



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 08:58 AM UTC

PDB ID : 1SQB / pdb_00001sqb
Title : Crystal Structure Analysis of Bovine Bcl with Azoxystrobin
Authors : Esser, L.; Quinn, B.; Li, Y.F.; Zhang, M.; Elberry, M.; Yu, L.; Yu, C.A.; Xia, D.
Deposited on : 2004-03-18
Resolution : 2.69 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

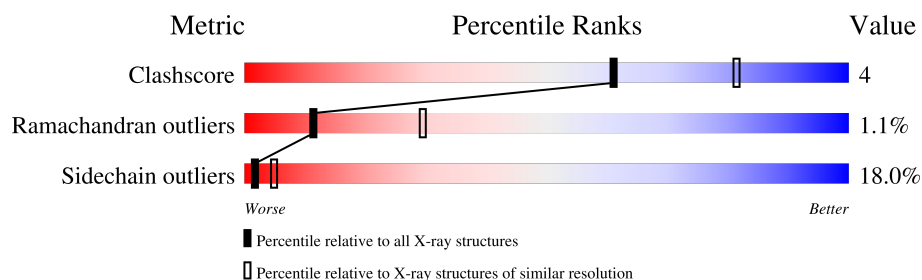
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)

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	480	72% 18% 7%
2	B	453	75% 15% 6%
3	C	379	75% 20% .
4	D	241	72% 24% .
5	E	196	71% 28% .
6	F	110	75% 18% 5%
7	G	81	63% 26% 7%
8	H	78	49% 32% 5% 14%

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Mol	Chain	Length	Quality of chain
9	I	78	
10	J	62	
11	K	56	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 16897 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 Ubiquinol-cytochrome C reductase complex core protein I, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	446	Total	C	N	O	S	0	0	0
			3458	2161	609	668	20			

- Molecule 2 is a protein called Ubiquinol-cytochrome C reductase complex core protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	425	Total	C	N	O	S	0	0	0
			3181	1998	564	612	7			

- Molecule 3 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	378	Total	C	N	O	S	0	0	0
			3003	2013	471	501	18			

- Molecule 4 is a protein called Cytochrome c1, heme protein, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	241	Total	C	N	O	S	0	0	0
			1919	1225	330	349	15			

- Molecule 5 is a protein called Ubiquinol-cytochrome c reductase iron-sulfur subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	196	Total	C	N	O	S	0	0	0
			1519	957	263	291	8			

- Molecule 6 is a protein called Ubiquinol-cytochrome C reductase complex 14 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	105	Total	C	N	O	S	0	0	0
			911	576	165	168	2			

- Molecule 7 is a protein called Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	75	Total	C	N	O	S	0	0	0
			628	410	118	99	1			

- Molecule 8 is a protein called Ubiquinol-cytochrome C reductase complex 11 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	67	Total	C	N	O	S	0	0	0
			548	332	99	112	5			

- Molecule 9 is a protein called Ubiquinol-cytochrome c reductase 8 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	57	Total	C	N	O	S	0	0	0
			406	253	77	74	2			

- Molecule 10 is a protein called Ubiquinol-cytochrome C reductase complex 7.2 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	61	Total	C	N	O		0	0	0
			502	329	87	86				

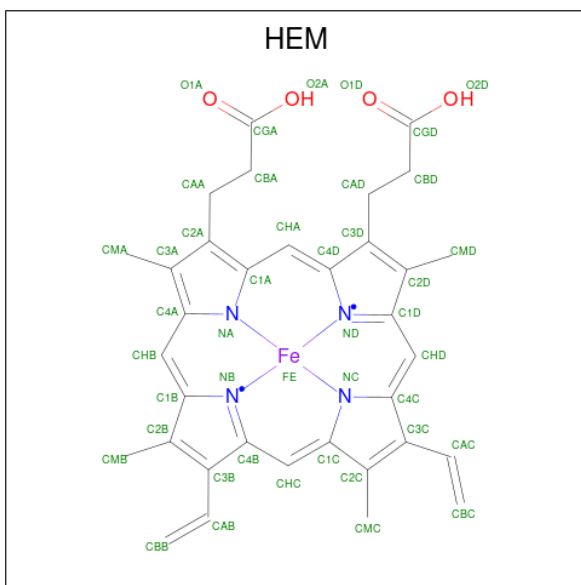
- Molecule 11 is a protein called Ubiquinol-cytochrome C reductase complex 6.4 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	52	Total	C	N	O		0	0	0
			425	282	77	66				

There is a discrepancy between the modelled and reference sequences:

