



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 13, 2026 – 08:14 AM EDT

PDB ID : 9O4D / pdb\_00009o4d  
Title : GutD in complex with guanine and cWW  
Authors : Gering, H.E.; Makris, T.M.; Phan, H.N.  
Deposited on : 2025-04-08  
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](mailto: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

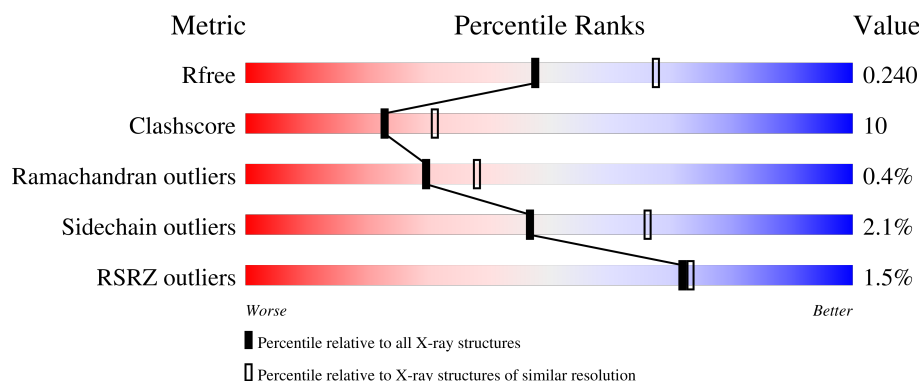
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

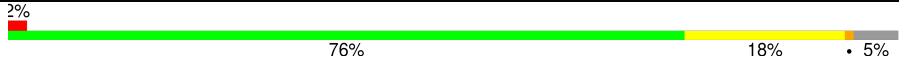

The reported resolution of this entry is 2.30 Å.

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))
$R_{free}$	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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  $\geq 3$ , 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	414	
1	B	414	

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
3	GUN	A	502	-	X	-	-
3	GUN	B	503	-	X	-	-

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 7470 atoms, of which 492 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 Cytochrome P450 121.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	3	0
			3069	1946	560	550	13			
1	B	395	Total	C	N	O	S	8	3	0
			3083	1954	562	555	12			

There are 36 discrepancies between the modelled and reference sequences:

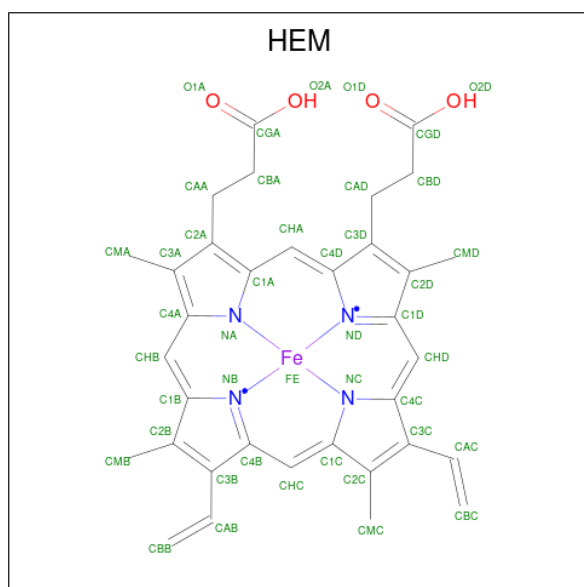
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP A0A918H2T3
A	1	GLY	-	expression tag	UNP A0A918H2T3
A	109	ALA	ASP	conflict	UNP A0A918H2T3
A	399	LEU	-	expression tag	UNP A0A918H2T3
A	400	VAL	-	expression tag	UNP A0A918H2T3
A	401	PRO	-	expression tag	UNP A0A918H2T3
A	402	ARG	-	expression tag	UNP A0A918H2T3
A	403	GLY	-	expression tag	UNP A0A918H2T3
A	404	SER	-	expression tag	UNP A0A918H2T3
A	405	GLY	-	expression tag	UNP A0A918H2T3
A	406	SER	-	expression tag	UNP A0A918H2T3
A	407	SER	-	expression tag	UNP A0A918H2T3
A	408	HIS	-	expression tag	UNP A0A918H2T3
A	409	HIS	-	expression tag	UNP A0A918H2T3
A	410	HIS	-	expression tag	UNP A0A918H2T3
A	411	HIS	-	expression tag	UNP A0A918H2T3
A	412	HIS	-	expression tag	UNP A0A918H2T3
A	413	HIS	-	expression tag	UNP A0A918H2T3
B	0	MET	-	initiating methionine	UNP A0A918H2T3
B	1	GLY	-	expression tag	UNP A0A918H2T3
B	109	ALA	ASP	conflict	UNP A0A918H2T3
B	399	LEU	-	expression tag	UNP A0A918H2T3
B	400	VAL	-	expression tag	UNP A0A918H2T3
B	401	PRO	-	expression tag	UNP A0A918H2T3
B	402	ARG	-	expression tag	UNP A0A918H2T3

*Continued on next page...*

Continued from previous page...

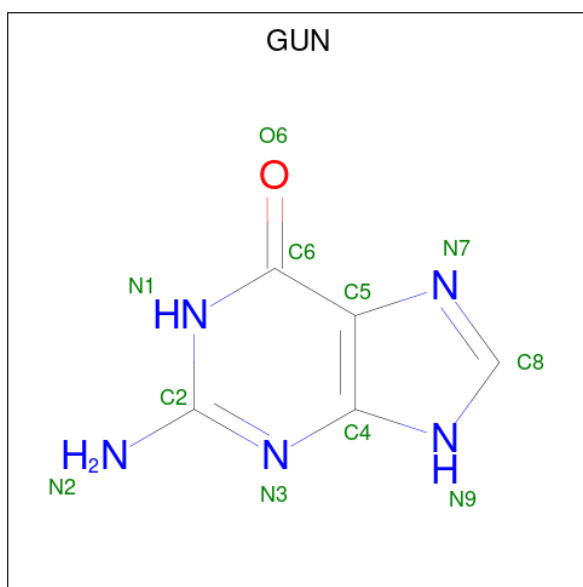
Chain	Residue	Modelled	Actual	Comment	Reference
B	403	GLY	-	expression tag	UNP A0A918H2T3
B	404	SER	-	expression tag	UNP A0A918H2T3
B	405	GLY	-	expression tag	UNP A0A918H2T3
B	406	SER	-	expression tag	UNP A0A918H2T3
B	407	SER	-	expression tag	UNP A0A918H2T3
B	408	HIS	-	expression tag	UNP A0A918H2T3
B	409	HIS	-	expression tag	UNP A0A918H2T3
B	410	HIS	-	expression tag	UNP A0A918H2T3
B	411	HIS	-	expression tag	UNP A0A918H2T3
B	412	HIS	-	expression tag	UNP A0A918H2T3
B	413	HIS	-	expression tag	UNP A0A918H2T3

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



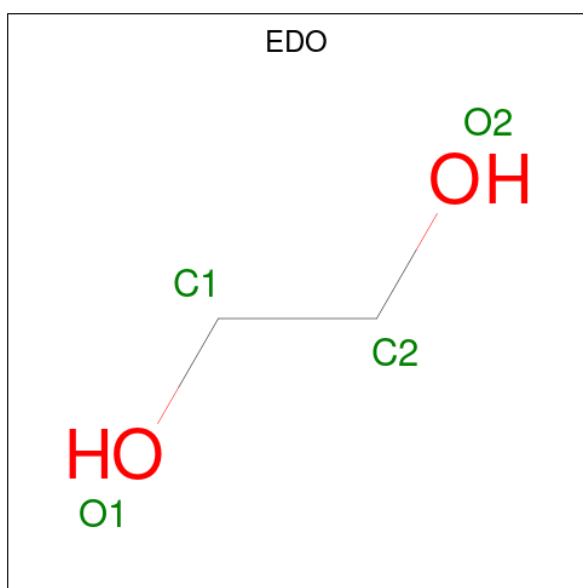
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Fe	H	N	O	0	0
			75	34	1	32	4	4		
2	B	1	Total	C	Fe	H	N	O	0	0
			75	34	1	32	4	4		

- Molecule 3 is GUANINE (CCD ID: GUN) (formula:  $C_5H_5N_5O$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			16	5	5	5	1		
3	B	1	Total	C	H	N	O	0	0
			16	5	5	5	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		

