



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 01:15 PM UTC

PDB ID : 4HHB / pdb_00004hhb
Title : THE CRYSTAL STRUCTURE OF HUMAN DEOXYHAEMOGLOBIN AT
1.74 ANGSTROMS RESOLUTION
Authors : Fermi, G.; Perutz, M.F.
Deposited on : 1984-03-07
Resolution : 1.74 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 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) : **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

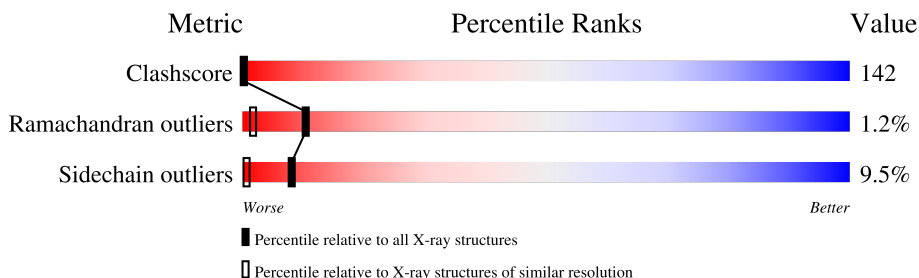
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.74 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	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	141	45% 28% 27%
1	C	141	40% 40% 18%
2	B	146	48% 30% 22%
2	D	146	38% 25% 34%

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
3	HEM	C	142	-	X	-	-
3	HEM	D	148	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4779 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.

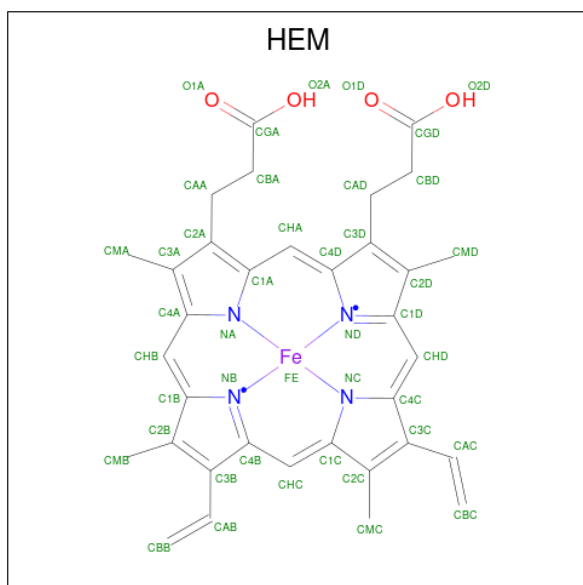
- Molecule 1 is a protein called Hemoglobin subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	0	0
			1069	685	187	194	3			
1	C	141	Total	C	N	O	S	0	0	0
			1069	685	187	194	3			

- Molecule 2 is a protein called Hemoglobin subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	146	Total	C	N	O	S	0	0	0
			1123	724	195	201	3			
2	D	146	Total	C	N	O	S	0	0	0
			1123	724	195	201	3			

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	P		
			1	1	0	0
4	D	1	Total	P		
			1	1	0	0

- Molecule 5 is water.

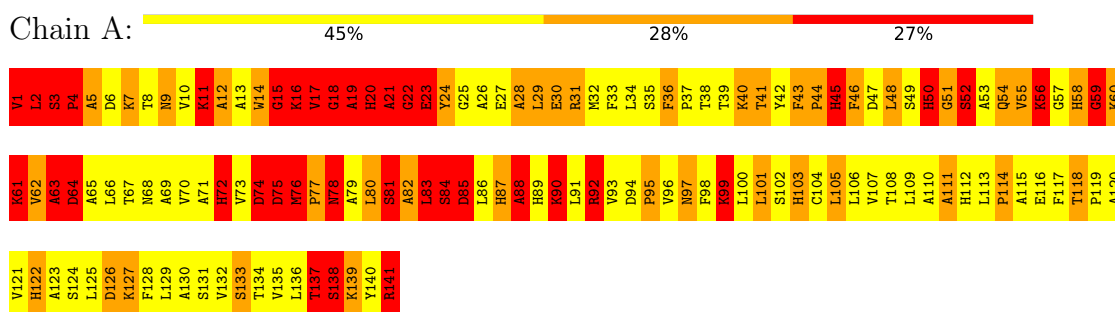
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	56	Total	O		
			56	56	0	0
5	B	57	Total	O		
			57	57	0	0
5	C	59	Total	O		
			59	59	0	0
5	D	49	Total	O		
			49	49	0	0

