



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:36 PM UTC

PDB ID : 4NKY / pdb_00004nky
Title : Human steroidogenic cytochrome P450 17A1 mutant A105L with substrate 17alpha-hydroxyprogesterone
Authors : Scott, E.E.; Petrunak, E.M.
Deposited on : 2013-11-13
Resolution : 2.55 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) : 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 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

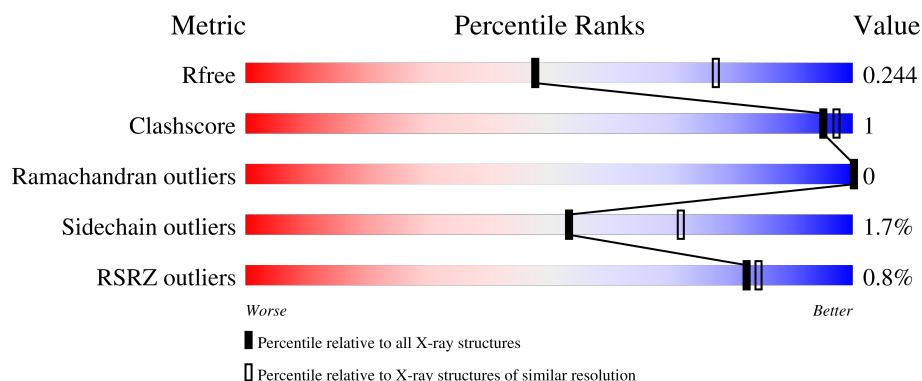
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	494	% 89% 6%
1	B	494	89% 6%
1	C	494	% 90% 5%
1	D	494	% 90% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 30605 atoms, of which 15344 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 Steroid 17-alpha-hydroxylase/17,20 lyase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	462	Total	C	H	N	O	S	0	0	0
			7473	2373	3782	638	665	15			
1	B	464	Total	C	H	N	O	S	0	0	0
			7496	2379	3793	640	669	15			
1	C	467	Total	C	H	N	O	S	0	0	0
			7466	2393	3739	645	674	15			
1	D	465	Total	C	H	N	O	S	0	0	0
			7501	2383	3790	641	672	15			

There are 40 discrepancies between the modelled and reference sequences:

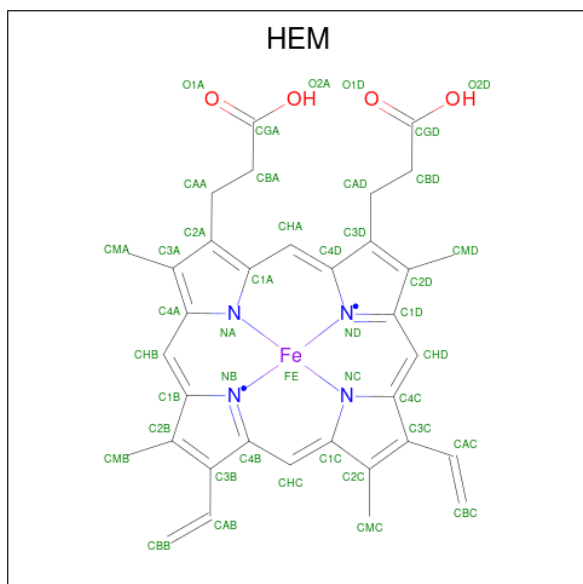
Chain	Residue	Modelled	Actual	Comment	Reference
A	19	MET	-	expression tag	UNP P05093
A	20	ALA	-	expression tag	UNP P05093
A	21	LYS	-	expression tag	UNP P05093
A	22	LYS	-	expression tag	UNP P05093
A	23	THR	-	expression tag	UNP P05093
A	105	LEU	ALA	engineered mutation	UNP P05093
A	509	HIS	-	expression tag	UNP P05093
A	510	HIS	-	expression tag	UNP P05093
A	511	HIS	-	expression tag	UNP P05093
A	512	HIS	-	expression tag	UNP P05093
B	19	MET	-	expression tag	UNP P05093
B	20	ALA	-	expression tag	UNP P05093
B	21	LYS	-	expression tag	UNP P05093
B	22	LYS	-	expression tag	UNP P05093
B	23	THR	-	expression tag	UNP P05093
B	105	LEU	ALA	engineered mutation	UNP P05093
B	509	HIS	-	expression tag	UNP P05093
B	510	HIS	-	expression tag	UNP P05093
B	511	HIS	-	expression tag	UNP P05093
B	512	HIS	-	expression tag	UNP P05093
C	19	MET	-	expression tag	UNP P05093

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Chain	Residue	Modelled	Actual	Comment	Reference
C	20	ALA	-	expression tag	UNP P05093
C	21	LYS	-	expression tag	UNP P05093
C	22	LYS	-	expression tag	UNP P05093
C	23	THR	-	expression tag	UNP P05093
C	105	LEU	ALA	engineered mutation	UNP P05093
C	509	HIS	-	expression tag	UNP P05093
C	510	HIS	-	expression tag	UNP P05093
C	511	HIS	-	expression tag	UNP P05093
C	512	HIS	-	expression tag	UNP P05093
D	19	MET	-	expression tag	UNP P05093
D	20	ALA	-	expression tag	UNP P05093
D	21	LYS	-	expression tag	UNP P05093
D	22	LYS	-	expression tag	UNP P05093
D	23	THR	-	expression tag	UNP P05093
D	105	LEU	ALA	engineered mutation	UNP P05093
D	509	HIS	-	expression tag	UNP P05093
D	510	HIS	-	expression tag	UNP P05093
D	511	HIS	-	expression tag	UNP P05093
D	512	HIS	-	expression tag	UNP P05093

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



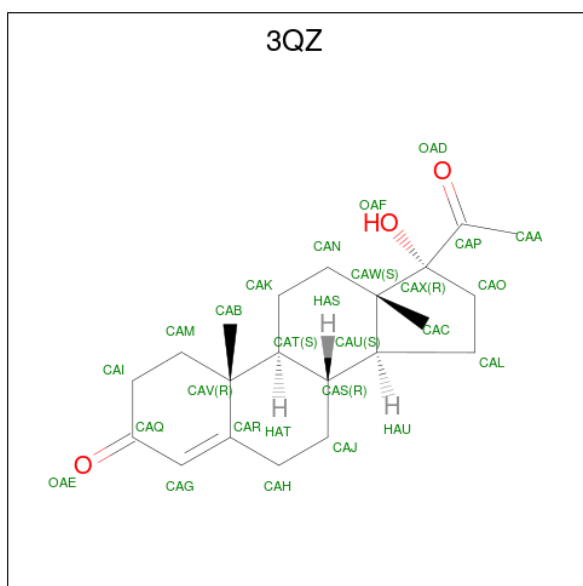
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
2	C	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
2	D	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		

- Molecule 3 is (9beta)-17-hydroxypregn-4-ene-3,20-dione (CCD ID: 3QZ) (formula: $C_{21}H_{30}O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			54	21	30	3		
3	B	1	Total	C	H	O	0	0
			54	21	30	3		
3	C	1	Total	C	H	O	0	0
			54	21	30	3		
3	D	1	Total	C	H	O	0	0
			54	21	30	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	40	Total	O	0
			40	40	
4	B	36	Total	O	0
			36	36	

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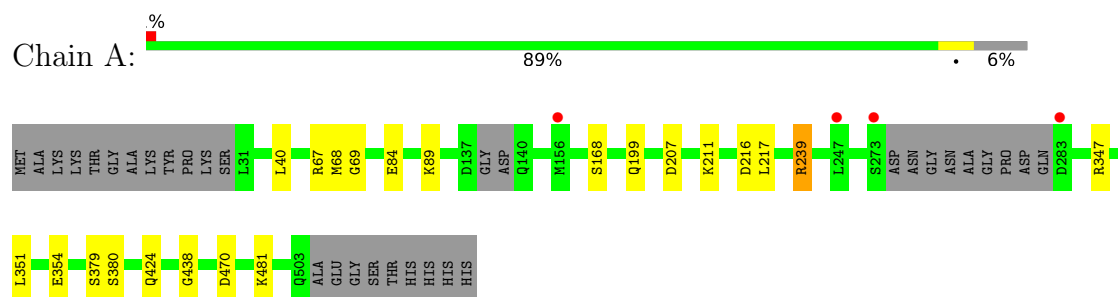
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	53	Total	O	0	0
			53	53		
4	D	32	Total	O	0	0
			32	32		

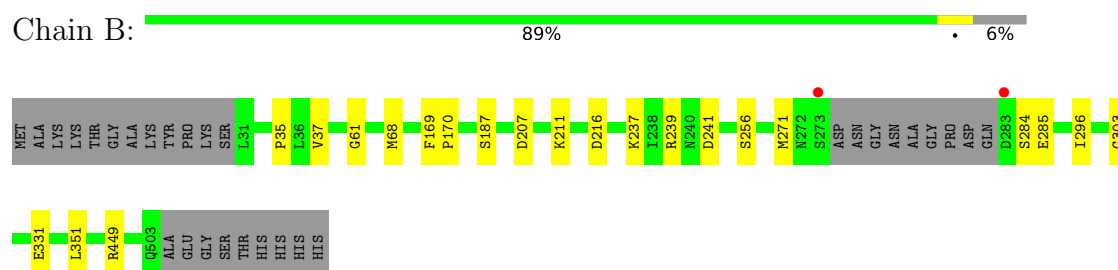
3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

