



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 20, 2026 – 12:00 pm BST

PDB ID : 9HKB / pdb\_00009hkb  
Title : Crystal structure of IMPDH from Burkholderia thailandensis  
Authors : Gelin, M.; Labesse, G.; Ayoub, N.; Haouz, A.; Munier-Lehmann, H.  
Deposited on : 2024-12-03  
Resolution : 1.44 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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 : 4-5-2 with Phenix2.0  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

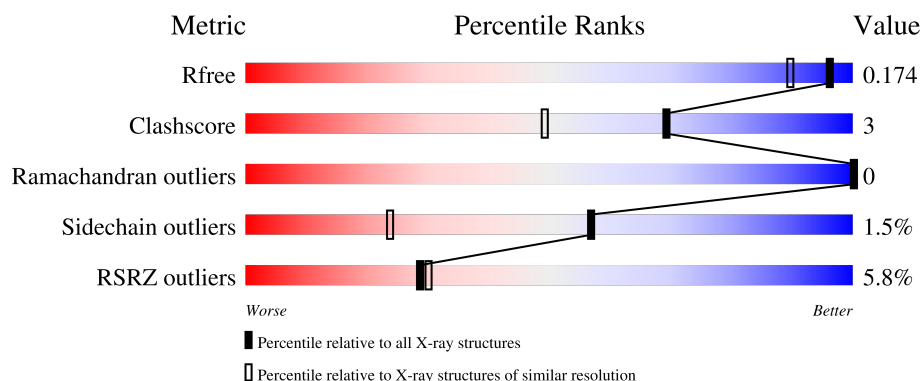
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.44 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))
$R_{free}$	180053	3234 (1.46-1.42)
Clashscore	190562	3289 (1.46-1.42)
Ramachandran outliers	187476	3248 (1.46-1.42)
Sidechain outliers	187428	3248 (1.46-1.42)
RSRZ outliers	180081	3234 (1.46-1.42)

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  $\geq 3$ , 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	B	397	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>5% • 10%</div> </div> </div>
1	C	397	<div> <div>5%</div> <div> <div></div> <div>83%</div> <div>6% • 11%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5876 atoms, of which 24 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	B	356	Total	C	N	O	S	0	2	0
			2615	1640	465	494	16			
1	C	355	Total	C	N	O	S	0	6	0
			2625	1650	469	490	16			

