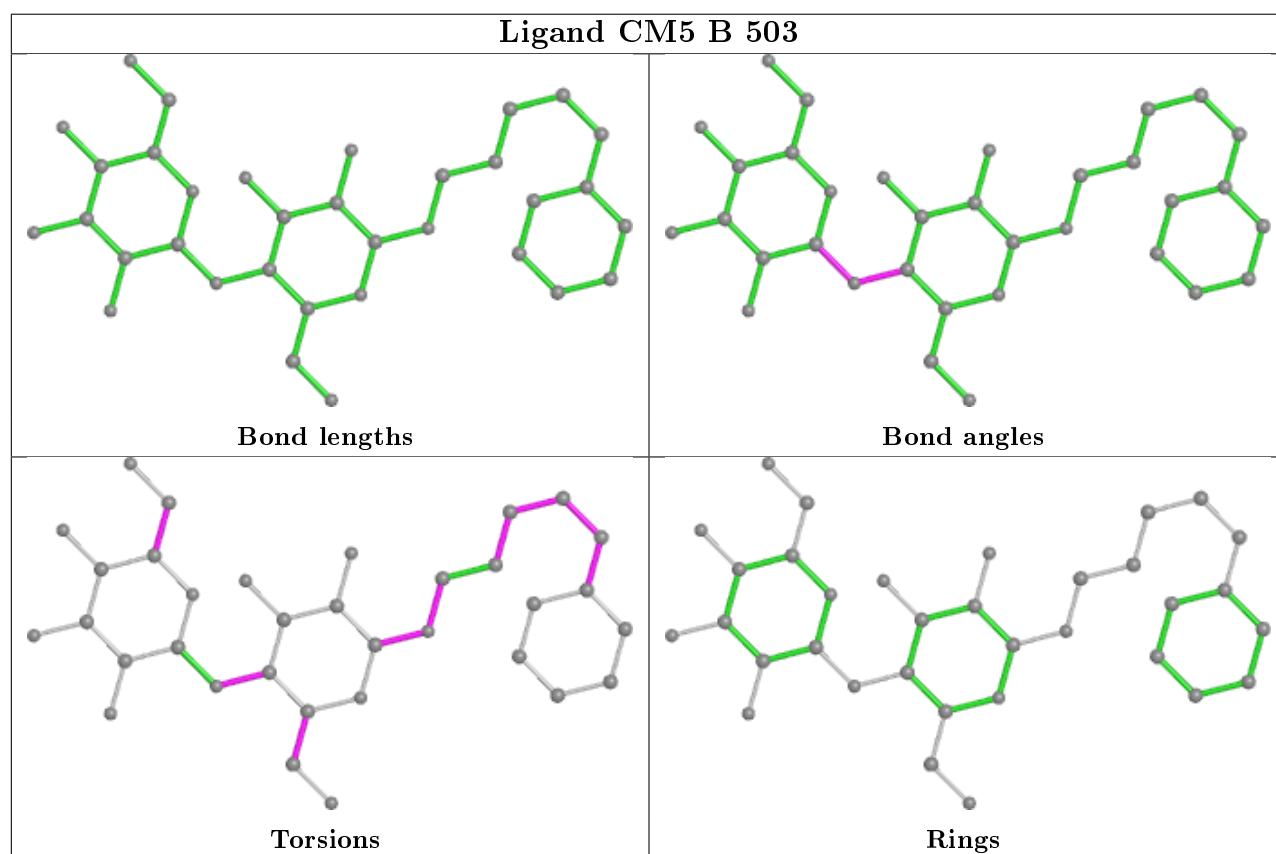
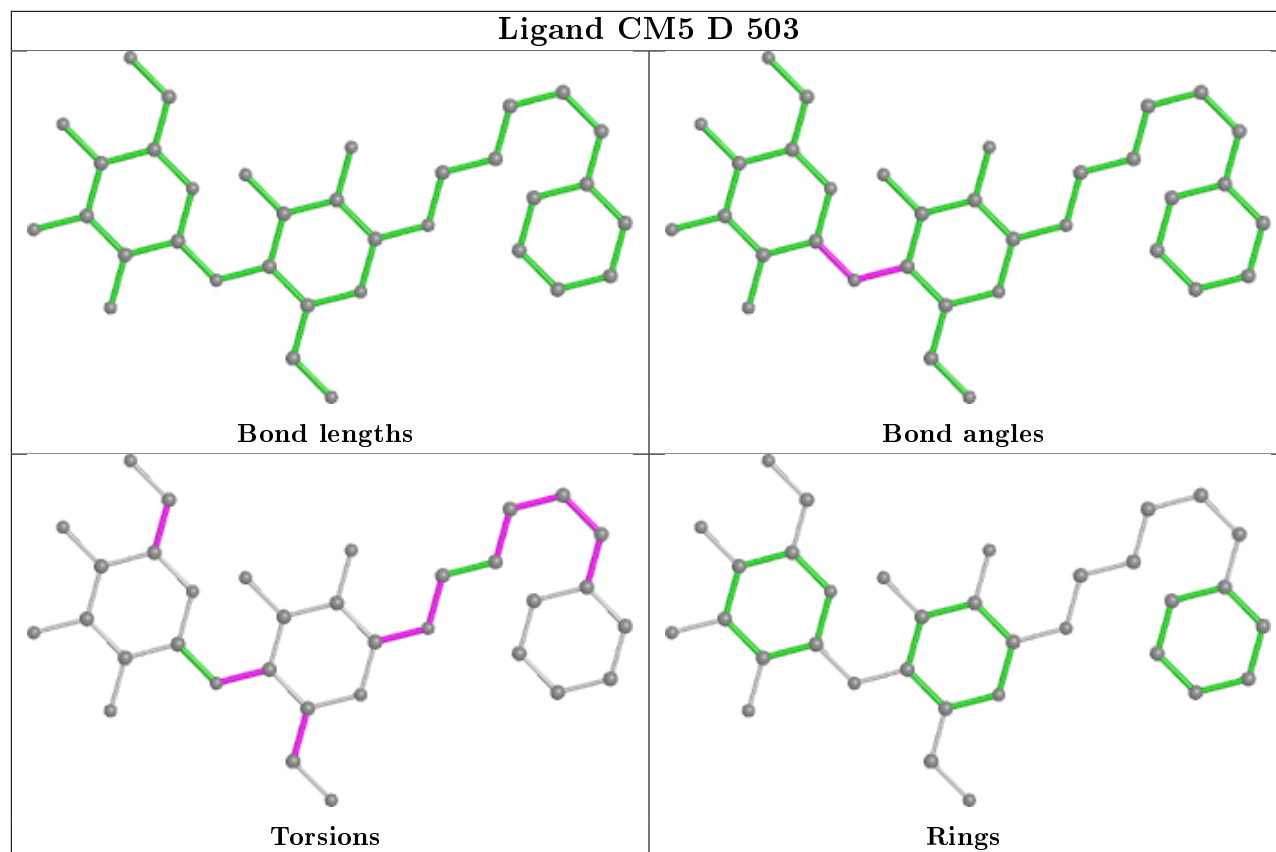


