wwPDB NMR Structure Validation Summary Report

Jun 14, 2020 – 02:07 am BST

PDB ID	:	1GX7
Title	:	Best model of the electron transfer complex between cytochrome c3 and [Fe]-hydrogenase
Authors	:	Elantak, L.; Morelli, X.; Bornet, O.; Hatchikian, C.; Czjzek, M.; Dolla, A.; Guerlesquin, F.
Deposited on	:	2002-03-28

This is a wwPDB NMR 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/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

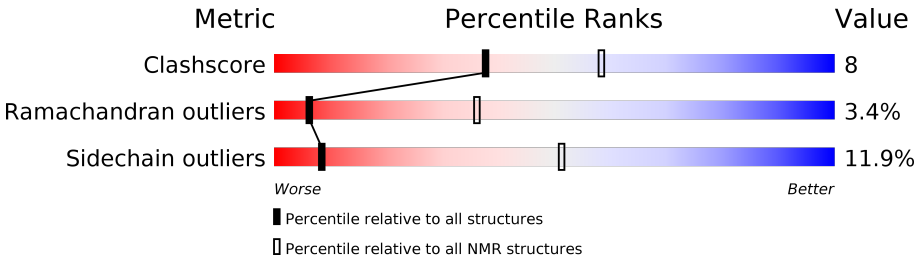
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
SOLUTION NMR, THEORETICAL MODEL

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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%

Mol	Chain	Length	Quality of chain
1	A	371	69% 25% 6% •
2	D	88	74% 19% 7%
3	E	107	72% 20% 7% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
5	A	PDT	4	-	1

2 Ensemble composition and analysis (i)

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 5509 atoms, of which 968 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PERIPLASMIC [FE] HYDROGENASE LARGE SUBUNIT.

Mol	Chain	Residues	Atoms						Trace
1	A	371	Total	C	H	N	O	S	0
			3394	1783	587	465	527	32	

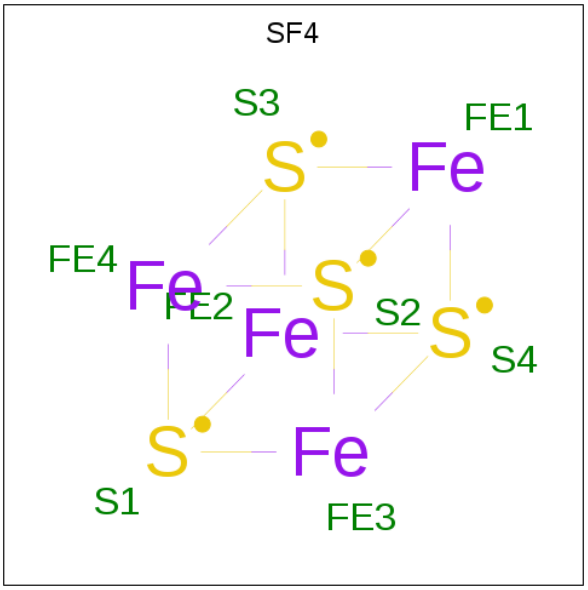
- Molecule 2 is a protein called PERIPLASMIC [FE] HYDROGENASE SMALL SUBUNIT.

Mol	Chain	Residues	Atoms						Trace
2	D	88	Total	C	H	N	O	S	0
			877	457	164	123	132	1	

- Molecule 3 is a protein called CYTOCHROME C3.

Mol	Chain	Residues	Atoms						Trace
3	E	107	Total	C	H	N	O	S	0
			1011	495	201	152	152	11	

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



Mol	Chain	Residues	Atoms		
4	A	1	Total	Fe	S
			8	4	4

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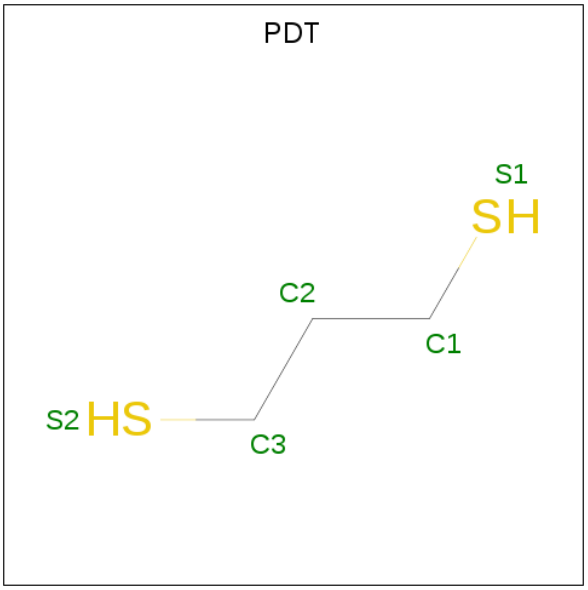
Mol	Chain	Residues	Atoms		
4	A	1	Total	Fe	S
			8	4	4
4	A	1	Total	Fe	S
			8	4	4

- Molecule 5 is 1,3-PROPANEDITHIOL (three-letter code: PDT) (formula: $C_3H_8S_2$).