There are 258 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	initiating methionine	UNP Q2SWW9
B	-18	GLY	-	expression tag	UNP Q2SWW9
B	-17	SER	-	expression tag	UNP Q2SWW9
B	-16	SER	-	expression tag	UNP Q2SWW9
B	-15	HIS	-	expression tag	UNP Q2SWW9
B	-14	HIS	-	expression tag	UNP Q2SWW9
B	-13	HIS	-	expression tag	UNP Q2SWW9
B	-12	HIS	-	expression tag	UNP Q2SWW9
B	-11	HIS	-	expression tag	UNP Q2SWW9
B	-10	HIS	-	expression tag	UNP Q2SWW9
B	-9	SER	-	expression tag	UNP Q2SWW9
B	-8	SER	-	expression tag	UNP Q2SWW9
B	-7	GLY	-	expression tag	UNP Q2SWW9
B	-6	LEU	-	expression tag	UNP Q2SWW9
B	-5	VAL	-	expression tag	UNP Q2SWW9
B	-4	PRO	-	expression tag	UNP Q2SWW9
B	-3	ARG	-	expression tag	UNP Q2SWW9
B	-2	GLY	-	expression tag	UNP Q2SWW9
B	-1	SER	-	expression tag	UNP Q2SWW9
B	0	HIS	-	expression tag	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	ARG	deletion	UNP Q2SWW9
B	?	-	ASP	deletion	UNP Q2SWW9
B	?	-	PRO	deletion	UNP Q2SWW9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	ILE	deletion	UNP Q2SWW9
B	?	-	THR	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	PRO	deletion	UNP Q2SWW9
B	?	-	PRO	deletion	UNP Q2SWW9
B	?	-	SER	deletion	UNP Q2SWW9
B	?	-	MET	deletion	UNP Q2SWW9
B	?	-	LYS	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	ARG	deletion	UNP Q2SWW9
B	?	-	ASP	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	ILE	deletion	UNP Q2SWW9
B	?	-	ALA	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	SER	deletion	UNP Q2SWW9
B	?	-	ARG	deletion	UNP Q2SWW9
B	?	-	GLN	deletion	UNP Q2SWW9
B	?	-	HIS	deletion	UNP Q2SWW9
B	?	-	GLY	deletion	UNP Q2SWW9
B	?	-	ILE	deletion	UNP Q2SWW9
B	?	-	SER	deletion	UNP Q2SWW9
B	?	-	GLY	deletion	UNP Q2SWW9
B	?	-	PHE	deletion	UNP Q2SWW9
B	?	-	PRO	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	GLU	deletion	UNP Q2SWW9
B	?	-	GLY	deletion	UNP Q2SWW9
B	?	-	PRO	deletion	UNP Q2SWW9
B	?	-	LYS	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	GLY	deletion	UNP Q2SWW9
B	?	-	ILE	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	THR	deletion	UNP Q2SWW9
B	?	-	ASN	deletion	UNP Q2SWW9
B	?	-	ARG	deletion	UNP Q2SWW9
B	?	-	ASP	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	ARG	deletion	UNP Q2SWW9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	PHE	deletion	UNP Q2SWW9
B	?	-	GLU	deletion	UNP Q2SWW9
B	?	-	THR	deletion	UNP Q2SWW9
B	?	-	ARG	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	ASP	deletion	UNP Q2SWW9
B	?	-	GLU	deletion	UNP Q2SWW9
B	?	-	PRO	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	LYS	deletion	UNP Q2SWW9
B	?	-	SER	deletion	UNP Q2SWW9
B	?	-	ILE	deletion	UNP Q2SWW9
B	?	-	MET	deletion	UNP Q2SWW9
B	?	-	THR	deletion	UNP Q2SWW9
B	?	-	PRO	deletion	UNP Q2SWW9
B	?	-	ARG	deletion	UNP Q2SWW9
B	?	-	GLU	deletion	UNP Q2SWW9
B	?	-	ARG	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	THR	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	ALA	deletion	UNP Q2SWW9
B	?	-	GLU	deletion	UNP Q2SWW9
B	?	-	GLY	deletion	UNP Q2SWW9
B	?	-	THR	deletion	UNP Q2SWW9
B	?	-	PRO	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	ALA	deletion	UNP Q2SWW9
B	?	-	GLU	deletion	UNP Q2SWW9
B	?	-	ALA	deletion	UNP Q2SWW9
B	?	-	LYS	deletion	UNP Q2SWW9
B	?	-	ALA	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	MET	deletion	UNP Q2SWW9
B	?	-	HIS	deletion	UNP Q2SWW9
B	?	-	SER	deletion	UNP Q2SWW9
B	?	-	HIS	deletion	UNP Q2SWW9
B	?	-	ARG	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	GLU	deletion	UNP Q2SWW9
B	?	-	ARG	deletion	UNP Q2SWW9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	ASN	deletion	UNP Q2SWW9
B	?	-	ASP	deletion	UNP Q2SWW9
B	?	-	ALA	deletion	UNP Q2SWW9
B	?	-	PHE	deletion	UNP Q2SWW9
B	?	-	GLU	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	ARG	deletion	UNP Q2SWW9
B	?	-	GLY	deletion	UNP Q2SWW9
B	?	-	LEU	deletion	UNP Q2SWW9
B	?	-	MET	deletion	UNP Q2SWW9
B	?	-	THR	deletion	UNP Q2SWW9
B	?	-	VAL	deletion	UNP Q2SWW9
B	?	-	LYS	deletion	UNP Q2SWW9
B	?	-	ASP	deletion	UNP Q2SWW9
B	?	-	ILE	deletion	UNP Q2SWW9
B	?	-	THR	deletion	UNP Q2SWW9
C	-19	MET	-	initiating methionine	UNP Q2SWW9
C	-18	GLY	-	expression tag	UNP Q2SWW9
C	-17	SER	-	expression tag	UNP Q2SWW9
C	-16	SER	-	expression tag	UNP Q2SWW9
C	-15	HIS	-	expression tag	UNP Q2SWW9
C	-14	HIS	-	expression tag	UNP Q2SWW9
C	-13	HIS	-	expression tag	UNP Q2SWW9
C	-12	HIS	-	expression tag	UNP Q2SWW9
C	-11	HIS	-	expression tag	UNP Q2SWW9
C	-10	HIS	-	expression tag	UNP Q2SWW9
C	-9	SER	-	expression tag	UNP Q2SWW9
C	-8	SER	-	expression tag	UNP Q2SWW9
C	-7	GLY	-	expression tag	UNP Q2SWW9
C	-6	LEU	-	expression tag	UNP Q2SWW9
C	-5	VAL	-	expression tag	UNP Q2SWW9
C	-4	PRO	-	expression tag	UNP Q2SWW9
C	-3	ARG	-	expression tag	UNP Q2SWW9
C	-2	GLY	-	expression tag	UNP Q2SWW9
C	-1	SER	-	expression tag	UNP Q2SWW9
C	0	HIS	-	expression tag	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	ARG	deletion	UNP Q2SWW9
C	?	-	ASP	deletion	UNP Q2SWW9
C	?	-	PRO	deletion	UNP Q2SWW9
C	?	-	ILE	deletion	UNP Q2SWW9
C	?	-	THR	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	PRO	deletion	UNP Q2SWW9
C	?	-	PRO	deletion	UNP Q2SWW9
C	?	-	SER	deletion	UNP Q2SWW9
C	?	-	MET	deletion	UNP Q2SWW9
C	?	-	LYS	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	ARG	deletion	UNP Q2SWW9
C	?	-	ASP	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	ILE	deletion	UNP Q2SWW9
C	?	-	ALA	deletion	UNP Q2SWW9
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	SER	deletion	UNP Q2SWW9
C	?	-	ARG	deletion	UNP Q2SWW9
C	?	-	GLN	deletion	UNP Q2SWW9
C	?	-	HIS	deletion	UNP Q2SWW9
C	?	-	GLY	deletion	UNP Q2SWW9
C	?	-	ILE	deletion	UNP Q2SWW9
C	?	-	SER	deletion	UNP Q2SWW9
C	?	-	GLY	deletion	UNP Q2SWW9
C	?	-	PHE	deletion	UNP Q2SWW9
C	?	-	PRO	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	GLU	deletion	UNP Q2SWW9
C	?	-	GLY	deletion	UNP Q2SWW9
C	?	-	PRO	deletion	UNP Q2SWW9
C	?	-	LYS	deletion	UNP Q2SWW9
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	GLY	deletion	UNP Q2SWW9
C	?	-	ILE	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	THR	deletion	UNP Q2SWW9
C	?	-	ASN	deletion	UNP Q2SWW9
C	?	-	ARG	deletion	UNP Q2SWW9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	ASP	deletion	UNP Q2SWW9
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	ARG	deletion	UNP Q2SWW9
C	?	-	PHE	deletion	UNP Q2SWW9
C	?	-	GLU	deletion	UNP Q2SWW9
C	?	-	THR	deletion	UNP Q2SWW9
C	?	-	ARG	deletion	UNP Q2SWW9
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	ASP	deletion	UNP Q2SWW9
C	?	-	GLU	deletion	UNP Q2SWW9
C	?	-	PRO	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	LYS	deletion	UNP Q2SWW9
C	?	-	SER	deletion	UNP Q2SWW9
C	?	-	ILE	deletion	UNP Q2SWW9
C	?	-	MET	deletion	UNP Q2SWW9
C	?	-	THR	deletion	UNP Q2SWW9
C	?	-	PRO	deletion	UNP Q2SWW9
C	?	-	ARG	deletion	UNP Q2SWW9
C	?	-	GLU	deletion	UNP Q2SWW9
C	?	-	ARG	deletion	UNP Q2SWW9
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	THR	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	ALA	deletion	UNP Q2SWW9
C	?	-	GLU	deletion	UNP Q2SWW9
C	?	-	GLY	deletion	UNP Q2SWW9
C	?	-	THR	deletion	UNP Q2SWW9
C	?	-	PRO	deletion	UNP Q2SWW9
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	ALA	deletion	UNP Q2SWW9
C	?	-	GLU	deletion	UNP Q2SWW9
C	?	-	ALA	deletion	UNP Q2SWW9
C	?	-	LYS	deletion	UNP Q2SWW9
C	?	-	ALA	deletion	UNP Q2SWW9
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	MET	deletion	UNP Q2SWW9
C	?	-	HIS	deletion	UNP Q2SWW9
C	?	-	SER	deletion	UNP Q2SWW9
C	?	-	HIS	deletion	UNP Q2SWW9
C	?	-	ARG	deletion	UNP Q2SWW9

