



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 07:56 PM EDT

PDB ID : 1QSI / pdb_00001qsi
Title : MAGNESIUM(II)-AND ZINC(II)-PROTOPORPHYRIN IX'S STABILIZE
THE LOWEST OXYGEN AFFINITY STATE OF HUMAN HEMOGLOBIN
EVEN MORE STRONGLY THAN DEOXYHEME
Authors : Miyazaki, G.; Morimoto, H.; Yun, K.-M.; Park, S.-Y.; Nakagawa, A.; Mina-
gawa, H.; Shibayama, N.
Deposited on : 1999-06-22
Resolution : 1.70 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	:	4-5-2 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

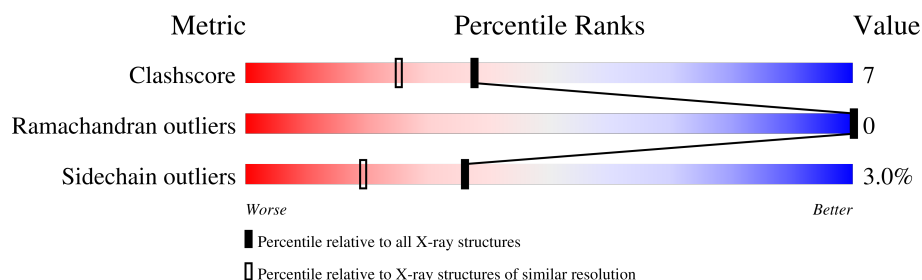
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)

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.

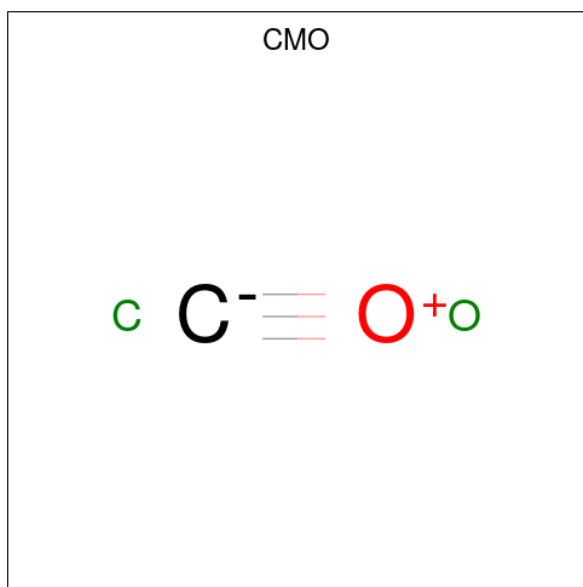
Mol	Chain	Length	Quality of chain
1	A	141	 65% 33% ..
1	C	141	 67% 29% ..
2	B	146	 73% 25% .
2	D	146	 74% 21% ..

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	HEG	B	147	X	-	-	-
5	HEG	D	147	X	-	-	-

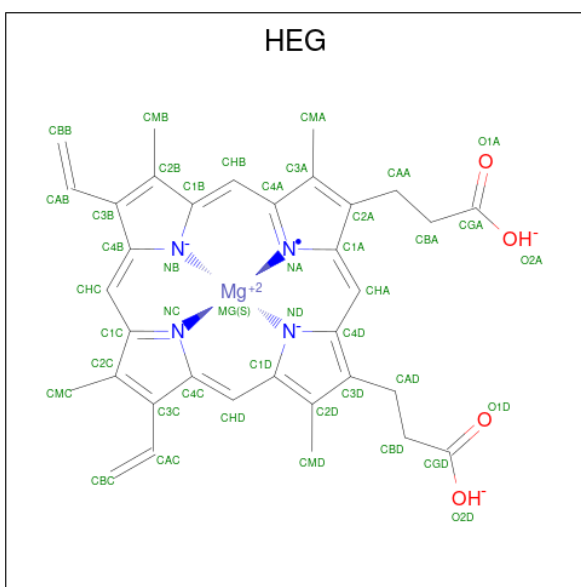
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	
3	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 4 is CARBON MONOXIDE (CCD ID: CMO) (formula: CO).



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

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING MG (CCD ID: HEG) (formula: C₃₄H₃₂MgN₄O₄).



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

- Molecule 6 is water.

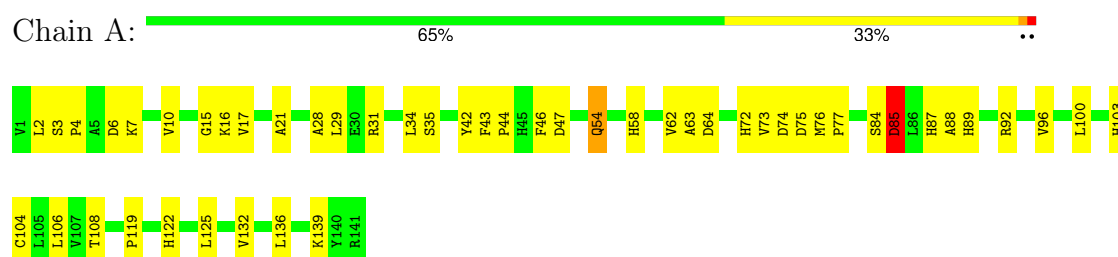
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	107	Total O 107 107	0	0
6	B	119	Total O 119 119	0	0
6	C	101	Total O 101 101	0	0
6	D	78	Total O 78 78	0	0

3 Residue-property plots

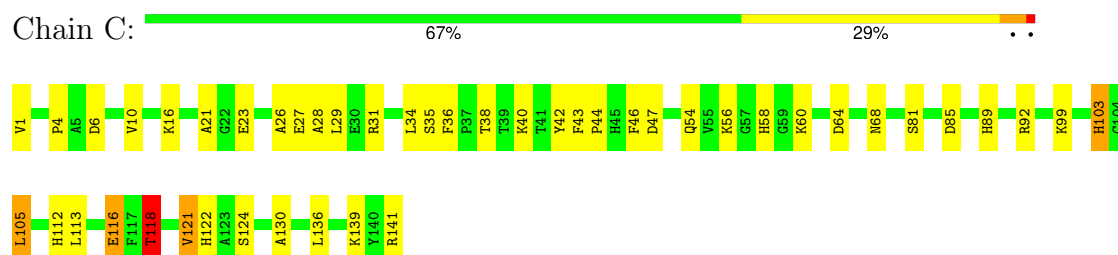
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