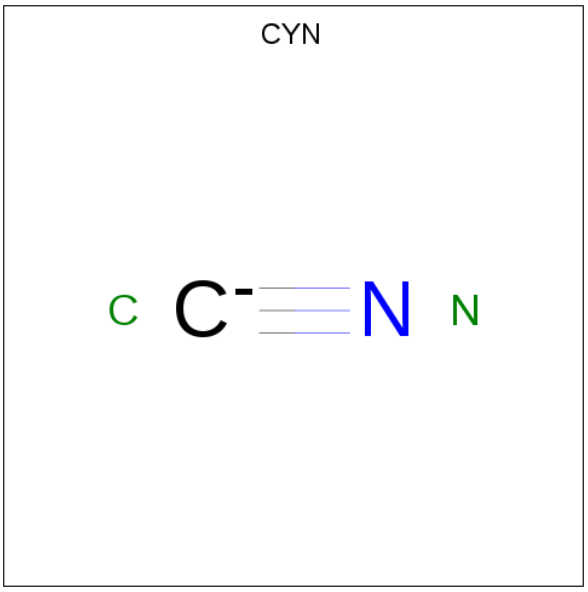


Mol	Chain	Residues	Atoms		
5	A	1	Total	C	S
			5	3	2

- Molecule 6 is FE (II) ION (three-letter code: FE2) (formula: Fe).

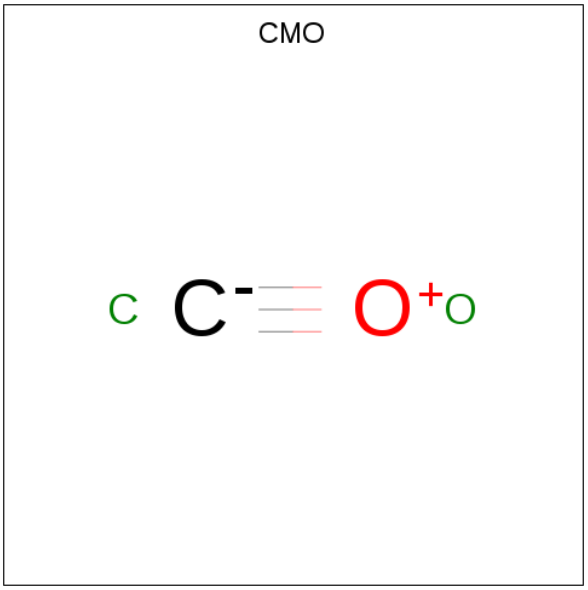
Mol	Chain	Residues	Atoms	
6	A	2	Total	Fe
			2	2

- Molecule 7 is CYANIDE ION (three-letter code: CYN) (formula: CN).



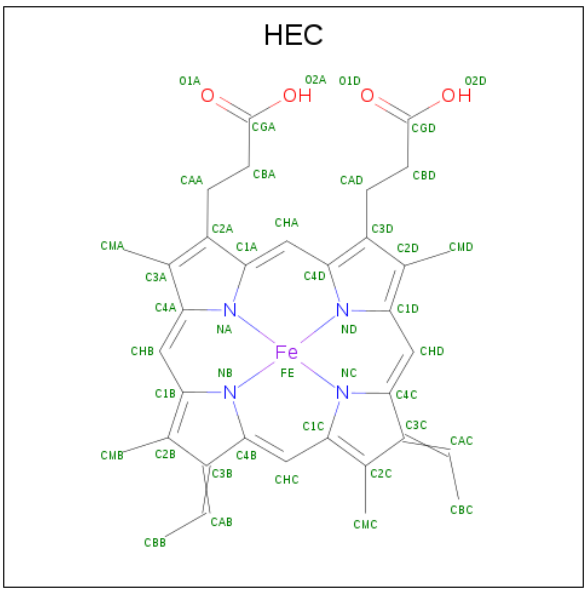
Mol	Chain	Residues	Atoms		
7	A	1	Total	C	N
			2	1	1
7	A	1	Total	C	N
			2	1	1

- Molecule 8 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO).



