wwPDB X-ray Structure Validation Summary Report (i)

Feb 3, 2024 – 01:00 PM EST

PDB ID	:	1KQG
Title	:	FORMATE DEHYDROGENASE N FROM E. COLI
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Deposited on	:	2002-01-05
Resolution	:	2.80 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 (i) 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 (1)) were used in the production of this report:

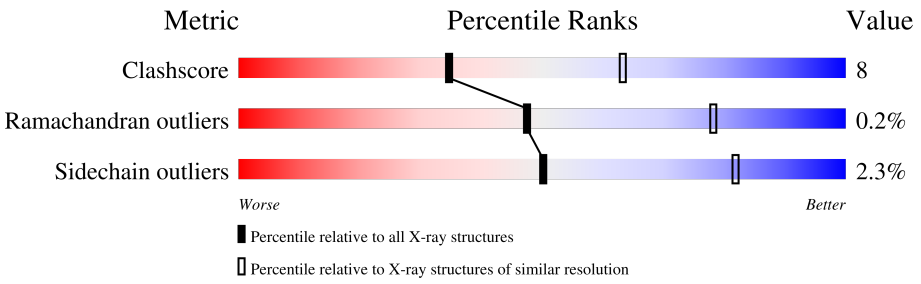
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1015	73% 21% • •
2	B	294	78% 17% • •
3	C	217	61% 32% 6% •

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 14003 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 FORMATE DEHYDROGENASE, NITRATE-INDUCIBLE, MAJOR SUBUNIT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	982	7719	4872	1352	1457	37	1	0	0	0

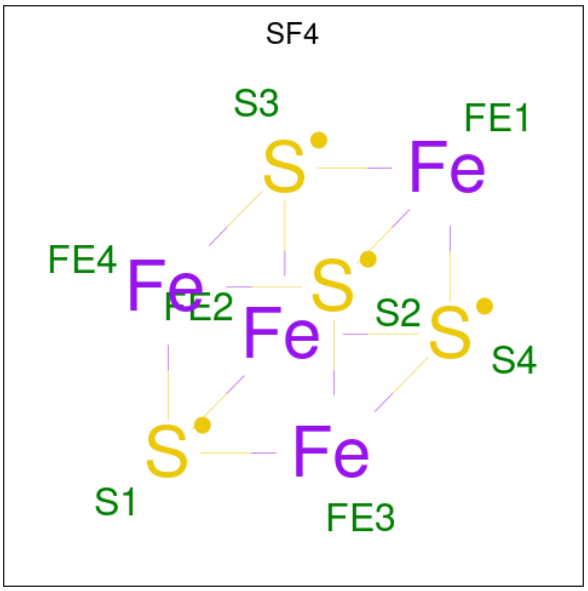
- Molecule 2 is a protein called FORMATE DEHYDROGENASE, NITRATE-INDUCIBLE, IRON-SULFUR SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	289	2207	1383	381	421	22	0	0	0

- Molecule 3 is a protein called FORMATE DEHYDROGENASE, NITRATE-INDUCIBLE, CYTOCHROME B556(FDN) SUBUNIT.

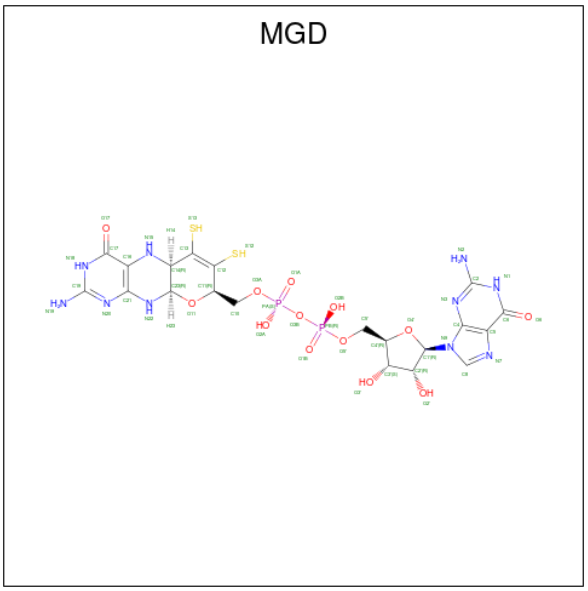
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	216	1783	1192	301	276	14	0	0	0

- Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
4	A	1	8	4	4	0	0
			Total	Fe	S		
4	B	1	8	4	4	0	0
			Total	Fe	S		
4	B	1	8	4	4	0	0
			Total	Fe	S		
4	B	1	8	4	4	0	0
			Total	Fe	S		
4	B	1	8	4	4	0	0

- Molecule 5 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (three-letter code: MGD) (formula: $C_{20}H_{26}N_{10}O_{13}P_2S_2$).

