



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 19, 2026 – 01:42 AM UTC

PDB ID : 5UGF / pdb_00005ugf
Title : Crystal structure of human purine nucleoside phosphorylase (F159Y) mutant complexed with DADMe-ImmG and phosphate
Authors : Harijan, R.K.; Cameron, S.A.; Bonanno, J.B.; Almo, S.C.; Schramm, V.L.
Deposited on : 2017-01-08
Resolution : 2.20 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

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

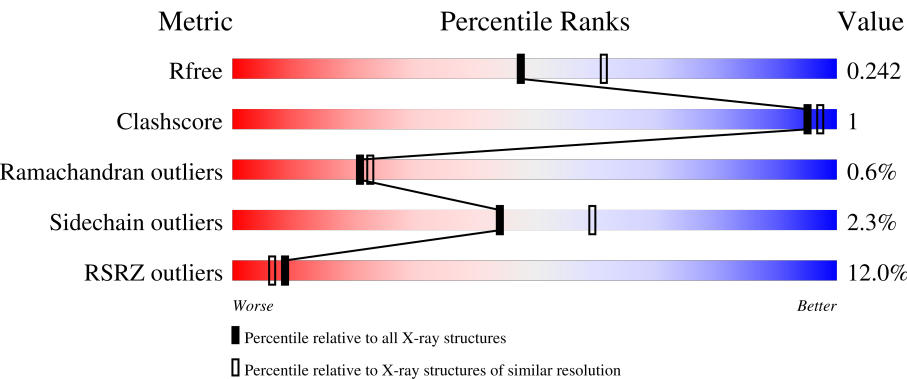
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

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

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 $\leq 5\%$. 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	320	7% 85% 11%
1	B	320	13% 83% 10%
1	C	320	8% 85% 10%
1	D	320	9% 86% 11%
1	E	320	17% 86% 10%

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Mol	Chain	Length	Quality of chain
1	F	320	11% 83% 5% • 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14370 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 Purine nucleoside phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	1	0
			2238	1421	390	412	15			
1	B	287	Total	C	N	O	S	0	2	0
			2244	1425	388	416	15			
1	C	288	Total	C	N	O	S	0	0	0
			2246	1427	391	412	16			
1	D	286	Total	C	N	O	S	0	1	0
			2219	1409	385	410	15			
1	E	287	Total	C	N	O	S	0	1	0
			2225	1414	383	413	15			
1	F	287	Total	C	N	O	S	0	0	0
			2220	1413	384	408	15			

