



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 9, 2021 – 08:48 AM GMT

PDB ID : 6TV9
Title : Heme d1 biosynthesis associated Protein NirF in complex with dihydro-heme d1
Authors : Kluenemann, T.; Layer, G.; Blankenfeldt, W.
Deposited on : 2020-01-09
Resolution : 1.89 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.16
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.16

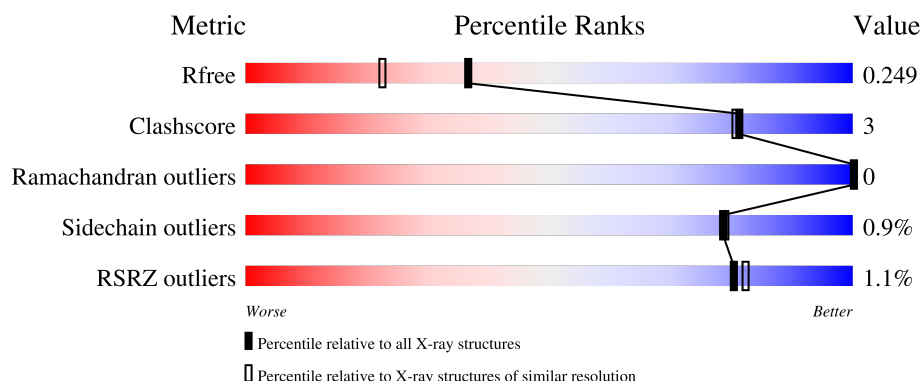
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	378	<div> <div>%</div> <div>95%</div> <div>..</div> </div>
1	B	378	<div> <div>3%</div> <div>89%</div> <div>10%</div> <div>.</div> </div>
1	C	378	<div> <div>94%</div> <div>5%</div> <div>.</div> </div>
1	D	378	<div> <div>%</div> <div>92%</div> <div>6%</div> <div>.</div> </div>
1	E	378	<div> <div>%</div> <div>91%</div> <div>7%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	378	<div><div></div><div>94%</div><div><div></div><div></div></div><div>• •</div></div>
1	G	378	<div><div>%</div><div><div></div><div></div></div><div>94%</div><div>5% •</div></div>
1	H	378	<div><div>2%</div><div><div></div><div></div></div><div>94%</div><div>• •</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 48716 atoms, of which 23314 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 Protein NirF,Protein NirF.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	372	Total	C	H	N	O	S	0	5	0
			5834	1854	2896	535	542	7			
1	B	372	Total	C	H	N	O	S	0	1	0
			5781	1842	2862	531	540	6			
1	C	372	Total	C	H	N	O	S	0	4	0
			5842	1857	2897	537	544	7			
1	D	372	Total	C	H	N	O	S	0	3	0
			5828	1853	2890	536	542	7			
1	E	372	Total	C	H	N	O	S	0	2	0
			5796	1845	2871	532	542	6			
1	F	372	Total	C	H	N	O	S	0	3	0
			5835	1854	2894	539	542	6			
1	G	372	Total	C	H	N	O	S	0	4	0
			5845	1857	2901	539	542	6			
1	H	372	Total	C	H	N	O	S	0	2	0
			5806	1847	2879	534	540	6			

There are 24 discrepancies between the modelled and reference sequences:

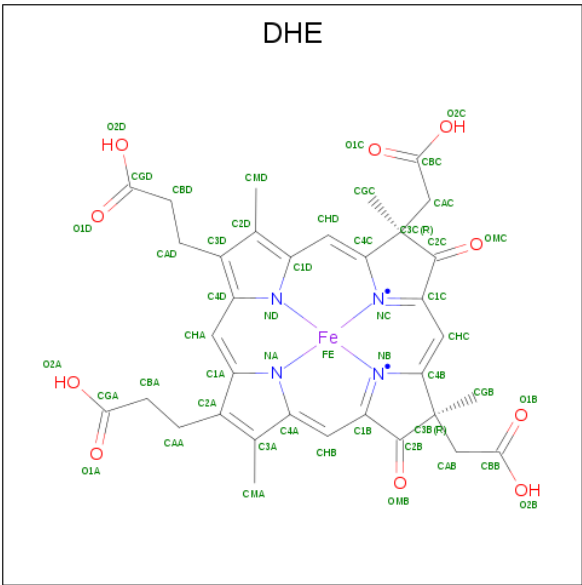
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	HIS	-	expression tag	UNP Q51480
A	2	MET	-	expression tag	UNP Q51480
A	3	MET	-	expression tag	UNP Q51480
B	1	HIS	-	expression tag	UNP Q51480
B	2	MET	-	expression tag	UNP Q51480
B	3	MET	-	expression tag	UNP Q51480
C	1	HIS	-	expression tag	UNP Q51480
C	2	MET	-	expression tag	UNP Q51480
C	3	MET	-	expression tag	UNP Q51480
D	1	HIS	-	expression tag	UNP Q51480
D	2	MET	-	expression tag	UNP Q51480
D	3	MET	-	expression tag	UNP Q51480
E	1	HIS	-	expression tag	UNP Q51480

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Chain	Residue	Modelled	Actual	Comment	Reference
E	2	MET	-	expression tag	UNP Q51480
E	3	MET	-	expression tag	UNP Q51480
F	1	HIS	-	expression tag	UNP Q51480
F	2	MET	-	expression tag	UNP Q51480
F	3	MET	-	expression tag	UNP Q51480
G	1	HIS	-	expression tag	UNP Q51480
G	2	MET	-	expression tag	UNP Q51480
G	3	MET	-	expression tag	UNP Q51480
H	1	HIS	-	expression tag	UNP Q51480
H	2	MET	-	expression tag	UNP Q51480
H	3	MET	-	expression tag	UNP Q51480

- Molecule 2 is HEME D (three-letter code: DHE) (formula: C₃₄H₃₂FeN₄O₁₀) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 77	C 34	Fe 1	H 28	N 4	O 10	0	0
2	B	1	Total 77	C 34	Fe 1	H 28	N 4	O 10	0	0
2	C	1	Total 77	C 34	Fe 1	H 28	N 4	O 10	0	0
2	D	1	Total 77	C 34	Fe 1	H 28	N 4	O 10	0	0
2	E	1	Total 77	C 34	Fe 1	H 28	N 4	O 10	0	0

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	F	1	Total	C	Fe	H	N	O	0	0
			77	34	1	28	4	10		
2	G	1	Total	C	Fe	H	N	O	0	0
			77	34	1	28	4	10		
2	H	1	Total	C	Fe	H	N	O	0	0
			77	34	1	28	4	10		

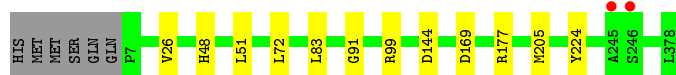
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	195	Total	O	0	0
			195	195		
3	B	117	Total	O	0	0
			117	117		
3	C	264	Total	O	0	0
			264	264		
3	D	242	Total	O	0	0
			242	242		
3	E	151	Total	O	0	0
			151	151		
3	F	208	Total	O	0	0
			208	208		
3	G	222	Total	O	0	0
			222	222		
3	H	134	Total	O	0	0
			134	134		

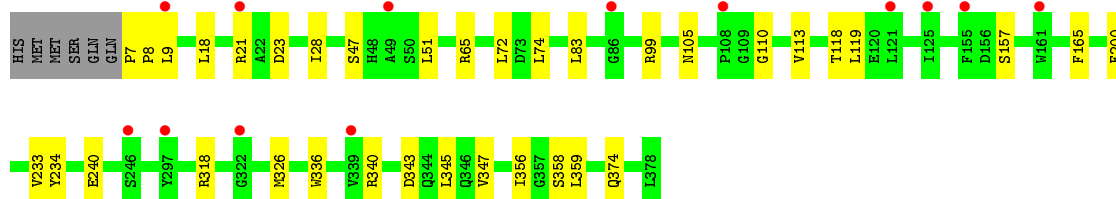
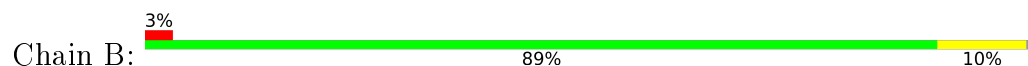
3 Residue-property plots [i](#)