3 Residue-property plots

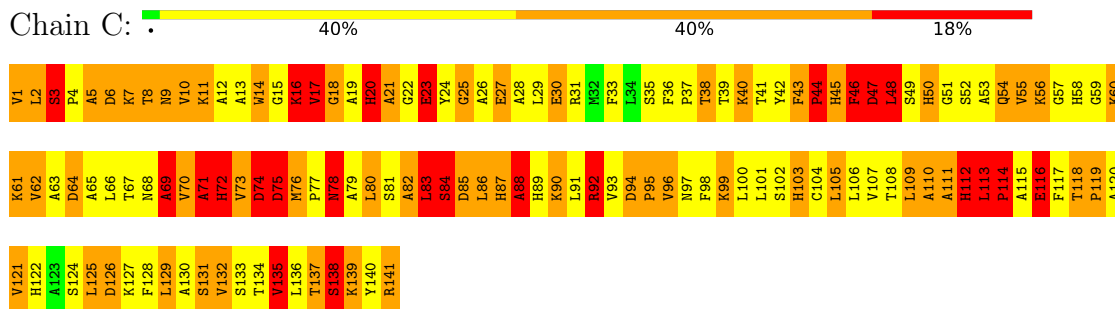
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

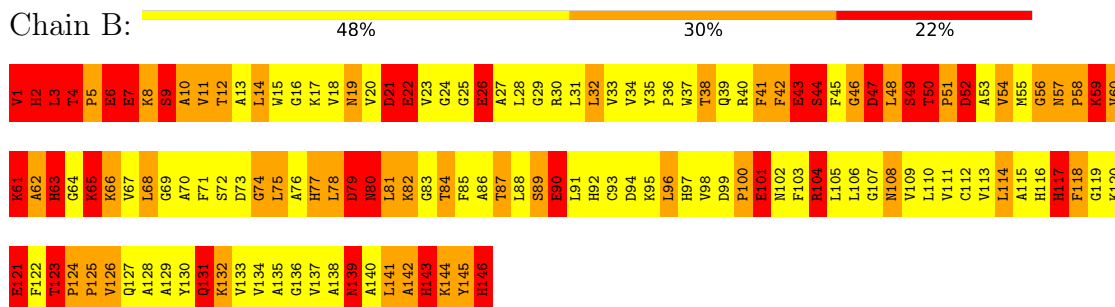
- Molecule 1: Hemoglobin subunit alpha



- Molecule 1: Hemoglobin subunit alpha



- Molecule 2: Hemoglobin subunit beta



- Molecule 2: Hemoglobin subunit beta





4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.15Å 83.59Å 53.80Å 90.00° 99.34° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.74	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.74)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	unknown	Depositor
R, R_{free}	0.135 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4779	wwPDB-VP
Average B, all atoms (Å ²)	24.0	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: PO4, 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	9.87	528/1097 (48.1%)	7.13	602/1491 (40.4%)
1	C	9.98	511/1097 (46.6%)	7.37	563/1491 (37.8%)
2	B	11.66	521/1153 (45.2%)	7.56	637/1566 (40.7%)
2	D	12.76	567/1153 (49.2%)	8.54	658/1566 (42.0%)
All	All	11.16	2127/4500 (47.3%)	7.68	2460/6114 (40.2%)

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	A	1	50
1	C	2	45
2	B	2	49
2	D	5	62
All	All	10	206

The worst 5 of 2127 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	92	ARG	NE-CZ	149.01	2.96	1.33
2	D	104	ARG	NE-CZ	113.64	2.58	1.33
1	A	92	ARG	NE-CZ	113.03	2.57	1.33
2	D	2	HIS	CG-ND1	100.10	2.48	1.38
2	B	2	HIS	ND1-CE1	85.56	2.18	1.32