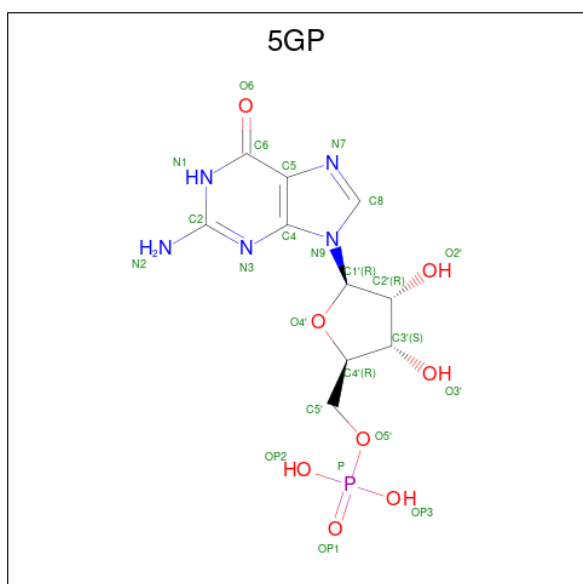
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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	GLU	deletion	UNP Q2SWW9
C	?	-	ARG	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	ASN	deletion	UNP Q2SWW9
C	?	-	ASP	deletion	UNP Q2SWW9
C	?	-	ALA	deletion	UNP Q2SWW9
C	?	-	PHE	deletion	UNP Q2SWW9
C	?	-	GLU	deletion	UNP Q2SWW9
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	ARG	deletion	UNP Q2SWW9
C	?	-	GLY	deletion	UNP Q2SWW9
C	?	-	LEU	deletion	UNP Q2SWW9
C	?	-	MET	deletion	UNP Q2SWW9
C	?	-	THR	deletion	UNP Q2SWW9
C	?	-	VAL	deletion	UNP Q2SWW9
C	?	-	LYS	deletion	UNP Q2SWW9
C	?	-	ASP	deletion	UNP Q2SWW9
C	?	-	ILE	deletion	UNP Q2SWW9
C	?	-	THR	deletion	UNP Q2SWW9

