



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 12:21 AM UTC

PDB ID : 1EZV / pdb_00001ezv
Title : STRUCTURE OF THE YEAST CYTOCHROME BC1 COMPLEX CO-CRYSTALLIZED WITH AN ANTIBODY FV-FRAGMENT
Authors : Hunte, C.; Koepke, J.; Lange, C.; Rossmann, T.; Michel, H.
Deposited on : 2000-05-12
Resolution : 2.30 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

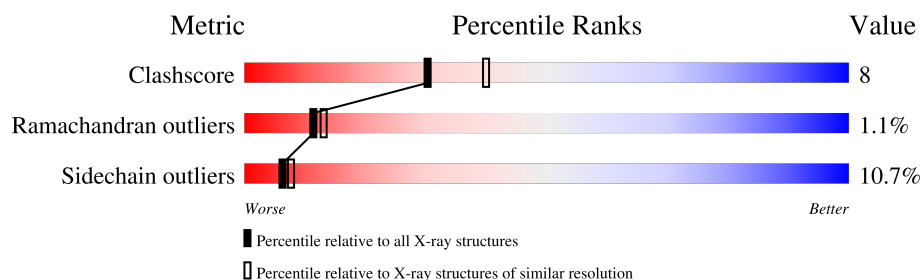
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (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	430	71% 25% . .
2	B	352	60% 34% 6%
3	C	385	84% 15% .
4	D	245	84% 14% .
5	E	185	81% 17% .
6	H	74	77% 18% 5%
7	F	125	80% 16% .
8	G	93	76% 20% .

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Mol	Chain	Length	Quality of chain
9	I	55	 84% 15% •
10	X	127	 74% 21% 5%
11	Y	107	 67% 31% •

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
13	SMA	C	505	X	-	-	-

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 17781 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	430	Total	C	N	O	S	0	0	0
			3338	2106	575	651	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	SER	deletion	UNP P07256
A	152	ASP	GLU	conflict	UNP P07256

- Molecule 2 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	352	Total	C	N	O	S	0	0	0
			2735	1747	453	534	1			

- Molecule 3 is a protein called CYTOCHROME B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	385	Total	C	N	O	S	0	0	0
			3089	2080	484	504	21			

- Molecule 4 is a protein called CYTOCHROME C1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	245	Total	C	N	O	S	0	0	0
			1934	1232	333	360	9			

- Molecule 5 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	185	Total	C	N	O	S	0	0	0
			1411	893	242	266	10			

- Molecule 6 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 17 KD PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	74	Total	C	N	O	S	0	0	0
			624	391	108	123	2			

- Molecule 7 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	F	125	Total	C	N	O	S	0	0	0
			1012	648	172	190	2			

- Molecule 8 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	G	93	Total	C	N	O	S	98	0	0
			773	510	131	130	2			

- Molecule 9 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.3 KD PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	I	55	Total	C	N	O	0	0	0
			449	298	75	76			

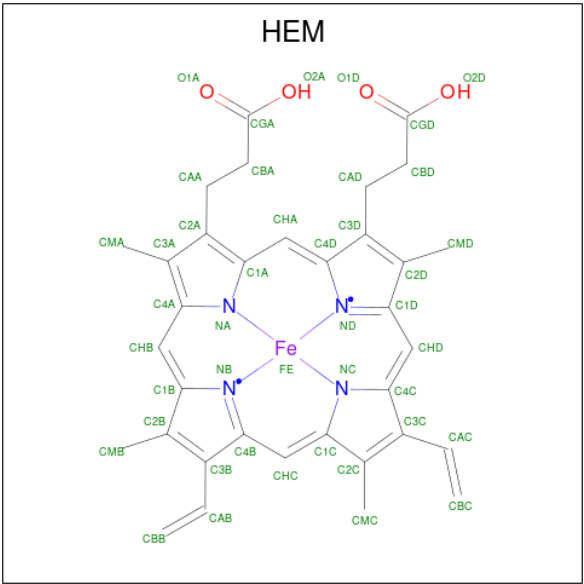
- Molecule 10 is a protein called HEAVY CHAIN (VH) OF FV-FRAGMENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	127	Total	C	N	O	S	0	0	0
			1015	644	167	201	3			

- Molecule 11 is a protein called LIGHT CHAIN (VL) OF FV-FRAGMENT.

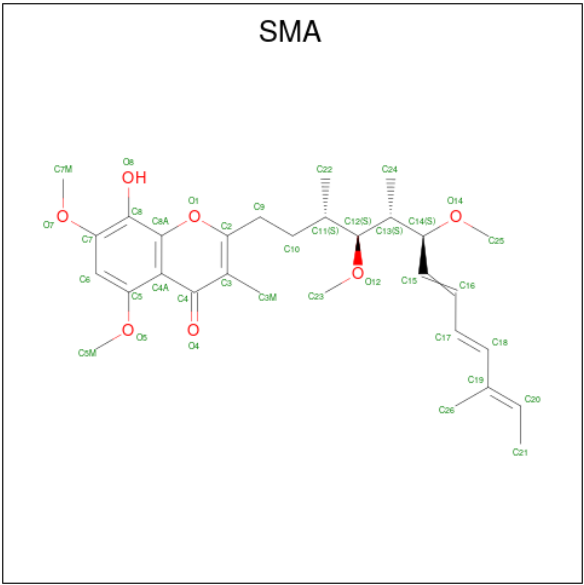
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	Y	107	Total	C	N	O	S	0	0	0
			842	536	141	163	2			