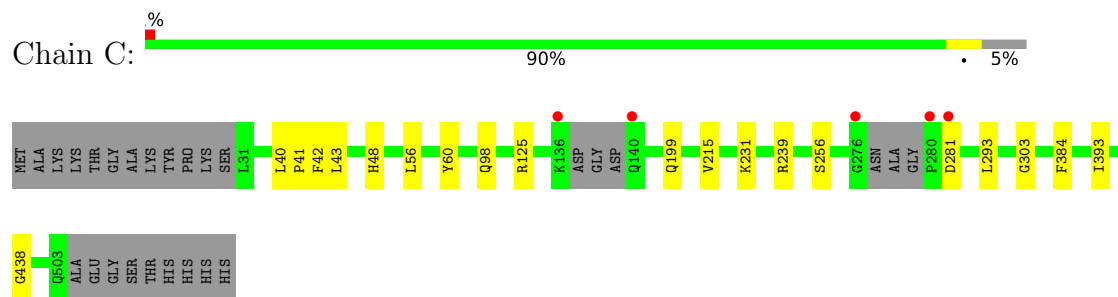
- Molecule 1: Steroid 17-alpha-hydroxylase/17,20 lyase



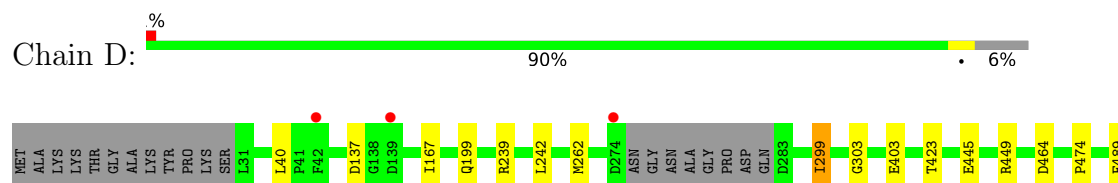
- Molecule 1: Steroid 17-alpha-hydroxylase/17,20 lyase



- Molecule 1: Steroid 17-alpha-hydroxylase/17,20 lyase



- Molecule 1: Steroid 17-alpha-hydroxylase/17,20 lyase



Q497	R500	Q503	ALA	GLU	GLY	SER	THR	HIS	HIS	HIS	HIS
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.28Å 151.78Å 168.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.15 – 2.55 39.15 – 2.55	Depositor EDS
% Data completeness (in resolution range)	98.8 (39.15-2.55) 98.8 (39.15-2.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.54Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.178 , 0.244 0.182 , 0.244	Depositor DCC
R_{free} test set	3806 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	52.4	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	30605	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% of the height of the origin peak. No significant pseudotranslation is detected.*

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: 3QZ, 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	0.45	0/3770	0.74	2/5102 (0.0%)
1	B	0.46	0/3783	0.75	2/5121 (0.0%)
1	C	0.50	0/3807	0.75	2/5152 (0.0%)
1	D	0.48	0/3791	0.75	0/5132
All	All	0.47	0/15151	0.75	6/20507 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	61	GLY	CA-C-N	5.69	126.77	120.45
1	B	61	GLY	C-N-CA	5.69	126.77	120.45
1	C	438	GLY	CA-C-N	5.55	125.91	119.47
1	C	438	GLY	C-N-CA	5.55	125.91	119.47
1	A	438	GLY	CA-C-N	5.35	125.42	119.32
1	A	438	GLY	C-N-CA	5.35	125.42	119.32

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	3691	3782	3773	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3703	3793	3781	9	0
1	C	3727	3739	3802	10	0
1	D	3711	3790	3785	7	0
2	A	43	30	30	2	0
2	B	43	30	30	1	0
2	C	43	30	30	2	0
2	D	43	30	30	1	0
3	A	24	30	30	2	0
3	B	24	30	30	0	0
3	C	24	30	30	0	0
3	D	24	30	30	0	0
4	A	40	0	0	1	0
4	B	36	0	0	0	0
4	C	53	0	0	1	0
4	D	32	0	0	0	0
All	All	15261	15344	15381	35	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 1.

All (35) 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)
3:A:601:3QZ:HAA	3:A:601:3QZ:HAN	1.70	0.71
1:D:445:GLU:OE2	1:D:449:ARG:NH2	2.29	0.65
1:A:239:ARG:NH2	4:A:733:HOH:O	2.29	0.65
1:A:84:GLU:OE2	1:A:89:LYS:NZ	2.31	0.64
2:A:600:HEM:HBB2	2:A:600:HEM:HHC	1.80	0.62
2:A:600:HEM:HBC2	2:A:600:HEM:HHD	1.82	0.61
1:C:42:PHE:O	1:C:43:LEU:HG	2.03	0.59
1:B:303:GLY:HA2	2:B:600:HEM:HMC2	1.85	0.58
1:C:125:ARG:NH1	2:C:600:HEM:O1D	2.37	0.58
3:A:601:3QZ:HAA	3:A:601:3QZ:CAN	2.35	0.57
1:A:470:ASP:O	1:C:231:LYS:NZ	2.35	0.56
1:D:497:GLN:OE1	1:D:500:ARG:NH1	2.42	0.52
1:D:303:GLY:HA2	2:D:600:HEM:HMC3	1.92	0.52
1:A:347:ARG:NH2	1:A:354:GLU:OE1	2.44	0.51
1:C:48:HIS:HD2	4:C:734:HOH:O	1.94	0.51
1:A:40:LEU:HD21	1:A:68:MET:HE1	1.94	0.48
1:D:474:PRO:HB3	1:D:489:PHE:CG	2.48	0.48
1:A:211:LYS:O	1:A:481:LYS:NZ	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:262:MET:SD	1:D:299:ILE:HD13	2.54	0.47
1:B:256:SER:OG	1:B:271:MET:SD	2.73	0.47
1:D:137:ASP:N	1:D:137:ASP:OD1	2.49	0.46
1:B:237:LYS:NZ	1:B:241:ASP:OD2	2.50	0.44
1:A:351:LEU:HD13	1:A:424:GLN:HA	2.00	0.43
1:A:379:SER:OG	1:A:380:SER:N	2.49	0.43
1:B:169:PHE:HB3	1:B:170:PRO:HD3	1.99	0.43
1:A:67:ARG:NH1	1:A:69:GLY:O	2.52	0.43
1:B:68:MET:HE1	1:C:40:LEU:HG	2.00	0.42
1:B:211:LYS:C	1:B:211:LYS:HD3	2.44	0.42
1:B:37:VAL:O	1:C:41:PRO:HD2	2.20	0.42
1:C:42:PHE:HE2	1:C:60:TYR:HH	1.67	0.41
1:B:331:GLU:OE2	1:B:351:LEU:N	2.54	0.41
1:C:303:GLY:HA2	2:C:600:HEM:HMC2	2.02	0.41
1:B:35:PRO:HD3	1:C:384:PHE:CE1	2.55	0.41
1:C:215:VAL:HG13	1:C:393:ILE:CD1	2.52	0.40
1:D:242:LEU:C	1:D:242:LEU:HD23	2.47	0.40

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	456/494 (92%)	441 (97%)	15 (3%)	0	100	100
1	B	460/494 (93%)	442 (96%)	18 (4%)	0	100	100
1	C	461/494 (93%)	450 (98%)	11 (2%)	0	100	100
1	D	461/494 (93%)	440 (95%)	21 (5%)	0	100	100
All	All	1838/1976 (93%)	1773 (96%)	65 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	414/437 (95%)	408 (99%)	6 (1%)	59	75
1	B	415/437 (95%)	407 (98%)	8 (2%)	50	69
1	C	418/437 (96%)	411 (98%)	7 (2%)	53	72
1	D	416/437 (95%)	408 (98%)	8 (2%)	50	69
All	All	1663/1748 (95%)	1634 (98%)	29 (2%)	53	72

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	168	SER
1	A	199	GLN
1	A	207	ASP
1	A	216	ASP
1	A	217	LEU
1	A	239	ARG
1	B	187	SER
1	B	207	ASP
1	B	216	ASP
1	B	239	ARG
1	B	284	SER
1	B	285	GLU
1	B	296	ILE
1	B	449	ARG
1	C	56	LEU
1	C	98	GLN
1	C	199	GLN
1	C	239	ARG
1	C	256	SER
1	C	281	ASP
1	C	293	LEU
1	D	40	LEU
1	D	167	ILE
1	D	199	GLN

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Mol	Chain	Res	Type
1	D	239	ARG
1	D	299	ILE
1	D	403	GLU
1	D	423	THR
1	D	464	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	HIS
1	A	79	HIS
1	A	98	GLN
1	A	202	ASN
1	A	208	ASN
1	B	50	HIS
1	B	140	GLN
1	B	148	GLN
1	B	202	ASN
1	B	407	HIS
1	B	408	GLN
1	B	503	GLN
1	C	50	HIS
1	C	196	ASN
1	C	200	ASN
1	C	202	ASN
1	C	411	GLN
1	D	50	HIS
1	D	160	HIS
1	D	196	ASN
1	D	202	ASN
1	D	401	HIS
1	D	407	HIS
1	D	408	GLN
1	D	411	GLN

