



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2026 – 09:04 AM JST

PDB ID : 9VTF / pdb_00009vtf
Title : Structural basis for the inhibition of cystathionine- β -synthase by isoflurane
Authors : Xu, K.
Deposited on : 2025-07-10
Resolution : 3.03 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

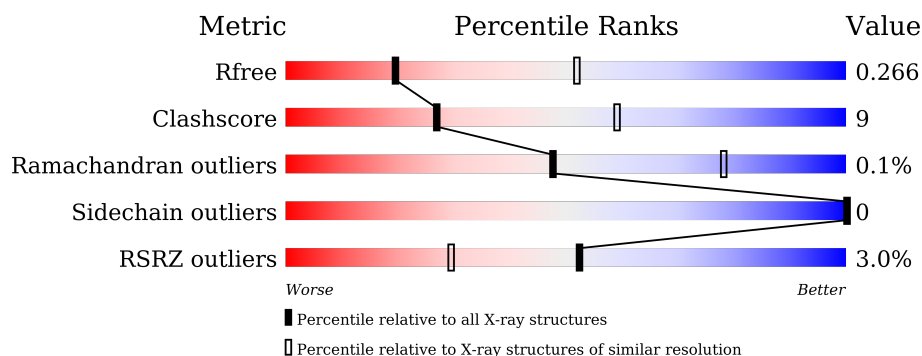
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.03 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))
R_{free}	180053	3685 (3.08-3.00)
Clashscore	190562	4007 (3.08-3.00)
Ramachandran outliers	187476	3834 (3.08-3.00)
Sidechain outliers	187428	3836 (3.08-3.00)
RSRZ outliers	180081	3684 (3.08-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	573	3% 71%15%14%
1	B	573	2% 70%14%15%
1	C	573	3% 74%12%14%
1	D	573	2% 74%11%15%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15265 atoms, of which 2 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 Cystathionine beta-synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	493	Total	C	N	O	P	S	0	0	0
			3792	2402	657	710	1	22			
1	B	485	Total	C	N	O	P	S	0	1	0
			3734	2369	646	696	1	22			
1	C	493	Total	C	N	O	P	S	0	1	0
			3800	2407	660	710	1	22			
1	D	488	Total	C	N	O	P	S	0	1	0
			3755	2381	653	698	1	22			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	initiating methionine	UNP P35520
A	-20	HIS	-	expression tag	UNP P35520
A	-19	HIS	-	expression tag	UNP P35520
A	-18	HIS	-	expression tag	UNP P35520
A	-17	HIS	-	expression tag	UNP P35520
A	-16	HIS	-	expression tag	UNP P35520
A	-15	HIS	-	expression tag	UNP P35520
A	-14	SER	-	expression tag	UNP P35520
A	-13	SER	-	expression tag	UNP P35520
A	-12	GLY	-	expression tag	UNP P35520
A	-11	VAL	-	expression tag	UNP P35520
A	-10	ASP	-	expression tag	UNP P35520
A	-9	LEU	-	expression tag	UNP P35520
A	-8	GLY	-	expression tag	UNP P35520
A	-7	THR	-	expression tag	UNP P35520
A	-6	GLU	-	expression tag	UNP P35520
A	-5	ASN	-	expression tag	UNP P35520
A	-4	LEU	-	expression tag	UNP P35520
A	-3	TYR	-	expression tag	UNP P35520
A	-2	PHE	-	expression tag	UNP P35520
A	-1	GLN	-	expression tag	UNP P35520

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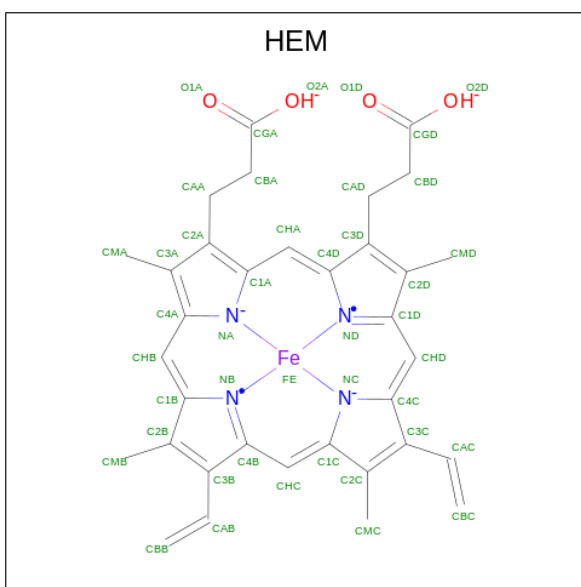
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP P35520
B	-21	MET	-	initiating methionine	UNP P35520
B	-20	HIS	-	expression tag	UNP P35520
B	-19	HIS	-	expression tag	UNP P35520
B	-18	HIS	-	expression tag	UNP P35520
B	-17	HIS	-	expression tag	UNP P35520
B	-16	HIS	-	expression tag	UNP P35520
B	-15	HIS	-	expression tag	UNP P35520
B	-14	SER	-	expression tag	UNP P35520
B	-13	SER	-	expression tag	UNP P35520
B	-12	GLY	-	expression tag	UNP P35520
B	-11	VAL	-	expression tag	UNP P35520
B	-10	ASP	-	expression tag	UNP P35520
B	-9	LEU	-	expression tag	UNP P35520
B	-8	GLY	-	expression tag	UNP P35520
B	-7	THR	-	expression tag	UNP P35520
B	-6	GLU	-	expression tag	UNP P35520
B	-5	ASN	-	expression tag	UNP P35520
B	-4	LEU	-	expression tag	UNP P35520
B	-3	TYR	-	expression tag	UNP P35520
B	-2	PHE	-	expression tag	UNP P35520
B	-1	GLN	-	expression tag	UNP P35520
B	0	SER	-	expression tag	UNP P35520
C	-21	MET	-	initiating methionine	UNP P35520
C	-20	HIS	-	expression tag	UNP P35520
C	-19	HIS	-	expression tag	UNP P35520
C	-18	HIS	-	expression tag	UNP P35520
C	-17	HIS	-	expression tag	UNP P35520
C	-16	HIS	-	expression tag	UNP P35520
C	-15	HIS	-	expression tag	UNP P35520
C	-14	SER	-	expression tag	UNP P35520
C	-13	SER	-	expression tag	UNP P35520
C	-12	GLY	-	expression tag	UNP P35520
C	-11	VAL	-	expression tag	UNP P35520
C	-10	ASP	-	expression tag	UNP P35520
C	-9	LEU	-	expression tag	UNP P35520
C	-8	GLY	-	expression tag	UNP P35520
C	-7	THR	-	expression tag	UNP P35520
C	-6	GLU	-	expression tag	UNP P35520
C	-5	ASN	-	expression tag	UNP P35520
C	-4	LEU	-	expression tag	UNP P35520
C	-3	TYR	-	expression tag	UNP P35520