- Molecule 12 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



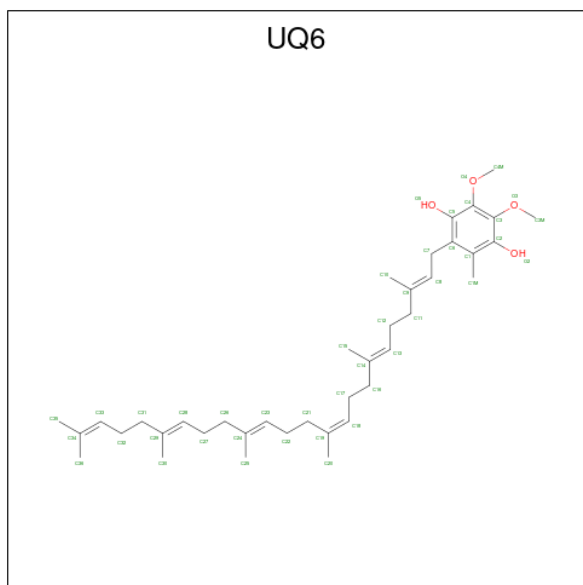
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	0
12	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	0

- Molecule 13 is STIGMATELLIN A (CCD ID: SMA) (formula: $C_{30}H_{42}O_7$).



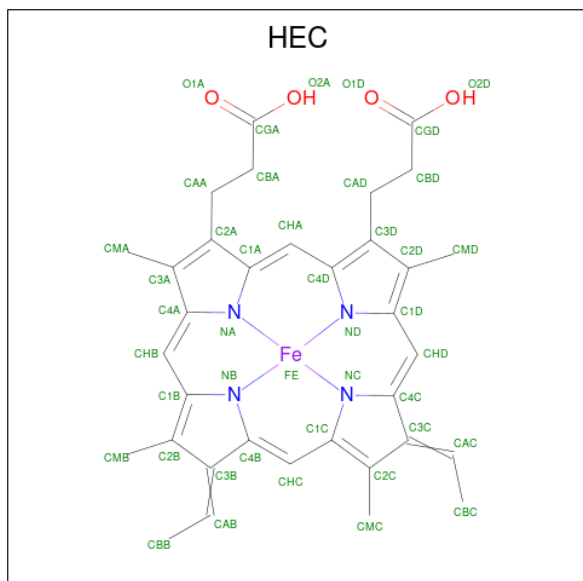
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	C	1	Total	C	O	0	0
			37	30	7		

- Molecule 14 is 5-(3,7,11,15,19,23-HEXAMETHYL-TETRACOSA-2,6,10,14,18,22-HEXA ENYL)-2,3-DIMETHOXY-6-METHYL-BENZENE-1,4-DIOL (CCD ID: UQ6) (formula: $C_{39}H_{60}O_4$).



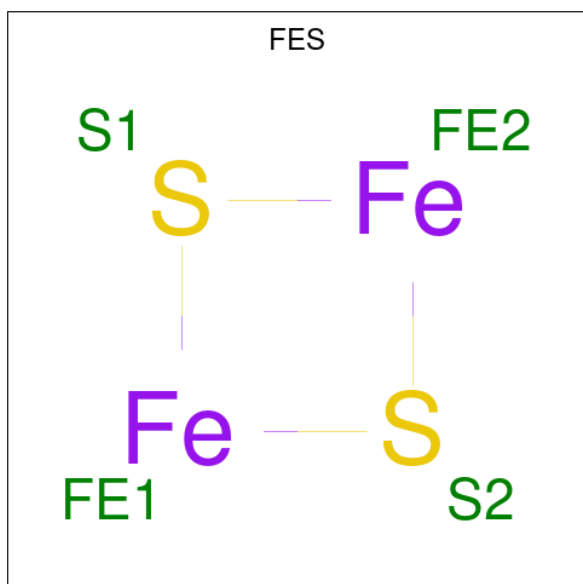
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	C	1	Total	C	O	0	0
			43	39	4		

- Molecule 15 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



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

- Molecule 16 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



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

- Molecule 17 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	47	Total	O	0	0
			47	47		
17	B	11	Total	O	0	0
			11	11		
17	C	114	Total	O	0	0
			114	114		
17	D	71	Total	O	0	0
			71	71		
17	E	33	Total	O	0	0
			33	33		
17	H	6	Total	O	0	0
			6	6		
17	F	36	Total	O	0	0
			36	36		
17	G	20	Total	O	0	0
			20	20		

