wwPDB X-ray Structure Validation Summary Report (i)

Mar 8, 2026 – 05:43 PM UTC

PDB ID	:	1NOD / pdb_00001nod
Title	:	MURINE INDUCIBLE NITRIC OXIDE SYNTHASE OXYGENASE DIMER (DELTA 65) WITH TETRAHYDROBIOPTERIN AND SUBSTRATE L-ARGININE
Authors	:	Crane, B.R.; Arvai, A.S.; Getzoff, E.D.; Stuehr, D.J.; Tainer, J.A.
Deposited on	:	1998-03-05
Resolution	:	2.60 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:

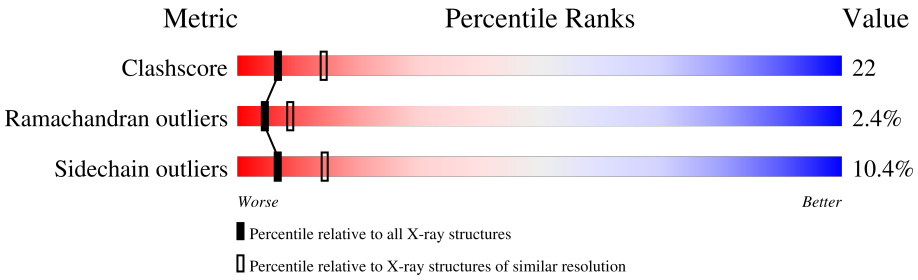
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.60 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	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)

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	423	55% 34% 7%
1	B	423	54% 36% 7%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	H4B	B	902	X	-	-	-

2 Entry composition (i)

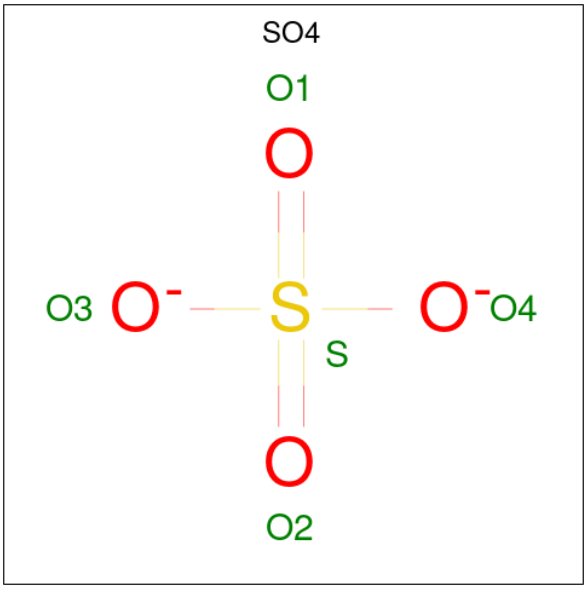
There are 6 unique types of molecules in this entry. The entry contains 7208 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 NITRIC OXIDE SYNTHASE.

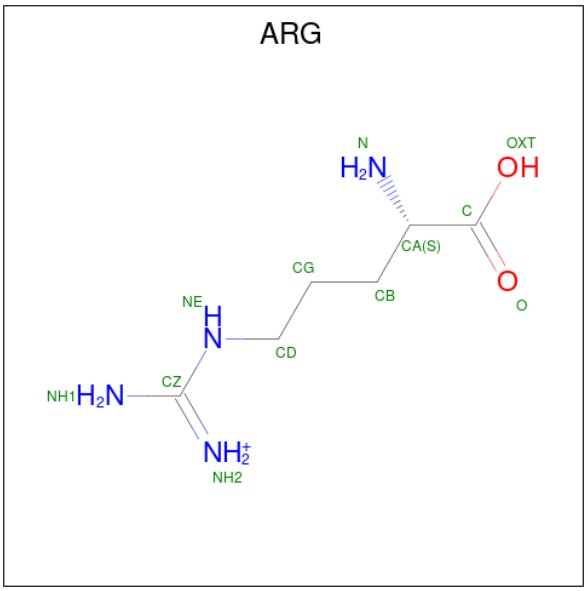
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	S	0	0	0
			3373	2162	582	609	20			
1	B	413	Total	C	N	O	S	0	0	0
			3368	2159	581	608	20			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



