



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 5, 2026 – 03:30 PM EDT

PDB ID : 1HBS / pdb_00001hbs
Title : REFINED CRYSTAL STRUCTURE OF DEOXYHEMOGLOBIN S. I. RE-
STRAINED LEAST-SQUARES REFINEMENT AT 3.0-ANGSTROMS RES-
OLUTION
Authors : Padlan, E.A.; Love, W.E.
Deposited on : 1982-06-02
Resolution : 3.00 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)	:	2.50

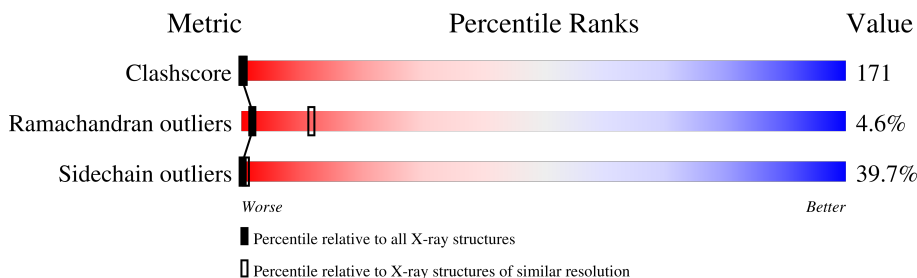
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)

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	13% 62% 26%
1	C	141	9% 55% 36%
1	E	141	13% 53% 34%
1	G	141	12% 51% 37%
2	B	146	8% 63% 29%
2	D	146	10% 64% 26%
2	F	146	12% 58% 30%
2	H	146	11% 51% 38%

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	A	142	-	-	X	-
3	HEM	B	147	-	X	-	-
3	HEM	D	147	-	-	X	-
3	HEM	E	142	-	X	X	-
3	HEM	F	147	-	X	-	-
3	HEM	G	142	-	-	X	-
3	HEM	H	147	-	X	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9104 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 S (DEOXY) (ALPHA CHAIN).

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			
1	E	141	Total	C	N	O	S	0	0	0
			1069	685	187	194	3			
1	G	141	Total	C	N	O	S	0	0	0
			1069	685	187	194	3			

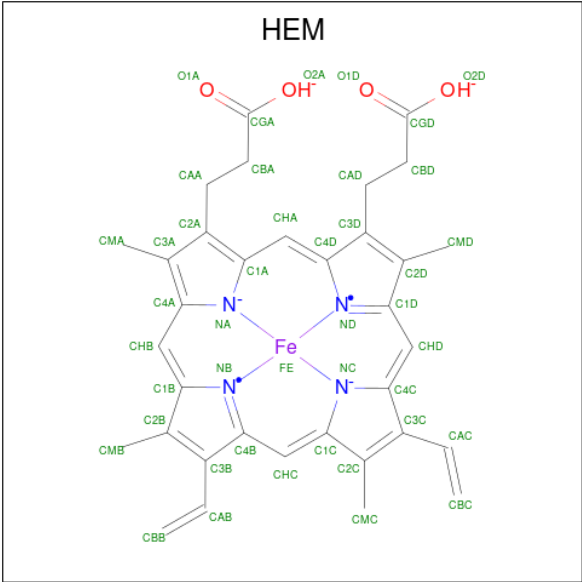
- Molecule 2 is a protein called HEMOGLOBIN S (DEOXY) (BETA CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	146	Total	C	N	O	S	0	0	0
			1121	724	195	199	3			
2	D	146	Total	C	N	O	S	0	0	0
			1121	724	195	199	3			
2	F	146	Total	C	N	O	S	0	0	0
			1121	724	195	199	3			
2	H	146	Total	C	N	O	S	0	0	0
			1121	724	195	199	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	6	VAL	GLU	conflict	UNP P68871
D	6	VAL	GLU	conflict	UNP P68871
F	6	VAL	GLU	conflict	UNP P68871
H	6	VAL	GLU	conflict	UNP P68871

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



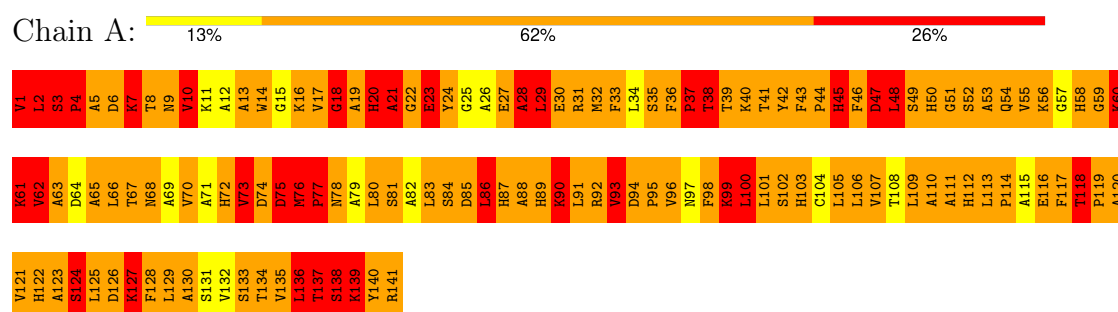
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	E	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	F	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	G	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	H	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

3 Residue-property plots

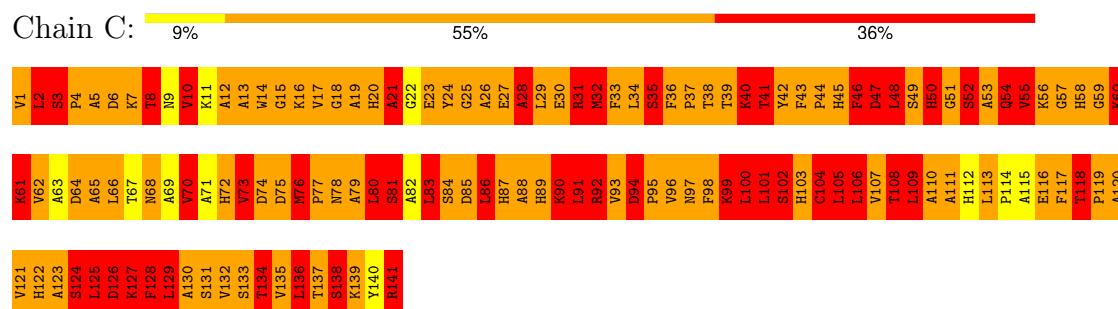
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