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: Protein NirF,Protein NirF



- Molecule 1: Protein NirF,Protein NirF



- Molecule 1: Protein NirF,Protein NirF

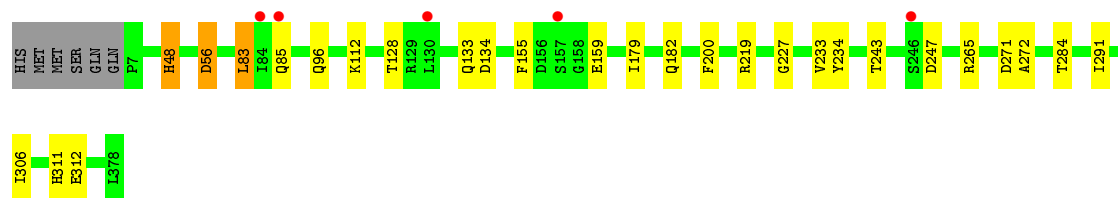


- Molecule 1: Protein NirF,Protein NirF



- Molecule 1: Protein NirF,Protein NirF





- Molecule 1: Protein NirF,Protein NirF

Chain F: 94%



- Molecule 1: Protein NirF,Protein NirF

Chain G: 94% 5%



- Molecule 1: Protein NirF,Protein NirF

Chain H: 94% 2%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	101.20Å 149.44Å 110.17Å 90.00° 98.48° 90.00°	Depositor
Resolution (Å)	100.09 – 1.89 100.09 – 1.89	Depositor EDS
% Data completeness (in resolution range)	58.3 (100.09-1.89) 58.4 (100.09-1.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 1.90Å)	Xtriage
Refinement program	PHENIX dev 3742	Depositor
R, R_{free}	0.215 , 0.258 0.208 , 0.249	Depositor DCC
R_{free} test set	7424 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	18.0	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 41.4	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	0.94	EDS
Total number of atoms	48716	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.57 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.3174e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.44	0/3023	0.52	0/4096
1	B	0.40	0/2991	0.51	0/4054
1	C	0.51	0/3017	0.56	0/4088
1	D	0.47	0/3010	0.54	0/4078
1	E	0.42	0/2997	0.52	0/4062
1	F	0.51	0/3013	0.54	0/4082
1	G	0.49	0/3022	0.53	0/4096
1	H	0.43	0/3002	0.52	0/4068
All	All	0.46	0/24075	0.53	0/32624

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2938	2896	2888	10	0
1	B	2919	2862	2868	25	0
1	C	2945	2897	2894	17	0
1	D	2938	2890	2888	14	0
1	E	2925	2871	2872	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2941	2894	2892	12	0
1	G	2944	2901	2902	17	0
1	H	2927	2879	2881	8	0
2	A	49	28	28	3	0
2	B	49	28	28	2	0
2	C	49	28	28	1	0
2	D	49	28	28	0	0
2	E	49	28	28	3	0
2	F	49	28	28	2	0
2	G	49	28	28	2	0
2	H	49	28	28	3	0
3	A	195	0	0	4	3
3	B	117	0	0	7	0
3	C	264	0	0	4	1
3	D	242	0	0	5	0
3	E	151	0	0	4	1
3	F	208	0	0	5	2
3	G	222	0	0	8	0
3	H	134	0	0	3	1
All	All	25402	23314	23309	124	4

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 124 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:C:10[B]:ARG:NH1	3:C:501:HOH:O	2.13	0.80
1:H:355[B]:ARG:NH1	3:H:502:HOH:O	2.17	0.78
1:D:309:GLU:OE1	3:D:501:HOH:O	2.02	0.78
1:C:246:SER:HG	1:G:246:SER:HG	1.31	0.77
1:B:105:ASN:OD1	1:B:110:GLY:N	2.18	0.77

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:689:HOH:O	3:H:611:HOH:O[2_645]	2.04	0.16
3:A:680:HOH:O	3:F:683:HOH:O[1_655]	2.04	0.16
3:A:585:HOH:O	3:F:697:HOH:O[1_655]	2.11	0.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:676:HOH:O	3:E:547:HOH:O[1_455]	2.18	0.02

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	375/378 (99%)	365 (97%)	10 (3%)	0	100	100
1	B	371/378 (98%)	363 (98%)	8 (2%)	0	100	100
1	C	374/378 (99%)	363 (97%)	11 (3%)	0	100	100
1	D	373/378 (99%)	365 (98%)	8 (2%)	0	100	100
1	E	372/378 (98%)	357 (96%)	15 (4%)	0	100	100
1	F	373/378 (99%)	360 (96%)	13 (4%)	0	100	100
1	G	374/378 (99%)	364 (97%)	10 (3%)	0	100	100
1	H	372/378 (98%)	362 (97%)	10 (3%)	0	100	100
All	All	2984/3024 (99%)	2899 (97%)	85 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	311/312 (100%)	311 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	307/312 (98%)	305 (99%)	2 (1%)	84	84
1	C	310/312 (99%)	308 (99%)	2 (1%)	86	87
1	D	309/312 (99%)	305 (99%)	4 (1%)	69	68
1	E	308/312 (99%)	304 (99%)	4 (1%)	69	68
1	F	309/312 (99%)	306 (99%)	3 (1%)	76	76
1	G	310/312 (99%)	309 (100%)	1 (0%)	92	93
1	H	308/312 (99%)	303 (98%)	5 (2%)	62	60
All	All	2472/2496 (99%)	2451 (99%)	21 (1%)	78	82

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	56	ASP
1	E	134	ASP
1	H	65	ARG
1	E	48	HIS
1	H	81	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	375	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

8 ligands are modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

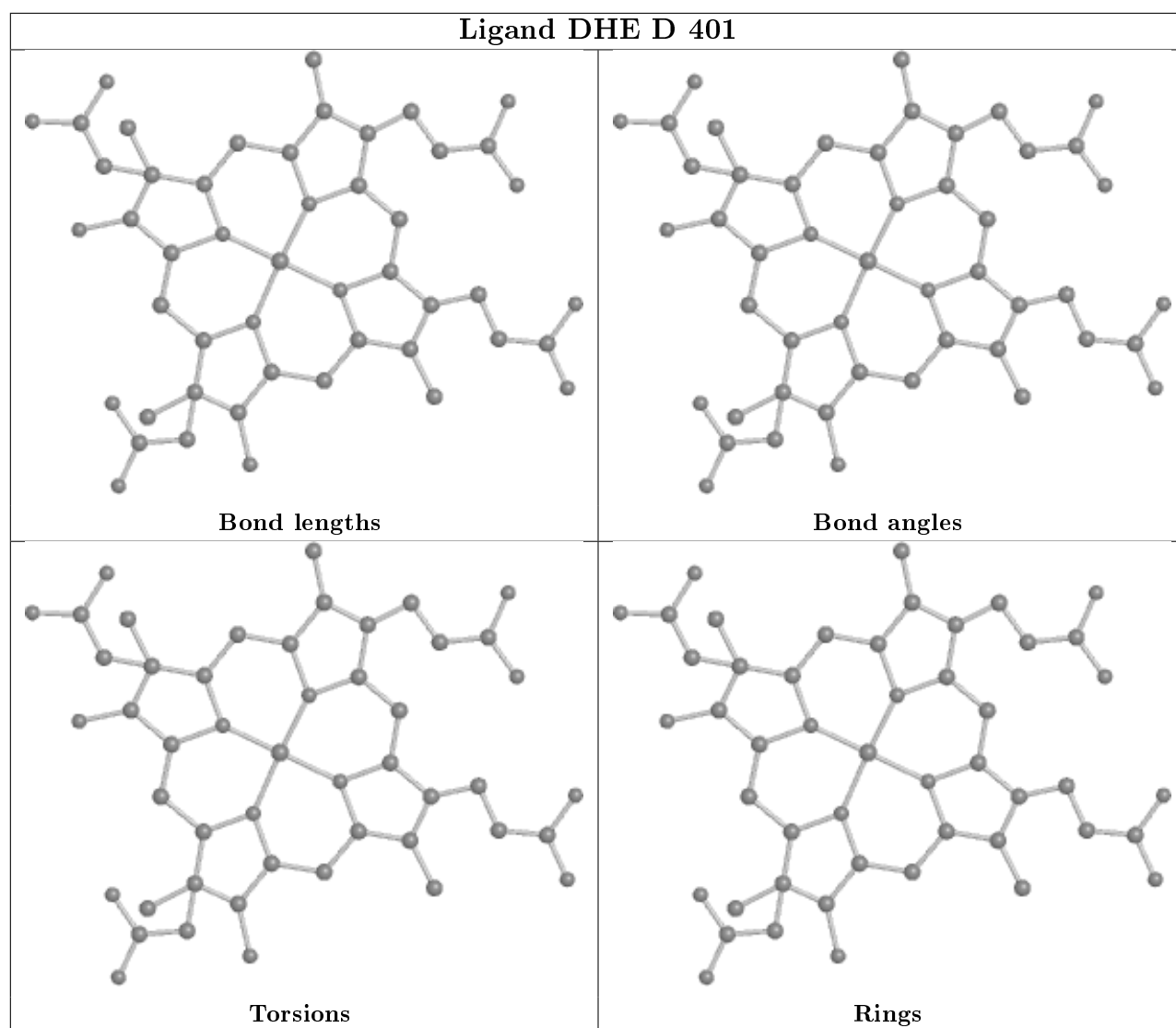
There are no chirality outliers.