5.3.3 RNA ⓘ

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](#)

8 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	D	600	1	50,50,50	1.99	10 (20%)	67,82,82	1.30	6 (8%)
3	3QZ	C	601	-	27,27,27	4.45	18 (66%)	44,45,45	4.15	18 (40%)
3	3QZ	D	601	-	27,27,27	4.54	19 (70%)	44,45,45	4.08	18 (40%)
3	3QZ	B	601	-	27,27,27	4.40	18 (66%)	44,45,45	4.09	21 (47%)
2	HEM	A	600	1	50,50,50	2.10	9 (18%)	67,82,82	1.43	10 (14%)
2	HEM	C	600	1	50,50,50	2.07	11 (22%)	67,82,82	1.35	7 (10%)
2	HEM	B	600	1	50,50,50	1.84	9 (18%)	67,82,82	1.28	5 (7%)
3	3QZ	A	601	-	27,27,27	4.44	17 (62%)	44,45,45	4.10	16 (36%)

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	D	600	1	-	3/14/54/54	-
3	3QZ	C	601	-	-	4/6/68/68	0/4/4/4
3	3QZ	D	601	-	-	4/6/68/68	0/4/4/4
3	3QZ	B	601	-	-	4/6/68/68	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	A	600	1	-	2/14/54/54	-
2	HEM	C	600	1	-	2/14/54/54	-
2	HEM	B	600	1	-	3/14/54/54	-
3	3QZ	A	601	-	-	4/6/68/68	0/4/4/4

All (111) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	601	3QZ	CAK-CAT	10.76	1.71	1.53
3	B	601	3QZ	CAK-CAT	10.75	1.71	1.53
3	D	601	3QZ	CAK-CAT	10.37	1.70	1.53
3	A	601	3QZ	CAK-CAT	10.17	1.70	1.53
3	B	601	3QZ	CAO-CAX	9.66	1.69	1.54
3	A	601	3QZ	CAO-CAX	9.15	1.68	1.54
3	D	601	3QZ	CAO-CAX	8.94	1.68	1.54
3	C	601	3QZ	CAO-CAX	8.87	1.67	1.54
3	D	601	3QZ	CAN-CAK	8.82	1.71	1.53
3	C	601	3QZ	CAN-CAK	8.68	1.70	1.53
3	B	601	3QZ	CAN-CAK	8.59	1.70	1.53
3	A	601	3QZ	CAN-CAK	8.52	1.70	1.53
2	C	600	HEM	C3D-C2D	8.29	1.54	1.36
2	A	600	HEM	C3D-C2D	7.88	1.53	1.36
2	B	600	HEM	C3D-C2D	7.83	1.53	1.36
2	D	600	HEM	C3D-C2D	7.61	1.53	1.36
3	D	601	3QZ	CAV-CAT	-6.62	1.45	1.56
3	A	601	3QZ	CAJ-CAH	6.26	1.66	1.53
3	D	601	3QZ	CAJ-CAH	6.24	1.66	1.53
2	C	600	HEM	FE-NA	6.21	2.15	1.95
2	A	600	HEM	FE-NA	6.17	2.15	1.95
3	C	601	3QZ	CAV-CAT	-6.11	1.46	1.56
3	A	601	3QZ	CAV-CAT	-6.09	1.46	1.56
2	D	600	HEM	FE-ND	6.08	2.13	1.94
3	C	601	3QZ	CAJ-CAH	6.04	1.65	1.53
3	D	601	3QZ	CAX-CAP	-5.85	1.49	1.53
3	A	601	3QZ	CAX-CAP	-5.77	1.49	1.53
3	B	601	3QZ	CAJ-CAH	5.68	1.65	1.53
3	B	601	3QZ	CAV-CAT	-5.61	1.47	1.56
3	C	601	3QZ	CAX-CAP	-5.45	1.49	1.53
2	A	600	HEM	FE-NB	5.16	2.10	1.94
3	D	601	3QZ	CAJ-CAS	5.06	1.62	1.53
3	A	601	3QZ	CAW-CAU	-4.92	1.46	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	600	HEM	FE-ND	4.91	2.10	1.94
2	C	600	HEM	FE-ND	4.91	2.10	1.94
2	A	600	HEM	FE-ND	4.87	2.09	1.94
2	D	600	HEM	FE-NA	4.77	2.10	1.95
3	A	601	3QZ	CAJ-CAS	4.77	1.61	1.53
3	B	601	3QZ	CAJ-CAS	4.76	1.61	1.53
3	B	601	3QZ	CAX-CAP	-4.59	1.50	1.53
3	C	601	3QZ	CAJ-CAS	4.56	1.61	1.53
3	D	601	3QZ	CAW-CAU	-4.54	1.46	1.54
3	C	601	3QZ	CAW-CAU	-4.44	1.46	1.54
3	B	601	3QZ	CAH-CAR	4.42	1.57	1.50
3	A	601	3QZ	CAH-CAR	4.36	1.57	1.50
3	D	601	3QZ	CAH-CAR	4.33	1.57	1.50
3	B	601	3QZ	CAW-CAU	-4.24	1.47	1.54
3	C	601	3QZ	CAH-CAR	4.21	1.57	1.50
3	D	601	3QZ	CAI-CAQ	4.10	1.58	1.50
3	C	601	3QZ	CAV-CAR	-4.00	1.45	1.52
3	A	601	3QZ	CAM-CAV	4.00	1.61	1.54
3	D	601	3QZ	CAV-CAR	-3.97	1.45	1.52
3	D	601	3QZ	CAM-CAV	3.97	1.61	1.54
2	C	600	HEM	FE-NB	3.78	2.06	1.94
3	A	601	3QZ	CAV-CAR	-3.74	1.45	1.52
3	B	601	3QZ	CAI-CAQ	3.73	1.57	1.50
2	D	600	HEM	FE-NC	3.63	2.07	1.95
3	B	601	3QZ	CAG-CAQ	3.62	1.53	1.45
3	D	601	3QZ	CAS-CAT	-3.62	1.46	1.53
3	B	601	3QZ	CAM-CAV	3.62	1.60	1.54
3	C	601	3QZ	CAS-CAT	-3.60	1.46	1.53
2	B	600	HEM	FE-NB	3.60	2.06	1.94
3	B	601	3QZ	CAV-CAR	-3.59	1.46	1.52
3	A	601	3QZ	CAS-CAT	-3.57	1.46	1.53
3	C	601	3QZ	CAM-CAV	3.51	1.60	1.54
3	C	601	3QZ	CAI-CAQ	3.48	1.57	1.50
3	C	601	3QZ	CAG-CAQ	3.41	1.52	1.45
3	A	601	3QZ	CAG-CAQ	3.41	1.52	1.45
2	A	600	HEM	CAC-C3C	3.31	1.56	1.47
3	B	601	3QZ	CAS-CAT	-3.29	1.47	1.53
3	A	601	3QZ	CAI-CAQ	3.29	1.56	1.50
2	A	600	HEM	CAB-C3B	3.23	1.56	1.47
2	D	600	HEM	CAB-C3B	3.18	1.55	1.47
2	D	600	HEM	CAC-C3C	3.18	1.55	1.47
3	C	601	3QZ	CAN-CAW	-3.15	1.48	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	601	3QZ	CAG-CAQ	3.14	1.52	1.45
2	C	600	HEM	FE-NC	3.12	2.05	1.95
2	C	600	HEM	CAC-C3C	3.08	1.55	1.47
2	B	600	HEM	CAB-C3B	3.05	1.55	1.47
3	A	601	3QZ	CAN-CAW	-3.00	1.49	1.54
2	B	600	HEM	FE-NA	2.97	2.05	1.95
3	D	601	3QZ	CAN-CAW	-2.93	1.49	1.54
3	D	601	3QZ	CAM-CAI	2.82	1.59	1.53
2	B	600	HEM	FE-NC	2.82	2.04	1.95
2	C	600	HEM	CAB-C3B	2.79	1.54	1.47
2	B	600	HEM	CAC-C3C	2.68	1.54	1.47
3	C	601	3QZ	CAA-CAP	2.62	1.56	1.50
3	A	601	3QZ	CAO-CAL	2.60	1.62	1.54
3	C	601	3QZ	CAM-CAI	2.57	1.58	1.53
3	B	601	3QZ	CAO-CAL	2.54	1.62	1.54
3	A	601	3QZ	CAM-CAI	2.52	1.58	1.53
3	B	601	3QZ	CAA-CAP	2.51	1.56	1.50
2	A	600	HEM	FE-NC	2.50	2.03	1.95
3	D	601	3QZ	CAO-CAL	2.49	1.62	1.54
3	C	601	3QZ	CAO-CAL	2.44	1.62	1.54
3	B	601	3QZ	CAN-CAW	-2.44	1.50	1.54
2	C	600	HEM	CMC-C2C	2.34	1.55	1.50
3	D	601	3QZ	CAA-CAP	2.32	1.55	1.50
2	D	600	HEM	FE-NB	2.31	2.02	1.94
3	B	601	3QZ	CAM-CAI	2.28	1.57	1.53
2	C	600	HEM	CMB-C2B	2.26	1.55	1.50
2	B	600	HEM	CMC-C2C	2.22	1.55	1.50
2	A	600	HEM	CMC-C2C	2.22	1.55	1.50
2	C	600	HEM	CMD-C2D	2.14	1.55	1.50
2	D	600	HEM	CMD-C2D	2.13	1.55	1.50
2	D	600	HEM	CMC-C2C	2.12	1.55	1.50
3	D	601	3QZ	CAS-CAU	-2.11	1.49	1.53
2	A	600	HEM	CMA-C3A	2.11	1.55	1.50
2	C	600	HEM	CMA-C3A	2.08	1.55	1.50
2	D	600	HEM	CMB-C2B	2.08	1.55	1.50
2	B	600	HEM	CMA-C3A	2.01	1.54	1.50