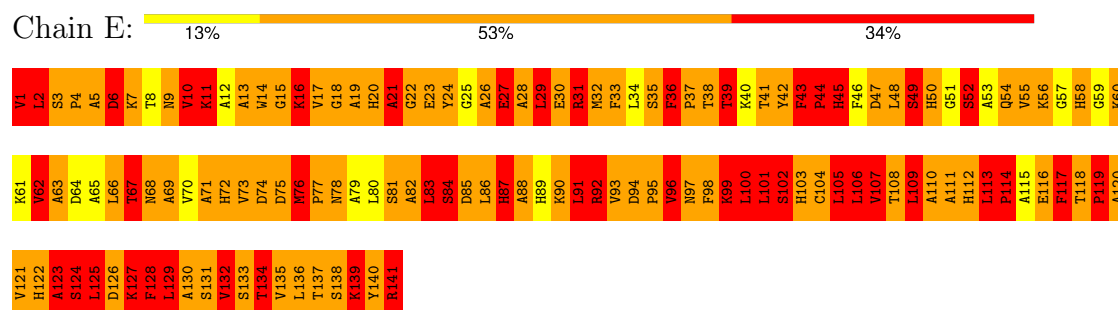
• Molecule 1: HEMOGLOBIN S (DEOXY) (ALPHA CHAIN)



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Category	Percentage
Very bad	12%
Bad	51%
Good	37%



Response	Percentage
Not a democracy	8%
Is a democracy	63%
Unsure	29%



Threat Level	Percentage
Not a threat	10%
Somewhat of a threat	64%
A major threat	26%



Response	Percentage
Yes	12%
No	58%
Don't know	30%



Category	Percentage
Very bad	11%
Bad	51%
Good	38%

E121	K61	V1
	A62	H2
	H63	L3
	G64	T4
	K65	P5
	K66	V6
	V67	E7
	L68	K8
	G69	S9
	A70	A10
Y130	F71	V11
	S72	T12
	D73	A13
	G74	L14
	L75	V15
	A76	G16
	H77	K17
	L78	V18
	D79	N19
	M80	V20
A142	L81	D21
	K82	E22
	G83	V23
	T84	G24
	F85	G25
	A86	E26
	T87	A27
	L88	L28
	S89	G29
	E90	R30
K95	L91	L31
	H92	L32
	C93	V33
	D94	V34
	K95	Y35
	L96	P36
	H97	K37
	V98	T38
	D99	Q39
	P100	R40
F101	F101	F41
	M102	E42
	F103	E43
	R104	S44
	L105	F45
	L106	C46
	G107	D47
	M108	L48
	V109	S49
	L110	T50
G112	V111	P51
	G112	D52
	V113	A53
	L114	V54
	A115	M55
	H116	G56
	H117	M57
	F118	P58
	G119	K59
	Z120	M60

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	63.33Å 185.66Å 52.97Å 90.00° 92.69° 90.00°	Depositor
Resolution (Å)	(Not available) – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	unknown	Depositor
R, R_{free}	0.254 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9104	wwPDB-VP
Average B, all atoms (Å ²)	22.0	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

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	5.80	354/1097 (32.3%)	7.44	642/1491 (43.1%)
1	C	5.93	364/1097 (33.2%)	8.66	704/1491 (47.2%)
1	E	5.33	322/1097 (29.4%)	8.11	702/1491 (47.1%)
1	G	5.61	339/1097 (30.9%)	8.09	681/1491 (45.7%)
2	B	5.35	361/1151 (31.4%)	7.54	665/1564 (42.5%)
2	D	5.71	377/1151 (32.8%)	7.46	695/1564 (44.4%)
2	F	5.61	356/1151 (30.9%)	7.79	707/1564 (45.2%)
2	H	5.24	335/1151 (29.1%)	8.02	704/1564 (45.0%)
All	All	5.57	2808/8992 (31.2%)	7.89	5500/12220 (45.0%)

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	0
1	C	0	1
2	F	0	2
All	All	1	3

The worst 5 of 2808 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	38	THR	C-O	30.85	1.65	1.24
1	A	122	HIS	CE1-NE2	27.81	1.60	1.32
2	F	143	HIS	CE1-NE2	26.50	1.59	1.32
2	B	41	PHE	C-O	24.63	1.56	1.24
1	E	132	VAL	C-O	24.42	1.55	1.24

The worst 5 of 5500 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	47	ASP	CA-CB-CG	55.17	167.77	112.60
1	E	31	ARG	NE-CZ-NH1	50.69	172.19	121.50
2	B	45	PHE	CA-CB-CG	46.21	160.01	113.80
1	E	10	VAL	CA-C-N	43.85	177.45	120.44
1	E	10	VAL	C-N-CA	43.85	177.45	120.44

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	20	HIS	CA

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	141	ARG	Sidechain
2	F	23	VAL	Mainchain,Peptide

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	1069	0	1060	340	0
1	C	1069	0	1048	410	3
1	E	1069	0	1058	341	0
1	G	1069	0	1056	418	0
2	B	1121	0	1111	385	0
2	D	1121	0	1103	481	3
2	F	1121	0	1101	360	3
2	H	1121	0	1103	445	0
3	A	43	0	30	23	0
3	B	43	0	30	14	0
3	C	43	0	30	15	0
3	D	43	0	30	25	0
3	E	43	0	30	24	0
3	F	43	0	30	16	1
3	G	43	0	30	21	0
3	H	43	0	30	7	0
All	All	9104	0	8880	3081	5

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 171.

