



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:40 PM UTC

PDB ID : 2NOX / pdb_00002nox
Title : Crystal structure of tryptophan 2,3-dioxygenase from *Ralstonia metallidurans*
Authors : Zhang, Y.; Kang, S.A.; Mukherjee, T.; Bale, S.; Crane, B.R.; Begley, T.P.; Ealick, S.E.
Deposited on : 2006-10-26
Resolution : 2.40 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

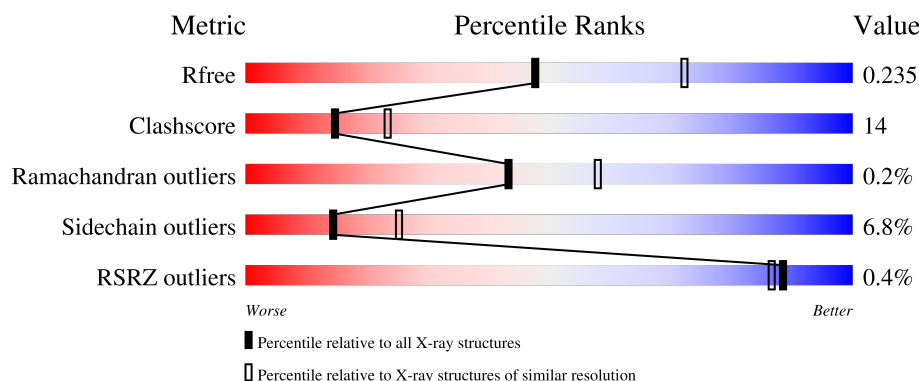
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



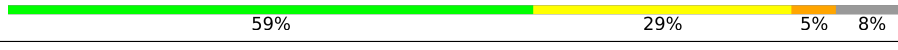
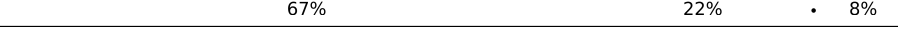
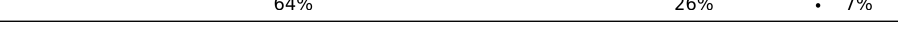
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	281	69% 21% • 7%
1	B	281	70% 21% • 5%
1	C	281	69% 19% • 9%
1	D	281	% 69% 20% • 8%
1	E	281	68% 21% • 9%

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Mol	Chain	Length	Quality of chain
1	F	281	% 
1	G	281	
1	H	281	
1	I	281	
1	J	281	% 
1	K	281	
1	L	281	
1	M	281	% 
1	N	281	% 
1	O	281	
1	P	281	

2 Entry composition [i](#)

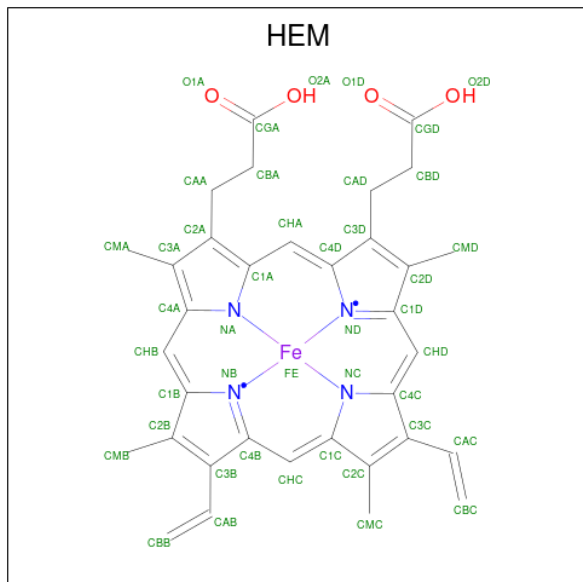
There are 3 unique types of molecules in this entry. The entry contains 36423 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Tryptophan 2,3-dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total	C	N	O	S	0	1	0
			2160	1375	382	390	13			
1	B	266	Total	C	N	O	S	0	0	0
			2192	1400	384	395	13			
1	C	255	Total	C	N	O	S	0	0	0
			2106	1344	368	382	12			
1	D	259	Total	C	N	O	S	0	0	0
			2133	1360	376	385	12			
1	E	256	Total	C	N	O	S	0	0	0
			2126	1356	376	382	12			
1	F	260	Total	C	N	O	S	0	0	0
			2152	1371	380	388	13			
1	G	259	Total	C	N	O	S	0	0	0
			2137	1362	376	387	12			
1	H	259	Total	C	N	O	S	0	2	0
			2147	1368	380	387	12			
1	I	259	Total	C	N	O	S	0	0	0
			2133	1360	376	385	12			
1	J	257	Total	C	N	O	S	0	0	0
			2126	1356	374	384	12			
1	K	255	Total	C	N	O	S	0	1	0
			2119	1352	372	383	12			
1	L	260	Total	C	N	O	S	0	0	0
			2141	1364	377	388	12			
1	M	255	Total	C	N	O	S	0	1	0
			2111	1349	370	380	12			
1	N	260	Total	C	N	O	S	0	1	0
			2150	1370	379	389	12			
1	O	257	Total	C	N	O	S	0	0	0
			2126	1356	374	384	12			
1	P	259	Total	C	N	O	S	0	0	0
			2133	1360	376	385	12			

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: 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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	M	1	Total	C	Fe	N	O	
			43	34	1	4	4	0
2	N	1	Total	C	Fe	N	O	
			43	34	1	4	4	0
2	O	1	Total	C	Fe	N	O	
			43	34	1	4	4	0
2	P	1	Total	C	Fe	N	O	
			43	34	1	4	4	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	130	Total	O	0	0
			130	130		
3	B	126	Total	O	0	0
			126	126		
3	C	107	Total	O	0	0
			107	107		
3	D	158	Total	O	0	0
			158	158		
3	E	107	Total	O	0	0
			107	107		
3	F	72	Total	O	0	0
			72	72		
3	G	56	Total	O	0	0
			56	56		
3	H	114	Total	O	0	0
			114	114		
3	I	85	Total	O	0	0
			85	85		
3	J	82	Total	O	0	0
			82	82		
3	K	74	Total	O	0	0
			74	74		
3	L	81	Total	O	0	0
			81	81		
3	M	116	Total	O	0	0
			116	116		
3	N	66	Total	O	0	0
			66	66		
3	O	61	Total	O	0	0
			61	61		

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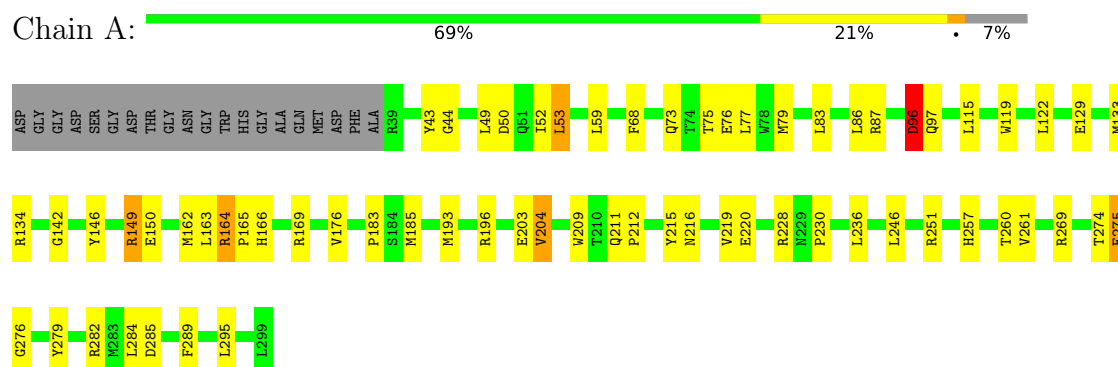
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	P	108	Total 108	O 108	0	0

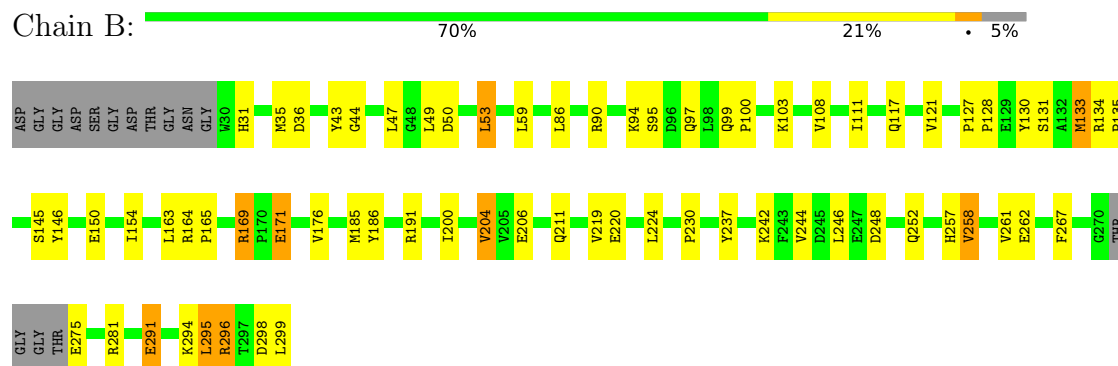
3 Residue-property plots [i](#)

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.

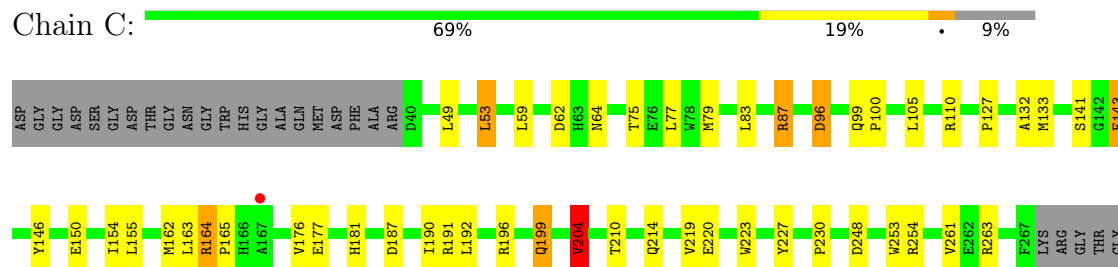
• Molecule 1: Tryptophan 2,3-dioxygenase



• Molecule 1: Tryptophan 2,3-dioxygenase

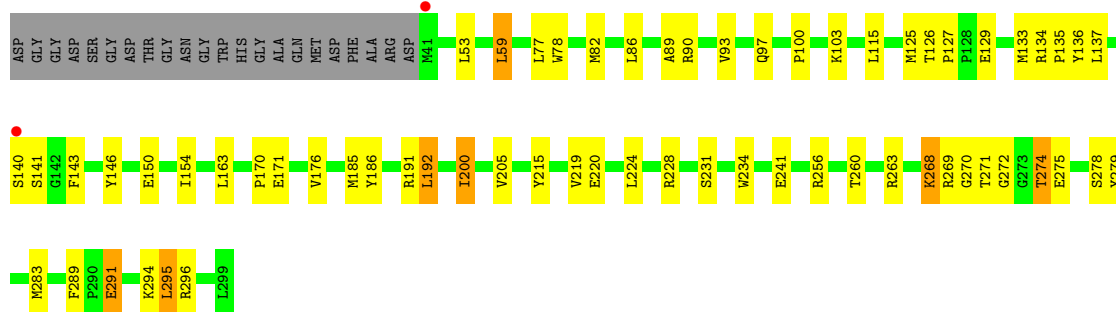


• Molecule 1: Tryptophan 2,3-dioxygenase

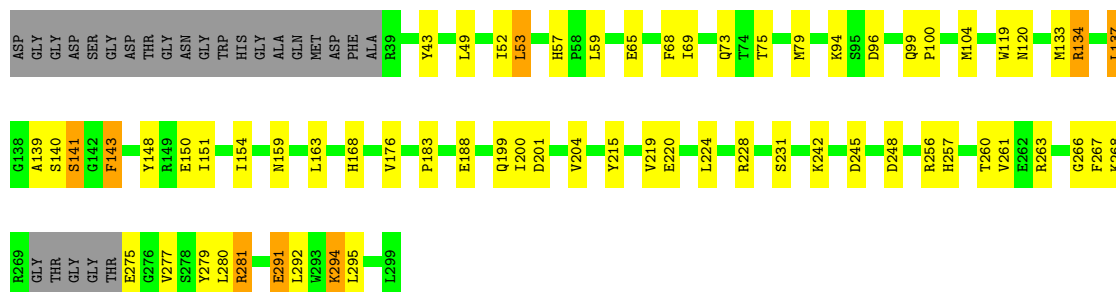




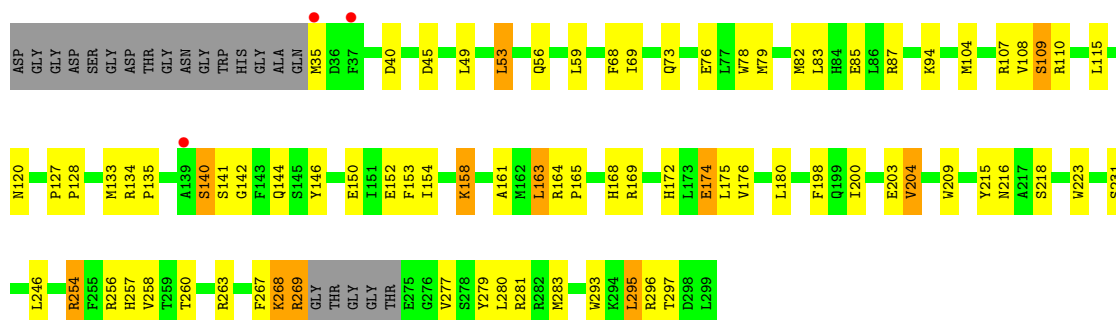
- Molecule 1: Tryptophan 2,3-dioxygenase



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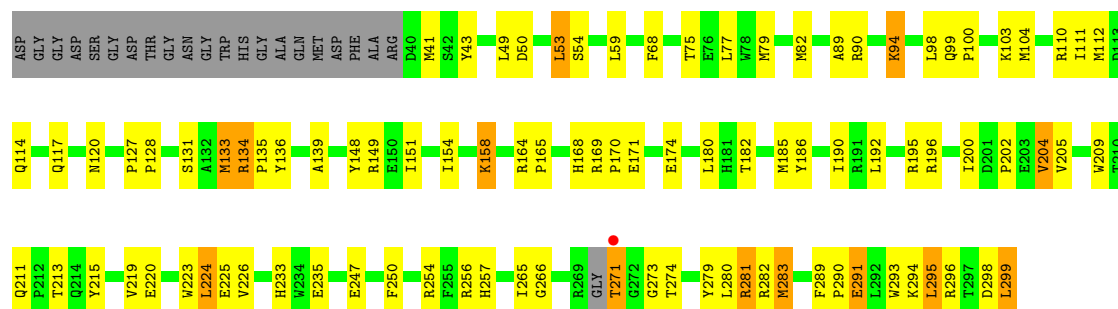


- Molecule 1: Tryptophan 2,3-dioxygenase

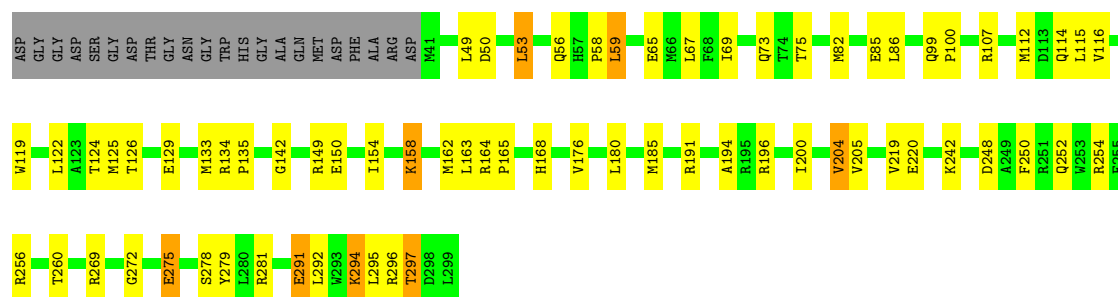


- Molecule 1: Tryptophan 2,3-dioxygenase

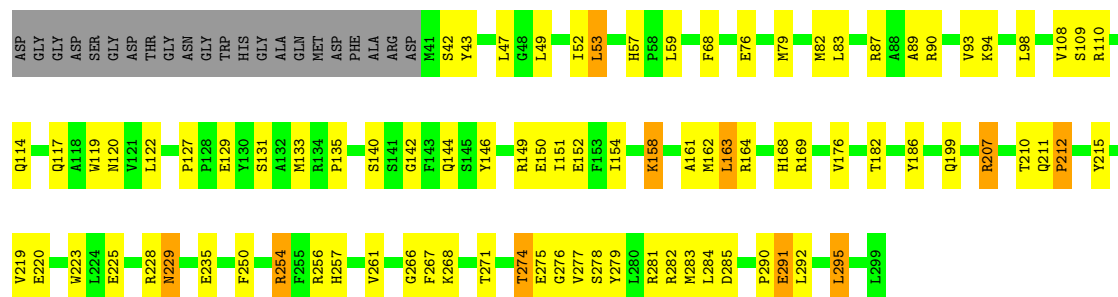




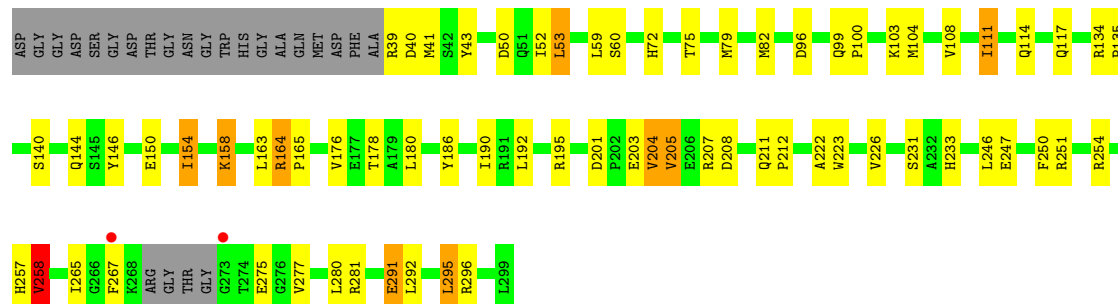
• Molecule 1: Tryptophan 2,3-dioxygenase



• Molecule 1: Tryptophan 2,3-dioxygenase

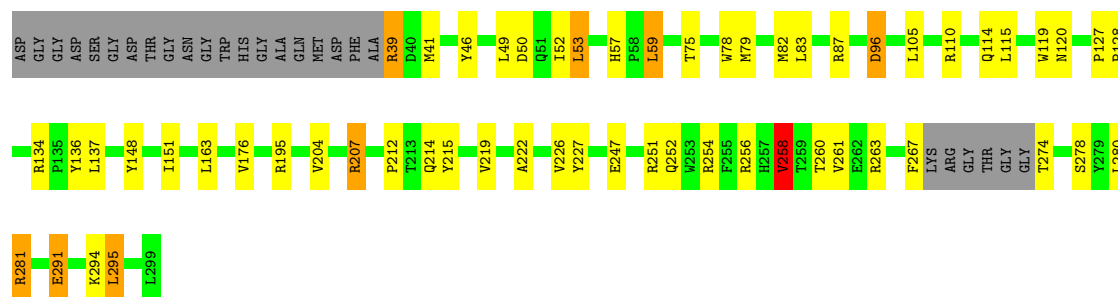


• Molecule 1: Tryptophan 2,3-dioxygenase



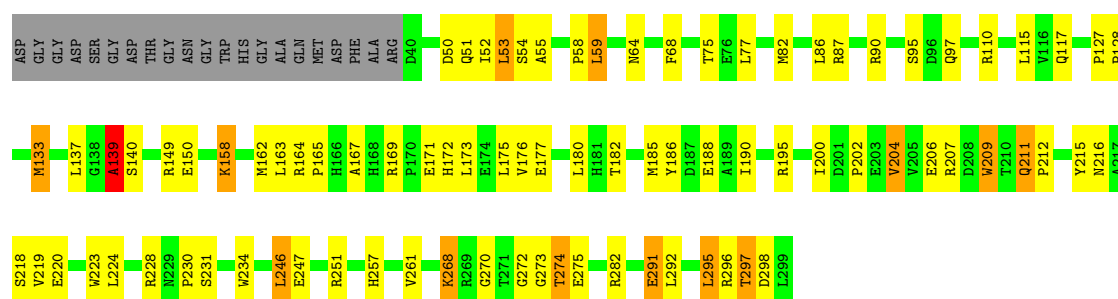
- Molecule 1: Tryptophan 2,3-dioxygenase

Chain K:  70% 17% 9%



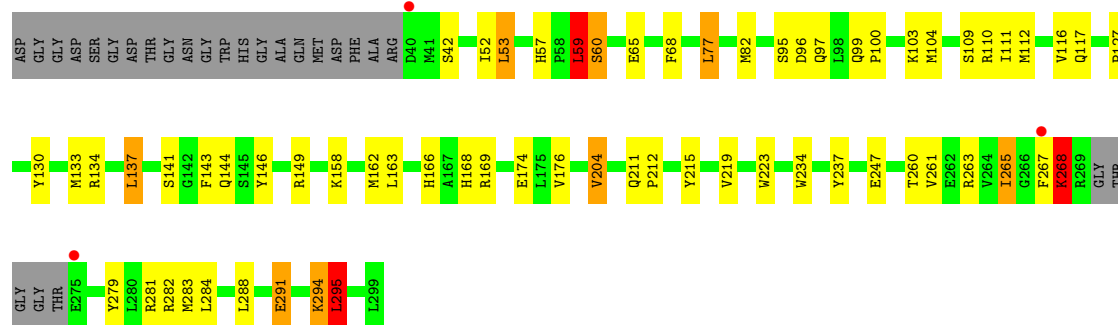
- Molecule 1: Tryptophan 2,3-dioxygenase

Chain L:  62% 26% 5% 7%



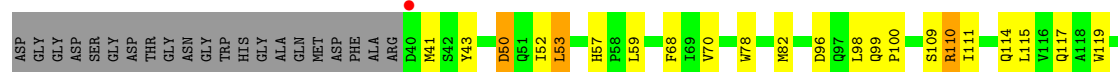
- Molecule 1: Tryptophan 2,3-dioxygenase

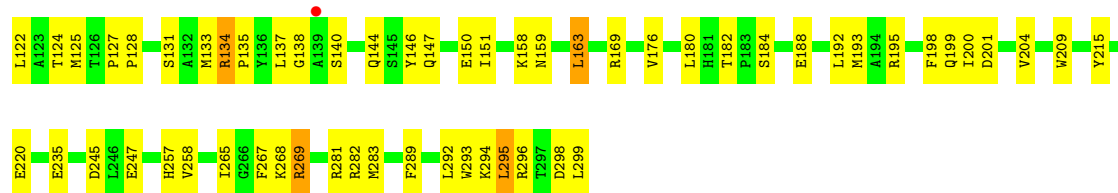
Chain M:  68% 19% 9%



- Molecule 1: Tryptophan 2,3-dioxygenase

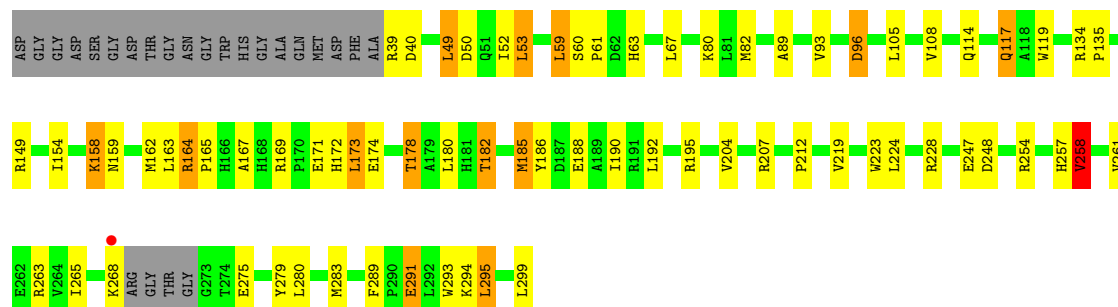
Chain N:  64% 26% 7%





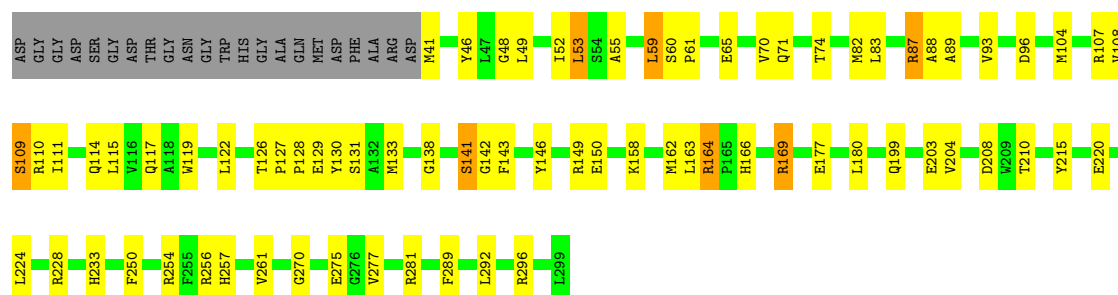
• Molecule 1: Tryptophan 2,3-dioxygenase

Chain O: 66% 21% 5% 9%



• Molecule 1: Tryptophan 2,3-dioxygenase

Chain P: 65% 25% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	72.54Å 132.12Å 139.95Å 66.97° 85.06° 89.89°	Depositor
Resolution (Å)	50.12 – 2.40 50.12 – 2.40	Depositor EDS
% Data completeness (in resolution range)	93.5 (50.12-2.40) 91.4 (50.12-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.22Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.210 , 0.270 0.163 , 0.235	Depositor DCC
R_{free} test set	11190 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	38.1	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 53.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	36423	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.97% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: HEM

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.88	0/2217	1.02	4/3004 (0.1%)
1	B	0.80	1/2252 (0.0%)	1.01	3/3053 (0.1%)
1	C	0.77	0/2162	1.04	4/2932 (0.1%)
1	D	0.86	0/2190	1.03	4/2969 (0.1%)
1	E	0.77	1/2182 (0.0%)	0.94	1/2956 (0.0%)
1	F	0.73	0/2208	0.96	0/2991
1	G	0.68	0/2193	0.96	4/2972 (0.1%)
1	H	0.76	0/2207	0.99	1/2992 (0.0%)
1	I	0.72	0/2190	0.94	1/2969 (0.0%)
1	J	0.68	1/2182 (0.0%)	0.96	5/2957 (0.2%)
1	K	0.68	0/2178	0.94	2/2953 (0.1%)
1	L	0.68	0/2198	0.96	3/2980 (0.1%)
1	M	0.81	1/2167 (0.0%)	1.00	5/2938 (0.2%)
1	N	0.68	0/2207	0.97	5/2991 (0.2%)
1	O	0.70	1/2182 (0.0%)	0.95	4/2957 (0.1%)
1	P	0.78	0/2190	1.01	4/2969 (0.1%)
All	All	0.75	5/35105 (0.0%)	0.98	50/47583 (0.1%)

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	L	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	O	265	ILE	CA-CB	5.64	1.60	1.54
1	B	244	VAL	CA-CB	5.30	1.61	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	258	VAL	CA-CB	5.18	1.60	1.54
1	M	127	PRO	CA-C	5.07	1.56	1.52
1	E	52	ILE	CA-CB	5.03	1.59	1.54

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	258	VAL	CB-CA-C	-9.38	99.97	111.97
1	P	289	PHE	CA-C-N	8.99	128.59	119.24
1	P	289	PHE	C-N-CA	8.99	128.59	119.24
1	C	289	PHE	CA-C-N	8.75	128.34	119.24
1	C	289	PHE	C-N-CA	8.75	128.34	119.24
1	K	258	VAL	CB-CA-C	-7.60	102.15	111.88
1	J	258	VAL	CB-CA-C	-7.58	102.27	111.97
1	N	289	PHE	CA-C-N	7.22	127.56	119.32
1	N	289	PHE	C-N-CA	7.22	127.56	119.32
1	D	289	PHE	CA-C-N	7.12	127.44	119.32
1	D	289	PHE	C-N-CA	7.12	127.44	119.32
1	L	140	SER	N-CA-C	7.08	120.14	109.95
1	M	211	GLN	CA-C-N	7.04	127.03	119.78
1	M	211	GLN	C-N-CA	7.04	127.03	119.78
1	N	57	HIS	CA-C-N	6.98	127.37	119.83
1	N	57	HIS	C-N-CA	6.98	127.37	119.83
1	E	245	ASP	CB-CA-C	-6.65	100.17	110.81
1	M	204	VAL	CB-CA-C	6.53	117.05	110.65
1	P	169	ARG	CA-C-N	6.29	126.50	119.32
1	P	169	ARG	C-N-CA	6.29	126.50	119.32
1	J	258	VAL	N-CA-CB	6.28	117.90	110.55
1	G	289	PHE	CA-C-N	6.04	125.52	119.24
1	G	289	PHE	C-N-CA	6.04	125.52	119.24
1	I	127	PRO	N-CA-C	6.00	118.03	110.70
1	C	204	VAL	N-CA-C	-5.74	107.90	113.53
1	O	289	PHE	CA-C-N	5.72	124.92	118.97
1	O	289	PHE	C-N-CA	5.72	124.92	118.97
1	O	258	VAL	CB-CA-C	-5.71	104.57	111.88
1	D	295	LEU	CA-CB-CG	5.68	136.17	116.30
1	K	258	VAL	N-CA-CB	5.64	116.77	110.51
1	D	127	PRO	N-CA-C	5.55	117.47	110.70
1	A	96	ASP	N-CA-C	5.55	119.22	111.90
1	H	204	VAL	N-CA-C	-5.52	106.96	113.42
1	B	258	VAL	N-CA-CB	5.52	117.01	110.55
1	L	169	ARG	CA-C-N	5.48	125.83	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	169	ARG	C-N-CA	5.48	125.83	119.47
1	M	295	LEU	CA-CB-CG	5.45	135.36	116.30
1	N	137	LEU	N-CA-C	5.37	118.69	110.36
1	J	111	ILE	CB-CA-C	-5.34	104.92	112.14
1	G	265	ILE	N-CA-C	5.24	118.76	113.47
1	A	289	PHE	CA-C-N	5.20	124.83	119.05
1	A	289	PHE	C-N-CA	5.20	124.83	119.05
1	B	36	ASP	N-CA-C	5.19	117.19	108.73
1	C	253	TRP	N-CA-C	-5.15	105.75	111.36
1	A	204	VAL	CB-CA-C	5.12	116.15	110.62
1	M	59	LEU	N-CA-C	-5.11	107.22	113.50
1	G	111	ILE	CB-CA-C	-5.02	105.30	112.22
1	O	190	ILE	CB-CA-C	-5.01	105.31	112.22
1	J	60	SER	CA-C-N	-5.01	113.58	119.84
1	J	60	SER	C-N-CA	-5.01	113.58	119.84

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	139	ALA	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2160	0	2108	69	0
1	B	2192	0	2117	52	0
1	C	2106	0	2047	54	0
1	D	2133	0	2083	48	0
1	E	2126	0	2076	59	0
1	F	2152	0	2096	69	0
1	G	2137	0	2083	82	0
1	H	2147	0	2101	42	0
1	I	2133	0	2083	90	0
1	J	2126	0	2073	56	0
1	K	2119	0	2065	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	2141	0	2087	82	0
1	M	2111	0	2051	53	0
1	N	2150	0	2099	69	0
1	O	2126	0	2073	61	0
1	P	2133	0	2083	68	0
2	A	43	0	30	6	0
2	B	43	0	30	0	0
2	C	43	0	30	2	0
2	D	43	0	30	2	0
2	E	43	0	30	7	0
2	F	43	0	30	3	0
2	G	43	0	30	3	0
2	H	43	0	30	2	0
2	I	43	0	30	9	0
2	J	43	0	30	1	0
2	K	43	0	30	4	0
2	L	43	0	30	5	0
2	M	43	0	30	2	0
2	N	43	0	30	1	0
2	O	43	0	30	4	0
2	P	43	0	30	7	0
3	A	130	0	0	10	0
3	B	126	0	0	6	0
3	C	107	0	0	7	0
3	D	158	0	0	4	0
3	E	107	0	0	4	0
3	F	72	0	0	5	0
3	G	56	0	0	8	0
3	H	114	0	0	3	0
3	I	85	0	0	8	0
3	J	82	0	0	6	0
3	K	74	0	0	7	0
3	L	81	0	0	10	0
3	M	116	0	0	5	0
3	N	66	0	0	1	0
3	O	61	0	0	4	0
3	P	108	0	0	5	0
All	All	36423	0	33805	957	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 14.