The worst 5 of 2460 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	92	ARG	NE-CZ-NH2	-90.86	37.43	119.20
2	D	80	ASN	CA-CB-CG	63.24	175.84	112.60
2	B	139	ASN	OD1-CG-ND2	-59.66	62.94	122.60
1	A	92	ARG	CD-NE-CZ	-52.47	50.94	124.40
2	B	143	HIS	ND1-CG-CD2	48.68	154.78	106.10

5 of 10 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	137	THR	CB
2	B	12	THR	CB
2	B	50	THR	CB
1	C	78	ASN	CA
1	C	118	THR	CB

5 of 206 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	VAL	Mainchain
1	A	11	LYS	Mainchain
1	A	3	SER	Mainchain
1	A	4	PRO	Mainchain
1	A	9	ASN	Mainchain

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	1069	0	1069	242	0
1	C	1069	0	1066	255	1
2	B	1123	0	1107	327	0
2	D	1123	0	1116	427	0
3	A	43	0	30	6	0
3	B	43	0	30	10	0
3	C	43	0	30	15	0
3	D	43	0	30	12	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	56	0	0	1	0
5	B	57	0	0	1	2
5	C	59	0	0	0	1
5	D	49	0	0	1	0
All	All	4779	0	4478	1286	2

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 142.

The worst 5 of 1286 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:118:THR:CA	1:C:118:THR:CB	1.75	1.63
1:C:113:LEU:CD1	1:C:113:LEU:CG	1.75	1.63
2:D:2:HIS:CD2	2:D:2:HIS:CG	1.85	1.63
2:B:50:THR:CG2	2:B:50:THR:CB	1.75	1.63
1:A:40:LYS:CA	1:A:40:LYS:CB	1.75	1.61

All (2) 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)
1:C:85:ASP:OD2	5:B:204:HOH:O[2_657]	1.41	0.79
5:B:204:HOH:O	5:C:161:HOH:O[2_647]	2.02	0.18

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	139/141 (99%)	122 (88%)	14 (10%)	3 (2%)	5 0
1	C	139/141 (99%)	126 (91%)	13 (9%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	144/146 (99%)	129 (90%)	14 (10%)	1 (1%)	18	6
2	D	144/146 (99%)	128 (89%)	13 (9%)	3 (2%)	5	0
All	All	566/574 (99%)	505 (89%)	54 (10%)	7 (1%)	10	2

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	16	LYS
2	D	73	ASP
1	A	21	ALA
2	D	77	HIS
2	B	4	THR

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	113/113 (100%)	104 (92%)	9 (8%)	11	1
1	C	113/113 (100%)	109 (96%)	4 (4%)	32	9
2	B	118/118 (100%)	107 (91%)	11 (9%)	8	1
2	D	118/118 (100%)	98 (83%)	20 (17%)	2	0
All	All	462/462 (100%)	418 (90%)	44 (10%)	8	0

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	21	ASP
2	D	67	VAL
2	D	22	GLU
2	D	47	ASP
2	D	72	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	68	ASN
2	D	80	ASN
1	C	72	HIS
2	D	139	ASN
2	D	63	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](#)

Of 6 ligands modelled in this entry, 2 are modelled with single atom - leaving 4 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	$\# Z > 2$
3	HEM	B	148	2	50,50,50	5.47	26 (52%)	67,82,82	5.59	43 (64%)
3	HEM	C	142	1	50,50,50	6.85	35 (70%)	67,82,82	4.54	42 (62%)
3	HEM	D	148	2	50,50,50	8.46	37 (74%)	67,82,82	4.73	42 (62%)
3	HEM	A	142	1	50,50,50	7.85	32 (64%)	67,82,82	6.01	40 (59%)

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	HEM	B	148	2	-	3/14/54/54	-
3	HEM	C	142	1	-	3/14/54/54	-
3	HEM	D	148	2	-	5/14/54/54	-
3	HEM	A	142	1	-	5/14/54/54	-

The worst 5 of 130 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	148	HEM	CBA-CGA	38.36	2.39	1.50
3	A	142	HEM	CBA-CGA	35.57	2.32	1.50
3	C	142	HEM	CBA-CGA	34.03	2.29	1.50
3	A	142	HEM	CBD-CGD	25.29	2.09	1.50
3	D	148	HEM	CBD-CGD	22.13	2.01	1.50