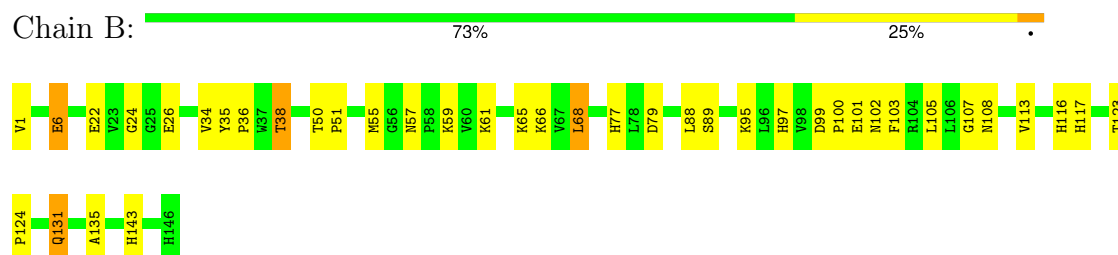
• Molecule 1: PROTEIN (HEMOGLOBIN ALPHA CHAIN)



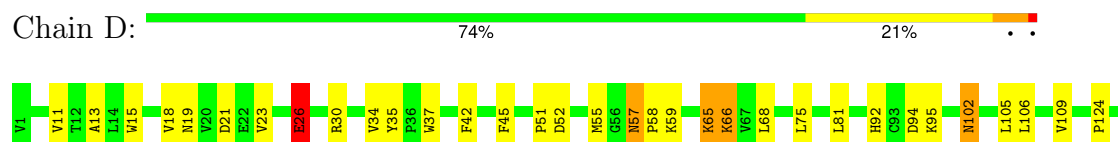
• Molecule 1: PROTEIN (HEMOGLOBIN ALPHA CHAIN)



• Molecule 2: PROTEIN (HEMOGLOBIN BETA CHAIN)



• Molecule 2: PROTEIN (HEMOGLOBIN BETA CHAIN)



Y130	Q131	V134	M139	Y145	H146
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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)	10.00 – 1.70	Depositor
% Data completeness (in resolution range)	91.6 (10.00-1.70)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.186 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4965	wwPDB-VP
Average B, all atoms (Å ²)	16.0	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: HEM, HEG, CMO

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	1.38	3/1097 (0.3%)	1.96	35/1491 (2.3%)
1	C	1.39	7/1097 (0.6%)	1.99	30/1491 (2.0%)
2	B	1.38	2/1153 (0.2%)	1.98	27/1566 (1.7%)
2	D	1.29	0/1153	1.94	30/1566 (1.9%)
All	All	1.36	12/4500 (0.3%)	1.97	122/6114 (2.0%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	36	PHE	N-CA	6.63	1.54	1.46
1	A	87	HIS	CD2-NE2	6.03	1.44	1.37
2	B	99	ASP	N-CA	5.95	1.54	1.46
1	C	92	ARG	NE-CZ	5.94	1.39	1.33
1	A	31	ARG	CZ-NH2	5.88	1.41	1.33
1	C	31	ARG	CZ-NH2	5.86	1.41	1.33
1	C	124	SER	C-O	5.79	1.30	1.24
1	C	118	THR	CA-CB	5.69	1.61	1.53
1	C	38	THR	N-CA	5.69	1.53	1.46
1	C	103	HIS	ND1-CE1	5.58	1.38	1.32
1	A	29	LEU	N-CA	5.52	1.53	1.46
2	B	113	VAL	C-O	5.29	1.30	1.24