- Molecule 2 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula:  $C_{10}H_{14}N_5O_8P$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	H	N	O	P	0	0
			36	10	12	5	8	1		
2	C	1	Total	C	H	N	O	P	0	0
			36	10	12	5	8	1		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Cl	0	0
			2	2		
3	C	2	Total	Cl	0	0
			2	2		

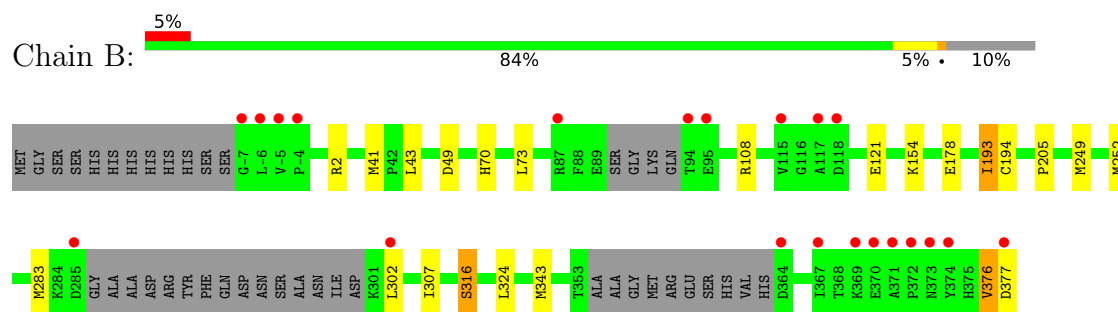
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	278	Total	O	0	0
			278	278		
4	C	282	Total	O	0	0
			282	282		

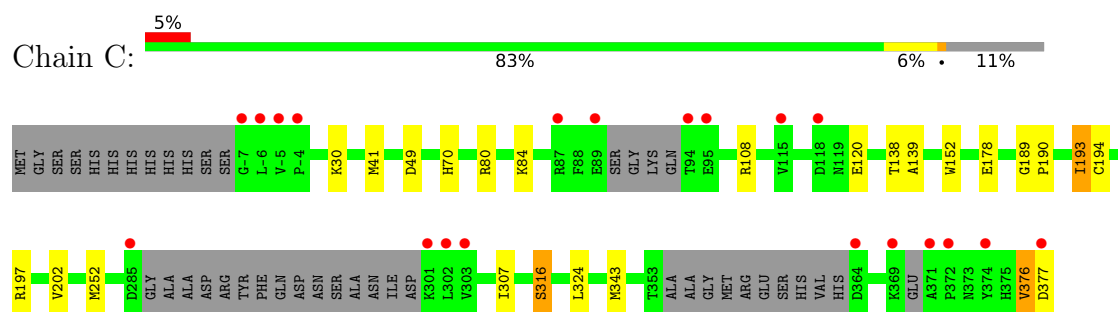
### 3 Residue-property plots [i](#)

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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.51Å 91.51Å 86.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.76 – 1.44 45.76 – 1.44	Depositor EDS
% Data completeness (in resolution range)	99.7 (45.76-1.44) 99.6 (45.76-1.44)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.07 (at 1.44Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.160 , 0.175 0.161 , 0.174	Depositor DCC
$R_{free}$ test set	6440 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.1	Xtriage
Anisotropy	0.195	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 47.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.042 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5876	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 95.39 % 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 1.4161e-09. 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5GP, CL

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	B	0.68	0/2657	0.78	2/3590 (0.1%)
1	C	0.66	0/2678	0.77	2/3615 (0.1%)
All	All	0.67	0/5335	0.77	4/7205 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2
1	C	0	1
All	All	0	3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	376	VAL	CA-C-N	5.40	131.41	121.70
1	B	376	VAL	C-N-CA	5.40	131.41	121.70
1	C	376	VAL	CA-C-N	5.21	131.09	121.70
1	C	376	VAL	C-N-CA	5.21	131.09	121.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	108	ARG	Sidechain
1	B	2	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	C	108	ARG	Sidechain