All (957) 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:P:88:ALA:CB	1:P:104:MET:HE1	1.73	1.18
1:N:109:SER:HB3	1:N:110:ARG:NH1	1.56	1.17
1:P:65:GLU:HG3	1:P:133:MET:CE	1.77	1.15
1:C:219:VAL:HG12	1:C:291:GLU:HG3	1.31	1.09
1:E:281:ARG:HG2	1:E:281:ARG:HH11	1.05	1.09
1:P:65:GLU:HG3	1:P:133:MET:HE3	1.09	1.09
1:G:82:MET:HE1	1:G:112:MET:SD	1.91	1.09
1:C:199:GLN:O	1:C:199:GLN:HG3	1.52	1.07
1:G:283:MET:HA	1:G:283:MET:HE3	1.38	1.04
1:P:88:ALA:HB3	1:P:104:MET:CE	1.88	1.04
1:I:207:ARG:HH11	1:I:207:ARG:HG3	1.19	1.01
1:P:88:ALA:HB1	1:P:104:MET:HE1	1.37	1.00
1:I:279:TYR:CE1	1:I:283:MET:HE3	1.96	1.00
1:N:109:SER:CB	1:N:110:ARG:NH1	2.25	0.99
1:N:109:SER:HB3	1:N:110:ARG:HH12	1.16	0.97
1:A:274:THR:HG22	1:A:276:GLY:H	1.30	0.96
1:I:164:ARG:HD2	3:I:583:HOH:O	1.63	0.96
1:G:82:MET:CE	1:G:112:MET:HG2	1.96	0.96
1:E:79:MET:HE2	1:E:151:ILE:HD12	1.48	0.95
1:G:283:MET:HA	1:G:283:MET:CE	1.96	0.94
1:I:274:THR:HG22	1:I:276:GLY:H	1.29	0.94
1:B:219:VAL:HG12	1:B:291:GLU:HG3	1.52	0.92
1:J:96:ASP:HB2	3:J:534:HOH:O	1.68	0.92
1:C:219:VAL:CG1	1:C:291:GLU:HG3	1.99	0.91
1:K:278:SER:HB2	3:K:513:HOH:O	1.70	0.91
1:F:109:SER:HB2	3:F:543:HOH:O	1.68	0.91
1:C:181:HIS:HE1	3:C:584:HOH:O	1.52	0.91
1:G:82:MET:HE2	1:G:112:MET:HG2	1.54	0.90
1:K:57:HIS:HD2	3:K:570:HOH:O	1.52	0.90
1:O:169:ARG:HD2	1:O:171:GLU:OE2	1.70	0.90
1:M:60:SER:HB3	1:M:65:GLU:OE1	1.72	0.90
1:P:88:ALA:CB	1:P:104:MET:CE	2.47	0.90
1:K:83:LEU:O	1:K:87:ARG:HG3	1.72	0.89
1:N:138:GLY:C	1:N:140:SER:H	1.79	0.89
1:E:281:ARG:HG2	1:E:281:ARG:NH1	1.82	0.88
1:I:149:ARG:CZ	1:I:162:MET:HE2	2.02	0.88
1:N:269:ARG:HB3	1:N:269:ARG:NH1	1.88	0.88
1:A:86:LEU:HD22	1:A:185:MET:HE1	1.56	0.88
1:K:295:LEU:HD23	1:K:295:LEU:C	2.00	0.87
1:G:158:LYS:HG3	1:G:180:LEU:HD12	1.57	0.86
1:I:219:VAL:HG12	1:I:291:GLU:HG3	1.55	0.86
1:I:274:THR:CG2	1:I:276:GLY:H	1.89	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:87:ARG:NH2	1:L:150:GLU:OE2	2.10	0.85
1:C:96:ASP:HB2	3:C:549:HOH:O	1.75	0.85
1:D:219:VAL:HG12	1:D:291:GLU:HG3	1.59	0.84
1:L:275:GLU:HB2	2:L:500:HEM:O1A	1.75	0.84
1:I:207:ARG:HH11	1:I:207:ARG:CG	1.88	0.84
1:L:68:PHE:HB2	1:L:133:MET:HE1	1.59	0.84
1:I:274:THR:HB	2:I:500:HEM:O1A	1.77	0.84
1:P:164:ARG:HG3	1:P:164:ARG:HH11	1.43	0.84
1:N:122:LEU:HD21	2:N:500:HEM:HAB	1.60	0.83
1:G:283:MET:HE3	1:G:283:MET:CA	2.08	0.83
2:P:500:HEM:HMB1	2:P:500:HEM:HBB2	1.57	0.83
1:J:163:LEU:HD22	1:J:176:VAL:HG12	1.60	0.83
1:O:254:ARG:O	1:O:258:VAL:HG23	1.79	0.81
1:C:177:GLU:HG2	3:C:520:HOH:O	1.80	0.81
1:O:158:LYS:HG3	1:O:180:LEU:HD12	1.62	0.81
1:C:163:LEU:HD22	1:C:176:VAL:HG12	1.61	0.80
1:G:68:PHE:CB	1:G:133:MET:HE1	2.12	0.80
1:G:134:ARG:HG3	1:G:135:PRO:HD3	1.62	0.80
1:N:299:LEU:HG	1:N:299:LEU:OXT	1.80	0.80
1:L:51:GLN:HG3	3:L:530:HOH:O	1.82	0.79
1:O:89:ALA:HB3	1:O:185:MET:CE	2.12	0.79
1:C:110:ARG:HD3	3:C:582:HOH:O	1.82	0.79
1:F:127:PRO:HG3	1:G:296:ARG:CD	2.13	0.79
1:K:79:MET:HE2	1:K:151:ILE:HD12	1.65	0.78
1:G:50:ASP:HB2	3:G:524:HOH:O	1.83	0.78
1:L:295:LEU:C	1:L:295:LEU:HD23	2.07	0.78
1:K:207:ARG:HG3	1:K:207:ARG:HH11	1.49	0.78
1:F:127:PRO:HG3	1:G:296:ARG:NE	1.99	0.77
1:J:52:ILE:HG22	1:J:53:LEU:HD13	1.67	0.77
1:G:139:ALA:HA	3:G:545:HOH:O	1.85	0.76
1:L:295:LEU:HD23	1:L:296:ARG:N	2.01	0.76
1:J:150:GLU:O	1:J:154:ILE:HG12	1.86	0.76
1:B:171:GLU:HG2	3:B:553:HOH:O	1.85	0.76
1:L:206:GLU:HG2	3:L:544:HOH:O	1.86	0.76
1:B:150:GLU:O	1:B:154:ILE:HG13	1.86	0.76
2:E:500:HEM:HMB2	2:E:500:HEM:HBB2	1.67	0.76
1:L:82:MET:HE1	1:L:115:LEU:CD1	2.16	0.75
2:I:500:HEM:HBB2	2:I:500:HEM:HMB2	1.69	0.75
1:I:82:MET:HG3	1:I:108:VAL:HG13	1.67	0.75
1:E:79:MET:CE	1:E:151:ILE:HD12	2.16	0.75
1:D:146:TYR:O	1:D:150:GLU:HG3	1.85	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:219:VAL:HG12	1:M:291:GLU:HG3	1.68	0.74
1:P:166:HIS:HD2	3:P:579:HOH:O	1.71	0.74
1:I:122:LEU:HD21	2:I:500:HEM:HAB	1.70	0.74
1:H:150:GLU:O	1:H:154:ILE:HG13	1.87	0.73
1:M:53:LEU:HD21	1:N:147:GLN:NE2	2.03	0.73
1:N:295:LEU:C	1:N:295:LEU:HD23	2.13	0.73
1:G:82:MET:HE1	1:G:112:MET:CG	2.17	0.73
1:I:219:VAL:CG1	1:I:291:GLU:HG3	2.17	0.73
1:L:149:ARG:NH2	1:L:162:MET:HE2	2.04	0.73
1:N:138:GLY:C	1:N:140:SER:N	2.43	0.73
1:I:274:THR:HG22	1:I:276:GLY:N	2.04	0.73
1:O:149:ARG:NH1	3:O:529:HOH:O	2.21	0.72
1:L:68:PHE:CB	1:L:133:MET:HE1	2.18	0.72
1:A:96:ASP:OD1	1:A:196:ARG:NH2	2.17	0.72
1:A:274:THR:HG21	1:A:279:TYR:CG	2.24	0.72
1:H:65:GLU:HG3	1:H:133:MET:HE3	1.72	0.72
1:J:158:LYS:HG3	1:J:180:LEU:HD12	1.69	0.72
1:K:96:ASP:OD2	1:K:195:ARG:NH2	2.22	0.72
1:E:79:MET:HE2	1:E:151:ILE:CD1	2.18	0.72
1:L:257:HIS:O	1:L:261:VAL:HG23	1.89	0.72
1:K:295:LEU:HD23	1:K:295:LEU:O	1.89	0.71
3:A:507:HOH:O	1:D:256:ARG:HD2	1.90	0.71
1:A:274:THR:HB	2:A:500:HEM:O1A	1.91	0.71
1:E:267:PHE:HE2	1:E:281:ARG:HE	1.36	0.71
1:I:211:GLN:O	1:I:212:PRO:O	2.08	0.71
1:J:277:VAL:O	1:J:281:ARG:HG3	1.91	0.71
1:L:82:MET:HE1	1:L:115:LEU:HD12	1.73	0.71
1:N:295:LEU:C	1:N:295:LEU:CD2	2.64	0.71
2:I:500:HEM:HBB2	2:I:500:HEM:CMB	2.21	0.71
1:K:79:MET:HE1	1:K:148:TYR:HA	1.73	0.71
1:D:192:LEU:HD12	1:D:192:LEU:O	1.92	0.70
1:L:273:GLY:HA3	1:N:41:MET:HE2	1.73	0.70
1:F:267:PHE:HD2	1:F:268:LYS:H	1.37	0.70
1:G:134:ARG:HG3	1:G:135:PRO:CD	2.20	0.70
1:J:258:VAL:HG13	1:J:280:LEU:HB3	1.74	0.70
1:E:150:GLU:O	1:E:154:ILE:HG13	1.91	0.70
1:G:219:VAL:HG12	1:G:291:GLU:HG3	1.74	0.70
3:M:510:HOH:O	1:P:256:ARG:HD2	1.92	0.70
1:P:149:ARG:HD2	1:P:162:MET:HB3	1.73	0.70
1:C:164:ARG:HH11	1:C:164:ARG:HG3	1.56	0.69
1:P:52:ILE:HG22	1:P:53:LEU:HD13	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:192:LEU:HD12	1:J:195:ARG:NH2	2.06	0.69
1:K:295:LEU:C	1:K:295:LEU:CD2	2.65	0.69
1:B:95:SER:OG	1:B:97:GLN:HG3	1.92	0.69
1:G:117:GLN:HG2	1:H:114:GLN:OE1	1.92	0.69
2:E:500:HEM:HBB2	2:E:500:HEM:CMB	2.22	0.69
1:J:250:PHE:O	1:J:254:ARG:HG3	1.92	0.69
1:M:42:SER:HB2	1:N:144:GLN:OE1	1.91	0.69
1:G:169:ARG:HH21	1:G:171:GLU:HG3	1.57	0.69
1:C:290:PRO:HG3	3:C:580:HOH:O	1.91	0.69
1:N:269:ARG:HB3	1:N:269:ARG:HH11	1.56	0.69
1:E:295:LEU:C	1:E:295:LEU:HD12	2.17	0.69
1:G:219:VAL:CG1	1:G:291:GLU:HG3	2.23	0.69
2:H:500:HEM:HMB2	2:H:500:HEM:HBB2	1.75	0.69
1:A:274:THR:CG2	1:A:279:TYR:CB	2.71	0.68
1:D:89:ALA:HB3	1:D:185:MET:HE1	1.75	0.68
1:D:89:ALA:HB3	1:D:185:MET:CE	2.22	0.68
1:L:224:LEU:O	1:L:228:ARG:HG3	1.93	0.68
1:A:68:PHE:CD2	1:A:133[A]:MET:HE1	2.27	0.68
1:J:295:LEU:C	1:J:295:LEU:HD23	2.18	0.68
1:D:275:GLU:HB2	2:D:500:HEM:O1A	1.94	0.68
1:G:82:MET:CE	1:G:112:MET:CG	2.69	0.68
1:K:219:VAL:HG12	1:K:291:GLU:HG3	1.76	0.68
1:J:146:TYR:O	1:J:150:GLU:HG3	1.94	0.67
1:C:181:HIS:CE1	3:C:584:HOH:O	2.33	0.67
1:L:275:GLU:HB2	2:L:500:HEM:CGA	2.24	0.67
1:I:120:ASN:OD1	1:I:256:ARG:NH2	2.20	0.67
1:B:275:GLU:HG3	3:B:615:HOH:O	1.93	0.67
1:A:274:THR:HG21	1:A:279:TYR:CD2	2.30	0.67
1:J:163:LEU:CD2	1:J:176:VAL:HG12	2.25	0.67
1:A:274:THR:HG21	1:A:279:TYR:CB	2.25	0.67
1:L:86:LEU:HD22	1:L:185:MET:HE1	1.77	0.67
1:P:65:GLU:CG	1:P:133:MET:CE	2.65	0.67
1:B:219:VAL:CG1	1:B:291:GLU:HG3	2.23	0.67
1:F:82:MET:HG3	1:F:108:VAL:HG13	1.77	0.67
1:B:134:ARG:N	1:B:135:PRO:HD2	2.11	0.66
1:G:68:PHE:HB2	1:G:133:MET:HE1	1.77	0.66
1:L:58:PRO:HD2	3:L:581:HOH:O	1.94	0.66
1:M:267:PHE:CE1	1:M:281:ARG:NH1	2.64	0.66
1:E:75:THR:O	1:E:79:MET:HG3	1.94	0.66
1:F:168:HIS:CD2	1:F:169:ARG:HG2	2.31	0.66
1:A:52:ILE:HG22	1:A:53:LEU:HD13	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:ARG:HH21	1:B:31:HIS:CD2	2.14	0.66
1:I:199:GLN:HG3	3:I:552:HOH:O	1.96	0.66
1:A:274:THR:CG2	1:A:275:GLU:N	2.58	0.66
1:P:82:MET:HE1	1:P:115:LEU:HD12	1.77	0.65
1:C:295:LEU:C	1:C:295:LEU:HD23	2.21	0.65
1:I:163:LEU:HD22	1:I:176:VAL:HG12	1.78	0.65
1:P:52:ILE:HG22	1:P:53:LEU:CD1	2.26	0.65
1:C:162:MET:HA	1:C:162:MET:HE2	1.79	0.65
1:K:79:MET:CE	1:K:151:ILE:HD12	2.25	0.65
1:P:250:PHE:CE1	1:P:254:ARG:NH2	2.64	0.65
1:F:49:LEU:O	1:F:53:LEU:HB2	1.96	0.65
1:M:219:VAL:HG12	1:M:291:GLU:CG	2.27	0.65
1:A:274:THR:HG22	1:A:275:GLU:N	2.10	0.65
1:P:199:GLN:HG3	3:P:571:HOH:O	1.97	0.65
1:B:220:GLU:HG2	1:B:224:LEU:HD12	1.78	0.64
1:G:90:ARG:O	1:G:94:LYS:HG2	1.95	0.64
1:I:149:ARG:NH2	1:I:162:MET:HE2	2.11	0.64
1:F:257:HIS:HE1	2:F:500:HEM:C4D	2.15	0.64
1:H:250:PHE:O	1:H:254:ARG:HG3	1.97	0.64
1:K:87:ARG:HD2	3:K:569:HOH:O	1.96	0.64
1:L:247:GLU:O	1:L:251:ARG:HG3	1.97	0.64
1:A:149:ARG:NE	1:A:162:MET:HE2	2.12	0.64
1:E:134:ARG:HA	1:E:137:LEU:HD22	1.77	0.64
1:M:267:PHE:HE1	1:M:281:ARG:NH1	1.96	0.64
1:O:82:MET:HG3	1:O:108:VAL:HG13	1.79	0.64
1:N:109:SER:CB	1:N:110:ARG:HH11	2.09	0.64
1:B:164:ARG:HB3	1:B:165:PRO:HD3	1.80	0.64
1:I:186:TYR:OH	1:I:291:GLU:HG2	1.97	0.64
1:A:68:PHE:HE1	2:A:500:HEM:HAB	1.63	0.64
1:O:89:ALA:HB3	1:O:185:MET:HE1	1.79	0.64
1:D:126:THR:OG1	1:D:129:GLU:HG3	1.98	0.63
1:K:52:ILE:HD11	1:L:55:ALA:HB3	1.80	0.63
1:P:65:GLU:CG	1:P:133:MET:HE3	2.05	0.63
1:J:231:SER:HB2	3:J:540:HOH:O	1.97	0.63
1:M:166:HIS:HD2	3:M:582:HOH:O	1.81	0.63
1:N:138:GLY:HA3	1:N:140:SER:OG	1.97	0.63
1:H:272:GLY:HA3	1:I:57:HIS:CD2	2.33	0.63
2:L:500:HEM:HBC2	2:L:500:HEM:HHD	1.79	0.63
1:A:146:TYR:HE2	3:A:597:HOH:O	1.80	0.63
1:K:207:ARG:HH11	1:K:207:ARG:CG	2.11	0.63
1:P:166:HIS:HE1	3:P:558:HOH:O	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:178:THR:O	1:O:182:THR:OG1	2.17	0.62
1:O:219:VAL:HG12	1:O:291:GLU:HG3	1.81	0.62
1:O:295:LEU:C	1:O:295:LEU:HD23	2.24	0.62
1:G:100:PRO:O	1:G:104:MET:HG3	1.98	0.62
1:A:68:PHE:CE1	2:A:500:HEM:HAB	2.33	0.62
1:G:281:ARG:NH2	3:G:520:HOH:O	2.33	0.62
1:L:200:ILE:HA	1:L:218:SER:OG	1.98	0.62
1:L:207:ARG:HG2	1:L:209:TRP:CZ3	2.35	0.62
1:B:248:ASP:O	1:B:252:GLN:HG3	1.99	0.62
1:E:168:HIS:HA	1:F:35:MET:HA	1.82	0.62
1:F:87:ARG:HD2	3:F:562:HOH:O	1.99	0.62
1:O:257:HIS:O	1:O:261:VAL:HG23	2.00	0.62
1:C:295:LEU:HD23	1:C:295:LEU:O	2.00	0.62
1:B:49:LEU:O	1:B:53:LEU:HB2	2.00	0.62
1:E:99:GLN:HB2	1:E:100:PRO:HD3	1.82	0.61
1:D:192:LEU:HD12	1:D:192:LEU:C	2.26	0.61
1:M:141:SER:OG	1:M:143:PHE:HB2	2.00	0.61
1:M:149:ARG:CZ	1:M:162:MET:CE	2.78	0.61
1:P:292:LEU:O	1:P:296:ARG:NH1	2.32	0.61
1:P:88:ALA:HB3	1:P:104:MET:HE2	1.79	0.61
1:C:164:ARG:HH11	1:C:164:ARG:CG	2.14	0.61
1:M:219:VAL:CG1	1:M:291:GLU:HG3	2.29	0.61
1:A:149:ARG:CZ	1:A:162:MET:HE2	2.31	0.61
1:L:219:VAL:HG12	1:L:291:GLU:HG3	1.81	0.61
1:F:164:ARG:N	1:F:165:PRO:HD2	2.16	0.61
1:L:220:GLU:OE2	1:L:298:ASP:OD2	2.18	0.61
1:N:109:SER:CB	1:N:110:ARG:HH12	1.95	0.61
1:A:163:LEU:HD22	1:A:176:VAL:HG12	1.81	0.61
1:H:158:LYS:HG3	1:H:180:LEU:HD12	1.83	0.60
1:J:75:THR:O	1:J:79:MET:HG3	2.01	0.60
1:J:39:ARG:HA	3:J:541:HOH:O	2.01	0.60
1:P:49:LEU:O	1:P:53:LEU:HB2	2.01	0.60
1:F:150:GLU:O	1:F:154:ILE:HG13	2.01	0.60
1:J:186:TYR:OH	1:J:291:GLU:HG2	2.01	0.60
1:H:134:ARG:HG2	1:H:135:PRO:HD3	1.83	0.60
2:K:500:HEM:HBC2	2:K:500:HEM:HHD	1.83	0.60
1:C:146:TYR:O	1:C:150:GLU:HG3	2.01	0.60
1:C:275:GLU:OE2	1:C:275:GLU:N	2.35	0.60
1:O:119:TRP:CH2	1:O:257:HIS:HD2	2.20	0.60
1:E:219:VAL:CG1	1:E:291:GLU:HG3	2.32	0.60
1:F:83:LEU:O	1:F:87:ARG:HG3	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:163:LEU:HD22	1:K:176:VAL:HG12	1.84	0.60
1:L:90:ARG:HB3	3:L:534:HOH:O	2.01	0.60
1:N:269:ARG:HH11	1:N:269:ARG:CB	2.15	0.60
1:J:222:ALA:O	1:J:226:VAL:HG23	2.02	0.60
1:K:258:VAL:HG13	1:K:280:LEU:CB	2.32	0.60
1:B:146:TYR:O	1:B:150:GLU:HG3	2.01	0.60
1:C:150:GLU:O	1:C:154:ILE:HG13	2.02	0.60
1:D:274:THR:HG21	3:E:550:HOH:O	2.01	0.60
1:O:114:GLN:OE1	1:P:117:GLN:HG2	2.02	0.60
1:C:77:LEU:HD12	1:D:77:LEU:HD12	1.84	0.59
1:L:270:GLY:HA3	1:N:50:ASP:HB2	1.84	0.59
1:P:122:LEU:HD21	2:P:500:HEM:HAB	1.84	0.59
1:P:126:THR:OG1	1:P:129:GLU:HG3	2.01	0.59
1:F:127:PRO:HG3	1:G:296:ARG:HD2	1.84	0.59
1:F:279:TYR:CE1	1:F:283:MET:HE3	2.37	0.59
1:P:89:ALA:O	1:P:93:VAL:HG23	2.03	0.59
2:P:500:HEM:HBB2	2:P:500:HEM:CMB	2.31	0.59
1:N:109:SER:HB2	1:N:110:ARG:HH11	1.67	0.59
1:A:261:VAL:HG22	2:A:500:HEM:C1B	2.37	0.59
1:L:86:LEU:CD2	1:L:185:MET:HE1	2.33	0.59
1:G:120:ASN:OD1	1:G:256:ARG:NH2	2.26	0.59
1:G:151:ILE:O	1:G:154:ILE:HG22	2.02	0.59
1:I:89:ALA:O	1:I:93:VAL:HG23	2.03	0.59
1:L:186:TYR:O	1:L:190:ILE:HG13	2.02	0.59
1:M:149:ARG:CZ	1:M:162:MET:HE2	2.33	0.59
1:C:141:SER:OG	1:C:143:PHE:HB2	2.02	0.59
1:D:219:VAL:CG1	1:D:291:GLU:HG3	2.29	0.59
1:K:75:THR:O	1:K:79:MET:HG3	2.03	0.58
1:I:211:GLN:C	1:I:212:PRO:O	2.44	0.58
1:J:295:LEU:HD23	1:J:295:LEU:O	2.03	0.58
1:P:162:MET:HE3	1:P:162:MET:HA	1.85	0.58
1:O:49:LEU:O	1:O:53:LEU:HB2	2.01	0.58
1:E:183:PRO:HG2	3:E:502:HOH:O	2.03	0.58
1:B:99:GLN:HB2	1:B:100:PRO:HD3	1.84	0.58
2:O:500:HEM:HBB2	2:O:500:HEM:CMB	2.34	0.58
1:E:100:PRO:O	1:E:104:MET:HG3	2.04	0.58
1:K:214:GLN:HG2	3:K:553:HOH:O	2.04	0.58
1:K:119:TRP:CD1	1:K:256:ARG:HG2	2.39	0.58
1:C:49:LEU:O	1:C:53:LEU:HB2	2.03	0.58
1:C:295:LEU:C	1:C:295:LEU:CD2	2.77	0.58
1:J:190:ILE:HG21	1:J:204:VAL:CG1	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:163:LEU:HD23	1:L:176:VAL:HG12	1.85	0.58
1:A:282:ARG:HH21	1:B:31:HIS:HD2	1.52	0.58
1:D:141:SER:OG	1:D:143:PHE:HB2	2.04	0.58
1:I:52:ILE:HG22	1:I:53:LEU:HD13	1.85	0.58
1:P:166:HIS:CE1	3:P:558:HOH:O	2.55	0.58
1:A:212:PRO:HB2	3:A:586:HOH:O	2.04	0.57
1:L:274:THR:HG22	1:L:275:GLU:OE2	2.04	0.57
1:L:295:LEU:C	1:L:295:LEU:CD2	2.77	0.57
1:N:163:LEU:HD22	1:N:176:VAL:HG12	1.85	0.57
1:D:103:LYS:HG2	3:D:520:HOH:O	2.04	0.57
1:G:99:GLN:HB2	1:G:100:PRO:HD3	1.86	0.57
1:I:43:TYR:HB3	1:J:144:GLN:HB2	1.86	0.57
1:I:109:SER:HB3	1:I:110:ARG:HH21	1.68	0.57
1:K:222:ALA:O	1:K:226:VAL:HG23	2.04	0.57
1:N:158[A]:LYS:NZ	1:N:209:TRP:O	2.37	0.57
1:B:296:ARG:HD3	1:C:127:PRO:HG3	1.86	0.57
1:E:79:MET:HE1	1:E:148:TYR:HA	1.85	0.57
1:L:167:ALA:HA	1:L:173:LEU:HD22	1.86	0.57
1:O:224:LEU:O	1:O:228:ARG:HG3	2.05	0.57
1:I:158:LYS:NZ	1:I:182:THR:O	2.29	0.57
1:L:95:SER:HB3	1:L:97:GLN:HG3	1.86	0.57
1:D:86:LEU:O	1:D:185:MET:HE3	2.04	0.57
1:N:292:LEU:HA	1:N:295:LEU:HD13	1.87	0.57
1:E:68:PHE:CB	1:E:133:MET:HE1	2.35	0.57
1:E:219:VAL:HG12	1:E:291:GLU:HG3	1.87	0.57
1:J:258:VAL:HG13	1:J:280:LEU:CB	2.35	0.57
1:P:250:PHE:CD1	1:P:254:ARG:NH2	2.72	0.57
1:K:50:ASP:HB2	3:K:563:HOH:O	2.05	0.57
1:K:258:VAL:HG13	1:K:280:LEU:HB3	1.87	0.57
1:A:216:ASN:OD1	1:A:219:VAL:HG23	2.04	0.57
1:F:146:TYR:O	1:F:150:GLU:HG3	2.05	0.57
1:H:248:ASP:O	1:H:252:GLN:HG3	2.05	0.57
1:O:188:GLU:OE2	3:O:516:HOH:O	2.17	0.56
1:I:82:MET:CG	1:I:108:VAL:HG13	2.35	0.56
1:I:140:SER:O	1:I:271:THR:OG1	2.22	0.56
1:L:268:LYS:HG3	3:L:573:HOH:O	2.05	0.56
1:O:50:ASP:OD1	1:P:169:ARG:NH2	2.38	0.56
1:O:52:ILE:HD11	1:P:55:ALA:HB3	1.87	0.56
1:O:279:TYR:HD2	1:O:280:LEU:HD23	1.70	0.56
1:G:127:PRO:HB2	1:G:128:PRO:HD3	1.87	0.56
1:J:267:PHE:CE1	1:J:281:ARG:HD2	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:90:ARG:HB2	1:D:185:MET:HG3	1.87	0.56
1:P:146:TYR:O	1:P:150:GLU:HG3	2.05	0.56
1:B:163:LEU:HD23	1:B:176:VAL:HG12	1.88	0.56
1:J:207:ARG:HG3	1:J:208:ASP:N	2.21	0.56
1:G:186:TYR:OH	1:G:291:GLU:HG2	2.06	0.55
1:J:201:ASP:HB3	1:J:203:GLU:HG2	1.88	0.55
1:F:216:ASN:OD1	1:F:218:SER:HB3	2.05	0.55
1:I:207:ARG:CG	1:I:207:ARG:NH1	2.57	0.55
2:O:500:HEM:HBB2	2:O:500:HEM:HMB2	1.88	0.55
1:H:191:ARG:HG2	1:H:205:VAL:HG13	1.88	0.55
1:I:207:ARG:HG3	1:I:207:ARG:NH1	2.01	0.55
1:F:267:PHE:HD2	1:F:268:LYS:N	2.04	0.55
1:J:192:LEU:HD12	1:J:195:ARG:HH21	1.71	0.55
2:G:500:HEM:HBC2	2:G:500:HEM:HHD	1.89	0.55
1:I:168:HIS:CE1	1:I:169:ARG:HG2	2.41	0.55
2:L:500:HEM:HHD	2:L:500:HEM:CBC	2.36	0.55
1:H:49:LEU:O	1:H:53:LEU:HB2	2.07	0.55
1:O:167:ALA:HA	1:O:173:LEU:HD22	1.89	0.55
1:N:109:SER:HB2	1:N:110:ARG:NH1	2.17	0.55
1:I:290:PRO:HG3	3:I:577:HOH:O	2.06	0.55
1:D:133:MET:HE2	1:D:137:LEU:HD11	1.88	0.55
1:L:149:ARG:CZ	1:L:162:MET:HE2	2.37	0.55
1:P:65:GLU:HA	1:P:133:MET:HE1	1.89	0.55
1:A:146:TYR:HD2	3:A:595:HOH:O	1.90	0.54
1:C:192:LEU:O	1:C:196:ARG:HG3	2.06	0.54
1:E:256:ARG:HD2	3:H:502:HOH:O	2.06	0.54
1:G:283:MET:CE	1:G:283:MET:CA	2.77	0.54
1:N:247:GLU:CD	1:N:293:TRP:HE1	2.14	0.54
1:N:293:TRP:CZ3	1:O:263:ARG:HB3	2.42	0.54
1:M:282:ARG:NH2	3:M:536:HOH:O	2.40	0.54
1:D:200:ILE:HG22	1:D:205:VAL:HG23	1.88	0.54
1:I:266:GLY:HA3	1:L:297:THR:HG22	1.90	0.54
1:A:274:THR:CG2	1:A:279:TYR:HB2	2.38	0.54
1:L:219:VAL:CG1	1:L:291:GLU:HG3	2.38	0.54
1:G:59:LEU:HD23	1:G:136:TYR:O	2.07	0.54
1:L:295:LEU:CD2	1:L:296:ARG:N	2.70	0.54
1:G:223:TRP:HB3	1:G:295:LEU:HD12	1.90	0.54
1:I:250:PHE:O	1:I:254:ARG:CD	2.56	0.54
1:K:261:VAL:HG22	2:K:500:HEM:C2B	2.43	0.54
1:M:247:GLU:HG3	1:M:288:LEU:HD12	1.90	0.54
1:N:131:SER:HB2	1:O:299:LEU:HD23	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:172:HIS:O	1:F:176:VAL:HG23	2.08	0.53
1:G:254:ARG:NH1	3:G:537:HOH:O	2.41	0.53
1:H:126:THR:OG1	1:H:129:GLU:HG3	2.07	0.53
1:A:275:GLU:HB2	3:A:572:HOH:O	2.06	0.53
1:D:215:TYR:OH	1:D:220:GLU:OE1	2.21	0.53
1:M:279:TYR:CE1	1:M:283:MET:HE3	2.43	0.53
1:I:254:ARG:HB2	3:I:521:HOH:O	2.07	0.53
1:N:192:LEU:HD13	1:N:195:ARG:NH2	2.23	0.53
1:B:262:GLU:OE1	1:B:281:ARG:NH2	2.40	0.53
1:I:122:LEU:HD21	2:I:500:HEM:CAB	2.35	0.53
1:C:275:GLU:OE2	1:C:275:GLU:CA	2.57	0.53
1:K:114:GLN:OE1	1:L:117:GLN:HG2	2.08	0.53
1:M:267:PHE:HE1	1:M:281:ARG:HH11	1.54	0.53
1:A:119:TRP:CH2	1:A:257:HIS:HD2	2.27	0.53
1:G:148:TYR:CE1	1:G:250:PHE:HZ	2.26	0.53
1:L:291:GLU:O	1:L:295:LEU:HB3	2.09	0.53
1:O:159:ASN:OD1	1:O:162:MET:HG2	2.09	0.53
1:O:171:GLU:CD	1:O:171:GLU:H	2.16	0.53
1:M:99:GLN:HB2	1:M:100:PRO:HD3	1.91	0.53
1:G:279:TYR:O	1:G:282:ARG:HB2	2.08	0.53
1:P:65:GLU:HG3	1:P:133:MET:HE1	1.84	0.53
1:E:266:GLY:HA3	1:H:297:THR:HG22	1.90	0.53
1:O:223:TRP:HB3	1:O:295:LEU:HD12	1.91	0.53
1:D:272:GLY:HA3	3:D:589:HOH:O	2.08	0.53
1:F:110:ARG:CD	3:F:534:HOH:O	2.56	0.52
1:P:83:LEU:HD21	1:P:150:GLU:HB2	1.92	0.52
1:D:150:GLU:O	1:D:154:ILE:HG13	2.09	0.52
1:E:79:MET:CE	1:E:151:ILE:CD1	2.82	0.52
1:I:120:ASN:CG	1:I:256:ARG:HH22	2.14	0.52
1:K:127:PRO:N	1:K:128:PRO:HD2	2.24	0.52
1:K:39:ARG:HH11	1:K:39:ARG:HA	1.73	0.52
1:L:195:ARG:NH1	3:L:548:HOH:O	2.42	0.52
1:O:186:TYR:OH	1:O:291:GLU:HG2	2.10	0.52
1:C:75:THR:O	1:C:79:MET:HG3	2.09	0.52
1:E:68:PHE:CG	1:E:133:MET:HE1	2.44	0.52
1:F:158:LYS:HG3	1:F:180:LEU:HD12	1.91	0.52
1:I:267:PHE:H	1:L:297:THR:CG2	2.23	0.52
1:P:164:ARG:HG3	1:P:164:ARG:NH1	2.19	0.52
1:E:163:LEU:HD23	1:E:176:VAL:HG12	1.92	0.52
1:L:75:THR:HG23	1:L:115:LEU:HD22	1.91	0.52
1:L:273:GLY:HA3	1:N:41:MET:CE	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:146:TYR:O	1:N:150:GLU:HG3	2.09	0.52
1:B:296:ARG:HD3	1:C:127:PRO:CG	2.40	0.52
1:F:127:PRO:N	1:F:128:PRO:HD2	2.25	0.52
1:F:215:TYR:CD2	1:F:215:TYR:C	2.87	0.52
1:G:75:THR:HG22	1:G:79:MET:HE2	1.92	0.52
2:H:500:HEM:HBB2	2:H:500:HEM:CMB	2.39	0.52
1:I:114:GLN:OE1	1:J:117:GLN:HG2	2.10	0.52
1:J:163:LEU:HD22	1:J:176:VAL:CG1	2.35	0.52
1:F:254:ARG:HD2	3:F:506:HOH:O	2.10	0.52
1:H:99:GLN:HB2	1:H:100:PRO:HD3	1.91	0.52
1:I:163:LEU:CD2	1:I:176:VAL:HG12	2.40	0.52
1:L:64:ASN:HA	3:L:529:HOH:O	2.09	0.52
1:G:283:MET:HE3	1:G:283:MET:N	2.24	0.52
1:P:215:TYR:OH	1:P:220:GLU:OE1	2.27	0.52
1:O:169:ARG:HH21	1:O:172:HIS:CE1	2.28	0.51
1:D:279:TYR:CE1	1:D:283:MET:HE3	2.44	0.51
1:K:261:VAL:HG22	2:K:500:HEM:C1B	2.44	0.51
1:N:292:LEU:O	1:N:296:ARG:NH1	2.41	0.51
1:N:269:ARG:HB3	1:N:269:ARG:CZ	2.40	0.51
1:H:275:GLU:HG2	3:H:595:HOH:O	2.10	0.51
1:I:90:ARG:O	1:I:94:LYS:HG3	2.10	0.51
1:J:82:MET:HG3	1:J:111:ILE:HG21	1.92	0.51
1:B:295:LEU:C	1:B:295:LEU:CD2	2.84	0.51
1:E:261:VAL:HG22	2:E:500:HEM:C1B	2.45	0.51
1:E:267:PHE:CE2	1:E:281:ARG:NE	2.77	0.51
1:A:146:TYR:O	1:A:150:GLU:HG3	2.11	0.51
1:C:279:TYR:CE1	1:C:283:MET:HE3	2.46	0.51
1:I:275:GLU:HB3	1:I:278:SER:OG	2.10	0.51
1:C:99:GLN:HB2	1:C:100:PRO:HD3	1.92	0.51
1:H:67:LEU:HD23	1:H:125:MET:HE3	1.93	0.51
1:H:168:HIS:CD2	1:H:168:HIS:H	2.29	0.51
1:I:223:TRP:CD2	1:I:292:LEU:HD21	2.46	0.51
1:M:261:VAL:HG22	2:M:500:HEM:C1B	2.46	0.51
1:M:281:ARG:O	1:M:284:LEU:HB2	2.10	0.51
1:O:40:ASP:CG	1:O:40:ASP:O	2.53	0.51
1:E:215:TYR:CE1	1:E:294:LYS:HD3	2.46	0.51
1:G:226:VAL:HG13	1:G:233:HIS:HB2	1.93	0.51
1:M:168:HIS:CE1	1:M:169:ARG:HG2	2.47	0.51
1:N:99:GLN:HB2	1:N:100:PRO:HD3	1.92	0.51
1:F:152:GLU:OE2	1:F:254:ARG:NH1	2.41	0.50
1:G:158:LYS:CG	1:G:180:LEU:HD12	2.36	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:188:GLU:OE2	1:L:188:GLU:HA	2.12	0.50
1:N:119:TRP:CH2	1:N:257:HIS:HD2	2.29	0.50
1:P:119:TRP:CH2	1:P:257:HIS:CD2	3.00	0.50
1:D:269:ARG:NH1	1:F:45:ASP:OD1	2.45	0.50
1:N:295:LEU:HD23	1:N:295:LEU:O	2.10	0.50
1:O:163:LEU:HD22	1:O:173:LEU:CD1	2.41	0.50
1:C:164:ARG:HB2	1:C:164:ARG:CZ	2.41	0.50
1:F:200:ILE:HG22	1:F:204:VAL:HG23	1.92	0.50
1:F:258:VAL:HG21	1:F:281:ARG:HG2	1.93	0.50
1:J:295:LEU:C	1:J:295:LEU:CD2	2.84	0.50
1:G:257:HIS:HE1	2:G:500:HEM:C4D	2.29	0.50
1:I:49:LEU:HB3	1:I:53:LEU:HD22	1.94	0.50
1:M:261:VAL:HG22	2:M:500:HEM:C2B	2.47	0.50
1:N:125:MET:HE2	1:N:133:MET:HE1	1.94	0.50
1:F:163:LEU:CD2	1:F:176:VAL:HG12	2.41	0.50
1:G:131:SER:HA	1:G:134:ARG:HG2	1.93	0.50
1:I:250:PHE:O	1:I:254:ARG:HD2	2.11	0.50
1:O:247:GLU:OE1	1:O:293:TRP:NE1	2.40	0.50
1:O:89:ALA:CB	1:O:185:MET:HE1	2.41	0.50
1:P:119:TRP:CH2	1:P:257:HIS:HD2	2.30	0.50
1:P:149:ARG:HD2	1:P:162:MET:CB	2.42	0.50
1:F:142:GLY:C	1:F:144:GLN:H	2.20	0.50
1:G:134:ARG:N	1:G:135:PRO:HD2	2.27	0.50
1:N:119:TRP:CH2	1:N:257:HIS:CD2	3.00	0.49
1:E:248:ASP:C	1:E:248:ASP:OD1	2.56	0.49
1:A:86:LEU:CD2	1:A:185:MET:HE1	2.35	0.49
1:B:267:PHE:CE1	1:B:281:ARG:CD	2.95	0.49
1:D:274:THR:HG22	1:D:275:GLU:OE2	2.13	0.49
1:F:174:GLU:HG2	1:F:175:LEU:N	2.27	0.49
1:G:209:TRP:C	1:G:211:GLN:H	2.19	0.49
1:A:165:PRO:HA	1:B:35:MET:O	2.13	0.49
1:F:158:LYS:HG2	1:F:209:TRP:O	2.12	0.49
1:F:161:ALA:O	1:F:164:ARG:HG2	2.12	0.49
1:A:282:ARG:HG2	3:A:623:HOH:O	2.12	0.49
1:D:163:LEU:HD23	1:D:176:VAL:HG12	1.95	0.49
