



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 08:42 AM BST

PDB ID : 4FDH  
Title : Structure of human aldosterone synthase, CYP11B2, in complex with fadrozole  
Authors : Strushkevich, N.; Shen, L.; Tempel, W.; Arrowsmith, C.; Edwards, A.; Usanov, S.A.; Park, H.-W.  
Deposited on : 2012-05-28  
Resolution : 2.71 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.

---

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 : 2.13.1  
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) : 2.13.1

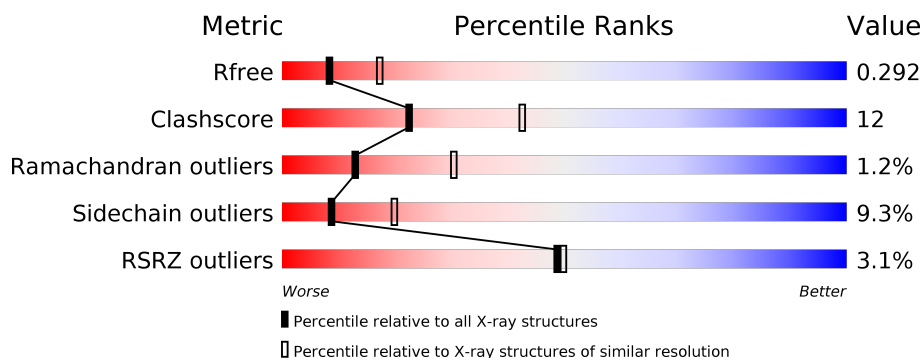
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.71 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	3359 (2.74-2.70)
Clashscore	141614	3686 (2.74-2.70)
Ramachandran outliers	138981	3622 (2.74-2.70)
Sidechain outliers	138945	3623 (2.74-2.70)
RSRZ outliers	127900	3276 (2.74-2.70)

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	483	<div> <div>%</div> <div> <div></div> <div>74%</div> <div>19%</div> <div>• •</div> </div> </div>
1	B	483	<div> <div>%</div> <div> <div></div> <div>66%</div> <div>26%</div> <div>• •</div> </div> </div>
1	C	483	<div> <div>%</div> <div> <div></div> <div>71%</div> <div>22%</div> <div>• •</div> </div> </div>
1	D	483	<div> <div></div> <div> <div>70%</div> <div>24%</div> <div>• •</div> </div> </div>
1	E	483	<div> <div>%</div> <div> <div></div> <div>69%</div> <div>25%</div> <div>• •</div> </div> </div>
1	F	483	<div> <div>%</div> <div> <div></div> <div>63%</div> <div>30%</div> <div>• •</div> </div> </div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	483	<div><div></div><div>3%</div><div>71%</div><div>21%</div><div>•</div><div>•</div></div>
1	H	483	<div><div></div><div>4%</div><div>67%</div><div>26%</div><div>•</div><div>•</div></div>
1	I	483	<div><div></div><div>5%</div><div>66%</div><div>25%</div><div>5%</div><div>•</div></div>
1	J	483	<div><div></div><div>7%</div><div>65%</div><div>27%</div><div>•</div><div>•</div></div>
1	K	483	<div><div></div><div>8%</div><div>64%</div><div>28%</div><div>5%</div><div>•</div></div>
1	L	483	<div><div></div><div>2%</div><div>69%</div><div>21%</div><div>•</div><div>6%</div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 46075 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 11B2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	463	Total	C	N	O	S	0	0	0
			3758	2429	663	646	20			
1	B	465	Total	C	N	O	S	0	0	0
			3777	2441	668	648	20			
1	C	462	Total	C	N	O	S	0	0	0
			3750	2425	661	644	20			
1	D	465	Total	C	N	O	S	0	0	0
			3777	2441	668	648	20			
1	E	470	Total	C	N	O	S	0	0	0
			3826	2469	683	654	20			
1	F	469	Total	C	N	O	S	0	0	0
			3818	2465	681	652	20			
1	G	463	Total	C	N	O	S	0	0	0
			3758	2429	663	646	20			
1	H	462	Total	C	N	O	S	0	0	0
			3750	2425	661	644	20			
1	I	462	Total	C	N	O	S	0	0	0
			3750	2425	661	644	20			
1	J	462	Total	C	N	O	S	0	0	0
			3750	2425	661	644	20			
1	K	469	Total	C	N	O	S	0	0	0
			3802	2454	675	653	20			
1	L	456	Total	C	N	O	S	0	0	0
			3712	2402	654	636	20			

There are 156 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	MET	-	EXPRESSION TAG	UNP P19099
A	28	ALA	-	EXPRESSION TAG	UNP P19099
A	29	LYS	-	EXPRESSION TAG	UNP P19099
A	30	LYS	-	EXPRESSION TAG	UNP P19099
A	31	THR	-	EXPRESSION TAG	UNP P19099

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	SER	-	EXPRESSION TAG	UNP P19099
A	33	SER	-	EXPRESSION TAG	UNP P19099
A	504	HIS	-	EXPRESSION TAG	UNP P19099
A	505	HIS	-	EXPRESSION TAG	UNP P19099
A	506	HIS	-	EXPRESSION TAG	UNP P19099
A	507	HIS	-	EXPRESSION TAG	UNP P19099
A	508	HIS	-	EXPRESSION TAG	UNP P19099
A	509	HIS	-	EXPRESSION TAG	UNP P19099
B	27	MET	-	EXPRESSION TAG	UNP P19099
B	28	ALA	-	EXPRESSION TAG	UNP P19099
B	29	LYS	-	EXPRESSION TAG	UNP P19099
B	30	LYS	-	EXPRESSION TAG	UNP P19099
B	31	THR	-	EXPRESSION TAG	UNP P19099
B	32	SER	-	EXPRESSION TAG	UNP P19099
B	33	SER	-	EXPRESSION TAG	UNP P19099
B	504	HIS	-	EXPRESSION TAG	UNP P19099
B	505	HIS	-	EXPRESSION TAG	UNP P19099
B	506	HIS	-	EXPRESSION TAG	UNP P19099
B	507	HIS	-	EXPRESSION TAG	UNP P19099
B	508	HIS	-	EXPRESSION TAG	UNP P19099
B	509	HIS	-	EXPRESSION TAG	UNP P19099
C	27	MET	-	EXPRESSION TAG	UNP P19099
C	28	ALA	-	EXPRESSION TAG	UNP P19099
C	29	LYS	-	EXPRESSION TAG	UNP P19099
C	30	LYS	-	EXPRESSION TAG	UNP P19099
C	31	THR	-	EXPRESSION TAG	UNP P19099
C	32	SER	-	EXPRESSION TAG	UNP P19099
C	33	SER	-	EXPRESSION TAG	UNP P19099
C	504	HIS	-	EXPRESSION TAG	UNP P19099
C	505	HIS	-	EXPRESSION TAG	UNP P19099
C	506	HIS	-	EXPRESSION TAG	UNP P19099
C	507	HIS	-	EXPRESSION TAG	UNP P19099
C	508	HIS	-	EXPRESSION TAG	UNP P19099
C	509	HIS	-	EXPRESSION TAG	UNP P19099
D	27	MET	-	EXPRESSION TAG	UNP P19099
D	28	ALA	-	EXPRESSION TAG	UNP P19099
D	29	LYS	-	EXPRESSION TAG	UNP P19099
D	30	LYS	-	EXPRESSION TAG	UNP P19099
D	31	THR	-	EXPRESSION TAG	UNP P19099
D	32	SER	-	EXPRESSION TAG	UNP P19099
D	33	SER	-	EXPRESSION TAG	UNP P19099
D	504	HIS	-	EXPRESSION TAG	UNP P19099

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
D	505	HIS	-	EXPRESSION TAG	UNP P19099
D	506	HIS	-	EXPRESSION TAG	UNP P19099
D	507	HIS	-	EXPRESSION TAG	UNP P19099
D	508	HIS	-	EXPRESSION TAG	UNP P19099
D	509	HIS	-	EXPRESSION TAG	UNP P19099
E	27	MET	-	EXPRESSION TAG	UNP P19099
E	28	ALA	-	EXPRESSION TAG	UNP P19099
E	29	LYS	-	EXPRESSION TAG	UNP P19099
E	30	LYS	-	EXPRESSION TAG	UNP P19099
E	31	THR	-	EXPRESSION TAG	UNP P19099
E	32	SER	-	EXPRESSION TAG	UNP P19099
E	33	SER	-	EXPRESSION TAG	UNP P19099
E	504	HIS	-	EXPRESSION TAG	UNP P19099
E	505	HIS	-	EXPRESSION TAG	UNP P19099
E	506	HIS	-	EXPRESSION TAG	UNP P19099
E	507	HIS	-	EXPRESSION TAG	UNP P19099
E	508	HIS	-	EXPRESSION TAG	UNP P19099
E	509	HIS	-	EXPRESSION TAG	UNP P19099
F	27	MET	-	EXPRESSION TAG	UNP P19099
F	28	ALA	-	EXPRESSION TAG	UNP P19099
F	29	LYS	-	EXPRESSION TAG	UNP P19099
F	30	LYS	-	EXPRESSION TAG	UNP P19099
F	31	THR	-	EXPRESSION TAG	UNP P19099
F	32	SER	-	EXPRESSION TAG	UNP P19099
F	33	SER	-	EXPRESSION TAG	UNP P19099
F	504	HIS	-	EXPRESSION TAG	UNP P19099
F	505	HIS	-	EXPRESSION TAG	UNP P19099
F	506	HIS	-	EXPRESSION TAG	UNP P19099
F	507	HIS	-	EXPRESSION TAG	UNP P19099
F	508	HIS	-	EXPRESSION TAG	UNP P19099
F	509	HIS	-	EXPRESSION TAG	UNP P19099
G	27	MET	-	EXPRESSION TAG	UNP P19099
G	28	ALA	-	EXPRESSION TAG	UNP P19099
G	29	LYS	-	EXPRESSION TAG	UNP P19099
G	30	LYS	-	EXPRESSION TAG	UNP P19099
G	31	THR	-	EXPRESSION TAG	UNP P19099
G	32	SER	-	EXPRESSION TAG	UNP P19099
G	33	SER	-	EXPRESSION TAG	UNP P19099
G	504	HIS	-	EXPRESSION TAG	UNP P19099
G	505	HIS	-	EXPRESSION TAG	UNP P19099
G	506	HIS	-	EXPRESSION TAG	UNP P19099
G	507	HIS	-	EXPRESSION TAG	UNP P19099

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
G	508	HIS	-	EXPRESSION TAG	UNP P19099
G	509	HIS	-	EXPRESSION TAG	UNP P19099
H	27	MET	-	EXPRESSION TAG	UNP P19099
H	28	ALA	-	EXPRESSION TAG	UNP P19099
H	29	LYS	-	EXPRESSION TAG	UNP P19099
H	30	LYS	-	EXPRESSION TAG	UNP P19099
H	31	THR	-	EXPRESSION TAG	UNP P19099
H	32	SER	-	EXPRESSION TAG	UNP P19099
H	33	SER	-	EXPRESSION TAG	UNP P19099
H	504	HIS	-	EXPRESSION TAG	UNP P19099
H	505	HIS	-	EXPRESSION TAG	UNP P19099
H	506	HIS	-	EXPRESSION TAG	UNP P19099
H	507	HIS	-	EXPRESSION TAG	UNP P19099
H	508	HIS	-	EXPRESSION TAG	UNP P19099
H	509	HIS	-	EXPRESSION TAG	UNP P19099
I	27	MET	-	EXPRESSION TAG	UNP P19099
I	28	ALA	-	EXPRESSION TAG	UNP P19099
I	29	LYS	-	EXPRESSION TAG	UNP P19099
I	30	LYS	-	EXPRESSION TAG	UNP P19099
I	31	THR	-	EXPRESSION TAG	UNP P19099
I	32	SER	-	EXPRESSION TAG	UNP P19099
I	33	SER	-	EXPRESSION TAG	UNP P19099
I	504	HIS	-	EXPRESSION TAG	UNP P19099
I	505	HIS	-	EXPRESSION TAG	UNP P19099
I	506	HIS	-	EXPRESSION TAG	UNP P19099
I	507	HIS	-	EXPRESSION TAG	UNP P19099
I	508	HIS	-	EXPRESSION TAG	UNP P19099
I	509	HIS	-	EXPRESSION TAG	UNP P19099
J	27	MET	-	EXPRESSION TAG	UNP P19099
J	28	ALA	-	EXPRESSION TAG	UNP P19099
J	29	LYS	-	EXPRESSION TAG	UNP P19099
J	30	LYS	-	EXPRESSION TAG	UNP P19099
J	31	THR	-	EXPRESSION TAG	UNP P19099
J	32	SER	-	EXPRESSION TAG	UNP P19099
J	33	SER	-	EXPRESSION TAG	UNP P19099
J	504	HIS	-	EXPRESSION TAG	UNP P19099
J	505	HIS	-	EXPRESSION TAG	UNP P19099
J	506	HIS	-	EXPRESSION TAG	UNP P19099
J	507	HIS	-	EXPRESSION TAG	UNP P19099
J	508	HIS	-	EXPRESSION TAG	UNP P19099
J	509	HIS	-	EXPRESSION TAG	UNP P19099
K	27	MET	-	EXPRESSION TAG	UNP P19099

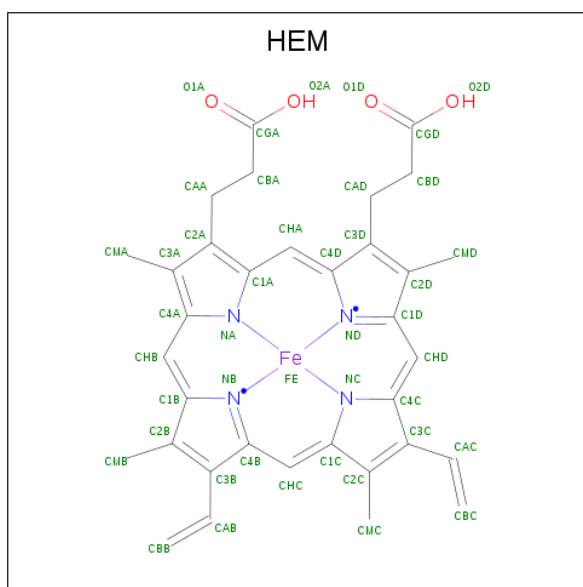
*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
K	28	ALA	-	EXPRESSION TAG	UNP P19099
K	29	LYS	-	EXPRESSION TAG	UNP P19099
K	30	LYS	-	EXPRESSION TAG	UNP P19099
K	31	THR	-	EXPRESSION TAG	UNP P19099
K	32	SER	-	EXPRESSION TAG	UNP P19099
K	33	SER	-	EXPRESSION TAG	UNP P19099
K	504	HIS	-	EXPRESSION TAG	UNP P19099
K	505	HIS	-	EXPRESSION TAG	UNP P19099
K	506	HIS	-	EXPRESSION TAG	UNP P19099
K	507	HIS	-	EXPRESSION TAG	UNP P19099
K	508	HIS	-	EXPRESSION TAG	UNP P19099
K	509	HIS	-	EXPRESSION TAG	UNP P19099
L	27	MET	-	EXPRESSION TAG	UNP P19099
L	28	ALA	-	EXPRESSION TAG	UNP P19099
L	29	LYS	-	EXPRESSION TAG	UNP P19099
L	30	LYS	-	EXPRESSION TAG	UNP P19099
L	31	THR	-	EXPRESSION TAG	UNP P19099
L	32	SER	-	EXPRESSION TAG	UNP P19099
L	33	SER	-	EXPRESSION TAG	UNP P19099
L	504	HIS	-	EXPRESSION TAG	UNP P19099
L	505	HIS	-	EXPRESSION TAG	UNP P19099
L	506	HIS	-	EXPRESSION TAG	UNP P19099
L	507	HIS	-	EXPRESSION TAG	UNP P19099
L	508	HIS	-	EXPRESSION TAG	UNP P19099
L	509	HIS	-	EXPRESSION TAG	UNP P19099

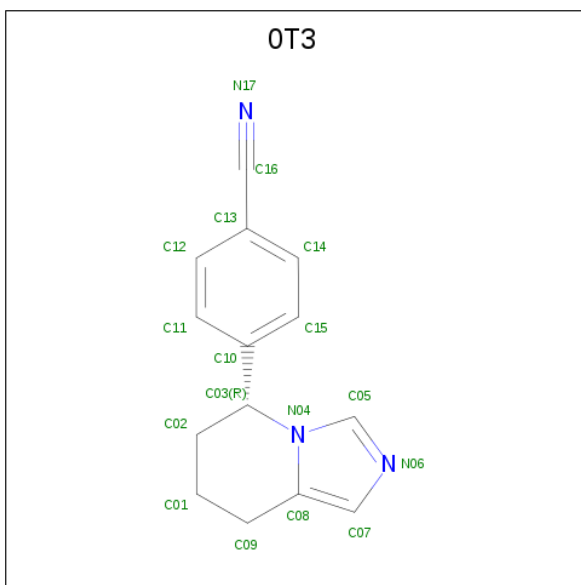
- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).





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
2	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	H	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	I	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	J	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	K	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	L	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is 4-[(5R)-5,6,7,8-tetrahydroimidazo[1,5-a]pyridin-5-yl]benzonitrile (three-letter code: 0T3) (formula: C<sub>14</sub>H<sub>13</sub>N<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			17	14	3		
3	B	1	Total	C	N	0	0
			17	14	3		
3	C	1	Total	C	N	0	0
			17	14	3		
3	D	1	Total	C	N	0	0
			17	14	3		
3	E	1	Total	C	N	0	0
			17	14	3		
3	F	1	Total	C	N	0	0
			17	14	3		
3	G	1	Total	C	N	0	0
			17	14	3		
3	H	1	Total	C	N	0	0
			17	14	3		
3	I	1	Total	C	N	0	0
			17	14	3		
3	J	1	Total	C	N	0	0
			17	14	3		
3	K	1	Total	C	N	0	0
			17	14	3		
3	L	1	Total	C	N	0	0
			17	14	3		

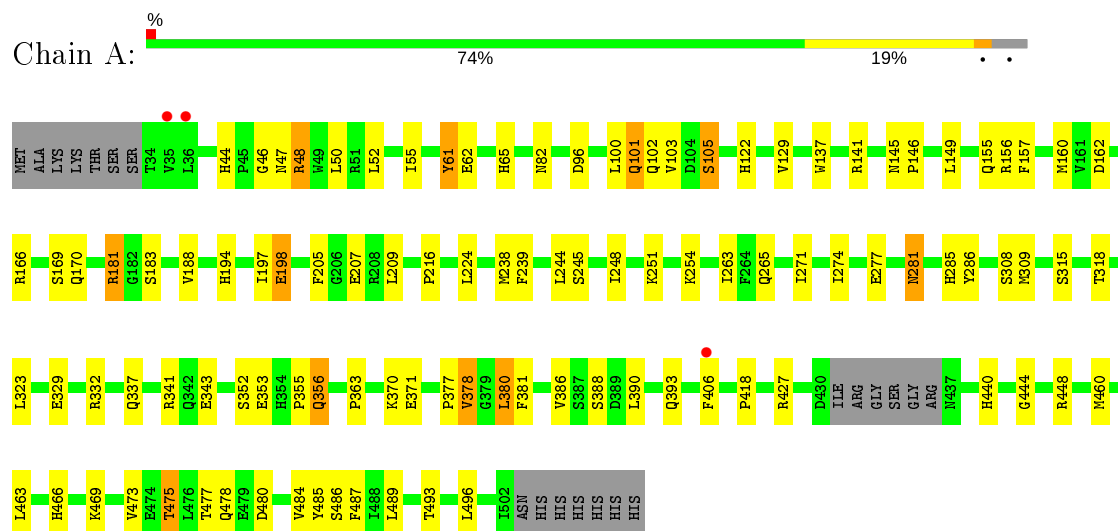
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	14	Total 14	O 14	0	0
4	B	6	Total 6	O 6	0	0
4	C	17	Total 17	O 17	0	0
4	D	9	Total 9	O 9	0	0
4	E	12	Total 12	O 12	0	0
4	F	17	Total 17	O 17	0	0
4	G	3	Total 3	O 3	0	0
4	H	13	Total 13	O 13	0	0
4	I	9	Total 9	O 9	0	0
4	J	3	Total 3	O 3	0	0
4	K	4	Total 4	O 4	0	0
4	L	20	Total 20	O 20	0	0

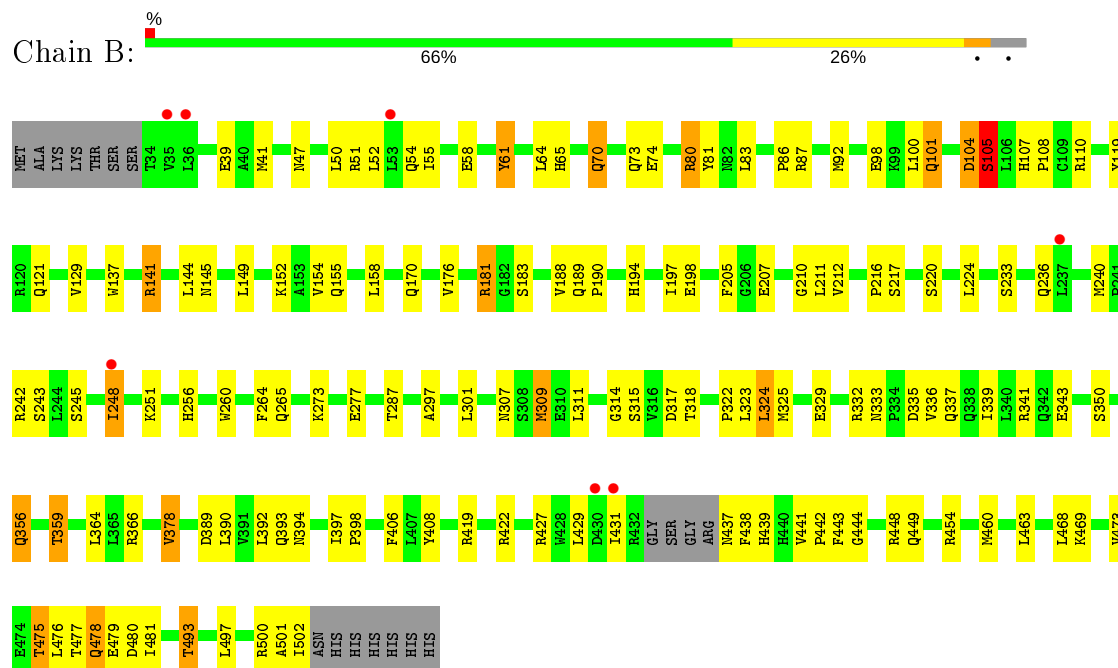
### 3 Residue-property plots [i](#)

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

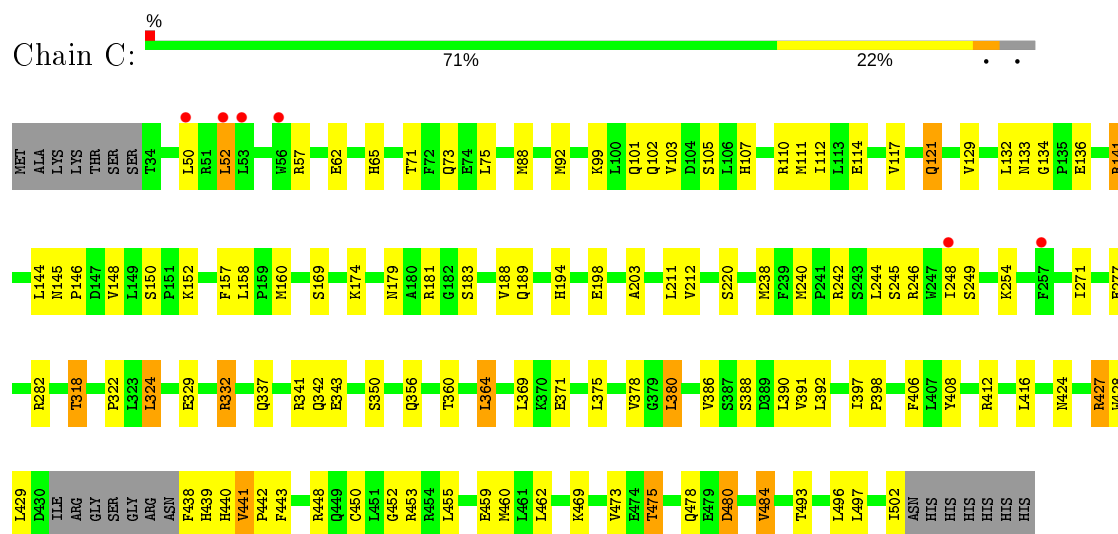
- Molecule 1: Cytochrome P450 11B2, mitochondrial



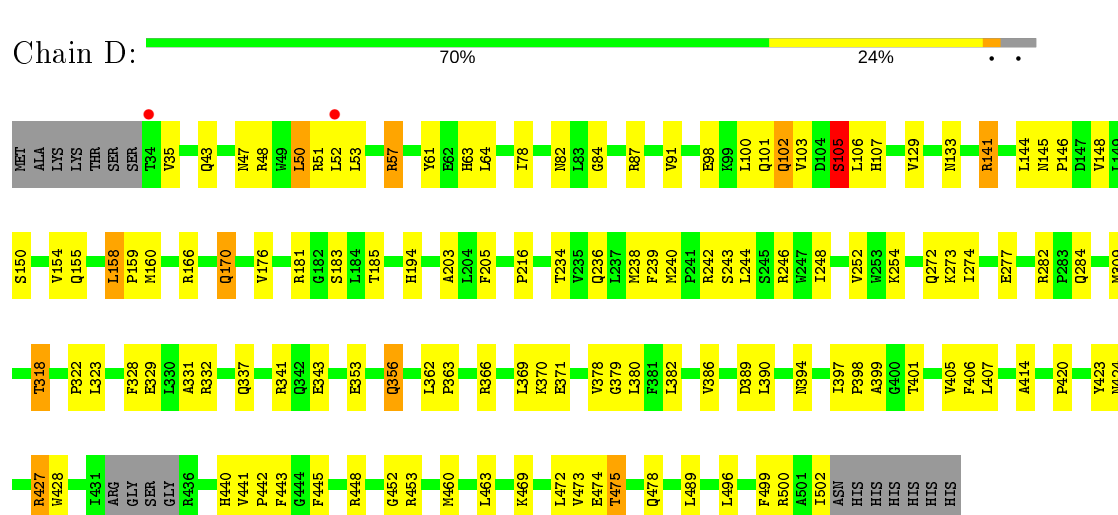
- Molecule 1: Cytochrome P450 11B2, mitochondrial



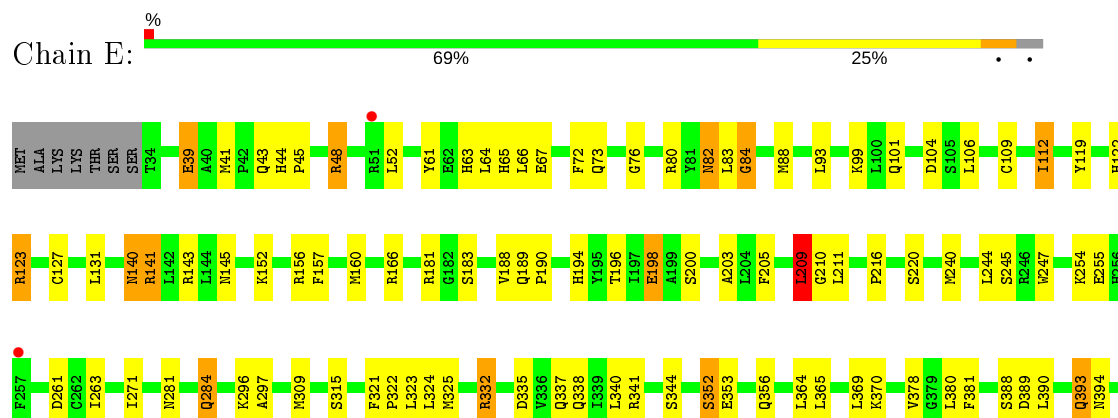
- Molecule 1: Cytochrome P450 11B2, mitochondrial