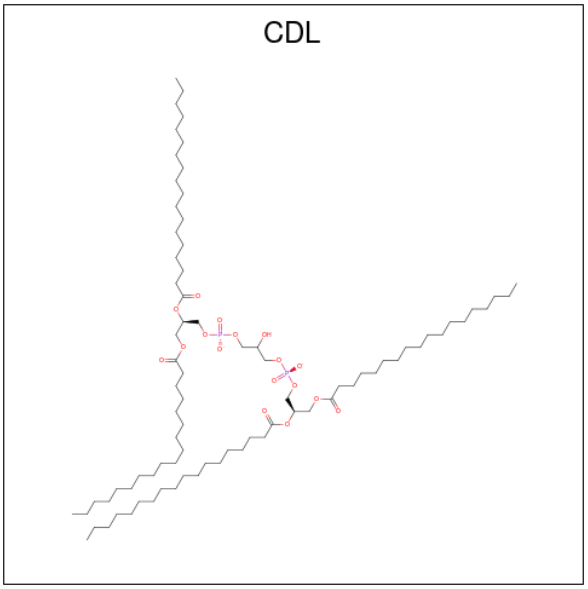


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
5	A	1	47	20	10	13	2	2	0	0
			Total	C	N	O	P	S		
5	A	1	47	20	10	13	2	2	0	0

- Molecule 6 is MOLYBDENUM(VI) ION (three-letter code: 6MO) (formula: Mo).

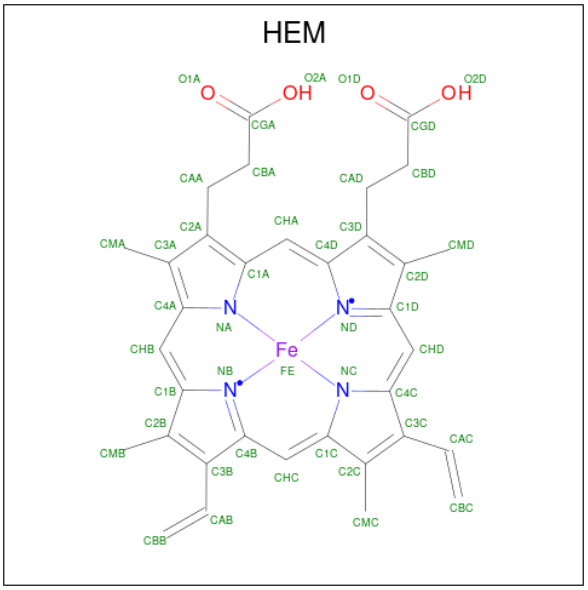
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mo		
6	A	1	1	1	0	0

- Molecule 7 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



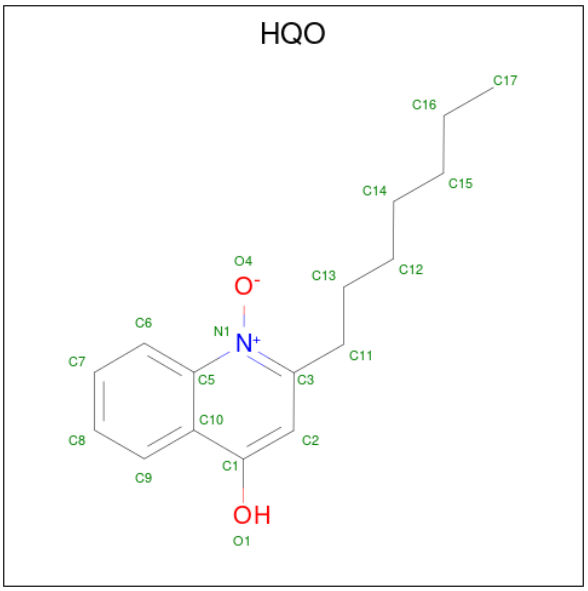
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
7	B	1	70	51	17	2	0	0

- Molecule 8 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 9 is 2-HEPTYL-4-HYDROXY QUINOLINE N-OXIDE (three-letter code: HQO) (formula: $C_{16}H_{21}NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
9	C	1	19	16	1	2	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
10	A	1493	1493	1493	0	0
			Total	O		
10	B	410	410	410	0	0
			Total	O		
10	C	81	81	81	0	0

