



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 21, 2021 – 06:03 PM EST

PDB ID : 6P5Z  
Title : Cobalt-sirohydrochlorin-bound *S. typhimurium* siroheme synthase  
Authors : Pennington, J.M.; Stroupe, M.E.  
Deposited on : 2019-05-31  
Resolution : 2.26 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](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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.25  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.25

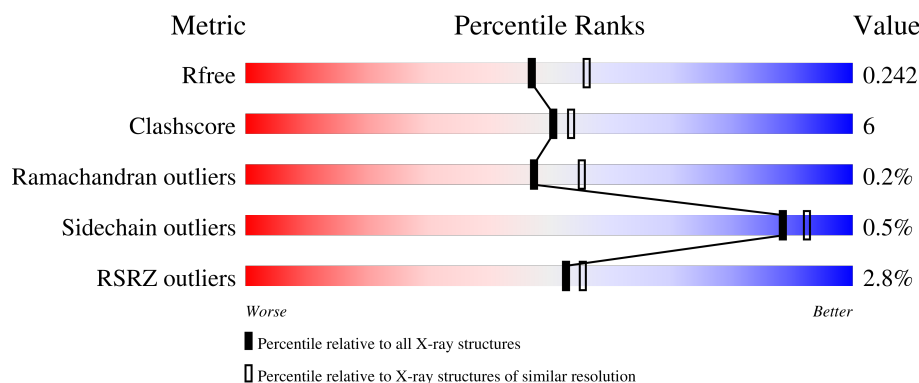
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 2.26 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))
$R_{free}$	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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	457	
1	B	457	

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	F0X	A	502	X	-	-	-
3	F0X	A	503	X	-	-	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7160 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

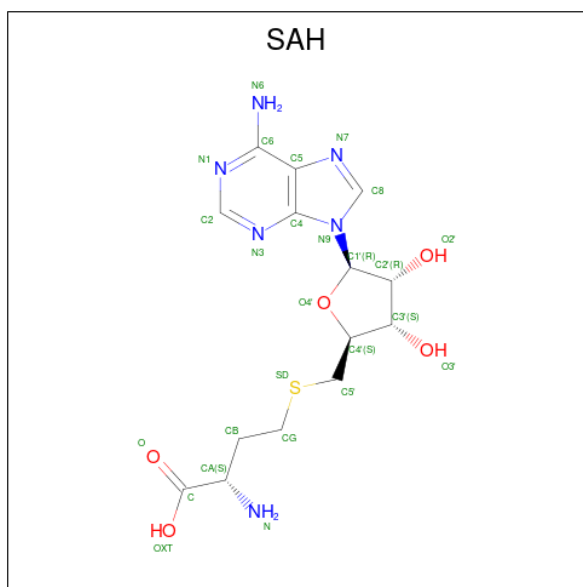
- Molecule 1 is a protein called Siroheme synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	450	Total	C	N	O	S	0	2	0
			3487	2197	627	647	16			
1	B	446	Total	C	N	O	S	0	1	0
			3440	2166	618	640	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	128	ALA	SER	conflict	UNP A0A3V0JC15
B	128	ALA	SER	conflict	UNP A0A3V0JC15

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula:  $C_{14}H_{20}N_6O_5S$ ).



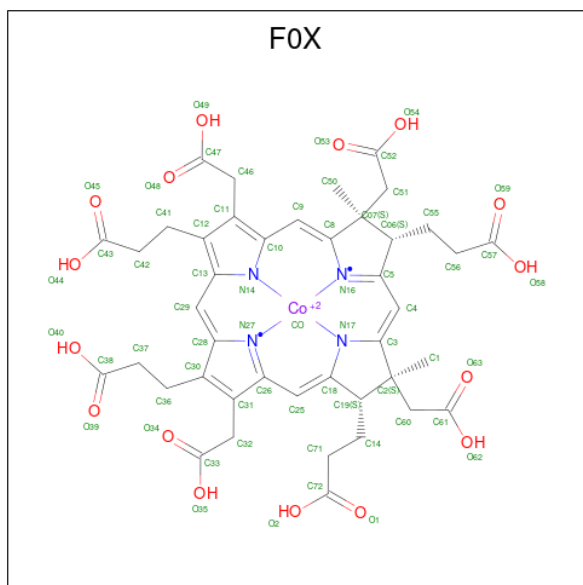
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 3 is cobalt-sirohydrochlorin (three-letter code: F0X) (formula:  $C_{42}H_{44}CoN_4O_{16}$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Co	N	O	0	0
			63	42	1	4	16		
3	A	1	Total	C	Co	N	O	0	0
			63	42	1	4	16		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula:  $Cl$ ).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	29	Total	O	0	0
			29	29		

Continued on next page...

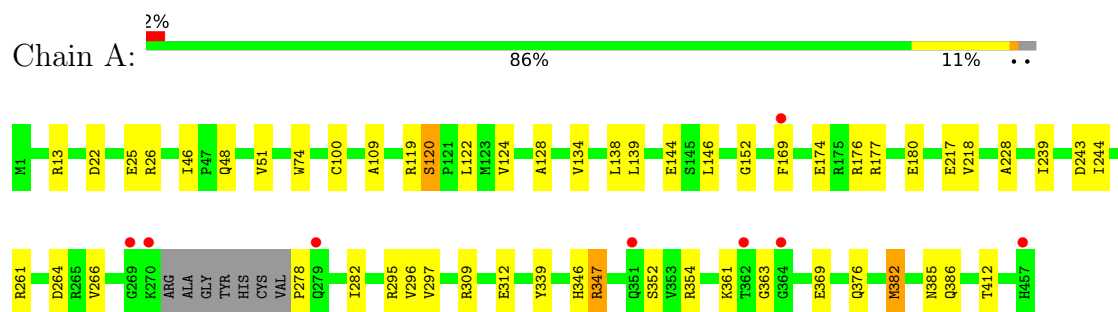
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	24	Total	O	0	0
			24	24		