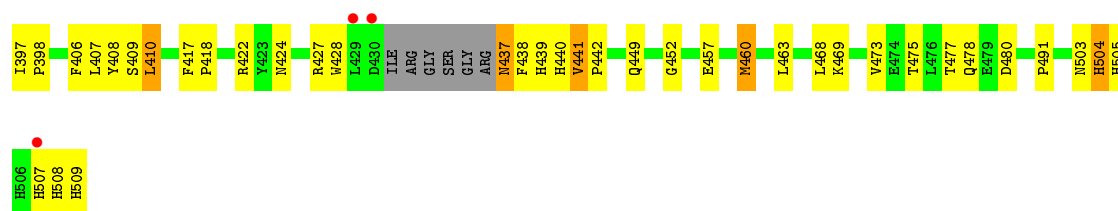


- Molecule 1: Cytochrome P450 11B2, mitochondrial

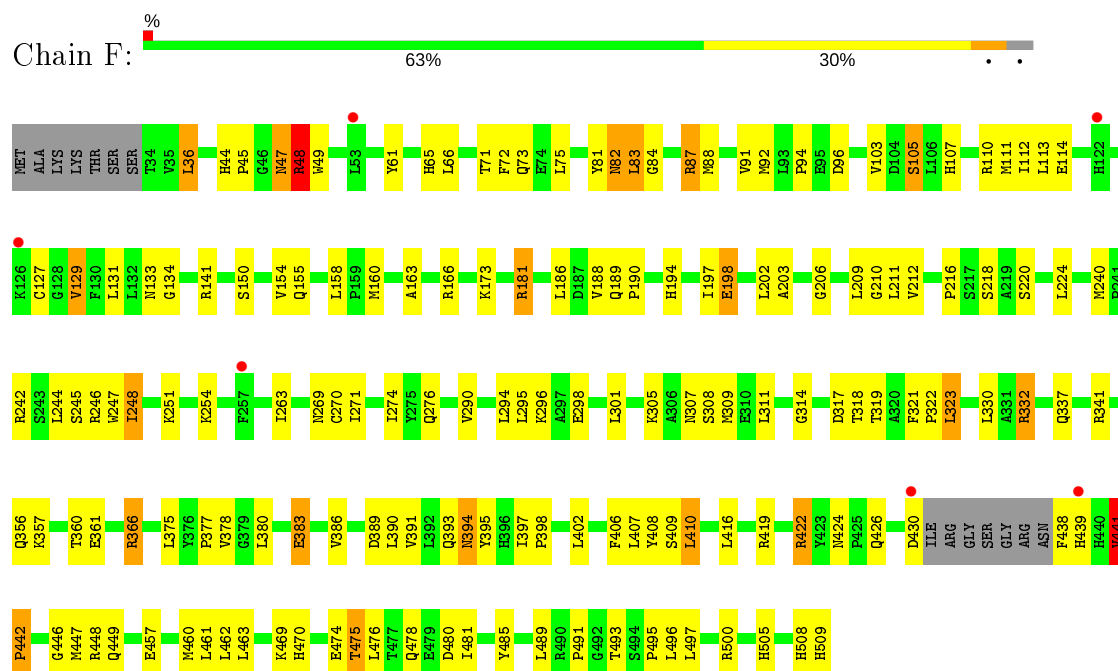


- Molecule 1: Cytochrome P450 11B2, mitochondrial

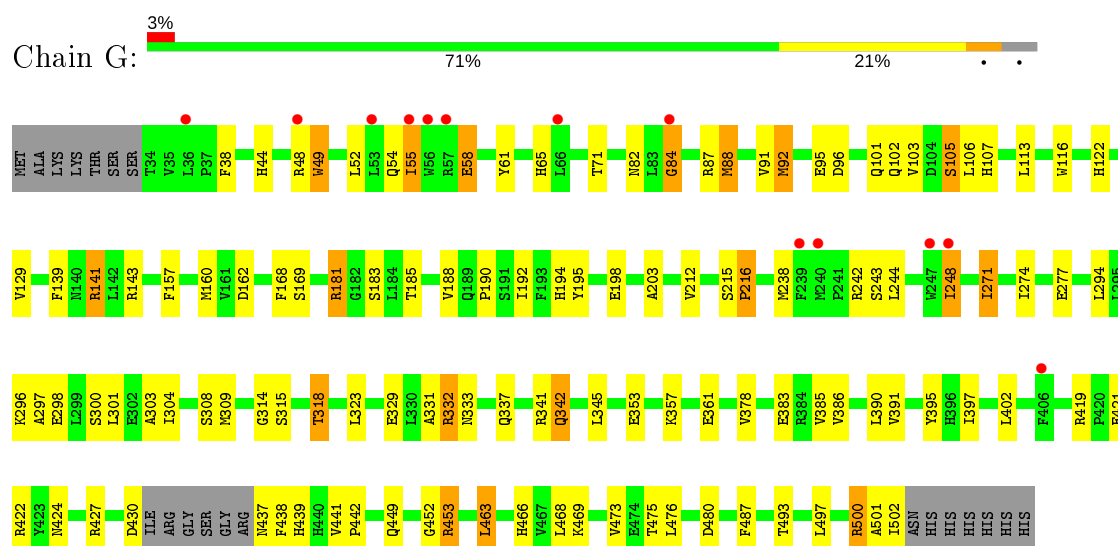




• Molecule 1: Cytochrome P450 11B2, mitochondrial

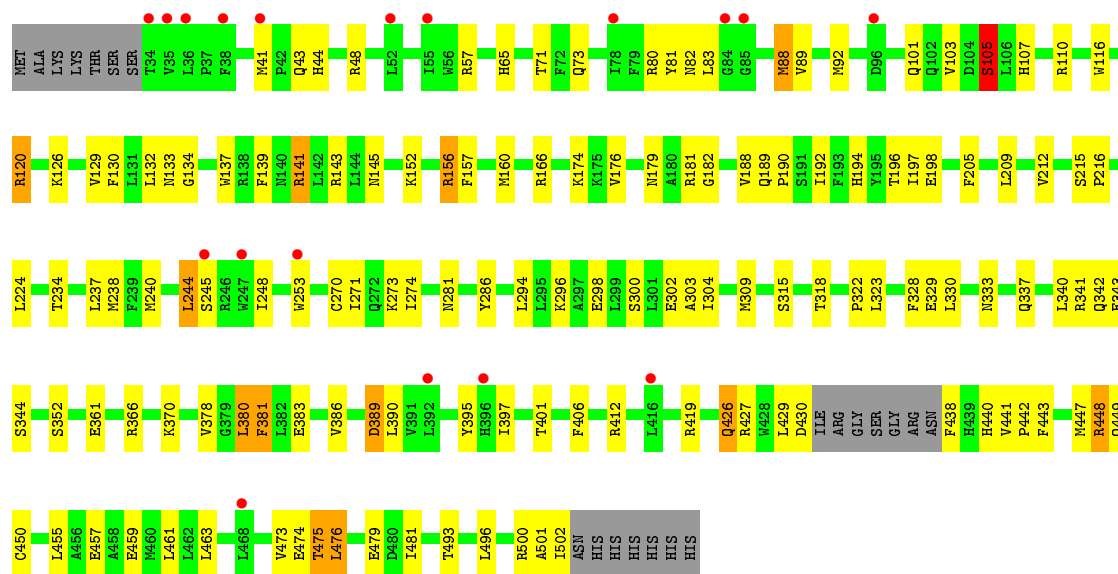


• Molecule 1: Cytochrome P450 11B2, mitochondrial

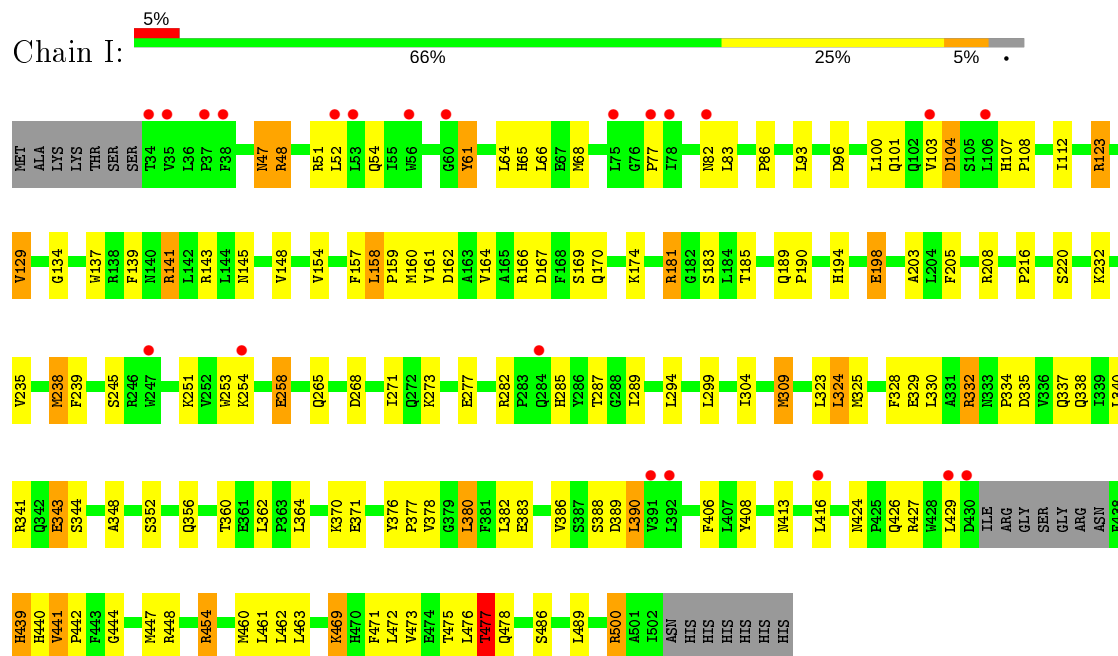


• Molecule 1: Cytochrome P450 11B2, mitochondrial

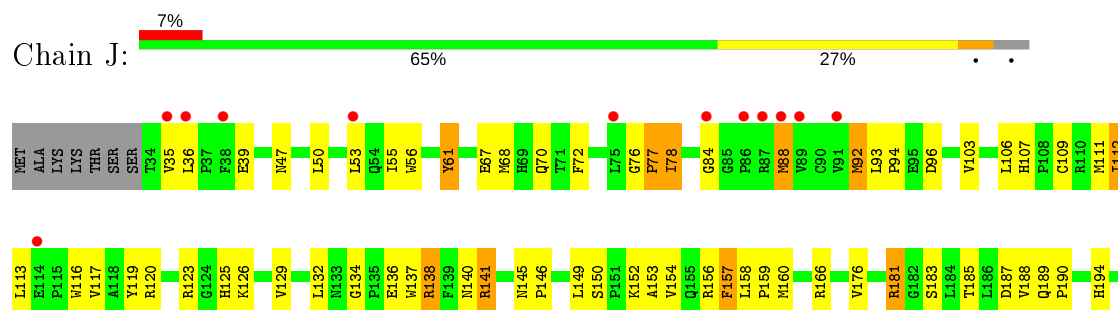


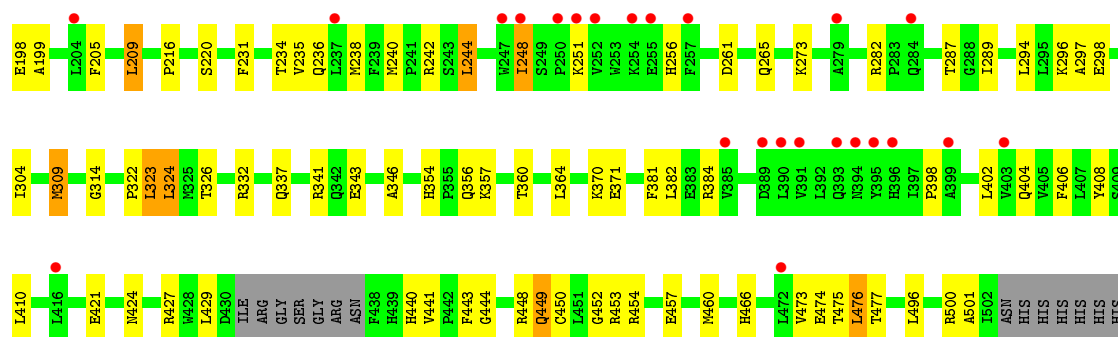


- Molecule 1: Cytochrome P450 11B2, mitochondrial

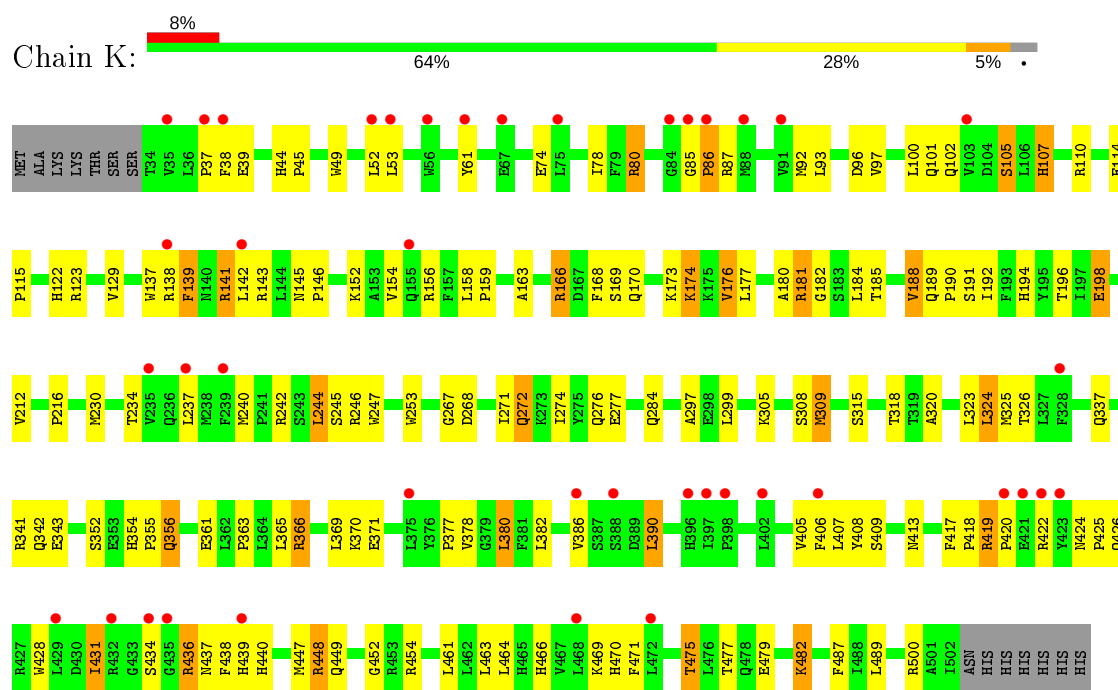


- Molecule 1: Cytochrome P450 11B2, mitochondrial

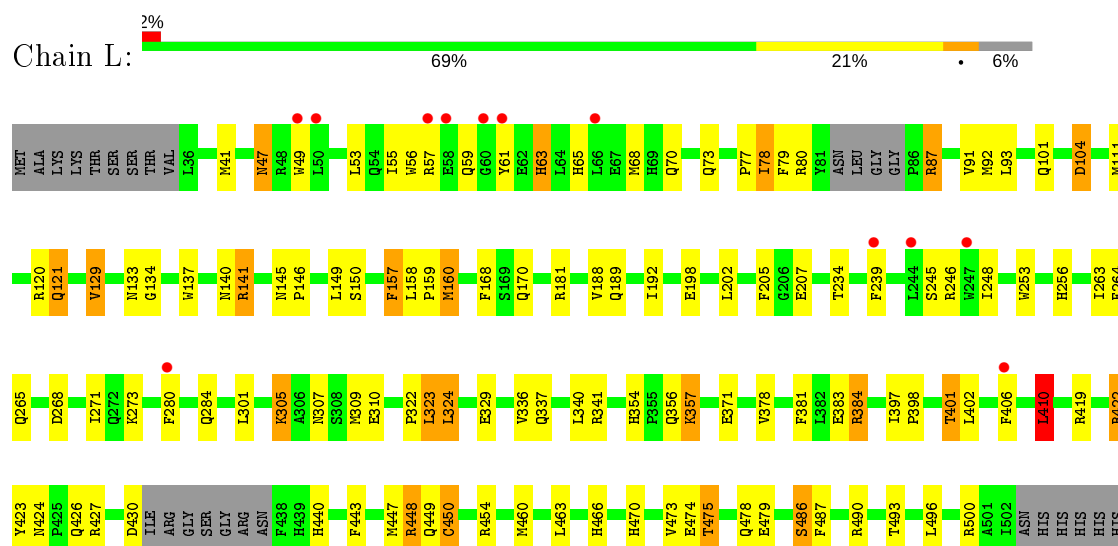




• Molecule 1: Cytochrome P450 11B2, mitochondrial



• Molecule 1: Cytochrome P450 11B2, mitochondrial





HIS

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	129.75Å 199.09Å 150.02Å 90.00° 112.08° 90.00°	Depositor
Resolution (Å)	48.89 – 2.71 48.00 – 2.71	Depositor EDS
% Data completeness (in resolution range)	(Not available) (48.89-2.71) 98.9 (48.00-2.71)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.55 (at 2.73Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.224 , 0.300 0.221 , 0.292	Depositor DCC
$R_{free}$ test set	9381 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	64.9	Xtrriage
Anisotropy	0.045	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 34.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	46075	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 39.94 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9437e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, OT3

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	0.58	0/3858	0.70	1/5235 (0.0%)
1	B	0.53	0/3877	0.67	0/5260
1	C	0.57	0/3850	0.71	0/5224
1	D	0.56	0/3877	0.69	0/5260
1	E	0.56	0/3932	0.68	1/5336 (0.0%)
1	F	0.54	1/3924 (0.0%)	0.67	0/5325
1	G	0.52	0/3858	0.65	0/5235
1	H	0.55	1/3850 (0.0%)	0.69	1/5224 (0.0%)
1	I	0.51	0/3850	0.65	0/5224
1	J	0.50	0/3850	0.64	0/5224
1	K	0.49	0/3903	0.64	0/5295
1	L	0.55	0/3811	0.68	1/5168 (0.0%)
All	All	0.54	2/46440 (0.0%)	0.67	4/63010 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	270	CYS	CB-SG	-6.33	1.71	1.82
1	F	270	CYS	CB-SG	-5.89	1.72	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	83	LEU	CA-CB-CG	5.45	127.83	115.30
1	L	410	LEU	CA-CB-CG	5.44	127.80	115.30
1	A	149	LEU	CB-CG-CD2	-5.14	102.27	111.00
1	E	209	LEU	CA-CB-CG	5.06	126.93	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	501	ALA	Peptide

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3758	0	3791	66	0
1	B	3777	0	3815	93	0
1	C	3750	0	3785	74	0
1	D	3777	0	3815	88	0
1	E	3826	0	3839	85	0
1	F	3818	0	3833	111	0
1	G	3758	0	3791	95	0
1	H	3750	0	3785	92	0
1	I	3750	0	3785	98	0
1	J	3750	0	3785	95	0
1	K	3802	0	3840	99	0
1	L	3712	0	3746	85	0
2	A	43	0	30	6	0
2	B	43	0	30	9	0
2	C	43	0	30	6	0
2	D	43	0	30	3	0
2	E	43	0	30	5	0
2	F	43	0	30	9	0
2	G	43	0	30	5	0
2	H	43	0	30	2	0
2	I	43	0	30	6	0
2	J	43	0	30	2	0
2	K	43	0	30	4	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	43	0	30	7	0
3	A	17	0	13	2	0
3	B	17	0	13	3	0
3	C	17	0	13	2	0
3	D	17	0	13	1	0
3	E	17	0	13	2	0
3	F	17	0	13	3	0
3	G	17	0	13	2	0
3	H	17	0	13	2	0
3	I	17	0	13	2	0
3	J	17	0	13	1	0
3	K	17	0	13	1	0
3	L	17	0	13	5	0
4	A	14	0	0	1	0
4	B	6	0	0	0	0
4	C	17	0	0	1	0
4	D	9	0	0	0	0
4	E	12	0	0	0	0
4	F	17	0	0	2	0
4	G	3	0	0	0	0
4	H	13	0	0	1	0
4	I	9	0	0	0	0
4	J	3	0	0	0	0
4	K	4	0	0	0	0
4	L	20	0	0	1	0
All	All	46075	0	46126	1065	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 12.

All (1065) 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:G:181:ARG:HH21	1:K:274:ILE:HG13	1.03	1.13
1:G:183:SER:HB3	1:G:500:ARG:HG2	1.35	1.09
1:L:55:ILE:HD11	1:L:239:PHE:HD1	1.17	1.08
1:L:55:ILE:HD11	1:L:239:PHE:CD1	1.89	1.07
1:G:181:ARG:NH2	1:K:274:ILE:HG13	1.72	1.05
1:I:123:ARG:HH21	1:I:123:ARG:HG2	1.15	1.03
1:J:337:GLN:HE22	1:J:473:VAL:H	1.02	0.99
1:G:181:ARG:HH21	1:K:274:ILE:CG1	1.74	0.99

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:GLN:NE2	1:A:356:GLN:H	1.62	0.96
1:A:356:GLN:HE21	1:A:356:GLN:H	1.14	0.96
1:F:194:HIS:CE1	1:F:220:SER:OG	2.21	0.94
1:G:337:GLN:HE22	1:G:473:VAL:H	0.94	0.93
1:G:183:SER:CB	1:G:500:ARG:HG2	1.98	0.93
1:G:419:ARG:NH2	1:G:422:ARG:HD2	1.84	0.92
1:I:337:GLN:HE22	1:I:473:VAL:H	1.17	0.92
1:E:503:ASN:O	1:E:504:HIS:HB2	1.70	0.90
1:K:356:GLN:HE21	1:K:356:GLN:H	1.21	0.88
1:B:337:GLN:HE22	1:B:473:VAL:H	1.14	0.88
1:I:181:ARG:HB2	1:I:181:ARG:HH11	1.37	0.88
1:G:337:GLN:NE2	1:G:473:VAL:H	1.70	0.88
1:B:389:ASP:OD1	1:B:398:PRO:HA	1.73	0.87
1:D:356:GLN:HE21	1:D:356:GLN:H	1.23	0.87
1:L:337:GLN:HE22	1:L:473:VAL:H	1.19	0.87
1:H:160:MET:HE1	1:H:286:TYR:HE2	1.41	0.85
1:I:183:SER:HB3	1:I:500:ARG:HG2	1.56	0.85
1:B:181:ARG:HH11	1:B:181:ARG:HB2	1.41	0.84
1:A:181:ARG:HB2	1:A:181:ARG:HH11	1.42	0.84
1:L:189:GLN:HA	1:L:324:LEU:HD11	1.58	0.83
1:C:198:GLU:HG3	1:C:212:VAL:HG23	1.61	0.83
1:E:337:GLN:HE22	1:E:473:VAL:H	1.27	0.83
1:L:65:HIS:HA	1:L:406:PHE:HZ	1.43	0.83
1:F:181:ARG:HB2	1:F:181:ARG:HH11	1.43	0.82
1:B:197:ILE:HD11	1:B:224:LEU:HD21	1.62	0.82
1:G:337:GLN:HE22	1:G:473:VAL:N	1.76	0.82
1:C:158:LEU:HD23	1:C:462:LEU:HD11	1.62	0.81
1:C:475:THR:HG23	1:C:497:LEU:HD23	1.62	0.81
1:L:263:ILE:HG22	1:L:309:MET:HE1	1.63	0.81
1:H:323:LEU:HD21	1:H:463:LEU:HD22	1.61	0.81
1:A:281:ASN:C	1:A:281:ASN:HD22	1.84	0.81
1:F:441:VAL:N	1:F:442:PRO:HD2	1.97	0.80
1:A:356:GLN:N	1:A:356:GLN:HE21	1.78	0.80
1:G:315:SER:HB3	2:G:601:HEM:HBC2	1.64	0.80
1:E:112:ILE:HD12	1:E:112:ILE:H	1.47	0.79
1:E:505:HIS:HD2	1:E:508:HIS:H	1.28	0.79
1:J:181:ARG:HH11	1:J:181:ARG:HB2	1.47	0.79
1:F:107:HIS:HB3	1:F:134:GLY:HA2	1.64	0.78
2:A:601:HEM:HMB2	2:A:601:HEM:HBB2	1.63	0.78
1:F:111:MET:HG3	1:F:402:LEU:HD22	1.64	0.78
1:C:189:GLN:HG3	1:C:324:LEU:HD21	1.66	0.77

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:322:PRO:HB2	1:L:460:MET:HE3	1.64	0.77
1:I:123:ARG:NH2	1:I:123:ARG:HG2	1.93	0.77
1:K:309:MET:HA	1:K:309:MET:CE	2.16	0.76
1:H:330:LEU:HD22	1:H:340:LEU:HD12	1.67	0.76
1:K:323:LEU:HD21	1:K:463:LEU:HD22	1.67	0.76
1:E:315:SER:HA	2:E:601:HEM:HMC2	1.68	0.75
1:I:277:GLU:OE1	1:L:181:ARG:NH1	2.20	0.75
1:H:245:SER:HA	1:H:248:ILE:HG22	1.68	0.75
1:L:245:SER:HB3	1:L:253:TRP:HE1	1.50	0.75
1:D:337:GLN:HE21	1:D:341:ARG:HH22	1.35	0.75
1:G:181:ARG:HH11	1:G:181:ARG:HB2	1.51	0.75
1:L:424:ASN:O	1:L:427:ARG:HG3	1.87	0.75
1:A:337:GLN:HE21	1:A:341:ARG:HH22	1.32	0.74
1:K:268:ASP:O	1:K:272:GLN:HB2	1.87	0.74
1:E:263:ILE:HG22	1:E:309:MET:HE1	1.68	0.74
1:H:198:GLU:HG3	1:H:212:VAL:HG23	1.70	0.74
1:L:474:GLU:OE1	1:L:500:ARG:NH1	2.21	0.74
2:L:601:HEM:NA	3:L:602:OT3:H7	2.02	0.74
1:C:332:ARG:NH1	1:C:480:ASP:OD2	2.20	0.74
1:L:419:ARG:HH12	1:L:422:ARG:HG3	1.53	0.73
1:L:55:ILE:CD1	1:L:239:PHE:HD1	1.99	0.73
1:F:475:THR:HG23	1:F:497:LEU:HD23	1.71	0.73
1:H:160:MET:CE	1:H:286:TYR:HE2	2.01	0.73
1:C:244:LEU:O	1:C:248:ILE:HG13	1.89	0.73
1:J:141:ARG:HD2	1:J:145:ASN:OD1	1.89	0.73
1:H:179:ASN:HB3	4:H:702:HOH:O	1.90	0.72
1:K:380:LEU:O	1:K:407:LEU:HB2	1.88	0.72
1:A:48:ARG:O	1:A:52:LEU:HG	1.89	0.72
1:F:406:PHE:HD2	1:F:409:SER:HB2	1.53	0.72
1:G:141:ARG:NH1	1:G:449:GLN:O	2.22	0.72
1:H:337:GLN:HE22	1:H:473:VAL:H	1.37	0.72
1:H:190:PRO:O	1:H:194:HIS:HD2	1.70	0.72
1:L:322:PRO:HB2	1:L:460:MET:CE	2.19	0.71
1:D:141:ARG:HD2	1:D:145:ASN:OD1	1.90	0.71
1:F:45:PRO:HD3	1:F:75:LEU:HD11	1.72	0.71
1:G:475:THR:HB	1:G:497:LEU:HD23	1.70	0.71
1:E:505:HIS:CD2	1:E:508:HIS:H	2.09	0.71
2:C:601:HEM:HMB2	2:C:601:HEM:HBB2	1.72	0.71
1:C:158:LEU:CD2	1:C:462:LEU:HD11	2.20	0.71
1:K:141:ARG:NH1	1:K:449:GLN:O	2.24	0.70
1:A:281:ASN:ND2	1:A:281:ASN:C	2.45	0.70

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:382:LEU:HD22	1:J:444:GLY:HA2	1.71	0.70
1:B:301:LEU:H	1:L:426:GLN:HE22	1.37	0.70
1:K:337:GLN:HE21	1:K:341:ARG:HH12	1.38	0.70
1:L:337:GLN:HE21	1:L:341:ARG:HH22	1.39	0.70
1:K:452:GLY:HA3	2:K:601:HEM:HBC2	1.73	0.69
1:H:105:SER:HB3	1:H:107:HIS:H	1.56	0.69
1:K:356:GLN:NE2	1:K:356:GLN:H	1.90	0.69
1:A:101:GLN:HG2	4:A:704:HOH:O	1.92	0.69
1:F:332:ARG:NH1	1:F:480:ASP:OD2	2.26	0.69
1:F:194:HIS:HE1	1:F:220:SER:OG	1.72	0.69
1:I:337:GLN:NE2	1:I:473:VAL:H	1.90	0.69
1:J:107:HIS:HB3	1:J:134:GLY:HA2	1.73	0.69
1:J:296:LYS:HD3	1:J:298:GLU:OE1	1.91	0.69
1:C:99:LYS:HD2	1:C:392:LEU:HD23	1.74	0.69
1:H:157:PHE:HA	1:H:160:MET:CE	2.23	0.69
1:A:162:ASP:OD1	1:A:466:HIS:HE1	1.75	0.69
1:J:449:GLN:OE1	1:J:453:ARG:HD3	1.93	0.69
1:E:406:PHE:CE2	1:E:408:TYR:HB3	2.28	0.68
1:G:181:ARG:HH11	1:G:181:ARG:CB	2.06	0.68
1:A:370:LYS:HG2	1:A:440:HIS:CE1	2.28	0.68
1:G:318:THR:HA	1:G:378:VAL:HG11	1.73	0.68
1:L:101:GLN:O	1:L:104:ASP:HB2	1.93	0.68
1:B:183:SER:HB3	1:B:500:ARG:HA	1.73	0.68
1:C:475:THR:HG22	1:C:496:LEU:O	1.93	0.68
1:B:277:GLU:OE1	1:D:181:ARG:NH1	2.27	0.68
1:D:337:GLN:HE22	1:D:473:VAL:H	1.39	0.68
1:G:500:ARG:HH11	1:G:500:ARG:CB	2.07	0.68
1:I:194:HIS:CE1	1:I:216:PRO:HB3	2.28	0.68
1:K:245:SER:HB2	1:K:253:TRP:HE1	1.59	0.68
1:L:383:GLU:HG2	1:L:402:LEU:HD11	1.75	0.68
1:B:217:SER:OG	1:B:220:SER:HB2	1.94	0.68
1:C:337:GLN:HE21	1:C:341:ARG:HH22	1.40	0.67
1:I:441:VAL:N	1:I:442:PRO:CD	2.57	0.67
1:B:448:ARG:HD3	2:B:601:HEM:O2D	1.94	0.67
1:L:140:ASN:HD22	1:L:307:ASN:HD21	1.42	0.67
1:C:369:LEU:HD22	1:C:460:MET:HE1	1.76	0.67
1:B:337:GLN:NE2	1:B:473:VAL:H	1.91	0.67
1:B:475:THR:HG23	1:B:497:LEU:HD23	1.77	0.67
1:J:337:GLN:NE2	1:J:473:VAL:H	1.84	0.67
1:H:181:ARG:NH2	1:L:205:PHE:O	2.28	0.67
1:F:194:HIS:CE1	1:F:216:PRO:HB3	2.30	0.67

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:137:TRP:CZ2	1:J:448:ARG:HD3	2.30	0.67
1:D:48:ARG:HH21	1:D:84:GLY:HA3	1.59	0.67
1:E:160:MET:HE3	1:E:203:ALA:HA	1.77	0.67
1:J:234:THR:O	1:J:238:MET:HG3	1.95	0.67
1:J:424:ASN:O	1:J:427:ARG:HG2	1.95	0.66
1:K:309:MET:HA	1:K:309:MET:HE3	1.73	0.66
1:B:52:LEU:HD11	1:B:240:MET:SD	2.35	0.66
1:D:328:PHE:O	1:D:332:ARG:HG3	1.95	0.66
1:E:209:LEU:O	1:E:211:LEU:HG	1.96	0.66
1:F:318:THR:HA	1:F:378:VAL:HG11	1.76	0.66
1:J:273:LYS:HG2	1:K:185:THR:HB	1.77	0.66
1:D:242:ARG:O	1:D:246:ARG:HB2	1.96	0.66
1:D:356:GLN:N	1:D:356:GLN:HE21	1.94	0.66
1:F:441:VAL:N	1:F:442:PRO:CD	2.58	0.66
1:K:105:SER:HB3	1:K:107:HIS:H	1.59	0.66
1:D:52:LEU:HD22	1:D:240:MET:HB3	1.77	0.66
1:F:65:HIS:HB3	1:F:380:LEU:HD11	1.77	0.66
1:G:181:ARG:HH11	1:G:181:ARG:CG	2.08	0.66
1:D:236:GLN:HB2	1:D:252:VAL:HG11	1.77	0.66
1:E:43:GLN:HE21	1:E:82:ASN:HB2	1.60	0.66
1:H:160:MET:HE1	1:H:286:TYR:CE2	2.27	0.66
1:D:244:LEU:O	1:D:248:ILE:HG13	1.95	0.65
1:H:141:ARG:HD2	1:H:145:ASN:OD1	1.97	0.65
1:J:231:PHE:O	1:J:235:VAL:HG23	1.95	0.65
1:J:294:LEU:HD23	1:J:304:ILE:HD13	1.78	0.65
1:A:271:ILE:HD11	1:A:308:SER:HB3	1.78	0.65
1:G:65:HIS:CD2	1:G:65:HIS:H	2.14	0.65
1:C:52:LEU:CD2	1:C:240:MET:HB3	2.26	0.65
1:D:176:VAL:HG13	1:D:183:SER:HA	1.79	0.65
1:D:380:LEU:HD13	1:D:489:LEU:HD22	1.78	0.65
1:G:181:ARG:HH21	1:K:274:ILE:CD1	2.09	0.65
1:G:271:ILE:HD11	1:G:308:SER:HB3	1.77	0.65
2:A:601:HEM:HBB2	2:A:601:HEM:CMB	2.27	0.65
2:F:601:HEM:HBC2	2:F:601:HEM:HMC2	1.79	0.65
1:I:205:PHE:O	1:L:181:ARG:NH2	2.29	0.65
1:B:318:THR:HA	1:B:378:VAL:HG11	1.79	0.64
1:K:323:LEU:HD21	1:K:463:LEU:CD2	2.26	0.64
1:K:194:HIS:CE1	1:K:216:PRO:HB3	2.33	0.64
1:D:183:SER:HB3	1:D:500:ARG:HG3	1.80	0.64
1:F:441:VAL:H	1:F:442:PRO:HD2	1.61	0.64
1:E:189:GLN:HB3	1:E:190:PRO:HD3	1.78	0.64