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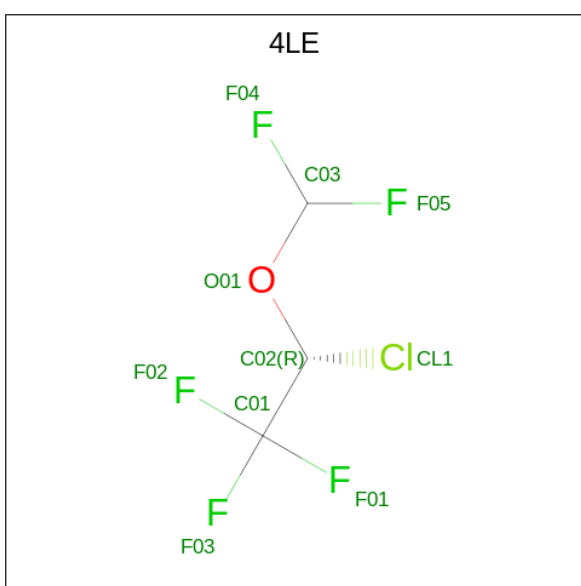
Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	PHE	-	expression tag	UNP P35520
C	-1	GLN	-	expression tag	UNP P35520
C	0	SER	-	expression tag	UNP P35520
D	-21	MET	-	initiating methionine	UNP P35520
D	-20	HIS	-	expression tag	UNP P35520
D	-19	HIS	-	expression tag	UNP P35520
D	-18	HIS	-	expression tag	UNP P35520
D	-17	HIS	-	expression tag	UNP P35520
D	-16	HIS	-	expression tag	UNP P35520
D	-15	HIS	-	expression tag	UNP P35520
D	-14	SER	-	expression tag	UNP P35520
D	-13	SER	-	expression tag	UNP P35520
D	-12	GLY	-	expression tag	UNP P35520
D	-11	VAL	-	expression tag	UNP P35520
D	-10	ASP	-	expression tag	UNP P35520
D	-9	LEU	-	expression tag	UNP P35520
D	-8	GLY	-	expression tag	UNP P35520
D	-7	THR	-	expression tag	UNP P35520
D	-6	GLU	-	expression tag	UNP P35520
D	-5	ASN	-	expression tag	UNP P35520
D	-4	LEU	-	expression tag	UNP P35520
D	-3	TYR	-	expression tag	UNP P35520
D	-2	PHE	-	expression tag	UNP P35520
D	-1	GLN	-	expression tag	UNP P35520
D	0	SER	-	expression tag	UNP P35520

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).

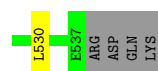


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

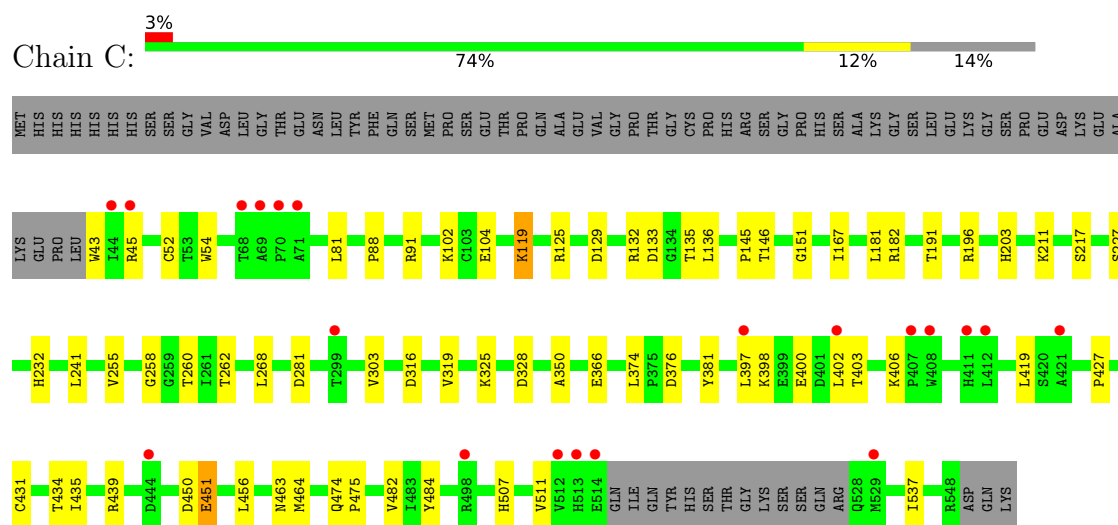
- Molecule 3 is (2R)-2-chloro-2-(difluoromethoxy)-1,1,1-trifluoroethane (CCD ID: 4LE) (formula: C₃H₂ClF₅O) (labeled as "Ligand of Interest" by depositor).



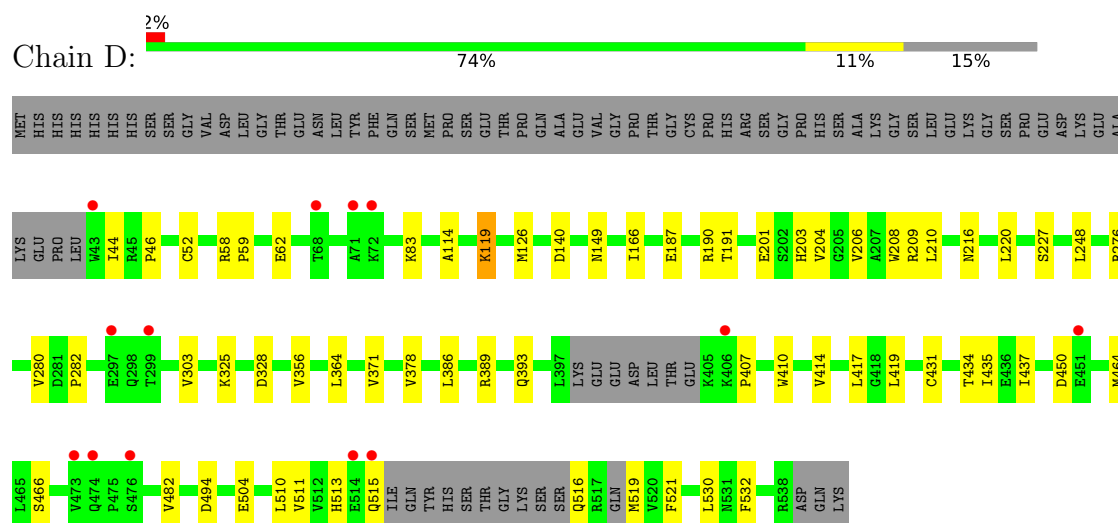
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	D	1	Total	C	Cl	F	H	O	0	0
			12	3	1	5	2	1		