The worst 5 of 167 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	142	HEM	O2A-CGA-O1A	-23.84	62.01	123.33
3	D	148	HEM	O1A-CGA-CBA	-18.59	64.13	123.09
3	B	148	HEM	C4C-C3C-C2C	-16.82	92.23	106.81
3	A	142	HEM	O1A-CGA-CBA	-16.32	71.34	123.09
3	C	142	HEM	O2A-CGA-CBA	-14.12	69.38	114.00

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	148	HEM	C4D-C3D-CAD-CBD
3	A	142	HEM	C2B-C3B-CAB-CBB
3	D	148	HEM	C2B-C3B-CAB-CBB
3	C	142	HEM	CAA-CBA-CGA-O1A
3	C	142	HEM	CAD-CBD-CGD-O2D

There are no ring outliers.

4 monomers are involved in 43 short contacts:

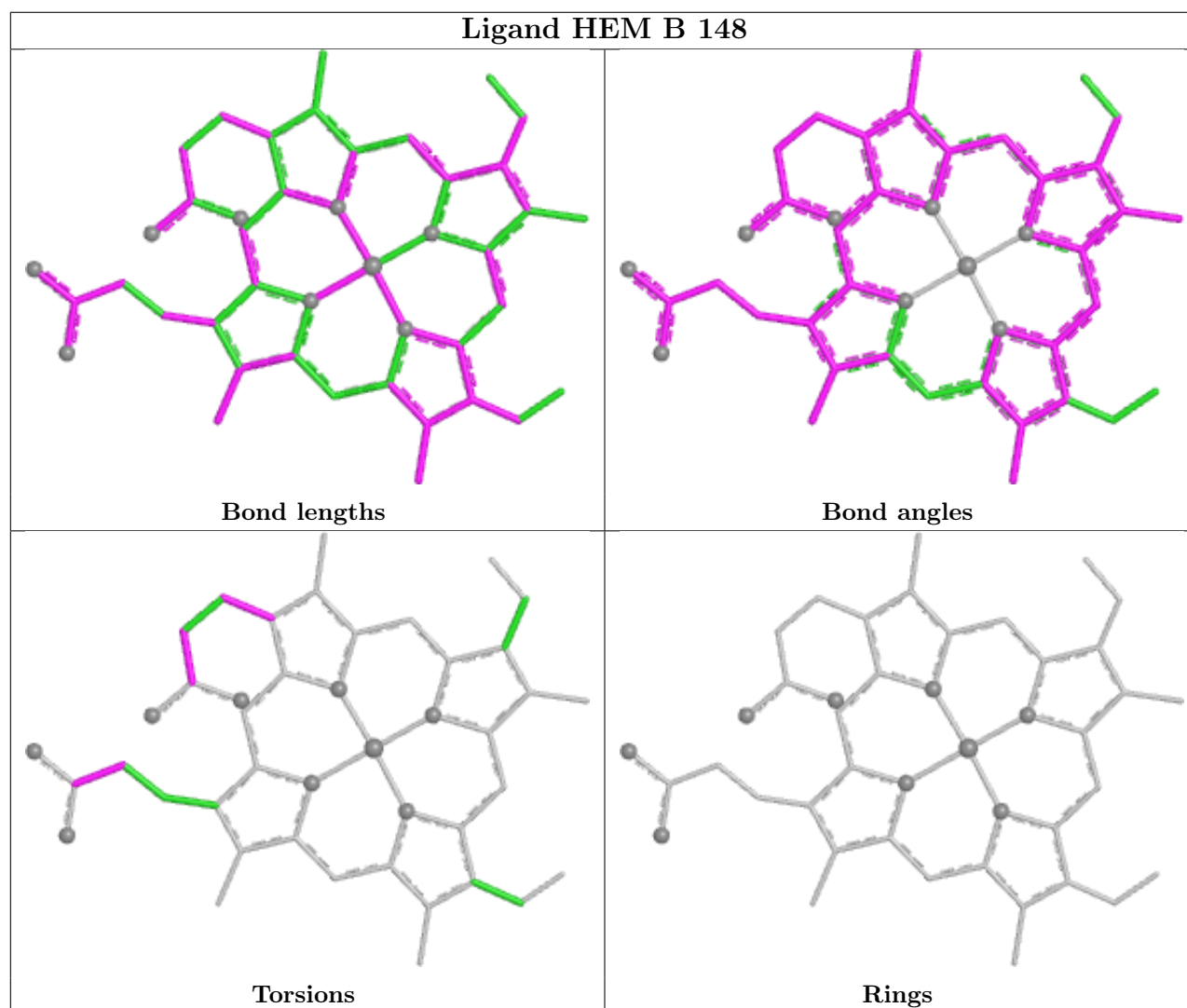
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	148	HEM	10	0
3	C	142	HEM	15	0