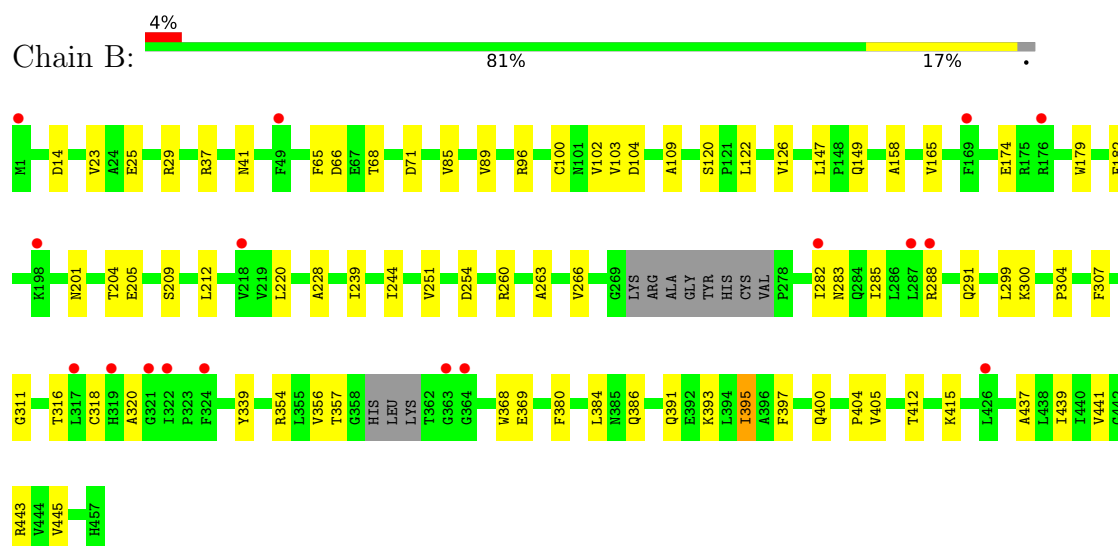
### 3 Residue-property plots [i](#)

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: Siroheme synthase



#### • Molecule 1: Siroheme synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.60Å 100.45Å 146.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.34 – 2.26 48.38 – 2.26	Depositor EDS
% Data completeness (in resolution range)	98.9 (35.34-2.26) 94.8 (48.38-2.26)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.48 (at 2.27Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, $R_{free}$	0.179 , 0.242 0.179 , 0.242	Depositor DCC
$R_{free}$ test set	1998 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.8	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 49.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7160	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% 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: SAH, CL, F0X

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	0.40	0/3543	0.58	0/4793
1	B	0.38	0/3494	0.56	0/4728
All	All	0.39	0/7037	0.57	0/9521

There are no bond length outliers.

There are no bond angle outliers.

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	3487	0	3532	38	0
1	B	3440	0	3480	49	0
2	A	26	0	19	0	0
2	B	26	0	19	0	0
3	A	126	0	0	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	29	0	0	2	0
5	B	24	0	0	1	0
All	All	7160	0	7050	80	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 6.

All (80) 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:A:244:ILE:HD11	1:A:266:VAL:HG23	1.60	0.84
1:B:283:ASN:HB3	1:B:316:THR:HG21	1.69	0.74
1:A:352:SER:HB3	1:B:356:VAL:HG12	1.68	0.73
1:A:169:PHE:HB3	1:A:174:GLU:HG3	1.70	0.72
1:B:400:GLN:OE1	1:B:443:ARG:NH2	2.23	0.70
1:B:102:VAL:HG23	1:B:109:ALA:HB2	1.71	0.70
1:B:405:VAL:HG23	1:B:441:VAL:HG22	1.74	0.68
1:A:385:ASN:ND2	3:A:503:F0X:O63	2.27	0.66
1:B:228:ALA:HB2	1:B:254:ASP:HB3	1.79	0.64
1:B:288:ARG:HA	1:B:291:GLN:HB2	1.80	0.63
1:A:346:HIS:HD2	1:B:311:GLY:HA3	1.64	0.62
1:B:201:ASN:HA	1:B:204:THR:HB	1.84	0.60
1:A:180:GLU:OE2	1:A:295:ARG:NH2	2.36	0.58
1:B:307:PHE:CE2	1:B:357:THR:HG23	2.40	0.57
1:B:384:LEU:HD11	1:B:437:ALA:HB3	1.87	0.56
1:A:139:LEU:HD21	1:B:147:LEU:HD21	1.87	0.56
1:A:124:VAL:HG22	1:B:126:VAL:HG22	1.86	0.56
1:B:368:TRP:CE2	1:B:393:LYS:HG2	2.41	0.55
1:B:300:LYS:HD3	1:B:304:PRO:HB3	1.88	0.55
1:A:309:ARG:HG2	1:A:312:GLU:OE1	2.07	0.55
1:A:176:ARG:HH12	1:A:243:ASP:CG	2.10	0.54
1:A:100:CYS:O	1:A:109:ALA:HB1	2.09	0.52
1:A:120:SER:O	1:A:120:SER:OG	2.22	0.52
1:A:228:ALA:HB3	1:B:149:GLN:HG3	1.92	0.52
1:A:244:ILE:HD12	1:A:264:ASP:O	2.08	0.52
1:B:354:ARG:HG3	1:B:356:VAL:HG13	1.91	0.52
1:B:369:GLU:HG2	1:B:397:PHE:CD2	2.45	0.51
1:B:282:ILE:HA	1:B:285:ILE:HD12	1.91	0.51
1:A:369:GLU:HG2	5:A:618:HOH:O	2.10	0.51
1:A:354:ARG:HG2	1:B:354:ARG:HD3	1.92	0.51
1:B:251:VAL:HG11	1:B:299:LEU:HD13	1.93	0.50
1:A:176:ARG:NH1	1:A:243:ASP:OD2	2.41	0.50
1:B:239:ILE:HD11	1:B:299:LEU:HD21	1.92	0.50
1:A:176:ARG:HG2	1:A:177:ARG:N	2.28	0.49
1:B:368:TRP:CD2	1:B:393:LYS:HG2	2.47	0.49
1:B:85:VAL:O	1:B:89:VAL:HG23	2.13	0.48
1:B:369:GLU:HG2	1:B:397:PHE:CE2	2.49	0.48
1:B:41:ASN:OD1	1:B:65:PHE:HA	2.14	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:ASP:OD1	1:B:37:ARG:HD2	2.14	0.47
1:B:391:GLN:O	1:B:395:ILE:HG22	2.14	0.47
1:B:100:CYS:O	1:B:109:ALA:HB1	2.15	0.47
1:B:260:ARG:HB3	1:B:263:ALA:HB2	1.96	0.47
1:B:339:TYR:CD2	1:B:412:THR:HA	2.50	0.47
1:B:165:VAL:HG11	1:B:179:TRP:CZ2	2.50	0.46
1:A:119:ARG:HB2	1:A:122:LEU:HB3	1.98	0.46
1:B:356:VAL:HG23	1:B:380:PHE:HA	1.97	0.46
1:A:239:ILE:HG22	1:A:297:VAL:HG11	1.98	0.46
1:A:22:ASP:O	1:A:26:ARG:HG3	2.16	0.45
1:B:174:GLU:HG3	1:B:212:LEU:HD11	1.98	0.45
1:A:134:VAL:O	1:A:138:LEU:HG	2.16	0.45
1:B:102:VAL:HG12	1:B:104:ASP:OD1	2.17	0.45
1:B:404:PRO:HB2	1:B:445:VAL:HB	1.98	0.44
1:A:382:MET:HB3	3:A:503:F0X:C50	2.47	0.44
1:B:244:ILE:HD11	1:B:266:VAL:HG23	1.99	0.44
1:A:354:ARG:HD2	1:A:376:GLN:OE1	2.18	0.44
1:A:261:ARG:NH1	5:A:601:HOH:O	2.46	0.43
1:B:220:LEU:HA	1:B:220:LEU:HD23	1.75	0.43
1:A:339:TYR:CD2	1:A:412:THR:HA	2.53	0.43
1:B:66:ASP:OD1	1:B:68:THR:OG1	2.37	0.42
1:A:278:PRO:O	1:A:282:ILE:HG13	2.19	0.42
1:B:158:ALA:HB2	1:B:182:PHE:CE2	2.54	0.42
1:A:25:GLU:HB2	1:A:46:ILE:HD11	2.01	0.42
1:B:25:GLU:OE1	1:B:29:ARG:NH1	2.52	0.42
1:B:205:GLU:O	1:B:209:SER:OG	2.30	0.42
1:A:361:LYS:O	1:A:363:GLY:N	2.52	0.41
1:A:48:GLN:HA	1:A:51:VAL:HG22	2.02	0.41
1:A:144:GLU:C	1:A:146:LEU:H	2.23	0.41
1:A:346:HIS:O	1:A:347:ARG:C	2.58	0.41
1:B:147:LEU:HD23	1:B:147:LEU:HA	1.85	0.41
1:B:380:PHE:HB2	1:B:439:ILE:HB	2.02	0.41
1:A:218:VAL:HA	1:A:296:VAL:HG13	2.02	0.41
1:A:217:GLU:HG2	1:A:295:ARG:HG2	2.01	0.41
1:A:119:ARG:O	1:A:152:GLY:HA3	2.21	0.41
1:A:13:ARG:HB3	1:A:74:TRP:CD1	2.56	0.41
1:B:318:CYS:C	1:B:320:ALA:H	2.25	0.41
1:A:386:GLN:OE1	1:A:386:GLN:HA	2.20	0.41
1:B:71:ASP:OD1	1:B:96:ARG:NH1	2.53	0.41
1:B:23:VAL:CG1	1:B:103:VAL:HG11	2.51	0.40
1:B:386:GLN:NE2	5:B:601:HOH:O	2.50	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:ALA:HA	1:B:122:LEU:HA	2.04	0.40