• Molecule 1: Cystathionine beta-synthase



• Molecule 1: Cystathionine beta-synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	109.79Å 130.51Å 207.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.55 – 3.03 48.55 – 3.03	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.55-3.03) 85.9 (48.55-3.03)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.219 , 0.266 0.222 , 0.266	Depositor DCC
R_{free} test set	2000 reflections (3.39%)	wwPDB-VP
Wilson B-factor (Å ²)	49.0	Xtriage
Anisotropy	0.866	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15265	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.30 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.7904e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: 4LE, LLP, 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	0.54	0/3838	0.87	2/5203 (0.0%)
1	B	0.50	0/3780	0.91	3/5125 (0.1%)
1	C	0.51	0/3849	0.86	1/5218 (0.0%)
1	D	0.50	0/3801	0.90	0/5153
All	All	0.51	0/15268	0.88	6/20699 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	68	THR	CA-C-N	-6.09	103.05	121.98
1	B	68	THR	C-N-CA	-6.09	103.05	121.98
1	A	55	GLN	CA-CB-CG	6.03	126.17	114.10
1	B	71	ALA	N-CA-C	5.45	117.40	108.52
1	C	451	GLU	CA-CB-CG	5.35	124.79	114.10

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	3792	0	3815	82	0
1	B	3734	0	3743	76	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3800	0	3827	58	0
1	D	3755	0	3764	67	0
2	A	43	0	30	11	0
2	B	43	0	30	6	0
2	C	43	0	30	4	0
2	D	43	0	30	3	0
3	D	10	2	1	3	0
All	All	15263	2	15270	281	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 9.

The worst 5 of 281 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:A:601:HEM:HBC2	2:A:601:HEM:HMC2	1.34	1.08
1:A:91:ARG:NH1	1:A:104:GLU:OE2	1.96	0.97
1:D:419:LEU:HD13	1:D:511:VAL:HG21	1.53	0.91
1:B:513:HIS:HB2	1:B:521:PHE:HE1	1.35	0.91
1:C:88:PRO:HG3	1:D:83:LYS:HE3	1.54	0.90

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	488/573 (85%)	478 (98%)	9 (2%)	1 (0%)	43	73
1	B	479/573 (84%)	469 (98%)	10 (2%)	0	100	100
1	C	489/573 (85%)	478 (98%)	11 (2%)	0	100	100
1	D	482/573 (84%)	469 (97%)	13 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1938/2292 (85%)	1894 (98%)	43 (2%)	1 (0%)	48 78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	528	GLN

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	406/484 (84%)	406 (100%)	0	100	100
1	B	397/484 (82%)	397 (100%)	0	100	100
1	C	407/484 (84%)	407 (100%)	0	100	100
1	D	398/484 (82%)	398 (100%)	0	100	100
All	All	1608/1936 (83%)	1608 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	149	ASN
1	D	380	ASN
1	D	411	HIS
1	B	463	ASN
1	C	232	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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
1	LLP	C	119	1	23,24,25	1.62	5 (21%)	25,32,34	1.71	6 (24%)
1	LLP	B	119	1	23,24,25	1.51	3 (13%)	25,32,34	2.91	11 (44%)
1	LLP	A	119	1	23,24,25	1.65	5 (21%)	25,32,34	1.53	6 (24%)
1	LLP	D	119	1	23,24,25	1.44	3 (13%)	25,32,34	1.77	5 (20%)

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
1	LLP	C	119	1	-	3/16/17/19	0/1/1/1
1	LLP	B	119	1	-	5/16/17/19	0/1/1/1
1	LLP	A	119	1	-	5/16/17/19	0/1/1/1
1	LLP	D	119	1	-	3/16/17/19	0/1/1/1

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	119	LLP	C4'-NZ	4.85	1.43	1.27
1	A	119	LLP	C4'-NZ	4.83	1.43	1.27
1	B	119	LLP	C4'-NZ	4.79	1.43	1.27
1	C	119	LLP	C4'-NZ	4.77	1.43	1.27
1	A	119	LLP	C2-N1	3.06	1.39	1.33

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	119	LLP	CE-NZ-C4'	-10.20	87.57	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	119	LLP	CE-NZ-C4'	-4.61	104.75	118.90
1	B	119	LLP	C4-C3-C2	-4.30	117.53	120.19
1	D	119	LLP	OP3-P-OP2	4.20	123.69	107.64
1	B	119	LLP	OP4-C5'-C5	4.08	117.12	109.35

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	119	LLP	C4-C5-C5'-OP4
1	A	119	LLP	C6-C5-C5'-OP4
1	C	119	LLP	C4-C5-C5'-OP4
1	C	119	LLP	C6-C5-C5'-OP4
1	D	119	LLP	C4-C5-C5'-OP4

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	119	LLP	1	0
1	B	119	LLP	3	0
1	A	119	LLP	1	0
1	D	119	LLP	4	0

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
2	HEM	A	601	1	50,50,50	1.71	8 (16%)	66,82,82	1.53	9 (13%)
3	4LE	D	602	-	6,9,9	1.33	0	7,13,13	2.13	3 (42%)
2	HEM	C	601	1	50,50,50	2.00	8 (16%)	66,82,82	1.58	16 (24%)
2	HEM	D	601	1	50,50,50	1.55	9 (18%)	66,82,82	1.62	11 (16%)
2	HEM	B	601	1	50,50,50	1.53	6 (12%)	66,82,82	1.47	10 (15%)

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
2	HEM	A	601	1	-	3/14/54/54	-
3	4LE	D	602	-	-	1/8/10/10	-
2	HEM	C	601	1	-	3/14/54/54	-
2	HEM	D	601	1	-	0/14/54/54	-
2	HEM	B	601	1	-	0/14/54/54	-

