wwPDB X-ray Structure Validation Summary Report (i)

Oct 9, 2023 – 11:05 PM EDT

PDB ID	:	7MTX
Title	:	Crystal Structure of the Catalytic Domain of the Inosine Monophosphate Dehydrogenase from Bacillus anthracis in the complex with IMP and the inhibitor P176
Authors	:	Kim, Y.; Maltseva, N.; Makowska-Grzyska, M.; Gu, M.; Gollapalli, D.; Hedstrom, L.; Anderson, W.F.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on	:	2021-05-13
Resolution	:	2.44 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

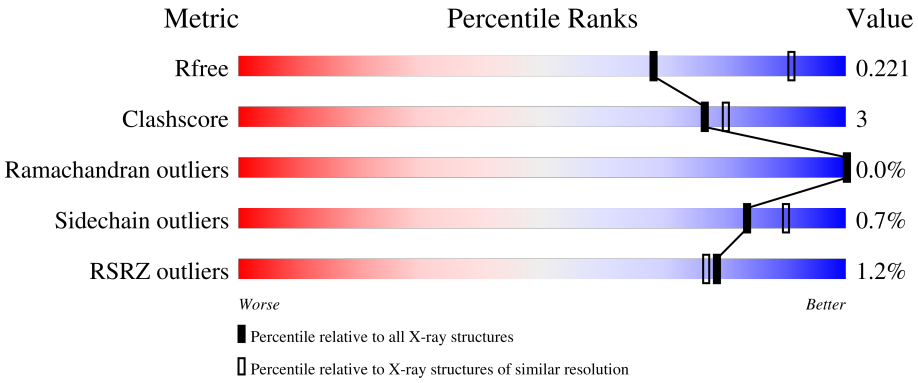
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.44 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	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	384	83% 8% 9%
1	B	384	84% 7% 9%
1	C	384	83% 9% 8%

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Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

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Mol	Chain	Length	Quality of chain
1	D	384	83% 9% 9%
1	E	384	% 85% 6% 8%
1	F	384	3% 83% 9% 8%
1	G	384	2% 83% 8% 9%
1	H	384	84% 7% 9%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 21542 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 Inosine-5'-monophosphate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	0	0
			2570	1615	451	488	16			
1	B	350	Total	C	N	O	S	0	1	0
			2578	1619	453	490	16			
1	C	354	Total	C	N	O	S	0	0	0
			2597	1631	455	495	16			
1	D	351	Total	C	N	O	S	0	1	0
			2580	1619	453	492	16			
1	E	352	Total	C	N	O	S	0	0	0
			2585	1623	454	492	16			
1	F	355	Total	C	N	O	S	0	1	0
			2614	1642	458	497	17			
1	G	349	Total	C	N	O	S	0	1	0
			2572	1615	453	488	16			
1	H	349	Total	C	N	O	S	0	0	0
			2561	1609	449	487	16			

There are 208 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	initiating methionine	UNP A0A6H3A7R4
A	-22	HIS	-	expression tag	UNP A0A6H3A7R4
A	-21	HIS	-	expression tag	UNP A0A6H3A7R4
A	-20	HIS	-	expression tag	UNP A0A6H3A7R4
A	-19	HIS	-	expression tag	UNP A0A6H3A7R4
A	-18	HIS	-	expression tag	UNP A0A6H3A7R4
A	-17	HIS	-	expression tag	UNP A0A6H3A7R4
A	-16	SER	-	expression tag	UNP A0A6H3A7R4
A	-15	SER	-	expression tag	UNP A0A6H3A7R4
A	-14	GLY	-	expression tag	UNP A0A6H3A7R4
A	-13	VAL	-	expression tag	UNP A0A6H3A7R4
A	-12	ASP	-	expression tag	UNP A0A6H3A7R4
A	-11	LEU	-	expression tag	UNP A0A6H3A7R4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLY	-	expression tag	UNP A0A6H3A7R4
A	-9	THR	-	expression tag	UNP A0A6H3A7R4
A	-8	GLU	-	expression tag	UNP A0A6H3A7R4
A	-7	ASN	-	expression tag	UNP A0A6H3A7R4
A	-6	LEU	-	expression tag	UNP A0A6H3A7R4
A	-5	TYR	-	expression tag	UNP A0A6H3A7R4
A	-4	PHE	-	expression tag	UNP A0A6H3A7R4
A	-3	GLN	-	expression tag	UNP A0A6H3A7R4
A	-2	SER	-	expression tag	UNP A0A6H3A7R4
A	-1	ASN	-	expression tag	UNP A0A6H3A7R4
A	0	ALA	-	expression tag	UNP A0A6H3A7R4
A	92	GLY	-	linker	UNP A0A6H3A7R4
A	220	GLY	-	linker	UNP A0A6H3A7R4
B	-23	MET	-	initiating methionine	UNP A0A6H3A7R4
B	-22	HIS	-	expression tag	UNP A0A6H3A7R4
B	-21	HIS	-	expression tag	UNP A0A6H3A7R4
B	-20	HIS	-	expression tag	UNP A0A6H3A7R4
B	-19	HIS	-	expression tag	UNP A0A6H3A7R4
B	-18	HIS	-	expression tag	UNP A0A6H3A7R4
B	-17	HIS	-	expression tag	UNP A0A6H3A7R4
B	-16	SER	-	expression tag	UNP A0A6H3A7R4
B	-15	SER	-	expression tag	UNP A0A6H3A7R4
B	-14	GLY	-	expression tag	UNP A0A6H3A7R4
B	-13	VAL	-	expression tag	UNP A0A6H3A7R4
B	-12	ASP	-	expression tag	UNP A0A6H3A7R4
B	-11	LEU	-	expression tag	UNP A0A6H3A7R4
B	-10	GLY	-	expression tag	UNP A0A6H3A7R4
B	-9	THR	-	expression tag	UNP A0A6H3A7R4
B	-8	GLU	-	expression tag	UNP A0A6H3A7R4
B	-7	ASN	-	expression tag	UNP A0A6H3A7R4
B	-6	LEU	-	expression tag	UNP A0A6H3A7R4
B	-5	TYR	-	expression tag	UNP A0A6H3A7R4
B	-4	PHE	-	expression tag	UNP A0A6H3A7R4
B	-3	GLN	-	expression tag	UNP A0A6H3A7R4
B	-2	SER	-	expression tag	UNP A0A6H3A7R4
B	-1	ASN	-	expression tag	UNP A0A6H3A7R4
B	0	ALA	-	expression tag	UNP A0A6H3A7R4
B	92	GLY	-	linker	UNP A0A6H3A7R4
B	220	GLY	-	linker	UNP A0A6H3A7R4
C	-23	MET	-	initiating methionine	UNP A0A6H3A7R4
C	-22	HIS	-	expression tag	UNP A0A6H3A7R4
C	-21	HIS	-	expression tag	UNP A0A6H3A7R4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-20	HIS	-	expression tag	UNP A0A6H3A7R4
C	-19	HIS	-	expression tag	UNP A0A6H3A7R4
C	-18	HIS	-	expression tag	UNP A0A6H3A7R4
C	-17	HIS	-	expression tag	UNP A0A6H3A7R4
C	-16	SER	-	expression tag	UNP A0A6H3A7R4
C	-15	SER	-	expression tag	UNP A0A6H3A7R4
C	-14	GLY	-	expression tag	UNP A0A6H3A7R4
C	-13	VAL	-	expression tag	UNP A0A6H3A7R4
C	-12	ASP	-	expression tag	UNP A0A6H3A7R4
C	-11	LEU	-	expression tag	UNP A0A6H3A7R4
C	-10	GLY	-	expression tag	UNP A0A6H3A7R4
C	-9	THR	-	expression tag	UNP A0A6H3A7R4
C	-8	GLU	-	expression tag	UNP A0A6H3A7R4
C	-7	ASN	-	expression tag	UNP A0A6H3A7R4
C	-6	LEU	-	expression tag	UNP A0A6H3A7R4
C	-5	TYR	-	expression tag	UNP A0A6H3A7R4
C	-4	PHE	-	expression tag	UNP A0A6H3A7R4
C	-3	GLN	-	expression tag	UNP A0A6H3A7R4
C	-2	SER	-	expression tag	UNP A0A6H3A7R4
C	-1	ASN	-	expression tag	UNP A0A6H3A7R4
C	0	ALA	-	expression tag	UNP A0A6H3A7R4
C	92	GLY	-	linker	UNP A0A6H3A7R4
C	220	GLY	-	linker	UNP A0A6H3A7R4
D	-23	MET	-	initiating methionine	UNP A0A6H3A7R4
D	-22	HIS	-	expression tag	UNP A0A6H3A7R4
D	-21	HIS	-	expression tag	UNP A0A6H3A7R4
D	-20	HIS	-	expression tag	UNP A0A6H3A7R4
D	-19	HIS	-	expression tag	UNP A0A6H3A7R4
D	-18	HIS	-	expression tag	UNP A0A6H3A7R4
D	-17	HIS	-	expression tag	UNP A0A6H3A7R4
D	-16	SER	-	expression tag	UNP A0A6H3A7R4
D	-15	SER	-	expression tag	UNP A0A6H3A7R4
D	-14	GLY	-	expression tag	UNP A0A6H3A7R4
D	-13	VAL	-	expression tag	UNP A0A6H3A7R4
D	-12	ASP	-	expression tag	UNP A0A6H3A7R4
D	-11	LEU	-	expression tag	UNP A0A6H3A7R4
D	-10	GLY	-	expression tag	UNP A0A6H3A7R4
D	-9	THR	-	expression tag	UNP A0A6H3A7R4
D	-8	GLU	-	expression tag	UNP A0A6H3A7R4
D	-7	ASN	-	expression tag	UNP A0A6H3A7R4
D	-6	LEU	-	expression tag	UNP A0A6H3A7R4
D	-5	TYR	-	expression tag	UNP A0A6H3A7R4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-4	PHE	-	expression tag	UNP A0A6H3A7R4
D	-3	GLN	-	expression tag	UNP A0A6H3A7R4
D	-2	SER	-	expression tag	UNP A0A6H3A7R4
D	-1	ASN	-	expression tag	UNP A0A6H3A7R4
D	0	ALA	-	expression tag	UNP A0A6H3A7R4
D	92	GLY	-	linker	UNP A0A6H3A7R4
D	220	GLY	-	linker	UNP A0A6H3A7R4
E	-23	MET	-	initiating methionine	UNP A0A6H3A7R4
E	-22	HIS	-	expression tag	UNP A0A6H3A7R4
E	-21	HIS	-	expression tag	UNP A0A6H3A7R4
E	-20	HIS	-	expression tag	UNP A0A6H3A7R4
E	-19	HIS	-	expression tag	UNP A0A6H3A7R4
E	-18	HIS	-	expression tag	UNP A0A6H3A7R4
E	-17	HIS	-	expression tag	UNP A0A6H3A7R4
E	-16	SER	-	expression tag	UNP A0A6H3A7R4
E	-15	SER	-	expression tag	UNP A0A6H3A7R4
E	-14	GLY	-	expression tag	UNP A0A6H3A7R4
E	-13	VAL	-	expression tag	UNP A0A6H3A7R4
E	-12	ASP	-	expression tag	UNP A0A6H3A7R4
E	-11	LEU	-	expression tag	UNP A0A6H3A7R4
E	-10	GLY	-	expression tag	UNP A0A6H3A7R4
E	-9	THR	-	expression tag	UNP A0A6H3A7R4
E	-8	GLU	-	expression tag	UNP A0A6H3A7R4
E	-7	ASN	-	expression tag	UNP A0A6H3A7R4
E	-6	LEU	-	expression tag	UNP A0A6H3A7R4
E	-5	TYR	-	expression tag	UNP A0A6H3A7R4
E	-4	PHE	-	expression tag	UNP A0A6H3A7R4
E	-3	GLN	-	expression tag	UNP A0A6H3A7R4
E	-2	SER	-	expression tag	UNP A0A6H3A7R4
E	-1	ASN	-	expression tag	UNP A0A6H3A7R4
E	0	ALA	-	expression tag	UNP A0A6H3A7R4
E	92	GLY	-	linker	UNP A0A6H3A7R4
E	220	GLY	-	linker	UNP A0A6H3A7R4
F	-23	MET	-	initiating methionine	UNP A0A6H3A7R4
F	-22	HIS	-	expression tag	UNP A0A6H3A7R4
F	-21	HIS	-	expression tag	UNP A0A6H3A7R4
F	-20	HIS	-	expression tag	UNP A0A6H3A7R4
F	-19	HIS	-	expression tag	UNP A0A6H3A7R4
F	-18	HIS	-	expression tag	UNP A0A6H3A7R4
F	-17	HIS	-	expression tag	UNP A0A6H3A7R4
F	-16	SER	-	expression tag	UNP A0A6H3A7R4
F	-15	SER	-	expression tag	UNP A0A6H3A7R4

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-14	GLY	-	expression tag	UNP A0A6H3A7R4
F	-13	VAL	-	expression tag	UNP A0A6H3A7R4
F	-12	ASP	-	expression tag	UNP A0A6H3A7R4
F	-11	LEU	-	expression tag	UNP A0A6H3A7R4
F	-10	GLY	-	expression tag	UNP A0A6H3A7R4
F	-9	THR	-	expression tag	UNP A0A6H3A7R4
F	-8	GLU	-	expression tag	UNP A0A6H3A7R4
F	-7	ASN	-	expression tag	UNP A0A6H3A7R4
F	-6	LEU	-	expression tag	UNP A0A6H3A7R4
F	-5	TYR	-	expression tag	UNP A0A6H3A7R4
F	-4	PHE	-	expression tag	UNP A0A6H3A7R4
F	-3	GLN	-	expression tag	UNP A0A6H3A7R4
F	-2	SER	-	expression tag	UNP A0A6H3A7R4
F	-1	ASN	-	expression tag	UNP A0A6H3A7R4
F	0	ALA	-	expression tag	UNP A0A6H3A7R4
F	92	GLY	-	linker	UNP A0A6H3A7R4
F	220	GLY	-	linker	UNP A0A6H3A7R4
G	-23	MET	-	initiating methionine	UNP A0A6H3A7R4
G	-22	HIS	-	expression tag	UNP A0A6H3A7R4
G	-21	HIS	-	expression tag	UNP A0A6H3A7R4
G	-20	HIS	-	expression tag	UNP A0A6H3A7R4
G	-19	HIS	-	expression tag	UNP A0A6H3A7R4
G	-18	HIS	-	expression tag	UNP A0A6H3A7R4
G	-17	HIS	-	expression tag	UNP A0A6H3A7R4
G	-16	SER	-	expression tag	UNP A0A6H3A7R4
G	-15	SER	-	expression tag	UNP A0A6H3A7R4
G	-14	GLY	-	expression tag	UNP A0A6H3A7R4
G	-13	VAL	-	expression tag	UNP A0A6H3A7R4
G	-12	ASP	-	expression tag	UNP A0A6H3A7R4
G	-11	LEU	-	expression tag	UNP A0A6H3A7R4
G	-10	GLY	-	expression tag	UNP A0A6H3A7R4
G	-9	THR	-	expression tag	UNP A0A6H3A7R4
G	-8	GLU	-	expression tag	UNP A0A6H3A7R4
G	-7	ASN	-	expression tag	UNP A0A6H3A7R4
G	-6	LEU	-	expression tag	UNP A0A6H3A7R4
G	-5	TYR	-	expression tag	UNP A0A6H3A7R4
G	-4	PHE	-	expression tag	UNP A0A6H3A7R4
G	-3	GLN	-	expression tag	UNP A0A6H3A7R4
G	-2	SER	-	expression tag	UNP A0A6H3A7R4
G	-1	ASN	-	expression tag	UNP A0A6H3A7R4
G	0	ALA	-	expression tag	UNP A0A6H3A7R4
G	92	GLY	-	linker	UNP A0A6H3A7R4