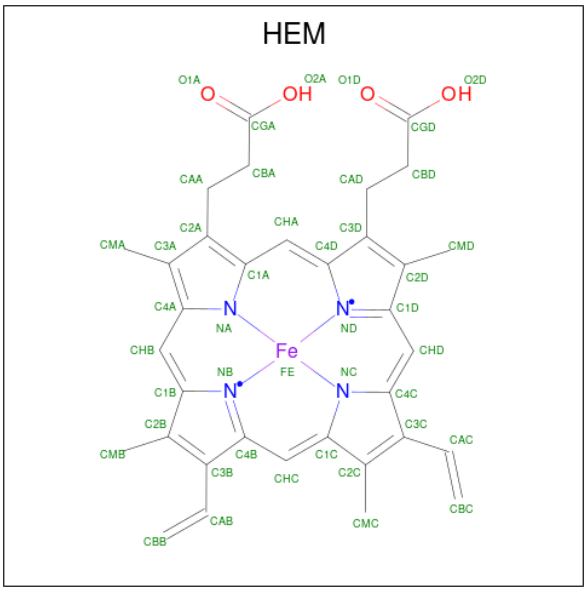
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	O	S		0	0
			5	4	1			

- Molecule 3 is ARGININE (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			12	6	4	2		
3	B	1	Total	C	N	O	0	0
			12	6	4	2		

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

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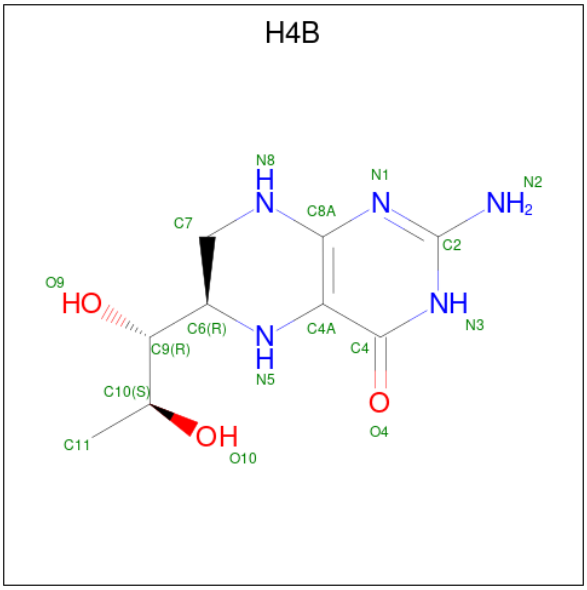
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 5 is 5,6,7,8-TETRAHYDROBIOPTERIN (CCD ID: H4B) (formula: $C_9H_{15}N_5O_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O		0	0
			17	9	5	3			
5	B	1	Total	C	N	O		0	0
			17	9	5	3			

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	148	Total	O	0	0
			148	148		
6	B	170	Total	O	0	0
			170	170		

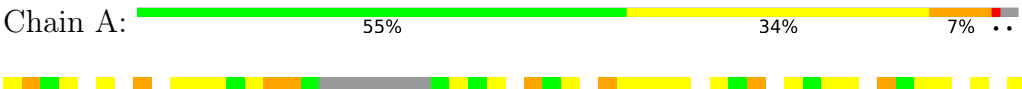
3 Residue-property plots (i)