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	HEM	FE-NA	8.14	2.22	1.95
2	C	601	HEM	FE-NB	7.22	2.17	1.94
2	A	601	HEM	FE-NB	6.40	2.14	1.94
2	A	601	HEM	FE-NA	5.33	2.13	1.95
2	B	601	HEM	FE-ND	5.14	2.10	1.94

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	HEM	CAA-CBA-CGA	-5.09	102.65	113.60
2	C	601	HEM	C3B-C2B-C1B	4.19	109.59	106.49
2	D	601	HEM	CAA-CBA-CGA	-4.19	104.59	113.60
2	D	601	HEM	C4A-NA-C1A	4.13	109.39	105.35
2	A	601	HEM	C4C-NC-C1C	4.09	109.36	105.35

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

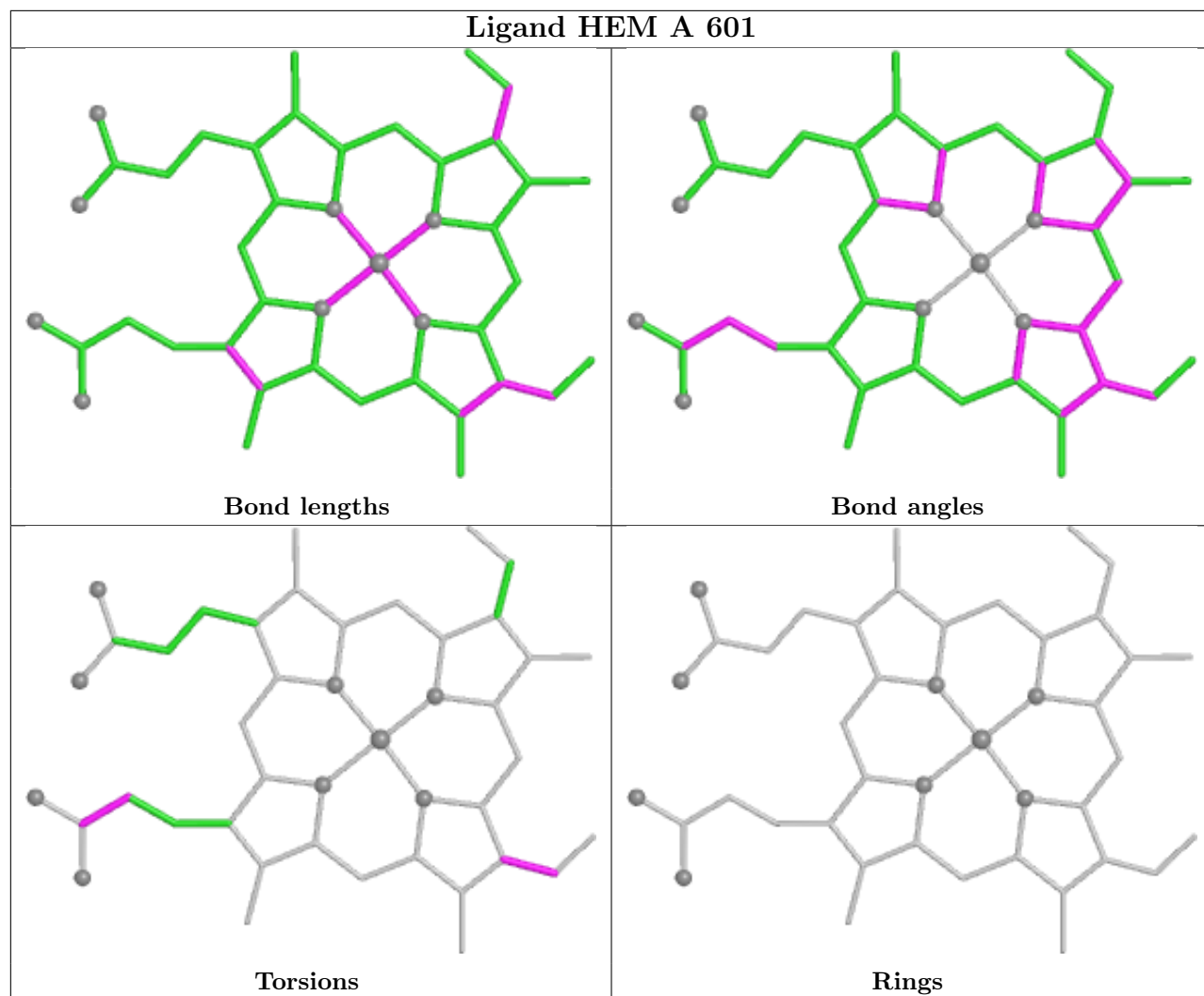
Mol	Chain	Res	Type	Atoms
3	D	602	4LE	F05-C03-O01-C02
2	A	601	HEM	C4B-C3B-CAB-CBB
2	A	601	HEM	CAA-CBA-CGA-O1A
2	A	601	HEM	CAA-CBA-CGA-O2A
2	C	601	HEM	CAA-CBA-CGA-O2A