## 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	B	2615	0	2647	17	0
1	C	2625	0	2670	20	0
2	B	24	12	12	1	0
2	C	24	12	12	1	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
4	B	278	0	0	5	0
4	C	282	0	0	4	0
All	All	5852	24	5341	37	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (37) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:316:SER:HB2	1:B:377:ASP:C	2.03	0.84
1:B:283:MET:HE3	1:B:302:LEU:HD13	1.60	0.82
1:B:154:LYS:HE2	4:B:504:HOH:O	1.85	0.74
1:B:178:GLU:HG3	4:B:516:HOH:O	1.90	0.71
1:B:194:CYS:SG	2:B:401:5GP:N2	2.64	0.71
1:C:178:GLU:HG3	4:C:545:HOH:O	1.92	0.70
1:C:194:CYS:SG	2:C:401:5GP:N2	2.67	0.67
1:C:189:GLY:HA3	1:C:197[A]:ARG:HE	1.58	0.66
1:C:376:VAL:O	1:C:377:ASP:HB2	1.99	0.61
1:B:376:VAL:O	1:B:377:ASP:HB2	2.04	0.58
1:C:193:ILE:HG22	1:C:307:ILE:HD11	1.85	0.57
1:C:307:ILE:C	1:C:307:ILE:HD12	2.29	0.57
1:C:189:GLY:HA3	1:C:197[A]:ARG:NE	2.20	0.56
1:C:138:THR:HG22	1:C:139:ALA:N	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:30:LYS:HE2	4:C:577:HOH:O	2.07	0.54
1:C:316:SER:HB2	1:C:377:ASP:C	2.33	0.54
1:B:316:SER:HB2	1:B:377:ASP:OXT	2.08	0.54
1:B:252:MET:HE2	1:B:324:LEU:HD21	1.90	0.53
4:B:516:HOH:O	1:C:376:VAL:HG23	2.09	0.52
1:B:43:LEU:HD22	1:B:249:MET:HE1	1.91	0.51
1:B:307:ILE:C	1:B:307:ILE:HD12	2.36	0.51
1:B:193:ILE:HG22	1:B:307:ILE:HD11	1.93	0.49
1:B:316:SER:HB2	1:B:377:ASP:O	2.13	0.48
1:C:80:ARG:O	1:C:84:LYS:HG3	2.13	0.48
1:C:343:MET:HE2	4:C:663:HOH:O	2.14	0.47
1:C:252:MET:HE2	1:C:324:LEU:HD21	1.96	0.47
1:C:197[A]:ARG:HG2	1:C:202:VAL:O	2.15	0.45
1:C:252:MET:HG2	4:C:606:HOH:O	2.17	0.44
1:B:343:MET:HE2	4:B:681:HOH:O	2.17	0.43
1:C:120:GLU:HG2	1:C:152:TRP:CH2	2.53	0.43
1:B:252:MET:HG2	4:B:610:HOH:O	2.18	0.43
1:B:49:ASP:HA	1:B:70:HIS:CD2	2.54	0.42
1:B:252:MET:HB3	1:B:252:MET:HE3	1.79	0.42
1:C:120:GLU:HG2	1:C:152:TRP:CZ2	2.54	0.42
1:C:49:ASP:HA	1:C:70:HIS:CD2	2.55	0.41
1:B:70:HIS:CE1	1:B:73:LEU:HG	2.56	0.40
1:C:189:GLY:N	1:C:190:PRO:CD	2.84	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	350/397 (88%)	342 (98%)	8 (2%)	0	100	100
1	C	351/397 (88%)	343 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	701/794 (88%)	685 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	270/305 (88%)	265 (98%)	5 (2%)	50	16
1	C	271/305 (89%)	268 (99%)	3 (1%)	65	35
All	All	541/610 (89%)	533 (98%)	8 (2%)	57	24

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	41	MET
1	B	121	GLU
1	B	193	ILE
1	B	205	PRO
1	B	316	SER
1	C	41	MET
1	C	193	ILE
1	C	316	SER

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

Mol	Chain	Res	Type
1	C	96	HIS

### 5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	5GP	C	401	-	26,26,26	1.12	3 (11%)	40,40,40	1.69	9 (22%)
2	5GP	B	401	-	26,26,26	1.08	2 (7%)	40,40,40	1.56	6 (15%)

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	5GP	C	401	-	-	0/10/26/26	0/3/3/3
2	5GP	B	401	-	-	0/10/26/26	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	5GP	C6-N1	-3.15	1.33	1.38
2	C	401	5GP	C6-N1	-2.95	1.33	1.38
2	B	401	5GP	C4-N9	-2.54	1.31	1.38
2	C	401	5GP	C4-N9	-2.42	1.31	1.38
2	C	401	5GP	C5-N7	-2.13	1.34	1.39

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	5GP	C5-C4-N3	-4.42	121.28	128.46
2	C	401	5GP	N9-C8-N7	-4.30	105.29	113.39
2	B	401	5GP	N9-C8-N7	-4.03	105.79	113.39
2	B	401	5GP	C4-C5-N7	-4.01	104.37	110.72
2	B	401	5GP	C5-C4-N3	-3.97	122.02	128.46
2	C	401	5GP	C8-N7-C5	3.76	111.05	104.24
2	C	401	5GP	C4-C5-N7	-3.73	104.82	110.72
2	B	401	5GP	C8-N7-C5	3.71	110.96	104.24
2	C	401	5GP	C6-C5-N7	2.46	134.83	130.25
2	C	401	5GP	C2-N1-C6	-2.33	120.85	125.10
2	B	401	5GP	C6-C5-N7	2.23	134.40	130.25
2	C	401	5GP	C8-N9-C4	2.14	110.13	106.05
2	C	401	5GP	N9-C4-N3	2.03	130.02	125.94
2	B	401	5GP	C5-C4-N9	2.02	109.29	105.63
2	C	401	5GP	C2-N3-C4	2.01	115.87	112.30

There are no chirality outliers.

