



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 26, 2023 – 03:24 AM EDT

PDB ID : 1BIJ
Title : CROSSLINKED, DEOXY HUMAN HEMOGLOBIN A
Authors : Fernandez, E.J.; Abad-Zapatero, C.; Olsen, K.W.
Deposited on : 1998-06-18
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (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) : 2.34

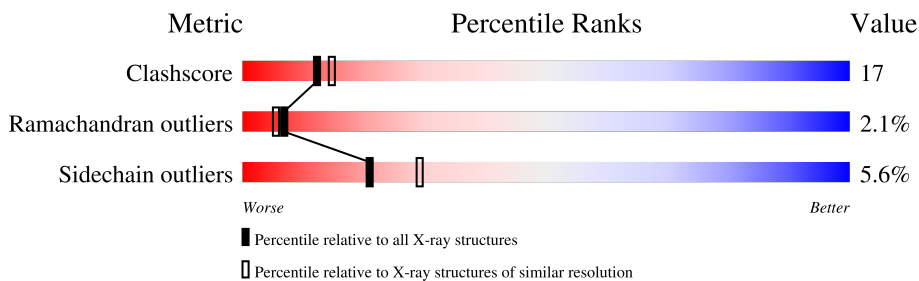
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

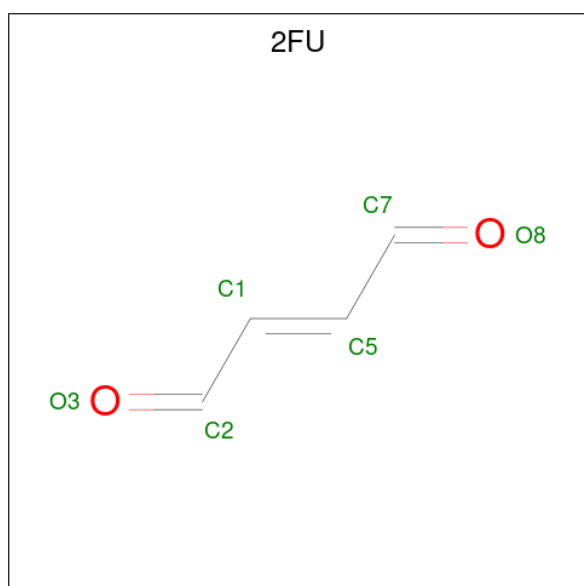
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	69% 26% 5% •
1	C	141	66% 33% •
2	B	146	52% 42% 5% •
2	D	146	64% 34% •

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		

- Molecule 4 is BUT-2-ENEDIAL (three-letter code: 2FU) (formula: C₄H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			6	4	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	57	Total	O	0	0
			57	57		
5	B	60	Total	O	0	0
			60	60		
5	C	32	Total	O	0	0
			32	32		
5	D	38	Total	O	0	0
			38	38		

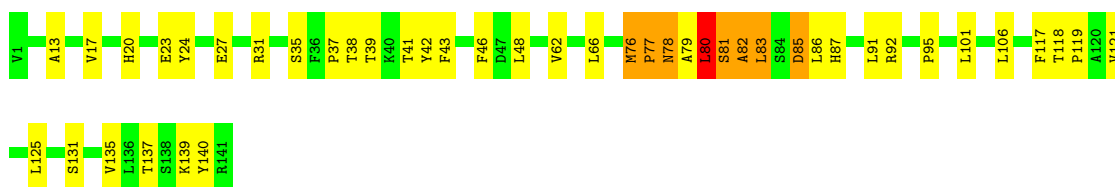
3 Residue-property plots [i](#)

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.

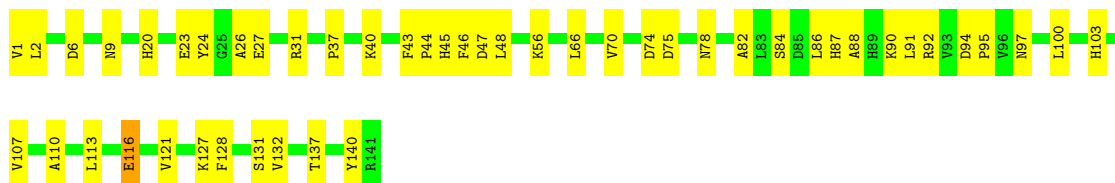
- Molecule 1: HEMOGLOBIN A

Chain A: 



- Molecule 1: HEMOGLOBIN A

Chain C: 



- Molecule 2: HEMOGLOBIN A

Chain B: 



- Molecule 2: HEMOGLOBIN A

Chain D: 



R104	L105	L106	L110	A115	H116	H117	F118	E121	P124	P125	V126	Q127	Y130	Q131	R132	V133	V134	V137	Y145	H146
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

4 Data and refinement statistics

Xtrriage (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	65.30Å 96.00Å 101.50Å 90.00° 101.50° 90.00°	Depositor
Resolution (Å)	5.00 – 2.30	Depositor
% Data completeness (in resolution range)	73.0 (5.00-2.30)	Depositor
R_{merge}	0.11	Depositor
R_{sym}	0.04	Depositor
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.190 , 0.263	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	4749	wwPDB-VP
Average B, all atoms (Å ²)	19.0	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: 2FU, 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	0.50	0/1097	0.77	2/1491 (0.1%)
1	C	0.50	0/1097	0.71	0/1491
2	B	0.56	0/1153	0.75	0/1566
2	D	0.53	0/1153	0.72	0/1566
All	All	0.52	0/4500	0.74	2/6114 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	LEU	CA-CB-CG	5.33	127.56	115.30
1	A	76	MET	N-CA-C	5.32	125.37	111.00

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	1069	0	1073	33	0
1	C	1069	0	1073	34	0
2	B	1123	0	1116	62	0
2	D	1123	0	1115	35	0
3	A	43	0	30	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	43	0	30	8	0
3	C	43	0	30	0	0
3	D	43	0	30	1	0
4	D	6	0	2	0	0
5	A	57	0	0	4	0
5	B	60	0	0	8	0
5	C	32	0	0	2	0
5	D	38	0	0	2	0
All	All	4749	0	4499	154	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 17.