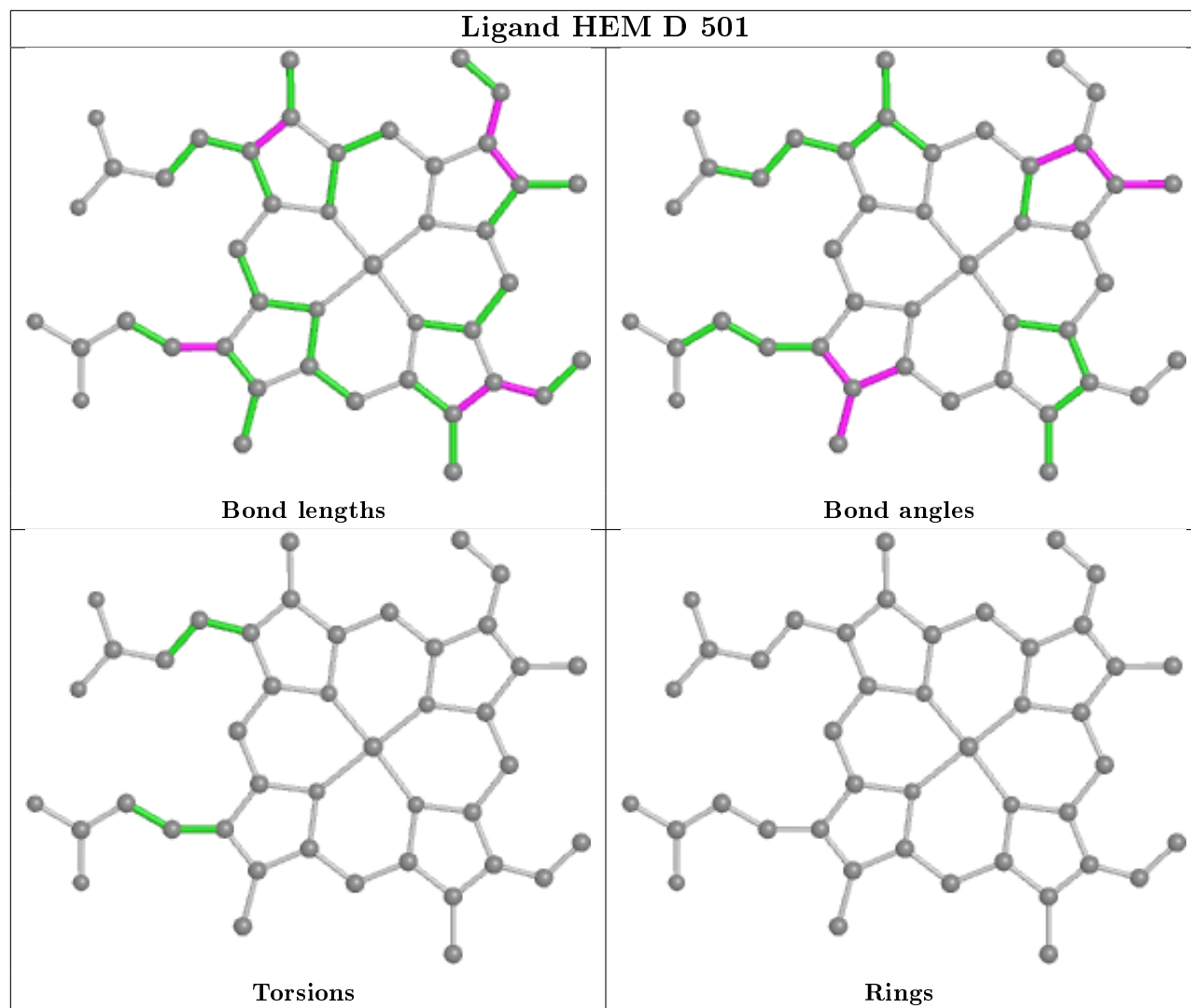




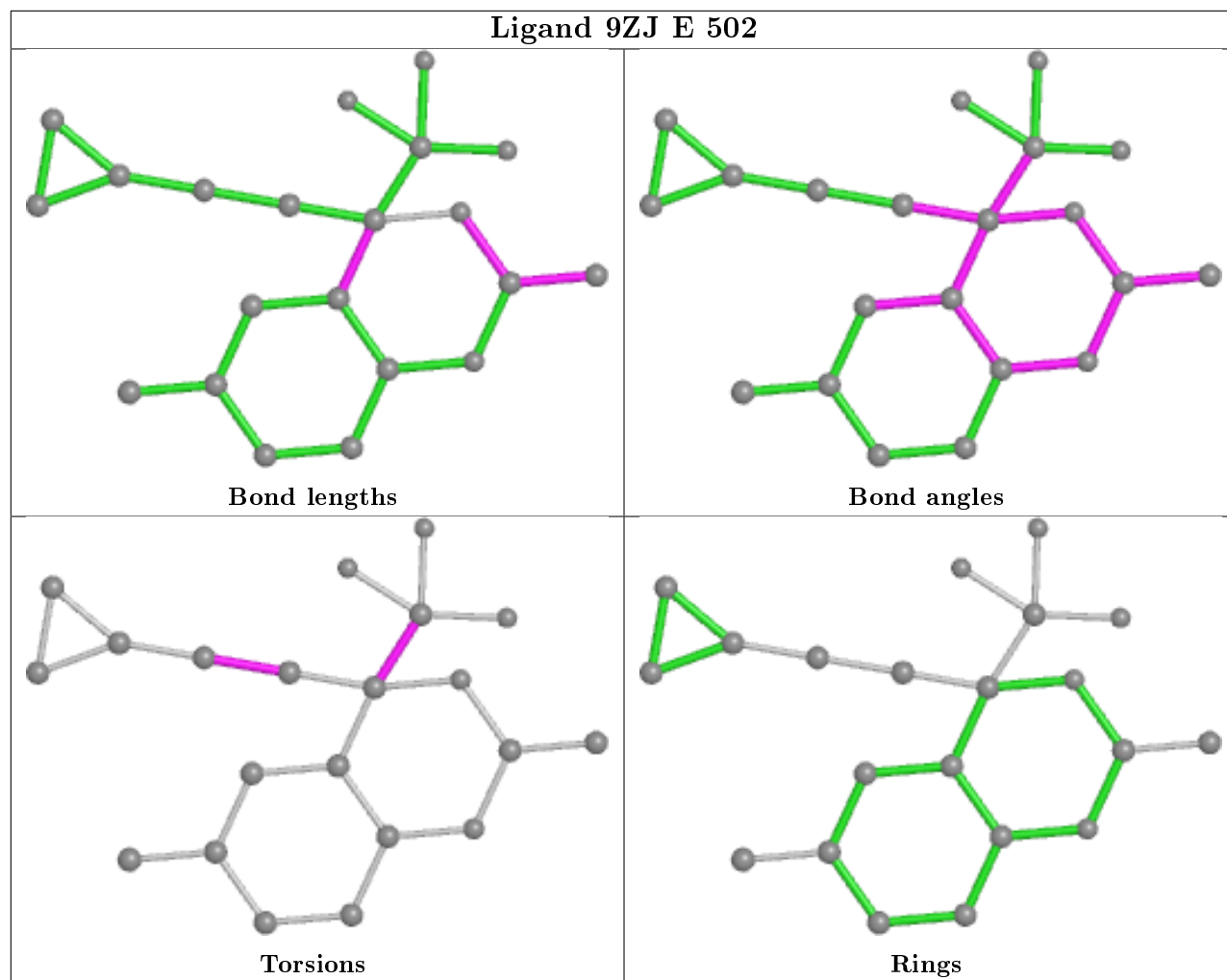
## Ligand 9ZJ F 503

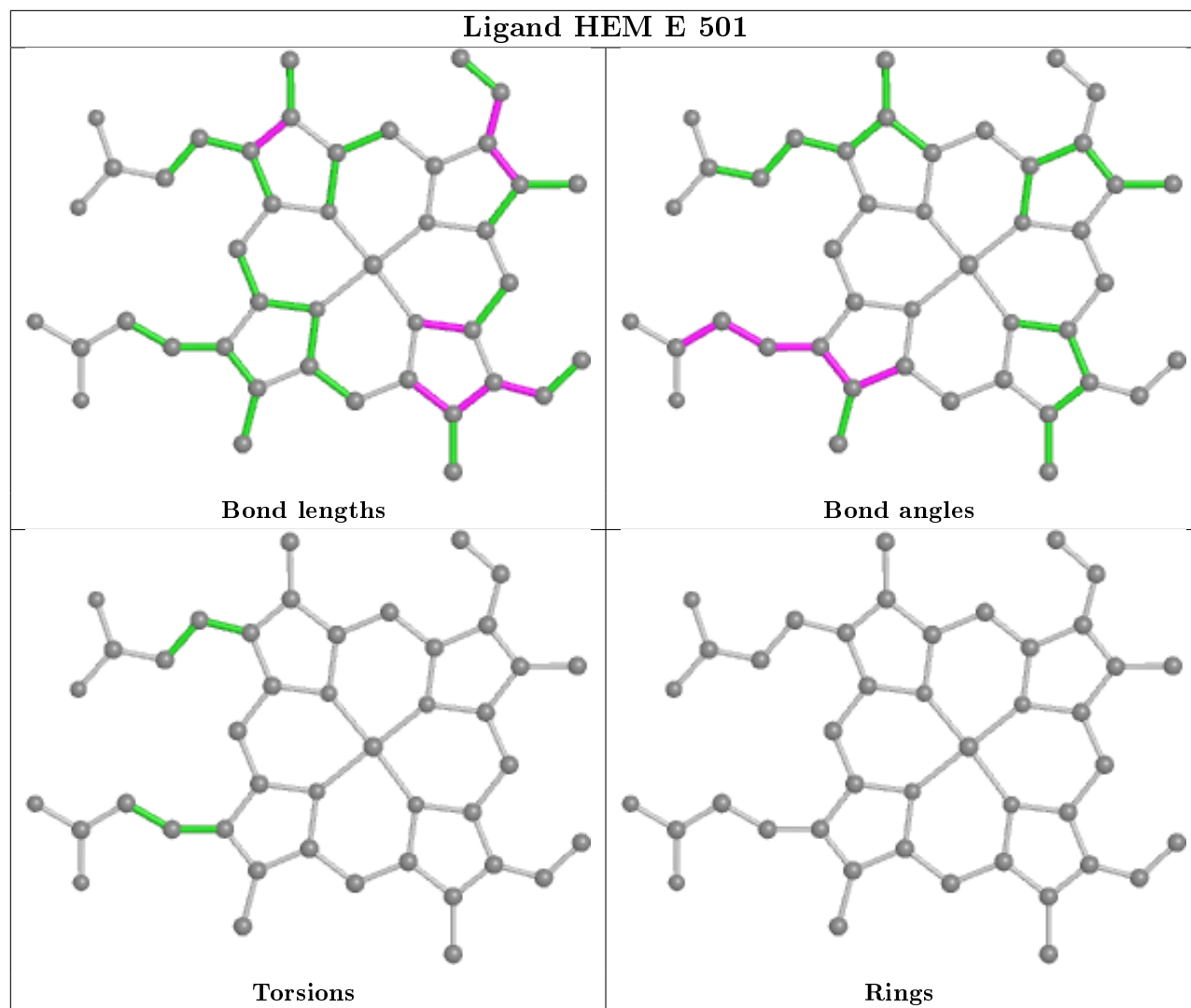




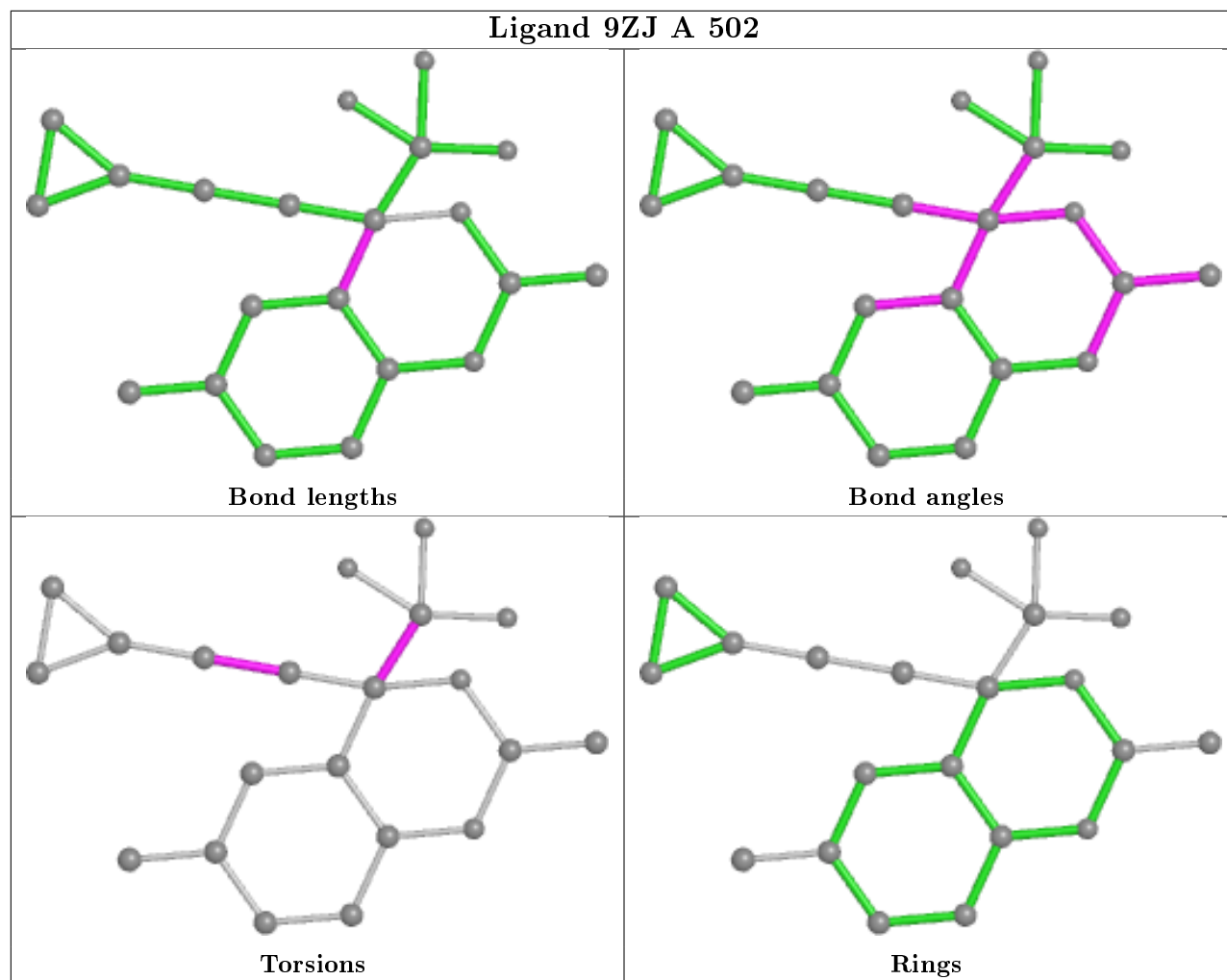


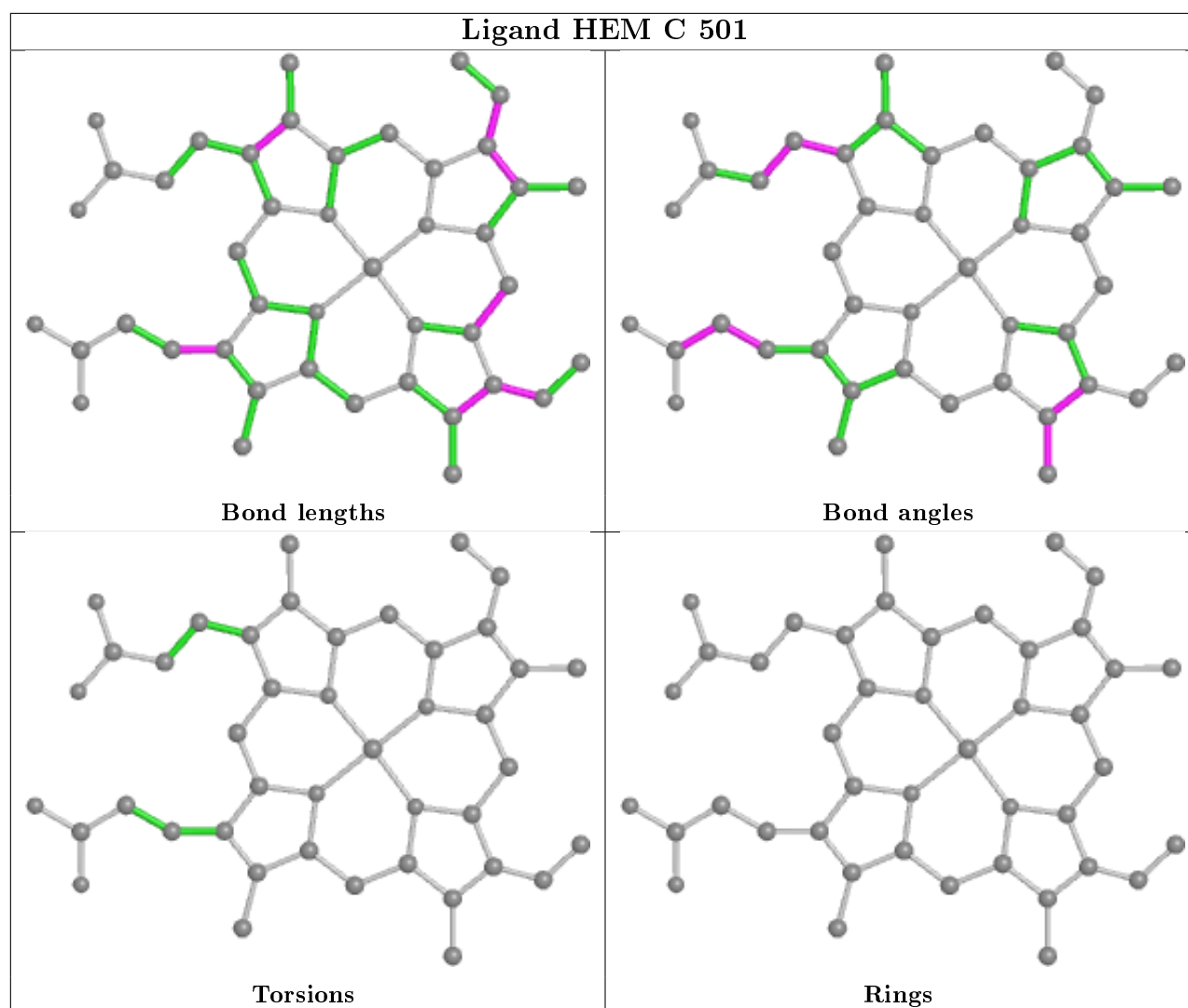
## Ligand 9ZJ E 502





## Ligand 9ZJ A 502





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	463/476 (97%)	-0.04	11 (2%) 59 30	18, 45, 71, 106	0
1	B	464/476 (97%)	-0.10	5 (1%) 80 56	17, 41, 66, 93	0
1	C	464/476 (97%)	0.03	10 (2%) 62 33	24, 48, 72, 98	0
1	D	464/476 (97%)	0.03	14 (3%) 50 22	26, 49, 73, 115	0
1	E	463/476 (97%)	-0.05	13 (2%) 53 25	22, 46, 72, 108	0
1	F	464/476 (97%)	0.17	20 (4%) 35 13	27, 56, 84, 114	0
All	All	2782/2856 (97%)	0.01	73 (2%) 56 27	17, 47, 77, 115	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	335	HIS	5.0
1	D	335	HIS	4.6
1	D	140	ARG	4.5
1	A	335	HIS	4.3
1	A	417	ASN	4.1
1	C	163	ALA	4.0
1	A	416	ALA	3.7
1	F	277	SER	3.6
1	E	138	GLY	3.5
1	F	489	LEU	3.3
1	A	137	MET	3.3
1	F	335	HIS	3.3
1	E	139	LYS	3.3
1	A	419	ALA	3.2
1	C	417	ASN	3.2
1	F	461	SER	3.1
1	F	462	PRO	3.1