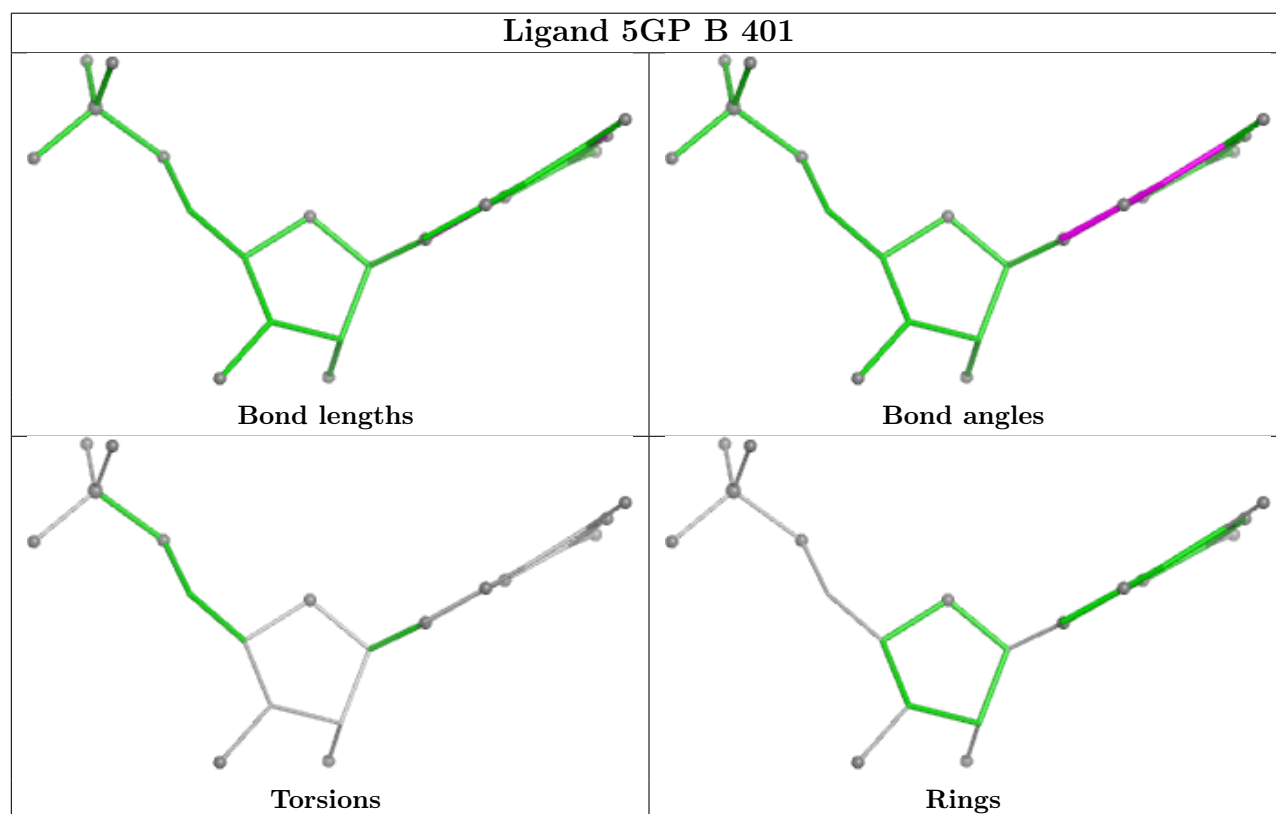
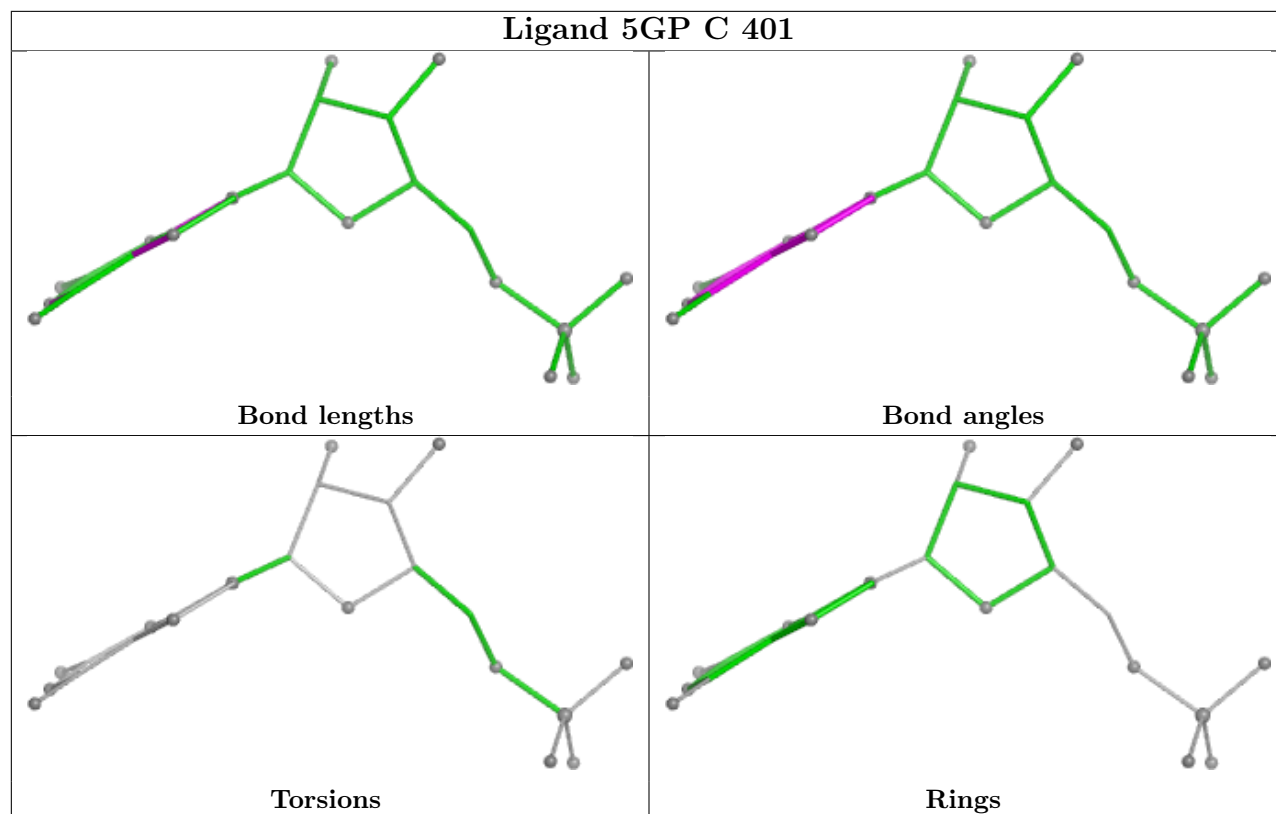
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	5GP	1	0
2	B	401	5GP	1	0