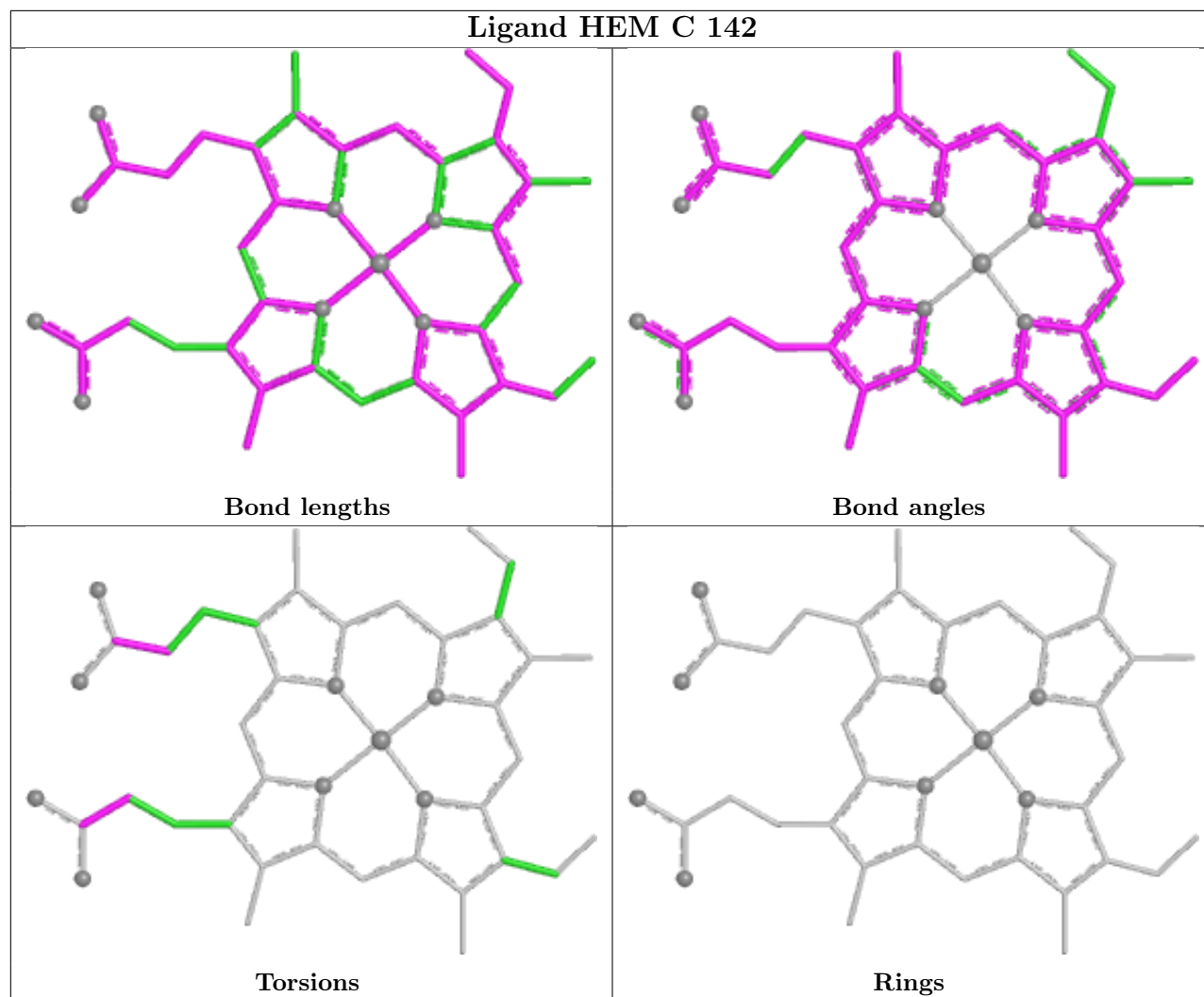
Continued on next page...