1	A	136	GLY	3.1
1	F	163	ALA	3.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	E	136	GLY	3.0
1	D	138	GLY	2.9
1	F	416	ALA	2.9
1	F	136	GLY	2.9
1	F	460	ALA	2.9
1	E	260	ALA	2.9
1	D	193	GLN	2.8
1	E	400	HIS	2.8
1	D	416	ALA	2.8
1	E	330	GLN	2.7
1	F	280	HIS	2.7
1	C	255	THR	2.7
1	E	137	MET	2.7
1	D	136	GLY	2.7
1	E	329	GLU	2.6
1	A	330	GLN	2.6
1	F	487	ARG	2.6
1	E	140	ARG	2.6
1	D	333	GLY	2.6
1	B	140	ARG	2.6
1	E	277	SER	2.6
1	F	463	VAL	2.6
1	B	254	GLU	2.6
1	F	260	ALA	2.6
1	C	133	ARG	2.5
1	E	132	MET	2.5
1	D	139	LYS	2.5
1	F	255	THR	2.5
1	B	137	MET	2.5
1	F	257	ASP	2.5
1	A	329	GLU	2.4
1	A	331	VAL	2.4
1	D	417	ASN	2.4
1	D	415	ASP	2.4
1	C	134	ASP	2.4
1	E	259	SER	2.3
1	C	132	MET	2.3
1	C	254	GLU	2.3
1	B	255	THR	2.3
1	F	485	GLN	2.3
1	D	277	SER	2.3
1	C	416	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	401	TYR	2.2
1	F	134	ASP	2.2
1	F	304	SER	2.2
1	C	140	ARG	2.1
1	A	260	ALA	2.1
1	F	302	THR	2.1
1	D	334	PRO	2.1
1	A	256	LEU	2.1
1	C	335	HIS	2.1
1	F	415	ASP	2.1
1	B	416	ALA	2.0
1	D	260	ALA	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	CM5	F	502	34/34	0.47	0.53	60,134,145,147	0