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:173:LYS:HE3	1:F:470:HIS:HB3	1.80	0.64
2:F:601:HEM:C4A	3:F:602:OT3:H7	2.33	0.64
1:A:337:GLN:HE22	1:A:473:VAL:H	1.44	0.64
1:D:328:PHE:CE2	1:D:332:ARG:HD2	2.32	0.64
1:K:38:PHE:HE2	1:K:80:ARG:HD3	1.62	0.64
1:E:43:GLN:NE2	1:E:82:ASN:HB2	2.14	0.63
1:F:129:VAL:HG12	2:F:601:HEM:HAD1	1.81	0.63
1:B:181:ARG:HH21	1:F:274:ILE:HD12	1.63	0.63
1:E:52:LEU:HD11	1:E:240:MET:SD	2.38	0.63
1:F:44:HIS:HD2	1:F:71:THR:HG21	1.63	0.63
1:F:47:ASN:C	1:F:49:TRP:H	2.01	0.63
1:I:441:VAL:H	1:I:442:PRO:HD3	1.63	0.63
1:B:441:VAL:N	1:B:442:PRO:HD3	2.13	0.63
1:D:356:GLN:NE2	1:D:356:GLN:H	1.94	0.63
1:G:315:SER:HB3	2:G:601:HEM:CBC	2.29	0.63
1:H:166:ARG:HH22	1:H:352:SER:HA	1.64	0.63
1:B:287:THR:HG21	1:D:181:ARG:HG3	1.81	0.63
1:D:47:ASN:HD21	1:D:50:LEU:HD12	1.63	0.62
1:K:122:HIS:HD2	1:K:123:ARG:HE	1.46	0.62
1:K:356:GLN:HE21	1:K:356:GLN:N	1.94	0.62
1:G:329:GLU:O	1:G:333:ASN:ND2	2.31	0.62
1:I:103:VAL:HG11	1:I:386:VAL:HG13	1.79	0.62
1:K:190:PRO:O	1:K:194:HIS:HD2	1.82	0.62
1:A:245:SER:HA	1:A:248:ILE:HG22	1.80	0.62
1:J:137:TRP:CE2	1:J:448:ARG:HD3	2.34	0.62
2:L:601:HEM:C4A	3:L:602:OT3:H7	2.34	0.62
1:I:386:VAL:HG11	1:I:390:LEU:CD2	2.30	0.62
1:H:330:LEU:CD2	1:H:340:LEU:HD12	2.30	0.62
1:C:242:ARG:O	1:C:246:ARG:HB2	1.98	0.62
1:K:318:THR:O	2:K:601:HEM:HAB	1.99	0.62
1:E:422:ARG:HE	1:E:424:ASN:HB2	1.65	0.61
1:D:443:PHE:CG	1:D:453:ARG:HG3	2.34	0.61
1:G:101:GLN:HE21	1:G:438:PHE:HZ	1.48	0.61
1:H:157:PHE:HA	1:H:160:MET:HE2	1.82	0.61
2:J:601:HEM:HBB2	2:J:601:HEM:HMB2	1.82	0.61
1:E:209:LEU:O	1:E:211:LEU:N	2.32	0.61
1:C:441:VAL:N	1:C:442:PRO:HD3	2.15	0.61
1:F:474:GLU:OE1	1:F:500:ARG:NH1	2.32	0.61
1:A:444:GLY:HA3	2:A:601:HEM:HBA1	1.81	0.61
1:B:141:ARG:HD2	1:B:145:ASN:OD1	2.00	0.61
1:B:273:LYS:HG2	1:D:185:THR:HB	1.82	0.61

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:GLU:OE1	1:C:181:ARG:NH1	2.33	0.61
1:B:315:SER:HB3	2:B:601:HEM:HBC2	1.81	0.61
1:G:194:HIS:CE1	1:G:216:PRO:HB3	2.35	0.61
1:B:158:LEU:HD23	1:B:356:GLN:HA	1.83	0.61
2:C:601:HEM:NA	3:C:602:OT3:H7	2.16	0.61
1:G:271:ILE:HD11	1:G:308:SER:CB	2.30	0.61
1:A:141:ARG:HD2	1:A:145:ASN:OD1	2.01	0.61
1:E:166:ARG:HH22	1:E:352:SER:HA	1.65	0.60
1:K:158:LEU:N	1:K:159:PRO:HD2	2.15	0.60
1:B:47:ASN:HB3	1:B:50:LEU:HD12	1.83	0.60
1:C:440:HIS:ND1	4:C:714:HOH:O	2.31	0.60
1:D:475:THR:CG2	1:D:496:LEU:O	2.50	0.60
1:I:123:ARG:HH21	1:I:123:ARG:CG	2.00	0.60
1:F:110:ARG:HB2	1:F:383:GLU:HB3	1.83	0.60
1:A:157:PHE:HA	1:A:160:MET:HE2	1.83	0.60
1:A:205:PHE:O	1:C:181:ARG:NH2	2.35	0.60
1:F:446:GLY:O	1:F:448:ARG:N	2.33	0.60
1:H:65:HIS:CD2	1:H:65:HIS:H	2.20	0.60
1:B:87:ARG:NE	1:B:398:PRO:HG2	2.17	0.60
1:I:52:LEU:HD22	1:I:239:PHE:O	2.00	0.60
1:I:65:HIS:HB3	1:I:380:LEU:HD11	1.84	0.60
1:F:481:ILE:HD11	1:F:495:PRO:HG3	1.83	0.60
1:B:481:ILE:HG23	1:B:493:THR:HG22	1.84	0.60
1:F:103:VAL:O	1:F:103:VAL:HG12	2.02	0.60
1:J:123:ARG:HB2	1:J:125:HIS:CD2	2.36	0.60
1:L:384:ARG:HH22	2:L:601:HEM:CGA	2.14	0.60
1:L:70:GLN:HA	1:L:73:GLN:HG2	1.84	0.60
1:A:475:THR:HG23	1:A:496:LEU:O	2.02	0.59
1:F:155:GLN:OE1	1:F:356:GLN:HB3	2.02	0.59
1:G:198:GLU:HG3	1:G:212:VAL:HG23	1.84	0.59
1:G:88:MET:HB2	1:G:402:LEU:HB3	1.83	0.59
1:L:378:VAL:HG12	2:L:601:HEM:HMB2	1.83	0.59
1:L:78:ILE:HD12	1:L:91:VAL:HG23	1.84	0.59
1:C:141:ARG:HD2	1:C:145:ASN:OD1	2.02	0.59
1:C:52:LEU:HD21	1:C:240:MET:HB3	1.85	0.59
1:K:325:MET:HA	1:K:325:MET:CE	2.32	0.59
1:C:62:GLU:HB3	1:C:484:VAL:HG22	1.84	0.59
1:H:475:THR:HG23	1:H:496:LEU:O	2.02	0.59
1:G:476:LEU:HB2	1:K:276:GLN:HG3	1.85	0.59
1:D:329:GLU:OE1	1:D:332:ARG:HD3	2.03	0.59
1:D:318:THR:HA	1:D:378:VAL:HG11	1.84	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:601:HEM:HBC2	2:F:601:HEM:CMC	2.33	0.58
1:I:343:GLU:OE1	1:I:362:LEU:HA	2.04	0.58
1:A:55:ILE:HD11	1:A:61:TYR:CD1	2.38	0.58
1:F:441:VAL:H	1:F:442:PRO:CD	2.15	0.58
1:L:447:MET:CE	1:L:447:MET:HA	2.33	0.58
1:B:233:SER:OG	1:B:256:HIS:HD2	1.87	0.58
1:C:441:VAL:N	1:C:442:PRO:CD	2.65	0.58
1:G:181:ARG:HD2	1:K:277:GLU:HB3	1.85	0.58
1:G:419:ARG:HH21	1:G:422:ARG:HD2	1.68	0.58
1:D:87:ARG:HB3	1:D:401:THR:HG23	1.86	0.58
1:E:190:PRO:O	1:E:194:HIS:HD2	1.86	0.58
1:F:103:VAL:HG21	1:F:390:LEU:HD22	1.83	0.58
1:H:240:MET:HE2	1:H:248:ILE:HG21	1.84	0.58
1:I:101:GLN:O	1:I:104:ASP:HB2	2.03	0.58
1:D:420:PRO:HD2	1:I:282:ARG:HH12	1.68	0.58
1:B:205:PHE:O	1:D:181:ARG:NH2	2.37	0.58
1:G:452:GLY:HA3	2:G:601:HEM:C3C	2.39	0.58
1:J:35:VAL:HG12	1:J:36:LEU:H	1.69	0.58
1:A:197:ILE:HD11	1:A:224:LEU:HD21	1.86	0.58
1:G:52:LEU:HA	1:G:55:ILE:HG22	1.86	0.58
1:H:81:TYR:HB3	1:H:88:MET:HG2	1.86	0.57
1:I:273:LYS:O	1:I:277:GLU:HG3	2.03	0.57
1:F:197:ILE:HD11	1:F:224:LEU:HD21	1.85	0.57
1:B:101:GLN:O	1:B:104:ASP:HB2	2.05	0.57
1:H:240:MET:CE	1:H:248:ILE:HG21	2.33	0.57
1:H:412:ARG:HG3	1:H:412:ARG:HH11	1.68	0.57
1:I:377:PRO:O	1:I:489:LEU:HB3	2.03	0.57
1:F:419:ARG:HH21	1:F:422:ARG:HD3	1.69	0.57
2:F:601:HEM:HBB2	2:F:601:HEM:HMB2	1.86	0.57
1:I:139:PHE:O	1:I:143:ARG:HD2	2.03	0.57
1:C:133:ASN:OD1	1:C:448:ARG:NH2	2.37	0.57
1:F:357:LYS:O	1:F:361:GLU:HG2	2.04	0.57
1:G:314:GLY:O	1:G:318:THR:OG1	2.21	0.57
1:I:161:VAL:HG12	1:I:462:LEU:HD12	1.86	0.57
1:J:296:LYS:O	1:J:298:GLU:N	2.38	0.57
1:J:371:GLU:OE2	1:J:427:ARG:NH1	2.37	0.57
1:K:173:LYS:O	1:K:177:LEU:HG	2.05	0.57
1:C:406:PHE:CZ	1:C:408:TYR:HB3	2.39	0.57
1:I:154:VAL:HG21	1:I:454:ARG:HD3	1.85	0.57
2:A:601:HEM:NA	3:A:602:OT3:H7	2.20	0.56
1:E:441:VAL:N	1:E:442:PRO:CD	2.68	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:154:VAL:O	1:F:158:LEU:HB2	2.04	0.56
1:F:380:LEU:HD12	1:F:485:TYR:CD1	2.40	0.56
1:F:65:HIS:CE1	1:F:66:LEU:HG	2.40	0.56
1:G:181:ARG:HG3	1:G:181:ARG:NH1	2.19	0.56
1:G:44:HIS:HD2	1:G:71:THR:HG21	1.69	0.56
1:I:309:MET:HE3	1:I:309:MET:HA	1.88	0.56
1:L:329:GLU:HA	1:L:329:GLU:OE1	2.06	0.56
1:A:198:GLU:CD	1:A:209:LEU:O	2.43	0.56
1:E:337:GLN:HE21	1:E:341:ARG:HH22	1.53	0.56
1:I:337:GLN:HE21	1:I:341:ARG:HH22	1.53	0.56
1:D:475:THR:HG23	1:D:496:LEU:O	2.06	0.56
1:F:82:ASN:O	1:F:84:GLY:N	2.39	0.56
1:H:176:VAL:HG11	1:H:501:ALA:HB2	1.86	0.56
1:I:141:ARG:HD2	1:I:145:ASN:OD1	2.06	0.56
1:J:323:LEU:HG	1:J:460:MET:HG2	1.86	0.56
1:H:386:VAL:HG21	1:H:390:LEU:HD22	1.87	0.56
1:A:418:PRO:O	1:A:427:ARG:NH2	2.38	0.56
1:B:233:SER:HA	1:B:236:GLN:OE1	2.05	0.56
1:F:189:GLN:HB3	1:F:190:PRO:HD3	1.88	0.56
1:F:391:VAL:HA	1:F:395:TYR:O	2.04	0.56
1:C:318:THR:HA	1:C:378:VAL:HG11	1.85	0.56
1:H:274:ILE:HD12	1:I:181:ARG:HH21	1.69	0.56
1:A:343:GLU:OE1	1:A:363:PRO:HD2	2.05	0.56
1:K:370:LYS:HG2	1:K:440:HIS:CE1	2.41	0.56
1:L:207:GLU:OE2	1:L:273:LYS:HE2	2.05	0.56
1:F:271:ILE:HA	1:F:274:ILE:HG22	1.87	0.56
1:F:322:PRO:HB2	1:F:460:MET:HE1	1.88	0.56
1:G:38:PHE:CE2	1:G:87:ARG:HG2	2.41	0.56
1:H:315:SER:HA	2:H:601:HEM:HMC2	1.88	0.56
1:J:205:PHE:O	1:K:181:ARG:NH2	2.39	0.56
1:B:307:ASN:O	1:B:311:LEU:HG	2.05	0.55
1:F:416:LEU:HB3	1:F:439:HIS:CE1	2.41	0.55
1:G:296:LYS:HB3	1:G:298:GLU:HG3	1.87	0.55
1:H:194:HIS:CE1	1:H:216:PRO:HB3	2.41	0.55
1:H:474:GLU:OE1	1:H:500:ARG:NH1	2.39	0.55
1:K:471:PHE:HA	1:K:500:ARG:O	2.06	0.55
2:D:601:HEM:HBB2	2:D:601:HEM:HMB2	1.86	0.55
1:E:122:HIS:HD2	1:E:123:ARG:HE	1.54	0.55
1:G:103:VAL:O	1:G:103:VAL:HG12	2.06	0.55
1:I:181:ARG:HB2	1:I:181:ARG:NH1	2.16	0.55
1:K:122:HIS:CD2	1:K:123:ARG:HE	2.25	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:337:GLN:HE22	1:C:473:VAL:H	1.54	0.55
1:H:244:LEU:HD21	1:K:53:LEU:HD13	1.88	0.55
1:D:98:GLU:O	1:D:102:GLN:HG2	2.07	0.55
1:L:487:PHE:HE2	3:L:602:OT3:H2	1.70	0.55
1:B:240:MET:CE	1:B:248:ILE:HG21	2.36	0.55
1:C:369:LEU:HD22	1:C:460:MET:CE	2.37	0.55
1:E:437:ASN:N	1:E:437:ASN:OD1	2.39	0.55
1:I:309:MET:CE	1:I:309:MET:HA	2.37	0.55
1:G:390:LEU:HB3	1:G:397:ILE:HB	1.89	0.55
1:H:271:ILE:HA	1:H:274:ILE:HG22	1.87	0.55
1:K:482:LYS:H	1:K:482:LYS:HD2	1.72	0.55
1:D:390:LEU:HD23	1:D:397:ILE:HB	1.88	0.55
1:E:338:GLN:NE2	1:E:341:ARG:HE	2.04	0.55
1:F:263:ILE:HG22	1:F:309:MET:CE	2.37	0.55
1:J:287:THR:HG22	1:K:180:ALA:HB1	1.89	0.55
1:J:453:ARG:HG2	1:J:457:GLU:OE1	2.07	0.55
1:D:166:ARG:O	1:D:170:GLN:HB2	2.07	0.54
1:A:62:GLU:HG2	1:A:484:VAL:HG13	1.89	0.54
1:B:65:HIS:HA	1:B:406:PHE:HZ	1.71	0.54
1:D:343:GLU:OE1	1:D:363:PRO:HD2	2.07	0.54
1:D:389:ASP:OD1	1:D:399:ALA:N	2.40	0.54
1:E:341:ARG:HD3	1:E:468:LEU:O	2.07	0.54
2:B:601:HEM:HBC2	2:B:601:HEM:HMC2	1.87	0.54
1:J:474:GLU:OE1	1:J:500:ARG:NH1	2.40	0.54
1:A:103:VAL:O	1:A:103:VAL:CG1	2.54	0.54
1:E:122:HIS:CD2	1:E:123:ARG:HE	2.25	0.54
1:E:52:LEU:HD11	1:E:240:MET:HB3	1.89	0.54
1:E:469:LYS:O	1:E:509:HIS:HB2	2.08	0.54
1:E:52:LEU:CD1	1:E:240:MET:HB3	2.38	0.54
1:B:406:PHE:CE2	1:B:408:TYR:HB3	2.43	0.54
1:D:103:VAL:CG1	1:D:103:VAL:O	2.55	0.54
1:G:500:ARG:HH11	1:G:500:ARG:HB3	1.72	0.54
1:F:390:LEU:HG	1:F:397:ILE:HB	1.90	0.54
2:F:601:HEM:CMB	2:F:601:HEM:HBB2	2.37	0.54
1:A:44:HIS:CD2	1:A:46:GLY:H	2.24	0.54
1:B:309:MET:HA	1:B:309:MET:HE3	1.89	0.54
1:D:234:THR:O	1:D:238:MET:HB2	2.07	0.54
1:D:382:LEU:HB2	1:D:405:VAL:HB	1.89	0.54
1:E:101:GLN:O	1:E:104:ASP:HB2	2.06	0.54
1:J:452:GLY:HA3	2:J:601:HEM:HBC2	1.90	0.54
1:L:159:PRO:HG3	1:L:356:GLN:HE21	1.71	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:601:HEM:C4A	3:C:602:OT3:H7	2.43	0.54
1:E:323:LEU:HG	1:E:460:MET:HG2	1.90	0.54
1:I:83:LEU:HD23	1:I:86:PRO:HB2	1.90	0.54
1:E:48:ARG:NE	1:E:84:GLY:HA2	2.22	0.54
2:F:601:HEM:NA	3:F:602:OT3:H7	2.22	0.54
1:C:158:LEU:HD23	1:C:462:LEU:CD1	2.36	0.53
1:C:475:THR:CG2	1:C:497:LEU:HD23	2.36	0.53
1:D:443:PHE:CD2	1:D:453:ARG:HG3	2.43	0.53
1:J:354:HIS:HB2	1:J:357:LYS:HD2	1.88	0.53
1:J:77:PRO:HB3	1:J:93:LEU:HD11	1.90	0.53
1:L:410:LEU:C	1:L:410:LEU:HD12	2.29	0.53
1:A:386:VAL:CG1	1:A:388:SER:O	2.56	0.53
2:C:601:HEM:CMB	2:C:601:HEM:HBB2	2.38	0.53
1:F:330:LEU:HB3	1:F:337:GLN:HG3	1.90	0.53
1:L:245:SER:CB	1:L:253:TRP:HE1	2.17	0.53
1:D:472:LEU:HG	1:D:502:ILE:CG2	2.37	0.53
1:I:107:HIS:HB3	1:I:134:GLY:HA2	1.89	0.53
1:J:244:LEU:O	1:J:248:ILE:HG22	2.08	0.53
1:E:325:MET:HA	1:E:325:MET:CE	2.39	0.53
1:I:245:SER:HB2	1:I:253:TRP:HE1	1.73	0.53
1:L:264:PHE:HA	1:L:309:MET:SD	2.49	0.53
1:F:186:LEU:H	1:F:186:LEU:HD23	1.73	0.53
1:H:160:MET:CE	1:H:286:TYR:CE2	2.88	0.53
2:I:601:HEM:C4A	3:I:602:OT3:H7	2.44	0.53
1:K:475:THR:HG22	1:K:477:THR:H	1.73	0.53
1:D:194:HIS:CE1	1:D:216:PRO:HB3	2.42	0.53
1:A:181:ARG:NH2	1:E:205:PHE:O	2.39	0.53
1:D:414:ALA:HB2	1:D:420:PRO:HG3	1.90	0.53
1:K:174:LYS:HA	1:K:177:LEU:HD12	1.90	0.53
1:L:384:ARG:NH2	2:L:601:HEM:O1A	2.42	0.53
1:J:183:SER:HB3	1:J:500:ARG:HA	1.90	0.53
1:E:332:ARG:NH1	1:E:480:ASP:OD2	2.41	0.53
1:G:54:GLN:HE22	1:G:58:GLU:HG3	1.74	0.53
1:B:264:PHE:HA	1:B:309:MET:SD	2.49	0.52
1:G:160:MET:CE	1:G:203:ALA:HA	2.38	0.52
1:I:330:LEU:HD21	1:I:340:LEU:HD12	1.91	0.52
1:J:72:PHE:HB3	1:J:92:MET:HE1	1.91	0.52
1:K:196:THR:HG21	1:K:320:ALA:HB2	1.91	0.52
1:B:242:ARG:HA	1:B:245:SER:OG	2.09	0.52
1:H:329:GLU:O	1:H:333:ASN:ND2	2.40	0.52
1:I:123:ARG:NH2	1:I:123:ARG:CG	2.64	0.52

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:284:GLN:H	1:E:284:GLN:CD	2.12	0.52
2:I:601:HEM:NA	3:I:602:0T3:H7	2.24	0.52
1:K:154:VAL:HG21	1:K:454:ARG:HB3	1.92	0.52
1:A:52:LEU:HD22	1:A:239:PHE:O	2.10	0.52
1:B:121:GLN:HE22	1:B:242:ARG:HH22	1.57	0.52
1:F:422:ARG:HH11	1:F:424:ASN:HB2	1.75	0.52
1:G:44:HIS:CD2	1:G:71:THR:HG21	2.44	0.52
1:K:237:LEU:HD22	1:K:253:TRP:NE1	2.25	0.52
1:F:47:ASN:C	1:F:49:TRP:N	2.62	0.52
1:J:159:PRO:HG3	1:J:356:GLN:HE21	1.73	0.52
1:J:189:GLN:HA	1:J:324:LEU:HD11	1.90	0.52
1:K:189:GLN:HB3	1:K:190:PRO:HD3	1.92	0.52
1:I:287:THR:HG21	1:L:181:ARG:HG3	1.92	0.52
1:A:380:LEU:HB3	1:A:381:PHE:HD2	1.74	0.52
2:I:601:HEM:HMB2	2:I:601:HEM:HBB2	1.91	0.52
1:L:284:GLN:CD	1:L:284:GLN:H	2.13	0.52
1:A:65:HIS:H	1:A:65:HIS:CD2	2.27	0.52
1:C:65:HIS:HB3	1:C:380:LEU:HD11	1.92	0.52
1:F:36:LEU:HB2	1:F:394:ASN:O	2.08	0.52
1:J:166:ARG:HG3	1:J:466:HIS:CE1	2.44	0.52
1:K:139:PHE:O	1:K:143:ARG:HD3	2.10	0.52
1:L:486:SER:HB3	1:L:490:ARG:HH21	1.74	0.52
1:B:83:LEU:HD23	1:B:86:PRO:HB2	1.92	0.52
1:J:322:PRO:HB2	1:J:460:MET:HE3	1.92	0.52
1:D:57:ARG:HD2	1:E:247:TRP:CE3	2.45	0.52
1:F:127:CYS:HB3	1:F:131:LEU:HB2	1.91	0.52
1:G:332:ARG:NH1	1:G:480:ASP:OD2	2.42	0.52
1:L:146:PRO:HA	1:L:150:SER:OG	2.10	0.52
1:B:194:HIS:CE1	1:B:216:PRO:HB3	2.45	0.51
1:J:475:THR:HG22	1:J:476:LEU:N	2.25	0.51
1:K:163:ALA:HA	1:K:166:ARG:NH1	2.25	0.51
1:D:337:GLN:NE2	1:D:341:ARG:HH12	2.08	0.51
1:F:406:PHE:CD2	1:F:409:SER:HB2	2.41	0.51
1:I:386:VAL:HG12	1:I:388:SER:H	1.74	0.51
1:J:157:PHE:HA	1:J:160:MET:HE2	1.92	0.51
1:B:198:GLU:OE2	1:B:210:GLY:N	2.43	0.51
1:G:181:ARG:CG	1:G:181:ARG:NH1	2.67	0.51
1:H:274:ILE:CD1	1:I:181:ARG:HH21	2.23	0.51
1:D:158:LEU:HD22	1:D:356:GLN:HA	1.92	0.51
1:F:406:PHE:CZ	1:F:408:TYR:HB3	2.46	0.51
1:I:325:MET:HB3	1:I:376:TYR:CD1	2.46	0.51