All (154) 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:66:LEU:O	1:C:70:VAL:HG23	1.76	0.85
1:A:82:ALA:O	1:A:86:LEU:HB2	1.82	0.79
2:B:28:LEU:HD23	2:B:60:VAL:HG13	1.65	0.78
1:A:80:LEU:HD13	1:A:81:SER:H	1.54	0.73
2:D:75:LEU:HA	2:D:78:LEU:HD13	1.70	0.72
2:B:100:PRO:HA	2:B:103:PHE:HD2	1.55	0.71
2:B:90:GLU:HB3	5:B:203:HOH:O	1.91	0.69
2:D:100:PRO:HD3	2:D:145:TYR:CE2	2.28	0.69
2:B:96:LEU:HD13	3:B:147:HEM:HAD1	1.77	0.67
2:B:103:PHE:HD1	3:B:147:HEM:HBB2	1.60	0.66
2:D:32:LEU:HG	2:D:39:GLN:HG2	1.77	0.66
1:C:43:PHE:HB3	1:C:46:PHE:HB2	1.79	0.65
1:C:113:LEU:HB3	1:C:116:GLU:HG2	1.79	0.64
2:B:100:PRO:HA	2:B:103:PHE:CD2	2.32	0.64
1:C:26:ALA:HB2	1:C:56:LYS:HA	1.80	0.63
1:C:75:ASP:OD2	1:C:78:ASN:HB2	1.97	0.63
2:B:14:LEU:HD23	2:B:14:LEU:O	1.98	0.63
2:D:14:LEU:O	2:D:14:LEU:HD13	1.99	0.63
1:A:118:THR:OG1	1:A:121:VAL:HG23	1.99	0.62
2:D:124:PRO:HB2	2:D:125:PRO:HD3	1.81	0.62
2:B:14:LEU:HD12	2:B:126:VAL:HG11	1.83	0.60
1:C:82:ALA:HB3	5:C:158:HOH:O	2.01	0.60
1:A:80:LEU:HB2	5:A:157:HOH:O	2.00	0.60
2:B:36:PRO:O	2:B:39:GLN:HG3	2.01	0.60
2:D:67:VAL:HG13	3:D:147:HEM:C3B	2.36	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:THR:HA	5:A:163:HOH:O	2.02	0.60
2:B:85:PHE:HA	5:B:189:HOH:O	2.01	0.60
1:C:20:HIS:O	1:C:23:GLU:HB3	2.02	0.59
2:D:79:ASP:HB3	5:D:149:HOH:O	2.00	0.59
2:B:85:PHE:HB3	2:B:141:LEU:CD2	2.33	0.59
2:B:120:LYS:HE2	5:B:158:HOH:O	2.03	0.59
1:C:110:ALA:O	2:D:116:HIS:HA	2.01	0.59
2:B:104:ARG:HH12	2:B:139:ASN:HD21	1.50	0.59
2:D:51:PRO:O	2:D:55:MET:HG2	2.03	0.58
2:D:72:SER:HA	2:D:75:LEU:HD23	1.84	0.58
2:B:61:LYS:HG2	5:B:168:HOH:O	2.03	0.58
2:B:23:VAL:HG22	2:B:117:HIS:CD2	2.39	0.57
1:A:131:SER:O	1:A:135:VAL:HG23	2.05	0.57
2:B:87:THR:HA	2:B:90:GLU:OE1	2.06	0.56
1:A:83:LEU:O	1:A:85:ASP:N	2.40	0.55
2:B:66:LYS:HD2	5:B:195:HOH:O	2.06	0.55
2:B:4:THR:HB	2:B:7:GLU:HB3	1.89	0.55
2:B:85:PHE:HD1	2:B:88:LEU:HD12	1.70	0.55
2:B:109:VAL:O	2:B:113:VAL:HG23	2.07	0.54
2:B:91:LEU:HG	2:B:96:LEU:HD12	1.90	0.54
2:B:75:LEU:O	2:B:78:LEU:HD22	2.08	0.54
2:B:103:PHE:CD1	3:B:147:HEM:HBB2	2.43	0.54
2:D:91:LEU:HD12	2:D:95:LYS:HG3	1.89	0.54
1:C:103:HIS:HE1	2:D:131:GLN:OE1	1.90	0.54
2:B:3:LEU:HD13	5:B:161:HOH:O	2.08	0.53
1:A:117:PHE:HB3	2:B:116:HIS:CE1	2.43	0.53
2:B:124:PRO:HB2	2:B:125:PRO:HD3	1.91	0.52
2:B:41:PHE:CE1	2:B:98:VAL:HG22	2.45	0.52
1:C:128:PHE:O	1:C:132:VAL:HG23	2.08	0.52
1:A:76:MET:HB2	1:A:135:VAL:HG21	1.91	0.52
2:D:101:GLU:OE1	2:D:104:ARG:NH1	2.44	0.51
2:D:118:PHE:HB3	2:D:121:GLU:HB2	1.93	0.51
2:B:30:ARG:O	2:B:34:VAL:HG23	2.11	0.51
2:B:41:PHE:HE2	2:B:102:ASN:ND2	2.09	0.50
2:B:42:PHE:HD1	2:B:45:PHE:CZ	2.28	0.50
1:C:37:PRO:O	1:C:40:LYS:HG2	2.11	0.50
1:A:77:PRO:HD3	1:A:135:VAL:HG11	1.94	0.50
1:C:31:ARG:HB3	2:D:127:GLN:OE1	2.10	0.50
1:C:97:ASN:O	1:C:100:LEU:HB2	2.11	0.50
1:A:81:SER:O	1:A:82:ALA:HB2	2.11	0.50
2:B:70:ALA:HB3	3:B:147:HEM:HMB3	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:LEU:CD1	1:A:81:SER:H	2.23	0.50
2:B:41:PHE:CE2	2:B:102:ASN:ND2	2.80	0.49
2:B:88:LEU:HB2	2:B:141:LEU:HD21	1.93	0.49
2:B:20:VAL:HG13	2:B:68:LEU:HB3	1.93	0.49
2:B:41:PHE:CE1	2:B:98:VAL:HA	2.47	0.49
2:D:31:LEU:HD22	2:D:106:LEU:HD13	1.94	0.48
1:A:13:ALA:O	1:A:17:VAL:HG23	2.13	0.48
2:B:66:LYS:HE2	3:B:147:HEM:HAA2	1.95	0.48
2:D:21:ASP:HA	2:D:65:LYS:HG2	1.95	0.48
2:B:18:VAL:HG13	2:B:23:VAL:HG21	1.96	0.48