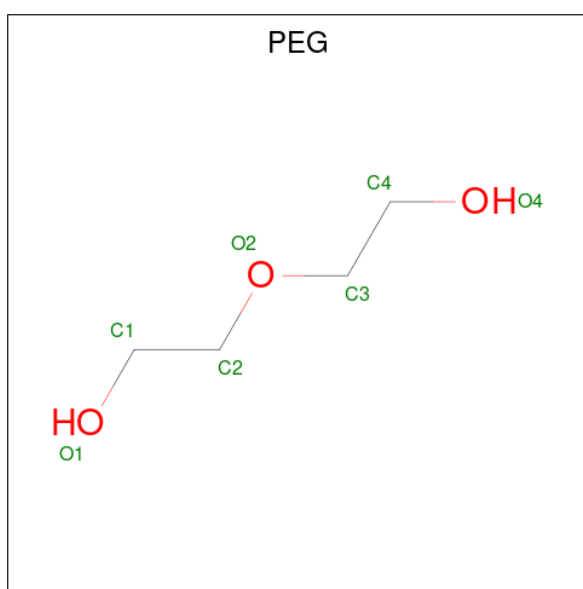
*Continued on next page...*



Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



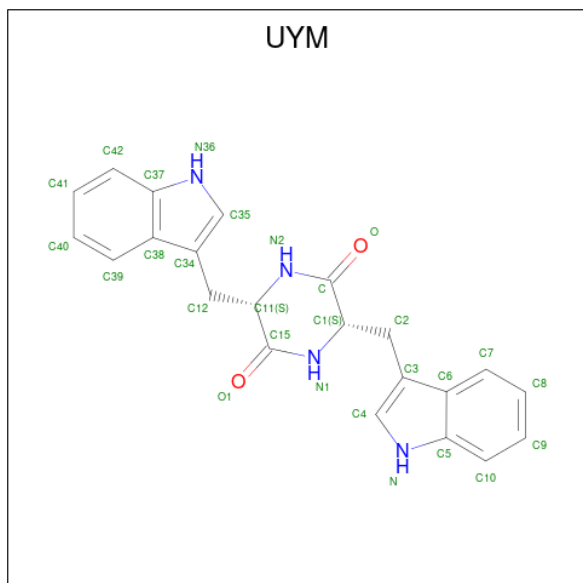
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			17	4	10	3		
5	A	1	Total	C	H	O	0	0
			17	4	10	3		
5	A	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 6 is (3S,6S)-3,6-bis[(1H-indol-3-yl)methyl]piperazine-2,5-dione (CCD ID: UYM) (formula: C<sub>22</sub>H<sub>20</sub>N<sub>4</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	H	N	O	0	0
			48	22	20	4	2		
6	B	1	Total	C	H	N	O	0	0
			48	22	20	4	2		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Cl	0	0
			1	1		
7	B	1	Total	Cl	0	0
			1	1		

- Molecule 8 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	3	Total 3	Mg 3	0	0

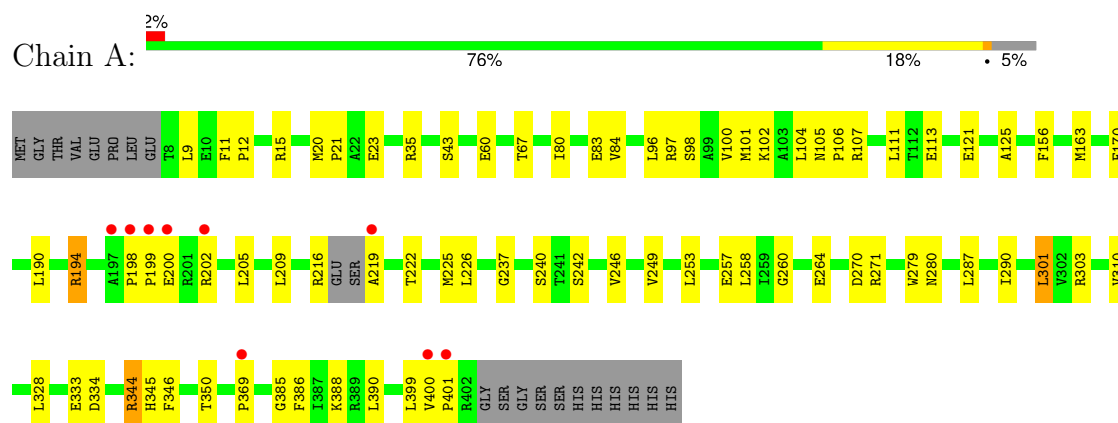
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	183	Total 183	O 183	0	0
9	B	219	Total 219	O 219	0	0

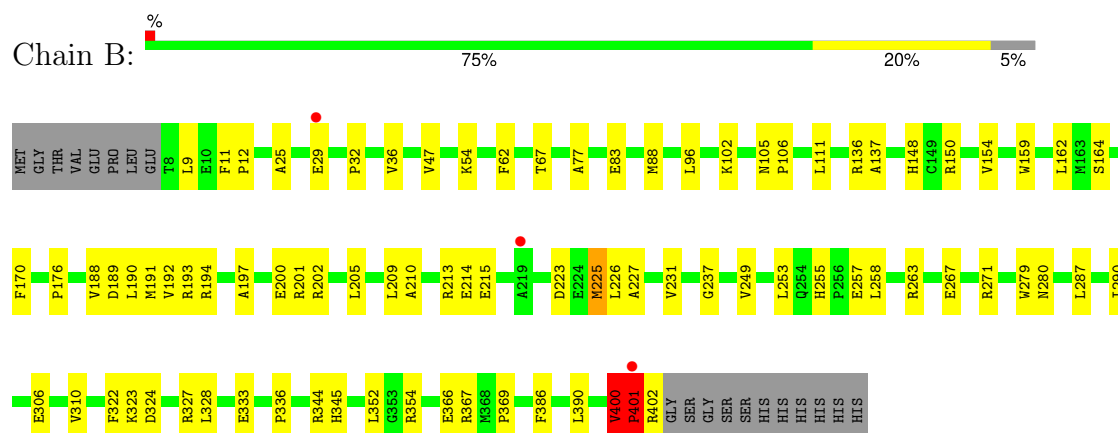
### 3 Residue-property plots [i](#)

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: Cytochrome P450 121



#### • Molecule 1: Cytochrome P450 121



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.29Å 101.32Å 121.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.18 – 2.30 17.18 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.0 (17.18-2.30) 96.6 (17.18-2.30)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.03 (at 2.30Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, $R_{free}$	0.199 , 0.239 0.200 , 0.240	Depositor DCC
$R_{free}$ test set	2000 reflections (3.58%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.8	Xtriage
Anisotropy	0.456	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 63.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7470	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PEG, UYM, EDO, MG, GUN, CL, 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	0.15	0/3135	0.36	0/4262
1	B	0.20	0/3150	0.43	1/4286 (0.0%)
All	All	0.18	0/6285	0.40	1/8548 (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	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	401	PRO	CA-N-CD	-6.30	103.18	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	402	ARG	Sidechain

### 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	3069	0	3106	65	0
1	B	3083	0	3119	73	0
2	A	43	32	30	1	0
2	B	43	32	30	3	0
3	A	11	5	5	0	0
3	B	11	5	5	0	0
4	A	108	162	162	4	0
4	B	84	126	126	13	0
5	A	21	30	30	1	0
5	B	42	60	60	3	0
6	A	28	20	0	0	0
6	B	28	20	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	3	0	0	0	0
9	A	183	0	0	4	0
9	B	219	0	0	3	0
All	All	6978	492	6673	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 10.

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)
1:B:400:VAL:HB	1:B:401:PRO:HD2	1.46	0.96
1:A:96:LEU:HD11	1:A:225[B]:MET:CE	2.12	0.79
1:A:96:LEU:HD11	1:A:225[B]:MET:HE2	1.67	0.77
1:A:105:ASN:HD21	1:A:107:ARG:HH21	1.37	0.71
1:A:100:VAL:O	1:A:104:LEU:HD13	1.93	0.69

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	392/414 (95%)	380 (97%)	11 (3%)	1 (0%)	36	46
1	B	396/414 (96%)	386 (98%)	8 (2%)	2 (0%)	24	31
All	All	788/828 (95%)	766 (97%)	19 (2%)	3 (0%)	30	38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	401	PRO
1	A	369	PRO
1	B	400	VAL

### 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	319/334 (96%)	313 (98%)	6 (2%)	50	69
1	B	321/334 (96%)	313 (98%)	8 (2%)	42	60
All	All	640/668 (96%)	626 (98%)	14 (2%)	47	65

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	105[A]	ASN
1	B	105[B]	ASN
1	B	401	PRO
1	B	280	ASN
1	B	400	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:



Mol	Chain	Res	Type
1	A	86	ASN
1	B	345	HIS

### 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 ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 68 ligands modelled in this entry, 5 are monoatomic - leaving 63 for Mogul analysis.