All (101) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	3QZ	CAW-CAX-CAP	14.05	129.72	112.93
3	C	601	3QZ	CAW-CAX-CAP	13.69	129.29	112.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	3QZ	OAF-CAX-CAP	-13.59	74.73	107.26
3	B	601	3QZ	CAW-CAX-CAP	13.25	128.76	112.93
3	D	601	3QZ	CAW-CAX-CAP	12.99	128.45	112.93
3	C	601	3QZ	OAF-CAX-CAP	-12.73	76.79	107.26
3	B	601	3QZ	OAF-CAX-CAP	-12.68	76.90	107.26
3	D	601	3QZ	OAF-CAX-CAP	-11.52	79.68	107.26
3	B	601	3QZ	OAF-CAX-CAO	-7.97	90.79	110.26
3	C	601	3QZ	OAF-CAX-CAO	-7.90	90.95	110.26
3	D	601	3QZ	OAF-CAX-CAO	-7.77	91.28	110.26
3	A	601	3QZ	CAX-CAW-CAU	7.76	108.50	99.93
3	D	601	3QZ	OAF-CAX-CAW	-7.64	90.97	108.01
3	A	601	3QZ	OAF-CAX-CAW	-7.33	91.65	108.01
3	C	601	3QZ	CAX-CAW-CAU	7.28	107.97	99.93
3	A	601	3QZ	CAM-CAI-CAQ	-6.86	97.62	111.60
3	A	601	3QZ	OAF-CAX-CAO	-6.67	93.96	110.26
3	B	601	3QZ	CAX-CAW-CAU	6.64	107.26	99.93
3	D	601	3QZ	CAC-CAW-CAX	-6.55	100.95	109.11
3	C	601	3QZ	CAC-CAW-CAX	-6.53	100.97	109.11
3	D	601	3QZ	CAX-CAW-CAU	6.50	107.11	99.93
3	B	601	3QZ	OAF-CAX-CAW	-6.47	93.59	108.01
3	C	601	3QZ	OAF-CAX-CAW	-6.30	93.96	108.01
3	C	601	3QZ	CAM-CAI-CAQ	-6.25	98.86	111.60
3	D	601	3QZ	CAH-CAR-CAG	-5.97	111.32	120.86
3	B	601	3QZ	CAM-CAI-CAQ	-5.78	99.82	111.60
3	B	601	3QZ	CAC-CAW-CAX	-5.45	102.32	109.11
2	C	600	HEM	C4D-ND-C1D	5.26	111.44	105.21
3	B	601	3QZ	CAL-CAU-CAS	-5.26	110.70	119.10
3	C	601	3QZ	CAL-CAU-CAS	-5.23	110.75	119.10
2	D	600	HEM	C4D-ND-C1D	5.22	111.39	105.21
3	A	601	3QZ	CAL-CAU-CAS	-5.02	111.08	119.10
3	D	601	3QZ	CAL-CAU-CAS	-5.00	111.12	119.10
3	D	601	3QZ	CAH-CAR-CAV	4.97	125.54	116.76
3	A	601	3QZ	CAC-CAW-CAX	-4.92	102.98	109.11
2	B	600	HEM	C4D-ND-C1D	4.71	110.78	105.21
3	D	601	3QZ	CAL-CAU-CAW	4.58	109.58	103.70
3	B	601	3QZ	CAJ-CAH-CAR	-4.54	103.61	111.93
2	A	600	HEM	C4D-ND-C1D	4.53	110.57	105.21
3	D	601	3QZ	CAM-CAI-CAQ	-4.42	102.60	111.60
3	D	601	3QZ	CAA-CAP-CAX	4.40	127.09	118.57
3	C	601	3QZ	CAL-CAU-CAW	4.34	109.27	103.70
3	B	601	3QZ	CAA-CAP-CAX	4.28	126.87	118.57
3	C	601	3QZ	CAA-CAP-CAX	4.25	126.80	118.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	601	3QZ	CAL-CAU-CAW	4.21	109.10	103.70
3	D	601	3QZ	OAD-CAP-CAX	-4.14	114.45	120.71
3	C	601	3QZ	CAH-CAR-CAG	-4.12	114.27	120.86
3	A	601	3QZ	CAH-CAR-CAG	-4.02	114.44	120.86
3	A	601	3QZ	CAH-CAR-CAV	3.68	123.25	116.76
3	C	601	3QZ	CAH-CAR-CAV	3.65	123.20	116.76
3	C	601	3QZ	OAD-CAP-CAX	-3.62	115.25	120.71
2	A	600	HEM	C3B-C2B-C1B	3.54	109.07	106.41
3	A	601	3QZ	CAL-CAU-CAW	3.52	108.23	103.70
3	B	601	3QZ	CAT-CAV-CAR	3.48	114.74	109.65
3	B	601	3QZ	CAH-CAJ-CAS	-3.42	105.64	111.64
3	B	601	3QZ	CAH-CAR-CAG	-3.29	115.60	120.86
3	C	601	3QZ	CAK-CAN-CAW	-3.29	107.18	112.85
3	B	601	3QZ	CAH-CAR-CAV	3.26	122.52	116.76
2	B	600	HEM	CAA-CBA-CGA	-3.10	105.44	113.67
3	B	601	3QZ	OAD-CAP-CAX	-3.08	116.06	120.71
2	A	600	HEM	CHC-C1C-NC	2.99	127.71	124.45
3	A	601	3QZ	CAJ-CAH-CAR	-2.99	106.45	111.93
3	C	601	3QZ	CAJ-CAH-CAR	-2.99	106.45	111.93
2	A	600	HEM	C1B-NB-C4B	2.90	108.64	105.21
3	B	601	3QZ	CAJ-CAS-CAT	-2.86	107.09	110.52
3	A	601	3QZ	CAK-CAN-CAW	-2.84	107.94	112.85
2	B	600	HEM	CMB-C2B-C1B	-2.79	120.68	125.03
3	D	601	3QZ	CAK-CAN-CAW	-2.78	108.05	112.85
2	D	600	HEM	CMB-C2B-C1B	-2.78	120.69	125.03
3	B	601	3QZ	CAI-CAM-CAV	-2.66	108.80	113.42
2	A	600	HEM	C3B-C4B-NB	-2.54	107.64	109.47
3	B	601	3QZ	CAK-CAN-CAW	-2.52	108.51	112.85
3	A	601	3QZ	CAA-CAP-CAX	2.50	123.41	118.57
2	C	600	HEM	CMB-C2B-C1B	-2.44	121.22	125.03
3	D	601	3QZ	CAK-CAT-CAS	-2.42	108.40	111.78
2	A	600	HEM	C3C-C2C-C1C	2.38	109.30	107.05
2	C	600	HEM	C2A-C1A-NA	-2.36	107.53	110.15
3	A	601	3QZ	CAK-CAT-CAS	-2.35	108.50	111.78
3	C	601	3QZ	CAJ-CAS-CAU	-2.32	108.23	112.08
3	B	601	3QZ	OAD-CAP-CAA	-2.30	117.03	121.39
3	B	601	3QZ	CAM-CAV-CAT	-2.29	105.71	108.74
3	D	601	3QZ	CAC-CAW-CAN	-2.26	106.60	109.69
2	C	600	HEM	CAC-C3C-C4C	-2.25	119.44	124.82
3	D	601	3QZ	CAC-CAW-CAU	2.19	115.96	111.72
2	C	600	HEM	CMC-C2C-C1C	-2.18	120.89	124.73
2	A	600	HEM	CAC-C3C-C4C	2.17	130.01	124.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	601	3QZ	CAK-CAT-CAS	-2.17	108.75	111.78
2	B	600	HEM	CMC-C2C-C1C	-2.14	120.95	124.73
3	C	601	3QZ	CAT-CAV-CAR	2.12	112.76	109.65
2	D	600	HEM	CMC-C2C-C1C	-2.12	121.00	124.73
2	A	600	HEM	C2B-C1B-NB	-2.11	107.42	109.84
2	A	600	HEM	CHB-C1B-NB	2.10	126.97	124.37
2	A	600	HEM	C4C-NC-C1C	2.10	109.25	105.82
2	B	600	HEM	CAC-C3C-C4C	-2.10	119.81	124.82
2	D	600	HEM	C1B-NB-C4B	2.08	107.67	105.21
3	D	601	3QZ	CAO-CAX-CAW	2.07	105.14	103.24
2	C	600	HEM	C1B-NB-C4B	2.04	107.62	105.21
3	A	601	3QZ	CAI-CAM-CAV	-2.03	109.90	113.42
2	D	600	HEM	C3B-C2B-C1B	2.01	107.92	106.41
2	C	600	HEM	CHD-C1D-ND	2.01	126.58	124.42
2	D	600	HEM	CAC-C3C-C4C	-2.00	120.04	124.82