2:B:107:GLY:O	2:B:111:VAL:HG23	2.14	0.48
1:A:35:SER:HB3	2:B:131:GLN:HG3	1.96	0.48
1:C:43:PHE:N	1:C:44:PRO:HD3	2.29	0.48
2:B:96:LEU:CD1	3:B:147:HEM:HAD1	2.42	0.48
2:D:94:ASP:O	2:D:97:HIS:CE1	2.67	0.48
1:A:121:VAL:O	1:A:125:LEU:HG	2.14	0.47
2:B:85:PHE:HB3	2:B:141:LEU:HD23	1.95	0.47
1:C:20:HIS:HB3	1:C:24:TYR:CE1	2.49	0.47
2:B:92:HIS:HA	2:B:96:LEU:HB2	1.96	0.47
1:C:6:ASP:OD2	1:C:127:LYS:HD3	2.15	0.47
1:A:62:VAL:O	1:A:66:LEU:HG	2.15	0.46
2:D:44:SER:O	2:D:45:PHE:HD1	1.98	0.46
1:A:83:LEU:HD22	5:A:157:HOH:O	2.15	0.46
2:D:30:ARG:O	2:D:34:VAL:HG23	2.14	0.46
2:B:82:LYS:C	2:B:84:THR:H	2.19	0.46
2:D:1:VAL:HG11	5:D:178:HOH:O	2.15	0.46
2:B:82:LYS:O	2:B:86:ALA:HB2	2.16	0.46
1:C:1:VAL:HG12	1:C:2:LEU:N	2.31	0.45
1:A:17:VAL:HG13	1:A:24:TYR:CD2	2.52	0.45
2:B:72:SER:HA	2:B:75:LEU:HD12	1.98	0.45
2:D:133:VAL:O	2:D:137:VAL:HG23	2.17	0.45
1:A:27:GLU:O	1:A:31:ARG:HG3	2.17	0.45
1:A:76:MET:HB2	1:A:135:VAL:HG11	1.99	0.45
2:B:122:PHE:HE2	2:B:127:GLN:HG3	1.82	0.45
1:A:17:VAL:HG13	1:A:24:TYR:CE2	2.52	0.45
1:A:92:ARG:HD3	2:D:40:ARG:HB3	1.99	0.45
1:C:87:HIS:O	1:C:92:ARG:N	2.50	0.45
2:B:10:ALA:HB1	2:B:126:VAL:HG22	1.99	0.44
2:D:91:LEU:HD12	2:D:95:LYS:CG	2.47	0.44
1:A:137:THR:HA	1:A:140:TYR:CE1	2.52	0.44
1:C:86:LEU:O	1:C:91:LEU:HG	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:TYR:HD2	5:A:163:HOH:O	2.00	0.44
2:B:41:PHE:HB3	3:B:147:HEM:HMD3	1.99	0.44
1:A:87:HIS:CD2	1:A:91:LEU:HD12	2.52	0.44
1:A:35:SER:C	1:A:37:PRO:HD3	2.38	0.44
2:B:144:LYS:HG2	2:B:144:LYS:O	2.17	0.44
1:C:9:ASN:HB3	1:C:121:VAL:HG22	2.00	0.44
1:C:27:GLU:O	1:C:31:ARG:HG3	2.18	0.44
2:D:81:LEU:HD22	2:D:85:PHE:HE2	1.82	0.44
1:A:119:PRO:O	2:B:33:VAL:HG11	2.17	0.44
2:B:1:VAL:N	5:B:170:HOH:O	2.50	0.43
1:C:1:VAL:HA	5:C:144:HOH:O	2.18	0.43
2:D:127:GLN:O	2:D:131:GLN:HG2	2.18	0.43
2:D:130:TYR:O	2:D:134:VAL:HG22	2.18	0.43
1:C:43:PHE:HA	1:C:45:HIS:CE1	2.54	0.43
2:B:3:LEU:HB3	2:B:8:LYS:HB2	2.00	0.43
2:B:133:VAL:HG22	5:B:161:HOH:O	2.19	0.43
1:C:137:THR:HA	1:C:140:TYR:CD1	2.52	0.42
1:A:43:PHE:HB3	1:A:46:PHE:HB2	2.00	0.42
2:B:85:PHE:O	2:B:88:LEU:N	2.53	0.42
1:A:20:HIS:O	1:A:23:GLU:HB3	2.20	0.42
1:A:101:LEU:HD12	1:A:101:LEU:O	2.20	0.42
1:A:35:SER:O	1:A:37:PRO:HD3	2.20	0.42
1:C:107:VAL:HG13	2:D:115:ALA:CB	2.50	0.42
2:B:14:LEU:HB3	2:B:130:TYR:OH	2.19	0.42
2:B:71:PHE:O	2:B:73:ASP:N	2.53	0.41
2:B:141:LEU:HD23	2:B:141:LEU:HA	1.75	0.41
2:D:23:VAL:HA	2:D:26:GLU:HB2	2.02	0.41
2:B:40:ARG:HB3	1:C:92:ARG:HD2	2.02	0.41
1:C:43:PHE:HB2	1:C:48:LEU:HD11	2.03	0.41
1:C:94:ASP:HA	1:C:95:PRO:HD3	1.92	0.41
1:C:137:THR:HA	1:C:140:TYR:CE1	2.56	0.41
1:C:88:ALA:HA	1:C:140:TYR:CZ	2.56	0.41
1:A:38:THR:O	1:A:41:THR:HG23	2.21	0.41
2:D:68:LEU:HD21	2:D:110:LEU:CD2	2.51	0.41
2:D:78:LEU:HD12	2:D:78:LEU:HA	1.93	0.41
1:C:88:ALA:HB2	1:C:140:TYR:CE1	2.56	0.41
2:D:45:PHE:HA	2:D:59:LYS:HD3	2.03	0.41
2:D:68:LEU:HA	2:D:71:PHE:HB3	2.03	0.41
1:C:40:LYS:HB2	1:C:48:LEU:HD13	2.03	0.41
2:B:39:GLN:C	1:C:92:ARG:HH11	2.23	0.40
2:B:41:PHE:HB3	3:B:147:HEM:CMD	2.50	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:ASN:O	1:A:79:ALA:HB2	2.22	0.40
2:B:68:LEU:O	2:B:71:PHE:HB3	2.21	0.40
2:D:68:LEU:HA	2:D:68:LEU:HD22	1.82	0.40
2:B:118:PHE:HB3	2:B:121:GLU:HB2	2.03	0.40
2:D:29:GLY:O	2:D:33:VAL:HG23	2.21	0.40
1:C:87:HIS:HA	1:C:91:LEU:HB2	2.03	0.40