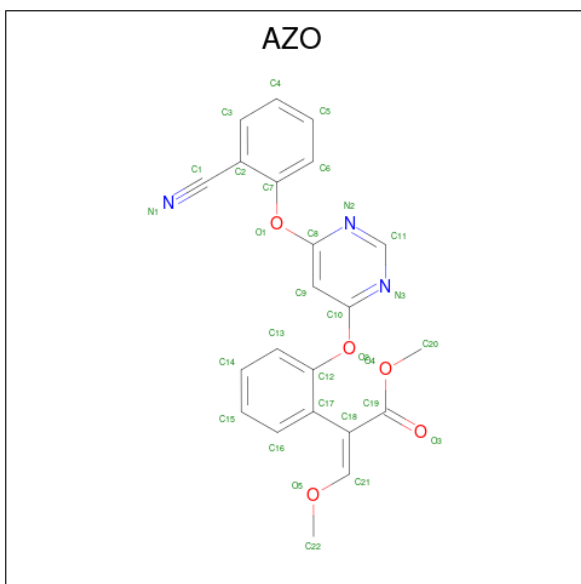
Chain	Residue	Modelled	Actual	Comment	Reference
K	34	TRP	SER	conflict	UNP P07552

- Molecule 12 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄).



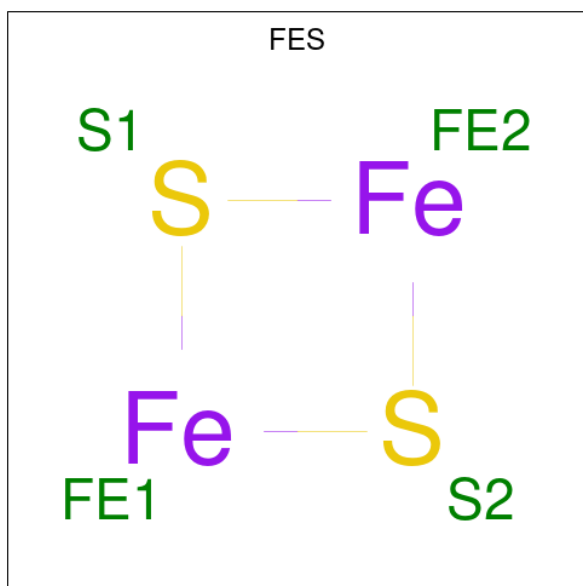
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
12	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
12	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 13 is METHYL (2Z)-2-(2-{[6-(2-CYANOPHENOXY)PYRIMIDIN-4-YL]OXY}PHENYL)-3-METHOXYACRYLATE (CCD ID: AZO) (formula: $C_{22}H_{17}N_3O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	C	1	Total	C	N	O	0	0
			30	22	3	5		

- Molecule 14 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	E	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 15 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	47	Total	O	0	0
			47	47		
15	B	82	Total	O	0	0
			82	82		
15	C	37	Total	O	0	0
			37	37		
15	D	19	Total	O	0	0
			19	19		
15	E	2	Total	O	0	0
			2	2		
15	F	21	Total	O	0	0
			21	21		
15	G	20	Total	O	0	0
			20	20		
15	H	1	Total	O	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	I	3	Total	O	0	0
			3	3		
15	K	2	Total	O	0	0
			2	2		

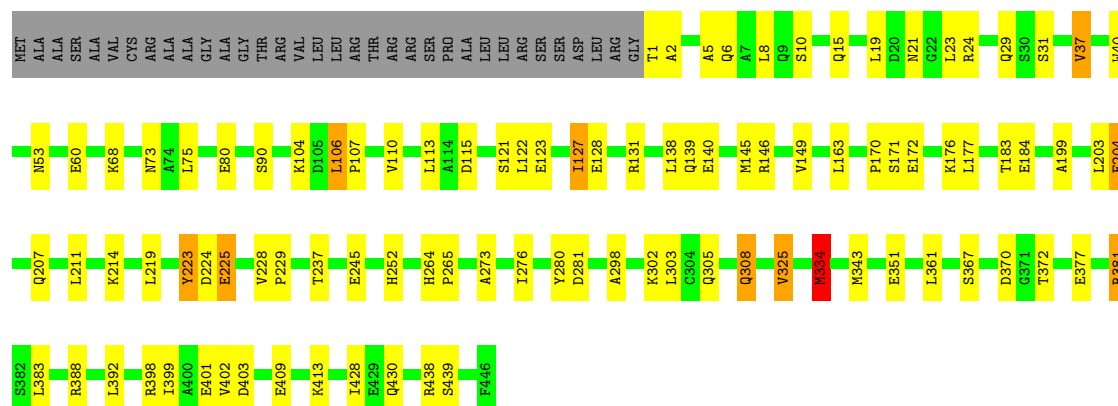
3 Residue-property plots [i](#)

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.