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:185:THR:CG2	1:J:496:LEU:HG	2.39	0.51
1:K:365:LEU:HG	1:K:461:LEU:HD23	1.93	0.51
1:L:160:MET:HB3	1:L:202:LEU:CD2	2.41	0.51
2:D:601:HEM:NA	3:D:602:OT3:H7	2.26	0.51
1:G:357:LYS:HG2	1:G:361:GLU:OE2	2.10	0.51
1:G:331:ALA:HB1	1:G:475:THR:HG22	1.92	0.51
1:C:52:LEU:HD22	1:C:240:MET:HB3	1.92	0.51
1:E:194:HIS:HE1	1:E:220:SER:OG	1.94	0.51
1:F:391:VAL:HG13	1:F:395:TYR:H	1.74	0.51
1:A:263:ILE:HG22	1:A:309:MET:HE1	1.93	0.51
2:B:601:HEM:HMB2	2:B:601:HEM:HBB2	1.93	0.51
1:D:274:ILE:HD12	1:F:181:ARG:HH21	1.75	0.51
1:F:87:ARG:HD3	1:F:398:PRO:HG2	1.93	0.51
1:H:132:LEU:O	1:H:448:ARG:NH2	2.44	0.51
1:I:254:LYS:O	1:I:258:GLU:HB2	2.11	0.51
1:I:162:ASP:HB2	1:I:462:LEU:HD13	1.91	0.51
1:L:41:MET:HB2	1:L:80:ARG:HD3	1.92	0.51
1:E:389:ASP:HA	1:E:397:ILE:O	2.11	0.50
1:F:240:MET:HG3	1:F:245:SER:HB3	1.93	0.50
1:I:475:THR:HG22	1:I:477:THR:N	2.26	0.50
1:F:209:LEU:O	1:F:211:LEU:N	2.44	0.50
1:F:244:LEU:O	1:F:248:ILE:CG2	2.59	0.50
1:I:190:PRO:O	1:I:194:HIS:HD2	1.94	0.50
1:C:475:THR:CG2	1:C:496:LEU:O	2.59	0.50
2:E:601:HEM:NA	3:E:602:OT3:H7	2.26	0.50
1:G:190:PRO:O	1:G:194:HIS:HD2	1.94	0.50
1:G:198:GLU:CG	1:G:212:VAL:HG23	2.40	0.50
1:J:322:PRO:O	1:J:326:THR:OG1	2.21	0.50
1:F:94:PRO:HG2	1:F:416:LEU:HD13	1.93	0.50
1:H:234:THR:O	1:H:238:MET:HB2	2.12	0.50
2:B:601:HEM:CMB	2:B:601:HEM:HBB2	2.42	0.50
1:C:277:GLU:OE1	1:E:181:ARG:NH1	2.44	0.50
1:C:322:PRO:HG3	1:C:378:VAL:CG2	2.42	0.50
1:H:139:PHE:O	1:H:143:ARG:HD2	2.12	0.50
1:H:337:GLN:HE21	1:H:341:ARG:HH22	1.59	0.50
1:H:281:ASN:HB2	1:I:500:ARG:NH2	2.27	0.50
1:E:369:LEU:HD22	1:E:460:MET:HE3	1.94	0.50
1:F:406:PHE:CE2	1:F:408:TYR:HB3	2.47	0.50
1:J:67:GLU:O	1:J:70:GLN:HB3	2.11	0.50
1:C:386:VAL:CG1	1:C:388:SER:O	2.60	0.50
1:H:89:VAL:HG21	1:H:397:ILE:HD12	1.93	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:322:PRO:HG3	1:B:378:VAL:CG2	2.41	0.50
1:D:329:GLU:OE1	1:D:329:GLU:HA	2.12	0.50
1:E:240:MET:HG3	1:E:245:SER:HB3	1.94	0.50
1:F:163:ALA:HA	1:F:166:ARG:NH1	2.26	0.50
1:H:273:LYS:HG2	1:I:185:THR:HB	1.93	0.50
1:B:149:LEU:HD12	1:B:454:ARG:HG3	1.94	0.50
1:F:301:LEU:HG	1:F:305:LYS:HE3	1.94	0.50
1:K:192:ILE:HG13	1:K:324:LEU:HD12	1.94	0.50
1:L:140:ASN:ND2	1:L:307:ASN:HD21	2.09	0.50
1:D:154:VAL:O	1:D:158:LEU:HB2	2.12	0.49
1:G:300:SER:O	1:G:301:LEU:C	2.49	0.49
1:G:49:TRP:HA	1:G:49:TRP:CE3	2.47	0.49
1:I:323:LEU:HG	1:I:460:MET:HG2	1.93	0.49
1:L:53:LEU:O	1:L:57:ARG:HB2	2.12	0.49
1:A:386:VAL:HG12	1:A:388:SER:O	2.12	0.49
1:D:273:LYS:O	1:D:277:GLU:HG3	2.11	0.49
1:D:78:ILE:HG13	1:D:91:VAL:HG12	1.94	0.49
1:G:244:LEU:HD23	1:G:248:ILE:HG23	1.94	0.49
1:I:370:LYS:HG2	1:I:440:HIS:CE1	2.46	0.49
1:K:101:GLN:HE21	1:K:438:PHE:HE2	1.60	0.49
1:C:132:LEU:HD22	1:C:136:GLU:HG2	1.94	0.49
1:H:137:TRP:CZ2	1:H:448:ARG:HG2	2.47	0.49
1:H:337:GLN:NE2	1:H:473:VAL:H	2.07	0.49
1:F:380:LEU:HG	1:F:489:LEU:HB2	1.94	0.49
1:J:88:MET:HB2	1:J:402:LEU:HB3	1.94	0.49
1:K:230:MET:O	1:K:234:THR:OG1	2.22	0.49
1:K:92:MET:CE	1:K:409:SER:HB3	2.43	0.49
1:D:48:ARG:NH2	1:D:84:GLY:HA3	2.25	0.49
1:F:150:SER:O	1:F:154:VAL:HG23	2.13	0.49
1:G:190:PRO:O	1:G:194:HIS:CD2	2.66	0.49
1:J:107:HIS:CB	1:J:134:GLY:HA2	2.41	0.49
1:J:35:VAL:HG12	1:J:36:LEU:N	2.27	0.49
1:K:267:GLY:HA3	1:K:309:MET:CE	2.43	0.49
1:B:87:ARG:HE	1:B:398:PRO:HG2	1.77	0.49
1:D:371:GLU:HA	1:D:371:GLU:OE1	2.13	0.49
1:L:268:ASP:HA	1:L:271:ILE:HG22	1.94	0.49
1:B:332:ARG:NH1	1:B:480:ASP:OD2	2.45	0.49
1:B:444:GLY:HA3	2:B:601:HEM:HBA1	1.94	0.49
1:C:424:ASN:O	1:C:427:ARG:HB2	2.12	0.49
1:E:325:MET:SD	1:E:491:PRO:HG3	2.53	0.49
1:F:263:ILE:HG22	1:F:309:MET:HE2	1.93	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:381:PHE:CD2	1:H:406:PHE:CE2	3.00	0.49
1:I:65:HIS:CE1	1:I:66:LEU:HG	2.47	0.49
1:J:154:VAL:HG21	1:J:454:ARG:HD3	1.94	0.49
1:G:181:ARG:NH2	1:K:274:ILE:CD1	2.74	0.49
1:A:122:HIS:O	1:A:122:HIS:CG	2.66	0.49
1:D:474:GLU:OE1	1:D:500:ARG:NH2	2.45	0.49
1:F:47:ASN:O	1:F:49:TRP:N	2.45	0.49
1:E:140:ASN:N	1:E:140:ASN:HD22	2.10	0.49
1:E:160:MET:CE	1:E:203:ALA:HA	2.43	0.49
1:G:54:GLN:NE2	1:G:58:GLU:HG3	2.27	0.49
1:J:406:PHE:CE2	1:J:408:TYR:HB3	2.48	0.49
1:L:487:PHE:CE2	3:L:602:OT3:H2	2.47	0.49
2:A:601:HEM:C4A	3:A:602:OT3:H7	2.48	0.49
1:B:105:SER:HB2	1:B:107:HIS:H	1.78	0.49
1:F:307:ASN:O	1:F:311:LEU:HG	2.13	0.49
1:I:181:ARG:CB	1:I:181:ARG:HH11	2.18	0.49
1:J:309:MET:CE	1:J:309:MET:HA	2.43	0.49
1:L:87:ARG:O	1:L:87:ARG:HD2	2.12	0.49
1:B:198:GLU:HG3	1:B:212:VAL:HG23	1.95	0.48
1:C:416:LEU:HD22	1:C:439:HIS:CE1	2.48	0.48
1:C:443:PHE:CG	1:C:453:ARG:HG3	2.48	0.48
1:H:133:ASN:OD1	1:H:448:ARG:NH2	2.45	0.48
1:I:348:ALA:HB2	1:I:469:LYS:HD2	1.94	0.48
1:B:318:THR:O	1:B:322:PRO:CD	2.61	0.48
1:B:392:LEU:HD12	1:B:397:ILE:HG13	1.95	0.48
1:J:364:LEU:HD12	1:J:429:LEU:HD11	1.94	0.48
1:K:366:ARG:O	1:K:369:LEU:HB2	2.11	0.48
1:F:375:LEU:O	1:F:377:PRO:HD3	2.13	0.48
1:D:52:LEU:CD2	1:D:239:PHE:O	2.62	0.48
1:C:240:MET:CE	1:C:245:SER:HB3	2.43	0.48
1:I:160:MET:HE3	1:I:203:ALA:HA	1.96	0.48
1:K:137:TRP:CD1	1:K:448:ARG:NH1	2.81	0.48
1:C:455:LEU:O	1:C:459:GLU:HG3	2.14	0.48
1:E:406:PHE:HD2	1:E:409:SER:HG	1.61	0.48
1:G:181:ARG:NH2	1:K:274:ILE:CG1	2.52	0.48
1:H:443:PHE:O	1:H:449:GLN:HG3	2.13	0.48
1:I:337:GLN:HE22	1:I:473:VAL:N	1.97	0.48
1:I:64:LEU:O	1:I:68:MET:HG2	2.13	0.48
1:L:378:VAL:HG12	2:L:601:HEM:CMB	2.44	0.48
1:L:63:HIS:CD2	1:L:63:HIS:H	2.31	0.48
1:C:416:LEU:HD22	1:C:439:HIS:HE1	1.78	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:237:LEU:HD22	1:H:253:TRP:NE1	2.28	0.48
1:J:109:CYS:O	1:J:384:ARG:HA	2.14	0.48
1:F:290:VAL:HG12	1:F:294:LEU:HD12	1.94	0.48
1:F:47:ASN:HD22	1:F:47:ASN:N	2.12	0.48
1:B:198:GLU:OE2	1:B:211:LEU:N	2.40	0.48
1:F:72:PHE:CD2	1:F:92:MET:HG2	2.49	0.48
1:H:294:LEU:HD23	1:H:304:ILE:HD13	1.95	0.48
1:D:146:PRO:HA	1:D:150:SER:OG	2.14	0.47
1:H:205:PHE:O	1:I:181:ARG:NH2	2.46	0.47
1:J:111:MET:O	1:J:112:ILE:C	2.52	0.47
1:L:133:ASN:OD1	1:L:448:ARG:NH2	2.47	0.47
1:E:39:GLU:HG2	1:E:39:GLU:H	1.44	0.47
1:F:389:ASP:OD1	1:F:398:PRO:HA	2.13	0.47
1:F:441:VAL:HA	4:F:712:HOH:O	2.14	0.47
1:H:328:PHE:CE2	1:H:481:ILE:HG13	2.48	0.47
1:I:424:ASN:O	1:I:427:ARG:HB2	2.13	0.47
1:G:48:ARG:HH21	1:L:49:TRP:HE3	1.60	0.47
1:C:371:GLU:HA	1:C:371:GLU:OE1	2.14	0.47
1:A:137:TRP:CD1	1:A:448:ARG:NH1	2.82	0.47
1:B:51:ARG:HD3	1:B:81:TYR:OH	2.15	0.47
1:L:234:THR:OG1	1:L:256:HIS:HE1	1.96	0.47
1:A:145:ASN:HB2	1:A:146:PRO:HD3	1.95	0.47
1:B:55:ILE:HD11	1:B:61:TYR:CD1	2.49	0.47
1:F:366:ARG:HG3	1:F:461:LEU:HD13	1.95	0.47
1:G:105:SER:HB2	1:G:107:HIS:H	1.79	0.47
1:G:274:ILE:CD1	1:J:181:ARG:NH2	2.78	0.47
1:I:47:ASN:HD22	1:I:48:ARG:N	2.13	0.47
1:B:475:THR:HB	1:B:477:THR:H	1.80	0.47
1:H:412:ARG:HG3	1:H:412:ARG:NH1	2.30	0.47
1:I:382:LEU:HD22	1:I:444:GLY:HA2	1.96	0.47
1:I:48:ARG:HB3	1:I:82:ASN:O	2.15	0.47
1:K:52:LEU:HD13	1:K:240:MET:HB3	1.97	0.47
1:F:393:GLN:O	1:F:394:ASN:HB2	2.14	0.47
1:G:139:PHE:O	1:G:143:ARG:HD2	2.15	0.47
1:K:168:PHE:CD2	1:K:463:LEU:HD11	2.50	0.47
1:H:43:GLN:HG3	1:H:80:ARG:HG3	1.97	0.47
1:I:167:ASP:OD2	1:I:208:ARG:NH2	2.48	0.47
1:L:192:ILE:HG23	1:L:323:LEU:HD13	1.96	0.47
1:C:443:PHE:CD2	1:C:453:ARG:HG3	2.50	0.47
1:E:370:LYS:HG2	1:E:440:HIS:CE1	2.50	0.47
1:F:190:PRO:O	1:F:194:HIS:HD2	1.98	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:ARG:NH2	1:F:274:ILE:HD12	2.29	0.47
1:J:337:GLN:HE21	1:J:341:ARG:HH22	1.63	0.47
1:K:354:HIS:HA	1:K:355:PRO:HD2	1.70	0.47
1:K:85:GLY:O	1:K:86:PRO:C	2.53	0.47
1:L:41:MET:HE1	1:L:78:ILE:HG13	1.97	0.47
1:A:47:ASN:HB2	1:A:50:LEU:HD12	1.96	0.47
1:C:329:GLU:OE1	1:C:329:GLU:HA	2.15	0.47
1:D:452:GLY:HA3	2:D:601:HEM:C3C	2.50	0.47
1:E:315:SER:HA	2:E:601:HEM:CMC	2.43	0.47
1:J:189:GLN:HB3	1:J:190:PRO:HD3	1.97	0.47
1:J:294:LEU:HD21	1:J:304:ILE:HG21	1.96	0.47
1:C:240:MET:HE2	1:C:245:SER:HB3	1.97	0.46
1:C:364:LEU:CD1	1:C:429:LEU:HD11	2.45	0.46
1:C:364:LEU:HD12	1:C:364:LEU:HA	1.79	0.46
1:D:43:GLN:HE21	1:D:82:ASN:HB2	1.80	0.46
1:I:448:ARG:HD3	2:I:601:HEM:O2D	2.14	0.46
1:K:198:GLU:HG3	1:K:212:VAL:HG23	1.97	0.46
1:A:315:SER:HA	2:A:601:HEM:HMC2	1.97	0.46
1:D:144:LEU:O	1:D:148:VAL:HG23	2.15	0.46
1:E:437:ASN:C	1:E:439:HIS:H	2.18	0.46
1:F:438:PHE:N	4:F:716:HOH:O	2.47	0.46
1:K:466:HIS:O	1:K:470:HIS:HD2	1.98	0.46
1:L:466:HIS:O	1:L:470:HIS:HD2	1.98	0.46
1:K:169:SER:O	1:K:170:GLN:C	2.52	0.46
1:K:97:VAL:HG22	1:K:405:VAL:HG11	1.97	0.46
2:K:601:HEM:HH A	2:K:601:HEM:HBD1	1.98	0.46
1:L:310:GLU:HG2	3:L:602:OT3:N17	2.31	0.46
1:B:341:ARG:HD3	1:B:468:LEU:O	2.16	0.46
1:I:471:PHE:HA	1:I:500:ARG:O	2.16	0.46
1:K:176:VAL:HG13	1:K:182:GLY:C	2.35	0.46
1:B:245:SER:HA	1:B:248:ILE:HG22	1.96	0.46
1:F:407:LEU:HD23	1:F:410:LEU:HD23	1.98	0.46
1:F:48:ARG:CZ	1:F:84:GLY:HA2	2.45	0.46
1:I:406:PHE:CE2	1:I:408:TYR:HB3	2.51	0.46
1:J:166:ARG:HG3	1:J:466:HIS:NE2	2.30	0.46
1:L:158:LEU:HD22	1:L:356:GLN:HA	1.97	0.46
1:A:160:MET:HE2	1:A:286:TYR:HE2	1.81	0.46
2:B:601:HEM:NA	3:B:602:OT3:H7	2.30	0.46
1:C:103:VAL:CG1	1:C:103:VAL:O	2.63	0.46
1:D:160:MET:CE	1:D:203:ALA:HA	2.46	0.46
1:K:114:GLU:HB2	1:K:115:PRO:HD3	1.97	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:343:GLU:OE2	1:K:365:LEU:N	2.48	0.46
1:B:314:GLY:HA2	3:B:602:OT3:C11	2.46	0.46
1:C:110:ARG:NH1	2:C:601:HEM:O2D	2.48	0.46
1:C:117:VAL:O	1:C:121:GLN:HG2	2.16	0.46
1:D:322:PRO:HD3	1:D:378:VAL:HG22	1.98	0.46
1:I:166:ARG:O	1:I:170:GLN:HG2	2.16	0.46
1:I:294:LEU:HD23	1:I:304:ILE:HD13	1.96	0.46
1:A:386:VAL:HG11	1:A:390:LEU:HD22	1.97	0.46
1:D:369:LEU:HD22	1:D:460:MET:HE2	1.97	0.46
1:D:331:ALA:HB2	1:D:473:VAL:HG12	1.98	0.46
1:E:141:ARG:HD2	1:E:145:ASN:OD1	2.16	0.46
1:H:107:HIS:HB3	1:H:134:GLY:HA2	1.97	0.46
1:H:245:SER:HA	1:H:248:ILE:CG2	2.43	0.46
1:I:389:ASP:O	1:I:390:LEU:HB3	2.15	0.46
1:J:194:HIS:NE2	1:J:216:PRO:HB3	2.31	0.46
1:L:419:ARG:NH1	1:L:422:ARG:HG3	2.26	0.46
1:B:65:HIS:HA	1:B:406:PHE:CZ	2.50	0.46
1:C:375:LEU:O	1:C:412:ARG:NH1	2.48	0.46
1:E:93:LEU:HD12	1:E:393:GLN:HE22	1.81	0.46
1:H:192:ILE:O	1:H:196:THR:HG23	2.16	0.46
1:H:245:SER:HB2	1:H:253:TRP:HE1	1.81	0.46
1:H:441:VAL:N	1:H:442:PRO:CD	2.79	0.46
1:J:181:ARG:CB	1:J:181:ARG:HH11	2.21	0.46
1:L:450:CYS:HB2	2:L:601:HEM:NA	2.31	0.46
1:L:78:ILE:HD12	1:L:91:VAL:CG2	2.46	0.46
1:A:318:THR:HA	1:A:378:VAL:HG11	1.97	0.45
1:C:111:MET:HE2	1:C:112:ILE:HG12	1.98	0.45
1:H:441:VAL:N	1:H:442:PRO:HD3	2.31	0.45
1:I:472:LEU:HD13	1:I:500:ARG:HH12	1.81	0.45
1:L:323:LEU:HD21	1:L:463:LEU:HD23	1.98	0.45
1:D:48:ARG:O	1:D:51:ARG:HB3	2.16	0.45
1:G:91:VAL:HG12	1:G:92:MET:H	1.81	0.45
1:I:143:ARG:HD3	1:I:299:LEU:HD21	1.99	0.45
1:I:416:LEU:HD22	1:I:439:HIS:HE1	1.82	0.45
1:K:190:PRO:O	1:K:194:HIS:CD2	2.66	0.45
1:L:68:MET:HB2	1:L:406:PHE:CZ	2.51	0.45
1:H:101:GLN:OE1	1:H:438:PHE:HZ	1.99	0.45
2:B:601:HEM:NC	3:B:602:OT3:H6	2.32	0.45
1:C:146:PRO:HA	1:C:150:SER:HB2	1.99	0.45
2:E:601:HEM:C4A	3:E:602:OT3:H7	2.51	0.45
1:F:160:MET:HE3	1:F:203:ALA:HA	1.99	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:386:VAL:HG21	1:H:390:LEU:CD2	2.46	0.45
1:H:455:LEU:O	1:H:459:GLU:HG3	2.16	0.45
1:I:475:THR:HG22	1:I:476:LEU:N	2.32	0.45
1:A:48:ARG:HG2	1:A:82:ASN:O	2.16	0.45
1:D:158:LEU:N	1:D:159:PRO:CD	2.79	0.45
1:I:103:VAL:O	1:I:104:ASP:C	2.55	0.45
1:A:329:GLU:OE2	1:A:332:ARG:NH2	2.50	0.45
1:B:419:ARG:HH21	1:B:422:ARG:HD2	1.81	0.45
1:E:338:GLN:HE22	1:E:341:ARG:HE	1.62	0.45
1:G:441:VAL:N	1:G:442:PRO:CD	2.80	0.45
1:G:487:PHE:HE2	3:G:602:OT3:H2	1.82	0.45
1:H:116:TRP:O	1:H:120:ARG:HD3	2.17	0.45
2:H:601:HEM:C4A	3:H:602:OT3:H7	2.52	0.45
1:L:443:PHE:O	1:L:449:GLN:HG3	2.16	0.45
1:C:160:MET:HE3	1:C:203:ALA:HA	1.98	0.45
1:K:406:PHE:CE2	1:K:408:TYR:HB3	2.52	0.45
1:B:129:VAL:HG13	1:B:137:TRP:CD1	2.51	0.45
1:B:110:ARG:NH1	1:B:448:ARG:HD2	2.31	0.45
1:C:198:GLU:HG2	1:C:211:LEU:HB2	1.99	0.45
1:D:53:LEU:HD13	1:E:244:LEU:HD11	1.98	0.45
1:E:141:ARG:NH1	1:E:449:GLN:O	2.28	0.45
1:F:424:ASN:OD1	1:F:426:GLN:HB3	2.17	0.45
1:H:197:ILE:HD11	1:H:224:LEU:HD21	1.99	0.45
1:H:89:VAL:HG23	1:H:401:THR:HG21	1.99	0.45
1:I:158:LEU:HD22	1:I:356:GLN:HA	1.97	0.45
1:I:371:GLU:OE1	1:I:371:GLU:HA	2.17	0.45
1:I:472:LEU:CD1	1:I:500:ARG:HH12	2.30	0.45
1:K:176:VAL:HG22	1:K:184:LEU:N	2.32	0.45
1:A:355:PRO:HD2	1:A:356:GLN:HE22	1.81	0.45
1:E:44:HIS:HA	1:E:45:PRO:HD3	1.82	0.45
1:F:163:ALA:HA	1:F:166:ARG:HH11	1.81	0.45
1:F:198:GLU:HG3	1:F:212:VAL:HG23	1.99	0.45
1:F:505:HIS:HD2	1:F:508:HIS:H	1.63	0.45
1:G:122:HIS:CG	1:G:122:HIS:O	2.69	0.45
1:G:162:ASP:OD1	1:G:466:HIS:HE1	1.99	0.45
1:G:500:ARG:CB	1:G:500:ARG:NH1	2.77	0.45
1:H:176:VAL:HG13	1:H:182:GLY:C	2.37	0.45
1:H:190:PRO:O	1:H:194:HIS:CD2	2.61	0.45
1:J:443:PHE:HB3	1:J:450:CYS:HB3	1.99	0.45
1:L:65:HIS:H	1:L:65:HIS:CD2	2.34	0.45
1:A:156:ARG:HD3	1:A:286:TYR:CD1	2.51	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:154:VAL:HG21	1:B:454:ARG:HD3	1.99	0.45
1:E:397:ILE:HA	1:E:398:PRO:HD3	1.69	0.45
1:C:103:VAL:O	1:C:103:VAL:HG12	2.17	0.44
1:G:49:TRP:HA	1:G:49:TRP:HE3	1.82	0.44
1:I:268:ASP:HA	1:I:271:ILE:HD12	1.99	0.44
1:I:426:GLN:HA	1:I:429:LEU:HD12	1.99	0.44
1:J:187:ASP:OD1	1:J:187:ASP:C	2.55	0.44
1:L:449:GLN:O	1:L:450:CYS:C	2.55	0.44
1:A:96:ASP:O	1:A:100:LEU:HB2	2.16	0.44
1:B:181:ARG:HH21	1:F:274:ILE:CD1	2.30	0.44
1:B:98:GLU:HG3	1:B:438:PHE:CE1	2.52	0.44
1:H:323:LEU:HD21	1:H:463:LEU:CD2	2.38	0.44
1:I:160:MET:CE	1:I:203:ALA:HA	2.47	0.44
1:I:329:GLU:OE1	1:I:329:GLU:HA	2.17	0.44
1:K:326:THR:HG21	1:K:464:LEU:CD1	2.48	0.44
1:B:189:GLN:HA	1:B:324:LEU:HD11	1.98	0.44
1:B:337:GLN:HE21	1:B:341:ARG:HH22	1.64	0.44
1:D:133:ASN:OD1	1:D:448:ARG:NH2	2.50	0.44
1:I:108:PRO:HD2	1:I:137:TRP:CZ3	2.52	0.44
1:J:145:ASN:N	1:J:146:PRO:HD2	2.32	0.44
1:K:158:LEU:N	1:K:159:PRO:CD	2.80	0.44
1:B:443:PHE:O	2:B:601:HEM:HBA1	2.17	0.44
1:D:370:LYS:HG2	1:D:440:HIS:CE1	2.53	0.44
1:G:300:SER:O	1:G:303:ALA:N	2.43	0.44
1:H:198:GLU:CG	1:H:212:VAL:HG23	2.44	0.44
1:J:116:TRP:O	1:J:120:ARG:NH2	2.51	0.44
1:K:188:VAL:O	1:K:192:ILE:HG12	2.17	0.44
1:K:371:GLU:OE1	1:K:428:TRP:NE1	2.47	0.44
1:K:93:LEU:HB2	1:K:96:ASP:OD1	2.17	0.44
1:H:476:LEU:HD13	1:L:280:PHE:HE1	1.83	0.44
1:A:207:GLU:OE2	1:C:179:ASN:ND2	2.51	0.44
1:B:176:VAL:HG13	1:B:183:SER:HA	2.00	0.44
1:B:309:MET:CE	1:B:309:MET:HA	2.48	0.44
1:E:335:ASP:OD1	1:E:335:ASP:N	2.51	0.44
1:F:158:LEU:CD2	1:F:462:LEU:HD11	2.48	0.44
1:G:452:GLY:O	1:G:453:ARG:C	2.56	0.44
1:L:475:THR:HG23	1:L:496:LEU:O	2.17	0.44
1:D:274:ILE:CD1	1:F:181:ARG:HH21	2.31	0.44
1:F:475:THR:HG22	1:F:496:LEU:O	2.17	0.44
1:G:113:LEU:HD23	1:G:116:TRP:CD2	2.53	0.44
1:H:110:ARG:NH2	1:H:130:PHE:O	2.51	0.44

