



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2021 – 12:10 PM EDT

PDB ID : 7LKK  
Title : Crystal structure of Helicobacter pylori aminofutalosine deaminase (AFLDA)  
in complex with Methylthio-coformycin  
Authors : Harijan, R.K.; Feng, M.; Bonanno, J.B.; Almo, S.C.; Schramm, V.L.  
Deposited on : 2021-02-02  
Resolution : 1.89 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.

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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 : 2.20  
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) : 2.20

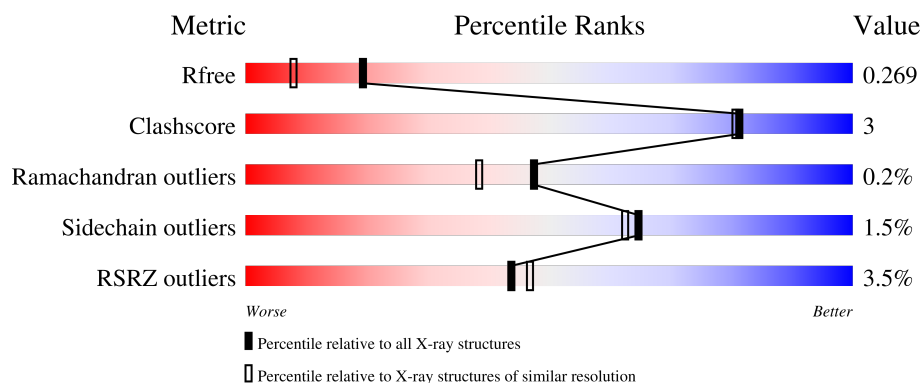
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.89 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	423	
1	B	423	
1	C	423	
1	D	423	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14015 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 Aminofutalosine deaminase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	411	Total	C	N	O	S	0	3	0
			3246	2087	541	609	9			
1	B	409	Total	C	N	O	S	6	5	0
			3243	2086	536	612	9			
1	C	408	Total	C	N	O	S	0	1	0
			3194	2057	530	599	8			
1	D	409	Total	C	N	O	S	0	1	0
			3221	2072	536	604	9			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP Q9ZMG8
A	-12	HIS	-	expression tag	UNP Q9ZMG8
A	-11	HIS	-	expression tag	UNP Q9ZMG8
A	-10	HIS	-	expression tag	UNP Q9ZMG8
A	-9	HIS	-	expression tag	UNP Q9ZMG8
A	-8	HIS	-	expression tag	UNP Q9ZMG8
A	-7	HIS	-	expression tag	UNP Q9ZMG8
A	-6	GLU	-	expression tag	UNP Q9ZMG8
A	-5	ASN	-	expression tag	UNP Q9ZMG8
A	-4	LEU	-	expression tag	UNP Q9ZMG8
A	-3	TYR	-	expression tag	UNP Q9ZMG8
A	-2	PHE	-	expression tag	UNP Q9ZMG8
A	-1	GLN	-	expression tag	UNP Q9ZMG8
A	0	GLY	-	expression tag	UNP Q9ZMG8
B	-13	MET	-	initiating methionine	UNP Q9ZMG8
B	-12	HIS	-	expression tag	UNP Q9ZMG8
B	-11	HIS	-	expression tag	UNP Q9ZMG8
B	-10	HIS	-	expression tag	UNP Q9ZMG8
B	-9	HIS	-	expression tag	UNP Q9ZMG8
B	-8	HIS	-	expression tag	UNP Q9ZMG8
B	-7	HIS	-	expression tag	UNP Q9ZMG8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	GLU	-	expression tag	UNP Q9ZMG8
B	-5	ASN	-	expression tag	UNP Q9ZMG8
B	-4	LEU	-	expression tag	UNP Q9ZMG8
B	-3	TYR	-	expression tag	UNP Q9ZMG8
B	-2	PHE	-	expression tag	UNP Q9ZMG8
B	-1	GLN	-	expression tag	UNP Q9ZMG8
B	0	GLY	-	expression tag	UNP Q9ZMG8
C	-13	MET	-	initiating methionine	UNP Q9ZMG8
C	-12	HIS	-	expression tag	UNP Q9ZMG8
C	-11	HIS	-	expression tag	UNP Q9ZMG8
C	-10	HIS	-	expression tag	UNP Q9ZMG8
C	-9	HIS	-	expression tag	UNP Q9ZMG8
C	-8	HIS	-	expression tag	UNP Q9ZMG8
C	-7	HIS	-	expression tag	UNP Q9ZMG8
C	-6	GLU	-	expression tag	UNP Q9ZMG8
C	-5	ASN	-	expression tag	UNP Q9ZMG8
C	-4	LEU	-	expression tag	UNP Q9ZMG8
C	-3	TYR	-	expression tag	UNP Q9ZMG8
C	-2	PHE	-	expression tag	UNP Q9ZMG8
C	-1	GLN	-	expression tag	UNP Q9ZMG8
C	0	GLY	-	expression tag	UNP Q9ZMG8
D	-13	MET	-	initiating methionine	UNP Q9ZMG8
D	-12	HIS	-	expression tag	UNP Q9ZMG8
D	-11	HIS	-	expression tag	UNP Q9ZMG8
D	-10	HIS	-	expression tag	UNP Q9ZMG8
D	-9	HIS	-	expression tag	UNP Q9ZMG8
D	-8	HIS	-	expression tag	UNP Q9ZMG8
D	-7	HIS	-	expression tag	UNP Q9ZMG8
D	-6	GLU	-	expression tag	UNP Q9ZMG8
D	-5	ASN	-	expression tag	UNP Q9ZMG8
D	-4	LEU	-	expression tag	UNP Q9ZMG8
D	-3	TYR	-	expression tag	UNP Q9ZMG8
D	-2	PHE	-	expression tag	UNP Q9ZMG8
D	-1	GLN	-	expression tag	UNP Q9ZMG8
D	0	GLY	-	expression tag	UNP Q9ZMG8

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Fe	0	0
			1	1		
2	C	1	Total	Fe	0	0
			1	1		
2	D	1	Total	Fe	0	0
			1	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



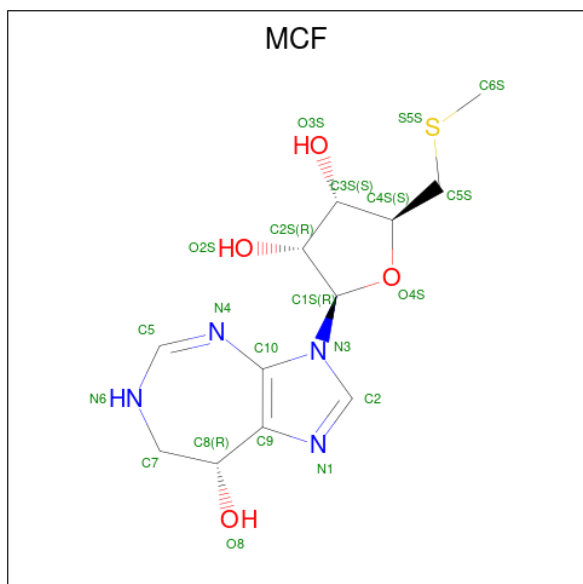
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is (8R)-3-(5-S-methyl-5-thio-beta-D-ribofuranosyl)-3,6,7,8-tetrahydroimidazo[4,5-d][1,3]diazepin-8-ol (three-letter code: MCF) (formula: C<sub>12</sub>H<sub>18</sub>N<sub>4</sub>O<sub>4</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			21	12	4	4	1		
4	B	1	Total	C	N	O	S	0	0
			21	12	4	4	1		
4	C	1	Total	C	N	O	S	0	0
			21	12	4	4	1		
4	D	1	Total	C	N	O	S	0	0
			21	12	4	4	1		

- Molecule 5 is water.

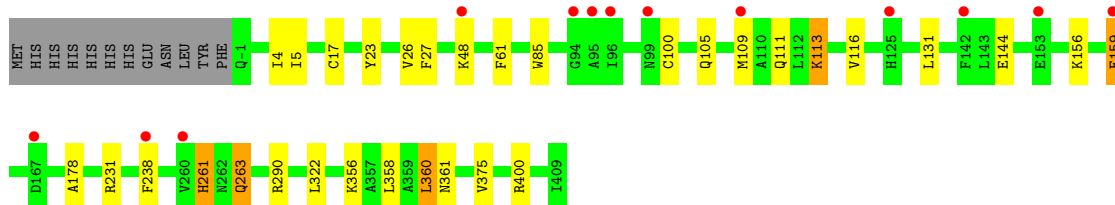
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	264	Total 264	O 264	0	0
5	B	248	Total 248	O 248	0	0
5	C	246	Total 246	O 246	0	0
5	D	213	Total 213	O 213	0	0

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

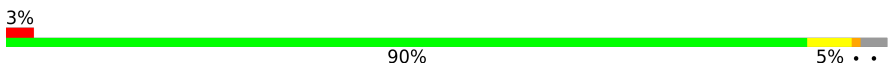
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

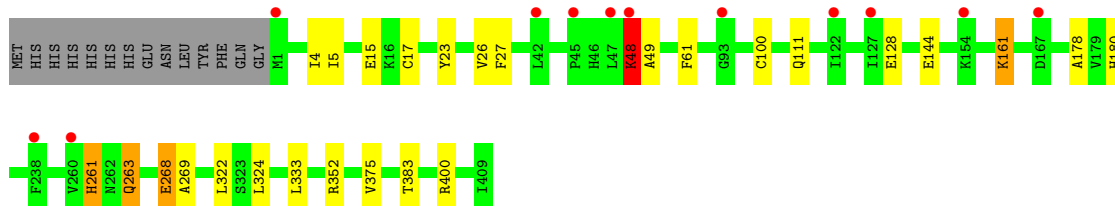
- Molecule 1: Aminofutalosine deaminase

Chain A: 

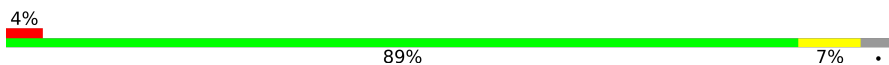


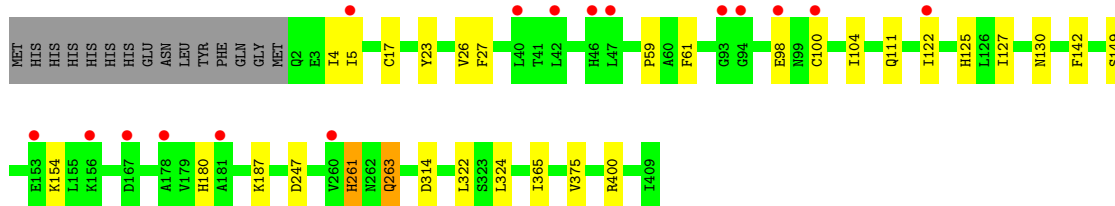
- Molecule 1: Aminofutalosine deaminase

Chain B: 

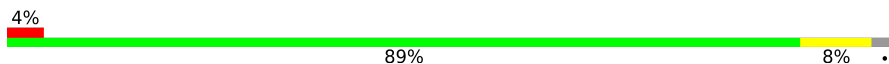


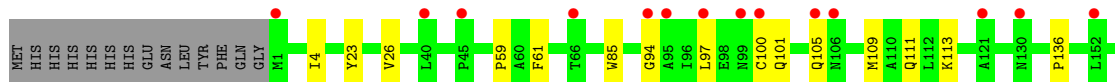
- Molecule 1: Aminofutalosine deaminase

Chain C: 



- Molecule 1: Aminofutalosine deaminase

Chain D: 







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	72.91Å 73.07Å 157.44Å 90.00° 98.30° 90.00°	Depositor
Resolution (Å)	28.59 – 1.89 28.59 – 1.89	Depositor EDS
% Data completeness (in resolution range)	98.7 (28.59-1.89) 98.7 (28.59-1.89)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.84 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, $R_{free}$	0.231 , 0.269 0.231 , 0.269	Depositor DCC
$R_{free}$ test set	6554 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.4	Xtriage
Anisotropy	0.658	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 44.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	14015	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.49% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MCF, EDO, FE

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	0.29	0/3307	0.48	3/4461 (0.1%)
1	B	0.27	0/3303	0.47	3/4455 (0.1%)
1	C	0.29	0/3255	0.47	1/4395 (0.0%)
1	D	0.25	0/3282	0.43	0/4426
All	All	0.28	0/13147	0.46	7/17737 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	48	LYS	CA-CB-CG	9.02	133.24	113.40
1	B	48	LYS	CG-CD-CE	7.81	135.34	111.90
1	A	159	GLU	CA-CB-CG	6.53	127.77	113.40
1	A	109	MET	CG-SD-CE	6.36	110.38	100.20
1	C	98	GLU	CG-CD-OE2	-5.25	107.79	118.30
1	A	360	LEU	CB-CG-CD2	-5.17	102.21	111.00
1	B	48	LYS	CD-CE-NZ	-5.03	100.14	111.70

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3246	0	3247	19	0
1	B	3243	0	3239	16	0
1	C	3194	0	3176	15	0
1	D	3221	0	3220	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	16	0	24	0	0
3	B	8	0	12	1	0
3	C	8	0	12	0	0
3	D	20	0	30	2	0
4	A	21	0	16	1	0
4	B	21	0	16	1	0
4	C	21	0	16	1	0
4	D	21	0	16	2	0
5	A	264	0	0	4	0
5	B	248	0	0	1	0
5	C	246	0	0	2	0
5	D	213	0	0	1	0
All	All	14015	0	13024	67	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 3.

All (67) 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:48:LYS:HE3	5:A:735:HOH:O	1.21	1.37
1:A:156:LYS:HD2	1:A:159:GLU:OE2	1.75	0.85
1:B:161:LYS:NZ	5:B:601:HOH:O	2.27	0.66
1:A:4:ILE:HG12	1:A:26:VAL:HG22	1.76	0.66
1:B:111:GLN:NE2	1:B:322:LEU:O	2.30	0.65
1:C:5[A]:ILE:HG12	1:C:27:PHE:HE1	1.62	0.65
1:C:130:ASN:ND2	5:C:604:HOH:O	2.30	0.64
1:A:156:LYS:HA	1:A:159:GLU:OE2	1.97	0.64
1:D:212:LEU:O	1:D:216:GLU:HG3	1.99	0.63
1:C:4:ILE:HG12	1:C:26:VAL:HG22	1.80	0.62
1:B:4:ILE:HG12	1:B:26:VAL:HG22	1.81	0.61
1:D:94:GLY:HA2	1:D:97:LEU:HD23	1.83	0.60
1:C:100:CYS:SG	1:C:104:ILE:HD11	2.41	0.60
1:C:111:GLN:NE2	1:C:322:LEU:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:321:SER:HB3	3:D:506:EDO:H12	1.85	0.57
1:D:111:GLN:NE2	1:D:322:LEU:O	2.37	0.57
1:A:111:GLN:NE2	1:A:322:LEU:O	2.37	0.57
1:B:268[B]:GLU:OE1	1:B:268[B]:GLU:N	2.35	0.56
1:A:358:LEU:O	1:A:360:LEU:HD23	2.06	0.55
1:B:261:HIS:HB3	1:B:263:GLN:OE1	2.07	0.55
1:A:261:HIS:HB3	1:A:263:GLN:OE1	2.07	0.54
1:D:101:GLN:O	1:D:105:GLN:HG3	2.07	0.54
1:A:361:ASN:OD1	5:A:601:HOH:O	2.18	0.54
1:C:5[A]:ILE:HG12	1:C:27:PHE:CE1	2.45	0.51
1:D:159:GLU:HG2	1:D:196:LEU:HD22	1.92	0.51
1:A:356:LYS:NZ	5:A:614:HOH:O	2.43	0.50
1:A:105:GLN:HG3	1:A:131:LEU:HD13	1.93	0.50
1:D:4:ILE:HG12	1:D:26:VAL:HG22	1.93	0.49
1:D:180:HIS:NE2	4:D:507:MCF:H5SA	2.29	0.48
1:D:59:PRO:HG3	1:D:365:ILE:HG13	1.95	0.48
1:D:109:MET:HG3	1:D:113:LYS:HD2	1.95	0.48
1:D:136:PRO:HA	1:D:172:LYS:HE3	1.96	0.47
1:D:261:HIS:HB3	1:D:263:GLN:OE1	2.14	0.47
1:C:61:PHE:HB3	1:C:324:LEU:HD23	1.95	0.47
1:B:4:ILE:O	1:B:49:ALA:HA	2.15	0.46
1:A:5:ILE:HG12	1:A:27:PHE:HE1	1.80	0.46
1:C:187:LYS:NZ	1:C:247:ASP:OD1	2.47	0.46
1:C:375:VAL:HB	1:C:400:ARG:HB2	1.97	0.46
1:B:180:HIS:NE2	4:B:504:MCF:H5SA	2.31	0.46
1:C:261:HIS:HB3	1:C:263:GLN:OE1	2.16	0.46
1:B:61:PHE:HB3	1:B:324:LEU:HD23	1.98	0.45
1:D:375:VAL:HB	1:D:400:ARG:HB2	1.98	0.45
1:D:61:PHE:HB3	1:D:324:LEU:HD23	1.99	0.45
1:B:144:GLU:HA	1:B:178:ALA:HB3	1.99	0.44
1:A:144:GLU:HA	1:A:178:ALA:HB3	2.00	0.44
1:B:15:GLU:OE2	1:B:352:ARG:NH1	2.50	0.44
1:A:238:PHE:O	1:A:238:PHE:CG	2.70	0.44
1:C:122:ILE:HD13	1:C:142:PHE:HB2	2.00	0.43
1:A:375:VAL:HB	1:A:400:ARG:HB2	1.99	0.43
1:B:375:VAL:HB	1:B:400:ARG:HB2	2.00	0.43
1:C:154:LYS:HD3	5:C:637:HOH:O	2.17	0.43
1:C:180:HIS:NE2	4:C:504:MCF:H5SA	2.34	0.43
1:A:231:ARG:NH2	5:A:627:HOH:O	2.52	0.43
1:A:113:LYS:HB3	1:A:113:LYS:HE2	1.90	0.43
1:C:125:HIS:HB2	1:C:127:ILE:HG12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:156:LYS:NZ	5:D:621:HOH:O	2.52	0.42
1:B:268[A]:GLU:HG3	1:B:269:ALA:N	2.35	0.42
1:B:383:THR:HA	3:B:502:EDO:H12	2.01	0.42
1:D:385:GLU:O	1:D:385:GLU:HG2	2.20	0.41
1:A:290:ARG:HG2	1:B:333:LEU:HD23	2.02	0.41
1:B:4:ILE:N	1:B:48:LYS:O	2.47	0.41
1:D:287:PHE:CE2	3:D:506:EDO:H22	2.56	0.41
1:B:5[A]:ILE:HG12	1:B:27:PHE:HE1	1.86	0.40
1:C:59:PRO:HG3	1:C:365:ILE:HG13	2.02	0.40
1:D:85:TRP:CH2	4:D:507:MCF:H7	2.56	0.40
1:A:61:PHE:HB2	1:A:116:VAL:HA	2.02	0.40
1:A:85:TRP:CH2	4:A:506:MCF:H7	2.57	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	412/423 (97%)	395 (96%)	16 (4%)	1 (0%)	47	38
1	B	412/423 (97%)	397 (96%)	14 (3%)	1 (0%)	47	38
1	C	407/423 (96%)	391 (96%)	15 (4%)	1 (0%)	47	38
1	D	408/423 (96%)	392 (96%)	15 (4%)	1 (0%)	47	38
All	All	1639/1692 (97%)	1575 (96%)	60 (4%)	4 (0%)	47	38

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	261	HIS
1	B	261	HIS
1	C	261	HIS

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Mol	Chain	Res	Type
1	D	261	HIS

### 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	350/362 (97%)	345 (99%)	5 (1%)	67	65
1	B	350/362 (97%)	341 (97%)	9 (3%)	46	39
1	C	342/362 (94%)	337 (98%)	5 (2%)	65	62
1	D	347/362 (96%)	344 (99%)	3 (1%)	78	79
All	All	1389/1448 (96%)	1367 (98%)	22 (2%)	65	60

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	CYS
1	A	23	TYR
1	A	100	CYS
1	A	113	LYS
1	A	263	GLN
1	B	17	CYS
1	B	23	TYR
1	B	48	LYS
1	B	100	CYS
1	B	128	GLU
1	B	161	LYS
1	B	263	GLN
1	B	268[A]	GLU
1	B	268[B]	GLU
1	C	17	CYS
1	C	23	TYR
1	C	149	SER
1	C	263	GLN
1	C	314	ASP
1	D	23	TYR

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Mol	Chain	Res	Type
1	D	100	CYS
1	D	243	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	368	ASN

### 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 21 ligands modelled in this entry, 4 are monoatomic - leaving 17 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$
3	EDO	C	502	-	3,3,3	0.43	0	2,2,2	0.36	0
3	EDO	D	502	-	3,3,3	0.45	0	2,2,2	0.38	0
4	MCF	A	506	2	15,23,23	4.44	6 (40%)	13,33,33	1.63	1 (7%)
3	EDO	D	506	-	3,3,3	0.45	0	2,2,2	0.32	0
4	MCF	D	507	2	15,23,23	4.47	6 (40%)	13,33,33	1.63	1 (7%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	B	503	-	3,3,3	0.45	0	2,2,2	0.31	0
3	EDO	D	503	-	3,3,3	0.46	0	2,2,2	0.29	0
4	MCF	C	504	2	15,23,23	4.45	6 (40%)	13,33,33	1.65	1 (7%)
3	EDO	A	505	-	3,3,3	0.47	0	2,2,2	0.26	0
3	EDO	D	504	-	3,3,3	0.45	0	2,2,2	0.31	0
3	EDO	A	504	-	3,3,3	0.45	0	2,2,2	0.35	0
3	EDO	B	502	-	3,3,3	0.47	0	2,2,2	0.35	0
3	EDO	A	502	-	3,3,3	0.46	0	2,2,2	0.28	0
3	EDO	C	503	-	3,3,3	0.47	0	2,2,2	0.34	0
4	MCF	B	504	2	15,23,23	4.43	6 (40%)	13,33,33	1.69	2 (15%)
3	EDO	D	505	-	3,3,3	0.46	0	2,2,2	0.34	0
3	EDO	A	503	-	3,3,3	0.46	0	2,2,2	0.33	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
3	EDO	C	502	-	-	1/1/1/1	-
3	EDO	D	502	-	-	0/1/1/1	-
4	MCF	A	506	2	-	3/3/34/34	0/2/3/3
3	EDO	D	506	-	-	1/1/1/1	-
4	MCF	D	507	2	-	3/3/34/34	0/2/3/3
3	EDO	B	503	-	-	0/1/1/1	-
3	EDO	D	503	-	-	0/1/1/1	-
4	MCF	C	504	2	-	2/3/34/34	0/2/3/3
3	EDO	A	505	-	-	0/1/1/1	-
3	EDO	D	504	-	-	0/1/1/1	-
3	EDO	A	504	-	-	0/1/1/1	-
3	EDO	B	502	-	-	0/1/1/1	-
3	EDO	A	502	-	-	0/1/1/1	-
3	EDO	C	503	-	-	0/1/1/1	-
4	MCF	B	504	2	-	3/3/34/34	0/2/3/3
3	EDO	D	505	-	-	0/1/1/1	-
3	EDO	A	503	-	-	0/1/1/1	-

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	504	MCF	O4S-C1S	-9.13	1.28	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	506	MCF	O4S-C1S	-9.06	1.28	1.41
4	C	504	MCF	O4S-C1S	-9.05	1.28	1.41
4	D	507	MCF	O4S-C1S	-9.04	1.28	1.41
4	D	507	MCF	C3S-C4S	-8.75	1.30	1.53
4	A	506	MCF	C3S-C4S	-8.74	1.30	1.53
4	C	504	MCF	C3S-C4S	-8.73	1.30	1.53
4	B	504	MCF	C3S-C4S	-8.70	1.30	1.53
4	D	507	MCF	O4S-C4S	7.90	1.62	1.45
4	C	504	MCF	O4S-C4S	7.82	1.62	1.45
4	A	506	MCF	O4S-C4S	7.81	1.62	1.45
4	B	504	MCF	O4S-C4S	7.80	1.62	1.45
4	D	507	MCF	C10-N4	7.43	1.49	1.41
4	C	504	MCF	C10-N4	7.36	1.48	1.41
4	A	506	MCF	C10-N4	7.30	1.48	1.41
4	B	504	MCF	C10-N4	7.15	1.48	1.41
4	D	507	MCF	O3S-C3S	3.53	1.51	1.43
4	C	504	MCF	O3S-C3S	3.51	1.51	1.43
4	B	504	MCF	O3S-C3S	3.51	1.51	1.43
4	A	506	MCF	O3S-C3S	3.50	1.51	1.43
4	D	507	MCF	O2S-C2S	-2.69	1.36	1.43
4	B	504	MCF	O2S-C2S	-2.69	1.36	1.43
4	A	506	MCF	O2S-C2S	-2.62	1.36	1.43
4	C	504	MCF	O2S-C2S	-2.62	1.36	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	507	MCF	C6S-S5S-C5S	4.57	109.69	101.30
4	C	504	MCF	C6S-S5S-C5S	4.52	109.61	101.30
4	B	504	MCF	C6S-S5S-C5S	4.36	109.33	101.30
4	A	506	MCF	C6S-S5S-C5S	4.28	109.18	101.30
4	B	504	MCF	O4S-C1S-C2S	-2.30	103.57	106.93

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	506	MCF	O4S-C4S-C5S-S5S
4	A	506	MCF	C3S-C4S-C5S-S5S
4	B	504	MCF	O4S-C4S-C5S-S5S
4	B	504	MCF	C3S-C4S-C5S-S5S
4	B	504	MCF	C4S-C5S-S5S-C6S

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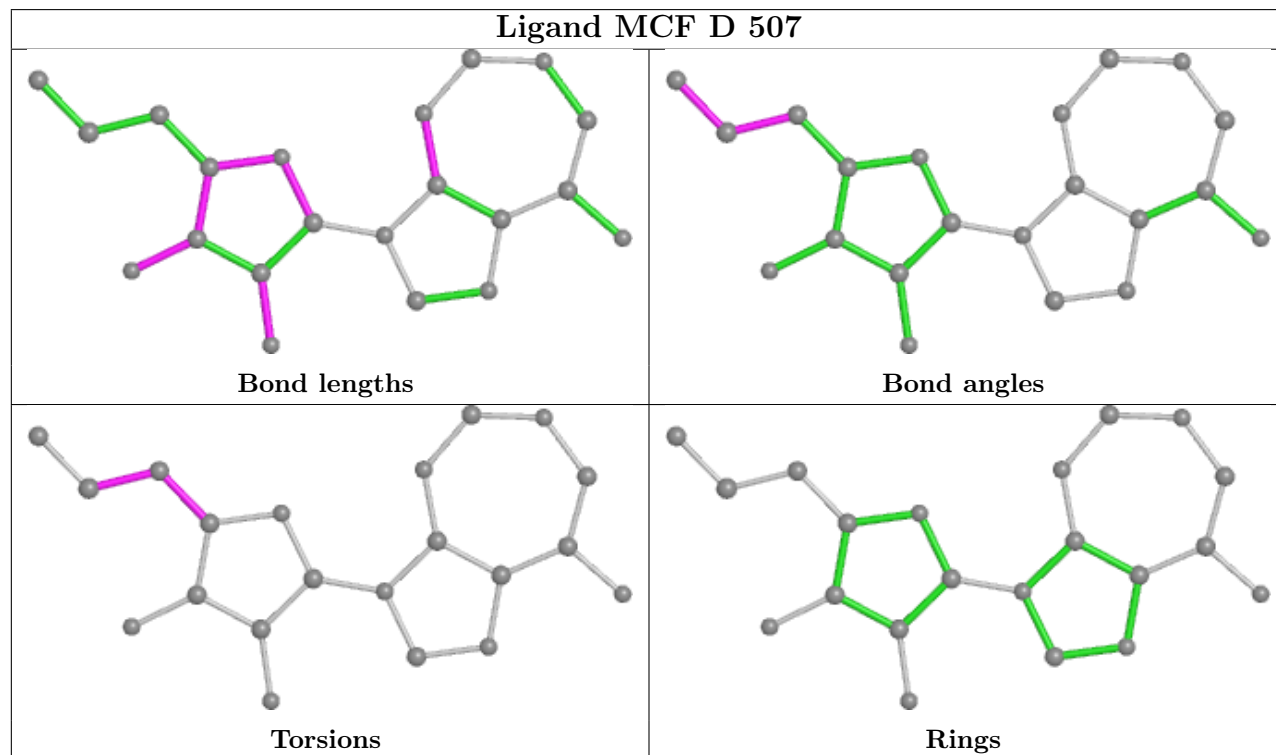
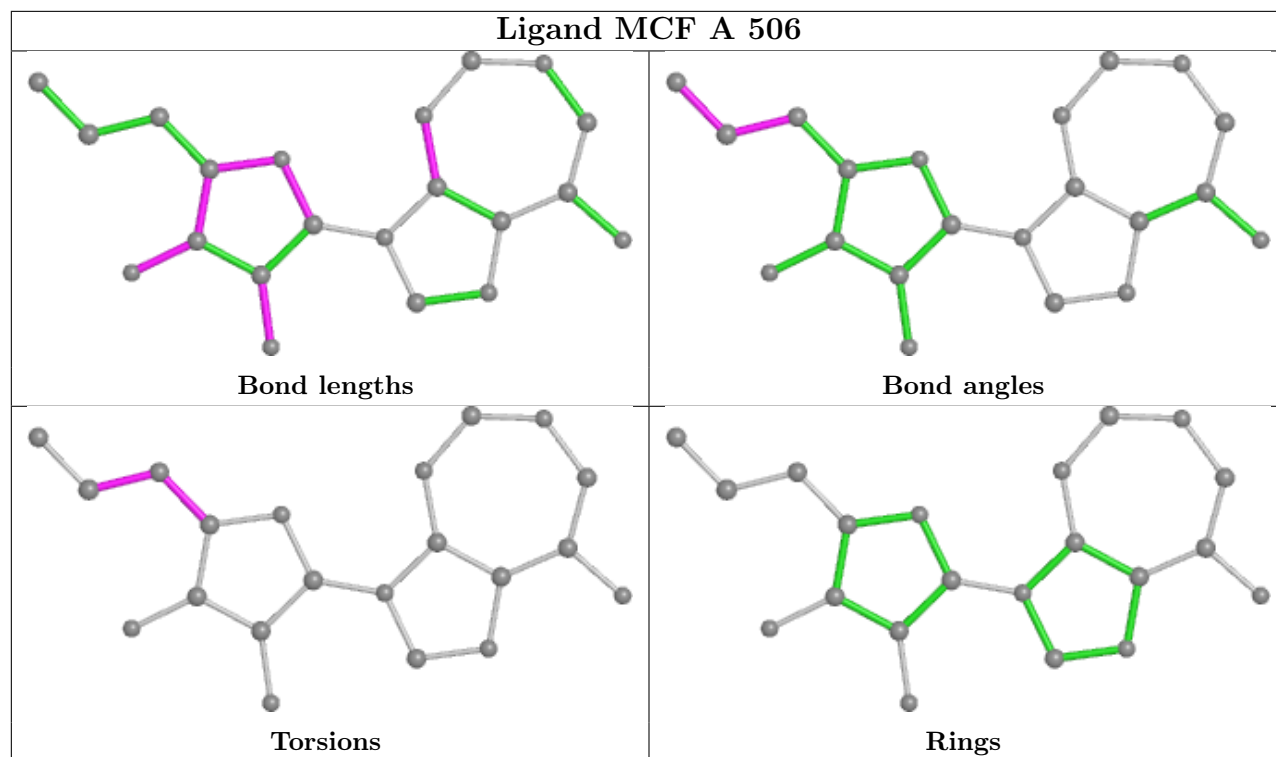
Mol	Chain	Res	Type	Atoms
4	C	504	MCF	O4S-C4S-C5S-S5S
4	C	504	MCF	C3S-C4S-C5S-S5S
4	D	507	MCF	O4S-C4S-C5S-S5S
4	D	507	MCF	C3S-C4S-C5S-S5S
4	D	507	MCF	C4S-C5S-S5S-C6S
4	A	506	MCF	C4S-C5S-S5S-C6S
3	D	506	EDO	O1-C1-C2-O2
3	C	502	EDO	O1-C1-C2-O2

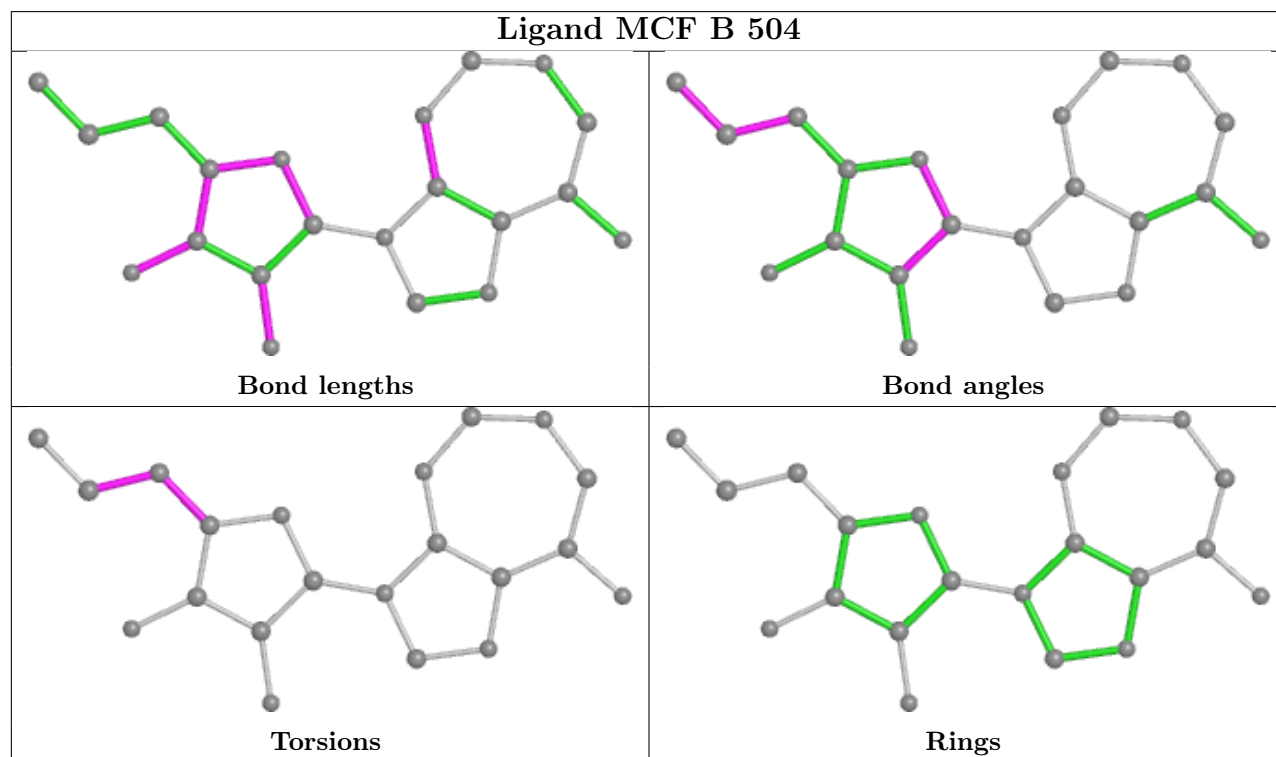
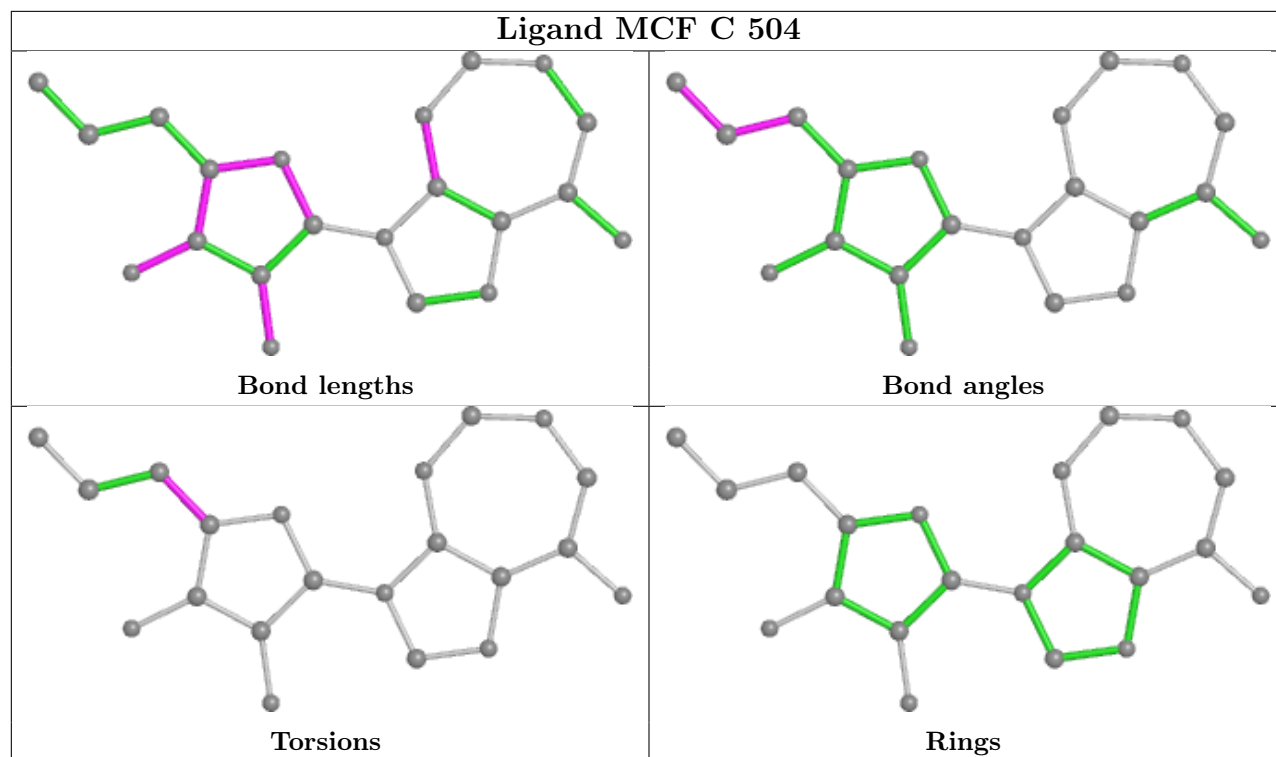
There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	506	MCF	1	0
3	D	506	EDO	2	0
4	D	507	MCF	2	0
4	C	504	MCF	1	0
3	B	502	EDO	1	0
4	B	504	MCF	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

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	411/423 (97%)	0.32	13 (3%) 47 50	15, 24, 36, 54	0
1	B	409/423 (96%)	0.36	12 (2%) 51 54	16, 23, 33, 46	0
1	C	408/423 (96%)	0.40	16 (3%) 39 42	18, 26, 36, 50	0
1	D	409/423 (96%)	0.46	16 (3%) 39 42	19, 27, 37, 48	0
All	All	1637/1692 (96%)	0.39	57 (3%) 44 47	15, 25, 36, 54	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	100	CYS	5.6
1	D	238	PHE	5.0
1	A	238	PHE	4.1
1	D	94	GLY	4.1
1	C	98	GLU	3.9
1	C	46	HIS	3.8
1	B	238	PHE	3.6
1	C	42	LEU	3.5
1	B	1	MET	3.4
1	A	95	ALA	3.4
1	D	97	LEU	3.3
1	A	96	ILE	3.3
1	B	167	ASP	3.2
1	B	93	GLY	3.2
1	C	122	ILE	3.1
1	C	153	GLU	3.1
1	D	105	GLN	3.0
1	D	40	LEU	3.0
1	A	109	MET	3.0
1	D	409	ILE	3.0
1	B	127	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	5[A]	ILE	2.7
1	A	159	GLU	2.7
1	C	47	LEU	2.7
1	A	167	ASP	2.7
1	B	42	LEU	2.7
1	D	152	LEU	2.6
1	D	99	ASN	2.6
1	B	260	VAL	2.6
1	C	94	GLY	2.6
1	C	100	CYS	2.6
1	A	260	VAL	2.5
1	D	1	MET	2.4
1	B	48	LYS	2.4
1	C	181	ALA	2.4
1	B	45	PRO	2.4
1	A	142	PHE	2.4
1	D	95	ALA	2.4
1	D	66	THR	2.3
1	C	40	LEU	2.3
1	D	121	ALA	2.3
1	A	94	GLY	2.3
1	A	99	ASN	2.3
1	D	106	ASN	2.3
1	A	125	HIS	2.2
1	C	178	ALA	2.2
1	C	167	ASP	2.2
1	B	154	LYS	2.2
1	C	260	VAL	2.2
1	A	48	LYS	2.1
1	B	122	ILE	2.1
1	D	130	ASN	2.1
1	D	45	PRO	2.1
1	C	93	GLY	2.1
1	B	47	LEU	2.1
1	A	153	GLU	2.1
1	C	156	LYS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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



## 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

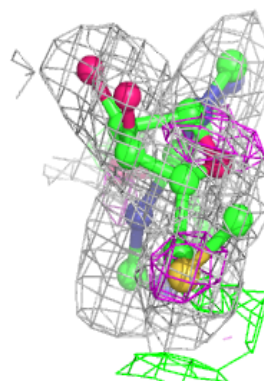
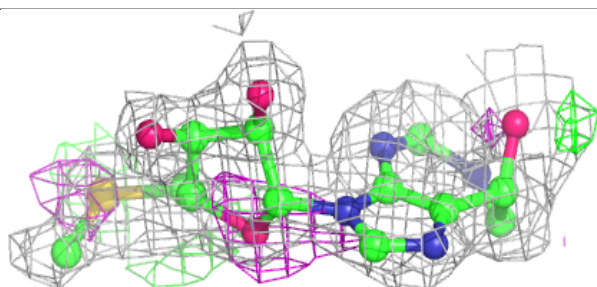
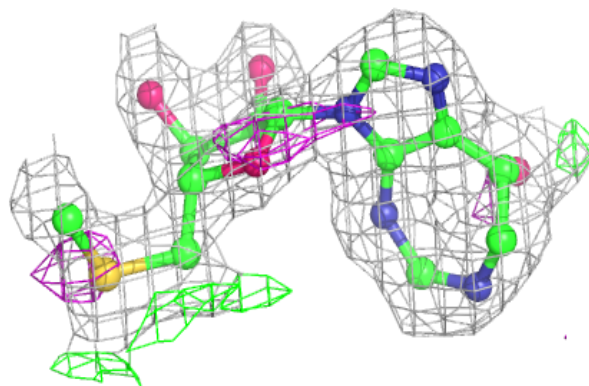
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
3	EDO	D	505	4/4	0.70	0.21	45,46,50,54	0
3	EDO	C	503	4/4	0.73	0.18	49,50,51,52	0
3	EDO	D	502	4/4	0.82	0.17	46,46,51,56	0
3	EDO	A	504	4/4	0.84	0.17	29,32,34,36	0
3	EDO	B	502	4/4	0.84	0.16	30,33,35,39	0
3	EDO	B	503	4/4	0.84	0.24	26,26,29,29	0
4	MCF	B	504	21/21	0.84	0.16	22,25,28,33	0
4	MCF	A	506	21/21	0.86	0.15	23,26,31,38	0
3	EDO	D	503	4/4	0.86	0.23	34,35,41,41	0
4	MCF	D	507	21/21	0.86	0.17	26,30,37,42	0
3	EDO	A	505	4/4	0.87	0.12	28,31,32,35	0
4	MCF	C	504	21/21	0.88	0.16	24,28,33,37	0
3	EDO	A	502	4/4	0.88	0.12	35,36,36,37	0
3	EDO	D	506	4/4	0.90	0.18	28,29,30,37	0
3	EDO	C	502	4/4	0.91	0.27	27,28,29,29	0
3	EDO	D	504	4/4	0.91	0.14	29,31,37,45	0
3	EDO	A	503	4/4	0.93	0.11	34,36,37,37	0
2	FE	D	501	1/1	0.98	0.08	32,32,32,32	0
2	FE	A	501	1/1	0.98	0.06	27,27,27,27	0
2	FE	B	501	1/1	0.99	0.07	26,26,26,26	0
2	FE	C	501	1/1	0.99	0.05	28,28,28,28	0

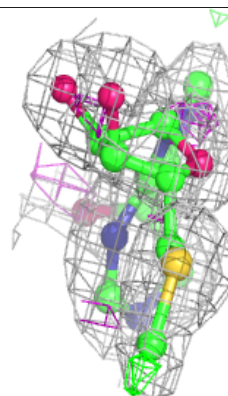
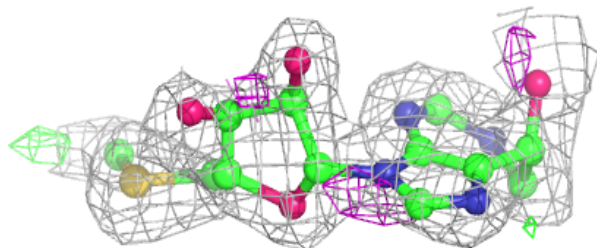
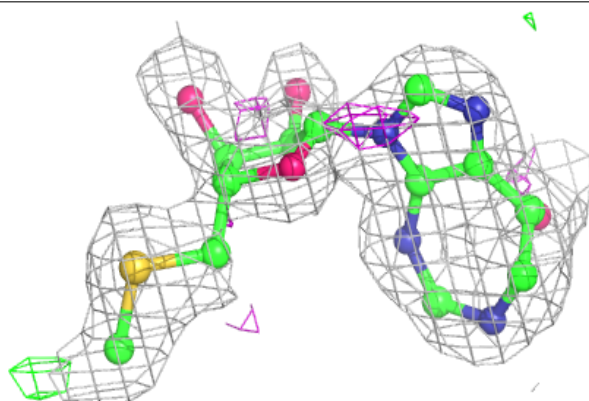
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around MCF B 504:**

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

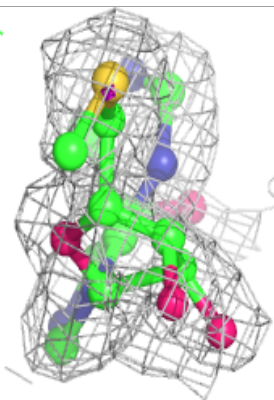
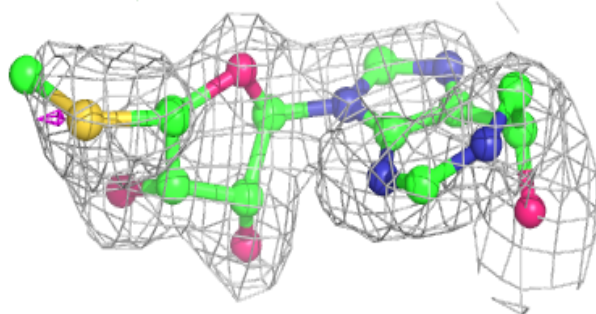
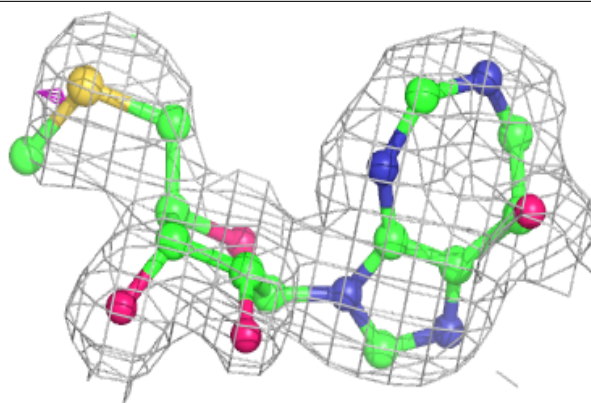
**Electron density around MCF A 506:**

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

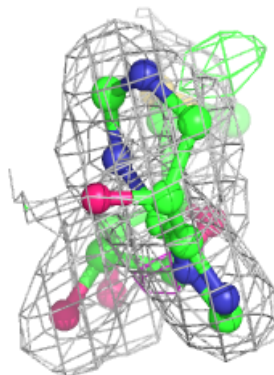
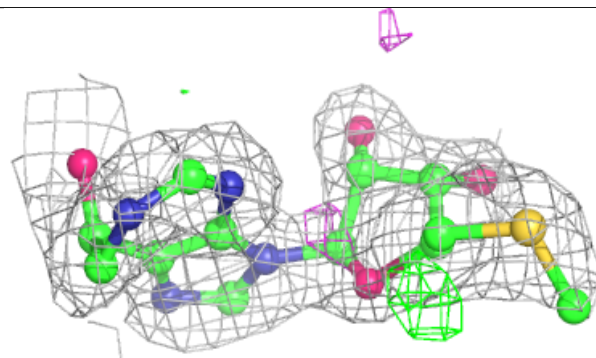
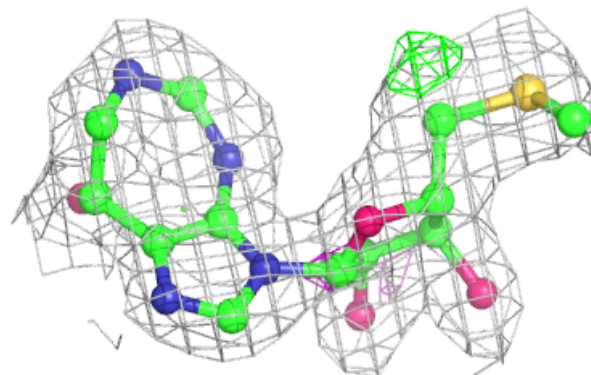


**Electron density around MCF D 507:**

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

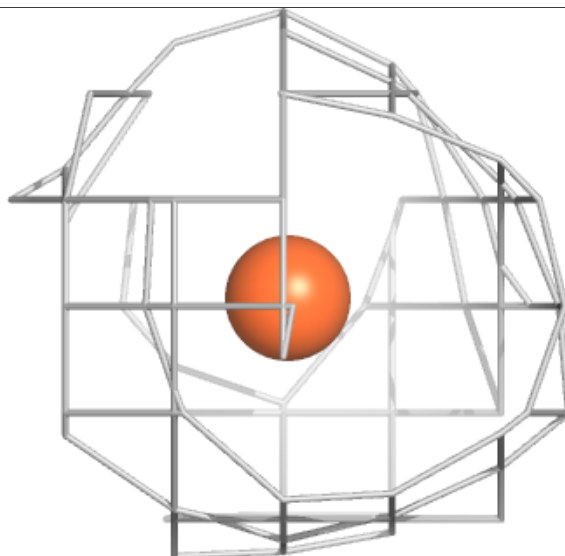
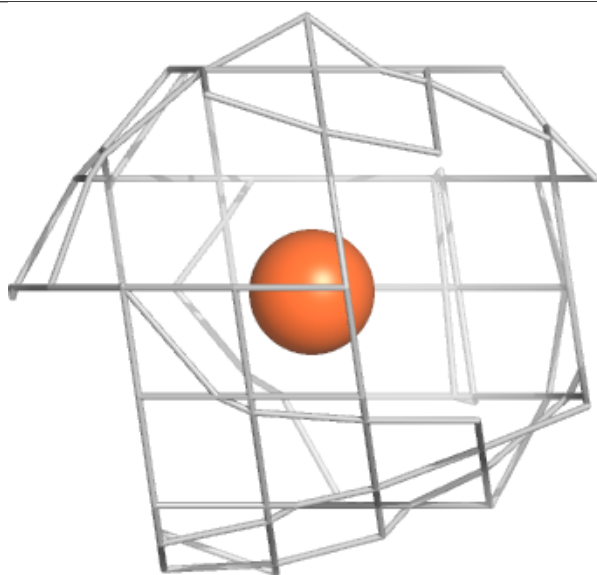
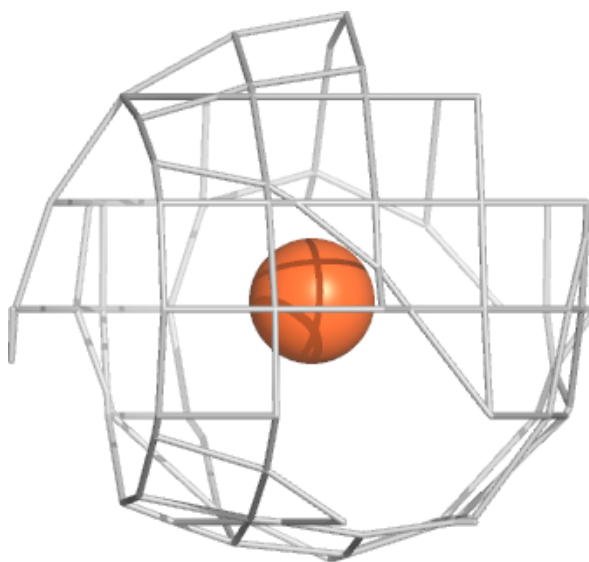
**Electron density around MCF C 504:**

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



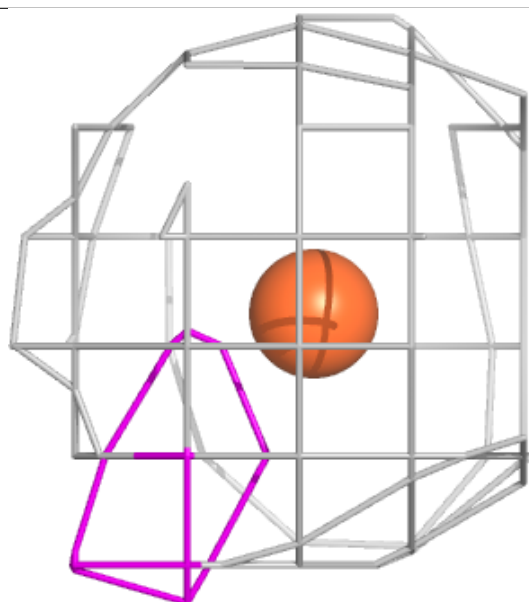
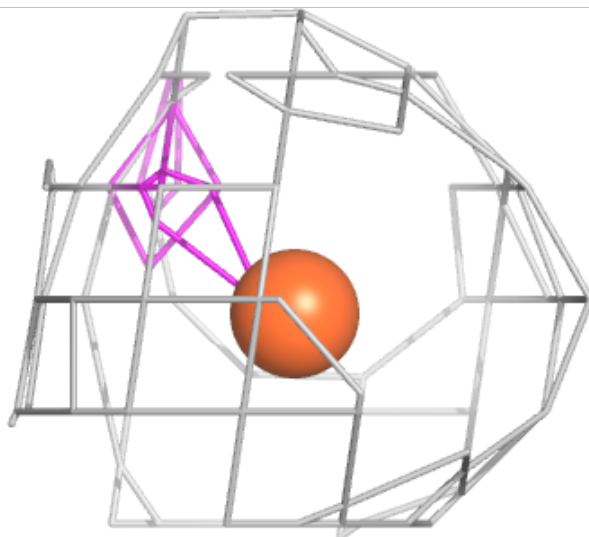
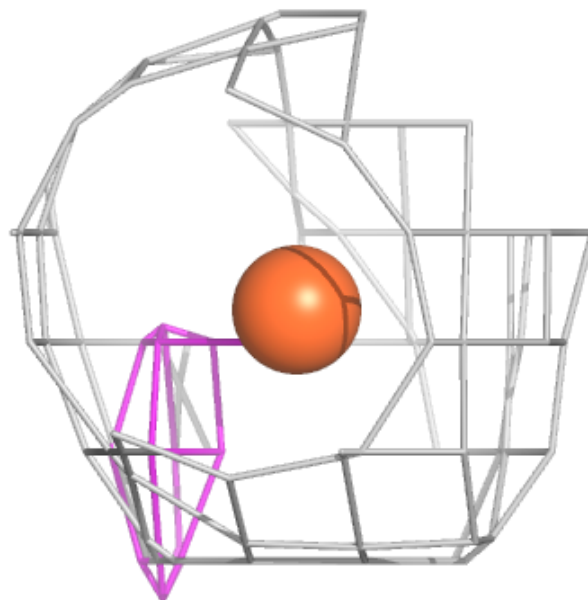
**Electron density around FE D 501:**

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



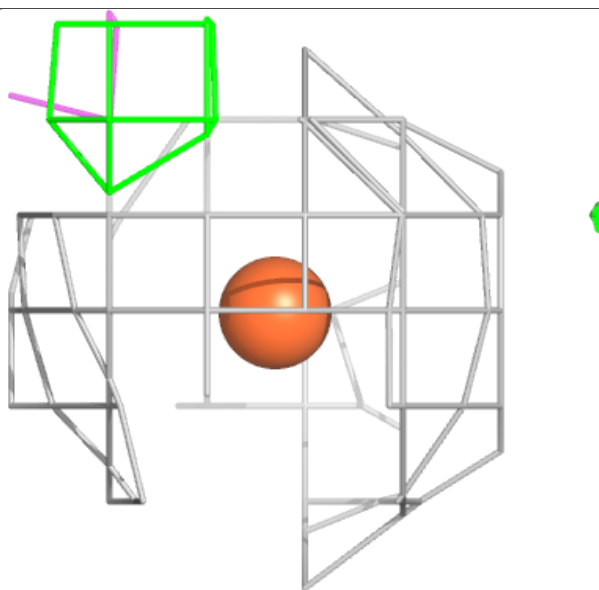
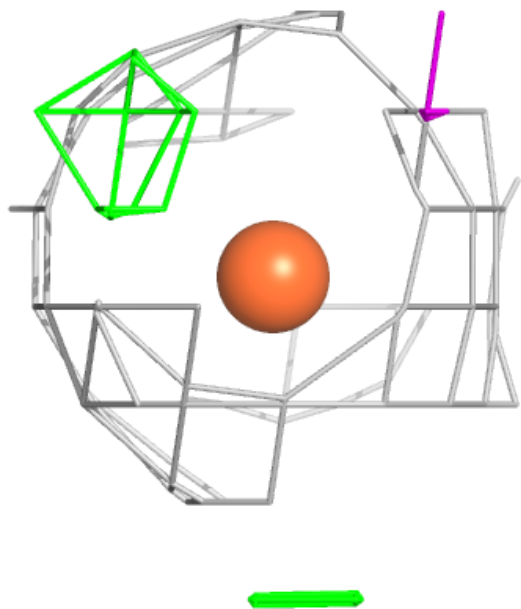
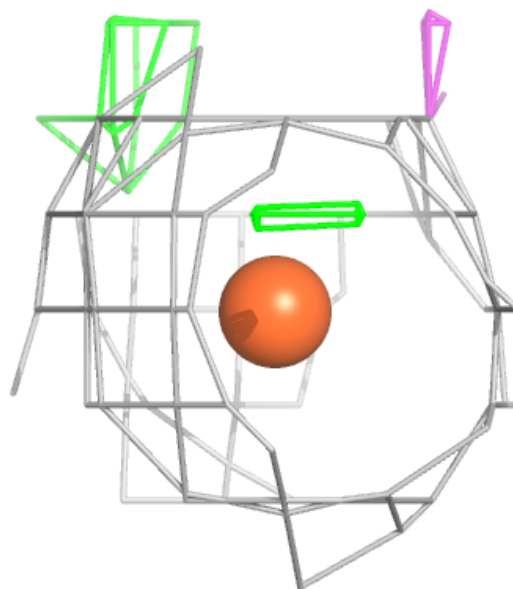
**Electron density around FE A 501:**

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

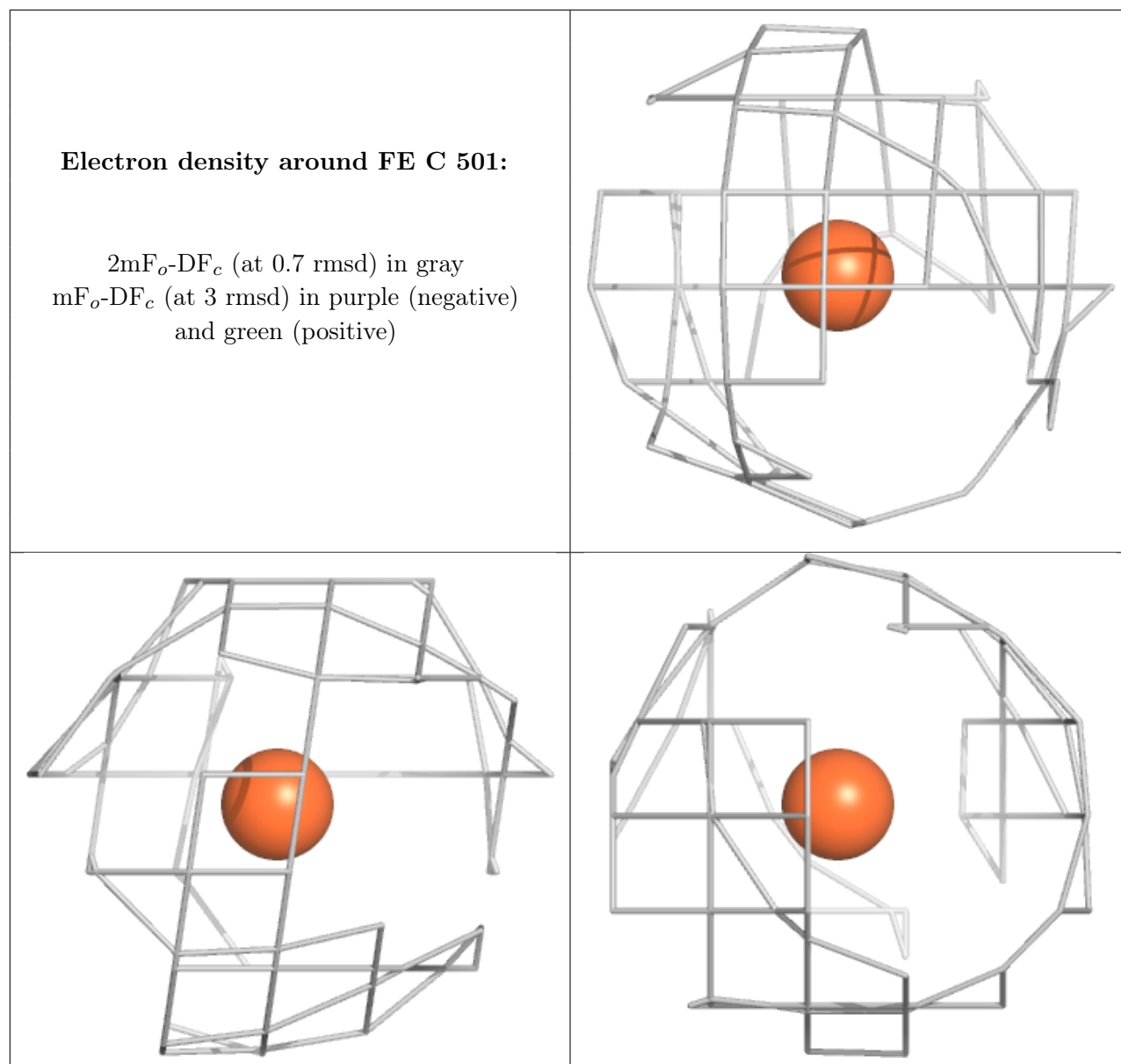


**Electron density around FE B 501:**

$2mF_o-DF_c$  (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.