1:G:202:PRO:HD2	3:G:540:HOH:O	2.13	0.49
1:E:143:PHE:HE2	1:E:279:TYR:CZ	2.31	0.49
1:G:247:GLU:OE1	1:G:293:TRP:NE1	2.45	0.49
1:K:120:ASN:OD1	1:K:256:ARG:NH1	2.31	0.49
1:D:133:MET:CE	1:D:137:LEU:HD11	2.42	0.49
1:F:153:PHE:O	1:F:158:LYS:HE3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:134:ARG:HA	1:K:137:LEU:HG	1.95	0.49
1:A:269:ARG:NH1	1:A:275:GLU:OE2	2.46	0.49
1:E:119:TRP:CH2	1:E:257:HIS:CD2	3.01	0.49
1:K:247:GLU:O	1:K:251:ARG:HG3	2.12	0.49
1:O:158:LYS:O	1:O:212:PRO:HG3	2.12	0.49
1:A:284:LEU:HD23	1:A:284:LEU:HA	1.38	0.48
1:C:83:LEU:O	1:C:87:ARG:HG3	2.13	0.48
1:G:68:PHE:HB3	1:G:133:MET:HE1	1.92	0.48
2:I:500:HEM:HBC2	2:I:500:HEM:HHD	1.95	0.48
1:K:49:LEU:O	1:K:53:LEU:HB2	2.13	0.48
1:L:272:GLY:HA3	1:M:57:HIS:CD2	2.48	0.48
1:M:133:MET:HE2	1:M:137:LEU:HD11	1.94	0.48
1:C:223:TRP:HB3	1:C:295:LEU:HD12	1.95	0.48
1:H:65:GLU:HG3	1:H:133:MET:CE	2.41	0.48
1:M:68:PHE:CG	1:M:133:MET:HE1	2.48	0.48
1:N:158[A]:LYS:HD2	1:N:180:LEU:HD12	1.94	0.48
1:B:99:GLN:HB3	1:D:234:TRP:NE1	2.28	0.48
1:B:257:HIS:O	1:B:261:VAL:HG23	2.13	0.48
1:L:202:PRO:HD2	3:L:547:HOH:O	2.13	0.48
1:P:158:LYS:HD2	1:P:180:LEU:HD12	1.94	0.48
1:A:282:ARG:NH2	1:B:31:HIS:HD2	2.11	0.48
1:C:227:TYR:O	1:C:230:PRO:HD3	2.14	0.48
1:E:267:PHE:CZ	1:E:281:ARG:HD2	2.47	0.48
1:H:149:ARG:CZ	1:H:162:MET:HE2	2.43	0.48
1:L:190:ILE:HG21	1:L:204:VAL:HG13	1.95	0.48
1:M:219:VAL:CG1	1:M:291:GLU:CG	2.89	0.48
1:O:39:ARG:O	1:P:138:GLY:HA3	2.13	0.48
2:E:500:HEM:HMB2	2:E:500:HEM:CBB	2.41	0.48
1:J:39:ARG:NH1	3:J:556:HOH:O	2.46	0.48
1:K:57:HIS:CD2	3:K:570:HOH:O	2.41	0.48
1:N:82:MET:HE2	1:N:151:ILE:HD13	1.94	0.48
1:G:54:SER:HA	3:G:551:HOH:O	2.14	0.48
1:M:149:ARG:CZ	1:M:162:MET:HE3	2.43	0.48
1:N:188:GLU:OE2	1:N:188:GLU:HA	2.14	0.48
1:G:223:TRP:HB3	1:G:295:LEU:CD1	2.44	0.48
1:E:69:ILE:O	1:E:73:GLN:HG3	2.14	0.48
1:E:295:LEU:HD12	1:E:295:LEU:O	2.12	0.48
1:I:49:LEU:O	1:I:53:LEU:HB2	2.13	0.48
1:O:117:GLN:HB3	1:P:114:GLN:OE1	2.13	0.48
1:O:195:ARG:NH2	3:O:516:HOH:O	2.47	0.48
1:C:220:GLU:OE2	1:C:298:ASP:OD2	2.32	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:261:VAL:HG22	2:E:500:HEM:C2B	2.49	0.48
1:H:122:LEU:HD23	1:H:260:THR:HG21	1.96	0.48
1:I:211:GLN:O	1:I:212:PRO:C	2.56	0.48
2:I:500:HEM:HMB2	2:I:500:HEM:CBB	2.40	0.47
1:A:164:ARG:C	1:A:166:HIS:H	2.22	0.47
1:C:62:ASP:OD1	1:C:64:ASN:HB2	2.14	0.47
1:D:171:GLU:HG2	3:D:600:HOH:O	2.14	0.47
1:I:117:GLN:HB2	3:I:547:HOH:O	2.13	0.47
1:I:142:GLY:HA3	2:I:500:HEM:C1D	2.48	0.47
1:L:246:LEU:HD13	3:L:579:HOH:O	2.14	0.47
1:O:223:TRP:HB3	1:O:295:LEU:CD1	2.44	0.47
1:P:48:GLY:HA2	3:P:568:HOH:O	2.14	0.47
1:E:281:ARG:NH1	1:E:281:ARG:CG	2.62	0.47
1:G:89:ALA:HB3	1:G:185:MET:HE1	1.95	0.47
1:M:96:ASP:HB3	3:M:594:HOH:O	2.13	0.47
1:O:275:GLU:HA	1:O:279:TYR:HB2	1.96	0.47
1:C:288:LEU:C	1:C:290:PRO:HD3	2.39	0.47
1:L:158:LYS:HG3	1:L:180:LEU:HD12	1.96	0.47
1:L:282:ARG:HD2	1:N:41:MET:HE3	1.96	0.47
1:O:283:MET:N	1:O:283:MET:HE2	2.29	0.47
1:I:267:PHE:H	1:L:297:THR:HG22	1.80	0.47
1:K:39:ARG:O	1:L:139:ALA:HB2	2.14	0.47
1:P:224:LEU:O	1:P:228:ARG:HG3	2.15	0.47
1:A:164:ARG:C	1:A:166:HIS:N	2.72	0.47
1:A:169:ARG:HD3	3:B:580:HOH:O	2.14	0.47
1:B:186:TYR:OH	1:B:291:GLU:HG2	2.15	0.47
1:C:164:ARG:CG	1:C:164:ARG:NH1	2.76	0.47
1:D:78:TRP:HB2	1:D:115:LEU:HD21	1.96	0.47
1:D:134:ARG:HB3	1:D:135:PRO:HD3	1.97	0.47
1:K:258:VAL:HG13	1:K:280:LEU:HB2	1.96	0.47
1:L:127:PRO:HB2	1:L:128:PRO:CD	2.45	0.47
1:N:293:TRP:O	1:N:296:ARG:HB2	2.14	0.47
1:P:70:VAL:O	1:P:74:THR:HG23	2.15	0.47
1:A:274:THR:CG2	1:A:279:TYR:HB3	2.44	0.47
1:G:103:LYS:NZ	3:G:534:HOH:O	2.40	0.47
1:G:170:PRO:O	1:G:174:GLU:HB2	2.15	0.47
1:I:215:TYR:OH	1:I:220:GLU:OE1	2.22	0.47
1:J:203:GLU:HB3	3:J:544:HOH:O	2.15	0.47
1:J:292:LEU:O	1:J:296:ARG:NH1	2.46	0.47
1:O:96:ASP:HB2	3:O:507:HOH:O	2.14	0.47
1:N:52:ILE:HG22	1:N:53:LEU:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:67:LEU:HD12	1:O:67:LEU:O	2.14	0.47
1:M:59:LEU:HD21	1:N:41:MET:HE1	1.96	0.47
1:M:260:THR:O	1:M:263:ARG:HB2	2.15	0.47
1:N:182:THR:HG22	3:N:532:HOH:O	2.15	0.47
1:O:119:TRP:CH2	1:O:257:HIS:CD2	3.01	0.47
1:I:279:TYR:HE1	1:I:283:MET:HE3	1.70	0.46
1:L:274:THR:HB	1:M:57:HIS:HB3	1.97	0.46
1:O:105:LEU:HD21	1:O:185:MET:HE1	1.96	0.46
1:C:164:ARG:HB2	1:C:164:ARG:NH1	2.30	0.46
1:G:220:GLU:OE2	1:G:298:ASP:OD2	2.32	0.46
1:O:134:ARG:N	1:O:135:PRO:HD2	2.30	0.46
1:H:112:MET:O	1:H:116:VAL:HG23	2.16	0.46
2:D:500:HEM:HBC2	2:D:500:HEM:HHD	1.96	0.46
1:F:76:GLU:HA	1:F:79:MET:HE2	1.98	0.46
1:F:267:PHE:CZ	1:F:281:ARG:HD2	2.51	0.46
1:G:49:LEU:O	1:G:53:LEU:HB2	2.15	0.46
1:M:212:PRO:HB3	3:M:588:HOH:O	2.15	0.46
1:O:134:ARG:HB3	1:O:135:PRO:CD	2.45	0.46
1:P:277:VAL:O	1:P:281:ARG:HG3	2.15	0.46
1:B:130:TYR:CE1	1:B:134:ARG:HG3	2.50	0.46
1:E:141:SER:HA	3:E:554:HOH:O	2.15	0.46
1:B:295:LEU:C	1:B:295:LEU:HD22	2.41	0.46
1:D:241:GLU:OE2	1:D:296:ARG:NH2	2.39	0.46
1:E:280:LEU:HD11	2:E:500:HEM:C2A	2.51	0.46
1:F:200:ILE:HA	1:F:218:SER:OG	2.14	0.46
1:F:296:ARG:HD3	1:G:127:PRO:HG3	1.98	0.46
1:I:149:ARG:HA	1:I:149:ARG:HD3	1.72	0.46
1:L:52:ILE:HG22	1:L:53:LEU:HD13	1.98	0.46
1:P:59:LEU:HD12	1:P:59:LEU:HA	1.68	0.46
1:A:68:PHE:CG	1:A:133[A]:MET:HE1	2.51	0.46
1:E:120:ASN:OD1	1:E:256:ARG:NH2	2.35	0.46
1:G:294:LYS:NZ	1:G:294:LYS:HB3	2.29	0.46
1:I:168:HIS:CD2	3:I:551:HOH:O	2.69	0.46
1:M:100:PRO:O	1:M:104:MET:HG3	2.15	0.46
1:A:183:PRO:HG3	1:A:209:TRP:CE2	2.51	0.46
1:J:207:ARG:CG	1:J:208:ASP:N	2.77	0.46
1:A:274:THR:HG21	1:A:279:TYR:HB3	1.96	0.46
1:B:103:LYS:HG2	3:B:533:HOH:O	2.16	0.46
1:F:164:ARG:HB2	1:F:165:PRO:HD3	1.96	0.46
1:I:42:SER:HB2	1:J:144:GLN:OE1	2.16	0.46
1:I:129:GLU:OE2	1:J:103:LYS:NZ	2.37	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:93:VAL:HG13	1:D:192:LEU:HD23	1.97	0.46
1:I:149:ARG:NH2	1:I:162:MET:CE	2.79	0.46
1:J:104:MET:O	1:J:108:VAL:HG23	2.15	0.46
1:J:134:ARG:N	1:J:135:PRO:CD	2.78	0.46
2:K:500:HEM:CMB	2:K:500:HEM:HBB2	2.46	0.46
2:O:500:HEM:HBC2	2:O:500:HEM:HHD	1.97	0.46
1:B:127:PRO:N	1:B:128:PRO:HD2	2.30	0.45
1:G:192:LEU:HD13	1:G:195:ARG:NH2	2.31	0.45
1:L:223:TRP:HB3	1:L:295:LEU:HD12	1.97	0.45
1:N:193:MET:O	1:N:198:PHE:HD1	1.98	0.45
1:A:149:ARG:HA	1:A:149:ARG:HD3	1.59	0.45
1:B:191:ARG:NH2	1:B:206:GLU:OE2	2.49	0.45
1:E:261:VAL:HG12	1:E:277:VAL:CG2	2.46	0.45
1:G:190:ILE:HG21	1:G:204:VAL:HG13	1.98	0.45
1:H:82:MET:HE3	1:H:82:MET:HB2	1.76	0.45
1:J:247:GLU:O	1:J:251:ARG:HG3	2.16	0.45
1:K:41:MET:O	1:L:139:ALA:HB3	2.16	0.45
1:L:186:TYR:OH	1:L:291:GLU:HG2	2.17	0.45
1:A:43:TYR:CE1	1:B:145:SER:HB2	2.51	0.45
1:A:129:GLU:O	1:A:133[B]:MET:HE3	2.16	0.45
1:B:267:PHE:HE1	1:B:281:ARG:CD	2.29	0.45
1:F:127:PRO:CD	1:F:128:PRO:HD2	2.46	0.45
1:F:152:GLU:CD	1:F:254:ARG:HH12	2.24	0.45
1:L:158:LYS:CG	1:L:180:LEU:HD12	2.47	0.45
1:I:161:ALA:O	1:I:164:ARG:HG3	2.16	0.45
1:J:257:HIS:HE1	2:J:500:HEM:C4D	2.34	0.45
1:O:169:ARG:CD	1:O:171:GLU:OE2	2.55	0.45
1:A:236:LEU:HD23	1:A:236:LEU:HA	1.87	0.45
1:F:198:PHE:HA	3:F:552:HOH:O	2.17	0.45
1:F:277:VAL:O	1:F:281:ARG:HG3	2.16	0.45
1:G:148:TYR:CE1	1:G:250:PHE:CZ	3.04	0.45
1:N:192:LEU:HD12	1:N:192:LEU:O	2.16	0.45
1:P:83:LEU:O	1:P:87:ARG:HG3	2.17	0.45
1:A:228:ARG:C	1:A:230:PRO:HD3	2.42	0.45
1:C:261:VAL:HG22	2:C:500:HEM:C1B	2.52	0.45
1:E:119:TRP:CH2	1:E:257:HIS:HD2	2.35	0.45
1:G:149:ARG:HD3	1:G:149:ARG:HA	1.70	0.45
1:H:163:LEU:HD22	1:H:176:VAL:HG12	1.98	0.45
1:L:50:ASP:O	1:L:54:SER:OG	2.32	0.45
1:L:228:ARG:C	1:L:230:PRO:HD3	2.42	0.45
1:L:292:LEU:HD23	1:L:292:LEU:HA	1.68	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:68:PHE:CB	1:M:133:MET:HE1	2.47	0.45
1:A:76:GLU:HA	1:A:79:MET:HE2	1.98	0.45
1:A:274:THR:CG2	1:A:275:GLU:H	2.30	0.45
1:C:133:MET:HB2	1:C:133:MET:HE2	1.72	0.45
1:E:260:THR:HA	1:E:263:ARG:HG2	1.99	0.45
1:G:77:LEU:HD23	1:G:77:LEU:HA	1.58	0.45
1:J:201:ASP:O	1:J:205:VAL:HG23	2.17	0.45
1:J:211:GLN:NE2	1:J:212:PRO:HD2	2.32	0.45
1:D:260:THR:HA	1:D:263:ARG:HG2	1.99	0.45
1:E:159:ASN:OD1	1:E:159:ASN:C	2.60	0.45
1:F:78:TRP:HB2	1:F:115:LEU:HD21	1.99	0.45
1:F:142:GLY:C	1:F:144:GLN:N	2.74	0.45
1:M:234:TRP:O	1:M:237:TYR:HB3	2.17	0.45
1:N:215:TYR:C	1:N:215:TYR:CD2	2.95	0.45
1:P:164:ARG:HH11	1:P:164:ARG:CG	2.20	0.45
1:D:59:LEU:HB3	1:D:136:TYR:HB3	1.98	0.45
1:F:104:MET:O	1:F:108:VAL:HG23	2.17	0.45
1:I:250:PHE:O	1:I:254:ARG:HD3	2.16	0.45
1:M:52:ILE:HG22	1:M:53:LEU:HD13	1.98	0.45
1:P:82:MET:HE1	1:P:115:LEU:CD1	2.44	0.45
1:P:142:GLY:HA3	2:P:500:HEM:C2D	2.52	0.45
1:B:230:PRO:HB3	1:B:237:TYR:CD2	2.53	0.44
1:L:295:LEU:HD22	1:L:296:ARG:HD2	1.99	0.44
1:A:122:LEU:HD21	2:A:500:HEM:CBB	2.48	0.44
1:G:98:LEU:HD12	1:G:235:GLU:OE1	2.18	0.44
1:J:226:VAL:HG13	1:J:233:HIS:HB2	1.98	0.44
1:M:65:GLU:HG3	1:M:133:MET:HE3	1.99	0.44
1:O:60:SER:CB	1:O:61:PRO:CD	2.95	0.44
1:P:261:VAL:HG22	2:P:500:HEM:C1B	2.52	0.44
1:B:296:ARG:H	1:B:296:ARG:HG2	1.68	0.44
1:K:82:MET:HE1	1:K:115:LEU:HD12	1.98	0.44
1:L:110:ARG:HA	1:L:110:ARG:HD3	1.84	0.44
1:M:279:TYR:O	1:M:283:MET:HG2	2.17	0.44
1:N:268:LYS:HE2	1:N:268:LYS:HB3	1.80	0.44
1:O:149:ARG:HD2	1:O:162:MET:HB3	1.99	0.44
1:F:120:ASN:OD1	1:F:256:ARG:NH2	2.40	0.44
1:F:200:ILE:CG2	1:F:204:VAL:HG23	2.47	0.44
1:F:295:LEU:HD23	1:F:295:LEU:C	2.42	0.44
1:N:134:ARG:HB3	1:N:135:PRO:HD3	1.99	0.44
1:A:146:TYR:HB3	1:A:166:HIS:CE1	2.52	0.44
1:A:274:THR:HG23	1:A:279:TYR:HB2	1.97	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:199:GLN:O	1:C:199:GLN:CG	2.42	0.44
1:I:87:ARG:HD2	3:I:584:HOH:O	2.16	0.44
1:M:82:MET:HG3	1:M:111:ILE:HG21	1.99	0.44
1:P:65:GLU:CG	1:P:133:MET:HE1	2.46	0.44
1:E:49:LEU:O	1:E:53:LEU:HB2	2.18	0.44
1:F:85:GLU:OE2	1:F:107:ARG:NH1	2.43	0.44
1:I:76:GLU:HA	1:I:79:MET:HE2	1.99	0.44
1:K:39:ARG:HH11	1:K:39:ARG:CA	2.31	0.44
1:M:223:TRP:HB3	1:M:295:LEU:HD12	1.99	0.44
1:O:280:LEU:HD21	2:O:500:HEM:HAA2	2.00	0.44
1:P:107:ARG:O	1:P:111:ILE:HG13	2.16	0.44
1:B:267:PHE:C	1:B:267:PHE:CD2	2.96	0.44
1:F:82:MET:HE3	1:F:82:MET:HB2	1.81	0.44
1:F:293:TRP:O	1:F:296:ARG:HG2	2.18	0.44
1:H:56:GLN:O	1:H:58:PRO:HD3	2.17	0.44
1:N:220:GLU:OE2	1:N:298:ASP:OD2	2.36	0.44
1:O:223:TRP:CB	1:O:295:LEU:HD12	2.48	0.44
1:D:270:GLY:HA2	1:F:45:ASP:HA	1.99	0.44
1:P:122:LEU:HD21	2:P:500:HEM:CAB	2.48	0.44
1:D:134:ARG:N	1:D:135:PRO:HD2	2.32	0.44
1:F:134:ARG:N	1:F:135:PRO:CD	2.81	0.44
1:M:163:LEU:CD2	1:M:176:VAL:HG12	2.48	0.44
1:N:78:TRP:HB2	1:N:115:LEU:HD21	2.00	0.44
1:O:117:GLN:HB3	1:O:117:GLN:HE21	1.71	0.44
1:C:190:ILE:HG21	1:C:204:VAL:HG13	2.00	0.43
1:I:163:LEU:HD22	1:I:176:VAL:CG1	2.46	0.43
1:I:268:LYS:HD2	1:L:297:THR:HA	1.99	0.43
1:I:274:THR:HG23	1:I:275:GLU:N	2.32	0.43
1:M:168:HIS:ND1	1:M:169:ARG:HG2	2.33	0.43
1:D:186:TYR:OH	1:D:291:GLU:HG2	2.18	0.43
1:I:47:LEU:HD13	1:J:72:HIS:HB3	2.00	0.43
1:I:68:PHE:CG	1:I:133:MET:HE1	2.53	0.43
1:I:131:SER:O	1:I:135:PRO:HD3	2.18	0.43
1:I:149:ARG:CZ	1:I:162:MET:CE	2.85	0.43
1:L:164:ARG:N	1:L:165:PRO:CD	2.81	0.43
1:O:279:TYR:CD2	1:O:280:LEU:HD23	2.53	0.43
1:E:224:LEU:HD22	1:E:228:ARG:CZ	2.48	0.43
2:I:500:HEM:CMB	2:I:500:HEM:CBB	2.95	0.43
1:D:97:GLN:O	1:D:100:PRO:HD2	2.18	0.43
1:E:65:GLU:HG3	1:E:133:MET:HE3	2.01	0.43
1:H:75:THR:HG23	1:H:115:LEU:HD22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:164[B]:ARG:HB3	1:H:165:PRO:HD3	1.99	0.43
1:M:144:GLN:HB2	1:N:43:TYR:HB3	1.99	0.43
1:O:167:ALA:HA	1:O:173:LEU:CD2	2.48	0.43
1:P:71:GLN:HG2	2:P:500:HEM:CMC	2.48	0.43
1:A:142:GLY:HA2	1:B:43:TYR:CE2	2.54	0.43
1:B:44:GLY:O	1:P:270:GLY:HA2	2.18	0.43
1:I:68:PHE:CB	1:I:133:MET:HE1	2.48	0.43
1:I:281:ARG:O	1:I:284:LEU:HB2	2.19	0.43
1:L:127:PRO:HB2	1:L:128:PRO:HD3	2.01	0.43
1:L:216:ASN:OD1	1:L:218:SER:HB3	2.18	0.43
1:D:224:LEU:O	1:D:228:ARG:HG3	2.19	0.43
1:G:41:MET:HE1	1:H:59:LEU:CD2	2.49	0.43
1:G:205:VAL:O	1:G:205:VAL:HG12	2.18	0.43
1:I:292:LEU:O	1:I:295:LEU:HD13	2.19	0.43
1:A:76:GLU:CD	1:A:79:MET:CE	2.91	0.43
1:A:203:GLU:HG2	3:A:573:HOH:O	2.18	0.43
1:D:143:PHE:HE2	1:D:279:TYR:CZ	2.37	0.43
1:F:269:ARG:HE	1:F:269:ARG:HB2	1.61	0.43
2:G:500:HEM:HHD	2:G:500:HEM:CBC	2.49	0.43
1:H:219:VAL:HB	1:H:291:GLU:HG3	1.99	0.43
1:I:266:GLY:O	1:I:277:VAL:HG21	2.19	0.43
1:M:163:LEU:HD22	1:M:176:VAL:HG12	2.01	0.43
1:N:258:VAL:HG21	1:N:281:ARG:HG3	2.01	0.43
1:O:169:ARG:HH21	1:O:172:HIS:HE1	1.65	0.43
1:A:77:LEU:HD23	1:A:77:LEU:HA	1.88	0.43
1:A:119:TRP:CH2	1:A:257:HIS:CD2	3.05	0.43
1:C:280:LEU:HD23	1:C:280:LEU:HA	1.69	0.43
1:E:141:SER:OG	1:E:143:PHE:HB2	2.18	0.43
1:I:151:ILE:O	1:I:154:ILE:HG22	2.18	0.43
1:I:168:HIS:HD2	3:I:551:HOH:O	2.01	0.43
1:K:105:LEU:HD23	1:K:105:LEU:HA	1.90	0.43
1:A:122:LEU:HD23	1:A:260:THR:HG21	2.00	0.43
1:A:282:ARG:O	1:A:285:ASP:HB2	2.19	0.43
1:A:134:ARG:NH2	1:A:269:ARG:O	2.51	0.43
1:D:134:ARG:HB3	1:D:135:PRO:CD	2.49	0.43
1:D:272:GLY:HA3	1:E:57:HIS:CD2	2.54	0.43
1:I:257:HIS:O	1:I:261:VAL:HG23	2.18	0.43
1:K:215:TYR:CD2	1:K:215:TYR:C	2.97	0.43
1:P:41:MET:HB2	1:P:41:MET:HE3	1.73	0.43
1:P:130:TYR:O	1:P:133:MET:HG2	2.18	0.43
1:A:49:LEU:O	1:A:53:LEU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:TYR:OH	1:A:220:GLU:OE1	2.28	0.42
1:E:280:LEU:HD11	2:E:500:HEM:C3A	2.54	0.42
1:F:141:SER:O	1:F:144:GLN:HB2	2.18	0.42
1:G:192:LEU:HD13	1:G:195:ARG:HH21	1.84	0.42
1:J:41:MET:HA	3:J:538:HOH:O	2.18	0.42
2:L:500:HEM:HBC2	2:L:500:HEM:CHD	2.47	0.42
1:O:295:LEU:C	1:O:295:LEU:CD2	2.91	0.42
1:A:50:ASP:OD1	1:B:169:ARG:NH2	2.52	0.42
1:A:83:LEU:O	1:A:87:ARG:HG3	2.19	0.42
1:B:267:PHE:C	1:B:267:PHE:HD2	2.26	0.42
1:E:43:TYR:HA	1:F:140:SER:HB2	2.00	0.42
1:G:280:LEU:HD23	1:G:280:LEU:HA	1.85	0.42
1:M:95:SER:O	1:M:97:GLN:HG3	2.19	0.42
1:P:109:SER:HB3	1:P:110:ARG:NH2	2.34	0.42
1:B:94:LYS:NZ	3:B:526:HOH:O	2.46	0.42
1:G:164:ARG:N	1:G:165:PRO:HD2	2.34	0.42
1:I:146:TYR:O	1:I:150:GLU:HG3	2.18	0.42
1:K:227:TYR:CD2	1:K:295:LEU:HD11	2.54	0.42
1:E:215:TYR:OH	1:E:220:GLU:OE1	2.28	0.42
1:F:83:LEU:HD23	1:F:83:LEU:HA	1.72	0.42
1:G:110:ARG:HG2	1:G:110:ARG:HH11	1.84	0.42
1:H:85:GLU:CD	1:H:107:ARG:HD2	2.45	0.42
1:F:68:PHE:CB	1:F:133:MET:HE1	2.49	0.42
1:H:292:LEU:O	1:H:296:ARG:NH1	2.51	0.42
1:O:89:ALA:CB	1:O:185:MET:CE	2.89	0.42
1:P:127:PRO:HB2	1:P:128:PRO:HD3	2.01	0.42
3:A:588:HOH:O	1:M:294:LYS:HE2	2.20	0.42
1:C:162:MET:O	1:C:165:PRO:HD2	2.20	0.42
1:F:164:ARG:N	1:F:165:PRO:CD	2.83	0.42
1:G:224:LEU:HD21	1:G:299:LEU:HA	2.01	0.42
1:P:141:SER:C	1:P:143:PHE:N	2.75	0.42
1:A:115:LEU:HD23	1:A:115:LEU:HA	1.63	0.42
1:C:132:ALA:HB1	3:C:587:HOH:O	2.18	0.42
1:D:59:LEU:HD23	1:D:136:TYR:O	2.18	0.42
1:F:297:THR:HG23	1:G:266:GLY:HA3	2.00	0.42
1:G:103:LYS:NZ	1:H:124:THR:O	2.43	0.42
1:G:168:HIS:CD2	1:G:168:HIS:H	2.38	0.42
1:H:275:GLU:N	1:H:279:TYR:HB2	2.34	0.42
1:I:144:GLN:HB2	1:J:43:TYR:HB3	2.02	0.42
1:K:78:TRP:HB2	1:K:115:LEU:HD21	2.00	0.42
1:K:252:GLN:O	1:K:256:ARG:HB2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:278:SER:CB	3:K:513:HOH:O	2.48	0.42
1:A:251:ARG:HG2	3:A:525:HOH:O	2.19	0.42
1:G:200:ILE:HG22	1:G:204:VAL:HG12	2.01	0.42
1:G:290:PRO:HD2	1:G:291:GLU:OE1	2.20	0.42
1:I:98:LEU:HD12	1:I:235:GLU:HB3	2.02	0.42
1:K:59:LEU:HD23	1:K:136:TYR:O	2.20	0.42
1:L:158:LYS:NZ	1:L:182:THR:O	2.33	0.42
1:N:163:LEU:HD22	1:N:176:VAL:CG1	2.48	0.42
1:N:269:ARG:NH1	1:N:269:ARG:CB	2.69	0.42
1:A:68:PHE:HE1	2:A:500:HEM:CAB	2.31	0.42
1:E:139:ALA:C	1:E:140:SER:O	2.60	0.42
1:J:164:ARG:HG2	1:J:165:PRO:HD3	2.02	0.42
1:N:111:ILE:O	1:N:114:GLN:HB2	2.20	0.42
1:B:220:GLU:OE2	1:B:298:ASP:OD2	2.38	0.42
1:E:141:SER:C	1:E:143:PHE:N	2.75	0.42
1:F:69:ILE:O	1:F:73:GLN:HG3	2.20	0.42
1:H:86:LEU:HD23	1:H:185:MET:HE1	2.02	0.42
1:I:110:ARG:HH12	1:K:110:ARG:CZ	2.33	0.42
1:I:149:ARG:NH1	1:I:152:GLU:OE2	2.52	0.42
1:I:149:ARG:NH1	1:I:162:MET:HE2	2.34	0.42
1:A:75:THR:O	1:A:79:MET:HG3	2.20	0.41
3:A:507:HOH:O	1:D:256:ARG:CD	2.60	0.41
1:B:90:ARG:HD2	3:B:556:HOH:O	2.19	0.41
1:D:170:PRO:HB2	3:D:600:HOH:O	2.20	0.41
1:F:56:GLN:CD	1:F:56:GLN:N	2.78	0.41
1:G:215:TYR:OH	1:G:220:GLU:OE1	2.23	0.41
1:G:295:LEU:C	1:G:295:LEU:HD23	2.45	0.41
1:I:282:ARG:O	1:I:285:ASP:HB2	2.20	0.41
1:J:99:GLN:HB2	1:J:100:PRO:HD3	2.02	0.41
1:J:99:GLN:HB3	1:L:234:TRP:NE1	2.35	0.41
1:K:267:PHE:HE1	1:K:281:ARG:HE	1.66	0.41
1:C:155:LEU:HD23	1:C:155:LEU:HA	1.90	0.41
1:E:200:ILE:O	1:E:201:ASP:C	2.62	0.41
1:G:192:LEU:O	1:G:196:ARG:HG3	2.20	0.41
1:I:292:LEU:HA	1:I:295:LEU:CD1	2.50	0.41
1:I:292:LEU:HA	1:I:295:LEU:HD12	2.02	0.41
1:M:146:TYR:HB3	1:M:166:HIS:CD2	2.54	0.41
1:D:274:THR:HB	1:E:57:HIS:HB3	2.01	0.41
1:F:223:TRP:HB3	1:F:295:LEU:HD12	2.02	0.41
1:H:220:GLU:HB2	1:H:291:GLU:HB2	2.03	0.41
1:H:269:ARG:HH22	1:J:39:ARG:HH21	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:219:VAL:CG1	1:K:291:GLU:HG3	2.49	0.41
1:M:215:TYR:CD2	1:M:215:TYR:C	2.97	0.41
1:N:267:PHE:C	1:N:267:PHE:CD2	2.99	0.41
1:O:248:ASP:C	1:O:248:ASP:OD1	2.62	0.41
1:B:133:MET:HE2	1:B:133:MET:HB3	1.82	0.41
1:M:149:ARG:NH1	1:M:162:MET:HE2	2.35	0.41
1:O:60:SER:HB2	1:O:61:PRO:HD2	2.01	0.41
1:A:44:GLY:HA2	1:A:49:LEU:HD12	2.02	0.41
1:C:163:LEU:CD2	1:C:176:VAL:HG12	2.42	0.41
1:H:69:ILE:O	1:H:73:GLN:HG3	2.21	0.41
1:K:46:TYR:CE1	1:L:59:LEU:HD22	2.55	0.41
1:L:295:LEU:CD2	1:L:296:ARG:HD2	2.50	0.41
1:N:133:MET:HE3	1:N:133:MET:HB2	1.99	0.41
1:N:158[B]:LYS:HE3	1:N:184:SER:HB3	2.02	0.41
1:J:192:LEU:O	1:J:192:LEU:HG	2.20	0.41
1:N:127:PRO:N	1:N:128:PRO:HD2	2.35	0.41
1:C:105:LEU:HD23	1:C:105:LEU:HA	1.76	0.41
1:F:164:ARG:HB2	1:F:165:PRO:CD	2.51	0.41
1:G:219:VAL:HG11	1:G:291:GLU:HG3	2.00	0.41
1:J:154:ILE:HG12	1:J:154:ILE:H	1.77	0.41
1:L:158:LYS:HD3	3:L:516:HOH:O	2.20	0.41
1:L:215:TYR:HE1	1:L:220:GLU:OE1	2.04	0.41
1:M:112:MET:O	1:M:116:VAL:HG23	2.21	0.41
1:P:104:MET:O	1:P:108:VAL:HG23	2.21	0.41
1:A:73:GLN:NE2	1:B:47:LEU:O	2.43	0.41
1:F:257:HIS:CE1	2:F:500:HEM:C4D	3.01	0.41
1:G:209:TRP:C	1:G:211:GLN:N	2.79	0.41
1:H:294:LYS:HE2	3:H:604:HOH:O	2.21	0.41
1:K:79:MET:HE1	1:K:148:TYR:CA	2.46	0.41
1:K:260:THR:HA	1:K:263:ARG:HG2	2.03	0.41
1:L:149:ARG:HD3	1:L:149:ARG:HA	1.69	0.41
1:M:103:LYS:NZ	1:N:124:THR:O	2.54	0.41
1:N:98:LEU:HD12	1:N:235:GLU:OE1	2.20	0.41
1:P:60:SER:HB2	1:P:61:PRO:HD2	2.03	0.41
1:C:261:VAL:HG22	2:C:500:HEM:C2B	2.55	0.41
1:D:268:LYS:HG3	1:D:271:THR:HG21	2.02	0.41
1:E:168:HIS:H	1:E:168:HIS:CD2	2.39	0.41
1:E:188:GLU:HA	1:E:188:GLU:OE2	2.21	0.41
1:E:292:LEU:HA	1:E:295:LEU:HD23	2.03	0.41
1:F:280:LEU:HD21	2:F:500:HEM:CHA	2.51	0.41
1:H:119:TRP:CD1	1:H:256:ARG:HB3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:134:ARG:N	1:H:135:PRO:HD2	2.36	0.41
1:I:83:LEU:HD23	1:I:83:LEU:HA	1.77	0.41
1:I:119:TRP:CH2	1:I:257:HIS:CD2	3.09	0.41
1:I:228:ARG:C	1:I:229:ASN:OD1	2.64	0.41
1:L:53:LEU:HD12	1:L:53:LEU:HA	1.90	0.41
1:M:268:LYS:H	1:M:268:LYS:HG2	1.55	0.41
1:N:159:ASN:C	1:N:159:ASN:OD1	2.63	0.41
1:B:200:ILE:HG22	1:B:204:VAL:HG12	2.03	0.41
1:G:295:LEU:HD22	1:G:296:ARG:HH11	1.84	0.41
1:H:86:LEU:O	1:H:185:MET:CE	2.69	0.41
1:H:194:ALA:C	1:H:196:ARG:H	2.29	0.41
1:L:82:MET:HE1	1:L:115:LEU:HD11	2.00	0.41
1:P:208:ASP:OD1	1:P:210:THR:HB	2.21	0.41
1:B:108:VAL:HA	1:B:111:ILE:HD12	2.03	0.40
1:B:134:ARG:N	1:B:135:PRO:CD	2.83	0.40
1:C:187:ASP:O	1:C:191:ARG:HG3	2.21	0.40
1:C:248:ASP:OD1	1:C:248:ASP:C	2.64	0.40
1:I:110:ARG:N	1:I:110:ARG:HE	2.19	0.40
1:J:111:ILE:O	1:J:114:GLN:HB2	2.21	0.40
1:N:68:PHE:HB2	1:N:125:MET:HE1	2.02	0.40
1:O:93:VAL:O	1:O:192:LEU:HD13	2.21	0.40
1:J:186:TYR:OH	1:J:291:GLU:CG	2.69	0.40
1:J:186:TYR:O	1:J:190:ILE:HG13	2.20	0.40
1:M:130:TYR:CE1	1:M:265:ILE:HG22	2.56	0.40
1:N:169:ARG:HE	1:N:169:ARG:HB3	1.77	0.40
1:B:86:LEU:O	1:B:185:MET:HE2	2.22	0.40
1:B:296:ARG:HD2	1:C:263:ARG:O	2.22	0.40
1:C:291:GLU:O	1:C:295:LEU:HB3	2.22	0.40
1:E:261:VAL:HG12	1:E:277:VAL:HG22	2.03	0.40
1:H:220:GLU:HB2	1:H:291:GLU:CB	2.51	0.40
1:I:129:GLU:CD	1:J:103:LYS:HZ2	2.26	0.40
1:I:274:THR:C	1:I:276:GLY:N	2.77	0.40
1:J:223:TRP:HB3	1:J:295:LEU:HD12	2.04	0.40
1:L:133:MET:HG3	1:L:137:LEU:HD11	2.02	0.40
1:L:211:GLN:HG3	1:L:212:PRO:CD	2.51	0.40
1:O:63:HIS:CE1	1:P:104:MET:HE3	2.56	0.40
1:O:164:ARG:N	1:O:165:PRO:CD	2.85	0.40
1:P:162:MET:HE3	1:P:162:MET:CA	2.52	0.40
1:B:224:LEU:HG	1:B:295:LEU:HB2	2.04	0.40
1:E:295:LEU:C	1:E:295:LEU:CD1	2.88	0.40
1:G:43:TYR:CE2	1:H:142:GLY:HA2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:77:LEU:HD23	1:L:77:LEU:HA	1.87	0.40
1:M:77:LEU:HD23	1:N:70:VAL:HG22	2.03	0.40
1:B:299:LEU:HD22	1:C:127:PRO:HB2	2.02	0.40
1:D:191:ARG:HG2	1:D:205:VAL:HG13	2.03	0.40
1:E:242:LYS:HD2	3:E:563:HOH:O	2.21	0.40
1:F:260:THR:HA	1:F:263:ARG:HG2	2.04	0.40
1:F:267:PHE:CD2	1:F:268:LYS:N	2.86	0.40
1:G:271:THR:HG23	3:G:554:HOH:O	2.22	0.40
1:K:207:ARG:CG	1:K:207:ARG:NH1	2.78	0.40
1:L:172:HIS:HA	1:L:175:LEU:HD12	2.02	0.40
1:N:200:ILE:O	1:N:201:ASP:C	2.62	0.40
1:N:282:ARG:HG3	1:N:283:MET:CE	2.51	0.40
1:O:59:LEU:HD22	1:P:46:TYR:HD1	1.86	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	260/281 (92%)	254 (98%)	6 (2%)	0	100	100
1	B	262/281 (93%)	254 (97%)	8 (3%)	0	100	100
1	C	251/281 (89%)	244 (97%)	7 (3%)	0	100	100
1	D	257/281 (92%)	248 (96%)	8 (3%)	1 (0%)	30	43
1	E	252/281 (90%)	241 (96%)	9 (4%)	2 (1%)	16	25
1	F	256/281 (91%)	249 (97%)	6 (2%)	1 (0%)	30	43
1	G	255/281 (91%)	242 (95%)	12 (5%)	1 (0%)	30	43
1	H	259/281 (92%)	254 (98%)	5 (2%)	0	100	100
1	I	257/281 (92%)	249 (97%)	7 (3%)	1 (0%)	30	43
1	J	253/281 (90%)	244 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K	252/281 (90%)	246 (98%)	5 (2%)	1 (0%)	30	43
1	L	258/281 (92%)	250 (97%)	6 (2%)	2 (1%)	16	25
1	M	252/281 (90%)	244 (97%)	7 (3%)	1 (0%)	30	43
1	N	259/281 (92%)	250 (96%)	9 (4%)	0	100	100
1	O	253/281 (90%)	238 (94%)	15 (6%)	0	100	100
1	P	257/281 (92%)	249 (97%)	8 (3%)	0	100	100
All	All	4093/4496 (91%)	3956 (97%)	127 (3%)	10 (0%)	43	58