Mol	Chain	Residues	Atoms		
8	A	1	Total	C	O
			2	1	1
8	A	1	Total	C	O
			2	1	1

- Molecule 9 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



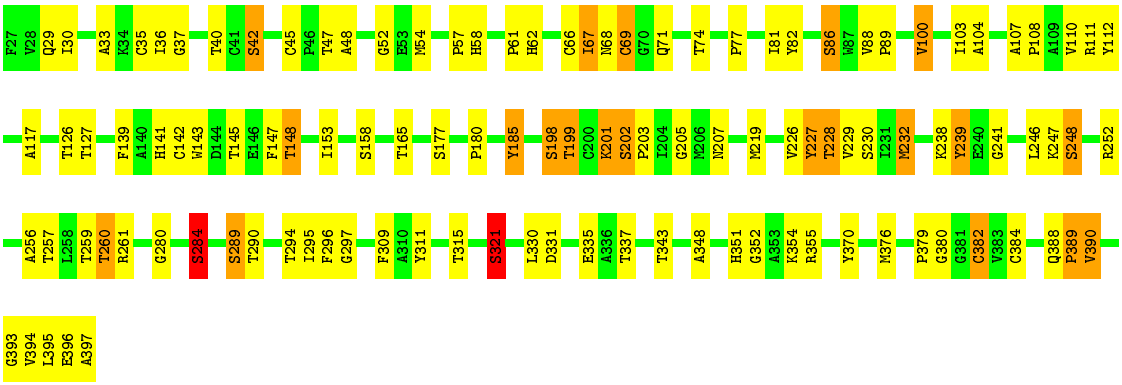
Mol	Chain	Residues	Atoms					
9	E	1	Total	C	Fe	H	N	O
			47	34	1	4	4	4
9	E	1	Total	C	Fe	H	N	O
			47	34	1	4	4	4
9	E	1	Total	C	Fe	H	N	O
			47	34	1	4	4	4
9	E	1	Total	C	Fe	H	N	O
			47	34	1	4	4	4

4 Residue-property plots (i)

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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 outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

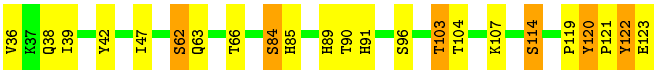
- Molecule 1: PERIPLASMIC [FE] HYDROGENASE LARGE SUBUNIT

Chain A:



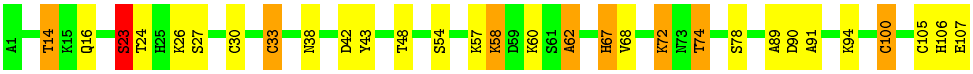
- Molecule 2: PERIPLASMIC [FE] HYDROGENASE SMALL SUBUNIT

Chain D:



- Molecule 3: CYTOCHROME C3

Chain E:



5 Refinement protocol and experimental data overview

The models were refined using the following method: *?*.

Of the ? calculated structures, 1 were deposited, based on the following criterion: *?*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR	refinement	

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CMO, SF4, PDT, FE2, HEC, CYN

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 (average) 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	0.57	0/2874 (0.0%)	1.23	17/3885 (0.4%)
2	D	0.58	0/733 (0.0%)	1.16	5/988 (0.5%)
3	E	0.54	0/827 (0.0%)	1.29	4/1101 (0.4%)
All	All	0.57	0/4434 (0.0%)	1.23	26/5974 (0.4%)

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	Planarity
1	A	2	20
2	D	1	4
3	E	0	6
All	All	3	30

There are no bond-length outliers.

5 of 26 angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	107	GLU	N-CA-C	-6.77	92.71	111.00
1	A	382	CYS	CA-CB-SG	-6.63	102.06	114.00
2	D	123	GLU	N-CA-C	-6.61	93.14	111.00
1	A	397	ALA	N-CA-C	-6.60	93.18	111.00
1	A	321	SER	N-CA-CB	-6.14	101.30	110.50

All chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms
1	A	50	ILE	CB

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Mol	Chain	Res	Type	Atoms
1	A	63	ILE	CB
2	D	39	ILE	CB

5 of 29 planar outliers are listed below.