There are 198 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-30	HIS	-	expression tag	UNP P00491
A	-29	HIS	-	expression tag	UNP P00491
A	-28	HIS	-	expression tag	UNP P00491
A	-27	HIS	-	expression tag	UNP P00491
A	-26	HIS	-	expression tag	UNP P00491
A	-25	HIS	-	expression tag	UNP P00491
A	-24	GLY	-	expression tag	UNP P00491
A	-23	MET	-	expression tag	UNP P00491
A	-22	ALA	-	expression tag	UNP P00491
A	-21	SER	-	expression tag	UNP P00491
A	-20	MET	-	expression tag	UNP P00491
A	-19	THR	-	expression tag	UNP P00491
A	-18	GLY	-	expression tag	UNP P00491
A	-17	GLY	-	expression tag	UNP P00491
A	-16	GLN	-	expression tag	UNP P00491
A	-15	GLN	-	expression tag	UNP P00491
A	-14	MET	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	GLY	-	expression tag	UNP P00491
A	-12	ARG	-	expression tag	UNP P00491
A	-11	ASP	-	expression tag	UNP P00491
A	-10	LEU	-	expression tag	UNP P00491
A	-9	TYR	-	expression tag	UNP P00491
A	-8	ASP	-	expression tag	UNP P00491
A	-7	ASP	-	expression tag	UNP P00491
A	-6	ASP	-	expression tag	UNP P00491
A	-5	ASP	-	expression tag	UNP P00491
A	-4	LYS	-	expression tag	UNP P00491
A	-3	ASP	-	expression tag	UNP P00491
A	-2	PRO	-	expression tag	UNP P00491
A	-1	THR	-	expression tag	UNP P00491
A	0	LEU	-	expression tag	UNP P00491
A	51	SER	GLY	conflict	UNP P00491
A	159	TYR	PHE	engineered mutation	UNP P00491
B	-30	HIS	-	expression tag	UNP P00491
B	-29	HIS	-	expression tag	UNP P00491
B	-28	HIS	-	expression tag	UNP P00491
B	-27	HIS	-	expression tag	UNP P00491
B	-26	HIS	-	expression tag	UNP P00491
B	-25	HIS	-	expression tag	UNP P00491
B	-24	GLY	-	expression tag	UNP P00491
B	-23	MET	-	expression tag	UNP P00491
B	-22	ALA	-	expression tag	UNP P00491
B	-21	SER	-	expression tag	UNP P00491
B	-20	MET	-	expression tag	UNP P00491
B	-19	THR	-	expression tag	UNP P00491
B	-18	GLY	-	expression tag	UNP P00491
B	-17	GLY	-	expression tag	UNP P00491
B	-16	GLN	-	expression tag	UNP P00491
B	-15	GLN	-	expression tag	UNP P00491
B	-14	MET	-	expression tag	UNP P00491
B	-13	GLY	-	expression tag	UNP P00491
B	-12	ARG	-	expression tag	UNP P00491
B	-11	ASP	-	expression tag	UNP P00491
B	-10	LEU	-	expression tag	UNP P00491
B	-9	TYR	-	expression tag	UNP P00491
B	-8	ASP	-	expression tag	UNP P00491
B	-7	ASP	-	expression tag	UNP P00491
B	-6	ASP	-	expression tag	UNP P00491
B	-5	ASP	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	LYS	-	expression tag	UNP P00491
B	-3	ASP	-	expression tag	UNP P00491
B	-2	PRO	-	expression tag	UNP P00491
B	-1	THR	-	expression tag	UNP P00491
B	0	LEU	-	expression tag	UNP P00491
B	51	SER	GLY	conflict	UNP P00491
B	159	TYR	PHE	engineered mutation	UNP P00491
C	-30	HIS	-	expression tag	UNP P00491
C	-29	HIS	-	expression tag	UNP P00491
C	-28	HIS	-	expression tag	UNP P00491
C	-27	HIS	-	expression tag	UNP P00491
C	-26	HIS	-	expression tag	UNP P00491
C	-25	HIS	-	expression tag	UNP P00491
C	-24	GLY	-	expression tag	UNP P00491
C	-23	MET	-	expression tag	UNP P00491
C	-22	ALA	-	expression tag	UNP P00491
C	-21	SER	-	expression tag	UNP P00491
C	-20	MET	-	expression tag	UNP P00491
C	-19	THR	-	expression tag	UNP P00491
C	-18	GLY	-	expression tag	UNP P00491
C	-17	GLY	-	expression tag	UNP P00491
C	-16	GLN	-	expression tag	UNP P00491
C	-15	GLN	-	expression tag	UNP P00491
C	-14	MET	-	expression tag	UNP P00491
C	-13	GLY	-	expression tag	UNP P00491
C	-12	ARG	-	expression tag	UNP P00491
C	-11	ASP	-	expression tag	UNP P00491
C	-10	LEU	-	expression tag	UNP P00491
C	-9	TYR	-	expression tag	UNP P00491
C	-8	ASP	-	expression tag	UNP P00491
C	-7	ASP	-	expression tag	UNP P00491
C	-6	ASP	-	expression tag	UNP P00491
C	-5	ASP	-	expression tag	UNP P00491
C	-4	LYS	-	expression tag	UNP P00491
C	-3	ASP	-	expression tag	UNP P00491
C	-2	PRO	-	expression tag	UNP P00491
C	-1	THR	-	expression tag	UNP P00491
C	0	LEU	-	expression tag	UNP P00491
C	51	SER	GLY	conflict	UNP P00491
C	159	TYR	PHE	engineered mutation	UNP P00491
D	-30	HIS	-	expression tag	UNP P00491
D	-29	HIS	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-28	HIS	-	expression tag	UNP P00491
D	-27	HIS	-	expression tag	UNP P00491
D	-26	HIS	-	expression tag	UNP P00491
D	-25	HIS	-	expression tag	UNP P00491
D	-24	GLY	-	expression tag	UNP P00491
D	-23	MET	-	expression tag	UNP P00491
D	-22	ALA	-	expression tag	UNP P00491
D	-21	SER	-	expression tag	UNP P00491
D	-20	MET	-	expression tag	UNP P00491
D	-19	THR	-	expression tag	UNP P00491
D	-18	GLY	-	expression tag	UNP P00491
D	-17	GLY	-	expression tag	UNP P00491
D	-16	GLN	-	expression tag	UNP P00491
D	-15	GLN	-	expression tag	UNP P00491
D	-14	MET	-	expression tag	UNP P00491
D	-13	GLY	-	expression tag	UNP P00491
D	-12	ARG	-	expression tag	UNP P00491
D	-11	ASP	-	expression tag	UNP P00491
D	-10	LEU	-	expression tag	UNP P00491
D	-9	TYR	-	expression tag	UNP P00491
D	-8	ASP	-	expression tag	UNP P00491
D	-7	ASP	-	expression tag	UNP P00491
D	-6	ASP	-	expression tag	UNP P00491
D	-5	ASP	-	expression tag	UNP P00491
D	-4	LYS	-	expression tag	UNP P00491
D	-3	ASP	-	expression tag	UNP P00491
D	-2	PRO	-	expression tag	UNP P00491
D	-1	THR	-	expression tag	UNP P00491
D	0	LEU	-	expression tag	UNP P00491
D	51	SER	GLY	conflict	UNP P00491
D	159	TYR	PHE	engineered mutation	UNP P00491
E	-30	HIS	-	expression tag	UNP P00491
E	-29	HIS	-	expression tag	UNP P00491
E	-28	HIS	-	expression tag	UNP P00491
E	-27	HIS	-	expression tag	UNP P00491
E	-26	HIS	-	expression tag	UNP P00491
E	-25	HIS	-	expression tag	UNP P00491
E	-24	GLY	-	expression tag	UNP P00491
E	-23	MET	-	expression tag	UNP P00491
E	-22	ALA	-	expression tag	UNP P00491
E	-21	SER	-	expression tag	UNP P00491
E	-20	MET	-	expression tag	UNP P00491