The worst 5 of 3081 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:76:MET:CA	1:A:76:MET:CB	1.76	1.64
2:D:104:ARG:CB	2:D:104:ARG:CG	1.74	1.64
2:F:29:GLY:HA3	2:F:55:MET:SD	1.32	1.64
2:H:14:LEU:CD2	2:H:14:LEU:CG	1.76	1.63
1:G:32:MET:CA	1:G:32:MET:CB	1.75	1.62

All (5) 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:53:ALA:CB	2:F:43:GLU:O[1_454]	1.28	0.92
2:D:6:VAL:CG2	2:F:73:ASP:OD2[1_455]	1.92	0.28
1:C:54:GLN:OE1	2:F:46:GLY:CA[1_454]	1.94	0.26
1:C:85:ASP:OD2	2:D:83:GLY:O[1_554]	2.00	0.20
2:D:9:SER:OG	3:F:147:HEM:O2A[1_455]	2.08	0.12

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	139/141 (99%)	121 (87%)	15 (11%)	3 (2%)	5	26
1	C	139/141 (99%)	116 (84%)	13 (9%)	10 (7%)	1	4
1	E	139/141 (99%)	113 (81%)	20 (14%)	6 (4%)	2	12
1	G	139/141 (99%)	105 (76%)	24 (17%)	10 (7%)	1	4
2	B	144/146 (99%)	120 (83%)	23 (16%)	1 (1%)	18	53
2	D	144/146 (99%)	120 (83%)	17 (12%)	7 (5%)	1	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	144/146 (99%)	123 (85%)	14 (10%)	7 (5%)	1	10
2	H	144/146 (99%)	114 (79%)	22 (15%)	8 (6%)	1	8
All	All	1132/1148 (99%)	932 (82%)	148 (13%)	52 (5%)	2	11

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	GLY
1	C	73	VAL
2	D	11	VAL
2	D	40	ARG
2	D	54	VAL

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%)	78 (69%)	35 (31%)	0	1
1	C	113/113 (100%)	66 (58%)	47 (42%)	0	0
1	E	113/113 (100%)	64 (57%)	49 (43%)	0	0
1	G	113/113 (100%)	65 (58%)	48 (42%)	0	0
2	B	118/118 (100%)	70 (59%)	48 (41%)	0	0
2	D	118/118 (100%)	79 (67%)	39 (33%)	0	1
2	F	118/118 (100%)	73 (62%)	45 (38%)	0	1
2	H	118/118 (100%)	62 (52%)	56 (48%)	0	0
All	All	924/924 (100%)	557 (60%)	367 (40%)	0	1

5 of 367 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	32	LEU
1	G	70	VAL

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Mol	Chain	Res	Type
2	F	54	VAL
2	F	137	VAL
1	G	108	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	108	ASN
2	H	39	GLN
2	F	143	HIS
1	G	72	HIS
2	H	80	ASN

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](#)

8 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	$\# Z > 2$
3	HEM	G	142	1	50,50,50	3.64	28 (56%)	67,82,82	3.66	38 (56%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HEM	A	142	1	50,50,50	3.69	26 (52%)	67,82,82	4.52	41 (61%)
3	HEM	B	147	2	50,50,50	3.94	37 (74%)	67,82,82	5.10	39 (58%)
3	HEM	E	142	1	50,50,50	3.51	30 (60%)	67,82,82	4.59	50 (74%)
3	HEM	F	147	2	50,50,50	3.57	28 (56%)	67,82,82	4.72	45 (67%)
3	HEM	D	147	2	50,50,50	2.96	25 (50%)	67,82,82	3.74	42 (62%)
3	HEM	H	147	2	50,50,50	3.65	29 (58%)	67,82,82	4.39	42 (62%)
3	HEM	C	142	1	50,50,50	3.10	25 (50%)	67,82,82	3.95	34 (50%)

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	G	142	1	-	3/14/54/54	-
3	HEM	A	142	1	-	4/14/54/54	-
3	HEM	B	147	2	-	5/14/54/54	-
3	HEM	E	142	1	-	4/14/54/54	-
3	HEM	F	147	2	-	7/14/54/54	-
3	HEM	D	147	2	-	5/14/54/54	-
3	HEM	H	147	2	-	8/14/54/54	-
3	HEM	C	142	1	-	4/14/54/54	-

The worst 5 of 228 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	142	HEM	C3C-C2C	11.24	1.60	1.37
3	E	142	HEM	CMC-C2C	10.43	1.72	1.50
3	F	147	HEM	CBD-CGD	10.12	1.74	1.50
3	D	147	HEM	C4D-C3D	10.09	1.62	1.45
3	G	142	HEM	FE-NB	10.08	2.25	1.94

The worst 5 of 331 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	147	HEM	CHD-C4C-NC	18.84	144.97	124.45
3	C	142	HEM	CMA-C3A-C4A	16.59	150.68	125.42
3	B	147	HEM	CHA-C4D-ND	15.21	143.19	124.37
3	F	147	HEM	CHC-C4B-NB	14.74	140.28	124.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	147	HEM	O2A-CGA-O1A	14.22	159.90	123.33