Mol	Chain	Res	Type	Group
3	E	62	ALA	Peptide
1	A	185	TYR	Sidechain
3	E	72	LYS	Peptide
1	A	37	GLY	Peptide
1	A	227	TYR	Sidechain

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	2807	587	2765	53
2	D	713	164	703	10
3	E	810	201	792	11
4	A	24	0	0	6
5	A	5	0	6	12
6	A	2	0	0	2
7	A	4	0	0	7
8	A	4	0	0	7
9	E	172	16	120	8
All	All	4541	968	4386	72

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.

5 of 72 clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:238:LYS:HG2	1:A:257:THR:HB	0.90	1.44
1:A:232:MET:SD	8:A:9:CMO:C	0.81	2.68
1:A:296:PHE:HB3	5:A:4:PDT:H11	0.80	1.51
1:A:232:MET:SD	7:A:7:CYN:C	0.78	2.70
1:A:104:ALA:HB2	1:A:139:PHE:HB3	0.75	1.58

6.3 Torsion angles

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	369/371 (99%)	311 (84%)	49 (13%)	9 (2%)	9 46
2	D	86/88 (98%)	75 (87%)	10 (12%)	1 (1%)	17 64
3	E	105/107 (98%)	76 (72%)	20 (19%)	9 (9%)	2 12
All	All	560/566 (99%)	462 (82%)	79 (14%)	19 (3%)	6 36

5 of 19 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	33	ALA
3	E	89	ALA
1	A	57	PRO
1	A	284	SER
1	A	295	ILE

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	297/297 (100%)	260 (88%)	37 (12%)	8 50
2	D	76/76 (100%)	68 (89%)	8 (11%)	10 55
3	E	88/88 (100%)	78 (89%)	10 (11%)	9 52
All	All	461/461 (100%)	406 (88%)	55 (12%)	8 51

5 of 55 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	201	LYS
1	A	74	THR
3	E	74	THR
1	A	248	SER
2	D	114	SER

6.3.3 RNA

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains

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

6.5 Carbohydrates

There are no carbohydrates in this entry.

6.6 Ligand geometry

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 for Mogul analysis.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
9	HEC	E	109	3	26,50,50	1.32	0 (0%)
9	HEC	E	112	3	26,50,50	1.42	0 (0%)
9	HEC	E	110	3	26,50,50	1.35	0 (0%)
4	SF4	A	3	1	0,12,12	0.00	-
9	HEC	E	111	3	26,50,50	1.49	0 (0%)
5	PDT	A	4	6	4,4,4	2.55	0 (0%)
7	CYN	A	7	8,6	0,1,1	0.00	-
4	SF4	A	1	1	0,12,12	0.00	-
8	CMO	A	10	7,6	0,1,1	0.00	-
8	CMO	A	9	7,6	0,1,1	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
4	SF4	A	2	1	0,12,12	0.00	-
7	CYN	A	8	8,6	0,1,1	0.00	-

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
9	HEC	E	109	3	18,82,82	1.82	0 (0%)
9	HEC	E	112	3	18,82,82	1.57	0 (0%)
9	HEC	E	110	3	18,82,82	1.47	0 (0%)
4	SF4	A	3	1	-	-	-
9	HEC	E	111	3	18,82,82	1.99	0 (0%)
5	PDT	A	4	6	3,3,3	1.36	0 (0%)
7	CYN	A	7	8,6	-	-	-
4	SF4	A	1	1	-	-	-
8	CMO	A	10	7,6	-	-	-
8	CMO	A	9	7,6	-	-	-
4	SF4	A	2	1	-	-	-
7	CYN	A	8	8,6	-	-	-

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
9	HEC	E	112	3	-	0,6,54,54	-
5	PDT	A	4	6	-	0,2,2,2	-
4	SF4	A	3	1	-	-	0,6,5,5
9	HEC	E	111	3	-	0,6,54,54	-
9	HEC	E	110	3	-	0,6,54,54	-
4	SF4	A	1	1	-	-	0,6,5,5
4	SF4	A	2	1	-	-	0,6,5,5
9	HEC	E	109	3	-	0,6,54,54	-

There are no bond-length outliers.

There are no bond-angle outliers.