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:386:VAL:HG12	1:I:388:SER:O	2.17	0.44
1:H:281:ASN:HB2	1:I:500:ARG:HH21	1.83	0.44
1:J:55:ILE:HG21	1:J:236:GLN:HA	2.00	0.44
1:L:41:MET:HE2	1:L:79:PHE:HA	1.99	0.44
1:D:183:SER:HB2	1:D:499:PHE:O	2.18	0.44
1:E:83:LEU:HG	1:E:84:GLY:H	1.82	0.44
1:G:101:GLN:NE2	1:G:438:PHE:HZ	2.15	0.44
1:I:96:ASP:O	1:I:100:LEU:HB2	2.18	0.44
1:J:149:LEU:HD12	1:J:454:ARG:HG3	2.00	0.44
1:J:72:PHE:HB3	1:J:92:MET:CE	2.48	0.44
1:K:152:LYS:O	1:K:156:ARG:HG3	2.18	0.44
1:K:271:ILE:HD13	1:K:305:LYS:HG3	2.00	0.44
1:A:103:VAL:O	1:A:103:VAL:HG12	2.17	0.44
1:D:441:VAL:N	1:D:442:PRO:HD3	2.32	0.44
1:F:296:LYS:HB3	1:F:298:GLU:HG3	2.00	0.44
1:H:41:MET:HA	1:H:395:TYR:CE2	2.53	0.44
1:J:137:TRP:CZ3	1:J:138:ARG:HG3	2.51	0.44
1:K:97:VAL:O	1:K:100:LEU:HB3	2.17	0.44
1:L:168:PHE:CD2	1:L:463:LEU:HD11	2.53	0.44
1:D:106:LEU:HA	1:D:106:LEU:HD12	1.89	0.44
1:E:65:HIS:CD2	1:E:66:LEU:HG	2.52	0.44
1:F:416:LEU:HB3	1:F:439:HIS:HE1	1.83	0.44
1:I:194:HIS:CE1	1:I:220:SER:OG	2.71	0.44
1:J:382:LEU:CD2	1:J:444:GLY:HA2	2.44	0.44
1:A:380:LEU:HB3	1:A:381:PHE:CD2	2.51	0.43
1:B:41:MET:O	1:B:80:ARG:NH2	2.48	0.43
1:C:101:GLN:OE1	1:C:438:PHE:HZ	2.00	0.43
1:F:105:SER:HB2	1:F:107:HIS:H	1.83	0.43
1:I:148:VAL:HG22	1:I:289:ILE:HG21	1.99	0.43
1:I:413:ASN:OD1	1:I:413:ASN:C	2.56	0.43
1:J:150:SER:O	1:J:153:ALA:N	2.50	0.43
1:J:198:GLU:O	1:J:199:ALA:C	2.55	0.43
1:B:158:LEU:HA	1:B:158:LEU:HD12	1.69	0.43
1:D:160:MET:HE3	1:D:203:ALA:HA	2.01	0.43
1:D:424:ASN:O	1:D:427:ARG:HB2	2.18	0.43
1:E:119:TYR:OH	1:E:261:ASP:OD1	2.30	0.43
1:E:321:PHE:CD2	1:E:491:PRO:HD2	2.53	0.43
1:H:426:GLN:HG3	1:H:429:LEU:HD12	2.00	0.43
1:I:328:PHE:CZ	1:I:332:ARG:HD2	2.53	0.43
1:K:123:ARG:HD3	1:K:123:ARG:HA	1.86	0.43
1:K:154:VAL:O	1:K:158:LEU:HB2	2.18	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:129:VAL:HG22	1:L:137:TRP:CD1	2.53	0.43
1:B:256:HIS:CE1	1:B:260:TRP:HE1	2.36	0.43
1:C:57:ARG:HD2	1:F:247:TRP:CE3	2.53	0.43
1:D:441:VAL:N	1:D:442:PRO:CD	2.81	0.43
1:E:323:LEU:HD22	1:E:463:LEU:HD22	1.98	0.43
1:H:157:PHE:HA	1:H:160:MET:HE3	1.96	0.43
1:J:370:LYS:HG2	1:J:440:HIS:CE1	2.53	0.43
1:L:157:PHE:C	1:L:157:PHE:CD2	2.91	0.43
1:B:437:ASN:C	1:B:439:HIS:H	2.22	0.43
1:F:475:THR:CG2	1:F:497:LEU:HD23	2.43	0.43
1:G:437:ASN:N	1:G:439:HIS:HD2	2.15	0.43
1:J:443:PHE:CD2	1:J:453:ARG:HG3	2.54	0.43
1:K:361:GLU:C	1:K:363:PRO:HD3	2.38	0.43
1:L:371:GLU:HA	1:L:371:GLU:OE1	2.18	0.43
1:A:274:ILE:HG13	1:C:181:ARG:CZ	2.49	0.43
1:F:240:MET:SD	1:F:245:SER:HB3	2.58	0.43
2:G:601:HEM:NA	3:G:602:OT3:H7	2.32	0.43
1:I:334:PRO:O	1:I:338:GLN:HG2	2.19	0.43
1:A:181:ARG:CB	1:A:181:ARG:HH11	2.23	0.43
1:B:240:MET:HE1	1:B:248:ILE:HG21	2.01	0.43
1:C:364:LEU:HD13	1:C:429:LEU:HD11	2.01	0.43
1:G:500:ARG:HB2	1:G:500:ARG:NH1	2.34	0.43
1:I:51:ARG:O	1:I:54:GLN:HB2	2.19	0.43
1:J:76:GLY:O	1:J:78:ILE:N	2.52	0.43
1:K:434:SER:C	1:K:436:ARG:H	2.21	0.43
1:C:429:LEU:HD23	1:C:429:LEU:HA	1.89	0.43
1:E:194:HIS:CE1	1:E:220:SER:OG	2.71	0.43
1:G:424:ASN:O	1:G:427:ARG:HB2	2.19	0.43
1:H:189:GLN:HB3	1:H:190:PRO:HD3	2.00	0.43
1:J:113:LEU:O	1:J:117:VAL:HG23	2.18	0.43
1:J:176:VAL:HG11	1:J:501:ALA:HB2	1.99	0.43
1:K:145:ASN:HB2	1:K:146:PRO:HD3	2.01	0.43
1:E:61:TYR:OH	1:E:67:GLU:OE2	2.37	0.43
1:H:457:GLU:O	1:H:461:LEU:HB2	2.19	0.43
1:I:371:GLU:HG2	1:I:424:ASN:H	1.84	0.43
1:J:181:ARG:HB2	1:J:181:ARG:NH1	2.25	0.43
1:J:53:LEU:C	1:J:55:ILE:H	2.20	0.43
1:A:371:GLU:OE2	1:A:427:ARG:HD2	2.19	0.43
1:C:107:HIS:HB3	1:C:134:GLY:HA2	1.99	0.43
1:E:127:CYS:HB3	1:E:131:LEU:HB2	2.00	0.43
1:H:380:LEU:HB3	1:H:381:PHE:CD2	2.54	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:44:HIS:HD2	1:H:71:THR:HG21	1.84	0.43
1:K:101:GLN:NE2	1:K:438:PHE:CE2	2.87	0.43
1:D:105:SER:HB2	1:D:107:HIS:H	1.83	0.43
1:F:202:LEU:O	1:F:206:GLY:N	2.49	0.43
1:F:44:HIS:CD2	1:F:71:THR:HG21	2.48	0.43
1:G:294:LEU:HD23	1:G:304:ILE:HD13	2.01	0.43
1:H:65:HIS:HD2	1:H:65:HIS:H	1.66	0.43
1:J:53:LEU:C	1:J:55:ILE:N	2.73	0.43
1:C:441:VAL:H	1:C:442:PRO:HD3	1.81	0.42
1:D:155:GLN:HG3	1:D:356:GLN:HG2	2.00	0.42
1:E:140:ASN:HD22	1:E:140:ASN:H	1.67	0.42
1:J:119:TYR:HE1	1:J:261:ASP:OD1	2.02	0.42
1:K:92:MET:HE1	1:K:409:SER:HB3	2.01	0.42
1:K:315:SER:HA	2:K:601:HEM:HMC2	2.01	0.42
1:D:379:GLY:O	1:D:407:LEU:HD12	2.19	0.42
1:I:469:LYS:HE2	1:I:469:LYS:HB3	1.88	0.42
1:J:309:MET:HA	1:J:309:MET:HE3	2.01	0.42
1:K:417:PHE:HA	1:K:418:PRO:HD3	1.88	0.42
1:K:431:ILE:HD12	1:K:436:ARG:HH21	1.84	0.42
1:A:323:LEU:HG	1:A:460:MET:CG	2.49	0.42
1:C:141:ARG:HD3	1:C:141:ARG:HA	1.94	0.42
1:D:309:MET:HE2	1:D:309:MET:HB3	1.64	0.42
1:E:452:GLY:HA3	2:E:601:HEM:C3C	2.54	0.42
1:H:156:ARG:HD3	1:H:286:TYR:CD1	2.53	0.42
1:I:137:TRP:CZ2	1:I:448:ARG:HG2	2.54	0.42
1:G:274:ILE:HD11	1:J:181:ARG:HH21	1.84	0.42
1:J:141:ARG:NH1	1:J:449:GLN:O	2.27	0.42
1:L:47:ASN:HD22	1:L:47:ASN:N	2.17	0.42
1:C:397:ILE:HA	1:C:398:PRO:HD3	1.82	0.42
1:D:362:LEU:O	1:D:366:ARG:HG3	2.18	0.42
1:F:48:ARG:HD3	1:F:84:GLY:H	1.83	0.42
1:K:386:VAL:HG21	1:K:390:LEU:HD22	2.01	0.42
1:D:63:HIS:O	1:D:64:LEU:C	2.57	0.42
1:K:424:ASN:HA	1:K:425:PRO:HD2	1.90	0.42
1:L:371:GLU:HG3	1:L:423:TYR:CD1	2.54	0.42
1:L:87:ARG:HG2	1:L:401:THR:HG22	2.02	0.42
1:B:190:PRO:O	1:B:194:HIS:HD2	2.03	0.42
1:B:356:GLN:H	1:B:356:GLN:NE2	2.17	0.42
1:E:321:PHE:HB2	1:E:322:PRO:HD3	2.02	0.42
1:A:181:ARG:HB2	1:A:181:ARG:NH1	2.23	0.42
1:E:41:MET:HB3	1:E:80:ARG:HD3	2.02	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:194:HIS:NE2	1:G:216:PRO:HB3	2.35	0.42
1:H:166:ARG:NH2	1:H:352:SER:HA	2.32	0.42
1:J:136:GLU:O	1:J:140:ASN:ND2	2.53	0.42
1:J:93:LEU:HB2	1:J:96:ASP:OD1	2.20	0.42
1:A:244:LEU:O	1:A:248:ILE:HG22	2.20	0.42
1:A:65:HIS:HA	1:A:406:PHE:CZ	2.55	0.42
1:C:452:GLY:HA3	2:C:601:HEM:C3C	2.55	0.42
1:G:441:VAL:N	1:G:442:PRO:HD3	2.35	0.42
1:H:370:LYS:HG2	1:H:440:HIS:CE1	2.54	0.42
1:I:462:LEU:HD23	1:I:462:LEU:HA	1.92	0.42
1:E:505:HIS:CD2	1:E:507:HIS:H	2.37	0.42
1:F:406:PHE:HD2	1:F:409:SER:CB	2.27	0.42
1:F:469:LYS:O	1:F:509:HIS:HB2	2.20	0.42
1:G:91:VAL:HG11	1:G:96:ASP:OD1	2.18	0.42
1:H:330:LEU:CD2	1:H:340:LEU:CD1	2.96	0.42
1:J:234:THR:OG1	1:J:256:HIS:HE1	2.03	0.42
1:K:242:ARG:O	1:K:246:ARG:HB2	2.19	0.42
1:L:354:HIS:O	1:L:357:LYS:HB2	2.19	0.42
1:B:441:VAL:N	1:B:442:PRO:CD	2.82	0.42
1:D:145:ASN:O	1:D:146:PRO:C	2.58	0.42
1:D:205:PHE:O	1:F:181:ARG:NH2	2.47	0.42
1:D:428:TRP:CZ3	1:D:440:HIS:HB2	2.54	0.42
1:E:325:MET:HA	1:E:325:MET:HE2	2.02	0.42
1:G:82:ASN:C	1:G:84:GLY:H	2.23	0.42
1:H:198:GLU:HG3	1:H:212:VAL:CG2	2.45	0.42
1:H:475:THR:CG2	1:H:496:LEU:O	2.68	0.42
1:A:337:GLN:HE22	1:A:473:VAL:N	2.15	0.41
1:B:108:PRO:HB2	1:B:448:ARG:HG3	2.02	0.41
1:G:341:ARG:HD3	1:G:468:LEU:O	2.20	0.41
1:I:158:LEU:N	1:I:159:PRO:HD2	2.35	0.41
1:J:189:GLN:HA	1:J:324:LEU:CD1	2.49	0.41
1:J:314:GLY:HA2	3:J:602:OT3:C11	2.50	0.41
1:A:157:PHE:HA	1:A:160:MET:CE	2.48	0.41
1:B:335:ASP:OD1	1:B:336:VAL:N	2.53	0.41
1:E:72:PHE:O	1:E:76:GLY:N	2.47	0.41
1:G:106:LEU:HB3	1:G:107:HIS:CD2	2.55	0.41
1:G:192:ILE:O	1:G:195:TYR:HB3	2.20	0.41
1:I:189:GLN:HA	1:I:324:LEU:HD11	2.02	0.41
1:I:164:VAL:HG22	1:I:208:ARG:HE	1.85	0.41
1:G:274:ILE:CD1	1:J:181:ARG:HH21	2.33	0.41
1:A:323:LEU:HD22	1:A:463:LEU:HD23	2.02	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:332:ARG:HG2	1:B:478:GLN:HG3	2.03	0.41
1:D:337:GLN:HE21	1:D:341:ARG:NH2	2.11	0.41
1:E:152:LYS:O	1:E:156:ARG:HG3	2.20	0.41
1:E:410:LEU:HD12	1:E:410:LEU:O	2.20	0.41
1:F:321:PHE:CD2	1:F:491:PRO:HD2	2.55	0.41
1:G:342:GLN:HE21	1:G:342:GLN:HB2	1.76	0.41
1:G:103:VAL:HG21	1:G:390:LEU:HD13	2.02	0.41
1:K:382:LEU:HB2	1:K:405:VAL:HB	2.02	0.41
1:L:121:GLN:HA	4:L:711:HOH:O	2.19	0.41
1:A:377:PRO:O	1:A:489:LEU:HB3	2.21	0.41
1:B:70:GLN:O	1:B:73:GLN:HB2	2.21	0.41
1:C:390:LEU:HG	1:C:391:VAL:N	2.36	0.41
1:F:186:LEU:HD23	1:F:186:LEU:N	2.33	0.41
1:J:294:LEU:CD2	1:J:304:ILE:HG21	2.50	0.41
1:A:323:LEU:HG	1:A:460:MET:HG2	2.02	0.41
1:B:100:LEU:HD12	1:B:100:LEU:HA	1.93	0.41
1:B:149:LEU:O	1:B:454:ARG:HD2	2.20	0.41
1:D:240:MET:CE	1:D:248:ILE:HD12	2.51	0.41
1:E:166:ARG:NH2	1:E:352:SER:HA	2.34	0.41
1:E:417:PHE:O	1:E:418:PRO:C	2.59	0.41
1:G:185:THR:OG1	1:K:277:GLU:HG3	2.21	0.41
1:J:132:LEU:HB3	1:J:137:TRP:HB2	2.02	0.41
1:L:149:LEU:O	1:L:454:ARG:HD2	2.21	0.41
1:D:331:ALA:HA	1:D:473:VAL:O	2.20	0.41
1:E:365:LEU:HD12	1:E:365:LEU:HA	1.93	0.41
1:E:63:HIS:O	1:E:64:LEU:C	2.58	0.41
1:F:323:LEU:HD21	1:F:463:LEU:HD22	2.02	0.41
1:G:315:SER:CB	2:G:601:HEM:HBC2	2.41	0.41
1:H:309:MET:HE2	1:H:309:MET:HB3	1.76	0.41
1:H:318:THR:O	1:H:322:PRO:CD	2.68	0.41
1:I:198:GLU:OE2	1:I:208:ARG:HG3	2.21	0.41
1:I:251:LYS:HD2	1:I:251:LYS:N	2.36	0.41
1:J:68:MET:HB2	1:J:406:PHE:CZ	2.55	0.41
1:B:176:VAL:HG11	1:B:501:ALA:HB2	2.01	0.41
1:B:339:ILE:CG2	1:B:364:LEU:HD21	2.51	0.41
1:E:196:THR:O	1:E:200:SER:HB2	2.21	0.41
1:F:337:GLN:HE21	1:F:341:ARG:HH22	1.67	0.41
2:F:601:HEM:HHA	2:F:601:HEM:HBD1	2.03	0.41
1:G:437:ASN:N	1:G:439:HIS:CD2	2.88	0.41
3:H:602:0T3:H13	3:H:602:0T3:C05	2.51	0.41
1:J:152:LYS:H	1:J:152:LYS:HD2	1.84	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:274:ILE:HD12	1:J:181:ARG:NH2	2.36	0.41
1:L:134:GLY:O	1:L:137:TRP:HB3	2.20	0.41
1:L:141:ARG:HD2	1:L:145:ASN:OD1	2.21	0.41
1:L:56:TRP:CZ2	1:L:248:ILE:HG22	2.56	0.41
1:L:77:PRO:HB2	1:L:93:LEU:HD11	2.03	0.41
1:C:71:THR:HG23	1:C:75:LEU:HD12	2.03	0.41
1:E:198:GLU:OE2	1:E:209:LEU:N	2.52	0.41
1:E:407:LEU:HA	1:E:410:LEU:HB3	2.03	0.41
1:G:341:ARG:HB2	1:G:341:ARG:CZ	2.50	0.41
1:J:198:GLU:OE2	1:J:209:LEU:O	2.39	0.41
1:L:336:VAL:O	1:L:340:LEU:HG	2.19	0.41
1:B:129:VAL:HG21	1:B:144:LEU:HD12	2.02	0.41
1:B:329:GLU:O	1:B:333:ASN:ND2	2.53	0.41
1:D:100:LEU:HD23	1:D:445:PHE:CZ	2.56	0.41
1:E:263:ILE:HG22	1:E:309:MET:CE	2.46	0.41
1:G:248:ILE:HG22	1:L:56:TRP:CG	2.56	0.41
1:H:300:SER:O	1:H:303:ALA:N	2.50	0.41
1:J:93:LEU:HA	1:J:94:PRO:HD3	1.93	0.41
1:A:485:TYR:CZ	1:A:487:PHE:HA	2.56	0.41
1:B:325:MET:CE	1:B:325:MET:HA	2.51	0.41
1:B:65:HIS:CD2	1:B:65:HIS:H	2.39	0.41
1:B:476:LEU:HD22	1:F:276:GLN:HA	2.03	0.41
1:K:487:PHE:HE2	3:K:602:OT3:H2	1.86	0.41
1:A:194:HIS:NE2	1:A:216:PRO:HB3	2.36	0.41
1:C:194:HIS:NE2	1:C:220:SER:HB3	2.35	0.41
1:E:194:HIS:CE1	1:E:216:PRO:HB3	2.56	0.41
1:F:314:GLY:HA2	3:F:602:OT3:C11	2.50	0.41
1:G:168:PHE:CD2	1:G:463:LEU:HD11	2.56	0.41
1:G:391:VAL:HA	1:G:395:TYR:O	2.21	0.41
1:L:301:LEU:O	1:L:305:LYS:HB2	2.21	0.41
1:E:428:TRP:CZ3	1:E:440:HIS:HB2	2.56	0.40
1:F:470:HIS:CD2	1:F:509:HIS:HB3	2.56	0.40
1:I:235:VAL:HA	1:I:238:MET:SD	2.61	0.40
2:I:601:HEM:HBB2	2:I:601:HEM:CMB	2.51	0.40
1:J:475:THR:HG23	1:J:496:LEU:O	2.20	0.40
1:K:105:SER:HB3	1:K:107:HIS:N	2.33	0.40
1:L:63:HIS:HD2	1:L:63:HIS:H	1.68	0.40
1:A:356:GLN:N	1:A:356:GLN:NE2	2.42	0.40
1:B:181:ARG:CB	1:B:181:ARG:HH11	2.22	0.40
1:C:65:HIS:CD2	1:C:65:HIS:H	2.40	0.40
1:D:371:GLU:HG3	1:D:423:TYR:CD1	2.56	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:397:ILE:HA	1:D:398:PRO:HD3	1.85	0.40
1:D:380:LEU:HD11	1:D:406:PHE:CE1	2.56	0.40
1:F:133:ASN:OD1	1:F:448:ARG:NH2	2.53	0.40
1:J:56:TRP:CD1	1:J:248:ILE:HD11	2.55	0.40
1:L:397:ILE:HA	1:L:398:PRO:HD3	1.91	0.40
1:B:119:TYR:CE2	1:B:260:TRP:HB3	2.57	0.40
1:C:329:GLU:OE2	1:C:332:ARG:NH2	2.54	0.40
1:C:428:TRP:CZ3	1:C:440:HIS:HB2	2.57	0.40
1:E:340:LEU:HD23	1:E:364:LEU:HB3	2.03	0.40
1:F:386:VAL:HG11	1:F:390:LEU:HD23	2.02	0.40
1:H:198:GLU:OE2	1:H:209:LEU:HB2	2.20	0.40
1:H:296:LYS:HB3	1:H:298:GLU:HG3	2.03	0.40
1:H:476:LEU:HD12	1:H:476:LEU:HA	1.84	0.40
1:I:129:VAL:HG13	2:I:601:HEM:HAD1	2.02	0.40
1:K:341:ARG:CZ	1:K:341:ARG:HB2	2.51	0.40
1:K:323:LEU:CD2	1:K:463:LEU:HD22	2.45	0.40
1:K:377:PRO:O	1:K:489:LEU:HB3	2.20	0.40
1:B:323:LEU:HG	1:B:460:MET:HG2	2.04	0.40
1:B:51:ARG:O	1:B:55:ILE:HD12	2.21	0.40
1:C:144:LEU:O	1:C:148:VAL:HG23	2.21	0.40
1:F:242:ARG:HH22	1:F:246:ARG:HH21	1.69	0.40
1:F:81:TYR:HD2	1:F:83:LEU:HB2	1.86	0.40
1:J:296:LYS:C	1:J:298:GLU:H	2.25	0.40
1:K:49:TRP:CZ3	1:K:244:LEU:HD11	2.57	0.40
1:K:44:HIS:HA	1:K:45:PRO:HD3	1.94	0.40
1:B:359:THR:O	1:B:366:ARG:HD2	2.22	0.40
1:F:422:ARG:HB3	1:F:422:ARG:HE	1.76	0.40
2:F:601:HEM:CBC	2:F:601:HEM:HMC2	2.49	0.40
1:G:345:LEU:HA	1:G:345:LEU:HD23	1.88	0.40
1:H:192:ILE:HA	1:H:192:ILE:HD13	1.88	0.40
1:J:47:ASN:HD22	1:J:50:LEU:HG	1.86	0.40
1:K:297:ALA:C	1:K:299:LEU:H	2.25	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	459/483 (95%)	436 (95%)	21 (5%)	2 (0%)	34	58
1	B	461/483 (95%)	422 (92%)	33 (7%)	6 (1%)	12	28
1	C	458/483 (95%)	436 (95%)	17 (4%)	5 (1%)	14	32
1	D	461/483 (95%)	433 (94%)	26 (6%)	2 (0%)	34	58
1	E	466/483 (96%)	433 (93%)	23 (5%)	10 (2%)	7	16
1	F	465/483 (96%)	424 (91%)	33 (7%)	8 (2%)	9	21
1	G	459/483 (95%)	422 (92%)	32 (7%)	5 (1%)	14	32
1	H	458/483 (95%)	429 (94%)	24 (5%)	5 (1%)	14	32
1	I	458/483 (95%)	422 (92%)	30 (7%)	6 (1%)	12	28
1	J	458/483 (95%)	418 (91%)	31 (7%)	9 (2%)	7	17
1	K	467/483 (97%)	418 (90%)	43 (9%)	6 (1%)	12	28
1	L	450/483 (93%)	418 (93%)	31 (7%)	1 (0%)	47	72
All	All	5520/5796 (95%)	5111 (93%)	344 (6%)	65 (1%)	13	30

All (65) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	477	THR
1	C	427	ARG
1	D	427	ARG
1	E	210	GLY
1	E	297	ALA
1	E	427	ARG
1	E	504	HIS
1	F	83	LEU
1	H	82	ASN
1	H	389	ASP
1	H	427	ARG
1	J	61	TYR
1	J	77	PRO
1	J	297	ALA
1	K	86	PRO
1	K	437	ASN
1	A	105	SER
1	B	297	ALA

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	B	427	ARG
1	C	450	CYS
1	E	438	PHE
1	F	210	GLY
1	F	447	MET
1	H	105	SER
1	I	61	TYR
1	I	477	THR
1	J	84	GLY
1	J	112	ILE
1	J	398	PRO
1	L	450	CYS
1	B	92	MET
1	B	243	SER
1	E	477	THR
1	F	48	ARG
1	G	95	GLU
1	G	297	ALA
1	H	450	CYS
1	I	104	ASP
1	I	439	HIS
1	J	346	ALA
1	J	477	THR
1	B	105	SER
1	C	105	SER
1	C	480	ASP
1	F	394	ASN
1	G	129	VAL
1	E	82	ASN
1	E	441	VAL
1	F	82	ASN
1	G	453	ARG
1	D	105	SER
1	E	296	LYS
1	I	77	PRO
1	I	441	VAL
1	K	419	ARG
1	E	84	GLY
1	J	289	ILE
1	K	37	PRO
1	F	441	VAL
1	F	442	PRO

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	K	420	PRO
1	B	431	ILE
1	G	84	GLY
1	K	431	ILE
1	C	441	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	408/425 (96%)	376 (92%)	32 (8%)	12	28
1	B	410/425 (96%)	369 (90%)	41 (10%)	7	17
1	C	407/425 (96%)	370 (91%)	37 (9%)	9	21
1	D	410/425 (96%)	384 (94%)	26 (6%)	18	38
1	E	415/425 (98%)	374 (90%)	41 (10%)	8	17
1	F	414/425 (97%)	372 (90%)	42 (10%)	7	17
1	G	408/425 (96%)	371 (91%)	37 (9%)	9	21
1	H	407/425 (96%)	369 (91%)	38 (9%)	9	20
1	I	407/425 (96%)	366 (90%)	41 (10%)	7	17
1	J	407/425 (96%)	369 (91%)	38 (9%)	9	20
1	K	412/425 (97%)	364 (88%)	48 (12%)	5	12
1	L	403/425 (95%)	366 (91%)	37 (9%)	9	20
All	All	4908/5100 (96%)	4450 (91%)	458 (9%)	9	20

All (458) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	ARG
1	A	61	TYR
1	A	101	GLN
1	A	102	GLN
1	A	105	SER

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	129	VAL
1	A	155	GLN
1	A	166	ARG
1	A	169	SER
1	A	170	GLN
1	A	181	ARG
1	A	183	SER
1	A	188	VAL
1	A	198	GLU
1	A	238	MET
1	A	251	LYS
1	A	254	LYS
1	A	265	GLN
1	A	281	ASN
1	A	285	HIS
1	A	352	SER
1	A	353	GLU
1	A	356	GLN
1	A	378	VAL
1	A	380	LEU
1	A	393	GLN
1	A	469	LYS
1	A	475	THR
1	A	478	GLN
1	A	480	ASP
1	A	486	SER
1	A	493	THR
1	B	39	GLU
1	B	54	GLN
1	B	58	GLU
1	B	61	TYR
1	B	64	LEU
1	B	70	GLN
1	B	74	GLU
1	B	80	ARG
1	B	101	GLN
1	B	104	ASP
1	B	105	SER
1	B	141	ARG
1	B	152	LYS
1	B	155	GLN
1	B	170	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	181	ARG
1	B	188	VAL
1	B	207	GLU
1	B	248	ILE
1	B	251	LYS
1	B	265	GLN
1	B	309	MET
1	B	317	ASP
1	B	324	LEU
1	B	343	GLU
1	B	350	SER
1	B	356	GLN
1	B	359	THR
1	B	378	VAL
1	B	390	LEU
1	B	393	GLN
1	B	394	ASN
1	B	429	LEU
1	B	449	GLN
1	B	463	LEU
1	B	469	LYS
1	B	475	THR
1	B	478	GLN
1	B	479	GLU
1	B	493	THR
1	B	502	ILE
1	C	50	LEU
1	C	52	LEU
1	C	73	GLN
1	C	88	MET
1	C	92	MET
1	C	102	GLN
1	C	114	GLU
1	C	121	GLN
1	C	129	VAL
1	C	141	ARG
1	C	152	LYS
1	C	157	PHE
1	C	169	SER
1	C	174	LYS
1	C	183	SER
1	C	188	VAL

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	238	MET
1	C	249	SER
1	C	254	LYS
1	C	271	ILE
1	C	282	ARG
1	C	318	THR
1	C	324	LEU
1	C	332	ARG
1	C	342	GLN
1	C	343	GLU
1	C	350	SER
1	C	356	GLN
1	C	360	THR
1	C	364	LEU
1	C	380	LEU
1	C	469	LYS
1	C	475	THR
1	C	478	GLN
1	C	484	VAL
1	C	493	THR
1	C	502	ILE
1	D	35	VAL
1	D	50	LEU
1	D	57	ARG
1	D	61	TYR
1	D	101	GLN
1	D	102	GLN
1	D	105	SER
1	D	129	VAL
1	D	141	ARG
1	D	158	LEU
1	D	170	GLN
1	D	243	SER
1	D	254	LYS
1	D	272	GLN
1	D	282	ARG
1	D	284	GLN
1	D	318	THR
1	D	323	LEU
1	D	353	GLU
1	D	356	GLN
1	D	386	VAL

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	D	394	ASN
1	D	463	LEU
1	D	469	LYS
1	D	475	THR
1	D	478	GLN
1	E	39	GLU
1	E	48	ARG
1	E	73	GLN
1	E	88	MET
1	E	99	LYS
1	E	106	LEU
1	E	109	CYS
1	E	112	ILE
1	E	123	ARG
1	E	140	ASN
1	E	141	ARG
1	E	143	ARG
1	E	157	PHE
1	E	183	SER
1	E	188	VAL
1	E	198	GLU
1	E	209	LEU
1	E	254	LYS
1	E	255	GLU
1	E	271	ILE
1	E	281	ASN
1	E	284	GLN
1	E	324	LEU
1	E	332	ARG
1	E	344	SER
1	E	352	SER
1	E	353	GLU
1	E	356	GLN
1	E	378	VAL
1	E	380	LEU
1	E	381	PHE
1	E	388	SER
1	E	390	LEU
1	E	393	GLN
1	E	394	ASN
1	E	410	LEU
1	E	437	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	E	457	GLU
1	E	460	MET
1	E	475	THR
1	E	478	GLN
1	F	36	LEU
1	F	47	ASN
1	F	48	ARG
1	F	61	TYR
1	F	73	GLN
1	F	87	ARG
1	F	88	MET
1	F	91	VAL
1	F	96	ASP
1	F	105	SER
1	F	112	ILE
1	F	113	LEU
1	F	114	GLU
1	F	129	VAL
1	F	141	ARG
1	F	181	ARG
1	F	188	VAL
1	F	198	GLU
1	F	218	SER
1	F	248	ILE
1	F	251	LYS
1	F	254	LYS
1	F	269	ASN
1	F	295	LEU
1	F	308	SER
1	F	317	ASP
1	F	319	THR
1	F	323	LEU
1	F	332	ARG
1	F	360	THR
1	F	366	ARG
1	F	383	GLU
1	F	410	LEU
1	F	422	ARG
1	F	430	ASP
1	F	441	VAL
1	F	449	GLN
1	F	457	GLU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	F	475	THR
1	F	476	LEU
1	F	478	GLN
1	F	493	THR
1	G	49	TRP
1	G	55	ILE
1	G	58	GLU
1	G	61	TYR
1	G	88	MET
1	G	92	MET
1	G	102	GLN
1	G	105	SER
1	G	141	ARG
1	G	157	PHE
1	G	169	SER
1	G	181	ARG
1	G	188	VAL
1	G	215	SER
1	G	216	PRO
1	G	238	MET
1	G	242	ARG
1	G	243	SER
1	G	248	ILE
1	G	271	ILE
1	G	277	GLU
1	G	309	MET
1	G	318	THR
1	G	323	LEU
1	G	332	ARG
1	G	342	GLN
1	G	353	GLU
1	G	383	GLU
1	G	385	VAL
1	G	386	VAL
1	G	421	GLU
1	G	430	ASP
1	G	463	LEU
1	G	469	LYS
1	G	493	THR
1	G	500	ARG
1	G	502	ILE
1	H	48	ARG

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	H	57	ARG
1	H	73	GLN
1	H	88	MET
1	H	92	MET
1	H	103	VAL
1	H	105	SER
1	H	120	ARG
1	H	126	LYS
1	H	129	VAL
1	H	141	ARG
1	H	152	LYS
1	H	156	ARG
1	H	174	LYS
1	H	188	VAL
1	H	215	SER
1	H	244	LEU
1	H	302	GLU
1	H	342	GLN
1	H	343	GLU
1	H	344	SER
1	H	361	GLU
1	H	366	ARG
1	H	378	VAL
1	H	380	LEU
1	H	381	PHE
1	H	383	GLU
1	H	389	ASP
1	H	419	ARG
1	H	426	GLN
1	H	430	ASP
1	H	447	MET
1	H	448	ARG
1	H	475	THR
1	H	476	LEU
1	H	479	GLU
1	H	493	THR
1	H	502	ILE
1	I	47	ASN
1	I	48	ARG
1	I	61	TYR
1	I	93	LEU
1	I	112	ILE

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	I	123	ARG
1	I	129	VAL
1	I	141	ARG
1	I	157	PHE
1	I	158	LEU
1	I	169	SER
1	I	174	LYS
1	I	181	ARG
1	I	198	GLU
1	I	232	LYS
1	I	238	MET
1	I	258	GLU
1	I	265	GLN
1	I	285	HIS
1	I	309	MET
1	I	324	LEU
1	I	332	ARG
1	I	335	ASP
1	I	343	GLU
1	I	344	SER
1	I	352	SER
1	I	360	THR
1	I	364	LEU
1	I	378	VAL
1	I	380	LEU
1	I	383	GLU
1	I	390	LEU
1	I	447	MET
1	I	454	ARG
1	I	461	LEU
1	I	463	LEU
1	I	469	LYS
1	I	477	THR
1	I	478	GLN
1	I	486	SER
1	I	500	ARG
1	J	39	GLU
1	J	61	TYR
1	J	78	ILE
1	J	88	MET
1	J	92	MET
1	J	103	VAL

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	J	106	LEU
1	J	126	LYS
1	J	129	VAL
1	J	138	ARG
1	J	141	ARG
1	J	156	ARG
1	J	157	PHE
1	J	158	LEU
1	J	181	ARG
1	J	188	VAL
1	J	209	LEU
1	J	220	SER
1	J	240	MET
1	J	242	ARG
1	J	244	LEU
1	J	248	ILE
1	J	251	LYS
1	J	265	GLN
1	J	282	ARG
1	J	309	MET
1	J	323	LEU
1	J	324	LEU
1	J	332	ARG
1	J	343	GLU
1	J	360	THR
1	J	381	PHE
1	J	404	GLN
1	J	410	LEU
1	J	421	GLU
1	J	441	VAL
1	J	449	GLN
1	J	476	LEU
1	K	39	GLU
1	K	61	TYR
1	K	74	GLU
1	K	78	ILE
1	K	80	ARG
1	K	87	ARG
1	K	102	GLN
1	K	105	SER
1	K	107	HIS
1	K	110	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	K	129	VAL
1	K	138	ARG
1	K	139	PHE
1	K	141	ARG
1	K	142	LEU
1	K	166	ARG
1	K	174	LYS
1	K	176	VAL
1	K	181	ARG
1	K	188	VAL
1	K	191	SER
1	K	198	GLU
1	K	244	LEU
1	K	247	TRP
1	K	272	GLN
1	K	284	GLN
1	K	308	SER
1	K	309	MET
1	K	324	LEU
1	K	342	GLN
1	K	352	SER
1	K	356	GLN
1	K	366	ARG
1	K	378	VAL
1	K	380	LEU
1	K	390	LEU
1	K	413	ASN
1	K	419	ARG
1	K	422	ARG
1	K	426	GLN
1	K	436	ARG
1	K	439	HIS
1	K	447	MET
1	K	448	ARG
1	K	469	LYS
1	K	475	THR
1	K	479	GLU
1	K	482	LYS
1	L	47	ASN
1	L	59	GLN
1	L	61	TYR
1	L	63	HIS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	L	78	ILE
1	L	87	ARG
1	L	92	MET
1	L	104	ASP
1	L	111	MET
1	L	120	ARG
1	L	121	GLN
1	L	129	VAL
1	L	141	ARG
1	L	157	PHE
1	L	160	MET
1	L	170	GLN
1	L	188	VAL
1	L	198	GLU
1	L	246	ARG
1	L	265	GLN
1	L	305	LYS
1	L	323	LEU
1	L	324	LEU
1	L	357	LYS
1	L	381	PHE
1	L	384	ARG
1	L	401	THR
1	L	410	LEU
1	L	422	ARG
1	L	430	ASP
1	L	440	HIS
1	L	448	ARG
1	L	475	THR
1	L	478	GLN
1	L	479	GLU
1	L	486	SER
1	L	493	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (139) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	HIS
1	A	65	HIS
1	A	265	GLN
1	A	281	ASN
1	A	337	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	356	GLN
1	A	394	ASN
1	A	440	HIS
1	A	466	HIS
1	A	470	HIS
1	B	65	HIS
1	B	121	GLN
1	B	170	GLN
1	B	194	HIS
1	B	256	HIS
1	B	337	GLN
1	B	356	GLN
1	C	65	HIS
1	C	102	GLN
1	C	122	HIS
1	C	170	GLN
1	C	333	ASN
1	C	337	GLN
1	C	356	GLN
1	C	396	HIS
1	C	439	HIS
1	C	440	HIS
1	C	470	HIS
1	D	43	GLN
1	D	65	HIS
1	D	82	ASN
1	D	125	HIS
1	D	337	GLN
1	D	356	GLN
1	D	394	ASN
1	D	440	HIS
1	E	43	GLN
1	E	125	HIS
1	E	140	ASN
1	E	155	GLN
1	E	194	HIS
1	E	201	ASN
1	E	265	GLN
1	E	281	ASN
1	E	307	ASN
1	E	337	GLN
1	E	338	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	E	356	GLN
1	E	393	GLN
1	E	394	ASN
1	E	396	HIS
1	E	437	ASN
1	E	449	GLN
1	E	505	HIS
1	F	47	ASN
1	F	102	GLN
1	F	194	HIS
1	F	272	GLN
1	F	281	ASN
1	F	337	GLN
1	F	394	ASN
1	F	404	GLN
1	F	439	HIS
1	F	466	HIS
1	F	470	HIS
1	F	505	HIS
1	G	44	HIS
1	G	47	ASN
1	G	65	HIS
1	G	101	GLN
1	G	140	ASN
1	G	194	HIS
1	G	236	GLN
1	G	307	ASN
1	G	337	GLN
1	G	342	GLN
1	G	404	GLN
1	G	439	HIS
1	G	466	HIS
1	H	47	ASN
1	H	65	HIS
1	H	155	GLN
1	H	170	GLN
1	H	194	HIS
1	H	337	GLN
1	H	342	GLN
1	H	394	ASN
1	I	47	ASN
1	I	59	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	I	65	HIS
1	I	82	ASN
1	I	194	HIS
1	I	265	GLN
1	I	337	GLN
1	I	439	HIS
1	I	466	HIS
1	J	47	ASN
1	J	65	HIS
1	J	107	HIS
1	J	122	HIS
1	J	125	HIS
1	J	155	GLN
1	J	201	ASN
1	J	281	ASN
1	J	333	ASN
1	J	337	GLN
1	J	342	GLN
1	J	356	GLN
1	J	404	GLN
1	J	439	HIS
1	J	440	HIS
1	J	466	HIS
1	J	470	HIS
1	K	54	GLN
1	K	101	GLN
1	K	121	GLN
1	K	122	HIS
1	K	194	HIS
1	K	276	GLN
1	K	337	GLN
1	K	342	GLN
1	K	356	GLN
1	K	393	GLN
1	K	404	GLN
1	K	424	ASN
1	L	47	ASN
1	L	63	HIS
1	L	65	HIS
1	L	73	GLN
1	L	125	HIS
1	L	140	ASN