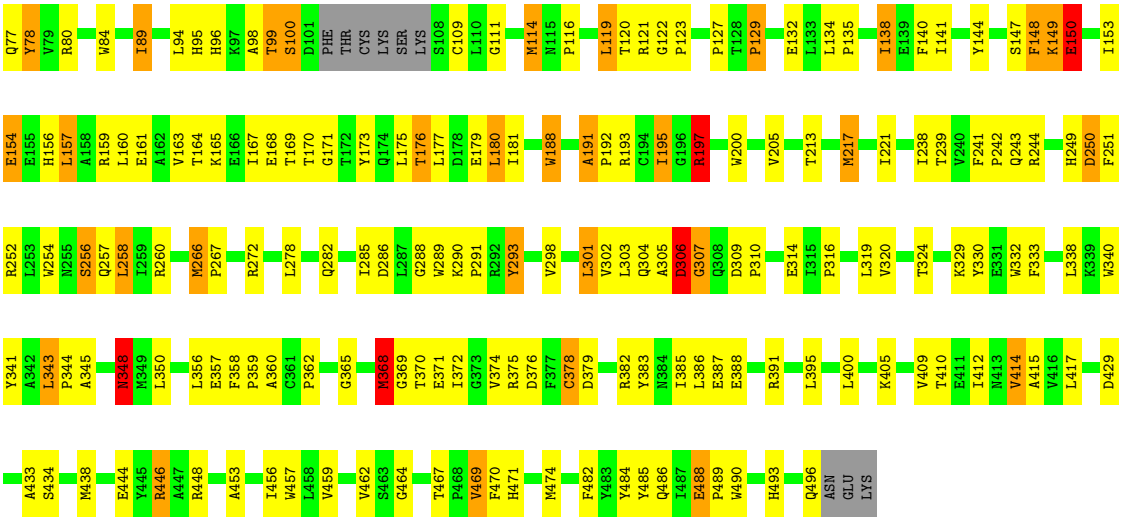
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: NITRIC OXIDE SYNTHASE

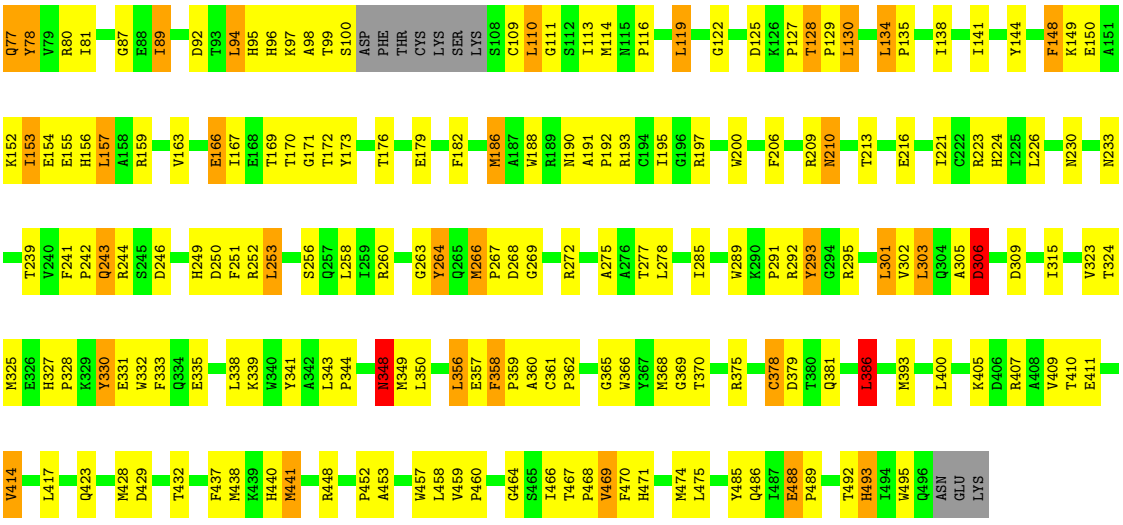
Chain A:





• Molecule 1: NITRIC OXIDE SYNTHASE

Chain B:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α, β, γ	213.00Å 213.00Å 114.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.60	Depositor
% Data completeness (in resolution range)	95.3 (20.00-2.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.229 , 0.288	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7208	wwPDB-VP
Average B, all atoms (Å^2)	64.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, H4B, SO4

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	0.48	0/3471	1.06	27/4719 (0.6%)
1	B	0.49	0/3466	1.06	34/4712 (0.7%)
All	All	0.48	0/6937	1.06	61/9431 (0.6%)

There are no bond length outliers.

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	87	GLY	N-CA-C	-7.80	104.99	115.36
1	B	122	GLY	N-CA-C	7.33	120.80	112.00
1	A	266	MET	CA-C-N	7.27	127.12	119.05
1	A	266	MET	C-N-CA	7.27	127.12	119.05
1	A	293	TYR	N-CA-C	7.11	121.19	111.17

There are no chirality outliers.