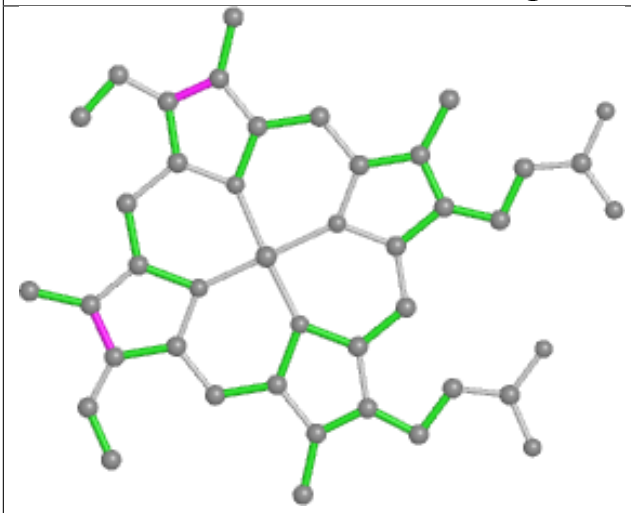
There are no chirality outliers.

There are no torsion outliers.

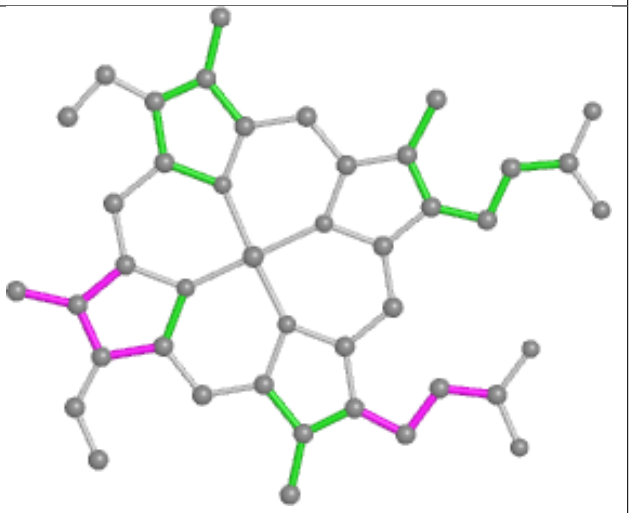
There are no ring outliers.

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.