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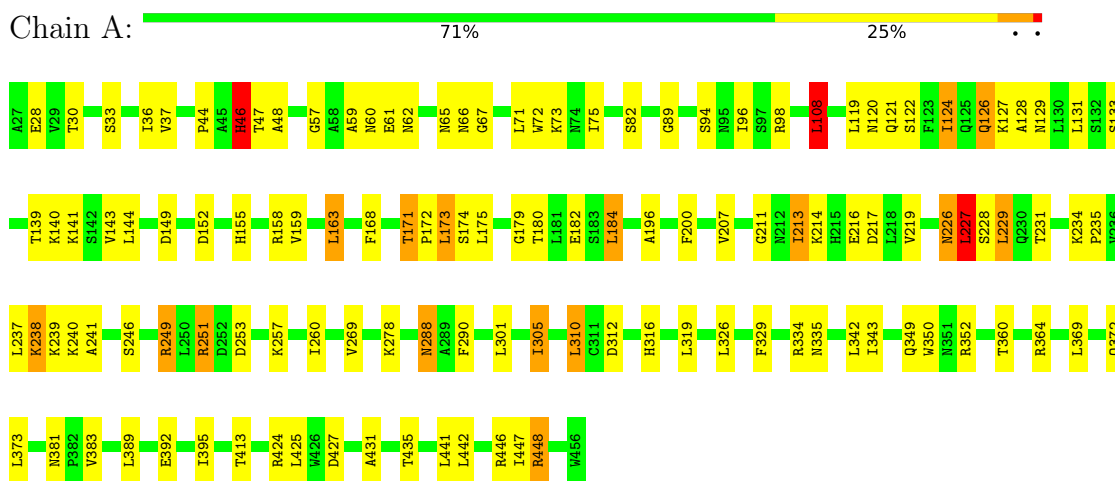
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	I	1	Total	O	0	0
			1	1		
17	X	5	Total	O	0	0
			5	5		
17	Y	2	Total	O	0	0
			2	2		

3 Residue-property plots

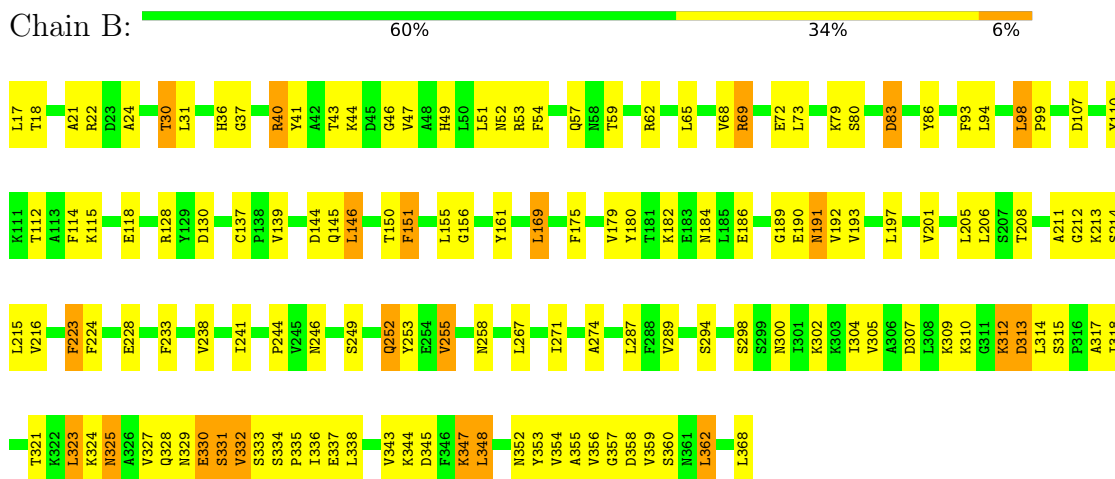
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

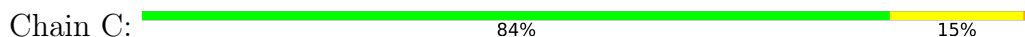
- Molecule 1: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN 1

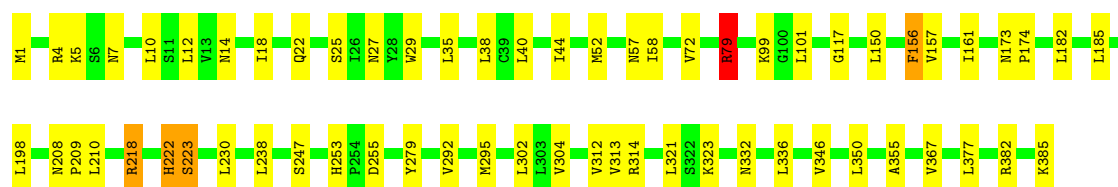


- Molecule 2: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN 2



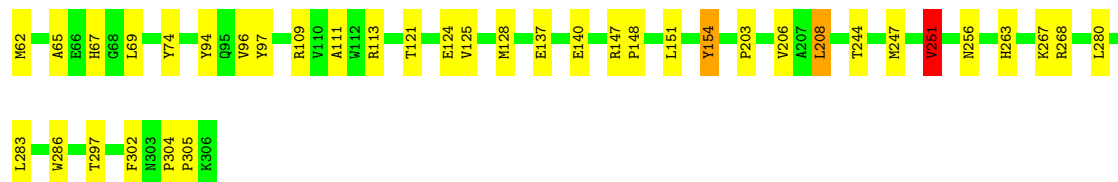
- Molecule 3: CYTOCHROME B





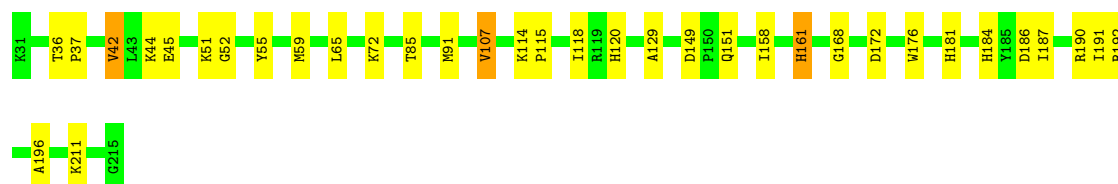
• Molecule 4: CYTOCHROME C1

Chain D: 84% 14% .