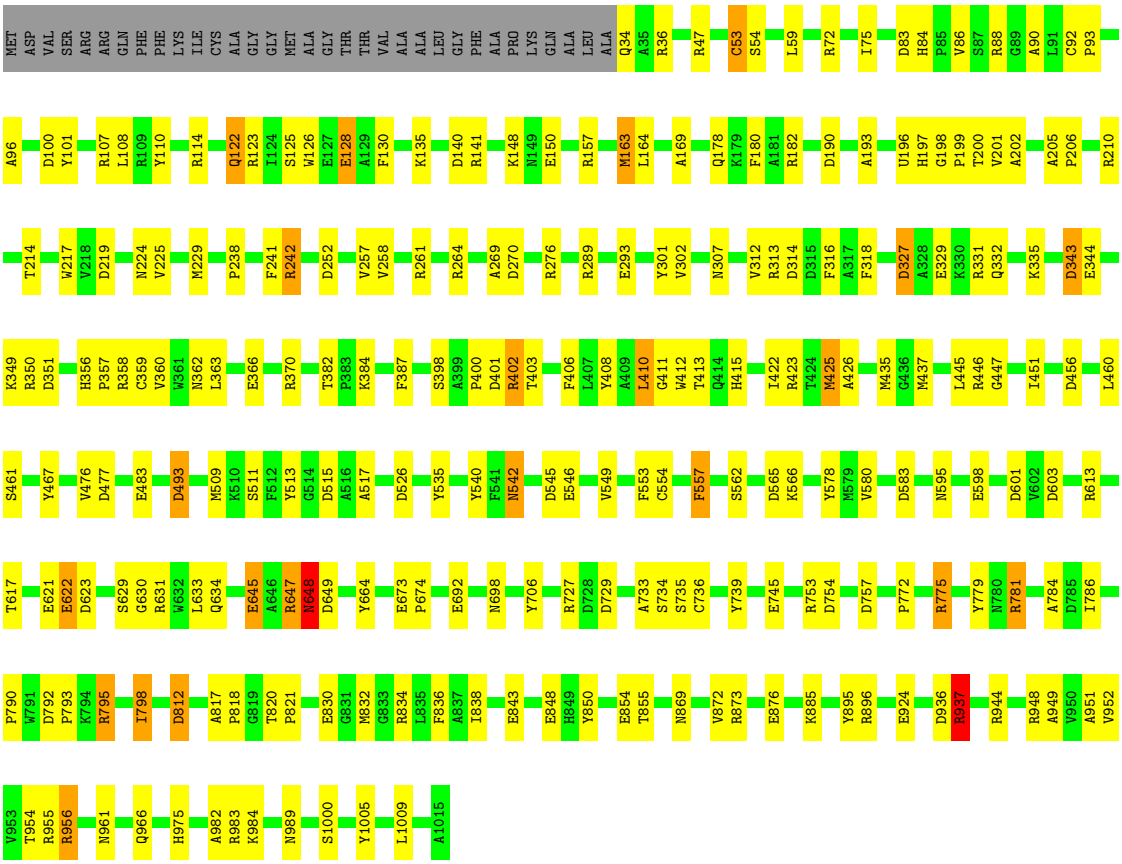
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

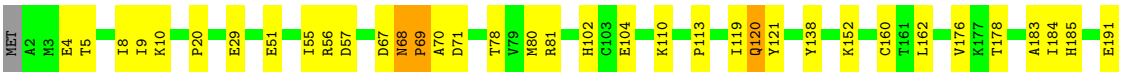
• Molecule 1: FORMATE DEHYDROGENASE, NITRATE-INDUCIBLE, MAJOR SUBUNIT

Chain A: 73% 21%



• Molecule 2: FORMATE DEHYDROGENASE, NITRATE-INDUCIBLE, IRON-SULFUR SUBUNIT

Chain B: 78% 17%



• Molecule 3: FORMATE DEHYDROGENASE, NITRATE-INDUCIBLE, CYTOCHROME B556(FDN) SUBUNIT

Chain C:

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α, β, γ	203.00Å 203.00Å 203.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.80	Depositor
% Data completeness (in resolution range)	90.8 (40.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.198 , 0.239	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14003	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

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: CDL, HEM, 6MO, SF4, SEC, HQO, MGD

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	0.75	1/7910 (0.0%)	1.88	205/10749 (1.9%)
2	B	0.76	0/2255	1.66	39/3056 (1.3%)
3	C	0.67	0/1840	1.65	28/2483 (1.1%)
All	All	0.74	1/12005 (0.0%)	1.81	272/16288 (1.7%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	622	GLU	CD-OE1	5.14	1.31	1.25

The worst 5 of 272 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	88	ARG	NE-CZ-NH2	-36.10	102.25	120.30
1	A	937	ARG	NE-CZ-NH2	-21.45	109.57	120.30
1	A	873	ARG	NE-CZ-NH1	18.68	129.64	120.30
1	A	157	ARG	NE-CZ-NH2	16.52	128.56	120.30
3	C	74	ARG	NE-CZ-NH2	-16.10	112.25	120.30

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	7719	0	7457	102	0
2	B	2207	0	2140	30	0
3	C	1783	0	1836	67	0
4	A	8	0	0	0	0
4	B	32	0	0	0	0
5	A	94	0	43	5	0
6	A	1	0	0	0	0
7	B	70	0	83	4	0
8	C	86	0	60	3	0
9	C	19	0	21	1	0
10	A	1493	0	0	27	0
10	B	410	0	0	11	0
10	C	81	0	0	9	0
All	All	14003	0	11640	196	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 8.

The worst 5 of 196 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:A:830:GLU:HG3	1:A:832:MET:HE2	1.40	0.98
1:A:356:HIS:HD2	1:A:358:ARG:H	1.11	0.89
1:A:869:ASN:HB3	1:A:872:VAL:HG23	1.58	0.85
1:A:224:ASN:HD22	1:A:403:THR:H	1.21	0.84
3:C:101:HIS:HD2	3:C:102:LYS:H	1.25	0.84

There are no symmetry-related clashes.

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	979/1015 (96%)	949 (97%)	29 (3%)	1 (0%)	51	81
2	B	287/294 (98%)	280 (98%)	7 (2%)	0	100	100
3	C	214/217 (99%)	206 (96%)	6 (3%)	2 (1%)	17	46
All	All	1480/1526 (97%)	1435 (97%)	42 (3%)	3 (0%)	47	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	208	GLU
1	A	838	ILE
3	C	198	PRO

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	815/837 (97%)	805 (99%)	10 (1%)	71	92
2	B	238/243 (98%)	225 (94%)	13 (6%)	21	52
3	C	188/189 (100%)	183 (97%)	5 (3%)	44	78
All	All	1241/1269 (98%)	1213 (98%)	28 (2%)	50	82

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	113	PRO
3	C	206	LYS
2	B	178	THR
3	C	105	ASP
2	B	162	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	185	HIS
3	C	101	HIS
3	C	196	HIS
3	C	164	HIS
1	A	356	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 1 is monoatomic - leaving 11 for Mogul analysis.