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	$\# Z  > 2$
4	EDO	B	522	-	3,3,3	0.44	0	2,2,2	0.40	0
4	EDO	B	510	-	3,3,3	0.44	0	2,2,2	0.37	0
5	PEG	B	516	-	6,6,6	0.49	0	5,5,5	0.46	0
4	EDO	A	517	-	3,3,3	0.43	0	2,2,2	0.40	0
4	EDO	B	515	-	3,3,3	0.44	0	2,2,2	0.39	0
4	EDO	A	510	-	3,3,3	0.45	0	2,2,2	0.35	0
4	EDO	A	507	-	3,3,3	0.44	0	2,2,2	0.38	0
4	EDO	B	509	-	3,3,3	0.44	0	2,2,2	0.39	0
4	EDO	B	523	-	3,3,3	0.45	0	2,2,2	0.37	0
4	EDO	B	512	-	3,3,3	0.44	0	2,2,2	0.36	0
4	EDO	A	518	-	3,3,3	0.43	0	2,2,2	0.36	0
4	EDO	A	529	-	3,3,3	0.44	0	2,2,2	0.38	0
6	UYM	B	502	-	32,32,32	1.63	3 (9%)	46,46,46	1.46	4 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	PEG	A	515	-	6,6,6	0.51	0	5,5,5	0.53	0
4	EDO	A	521	-	3,3,3	0.44	0	2,2,2	0.40	0
4	EDO	A	527	-	3,3,3	0.45	0	2,2,2	0.38	0
4	EDO	B	501	-	3,3,3	0.44	0	2,2,2	0.39	0
5	PEG	B	518	-	6,6,6	0.49	0	5,5,5	0.55	0
4	EDO	B	505	-	3,3,3	0.44	0	2,2,2	0.36	0
4	EDO	B	525	-	3,3,3	0.44	0	2,2,2	0.35	0
2	HEM	A	501	1	50,50,50	1.41	5 (10%)	67,82,82	0.76	0
4	EDO	A	519	-	3,3,3	0.44	0	2,2,2	0.39	0
4	EDO	A	505	-	3,3,3	0.44	0	2,2,2	0.37	0
4	EDO	B	528	-	3,3,3	0.44	0	2,2,2	0.37	0
3	GUN	A	502	-	12,12,12	3.72	8 (66%)	15,17,17	2.53	7 (46%)
2	HEM	B	526	1	50,50,50	1.41	5 (10%)	67,82,82	0.77	0
4	EDO	A	528	-	3,3,3	0.44	0	2,2,2	0.32	0
5	PEG	A	532	-	6,6,6	0.50	0	5,5,5	0.49	0
4	EDO	A	514	-	3,3,3	0.44	0	2,2,2	0.32	0
4	EDO	B	508	-	3,3,3	0.44	0	2,2,2	0.38	0
4	EDO	B	511	-	3,3,3	0.44	0	2,2,2	0.37	0
4	EDO	A	533	-	3,3,3	0.43	0	2,2,2	0.39	0
4	EDO	A	524	-	3,3,3	0.44	0	2,2,2	0.37	0
4	EDO	A	525	-	3,3,3	0.43	0	2,2,2	0.37	0
4	EDO	A	530	-	3,3,3	0.44	0	2,2,2	0.38	0
4	EDO	B	504	-	3,3,3	0.43	0	2,2,2	0.37	0
4	EDO	B	506	-	3,3,3	0.45	0	2,2,2	0.39	0
4	EDO	B	520	-	3,3,3	0.44	0	2,2,2	0.36	0
4	EDO	A	504	-	3,3,3	0.44	0	2,2,2	0.42	0
4	EDO	A	526	-	3,3,3	0.44	0	2,2,2	0.37	0
5	PEG	A	516	-	6,6,6	0.50	0	5,5,5	0.46	0
4	EDO	A	506	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	B	521	-	3,3,3	0.45	0	2,2,2	0.32	0
4	EDO	A	520	-	3,3,3	0.45	0	2,2,2	0.39	0
5	PEG	B	513	-	6,6,6	0.50	0	5,5,5	0.36	0
5	PEG	B	517	-	6,6,6	0.49	0	5,5,5	0.57	0
3	GUN	B	503	-	12,12,12	3.74	8 (66%)	15,17,17	2.53	7 (46%)
4	EDO	A	511	-	3,3,3	0.44	0	2,2,2	0.39	0
5	PEG	B	514	-	6,6,6	0.50	0	5,5,5	0.58	0
4	EDO	A	509	-	3,3,3	0.44	0	2,2,2	0.38	0
4	EDO	A	522	-	3,3,3	0.45	0	2,2,2	0.40	0
6	UYM	A	523	-	32,32,32	1.63	3 (9%)	46,46,46	1.47	3 (6%)
4	EDO	B	527	-	3,3,3	0.44	0	2,2,2	0.37	0
4	EDO	A	513	-	3,3,3	0.43	0	2,2,2	0.40	0
4	EDO	A	503	-	3,3,3	0.45	0	2,2,2	0.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	PEG	B	519	-	6,6,6	0.49	0	5,5,5	0.53	0
4	EDO	A	531	-	3,3,3	0.44	0	2,2,2	0.36	0
4	EDO	B	529	-	3,3,3	0.44	0	2,2,2	0.37	0
4	EDO	A	512	-	3,3,3	0.44	0	2,2,2	0.34	0
4	EDO	B	507	-	3,3,3	0.45	0	2,2,2	0.38	0
4	EDO	A	508	-	3,3,3	0.43	0	2,2,2	0.31	0
4	EDO	B	524	-	3,3,3	0.44	0	2,2,2	0.39	0
4	EDO	B	530	-	3,3,3	0.43	0	2,2,2	0.38	0

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
4	EDO	B	522	-	-	1/1/1/1	-
4	EDO	B	510	-	-	1/1/1/1	-
5	PEG	B	516	-	-	3/4/4/4	-
4	EDO	A	517	-	-	1/1/1/1	-
4	EDO	B	515	-	-	0/1/1/1	-
4	EDO	A	510	-	-	1/1/1/1	-
4	EDO	A	507	-	-	0/1/1/1	-
4	EDO	B	509	-	-	0/1/1/1	-
4	EDO	B	523	-	-	1/1/1/1	-
4	EDO	B	512	-	-	1/1/1/1	-
4	EDO	A	518	-	-	0/1/1/1	-
4	EDO	A	529	-	-	1/1/1/1	-
6	UYM	B	502	-	-	0/8/24/24	0/5/5/5
5	PEG	A	515	-	-	2/4/4/4	-
4	EDO	A	521	-	-	0/1/1/1	-
4	EDO	A	527	-	-	0/1/1/1	-
4	EDO	B	501	-	-	0/1/1/1	-
5	PEG	B	518	-	-	3/4/4/4	-
4	EDO	B	505	-	-	1/1/1/1	-
4	EDO	B	525	-	-	0/1/1/1	-
2	HEM	A	501	1	-	3/14/54/54	-
4	EDO	A	519	-	-	1/1/1/1	-
4	EDO	A	505	-	-	1/1/1/1	-
4	EDO	B	528	-	-	0/1/1/1	-
3	GUN	A	502	-	-	-	0/2/2/2
2	HEM	B	526	1	-	3/14/54/54	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	528	-	-	0/1/1/1	-
5	PEG	A	532	-	-	2/4/4/4	-
4	EDO	A	514	-	-	0/1/1/1	-
4	EDO	B	508	-	-	0/1/1/1	-
4	EDO	B	511	-	-	1/1/1/1	-
4	EDO	A	533	-	-	1/1/1/1	-
4	EDO	A	524	-	-	1/1/1/1	-
4	EDO	A	525	-	-	0/1/1/1	-
4	EDO	A	530	-	-	1/1/1/1	-
4	EDO	B	504	-	-	1/1/1/1	-
4	EDO	B	506	-	-	1/1/1/1	-
4	EDO	B	520	-	-	0/1/1/1	-
4	EDO	A	504	-	-	1/1/1/1	-
4	EDO	A	526	-	-	1/1/1/1	-
5	PEG	A	516	-	-	3/4/4/4	-
4	EDO	A	506	-	-	0/1/1/1	-
4	EDO	B	521	-	-	1/1/1/1	-
4	EDO	A	520	-	-	1/1/1/1	-
5	PEG	B	513	-	-	2/4/4/4	-
5	PEG	B	517	-	-	1/4/4/4	-
4	EDO	A	511	-	-	0/1/1/1	-
5	PEG	B	514	-	-	1/4/4/4	-
3	GUN	B	503	-	-	-	0/2/2/2
4	EDO	A	509	-	-	0/1/1/1	-
4	EDO	A	522	-	-	0/1/1/1	-
6	UYM	A	523	-	-	0/8/24/24	0/5/5/5
4	EDO	B	527	-	-	1/1/1/1	-
4	EDO	A	513	-	-	0/1/1/1	-
4	EDO	A	503	-	-	0/1/1/1	-
5	PEG	B	519	-	-	3/4/4/4	-
4	EDO	A	531	-	-	1/1/1/1	-
4	EDO	B	529	-	-	1/1/1/1	-
4	EDO	A	512	-	-	1/1/1/1	-
4	EDO	B	507	-	-	1/1/1/1	-
4	EDO	A	508	-	-	1/1/1/1	-
4	EDO	B	524	-	-	0/1/1/1	-
4	EDO	B	530	-	-	0/1/1/1	-