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	139/141 (99%)	123 (88%)	11 (8%)	5 (4%)	3	2
1	C	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
2	B	144/146 (99%)	118 (82%)	19 (13%)	7 (5%)	2	1
2	D	144/146 (99%)	131 (91%)	13 (9%)	0	100	100
All	All	566/574 (99%)	505 (89%)	49 (9%)	12 (2%)	7	5

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	83	LEU
1	A	80	LEU
1	A	81	SER
1	A	82	ALA
2	B	49	SER
2	B	72	SER
2	B	78	LEU
2	B	92	HIS
1	A	78	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	91	LEU
2	B	83	GLY
2	B	119	GLY

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	113/113 (100%)	107 (95%)	6 (5%)	22	31
1	C	113/113 (100%)	107 (95%)	6 (5%)	22	31
2	B	118/118 (100%)	111 (94%)	7 (6%)	19	27
2	D	118/118 (100%)	111 (94%)	7 (6%)	19	27
All	All	462/462 (100%)	436 (94%)	26 (6%)	21	29

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	LEU
1	A	77	PRO
1	A	80	LEU
1	A	85	ASP
1	A	95	PRO
1	A	139	LYS
2	B	3	LEU
2	B	17	LYS
2	B	32	LEU
2	B	40	ARG
2	B	78	LEU
2	B	117	HIS
2	B	141	LEU
1	C	47	ASP
1	C	74	ASP
1	C	84	SER
1	C	90	LYS
1	C	116	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	131	SER
2	D	2	HIS
2	D	5	PRO
2	D	44	SER
2	D	68	LEU
2	D	73	ASP
2	D	79	ASP
2	D	130	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	HIS
1	A	103	HIS
2	B	97	HIS
2	B	102	ASN
2	B	116	HIS
2	B	117	HIS
2	B	131	GLN
2	B	139	ASN
1	C	50	HIS
1	C	58	HIS
1	C	78	ASN
1	C	97	ASN
1	C	103	HIS
1	C	112	HIS
2	D	97	HIS
2	D	131	GLN
2	D	139	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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
4	2FU	D	148	2	5,5,5	1.25	1 (20%)	4,4,4	1.45	0
3	HEM	B	147	2	41,50,50	1.65	11 (26%)	45,82,82	2.11	8 (17%)
3	HEM	A	142	1	41,50,50	1.65	11 (26%)	45,82,82	1.80	13 (28%)
3	HEM	C	142	1	41,50,50	1.81	8 (19%)	45,82,82	1.55	8 (17%)
3	HEM	D	147	2	41,50,50	1.51	8 (19%)	45,82,82	1.92	13 (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
4	2FU	D	148	2	-	3/3/3/3	-
3	HEM	B	147	2	-	5/12/54/54	-
3	HEM	A	142	1	-	4/12/54/54	-
3	HEM	C	142	1	-	6/12/54/54	-
3	HEM	D	147	2	-	7/12/54/54	-