All (122) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	26	GLU	CB-CG-CD	10.78	130.93	112.60
1	C	58	HIS	CA-CB-CG	-10.64	103.16	113.80
2	D	124	PRO	CB-CA-C	9.76	122.82	110.92
1	C	122	HIS	CA-CB-CG	9.14	122.94	113.80
1	C	31	ARG	NE-CZ-NH1	8.85	130.35	121.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	94	ASP	N-CA-C	8.65	120.70	111.28
2	D	139	ASN	CA-CB-CG	-8.56	104.04	112.60
1	C	118	THR	OG1-CB-CG2	8.55	126.39	109.30
1	C	92	ARG	CD-NE-CZ	-8.41	112.62	124.40
1	A	122	HIS	CA-CB-CG	8.39	122.19	113.80
2	B	131	GLN	CB-CG-CD	8.23	126.60	112.60
1	A	75	ASP	CA-CB-CG	8.19	120.79	112.60
1	C	118	THR	N-CA-CB	-7.90	98.67	110.05
1	A	54	GLN	O-C-N	7.83	130.14	122.07
1	A	54	GLN	OE1-CD-NE2	-7.64	114.96	122.60
2	B	35	TYR	O-C-N	7.51	128.13	121.37
2	B	38	THR	O-C-N	7.47	132.77	122.46
1	A	31	ARG	O-C-N	7.47	130.66	122.15
2	B	79	ASP	CA-CB-CG	7.42	120.02	112.60
1	A	31	ARG	NE-CZ-NH1	7.34	128.84	121.50
1	C	54	GLN	O-C-N	7.33	130.50	122.15
1	A	85	ASP	CA-CB-CG	-7.29	105.31	112.60
1	C	121	VAL	O-C-N	7.24	129.29	121.83
2	D	105	LEU	O-C-N	7.23	130.39	122.15
1	A	104	CYS	CA-C-O	-7.11	112.89	120.42
2	D	145	TYR	O-C-N	7.08	131.36	123.01
1	A	28	ALA	O-C-N	7.03	130.17	122.15
2	D	105	LEU	CA-C-O	-6.89	113.12	120.42
1	A	17	VAL	O-C-N	6.83	128.61	121.91
2	B	108	ASN	O-C-N	6.81	129.91	122.15
1	C	68	ASN	OD1-CG-ND2	-6.77	115.83	122.60
1	A	35	SER	O-C-N	6.71	129.80	122.15
1	C	103	HIS	CB-CG-CD2	-6.69	122.51	131.20
2	B	124	PRO	CB-CA-C	6.67	119.06	110.92
1	C	31	ARG	O-C-N	6.67	129.19	122.12
1	C	36	PHE	O-C-N	6.65	127.36	121.37
2	B	97	HIS	CA-CB-CG	-6.62	107.18	113.80
2	B	135	ALA	CA-C-N	6.59	127.26	119.94
2	B	135	ALA	C-N-CA	6.59	127.26	119.94
2	D	134	VAL	O-C-N	6.58	128.61	121.83
2	B	101	GLU	O-C-N	6.55	129.88	122.22
1	C	85	ASP	CA-C-O	6.54	127.48	120.55
1	C	29	LEU	CA-C-O	6.46	127.27	120.42
1	A	125	LEU	O-C-N	6.41	129.45	122.15
1	A	119	PRO	O-C-N	-6.36	114.60	122.23
1	C	31	ARG	NE-CZ-NH2	-6.35	113.48	119.20
1	A	72	HIS	CA-CB-CG	-6.35	107.45	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	11	VAL	O-C-N	6.22	128.00	121.91
2	B	57	ASN	OD1-CG-ND2	6.21	128.81	122.60
1	C	89	HIS	CA-CB-CG	-6.18	107.61	113.80
1	A	15	GLY	N-CA-C	-6.18	105.33	112.50
1	C	47	ASP	N-CA-C	-6.16	98.49	108.41
2	D	30	ARG	O-C-N	6.13	128.62	122.12
2	D	130	TYR	O-C-N	6.12	129.38	122.22
1	A	31	ARG	CA-C-O	-6.08	113.98	120.42
1	C	26	ALA	CA-C-O	6.07	126.85	120.42
1	A	122	HIS	N-CA-C	-6.06	104.59	111.07
2	B	95	LYS	CA-C-O	6.04	126.62	119.67
2	D	145	TYR	CA-C-O	-6.01	114.20	121.05
2	B	77	HIS	CA-CB-CG	-5.96	107.84	113.80
2	B	88	LEU	O-C-N	5.89	129.51	122.27
2	D	109	VAL	O-C-N	5.88	127.58	121.87
1	C	141	ARG	NE-CZ-NH2	-5.88	113.91	119.20
1	A	46	PHE	CA-CB-CG	5.87	119.67	113.80
2	D	26	GLU	CG-CD-OE1	5.83	131.82	118.40
1	A	108	THR	O-C-N	5.83	128.07	122.07
2	D	139	ASN	OD1-CG-ND2	5.82	128.42	122.60
1	A	108	THR	CA-C-O	-5.75	114.78	120.82
2	B	105	LEU	CA-C-O	-5.68	114.85	120.82
2	D	57	ASN	CA-C-O	5.68	123.84	119.46
2	B	100	PRO	N-CA-CB	5.68	108.92	103.52
1	A	104	CYS	O-C-N	5.68	128.62	122.15
1	A	132	VAL	O-C-N	5.66	127.36	121.87
1	A	96	VAL	CA-C-N	5.65	128.41	120.28
1	A	96	VAL	C-N-CA	5.65	128.41	120.28
1	C	46	PHE	CA-CB-CG	5.64	119.44	113.80
2	B	61	LYS	CA-C-O	5.59	126.47	120.55
1	C	130	ALA	CA-C-N	5.59	128.04	120.44
1	C	130	ALA	C-N-CA	5.59	128.04	120.44
2	D	13	ALA	CA-C-O	5.56	126.66	120.82
1	A	46	PHE	CA-C-O	5.55	127.83	121.28
2	B	89	SER	CA-C-O	5.53	126.63	120.82
2	B	105	LEU	O-C-N	5.53	127.76	122.07
2	B	107	GLY	O-C-N	5.51	127.48	122.19
2	D	35	TYR	O-C-N	5.50	126.32	121.37
2	D	102	ASN	OD1-CG-ND2	5.47	128.07	122.60
2	B	143	HIS	N-CA-C	5.47	117.95	111.33
1	A	31	ARG	NE-CZ-NH2	-5.45	114.30	119.20
2	D	42	PHE	N-CA-C	5.44	117.84	110.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	106	LEU	O-C-N	5.43	127.88	122.12
2	D	15	TRP	O-C-N	5.37	128.50	122.22
1	A	62	VAL	O-C-N	5.37	127.17	121.91
1	C	118	THR	CA-CB-OG1	-5.36	101.56	109.60
2	B	103	PHE	O-C-N	5.35	128.25	122.15
2	D	92	HIS	O-C-N	5.32	128.44	122.22
2	D	34	VAL	CA-C-O	-5.32	114.51	120.25
1	A	88	ALA	N-CA-C	5.31	117.14	111.36
1	A	34	LEU	O-C-N	5.31	128.59	122.17
1	C	34	LEU	N-CA-C	5.28	116.84	111.14
2	D	131	GLN	OE1-CD-NE2	5.27	127.87	122.60
2	D	65	LYS	CA-C-O	5.27	126.35	120.82
1	C	68	ASN	CA-CB-CG	5.26	117.86	112.60
1	C	42	TYR	O-C-N	5.24	129.86	122.41
1	A	100	LEU	CA-C-O	-5.24	115.30	120.70
1	A	64	ASP	CA-C-O	5.20	126.06	120.55
2	D	81	LEU	CB-CA-C	5.16	118.99	110.88
2	B	50	THR	O-C-N	5.16	125.70	121.32
1	A	28	ALA	CA-C-N	-5.15	113.38	120.28
1	A	28	ALA	C-N-CA	-5.15	113.38	120.28
2	B	34	VAL	O-C-N	5.15	128.87	121.82
1	A	62	VAL	CA-C-O	-5.14	115.72	121.17
1	C	21	ALA	CA-C-N	5.13	125.67	119.98
1	C	21	ALA	C-N-CA	5.13	125.67	119.98
2	D	52	ASP	CB-CA-C	5.12	119.56	110.85
2	D	109	VAL	CA-C-O	-5.10	115.64	120.95
2	D	19	ASN	O-C-N	5.09	129.14	122.68
2	B	123	THR	O-C-N	5.07	128.32	121.12
2	B	36	PRO	N-CA-CB	5.06	108.54	103.48
2	B	22	GLU	O-C-N	5.05	127.55	122.09
1	A	42	TYR	CA-C-O	-5.04	113.18	119.18
1	C	35	SER	O-C-N	5.02	129.05	122.33
1	C	136	LEU	O-C-N	5.01	129.14	122.43