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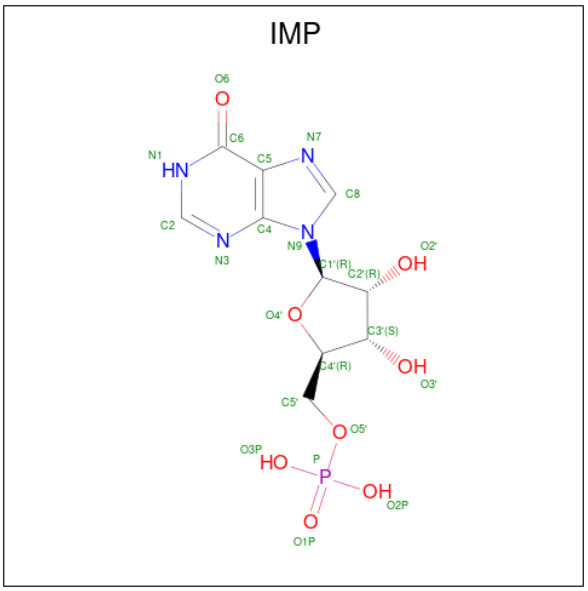
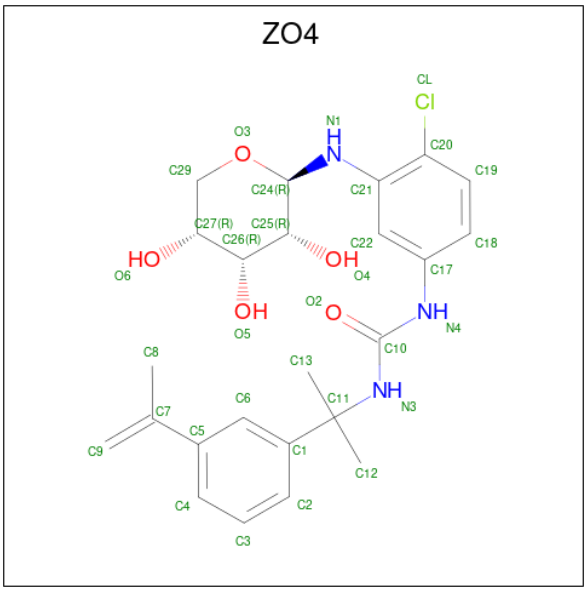
Chain	Residue	Modelled	Actual	Comment	Reference
G	220	GLY	-	linker	UNP A0A6H3A7R4
H	-23	MET	-	initiating methionine	UNP A0A6H3A7R4
H	-22	HIS	-	expression tag	UNP A0A6H3A7R4
H	-21	HIS	-	expression tag	UNP A0A6H3A7R4
H	-20	HIS	-	expression tag	UNP A0A6H3A7R4
H	-19	HIS	-	expression tag	UNP A0A6H3A7R4
H	-18	HIS	-	expression tag	UNP A0A6H3A7R4
H	-17	HIS	-	expression tag	UNP A0A6H3A7R4
H	-16	SER	-	expression tag	UNP A0A6H3A7R4
H	-15	SER	-	expression tag	UNP A0A6H3A7R4
H	-14	GLY	-	expression tag	UNP A0A6H3A7R4
H	-13	VAL	-	expression tag	UNP A0A6H3A7R4
H	-12	ASP	-	expression tag	UNP A0A6H3A7R4
H	-11	LEU	-	expression tag	UNP A0A6H3A7R4
H	-10	GLY	-	expression tag	UNP A0A6H3A7R4
H	-9	THR	-	expression tag	UNP A0A6H3A7R4
H	-8	GLU	-	expression tag	UNP A0A6H3A7R4
H	-7	ASN	-	expression tag	UNP A0A6H3A7R4
H	-6	LEU	-	expression tag	UNP A0A6H3A7R4
H	-5	TYR	-	expression tag	UNP A0A6H3A7R4
H	-4	PHE	-	expression tag	UNP A0A6H3A7R4
H	-3	GLN	-	expression tag	UNP A0A6H3A7R4
H	-2	SER	-	expression tag	UNP A0A6H3A7R4
H	-1	ASN	-	expression tag	UNP A0A6H3A7R4
H	0	ALA	-	expression tag	UNP A0A6H3A7R4
H	92	GLY	-	linker	UNP A0A6H3A7R4
H	220	GLY	-	linker	UNP A0A6H3A7R4

- Molecule 2 is INOSINIC ACID (three-letter code: IMP) (formula: $C_{10}H_{13}N_4O_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	B	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	C	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	D	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	E	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	F	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	G	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	H	1	Total	C	N	O	P	0	0
			23	10	4	8	1		

- Molecule 3 is N-{2-chloro-5-[({2-[3-(prop-1-en-2-yl)phenyl]propan-2-yl}carbamoyl)amino]phenyl}-beta-D-ribopyranosylamine (three-letter code: ZO4) (formula: $C_{24}H_{30}ClN_3O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0	0
			33	24	1	3	5		
3	B	1	Total	C	Cl	N	O	0	0
			33	24	1	3	5		
3	C	1	Total	C	Cl	N	O	0	0
			33	24	1	3	5		
3	D	1	Total	C	Cl	N	O	0	0
			33	24	1	3	5		
3	E	1	Total	C	Cl	N	O	0	0
			33	24	1	3	5		
3	F	1	Total	C	Cl	N	O	0	0
			33	24	1	3	5		
3	G	1	Total	C	Cl	N	O	0	0
			33	24	1	3	5		
3	H	1	Total	C	Cl	N	O	0	0
			33	24	1	3	5		

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	K	0	0
			1	1		
4	B	1	Total	K	0	0
			1	1		
4	C	1	Total	K	0	0
			1	1		
4	D	1	Total	K	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total K 1 1	0	0
4	F	1	Total K 1 1	0	0
4	G	1	Total K 1 1	0	0
4	H	1	Total K 1 1	0	0

- Molecule 5 is water.

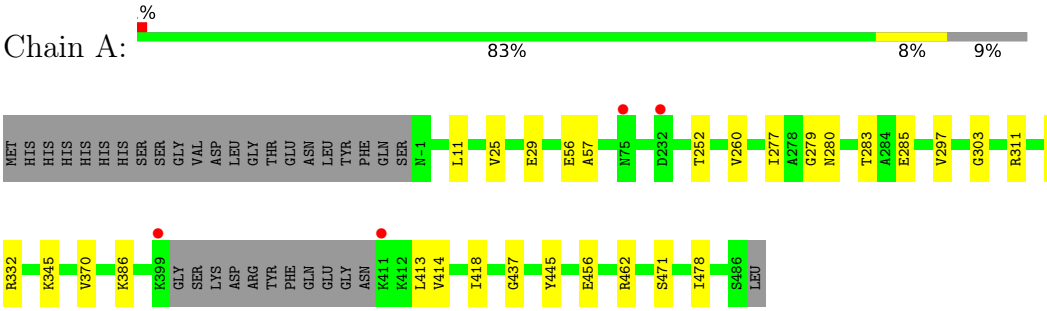
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	59	Total O 59 59	0	0
5	B	65	Total O 65 65	0	0
5	C	67	Total O 67 67	0	0
5	D	58	Total O 58 58	0	0
5	E	50	Total O 50 50	0	0
5	F	44	Total O 44 44	0	0
5	G	52	Total O 52 52	0	0
5	H	34	Total O 34 34	0	0

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.

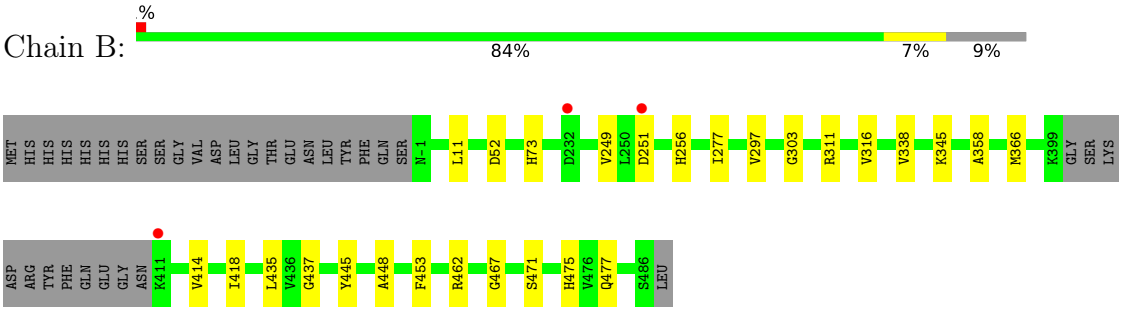
• Molecule 1: Inosine-5'-monophosphate dehydrogenase

Chain A:



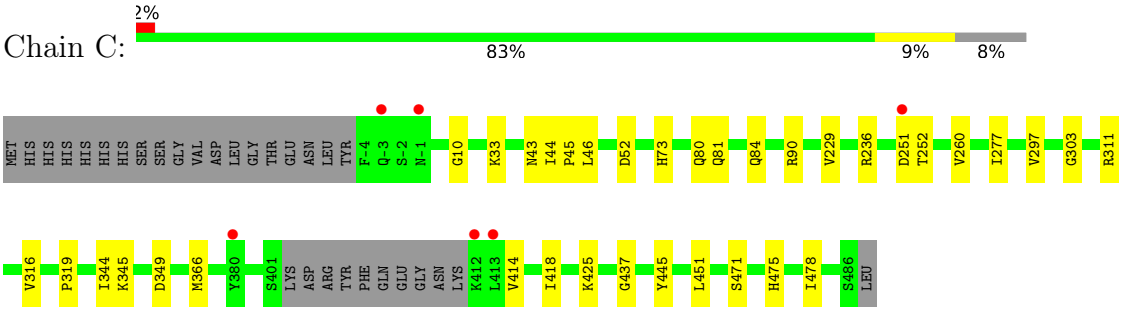
• Molecule 1: Inosine-5'-monophosphate dehydrogenase

Chain B:



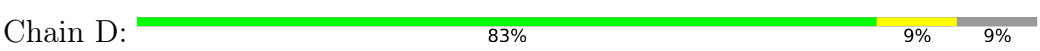
• Molecule 1: Inosine-5'-monophosphate dehydrogenase

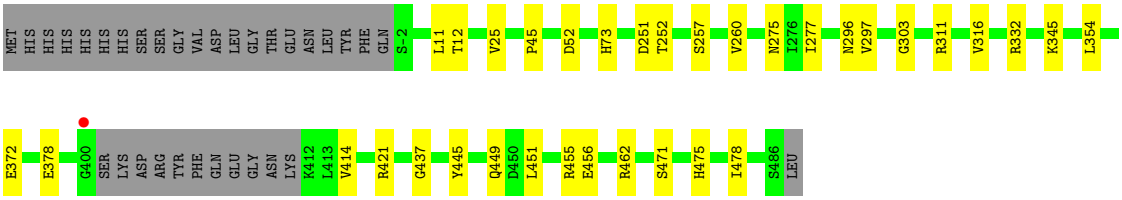
Chain C:



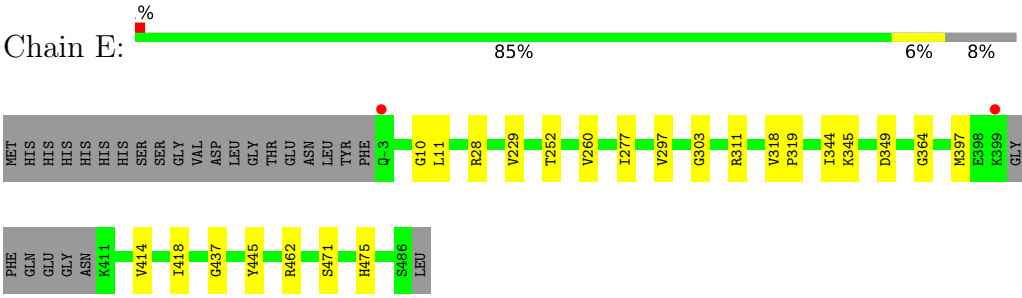
• Molecule 1: Inosine-5'-monophosphate dehydrogenase

Chain D:

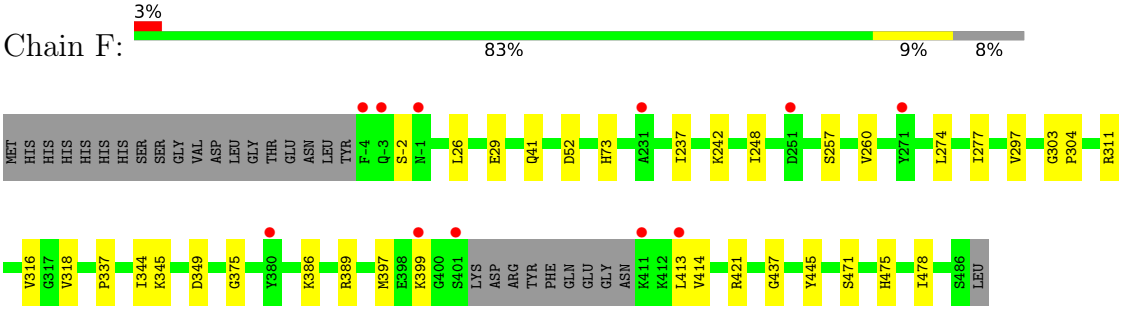




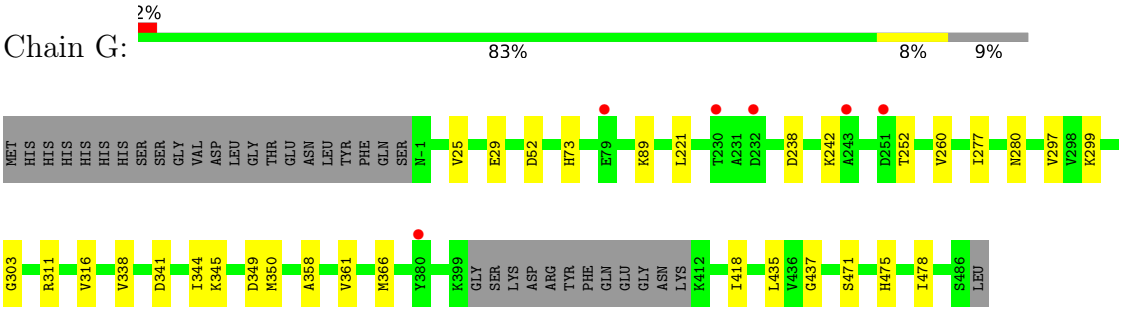
• Molecule 1: Inosine-5'-monophosphate dehydrogenase



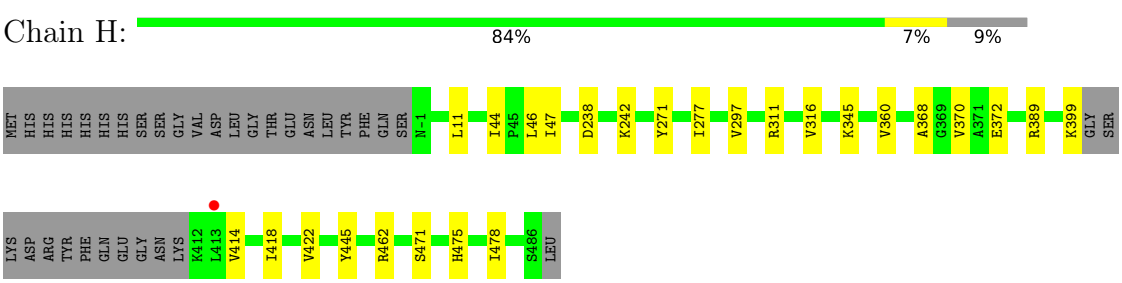
• Molecule 1: Inosine-5'-monophosphate dehydrogenase



• Molecule 1: Inosine-5'-monophosphate dehydrogenase



• Molecule 1: Inosine-5'-monophosphate dehydrogenase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	85.39Å 89.92Å 104.86Å 81.41° 90.03° 83.44°	Depositor
Resolution (Å)	40.08 – 2.44 48.33 – 2.44	Depositor EDS
% Data completeness (in resolution range)	91.2 (40.08-2.44) 91.2 (48.33-2.44)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.43 (at 2.42Å)	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
R, R_{free}	0.178 , 0.222 0.178 , 0.221	Depositor DCC
R_{free} test set	5155 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	35.4	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 36.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	21542	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: K, ZO4, IMP

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	0.24	0/2606	0.45	0/3521
1	B	0.24	0/2614	0.46	0/3532
1	C	0.24	0/2634	0.46	0/3559
1	D	0.24	0/2616	0.45	0/3535
1	E	0.24	0/2621	0.45	0/3541
1	F	0.24	0/2651	0.45	0/3580
1	G	0.24	0/2608	0.46	0/3524
1	H	0.23	0/2597	0.46	0/3510
All	All	0.24	0/20947	0.45	0/28302

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

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	2570	0	2634	21	0
1	B	2578	0	2639	18	0
1	C	2597	0	2651	23	0
1	D	2580	0	2636	24	0
1	E	2585	0	2647	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2614	0	2672	23	0
1	G	2572	0	2633	22	0
1	H	2561	0	2621	18	0
2	A	23	0	11	0	0
2	B	23	0	11	0	0
2	C	23	0	11	0	0
2	D	23	0	11	0	0
2	E	23	0	11	0	0
2	F	23	0	11	0	0
2	G	23	0	11	1	0
2	H	23	0	11	0	0
3	A	33	0	0	0	0
3	B	33	0	0	0	0
3	C	33	0	0	0	0
3	D	33	0	0	0	0
3	E	33	0	0	0	0
3	F	33	0	0	0	0
3	G	33	0	0	0	0
3	H	33	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	59	0	0	0	0
5	B	65	0	0	0	0
5	C	67	0	0	0	0
5	D	58	0	0	0	0
5	E	50	0	0	0	0
5	F	44	0	0	0	0
5	G	52	0	0	0	0
5	H	34	0	0	0	0
All	All	21542	0	21221	128	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.

The worst 5 of 128 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:C:414:VAL:HG21	1:D:437:GLY:HA3	1.71	0.72
1:E:437:GLY:HA3	1:F:414:VAL:HG21	1.77	0.66
1:F:437:GLY:HA3	1:H:414:VAL:HG21	1.77	0.66
1:D:332:ARG:NH2	1:D:456:GLU:OE2	2.31	0.62
1:A:418:ILE:HD13	1:C:478:ILE:HG12	1.83	0.61

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	346/384 (90%)	336 (97%)	10 (3%)	0	100	100
1	B	347/384 (90%)	340 (98%)	7 (2%)	0	100	100
1	C	350/384 (91%)	341 (97%)	9 (3%)	0	100	100
1	D	348/384 (91%)	338 (97%)	10 (3%)	0	100	100
1	E	348/384 (91%)	336 (97%)	11 (3%)	1 (0%)	41	49
1	F	352/384 (92%)	342 (97%)	10 (3%)	0	100	100
1	G	346/384 (90%)	337 (97%)	9 (3%)	0	100	100
1	H	345/384 (90%)	338 (98%)	7 (2%)	0	100	100
All	All	2782/3072 (91%)	2708 (97%)	73 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	364	GLY

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	268/298 (90%)	267 (100%)	1 (0%)	91 94
1	B	269/298 (90%)	267 (99%)	2 (1%)	84 90
1	C	271/298 (91%)	269 (99%)	2 (1%)	84 90
1	D	269/298 (90%)	267 (99%)	2 (1%)	84 90
1	E	270/298 (91%)	268 (99%)	2 (1%)	84 90
1	F	273/298 (92%)	269 (98%)	4 (2%)	65 76
1	G	268/298 (90%)	267 (100%)	1 (0%)	91 94
1	H	267/298 (90%)	267 (100%)	0	100 100
All	All	2155/2384 (90%)	2141 (99%)	14 (1%)	84 91

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

Mol	Chain	Res	Type
1	E	28	ARG
1	E	397	MET
1	G	366	MET
1	F	242	LYS
1	F	421	ARG

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 24 ligands modelled in this entry, 8 are monoatomic - leaving 16 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	IMP	F	501	-	21,25,25	1.46	2 (9%)	24,38,38	1.33	5 (20%)
3	ZO4	A	502	-	35,35,35	1.13	5 (14%)	50,51,51	3.10	6 (12%)
3	ZO4	F	502	-	35,35,35	1.04	4 (11%)	50,51,51	1.70	3 (6%)
3	ZO4	H	503	-	35,35,35	1.05	5 (14%)	50,51,51	1.24	4 (8%)
3	ZO4	C	503	-	35,35,35	1.14	5 (14%)	50,51,51	3.26	6 (12%)
3	ZO4	B	502	-	35,35,35	1.03	4 (11%)	50,51,51	1.80	4 (8%)
2	IMP	D	502	-	21,25,25	1.46	2 (9%)	24,38,38	1.33	5 (20%)
2	IMP	B	501	-	21,25,25	1.46	2 (9%)	24,38,38	1.30	4 (16%)
2	IMP	E	501	-	21,25,25	1.46	2 (9%)	24,38,38	1.34	5 (20%)
2	IMP	A	501	-	21,25,25	1.46	2 (9%)	24,38,38	1.33	5 (20%)
3	ZO4	E	502	-	35,35,35	1.03	4 (11%)	50,51,51	1.44	5 (10%)
3	ZO4	G	503	-	35,35,35	1.04	4 (11%)	50,51,51	1.64	3 (6%)
2	IMP	H	502	-	21,25,25	1.45	2 (9%)	24,38,38	1.35	5 (20%)
2	IMP	C	502	-	21,25,25	1.45	2 (9%)	24,38,38	1.30	5 (20%)
3	ZO4	D	503	-	35,35,35	1.04	4 (11%)	50,51,51	1.75	4 (8%)
2	IMP	G	502	-	21,25,25	1.47	2 (9%)	24,38,38	1.33	4 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	IMP	F	501	-	-	5/6/26/26	0/3/3/3
3	ZO4	A	502	-	-	4/23/40/40	0/3/3/3
3	ZO4	F	502	-	-	2/23/40/40	0/3/3/3
3	ZO4	H	503	-	-	3/23/40/40	0/3/3/3
3	ZO4	C	503	-	-	4/23/40/40	0/3/3/3
3	ZO4	B	502	-	-	2/23/40/40	0/3/3/3
2	IMP	D	502	-	-	4/6/26/26	0/3/3/3
2	IMP	B	501	-	-	5/6/26/26	0/3/3/3
2	IMP	E	501	-	-	3/6/26/26	0/3/3/3
2	IMP	A	501	-	-	5/6/26/26	0/3/3/3
3	ZO4	E	502	-	-	2/23/40/40	0/3/3/3
3	ZO4	G	503	-	-	2/23/40/40	0/3/3/3
2	IMP	H	502	-	-	4/6/26/26	0/3/3/3
2	IMP	C	502	-	-	5/6/26/26	0/3/3/3
3	ZO4	D	503	-	-	2/23/40/40	0/3/3/3
2	IMP	G	502	-	-	4/6/26/26	0/3/3/3

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	502	IMP	C2-N3	4.78	1.38	1.29
2	D	502	IMP	C2-N3	4.75	1.38	1.29
2	E	501	IMP	C2-N3	4.75	1.38	1.29
2	B	501	IMP	C2-N3	4.74	1.38	1.29
2	C	502	IMP	C2-N3	4.73	1.38	1.29

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	503	ZO4	C20-C21-N1	-16.96	112.36	120.43
3	A	502	ZO4	C20-C21-N1	-15.73	112.95	120.43
3	C	503	ZO4	C21-N1-C24	13.10	136.58	123.16
3	A	502	ZO4	C21-N1-C24	13.04	136.51	123.16
3	B	502	ZO4	C25-C24-N1	-8.89	102.65	110.71

There are no chirality outliers.

5 of 56 torsion outliers are listed below:

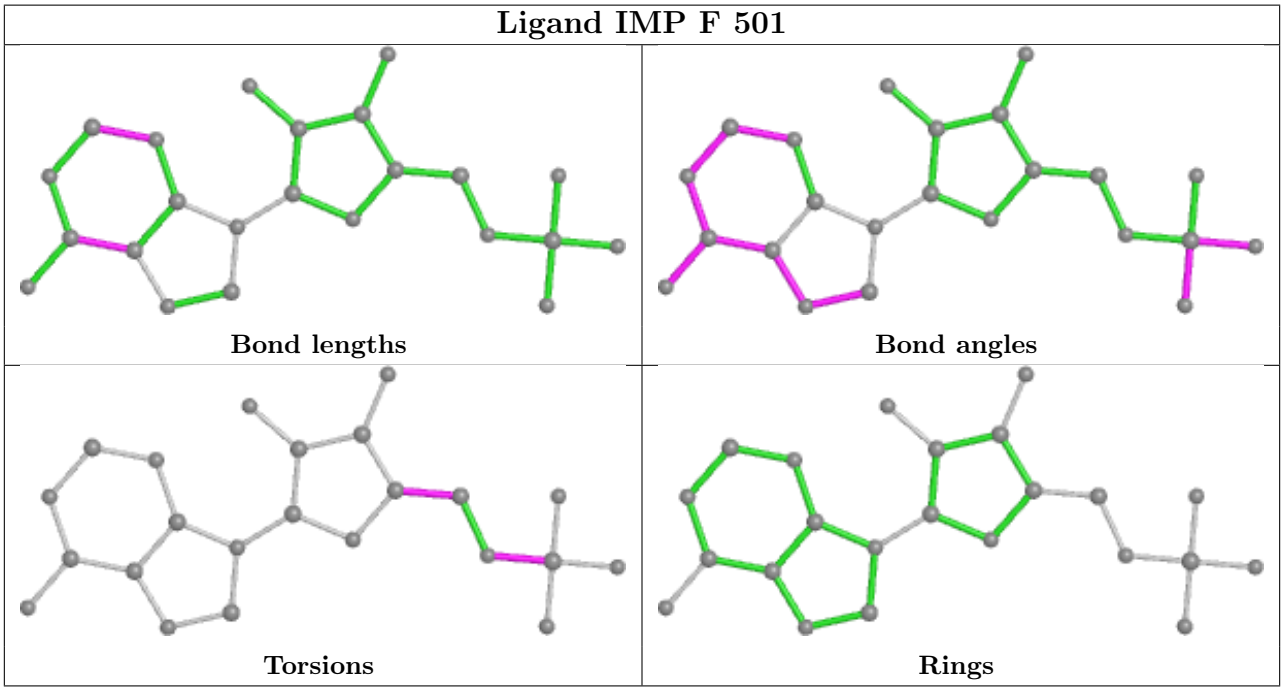
Mol	Chain	Res	Type	Atoms
2	A	501	IMP	C5'-O5'-P-O1P
2	A	501	IMP	C5'-O5'-P-O2P
2	A	501	IMP	C5'-O5'-P-O3P
2	B	501	IMP	C5'-O5'-P-O1P
2	B	501	IMP	C5'-O5'-P-O2P

There are no ring outliers.

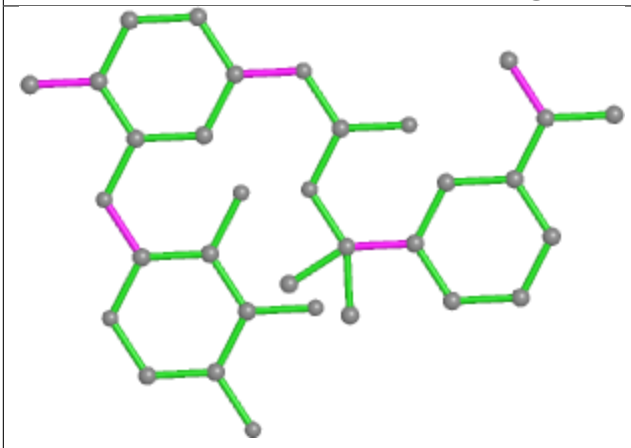
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	502	IMP	1	0

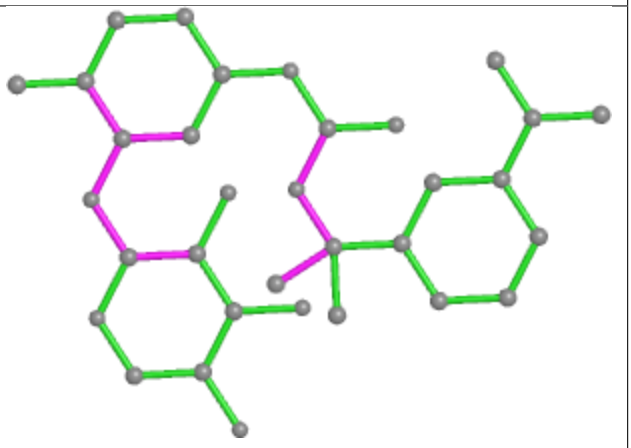
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



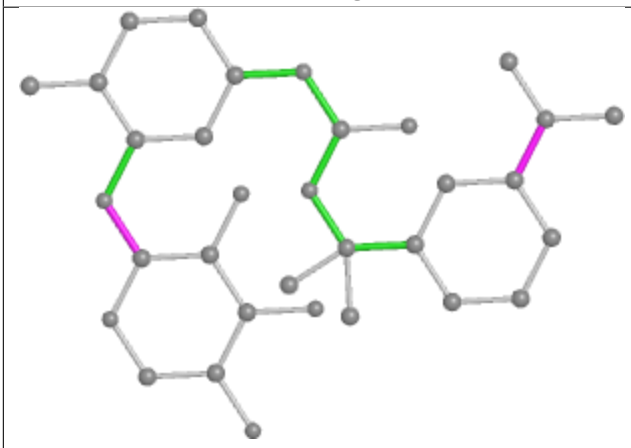
Ligand ZO4 A 502



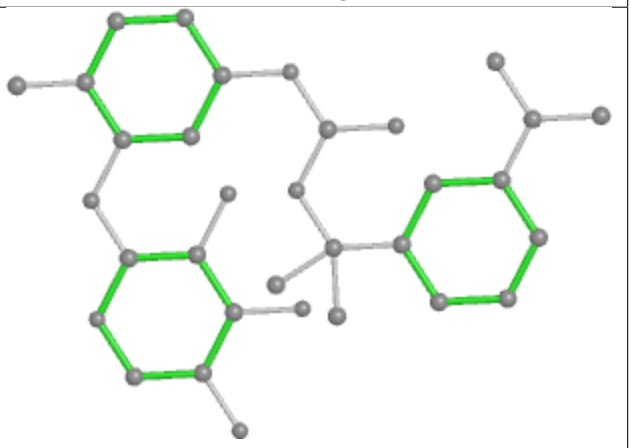
Bond lengths



Bond angles

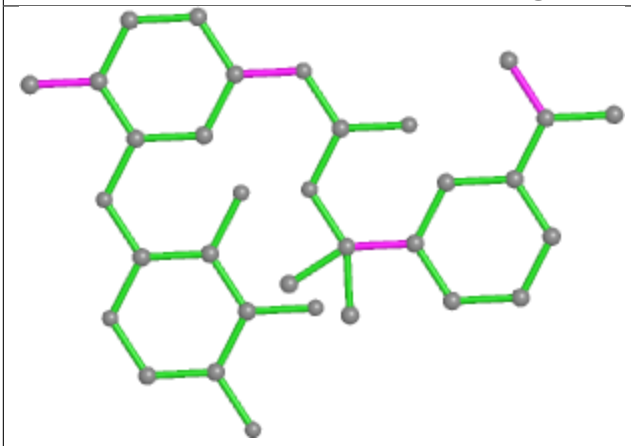


Torsions



Rings

Ligand ZO4 F 502



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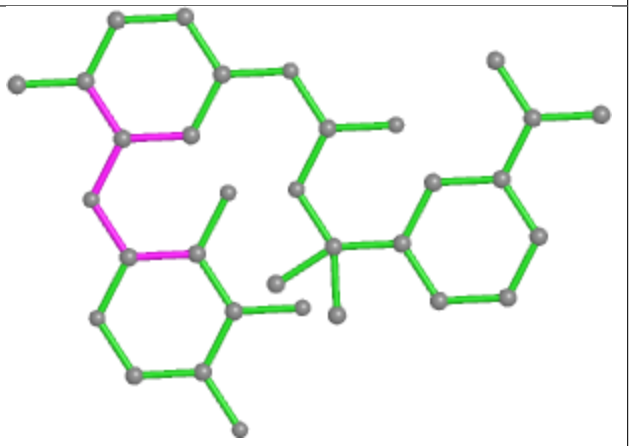
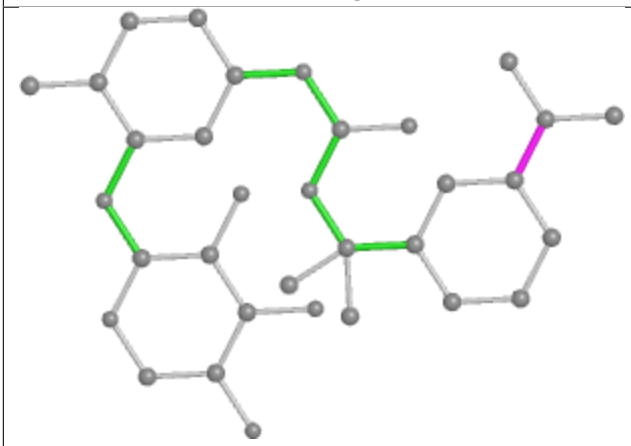


Bond angles



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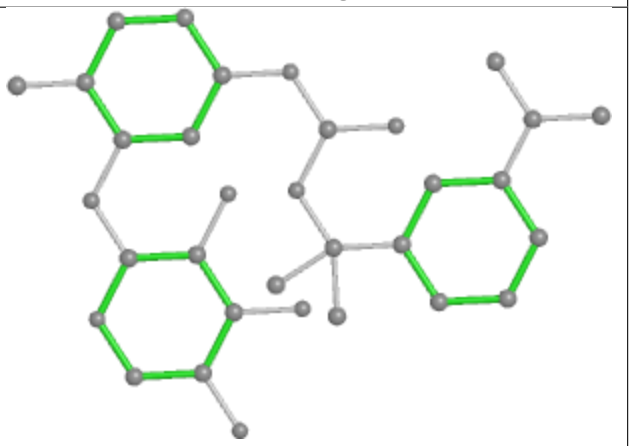
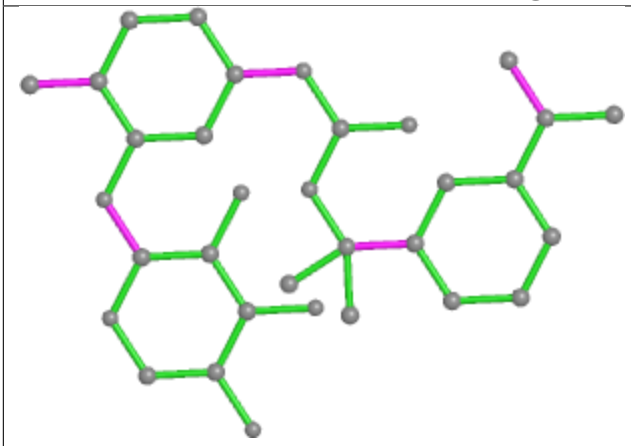


Rings

Ligand ZO4 H 503



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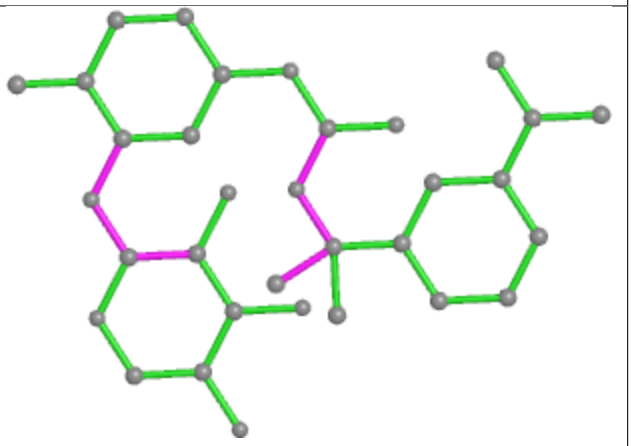

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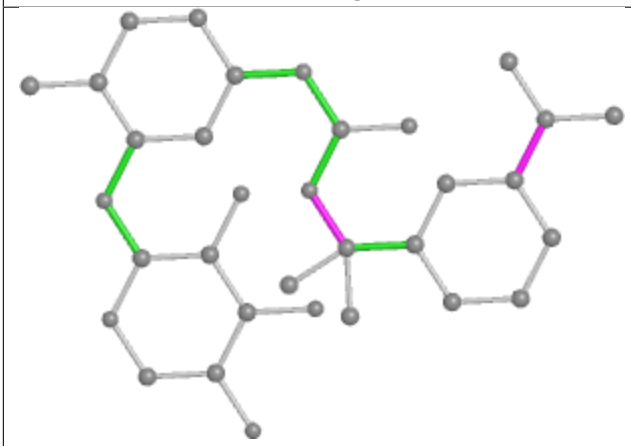

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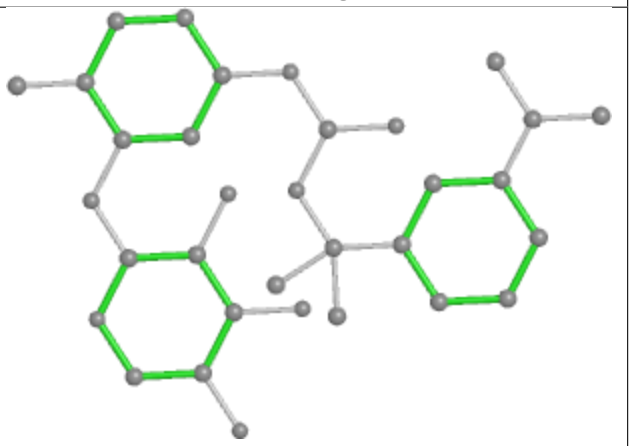
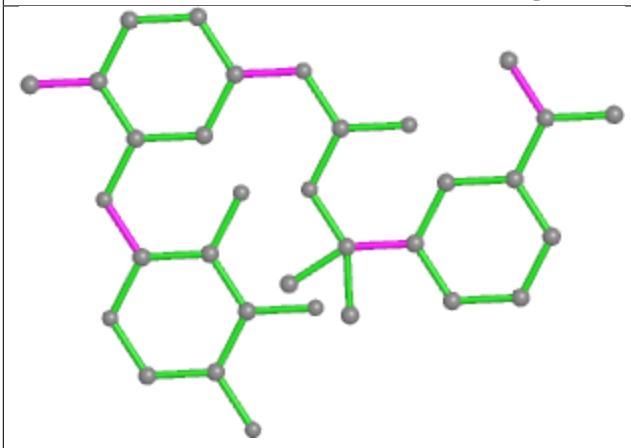


Rings

Ligand ZO4 C 503



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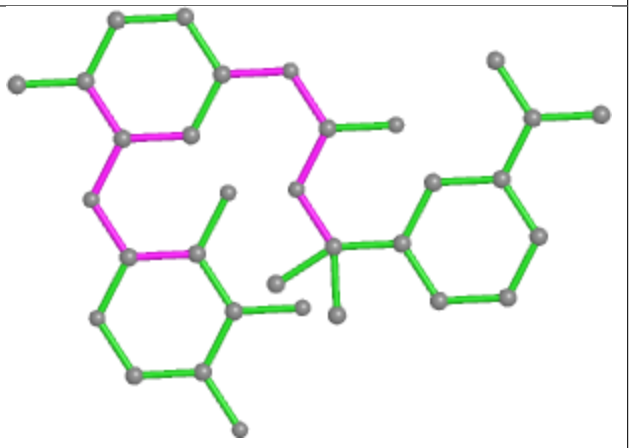

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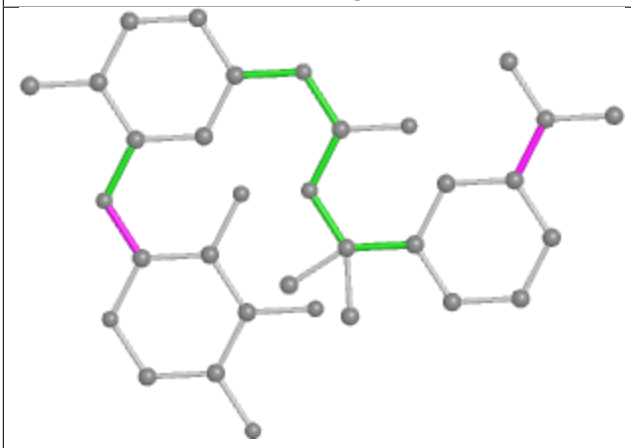

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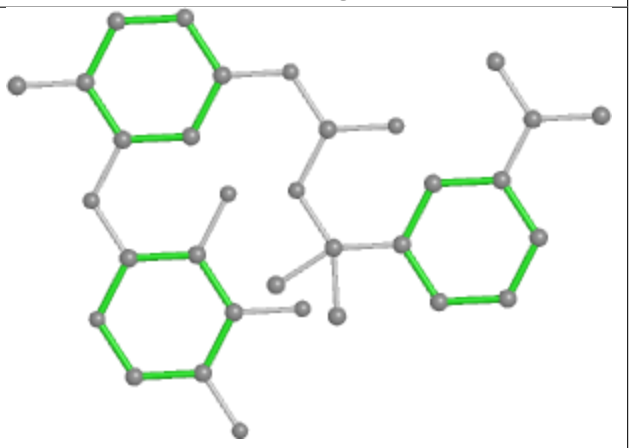
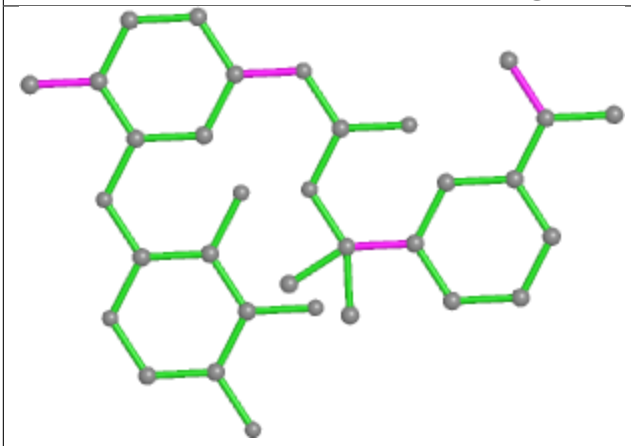


Rings

Ligand ZO4 B 502



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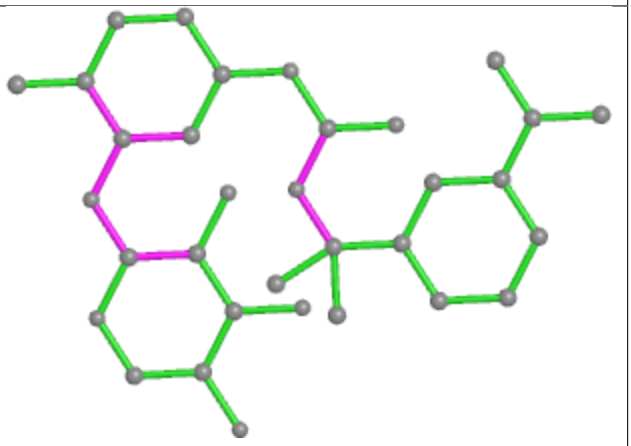

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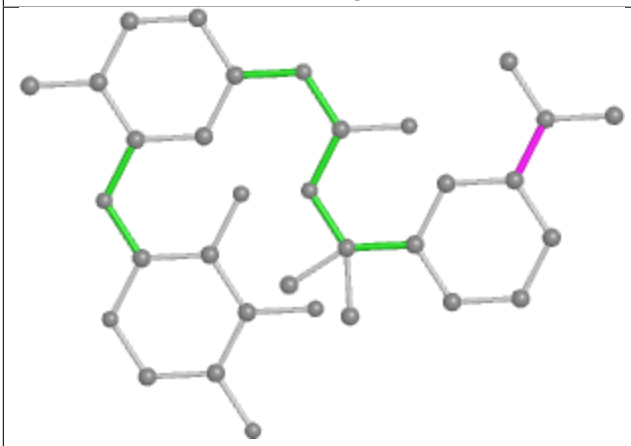

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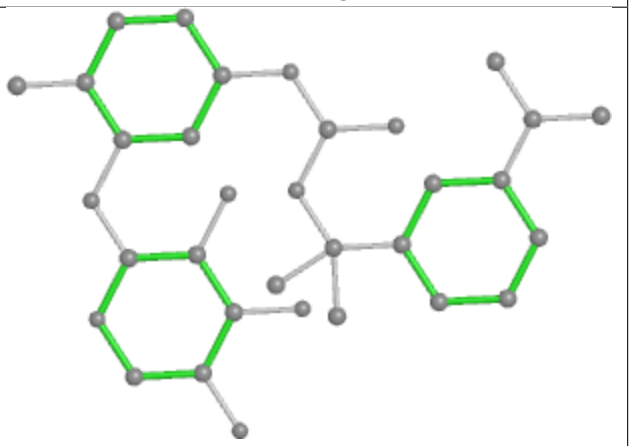
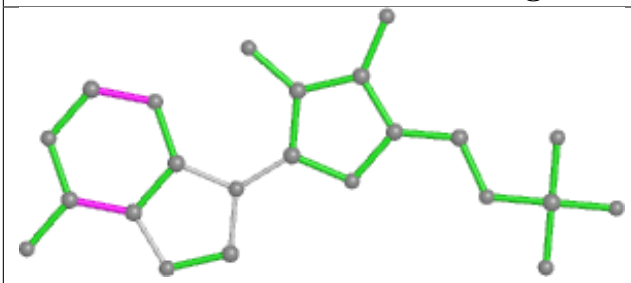


Rings

Ligand IMP D 502



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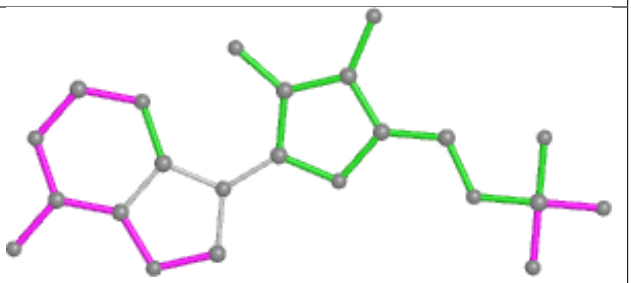

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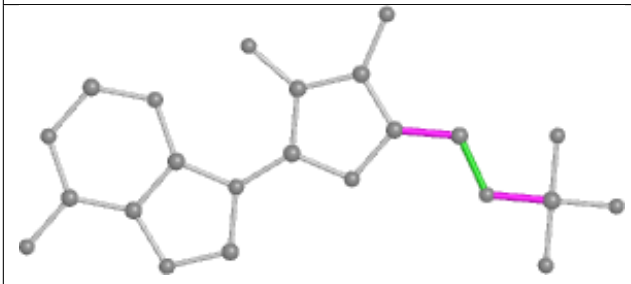

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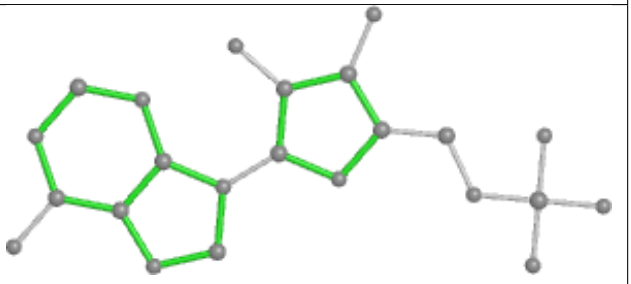

Rings

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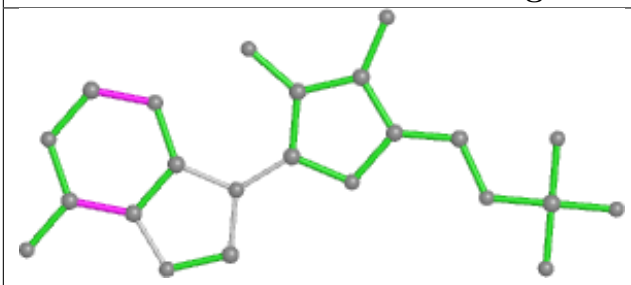

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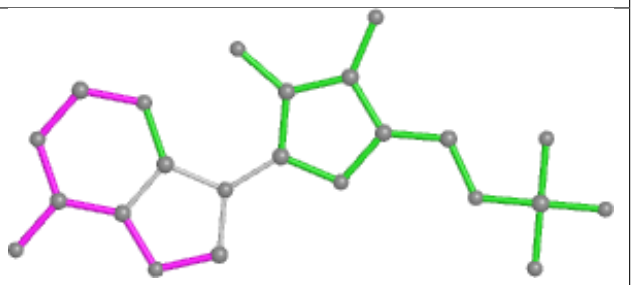

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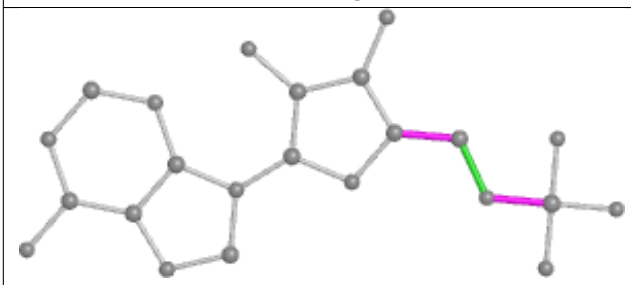

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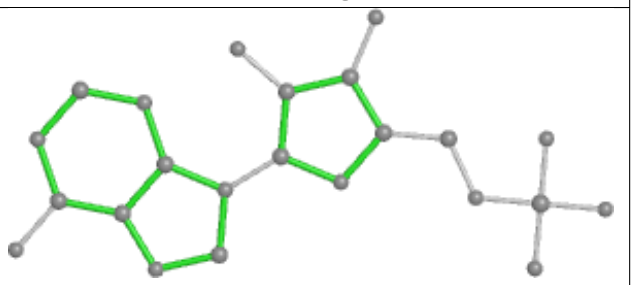
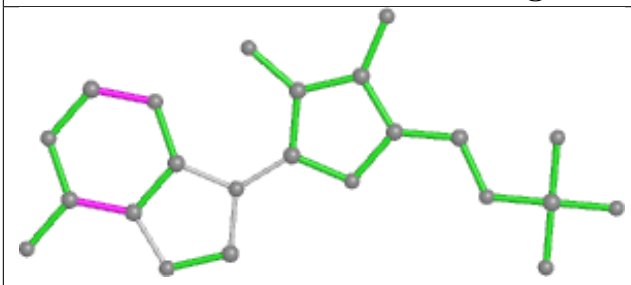


Rings

Ligand IMP E 501



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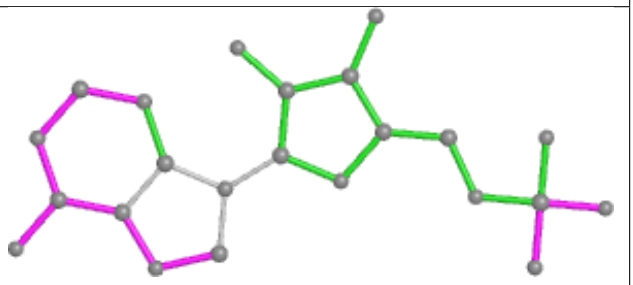

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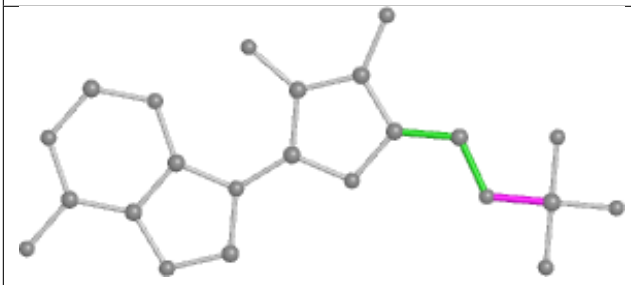

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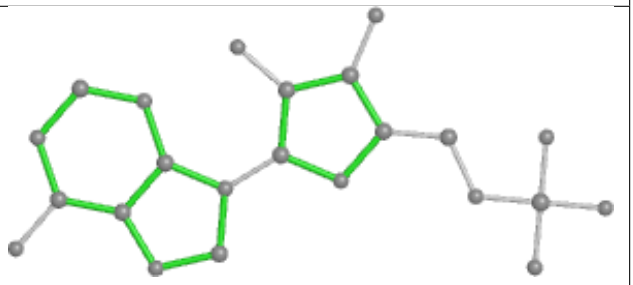

Rings

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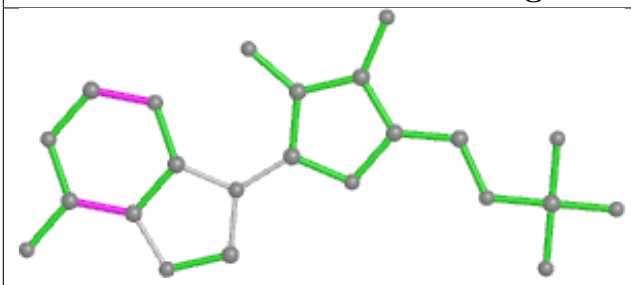

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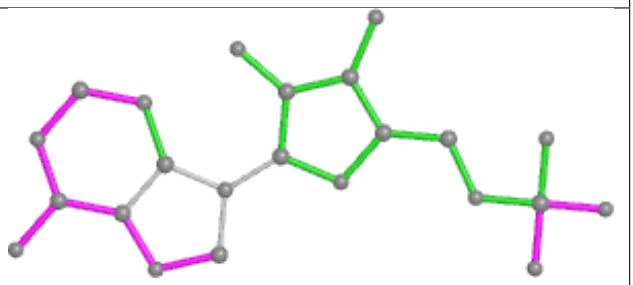

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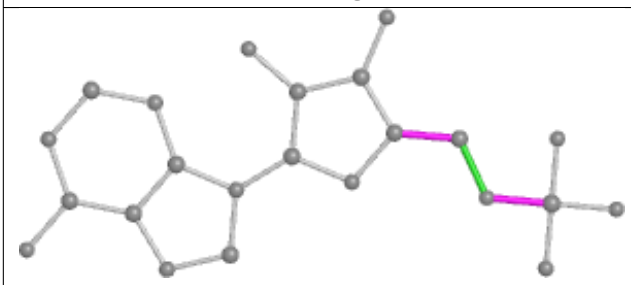

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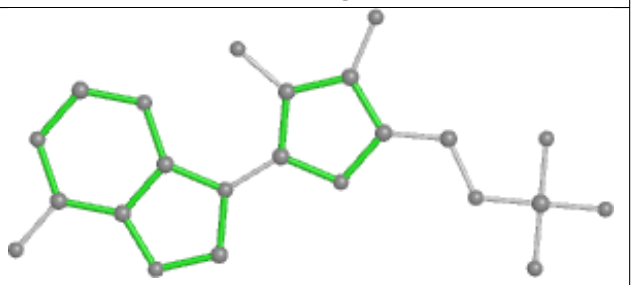
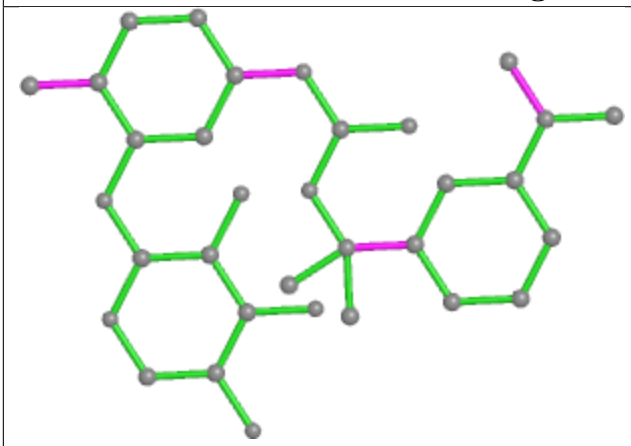


Rings

Ligand ZO4 E 502



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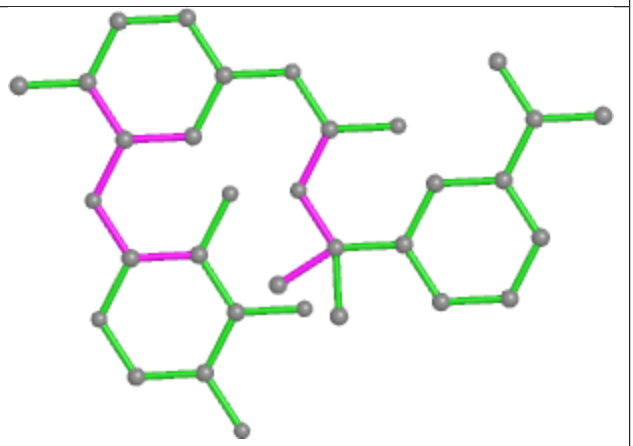

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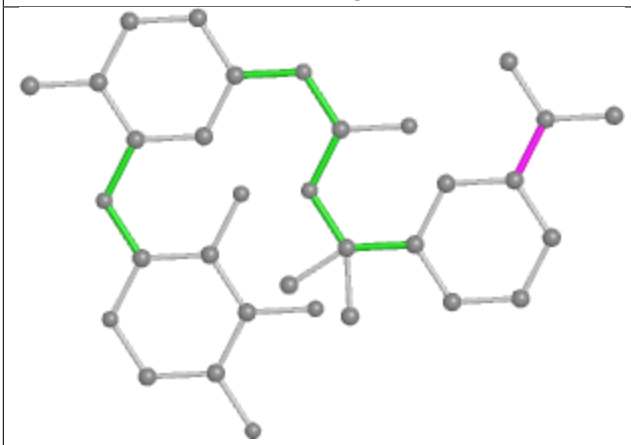

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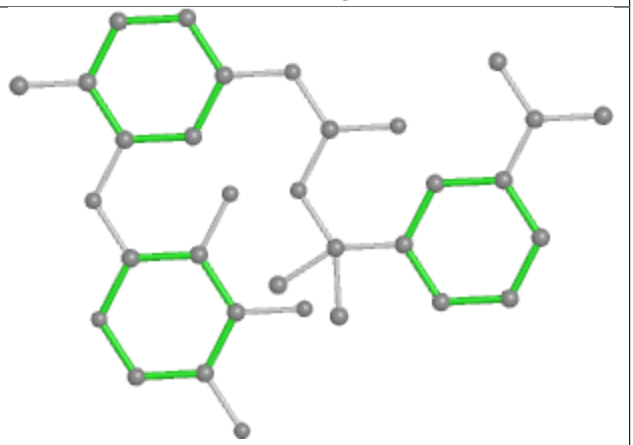
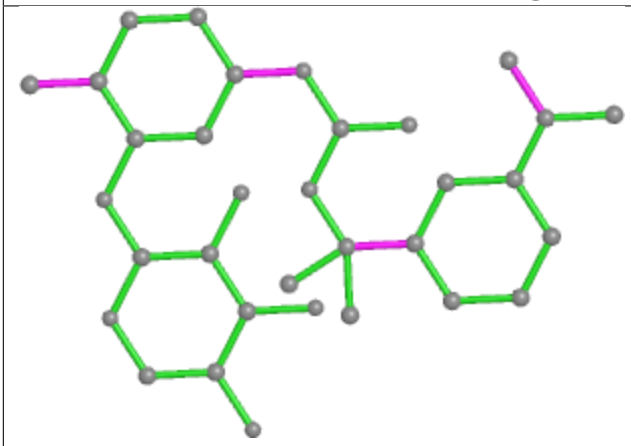


Rings

Ligand ZO4 G 503



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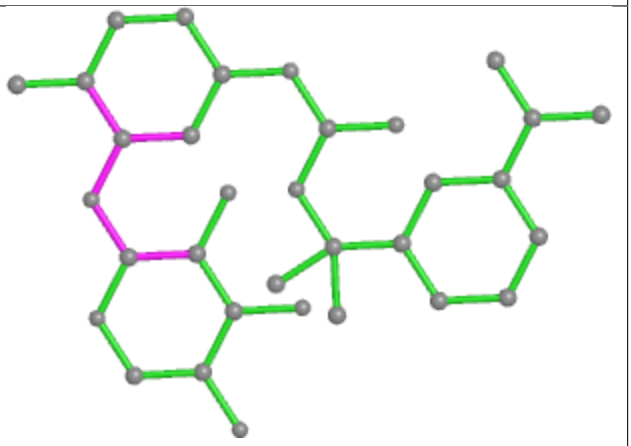

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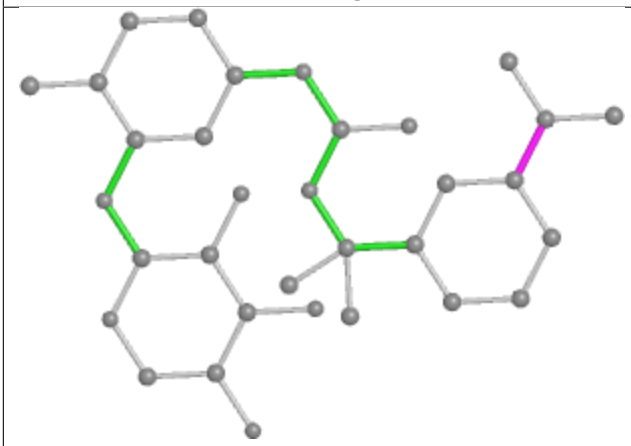

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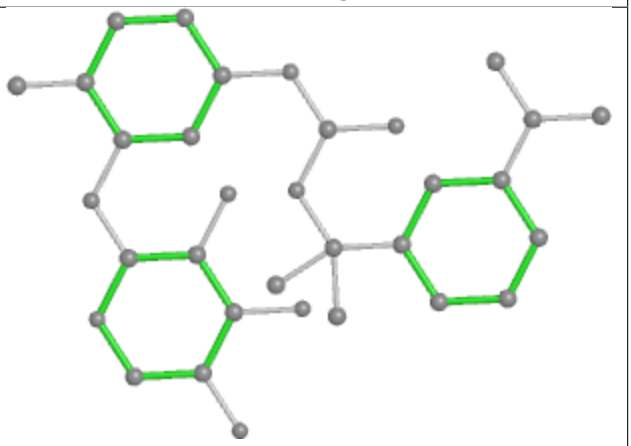
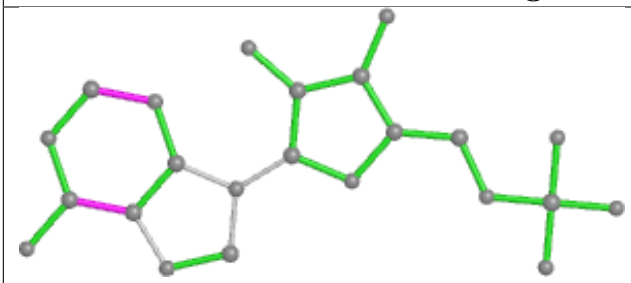


Rings

Ligand IMP H 502



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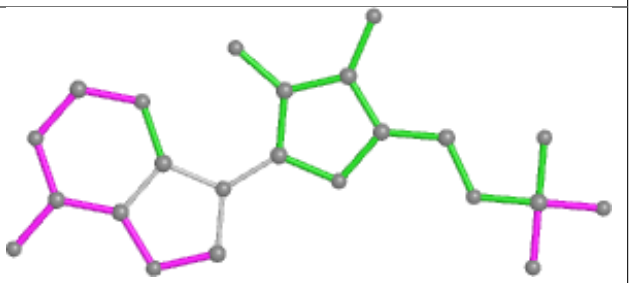

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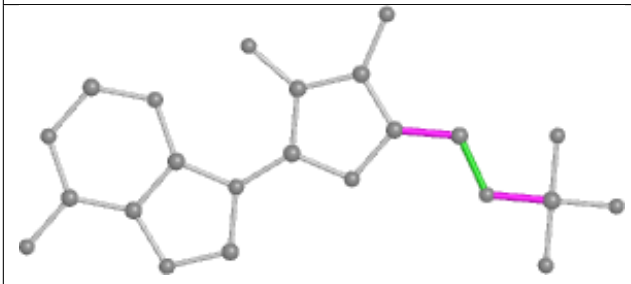

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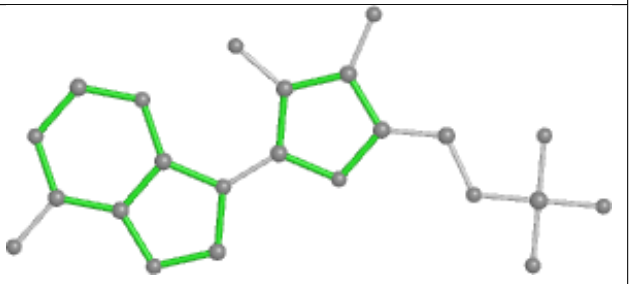
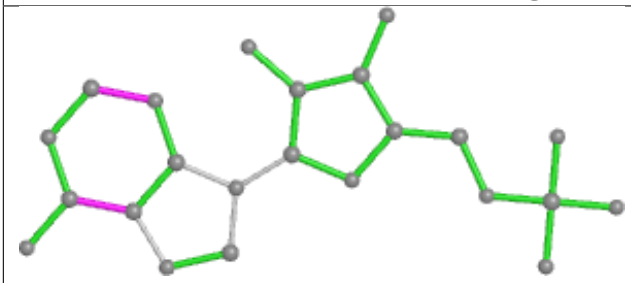


Rings

Ligand IMP C 502



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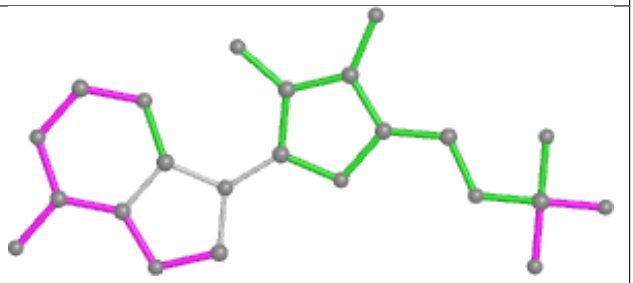
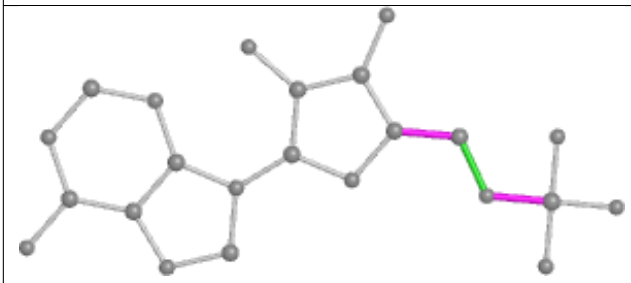


Bond angles



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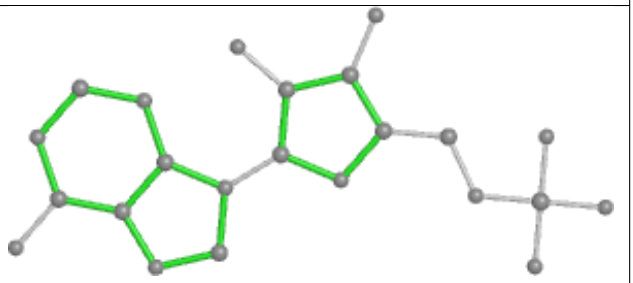
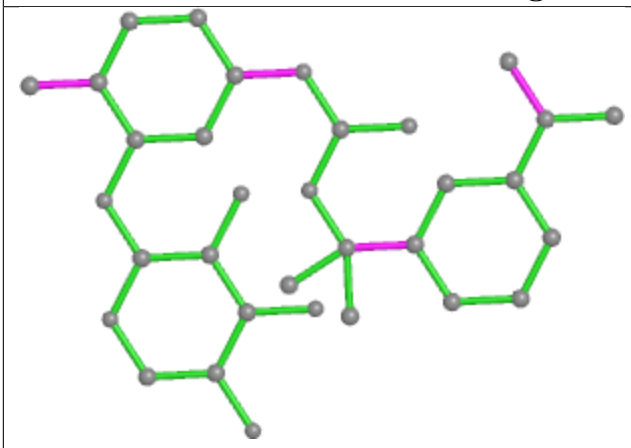


Rings

Ligand ZO4 D 503



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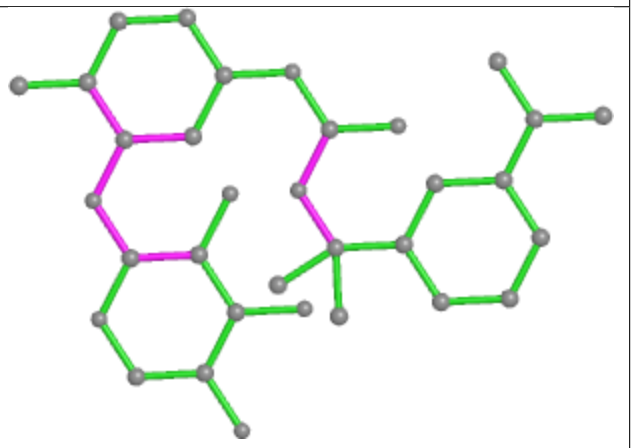
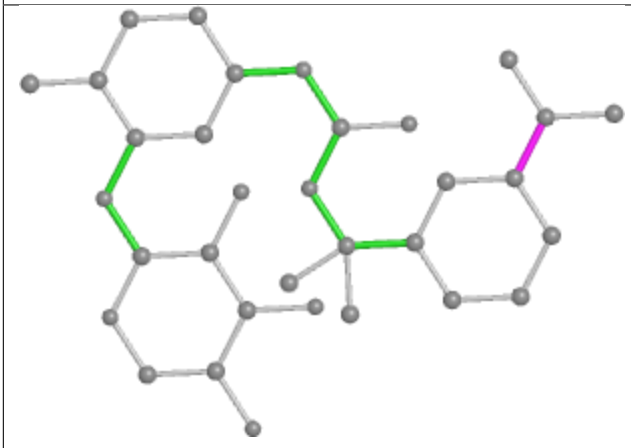


Bond angles



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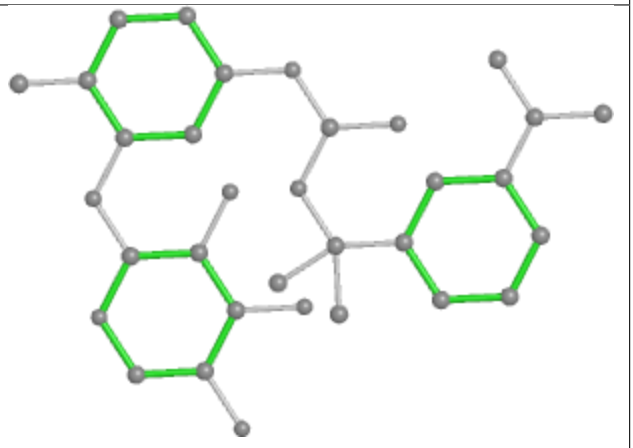
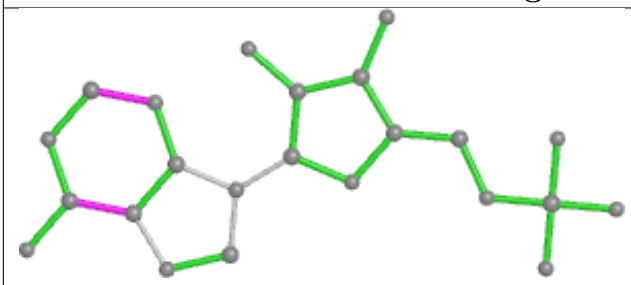
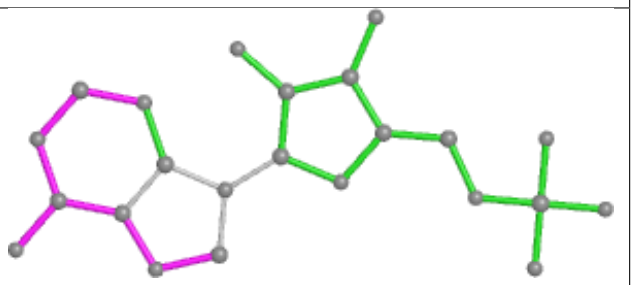
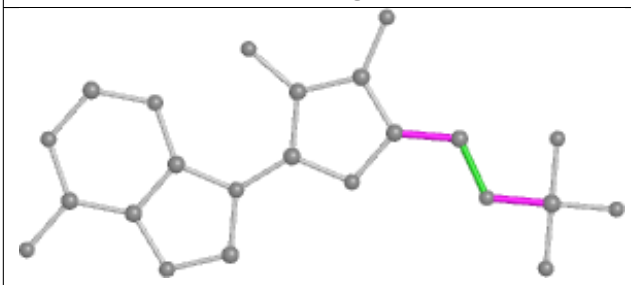
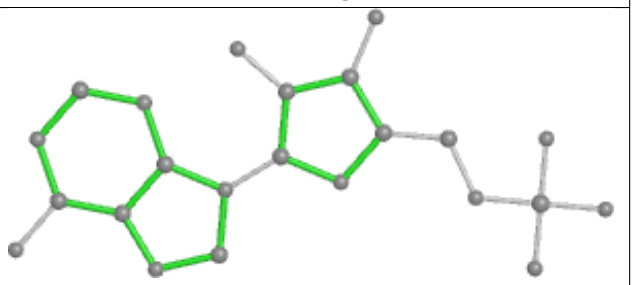


Rings

Ligand IMP G 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^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	350/384 (91%)	-0.07	4 (1%)	80	79	24, 37, 60, 89	0
1	B	350/384 (91%)	-0.13	3 (0%)	84	83	23, 35, 60, 80	0
1	C	354/384 (92%)	-0.10	6 (1%)	70	66	25, 35, 63, 104	0
1	D	351/384 (91%)	-0.20	1 (0%)	94	94	24, 37, 63, 95	0
1	E	352/384 (91%)	-0.17	2 (0%)	89	89	27, 38, 66, 90	0
1	F	355/384 (92%)	-0.00	11 (3%)	49	45	29, 40, 65, 101	0
1	G	349/384 (90%)	0.08	6 (1%)	70	66	29, 42, 67, 93	0
1	H	349/384 (90%)	-0.08	1 (0%)	94	94	30, 43, 64, 91	0
All	All	2810/3072 (91%)	-0.09	34 (1%)	79	77	23, 39, 64, 104	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	411	LYS	4.5
1	G	230	THR	4.2
1	F	401	SER	3.8
1	F	-4	PHE	3.7
1	G	232	ASP	3.2

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 (i)

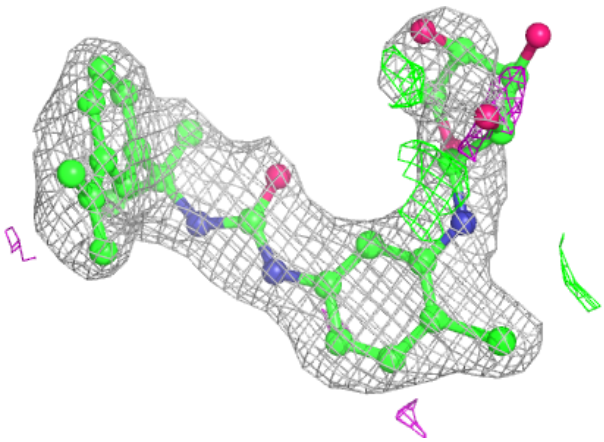
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

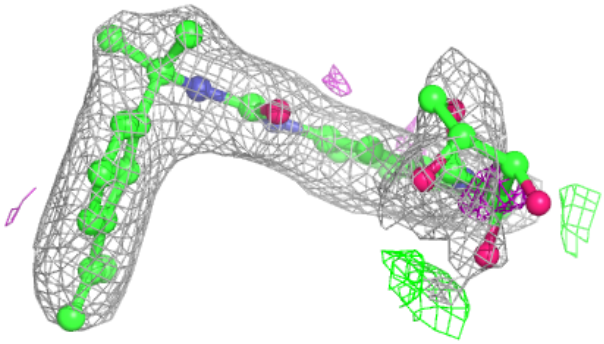
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	ZO4	H	503	33/33	0.87	0.25	30,44,80,82	0
3	ZO4	D	503	33/33	0.88	0.23	24,34,65,68	33
3	ZO4	A	502	33/33	0.88	0.23	27,35,65,72	33
3	ZO4	G	503	33/33	0.89	0.20	31,42,70,75	0
3	ZO4	F	502	33/33	0.89	0.21	26,40,64,68	33
3	ZO4	B	502	33/33	0.90	0.22	27,34,69,70	33
3	ZO4	E	502	33/33	0.92	0.17	26,37,66,76	0
3	ZO4	C	503	33/33	0.93	0.19	23,33,61,65	33
2	IMP	F	501	23/23	0.95	0.15	31,35,38,45	0
2	IMP	H	502	23/23	0.96	0.16	29,37,40,41	0
2	IMP	C	502	23/23	0.96	0.14	23,28,33,37	0
2	IMP	G	502	23/23	0.96	0.13	29,34,38,42	0
2	IMP	E	501	23/23	0.97	0.14	27,32,36,41	0
2	IMP	B	501	23/23	0.97	0.15	23,31,35,35	0
2	IMP	A	501	23/23	0.97	0.14	25,33,36,38	0
2	IMP	D	502	23/23	0.97	0.14	24,32,35,36	0
4	K	A	503	1/1	0.98	0.13	34,34,34,34	0
4	K	C	501	1/1	0.98	0.05	37,37,37,37	0
4	K	E	503	1/1	0.98	0.12	35,35,35,35	0
4	K	D	501	1/1	0.99	0.12	30,30,30,30	0
4	K	B	503	1/1	0.99	0.07	31,31,31,31	0
4	K	F	503	1/1	0.99	0.07	37,37,37,37	0
4	K	G	501	1/1	0.99	0.13	30,30,30,30	0
4	K	H	501	1/1	0.99	0.09	33,33,33,33	0

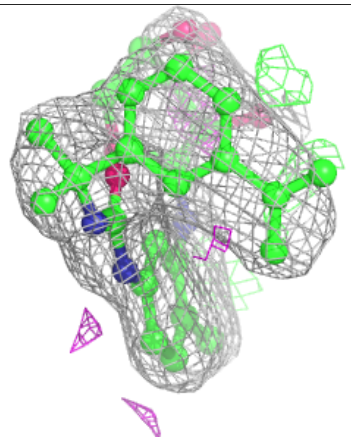
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ZO4 H 503:

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

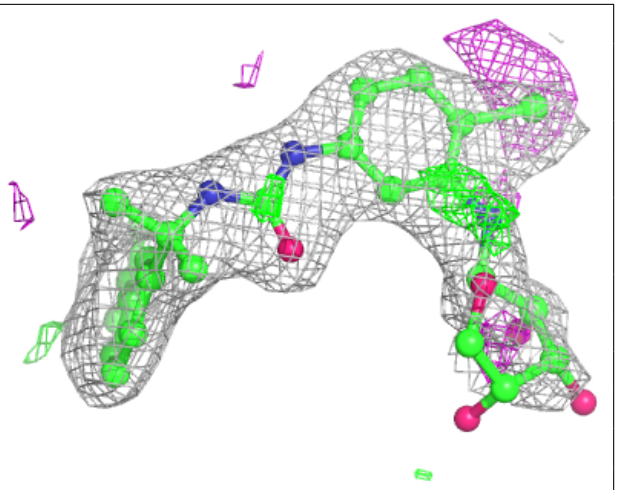


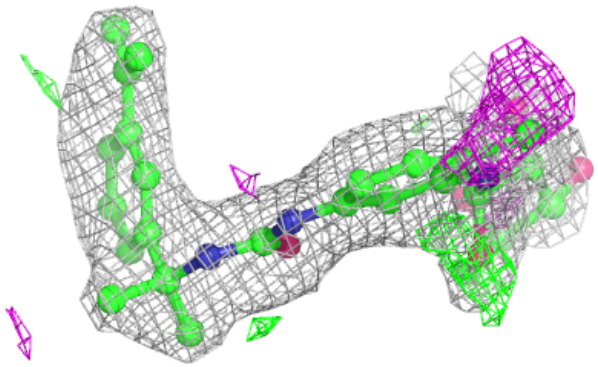


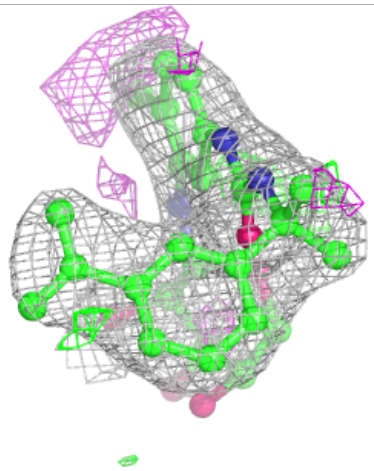


Electron density around ZO4 D 503:

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







Electron density around ZO4 A 502:

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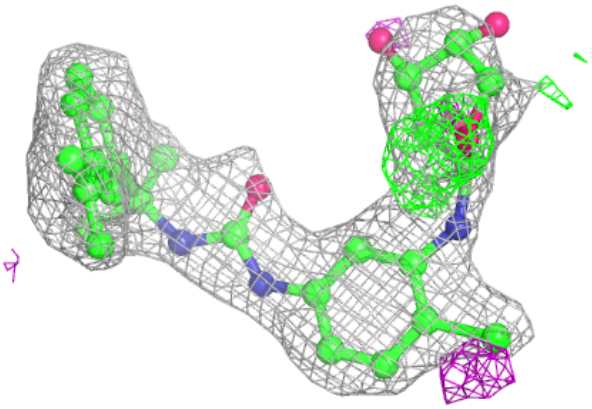
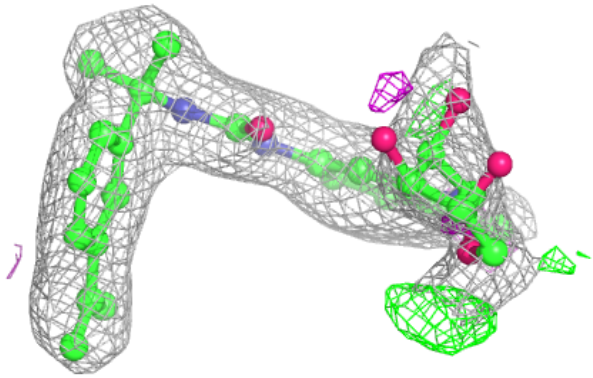
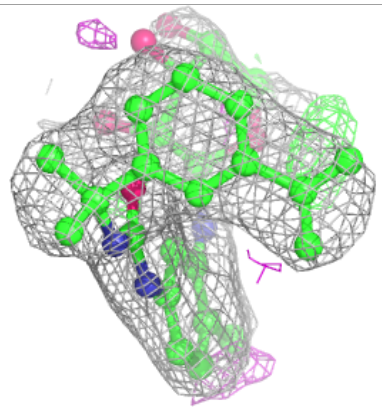
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)







Electron density around ZO4 G 503:

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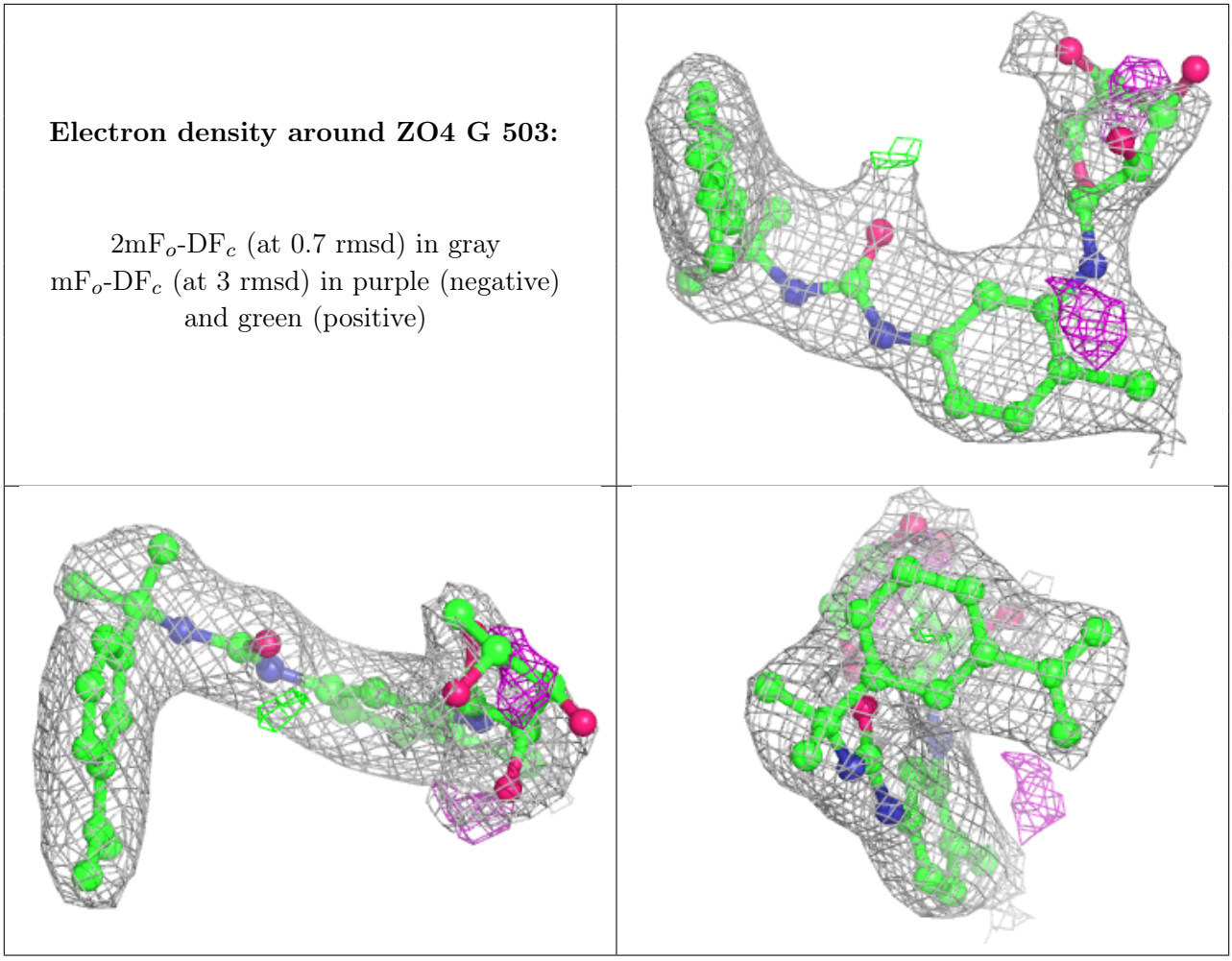
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around ZO4 F 502:

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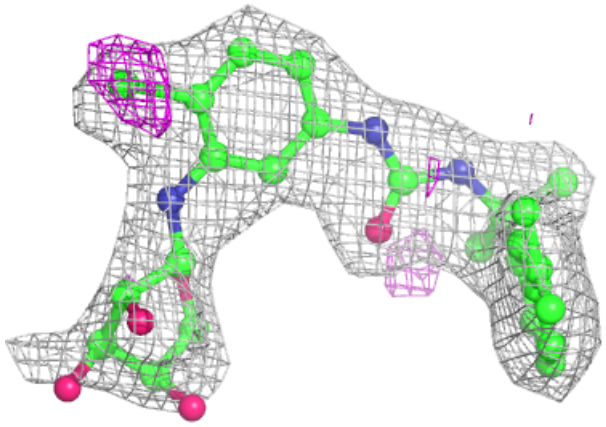
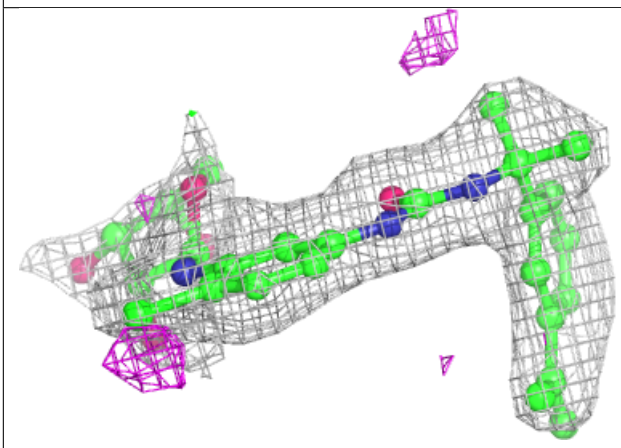
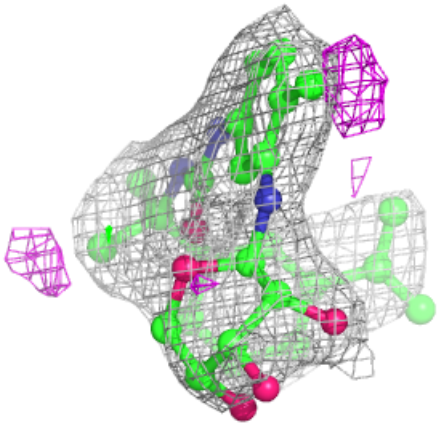
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)







Electron density around ZO4 B 502:

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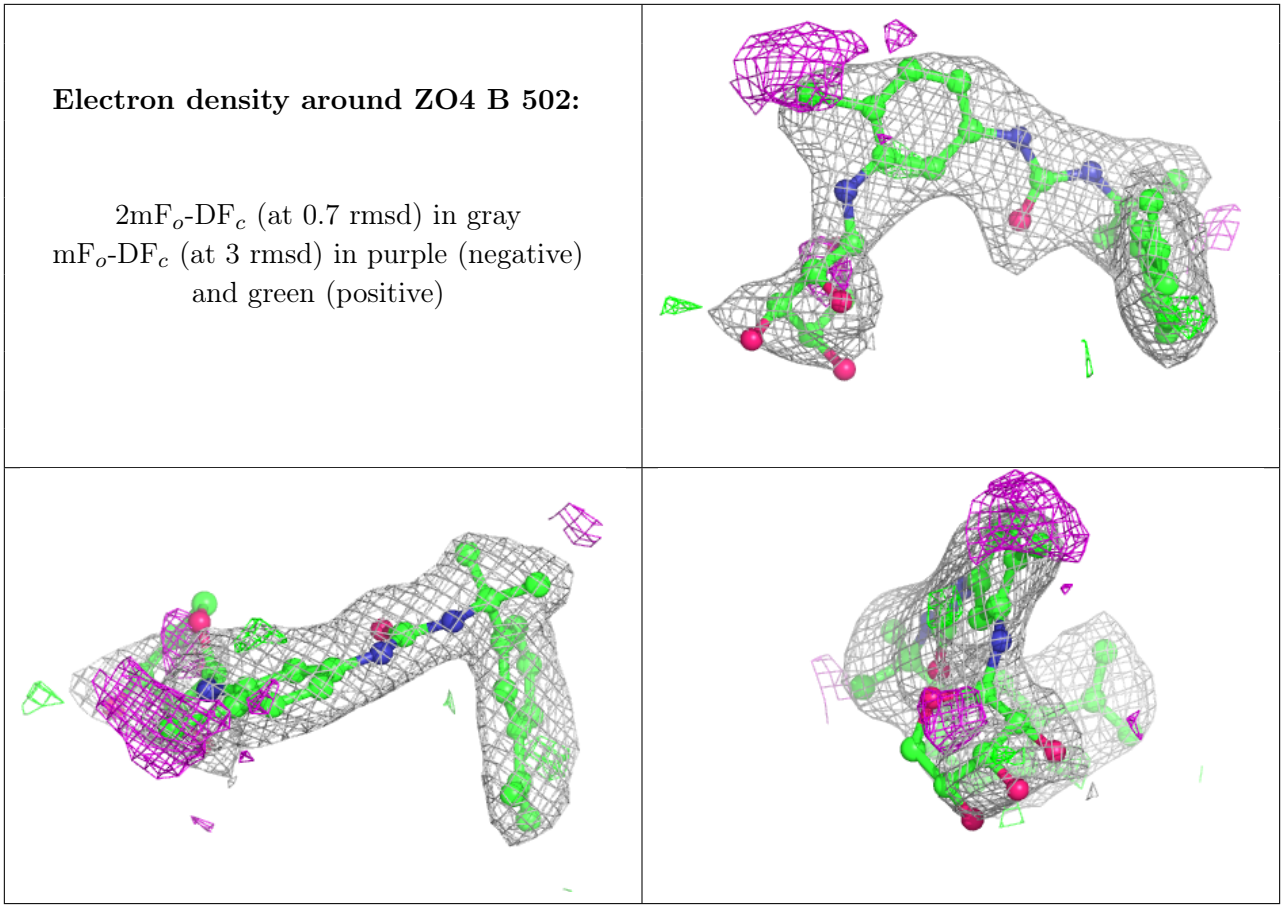
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around ZO4 E 502:

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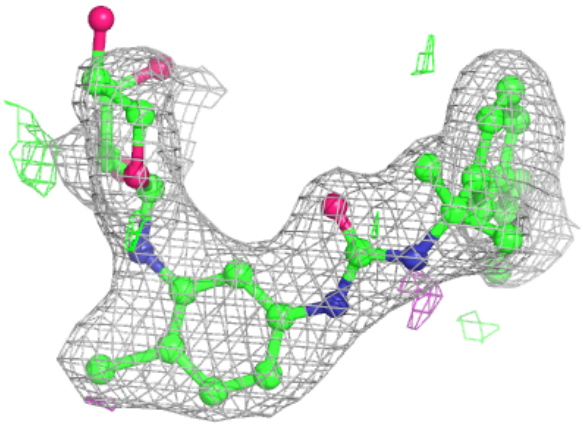
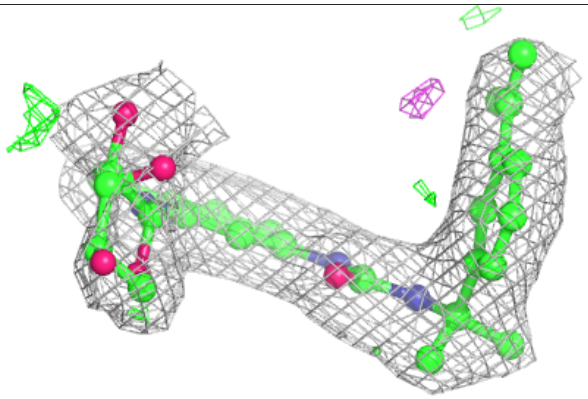
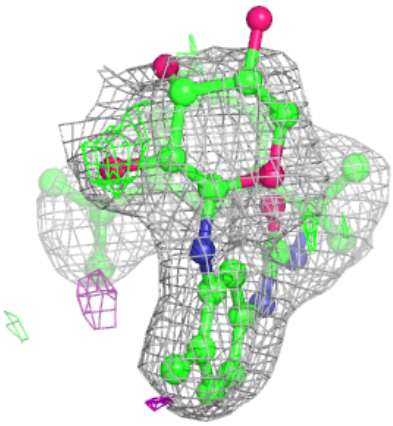
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)







Electron density around ZO4 C 503:

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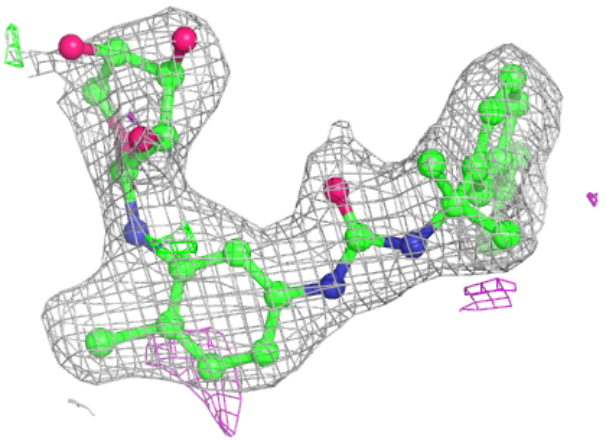
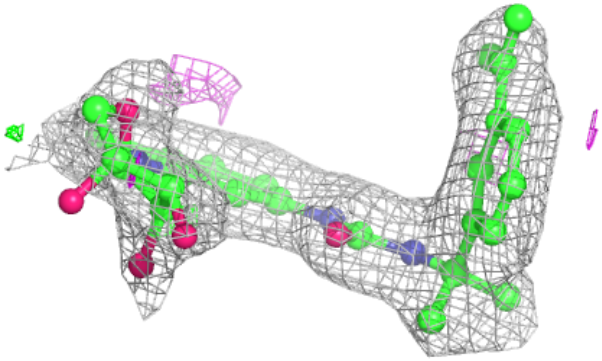
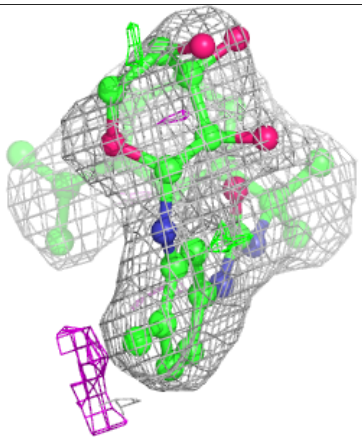
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)







Electron density around IMP F 501:

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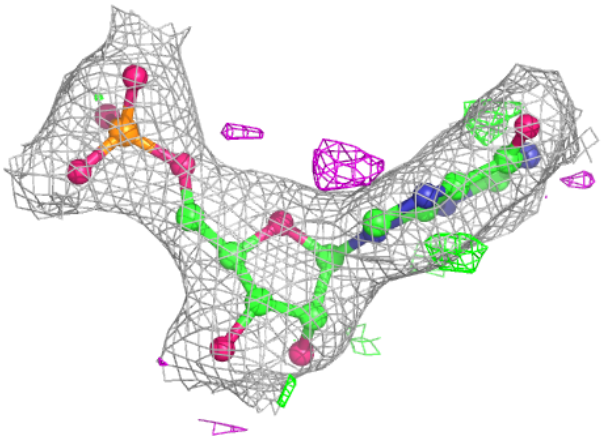
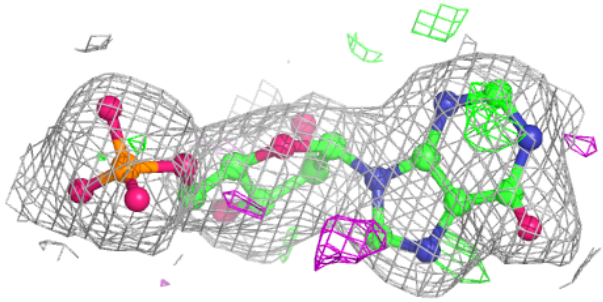
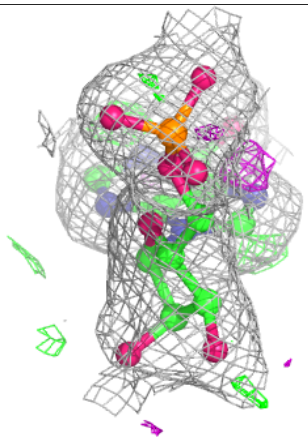
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)







Electron density around IMP H 502:

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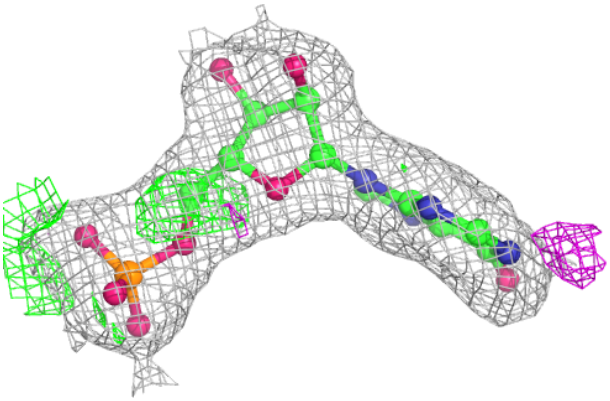

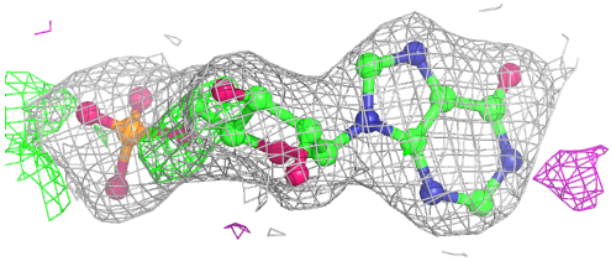

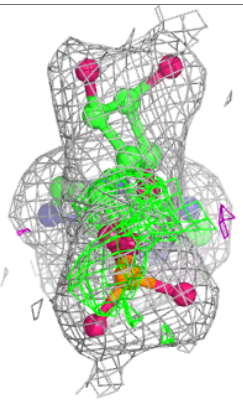

Electron density around IMP C 502:

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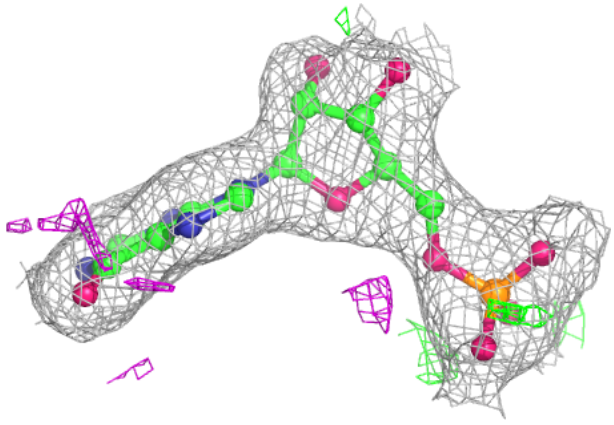
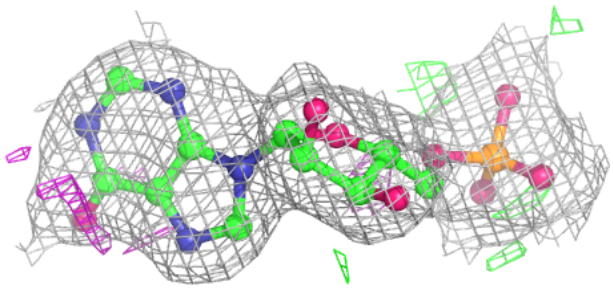
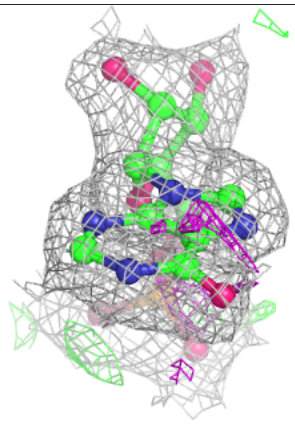
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)







Electron density around IMP G 502:

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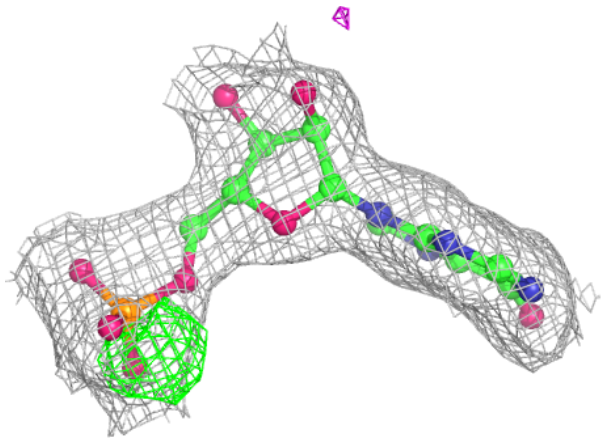
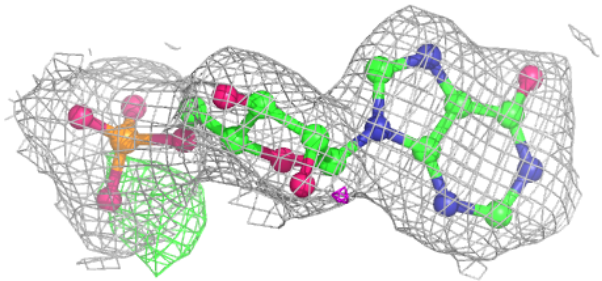
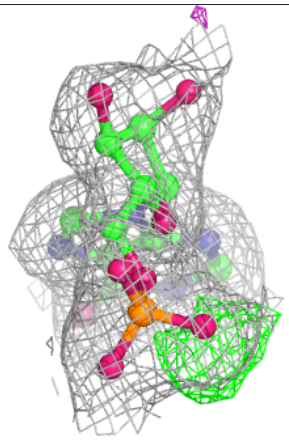
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)







Electron density around IMP E 501:

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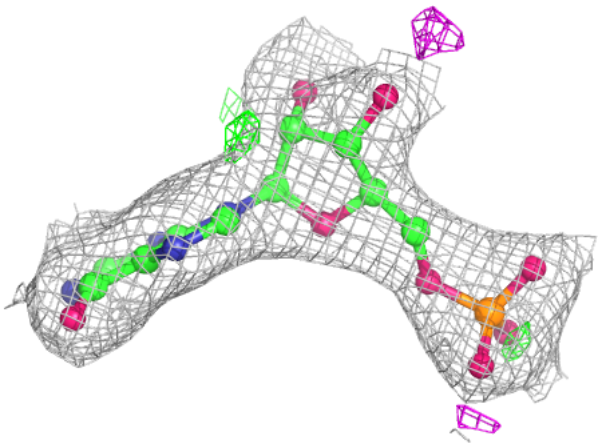
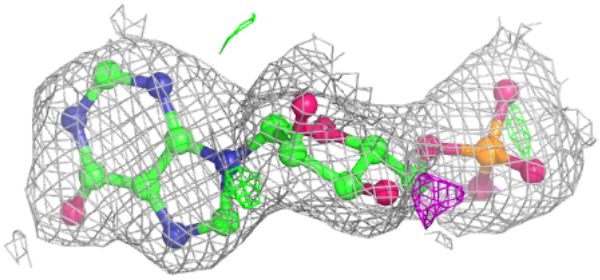
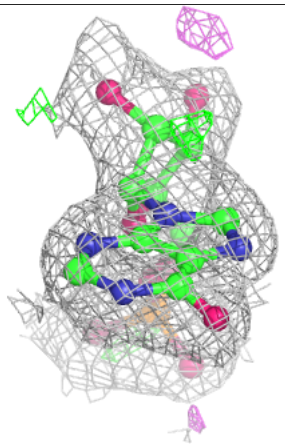
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)







Electron density around IMP B 501:

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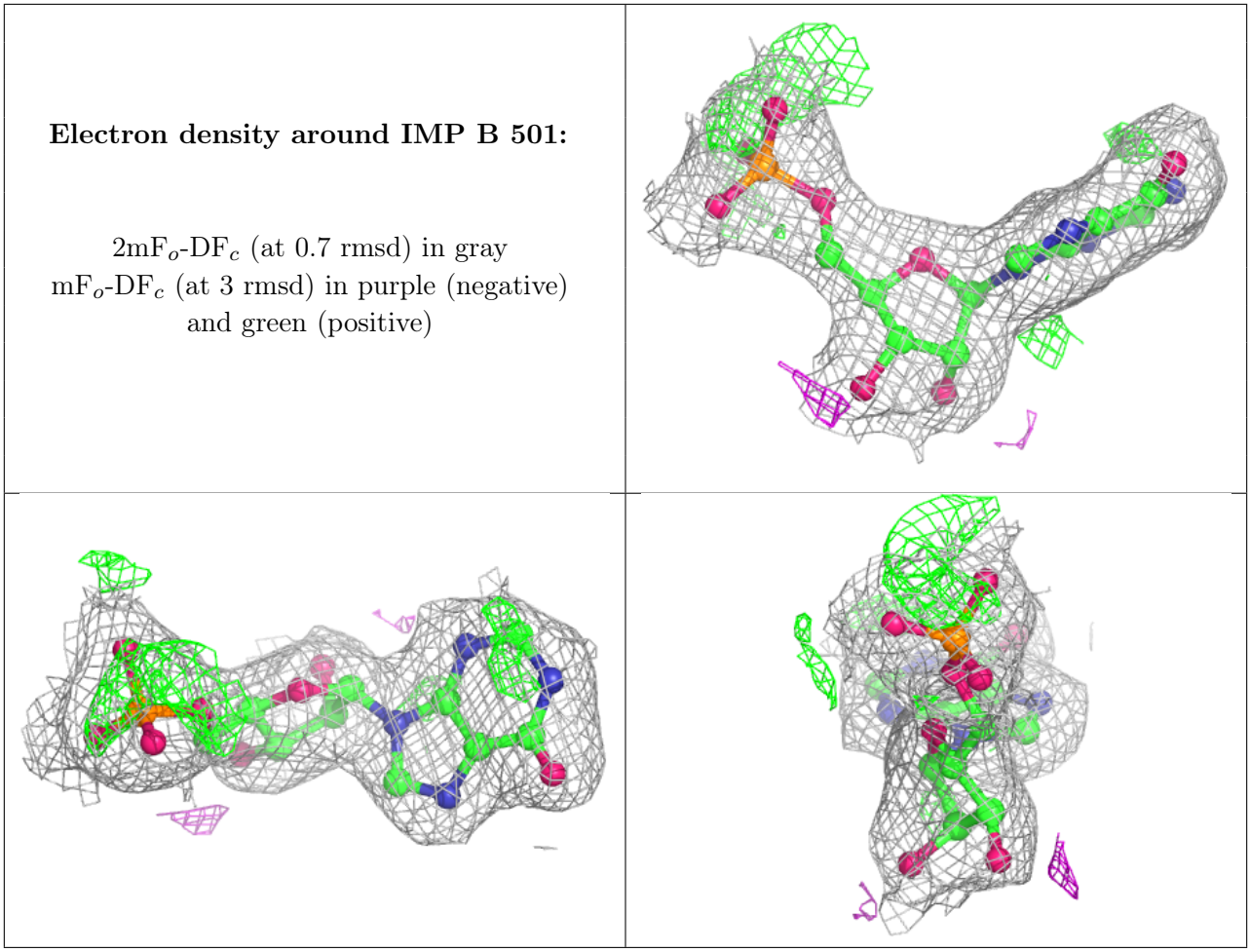
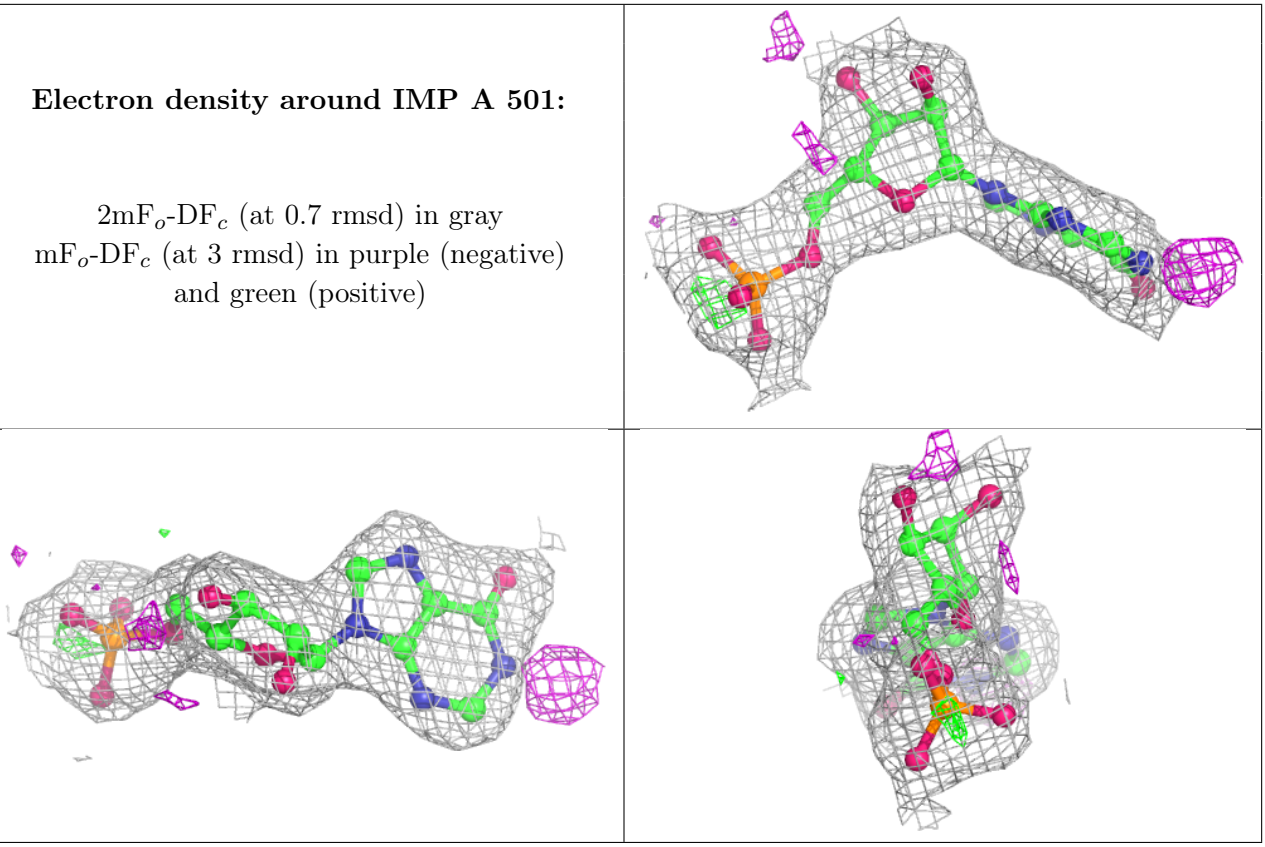
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



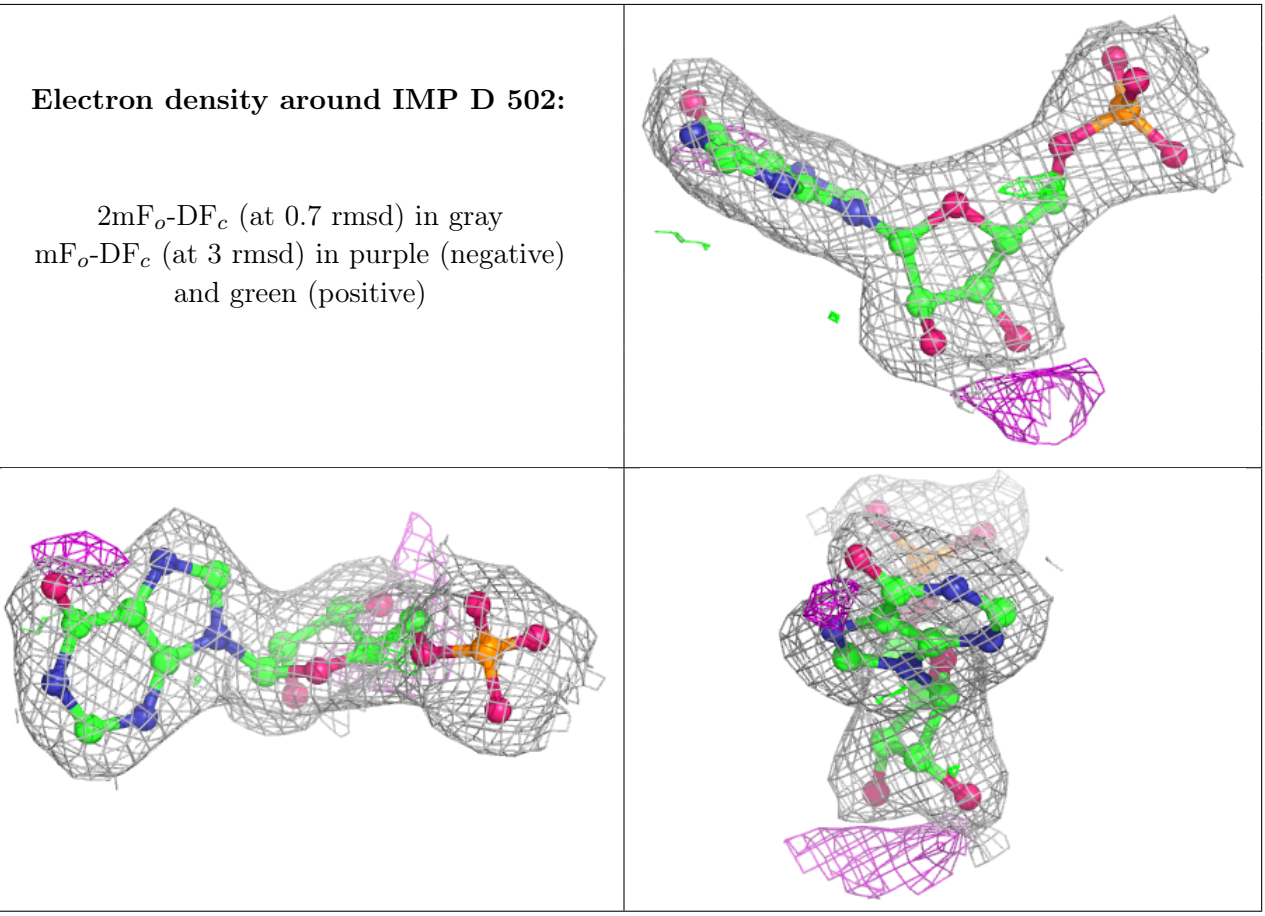
Electron density around IMP A 501:

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



Electron density around IMP D 502:

$2mF_o$-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.