• Molecule 5: UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT

Chain E: 81% 17% .



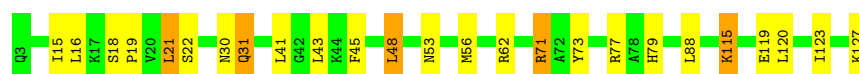
• Molecule 6: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 17 KD PROTEIN

Chain H: 77% 18% 5% .



• Molecule 7: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN

Chain F: 80% 16% .

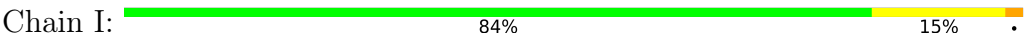


• Molecule 8: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C

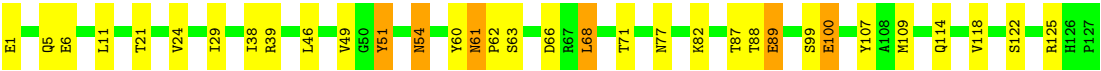
Chain G: 76% 20% .



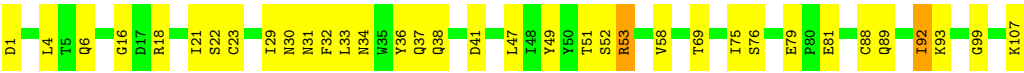
• Molecule 9: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.3 KD PROTEIN



● Molecule 10: HEAVY CHAIN (VH) OF FV-FRAGMENT



● Molecule 11: LIGHT CHAIN (VL) OF FV-FRAGMENT



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	214.47Å 163.92Å 147.27Å 90.00° 117.50° 90.00°	Depositor
Resolution (Å)	15.00 – 2.30	Depositor
% Data completeness (in resolution range)	84.7 (15.00-2.30)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.222 , 0.254	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	17781	wwPDB-VP
Average B, all atoms (Å ²)	70.0	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, FES, UQ6, SMA, HEC

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	0.41	0/3399	0.73	2/4606 (0.0%)
2	B	0.37	0/2781	0.74	0/3764
3	C	0.55	1/3191 (0.0%)	0.81	0/4353
4	D	0.42	0/1994	0.77	1/2714 (0.0%)
5	E	0.47	1/1444 (0.1%)	0.83	4/1957 (0.2%)
6	H	0.35	0/638	0.70	0/858
7	F	0.42	0/1032	0.75	0/1397
8	G	0.40	0/804	0.71	0/1088
9	I	0.40	0/462	0.74	0/622
10	X	0.37	0/1043	0.72	0/1422
11	Y	0.38	0/863	0.70	0/1172
All	All	0.43	2/17651 (0.0%)	0.76	7/23953 (0.0%)

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	0	4
2	B	0	2
3	C	0	5
4	D	0	4
5	E	0	1
6	H	0	1
7	F	0	1
8	G	0	1
10	X	0	1
11	Y	0	1
All	All	0	21

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	367	VAL	CA-CB	6.71	1.57	1.54
5	E	181	HIS	CE1-NE2	5.24	1.37	1.32

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	181	HIS	ND1-CG-CD2	7.13	113.23	106.10
5	E	161	HIS	ND1-CG-CD2	6.81	112.91	106.10
1	A	108	LEU	CA-C-N	5.77	125.44	119.56
1	A	108	LEU	C-N-CA	5.77	125.44	119.56
4	D	251	VAL	CB-CA-C	-5.42	104.83	112.14

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	LEU	Peptide
1	A	249	ARG	Sidechain
1	A	446	ARG	Sidechain
1	A	448	ARG	Sidechain
2	B	69	ARG	Sidechain

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	3338	0	3316	67	0
2	B	2735	0	2774	79	0
3	C	3089	0	3125	34	0
4	D	1934	0	1855	18	0
5	E	1411	0	1386	22	0
6	H	624	0	581	9	0
7	F	1012	0	1026	14	0
8	G	773	0	736	8	0
9	I	449	0	445	7	0
10	X	1015	0	959	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	Y	842	0	820	16	0
12	C	86	0	60	3	0
13	C	37	0	40	7	0
14	C	43	0	58	15	0
15	D	43	0	30	0	0
16	E	4	0	0	0	0
17	A	47	0	0	1	0
17	B	11	0	0	0	0
17	C	114	0	0	1	0
17	D	71	0	0	0	0
17	E	33	0	0	0	0
17	F	36	0	0	2	0
17	G	20	0	0	1	0
17	H	6	0	0	0	0
17	I	1	0	0	0	0
17	X	5	0	0	1	0
17	Y	2	0	0	0	0
All	All	17781	0	17211	290	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 8.