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	1069	0	1073	17	0
1	C	1069	0	1073	19	0
2	B	1123	0	1118	15	0
2	D	1123	0	1118	14	0
3	A	43	0	30	1	0
3	C	43	0	30	0	0
4	A	2	0	0	0	0
4	C	2	0	0	0	0
5	B	43	0	30	3	0
5	D	43	0	30	1	0
6	A	107	0	0	3	0
6	B	119	0	0	4	0
6	C	101	0	0	8	0
6	D	78	0	0	1	0
All	All	4965	0	4502	63	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 7.

All (63) 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)
2:D:66:LYS:HE3	6:D:219:HOH:O	1.50	1.11
1:C:118:THR:HG21	6:C:175:HOH:O	1.52	1.09
1:C:113:LEU:HB3	1:C:116:GLU:HG2	1.45	0.98
1:C:118:THR:HG22	1:C:121:VAL:H	1.41	0.86
1:C:4:PRO:HD2	6:C:185:HOH:O	1.82	0.78
1:C:23:GLU:HG2	6:C:220:HOH:O	1.86	0.75
2:B:116:HIS:HB3	6:B:225:HOH:O	1.86	0.75
1:A:47:ASP:HB3	1:A:54:GLN:OE1	1.87	0.75
2:B:59:LYS:HD3	6:B:171:HOH:O	1.93	0.68
2:D:21:ASP:CG	2:D:65:LYS:HD2	2.19	0.67
1:C:40:LYS:HE3	6:C:171:HOH:O	1.94	0.66
1:C:103:HIS:HE1	2:D:131:GLN:OE1	1.81	0.64
2:D:51:PRO:O	2:D:55:MET:HG2	1.99	0.63
1:C:103:HIS:HD2	6:C:144:HOH:O	1.82	0.62
1:C:27:GLU:OE2	1:C:112:HIS:HE1	1.81	0.62
1:C:60:LYS:HE3	1:C:64:ASP:OD2	2.02	0.60
1:A:47:ASP:CB	1:A:54:GLN:OE1	2.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:HIS:HD2	6:A:145:HOH:O	1.88	0.56
2:B:26:GLU:OE2	2:B:117:HIS:HE1	1.88	0.55
1:A:7:LYS:NZ	1:A:74:ASP:OD1	2.33	0.55
6:A:233:HOH:O	1:C:1:VAL:HG12	2.05	0.55
1:A:103:HIS:HE1	2:B:131:GLN:OE1	1.91	0.54
1:C:99:LYS:HD3	6:C:201:HOH:O	2.09	0.53
2:D:26:GLU:OE1	2:D:55:MET:CE	2.57	0.52
1:A:47:ASP:N	1:A:54:GLN:OE1	2.41	0.52
2:D:26:GLU:OE1	2:D:55:MET:HE2	2.11	0.51
1:A:84:SER:OG	1:A:139:LYS:HE3	2.10	0.51
1:A:21:ALA:HB1	1:A:63:ALA:HB1	1.92	0.50
2:B:51:PRO:O	2:B:55:MET:HG2	2.11	0.50
1:C:99:LYS:CD	6:C:201:HOH:O	2.58	0.50
1:C:56:LYS:HG3	6:C:192:HOH:O	2.12	0.50
1:C:28:ALA:CB	1:C:105:LEU:HD13	2.42	0.49
2:D:23:VAL:HG12	2:D:68:LEU:CD2	2.43	0.49
5:B:147:HEG:HMC1	5:B:147:HEG:HBC1	1.95	0.49
2:B:1:VAL:HG11	6:B:167:HOH:O	2.12	0.49
1:A:58:HIS:CE1	3:A:142:HEM:HBD2	2.48	0.48
6:A:233:HOH:O	1:C:1:VAL:CG1	2.61	0.48
2:B:66:LYS:HD3	5:B:147:HEG:CAA	2.43	0.47
1:A:85:ASP:OD1	1:A:89:HIS:HD2	1.97	0.47
2:B:6:GLU:H	2:B:6:GLU:CD	2.23	0.46
2:D:18:VAL:HG13	2:D:23:VAL:HG21	1.97	0.46
2:D:45:PHE:HA	2:D:59:LYS:HD3	1.96	0.46
2:B:26:GLU:OE2	2:B:117:HIS:CE1	2.68	0.46
2:D:57:ASN:HA	2:D:58:PRO:HD3	1.82	0.46
2:D:102:ASN:HB3	5:D:147:HEG:HMC3	1.98	0.46
1:C:81:SER:OG	1:C:139:LYS:NZ	2.48	0.45
2:B:55:MET:HE3	2:B:55:MET:HB3	1.83	0.45
2:B:24:GLY:HA2	2:B:68:LEU:HG	1.99	0.45
2:B:38:THR:HG22	2:B:102:ASN:OD1	2.17	0.44
1:A:43:PHE:N	1:A:44:PRO:CD	2.81	0.44
2:D:21:ASP:OD2	2:D:65:LYS:NZ	2.33	0.44
2:D:95:LYS:HA	2:D:95:LYS:HD3	1.90	0.43
1:A:6:ASP:O	1:A:10:VAL:HG23	2.18	0.43
1:A:136:LEU:HD23	1:A:136:LEU:HA	1.83	0.43
1:C:43:PHE:N	1:C:44:PRO:CD	2.81	0.42
1:A:92:ARG:HB3	2:D:37:TRP:HB2	2.02	0.42
2:B:65:LYS:HG3	2:B:66:LYS:N	2.35	0.41
1:A:16:LYS:HD2	1:A:16:LYS:HA	1.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:ASP:O	1:C:10:VAL:HG23	2.20	0.41
1:A:3:SER:HB2	1:A:4:PRO:HD2	2.03	0.40
2:B:65:LYS:CE	6:B:176:HOH:O	2.69	0.40
1:A:76:MET:N	1:A:77:PRO:CD	2.85	0.40
2:B:66:LYS:HD3	5:B:147:HEG:HAA2	2.04	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%)	136 (98%)	3 (2%)	0	100	100
1	C	139/141 (99%)	137 (99%)	2 (1%)	0	100	100
2	B	144/146 (99%)	143 (99%)	1 (1%)	0	100	100
2	D	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
All	All	566/574 (99%)	558 (99%)	8 (1%)	0	100	100

There are no Ramachandran outliers to report.