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	$\#\|Z\| > 2$
4	SF4	B	808	2	0,12,12	-	-	-		
4	SF4	B	805	2	0,12,12	-	-	-		
7	CDL	B	812	-	69,69,99	2.89	20 (28%)	75,81,111	2.66	17 (22%)
4	SF4	B	807	2	0,12,12	-	-	-		
5	MGD	A	1017	6	41,52,52	2.16	8 (19%)	40,81,81	2.50	13 (32%)
8	HEM	C	809	3	41,50,50	1.52	4 (9%)	45,82,82	1.23	5 (11%)
8	HEM	C	810	3	41,50,50	1.57	7 (17%)	45,82,82	1.73	9 (20%)
5	MGD	A	1018	6	41,52,52	2.31	8 (19%)	40,81,81	2.22	15 (37%)
4	SF4	A	1016	1	0,12,12	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
9	HQO	C	811	-	20,20,20	2.96	9 (45%)	18,26,26	3.56	7 (38%)
4	SF4	B	806	2	0,12,12	-	-	-		

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
4	SF4	B	808	2	-	-	0/6/5/5
4	SF4	B	805	2	-	-	0/6/5/5
7	CDL	B	812	-	-	41/80/80/110	-
4	SF4	B	807	2	-	-	0/6/5/5
5	MGD	A	1017	6	-	8/18/66/66	0/6/6/6
8	HEM	C	809	3	-	4/12/54/54	-
8	HEM	C	810	3	-	3/12/54/54	-
5	MGD	A	1018	6	-	5/18/66/66	0/6/6/6
4	SF4	A	1016	1	-	-	0/6/5/5
9	HQO	C	811	-	-	2/7/7/7	0/2/2/2
4	SF4	B	806	2	-	-	0/6/5/5

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	812	CDL	OB8-CB6	-15.23	1.10	1.45
5	A	1018	MGD	O3A-C10	-10.41	1.04	1.44
5	A	1017	MGD	O3A-C10	-10.00	1.06	1.44
7	B	812	CDL	OA6-CA5	8.44	1.58	1.34
9	C	811	HQO	C11-C3	7.71	1.71	1.50

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	B	812	CDL	OB6-CB5-C51	13.32	140.21	111.50
9	C	811	HQO	C11-C3-C2	10.85	139.33	120.74
5	A	1017	MGD	O11-C23-C14	8.49	114.63	108.96
7	B	812	CDL	C52-C51-CB5	-7.21	87.41	113.62
5	A	1018	MGD	O4'-C1'-C2'	-7.10	96.55	106.93

There are no chirality outliers.

5 of 63 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1017	MGD	PA-O3B-PB-O5'
5	A	1017	MGD	C5'-O5'-PB-O1B
5	A	1017	MGD	C10-O3A-PA-O1A
7	B	812	CDL	CA3-OA5-PA1-OA3
7	B	812	CDL	CA3-OA5-PA1-OA4

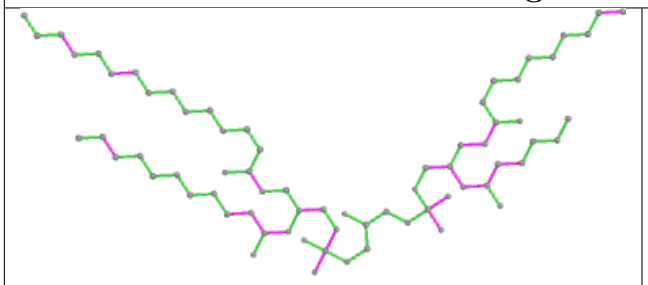
There are no ring outliers.

5 monomers are involved in 13 short contacts:

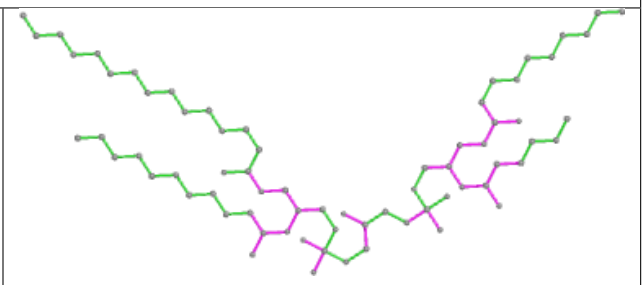
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	812	CDL	4	0
5	A	1017	MGD	3	0
8	C	810	HEM	3	0
5	A	1018	MGD	2	0
9	C	811	HQO	1	0

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 then 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.