The worst 5 of 290 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)
14:C:506:UQ6:C1M	14:C:506:UQ6:H103	1.93	0.98
14:C:506:UQ6:H103	14:C:506:UQ6:H1M3	1.46	0.95
6:H:77:GLN:HE21	6:H:77:GLN:H	1.11	0.91
2:B:347:LYS:H	2:B:347:LYS:HD3	1.43	0.82
1:A:316:HIS:HE1	1:A:350:TRP:HE1	1.29	0.81

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	428/430 (100%)	396 (92%)	27 (6%)	5 (1%)	10	12
2	B	350/352 (99%)	311 (89%)	31 (9%)	8 (2%)	5	4
3	C	383/385 (100%)	369 (96%)	13 (3%)	1 (0%)	36	46
4	D	243/245 (99%)	238 (98%)	5 (2%)	0	100	100
5	E	183/185 (99%)	174 (95%)	7 (4%)	2 (1%)	11	13
6	H	72/74 (97%)	68 (94%)	4 (6%)	0	100	100
7	F	123/125 (98%)	120 (98%)	3 (2%)	0	100	100
8	G	91/93 (98%)	76 (84%)	10 (11%)	5 (6%)	1	0
9	I	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
10	X	125/127 (98%)	116 (93%)	9 (7%)	0	100	100
11	Y	105/107 (98%)	91 (87%)	11 (10%)	3 (3%)	3	2
All	All	2156/2178 (99%)	2009 (93%)	123 (6%)	24 (1%)	11	13

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	336	ILE
8	G	52	PHE
8	G	93	ASN
2	B	313	ASP
2	B	329	ASN

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	369/369 (100%)	320 (87%)	49 (13%)	4	4
2	B	301/301 (100%)	253 (84%)	48 (16%)	2	2
3	C	338/338 (100%)	312 (92%)	26 (8%)	12	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	203/203 (100%)	194 (96%)	9 (4%)	25	38
5	E	151/151 (100%)	144 (95%)	7 (5%)	24	36
6	H	67/67 (100%)	58 (87%)	9 (13%)	4	4
7	F	109/109 (100%)	99 (91%)	10 (9%)	8	11
8	G	77/77 (100%)	67 (87%)	10 (13%)	4	4
9	I	45/45 (100%)	41 (91%)	4 (9%)	9	12
10	X	112/112 (100%)	96 (86%)	16 (14%)	3	3
11	Y	93/93 (100%)	82 (88%)	11 (12%)	5	6
All	All	1865/1865 (100%)	1666 (89%)	199 (11%)	6	8

5 of 199 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	312	VAL
6	H	94	LEU
3	C	350	LEU
4	D	280	LEU
7	F	30	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
10	X	54	ASN
10	X	61	ASN
11	Y	77	ASN
2	B	55	ASN
2	B	52	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	$\# Z > 2$
12	HEM	C	401	3	50,50,50	1.38	10 (20%)	67,82,82	1.02	3 (4%)
16	FES	E	4	5	0,4,4	-	-	-	-	-
14	UQ6	C	506	-	43,43,43	2.55	16 (37%)	54,55,55	2.09	13 (24%)
13	SMA	C	505	-	38,38,38	1.59	7 (18%)	47,52,52	2.12	11 (23%)
12	HEM	C	402	3	50,50,50	1.29	7 (14%)	67,82,82	0.71	0
15	HEC	D	3	4	46,50,50	1.38	2 (4%)	58,82,82	1.67	2 (3%)

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
12	HEM	C	401	3	-	5/14/54/54	-
16	FES	E	4	5	-	-	0/1/1/1
14	UQ6	C	506	-	-	13/39/39/39	0/1/1/1
13	SMA	C	505	-	2/2/5/10	21/34/34/34	0/2/2/2
12	HEM	C	402	3	-	4/14/54/54	-
15	HEC	D	3	4	-	6/14/54/54	-

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	C	506	UQ6	O5-C5	-7.05	1.20	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	C	506	UQ6	O2-C2	-5.88	1.23	1.36
14	C	506	UQ6	C7-C6	5.76	1.58	1.51
14	C	506	UQ6	C2-C3	5.75	1.48	1.39
15	D	3	HEC	CAB-C3B	5.42	1.52	1.35

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	D	3	HEC	CBB-CAB-C3B	-8.41	110.61	127.43
15	D	3	HEC	CBC-CAC-C3C	-7.77	111.91	127.43
14	C	506	UQ6	C3M-O3-C3	7.25	134.43	114.74
13	C	505	SMA	C26-C19-C18	-6.48	108.19	118.09
13	C	505	SMA	O14-C14-C15	6.42	129.71	111.05

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
13	C	505	SMA	C12
13	C	505	SMA	C14

5 of 49 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	C	505	SMA	C11-C12-C13-C24
13	C	505	SMA	O12-C12-C13-C14
13	C	505	SMA	O12-C12-C13-C24
13	C	505	SMA	C13-C14-C15-C16
13	C	505	SMA	C15-C14-O14-C25