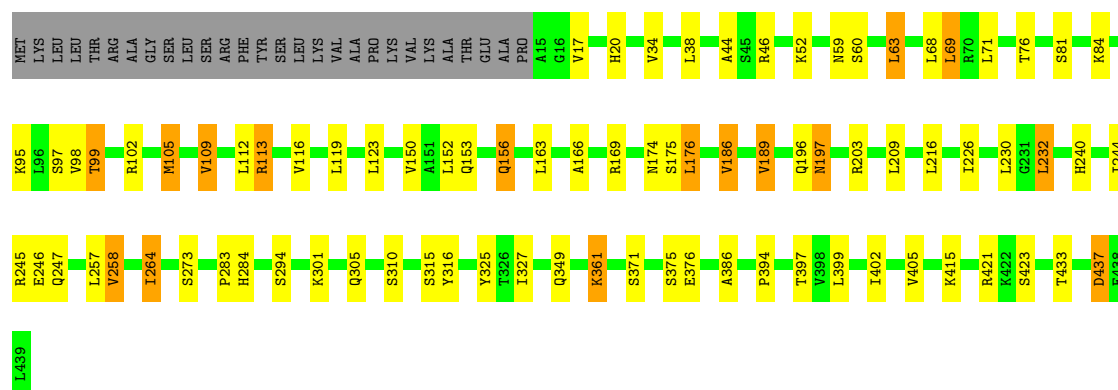
- Molecule 1: Ubiquinol-cytochrome C reductase complex core protein I, mitochondrial

Chain A: 



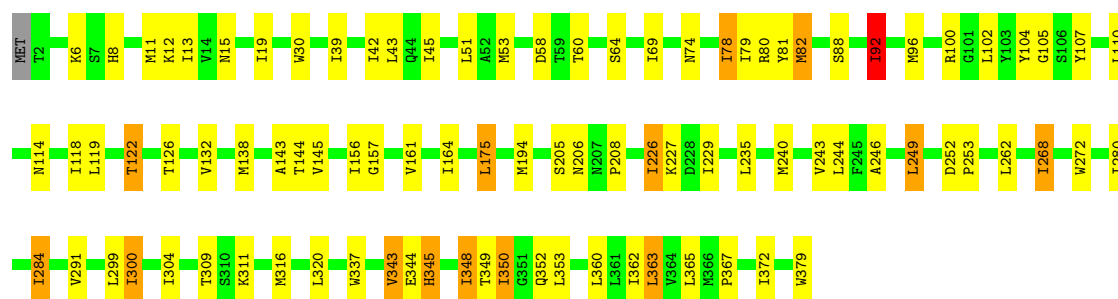
- Molecule 2: Ubiquinol-cytochrome C reductase complex core protein 2, mitochondrial

Chain B: 



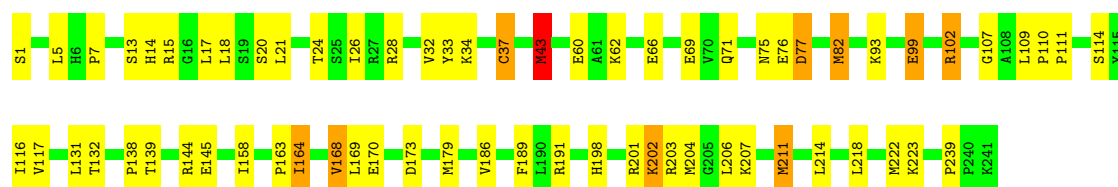
- Molecule 3: Cytochrome b

Chain C: 



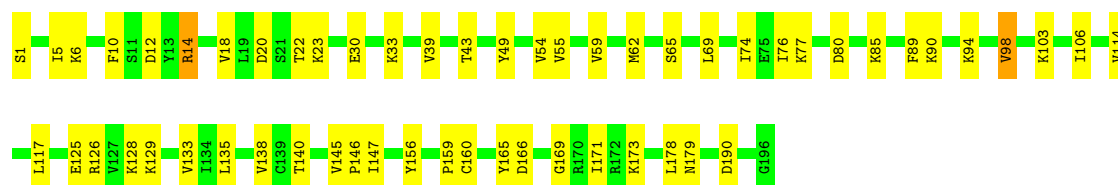
- Molecule 4: Cytochrome c1, heme protein, mitochondrial

Chain D: 72% 24% .



- Molecule 5: Ubiquinol-cytochrome c reductase iron-sulfur subunit

Chain E: 71% 28% .



- Molecule 6: Ubiquinol-cytochrome C reductase complex 14 kDa protein

Chain F: 75% 18% 5% .



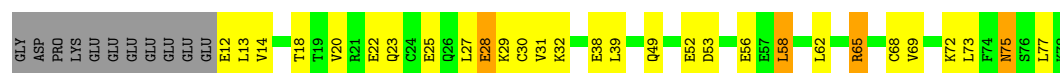
- Molecule 7: Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C

Chain G: 63% 26% 7% .