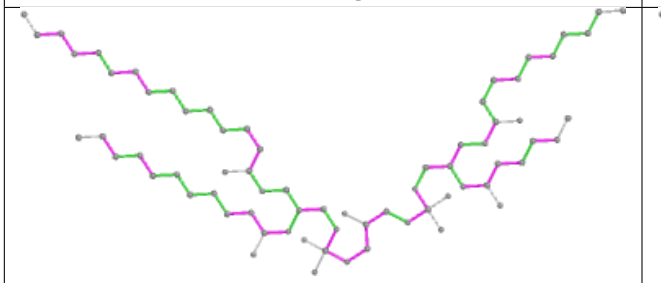
Ligand CDL B 812



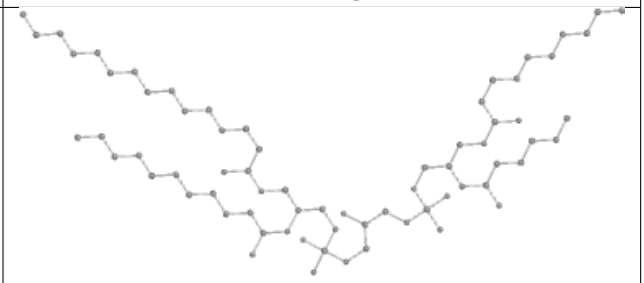
Bond lengths



Bond angles

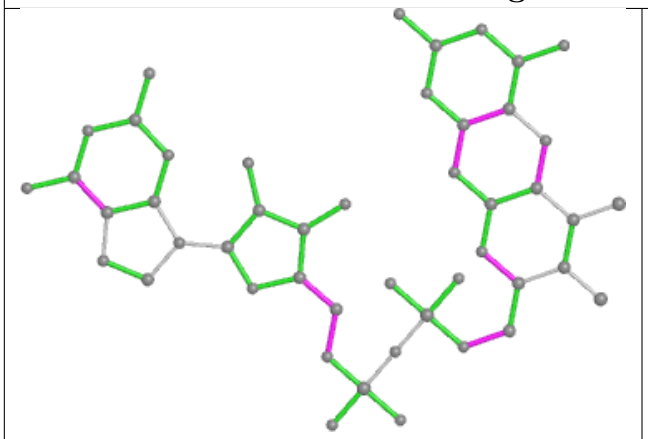


Torsions

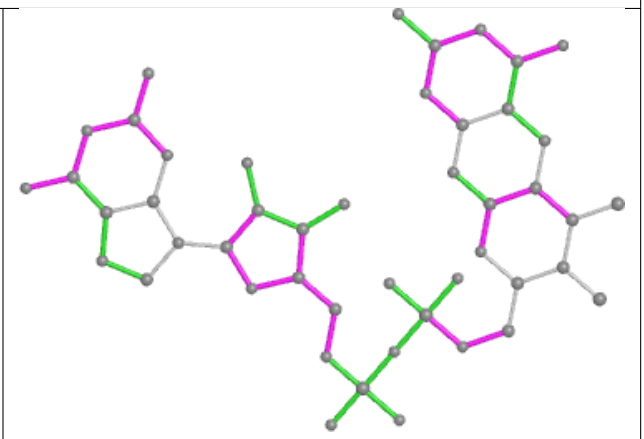


Rings

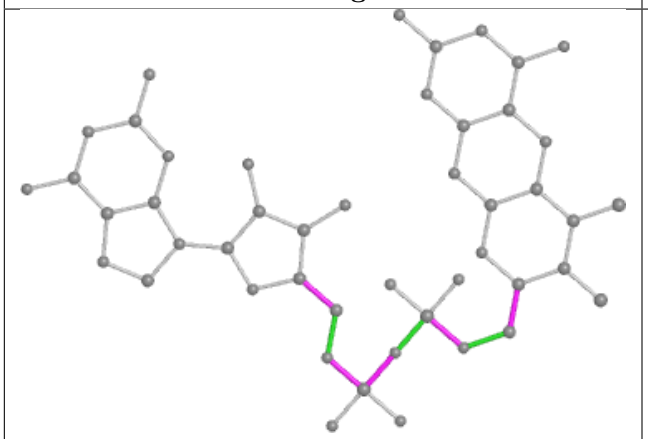
Ligand MGD A 1017