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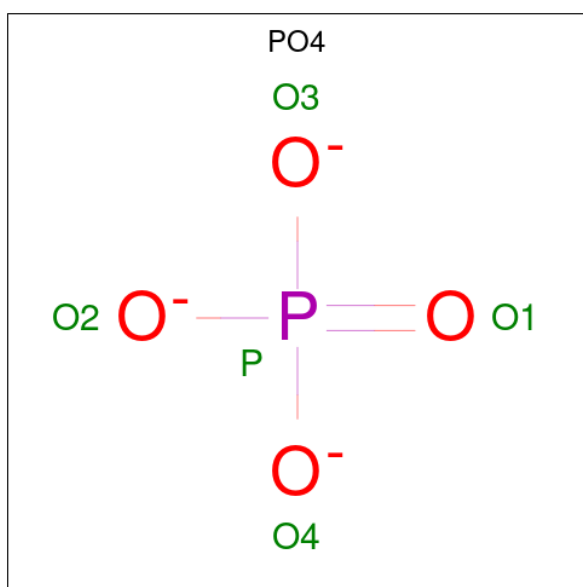
Chain	Residue	Modelled	Actual	Comment	Reference
E	-19	THR	-	expression tag	UNP P00491
E	-18	GLY	-	expression tag	UNP P00491
E	-17	GLY	-	expression tag	UNP P00491
E	-16	GLN	-	expression tag	UNP P00491
E	-15	GLN	-	expression tag	UNP P00491
E	-14	MET	-	expression tag	UNP P00491
E	-13	GLY	-	expression tag	UNP P00491
E	-12	ARG	-	expression tag	UNP P00491
E	-11	ASP	-	expression tag	UNP P00491
E	-10	LEU	-	expression tag	UNP P00491
E	-9	TYR	-	expression tag	UNP P00491
E	-8	ASP	-	expression tag	UNP P00491
E	-7	ASP	-	expression tag	UNP P00491
E	-6	ASP	-	expression tag	UNP P00491
E	-5	ASP	-	expression tag	UNP P00491
E	-4	LYS	-	expression tag	UNP P00491
E	-3	ASP	-	expression tag	UNP P00491
E	-2	PRO	-	expression tag	UNP P00491
E	-1	THR	-	expression tag	UNP P00491
E	0	LEU	-	expression tag	UNP P00491
E	51	SER	GLY	conflict	UNP P00491
E	159	TYR	PHE	engineered mutation	UNP P00491
F	-30	HIS	-	expression tag	UNP P00491
F	-29	HIS	-	expression tag	UNP P00491
F	-28	HIS	-	expression tag	UNP P00491
F	-27	HIS	-	expression tag	UNP P00491
F	-26	HIS	-	expression tag	UNP P00491
F	-25	HIS	-	expression tag	UNP P00491
F	-24	GLY	-	expression tag	UNP P00491
F	-23	MET	-	expression tag	UNP P00491
F	-22	ALA	-	expression tag	UNP P00491
F	-21	SER	-	expression tag	UNP P00491
F	-20	MET	-	expression tag	UNP P00491
F	-19	THR	-	expression tag	UNP P00491
F	-18	GLY	-	expression tag	UNP P00491
F	-17	GLY	-	expression tag	UNP P00491
F	-16	GLN	-	expression tag	UNP P00491
F	-15	GLN	-	expression tag	UNP P00491
F	-14	MET	-	expression tag	UNP P00491
F	-13	GLY	-	expression tag	UNP P00491
F	-12	ARG	-	expression tag	UNP P00491
F	-11	ASP	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-10	LEU	-	expression tag	UNP P00491
F	-9	TYR	-	expression tag	UNP P00491
F	-8	ASP	-	expression tag	UNP P00491
F	-7	ASP	-	expression tag	UNP P00491
F	-6	ASP	-	expression tag	UNP P00491
F	-5	ASP	-	expression tag	UNP P00491
F	-4	LYS	-	expression tag	UNP P00491
F	-3	ASP	-	expression tag	UNP P00491
F	-2	PRO	-	expression tag	UNP P00491
F	-1	THR	-	expression tag	UNP P00491
F	0	LEU	-	expression tag	UNP P00491
F	51	SER	GLY	conflict	UNP P00491
F	159	TYR	PHE	engineered mutation	UNP P00491