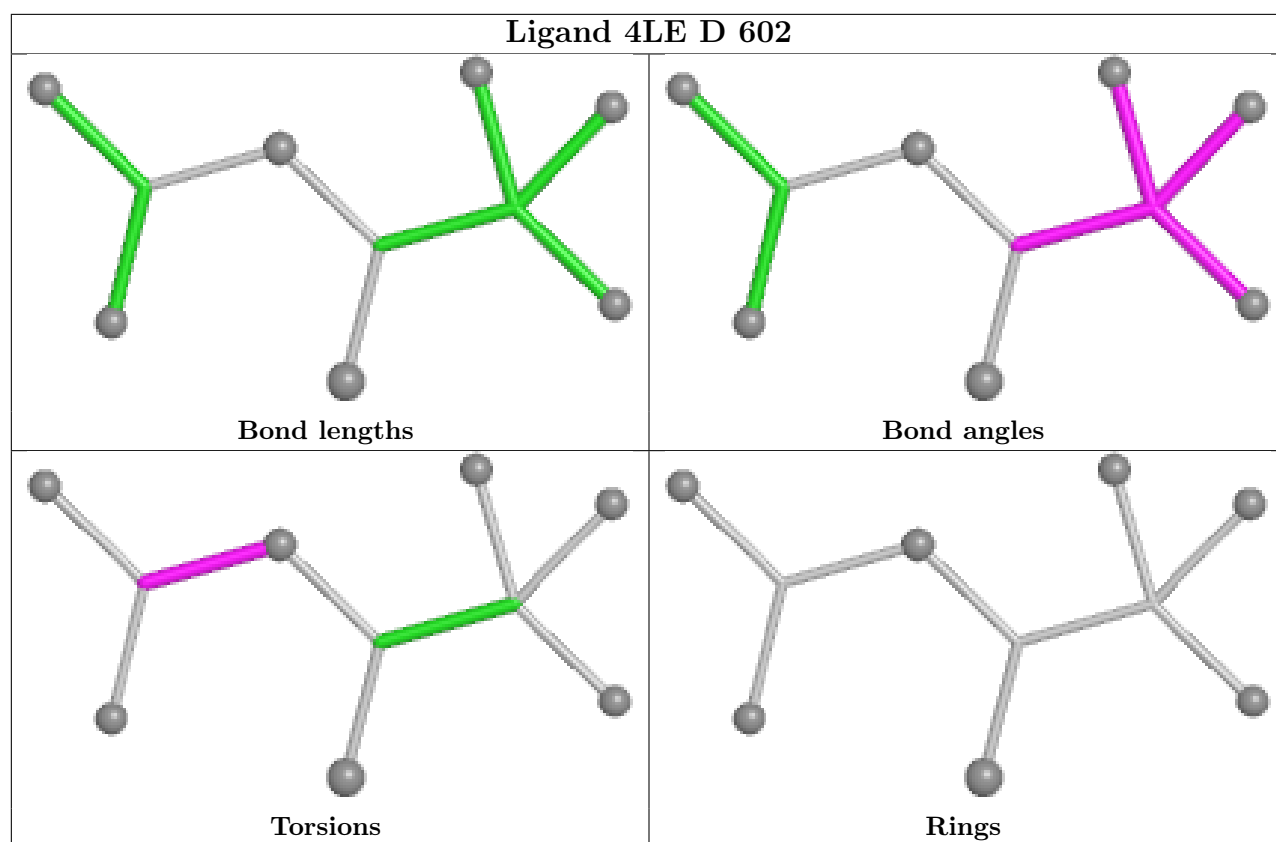
There are no ring outliers.

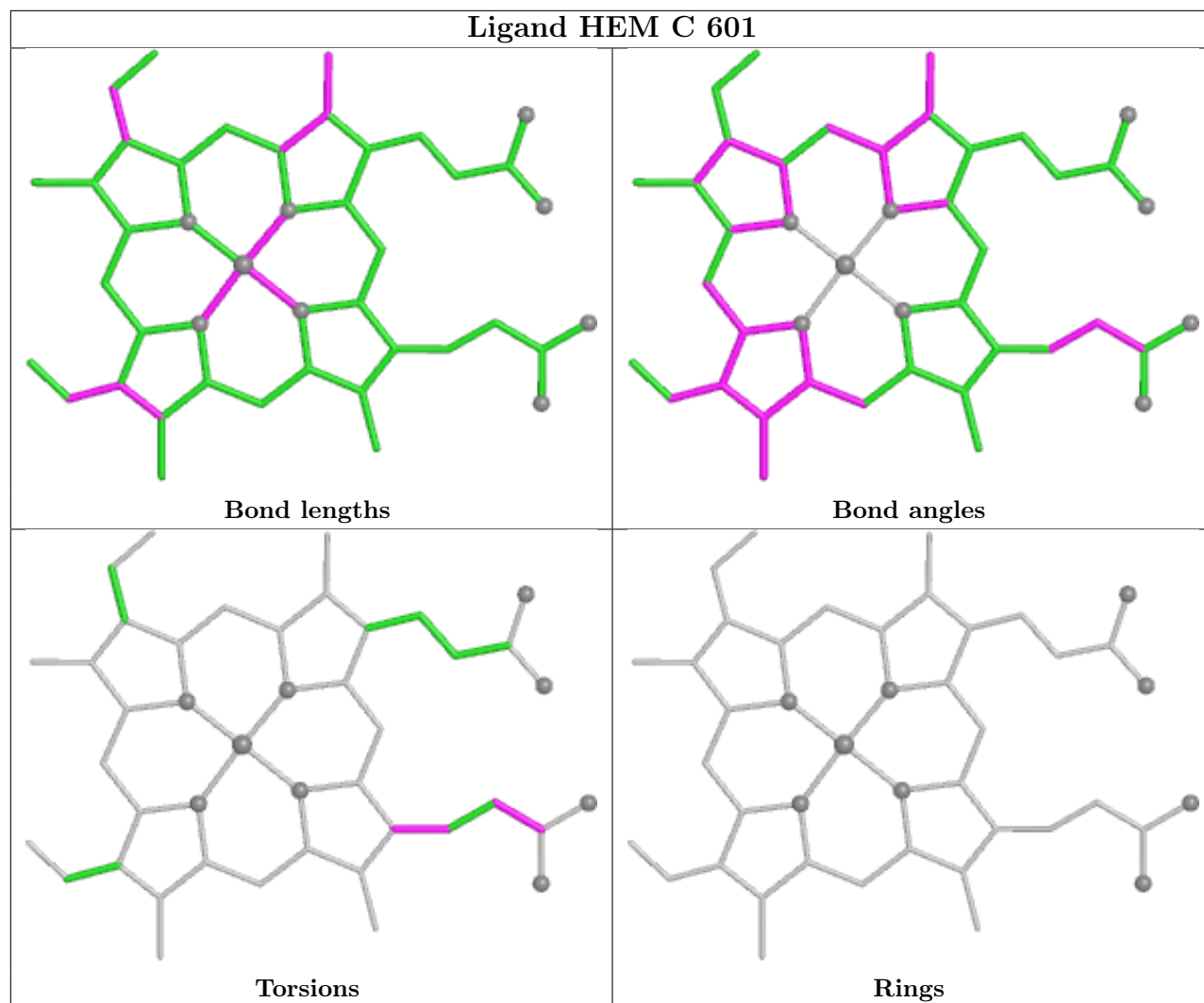
5 monomers are involved in 27 short contacts:

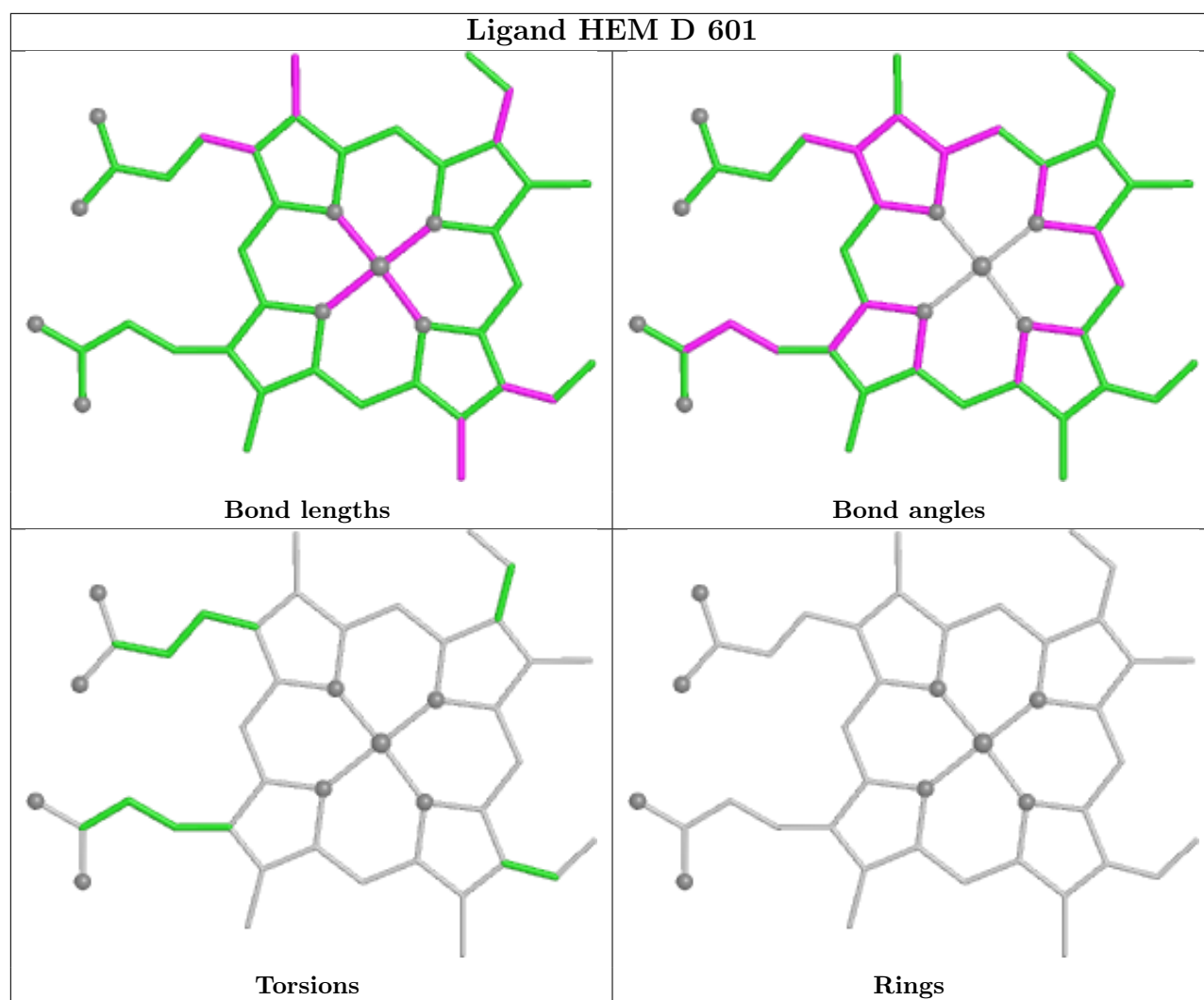
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	HEM	11	0
3	D	602	4LE	3	0
2	C	601	HEM	4	0
2	D	601	HEM	3	0
2	B	601	HEM	6	0

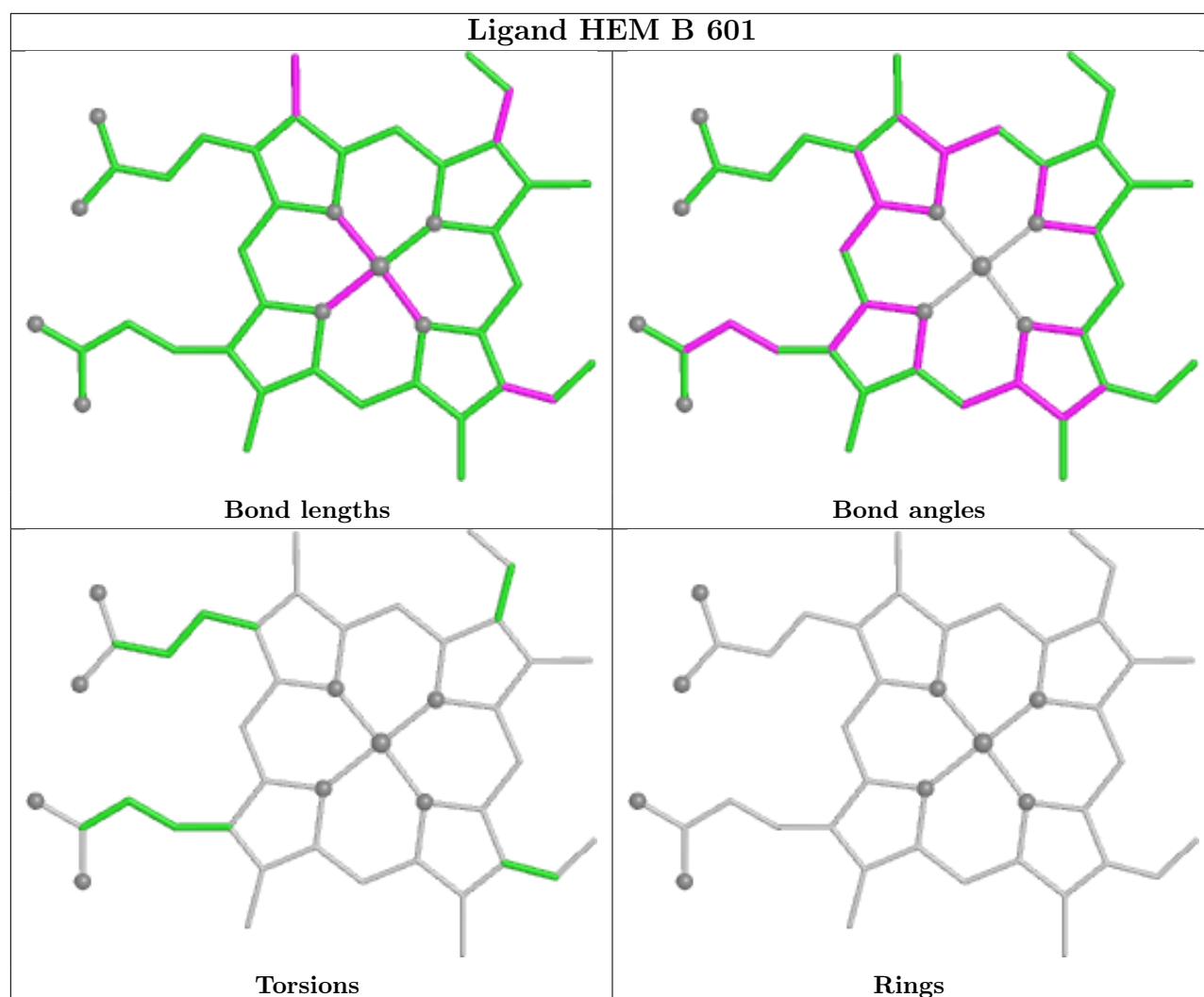
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	492/573 (85%)	0.32	15 (3%) 52 29	31, 49, 91, 125	0
1	B	484/573 (84%)	0.41	10 (2%) 63 39	19, 56, 88, 107	1 (0%)
1	C	492/573 (85%)	0.44	20 (4%) 41 22	31, 51, 93, 117	1 (0%)
1	D	487/573 (84%)	0.41	13 (2%) 56 32	20, 53, 92, 113	1 (0%)
All	All	1955/2292 (85%)	0.40	58 (2%) 52 29	19, 53, 91, 125	3 (0%)