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	448/457 (98%)	433 (97%)	13 (3%)	2 (0%)	34	37
1	B	441/457 (96%)	426 (97%)	15 (3%)	0	100	100
All	All	889/914 (97%)	859 (97%)	28 (3%)	2 (0%)	47	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	347	ARG
1	A	120	SER

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	369/372 (99%)	368 (100%)	1 (0%)	92	95
1	B	364/372 (98%)	361 (99%)	3 (1%)	81	88
All	All	733/744 (98%)	729 (100%)	4 (0%)	88	92

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	382	MET
1	B	120	SER
1	B	395	ILE
1	B	415	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\# Z  > 2$
2	SAH	A	501	-	21,28,28	1.19	2 (9%)	20,40,40	1.46	1 (5%)
2	SAH	B	501	-	21,28,28	1.30	2 (9%)	20,40,40	1.67	3 (15%)
3	F0X	A	502	1	38,70,70	2.51	13 (34%)	43,112,112	3.07	18 (41%)
3	F0X	A	503	1	38,70,70	2.63	15 (39%)	43,112,112	3.27	18 (41%)

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
3	F0X	A	503	1	2/2/19/23	9/22/126/126	-
2	SAH	A	501	-	-	0/7/31/31	0/3/3/3
3	F0X	A	502	1	2/2/19/23	11/22/126/126	-
2	SAH	B	501	-	-	1/7/31/31	0/3/3/3

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	503	F0X	C31-C30	9.24	1.48	1.37
3	A	502	F0X	C31-C30	8.74	1.48	1.37
3	A	503	F0X	C9-C8	7.46	1.48	1.35
3	A	502	F0X	C9-C8	7.04	1.47	1.35
2	B	501	SAH	C2-N3	4.31	1.39	1.32
3	A	503	F0X	C11-C12	3.84	1.48	1.39
2	A	501	SAH	C2-N3	3.77	1.38	1.32
3	A	502	F0X	C11-C12	3.56	1.47	1.39
3	A	503	F0X	C4-C5	3.43	1.48	1.39
3	A	503	F0X	C4-C3	3.39	1.48	1.38
3	A	502	F0X	C4-C5	3.17	1.48	1.39
3	A	502	F0X	C4-C3	3.15	1.48	1.38
2	B	501	SAH	C2-N1	2.93	1.39	1.33
3	A	503	F0X	C30-C28	2.89	1.49	1.42
3	A	502	F0X	C30-C28	2.85	1.49	1.42
3	A	502	F0X	CO-N14	2.80	2.10	1.97
3	A	502	F0X	C13-C29	2.73	1.48	1.41
3	A	502	F0X	C10-C9	2.69	1.48	1.41
3	A	503	F0X	C26-C25	2.68	1.48	1.41
3	A	502	F0X	C26-C25	2.66	1.48	1.41
3	A	503	F0X	C13-C29	2.62	1.48	1.41
3	A	503	F0X	C07-C06	-2.61	1.48	1.55
3	A	503	F0X	CO-N27	2.60	2.09	1.97
3	A	503	F0X	CO-N14	2.54	2.09	1.97
3	A	503	F0X	C10-C9	2.50	1.47	1.41
3	A	502	F0X	CO-N27	2.49	2.09	1.97
2	A	501	SAH	C2-N1	2.48	1.38	1.33
3	A	503	F0X	C2-C19	-2.42	1.48	1.55
3	A	502	F0X	C2-C19	-2.36	1.48	1.55
3	A	503	F0X	C5-N16	2.19	1.36	1.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	503	F0X	C19-C18	-2.04	1.47	1.51
3	A	502	F0X	C07-C06	-2.03	1.49	1.55