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		

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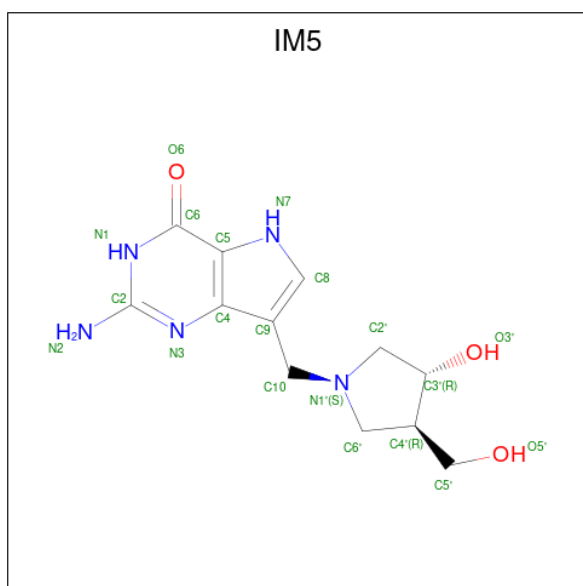
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	E	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is 2-amino-7-{[(3R,4R)-3-hydroxy-4-(hydroxymethyl)pyrrolidin-1-yl]methyl}-3,5-dihydro-4H-pyrrolo[3,2-d]pyrimidin-4-one (CCD ID: IM5) (formula: C₁₂H₁₇N₅O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			20	12	5	3		
3	B	1	Total	C	N	O	0	0
			20	12	5	3		
3	C	1	Total	C	N	O	0	0
			20	12	5	3		
3	D	1	Total	C	N	O	0	0
			20	12	5	3		
3	E	1	Total	C	N	O	0	0
			20	12	5	3		
3	F	1	Total	C	N	O	0	0
			20	12	5	3		

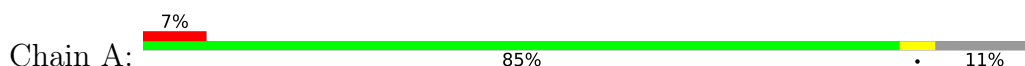
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	137	Total 137	O 137	0	0
4	B	135	Total 135	O 135	0	0
4	C	155	Total 155	O 155	0	0
4	D	104	Total 104	O 104	0	0
4	E	67	Total 67	O 67	0	0
4	F	115	Total 115	O 115	0	0

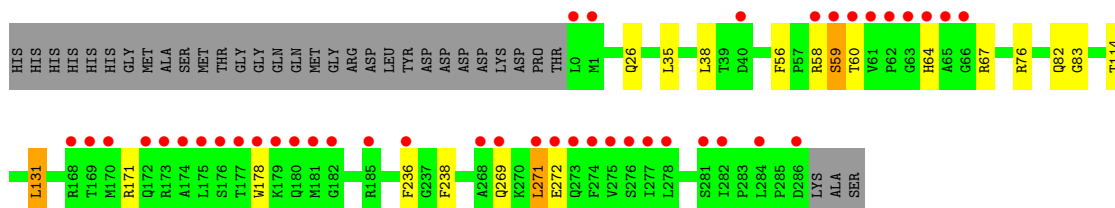
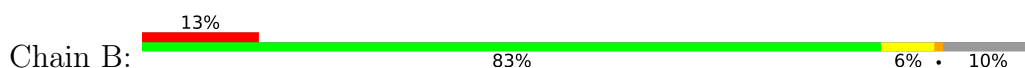
3 Residue-property plots [i](#)

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.