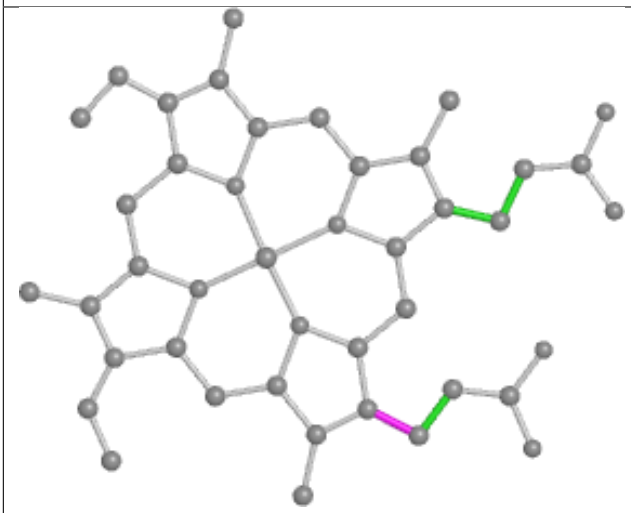
Ligand HEC E 112



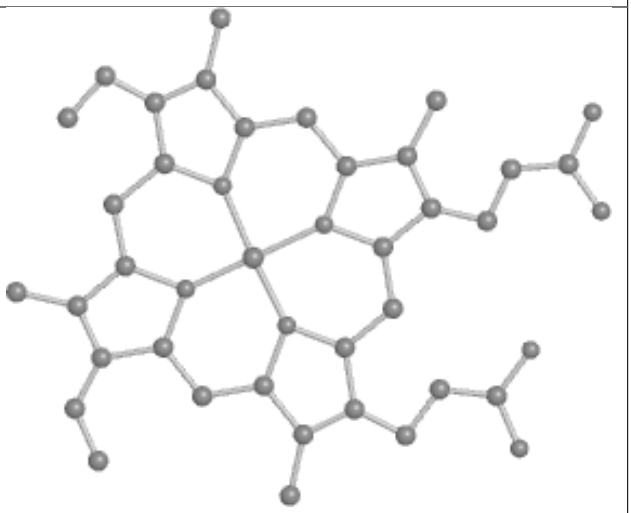
Bond lengths



Bond angles

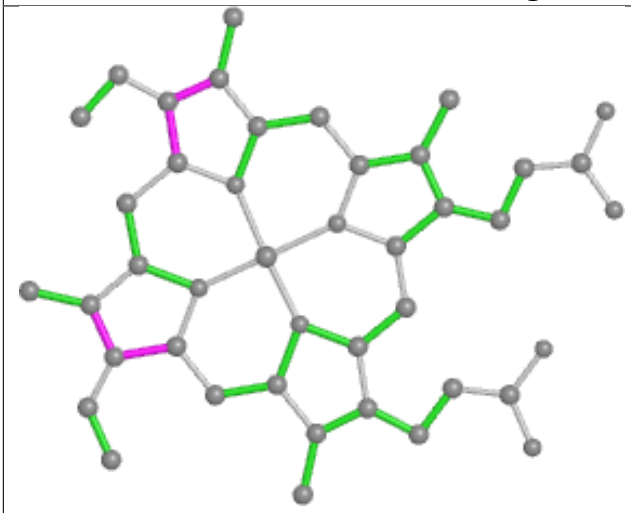


Torsions

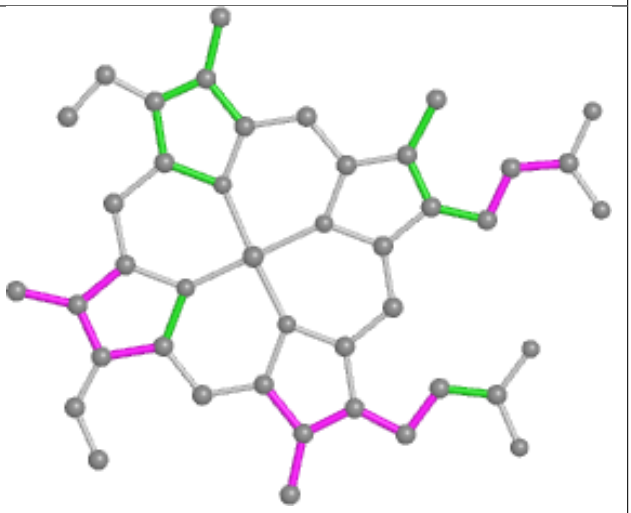


Rings

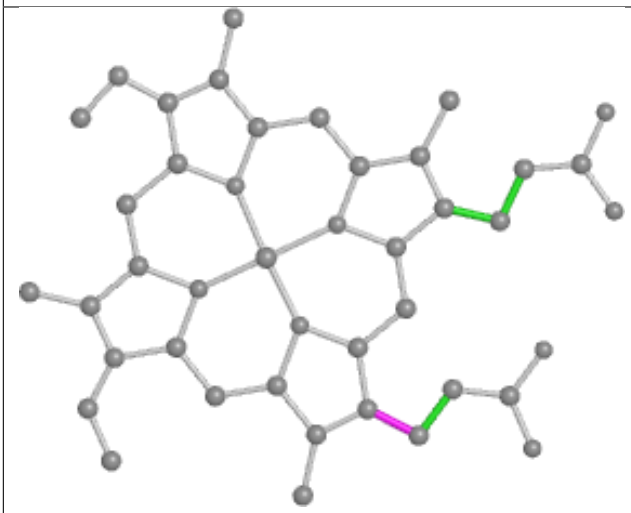
Ligand HEC E 111