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

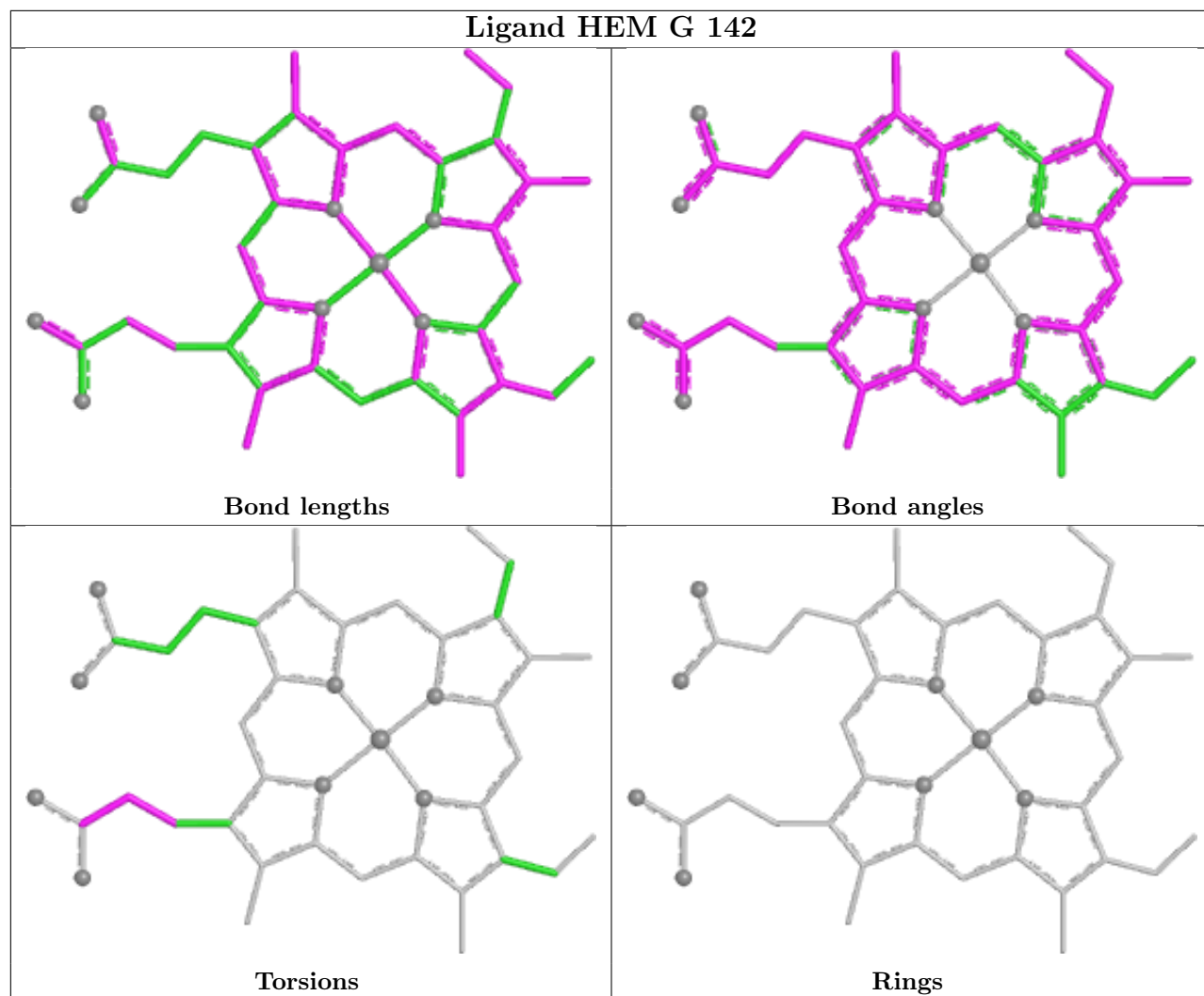
Mol	Chain	Res	Type	Atoms
3	B	147	HEM	C1A-C2A-CAA-CBA
3	F	147	HEM	C2B-C3B-CAB-CBB
3	F	147	HEM	C4B-C3B-CAB-CBB
3	F	147	HEM	C2C-C3C-CAC-CBC
3	F	147	HEM	C4C-C3C-CAC-CBC

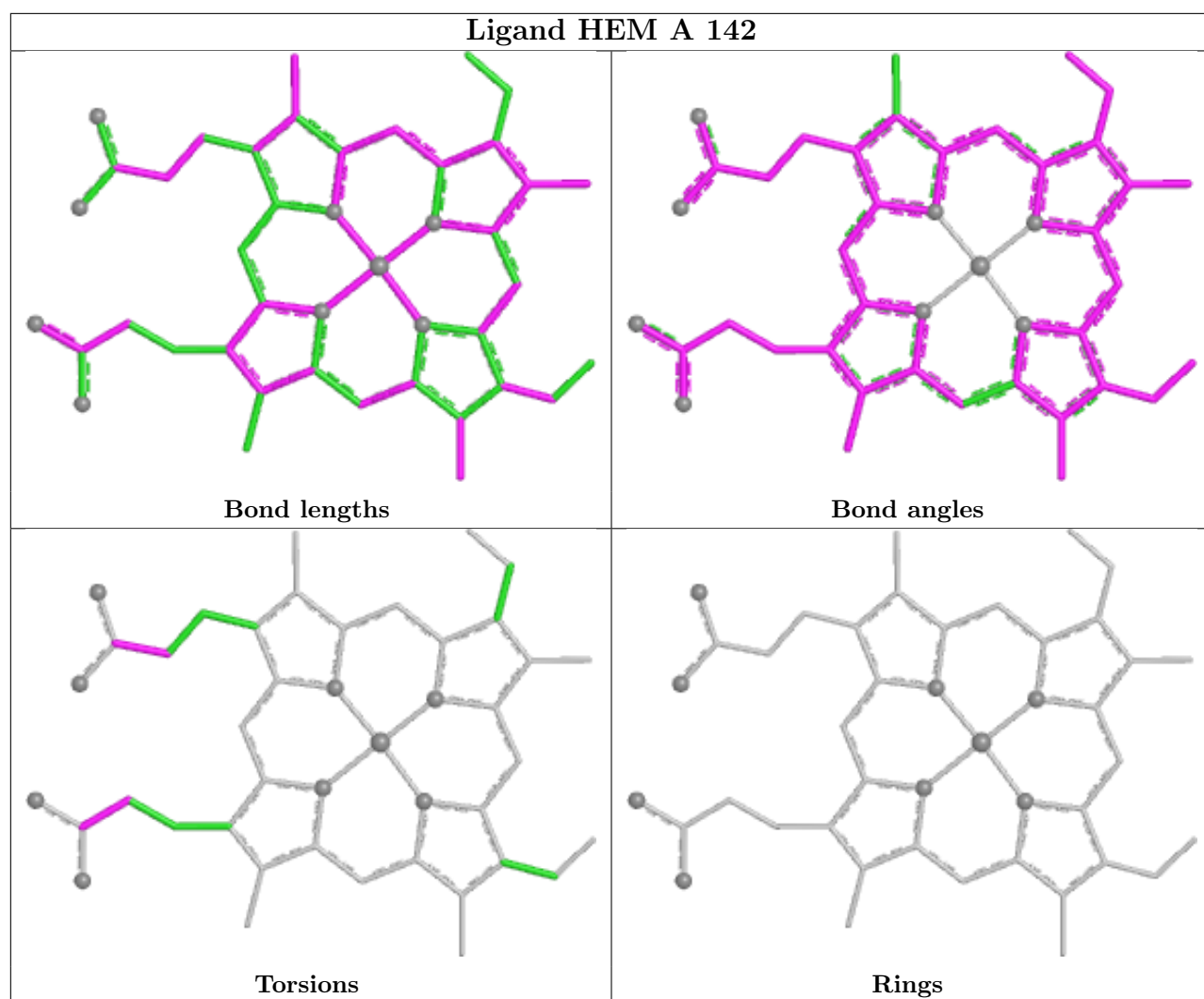
There are no ring outliers.