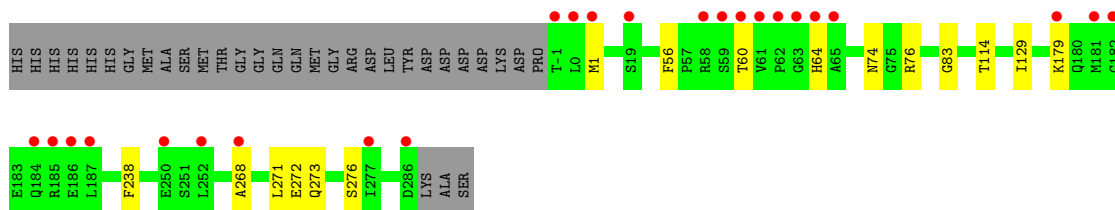
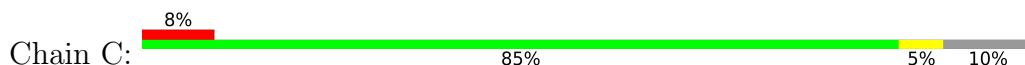
- Molecule 1: Purine nucleoside phosphorylase



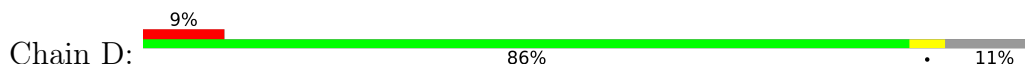
- Molecule 1: Purine nucleoside phosphorylase

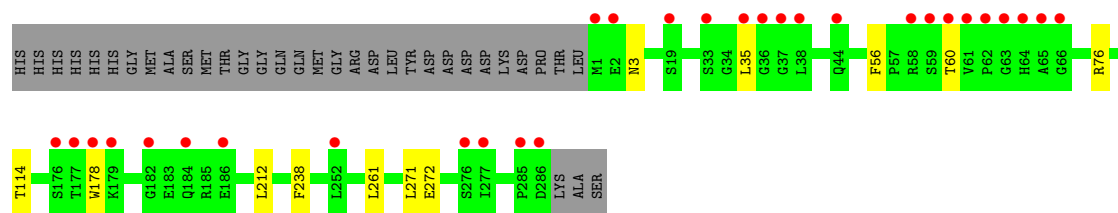


- Molecule 1: Purine nucleoside phosphorylase

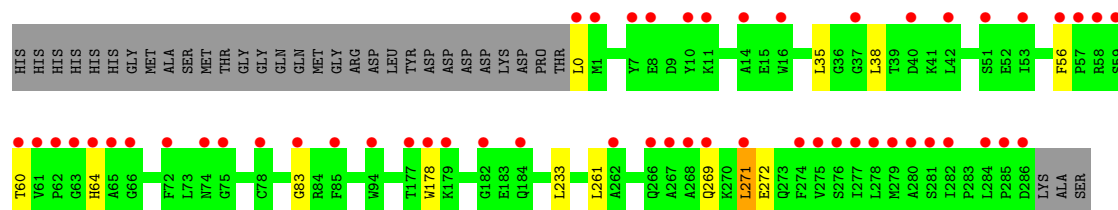
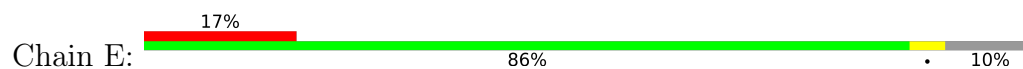


- Molecule 1: Purine nucleoside phosphorylase

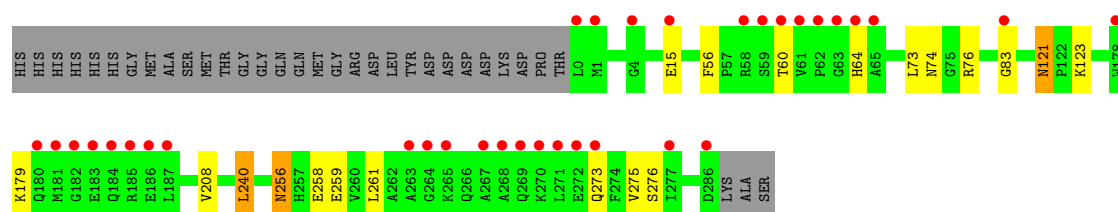
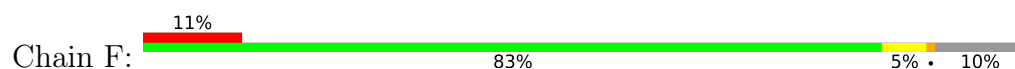