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	L	170	GLN
1	L	194	HIS
1	L	236	GLN
1	L	337	GLN
1	L	356	GLN
1	L	426	GLN
1	L	440	HIS
1	L	470	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

24 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	$\# Z  > 2$
2	HEM	B	601	1,3	27,50,50	2.01	5 (18%)	17,82,82	1.88	5 (29%)
3	OT3	E	602	2	15,19,19	0.44	0	18,26,26	0.43	0
3	OT3	B	602	2	15,19,19	0.35	0	18,26,26	0.42	0
3	OT3	L	602	2	15,19,19	0.49	0	18,26,26	0.41	0
3	OT3	J	602	2	15,19,19	0.39	0	18,26,26	0.35	0
3	OT3	D	602	2	15,19,19	0.39	0	18,26,26	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	HEM	L	601	1,3	27,50,50	2.14	6 (22%)	17,82,82	1.35	3 (17%)
3	OT3	A	602	2	15,19,19	0.38	0	18,26,26	0.44	0
2	HEM	A	601	1,3	27,50,50	2.02	6 (22%)	17,82,82	1.64	5 (29%)
3	OT3	H	602	2	15,19,19	0.48	0	18,26,26	0.38	0
2	HEM	E	601	1,3	27,50,50	2.23	6 (22%)	17,82,82	2.16	3 (17%)
3	OT3	K	602	2	15,19,19	0.38	0	18,26,26	0.39	0
2	HEM	I	601	1,3	27,50,50	2.20	7 (25%)	17,82,82	1.31	4 (23%)
2	HEM	H	601	1,3	27,50,50	2.15	6 (22%)	17,82,82	1.79	3 (17%)
3	OT3	C	602	2	15,19,19	0.40	0	18,26,26	0.42	0
3	OT3	G	602	2	15,19,19	0.47	0	18,26,26	0.41	0
2	HEM	G	601	1,3	27,50,50	2.06	7 (25%)	17,82,82	2.04	4 (23%)
2	HEM	C	601	1,3	27,50,50	2.03	6 (22%)	17,82,82	1.73	6 (35%)
2	HEM	J	601	1,3	27,50,50	2.07	5 (18%)	17,82,82	1.46	4 (23%)
2	HEM	D	601	1,3	27,50,50	1.99	6 (22%)	17,82,82	1.98	5 (29%)
2	HEM	K	601	1,3	27,50,50	2.10	5 (18%)	17,82,82	1.50	1 (5%)
3	OT3	F	602	2	15,19,19	0.39	0	18,26,26	0.38	0
3	OT3	I	602	2	15,19,19	0.39	0	18,26,26	0.40	0
2	HEM	F	601	1,3	27,50,50	2.11	6 (22%)	17,82,82	2.00	5 (29%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	B	601	1,3	-	0/6/54/54	-
3	OT3	E	602	2	-	0/6/16/16	0/2/3/3
3	OT3	B	602	2	-	0/6/16/16	0/2/3/3
3	OT3	L	602	2	-	0/6/16/16	0/2/3/3
3	OT3	J	602	2	-	0/6/16/16	0/2/3/3
3	OT3	D	602	2	-	0/6/16/16	0/2/3/3
2	HEM	L	601	1,3	-	0/6/54/54	-
3	OT3	A	602	2	-	0/6/16/16	0/2/3/3
2	HEM	A	601	1,3	-	0/6/54/54	-
3	OT3	H	602	2	-	1/6/16/16	0/2/3/3
2	HEM	E	601	1,3	-	0/6/54/54	-
3	OT3	K	602	2	-	0/6/16/16	0/2/3/3
2	HEM	I	601	1,3	-	0/6/54/54	-
2	HEM	H	601	1,3	-	0/6/54/54	-
3	OT3	C	602	2	-	0/6/16/16	0/2/3/3

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	0T3	G	602	2	-	0/6/16/16	0/2/3/3
2	HEM	G	601	1,3	-	0/6/54/54	-
2	HEM	C	601	1,3	-	1/6/54/54	-
2	HEM	J	601	1,3	-	0/6/54/54	-
2	HEM	D	601	1,3	-	0/6/54/54	-
2	HEM	K	601	1,3	-	2/6/54/54	-
3	0T3	F	602	2	-	0/6/16/16	0/2/3/3
3	0T3	I	602	2	-	0/6/16/16	0/2/3/3
2	HEM	F	601	1,3	-	1/6/54/54	-

All (71) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	601	HEM	C3D-C2D	5.80	1.54	1.37
2	B	601	HEM	C3D-C2D	5.53	1.54	1.37
2	I	601	HEM	C3C-C2C	-5.39	1.32	1.40
2	D	601	HEM	C3D-C2D	5.33	1.53	1.37
2	E	601	HEM	C3C-C2C	-5.30	1.33	1.40
2	L	601	HEM	C3D-C2D	5.27	1.53	1.37
2	E	601	HEM	C3B-C2B	-5.19	1.33	1.40
2	I	601	HEM	C3D-C2D	5.18	1.53	1.37
2	A	601	HEM	C3D-C2D	5.13	1.52	1.37
2	C	601	HEM	C3D-C2D	5.09	1.52	1.37
2	G	601	HEM	C3D-C2D	5.09	1.52	1.37
2	J	601	HEM	C3C-C2C	-5.09	1.33	1.40
2	K	601	HEM	C3D-C2D	5.03	1.52	1.37
2	J	601	HEM	C3D-C2D	5.00	1.52	1.37
2	F	601	HEM	C3D-C2D	4.99	1.52	1.37
2	F	601	HEM	C3C-C2C	-4.89	1.33	1.40
2	K	601	HEM	C3C-C2C	-4.78	1.33	1.40
2	E	601	HEM	C3D-C2D	4.71	1.51	1.37
2	K	601	HEM	C3B-C2B	-4.44	1.34	1.40
2	A	601	HEM	C3C-C2C	-4.38	1.34	1.40
2	C	601	HEM	C3C-C2C	-4.29	1.34	1.40
2	C	601	HEM	C3B-C2B	-4.29	1.34	1.40
2	H	601	HEM	C3C-C2C	-4.26	1.34	1.40
2	A	601	HEM	C3B-C2B	-4.23	1.34	1.40
2	D	601	HEM	C3C-C2C	-4.23	1.34	1.40
2	G	601	HEM	C3C-C2C	-4.21	1.34	1.40
2	L	601	HEM	C3C-C2C	-4.21	1.34	1.40
2	F	601	HEM	C3B-C2B	-4.12	1.34	1.40
2	L	601	HEM	C3C-CAC	3.99	1.56	1.47

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	601	HEM	C3B-CAB	3.97	1.56	1.47
2	H	601	HEM	C3B-C2B	-3.88	1.35	1.40
2	B	601	HEM	C3C-C2C	-3.75	1.35	1.40
2	I	601	HEM	C3B-CAB	3.75	1.55	1.47
2	I	601	HEM	C3B-C2B	-3.75	1.35	1.40
2	J	601	HEM	C3B-CAB	3.72	1.55	1.47
2	L	601	HEM	C3B-C2B	-3.71	1.35	1.40
2	H	601	HEM	C3B-CAB	3.69	1.55	1.47
2	J	601	HEM	C3B-C2B	-3.68	1.35	1.40
2	I	601	HEM	C3C-CAC	3.65	1.55	1.47
2	G	601	HEM	C3C-CAC	3.62	1.55	1.47
2	B	601	HEM	C3C-CAC	3.54	1.55	1.47
2	K	601	HEM	C3C-CAC	3.51	1.55	1.47
2	D	601	HEM	C3B-C2B	-3.43	1.35	1.40
2	H	601	HEM	C3C-CAC	3.43	1.54	1.47
2	G	601	HEM	C3B-C2B	-3.42	1.35	1.40
2	E	601	HEM	C3C-CAC	3.41	1.54	1.47
2	B	601	HEM	C3B-CAB	3.30	1.54	1.47
2	D	601	HEM	C3B-CAB	3.15	1.54	1.47
2	A	601	HEM	C3C-CAC	3.13	1.54	1.47
2	B	601	HEM	C3B-C2B	-3.12	1.36	1.40
2	G	601	HEM	C3B-CAB	3.12	1.54	1.47
2	F	601	HEM	C3C-CAC	3.11	1.54	1.47
2	J	601	HEM	C3C-CAC	3.02	1.54	1.47
2	E	601	HEM	C3B-CAB	3.01	1.54	1.47
2	C	601	HEM	C3C-CAC	2.96	1.53	1.47
2	C	601	HEM	C3B-CAB	2.88	1.53	1.47
2	A	601	HEM	C3B-CAB	2.86	1.53	1.47
2	K	601	HEM	C3B-CAB	2.75	1.53	1.47
2	D	601	HEM	C3C-CAC	2.71	1.53	1.47
2	I	601	HEM	CAA-C2A	2.55	1.55	1.52
2	F	601	HEM	C3B-CAB	2.44	1.52	1.47
2	H	601	HEM	CAA-C2A	2.42	1.55	1.52
2	F	601	HEM	CAA-C2A	2.34	1.55	1.52
2	C	601	HEM	CAA-C2A	2.34	1.55	1.52
2	E	601	HEM	CMB-C2B	2.22	1.56	1.51
2	A	601	HEM	CAA-C2A	2.11	1.55	1.52
2	G	601	HEM	CMB-C2B	2.09	1.56	1.51
2	D	601	HEM	CMA-C3A	2.08	1.56	1.51
2	L	601	HEM	CAA-C2A	2.08	1.55	1.52
2	G	601	HEM	CMA-C3A	2.05	1.55	1.51
2	I	601	HEM	C1B-C2B	2.00	1.47	1.42

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	601	HEM	CBD-CAD-C3D	-5.48	102.37	112.48
2	E	601	HEM	CBA-CAA-C2A	-5.17	102.94	112.49
2	D	601	HEM	CAA-CBA-CGA	-4.73	104.74	112.67
2	H	601	HEM	CBD-CAD-C3D	-4.56	104.07	112.48
2	G	601	HEM	C1D-C2D-C3D	-4.37	103.96	107.00
2	G	601	HEM	CBD-CAD-C3D	-4.15	104.83	112.48
2	K	601	HEM	CAD-CBD-CGD	-4.00	105.95	112.67
2	G	601	HEM	CBA-CAA-C2A	-3.97	105.17	112.49
2	F	601	HEM	C1D-C2D-C3D	-3.89	104.29	107.00
2	F	601	HEM	CBD-CAD-C3D	-3.88	105.33	112.48
2	F	601	HEM	CBA-CAA-C2A	-3.75	105.57	112.49
2	E	601	HEM	C1D-C2D-C3D	-3.74	104.39	107.00
2	B	601	HEM	CBD-CAD-C3D	-3.49	106.04	112.48
2	C	601	HEM	C4A-C3A-C2A	3.44	109.39	107.00
2	B	601	HEM	C1D-C2D-C3D	-3.12	104.82	107.00
2	D	601	HEM	CMB-C2B-C3B	3.07	130.43	124.68
2	B	601	HEM	CMB-C2B-C3B	3.02	130.33	124.68
2	L	601	HEM	CBD-CAD-C3D	-2.96	107.02	112.48
2	L	601	HEM	C1D-C2D-C3D	-2.93	104.95	107.00
2	C	601	HEM	C4C-C3C-C2C	2.91	108.93	106.90
2	C	601	HEM	CMA-C3A-C4A	-2.90	124.01	128.46
2	A	601	HEM	CBA-CAA-C2A	-2.88	107.18	112.49
2	H	601	HEM	CMA-C3A-C4A	-2.86	124.06	128.46
2	B	601	HEM	CBA-CAA-C2A	-2.84	107.25	112.49
2	D	601	HEM	CMA-C3A-C4A	-2.81	124.15	128.46
2	F	601	HEM	CMA-C3A-C4A	-2.78	124.20	128.46
2	J	601	HEM	CAD-CBD-CGD	-2.67	108.18	112.67
2	A	601	HEM	CMA-C3A-C4A	-2.61	124.45	128.46
2	I	601	HEM	C1D-C2D-C3D	-2.59	105.19	107.00
2	A	601	HEM	CMB-C2B-C3B	2.47	129.30	124.68
2	I	601	HEM	CAD-CBD-CGD	-2.46	108.55	112.67
2	J	601	HEM	CAA-CBA-CGA	-2.42	108.60	112.67
2	D	601	HEM	C1D-C2D-C3D	-2.42	105.31	107.00
2	C	601	HEM	CBD-CAD-C3D	-2.39	108.08	112.48
2	A	601	HEM	C4C-C3C-C2C	2.37	108.55	106.90
2	F	601	HEM	CMB-C2B-C3B	2.35	129.07	124.68
2	D	601	HEM	C4C-C3C-C2C	2.32	108.52	106.90
2	H	601	HEM	C1D-C2D-C3D	-2.25	105.43	107.00
2	I	601	HEM	CMA-C3A-C4A	-2.21	125.06	128.46
2	J	601	HEM	C1D-C2D-C3D	-2.21	105.46	107.00
2	L	601	HEM	C4A-C3A-C2A	2.19	108.52	107.00
2	J	601	HEM	CBA-CAA-C2A	-2.18	108.47	112.49

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	601	HEM	CMB-C2B-C3B	2.17	128.73	124.68
2	I	601	HEM	C4A-C3A-C2A	2.10	108.45	107.00
2	C	601	HEM	CMC-C2C-C3C	2.09	128.59	124.68
2	B	601	HEM	C4C-C3C-C2C	2.03	108.32	106.90
2	C	601	HEM	CMB-C2B-C3B	2.03	128.48	124.68
2	A	601	HEM	C1D-C2D-C3D	-2.01	105.60	107.00

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	K	601	HEM	C2D-C3D-CAD-CBD
2	K	601	HEM	C4D-C3D-CAD-CBD
2	C	601	HEM	C3A-C2A-CAA-CBA
2	F	601	HEM	C4D-C3D-CAD-CBD
3	H	602	0T3	N04-C03-C10-C15

There are no ring outliers.

24 monomers are involved in 73 short contacts:

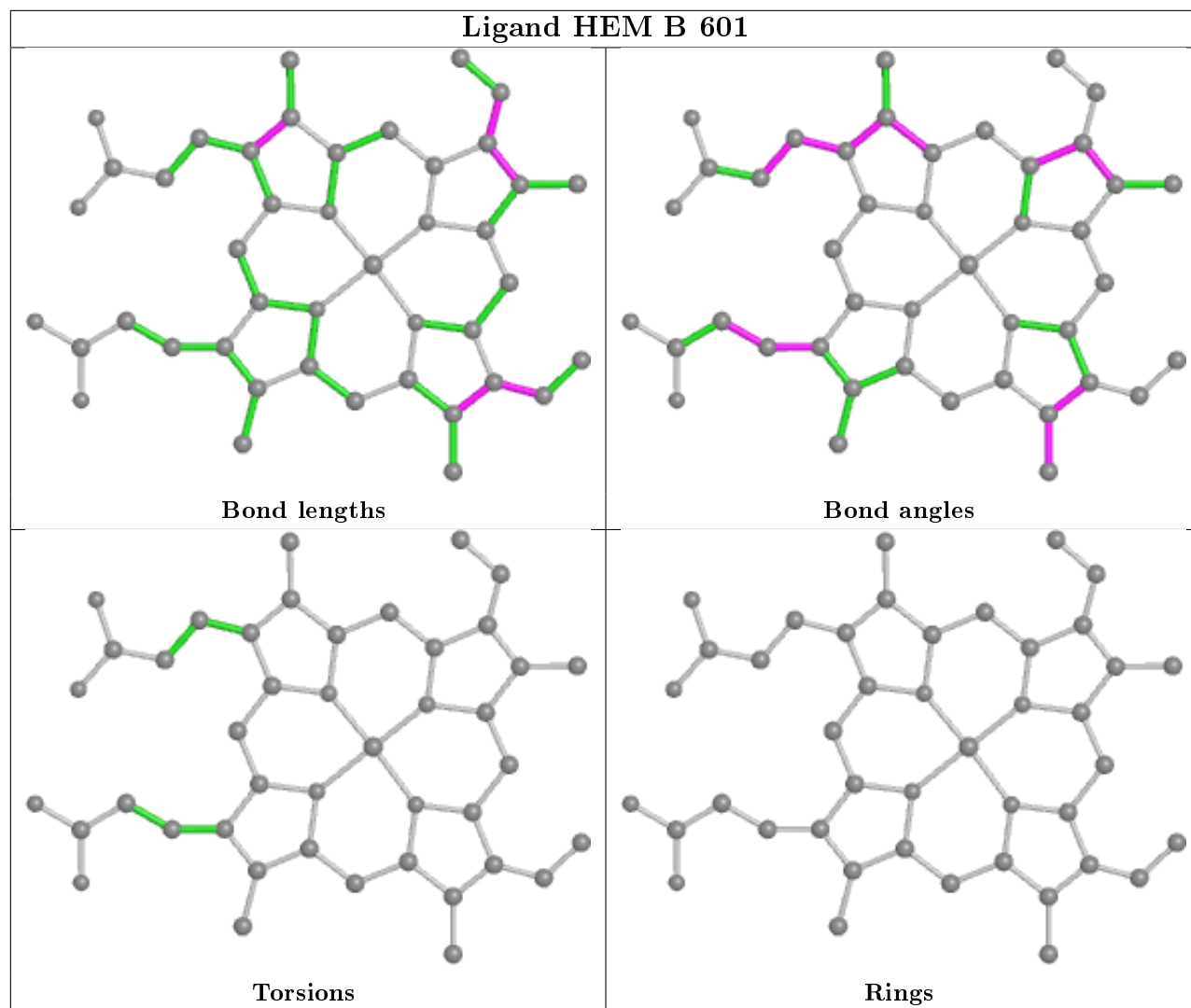
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	HEM	9	0
3	E	602	0T3	2	0
3	B	602	0T3	3	0
3	L	602	0T3	5	0
3	J	602	0T3	1	0
3	D	602	0T3	1	0
2	L	601	HEM	7	0
3	A	602	0T3	2	0
2	A	601	HEM	6	0
3	H	602	0T3	2	0
2	E	601	HEM	5	0
3	K	602	0T3	1	0
2	I	601	HEM	6	0
2	H	601	HEM	2	0
3	C	602	0T3	2	0
3	G	602	0T3	2	0
2	G	601	HEM	5	0
2	C	601	HEM	6	0
2	J	601	HEM	2	0
2	D	601	HEM	3	0

*Continued on next page...*

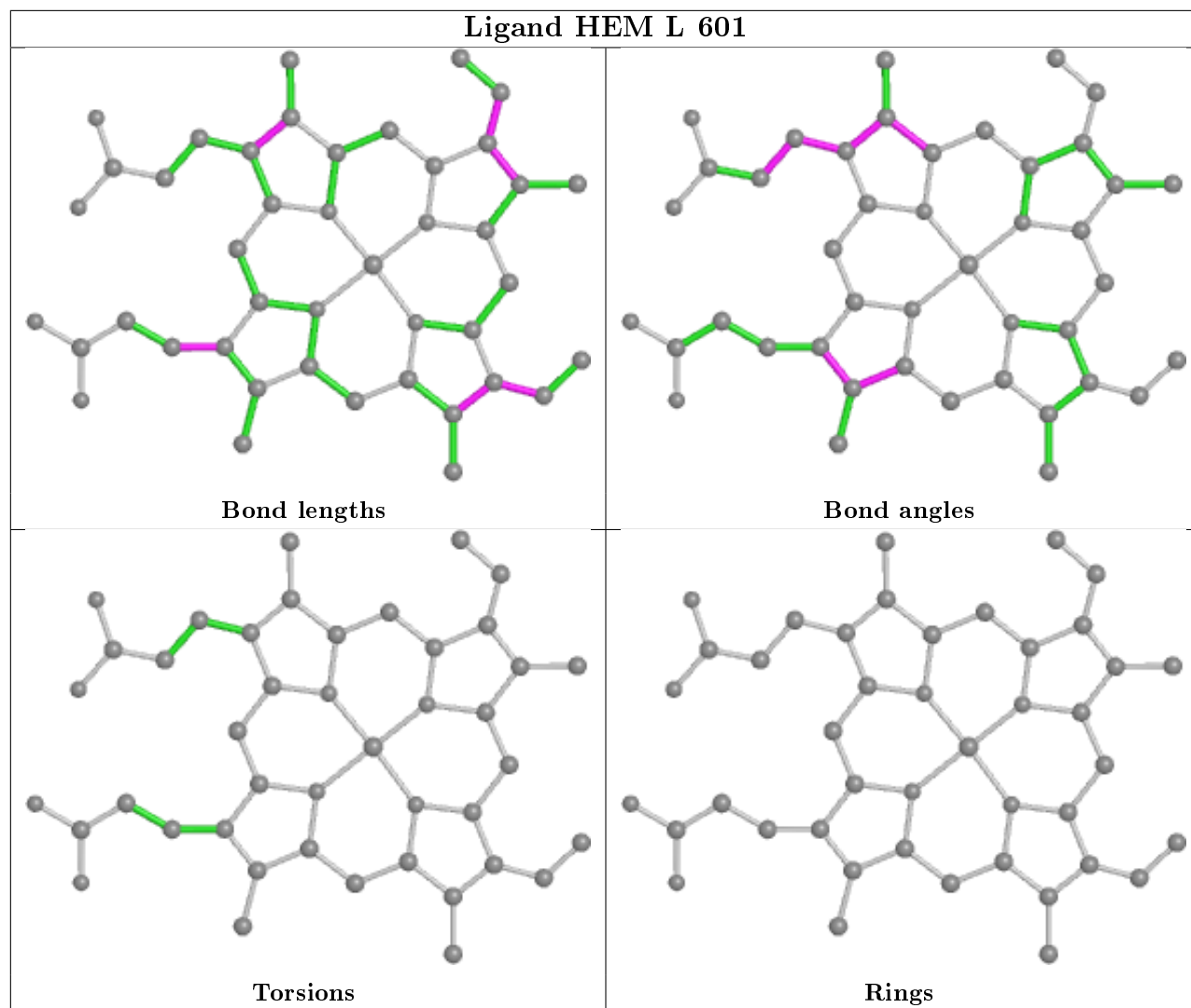
*Continued from previous page...*

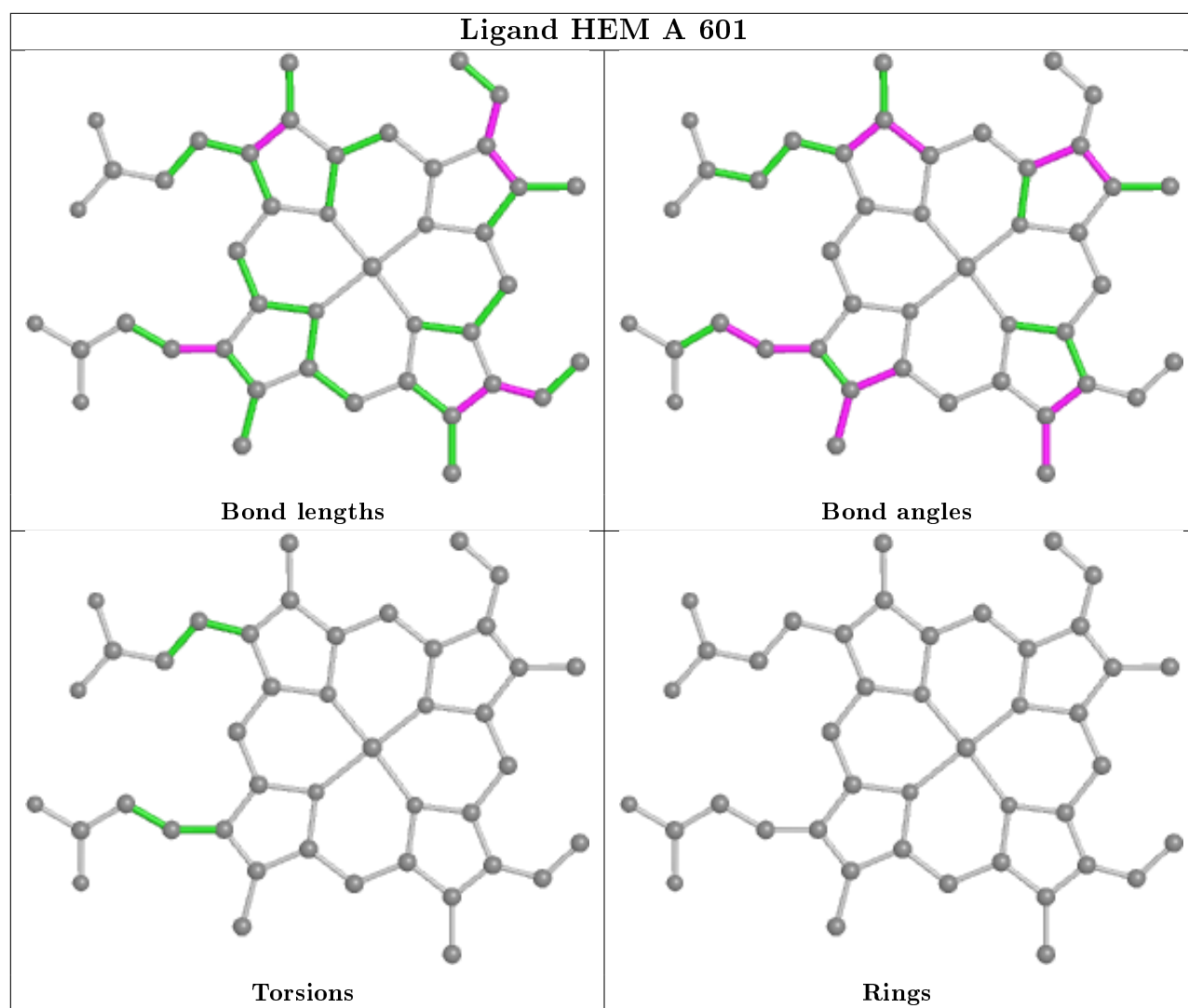
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	601	HEM	4	0
3	F	602	0T3	3	0
3	I	602	0T3	2	0
2	F	601	HEM	9	0

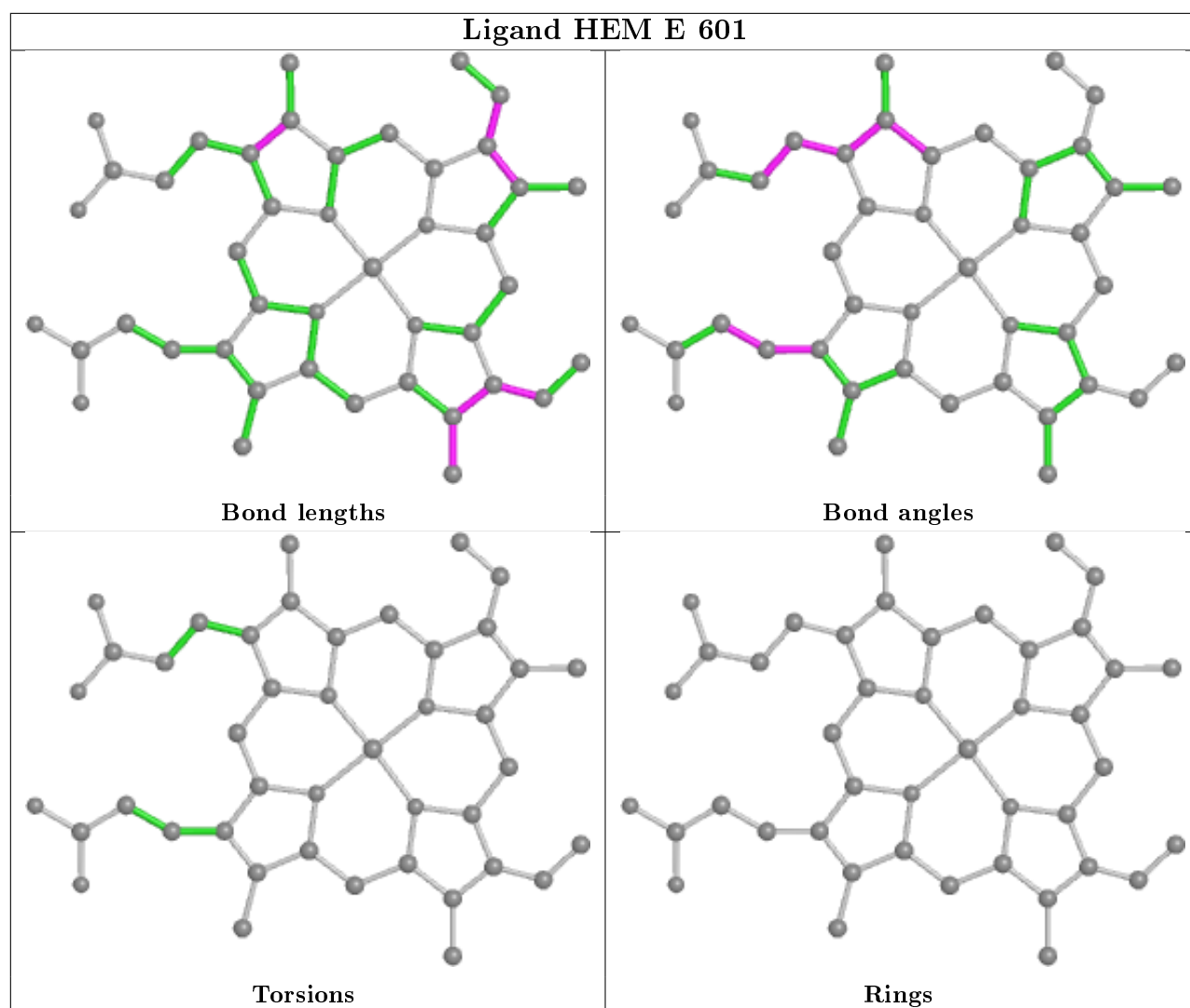
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