There are no planarity outliers.

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	3373	0	3267	147	0
1	B	3368	0	3265	141	0
2	A	5	0	0	1	0
3	A	12	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	12	0	12	1	0
4	A	43	0	30	1	0
4	B	43	0	30	2	0
5	A	17	0	14	1	0
5	B	17	0	14	1	0
6	A	148	0	0	15	0
6	B	170	0	0	15	0
All	All	7208	0	6644	291	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 22.

The worst 5 of 291 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:266:MET:SD	1:A:272:ARG:HD3	2.02	0.99
1:B:356:LEU:HD13	1:B:357:GLU:H	1.33	0.90
1:A:221:ILE:HG21	1:A:301:LEU:HD21	1.54	0.89
1:B:77:GLN:HE21	1:B:77:GLN:HA	1.39	0.86
1:B:243:GLN:HB2	1:B:356:LEU:HD12	1.58	0.86

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	410/423 (97%)	352 (86%)	49 (12%)	9 (2%)	5 10
1	B	409/423 (97%)	355 (87%)	43 (10%)	11 (3%)	4 7
All	All	819/846 (97%)	707 (86%)	92 (11%)	20 (2%)	4 9

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	306	ASP
1	B	306	ASP
1	A	111	GLY
1	B	111	GLY
1	B	150	GLU

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	361/371 (97%)	325 (90%)	36 (10%)	7 16
1	B	361/371 (97%)	324 (90%)	37 (10%)	7 15
All	All	722/742 (97%)	649 (90%)	73 (10%)	7 15

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	301	LEU
1	B	469	VAL
1	B	306	ASP
1	B	386	LEU
1	A	329	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	210	ASN
1	B	249	HIS
1	B	493	HIS
1	B	233	ASN
1	B	257	GLN

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)

7 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	SO4	A	907	-	4,4,4	0.50	0	6,6,6	0.48	0
3	ARG	A	906	-	10,11,11	0.72	0	9,13,13	0.42	0
4	HEM	B	901	1	50,50,50	1.44	8 (16%)	67,82,82	1.16	7 (10%)
5	H4B	B	902	-	17,18,18	2.75	5 (29%)	14,26,26	2.13	5 (35%)
3	ARG	B	906	-	10,11,11	0.71	0	9,13,13	0.41	0
4	HEM	A	901	1	50,50,50	1.49	12 (24%)	67,82,82	1.14	5 (7%)
5	H4B	A	902	-	17,18,18	2.63	5 (29%)	14,26,26	2.21	4 (28%)

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
3	ARG	A	906	-	-	2/11/11/11	-
4	HEM	B	901	1	-	2/14/54/54	-
5	H4B	B	902	-	1/1/3/5	2/8/17/17	0/2/2/2
3	ARG	B	906	-	-	2/11/11/11	-
4	HEM	A	901	1	-	3/14/54/54	-
5	H4B	A	902	-	-	2/8/17/17	0/2/2/2

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	902	H4B	C7-N8	-7.38	1.39	1.46
5	B	902	H4B	C7-C6	-7.05	1.45	1.52
5	A	902	H4B	C7-N8	-6.95	1.39	1.46
5	A	902	H4B	C7-C6	-6.43	1.46	1.52
4	B	901	HEM	CAB-C3B	-3.16	1.39	1.47

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	902	H4B	C2-N1-C8A	4.64	121.55	113.36
5	A	902	H4B	O4-C4-C4A	-4.56	116.27	127.26
5	A	902	H4B	C2-N1-C8A	4.36	121.06	113.36
5	B	902	H4B	O4-C4-C4A	-4.03	117.54	127.26
4	A	901	HEM	C3B-C4B-NB	3.81	112.20	109.47

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	B	902	H4B	C6

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	902	H4B	C7-C6-C9-O9
5	A	902	H4B	C7-C6-C9-C10
5	B	902	H4B	C7-C6-C9-O9
5	B	902	H4B	C7-C6-C9-C10
3	A	906	ARG	NE-CD-CG-CB