● Molecule 1: Purine nucleoside phosphorylase



● Molecule 1: Purine nucleoside phosphorylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.96Å 124.27Å 136.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.26 – 2.20 69.26 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (69.26-2.20) 100.0 (69.26-2.20)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.20Å)	Xtrriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.214 , 0.238 0.219 , 0.242	Depositor DCC
R_{free} test set	4492 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	27.1	Xtrriage
Anisotropy	0.104	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14370	wwPDB-VP
Average B, all atoms (Å ²)	36.0	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 48.97 % 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 7.9737e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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: IM5, PO4

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	0.69	1/2290 (0.0%)	0.87	1/3102 (0.0%)
1	B	0.63	1/2296 (0.0%)	0.84	1/3113 (0.0%)
1	C	0.64	0/2298	0.84	2/3113 (0.1%)
1	D	0.60	0/2271	0.82	0/3081
1	E	0.59	0/2277	0.81	0/3090
1	F	0.62	0/2272	0.86	3/3081 (0.1%)
All	All	0.63	2/13704 (0.0%)	0.84	7/18580 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	60	THR	CA-C	13.94	1.59	1.52
1	B	60	THR	CA-C	6.22	1.61	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	60	THR	N-CA-C	11.16	125.87	108.12
1	B	60	THR	N-CA-C	8.43	124.23	107.62
1	C	179	LYS	N-CA-C	-5.43	105.52	111.82
1	F	240	LEU	CB-CG-CD1	5.25	126.44	110.70
1	F	179	LYS	N-CA-C	-5.23	105.75	111.82
1	F	240	LEU	CB-CG-CD2	-5.22	95.03	110.70
1	C	268	ALA	N-CA-C	5.08	119.75	111.37

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	2238	0	2195	4	0
1	B	2244	0	2187	10	0
1	C	2246	0	2213	4	0
1	D	2219	0	2156	3	0
1	E	2225	0	2160	3	0
1	F	2220	0	2173	9	0
2	A	35	0	0	0	0
2	B	25	0	0	0	0
2	C	20	0	0	0	0
2	D	30	0	0	0	0
2	E	25	0	0	0	0
2	F	10	0	0	0	0
3	A	20	0	17	0	0
3	B	20	0	17	0	0
3	C	20	0	17	0	0
3	D	20	0	17	0	0
3	E	20	0	17	0	0
3	F	20	0	17	0	0
4	A	137	0	0	1	0
4	B	135	0	0	0	0
4	C	155	0	0	0	0
4	D	104	0	0	0	0
4	E	67	0	0	0	0
4	F	115	0	0	1	0
All	All	14370	0	13186	32	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 1.