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	140	SER
1	E	268	LYS
1	I	212	PRO
1	M	268	LYS
1	E	141	SER
1	L	139	ALA
1	F	140	SER
1	L	209	TRP
1	K	212	PRO
1	G	273	GLY

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	229/240 (95%)	217 (95%)	12 (5%)	21	36
1	B	230/240 (96%)	212 (92%)	18 (8%)	11	20
1	C	224/240 (93%)	208 (93%)	16 (7%)	13	23
1	D	226/240 (94%)	213 (94%)	13 (6%)	18	32
1	E	226/240 (94%)	212 (94%)	14 (6%)	16	29
1	F	228/240 (95%)	212 (93%)	16 (7%)	14	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	227/240 (95%)	209 (92%)	18 (8%)	11	19
1	H	228/240 (95%)	214 (94%)	14 (6%)	17	30
1	I	226/240 (94%)	214 (95%)	12 (5%)	20	36
1	J	226/240 (94%)	209 (92%)	17 (8%)	12	21
1	K	226/240 (94%)	213 (94%)	13 (6%)	18	32
1	L	227/240 (95%)	212 (93%)	15 (7%)	15	26
1	M	223/240 (93%)	206 (92%)	17 (8%)	12	21
1	N	228/240 (95%)	213 (93%)	15 (7%)	15	26
1	O	226/240 (94%)	205 (91%)	21 (9%)	8	14
1	P	226/240 (94%)	212 (94%)	14 (6%)	16	29
All	All	3626/3840 (94%)	3381 (93%)	245 (7%)	14	25

All (245) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	LEU
1	A	59	LEU
1	A	96	ASP
1	A	97	GLN
1	A	149	ARG
1	A	164	ARG
1	A	193	MET
1	A	204	VAL
1	A	211	GLN
1	A	246	LEU
1	A	275	GLU
1	A	295	LEU
1	B	50	ASP
1	B	53	LEU
1	B	59	LEU
1	B	117	GLN
1	B	121	VAL
1	B	131	SER
1	B	133	MET
1	B	169	ARG
1	B	171	GLU
1	B	204	VAL
1	B	211	GLN

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Mol	Chain	Res	Type
1	B	242	LYS
1	B	246	LEU
1	B	258	VAL
1	B	291	GLU
1	B	294	LYS
1	B	295	LEU
1	B	296	ARG
1	C	53	LEU
1	C	59	LEU
1	C	87	ARG
1	C	96	ASP
1	C	143	PHE
1	C	164	ARG
1	C	199	GLN
1	C	204	VAL
1	C	210	THR
1	C	214	GLN
1	C	254	ARG
1	C	275	GLU
1	C	281	ARG
1	C	291	GLU
1	C	294	LYS
1	C	295	LEU
1	D	53	LEU
1	D	59	LEU
1	D	82	MET
1	D	125	MET
1	D	192	LEU
1	D	200	ILE
1	D	231	SER
1	D	268	LYS
1	D	274	THR
1	D	278	SER
1	D	291	GLU
1	D	294	LYS
1	D	295	LEU
1	E	53	LEU
1	E	59	LEU
1	E	94	LYS
1	E	96	ASP
1	E	134	ARG
1	E	137	LEU

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Mol	Chain	Res	Type
1	E	143	PHE
1	E	199	GLN
1	E	204	VAL
1	E	231	SER
1	E	275	GLU
1	E	281	ARG
1	E	291	GLU
1	E	294	LYS
1	F	40	ASP
1	F	53	LEU
1	F	59	LEU
1	F	94	LYS
1	F	109	SER
1	F	158	LYS
1	F	163	LEU
1	F	174	GLU
1	F	203	GLU
1	F	204	VAL
1	F	231	SER
1	F	246	LEU
1	F	254	ARG
1	F	268	LYS
1	F	269	ARG
1	F	295	LEU
1	G	53	LEU
1	G	94	LYS
1	G	114	GLN
1	G	133	MET
1	G	134	ARG
1	G	158	LYS
1	G	182	THR
1	G	204	VAL
1	G	213	THR
1	G	224	LEU
1	G	225	GLU
1	G	271	THR
1	G	274	THR
1	G	281	ARG
1	G	283	MET
1	G	291	GLU
1	G	295	LEU
1	G	299	LEU

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Mol	Chain	Res	Type
1	H	50	ASP
1	H	53	LEU
1	H	59	LEU
1	H	158	LYS
1	H	200	ILE
1	H	204	VAL
1	H	242	LYS
1	H	275	GLU
1	H	278	SER
1	H	281	ARG
1	H	291	GLU
1	H	294	LYS
1	H	295	LEU
1	H	297	THR
1	I	53	LEU
1	I	59	LEU
1	I	158	LYS
1	I	163	LEU
1	I	207	ARG
1	I	210	THR
1	I	225	GLU
1	I	229	ASN
1	I	254	ARG
1	I	274	THR
1	I	291	GLU
1	I	295	LEU
1	J	40	ASP
1	J	50	ASP
1	J	53	LEU
1	J	59	LEU
1	J	140	SER
1	J	154	ILE
1	J	158	LYS
1	J	164	ARG
1	J	178	THR
1	J	204	VAL
1	J	205	VAL
1	J	246	LEU
1	J	258	VAL
1	J	265	ILE
1	J	275	GLU
1	J	291	GLU

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Mol	Chain	Res	Type
1	J	295	LEU
1	K	39	ARG
1	K	53	LEU
1	K	59	LEU
1	K	96	ASP
1	K	204	VAL
1	K	207	ARG
1	K	254	ARG
1	K	258	VAL
1	K	274	THR
1	K	281	ARG
1	K	291	GLU
1	K	294	LYS
1	K	295	LEU
1	L	53	LEU
1	L	59	LEU
1	L	133	MET
1	L	158	LYS
1	L	171	GLU
1	L	177	GLU
1	L	204	VAL
1	L	211	GLN
1	L	231	SER
1	L	246	LEU
1	L	268	LYS
1	L	274	THR
1	L	291	GLU
1	L	295	LEU
1	L	297	THR
1	M	53	LEU
1	M	59	LEU
1	M	60	SER
1	M	77	LEU
1	M	109	SER
1	M	110	ARG
1	M	117	GLN
1	M	134	ARG
1	M	137	LEU
1	M	158	LYS
1	M	174	GLU
1	M	204	VAL
1	M	265	ILE

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Mol	Chain	Res	Type
1	M	268	LYS
1	M	291	GLU
1	M	294	LYS
1	M	295	LEU
1	N	50	ASP
1	N	53	LEU
1	N	59	LEU
1	N	96	ASP
1	N	110	ARG
1	N	117	GLN
1	N	134	ARG
1	N	163	LEU
1	N	199	GLN
1	N	204	VAL
1	N	245	ASP
1	N	265	ILE
1	N	269	ARG
1	N	294	LYS
1	N	295	LEU
1	O	49	LEU
1	O	53	LEU
1	O	59	LEU
1	O	80	LYS
1	O	96	ASP
1	O	117	GLN
1	O	154	ILE
1	O	158	LYS
1	O	164	ARG
1	O	173	LEU
1	O	174	GLU
1	O	178	THR
1	O	182	THR
1	O	185	MET
1	O	204	VAL
1	O	207	ARG
1	O	258	VAL
1	O	268	LYS
1	O	291	GLU
1	O	294	LYS
1	O	295	LEU
1	P	53	LEU
1	P	59	LEU

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Mol	Chain	Res	Type
1	P	87	ARG
1	P	96	ASP
1	P	109	SER
1	P	131	SER
1	P	141	SER
1	P	163	LEU
1	P	164	ARG
1	P	177	GLU
1	P	203	GLU
1	P	204	VAL
1	P	233	HIS
1	P	275	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	GLN
1	A	168	HIS
1	B	31	HIS
1	B	34	GLN
1	B	97	GLN
1	B	168	HIS
1	C	117	GLN
1	C	172	HIS
1	C	252	GLN
1	D	211	GLN
1	E	51	GLN
1	E	57	HIS
1	E	172	HIS
1	F	51	GLN
1	F	172	HIS
1	G	117	GLN
1	G	181	HIS
1	G	211	GLN
1	H	51	GLN
1	H	99	GLN
1	I	117	GLN
1	I	168	HIS
1	I	252	GLN
1	J	51	GLN
1	J	97	GLN
1	J	99	GLN

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Mol	Chain	Res	Type
1	J	114	GLN
1	J	172	HIS
1	J	211	GLN
1	J	252	GLN
1	K	117	GLN
1	K	211	GLN
1	L	51	GLN
1	L	172	HIS
1	M	57	HIS
1	M	168	HIS
1	M	252	GLN
1	N	99	GLN
1	N	172	HIS
1	N	181	HIS
1	O	97	GLN
1	O	117	GLN
1	O	172	HIS
1	O	252	GLN
1	P	57	HIS
1	P	211	GLN
1	P	233	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

16 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	L	500	1	50,50,50	1.82	8 (16%)	67,82,82	1.42	7 (10%)
2	HEM	D	500	1,3	50,50,50	2.21	11 (22%)	67,82,82	1.69	11 (16%)
2	HEM	M	500	1	50,50,50	2.11	9 (18%)	67,82,82	1.45	8 (11%)
2	HEM	B	500	1	50,50,50	2.23	9 (18%)	67,82,82	1.35	6 (8%)
2	HEM	P	500	1,3	50,50,50	1.90	10 (20%)	67,82,82	1.41	5 (7%)
2	HEM	G	500	1	50,50,50	2.31	8 (16%)	67,82,82	1.56	8 (11%)
2	HEM	F	500	1	50,50,50	1.83	9 (18%)	67,82,82	1.35	6 (8%)
2	HEM	A	500	1,3	50,50,50	2.09	8 (16%)	67,82,82	1.56	9 (13%)
2	HEM	H	500	1	50,50,50	2.07	9 (18%)	67,82,82	1.52	11 (16%)
2	HEM	N	500	1	50,50,50	2.00	10 (20%)	67,82,82	1.32	5 (7%)
2	HEM	E	500	1,3	50,50,50	1.85	9 (18%)	67,82,82	1.32	6 (8%)
2	HEM	O	500	1	50,50,50	2.17	9 (18%)	67,82,82	1.38	9 (13%)
2	HEM	C	500	1	50,50,50	2.02	8 (16%)	67,82,82	1.41	8 (11%)
2	HEM	J	500	1	50,50,50	1.88	8 (16%)	67,82,82	1.30	6 (8%)
2	HEM	I	500	1	50,50,50	1.79	9 (18%)	67,82,82	1.37	9 (13%)
2	HEM	K	500	1	50,50,50	1.81	9 (18%)	67,82,82	1.33	5 (7%)

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	L	500	1	-	1/14/54/54	-
2	HEM	D	500	1,3	-	4/14/54/54	-
2	HEM	M	500	1	-	2/14/54/54	-
2	HEM	B	500	1	-	2/14/54/54	-
2	HEM	P	500	1,3	-	6/14/54/54	-
2	HEM	G	500	1	-	5/14/54/54	-
2	HEM	F	500	1	-	4/14/54/54	-
2	HEM	A	500	1,3	-	4/14/54/54	-
2	HEM	H	500	1	-	2/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	N	500	1	-	4/14/54/54	-
2	HEM	E	500	1,3	-	5/14/54/54	-
2	HEM	O	500	1	-	0/14/54/54	-
2	HEM	C	500	1	-	4/14/54/54	-
2	HEM	J	500	1	-	10/14/54/54	-
2	HEM	I	500	1	-	2/14/54/54	-
2	HEM	K	500	1	-	4/14/54/54	-