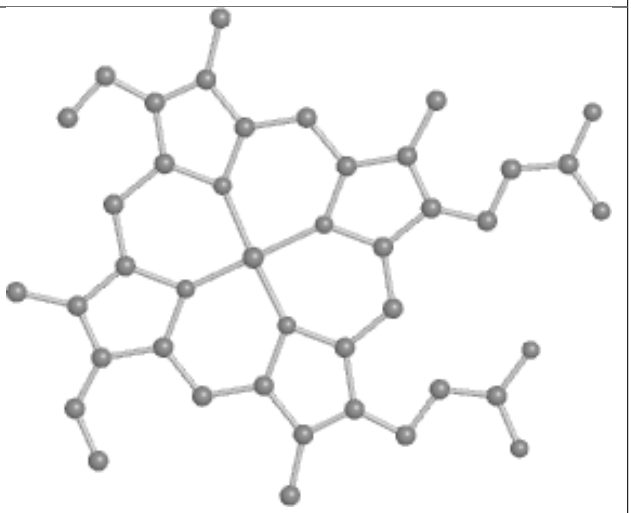
Bond lengths



Bond angles

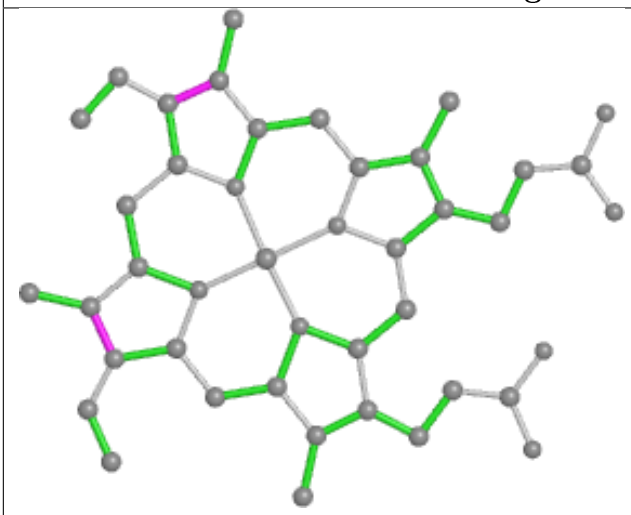


Torsions

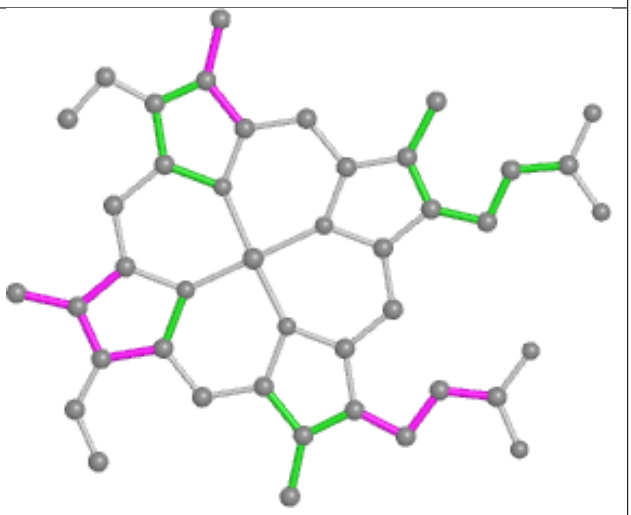


Rings

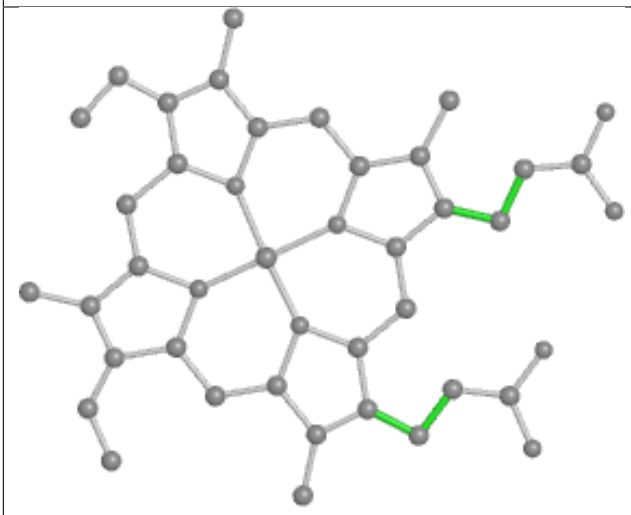
Ligand HEC E 110



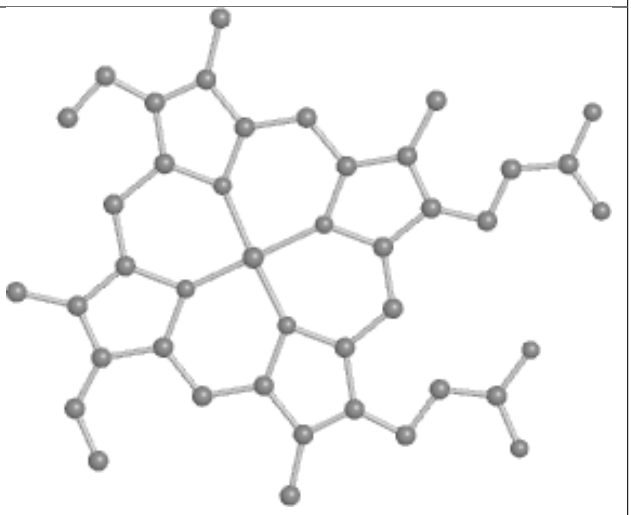
Bond lengths



Bond angles