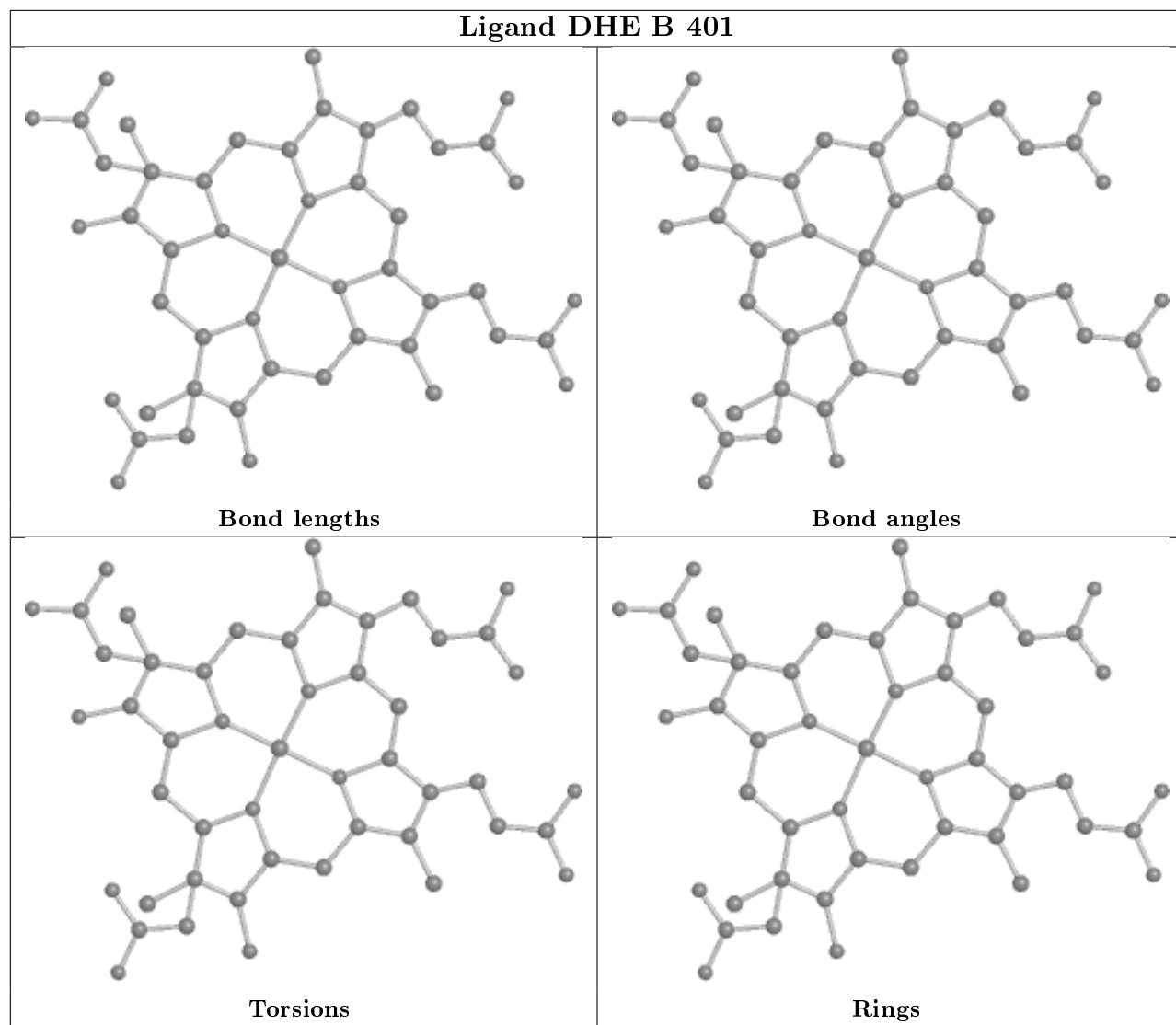
There are no torsion outliers.

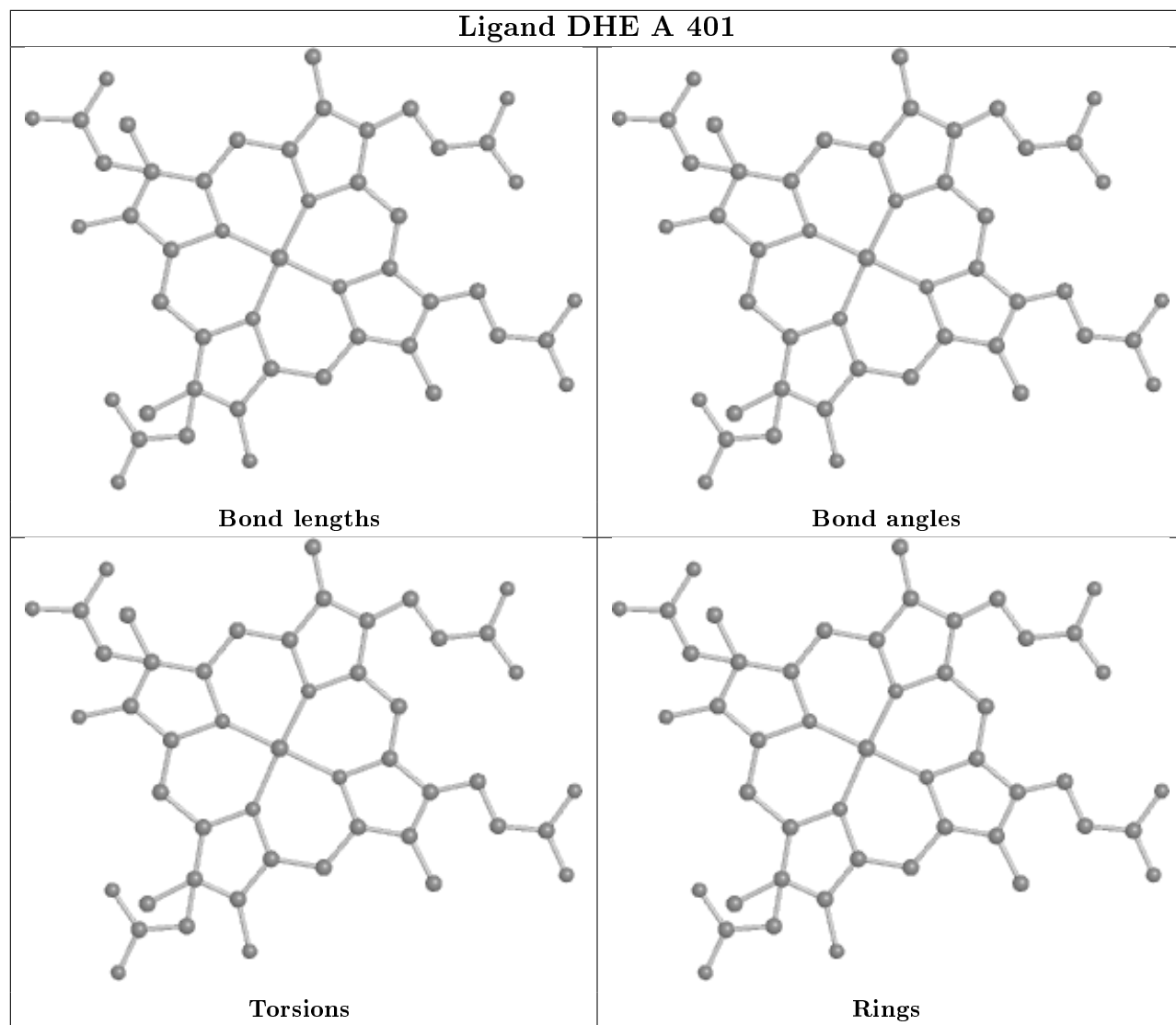
There are no ring outliers.