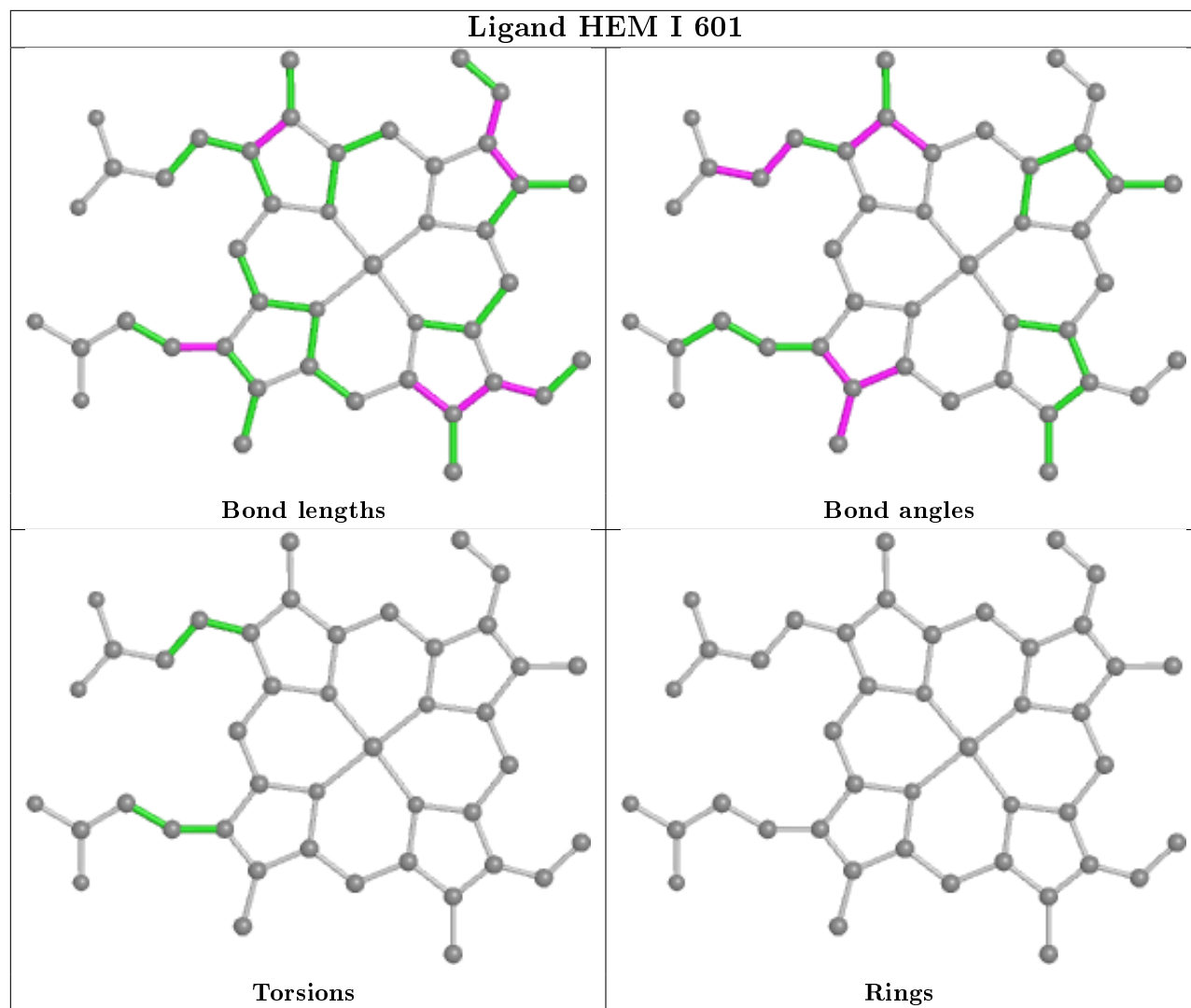


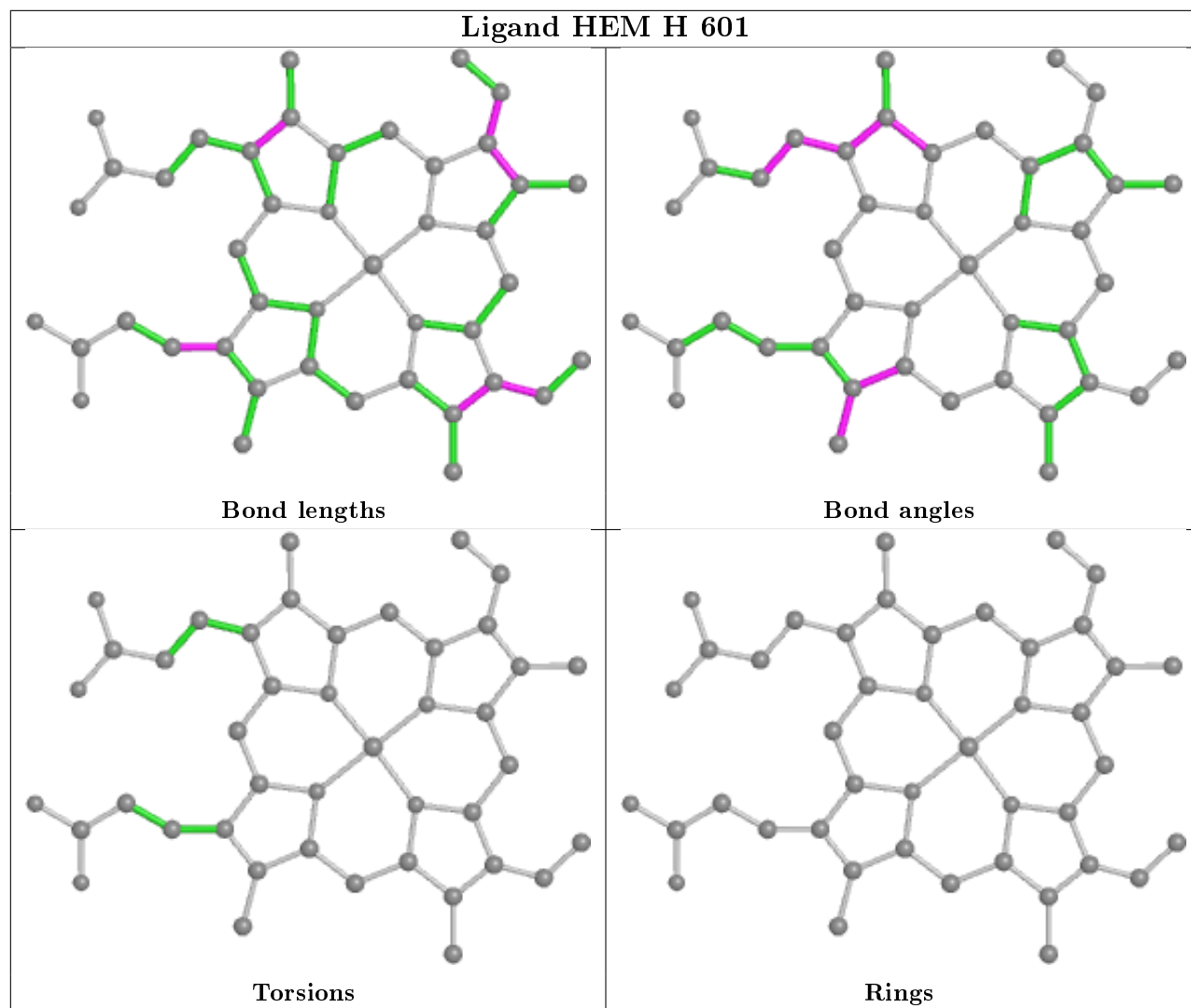


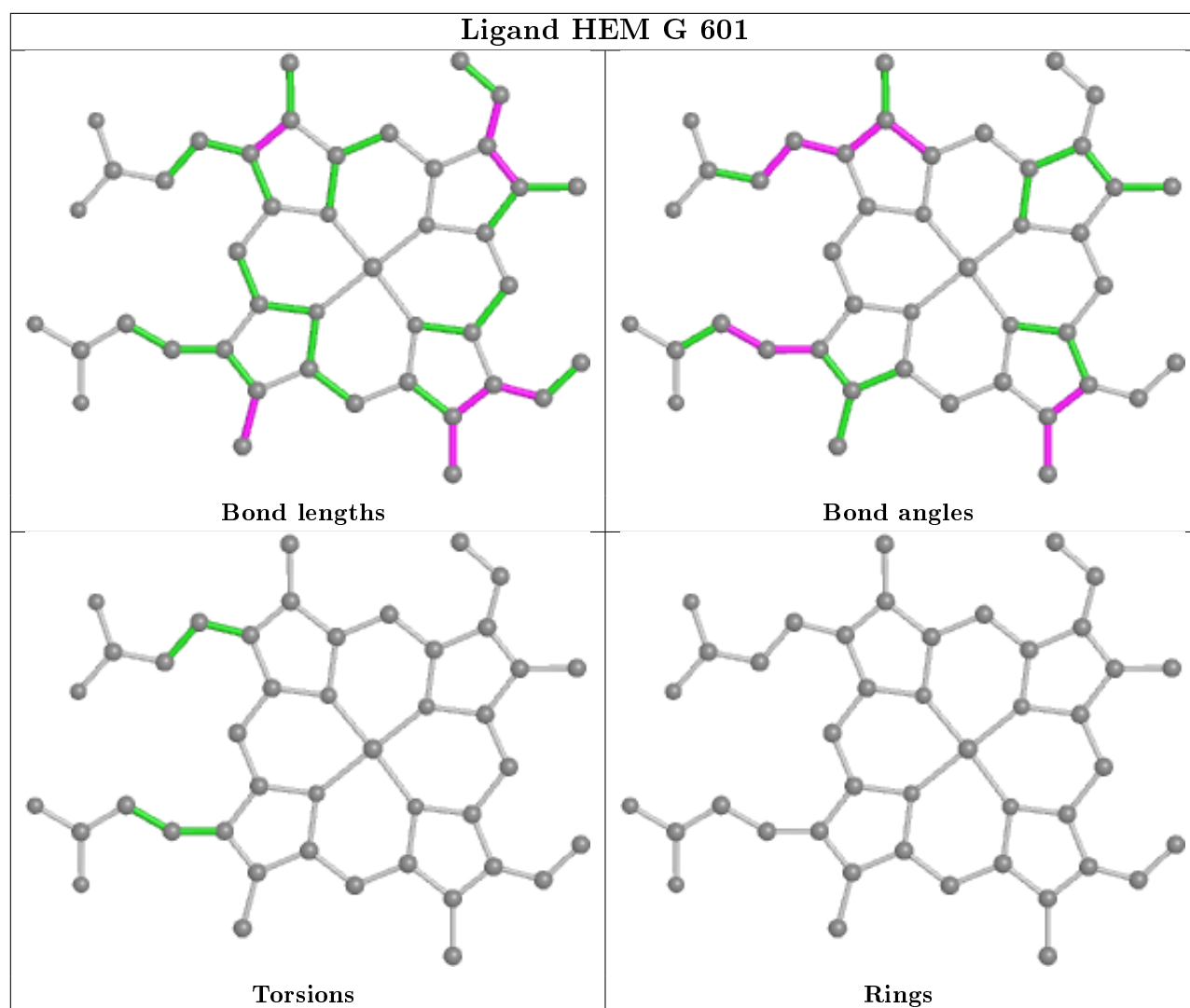


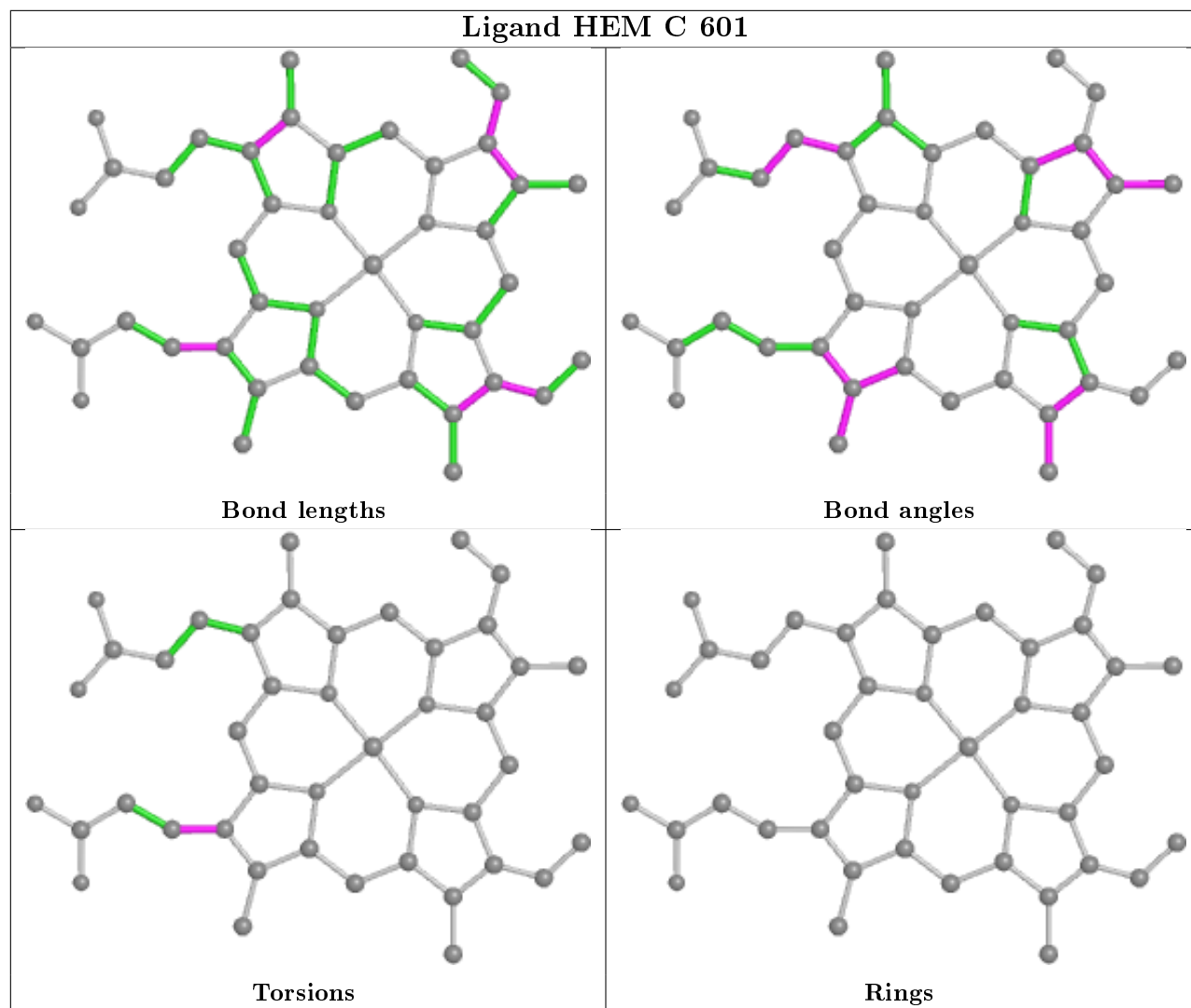


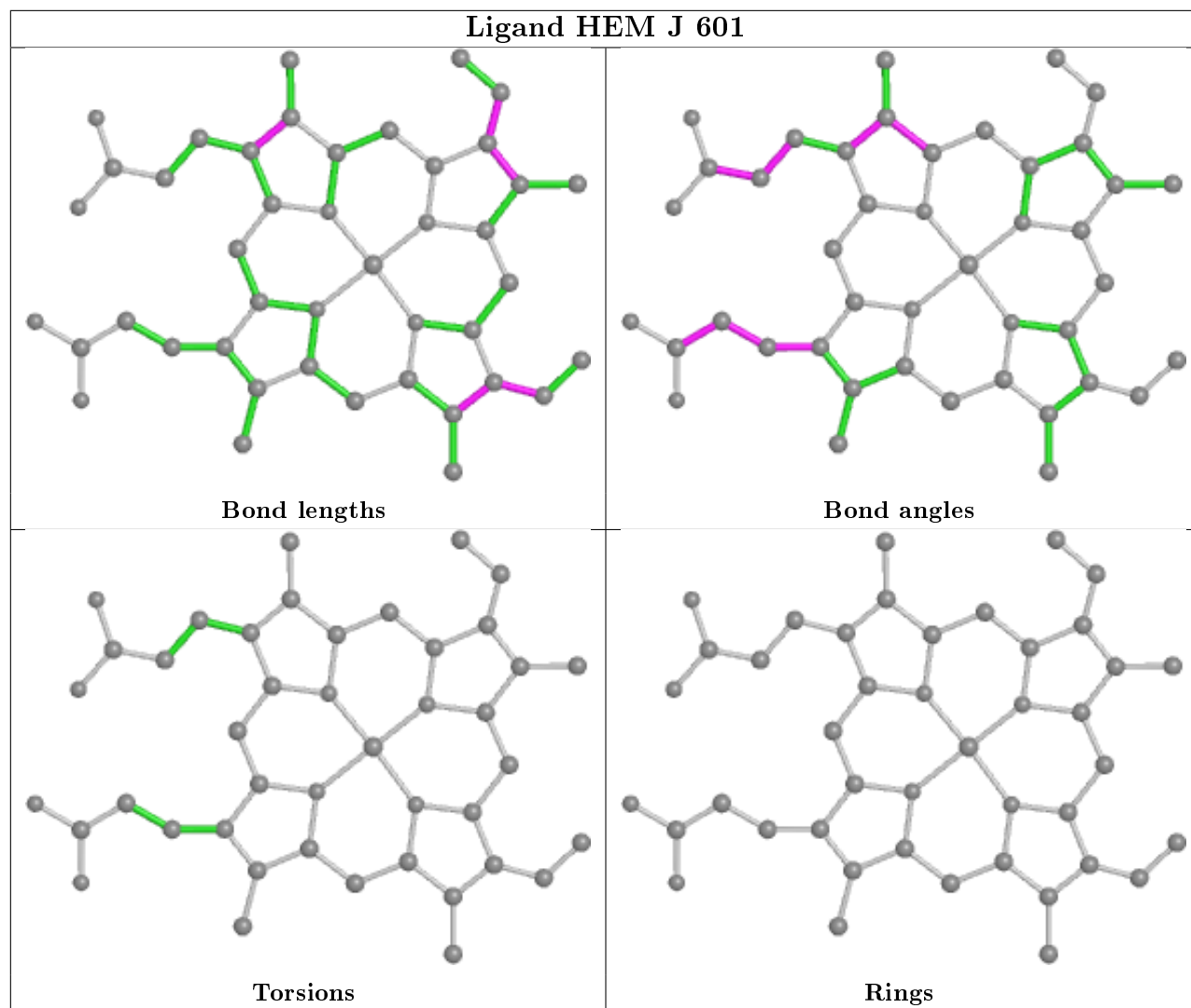
## Ligand HEM I 601



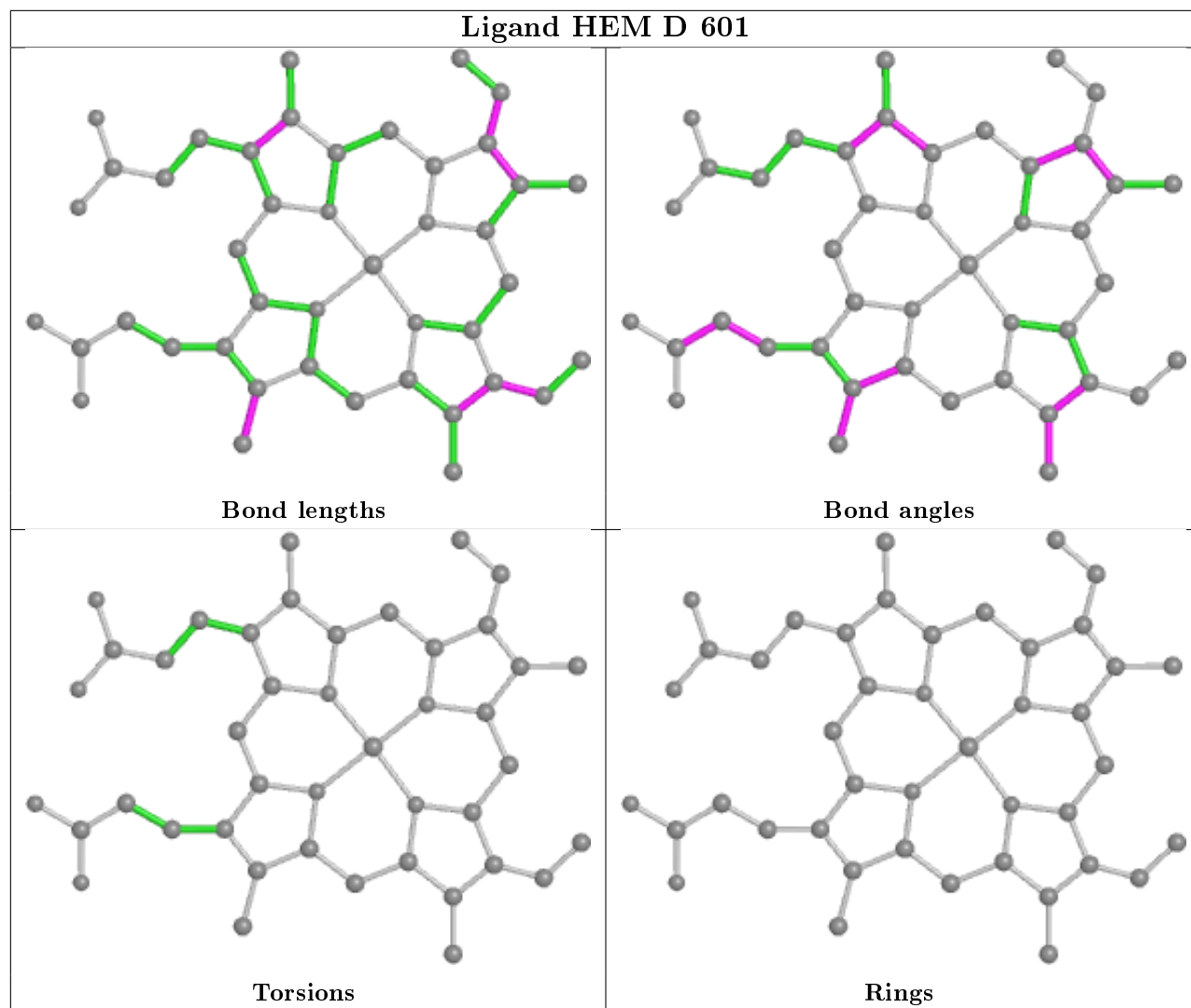


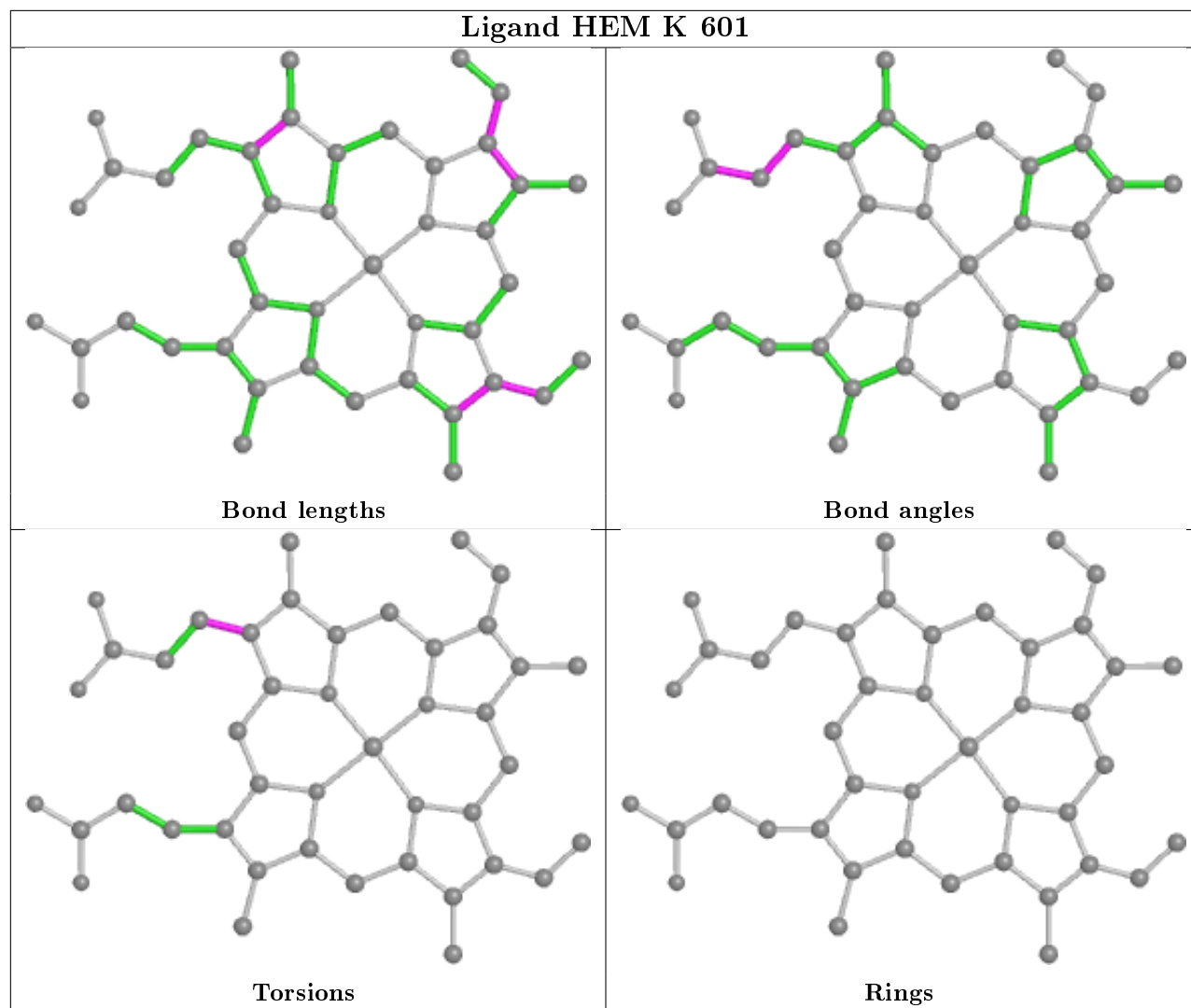


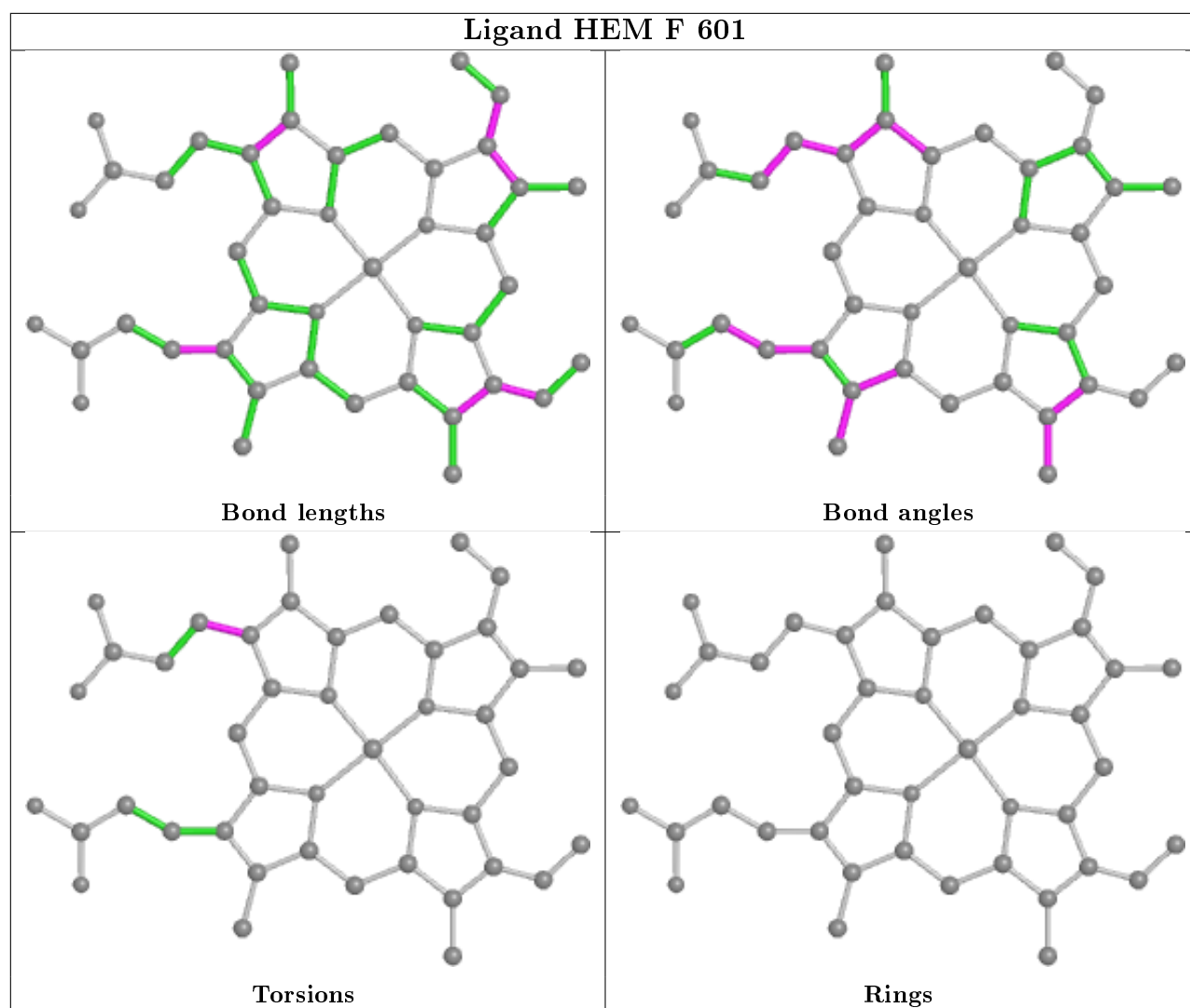












## 5.7 Other polymers [i](#)

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	463/483 (95%)	0.03	3 (0%) 89 90	37, 54, 71, 79	0
1	B	465/483 (96%)	0.10	7 (1%) 73 76	46, 63, 84, 103	0
1	C	462/483 (95%)	0.05	6 (1%) 77 78	42, 56, 77, 88	0
1	D	465/483 (96%)	-0.04	2 (0%) 92 93	41, 57, 75, 90	0
1	E	470/483 (97%)	0.12	5 (1%) 80 82	38, 58, 75, 86	0
1	F	469/483 (97%)	0.17	6 (1%) 77 78	41, 64, 88, 103	0
1	G	463/483 (95%)	0.19	13 (2%) 53 54	47, 67, 96, 115	0
1	H	462/483 (95%)	0.18	18 (3%) 39 39	40, 61, 94, 112	0
1	I	462/483 (95%)	0.31	22 (4%) 30 29	49, 68, 96, 118	0
1	J	462/483 (95%)	0.44	36 (7%) 13 11	52, 78, 101, 120	0
1	K	469/483 (97%)	0.54	41 (8%) 10 8	63, 83, 113, 123	0
1	L	456/483 (94%)	0.21	12 (2%) 56 57	47, 65, 93, 118	0
All	All	5568/5796 (96%)	0.19	171 (3%) 49 50	37, 64, 96, 123	0