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	3QZ	CAA-CAP-CAX-CAW
3	A	601	3QZ	OAD-CAP-CAX-CAW
3	B	601	3QZ	CAA-CAP-CAX-CAO
3	B	601	3QZ	CAA-CAP-CAX-CAW
3	B	601	3QZ	OAD-CAP-CAX-CAO
3	B	601	3QZ	OAD-CAP-CAX-CAW
3	C	601	3QZ	CAA-CAP-CAX-CAW
3	C	601	3QZ	OAD-CAP-CAX-CAW
3	D	601	3QZ	CAA-CAP-CAX-CAW
3	D	601	3QZ	OAD-CAP-CAX-CAW
3	C	601	3QZ	OAD-CAP-CAX-CAO
3	D	601	3QZ	CAA-CAP-CAX-CAO
3	D	601	3QZ	OAD-CAP-CAX-CAO
2	A	600	HEM	C4B-C3B-CAB-CBB
2	A	600	HEM	C4C-C3C-CAC-CBC
3	A	601	3QZ	OAD-CAP-CAX-OAF
3	A	601	3QZ	CAA-CAP-CAX-OAF
3	C	601	3QZ	CAA-CAP-CAX-CAO
2	B	600	HEM	CAA-CBA-CGA-O2A
2	B	600	HEM	CAA-CBA-CGA-O1A
2	C	600	HEM	CAA-CBA-CGA-O2A
2	C	600	HEM	CAA-CBA-CGA-O1A

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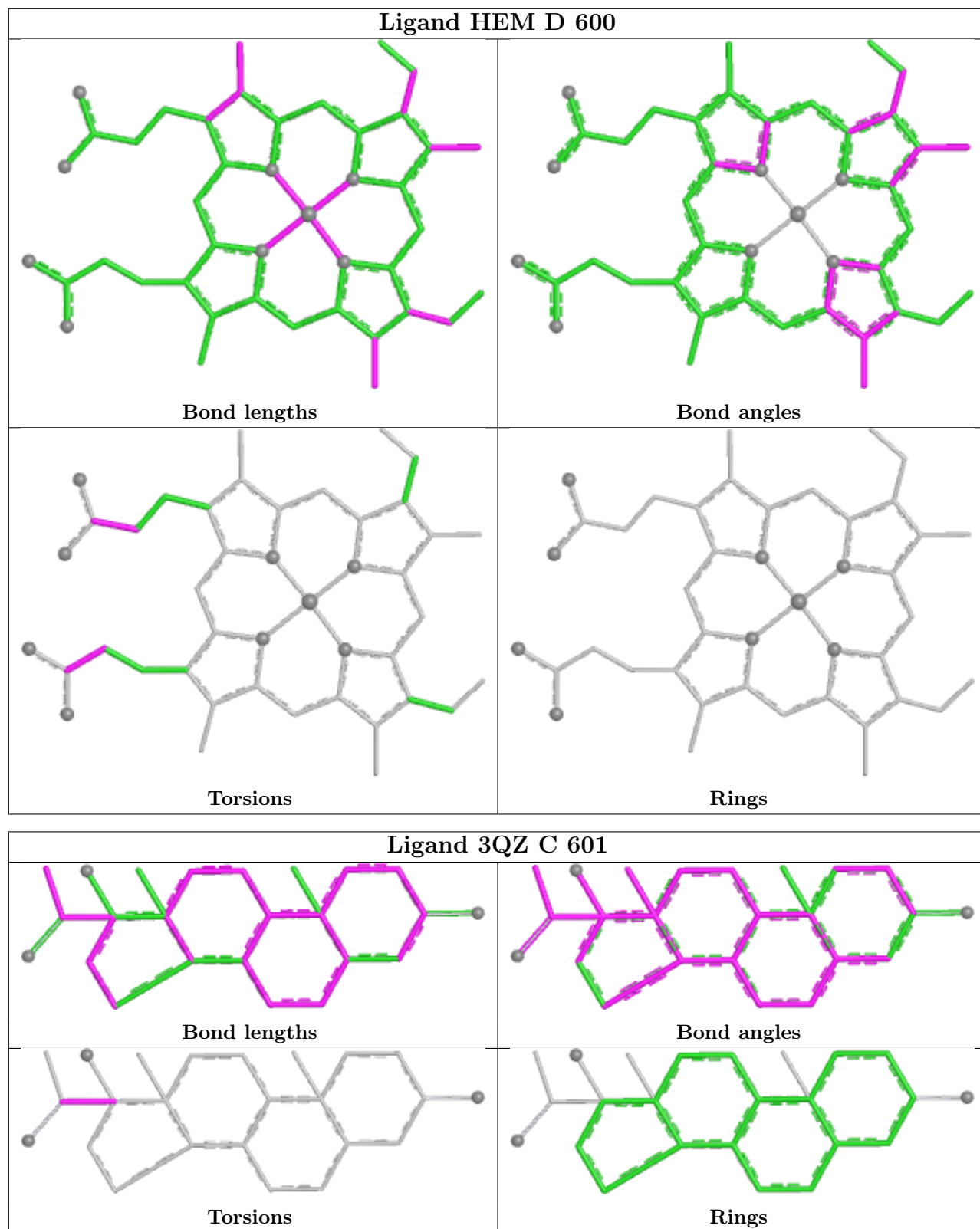
Mol	Chain	Res	Type	Atoms
2	B	600	HEM	CAD-CBD-CGD-O1D
2	D	600	HEM	CAA-CBA-CGA-O1A
2	D	600	HEM	CAA-CBA-CGA-O2A
2	D	600	HEM	CAD-CBD-CGD-O2D