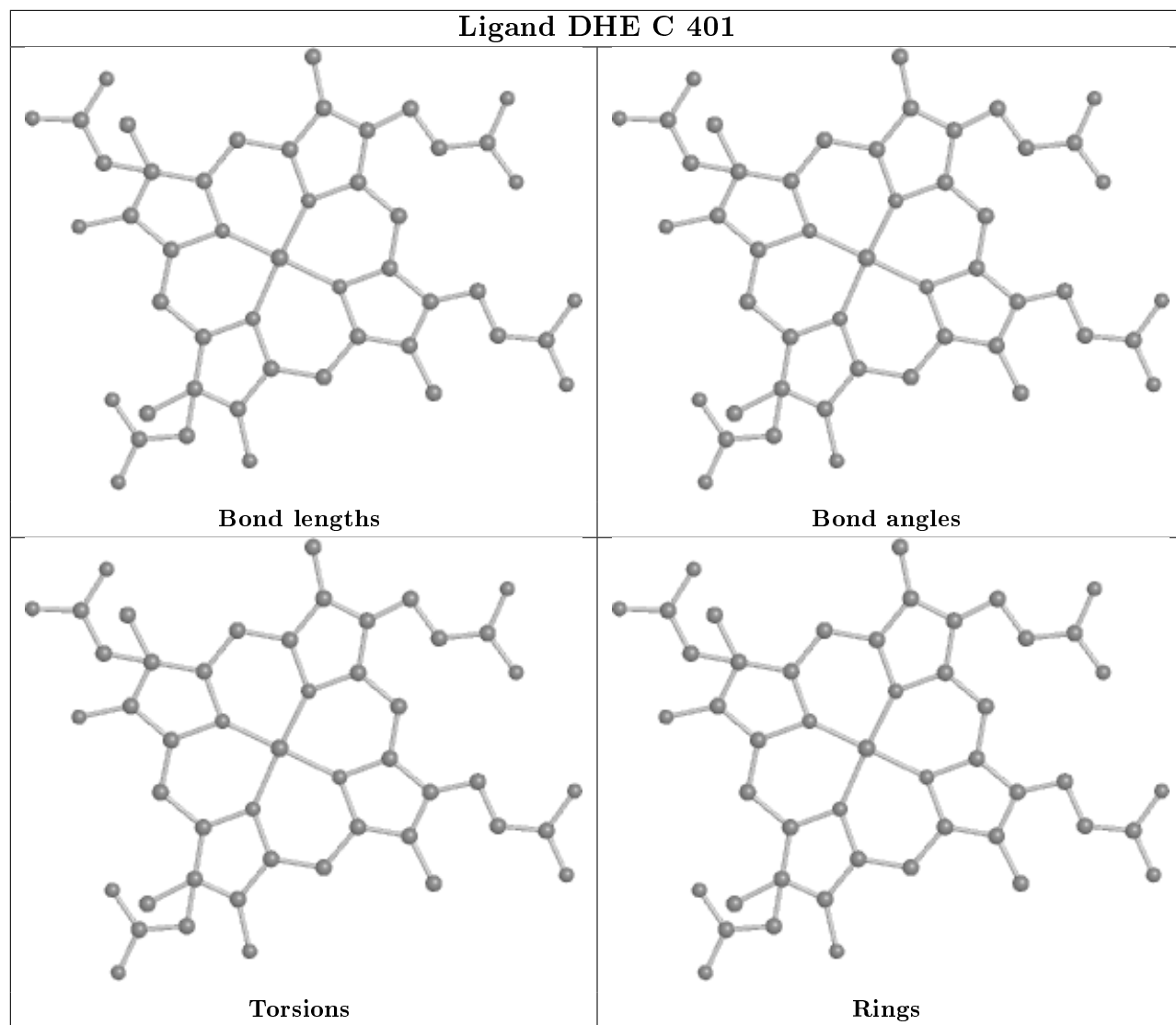
No monomer is involved in short contacts.

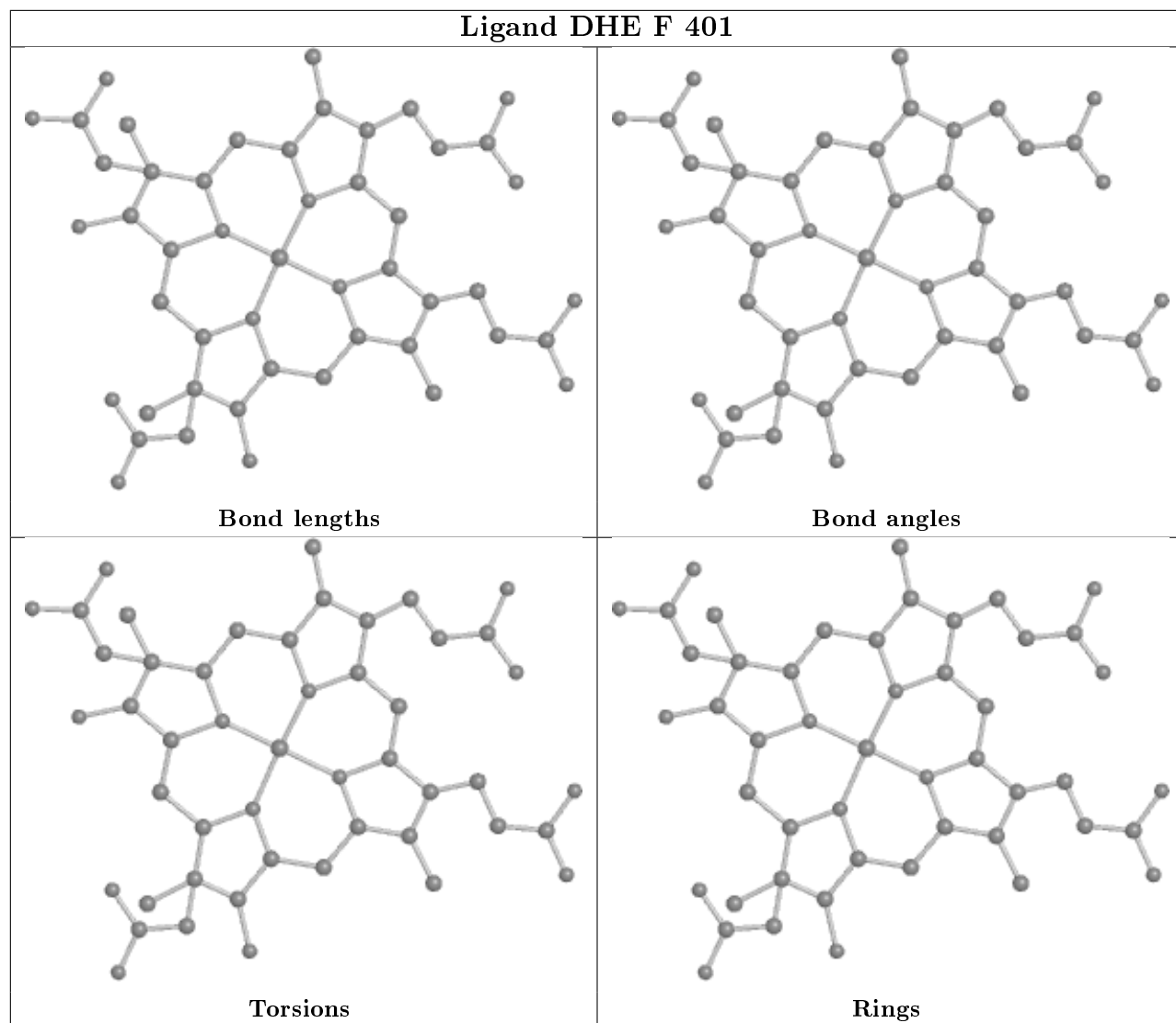
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