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	142	HEM	C3C-CAC	-4.93	1.37	1.47
3	C	142	HEM	C3C-C2C	-4.16	1.34	1.40
3	C	142	HEM	C1B-NB	-3.98	1.33	1.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	147	HEM	CBB-CAB	3.83	1.49	1.30
3	B	147	HEM	C4D-C3D	3.68	1.51	1.45
3	A	142	HEM	CHA-C4D	3.44	1.43	1.35
3	B	147	HEM	C3C-CAC	-3.44	1.40	1.47
3	C	142	HEM	CBB-CAB	3.43	1.47	1.30
3	D	147	HEM	C3C-CAC	-3.35	1.40	1.47
3	D	147	HEM	CBB-CAB	3.18	1.46	1.30
3	A	142	HEM	C1D-C2D	3.07	1.50	1.44
3	A	142	HEM	C3C-CAC	-2.97	1.41	1.47
3	A	142	HEM	C1B-NB	-2.96	1.35	1.40
3	B	147	HEM	CAB-C3B	-2.79	1.39	1.47
3	D	147	HEM	C1D-C2D	2.78	1.49	1.44
3	D	147	HEM	CBC-CAC	2.74	1.47	1.29
3	A	142	HEM	C3C-C2C	-2.74	1.36	1.40
3	D	147	HEM	CAB-C3B	-2.73	1.40	1.47
3	A	142	HEM	CBB-CAB	2.71	1.43	1.30
3	A	142	HEM	CBC-CAC	2.71	1.47	1.29
3	D	147	HEM	CMD-C2D	2.71	1.56	1.50
3	B	147	HEM	CBC-CAC	2.62	1.46	1.29
3	C	142	HEM	C1D-ND	-2.56	1.33	1.38
3	B	147	HEM	C3D-C2D	-2.51	1.31	1.36
3	C	142	HEM	C3B-C2B	-2.48	1.32	1.37
3	D	147	HEM	CHB-C1B	2.46	1.41	1.35
3	A	142	HEM	CAB-C3B	-2.37	1.41	1.47
3	A	142	HEM	CMB-C2B	2.32	1.55	1.50
3	C	142	HEM	CHD-C1D	-2.29	1.34	1.41
3	D	147	HEM	C1A-NA	2.28	1.40	1.36
4	D	148	2FU	C5-C1	2.24	1.41	1.36
3	B	147	HEM	CAA-C2A	2.21	1.55	1.52
3	A	142	HEM	C1B-C2B	2.21	1.48	1.44
3	C	142	HEM	CBC-CAC	2.20	1.43	1.29
3	B	147	HEM	C1D-ND	2.15	1.43	1.38
3	A	142	HEM	C2C-C1C	2.13	1.47	1.42
3	B	147	HEM	CHA-C4D	2.04	1.40	1.35
3	B	147	HEM	CHB-C1B	2.04	1.40	1.35
3	B	147	HEM	C1A-NA	2.01	1.40	1.36

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	147	HEM	CBA-CAA-C2A	9.89	129.50	112.62
3	D	147	HEM	CHC-C4B-NB	-5.50	118.45	124.43

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	142	HEM	C4C-CHD-C1D	4.49	128.48	122.56
3	A	142	HEM	CMD-C2D-C1D	4.38	131.72	125.04
3	B	147	HEM	CAD-C3D-C4D	4.32	132.20	124.66
3	A	142	HEM	C4B-C3B-C2B	-4.08	103.87	107.11
3	A	142	HEM	C1D-C2D-C3D	-3.68	103.09	106.96
3	C	142	HEM	C4B-C3B-C2B	-3.60	104.26	107.11
3	D	147	HEM	CBA-CAA-C2A	3.57	118.70	112.62
3	D	147	HEM	C1B-NB-C4B	-3.56	101.40	105.07
3	D	147	HEM	C4B-CHC-C1C	3.42	127.07	122.56
3	D	147	HEM	C2C-C3C-C4C	-3.40	104.52	106.90
3	B	147	HEM	C4A-C3A-C2A	3.37	109.34	107.00
3	D	147	HEM	C4A-C3A-C2A	3.37	109.34	107.00
3	A	142	HEM	C4D-C3D-C2D	3.25	111.63	106.90
3	B	147	HEM	CAD-C3D-C2D	-3.16	122.00	127.88
3	D	147	HEM	C4B-C3B-C2B	-3.12	104.63	107.11
3	A	142	HEM	C4B-CHC-C1C	3.04	126.57	122.56
3	A	142	HEM	CBA-CAA-C2A	2.85	117.48	112.62
3	A	142	HEM	C4A-C3A-C2A	-2.83	105.03	107.00
3	D	147	HEM	C2B-C1B-NB	2.83	113.19	109.84
3	B	147	HEM	C2C-C3C-C4C	-2.81	104.94	106.90
3	B	147	HEM	C4D-ND-C1D	-2.81	102.17	105.07
3	D	147	HEM	CAB-C3B-C2B	-2.69	119.75	128.60
3	B	147	HEM	C1D-C2D-C3D	2.68	109.78	106.96
3	C	142	HEM	C1B-NB-C4B	-2.64	102.34	105.07
3	C	142	HEM	CMA-C3A-C4A	-2.61	124.46	128.46
3	B	147	HEM	CHA-C4D-ND	-2.60	121.17	124.38
3	C	142	HEM	CBD-CAD-C3D	2.55	119.72	112.63
3	C	142	HEM	CMB-C2B-C1B	2.54	128.90	125.04
3	A	142	HEM	CAD-C3D-C4D	-2.51	120.28	124.66
3	A	142	HEM	C4C-CHD-C1D	2.45	125.79	122.56
3	A	142	HEM	C1B-NB-C4B	-2.44	102.56	105.07
3	A	142	HEM	CHC-C4B-NB	-2.39	121.84	124.43
3	A	142	HEM	C2B-C1B-NB	2.30	112.56	109.84
3	C	142	HEM	CHC-C4B-C3B	-2.29	121.07	124.57
3	D	147	HEM	CHC-C4B-C3B	2.28	128.06	124.57
3	D	147	HEM	C3D-C4D-ND	2.22	112.64	110.17
3	D	147	HEM	CHA-C4D-C3D	-2.16	121.28	125.33
3	A	142	HEM	CHB-C1B-NB	-2.09	121.80	124.38
3	C	142	HEM	C2B-C1B-NB	2.02	112.23	109.84
3	D	147	HEM	CMC-C2C-C3C	2.01	128.44	124.68