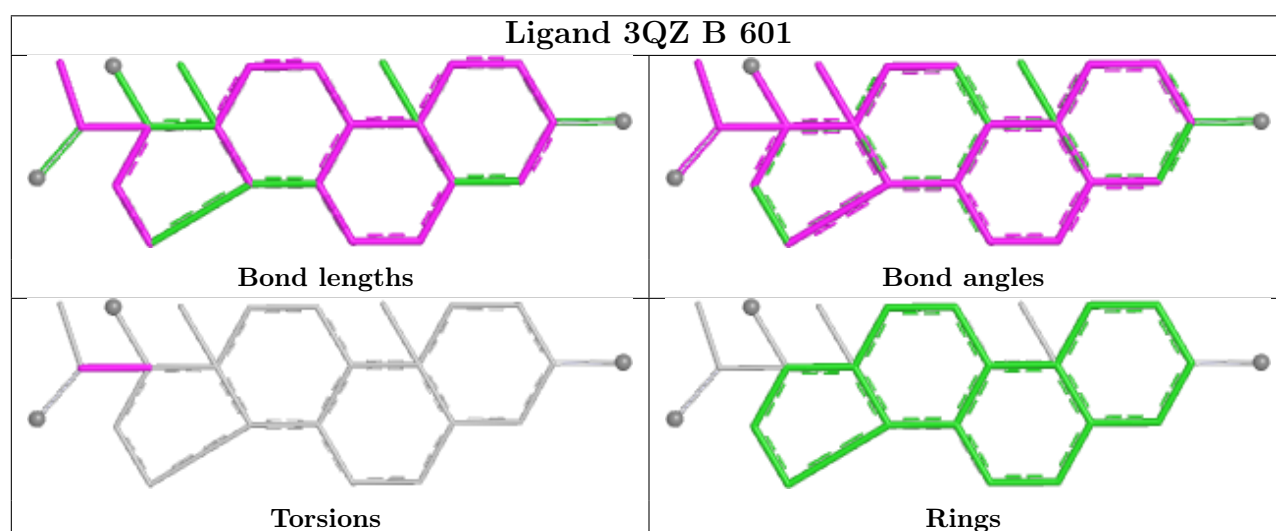
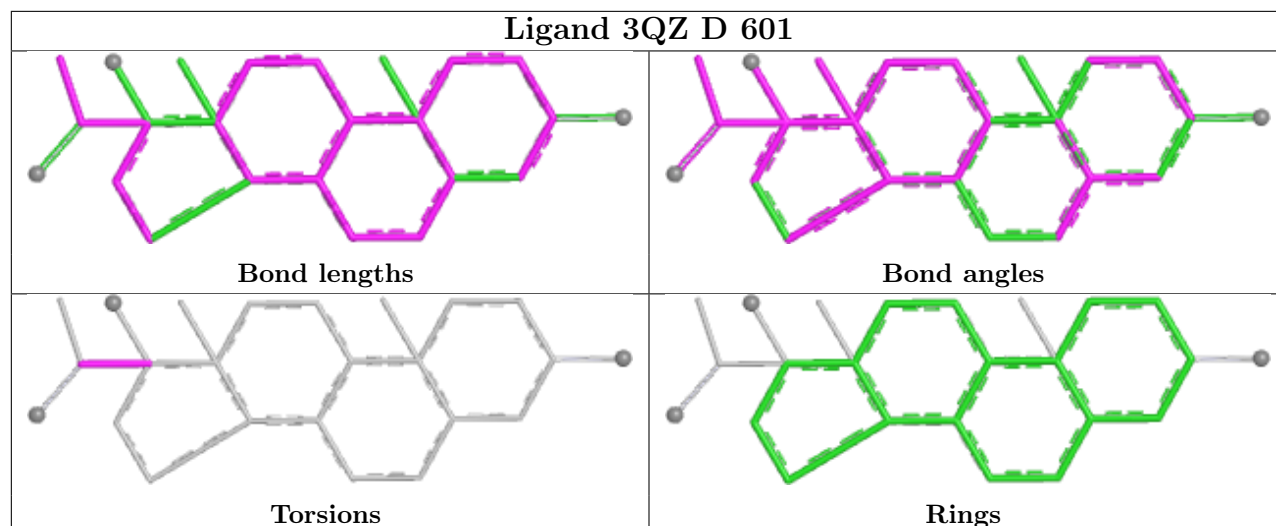
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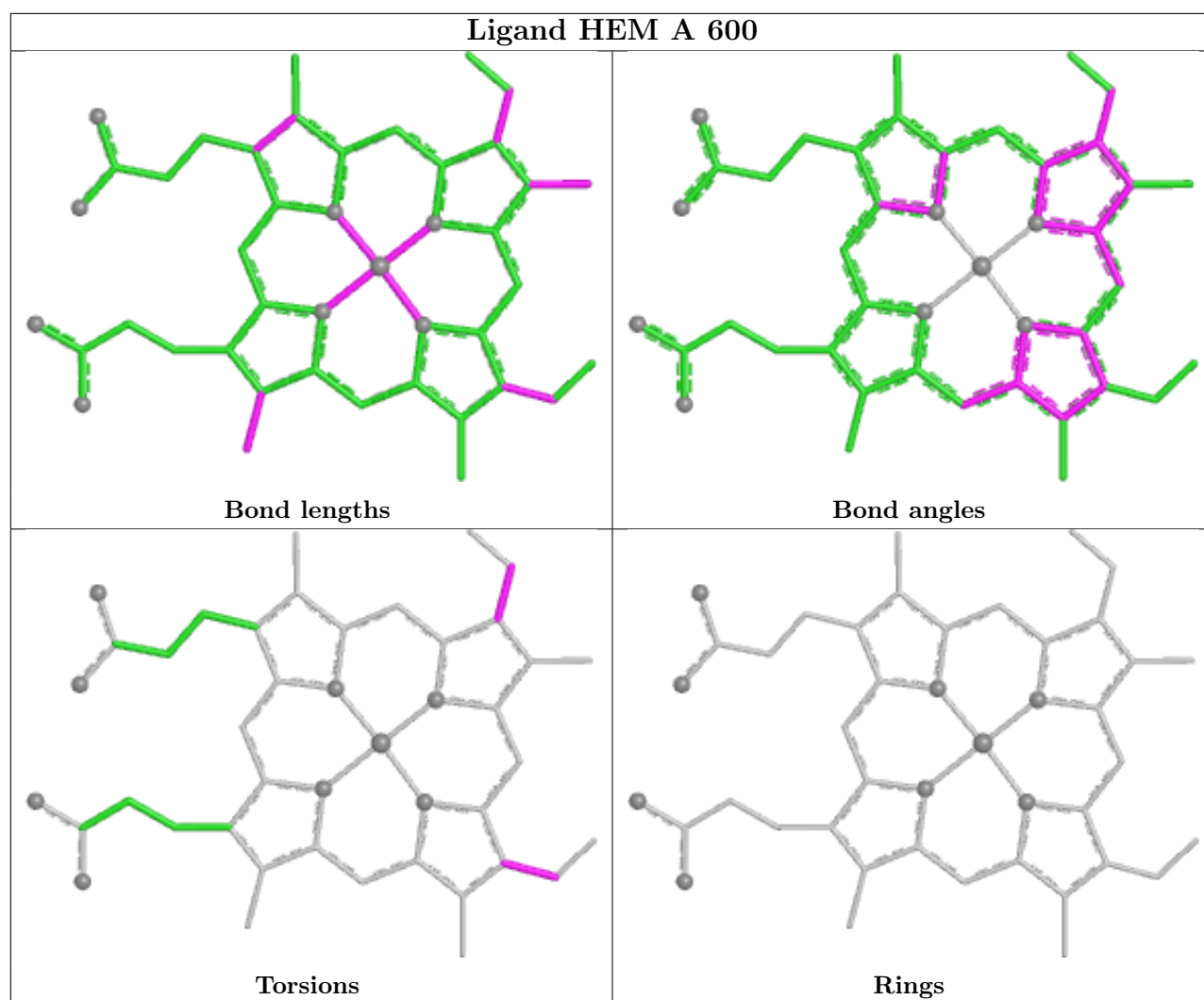
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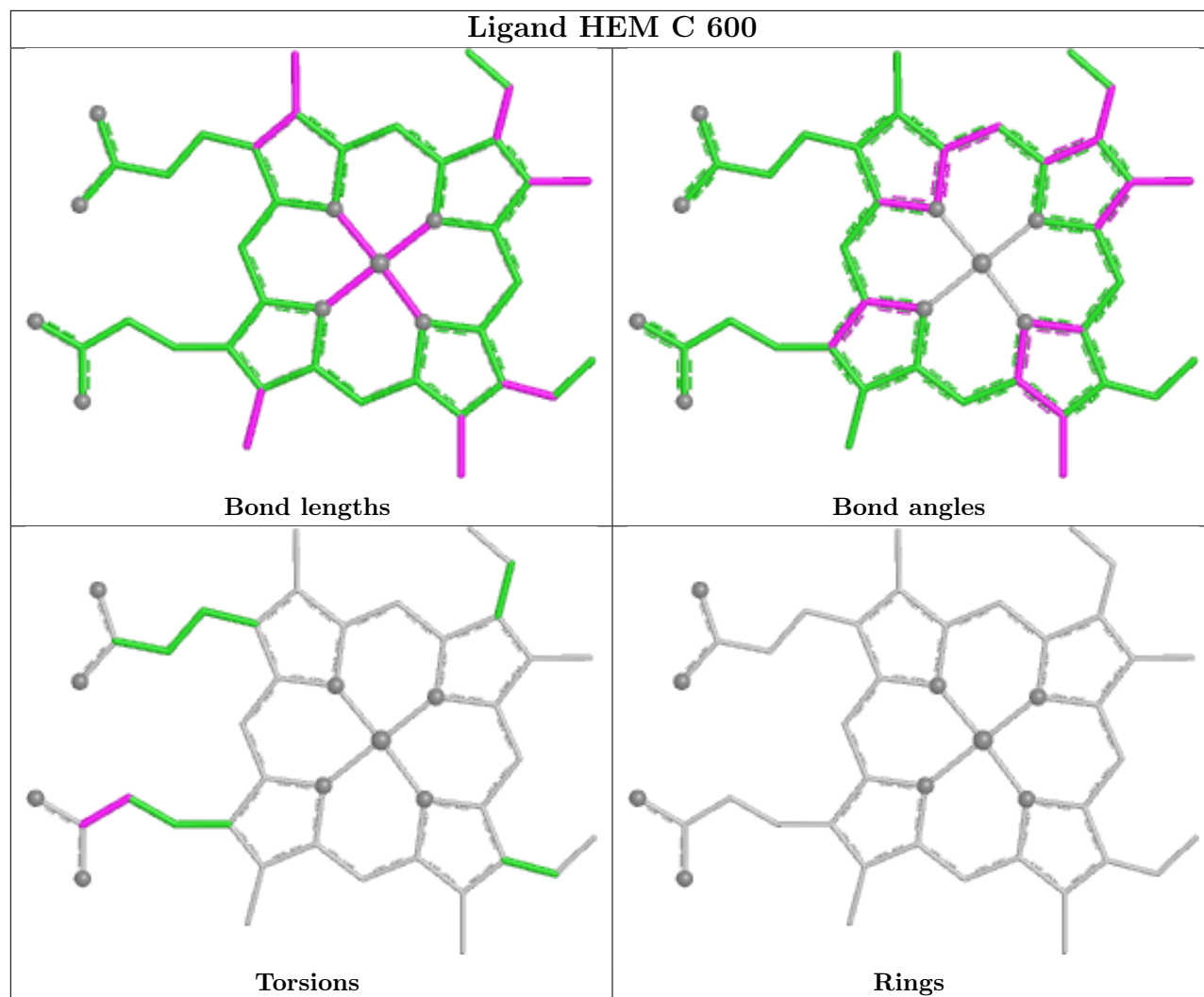
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	600	HEM	1	0
2	A	600	HEM	2	0
2	C	600	HEM	2	0
2	B	600	HEM	1	0
3	A	601	3QZ	2	0