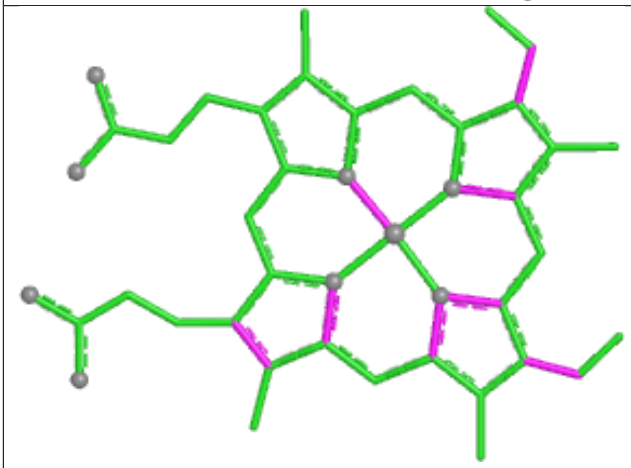
There are no ring outliers.

7 monomers are involved in 8 short contacts:

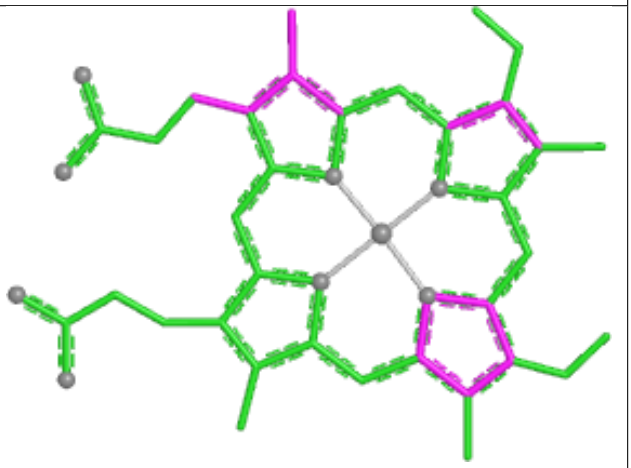
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	907	SO4	1	0
3	A	906	ARG	1	0
4	B	901	HEM	2	0
5	B	902	H4B	1	0
3	B	906	ARG	1	0
4	A	901	HEM	1	0
5	A	902	H4B	1	0

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.