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	70	PRO	3.7
1	D	72	LYS	3.7
1	C	70	PRO	3.6
1	A	71	ALA	3.4
1	C	69	ALA	3.3

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	LLP	B	119	24/25	0.90	0.12	38,45,54,58	0
1	LLP	D	119	24/25	0.92	0.10	30,35,40,43	0
1	LLP	C	119	24/25	0.93	0.10	31,41,46,50	0
1	LLP	A	119	24/25	0.93	0.11	31,37,44,45	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

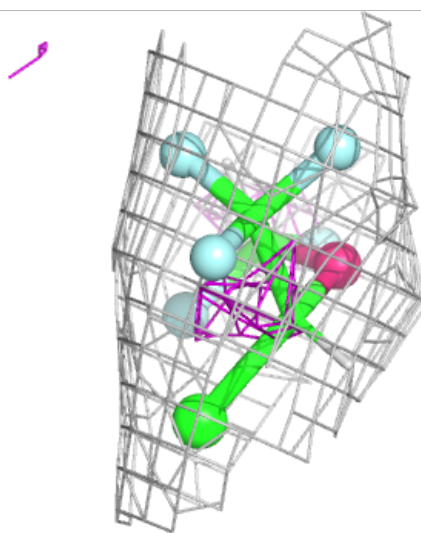
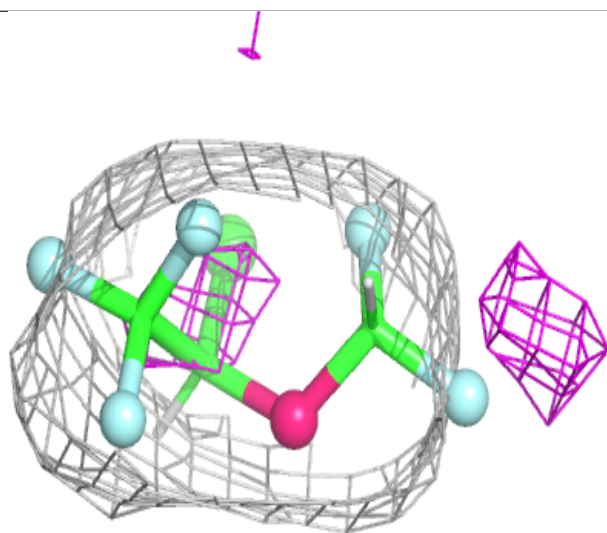
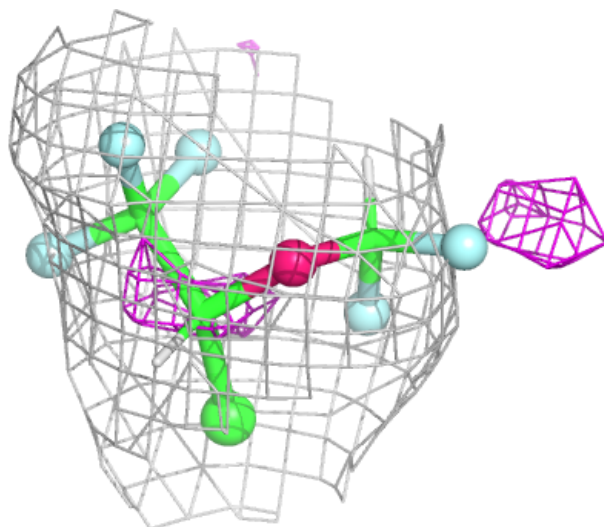
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	4LE	D	602	10/10	0.82	0.13	63,77,84,98	0
2	HEM	B	601	43/43	0.93	0.14	58,76,94,111	0
2	HEM	D	601	43/43	0.95	0.11	48,60,72,82	0
2	HEM	A	601	43/43	0.96	0.11	39,48,53,63	0
2	HEM	C	601	43/43	0.96	0.11	31,46,52,53	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

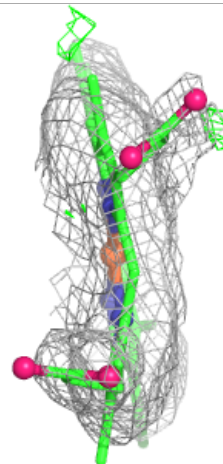
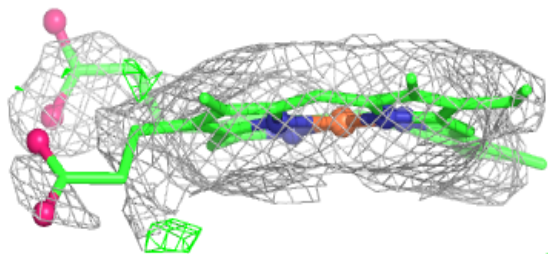
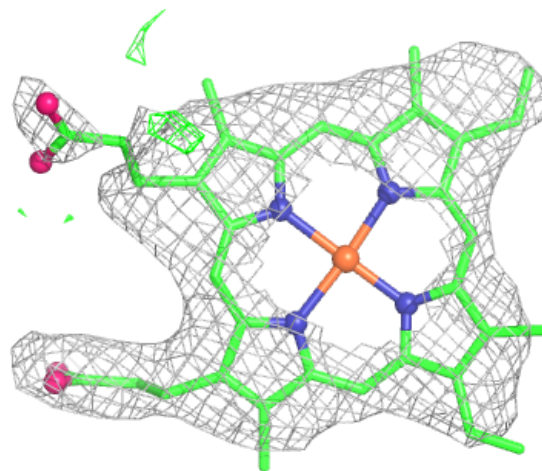
Electron density around 4LE D 602:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