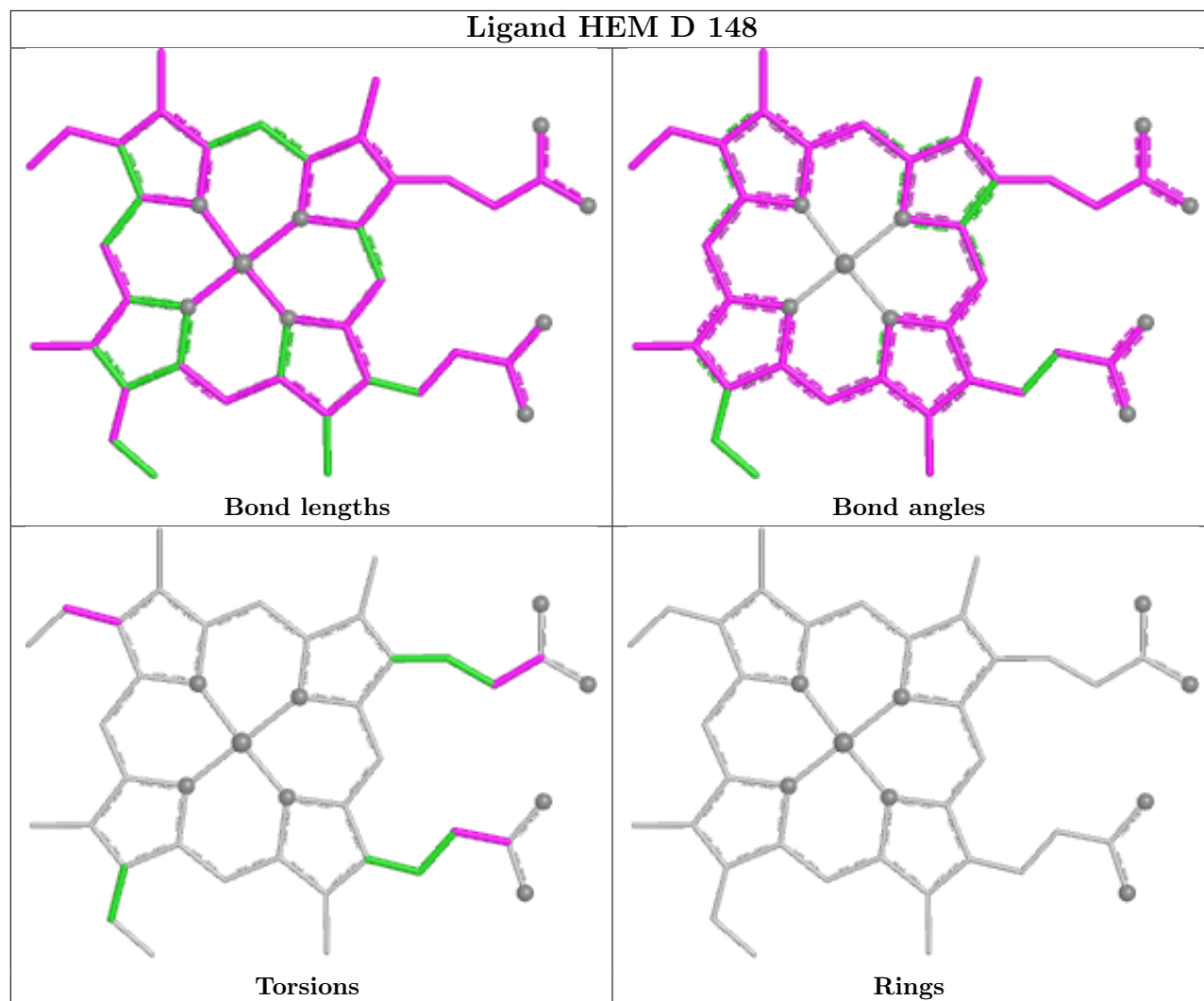
Continued from previous page...