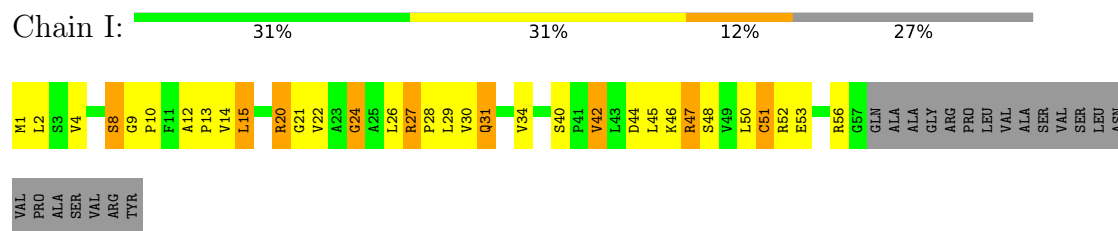


- Molecule 8: Ubiquinol-cytochrome C reductase complex 11 kDa protein

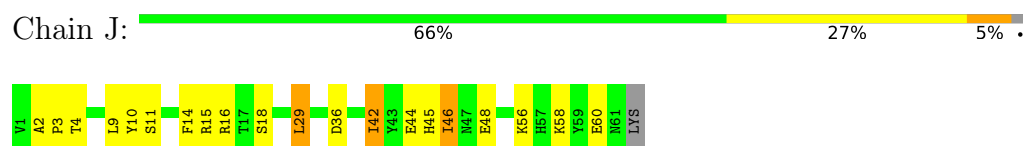
Chain H: 49% 32% 5% 14% .



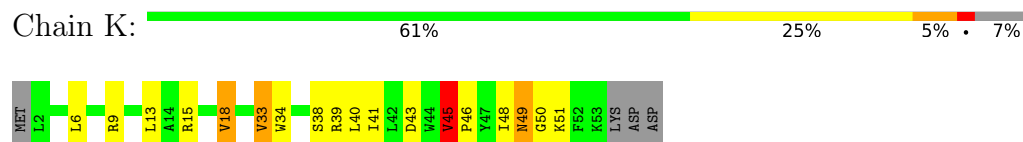
● Molecule 9: Ubiquinol-cytochrome c reductase 8 kDa protein



● Molecule 10: Ubiquinol-cytochrome C reductase complex 7.2 kDa protein



● Molecule 11: Ubiquinol-cytochrome C reductase complex 6.4 kDa protein



4 Data and refinement statistics

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

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	153.55Å 153.55Å 596.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.69	Depositor
% Data completeness (in resolution range)	95.6 (40.00-2.69)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.241 , 0.288	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16897	wwPDB-VP
Average B, all atoms (Å ²)	13.0	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: AZO, HEM, FES

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	0.96	6/3531 (0.2%)	1.09	3/4792 (0.1%)
2	B	1.00	7/3241 (0.2%)	1.08	4/4398 (0.1%)
3	C	1.10	11/3100 (0.4%)	1.17	1/4242 (0.0%)
4	D	1.07	6/1978 (0.3%)	1.09	3/2684 (0.1%)
5	E	1.20	8/1553 (0.5%)	1.08	0/2100
6	F	0.95	0/930	1.08	0/1246
7	G	1.25	4/649 (0.6%)	1.15	3/878 (0.3%)
8	H	1.07	3/553 (0.5%)	1.24	3/741 (0.4%)
9	I	1.50	3/411 (0.7%)	1.32	2/558 (0.4%)
10	J	1.07	1/515 (0.2%)	1.12	0/696
11	K	1.28	2/439 (0.5%)	1.27	2/600 (0.3%)
All	All	1.07	51/16900 (0.3%)	1.12	21/22935 (0.1%)

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
2	B	0	1

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	34	ILE	CA-CB	14.09	1.61	1.54
11	K	18	VAL	CA-CB	11.91	1.60	1.54
1	A	334	MET	SD-CE	-9.50	1.55	1.79
3	C	92	ILE	CA-CB	9.23	1.66	1.54
4	D	211	MET	SD-CE	-9.01	1.57	1.79

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	26	LEU	N-CA-C	11.24	127.11	110.48
11	K	45	VAL	N-CA-C	8.09	115.58	108.63
7	G	50	PRO	N-CA-C	6.83	119.03	110.70
3	C	345	HIS	N-CA-C	6.42	124.00	109.81
2	B	197	ASN	N-CA-C	5.91	120.61	113.17

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	174	ASN	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	3458	0	3356	27	0
2	B	3181	0	3160	32	0
3	C	3003	0	3065	28	0
4	D	1919	0	1870	24	0
5	E	1519	0	1504	12	0
6	F	911	0	904	8	0
7	G	628	0	636	3	0
8	H	548	0	530	2	0
9	I	406	0	437	21	0
10	J	502	0	505	5	0
11	K	425	0	433	4	0
12	C	86	0	60	5	0
12	D	43	0	30	1	0
13	C	30	0	17	2	0
14	E	4	0	0	0	0
15	A	47	0	0	0	0
15	B	82	0	0	4	0
15	C	37	0	0	1	0
15	D	19	0	0	1	0
15	E	2	0	0	0	0
15	F	21	0	0	0	0
15	G	20	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	H	1	0	0	0	0
15	I	3	0	0	0	0
15	K	2	0	0	0	0
All	All	16897	0	16507	138	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 4.