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%)	109 (96%)	4 (4%)	32	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	113/113 (100%)	109 (96%)	4 (4%)	32	15
2	B	118/118 (100%)	116 (98%)	2 (2%)	53	38
2	D	118/118 (100%)	114 (97%)	4 (3%)	32	16
All	All	462/462 (100%)	448 (97%)	14 (3%)	36	19

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LEU
1	A	73	VAL
1	A	85	ASP
1	A	106	LEU
2	B	6	GLU
2	B	68	LEU
1	C	16	LYS
1	C	105	LEU
1	C	116	GLU
1	C	118	THR
2	D	26	GLU
2	D	66	LYS
2	D	75	LEU
2	D	139	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	HIS
1	A	89	HIS
1	A	103	HIS
2	B	80	ASN
2	B	117	HIS
1	C	68	ASN
1	C	72	HIS
1	C	78	ASN
1	C	103	HIS
1	C	112	HIS
2	D	77	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](#)

6 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	$\# Z > 2$
5	HEG	B	147	2	48,50,50	1.49	9 (18%)	62,82,82	1.36	11 (17%)
4	CMO	C	143	-	0,1,1	-	-	-		
4	CMO	A	143	-	0,1,1	-	-	-		
3	HEM	A	142	1	50,50,50	1.53	11 (22%)	67,82,82	1.49	10 (14%)
5	HEG	D	147	2	48,50,50	1.34	3 (6%)	62,82,82	1.11	6 (9%)
3	HEM	C	142	1	50,50,50	1.46	7 (14%)	67,82,82	1.31	11 (16%)

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	A	142	1	-	2/14/54/54	-
5	HEG	B	147	2	3/3/3/9	2/14/54/54	-
5	HEG	D	147	2	2/2/3/9	4/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEM	C	142	1	-	4/14/54/54	-

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	147	HEG	CAB-C3B	3.44	1.56	1.47
3	C	142	HEM	FE-NB	3.44	2.05	1.94
3	A	142	HEM	CAB-C3B	3.28	1.56	1.47
3	C	142	HEM	CMB-C2B	3.05	1.57	1.50
3	A	142	HEM	FE-ND	2.84	2.03	1.94
5	D	147	HEG	CAC-C3C	2.83	1.54	1.47
5	B	147	HEG	CAA-C2A	2.76	1.58	1.51
3	C	142	HEM	C2A-C3A	-2.72	1.31	1.38
3	C	142	HEM	FE-ND	2.66	2.03	1.94
5	B	147	HEG	CAB-C3B	2.66	1.54	1.47
5	B	147	HEG	O1D-CGD	2.65	1.30	1.22
3	A	142	HEM	FE-NC	2.62	2.03	1.95
5	B	147	HEG	C3D-C2D	-2.54	1.32	1.38
3	C	142	HEM	CAB-C3B	2.54	1.54	1.47
5	D	147	HEG	C2A-C3A	-2.51	1.31	1.36
5	B	147	HEG	CAD-C3D	2.48	1.57	1.51
5	B	147	HEG	CAC-C3C	2.45	1.53	1.47
3	C	142	HEM	O2D-CGD	-2.37	1.23	1.30
3	A	142	HEM	CAC-C3C	2.36	1.53	1.47
3	A	142	HEM	CMC-C2C	2.32	1.55	1.50
3	A	142	HEM	CMA-C3A	2.30	1.55	1.50
3	A	142	HEM	FE-NB	2.28	2.01	1.94
5	B	147	HEG	CMC-C2C	2.26	1.55	1.50
5	B	147	HEG	C3C-C2C	-2.23	1.32	1.37
3	A	142	HEM	C2A-C3A	-2.21	1.33	1.38
3	C	142	HEM	CMC-C2C	2.21	1.55	1.50
5	B	147	HEG	C1D-C2D	2.20	1.48	1.43
3	A	142	HEM	C3D-C2D	-2.17	1.32	1.36
3	A	142	HEM	CAD-C3D	2.16	1.56	1.51
3	A	142	HEM	O2A-CGA	-2.04	1.24	1.30