All (143) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	HEM	C3D-C2D	8.35	1.54	1.36
2	G	500	HEM	C3D-C2D	8.19	1.54	1.36
2	I	500	HEM	C3D-C2D	8.13	1.54	1.36
2	C	500	HEM	C3D-C2D	8.06	1.54	1.36
2	J	500	HEM	C3D-C2D	8.03	1.54	1.36
2	D	500	HEM	C3D-C2D	7.95	1.53	1.36
2	F	500	HEM	C3D-C2D	7.91	1.53	1.36
2	O	500	HEM	C3D-C2D	7.80	1.53	1.36
2	M	500	HEM	FE-ND	7.80	2.18	1.94
2	O	500	HEM	FE-ND	7.73	2.18	1.94
2	N	500	HEM	C3D-C2D	7.73	1.53	1.36
2	H	500	HEM	C3D-C2D	7.71	1.53	1.36
2	M	500	HEM	C3D-C2D	7.68	1.53	1.36
2	E	500	HEM	C3D-C2D	7.63	1.53	1.36
2	H	500	HEM	FE-ND	7.58	2.18	1.94
2	A	500	HEM	C3D-C2D	7.45	1.52	1.36
2	K	500	HEM	C3D-C2D	7.45	1.52	1.36
2	D	500	HEM	FE-NB	7.41	2.17	1.94
2	L	500	HEM	C3D-C2D	7.31	1.52	1.36
2	A	500	HEM	FE-NB	7.29	2.17	1.94
2	B	500	HEM	FE-ND	7.11	2.16	1.94
2	P	500	HEM	C3D-C2D	6.97	1.51	1.36
2	G	500	HEM	FE-ND	6.89	2.16	1.94
2	B	500	HEM	FE-NC	6.60	2.17	1.95
2	D	500	HEM	FE-ND	6.45	2.14	1.94
2	G	500	HEM	FE-NA	5.92	2.14	1.95
2	G	500	HEM	FE-NB	5.90	2.13	1.94
2	P	500	HEM	FE-ND	5.79	2.12	1.94
2	O	500	HEM	FE-NA	5.53	2.13	1.95
2	N	500	HEM	FE-NB	5.46	2.11	1.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	500	HEM	FE-ND	5.39	2.11	1.94
2	C	500	HEM	FE-NA	5.27	2.12	1.95
2	F	500	HEM	FE-NB	4.95	2.10	1.94
2	M	500	HEM	FE-NA	4.93	2.11	1.95
2	N	500	HEM	FE-NC	4.82	2.11	1.95
2	O	500	HEM	FE-NC	4.72	2.10	1.95
2	K	500	HEM	FE-NA	4.72	2.10	1.95
2	A	500	HEM	FE-NC	4.64	2.10	1.95
2	A	500	HEM	FE-ND	4.60	2.09	1.94
2	J	500	HEM	FE-NC	4.55	2.10	1.95
2	J	500	HEM	FE-ND	4.54	2.08	1.94
2	E	500	HEM	FE-ND	4.41	2.08	1.94
2	P	500	HEM	FE-NA	4.36	2.09	1.95
2	M	500	HEM	FE-NB	4.35	2.08	1.94
2	K	500	HEM	FE-NC	4.32	2.09	1.95
2	L	500	HEM	FE-ND	4.29	2.08	1.94
2	I	500	HEM	FE-ND	4.26	2.08	1.94
2	G	500	HEM	FE-NC	4.21	2.09	1.95
2	L	500	HEM	FE-NB	4.06	2.07	1.94
2	N	500	HEM	FE-NA	4.02	2.08	1.95
2	H	500	HEM	FE-NA	3.94	2.08	1.95
2	H	500	HEM	FE-NC	3.83	2.07	1.95
2	C	500	HEM	FE-NC	3.81	2.07	1.95
2	L	500	HEM	FE-NA	3.80	2.07	1.95
2	D	500	HEM	FE-NC	3.71	2.07	1.95
2	B	500	HEM	FE-NB	3.57	2.05	1.94
2	P	500	HEM	FE-NB	3.44	2.05	1.94
2	L	500	HEM	CAB-C3B	3.31	1.56	1.47
2	E	500	HEM	FE-NB	3.31	2.05	1.94
2	F	500	HEM	FE-NA	3.30	2.06	1.95
2	E	500	HEM	FE-NA	3.28	2.06	1.95
2	D	500	HEM	CAB-C3B	3.26	1.56	1.47
2	A	500	HEM	CAC-C3C	3.25	1.56	1.47
2	N	500	HEM	CAC-C3C	3.16	1.55	1.47
2	G	500	HEM	CAB-C3B	3.16	1.55	1.47
2	J	500	HEM	CAB-C3B	3.15	1.55	1.47
2	C	500	HEM	CAB-C3B	3.14	1.55	1.47
2	E	500	HEM	CAC-C3C	3.13	1.55	1.47
2	G	500	HEM	CAC-C3C	3.11	1.55	1.47
2	N	500	HEM	CAB-C3B	3.07	1.55	1.47
2	P	500	HEM	CAC-C3C	3.06	1.55	1.47
2	O	500	HEM	CAC-C3C	3.00	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	500	HEM	CAB-C3B	2.97	1.55	1.47
2	C	500	HEM	CAC-C3C	2.97	1.55	1.47
2	I	500	HEM	CAC-C3C	2.95	1.55	1.47
2	M	500	HEM	CAC-C3C	2.95	1.55	1.47
2	I	500	HEM	FE-NB	2.94	2.04	1.94
2	A	500	HEM	CAB-C3B	2.94	1.55	1.47
2	F	500	HEM	CAB-C3B	2.92	1.55	1.47
2	E	500	HEM	CAB-C3B	2.83	1.54	1.47
2	H	500	HEM	CAC-C3C	2.83	1.54	1.47
2	F	500	HEM	FE-NC	2.77	2.04	1.95
2	H	500	HEM	CAB-C3B	2.74	1.54	1.47
2	E	500	HEM	CMB-C2B	2.72	1.56	1.50
2	B	500	HEM	CAB-C3B	2.72	1.54	1.47
2	D	500	HEM	CAC-C3C	2.71	1.54	1.47
2	B	500	HEM	CMD-C2D	2.68	1.56	1.50
2	K	500	HEM	CAC-C3C	2.65	1.54	1.47
2	O	500	HEM	CAB-C3B	2.64	1.54	1.47
2	C	500	HEM	FE-NB	2.64	2.03	1.94
2	H	500	HEM	FE-NB	2.64	2.03	1.94
2	B	500	HEM	CMB-C2B	2.63	1.56	1.50
2	P	500	HEM	CAB-C3B	2.62	1.54	1.47
2	B	500	HEM	CAC-C3C	2.59	1.54	1.47
2	M	500	HEM	CMA-C3A	2.59	1.56	1.50
2	I	500	HEM	CAB-C3B	2.57	1.54	1.47
2	D	500	HEM	FE-NA	2.54	2.03	1.95
2	F	500	HEM	CAC-C3C	2.52	1.54	1.47
2	J	500	HEM	CAC-C3C	2.52	1.54	1.47
2	L	500	HEM	FE-NC	2.52	2.03	1.95
2	K	500	HEM	CAB-C3B	2.50	1.54	1.47
2	M	500	HEM	CMB-C2B	2.48	1.55	1.50
2	O	500	HEM	CMA-C3A	2.40	1.55	1.50
2	C	500	HEM	CMA-C3A	2.39	1.55	1.50
2	N	500	HEM	FE-ND	2.35	2.02	1.94
2	I	500	HEM	FE-NA	2.35	2.02	1.95
2	O	500	HEM	CMB-C2B	2.35	1.55	1.50
2	F	500	HEM	CMB-C2B	2.35	1.55	1.50
2	P	500	HEM	CMA-C3A	2.31	1.55	1.50
2	L	500	HEM	CAC-C3C	2.30	1.53	1.47
2	G	500	HEM	CMD-C2D	2.28	1.55	1.50
2	N	500	HEM	CMA-C3A	2.25	1.55	1.50
2	J	500	HEM	C3B-C2B	-2.25	1.32	1.37
2	J	500	HEM	FE-NB	2.23	2.01	1.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	500	HEM	FE-NC	2.23	2.02	1.95
2	L	500	HEM	CMA-C3A	2.22	1.55	1.50
2	H	500	HEM	CMD-C2D	2.20	1.55	1.50
2	P	500	HEM	CAA-C2A	2.20	1.57	1.51
2	K	500	HEM	CMA-C3A	2.20	1.55	1.50
2	A	500	HEM	CMA-C3A	2.19	1.55	1.50
2	D	500	HEM	CMA-C3A	2.18	1.55	1.50
2	H	500	HEM	CMB-C2B	2.18	1.55	1.50
2	I	500	HEM	CMB-C2B	2.18	1.55	1.50
2	E	500	HEM	CMD-C2D	2.18	1.55	1.50
2	P	500	HEM	CMB-C2B	2.18	1.55	1.50
2	K	500	HEM	FE-ND	2.16	2.01	1.94
2	K	500	HEM	CMC-C2C	2.16	1.55	1.50
2	F	500	HEM	CMA-C3A	2.14	1.55	1.50
2	B	500	HEM	CMC-C2C	2.12	1.55	1.50
2	F	500	HEM	FE-ND	2.12	2.01	1.94
2	K	500	HEM	CMB-C2B	2.11	1.55	1.50
2	D	500	HEM	CMB-C2B	2.11	1.55	1.50
2	A	500	HEM	CMC-C2C	2.10	1.55	1.50
2	D	500	HEM	O1D-CGD	2.08	1.28	1.22
2	D	500	HEM	C2A-C3A	-2.08	1.33	1.38
2	I	500	HEM	CMA-C3A	2.07	1.55	1.50
2	N	500	HEM	CMD-C2D	2.07	1.55	1.50
2	J	500	HEM	FE-NA	2.05	2.01	1.95
2	M	500	HEM	CMC-C2C	2.05	1.55	1.50
2	N	500	HEM	CMC-C2C	2.04	1.55	1.50
2	P	500	HEM	CMD-C2D	2.03	1.54	1.50
2	I	500	HEM	FE-NC	2.00	2.01	1.95
2	O	500	HEM	CMD-C2D	2.00	1.54	1.50

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	HEM	C4D-ND-C1D	6.45	112.84	105.21
2	G	500	HEM	C4D-ND-C1D	5.88	112.18	105.21
2	A	500	HEM	C4D-ND-C1D	5.79	112.06	105.21
2	P	500	HEM	C4D-ND-C1D	5.52	111.75	105.21
2	N	500	HEM	C4D-ND-C1D	5.47	111.69	105.21
2	C	500	HEM	C4D-ND-C1D	5.28	111.46	105.21
2	B	500	HEM	C4D-ND-C1D	5.27	111.45	105.21
2	F	500	HEM	C4D-ND-C1D	5.21	111.37	105.21
2	O	500	HEM	C4D-ND-C1D	5.15	111.30	105.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	500	HEM	C4D-ND-C1D	4.98	111.11	105.21
2	M	500	HEM	C4D-ND-C1D	4.89	111.00	105.21
2	H	500	HEM	C4D-ND-C1D	4.72	110.80	105.21
2	E	500	HEM	C4D-ND-C1D	4.56	110.61	105.21
2	I	500	HEM	C4D-ND-C1D	4.55	110.59	105.21
2	A	500	HEM	CBD-CAD-C3D	-4.44	100.24	112.53
2	L	500	HEM	C4D-ND-C1D	4.32	110.33	105.21
2	J	500	HEM	C4D-ND-C1D	4.31	110.31	105.21
2	M	500	HEM	CBD-CAD-C3D	-4.15	101.05	112.53
2	H	500	HEM	CBD-CAD-C3D	-4.07	101.28	112.53
2	D	500	HEM	CHC-C1C-NC	3.76	128.55	124.45
2	D	500	HEM	CHD-C1D-ND	3.75	128.45	124.42
2	P	500	HEM	CBD-CAD-C3D	-3.70	102.30	112.53
2	M	500	HEM	CHC-C1C-NC	3.63	128.41	124.45
2	K	500	HEM	CHD-C1D-ND	3.60	128.30	124.42
2	I	500	HEM	CHC-C1C-NC	3.49	128.26	124.45
2	D	500	HEM	C2A-C1A-NA	-3.37	106.41	110.15
2	P	500	HEM	CHC-C4B-NB	3.31	127.99	124.42
2	C	500	HEM	CBD-CAD-C3D	-3.31	103.38	112.53
2	A	500	HEM	C1B-NB-C4B	3.30	109.11	105.21
2	G	500	HEM	C3B-C2B-C1B	3.29	108.88	106.41
2	A	500	HEM	C3B-C4B-NB	-3.22	107.16	109.47
2	F	500	HEM	CBD-CAD-C3D	-3.22	103.64	112.53
2	O	500	HEM	CBD-CAD-C3D	-3.15	103.81	112.53
2	C	500	HEM	CHD-C1D-ND	3.14	127.80	124.42
2	A	500	HEM	CAA-CBA-CGA	-3.13	105.36	113.67
2	E	500	HEM	CHD-C1D-ND	3.10	127.76	124.42
2	L	500	HEM	CAA-CBA-CGA	-3.07	105.52	113.67
2	J	500	HEM	CHD-C1D-ND	3.05	127.71	124.42
2	L	500	HEM	C3B-C2B-C1B	3.02	108.68	106.41
2	D	500	HEM	C3B-C2B-C1B	3.01	108.67	106.41
2	B	500	HEM	CBD-CAD-C3D	-2.98	104.30	112.53
2	F	500	HEM	CAA-CBA-CGA	-2.96	105.82	113.67
2	D	500	HEM	C3C-C2C-C1C	2.95	109.84	107.05
2	H	500	HEM	CHC-C1C-NC	2.95	127.66	124.45
2	L	500	HEM	CHC-C1C-NC	2.95	127.66	124.45
2	L	500	HEM	CHA-C4D-ND	2.89	127.94	124.37
2	G	500	HEM	C2A-C1A-NA	-2.86	106.98	110.15
2	G	500	HEM	CHC-C1C-NC	2.85	127.55	124.45
2	I	500	HEM	CHD-C1D-ND	2.84	127.48	124.42
2	K	500	HEM	CHC-C4B-NB	2.83	127.47	124.42
2	I	500	HEM	CAD-C3D-C4D	2.74	129.47	124.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	HEM	C3B-C2B-C1B	2.71	108.45	106.41
2	D	500	HEM	CHB-C4A-NA	2.71	128.78	123.86
2	K	500	HEM	CHA-C4D-ND	2.70	127.70	124.37
2	D	500	HEM	C1B-NB-C4B	2.70	108.40	105.21
2	H	500	HEM	CMA-C3A-C4A	-2.69	121.32	125.42
2	L	500	HEM	CBD-CAD-C3D	-2.67	105.15	112.53
2	C	500	HEM	C3B-C2B-C1B	2.65	108.40	106.41
2	A	500	HEM	CHC-C1C-NC	2.64	127.33	124.45
2	N	500	HEM	CHD-C1D-ND	2.64	127.27	124.42
2	P	500	HEM	C3C-C2C-C1C	2.64	109.54	107.05
2	M	500	HEM	O1D-CGD-CBD	-2.62	114.79	123.09
2	O	500	HEM	C3B-C4B-NB	-2.60	107.60	109.47
2	C	500	HEM	O2D-CGD-CBD	2.51	121.92	114.00
2	O	500	HEM	CHB-C1B-NB	2.50	127.45	124.37
2	O	500	HEM	C2A-C1A-NA	-2.46	107.42	110.15
2	E	500	HEM	CAD-CBD-CGD	-2.46	107.14	113.67
2	G	500	HEM	C1B-NB-C4B	2.45	108.11	105.21
2	O	500	HEM	CHD-C1D-ND	2.43	127.04	124.42
2	G	500	HEM	C3B-C4B-NB	-2.41	107.74	109.47
2	O	500	HEM	C1B-NB-C4B	2.40	108.05	105.21
2	N	500	HEM	C3B-C4B-NB	-2.39	107.75	109.47
2	H	500	HEM	O2D-CGD-CBD	2.39	121.54	114.00
2	F	500	HEM	CHA-C4D-ND	2.36	127.29	124.37
2	D	500	HEM	C2B-C1B-NB	-2.35	107.14	109.84
2	I	500	HEM	C3C-C2C-C1C	2.35	109.27	107.05
2	M	500	HEM	CHA-C1A-NA	2.32	128.07	123.86
2	B	500	HEM	C4C-C3C-C2C	2.30	108.81	106.81
2	M	500	HEM	C1B-NB-C4B	2.26	107.88	105.21
2	J	500	HEM	CAD-C3D-C4D	2.23	128.58	124.70
2	C	500	HEM	C1B-NB-C4B	2.21	107.83	105.21
2	B	500	HEM	C1B-NB-C4B	2.21	107.82	105.21
2	L	500	HEM	CHD-C4C-NC	2.19	126.83	124.45
2	D	500	HEM	C3A-C4A-NA	-2.18	106.65	110.14
2	E	500	HEM	CBD-CAD-C3D	-2.18	106.51	112.53
2	J	500	HEM	C2A-C1A-NA	-2.17	107.74	110.15
2	I	500	HEM	CMA-C3A-C2A	2.17	130.23	125.62
2	O	500	HEM	C3B-C2B-C1B	2.17	108.04	106.41
2	H	500	HEM	C3B-C2B-C1B	2.17	108.04	106.41
2	F	500	HEM	O2D-CGD-CBD	2.15	120.80	114.00
2	C	500	HEM	C2A-C1A-NA	-2.14	107.77	110.15
2	A	500	HEM	C2B-C1B-NB	-2.14	107.38	109.84
2	H	500	HEM	C1B-NB-C4B	2.13	107.73	105.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	HEM	CBD-CAD-C3D	-2.13	106.64	112.53
2	I	500	HEM	O1A-CGA-CBA	-2.13	116.35	123.09
2	O	500	HEM	CHC-C4B-NB	2.12	126.71	124.42
2	H	500	HEM	CHA-C4D-ND	2.10	126.97	124.37
2	J	500	HEM	O2D-CGD-CBD	2.10	120.63	114.00
2	K	500	HEM	CHD-C4C-C3C	2.09	128.73	125.21
2	J	500	HEM	C3B-C2B-C1B	2.08	107.97	106.41
2	C	500	HEM	O1D-CGD-CBD	-2.07	116.52	123.09
2	N	500	HEM	C1B-NB-C4B	2.06	107.65	105.21
2	G	500	HEM	O2D-CGD-CBD	2.06	120.52	114.00
2	P	500	HEM	O1D-CGD-CBD	-2.06	116.55	123.09
2	F	500	HEM	O1D-CGD-CBD	-2.06	116.57	123.09
2	M	500	HEM	O2D-CGD-CBD	2.05	120.48	114.00
2	H	500	HEM	CAD-C3D-C4D	2.05	128.26	124.70
2	A	500	HEM	CHD-C1D-ND	2.05	126.63	124.42
2	N	500	HEM	O1D-CGD-CBD	-2.04	116.61	123.09
2	H	500	HEM	CAD-CBD-CGD	2.04	119.08	113.67
2	B	500	HEM	O2D-CGD-CBD	2.04	120.43	114.00
2	G	500	HEM	C2B-C1B-NB	-2.03	107.50	109.84
2	E	500	HEM	C4A-C3A-C2A	2.03	109.14	106.82
2	E	500	HEM	CHB-C4A-NA	2.03	127.54	123.86
2	H	500	HEM	C2A-C1A-NA	-2.03	107.91	110.15
2	I	500	HEM	O2D-CGD-CBD	2.02	120.40	114.00
2	M	500	HEM	C2A-C1A-NA	-2.02	107.91	110.15
2	I	500	HEM	O2A-CGA-CBA	2.01	120.36	114.00
2	B	500	HEM	O2A-CGA-CBA	2.01	120.35	114.00

There are no chirality outliers.

All (59) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	HEM	C2B-C3B-CAB-CBB
2	F	500	HEM	C2C-C3C-CAC-CBC
2	J	500	HEM	C2C-C3C-CAC-CBC
2	A	500	HEM	C4B-C3B-CAB-CBB
2	J	500	HEM	C4C-C3C-CAC-CBC
2	N	500	HEM	C4C-C3C-CAC-CBC
2	J	500	HEM	C4D-C3D-CAD-CBD
2	N	500	HEM	C2C-C3C-CAC-CBC
2	P	500	HEM	C2C-C3C-CAC-CBC
2	M	500	HEM	CAA-CBA-CGA-O2A
2	F	500	HEM	C4C-C3C-CAC-CBC

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Mol	Chain	Res	Type	Atoms
2	P	500	HEM	C4C-C3C-CAC-CBC
2	A	500	HEM	CAA-CBA-CGA-O2A
2	M	500	HEM	CAA-CBA-CGA-O1A
2	J	500	HEM	C3D-CAD-CBD-CGD
2	K	500	HEM	CAA-CBA-CGA-O2A
2	C	500	HEM	CAA-CBA-CGA-O1A
2	E	500	HEM	CAA-CBA-CGA-O1A
2	I	500	HEM	CAA-CBA-CGA-O1A
2	A	500	HEM	CAA-CBA-CGA-O1A
2	E	500	HEM	CAA-CBA-CGA-O2A
2	C	500	HEM	CAA-CBA-CGA-O2A
2	I	500	HEM	CAA-CBA-CGA-O2A
2	J	500	HEM	C2D-C3D-CAD-CBD
2	K	500	HEM	CAA-CBA-CGA-O1A
2	E	500	HEM	CAD-CBD-CGD-O2D
2	H	500	HEM	CAA-CBA-CGA-O2A
2	B	500	HEM	CAA-CBA-CGA-O2A
2	K	500	HEM	CAD-CBD-CGD-O1D
2	G	500	HEM	CAA-CBA-CGA-O2A
2	J	500	HEM	CAA-CBA-CGA-O2A
2	E	500	HEM	CAD-CBD-CGD-O1D
2	E	500	HEM	C2C-C3C-CAC-CBC
2	N	500	HEM	CAA-CBA-CGA-O2A
2	F	500	HEM	CAA-CBA-CGA-O2A
2	H	500	HEM	CAA-CBA-CGA-O1A
2	B	500	HEM	CAA-CBA-CGA-O1A
2	G	500	HEM	CAA-CBA-CGA-O1A
2	J	500	HEM	CAD-CBD-CGD-O1D
2	D	500	HEM	CAA-CBA-CGA-O2A
2	G	500	HEM	C4B-C3B-CAB-CBB
2	J	500	HEM	CAA-CBA-CGA-O1A
2	D	500	HEM	CAA-CBA-CGA-O1A
2	P	500	HEM	CAA-CBA-CGA-O2A
2	N	500	HEM	CAA-CBA-CGA-O1A
2	J	500	HEM	CAD-CBD-CGD-O2D
2	K	500	HEM	CAD-CBD-CGD-O2D
2	C	500	HEM	CAD-CBD-CGD-O2D
2	D	500	HEM	CAD-CBD-CGD-O2D
2	F	500	HEM	CAA-CBA-CGA-O1A
2	P	500	HEM	CAA-CBA-CGA-O1A
2	L	500	HEM	CAA-CBA-CGA-O2A
2	P	500	HEM	CAD-CBD-CGD-O2D

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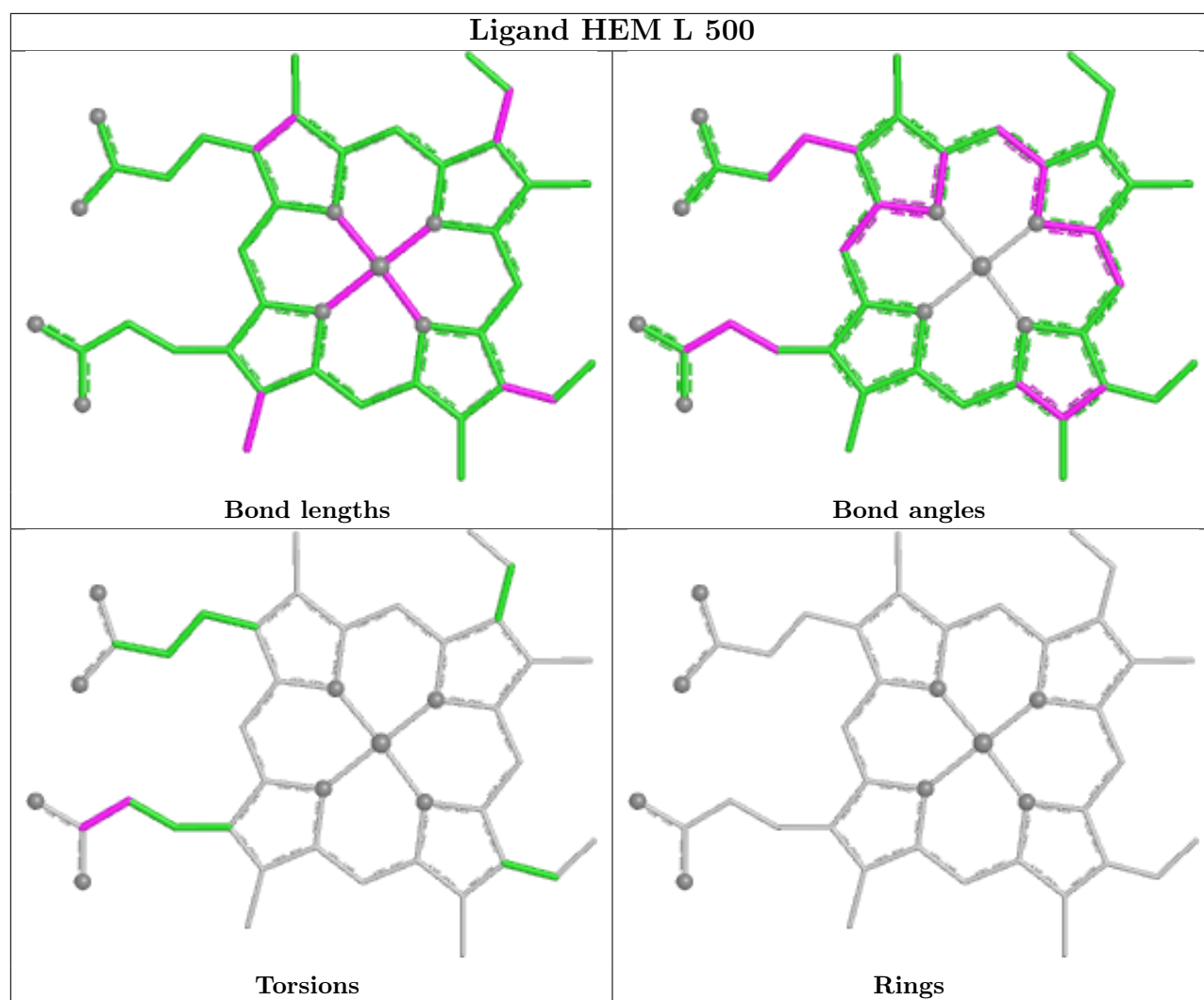
Mol	Chain	Res	Type	Atoms
2	P	500	HEM	CAD-CBD-CGD-O1D
2	C	500	HEM	CAD-CBD-CGD-O1D
2	D	500	HEM	CAD-CBD-CGD-O1D
2	G	500	HEM	C2B-C3B-CAB-CBB
2	J	500	HEM	C2B-C3B-CAB-CBB
2	G	500	HEM	CAD-CBD-CGD-O2D

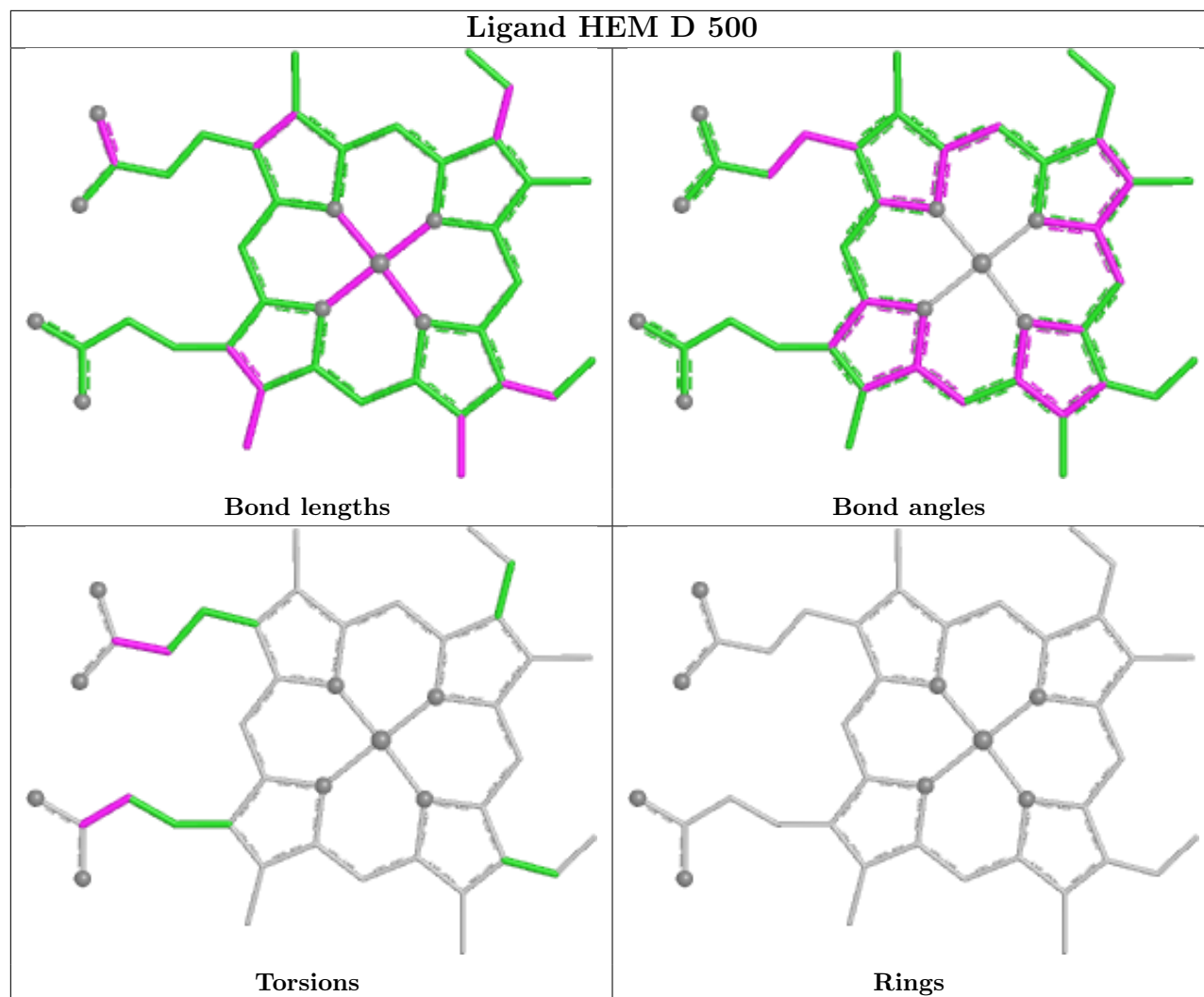
There are no ring outliers.