All (32) 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:58:ARG:O	1:B:59:SER:HB2	1.74	0.86
1:F:256:ASN:HD22	1:F:259:GLU:H	1.45	0.63
1:F:256:ASN:ND2	1:F:259:GLU:H	1.98	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:58:ARG:O	1:B:59:SER:CB	2.48	0.60
1:B:35:LEU:HD22	1:B:271:LEU:HD23	1.85	0.57
1:C:74:ASN:ND2	1:C:276:SER:HA	2.19	0.56
1:F:74:ASN:ND2	1:F:276:SER:HA	2.20	0.56
1:B:131:LEU:HD21	1:B:171:ARG:HG2	1.88	0.56
1:D:35:LEU:HD22	1:D:271:LEU:CD1	2.36	0.55
1:A:35:LEU:HD22	1:A:271:LEU:CD1	2.38	0.53
1:F:64:HIS:ND1	1:F:83:GLY:HA2	2.25	0.52
1:E:64:HIS:ND1	1:E:83:GLY:HA2	2.26	0.51
1:B:64:HIS:ND1	1:B:83:GLY:HA2	2.26	0.51
1:A:64:HIS:ND1	1:A:83:GLY:HA2	2.26	0.51
1:C:64:HIS:ND1	1:C:83:GLY:HA2	2.26	0.50
1:E:35:LEU:HD22	1:E:271:LEU:HD23	1.94	0.50
1:F:256:ASN:HD21	1:F:258:GLU:HB2	1.77	0.49
1:F:121:ASN:HD22	1:F:123:LYS:H	1.59	0.49
1:A:76:ARG:NH1	4:A:401:HOH:O	2.29	0.49
1:C:129:ILE:HD11	1:C:271:LEU:HD23	1.97	0.46
1:A:114:THR:HG22	1:A:238:PHE:CE2	2.51	0.46
1:B:131:LEU:HD21	1:B:236:PHE:CE1	2.51	0.45
1:B:26:GLN:OE1	1:B:76:ARG:NH1	2.45	0.45
1:F:121:ASN:ND2	4:F:405:HOH:O	2.51	0.44
1:B:67:ARG:HH11	1:B:82:GLN:HE22	1.68	0.41
1:C:114:THR:HG22	1:C:238:PHE:CE1	2.55	0.41
1:E:38:LEU:HD21	1:E:271:LEU:HB3	2.01	0.41
1:D:114:THR:HG22	1:D:238:PHE:CE1	2.56	0.41
1:D:212:LEU:HD22	1:F:208:VAL:HG13	2.03	0.40
1:F:73:LEU:HD21	1:F:275:VAL:HG11	2.03	0.40
1:B:38:LEU:HD21	1:B:271:LEU:HB3	2.03	0.40
1:B:114:THR:HG22	1:B:238:PHE:CE1	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	285/320 (89%)	278 (98%)	5 (2%)	2 (1%)	18	19
1	B	287/320 (90%)	282 (98%)	3 (1%)	2 (1%)	18	19
1	C	286/320 (89%)	282 (99%)	3 (1%)	1 (0%)	36	42
1	D	285/320 (89%)	279 (98%)	3 (1%)	3 (1%)	11	10
1	E	286/320 (89%)	281 (98%)	3 (1%)	2 (1%)	18	19
1	F	285/320 (89%)	282 (99%)	2 (1%)	1 (0%)	30	34
All	All	1714/1920 (89%)	1684 (98%)	19 (1%)	11 (1%)	21	23

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	59	SER
1	A	178	TRP
1	B	178	TRP
1	D	178	TRP
1	E	178	TRP
1	C	60	THR
1	D	60	THR
1	E	60	THR
1	F	60	THR
1	A	61	VAL
1	D	3	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	236/266 (89%)	233 (99%)	3 (1%)	61	76
1	B	236/266 (89%)	231 (98%)	5 (2%)	47	63
1	C	238/266 (90%)	233 (98%)	5 (2%)	47	63
1	D	232/266 (87%)	228 (98%)	4 (2%)	53	69
1	E	233/266 (88%)	226 (97%)	7 (3%)	36	49
1	F	233/266 (88%)	225 (97%)	8 (3%)	32	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1408/1596 (88%)	1376 (98%)	32 (2%)	44 59

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	PHE
1	A	212	LEU
1	A	272	GLU
1	B	56	PHE
1	B	131	LEU
1	B	269	GLN
1	B	271	LEU
1	B	272	GLU
1	C	1	MET
1	C	56	PHE
1	C	76	ARG
1	C	272	GLU
1	C	273	GLN
1	D	56	PHE
1	D	76	ARG
1	D	261	LEU
1	D	272	GLU
1	E	0	LEU
1	E	56	PHE
1	E	233	LEU
1	E	261	LEU
1	E	269	GLN
1	E	271	LEU
1	E	272	GLU
1	F	15	GLU
1	F	56	PHE
1	F	76	ARG
1	F	121	ASN
1	F	240	LEU
1	F	256	ASN
1	F	261	LEU
1	F	273	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	188	GLN
1	B	82	GLN
1	B	172	GLN
1	B	188	GLN
1	B	266	GLN
1	C	172	GLN
1	C	188	GLN
1	C	266	GLN
1	E	104	HIS
1	E	269	GLN
1	F	74	ASN
1	F	121	ASN
1	F	188	GLN
1	F	256	ASN
1	F	266	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