5	CM5	D	503	34/34	0.58	0.35	55,121,146,146	0
5	CM5	C	503	34/34	0.65	0.60	87,133,152,157	0
5	CM5	E	503	34/34	0.66	0.39	53,128,136,140	0
5	CM5	B	503	34/34	0.69	0.46	70,142,149,150	0
3	9ZJ	D	502	21/21	0.75	0.44	79,97,110,127	0
4	ZAZ	A	503	12/12	0.77	0.78	62,69,82,83	0
3	9ZJ	C	502	21/21	0.79	0.41	73,87,94,99	0
3	9ZJ	F	503	21/21	0.81	0.42	71,86,95,98	0
3	9ZJ	E	502	21/21	0.84	0.38	75,95,114,116	0
3	9ZJ	B	502	21/21	0.85	0.40	94,103,109,116	0

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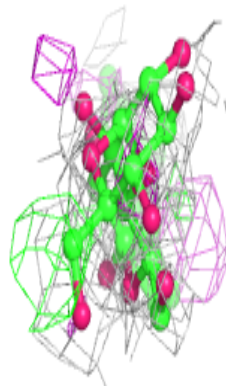
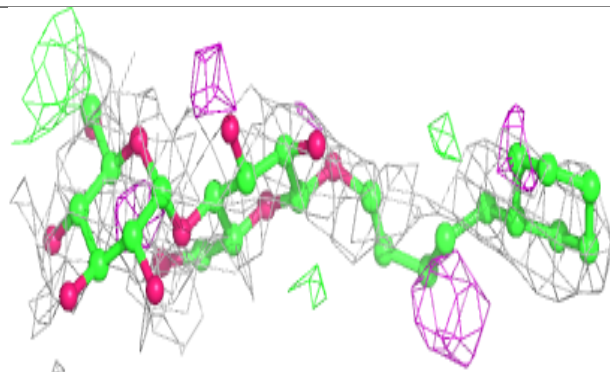
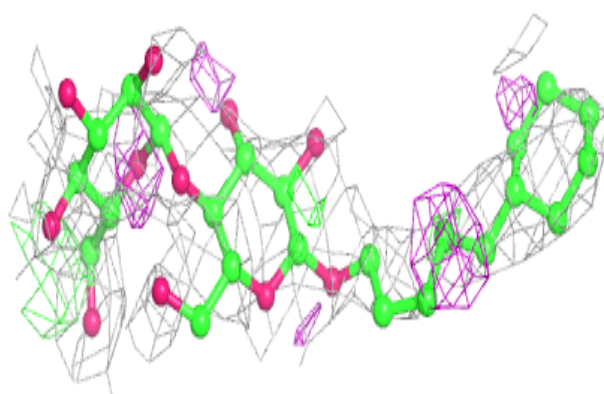
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	9ZJ	A	502	21/21	0.86	0.40	89,105,121,129	0
2	HEM	F	501	43/43	0.98	0.20	24,46,52,57	0
2	HEM	D	501	43/43	0.98	0.22	22,46,55,61	0
2	HEM	B	501	43/43	0.98	0.19	24,34,42,53	0
2	HEM	A	501	43/43	0.98	0.21	25,45,58,64	0
2	HEM	E	501	43/43	0.98	0.19	22,38,47,51	0
2	HEM	C	501	43/43	0.98	0.20	14,38,46,49	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.