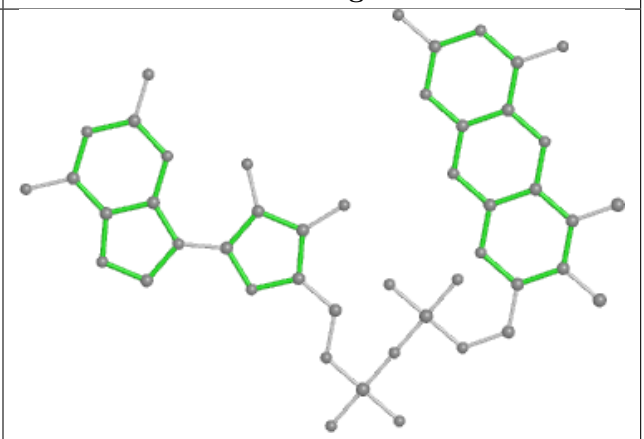
Bond lengths



Bond angles

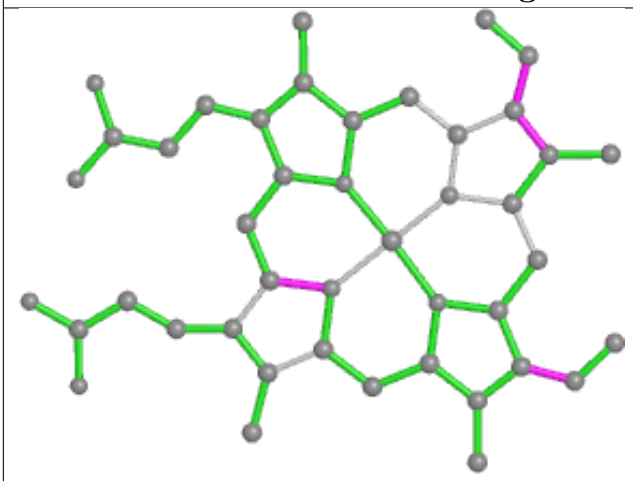


Torsions



Rings

Ligand HEM C 809



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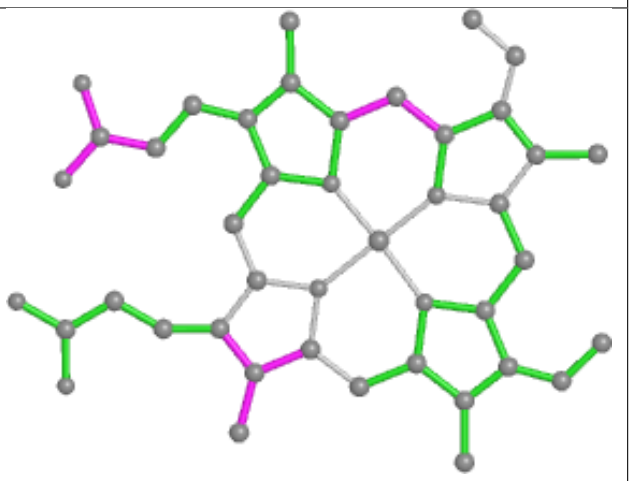
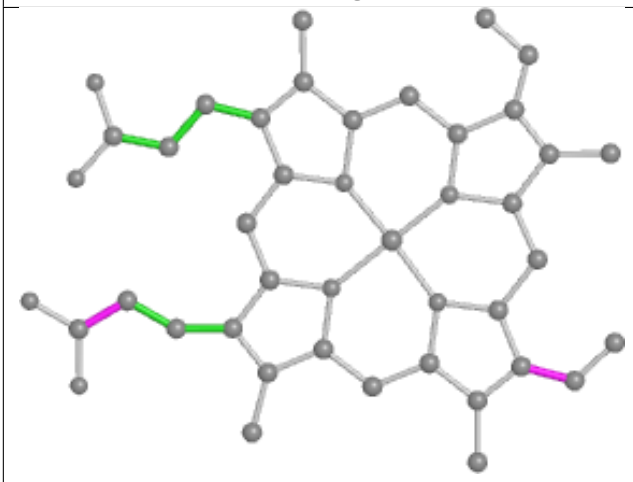
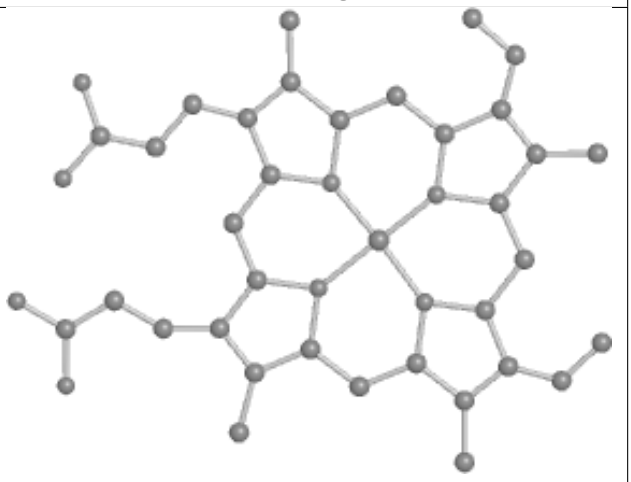