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	503	GUN	C4-N3	8.68	1.49	1.36

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	GUN	C4-N3	8.63	1.49	1.36
3	B	503	GUN	C2-N3	5.51	1.46	1.33
3	A	502	GUN	C2-N3	5.45	1.46	1.33
6	B	502	UYM	C-N2	5.05	1.41	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	523	UYM	O-C-N2	-5.06	115.97	122.67
3	B	503	GUN	N9-C4-N3	4.87	131.91	125.99
3	A	502	GUN	N9-C4-N3	4.85	131.89	125.99
6	B	502	UYM	O-C-N2	-4.67	116.49	122.67
6	B	502	UYM	O1-C15-N1	-4.45	116.78	122.67

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	HEM	C2B-C3B-CAB-CBB
2	A	501	HEM	C4B-C3B-CAB-CBB
2	B	526	HEM	C2B-C3B-CAB-CBB
2	B	526	HEM	C4B-C3B-CAB-CBB
5	A	516	PEG	O2-C3-C4-O4

There are no ring outliers.

16 monomers are involved in 25 short contacts:

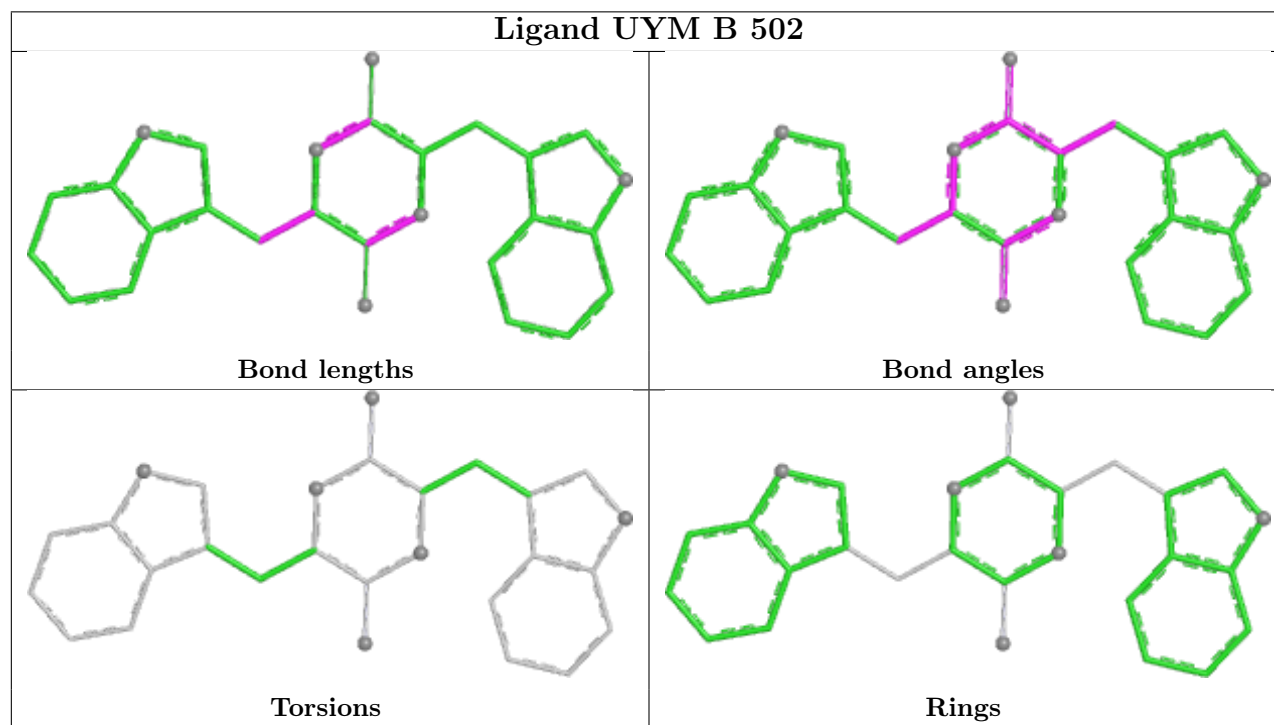
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	515	EDO	1	0
4	B	509	EDO	1	0
4	B	512	EDO	2	0
5	B	518	PEG	2	0
2	A	501	HEM	1	0
4	A	519	EDO	1	0
2	B	526	HEM	3	0
4	A	528	EDO	1	0
5	A	532	PEG	1	0
4	B	508	EDO	3	0
4	B	511	EDO	1	0
4	B	520	EDO	3	0
5	B	513	PEG	1	0