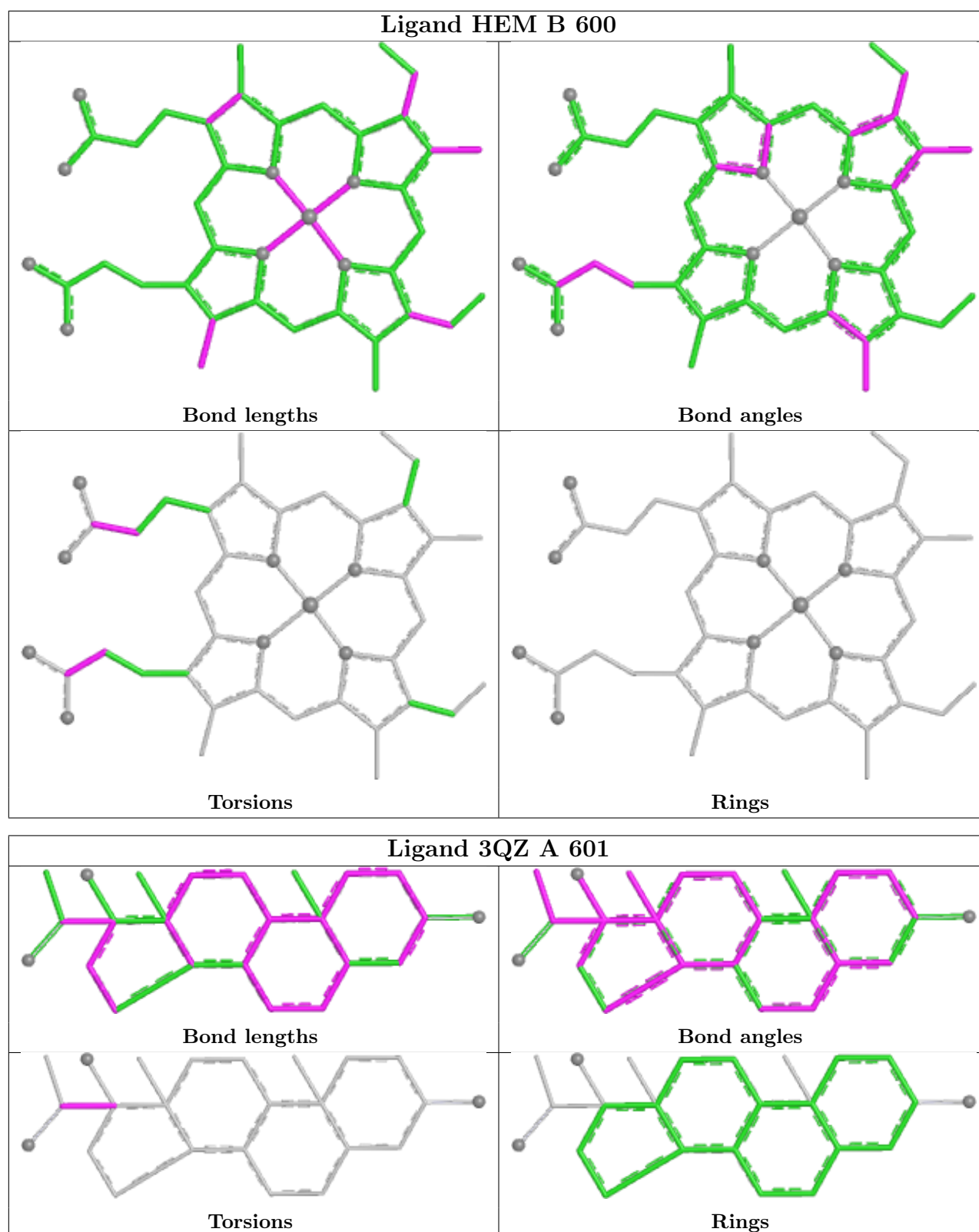
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	462/494 (93%)	-0.30	4 (0%) 81 83	37, 54, 87, 114	0
1	B	464/494 (93%)	-0.37	2 (0%) 88 90	37, 53, 83, 114	0
1	C	467/494 (94%)	-0.35	5 (1%) 78 79	36, 51, 76, 102	0
1	D	465/494 (94%)	-0.29	3 (0%) 85 88	35, 54, 85, 120	0
All	All	1858/1976 (94%)	-0.33	14 (0%) 82 84	35, 53, 84, 120	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	276	GLY	4.0
1	A	273	SER	3.4
1	B	273	SER	3.3
1	D	42	PHE	2.8
1	C	280	PRO	2.7
1	C	281	ASP	2.7
1	C	136	LYS	2.7
1	D	274	ASP	2.6
1	A	283	ASP	2.3
1	A	247	LEU	2.1
1	A	156	MET	2.1
1	C	140	GLN	2.1
1	B	283	ASP	2.0
1	D	139	ASP	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

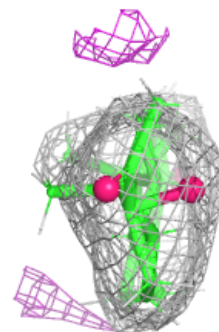
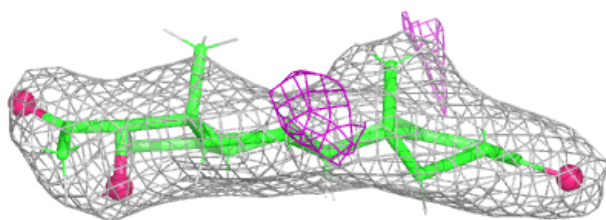
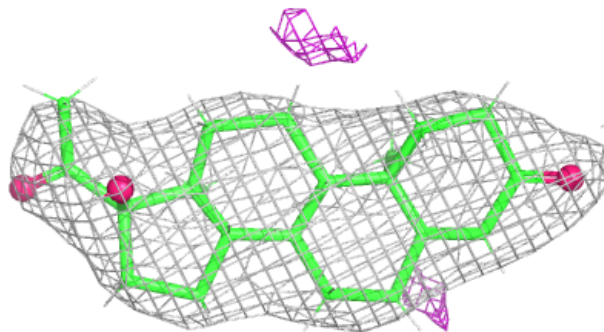
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	3QZ	B	601	24/24	0.94	0.09	45,54,61,69	0
3	3QZ	C	601	24/24	0.94	0.10	35,49,58,65	0
3	3QZ	A	601	24/24	0.96	0.08	43,60,72,74	0
3	3QZ	D	601	24/24	0.96	0.07	31,44,56,58	0
2	HEM	A	600	43/43	0.98	0.07	29,42,55,66	0
2	HEM	B	600	43/43	0.98	0.06	31,42,57,70	0
2	HEM	C	600	43/43	0.98	0.07	31,41,52,61	0
2	HEM	D	600	43/43	0.98	0.07	31,43,53,67	0

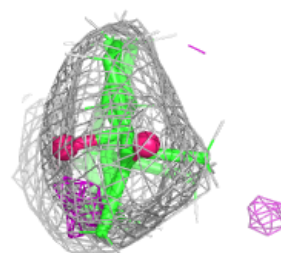
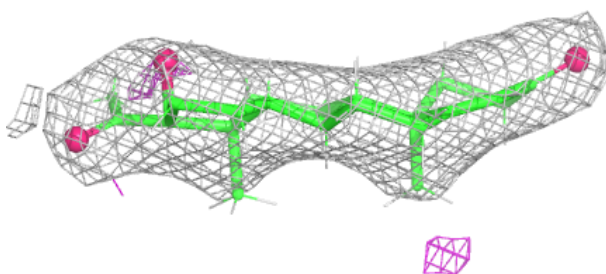
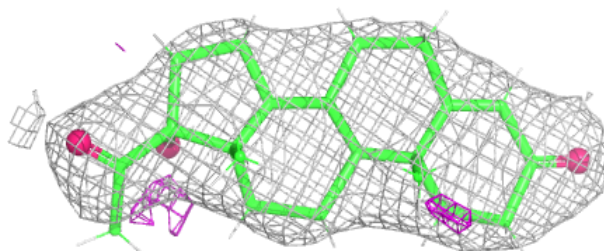
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 3QZ 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)

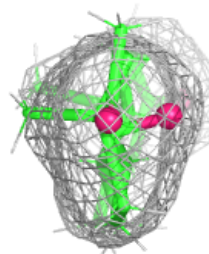
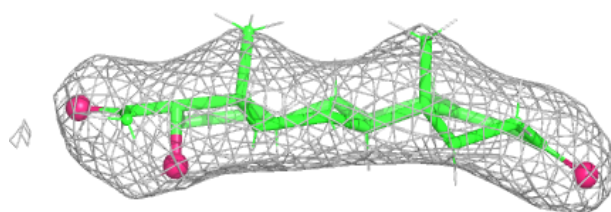
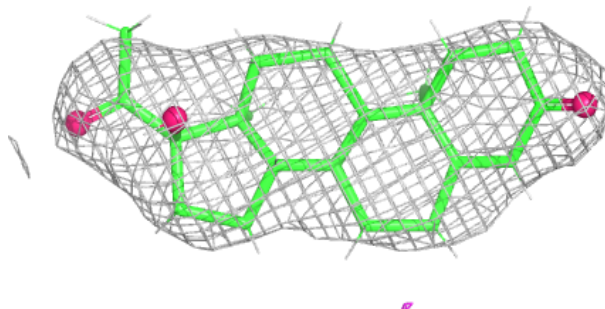
**Electron density around 3QZ C 601:**