The worst 5 of 138 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:B:176:LEU:HD21	9:I:13:PRO:HD3	1.65	0.77
4:D:37:CYS:SG	12:D:242:HEM:HAB	2.24	0.77
6:F:28:LYS:HB3	6:F:74:ILE:HG12	1.68	0.76
2:B:310:SER:HB3	9:I:28:PRO:HD3	1.69	0.75
1:A:149:VAL:HG21	1:A:252:HIS:HB3	1.73	0.70

There are no symmetry-related clashes.

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	444/480 (92%)	428 (96%)	13 (3%)	3 (1%)	18	41
2	B	423/453 (93%)	402 (95%)	18 (4%)	3 (1%)	18	41
3	C	376/379 (99%)	361 (96%)	13 (4%)	2 (0%)	24	48
4	D	239/241 (99%)	218 (91%)	19 (8%)	2 (1%)	16	37
5	E	194/196 (99%)	169 (87%)	23 (12%)	2 (1%)	12	32
6	F	103/110 (94%)	101 (98%)	2 (2%)	0	100	100
7	G	73/81 (90%)	69 (94%)	3 (4%)	1 (1%)	9	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	65/78 (83%)	63 (97%)	2 (3%)	0	100	100
9	I	55/78 (70%)	37 (67%)	11 (20%)	7 (13%)	0	0
10	J	59/62 (95%)	56 (95%)	2 (3%)	1 (2%)	7	19
11	K	50/56 (89%)	46 (92%)	3 (6%)	1 (2%)	6	16
All	All	2081/2214 (94%)	1950 (94%)	109 (5%)	22 (1%)	11	29

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	437	ASP
9	I	44	ASP
3	C	157	GLY
9	I	8	SER
9	I	29	LEU

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	370/394 (94%)	309 (84%)	61 (16%)	2	6
2	B	332/355 (94%)	287 (86%)	45 (14%)	3	9
3	C	326/327 (100%)	275 (84%)	51 (16%)	2	7
4	D	206/206 (100%)	170 (82%)	36 (18%)	2	5
5	E	168/168 (100%)	135 (80%)	33 (20%)	1	4
6	F	96/98 (98%)	85 (88%)	11 (12%)	5	14
7	G	66/71 (93%)	51 (77%)	15 (23%)	1	3
8	H	64/74 (86%)	39 (61%)	25 (39%)	0	0
9	I	44/60 (73%)	30 (68%)	14 (32%)	0	1
10	J	51/52 (98%)	36 (71%)	15 (29%)	0	1
11	K	42/46 (91%)	30 (71%)	12 (29%)	0	1
All	All	1765/1851 (95%)	1447 (82%)	318 (18%)	2	5

5 of 318 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	F	32	MET
9	I	47	ARG
7	G	18	LEU
8	H	28	GLU
10	J	44	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	121	GLN
11	K	12	GLN
5	E	122	HIS
7	G	64	GLN
2	B	290	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](#)

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
14	FES	E	200	5	0,4,4	-	-	-		
12	HEM	C	382	3	50,50,50	1.75	11 (22%)	67,82,82	1.85	18 (26%)
13	AZO	C	383	-	32,32,32	2.83	9 (28%)	42,42,42	2.93	11 (26%)
12	HEM	D	242	4	50,50,50	1.79	10 (20%)	67,82,82	1.91	19 (28%)
12	HEM	C	381	3	50,50,50	1.72	6 (12%)	67,82,82	1.86	18 (26%)

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
14	FES	E	200	5	-	-	0/1/1/1
12	HEM	C	382	3	-	9/14/54/54	-
13	AZO	C	383	-	-	0/23/23/23	0/3/3/3
12	HEM	D	242	4	-	12/14/54/54	-
12	HEM	C	381	3	-	6/14/54/54	-

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	C	383	AZO	C21-C18	8.27	1.51	1.34
13	C	383	AZO	C18-C19	-5.99	1.33	1.48
12	D	242	HEM	CBC-CAC	5.51	1.56	1.30
13	C	383	AZO	O4-C19	5.46	1.45	1.33
13	C	383	AZO	C17-C12	5.40	1.50	1.40

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	C	383	AZO	C11-N3-C10	9.41	121.67	114.50
13	C	383	AZO	C11-N2-C8	9.33	121.61	114.50
13	C	383	AZO	N2-C11-N3	-5.95	119.57	128.58
13	C	383	AZO	O4-C19-C18	5.53	119.58	112.05
13	C	383	AZO	O5-C21-C18	-4.89	112.40	121.30