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	142	HEM	C2B-C3B-CAB-CBB
3	A	142	HEM	C4B-C3B-CAB-CBB
3	B	147	HEM	C1A-C2A-CAA-CBA
3	B	147	HEM	C2B-C3B-CAB-CBB
3	B	147	HEM	C4B-C3B-CAB-CBB
3	C	142	HEM	C2B-C3B-CAB-CBB
3	C	142	HEM	C4B-C3B-CAB-CBB
3	D	147	HEM	C4B-C3B-CAB-CBB
4	D	148	2FU	C5-C1-C2-O3
4	D	148	2FU	C1-C5-C7-O8
3	D	147	HEM	C2B-C3B-CAB-CBB
4	D	148	2FU	C2-C1-C5-C7
3	C	142	HEM	CAA-CBA-CGA-O1A
3	C	142	HEM	CAA-CBA-CGA-O2A
3	B	147	HEM	CAD-CBD-CGD-O1D
3	C	142	HEM	CAD-CBD-CGD-O2D
3	A	142	HEM	CAD-CBD-CGD-O2D
3	A	142	HEM	CAD-CBD-CGD-O1D
3	C	142	HEM	CAD-CBD-CGD-O1D
3	B	147	HEM	CAD-CBD-CGD-O2D
3	D	147	HEM	C2D-C3D-CAD-CBD
3	D	147	HEM	CAA-CBA-CGA-O2A
3	D	147	HEM	CAA-CBA-CGA-O1A
3	D	147	HEM	CAD-CBD-CGD-O2D
3	D	147	HEM	CAD-CBD-CGD-O1D

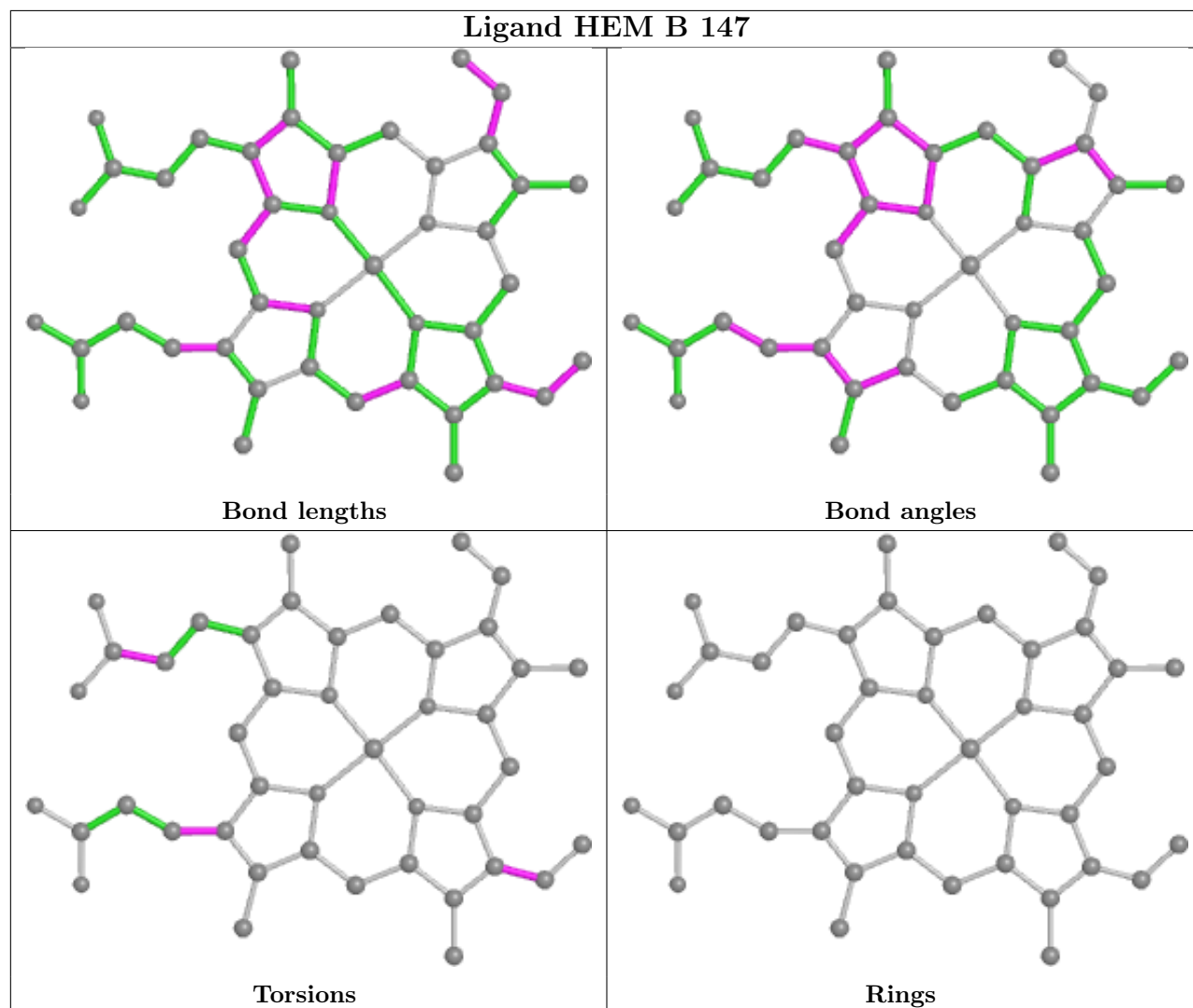
There are no ring outliers.