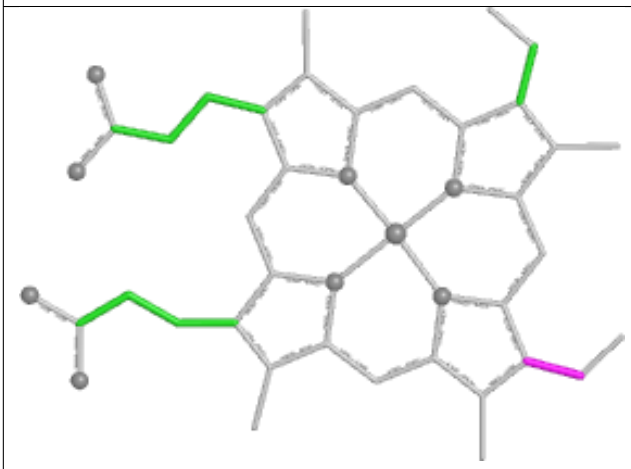
Ligand HEM B 901



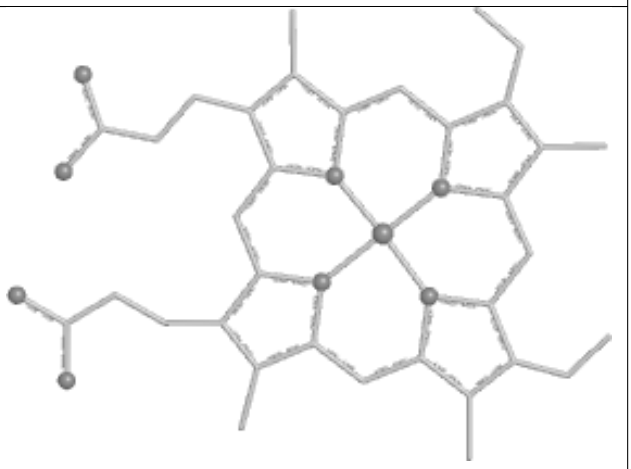
Bond lengths



Bond angles

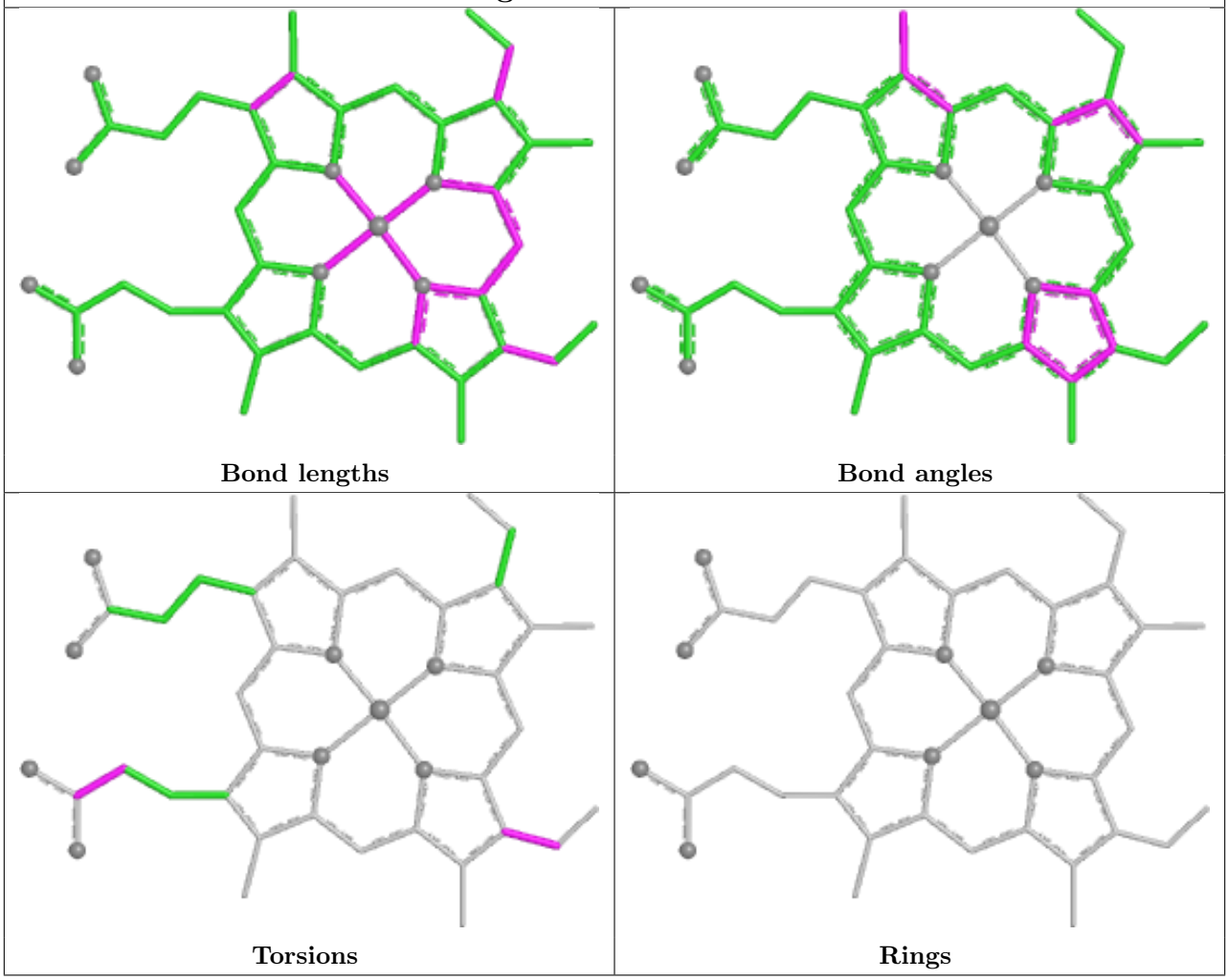


Torsions



Rings

Ligand HEM A 901



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.