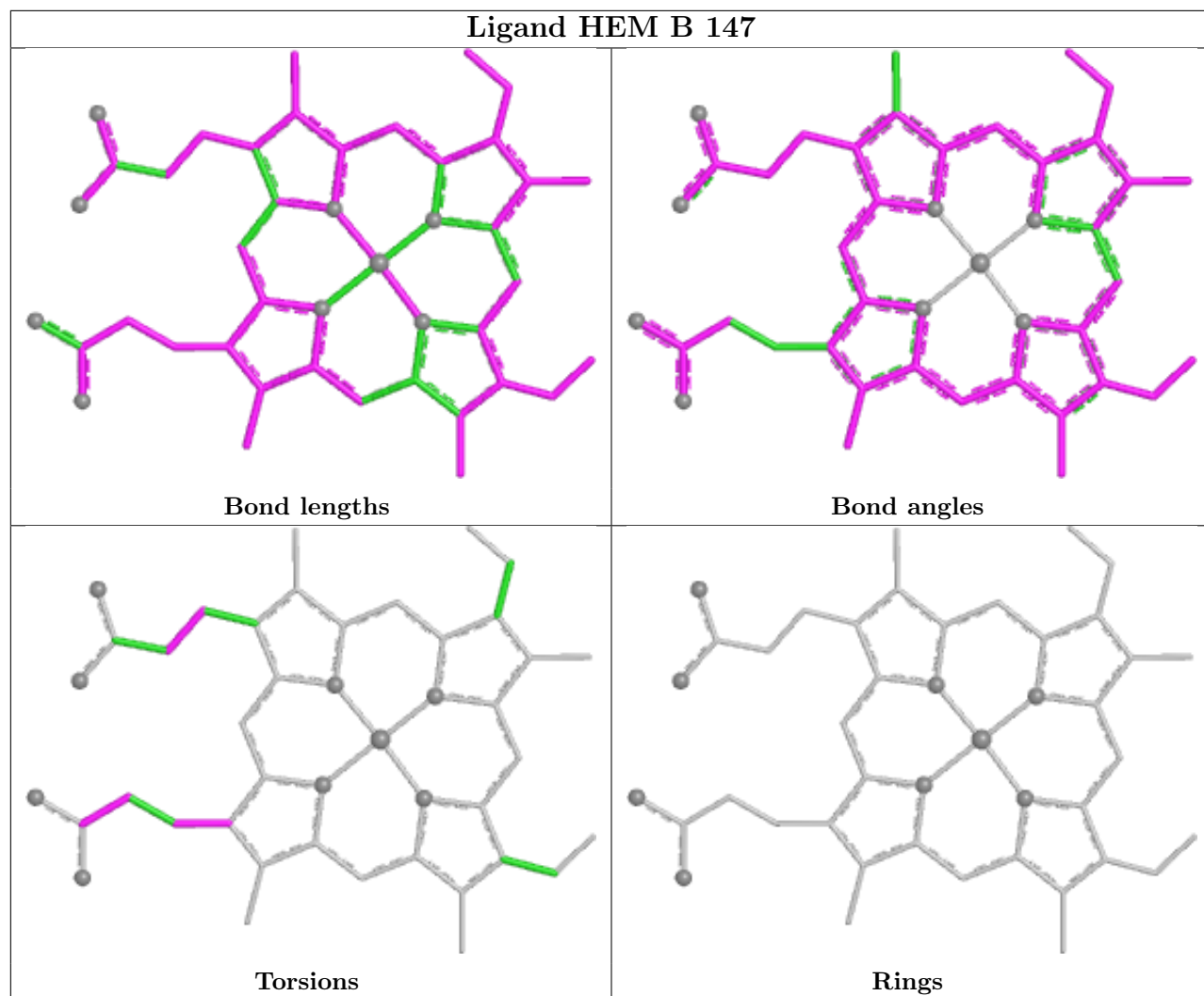
8 monomers are involved in 146 short contacts:

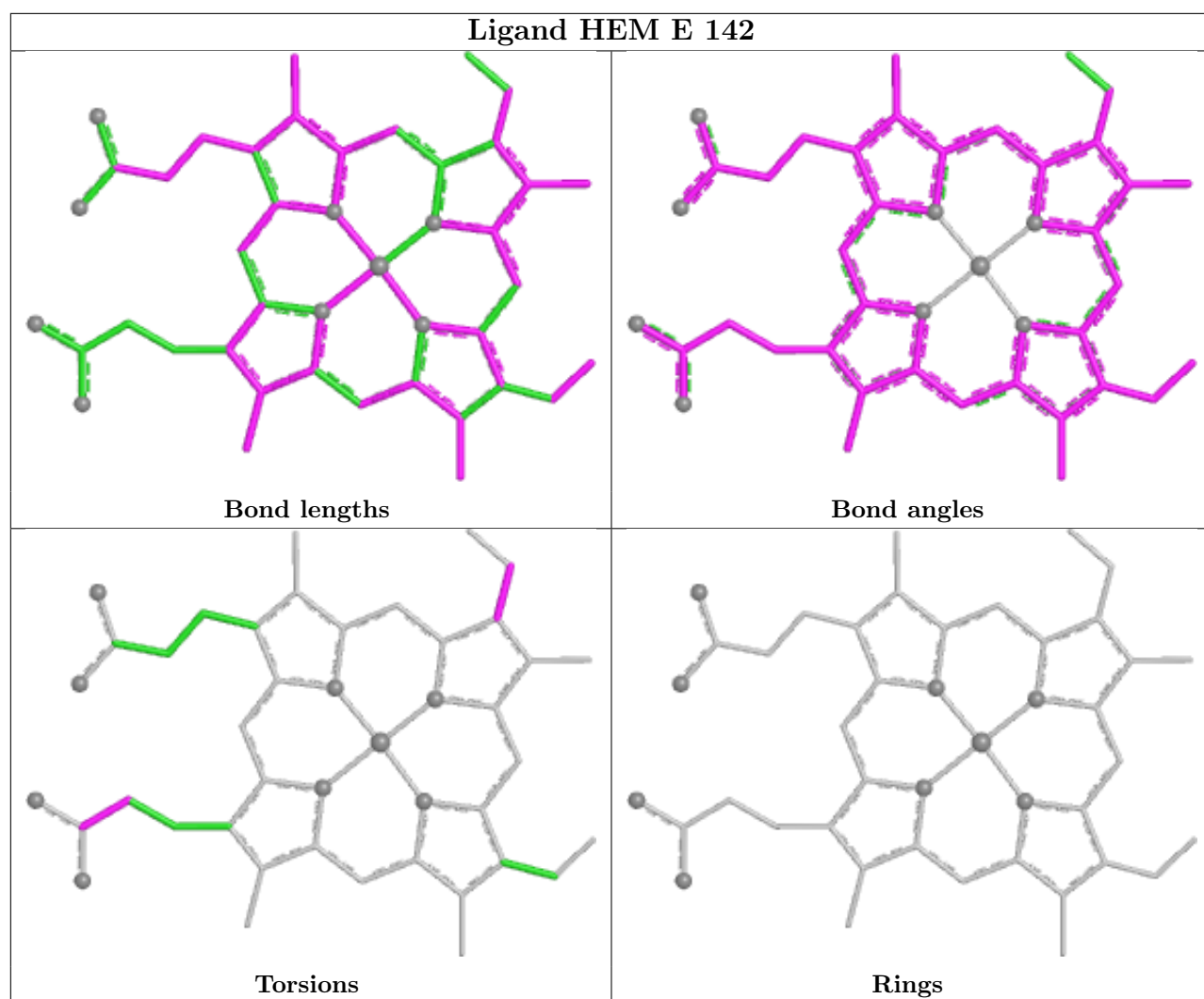
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	142	HEM	21	0
3	A	142	HEM	23	0
3	B	147	HEM	14	0
3	E	142	HEM	24	0
3	F	147	HEM	16	1
3	D	147	HEM	25	0
3	H	147	HEM	7	0
3	C	142	HEM	15	0

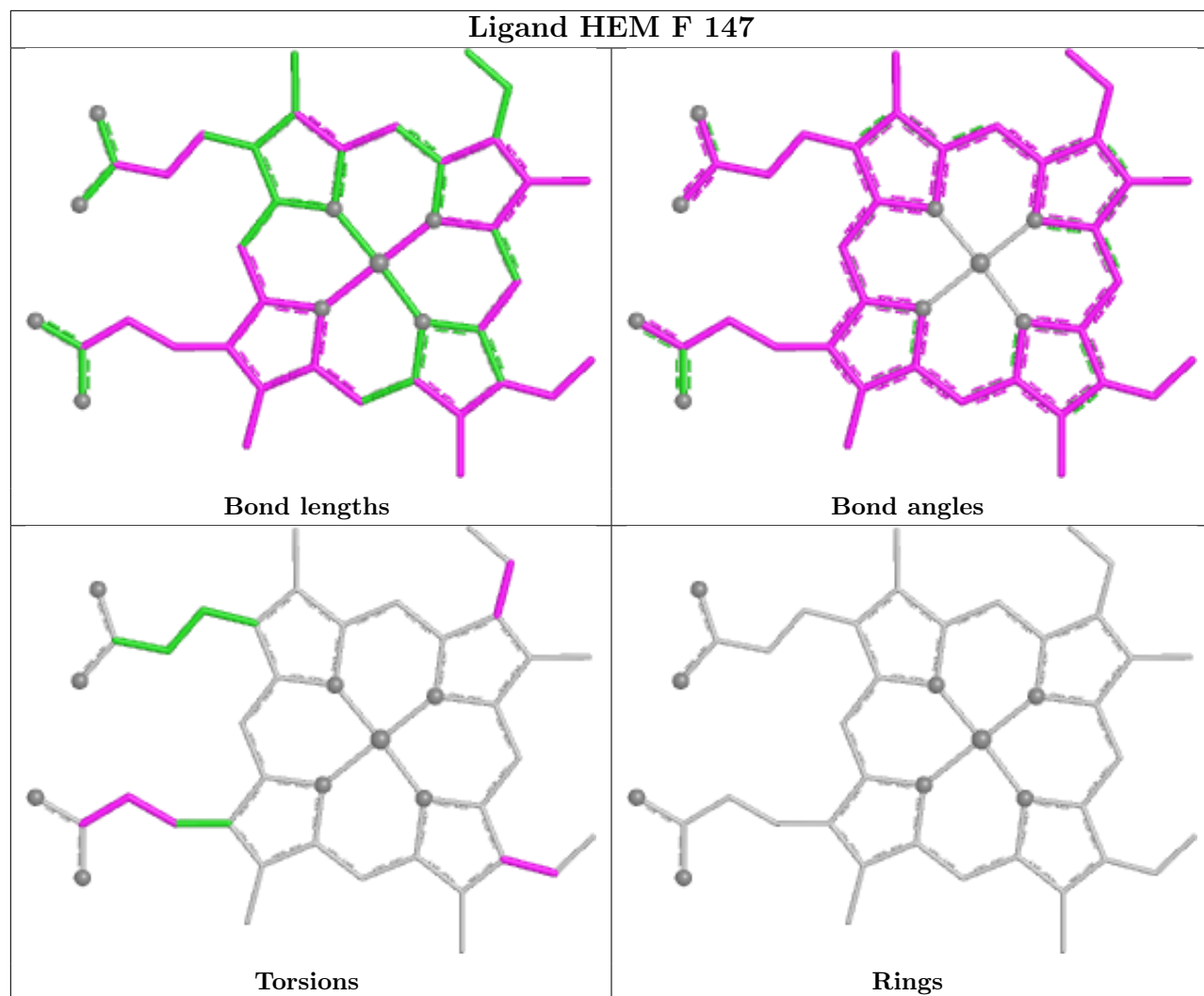
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