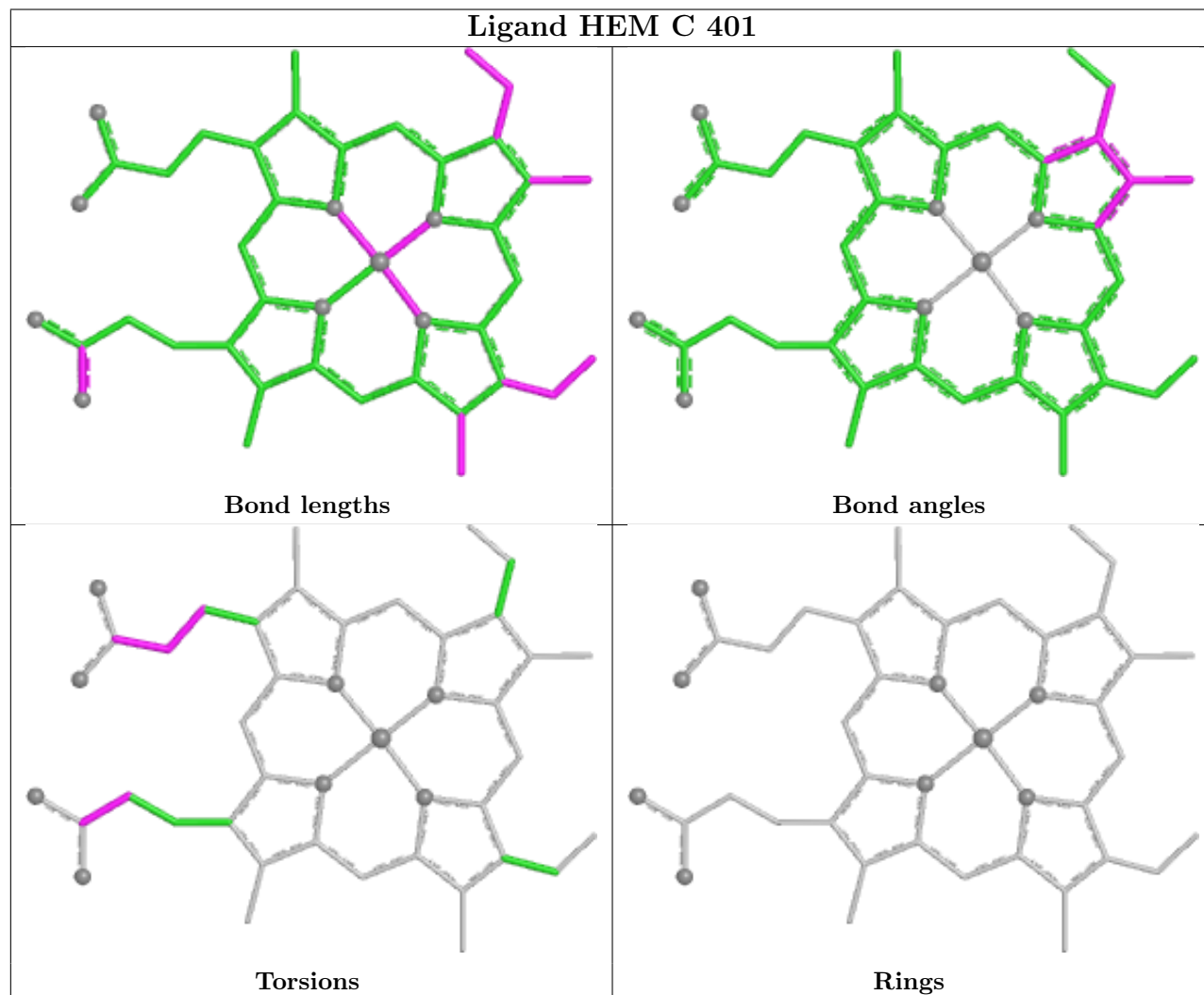
There are no ring outliers.