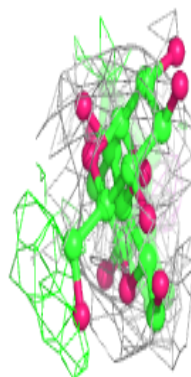
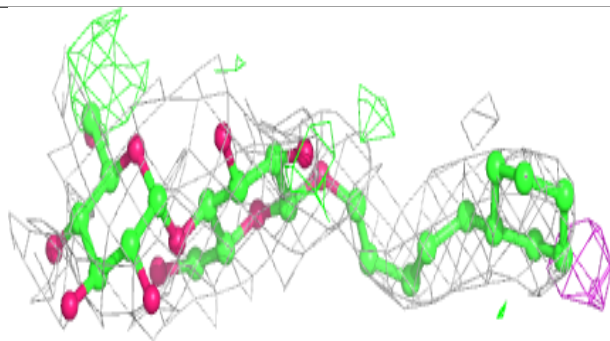
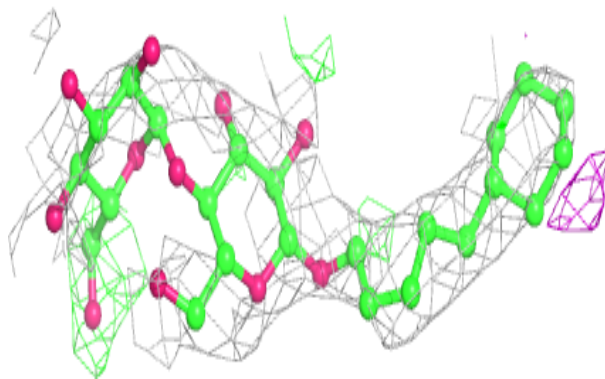
**Electron density around CM5 F 502:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

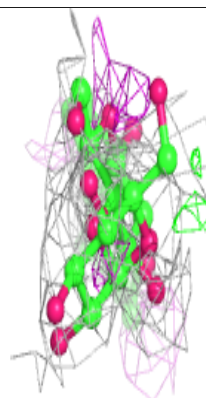
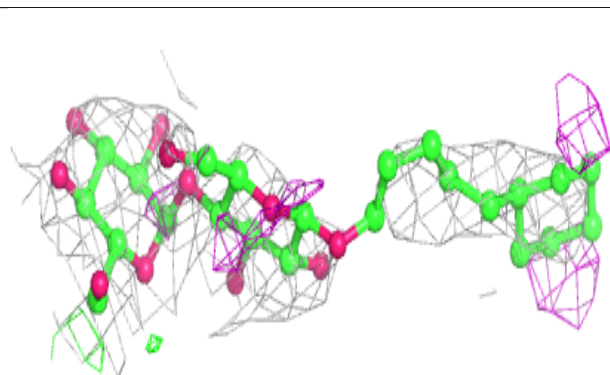
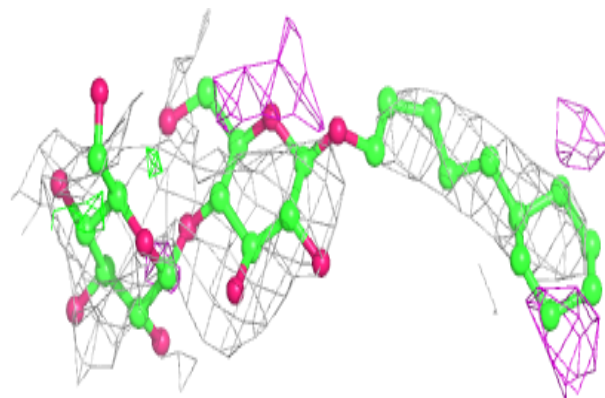


**Electron density around CM5 D 503:**

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

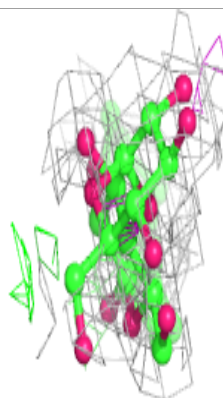
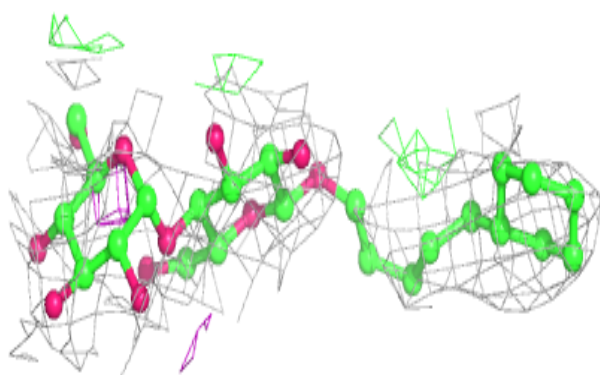
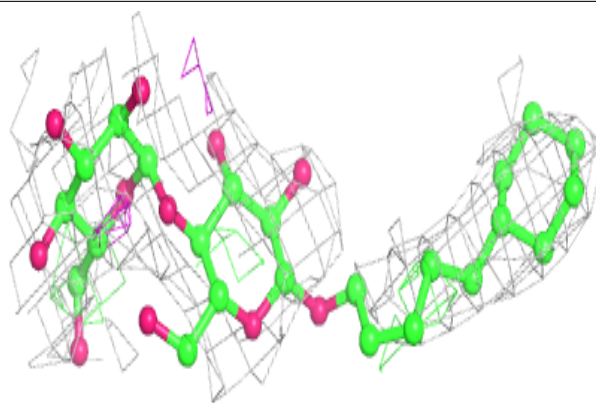
**Electron density around CM5 C 503:**

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and green (positive)

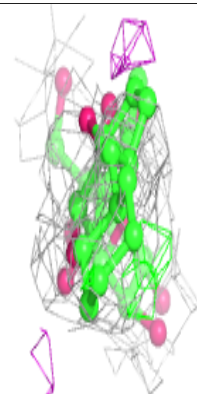
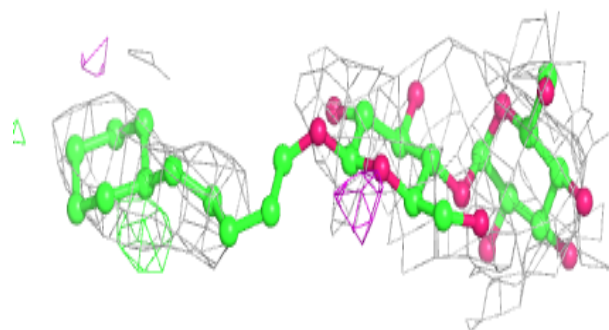
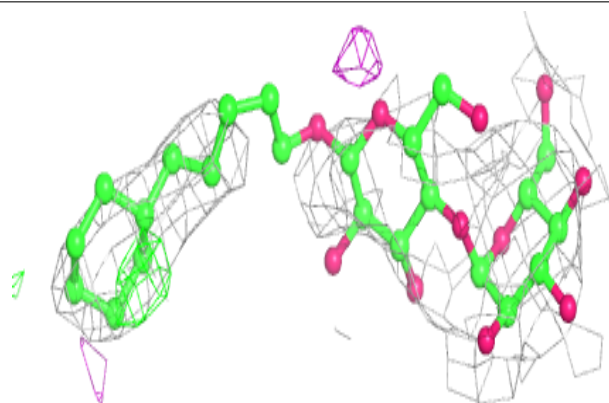


**Electron density around CM5 E 503:**

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and green (positive)