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



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å <sup>2</sup> )	Q < 0.9
1	B	356/397 (89%)	-0.10	21 (5%)	28 29	11, 19, 38, 59	27 (7%)
1	C	355/397 (89%)	-0.10	20 (5%)	30 31	10, 19, 37, 58	27 (7%)
All	All	711/794 (89%)	-0.10	41 (5%)	29 30	10, 19, 37, 59	54 (7%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	371	ALA	6.2
1	B	94	THR	4.4
1	B	371	ALA	4.4
1	C	94	THR	4.4
1	C	89	GLU	4.1
1	B	370	GLU	4.1
1	B	302	LEU	4.0
1	C	302	LEU	4.0
1	B	369	LYS	3.3
1	B	-7	GLY	3.2
1	B	364	ASP	3.1
1	C	364	ASP	2.9
1	B	374	TYR	2.9
1	C	369	LYS	2.9
1	B	377	ASP	2.9
1	B	-6	LEU	2.8
1	C	374	TYR	2.8
1	B	115	VAL	2.8
1	C	377	ASP	2.8
1	B	118	ASP	2.7
1	C	118	ASP	2.6
1	C	285	ASP	2.5
1	B	372	PRO	2.5
1	C	-6	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	-5	VAL	2.4
1	C	-7	GLY	2.4
1	C	-4	PRO	2.4
1	B	-4	PRO	2.4
1	B	87	ARG	2.4
1	B	285	ASP	2.3
1	C	115	VAL	2.3
1	C	303	VAL	2.3
1	B	117	ALA	2.3
1	C	95	GLU	2.3
1	B	95	GLU	2.2
1	B	367	ILE	2.2
1	B	373	ASN	2.2
1	C	301	LYS	2.1
1	C	372	PRO	2.1
1	C	87	ARG	2.0
1	B	-5	VAL	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 6.4 Ligands ⓘ