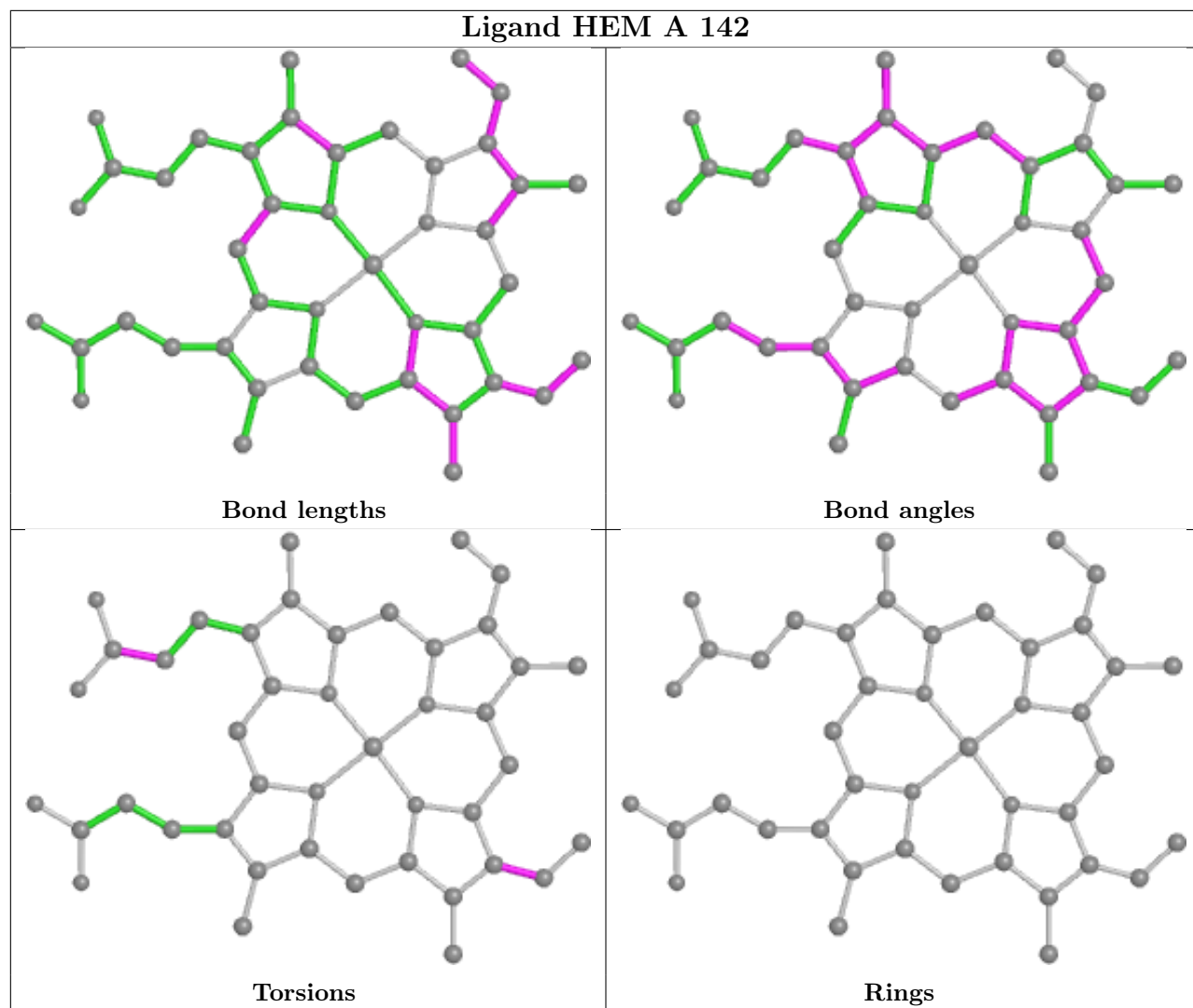
2 monomers are involved in 9 short contacts:

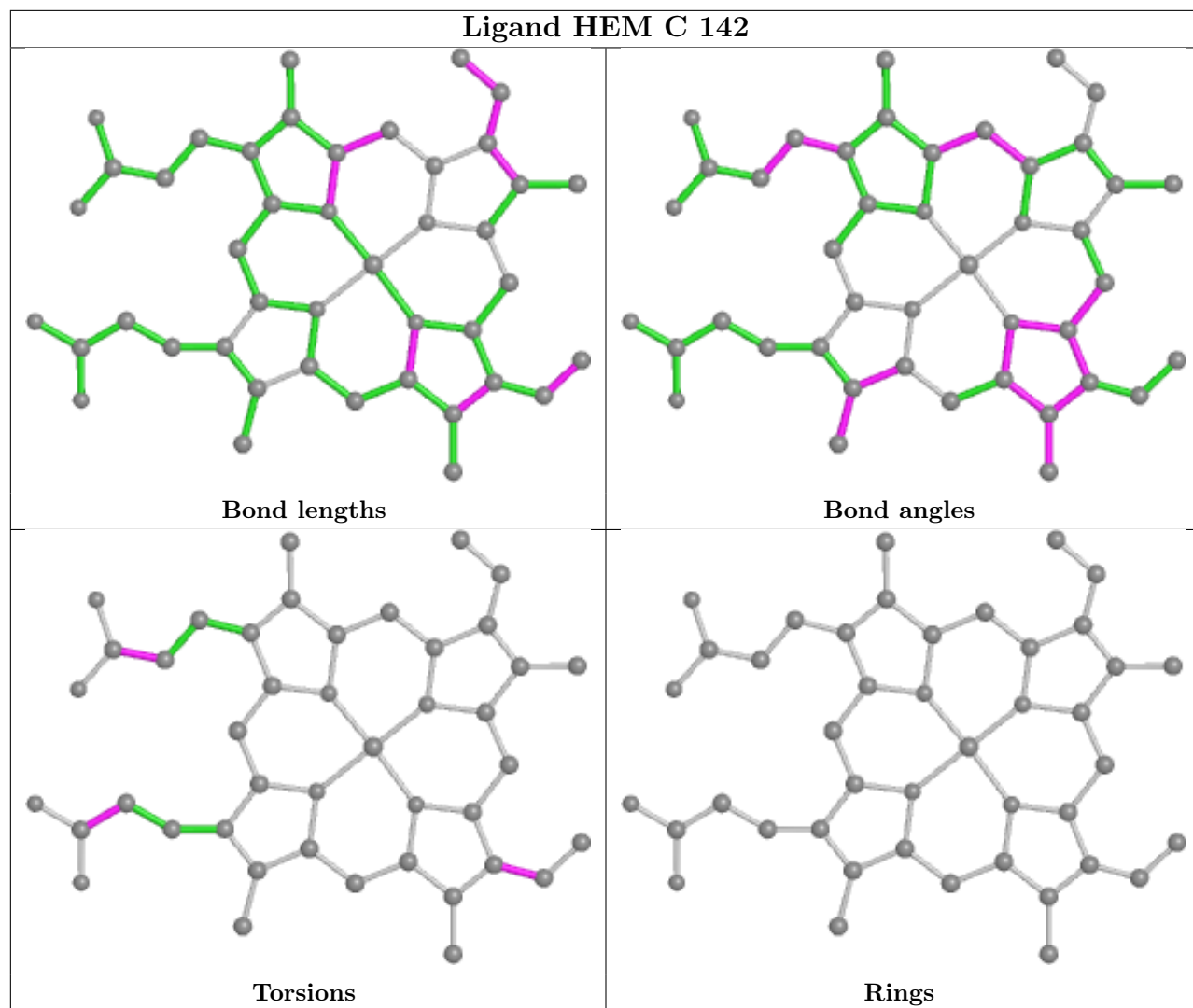
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	147	HEM	8	0
3	D	147	HEM	1	0