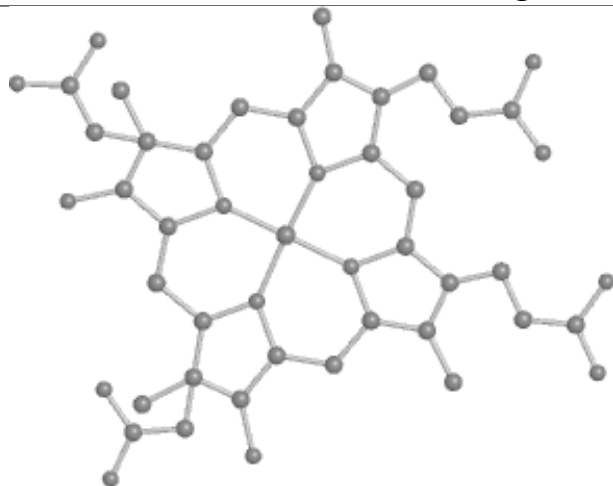




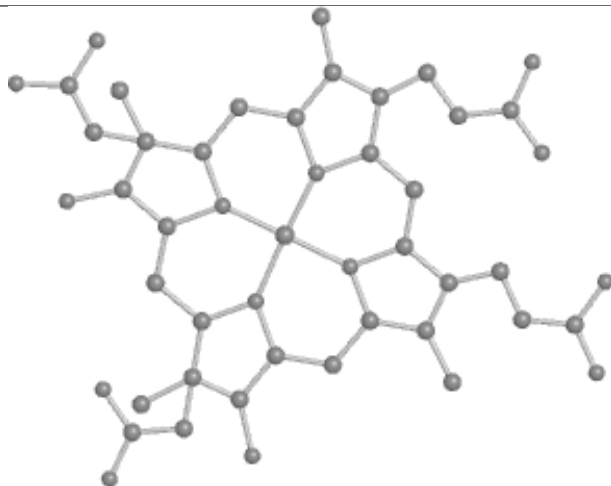




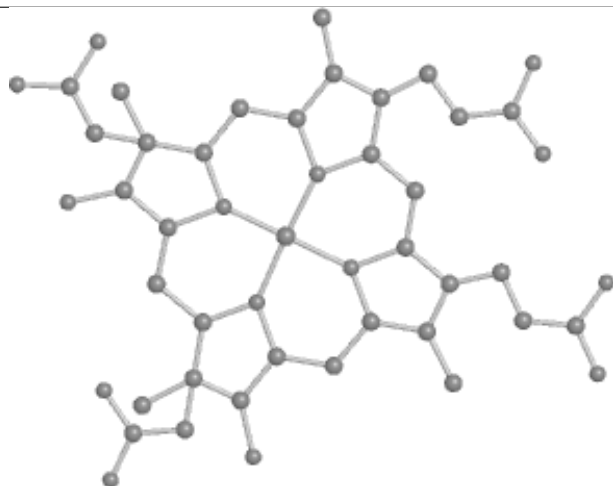
Ligand DHE E 401



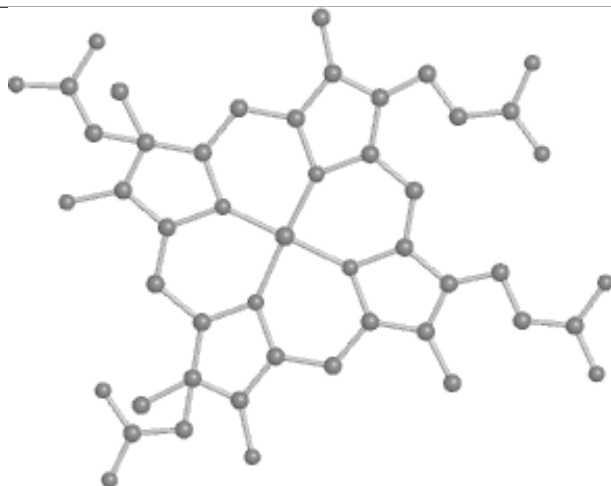
Bond lengths



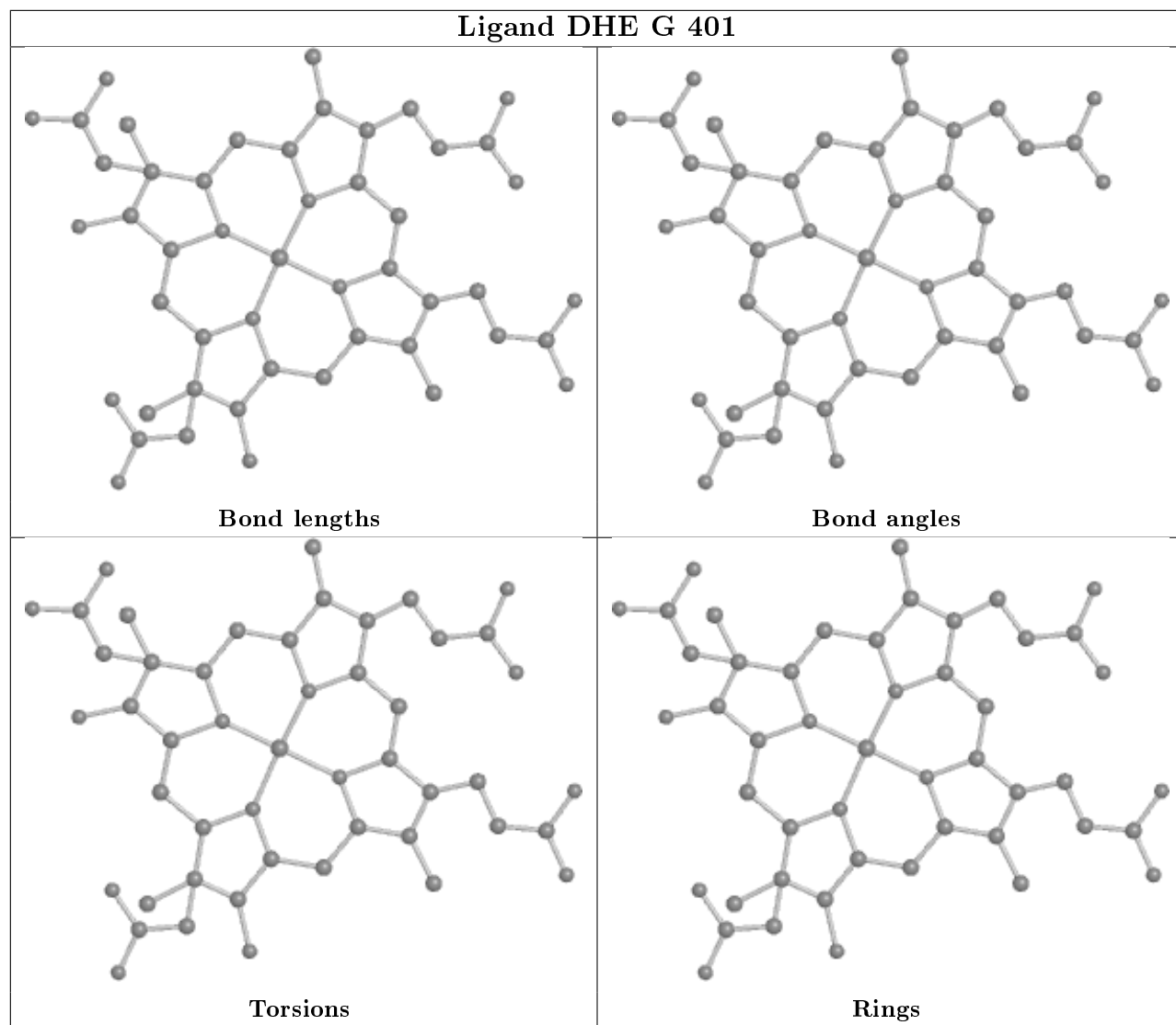
Bond angles

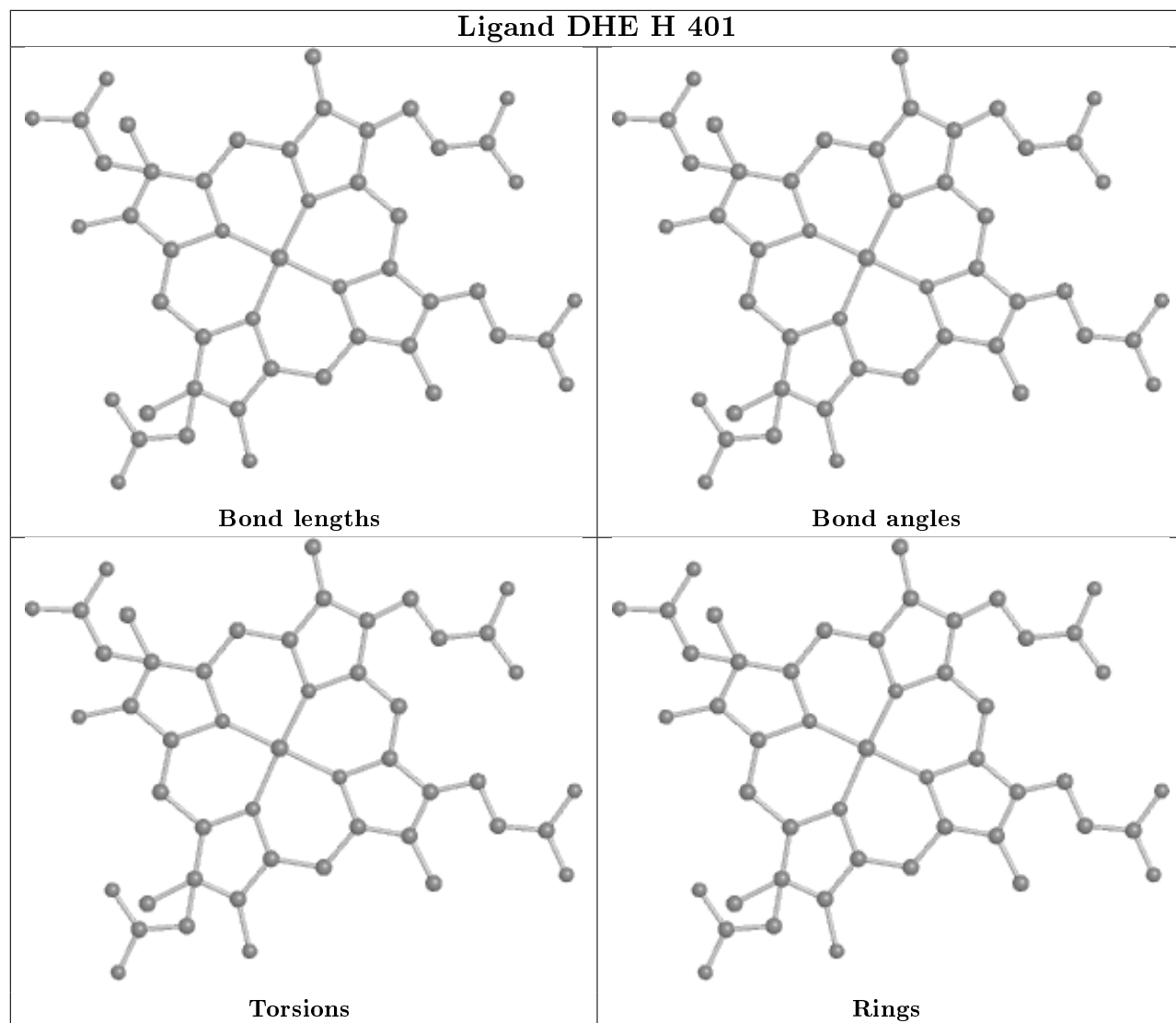


Torsions



Rings





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	372/378 (98%)	-0.14	2 (0%) 91 92	12, 21, 38, 64	0
1	B	372/378 (98%)	0.33	13 (3%) 44 47	15, 32, 50, 64	0
1	C	372/378 (98%)	-0.23	1 (0%) 94 94	4, 13, 29, 55	0
1	D	372/378 (98%)	-0.18	3 (0%) 86 87	6, 16, 32, 57	0
1	E	372/378 (98%)	0.10	5 (1%) 77 79	12, 27, 49, 71	0
1	F	372/378 (98%)	-0.19	0 100 100	5, 16, 34, 50	0
1	G	372/378 (98%)	-0.17	3 (0%) 86 87	5, 17, 35, 70	0
1	H	372/378 (98%)	0.04	7 (1%) 66 69	10, 25, 45, 73	0