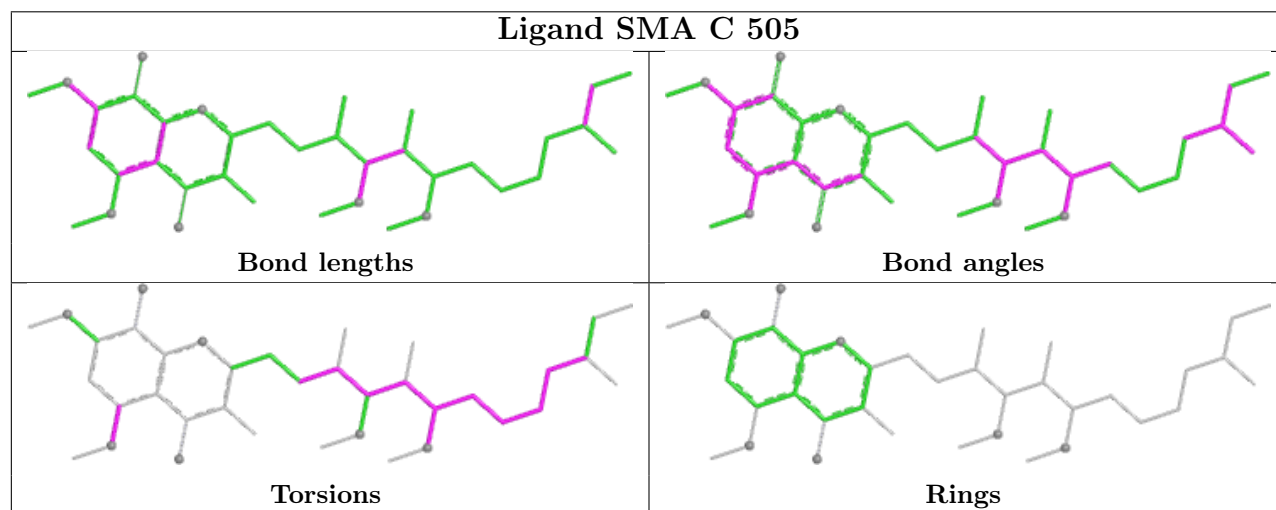
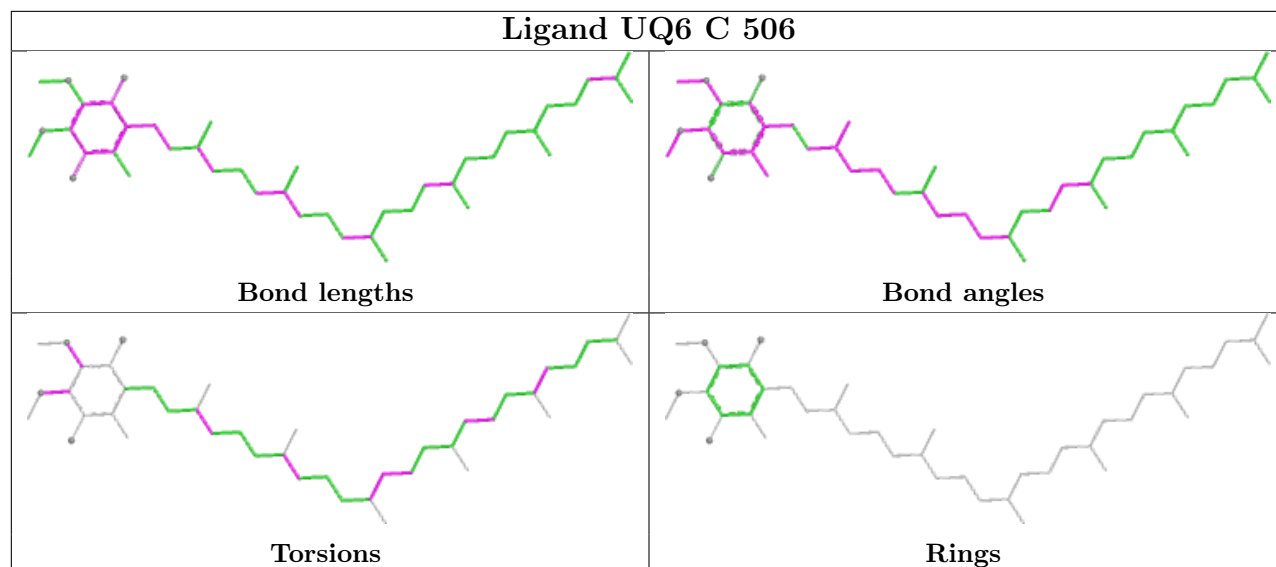
4 monomers are involved in 25 short contacts:

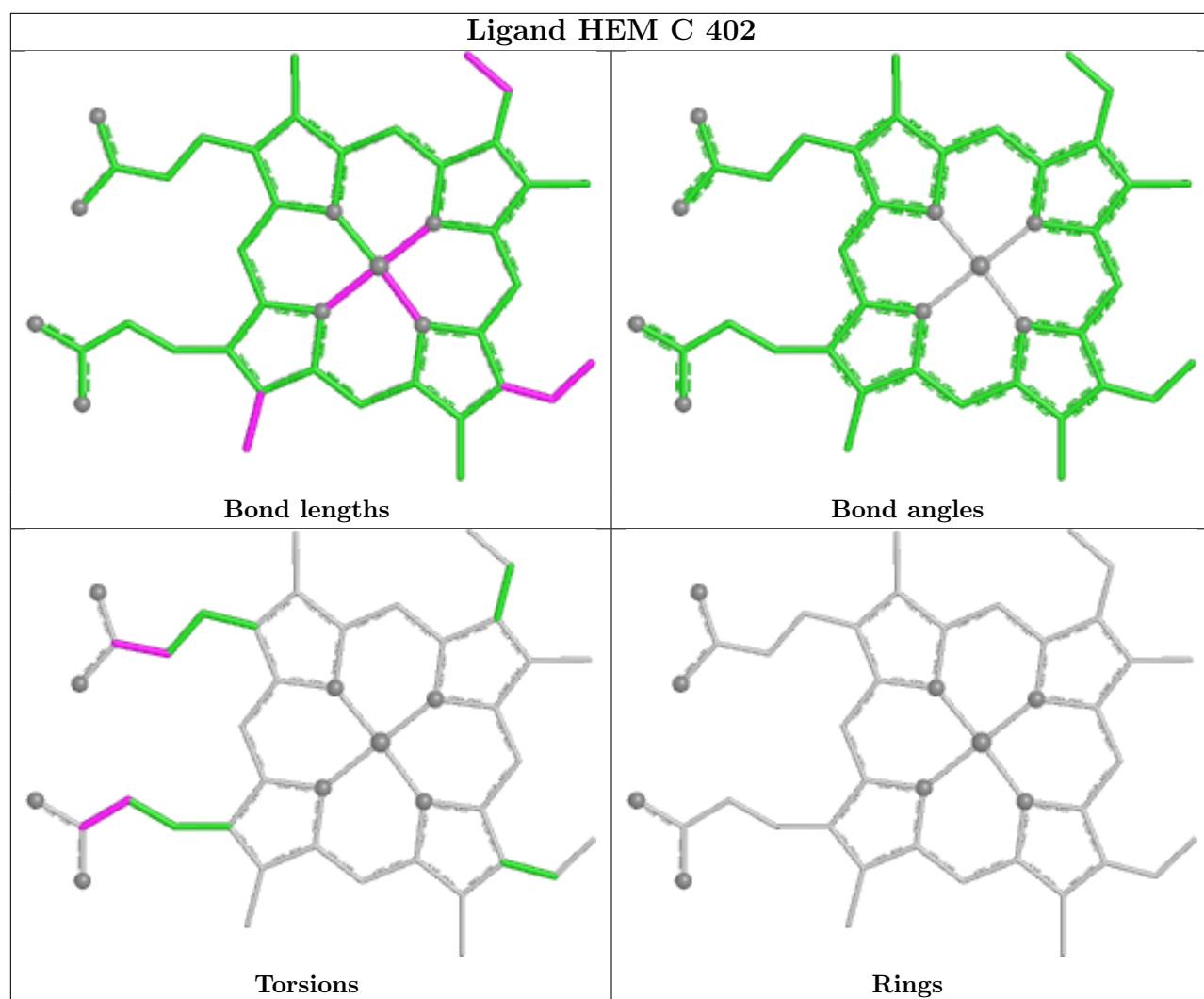
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	C	401	HEM	2	0
14	C	506	UQ6	15	0
13	C	505	SMA	7	0
12	C	402	HEM	1	0