15 monomers are involved in 58 short contacts:

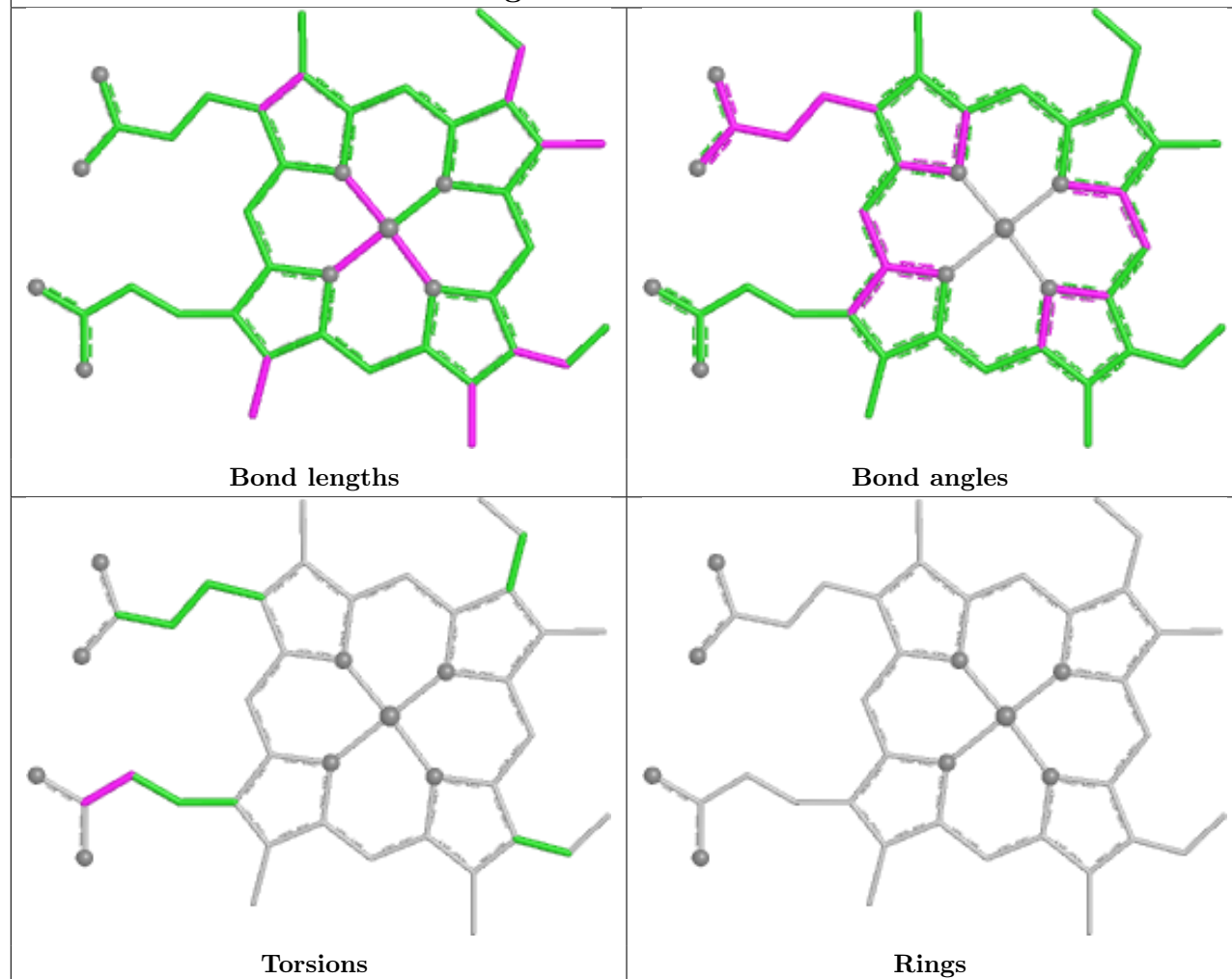
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	500	HEM	5	0
2	D	500	HEM	2	0
2	M	500	HEM	2	0
2	P	500	HEM	7	0
2	G	500	HEM	3	0
2	F	500	HEM	3	0
2	A	500	HEM	6	0
2	H	500	HEM	2	0
2	N	500	HEM	1	0
2	E	500	HEM	7	0
2	O	500	HEM	4	0
2	C	500	HEM	2	0
2	J	500	HEM	1	0
2	I	500	HEM	9	0
2	K	500	HEM	4	0

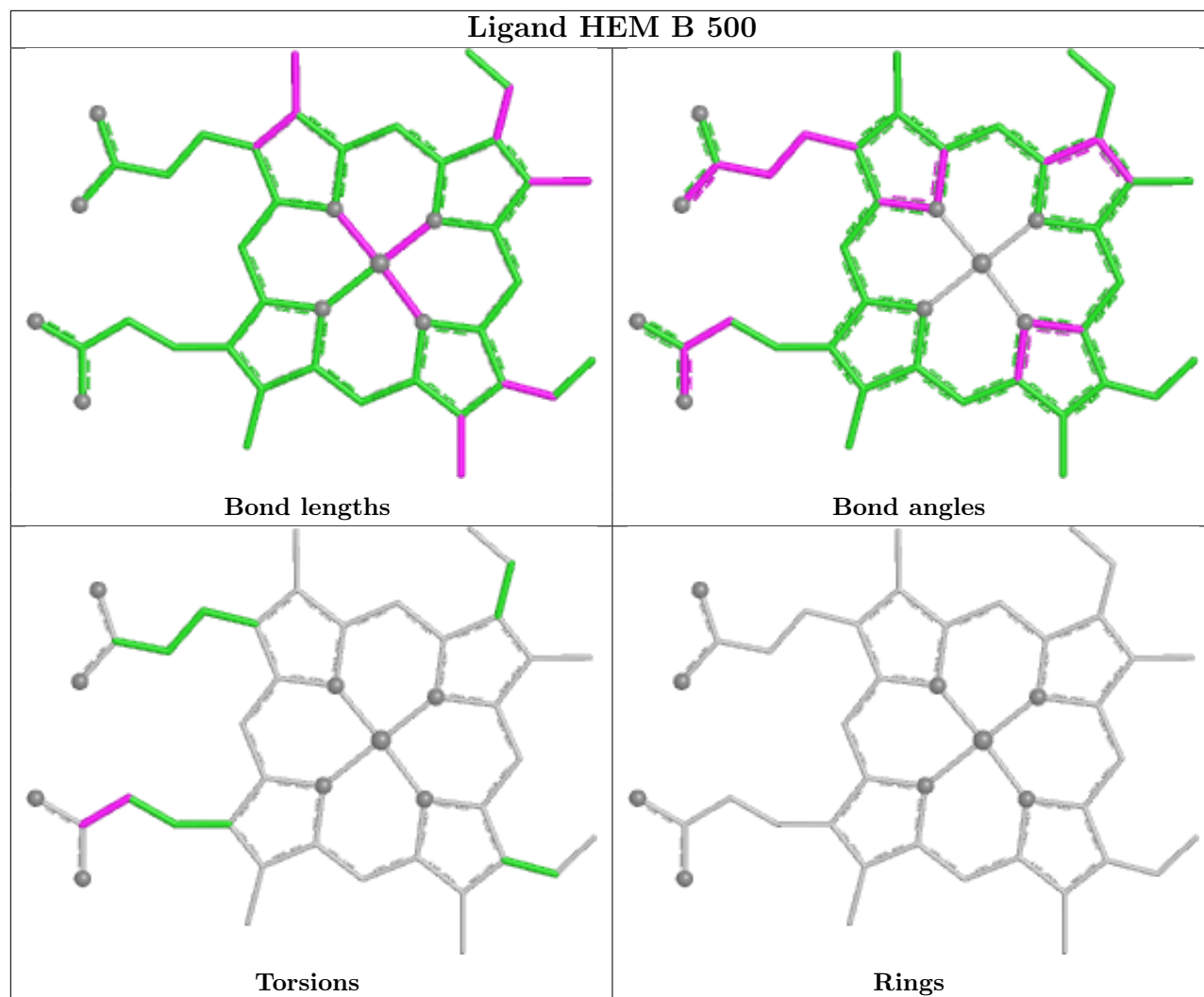
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