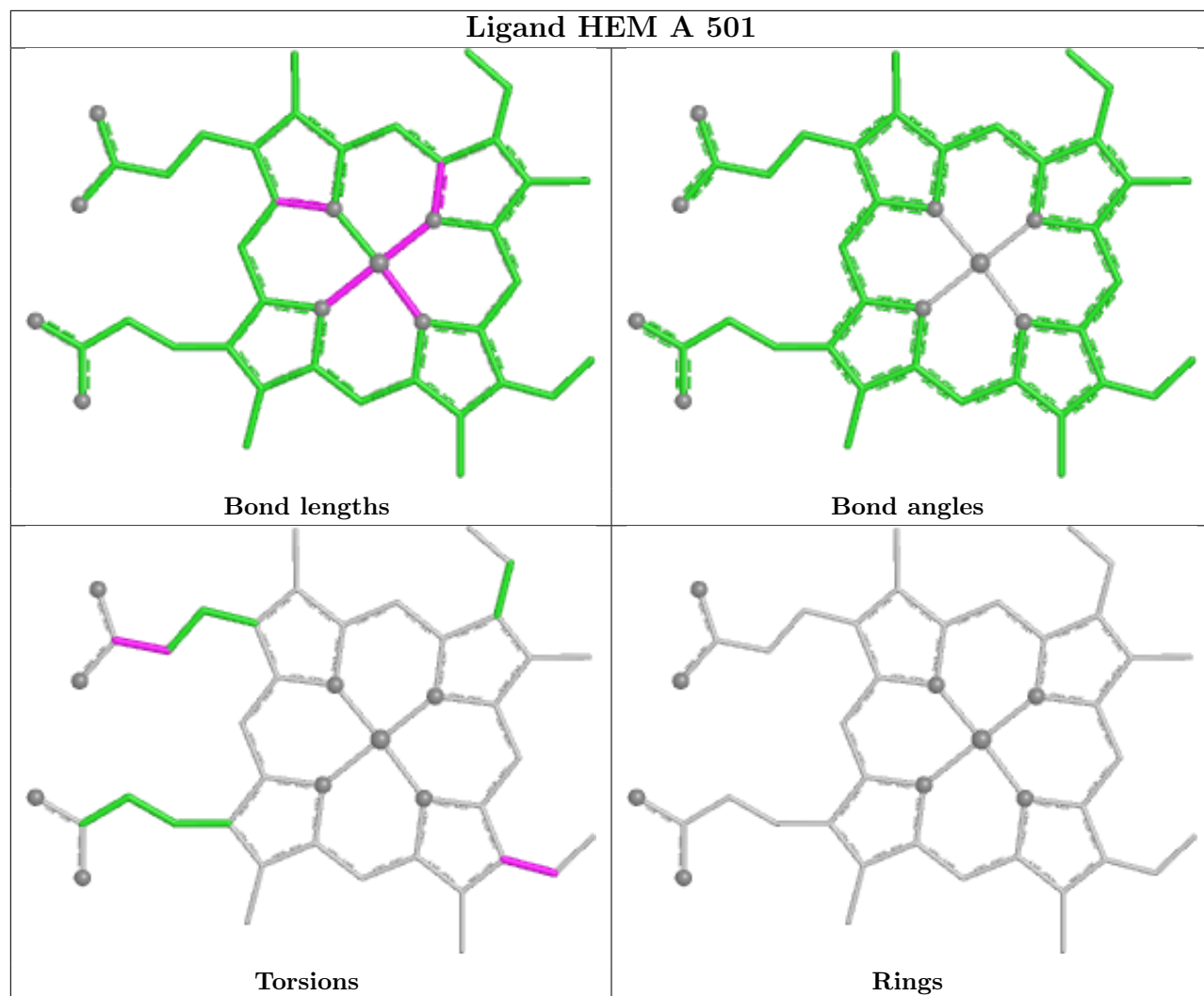
*Continued on next page...*

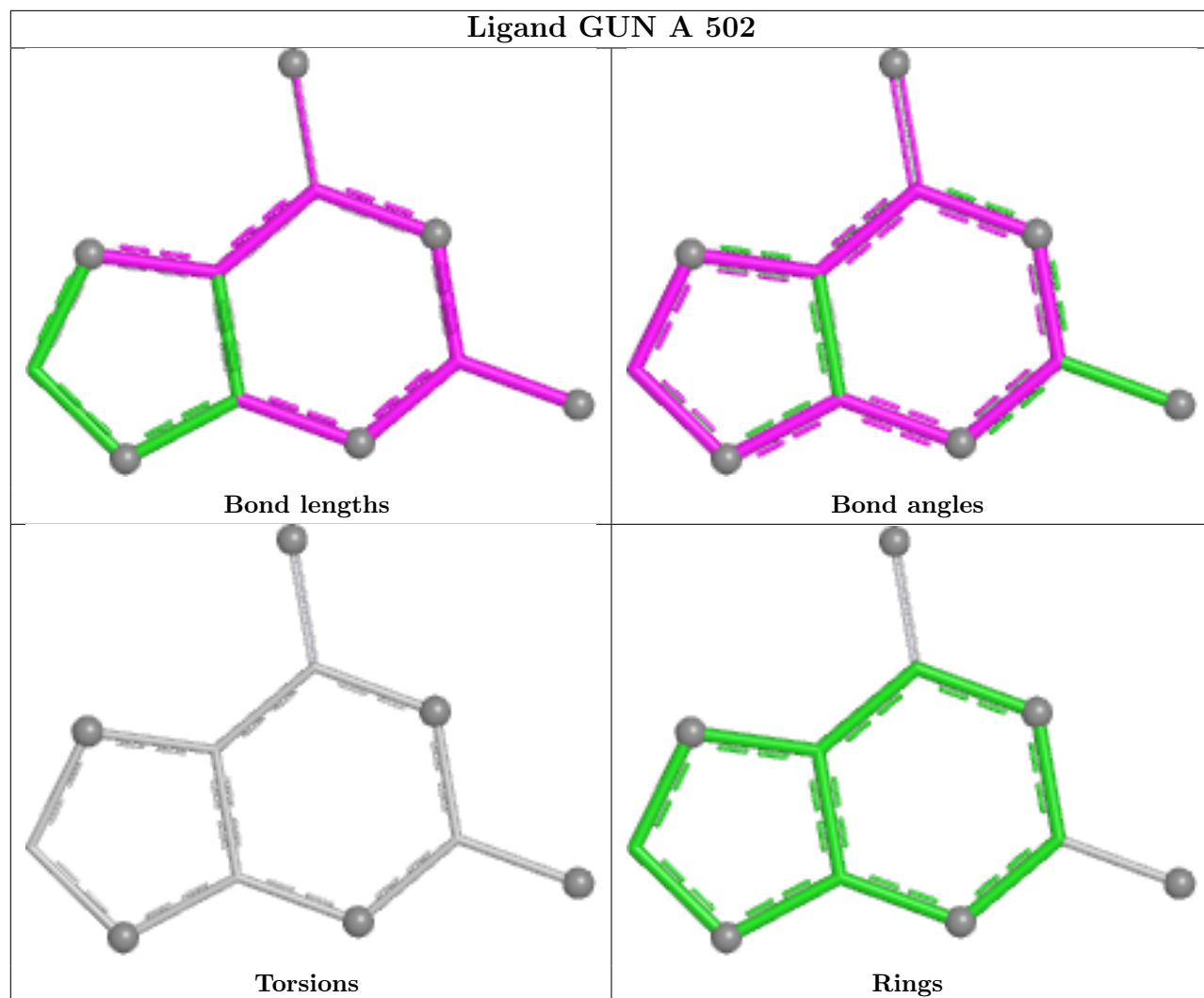
*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	527	EDO	1	0
4	A	503	EDO	2	0
4	B	530	EDO	1	0

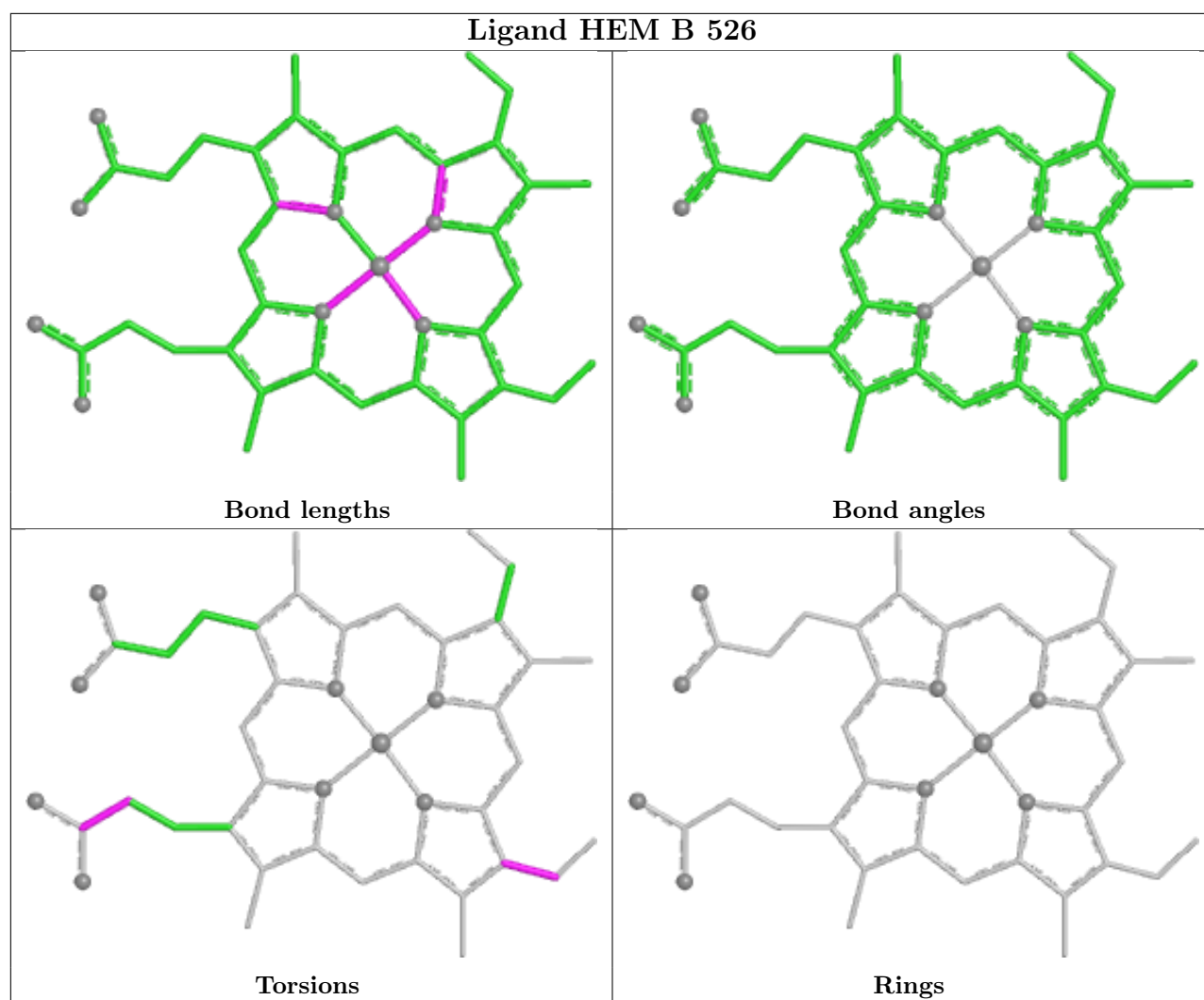
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