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	F0X	C55-C06-C5	13.35	134.73	111.19
3	A	502	F0X	C55-C06-C5	9.37	127.71	111.19
3	A	503	F0X	C07-C06-C5	8.10	111.27	100.90
3	A	502	F0X	C07-C06-C5	6.78	109.58	100.90
3	A	502	F0X	C07-C8-C9	-6.21	117.87	123.54
3	A	502	F0X	C07-C8-N16	5.99	118.61	111.38
2	B	501	SAH	N3-C2-N1	-5.46	120.14	128.68
2	A	501	SAH	N3-C2-N1	-5.38	120.27	128.68
3	A	503	F0X	C07-C8-N16	5.31	117.78	111.38
3	A	502	F0X	C51-C07-C06	5.25	122.46	108.39
3	A	503	F0X	C07-C8-C9	-5.17	118.83	123.54
3	A	502	F0X	C2-C3-C4	-5.02	116.83	123.37
3	A	502	F0X	C2-C3-N17	4.72	118.79	111.74
3	A	502	F0X	C37-C36-C30	-4.40	104.36	112.48
3	A	503	F0X	C51-C07-C06	4.24	119.76	108.39
3	A	503	F0X	C42-C41-C12	-4.00	105.11	112.49
3	A	503	F0X	C2-C3-N17	3.95	117.64	111.74
3	A	503	F0X	C2-C3-C4	-3.57	118.72	123.37
3	A	503	F0X	C31-C32-C33	-3.49	109.17	115.96
3	A	503	F0X	C50-C07-C06	-3.23	106.11	112.08
3	A	502	F0X	C41-C42-C43	-3.17	107.35	112.67
3	A	502	F0X	C46-C11-C10	3.15	132.14	127.36
3	A	503	F0X	C47-C46-C11	-3.11	109.92	115.96
3	A	502	F0X	C55-C06-C07	3.04	122.51	114.14
3	A	503	F0X	C06-C07-C8	-2.94	95.88	100.92
3	A	502	F0X	C1-C2-C60	2.92	115.58	110.77
3	A	502	F0X	C06-C07-C8	-2.92	95.91	100.92
2	B	501	SAH	C5'-SD-CG	-2.88	93.62	102.27
3	A	502	F0X	C50-C07-C06	-2.83	106.84	112.08
3	A	503	F0X	C51-C07-C8	2.82	115.98	107.12
3	A	503	F0X	C1-C2-C60	2.56	114.98	110.77
3	A	503	F0X	C4-C5-N16	-2.52	122.84	125.73
3	A	502	F0X	C4-C5-N16	-2.46	122.91	125.73
3	A	502	F0X	C1-C2-C19	2.38	116.47	112.08
3	A	502	F0X	C26-C25-C18	-2.37	125.43	130.12
3	A	503	F0X	C06-C5-C4	2.26	128.20	123.32

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	F0X	C26-C25-C18	-2.15	125.86	130.12
2	B	501	SAH	C3'-C2'-C1'	2.15	104.21	100.98
3	A	503	F0X	C10-C9-C8	-2.11	125.94	130.12
3	A	502	F0X	C32-C31-C30	2.02	130.09	126.49

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	502	F0X	C19
3	A	502	F0X	C06
3	A	503	F0X	C19
3	A	503	F0X	C06

All (21) torsion outliers are listed below:

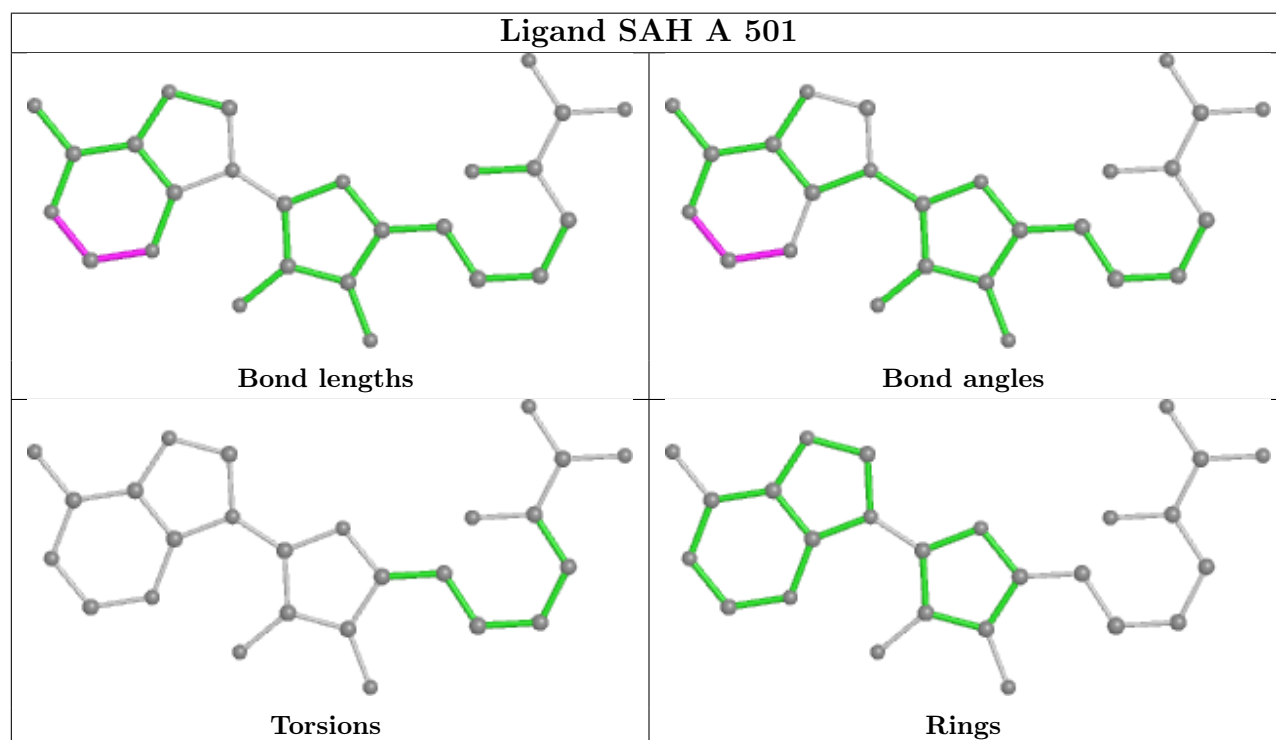
Mol	Chain	Res	Type	Atoms
3	A	502	F0X	C19-C2-C60-C61
3	A	502	F0X	C1-C2-C60-C61
3	A	502	F0X	C3-C2-C60-C61
3	A	502	F0X	C12-C41-C42-C43
3	A	502	F0X	C8-C07-C51-C52
3	A	502	F0X	C50-C07-C51-C52
3	A	502	F0X	C07-C06-C55-C56
3	A	502	F0X	C06-C55-C56-C57
3	A	503	F0X	C19-C2-C60-C61
3	A	503	F0X	C1-C2-C60-C61
3	A	503	F0X	C3-C2-C60-C61
3	A	503	F0X	C8-C07-C51-C52
3	A	503	F0X	C50-C07-C51-C52
3	A	503	F0X	C07-C06-C55-C56
3	A	503	F0X	C19-C14-C71-C72
3	A	503	F0X	C06-C55-C56-C57
3	A	502	F0X	C19-C14-C71-C72
3	A	502	F0X	C71-C14-C19-C2
2	B	501	SAH	C3'-C4'-C5'-SD
3	A	503	F0X	C71-C14-C19-C18
3	A	502	F0X	C10-C11-C46-C47