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

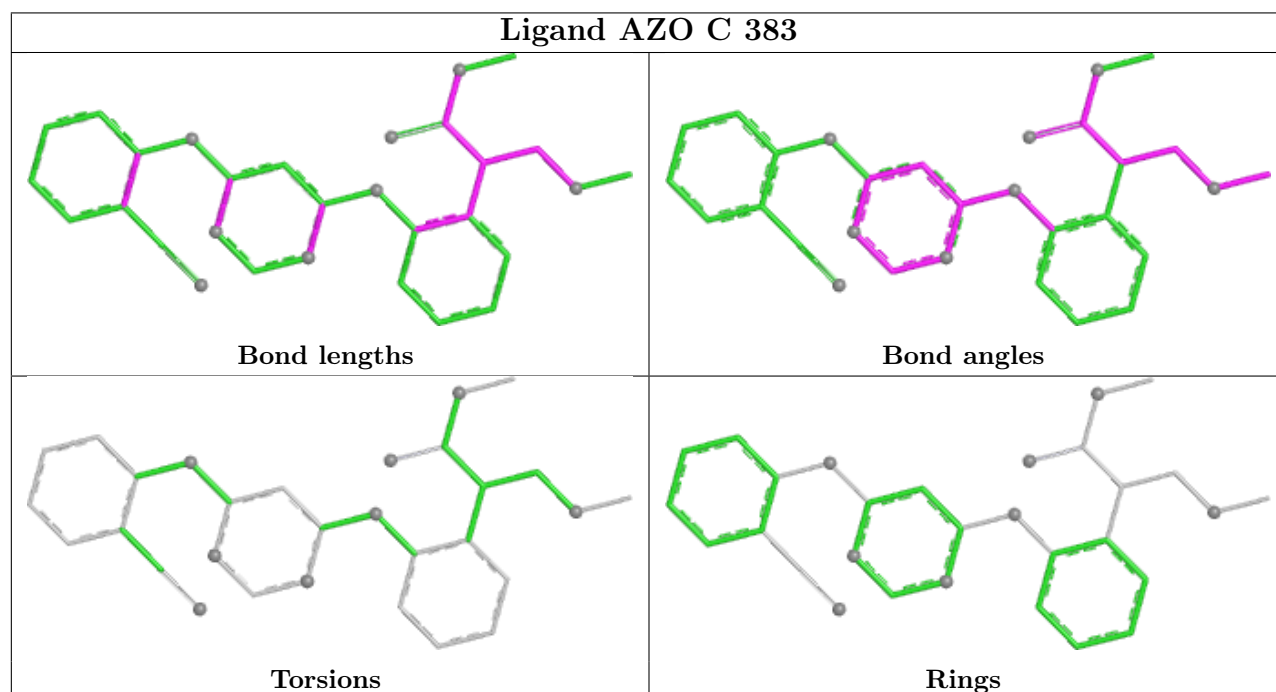
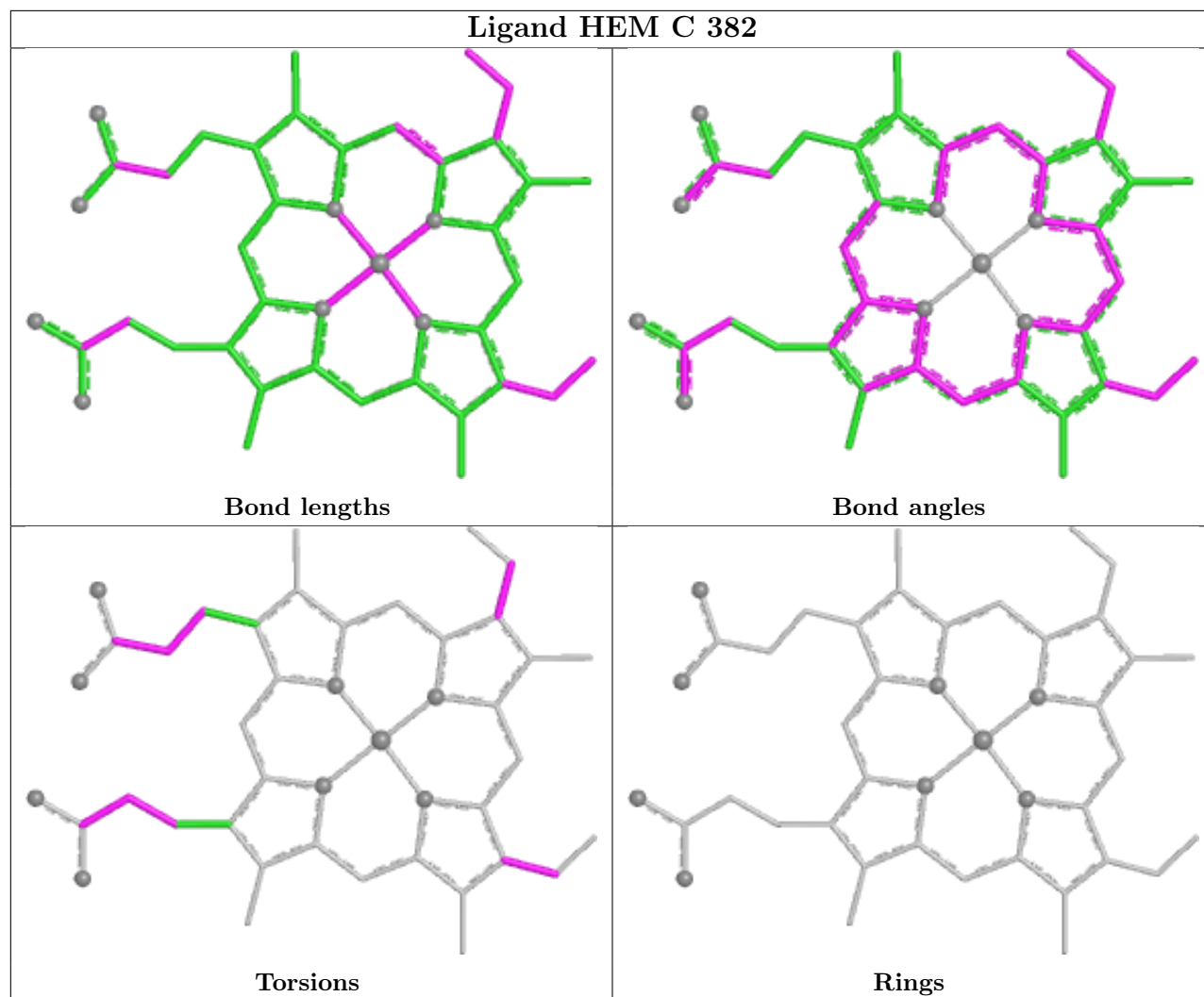
Mol	Chain	Res	Type	Atoms
12	C	381	HEM	C2B-C3B-CAB-CBB
12	C	381	HEM	C4B-C3B-CAB-CBB
12	C	382	HEM	C2B-C3B-CAB-CBB
12	D	242	HEM	C3A-C2A-CAA-CBA
12	D	242	HEM	C2B-C3B-CAB-CBB