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

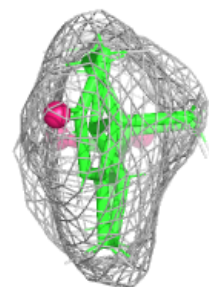
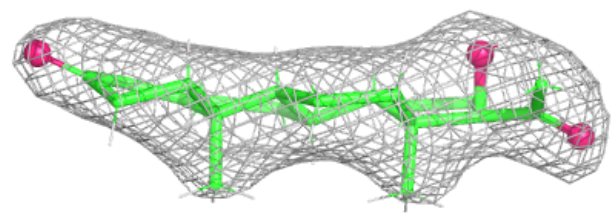
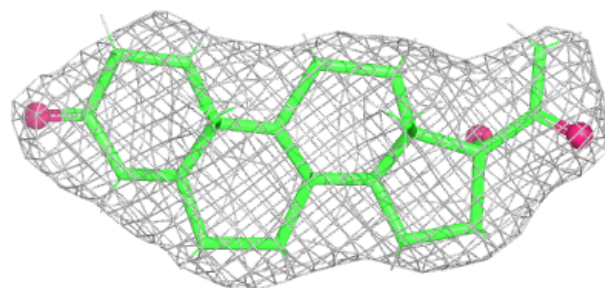


Electron density around 3QZ A 601:

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

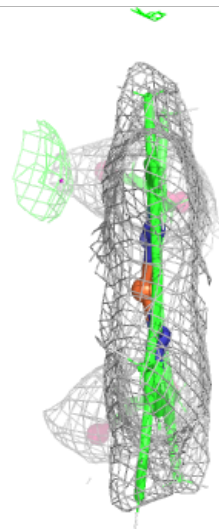
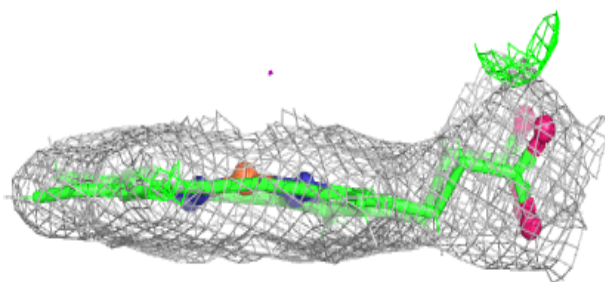
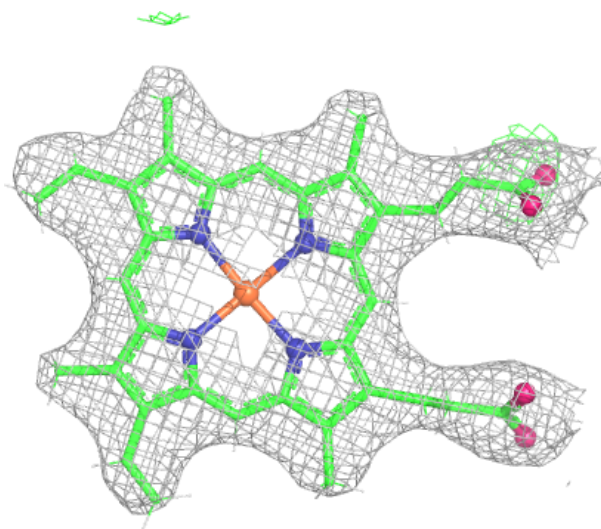
**Electron density around 3QZ D 601:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



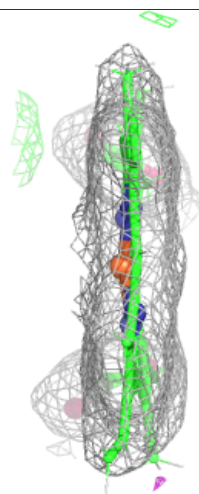
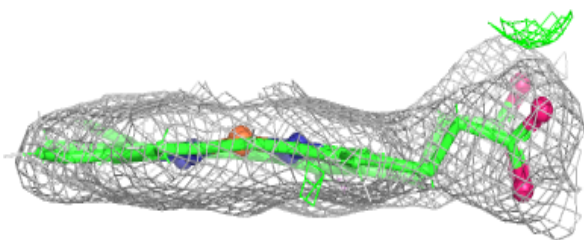
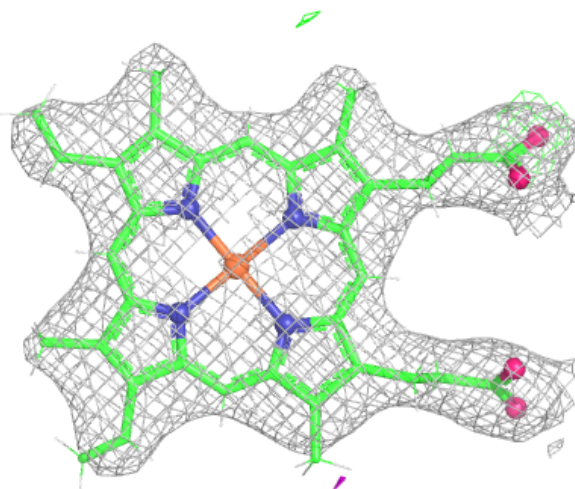
Electron density around HEM A 600:

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



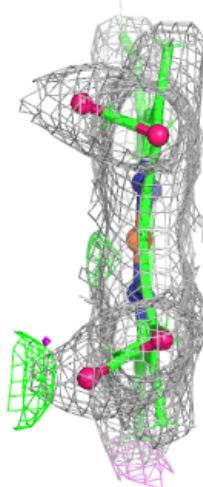
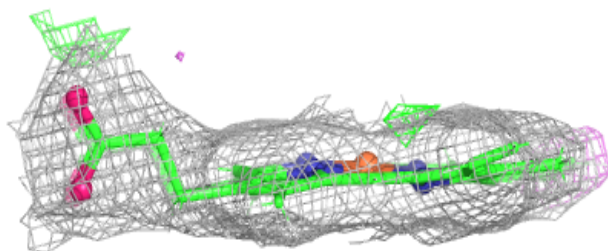
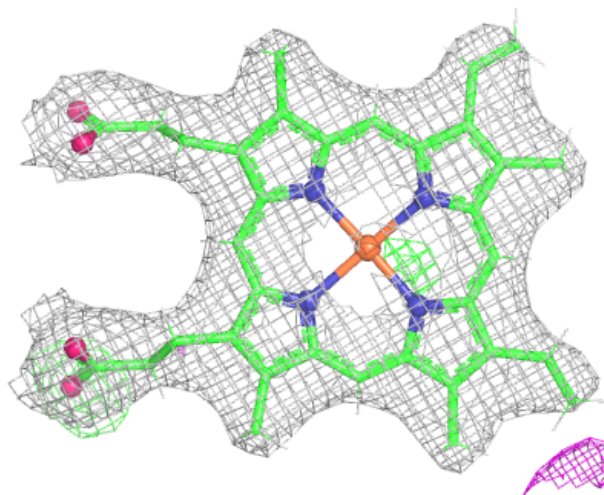
Electron density around HEM B 600:

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



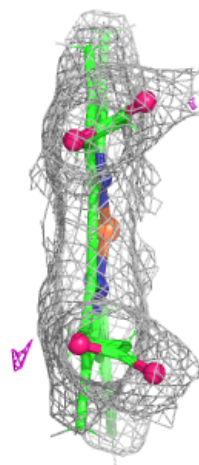
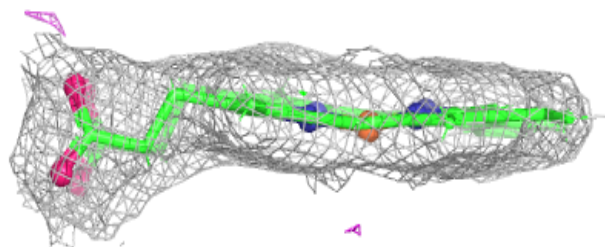
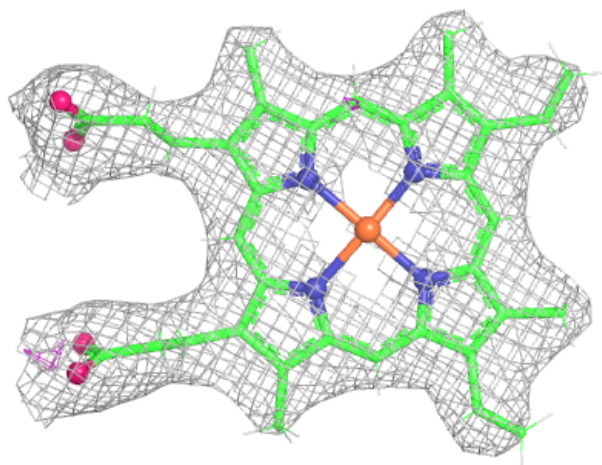
Electron density around HEM C 600:

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



Electron density around HEM D 600:

$2mF_o-DF_c$ (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.