All (171) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	37	PRO	5.6
1	J	35	VAL	5.5
1	K	103	VAL	4.8
1	L	49	TRP	4.6
1	F	53	LEU	4.5
1	K	56	TRP	4.3
1	J	391	VAL	4.3
1	H	55	ILE	4.2
1	I	35	VAL	4.1
1	G	55	ILE	4.1
1	H	392	LEU	4.0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	J	38	PHE	4.0
1	B	430	ASP	3.9
1	J	394	ASN	3.9
1	K	237	LEU	3.9
1	L	58	GLU	3.8
1	H	396	HIS	3.8
1	J	91	VAL	3.7
1	K	421	GLU	3.7
1	K	396	HIS	3.7
1	H	41	MET	3.6
1	I	53	LEU	3.6
1	K	435	GLY	3.5
1	J	251	LYS	3.5
1	K	398	PRO	3.5
1	H	36	LEU	3.4
1	K	52	LEU	3.4
1	J	257	PHE	3.3
1	J	399	ALA	3.3
1	J	84	GLY	3.3
1	H	52	LEU	3.3
1	K	239	PHE	3.3
1	K	434	SER	3.3
1	K	429	LEU	3.2
1	L	50	LEU	3.2
1	H	247	TRP	3.1
1	I	38	PHE	3.1
1	E	51	ARG	3.1
1	J	393	GLN	3.1
1	F	257	PHE	3.1
1	K	406	PHE	3.1
1	K	35	VAL	3.1
1	J	250	PRO	3.1
1	K	472	LEU	3.1
1	B	431	ILE	3.1
1	J	254	LYS	3.0
1	H	35	VAL	3.0
1	K	61	TYR	3.0
1	E	430	ASP	3.0
1	J	75	LEU	3.0
1	L	61	TYR	3.0
1	H	34	THR	3.0
1	G	247	TRP	3.0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	K	142	LEU	3.0
1	H	84	GLY	3.0
1	J	396	HIS	2.9
1	I	284	GLN	2.9
1	G	248	ILE	2.8
1	J	237	LEU	2.8
1	K	155	GLN	2.8
1	K	420	PRO	2.8
1	I	391	VAL	2.8
1	K	88	MET	2.8
1	J	252	VAL	2.8
1	K	422	ARG	2.8
1	J	247	TRP	2.7
1	K	86	PRO	2.7
1	G	57	ARG	2.7
1	G	48	ARG	2.7
1	H	38	PHE	2.7
1	I	52	LEU	2.7
1	J	385	VAL	2.7
1	J	403	VAL	2.7
1	K	84	GLY	2.7
1	J	36	LEU	2.7
1	L	60	GLY	2.6
1	G	36	LEU	2.6
1	J	87	ARG	2.6
1	L	57	ARG	2.6
1	I	247	TRP	2.6
1	J	86	PRO	2.6
1	E	429	LEU	2.6
1	L	406	PHE	2.6
1	I	103	VAL	2.6
1	L	244	LEU	2.6
1	J	248	ILE	2.6
1	I	430	ASP	2.6
1	J	114	GLU	2.5
1	A	36	LEU	2.5
1	A	35	VAL	2.5
1	K	138	ARG	2.5
1	K	432	ARG	2.5
1	J	89	VAL	2.5
1	K	423	TYR	2.5
1	D	34	THR	2.5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	I	60	GLY	2.5
1	B	53	LEU	2.5
1	B	35	VAL	2.5
1	G	239	PHE	2.5
1	I	37	PRO	2.5
1	I	429	LEU	2.5
1	C	53	LEU	2.4
1	I	416	LEU	2.4
1	J	472	LEU	2.4
1	C	56	TRP	2.4
1	G	84	GLY	2.4
1	F	122	HIS	2.4
1	J	389	ASP	2.4
1	I	392	LEU	2.4
1	K	91	VAL	2.4
1	J	53	LEU	2.4
1	K	386	VAL	2.4
1	E	257	PHE	2.3
1	K	85	GLY	2.3
1	A	406	PHE	2.3
1	K	38	PHE	2.3
1	K	402	LEU	2.3
1	G	406	PHE	2.3
1	F	439	HIS	2.3
1	K	388	SER	2.3
1	H	253	TRP	2.3
1	K	468	LEU	2.3
1	J	395	TYR	2.3
1	C	248	ILE	2.3
1	F	430	ASP	2.3
1	D	52	LEU	2.2
1	I	106	LEU	2.2
1	J	390	LEU	2.2
1	C	257	PHE	2.2
1	J	204	LEU	2.2
1	G	240	MET	2.2
1	K	397	ILE	2.2
1	H	245	SER	2.2
1	K	75	LEU	2.2
1	G	56	TRP	2.2
1	B	36	LEU	2.2
1	G	66	LEU	2.2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	J	284	GLN	2.2
1	B	248	ILE	2.2
1	F	126	LYS	2.2
1	I	56	TRP	2.2
1	J	279	ALA	2.2
1	H	78	ILE	2.1
1	K	235	VAL	2.1
1	E	507	HIS	2.1
1	H	468	LEU	2.1
1	I	82	ASN	2.1
1	I	77	PRO	2.1
1	B	237	LEU	2.1
1	J	88	MET	2.1
1	L	247	TRP	2.1
1	K	328	PHE	2.1
1	H	416	LEU	2.1
1	K	53	LEU	2.1
1	K	67	GLU	2.1
1	L	239	PHE	2.1
1	C	52	LEU	2.1
1	I	78	ILE	2.1
1	C	50	LEU	2.0
1	I	34	THR	2.0
1	L	280	PHE	2.0
1	G	53	LEU	2.0
1	L	66	LEU	2.0
1	I	75	LEU	2.0
1	I	254	LYS	2.0
1	H	85	GLY	2.0
1	H	96	ASP	2.0
1	J	255	GLU	2.0
1	J	416	LEU	2.0
1	K	375	LEU	2.0
1	K	439	HIS	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 monosaccharides in this entry.

## 6.4 Ligands ⓘ

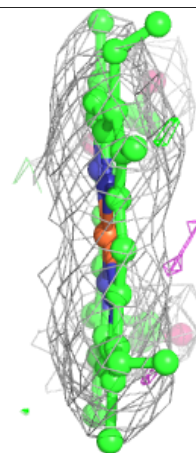
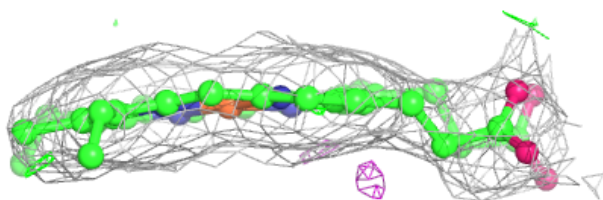
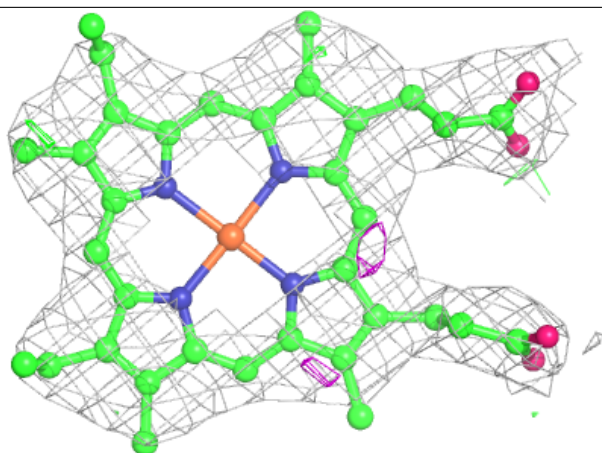
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
3	OT3	J	602	17/17	0.95	0.23	61,62,64,66	0
3	OT3	I	602	17/17	0.95	0.23	58,61,64,66	0
2	HEM	K	601	43/43	0.96	0.20	60,64,72,77	0
3	OT3	K	602	17/17	0.96	0.17	67,70,72,72	0
3	OT3	D	602	17/17	0.97	0.22	48,50,54,54	0
3	OT3	H	602	17/17	0.97	0.22	48,50,52,53	0
3	OT3	B	602	17/17	0.97	0.19	49,51,52,53	0
2	HEM	I	601	43/43	0.97	0.20	49,53,58,60	0
3	OT3	G	602	17/17	0.97	0.21	46,49,53,54	0
2	HEM	J	601	43/43	0.97	0.22	55,58,64,68	0
3	OT3	L	602	17/17	0.97	0.19	53,54,56,57	0
3	OT3	F	602	17/17	0.97	0.19	46,49,51,51	0
3	OT3	E	602	17/17	0.97	0.21	51,53,56,57	0
2	HEM	E	601	43/43	0.98	0.19	32,36,44,48	0
2	HEM	G	601	43/43	0.98	0.19	41,46,49,50	0
2	HEM	C	601	43/43	0.98	0.17	37,42,50,54	0
2	HEM	L	601	43/43	0.98	0.21	55,58,65,67	0
2	HEM	D	601	43/43	0.98	0.18	38,43,53,59	0
2	HEM	B	601	43/43	0.98	0.19	42,48,56,62	0
2	HEM	H	601	43/43	0.98	0.19	38,43,50,52	0
3	OT3	C	602	17/17	0.98	0.20	48,51,52,52	0
2	HEM	F	601	43/43	0.98	0.18	36,40,52,54	0
2	HEM	A	601	43/43	0.99	0.19	37,42,45,48	0
3	OT3	A	602	17/17	0.99	0.17	41,42,44,45	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

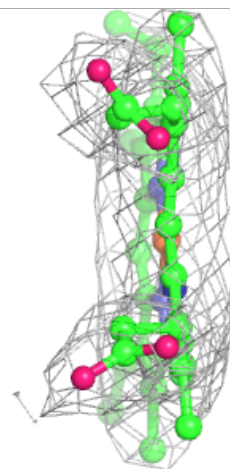
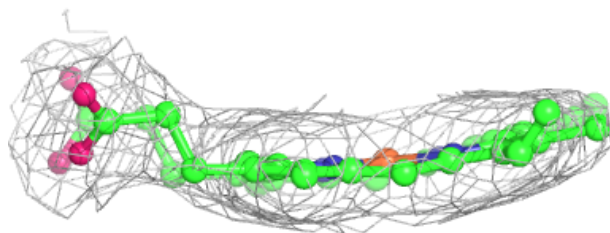
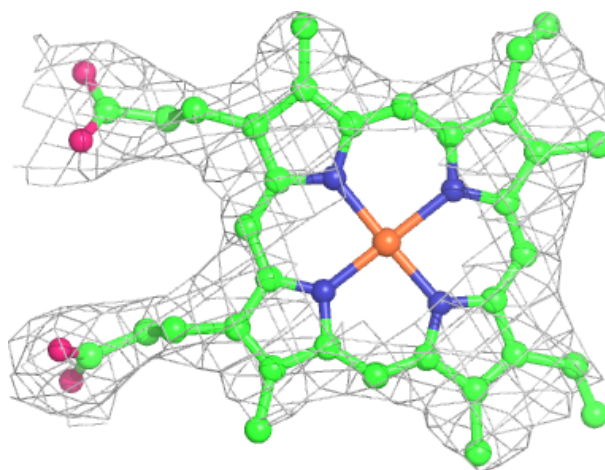
**Electron density around HEM K 601:**

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



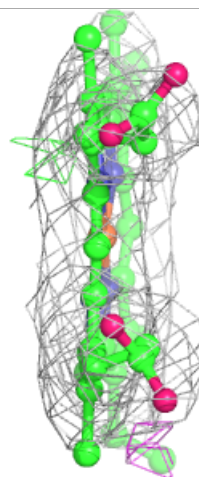
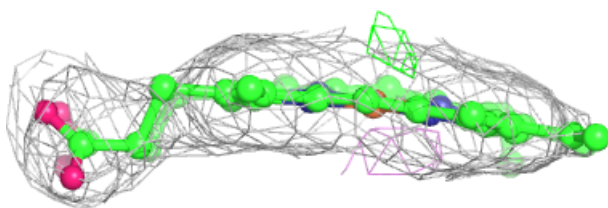
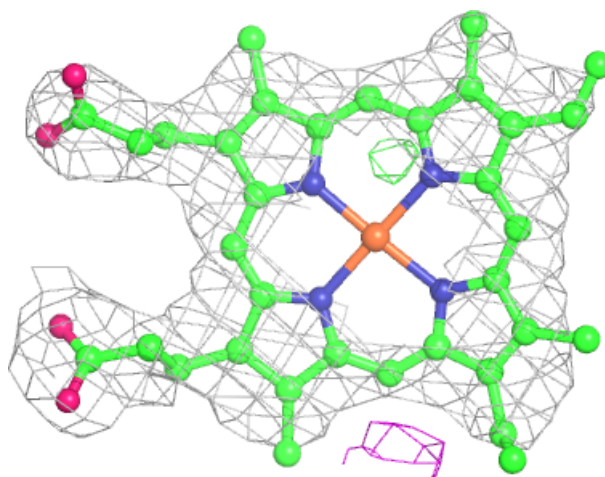
**Electron density around HEM I 601:**

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



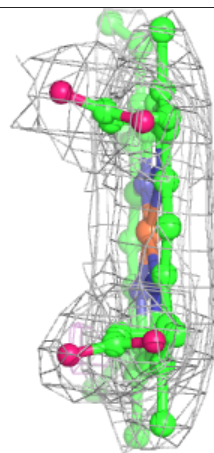
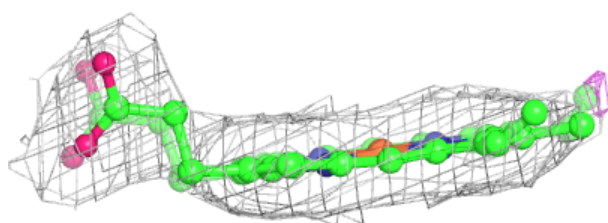
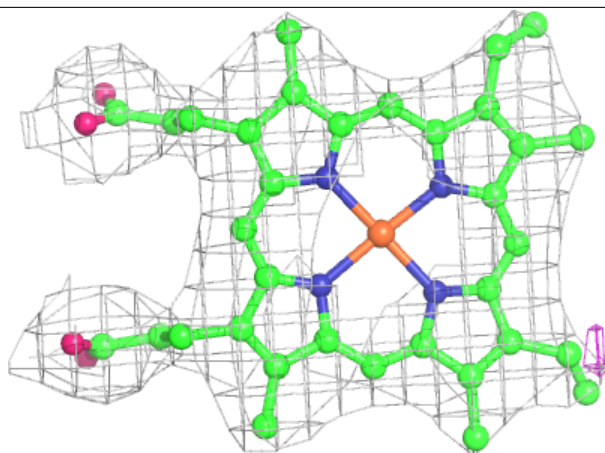
**Electron density around HEM J 601:**

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



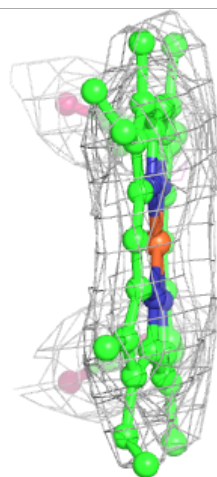
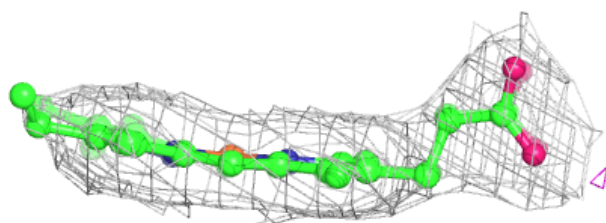
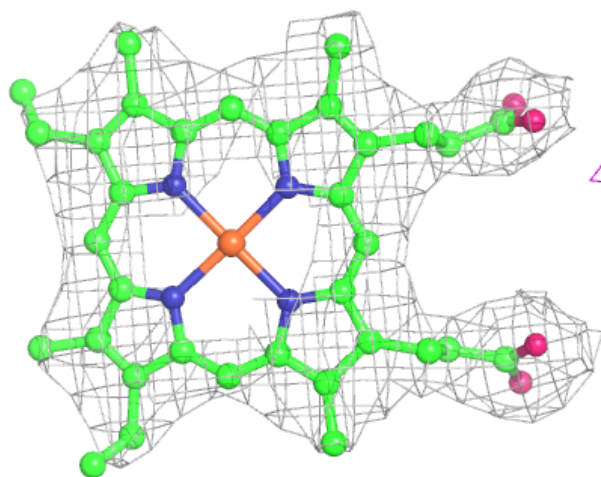
**Electron density around HEM E 601:**

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



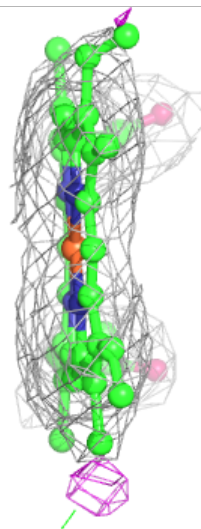
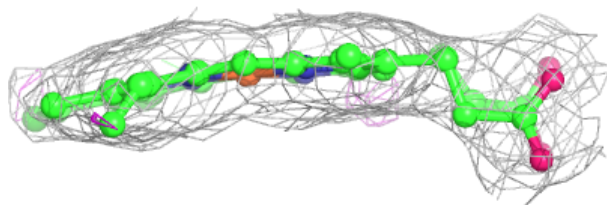
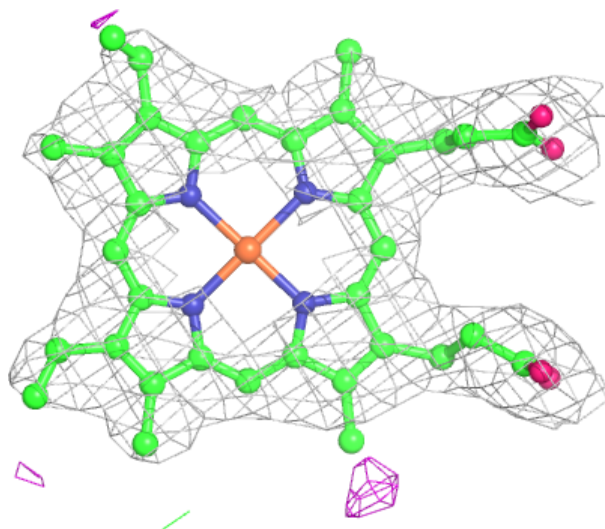
**Electron density around HEM G 601:**

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



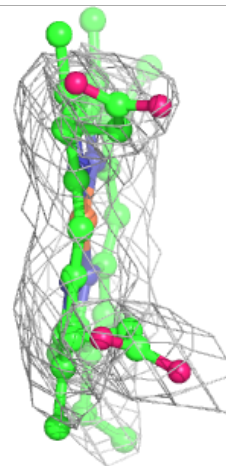
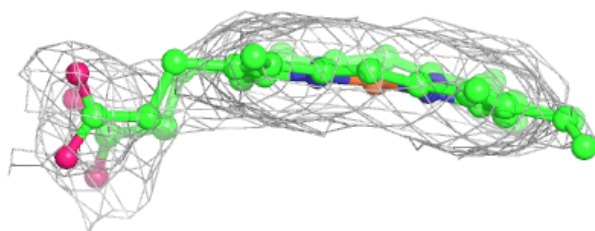
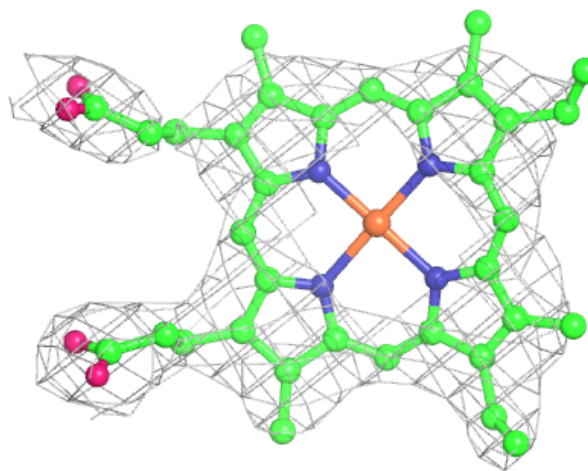
**Electron density around HEM C 601:**

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



**Electron density around HEM L 601:**

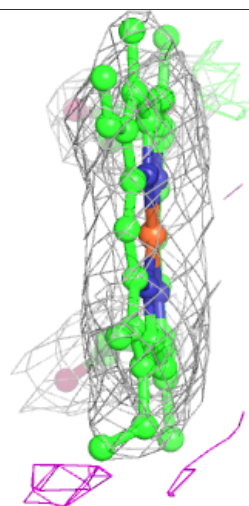
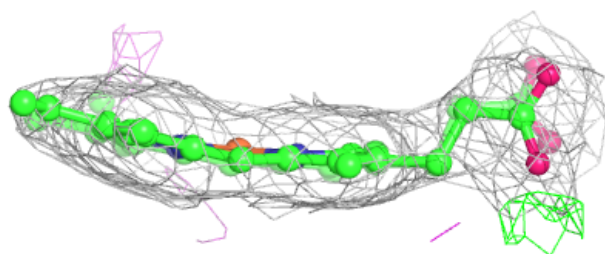
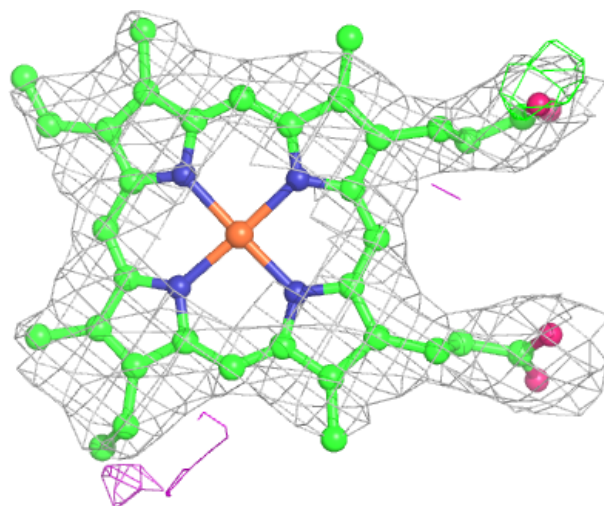
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





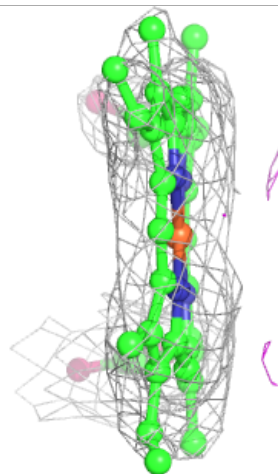
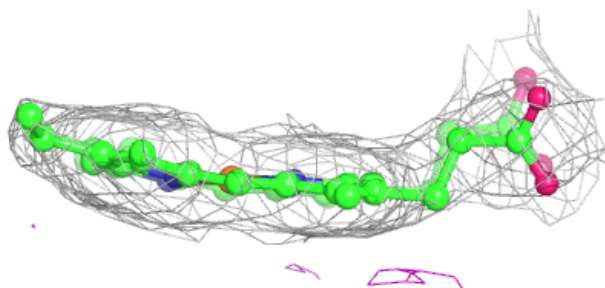
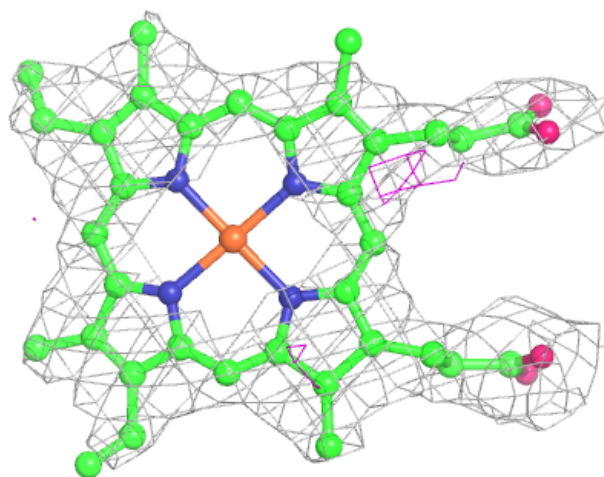
**Electron density around HEM D 601:**

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



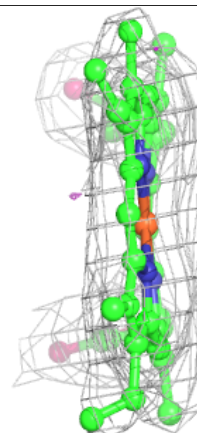
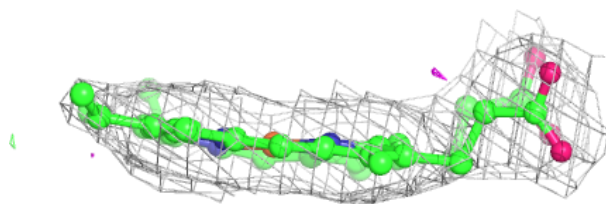
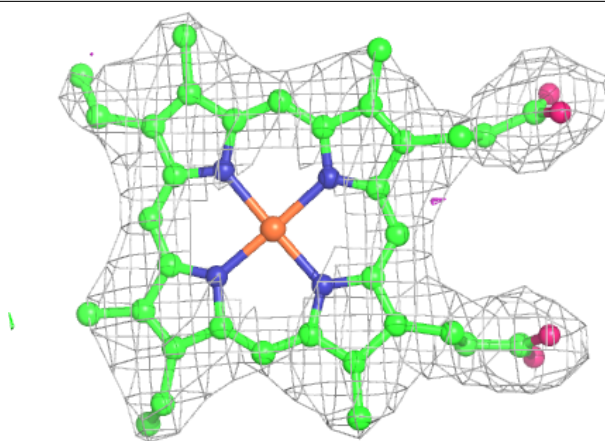
**Electron density around HEM B 601:**

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



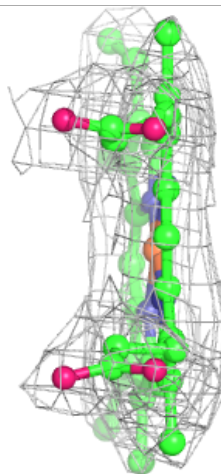
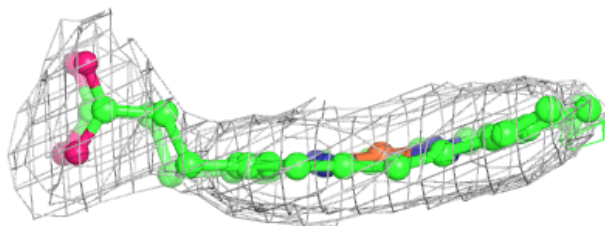
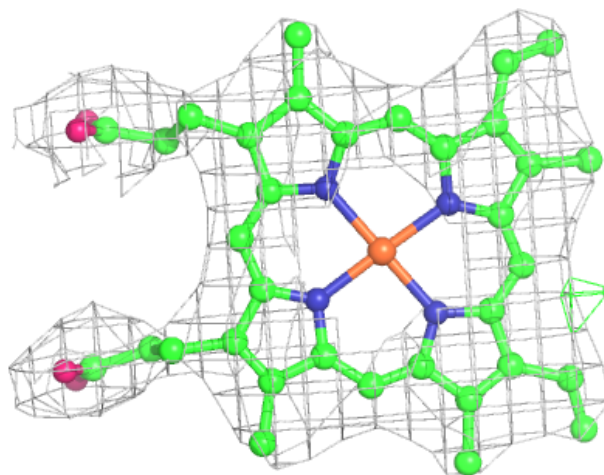
**Electron density around HEM H 601:**

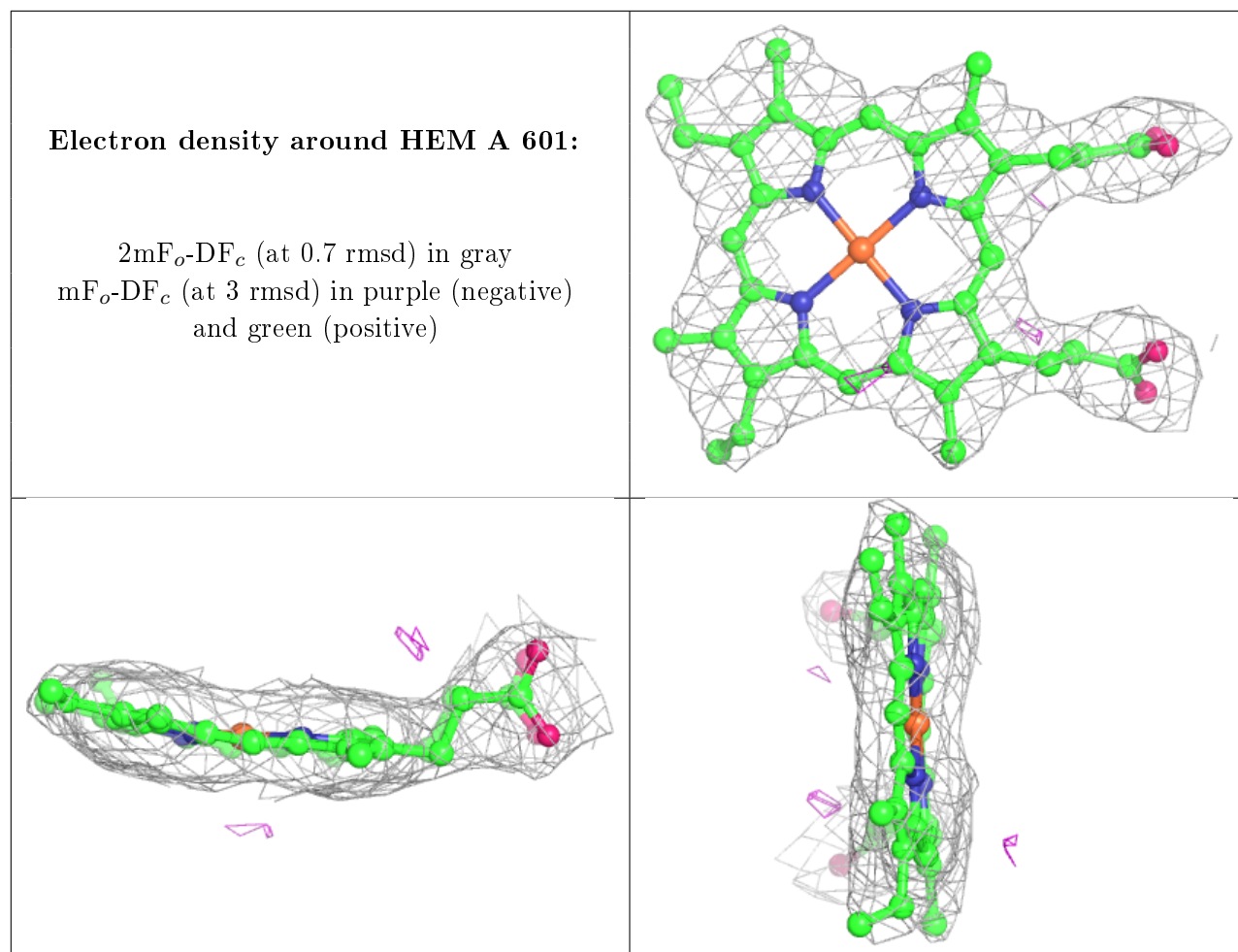
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around HEM F 601:**

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





## 6.5 Other polymers [i](#)

There are no such residues in this entry.