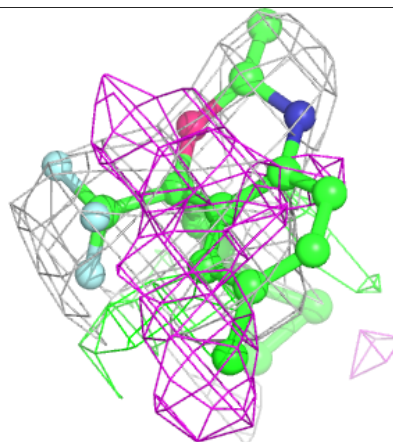
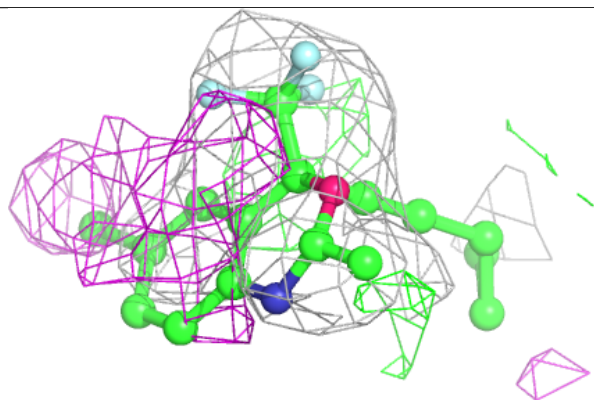
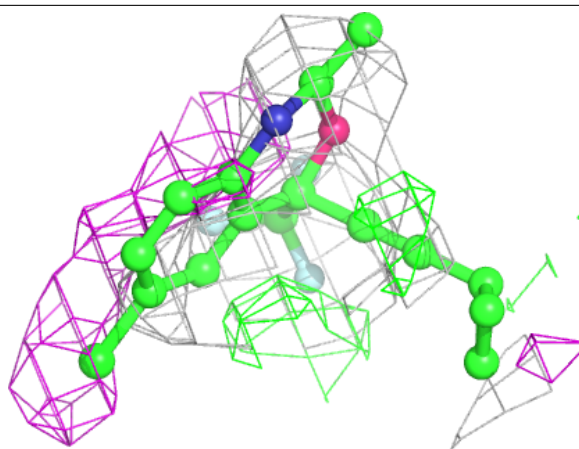
**Electron density around CM5 B 503:**

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and green (positive)



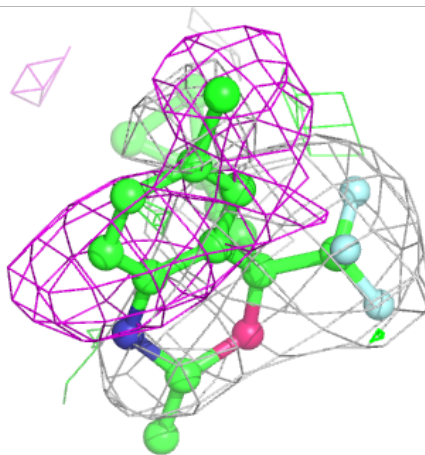
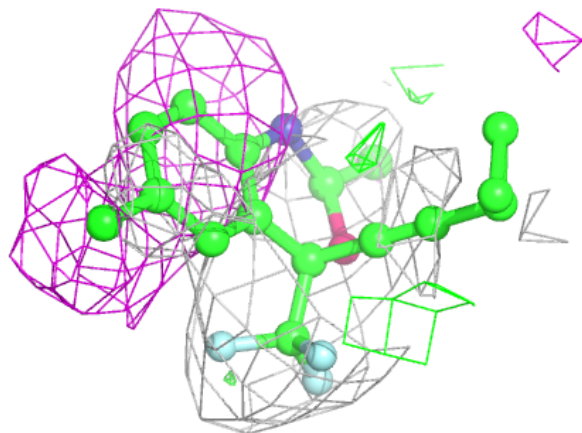
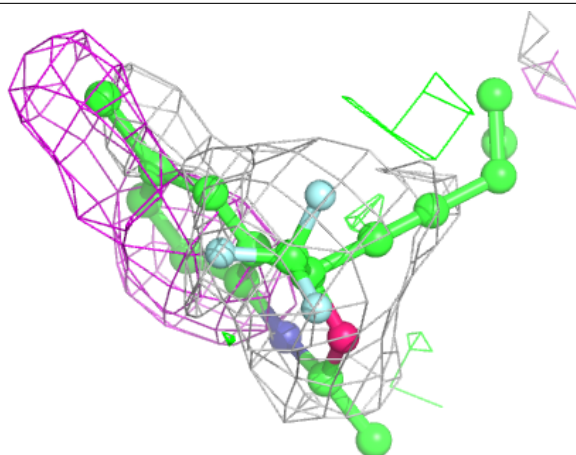
**Electron density around 9ZJ D 502:**

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



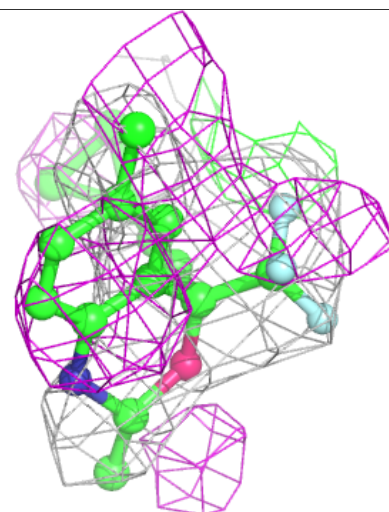
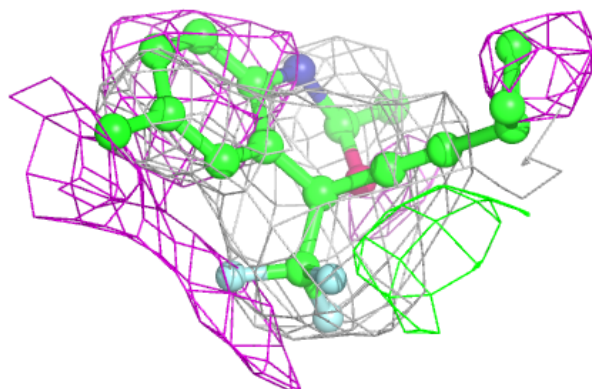
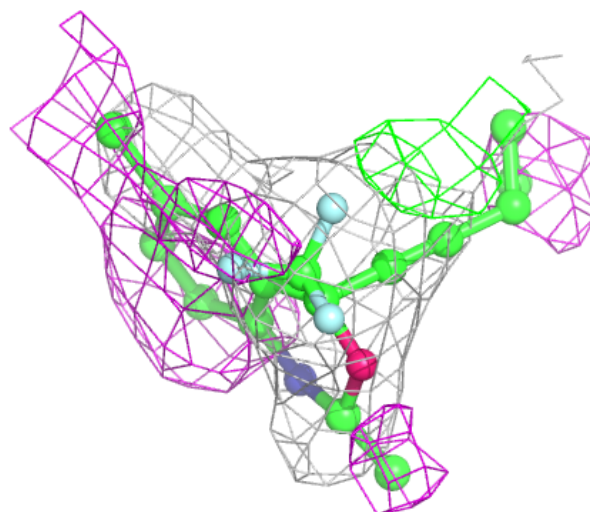
**Electron density around 9ZJ C 502:**

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mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



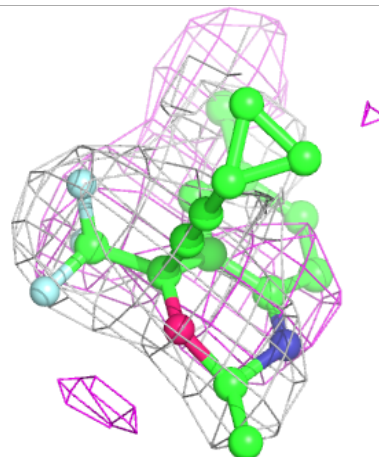
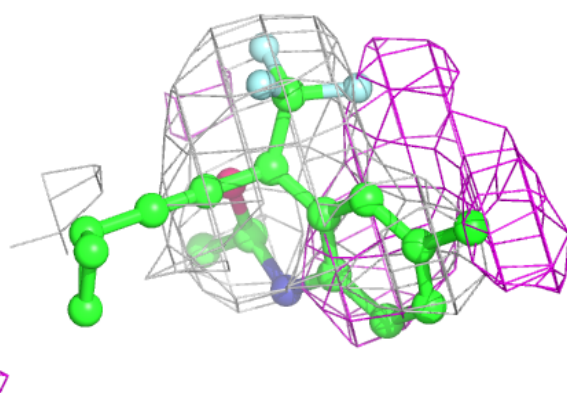
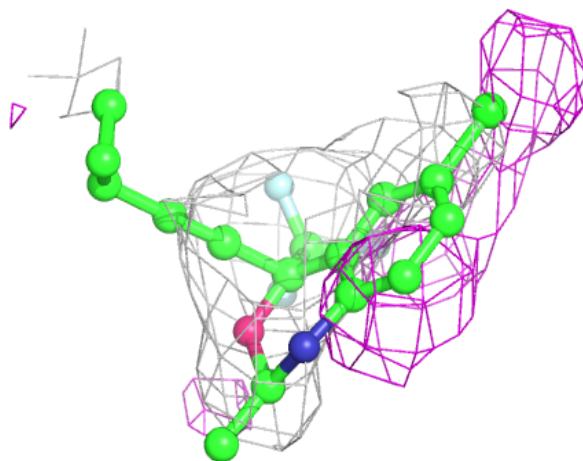
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and green (positive)