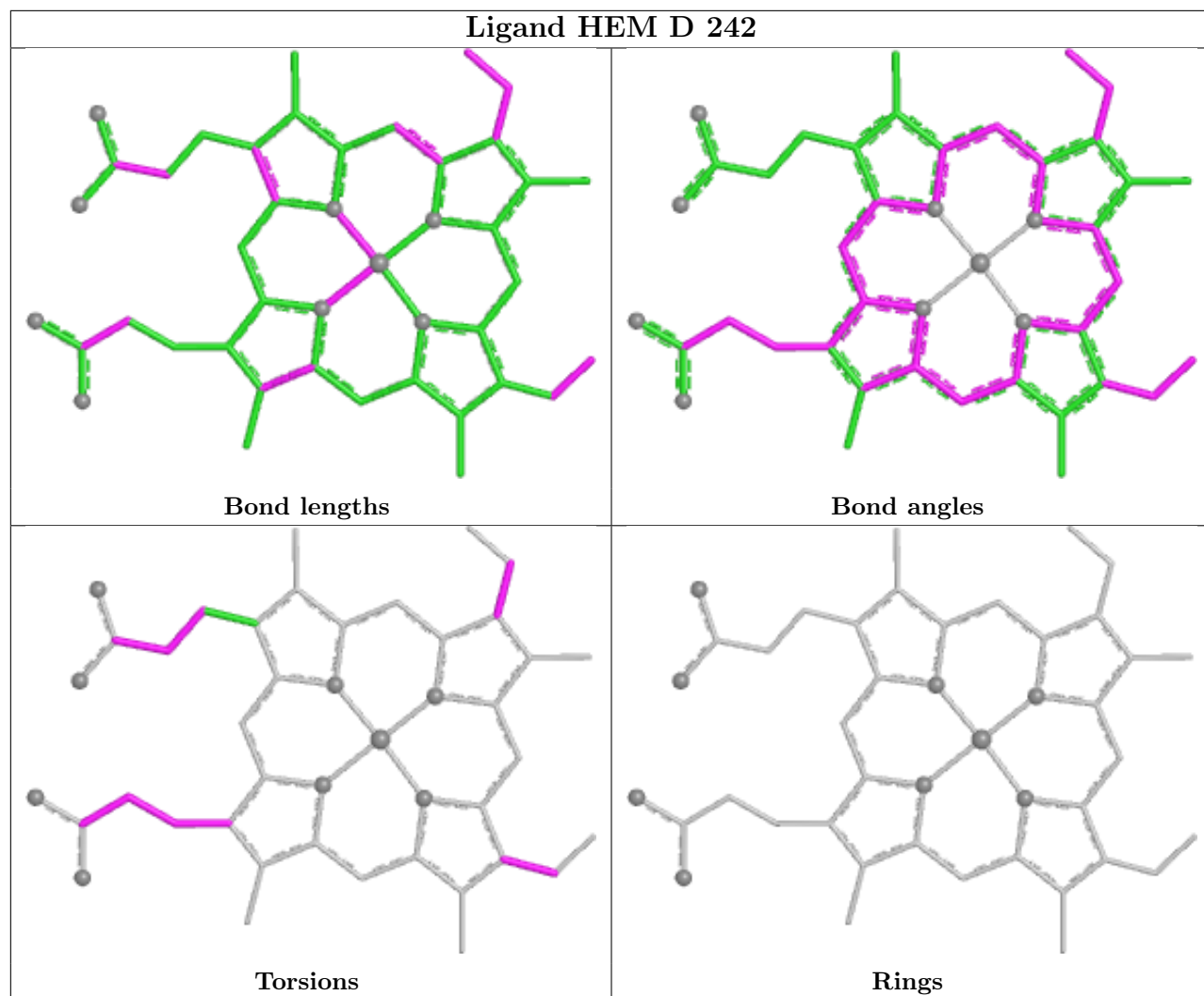
There are no ring outliers.