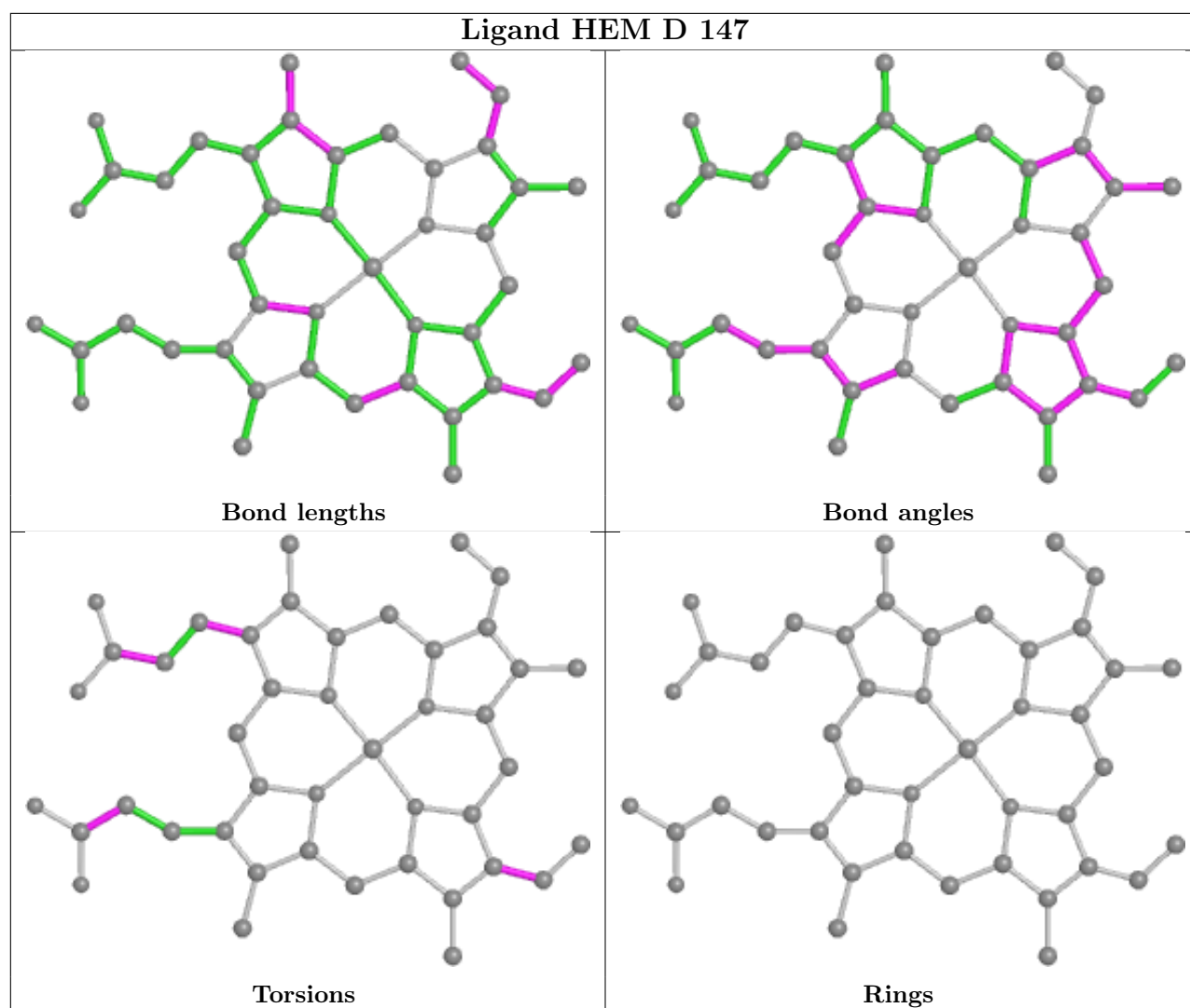
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

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.