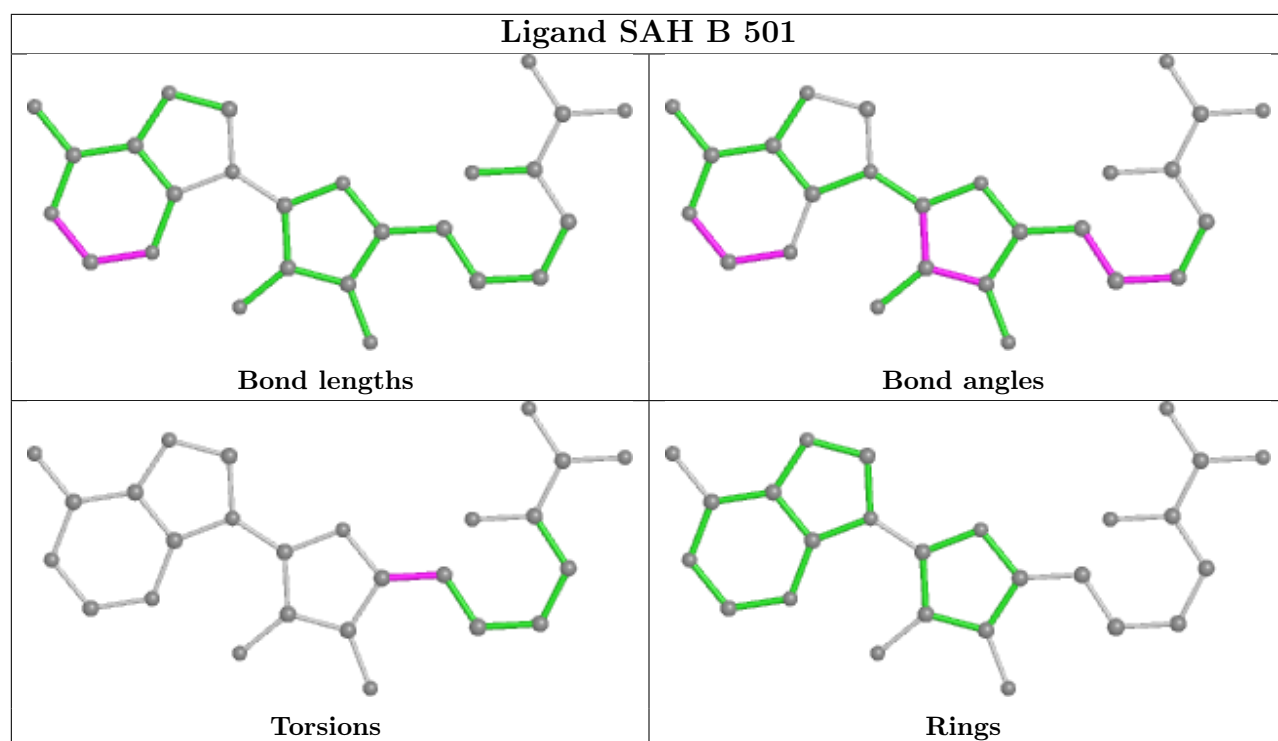
There are no ring outliers.

1 monomer is involved in 2 short contacts:

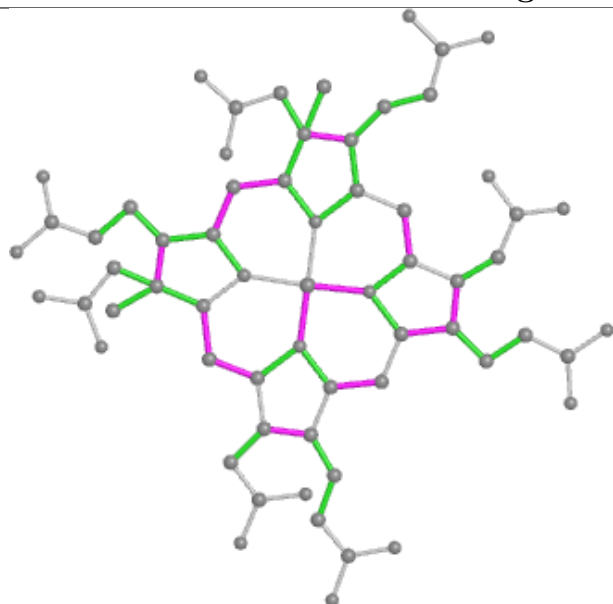
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	503	F0X	2	0

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.

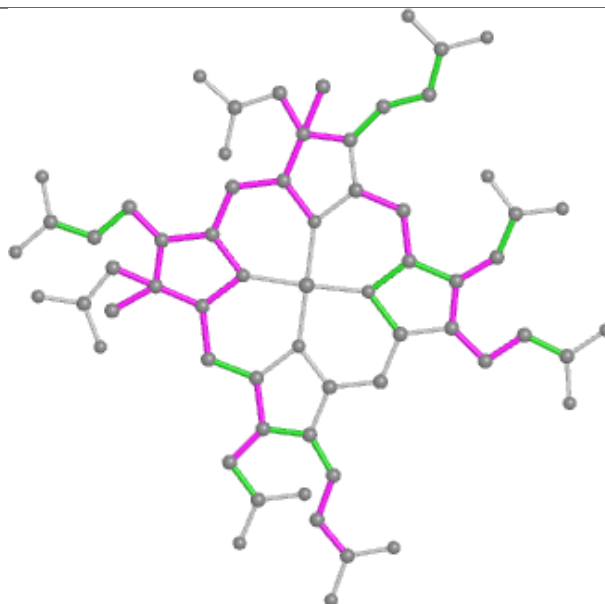




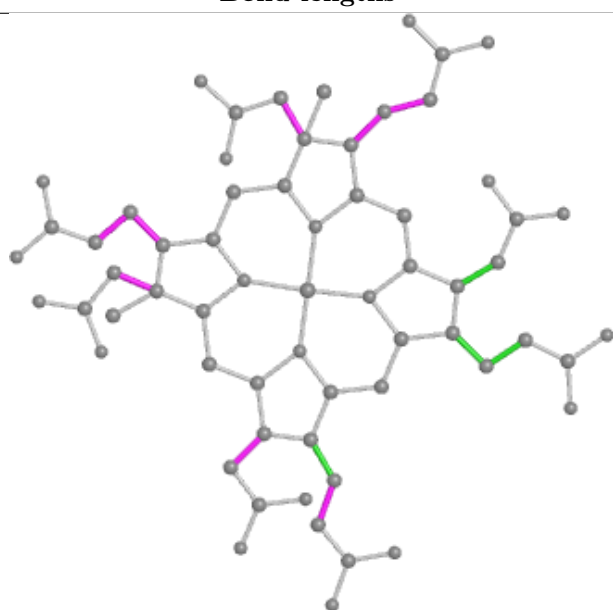
## Ligand F0X A 502



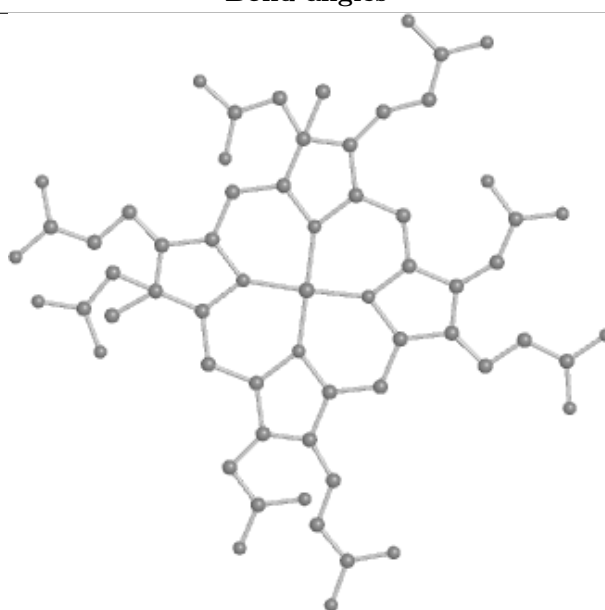
Bond lengths



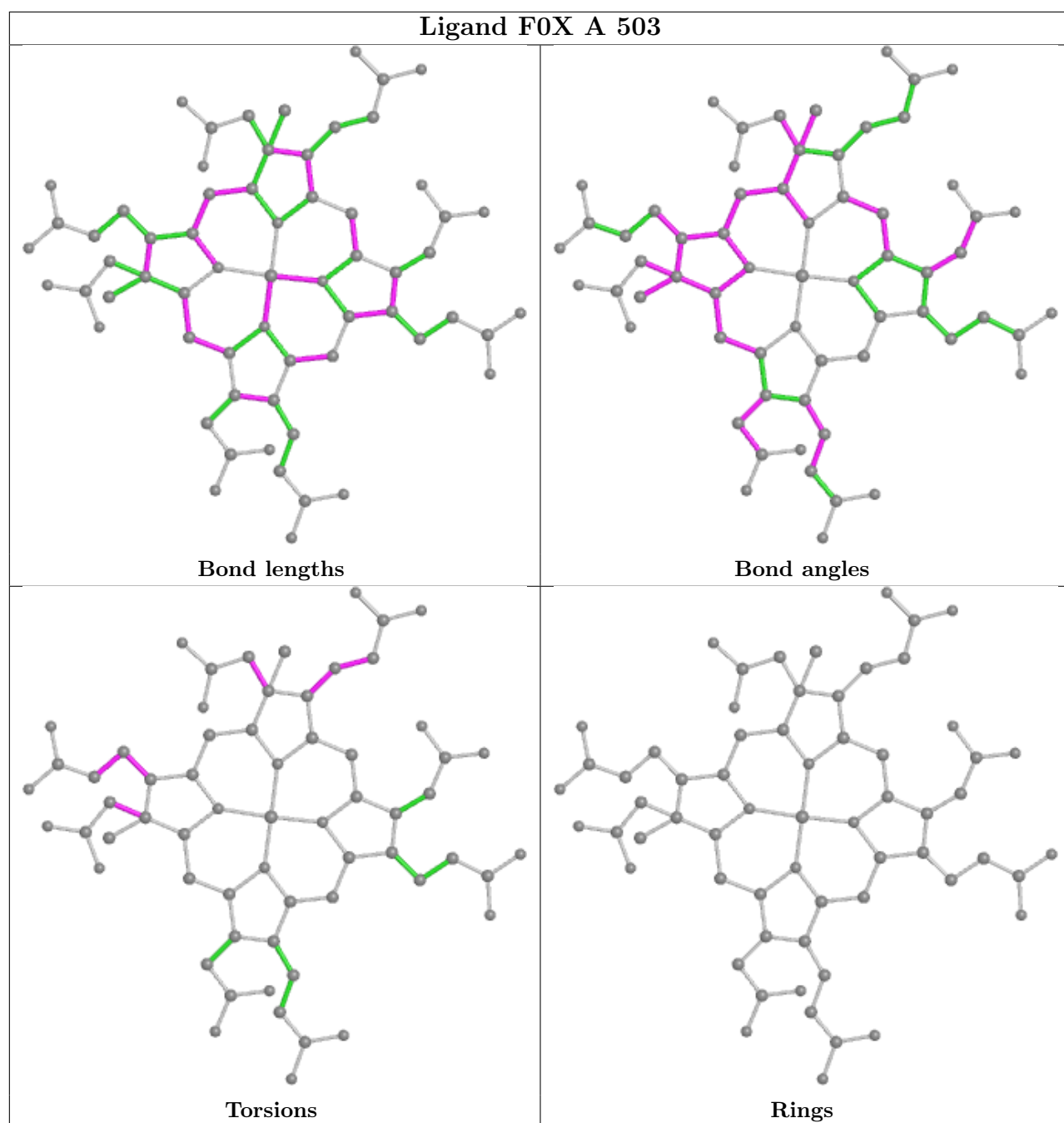
Bond angles



Torsions



Rings



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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	450/457 (98%)	0.03	8 (1%) 68 71	41, 68, 114, 163	0
1	B	446/457 (97%)	0.07	17 (3%) 40 43	42, 71, 128, 172	0
All	All	896/914 (98%)	0.05	25 (2%) 53 55	41, 70, 123, 172	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	362	THR	9.5
1	A	269	GLY	5.8
1	B	363	GLY	5.6
1	A	457	HIS	4.5
1	B	1	MET	4.2
1	B	282	ILE	3.5
1	B	322	ILE	3.4
1	B	287	LEU	3.3
1	B	324	PHE	3.3
1	B	321	GLY	3.2
1	B	319	HIS	3.1
1	A	279	GLN	2.9
1	A	270	LYS	2.8
1	B	198	LYS	2.6
1	B	364	GLY	2.6
1	B	176	ARG	2.5
1	B	426	LEU	2.5
1	B	169	PHE	2.5
1	B	317	LEU	2.5
1	B	218	VAL	2.4
1	A	351	GLN	2.3
1	A	169	PHE	2.2
1	B	288	ARG	2.1
1	B	49	PHE	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	364	GLY	2.1

## 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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

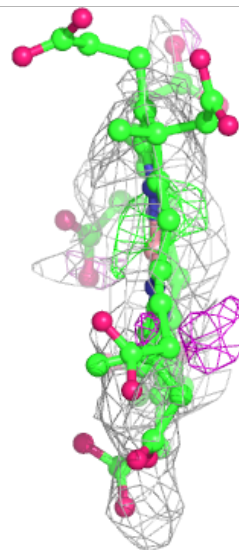
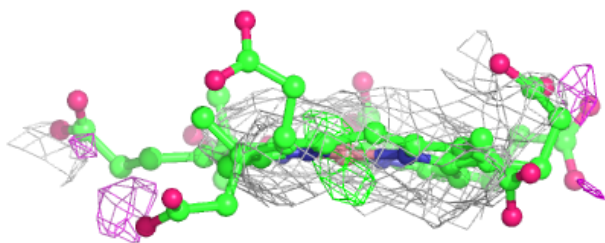
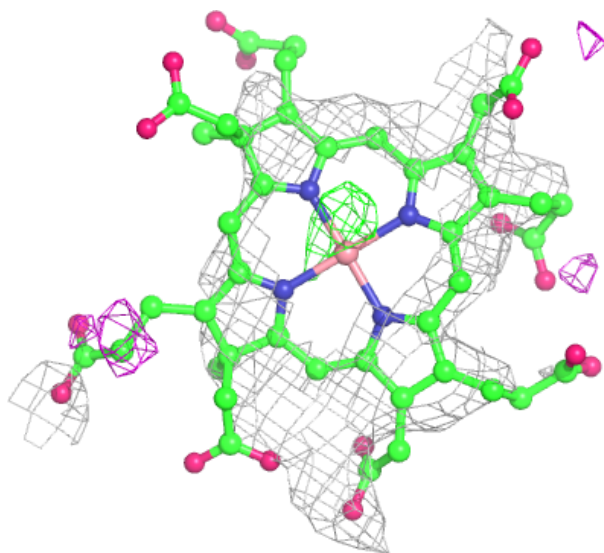
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	F0X	A	502	63/63	0.86	0.31	129,146,169,186	0
3	F0X	A	503	63/63	0.88	0.33	96,133,151,157	0
4	CL	A	504	1/1	0.92	0.27	105,105,105,105	0
2	SAH	A	501	26/26	0.96	0.11	41,53,62,67	0
2	SAH	B	501	26/26	0.97	0.11	43,56,67,69	0
4	CL	B	502	1/1	0.99	0.07	64,64,64,64	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.

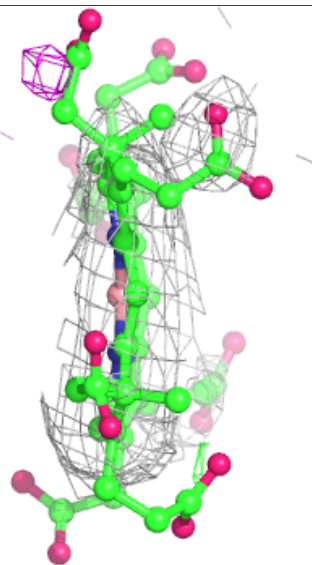
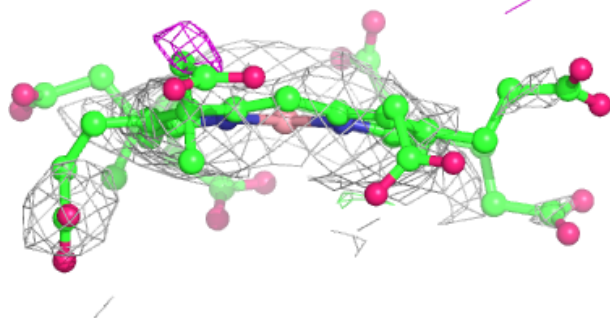
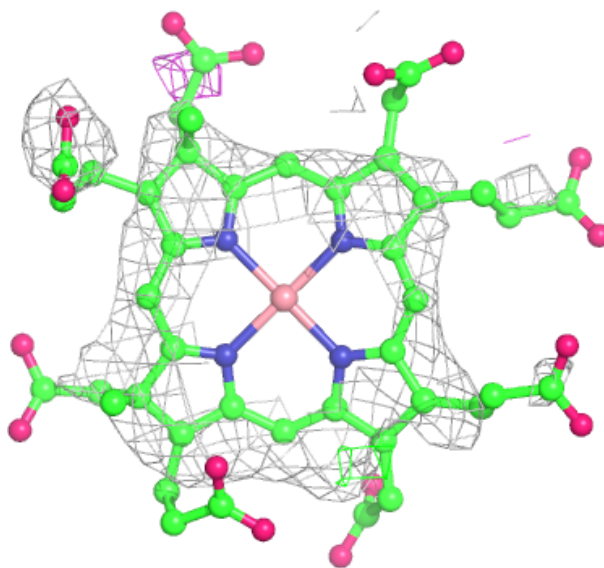
**Electron density around FOX A 502:**

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



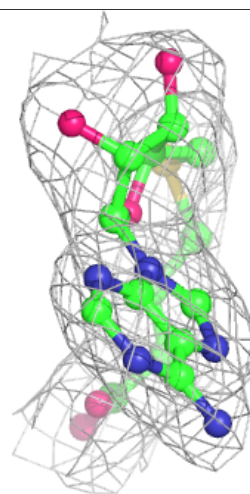
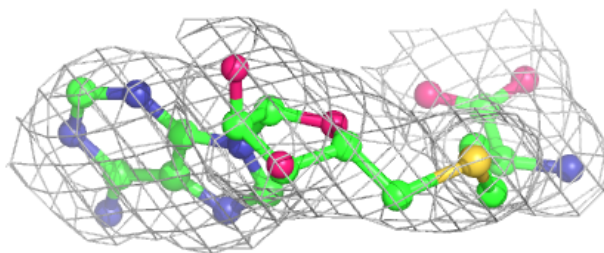
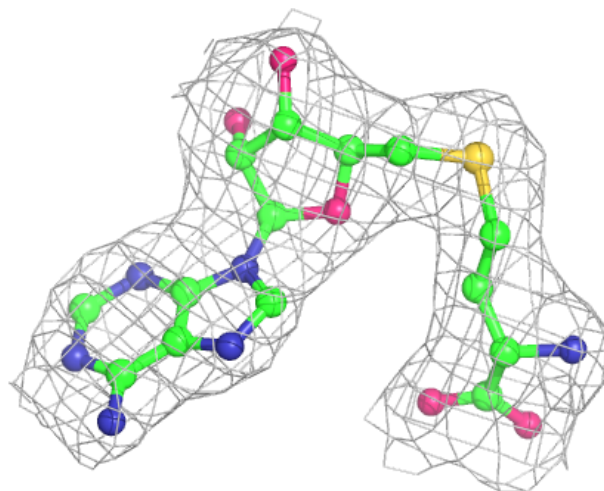
**Electron density around FOX A 503:**

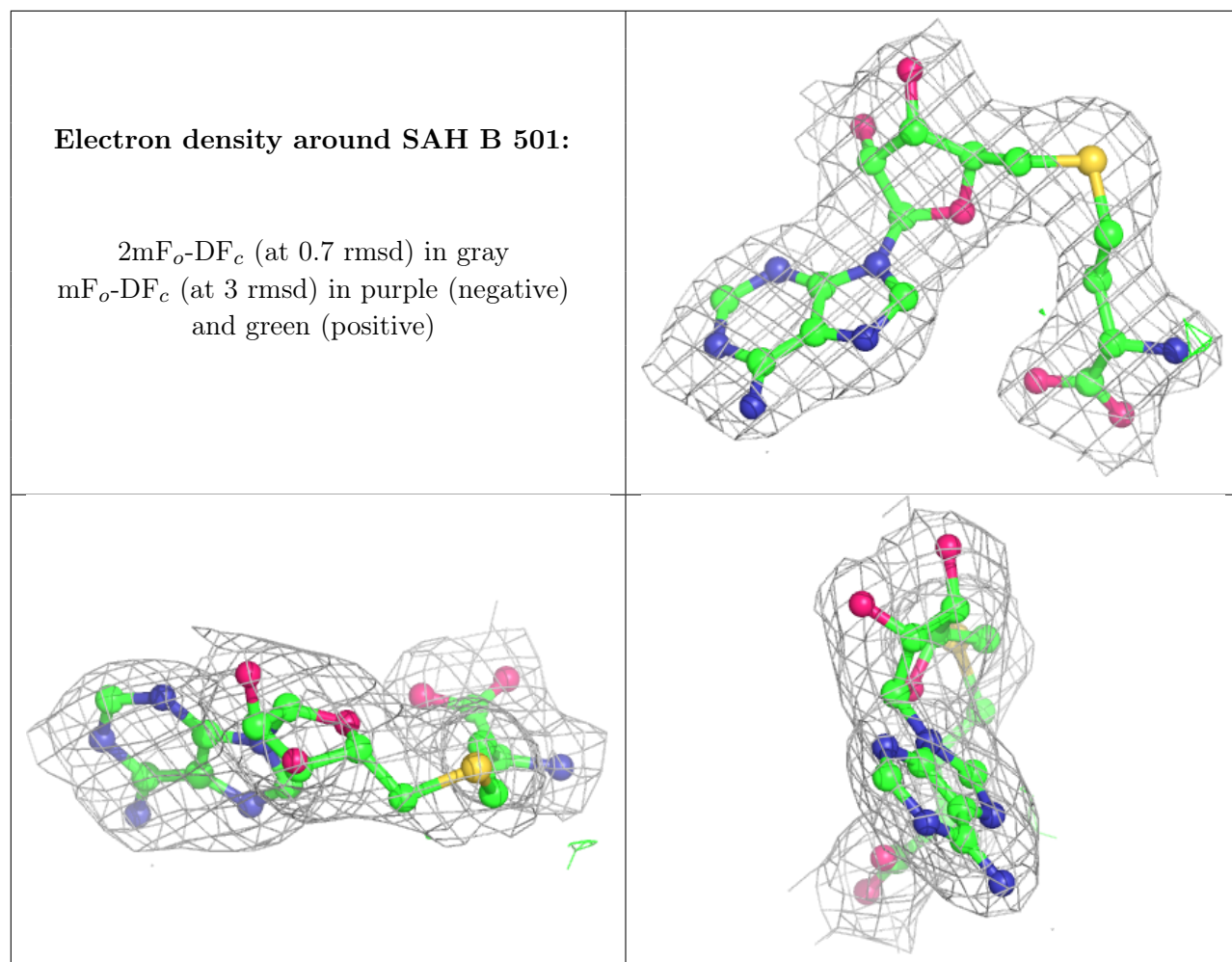
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around SAH 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)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.