Bond angles

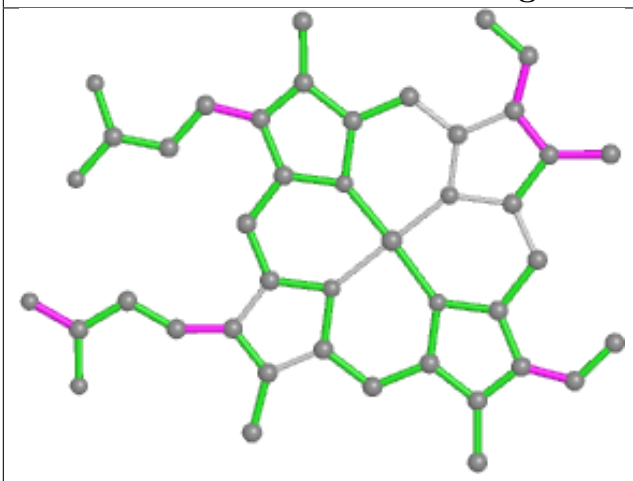


Torsions



Rings

Ligand HEM C 810



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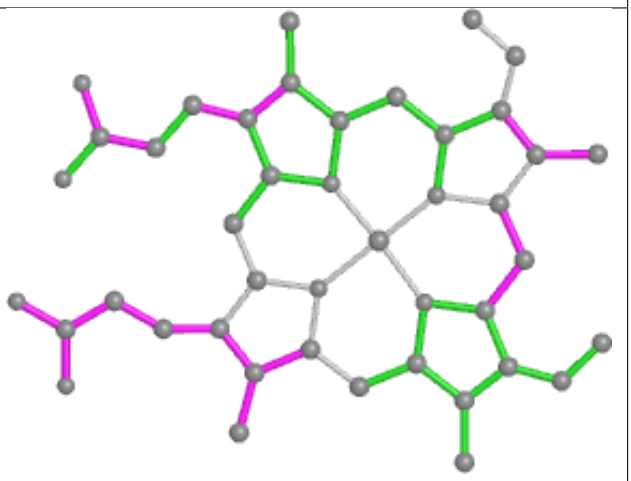
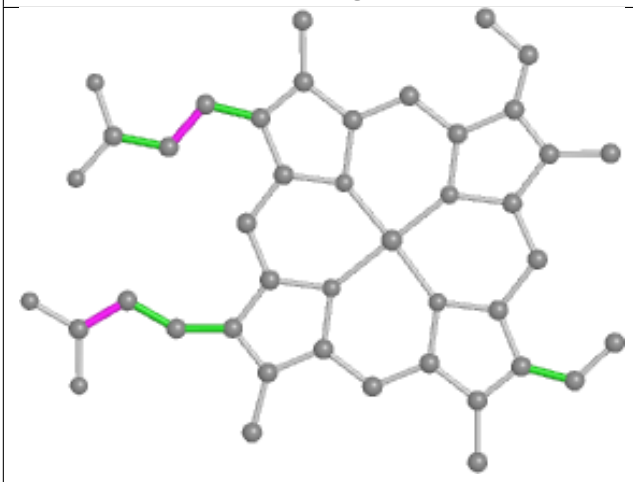
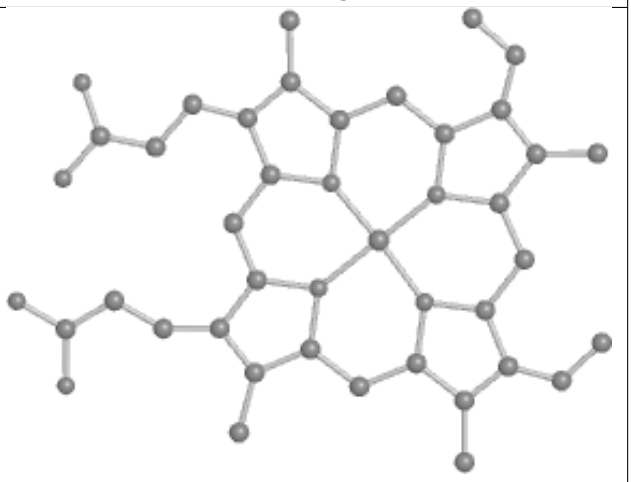