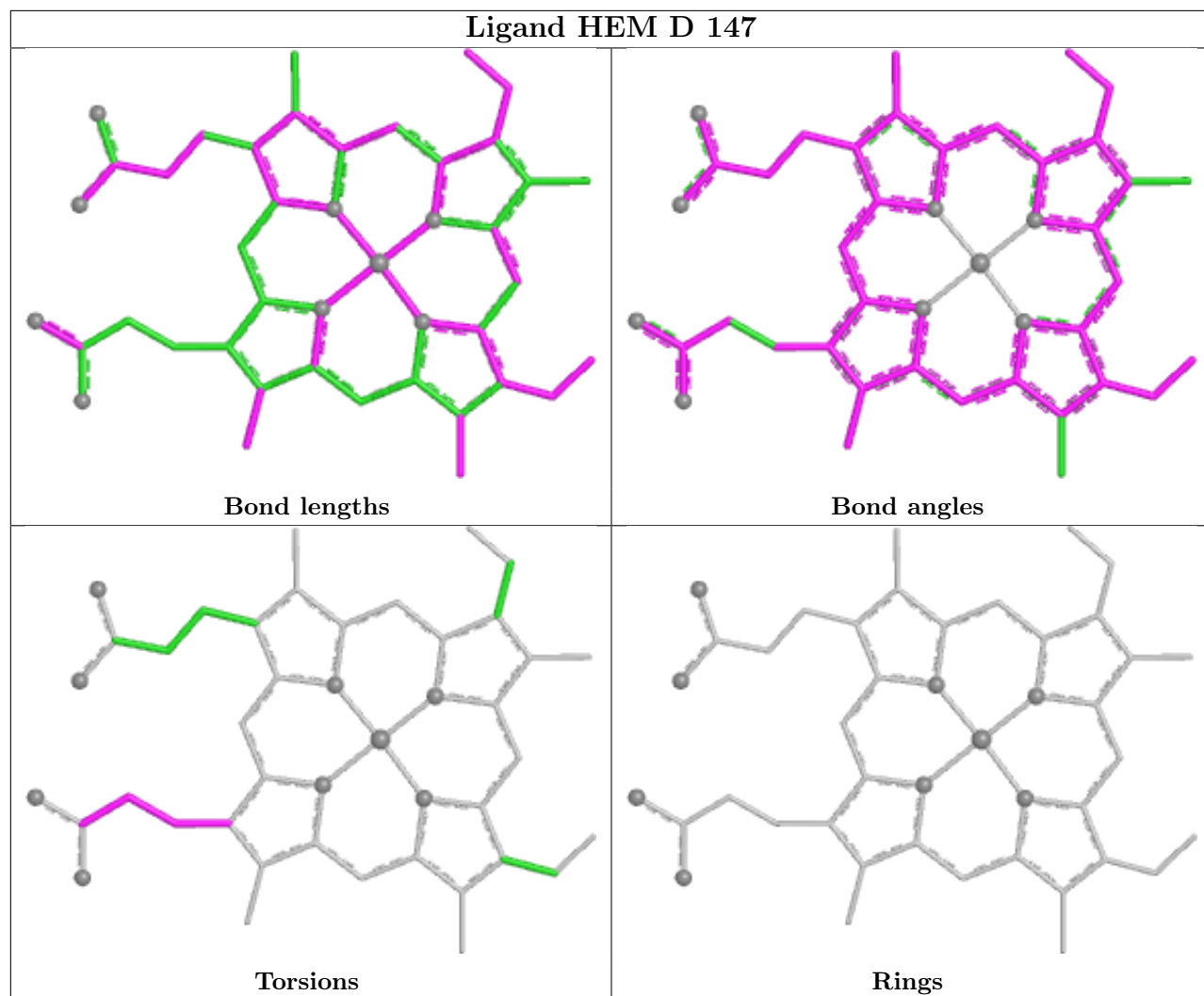


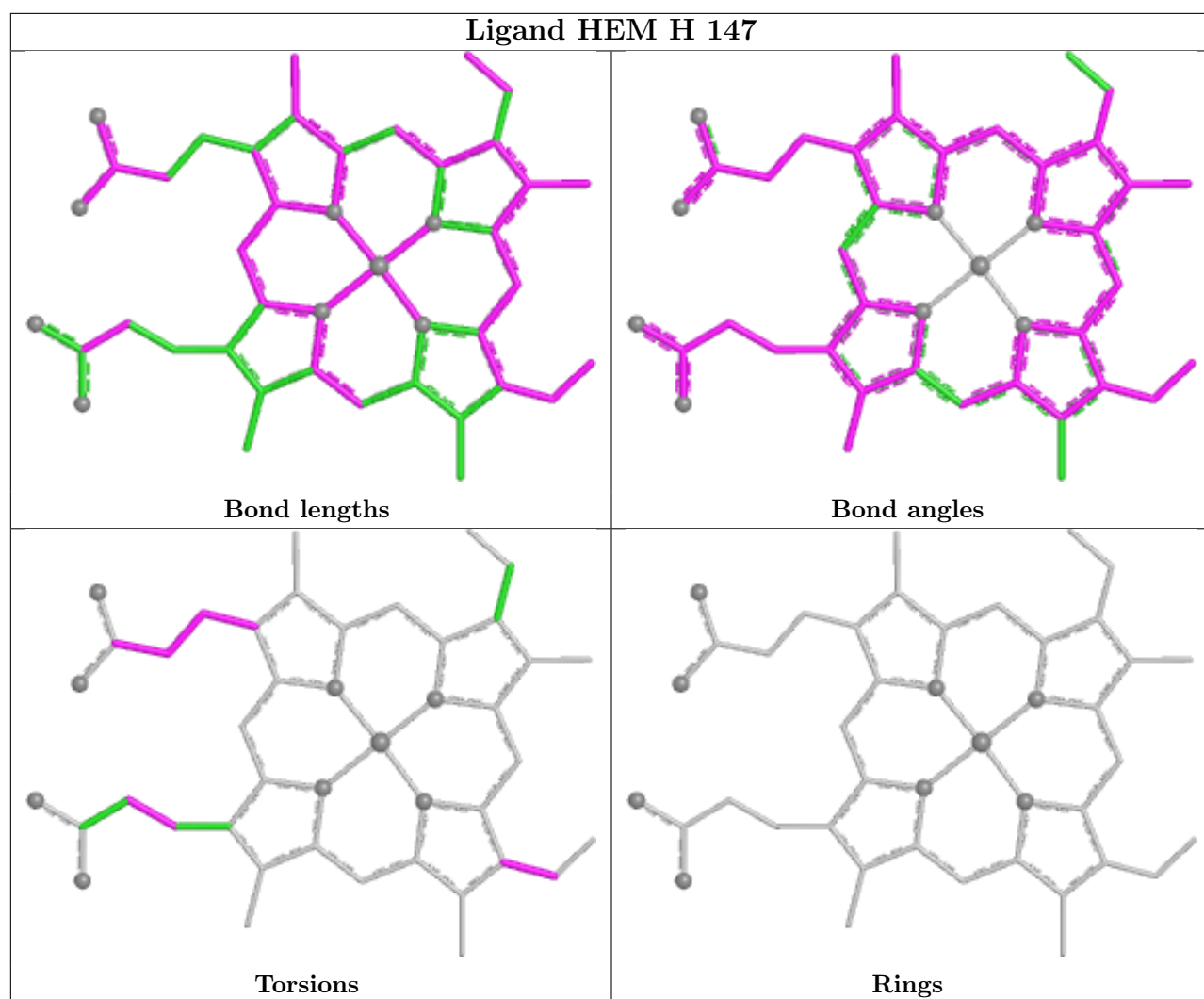


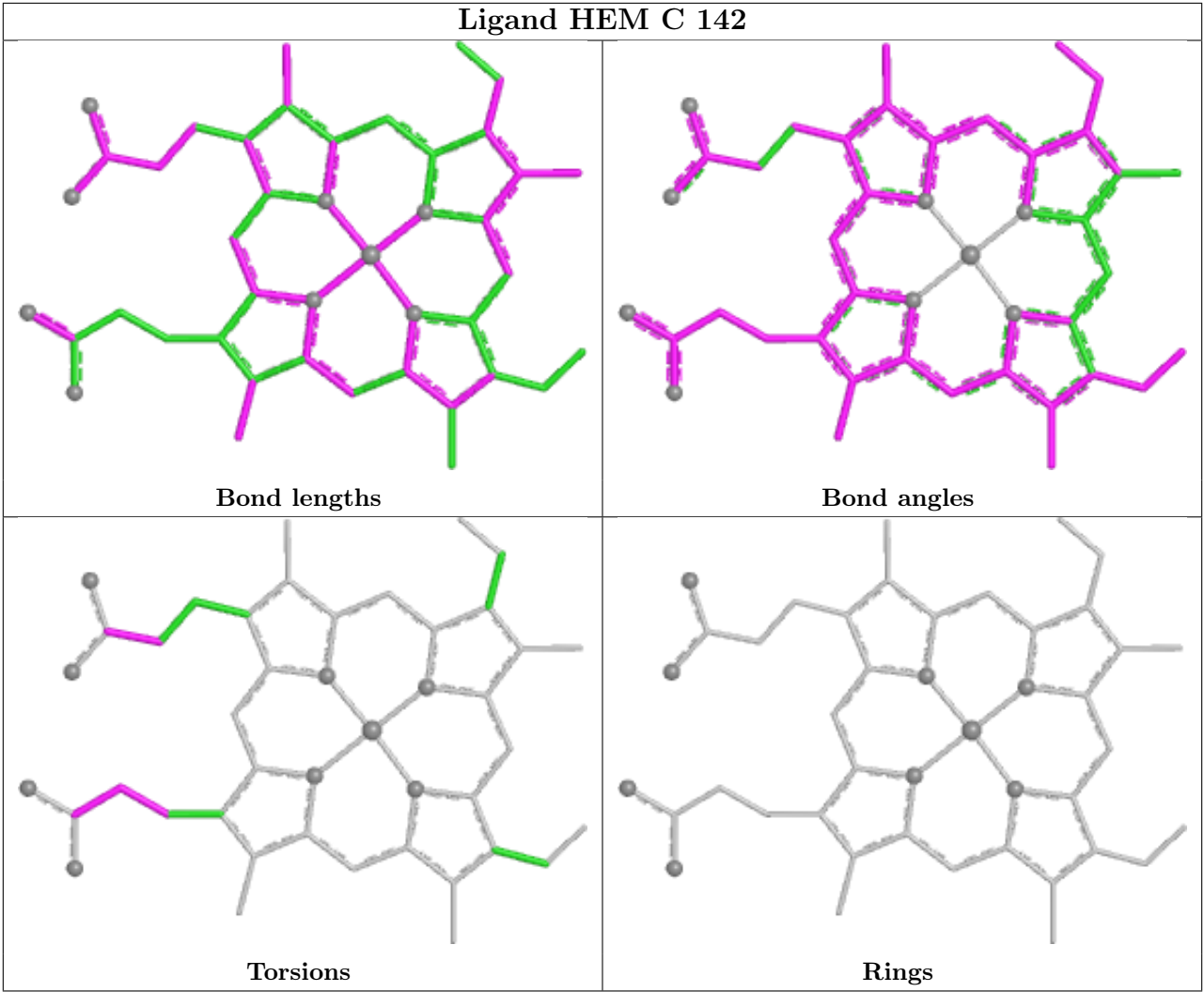












5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	12
2	D	12
1	C	12
2	F	11
1	G	11
1	E	10
2	H	10

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
2	B	2

The worst 5 of 80 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	125:LEU	C	126:ASP	N	1.62
1	F	145:TYR	C	146:HIS	N	1.62
1	D	129:ALA	C	130:TYR	N	1.61
1	C	37:PRO	C	38:THR	N	1.20
1	C	135:VAL	C	136:LEU	N	1.20

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.