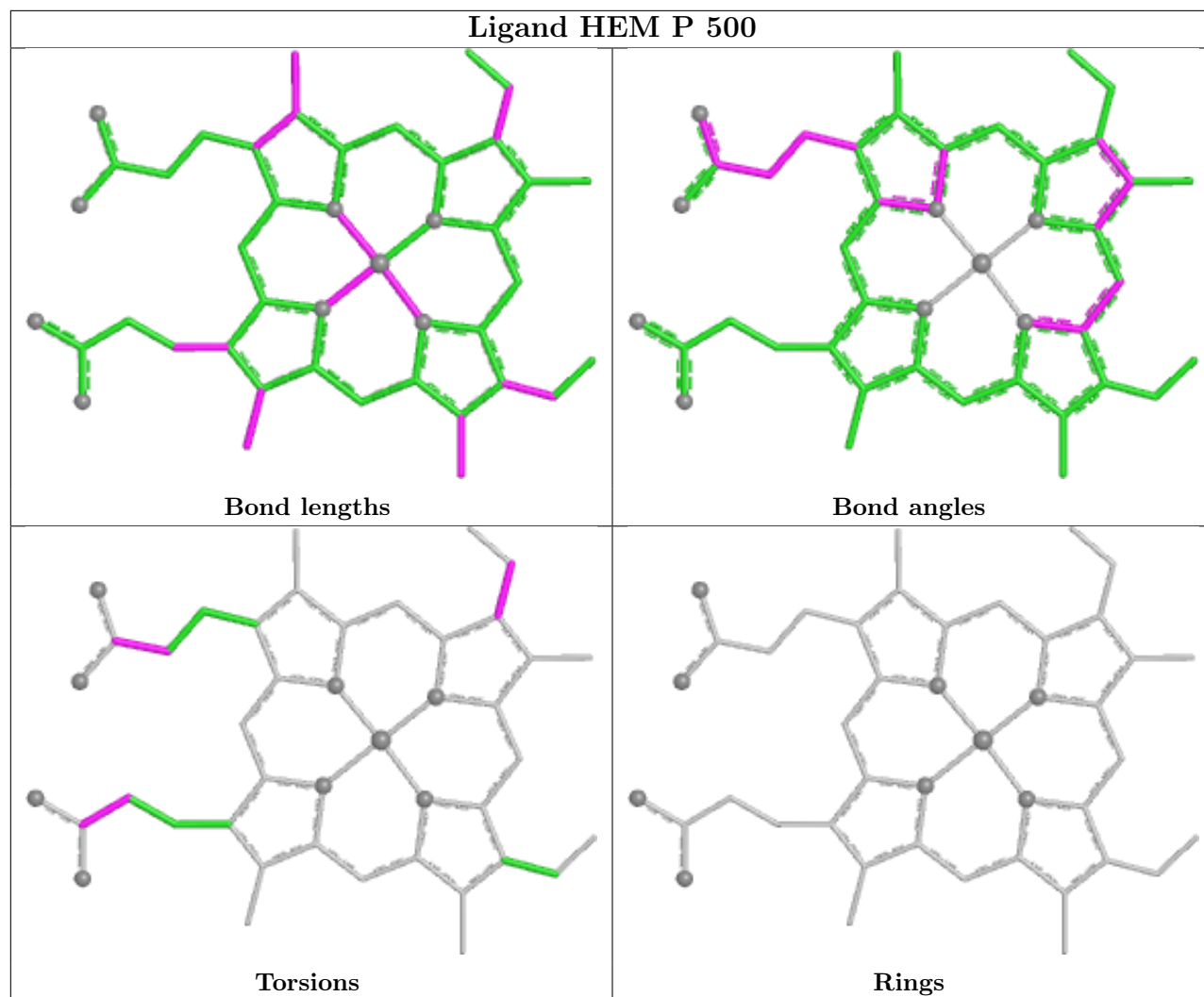


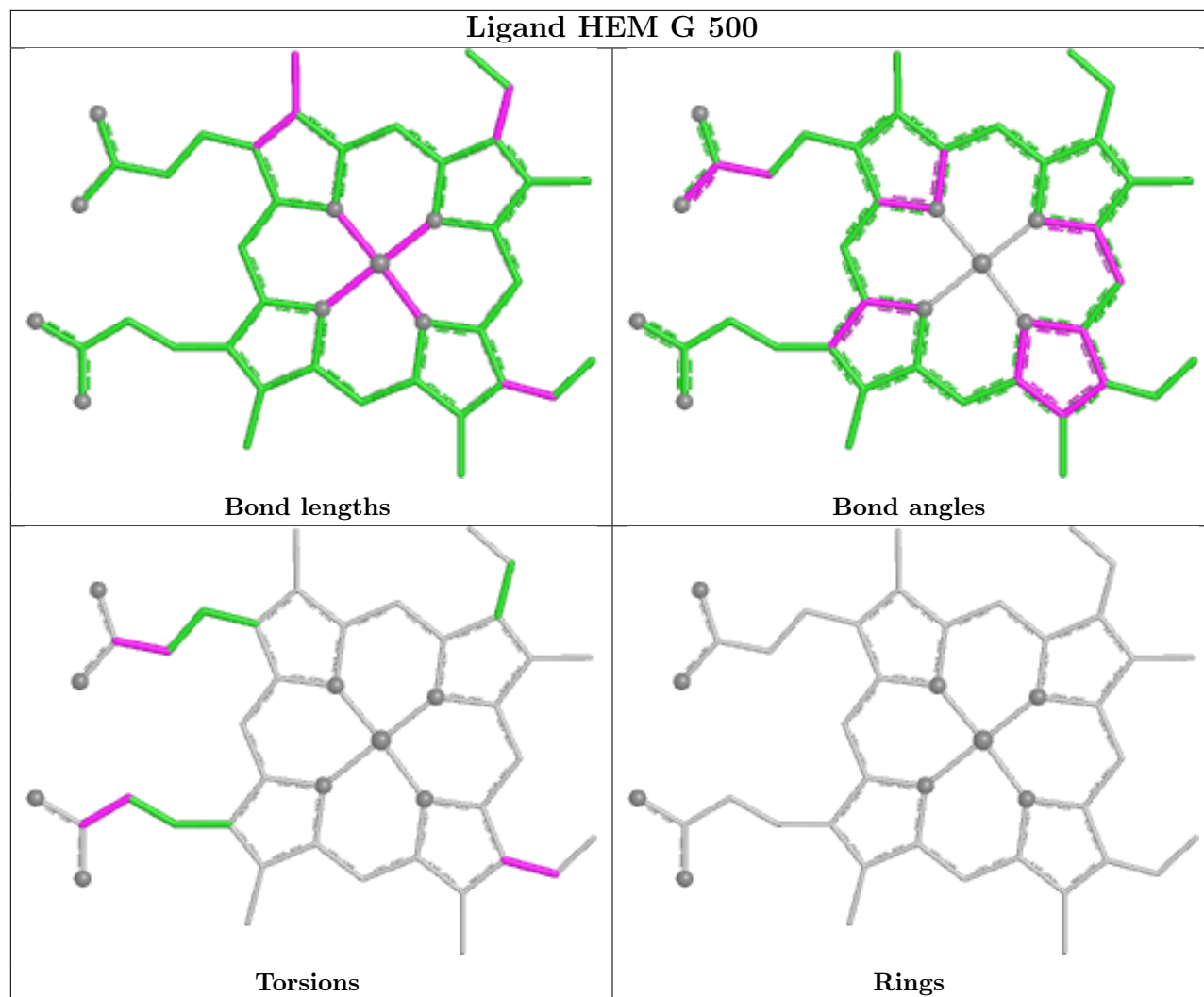


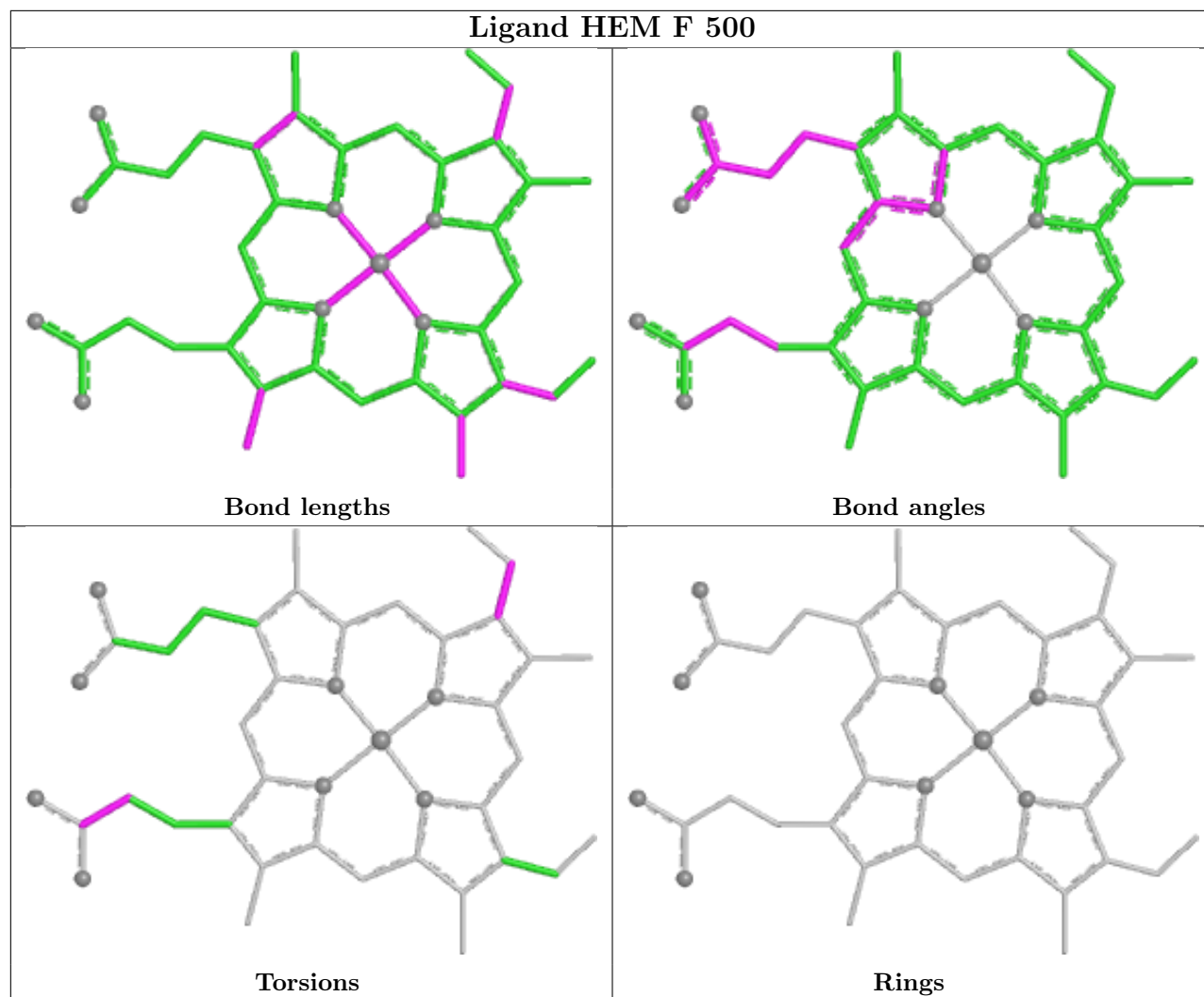
Ligand HEM M 500

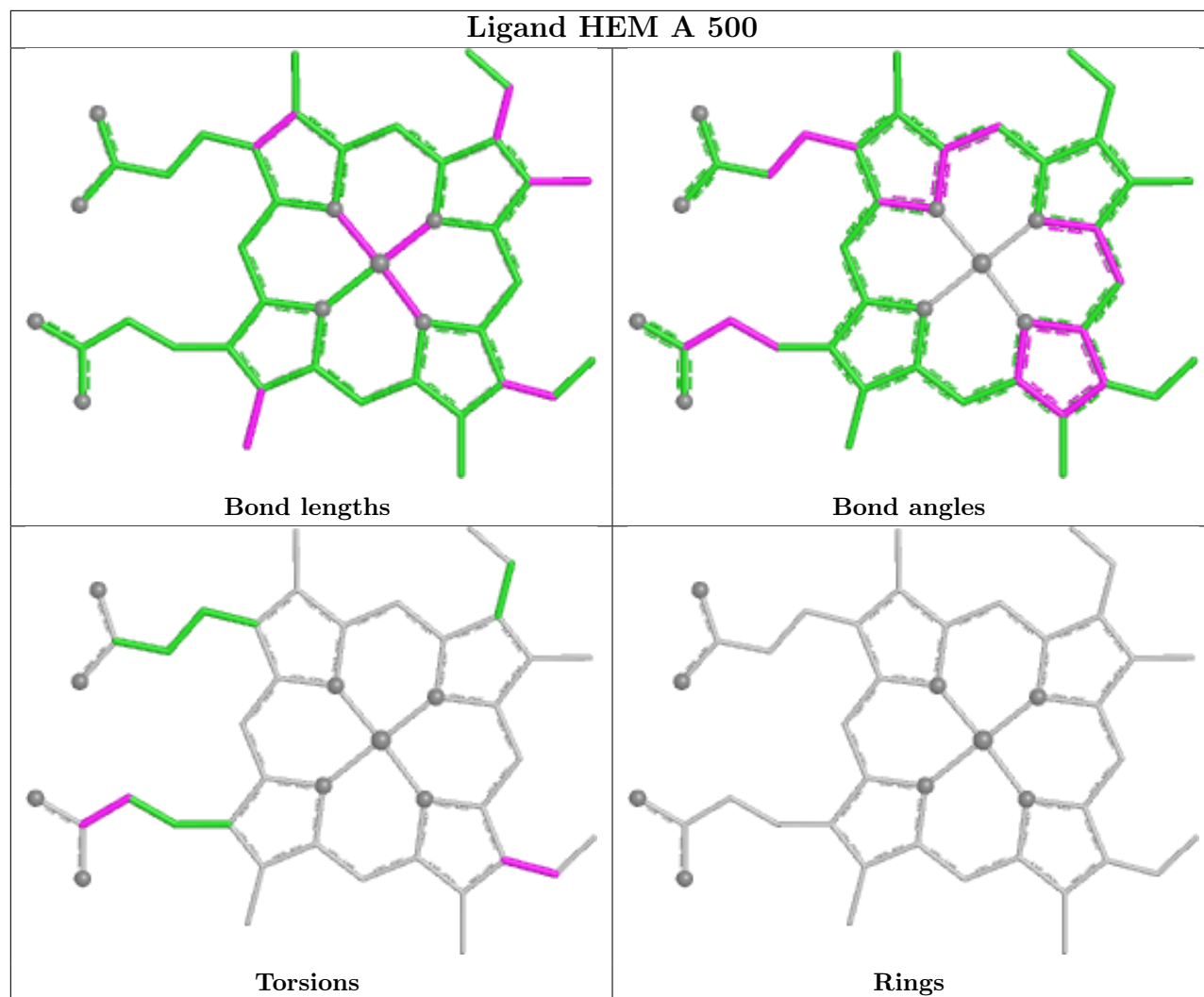


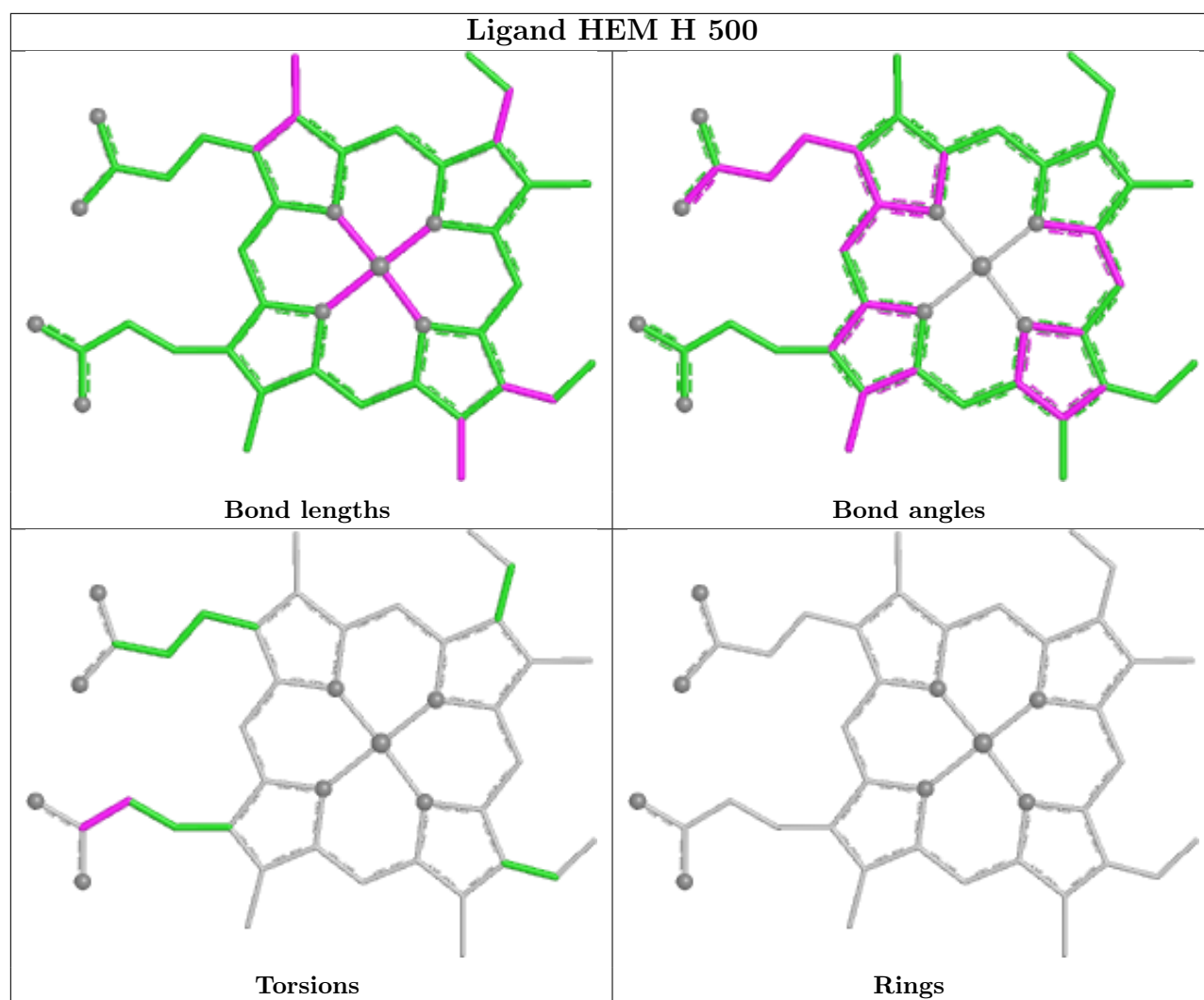


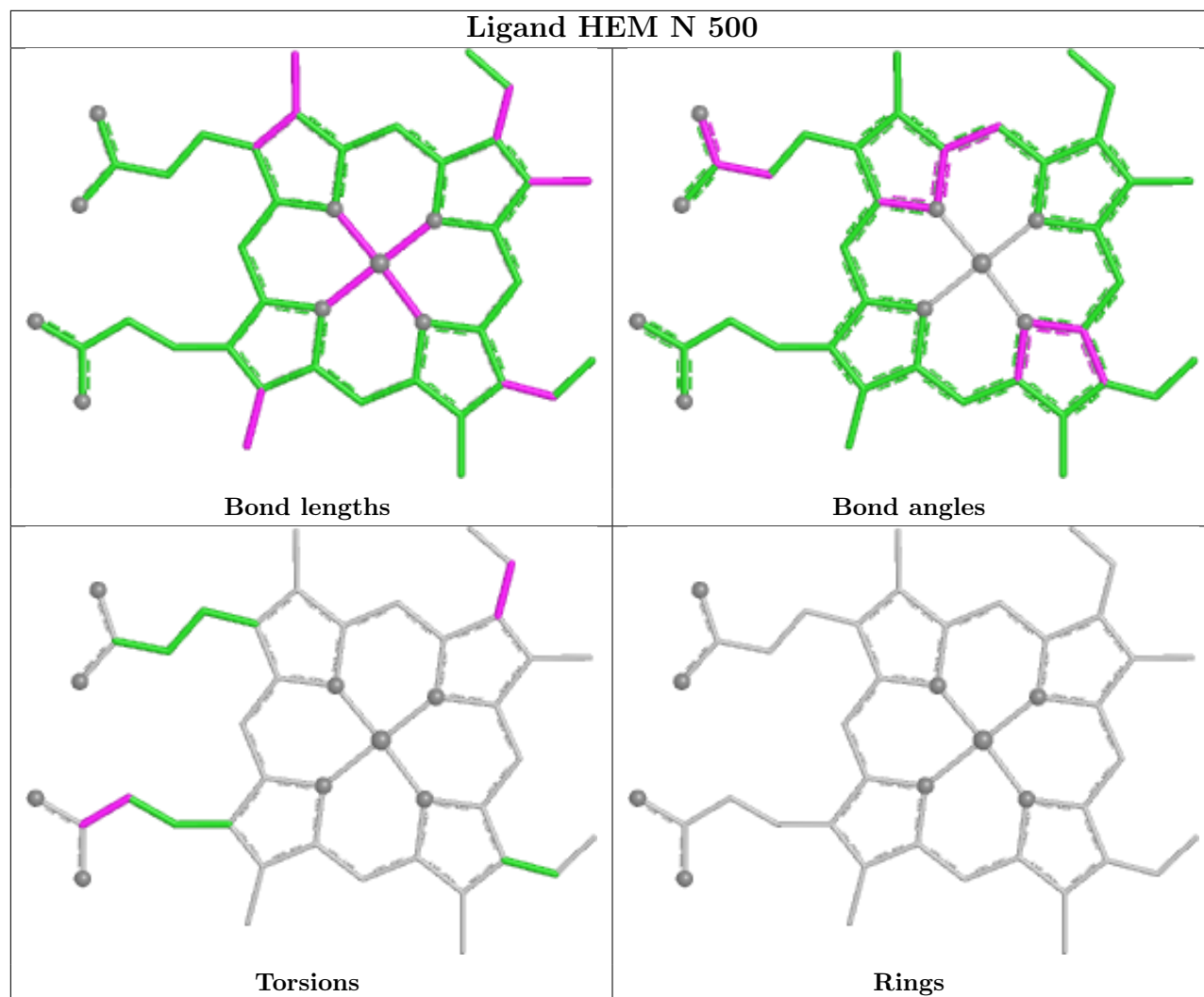


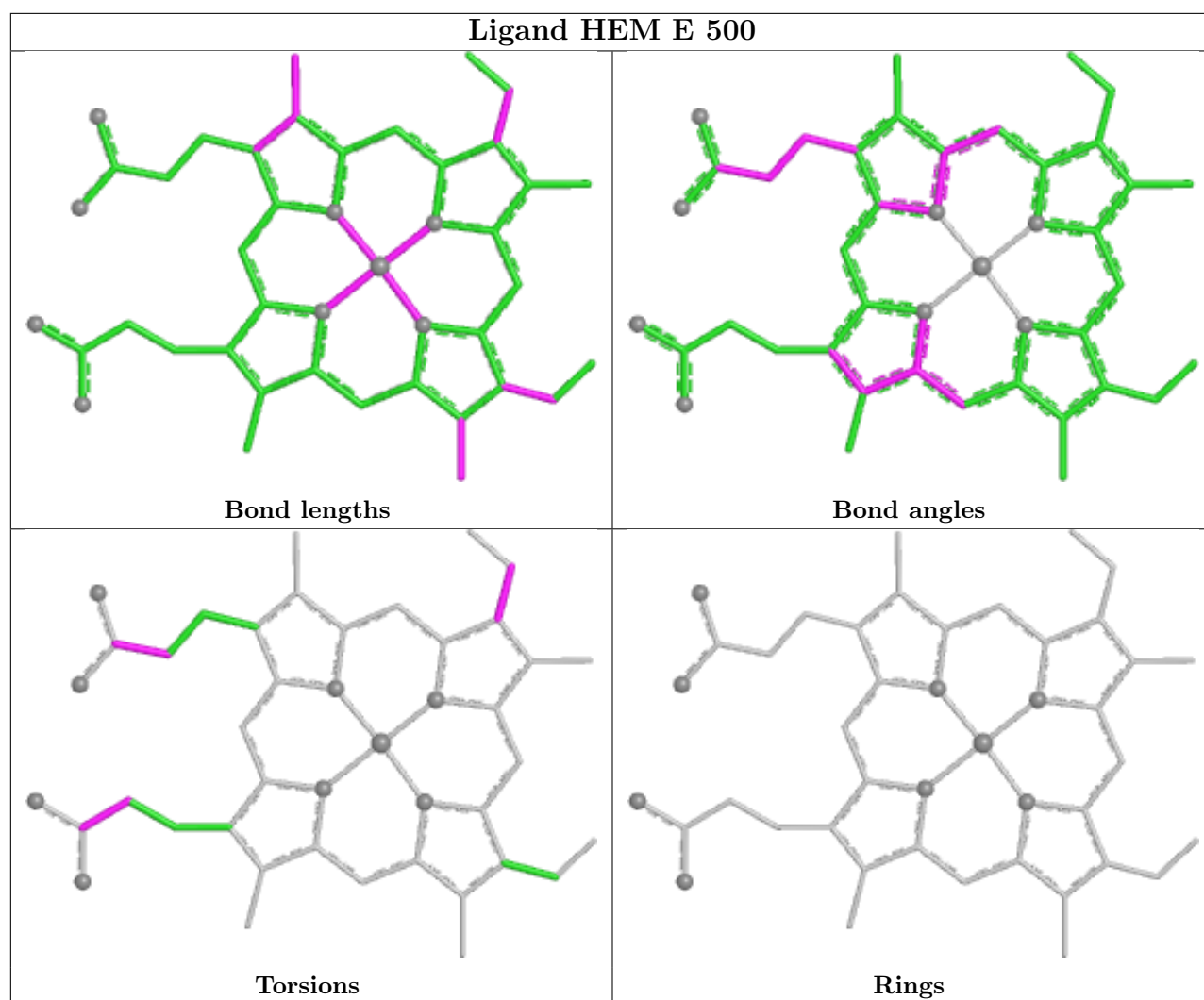


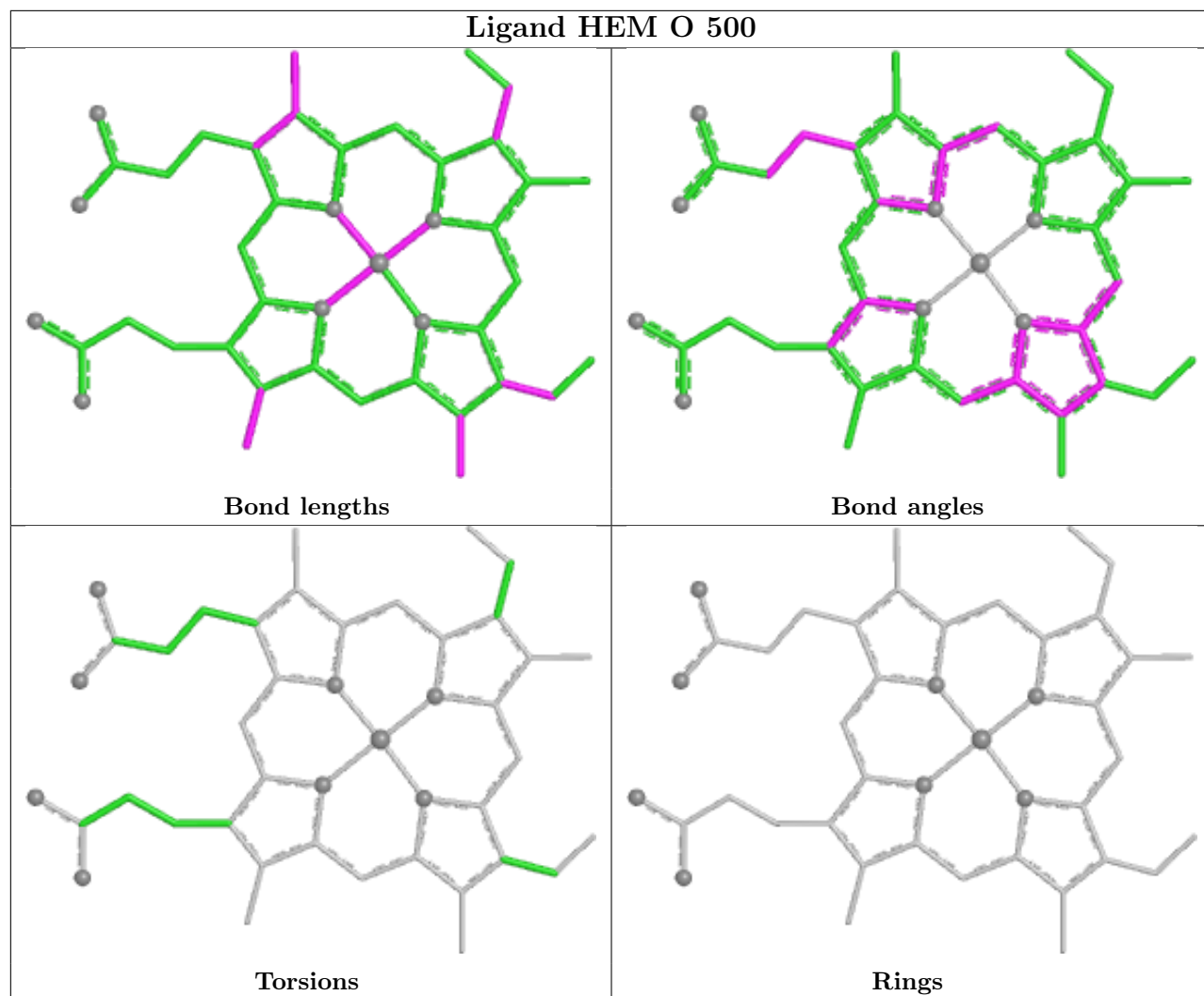


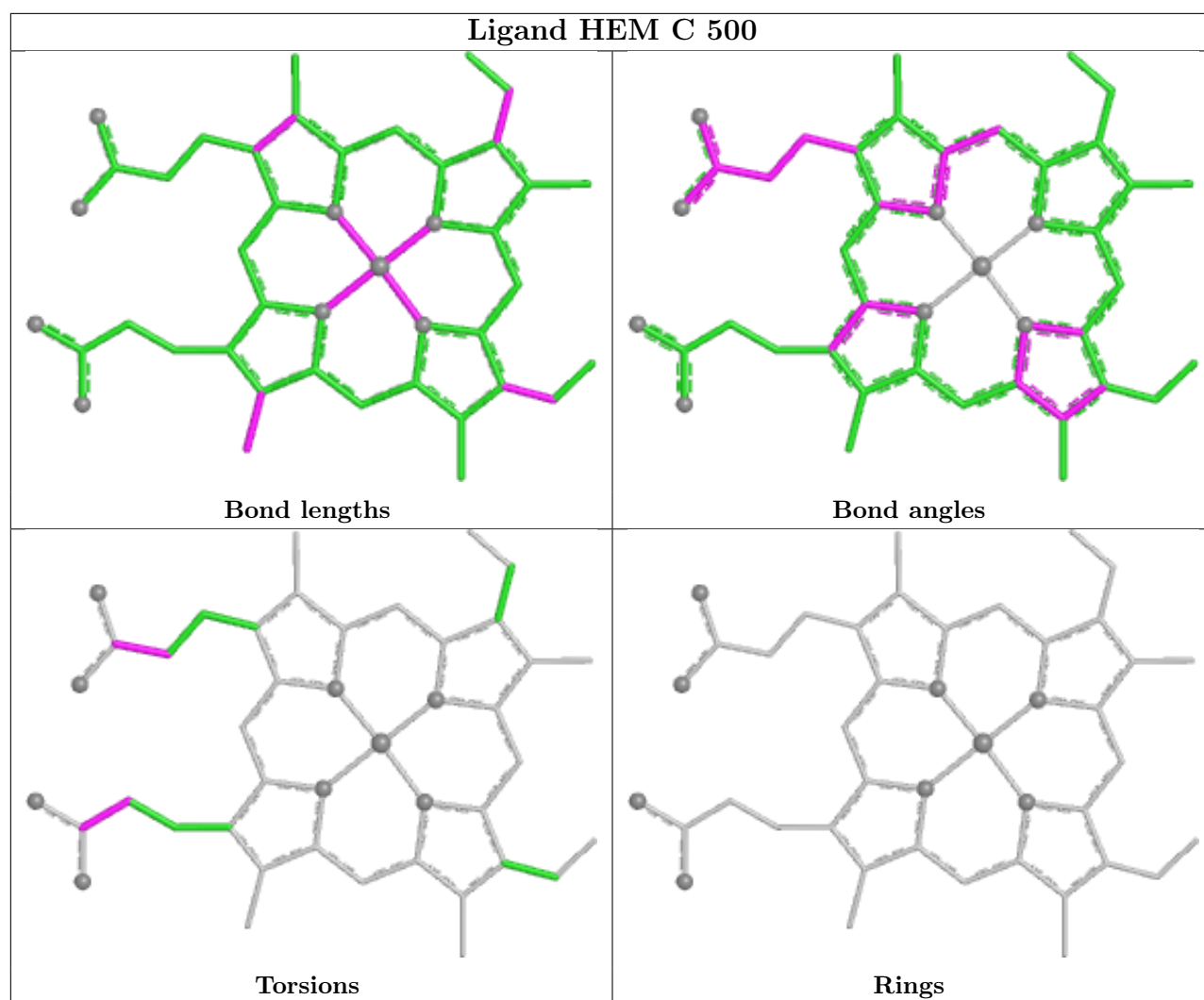


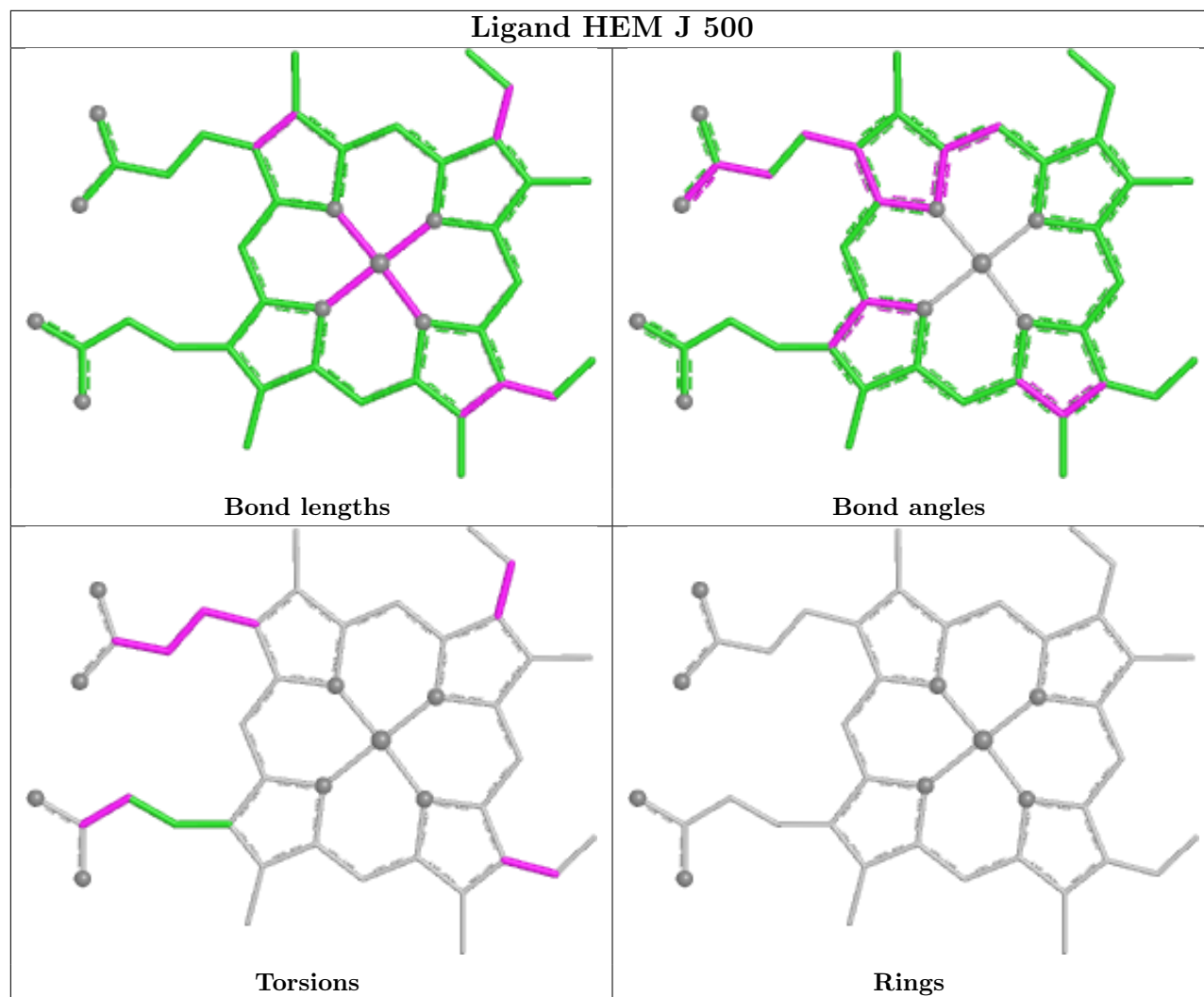




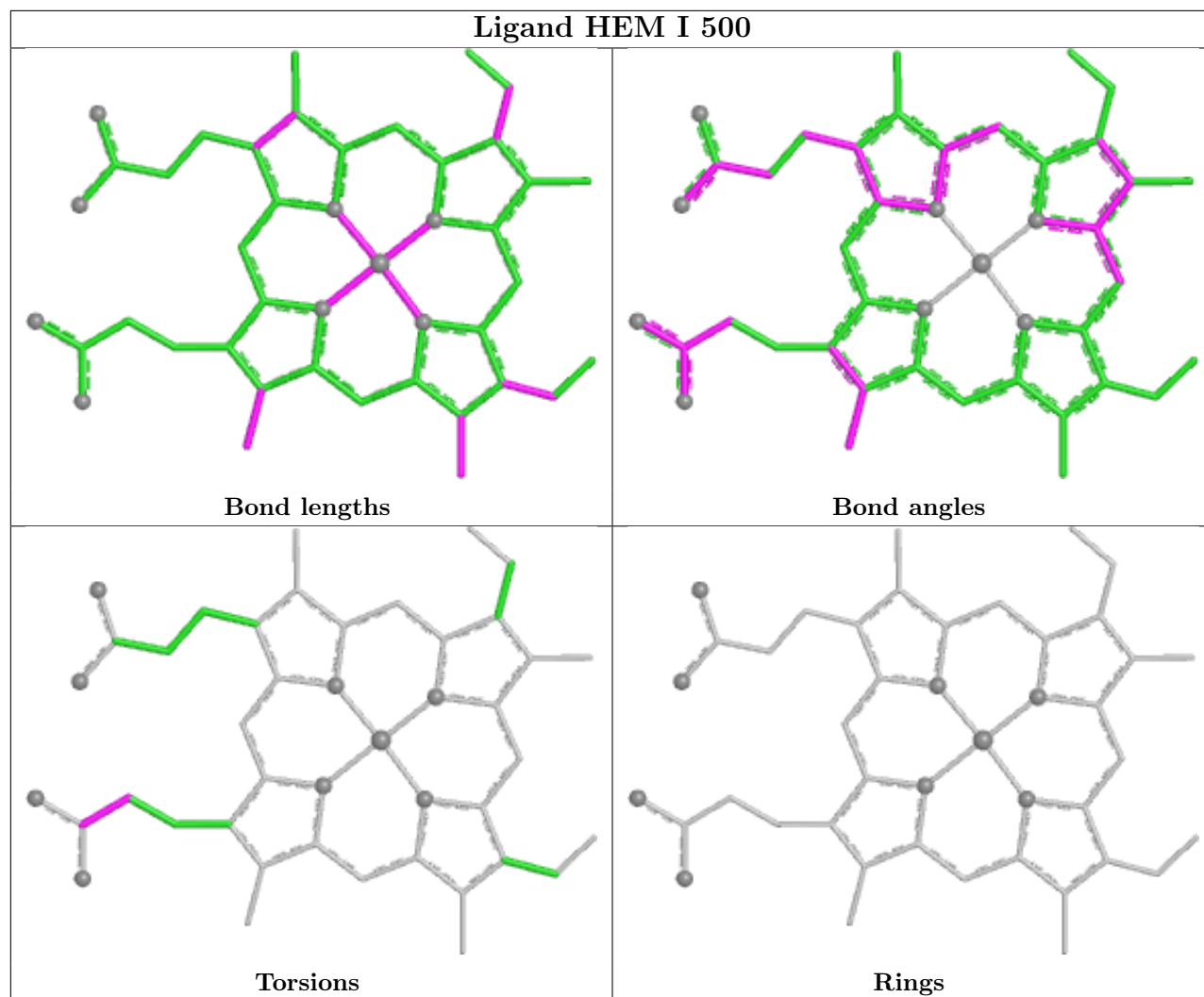


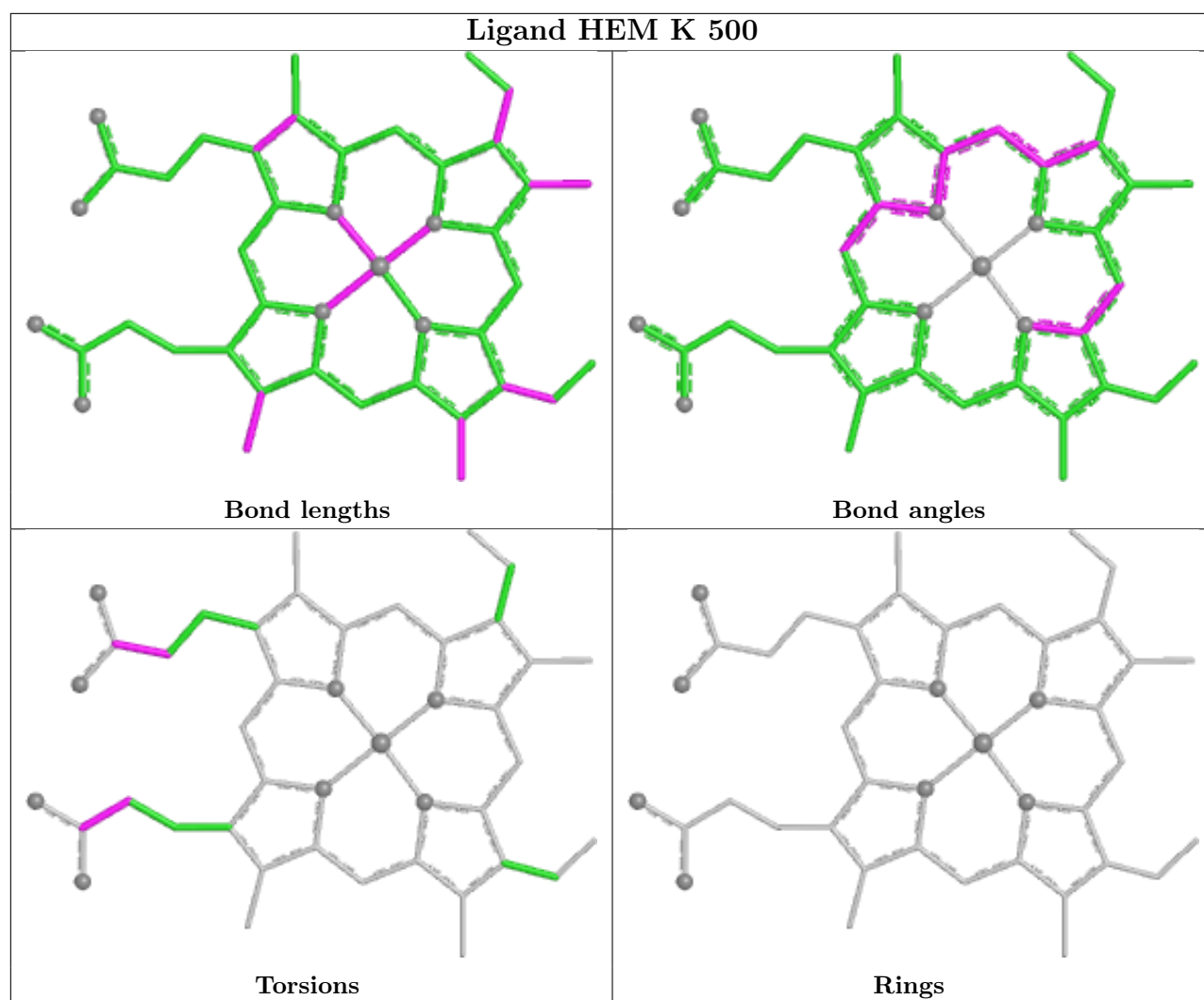






Ligand HEM I 500





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	261/281 (92%)	-0.30	0  	22, 41, 65, 121	1 (0%)
1	B	266/281 (94%)	-0.22	0  	30, 43, 70, 102	0
1	C	255/281 (90%)	-0.15	1 (0%)  	29, 43, 70, 101	0
1	D	259/281 (92%)	-0.16	2 (0%)  	27, 40, 64, 92	0
1	E	256/281 (91%)	-0.43	0  	26, 42, 70, 120	0
1	F	260/281 (92%)	-0.39	3 (1%)  	29, 44, 80, 106	0
1	G	259/281 (92%)	-0.27	1 (0%)  	29, 45, 76, 106	0
1	H	259/281 (92%)	-0.47	0  	26, 41, 63, 92	2 (0%)
1	I	259/281 (92%)	-0.36	0  	29, 44, 68, 83	0
1	J	257/281 (91%)	-0.30	2 (0%)  	28, 43, 71, 109	0
1	K	255/281 (90%)	-0.31	0  	23, 41, 66, 99	1 (0%)
1	L	260/281 (92%)	-0.33	0  	28, 43, 66, 91	0
1	M	255/281 (90%)	-0.39	3 (1%)  	24, 42, 70, 97	1 (0%)
1	N	260/281 (92%)	-0.26	2 (0%)  	16, 44, 74, 105	1 (0%)
1	O	257/281 (91%)	-0.24	1 (0%)  	28, 44, 74, 116	0
1	P	259/281 (92%)	-0.46	0  	27, 43, 65, 93	0
All	All	4137/4496 (92%)	-0.32	15 (0%)  	16, 43, 70, 121	6 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	37	PHE	4.1
1	O	268	LYS	2.9
1	C	167	ALA	2.7
1	D	140	SER	2.7
1	J	273	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	J	267	PHE	2.5
1	M	267	PHE	2.4
1	G	271	THR	2.2
1	M	275	GLU	2.2
1	D	41	MET	2.1
1	F	139	ALA	2.1
1	M	40	ASP	2.1
1	N	139	ALA	2.1
1	F	35	MET	2.0
1	N	40	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	HEM	O	500	43/43	0.96	0.08	48,58,68,80	0
2	HEM	G	500	43/43	0.97	0.07	43,52,63,70	0
2	HEM	I	500	43/43	0.97	0.07	24,37,57,60	0
2	HEM	N	500	43/43	0.97	0.08	37,56,65,74	0
2	HEM	F	500	43/43	0.97	0.07	39,47,58,74	0
2	HEM	A	500	43/43	0.98	0.06	18,28,39,57	0
2	HEM	B	500	43/43	0.98	0.06	32,43,56,62	0
2	HEM	H	500	43/43	0.98	0.06	16,29,37,43	0
2	HEM	C	500	43/43	0.98	0.06	28,42,62,68	0
2	HEM	J	500	43/43	0.98	0.06	27,42,57,67	0
2	HEM	K	500	43/43	0.98	0.06	28,43,61,71	0
2	HEM	L	500	43/43	0.98	0.06	20,34,53,63	0
2	HEM	M	500	43/43	0.98	0.06	25,37,48,52	0

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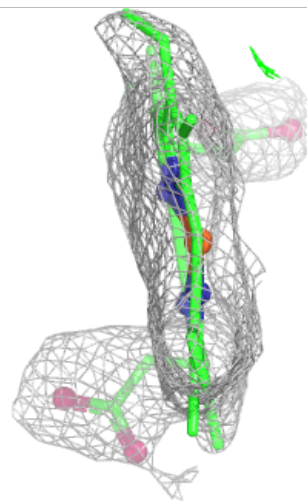
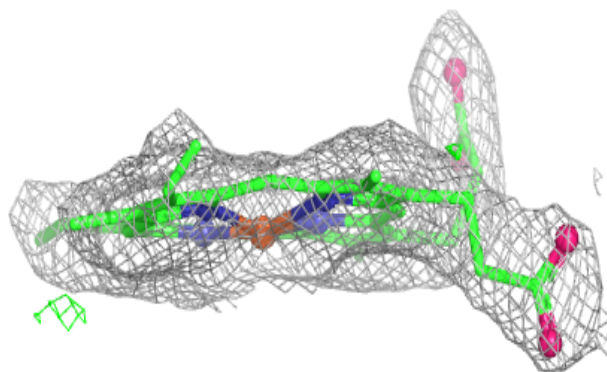
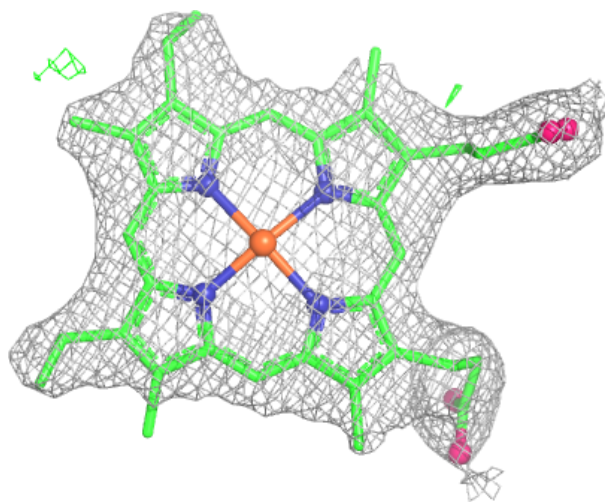
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	HEM	D	500	43/43	0.98	0.05	18,29,37,44	0
2	HEM	E	500	43/43	0.98	0.06	21,32,48,58	0
2	HEM	P	500	43/43	0.98	0.05	20,31,42,54	0

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.