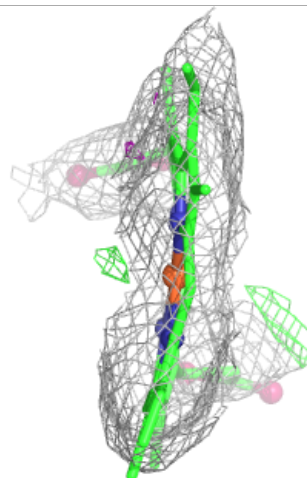
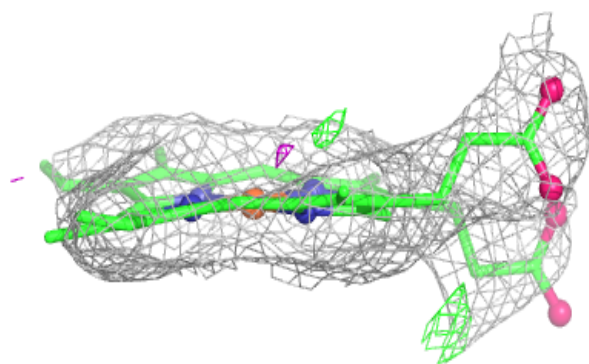
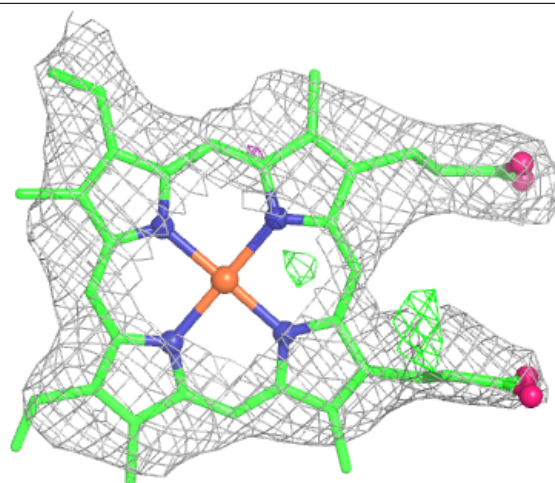
Electron density around HEM B 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



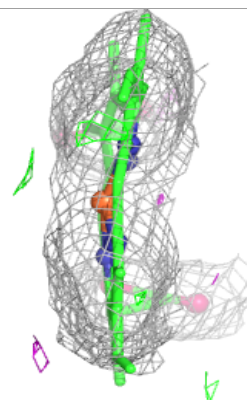
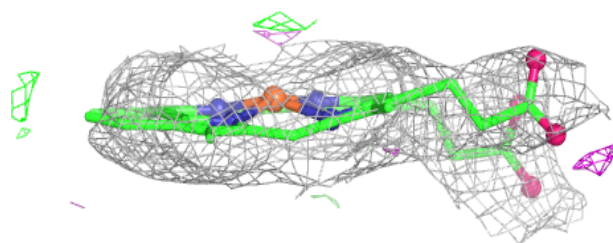
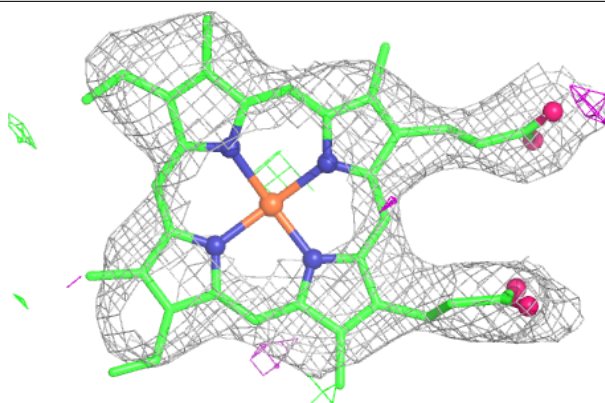
Electron density around HEM D 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

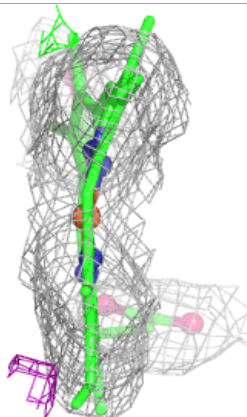
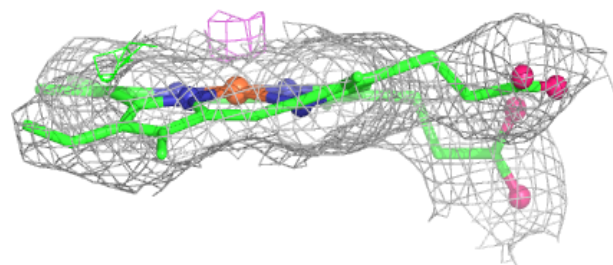
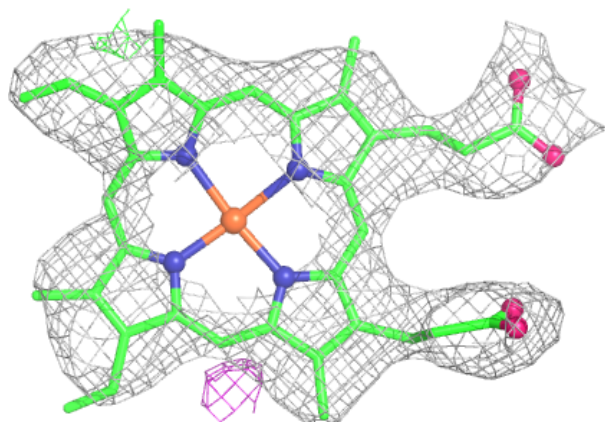


Electron density around HEM A 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around HEM C 601:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.