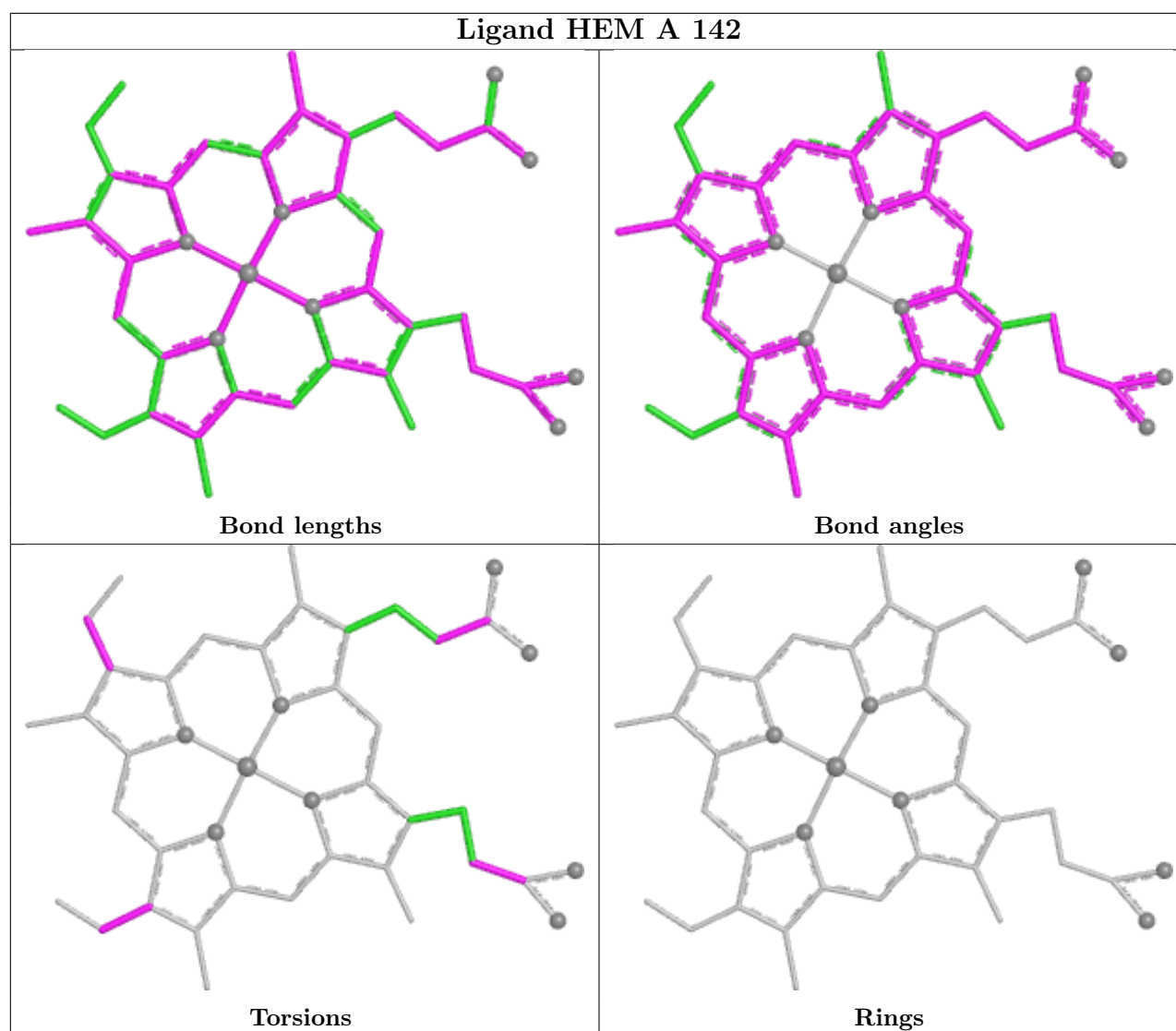
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	148	HEM	12	0
3	A	142	HEM	6	0

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.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	13
2	D	13
1	A	10
1	C	9

The worst 5 of 45 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	74:GLY	C	75:LEU	N	1.70
1	C	82:ALA	C	83:LEU	N	1.69
1	B	81:LEU	C	82:LYS	N	1.66
1	B	76:ALA	C	77:HIS	N	1.64
1	D	95:LYS	C	96:LEU	N	1.64

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.