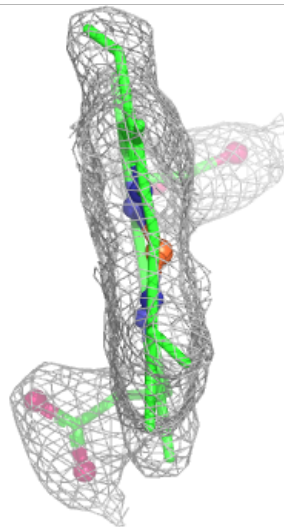
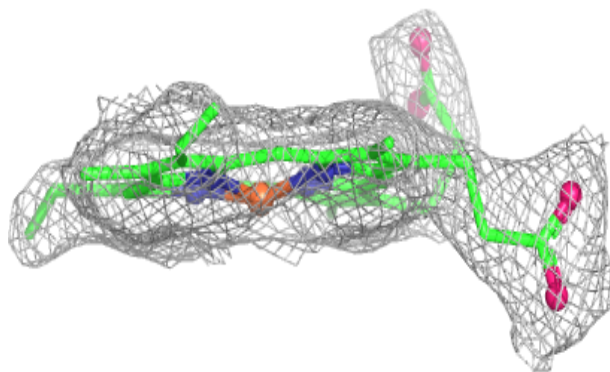
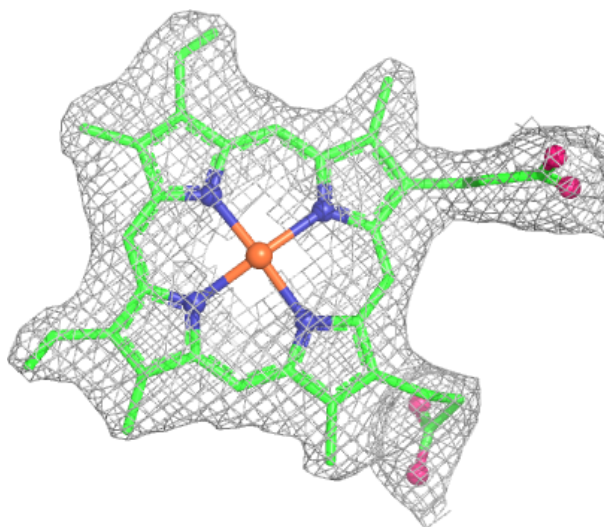
Electron density around HEM O 500:

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



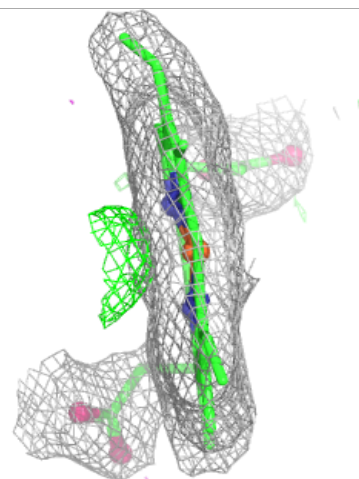
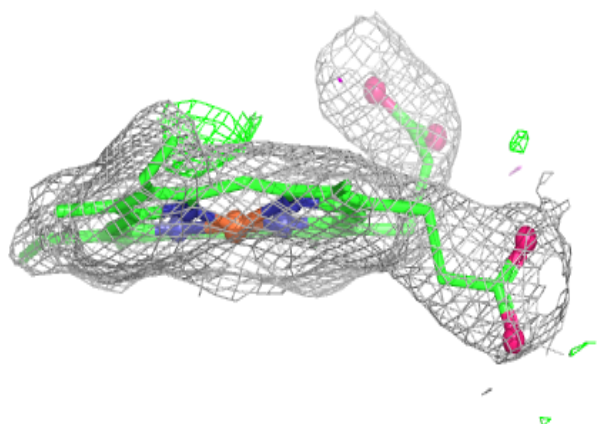
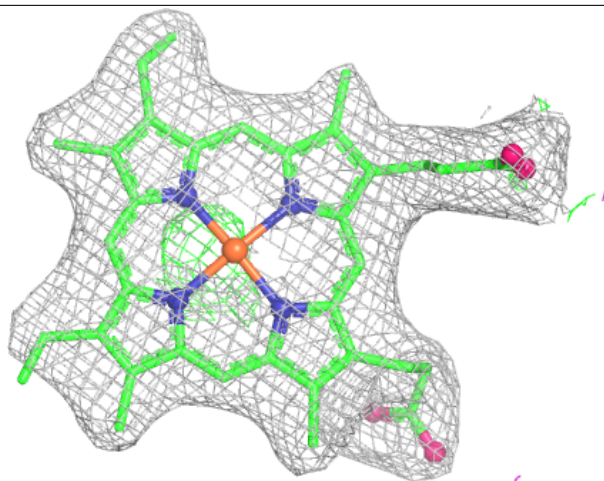
Electron density around HEM G 500:

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and green (positive)



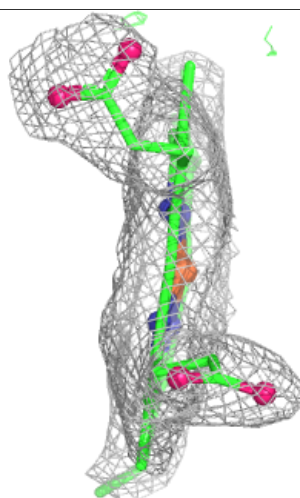
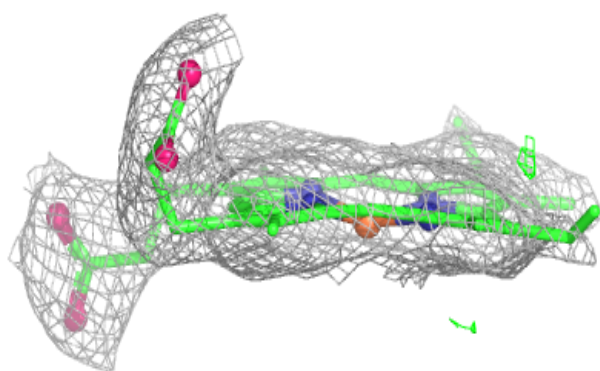
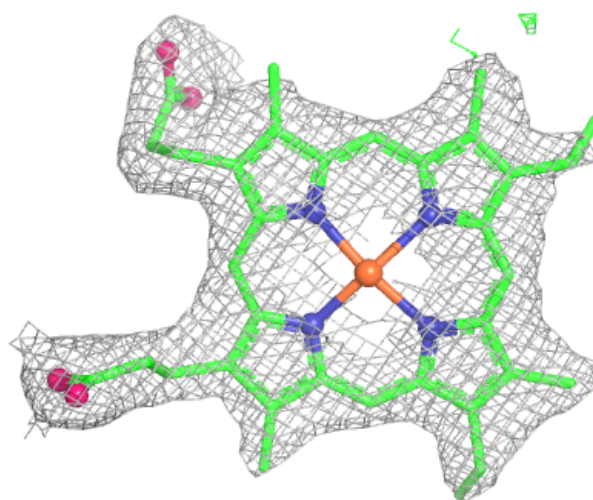
Electron density around HEM I 500:

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



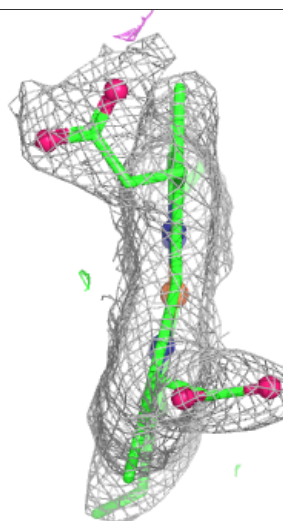
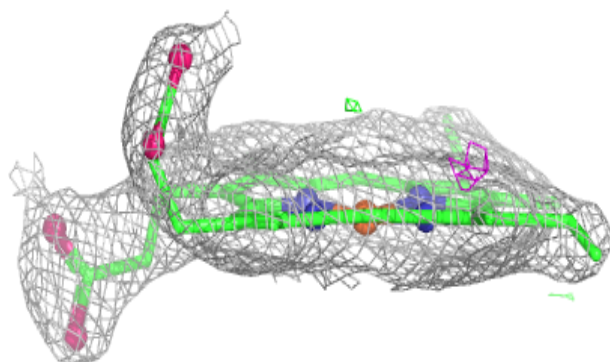
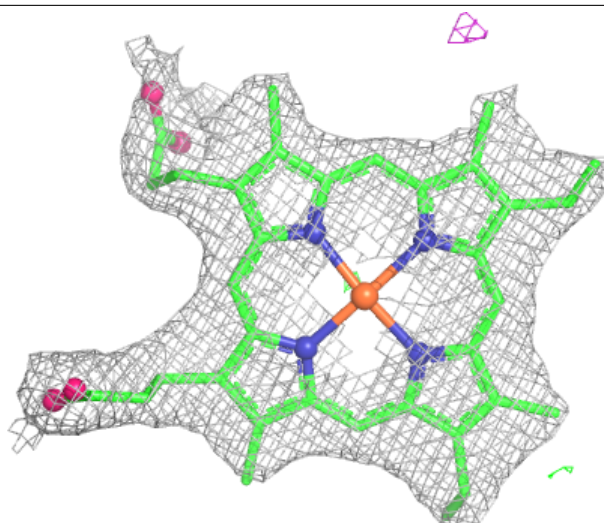
Electron density around HEM N 500:

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and green (positive)



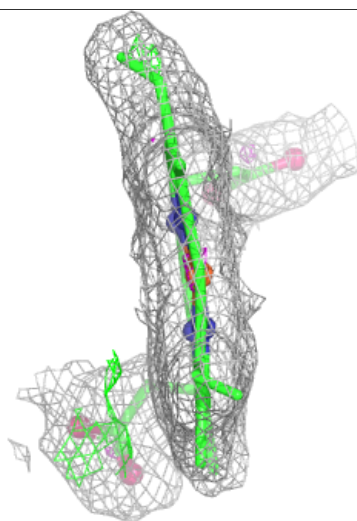
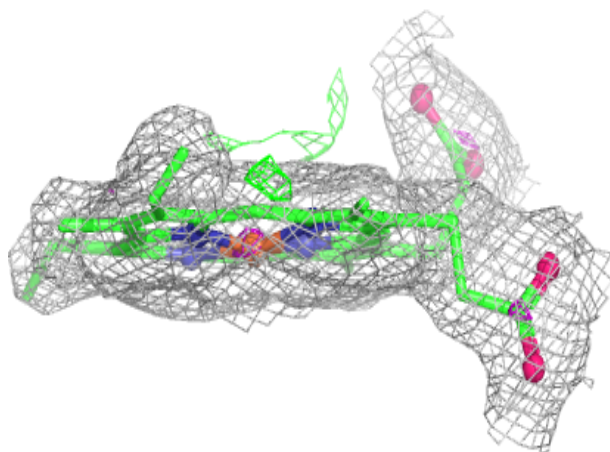
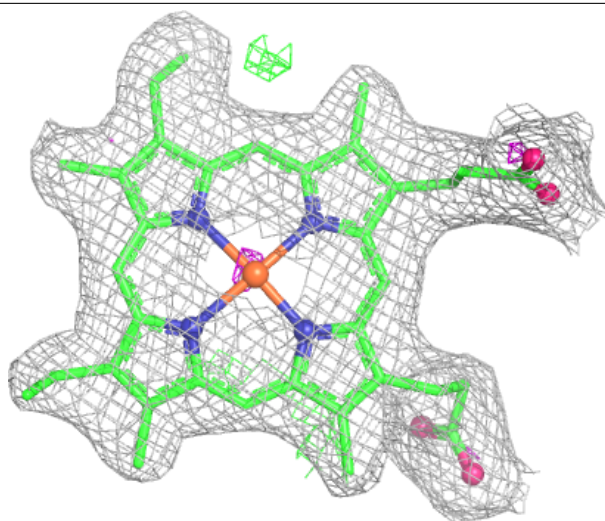
Electron density around HEM F 500:

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



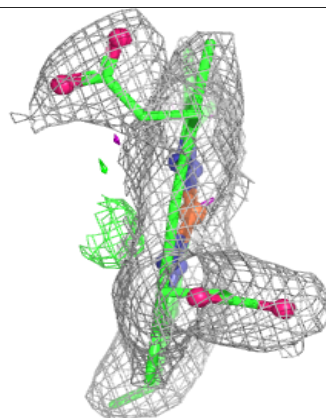
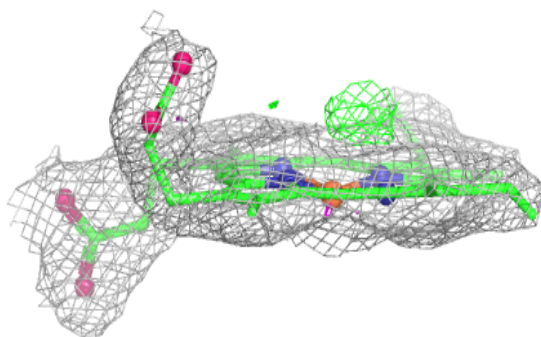
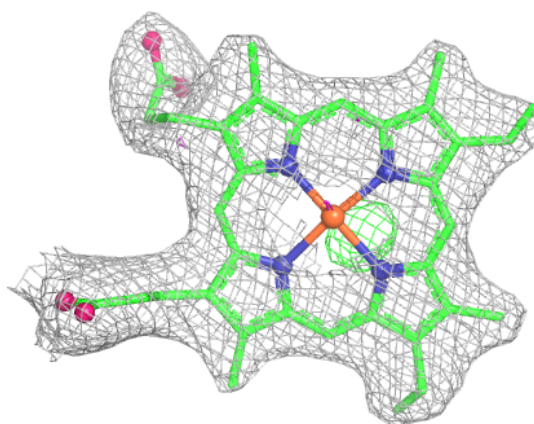
Electron density around HEM A 500:

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



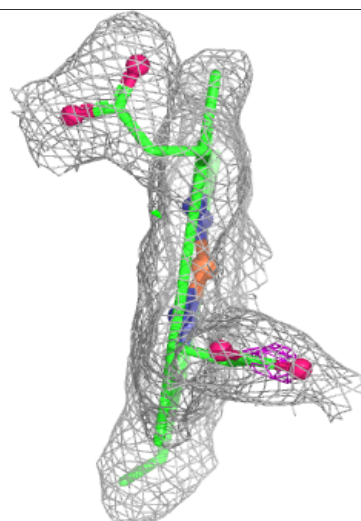
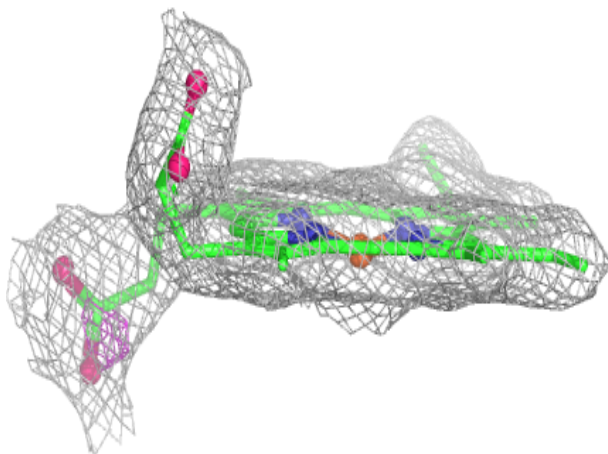
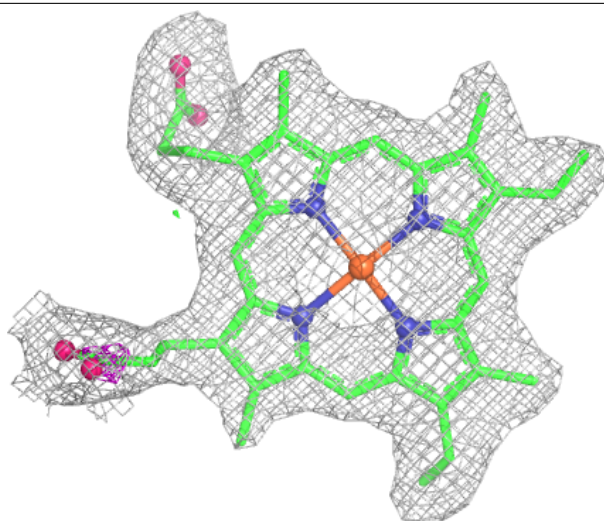
Electron density around HEM B 500:

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



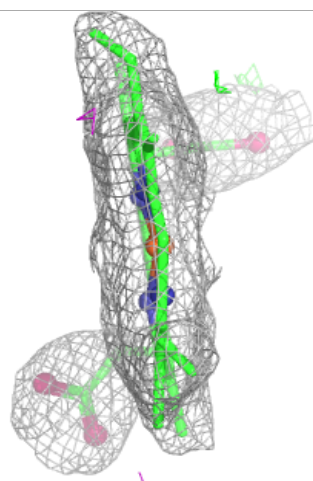
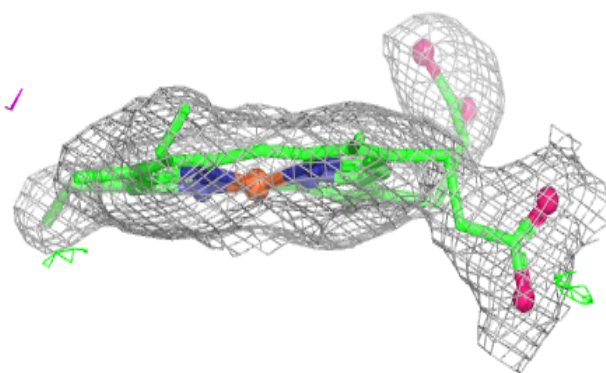
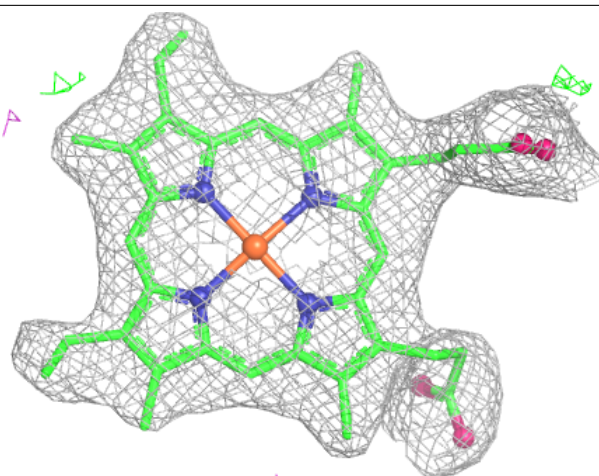
Electron density around HEM H 500:

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



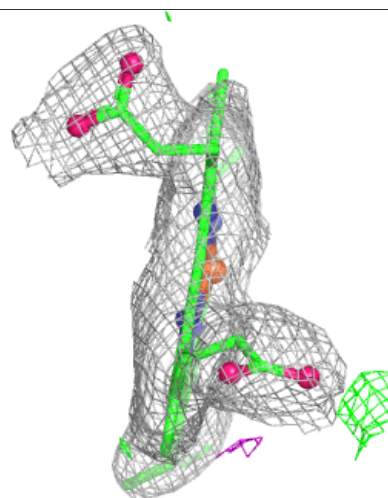
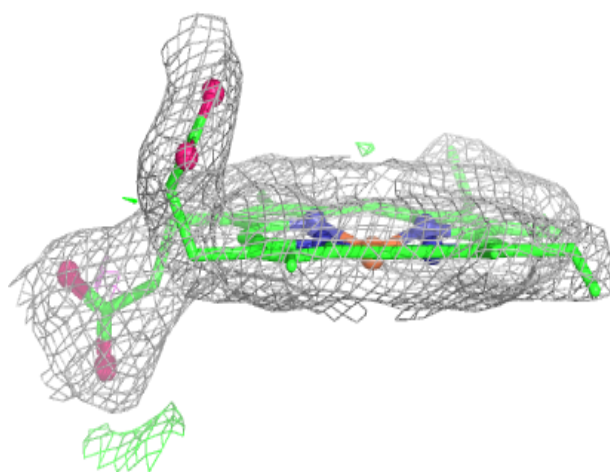
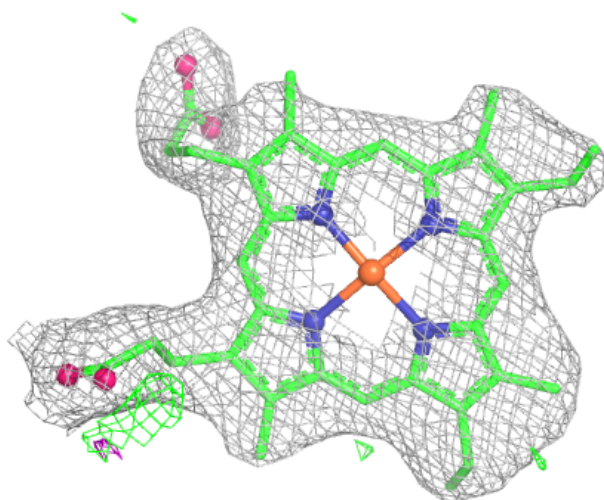
Electron density around HEM C 500:

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and green (positive)



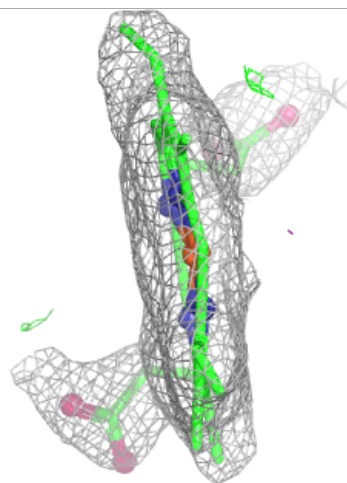
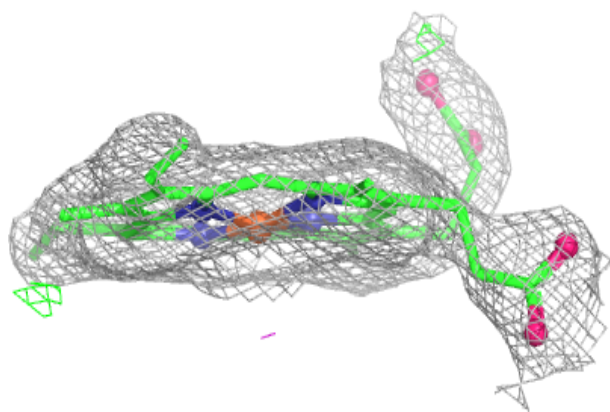
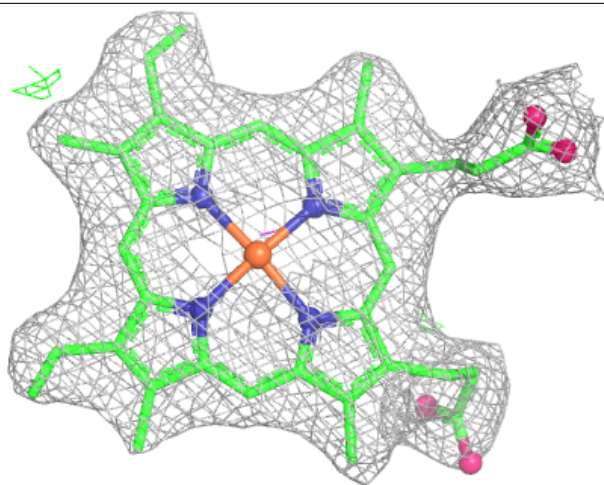
Electron density around HEM J 500:

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and green (positive)



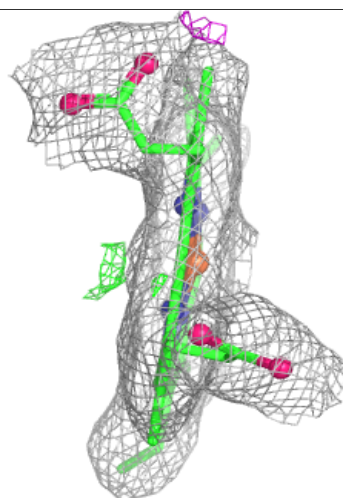
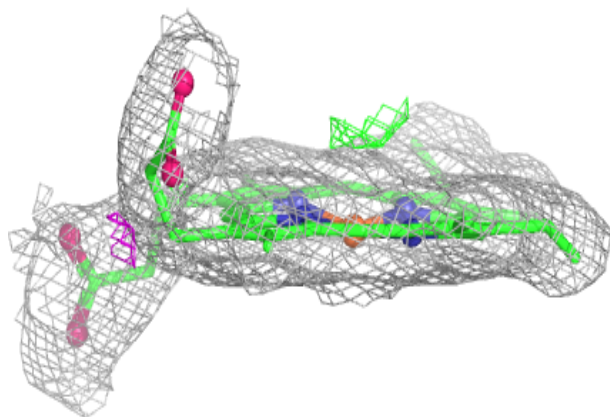
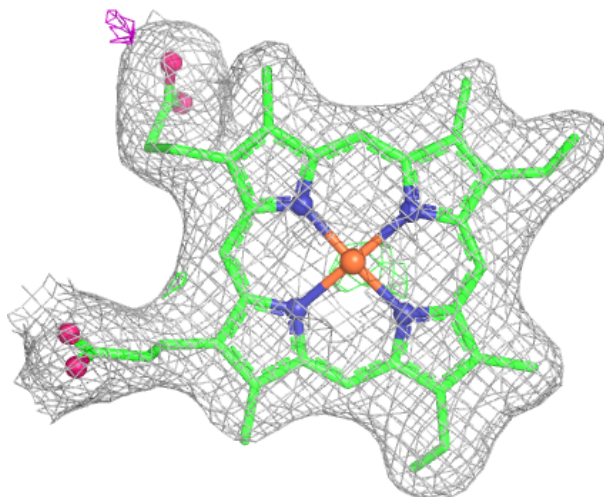
Electron density around HEM K 500:

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and green (positive)



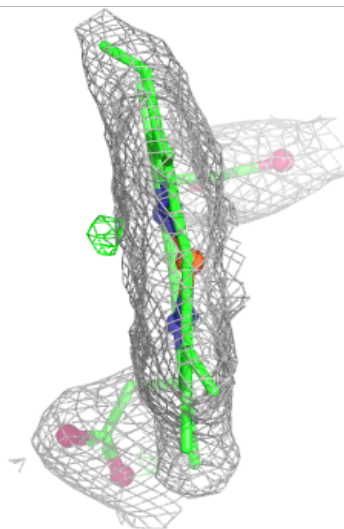
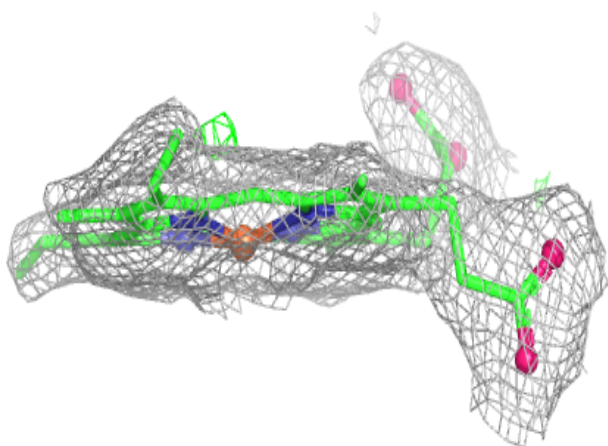
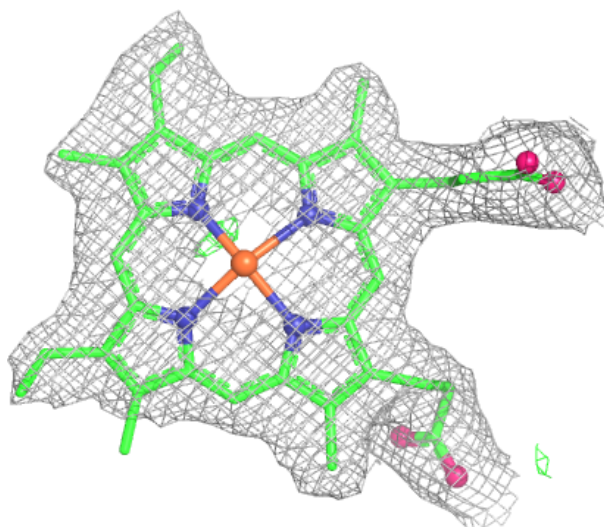
Electron density around HEM L 500:

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and green (positive)



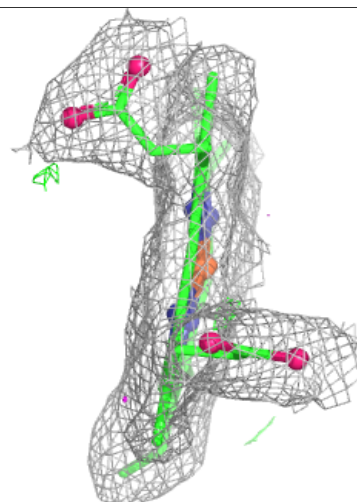
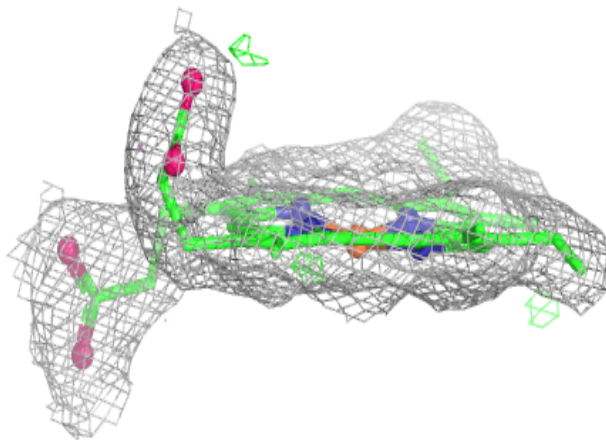
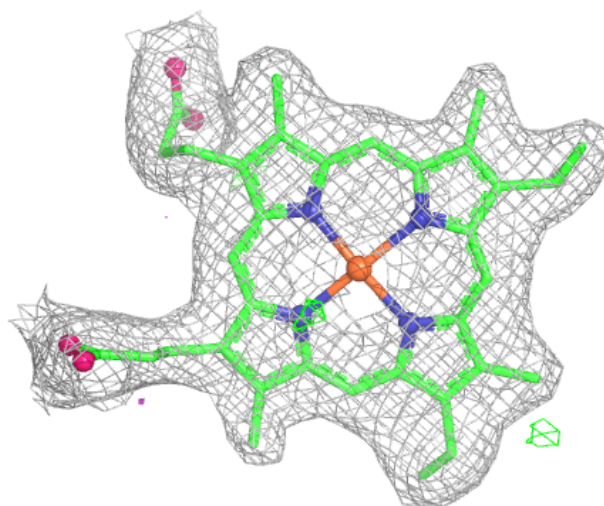
Electron density around HEM M 500:

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



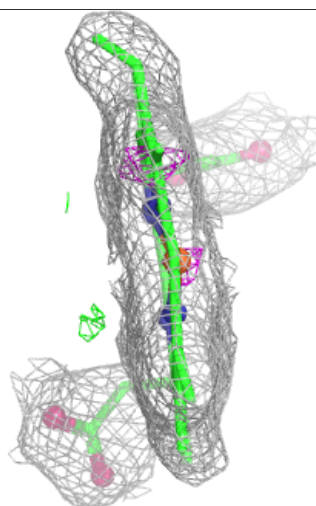
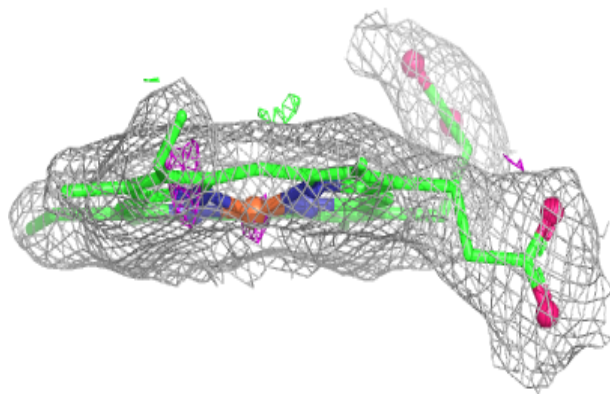
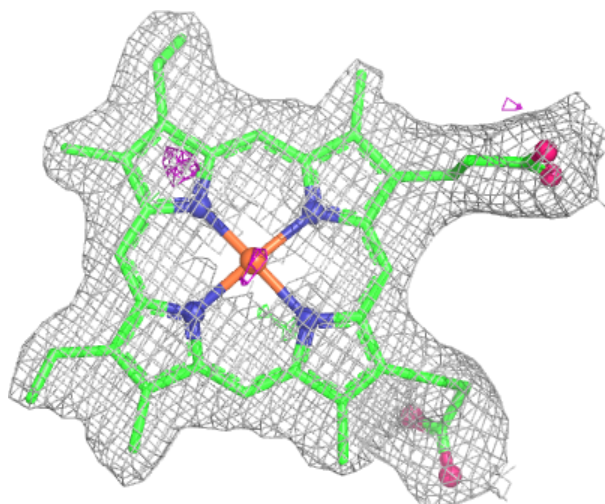
Electron density around HEM D 500:

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and green (positive)



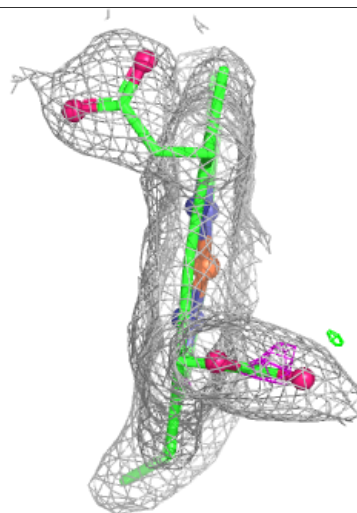
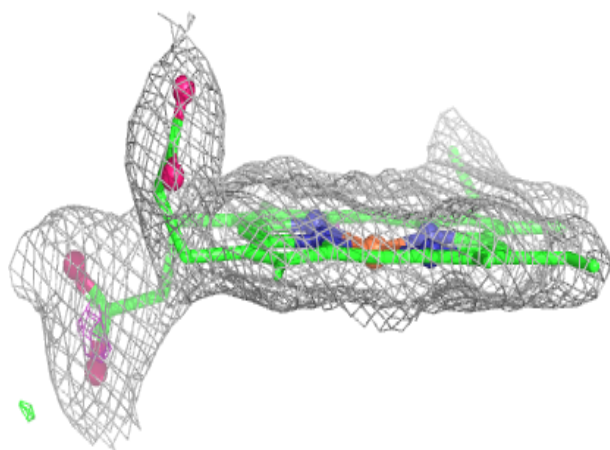
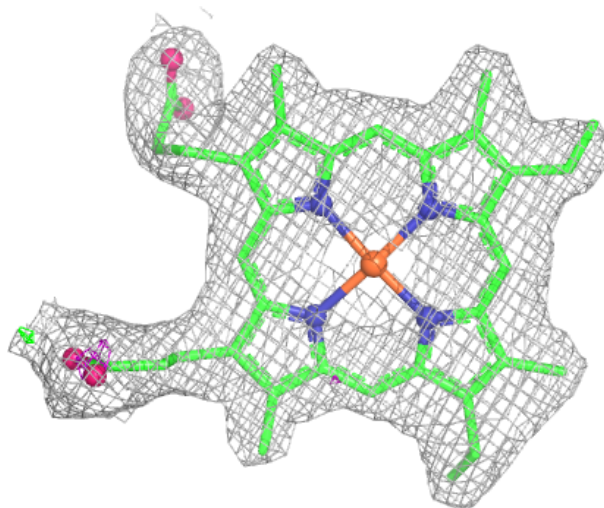
Electron density around HEM E 500:

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



Electron density around HEM P 500:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.