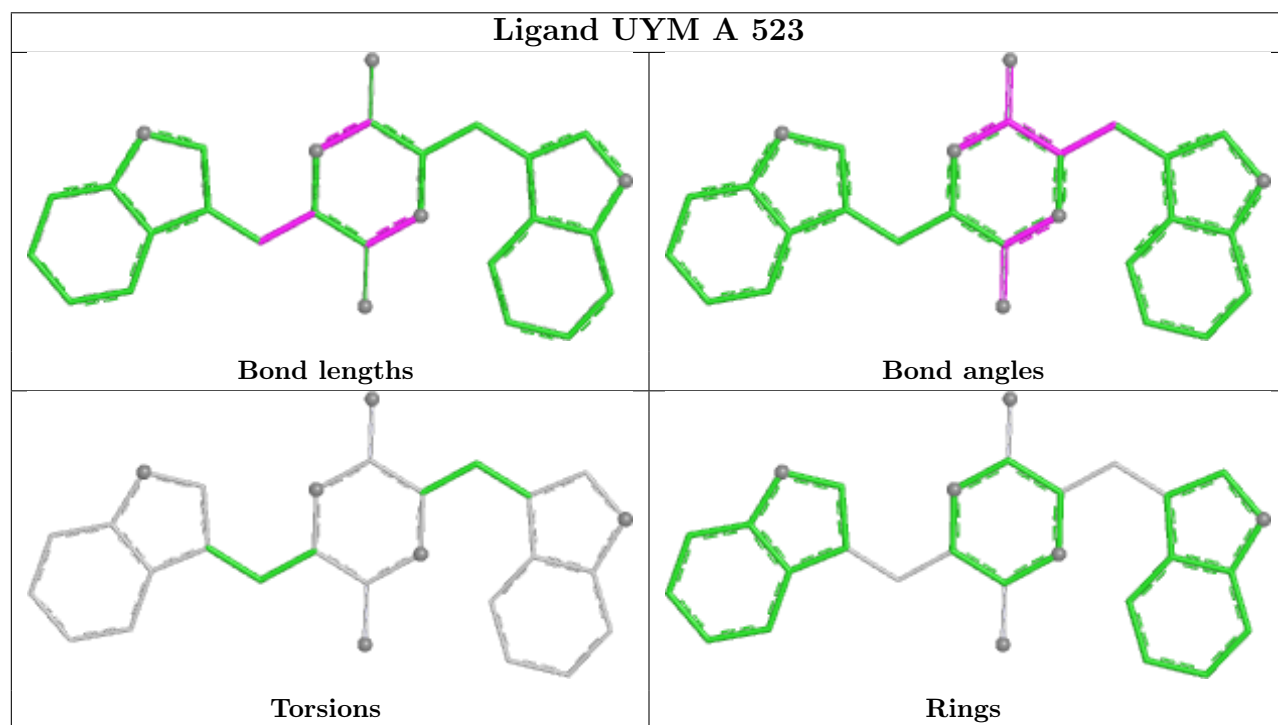
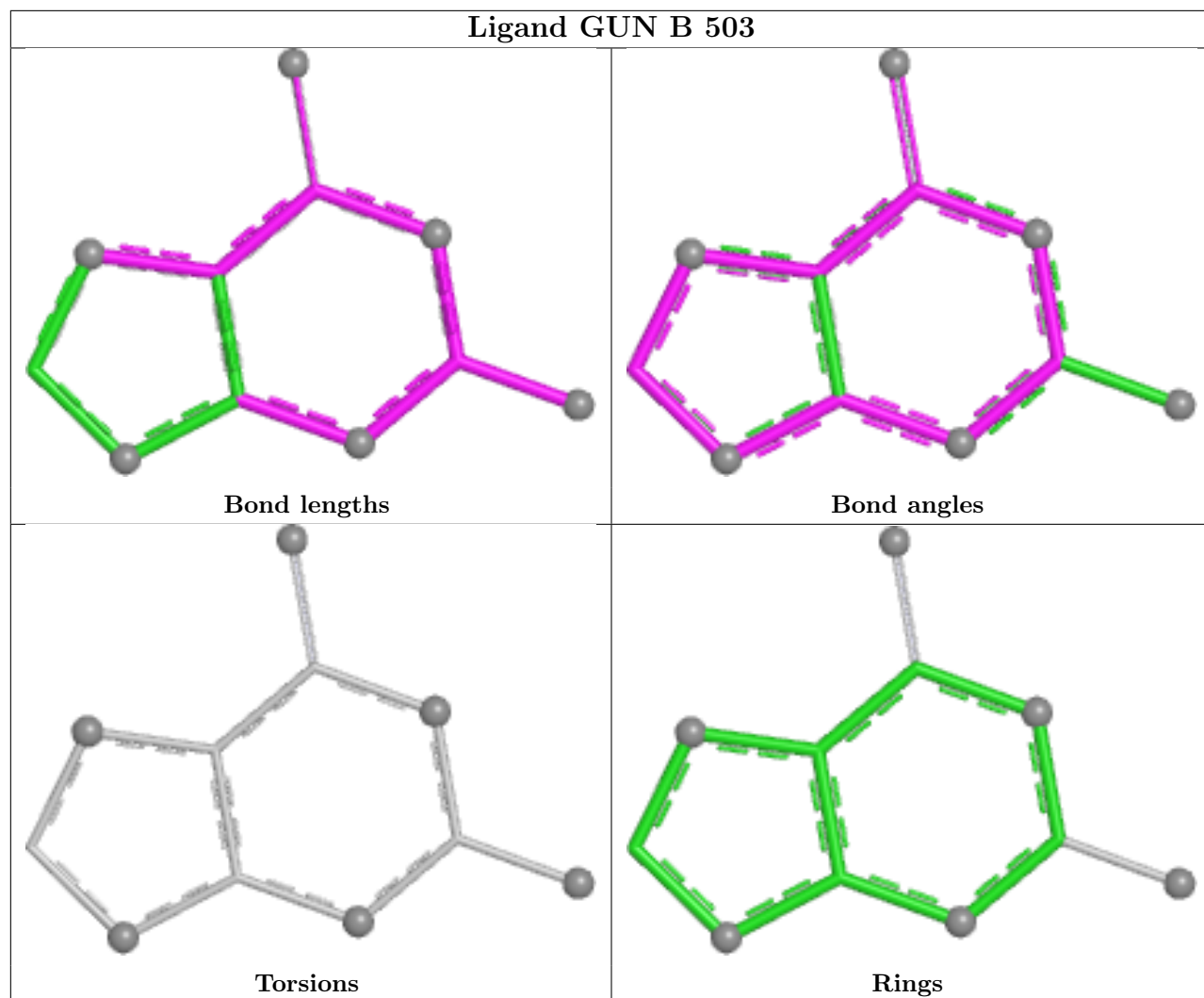












## 5.7 Other polymers [i](#)

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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	393/414 (94%)	0.14	9 (2%) 61 63	14, 32, 59, 116	3 (0%)
1	B	394/414 (95%)	0.01	3 (0%) 82 83	15, 30, 51, 89	2 (0%)
All	All	787/828 (95%)	0.07	12 (1%) 72 73	14, 31, 56, 116	5 (0%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	401	PRO	4.2
1	A	199	PRO	3.5
1	B	29	GLU	3.0
1	A	401	PRO	2.8
1	A	198	PRO	2.8