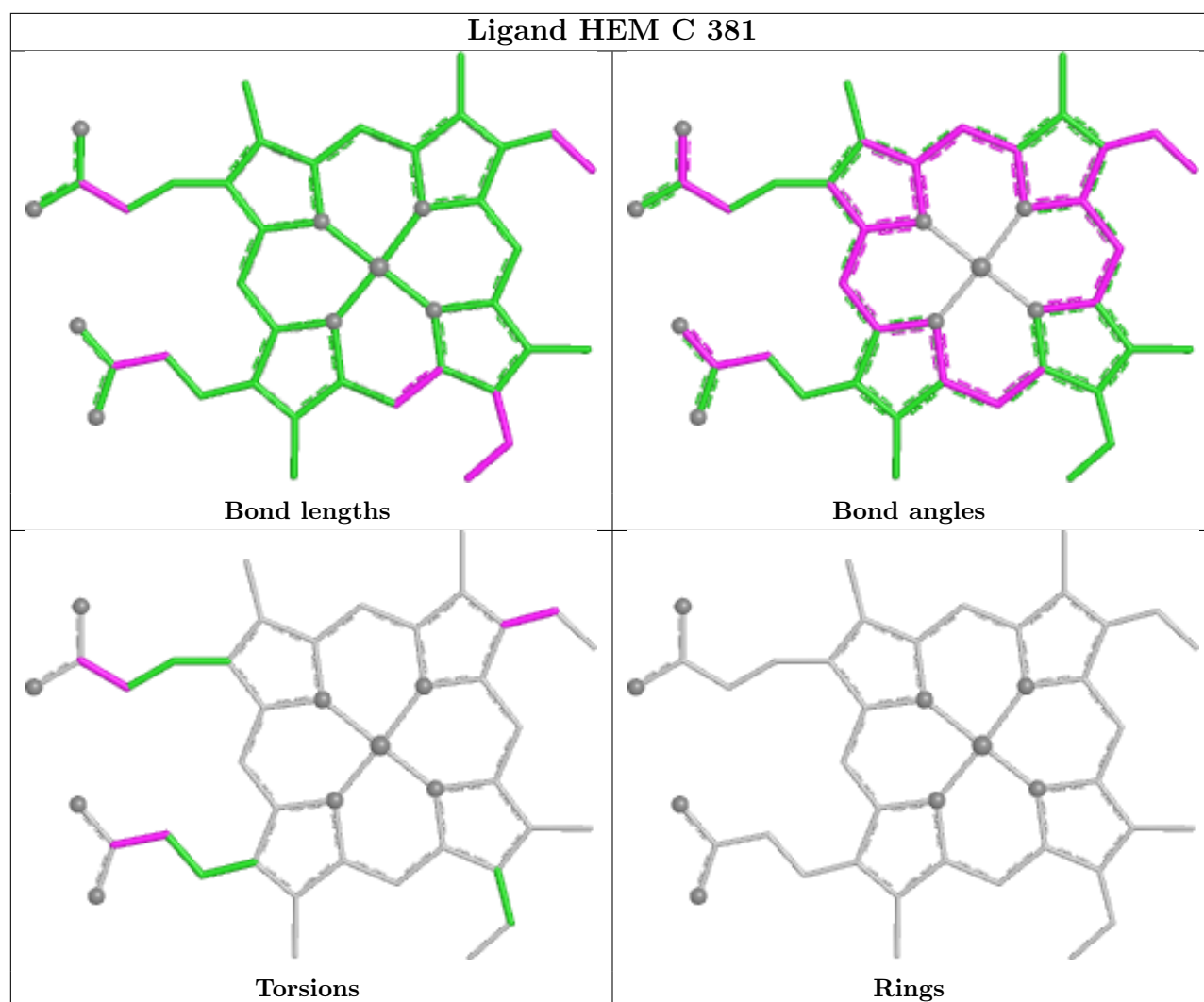
4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	C	382	HEM	2	0
13	C	383	AZO	2	0
12	D	242	HEM	1	0
12	C	381	HEM	3	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 [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.