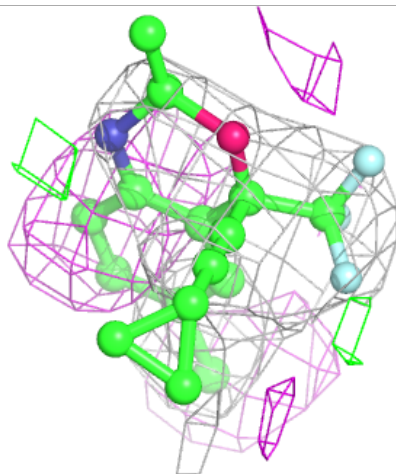
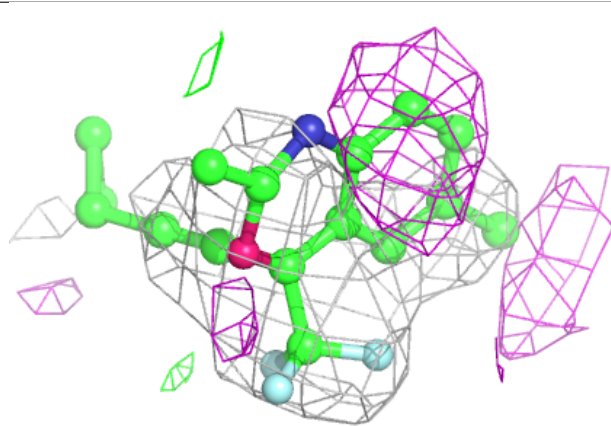
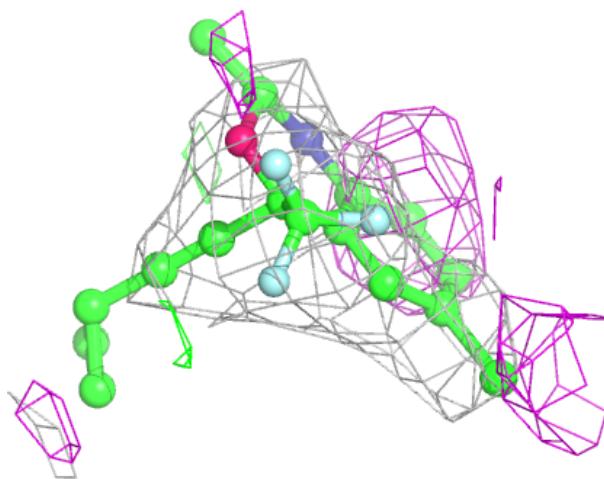
**Electron density around 9ZJ E 502:**

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



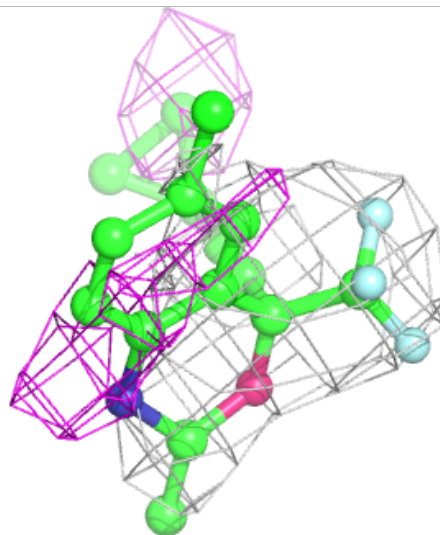
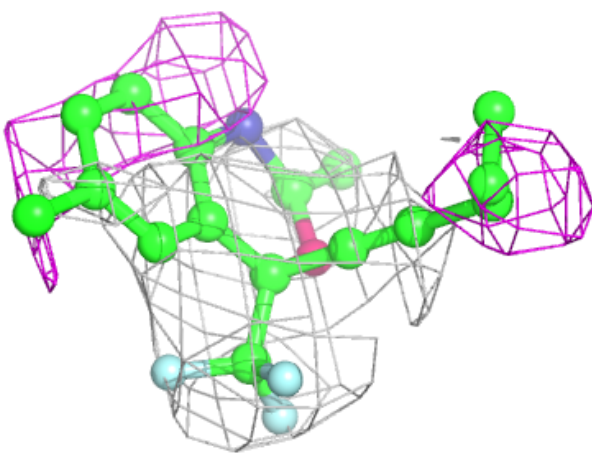
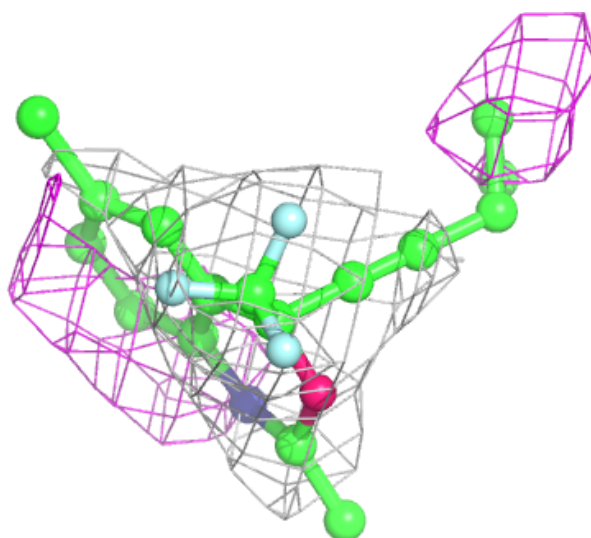
**Electron density around 9ZJ B 502:**

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and green (positive)



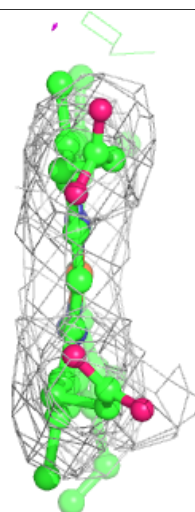
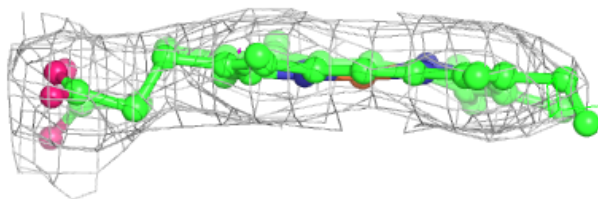
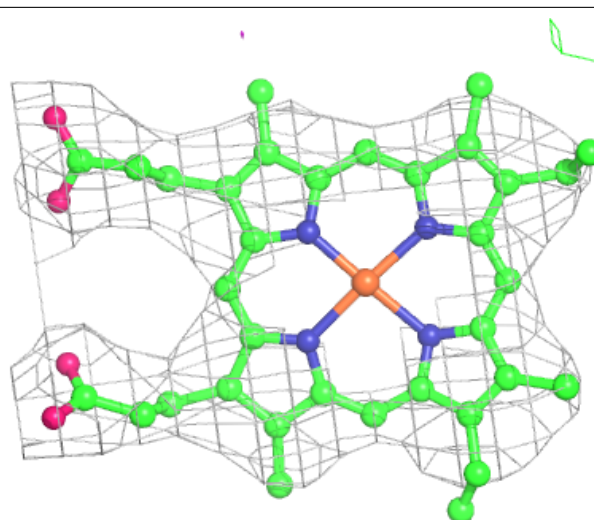
**Electron density around 9ZJ A 502:**

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and green (positive)