### 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, 95<sup>th</sup> 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
4	EDO	A	510	4/4	0.38	0.18	48,58,64,65	0
4	EDO	B	520	4/4	0.70	0.13	49,59,63,68	0
4	EDO	A	524	4/4	0.72	0.14	45,54,61,64	0
4	EDO	B	524	4/4	0.72	0.12	33,40,45,54	10
5	PEG	B	519	7/7	0.74	0.15	48,62,65,65	0
4	EDO	A	533	4/4	0.75	0.13	32,39,41,41	10
4	EDO	A	511	4/4	0.75	0.14	47,57,65,71	0
4	EDO	B	505	4/4	0.76	0.13	38,46,47,48	0
5	PEG	B	513	7/7	0.76	0.18	41,49,52,53	17
4	EDO	A	517	4/4	0.76	0.14	28,33,35,36	10
4	EDO	A	520	4/4	0.77	0.10	51,62,64,65	0
5	PEG	A	515	7/7	0.77	0.10	47,56,59,59	17
4	EDO	A	527	4/4	0.77	0.19	37,44,49,53	0
4	EDO	A	530	4/4	0.77	0.14	50,60,61,61	10
4	EDO	A	531	4/4	0.78	0.11	46,56,59,59	0
4	EDO	A	504	4/4	0.78	0.10	38,45,47,47	0
4	EDO	B	527	4/4	0.79	0.14	36,43,49,50	10
4	EDO	B	528	4/4	0.79	0.11	43,51,53,53	10
4	EDO	B	515	4/4	0.79	0.12	42,51,57,57	0
4	EDO	A	509	4/4	0.79	0.13	37,44,47,50	10
5	PEG	B	514	7/7	0.79	0.11	32,39,45,50	0
4	EDO	B	508	4/4	0.79	0.18	40,50,55,66	0
5	PEG	A	532	7/7	0.80	0.12	39,47,50,52	17
4	EDO	A	513	4/4	0.80	0.09	33,40,42,44	10
4	EDO	A	514	4/4	0.81	0.10	44,53,55,59	0
4	EDO	A	522	4/4	0.81	0.12	37,44,45,47	10
4	EDO	A	529	4/4	0.81	0.10	42,50,53,54	10
4	EDO	B	511	4/4	0.82	0.13	45,54,59,63	0
4	EDO	B	522	4/4	0.82	0.11	33,40,45,45	10
4	EDO	B	529	4/4	0.82	0.09	32,39,45,46	10
4	EDO	B	510	4/4	0.82	0.11	37,45,47,49	0
4	EDO	B	504	4/4	0.83	0.10	35,43,44,46	0
4	EDO	A	512	4/4	0.83	0.12	42,50,56,56	0
4	EDO	B	506	4/4	0.83	0.10	39,47,52,58	0
4	EDO	A	503	4/4	0.84	0.14	23,28,30,30	10
4	EDO	A	528	4/4	0.84	0.11	36,43,45,48	10
4	EDO	A	507	4/4	0.84	0.08	35,42,45,50	0
5	PEG	B	517	7/7	0.84	0.12	27,33,42,49	17
4	EDO	B	512	4/4	0.84	0.15	41,50,57,58	0
4	EDO	B	501	4/4	0.85	0.09	54,65,67,68	10
4	EDO	B	509	4/4	0.85	0.15	28,34,36,40	0
4	EDO	B	521	4/4	0.85	0.09	32,39,42,42	10
4	EDO	A	506	4/4	0.85	0.10	33,40,42,44	10

Continued on next page...

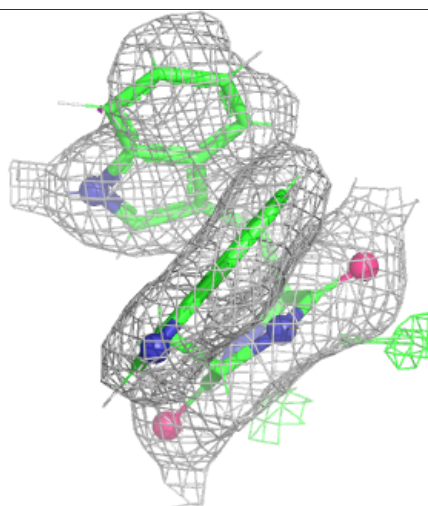
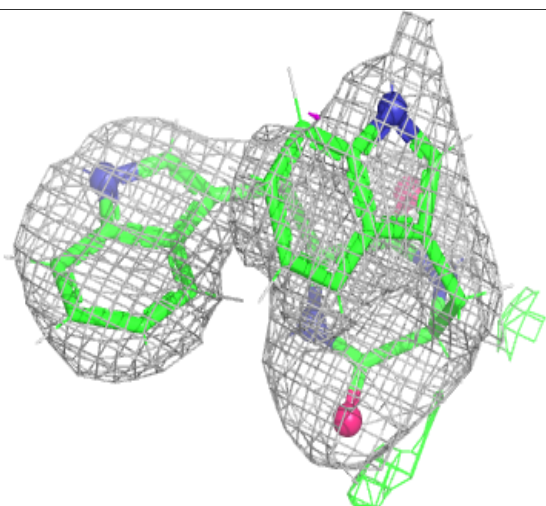
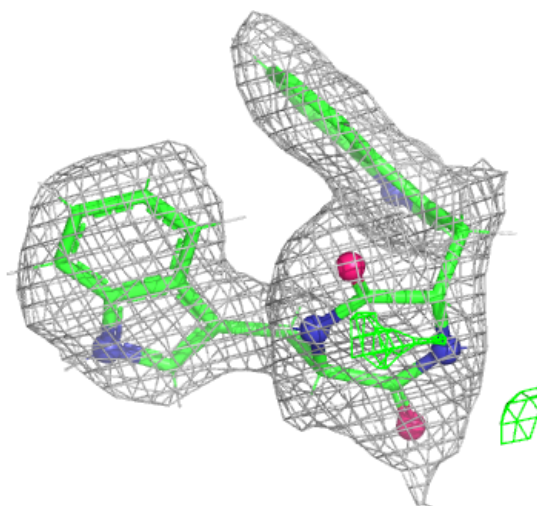
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	B	523	4/4	0.85	0.08	33,39,43,46	10
4	EDO	A	508	4/4	0.85	0.11	37,44,49,50	0
4	EDO	B	525	4/4	0.85	0.08	41,50,53,53	0
4	EDO	A	525	4/4	0.85	0.11	31,37,42,43	10
4	EDO	B	507	4/4	0.86	0.09	36,43,47,51	0
4	EDO	A	519	4/4	0.86	0.12	26,31,34,35	10
4	EDO	A	521	4/4	0.87	0.06	37,45,48,48	10
5	PEG	B	516	7/7	0.87	0.09	35,43,50,57	0
8	MG	A	536	1/1	0.87	0.10	49,49,49,49	0
5	PEG	B	518	7/7	0.88	0.11	22,26,28,28	17
4	EDO	A	505	4/4	0.88	0.08	47,57,62,66	0
4	EDO	B	530	4/4	0.88	0.10	47,56,58,58	0
6	UYM	A	523	28/28	0.89	0.09	25,29,35,36	48
4	EDO	A	518	4/4	0.90	0.13	25,30,31,32	10
4	EDO	A	526	4/4	0.90	0.08	36,43,51,51	0
5	PEG	A	516	7/7	0.90	0.12	29,35,38,40	0
6	UYM	B	502	28/28	0.92	0.07	23,24,29,30	0
8	MG	A	535	1/1	0.93	0.06	51,51,51,51	0
8	MG	A	537	1/1	0.93	0.05	33,33,33,33	0
3	GUN	A	502	11/11	0.94	0.07	24,25,30,31	0
7	CL	A	534	1/1	0.94	0.09	45,45,45,45	0
3	GUN	B	503	11/11	0.94	0.07	22,23,27,27	0
2	HEM	A	501	43/43	0.94	0.10	24,28,35,42	0
2	HEM	B	526	43/43	0.94	0.09	22,24,30,33	0
7	CL	B	531	1/1	0.98	0.13	36,36,36,36	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.