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	142	HEM	CHD-C1D-ND	3.96	128.68	124.42
3	A	142	HEM	C3D-C4D-ND	-3.86	105.93	110.17
3	A	142	HEM	C4D-ND-C1D	3.66	109.54	105.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	142	HEM	C4D-ND-C1D	3.24	109.04	105.21
3	C	142	HEM	CMA-C3A-C4A	-3.23	120.50	125.42
5	B	147	HEG	CAA-C2A-C1A	-3.11	119.28	124.70
5	B	147	HEG	C3C-C2C-C1C	3.03	108.68	106.41
5	B	147	HEG	C1A-C2A-C3A	3.01	111.27	106.89
3	C	142	HEM	CMA-C3A-C2A	2.85	131.66	125.62
3	C	142	HEM	C3D-C4D-ND	-2.82	107.08	110.17
3	C	142	HEM	O1D-CGD-CBD	-2.82	114.15	123.09
3	C	142	HEM	O2D-CGD-O1D	2.79	130.52	123.33
3	A	142	HEM	CBB-CAB-C3B	-2.73	113.91	127.53
3	C	142	HEM	CHD-C1D-ND	2.64	127.26	124.42
3	A	142	HEM	O1D-CGD-CBD	-2.62	114.78	123.09
5	B	147	HEG	CMD-C2D-C3D	2.60	131.14	125.62
5	B	147	HEG	C4A-C3A-C2A	-2.55	104.30	106.98
3	C	142	HEM	CMB-C2B-C1B	-2.54	121.06	125.03
5	D	147	HEG	CHD-C1D-ND	2.54	127.86	124.05
3	C	142	HEM	C3B-C2B-C1B	2.52	108.30	106.41
3	A	142	HEM	C4D-C3D-C2D	2.49	110.51	106.89
3	C	142	HEM	CMD-C2D-C1D	-2.43	121.24	125.03
3	A	142	HEM	C3C-C2C-C1C	2.39	109.31	107.05
3	A	142	HEM	O1A-CGA-CBA	-2.36	115.60	123.09
5	B	147	HEG	O1D-CGD-CBD	-2.34	115.66	123.09
5	D	147	HEG	O2A-CGA-O1A	2.25	129.11	123.33
5	D	147	HEG	O1A-CGA-CBA	-2.20	116.10	123.09
5	B	147	HEG	C2A-C1A-NA	-2.18	107.56	109.90
3	A	142	HEM	CMA-C3A-C4A	-2.16	122.14	125.42
3	A	142	HEM	CMA-C3A-C2A	2.15	130.19	125.62
5	B	147	HEG	CMD-C2D-C1D	-2.13	122.18	125.42
3	C	142	HEM	CMD-C2D-C3D	2.13	131.91	126.15
5	B	147	HEG	CHD-C1D-ND	2.10	127.20	124.05
5	B	147	HEG	C3B-C2B-C1B	-2.09	105.07	107.05
5	B	147	HEG	O1A-CGA-CBA	-2.08	116.49	123.09
5	D	147	HEG	CMA-C3A-C4A	-2.04	121.85	125.03
5	D	147	HEG	CMD-C2D-C3D	2.03	129.93	125.62
5	D	147	HEG	CAD-CBD-CGD	-2.01	108.34	113.67

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	B	147	HEG	NA
5	B	147	HEG	NC
5	B	147	HEG	NB

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Mol	Chain	Res	Type	Atom
5	D	147	HEG	NA
5	D	147	HEG	NC

All (12) torsion outliers are listed below:

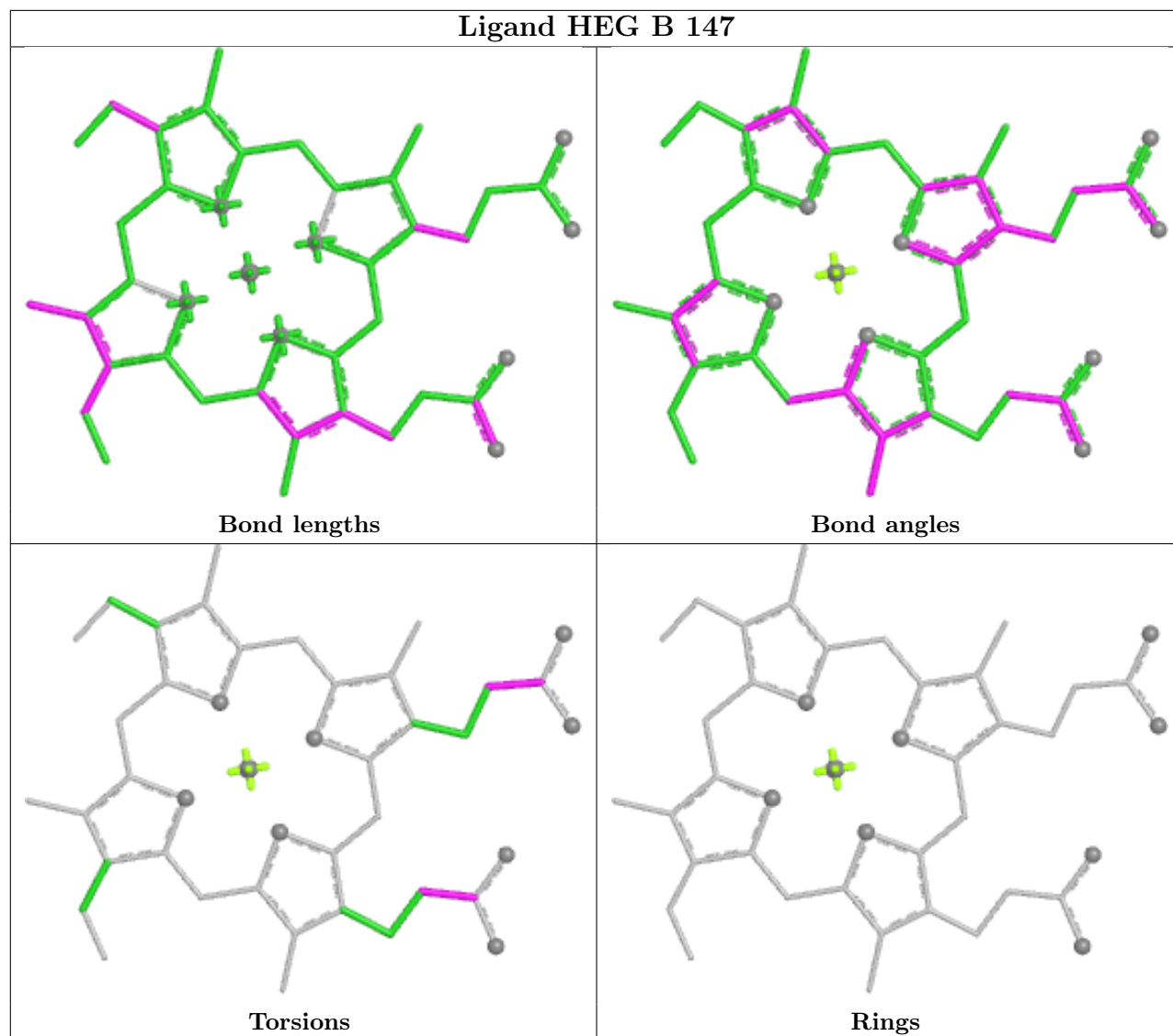
Mol	Chain	Res	Type	Atoms
5	D	147	HEG	C2B-C3B-CAB-CBB
3	C	142	HEM	CAD-CBD-CGD-O1D
3	A	142	HEM	CAD-CBD-CGD-O1D
5	D	147	HEG	CAD-CBD-CGD-O1D
3	C	142	HEM	CAD-CBD-CGD-O2D
5	D	147	HEG	CAD-CBD-CGD-O2D
3	A	142	HEM	CAD-CBD-CGD-O2D
5	B	147	HEG	CAD-CBD-CGD-O2D
5	D	147	HEG	C4B-C3B-CAB-CBB
3	C	142	HEM	CAA-CBA-CGA-O2A
3	C	142	HEM	CAA-CBA-CGA-O1A
5	B	147	HEG	CAA-CBA-CGA-O1A