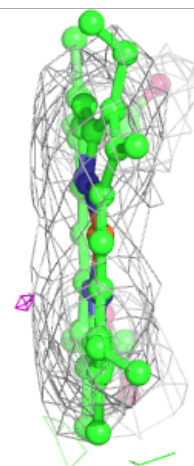
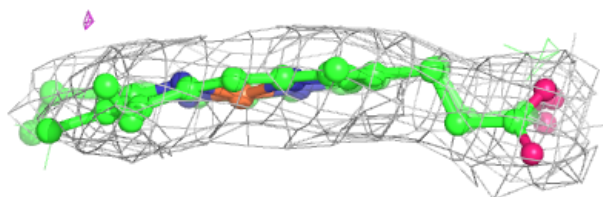
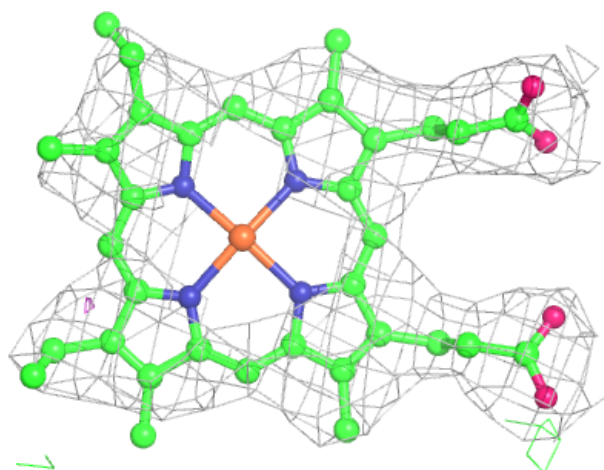
**Electron density around HEM F 501:**

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



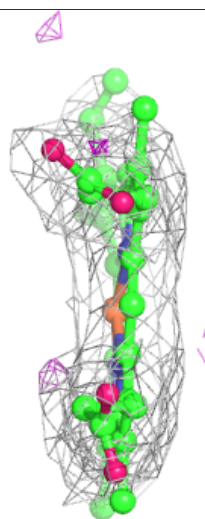
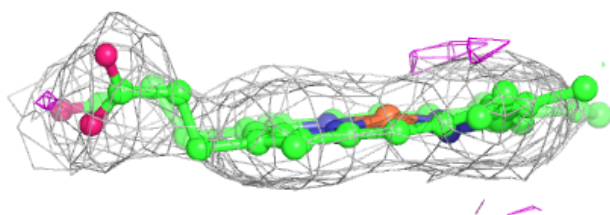
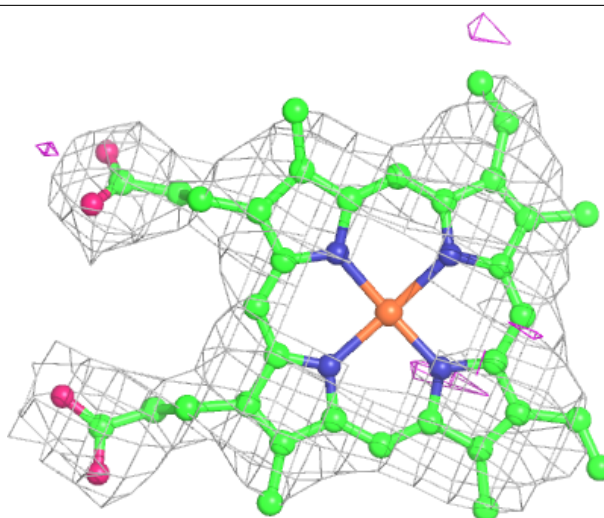
**Electron density around HEM D 501:**

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



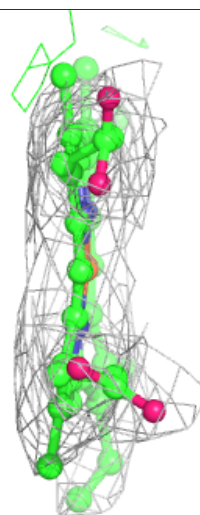
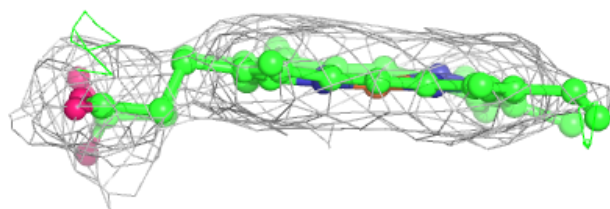
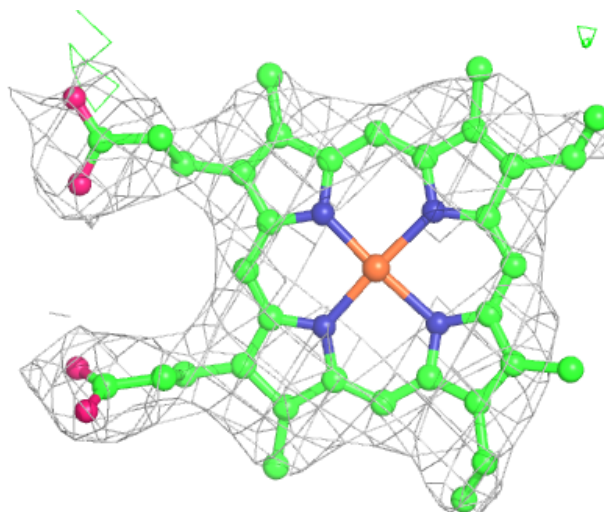
**Electron density around HEM B 501:**

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



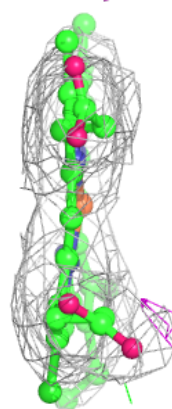
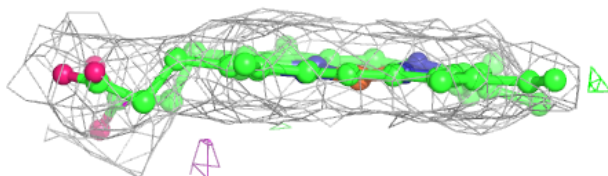
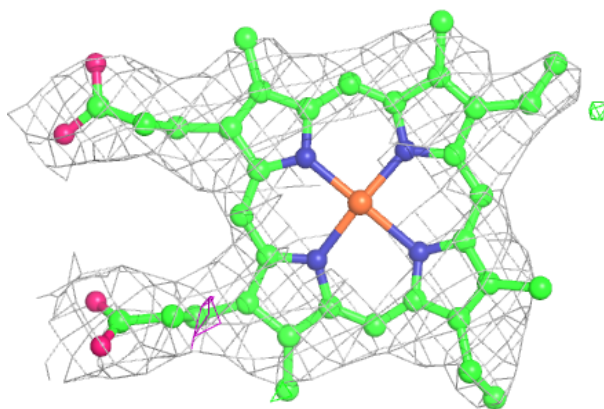
**Electron density around HEM A 501:**

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



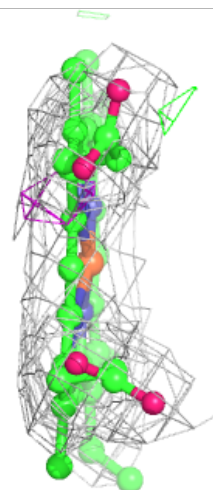
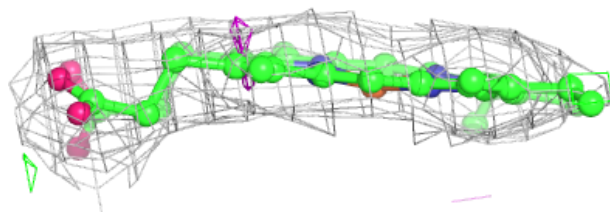
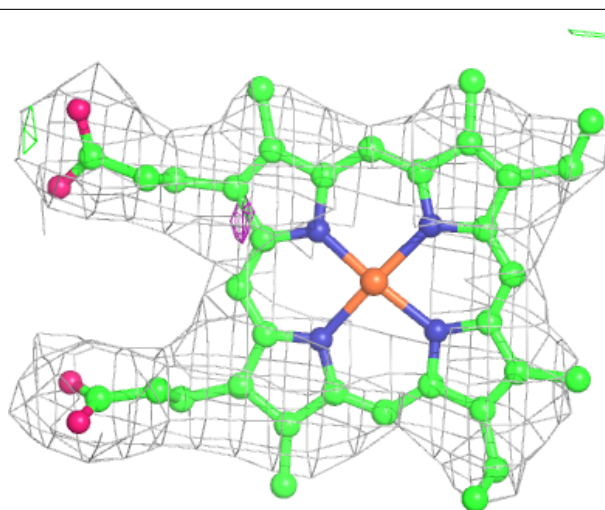
**Electron density around HEM E 501:**

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



**Electron density around HEM C 501:**

$2mF_o-DF_c$  (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.