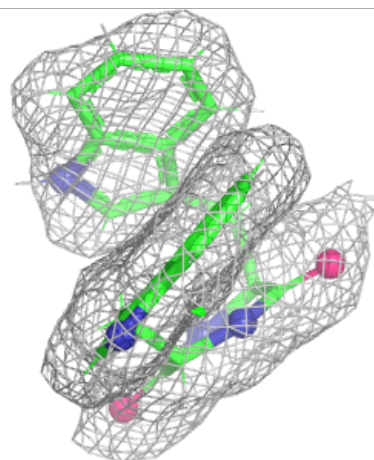
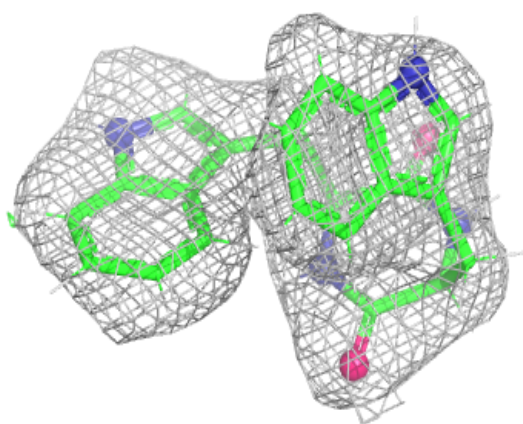
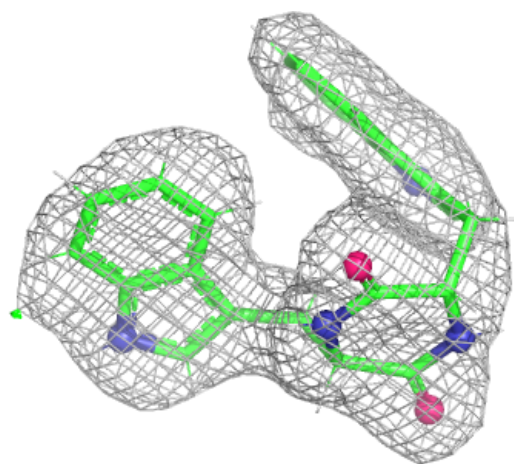
**Electron density around UYM A 523:**

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



**Electron density around UYM B 502:**

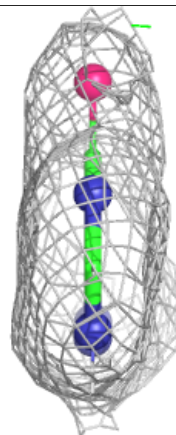
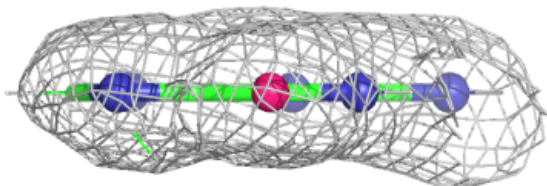
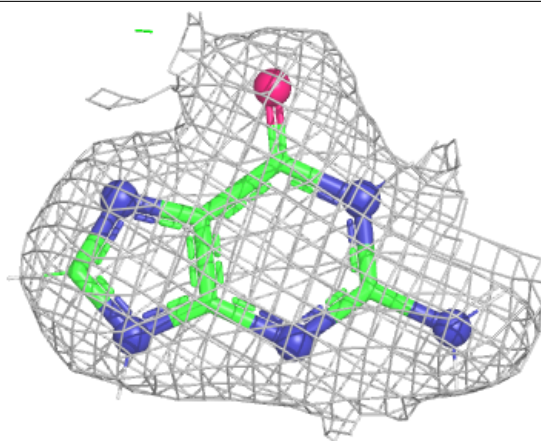
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





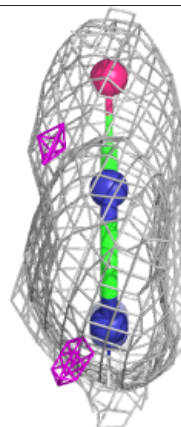
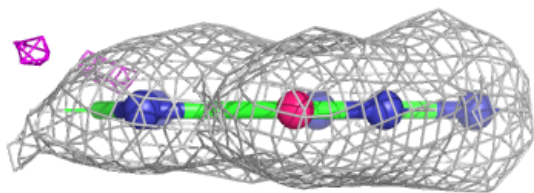
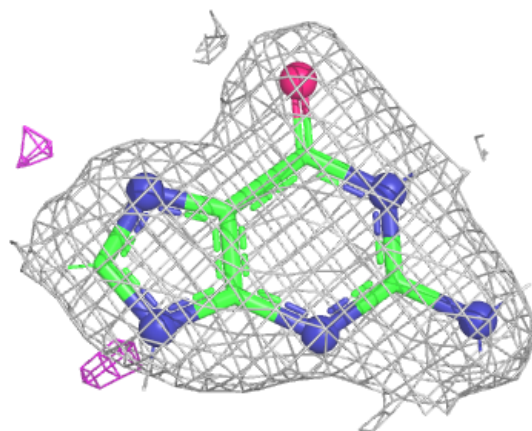
**Electron density around GUN A 502:**

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



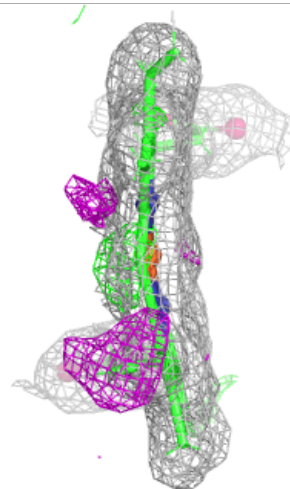
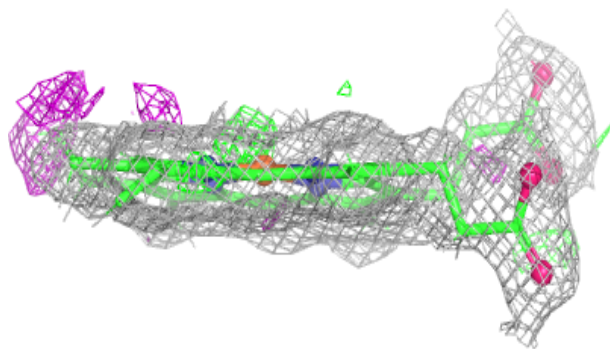
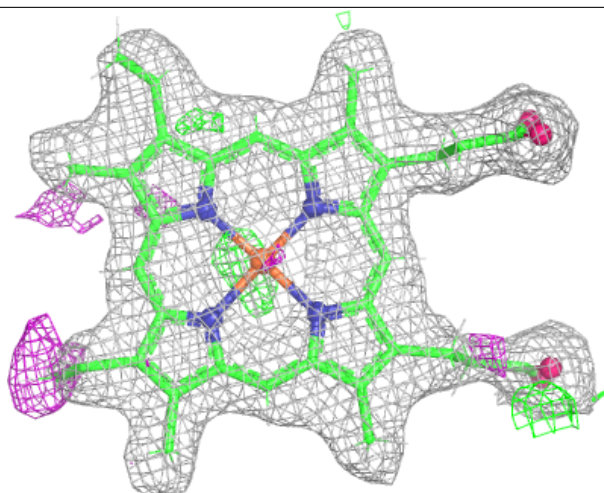
**Electron density around GUN B 503:**

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



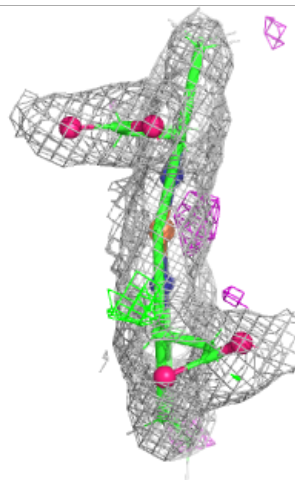
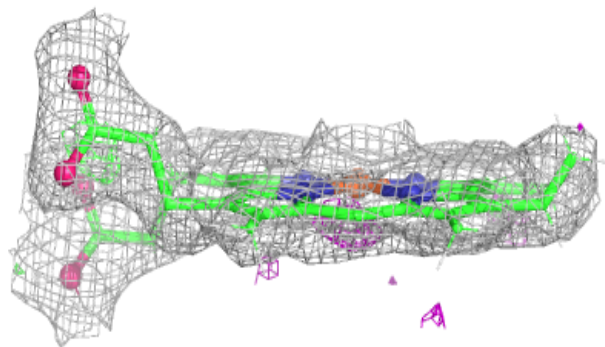
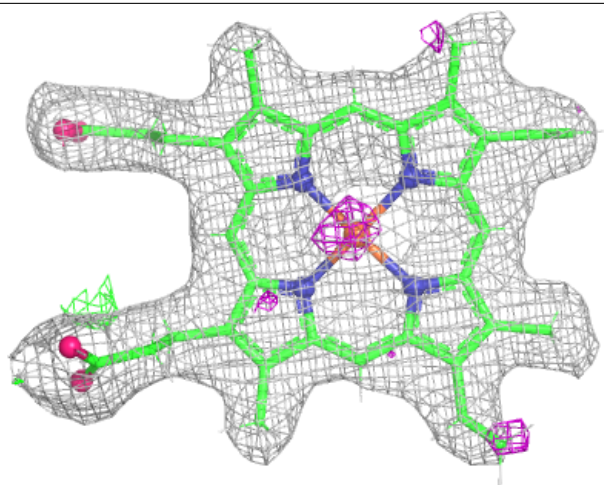
**Electron density around HEM A 501:**

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



**Electron density around HEM B 526:**

$2mF_o-DF_c$  (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.