All	All	2976/3024 (98%)	-0.06	34 (1%) 80 82	4, 20, 43, 73	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	132	GLY	4.7
1	A	246	SER	4.4
1	B	9	LEU	3.5
1	C	246	SER	3.4
1	G	132	GLY	3.3

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

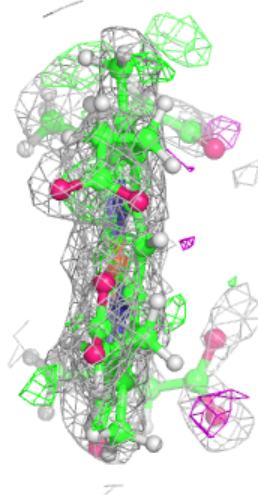
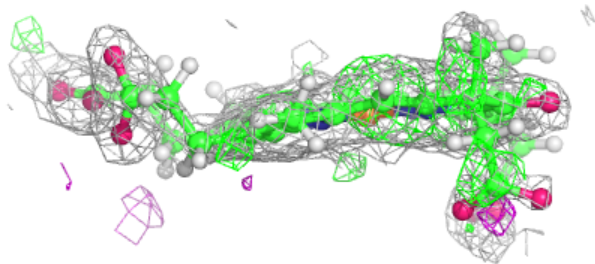
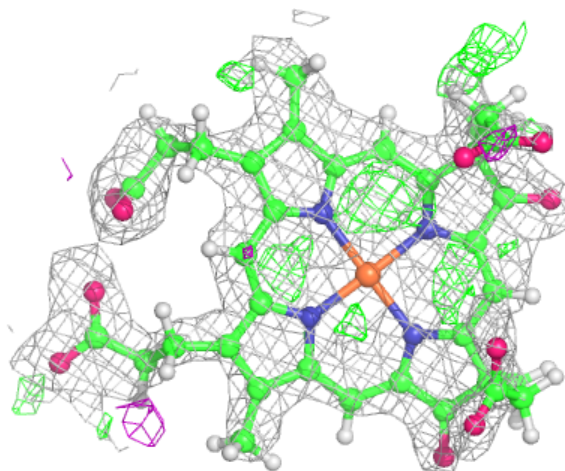
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	DHE	B	401	49/49	0.87	0.20	15,26,38,41	77
2	DHE	D	401	49/49	0.92	0.16	11,18,30,34	77
2	DHE	E	401	49/49	0.92	0.12	18,24,35,38	0
2	DHE	F	401	49/49	0.93	0.15	9,16,25,29	77
2	DHE	A	401	49/49	0.93	0.14	14,22,35,42	77
2	DHE	G	401	49/49	0.94	0.12	11,18,29,30	0
2	DHE	H	401	49/49	0.94	0.12	16,26,33,36	0
2	DHE	C	401	49/49	0.95	0.15	8,15,27,32	77

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.