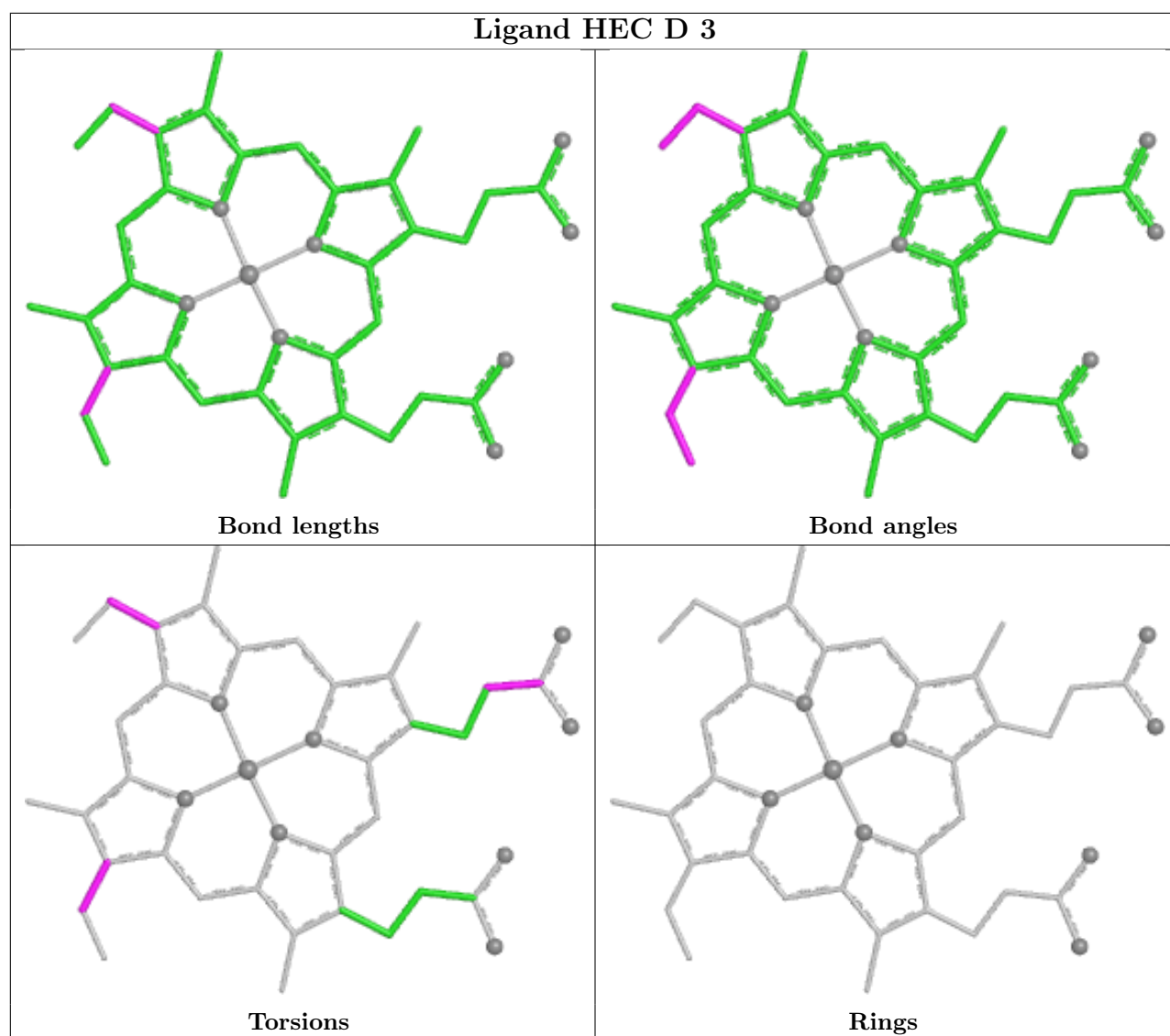
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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