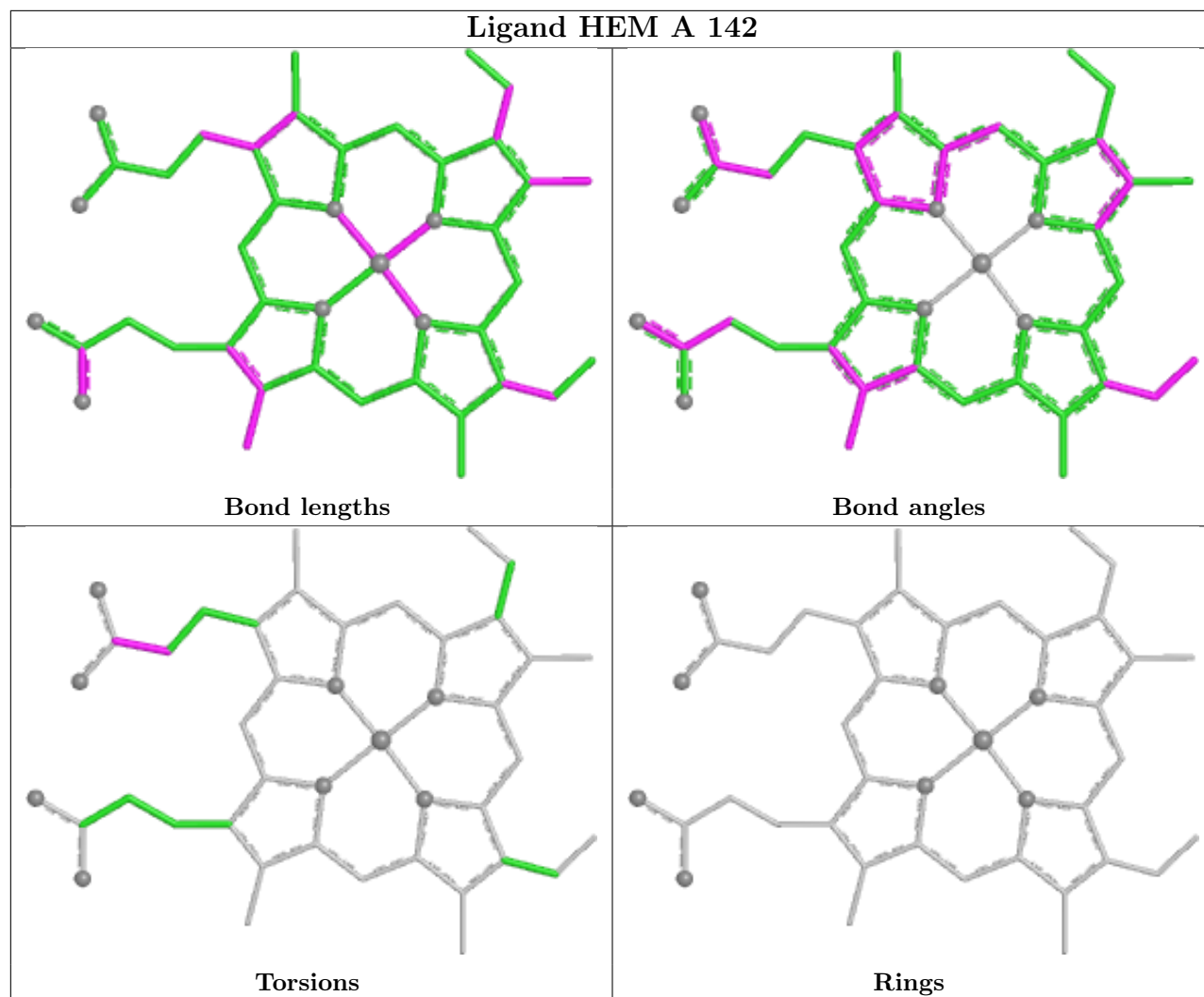
There are no ring outliers.