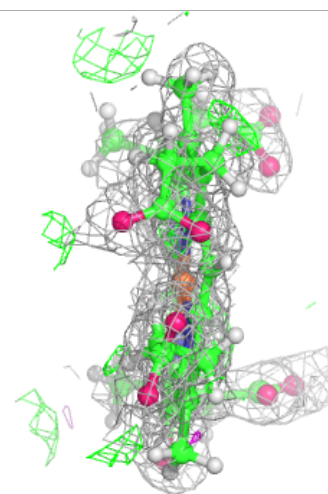
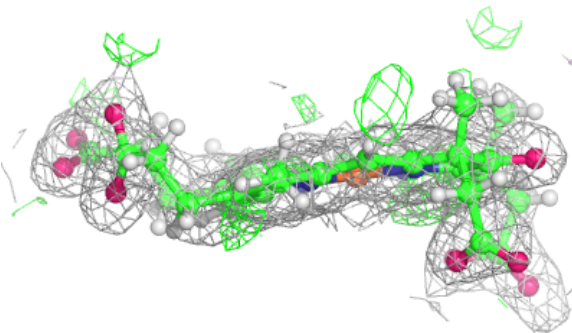
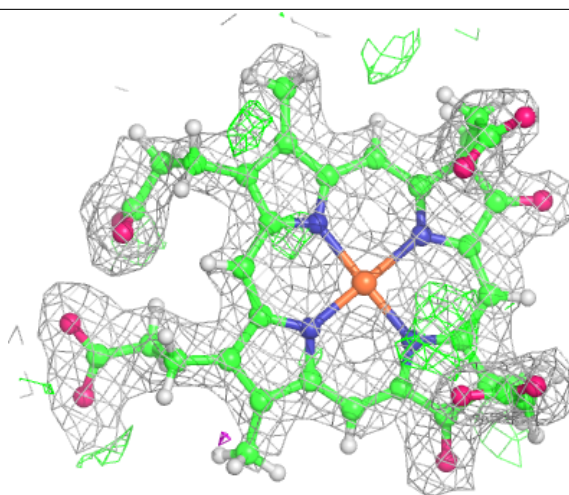
Electron density around DHE B 401:

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



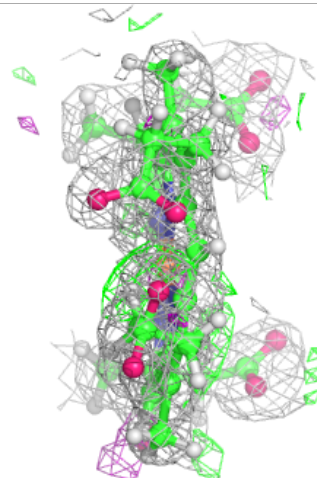
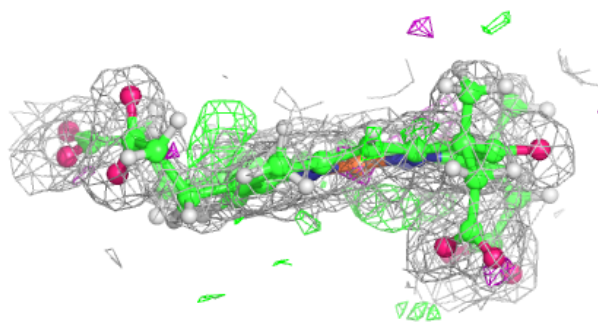
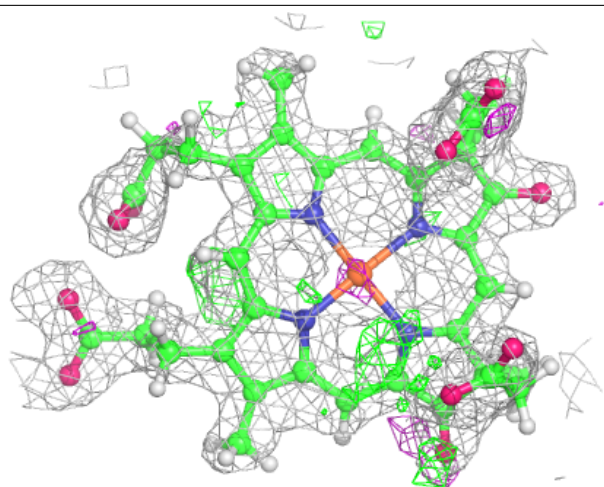
Electron density around DHE D 401:

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



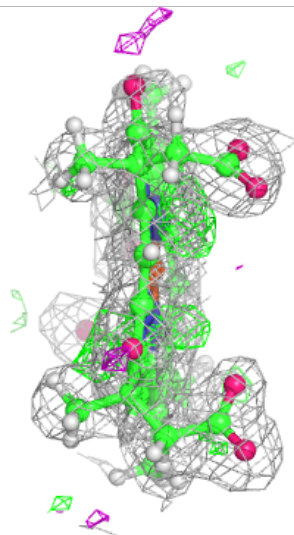
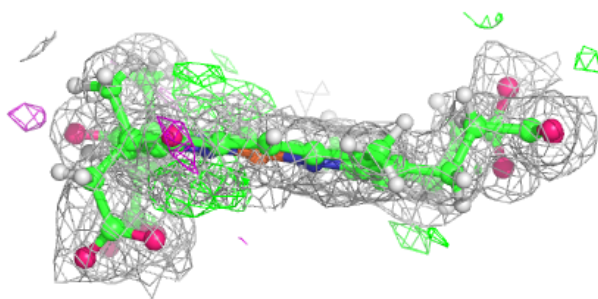
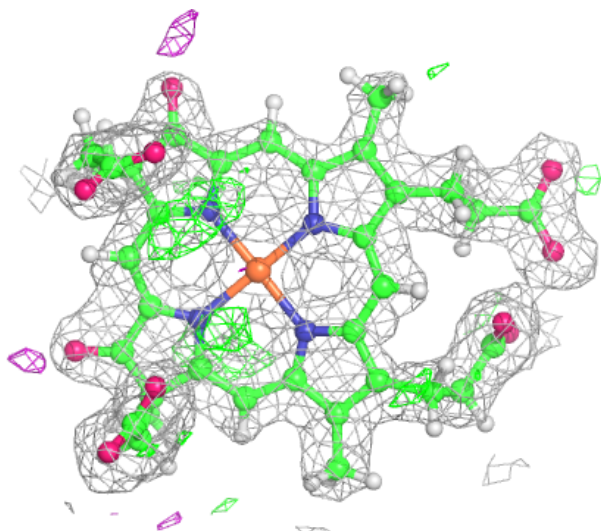
Electron density around DHE E 401:

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



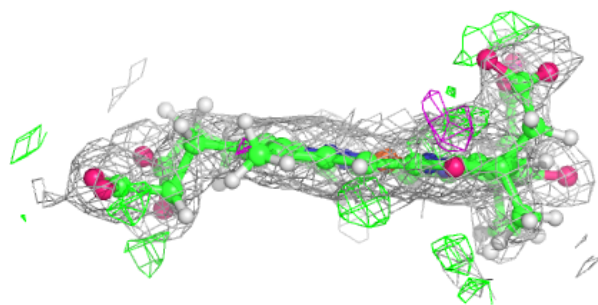
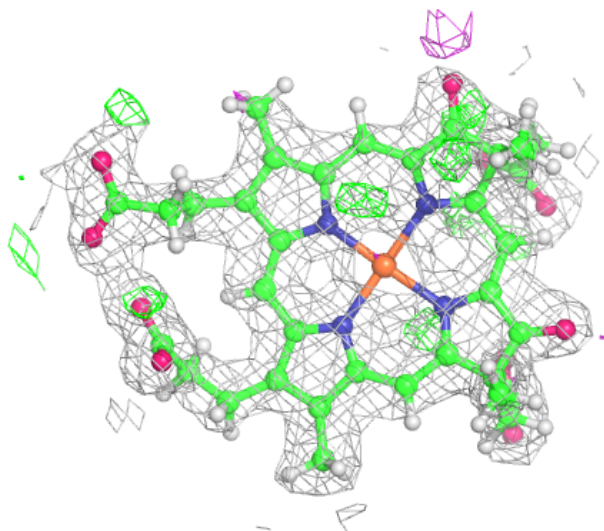
Electron density around DHE F 401:

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



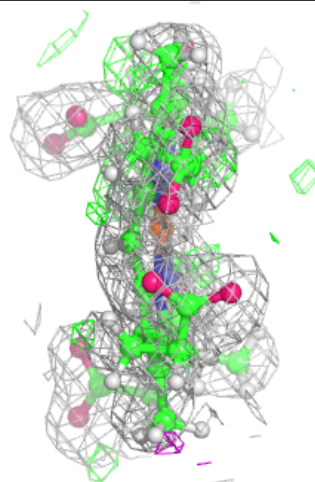
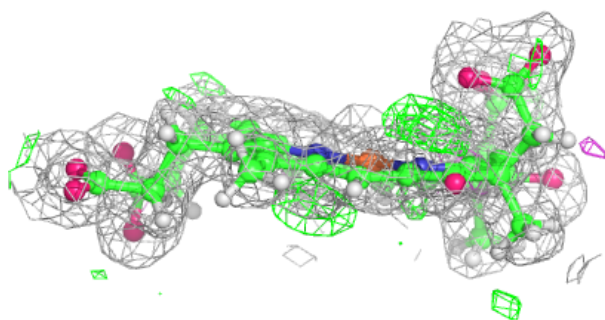
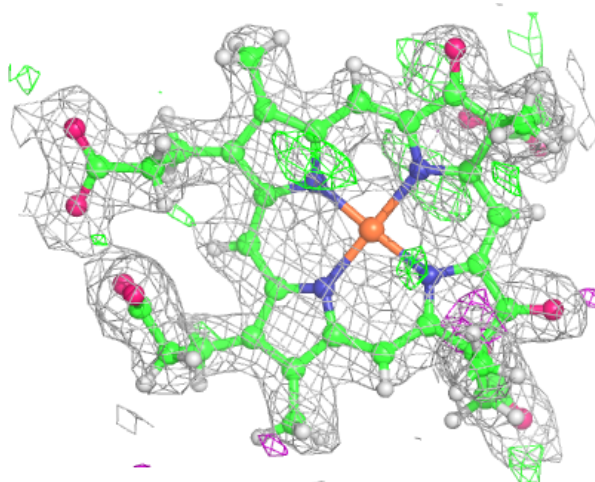
Electron density around DHE A 401:

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



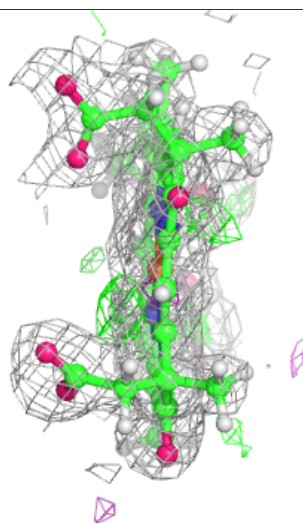
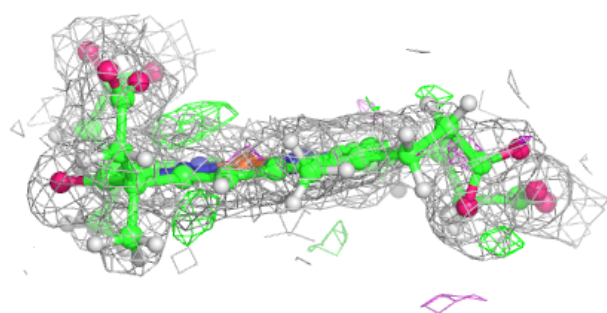
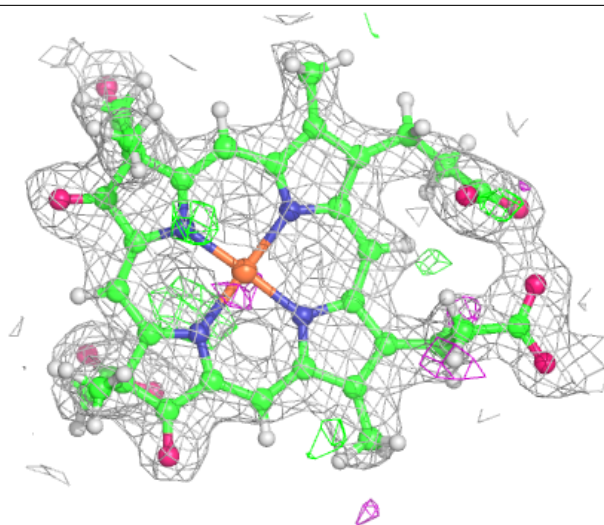
Electron density around DHE G 401:

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



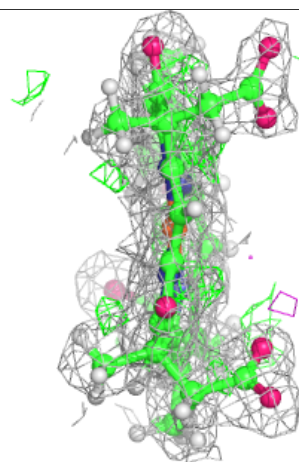
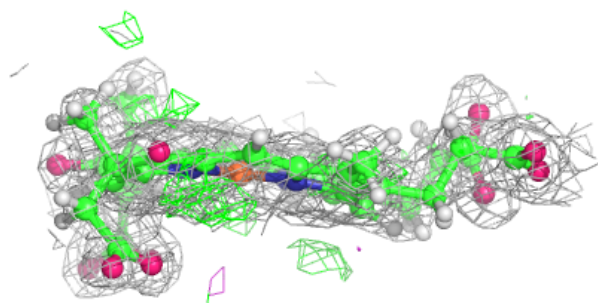
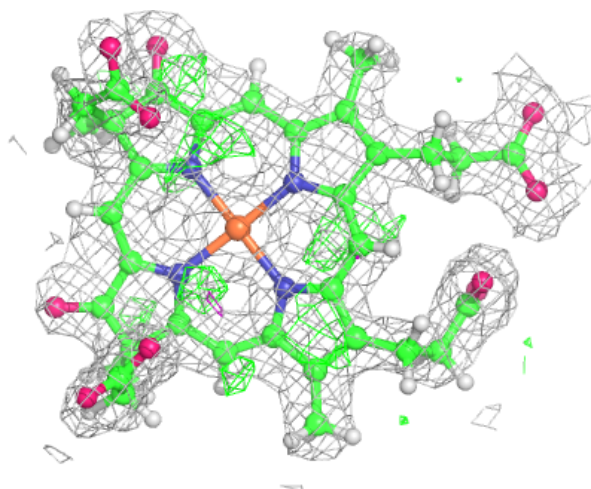
Electron density around DHE H 401:

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



Electron density around DHE C 401:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.