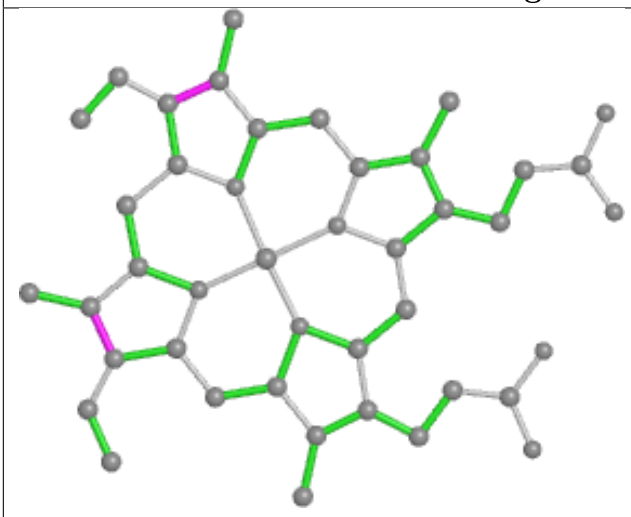


Torsions

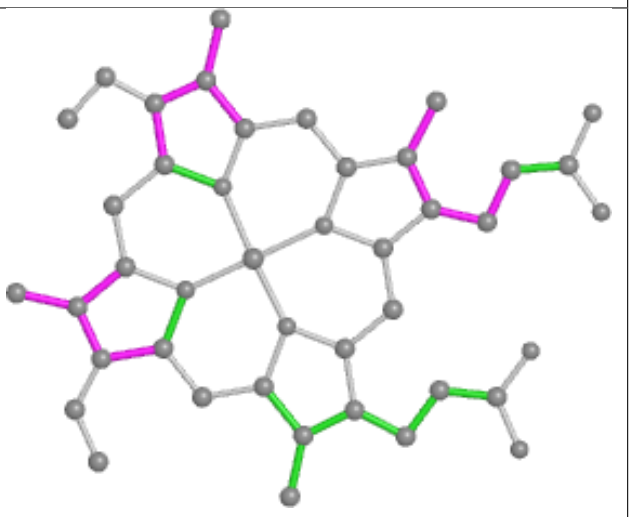


Rings

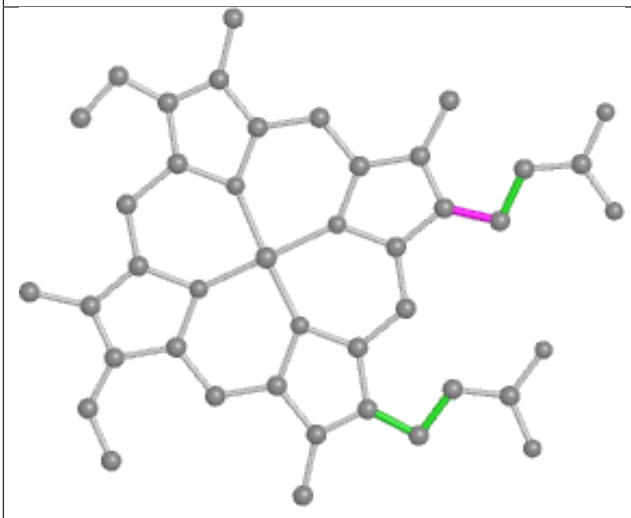
Ligand HEC E 109



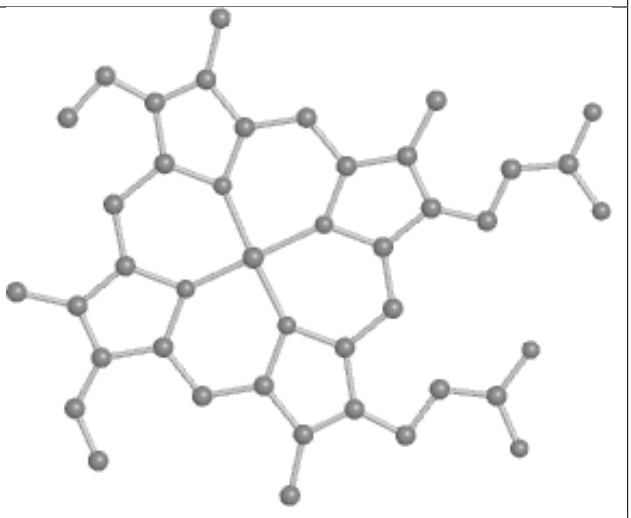
Bond lengths



Bond angles



Torsions



Rings

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided