



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 12, 2023 – 07:55 PM EDT

PDB ID : 4MY8  
Title : Crystal Structure of the Inosine 5'-monophosphate Dehydrogenase with an Internal Deletion of the CBS Domain from Bacillus anthracis str. Ames complexed with inhibitor Q21  
Authors : Kim, Y.; Makowska-Grzyska, M.; Gu, M.; Gorla, S.K.; Kavitha, M.; Cuny, G.; Hedstrom, L.; Anderson, W.F.; Joachimiak, A.; CSGID; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2013-09-27  
Resolution : 2.29 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2.35.1  
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)  
Ideal geometry (proteins) : Engh & Huber (2001)

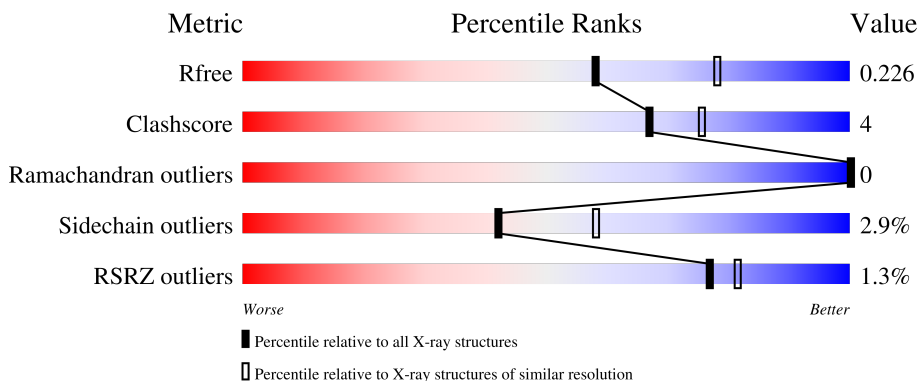
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


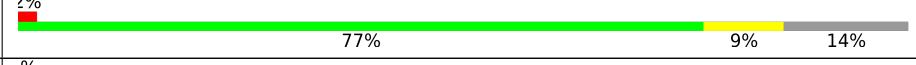

The reported resolution of this entry is 2.29 Å.

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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)


The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	384	
1	B	384	
1	C	384	

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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	 <p>A horizontal bar chart representing the quality of the chain. The bar is divided into three segments: a green segment representing 79%, a yellow segment representing 8%, and a grey segment representing 12%. A small red square is at the beginning of the bar, and a small black dot is at the end of the grey segment.</p>

## 2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 10378 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
			Total	C	N	O	S			
1	A	335	2469	1549	431	473	16	0	3	0
1	B	331	2423	1523	424	460	16	0	1	0
1	C	332	2440	1533	426	465	16	0	2	0
1	D	336	2475	1553	433	473	16	0	3	0

There are 104 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	expression tag	UNP Q81W29
A	-22	HIS	-	expression tag	UNP Q81W29
A	-21	HIS	-	expression tag	UNP Q81W29
A	-20	HIS	-	expression tag	UNP Q81W29
A	-19	HIS	-	expression tag	UNP Q81W29
A	-18	HIS	-	expression tag	UNP Q81W29
A	-17	HIS	-	expression tag	UNP Q81W29
A	-16	SER	-	expression tag	UNP Q81W29
A	-15	SER	-	expression tag	UNP Q81W29
A	-14	GLY	-	expression tag	UNP Q81W29
A	-13	VAL	-	expression tag	UNP Q81W29
A	-12	ASP	-	expression tag	UNP Q81W29
A	-11	LEU	-	expression tag	UNP Q81W29
A	-10	GLY	-	expression tag	UNP Q81W29
A	-9	THR	-	expression tag	UNP Q81W29
A	-8	GLU	-	expression tag	UNP Q81W29
A	-7	ASN	-	expression tag	UNP Q81W29
A	-6	LEU	-	expression tag	UNP Q81W29
A	-5	TYR	-	expression tag	UNP Q81W29
A	-4	PHE	-	expression tag	UNP Q81W29
A	-3	GLN	-	expression tag	UNP Q81W29

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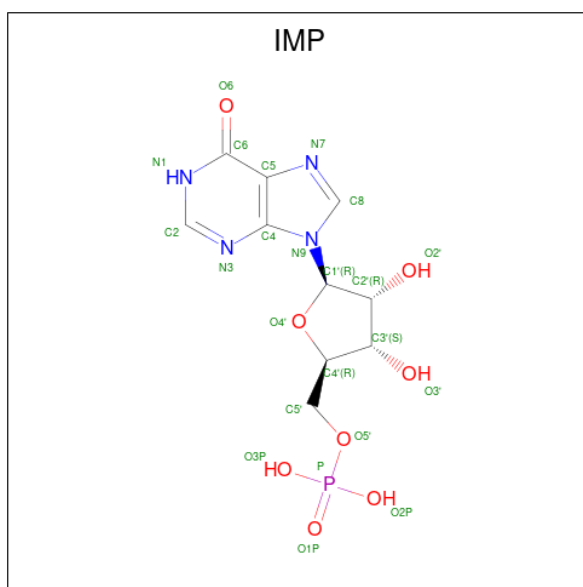
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q81W29
A	-1	ASN	-	expression tag	UNP Q81W29
A	0	ALA	-	expression tag	UNP Q81W29
A	92	GLY	-	linker	UNP Q81W29
A	220	GLY	-	linker	UNP Q81W29
B	-23	MET	-	expression tag	UNP Q81W29
B	-22	HIS	-	expression tag	UNP Q81W29
B	-21	HIS	-	expression tag	UNP Q81W29
B	-20	HIS	-	expression tag	UNP Q81W29
B	-19	HIS	-	expression tag	UNP Q81W29
B	-18	HIS	-	expression tag	UNP Q81W29
B	-17	HIS	-	expression tag	UNP Q81W29
B	-16	SER	-	expression tag	UNP Q81W29
B	-15	SER	-	expression tag	UNP Q81W29
B	-14	GLY	-	expression tag	UNP Q81W29
B	-13	VAL	-	expression tag	UNP Q81W29
B	-12	ASP	-	expression tag	UNP Q81W29
B	-11	LEU	-	expression tag	UNP Q81W29
B	-10	GLY	-	expression tag	UNP Q81W29
B	-9	THR	-	expression tag	UNP Q81W29
B	-8	GLU	-	expression tag	UNP Q81W29
B	-7	ASN	-	expression tag	UNP Q81W29
B	-6	LEU	-	expression tag	UNP Q81W29
B	-5	TYR	-	expression tag	UNP Q81W29
B	-4	PHE	-	expression tag	UNP Q81W29
B	-3	GLN	-	expression tag	UNP Q81W29
B	-2	SER	-	expression tag	UNP Q81W29
B	-1	ASN	-	expression tag	UNP Q81W29
B	0	ALA	-	expression tag	UNP Q81W29
B	92	GLY	-	linker	UNP Q81W29
B	220	GLY	-	linker	UNP Q81W29
C	-23	MET	-	expression tag	UNP Q81W29
C	-22	HIS	-	expression tag	UNP Q81W29
C	-21	HIS	-	expression tag	UNP Q81W29
C	-20	HIS	-	expression tag	UNP Q81W29
C	-19	HIS	-	expression tag	UNP Q81W29
C	-18	HIS	-	expression tag	UNP Q81W29
C	-17	HIS	-	expression tag	UNP Q81W29
C	-16	SER	-	expression tag	UNP Q81W29
C	-15	SER	-	expression tag	UNP Q81W29
C	-14	GLY	-	expression tag	UNP Q81W29
C	-13	VAL	-	expression tag	UNP Q81W29

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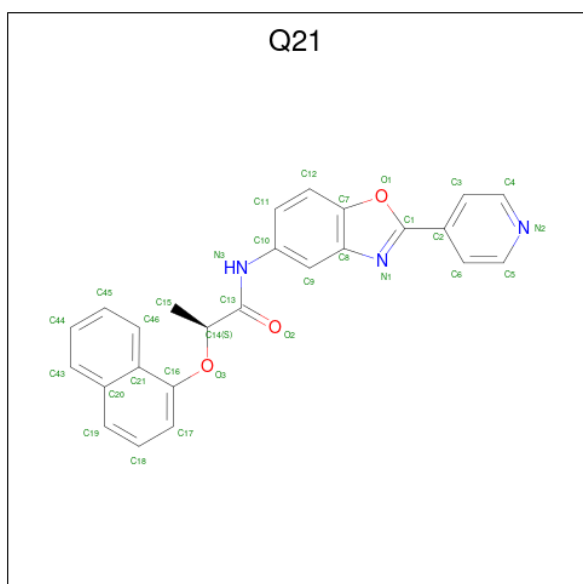
Chain	Residue	Modelled	Actual	Comment	Reference
C	-12	ASP	-	expression tag	UNP Q81W29
C	-11	LEU	-	expression tag	UNP Q81W29
C	-10	GLY	-	expression tag	UNP Q81W29
C	-9	THR	-	expression tag	UNP Q81W29
C	-8	GLU	-	expression tag	UNP Q81W29
C	-7	ASN	-	expression tag	UNP Q81W29
C	-6	LEU	-	expression tag	UNP Q81W29
C	-5	TYR	-	expression tag	UNP Q81W29
C	-4	PHE	-	expression tag	UNP Q81W29
C	-3	GLN	-	expression tag	UNP Q81W29
C	-2	SER	-	expression tag	UNP Q81W29
C	-1	ASN	-	expression tag	UNP Q81W29
C	0	ALA	-	expression tag	UNP Q81W29
C	92	GLY	-	linker	UNP Q81W29
C	220	GLY	-	linker	UNP Q81W29
D	-23	MET	-	expression tag	UNP Q81W29
D	-22	HIS	-	expression tag	UNP Q81W29
D	-21	HIS	-	expression tag	UNP Q81W29
D	-20	HIS	-	expression tag	UNP Q81W29
D	-19	HIS	-	expression tag	UNP Q81W29
D	-18	HIS	-	expression tag	UNP Q81W29
D	-17	HIS	-	expression tag	UNP Q81W29
D	-16	SER	-	expression tag	UNP Q81W29
D	-15	SER	-	expression tag	UNP Q81W29
D	-14	GLY	-	expression tag	UNP Q81W29
D	-13	VAL	-	expression tag	UNP Q81W29
D	-12	ASP	-	expression tag	UNP Q81W29
D	-11	LEU	-	expression tag	UNP Q81W29
D	-10	GLY	-	expression tag	UNP Q81W29
D	-9	THR	-	expression tag	UNP Q81W29
D	-8	GLU	-	expression tag	UNP Q81W29
D	-7	ASN	-	expression tag	UNP Q81W29
D	-6	LEU	-	expression tag	UNP Q81W29
D	-5	TYR	-	expression tag	UNP Q81W29
D	-4	PHE	-	expression tag	UNP Q81W29
D	-3	GLN	-	expression tag	UNP Q81W29
D	-2	SER	-	expression tag	UNP Q81W29
D	-1	ASN	-	expression tag	UNP Q81W29
D	0	ALA	-	expression tag	UNP Q81W29
D	92	GLY	-	linker	UNP Q81W29
D	220	GLY	-	linker	UNP Q81W29

- Molecule 2 is INOSINIC ACID (three-letter code: IMP) (formula: C<sub>10</sub>H<sub>13</sub>N<sub>4</sub>O<sub>8</sub>P).



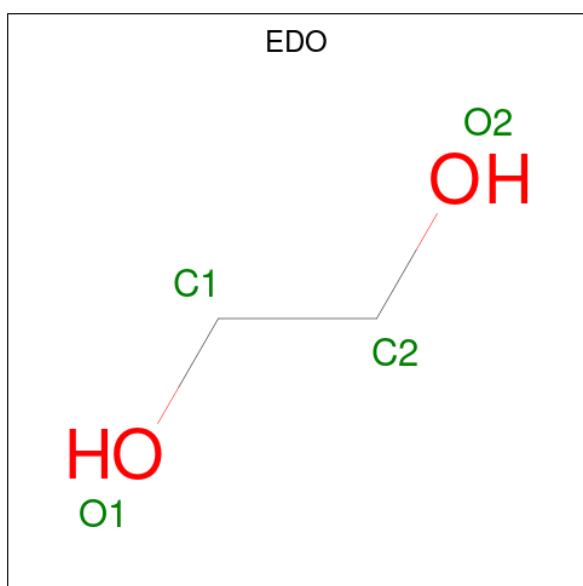
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	B	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	C	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
2	D	1	Total	C	N	O	P	0	0
			23	10	4	8	1		

- Molecule 3 is (2S)-2-(naphthalen-1-yloxy)-N-[2-(pyridin-4-yl)-1,3-benzoxazol-5-yl]propanamide (three-letter code: Q21) (formula: C<sub>25</sub>H<sub>19</sub>N<sub>3</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	31	25	3	3	0	0
3	B	1	31	25	3	3	0	0
3	B	1	31	25	3	3	0	0
3	D	1	31	25	3	3	0	0

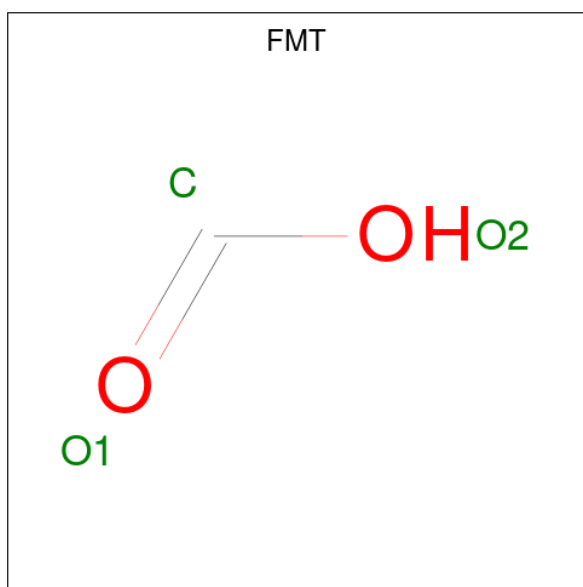
- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

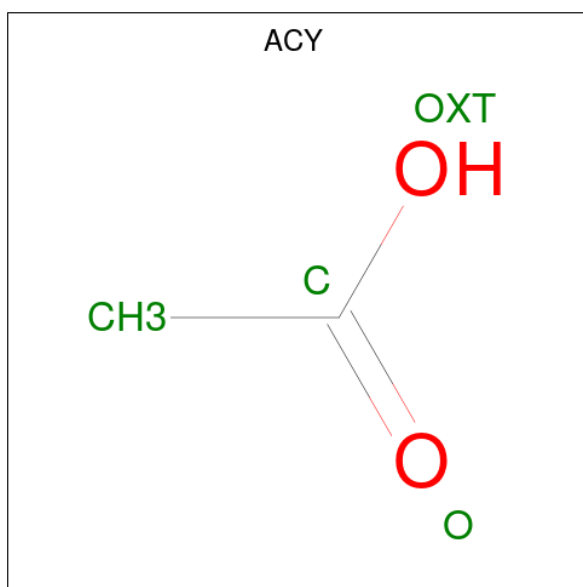
- Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula:  $CH_2O_2$ ).





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

- Molecule 6 is ACETIC ACID (three-letter code: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



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

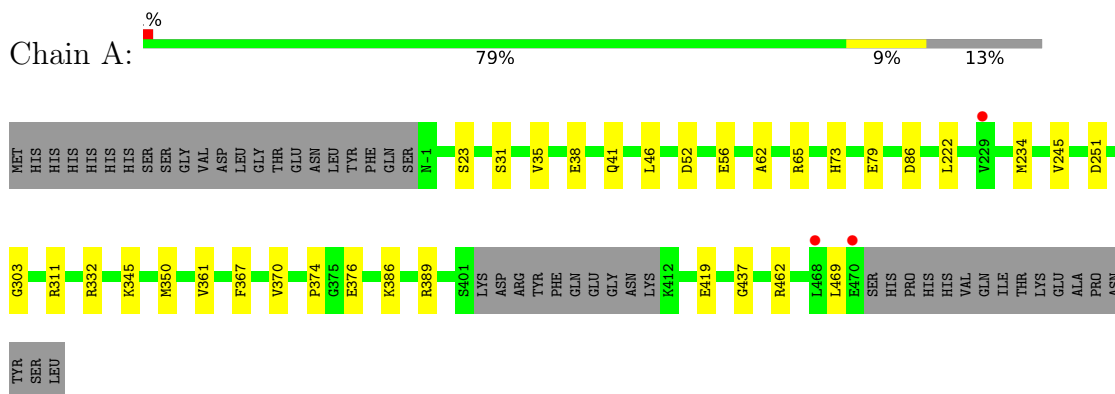
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	71	Total O 71 71	0	0
7	B	87	Total O 87 87	0	0
7	C	71	Total O 71 71	0	0
7	D	70	Total O 70 70	0	0

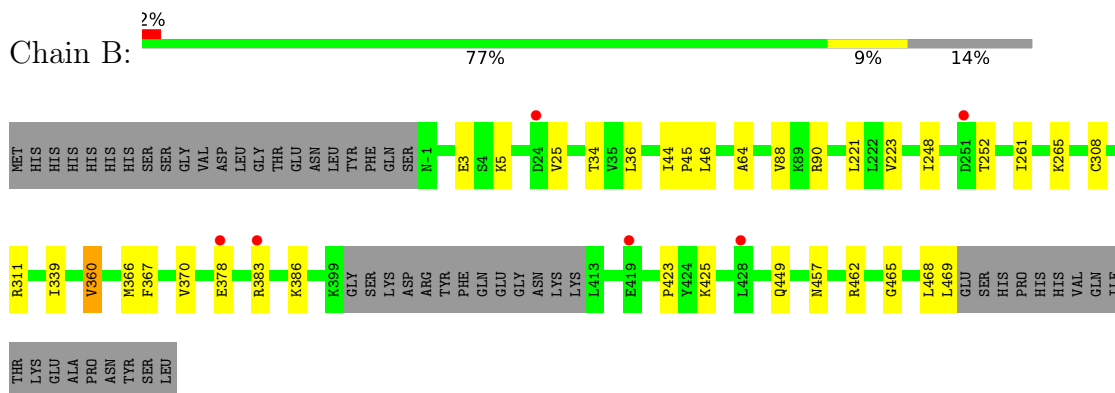
### 3 Residue-property plots [i](#)

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.

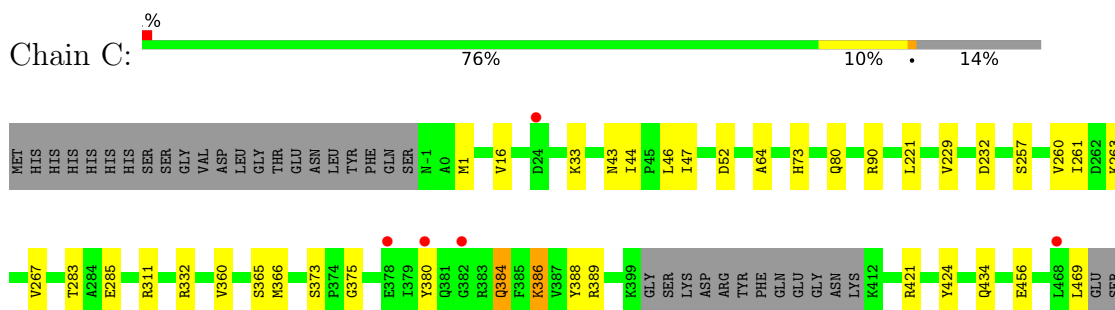
- Molecule 1: Inosine-5'-monophosphate dehydrogenase



- Molecule 1: Inosine-5'-monophosphate dehydrogenase




- Molecule 1: Inosine-5'-monophosphate dehydrogenase



HIS  
PRO  
HIS  
HIS  
HIS  
VAL  
GLN  
ILE  
THR  
LYS  
GLU  
ALA  
PRO  
ASN  
TYR  
SER  
LEU

● Molecule 1: Inosine-5'-monophosphate dehydrogenase

Chain D:  %

MET  
HIS  
HIS  
HIS  
HIS  
HIS  
HIS  
HIS  
SER  
SER  
GLY  
VAL  
ASP  
LEU  
GLY  
THR  
GLU  
GLU  
ASN  
LEU  
LEU  
TYR  
PHE  
GLN  
SER  
N-1  
E9  
V16  
V25  
E29  
I44  
P45  
L46  
M63  
E83  
G220  
V229  
T230  
I248  
D251  
S257  
V260  
L274  
N275  
G279  
N296

I307  
L321  
I339  
M350  
Y351  
K352  
V360  
G369  
Y380  
G390  
E398  
S401  
LYS  
ASP  
ARG  
TYR  
PHE  
GLN  
GLU  
GLY  
ASN  
LYS  
K412  
L413  
K425  
L428  
L439  
F460  
G467  
L468  
L469  
E470  
S471  
HIS  
PRO  
HIS  
HIS  
VAL  
GLN  
ILE  
THR  
LYS  
GLU  
ALA  
PRO  
ASN

TYR  
SER  
LEU

## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.43Å 56.23Å 111.39Å 90.00° 89.83° 90.00°	Depositor
Resolution (Å)	49.88 – 2.29 49.89 – 2.29	Depositor EDS
% Data completeness (in resolution range)	94.8 (49.88-2.29) 94.8 (49.89-2.29)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.41 (at 2.29Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1161)	Depositor
R, $R_{free}$	0.173 , 0.225 0.174 , 0.226	Depositor DCC
$R_{free}$ test set	2998 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.3	Xtrriage
Anisotropy	0.332	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 24.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.379 for l,k,-h 0.030 for -h,-k,l 0.033 for -l,-k,-h	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10378	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.60 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5078e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: Q21, IMP, ACY, FMT, EDO

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	0.39	0/2500	0.55	0/3375
1	B	0.38	0/2454	0.54	0/3315
1	C	0.38	0/2470	0.55	0/3335
1	D	0.39	0/2506	0.55	0/3382
All	All	0.39	0/9930	0.55	0/13407

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2469	0	2526	18	0
1	B	2423	0	2489	22	0
1	C	2440	0	2508	20	0
1	D	2475	0	2538	21	0
2	A	23	0	11	0	0
2	B	23	0	11	1	0
2	C	23	0	11	0	0
2	D	23	0	11	0	0
3	A	31	0	19	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	62	0	38	2	0
3	D	31	0	19	1	0
4	A	8	0	12	3	0
4	B	8	0	12	0	0
4	D	8	0	12	2	0
5	A	6	0	2	1	0
5	B	6	0	2	0	0
5	C	6	0	2	0	0
5	D	6	0	2	0	0
6	A	4	0	3	0	0
6	C	4	0	3	0	0
7	A	71	0	0	0	0
7	B	87	0	0	3	1
7	C	71	0	0	3	1
7	D	70	0	0	2	0
All	All	10378	0	10231	79	1

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 4.

The worst 5 of 79 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:65:ARG:HH11	4:A:504:EDO:H21	1.53	0.73
1:A:31:SER:HA	4:A:503:EDO:H11	1.70	0.71
1:C:384:GLN:HB3	1:C:424:TYR:HB3	1.72	0.71
1:C:90:ARG:NH2	7:C:659:HOH:O	2.25	0.68
1:B:457:ASN:HD22	1:C:1:MET:HG3	1.63	0.63

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:646:HOH:O	7:C:604:HOH:O[2_656]	2.19	0.01

## 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	334/384 (87%)	322 (96%)	12 (4%)	0	100	100
1	B	328/384 (85%)	318 (97%)	10 (3%)	0	100	100
1	C	330/384 (86%)	322 (98%)	8 (2%)	0	100	100
1	D	335/384 (87%)	325 (97%)	10 (3%)	0	100	100
All	All	1327/1536 (86%)	1287 (97%)	40 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	256/298 (86%)	248 (97%)	8 (3%)	40	55
1	B	251/298 (84%)	244 (97%)	7 (3%)	43	60
1	C	253/298 (85%)	244 (96%)	9 (4%)	35	49
1	D	257/298 (86%)	252 (98%)	5 (2%)	57	73
All	All	1017/1192 (85%)	988 (97%)	29 (3%)	42	58

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	425	LYS
1	D	321	LEU
1	C	366	MET

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Mol	Chain	Res	Type
1	D	16	VAL
1	C	232	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	HIS
1	B	258	GLN
1	B	457	ASN
1	D	275	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](#)

24 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	FMT	C	502	-	2,2,2	0.69	0	1,1,1	0.21	0
3	Q21	B	507	-	31,35,35	1.01	1 (3%)	43,49,49	1.33	5 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	IMP	C	501	-	21,25,25	1.39	2 (9%)	24,38,38	1.46	5 (20%)
5	FMT	A	505	-	2,2,2	0.60	0	1,1,1	0.07	0
5	FMT	D	504	-	2,2,2	0.72	0	1,1,1	0.26	0
5	FMT	B	506	-	2,2,2	0.70	0	1,1,1	0.24	0
2	IMP	D	502	-	21,25,25	1.44	2 (9%)	24,38,38	1.38	4 (16%)
4	EDO	A	503	-	3,3,3	0.46	0	2,2,2	0.34	0
5	FMT	B	504	-	2,2,2	0.69	0	1,1,1	0.26	0
5	FMT	A	506	-	2,2,2	0.69	0	1,1,1	0.19	0
4	EDO	B	503	-	3,3,3	0.46	0	2,2,2	0.45	0
2	IMP	B	501	-	21,25,25	1.44	2 (9%)	24,38,38	1.33	4 (16%)
3	Q21	D	503	-	31,35,35	0.99	1 (3%)	43,49,49	1.37	4 (9%)
3	Q21	B	502	-	31,35,35	1.01	1 (3%)	43,49,49	1.34	3 (6%)
4	EDO	D	505	-	3,3,3	0.53	0	2,2,2	0.26	0
5	FMT	C	504	-	2,2,2	0.69	0	1,1,1	0.25	0
2	IMP	A	501	-	21,25,25	1.40	2 (9%)	24,38,38	1.32	3 (12%)
3	Q21	A	502	-	31,35,35	1.03	1 (3%)	43,49,49	1.36	4 (9%)
4	EDO	B	505	-	3,3,3	0.61	0	2,2,2	0.13	0
6	ACY	C	503	-	3,3,3	0.68	0	3,3,3	1.03	0
4	EDO	D	501	-	3,3,3	0.51	0	2,2,2	0.25	0
5	FMT	D	506	-	2,2,2	0.68	0	1,1,1	0.18	0
4	EDO	A	504	-	3,3,3	0.50	0	2,2,2	0.17	0
6	ACY	A	507	-	3,3,3	0.78	0	3,3,3	0.84	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	Q21	A	502	-	-	0/14/16/16	0/5/5/5
3	Q21	B	507	-	-	0/14/16/16	0/5/5/5
4	EDO	B	505	-	-	0/1/1/1	-
4	EDO	D	501	-	-	1/1/1/1	-
2	IMP	B	501	-	-	0/6/26/26	0/3/3/3
2	IMP	C	501	-	-	0/6/26/26	0/3/3/3
3	Q21	B	502	-	-	0/14/16/16	0/5/5/5
3	Q21	D	503	-	-	0/14/16/16	0/5/5/5
4	EDO	A	503	-	-	0/1/1/1	-
4	EDO	B	503	-	-	1/1/1/1	-
4	EDO	D	505	-	-	0/1/1/1	-
4	EDO	A	504	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	IMP	A	501	-	-	0/6/26/26	0/3/3/3
2	IMP	D	502	-	-	0/6/26/26	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	IMP	C2-N3	4.90	1.38	1.29
2	C	501	IMP	C2-N3	4.72	1.38	1.29
2	D	502	IMP	C2-N3	4.55	1.38	1.29
2	A	501	IMP	C2-N3	4.47	1.37	1.29
2	A	501	IMP	C5-C6	-3.67	1.40	1.47

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	Q21	O3-C16-C21	5.30	121.19	114.22
3	B	507	Q21	O3-C16-C21	4.75	120.47	114.22
3	A	502	Q21	O3-C16-C21	4.75	120.47	114.22
3	D	503	Q21	O3-C16-C21	3.82	119.25	114.22
2	D	502	IMP	C8-N7-C5	3.50	109.66	102.99

There are no chirality outliers.

All (3) torsion outliers are listed below:

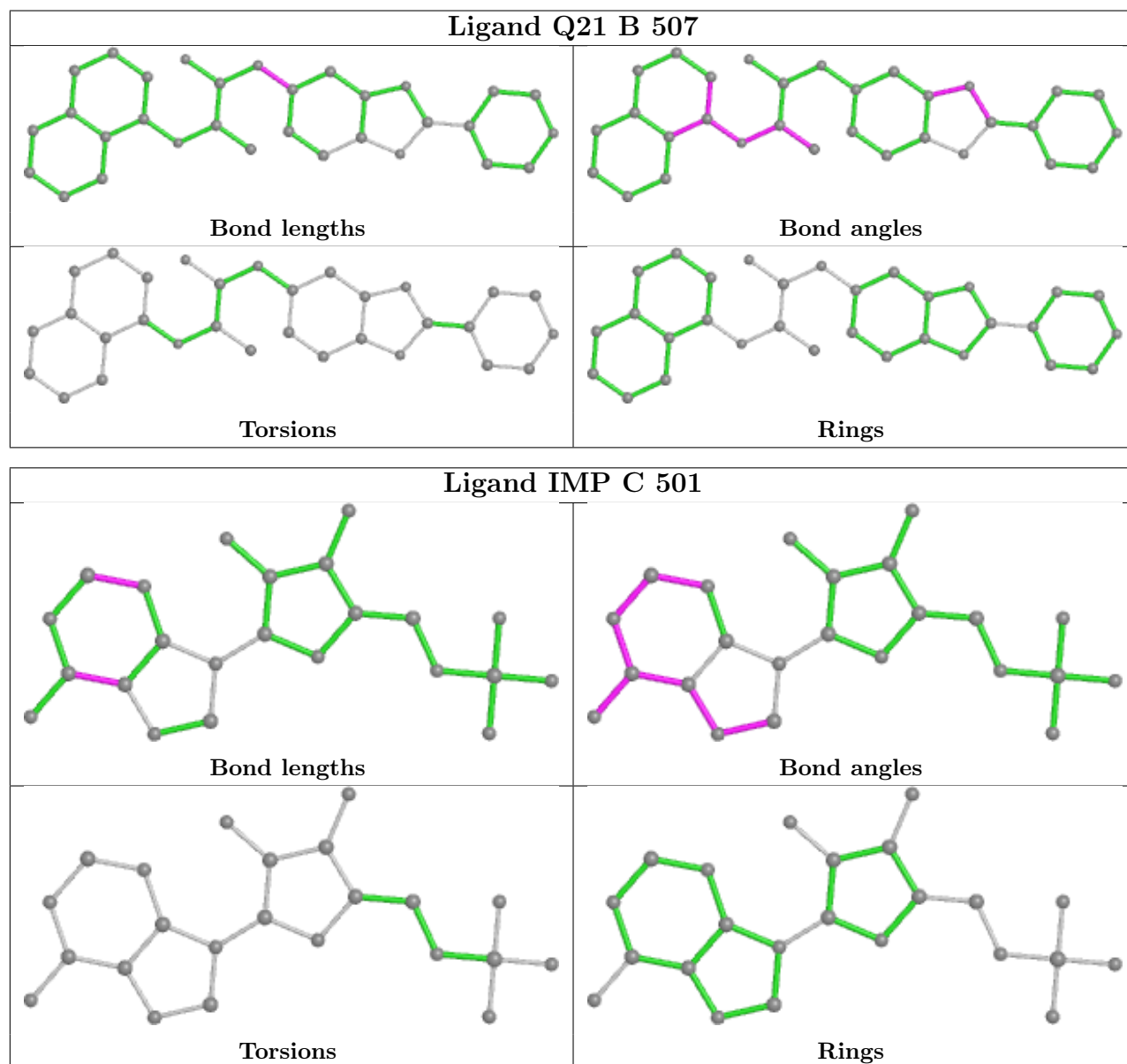
Mol	Chain	Res	Type	Atoms
4	B	503	EDO	O1-C1-C2-O2
4	A	504	EDO	O1-C1-C2-O2
4	D	501	EDO	O1-C1-C2-O2

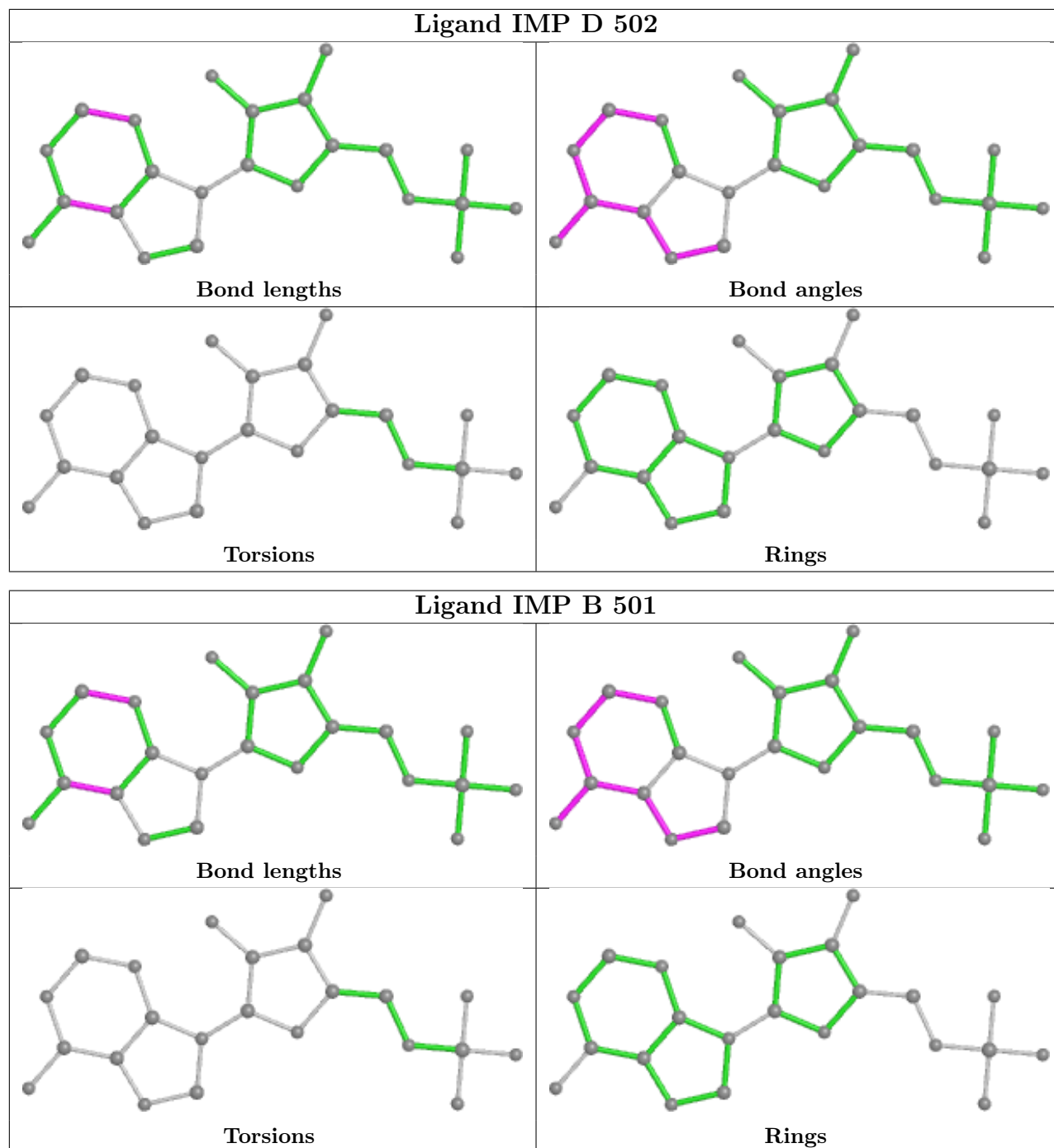
There are no ring outliers.

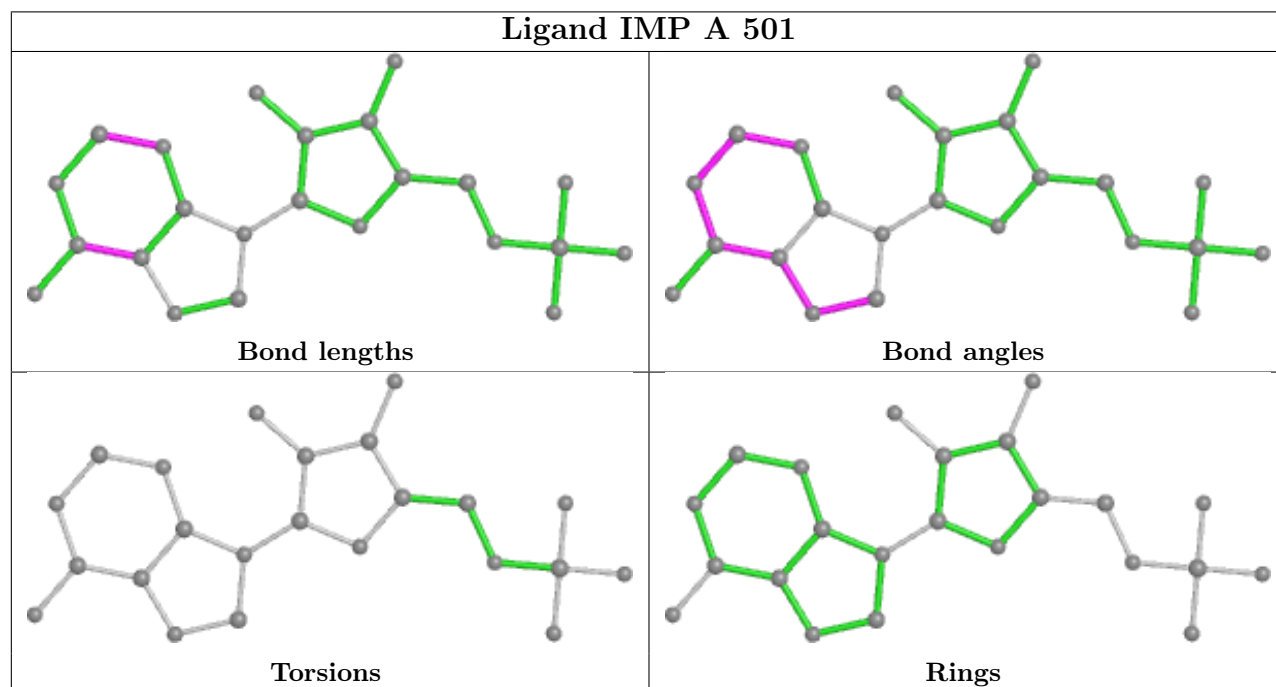
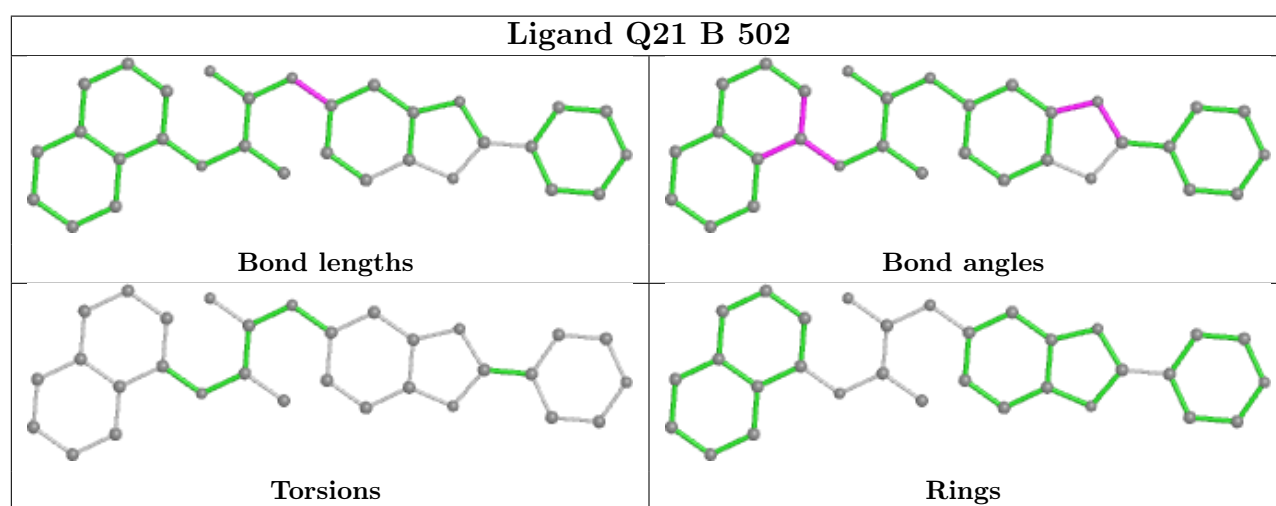
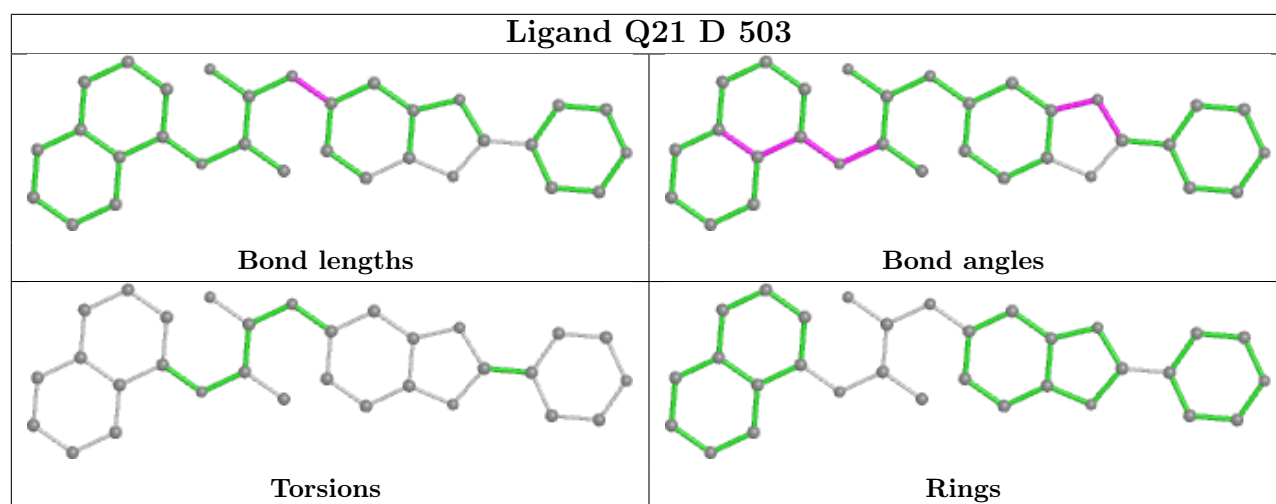
8 monomers are involved in 10 short contacts:

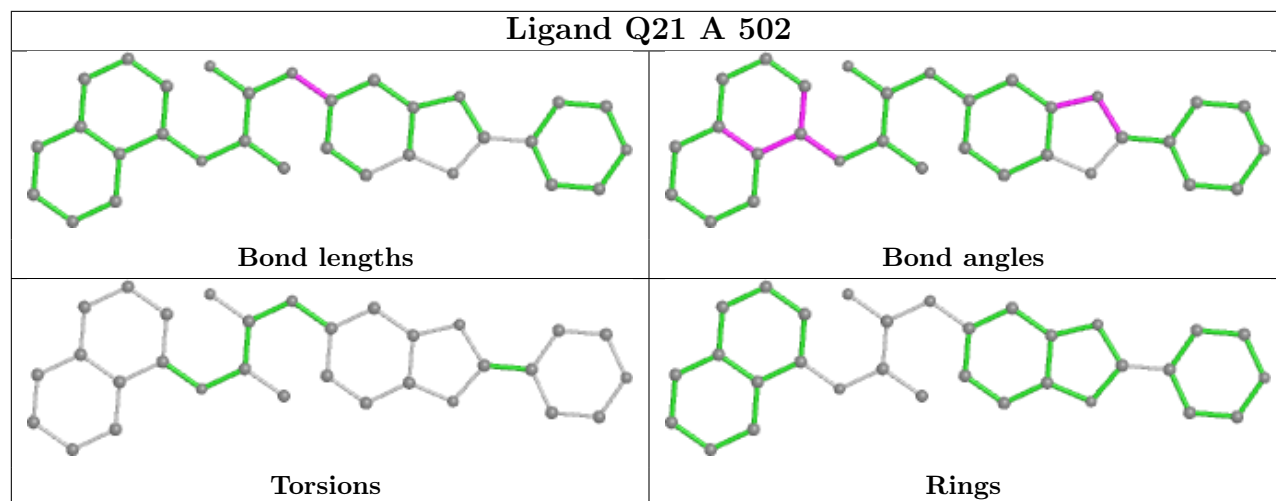
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	507	Q21	1	0
5	A	505	FMT	1	0
4	A	503	EDO	1	0
2	B	501	IMP	1	0
3	D	503	Q21	1	0
3	B	502	Q21	1	0
4	D	501	EDO	2	0
4	A	504	EDO	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	335/384 (87%)	-0.15	3 (0%) 84 88	22, 36, 73, 98	5 (1%)
1	B	331/384 (86%)	-0.10	6 (1%) 68 74	21, 38, 71, 106	4 (1%)
1	C	332/384 (86%)	-0.11	5 (1%) 73 79	22, 37, 78, 103	1 (0%)
1	D	336/384 (87%)	-0.17	4 (1%) 79 83	21, 36, 74, 104	3 (0%)
All	All	1334/1536 (86%)	-0.13	18 (1%) 77 81	21, 36, 75, 106	13 (0%)

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	467	GLY	5.3
1	C	382	GLY	4.2
1	C	380	TYR	4.1
1	D	469	LEU	3.4
1	D	470	GLU	3.1

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

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

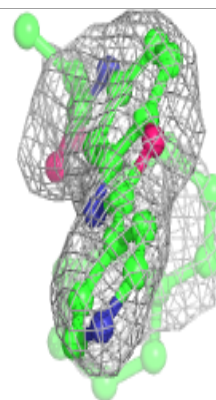
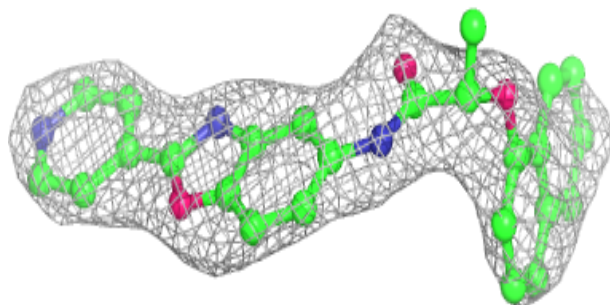
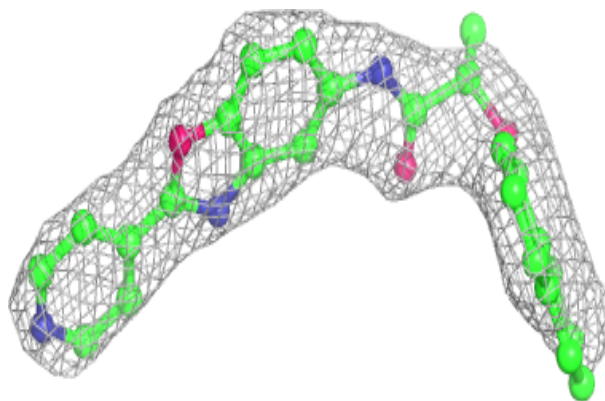


Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	FMT	A	505	3/3	0.81	0.24	50,50,54,54	0
4	EDO	D	501	4/4	0.83	0.23	58,61,65,67	0
5	FMT	C	502	3/3	0.83	0.22	75,75,76,76	0
4	EDO	A	503	4/4	0.84	0.31	60,62,62,62	0
5	FMT	D	506	3/3	0.84	0.10	64,64,64,64	0
6	ACY	A	507	4/4	0.84	0.35	64,65,67,71	0
4	EDO	D	505	4/4	0.85	0.12	55,56,57,57	0
4	EDO	B	505	4/4	0.87	0.14	43,47,49,49	0
5	FMT	C	504	3/3	0.88	0.15	71,71,71,71	0
4	EDO	A	504	4/4	0.91	0.39	55,58,60,62	0
5	FMT	D	504	3/3	0.91	0.12	65,65,66,67	0
6	ACY	C	503	4/4	0.91	0.27	51,54,54,56	0
4	EDO	B	503	4/4	0.92	0.11	55,55,56,56	0
5	FMT	B	506	3/3	0.92	0.07	74,74,74,74	0
3	Q21	B	507	31/31	0.93	0.26	53,59,67,68	0
5	FMT	A	506	3/3	0.94	0.09	58,58,59,60	0
5	FMT	B	504	3/3	0.94	0.14	64,64,66,67	0
3	Q21	D	503	31/31	0.94	0.16	42,48,52,52	0
3	Q21	A	502	31/31	0.95	0.11	35,38,44,45	0
3	Q21	B	502	31/31	0.95	0.17	42,50,62,62	0
2	IMP	C	501	23/23	0.96	0.11	28,37,40,41	0
2	IMP	B	501	23/23	0.97	0.09	27,33,38,39	0
2	IMP	A	501	23/23	0.97	0.12	26,32,36,36	0
2	IMP	D	502	23/23	0.98	0.11	24,32,36,37	0

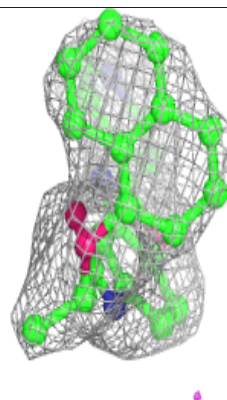
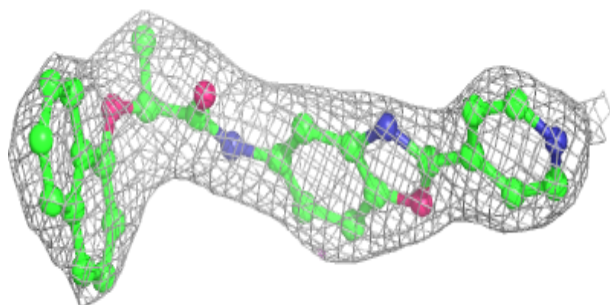
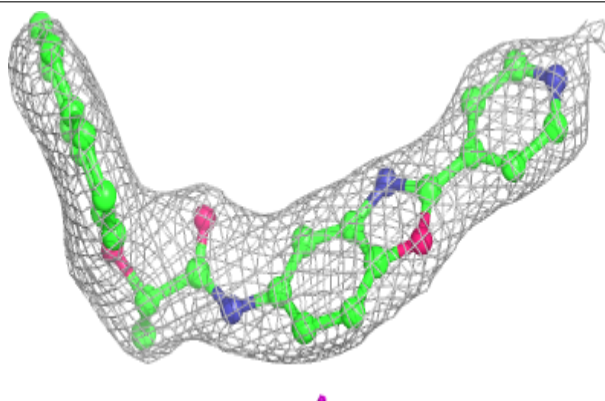
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around Q21 B 507:**

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

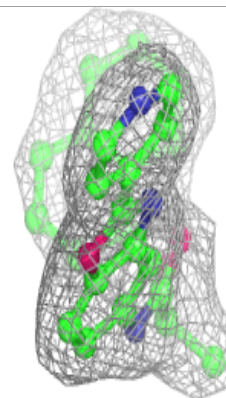
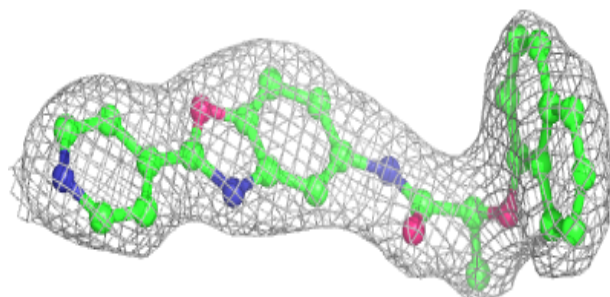
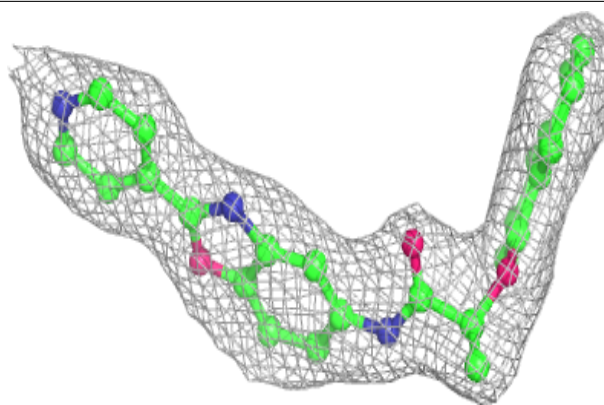
**Electron density around Q21 D 503:**

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

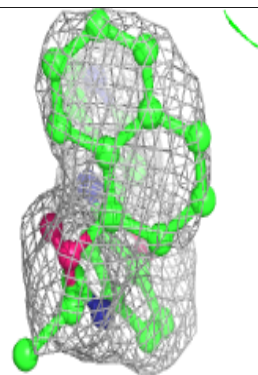
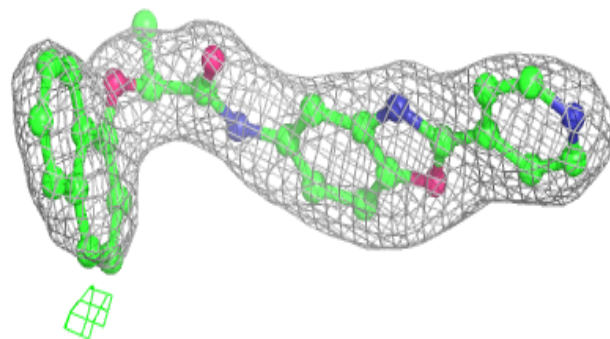
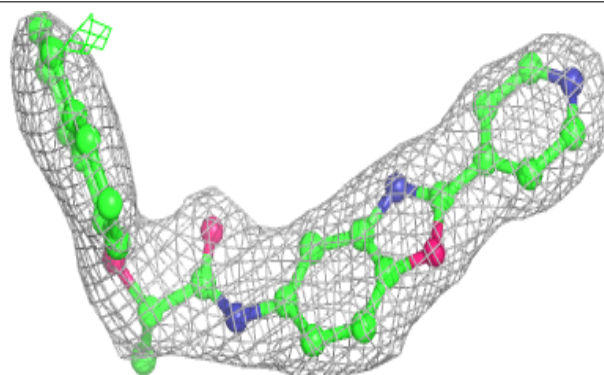


**Electron density around Q21 A 502:**

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

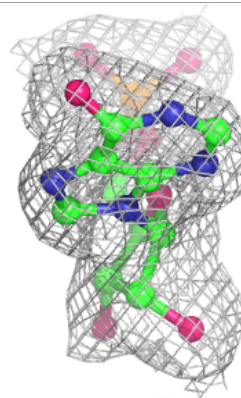
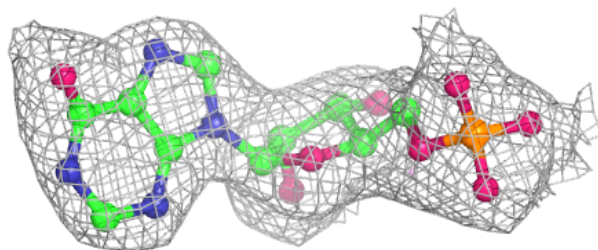
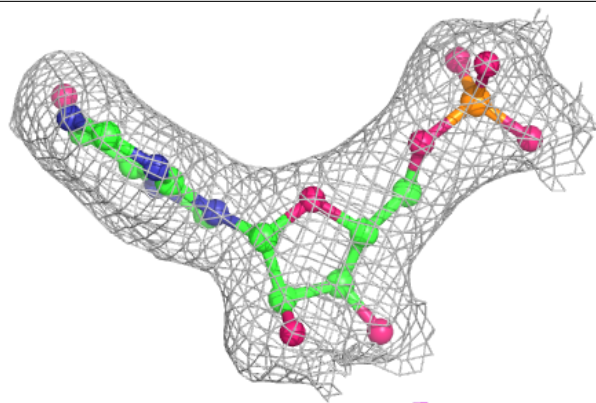
**Electron density around Q21 B 502:**

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and green (positive)

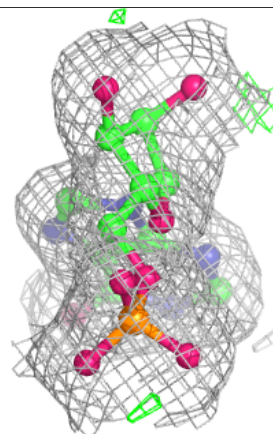
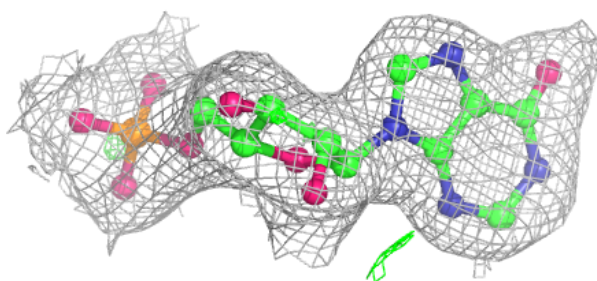
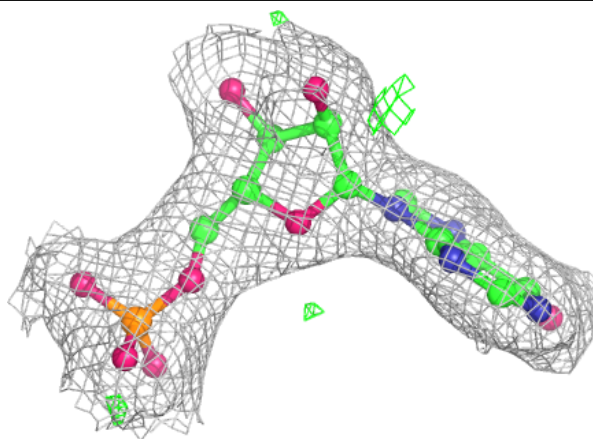


**Electron density around IMP C 501:**

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

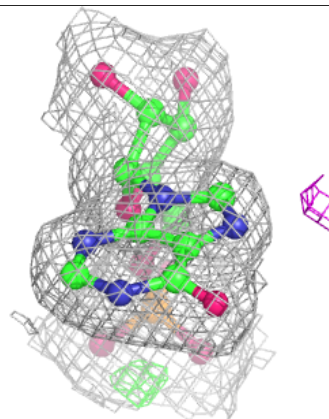
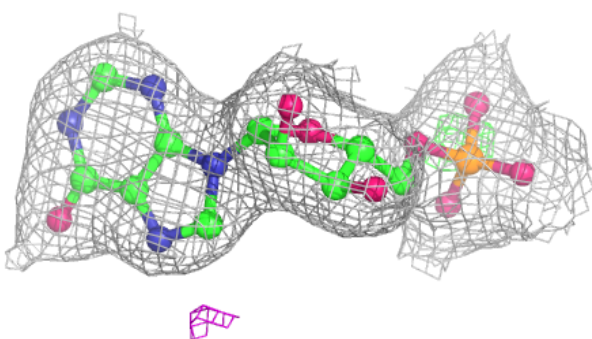
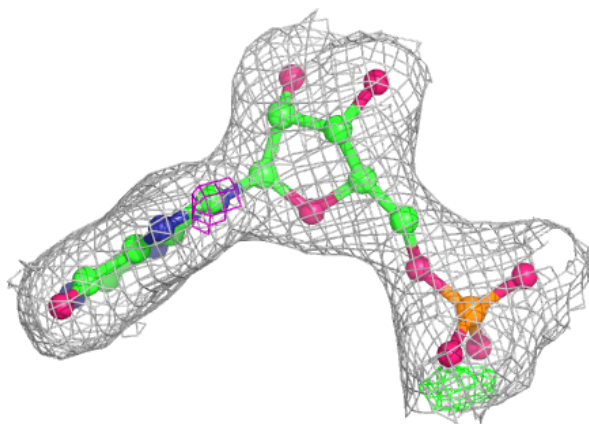
**Electron density around IMP B 501:**

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

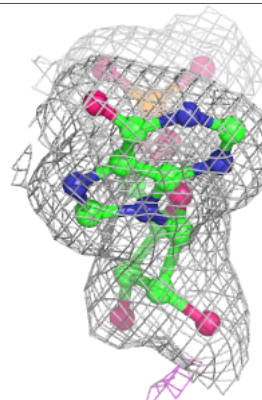
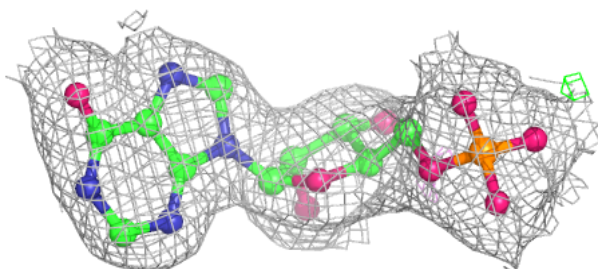
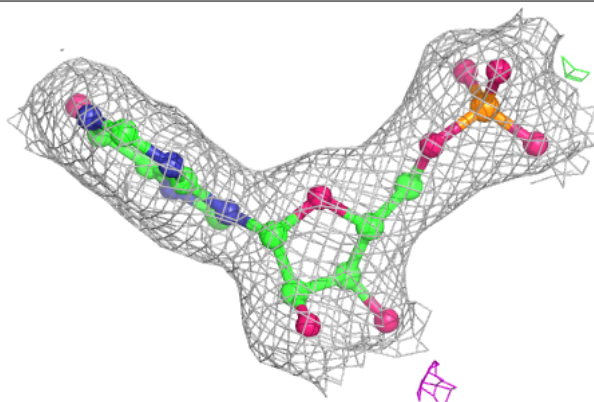


**Electron density around IMP A 501:**

$2mF_o-DF_c$  (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.