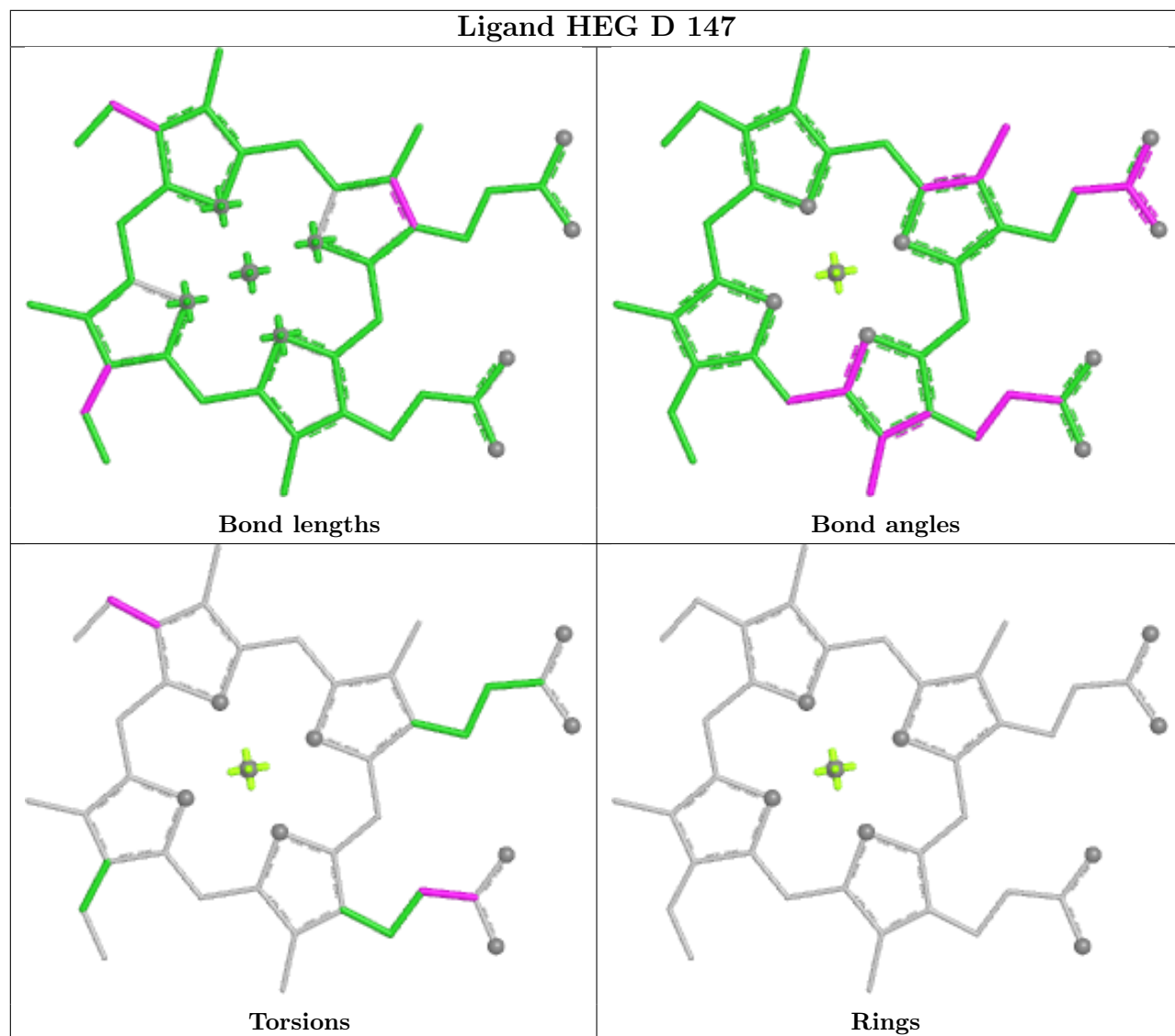
3 monomers are involved in 5 short contacts:

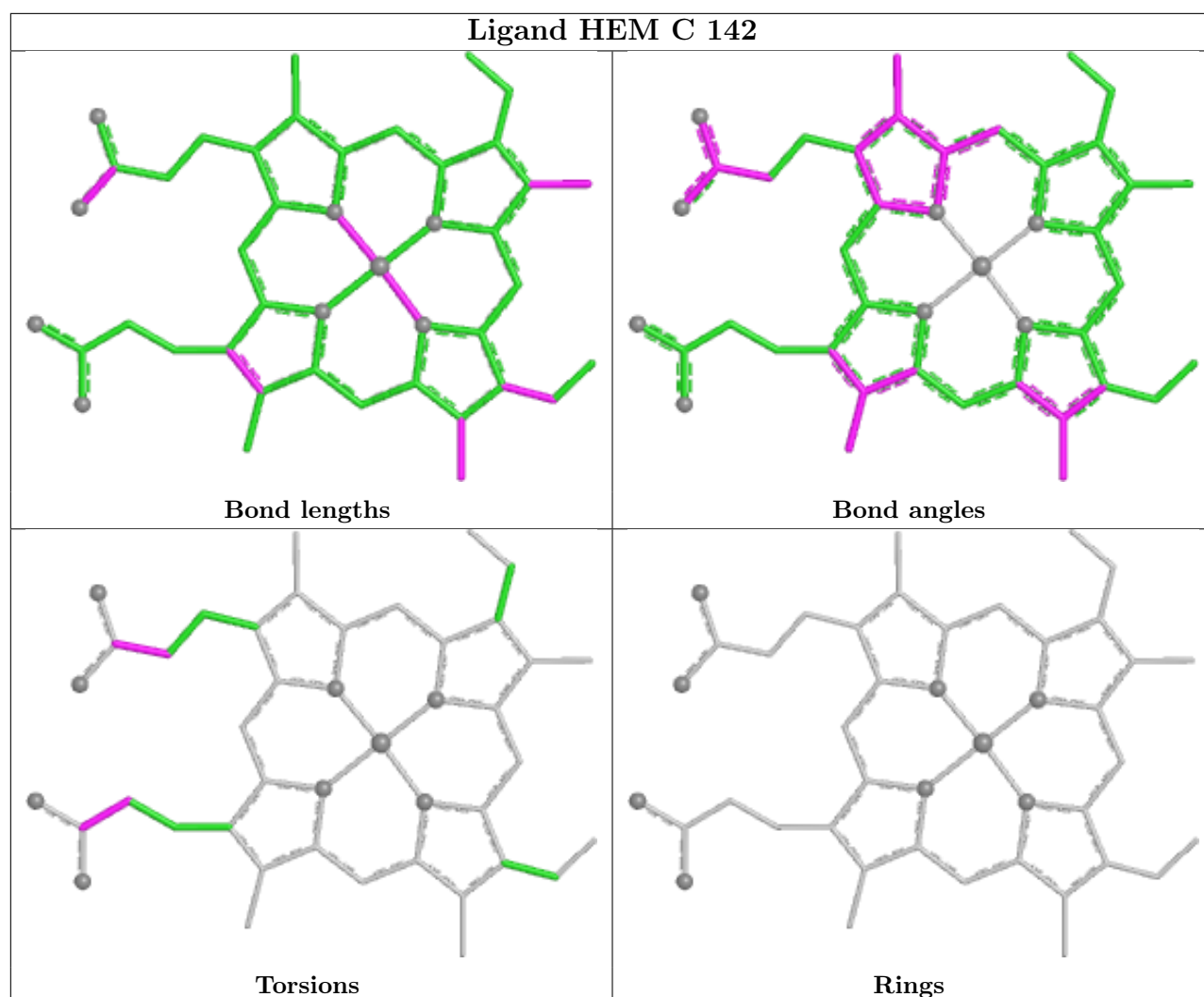
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	147	HEG	3	0
3	A	142	HEM	1	0
5	D	147	HEG	1	0

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.