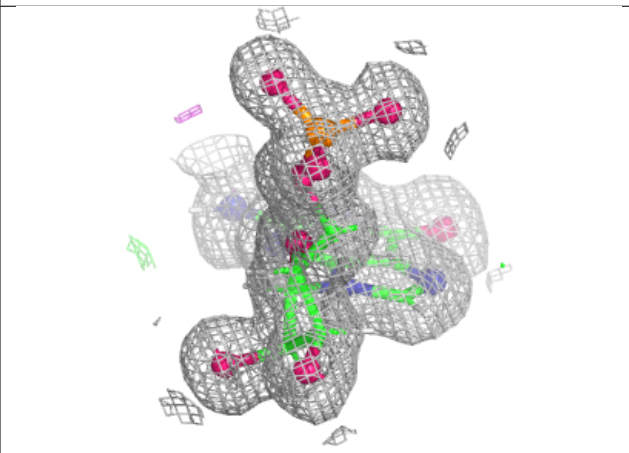
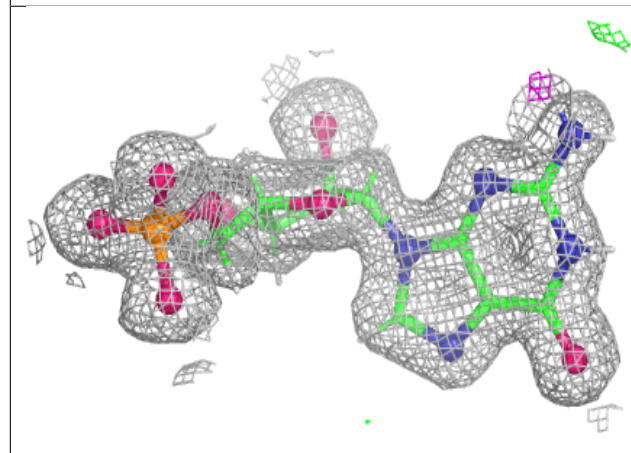
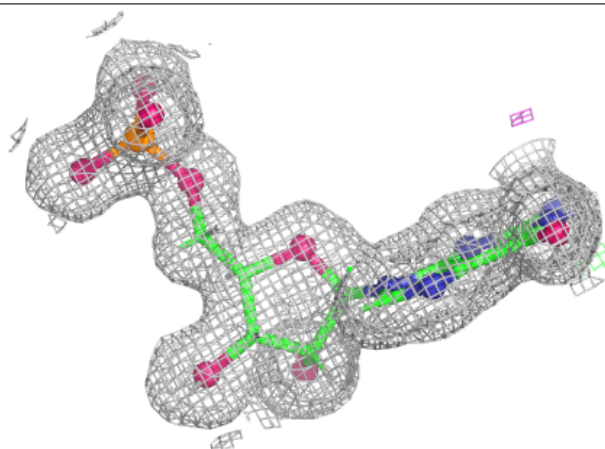
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	5GP	B	401	24/24	0.99	0.04	13,16,29,35	0
2	5GP	C	401	24/24	0.99	0.04	13,17,29,35	0
3	CL	B	402	1/1	0.99	0.03	19,19,19,19	0
3	CL	B	403	1/1	1.00	0.11	22,22,22,22	0
3	CL	C	402	1/1	1.00	0.03	19,19,19,19	0
3	CL	C	403	1/1	1.00	0.09	23,23,23,23	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.

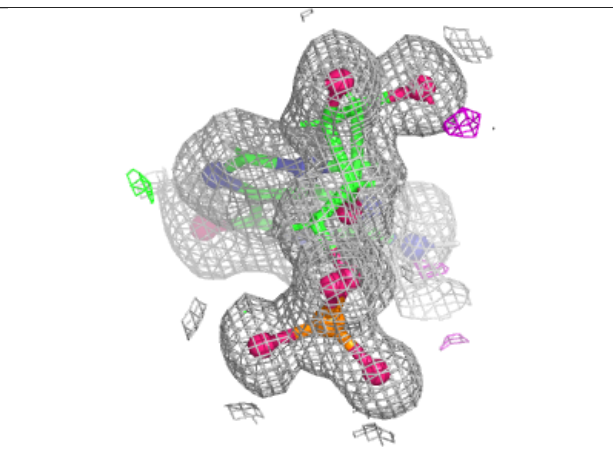
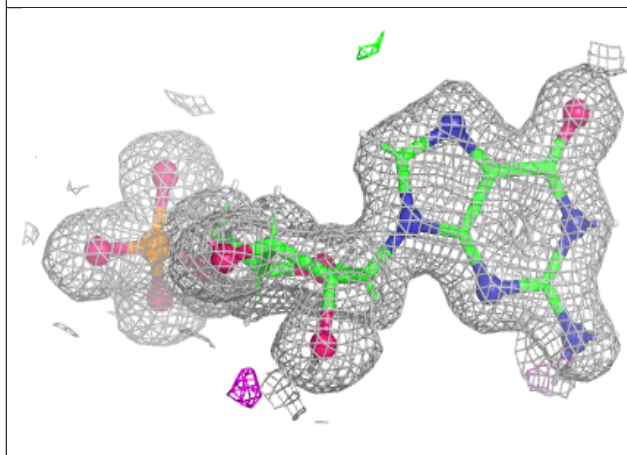
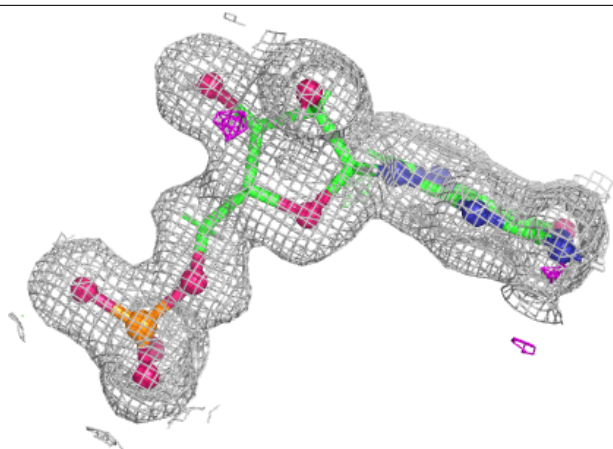
**Electron density around 5GP B 401:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around 5GP C 401:**

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



## 6.5 Other polymers ⓘ

There are no such residues in this entry.