Bond angles

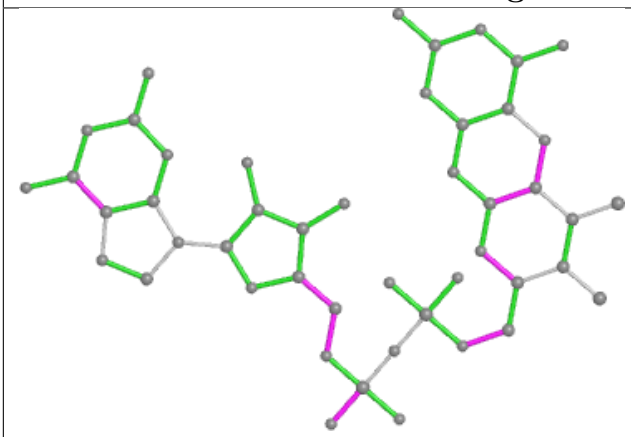


Torsions

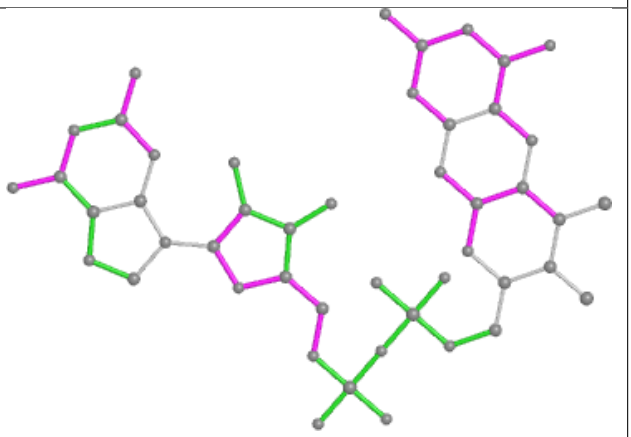


Rings

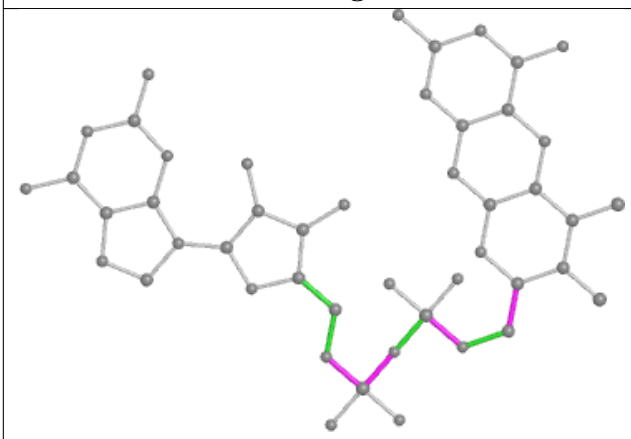
Ligand MGD A 1018



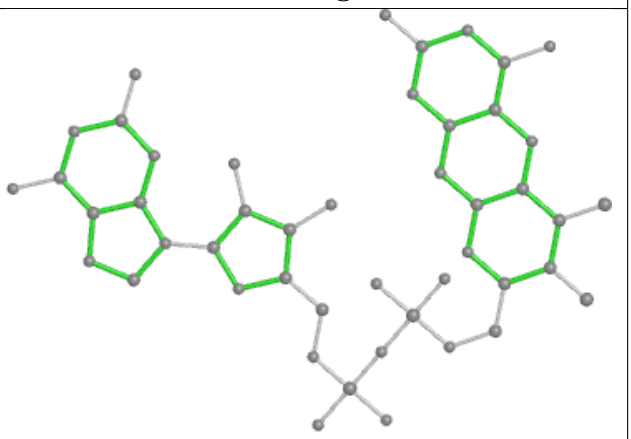
Bond lengths



Bond angles

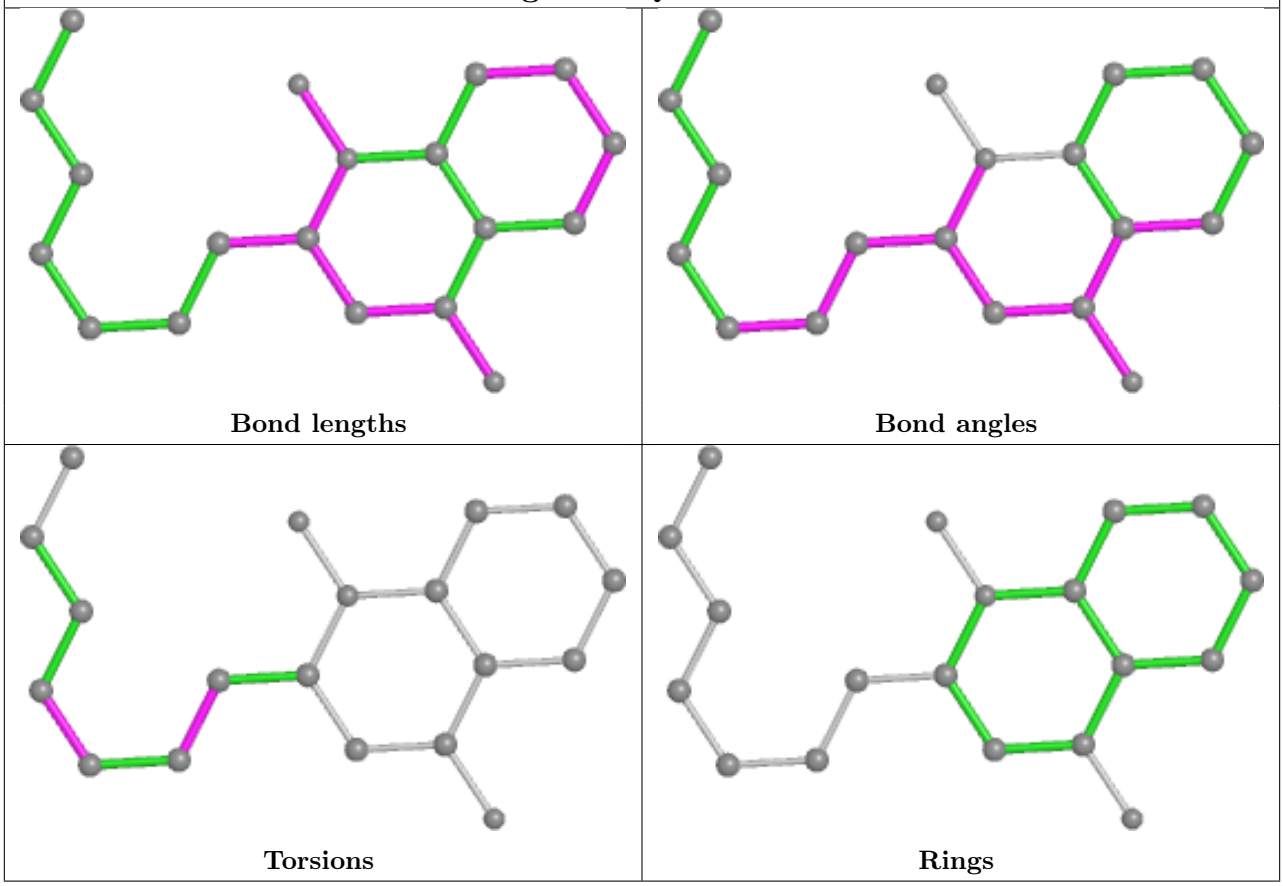


Torsions



Rings

Ligand HQO C 811



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.