35 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
2	PO4	C	304	-	4,4,4	0.84	0	6,6,6	0.61	0
2	PO4	E	301	-	4,4,4	1.04	0	6,6,6	0.56	0
2	PO4	D	303	-	4,4,4	1.03	0	6,6,6	0.38	0
3	IM5	F	303	-	22,22,22	1.93	3 (13%)	25,32,32	2.15	7 (28%)
2	PO4	A	304	-	4,4,4	0.88	0	6,6,6	0.51	0
2	PO4	B	304	-	4,4,4	0.87	0	6,6,6	0.76	0
2	PO4	F	302	-	4,4,4	0.92	0	6,6,6	0.43	0
3	IM5	B	306	-	22,22,22	2.07	3 (13%)	25,32,32	2.15	8 (32%)
3	IM5	A	308	-	22,22,22	1.92	3 (13%)	25,32,32	2.21	8 (32%)
2	PO4	A	305	-	4,4,4	0.93	0	6,6,6	0.54	0
2	PO4	B	305	-	4,4,4	0.87	0	6,6,6	0.54	0
2	PO4	E	303	-	4,4,4	0.96	0	6,6,6	0.40	0
2	PO4	D	304	-	4,4,4	0.99	0	6,6,6	0.56	0
2	PO4	E	302	-	4,4,4	1.04	0	6,6,6	0.56	0
2	PO4	B	301	-	4,4,4	1.03	0	6,6,6	0.76	0
3	IM5	D	307	-	22,22,22	1.81	3 (13%)	25,32,32	2.04	5 (20%)
2	PO4	D	301	-	4,4,4	1.08	0	6,6,6	0.72	0
2	PO4	A	307	-	4,4,4	0.90	0	6,6,6	0.52	0
2	PO4	E	304	-	4,4,4	0.91	0	6,6,6	0.46	0
2	PO4	E	305	-	4,4,4	0.92	0	6,6,6	0.52	0
2	PO4	B	302	-	4,4,4	1.03	0	6,6,6	0.54	0
2	PO4	A	306	-	4,4,4	0.87	0	6,6,6	0.62	0
2	PO4	D	302	-	4,4,4	1.05	0	6,6,6	0.44	0
2	PO4	F	301	-	4,4,4	0.99	0	6,6,6	0.63	0
2	PO4	C	302	-	4,4,4	0.99	0	6,6,6	0.64	0
3	IM5	C	305	-	22,22,22	2.11	3 (13%)	25,32,32	2.01	5 (20%)
2	PO4	C	301	-	4,4,4	1.14	0	6,6,6	0.56	0
2	PO4	A	301	-	4,4,4	0.98	0	6,6,6	0.47	0
2	PO4	D	306	-	4,4,4	0.98	0	6,6,6	0.50	0
2	PO4	D	305	-	4,4,4	0.90	0	6,6,6	0.56	0
3	IM5	E	306	-	22,22,22	2.04	3 (13%)	25,32,32	2.05	5 (20%)
2	PO4	A	302	-	4,4,4	1.11	0	6,6,6	0.53	0
2	PO4	C	303	-	4,4,4	0.96	0	6,6,6	0.56	0
2	PO4	A	303	-	4,4,4	0.98	0	6,6,6	0.56	0
2	PO4	B	303	-	4,4,4	0.92	0	6,6,6	0.41	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	IM5	A	308	-	-	0/6/18/18	0/3/3/3
3	IM5	F	303	-	-	0/6/18/18	0/3/3/3
3	IM5	B	306	-	-	0/6/18/18	0/3/3/3
3	IM5	E	306	-	-	1/6/18/18	0/3/3/3
3	IM5	C	305	-	-	0/6/18/18	0/3/3/3
3	IM5	D	307	-	-	1/6/18/18	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	305	IM5	C5-C4	8.57	1.46	1.38
3	B	306	IM5	C5-C4	8.38	1.46	1.38
3	E	306	IM5	C5-C4	8.30	1.46	1.38
3	F	303	IM5	C5-C4	7.95	1.46	1.38
3	A	308	IM5	C5-C4	7.66	1.45	1.38
3	D	307	IM5	C5-C4	7.06	1.45	1.38
3	A	308	IM5	C5-N7	-2.98	1.33	1.38
3	C	305	IM5	C5-N7	-2.91	1.33	1.38
3	E	306	IM5	C5-N7	-2.81	1.34	1.38
3	B	306	IM5	C5-N7	-2.64	1.34	1.38
3	D	307	IM5	C5-C6	2.40	1.49	1.41
3	E	306	IM5	C5-C6	2.31	1.48	1.41
3	F	303	IM5	C6-N1	-2.29	1.34	1.38
3	D	307	IM5	C5-N7	-2.29	1.34	1.38
3	C	305	IM5	C5-C6	2.18	1.48	1.41
3	F	303	IM5	C5-C6	2.12	1.48	1.41
3	B	306	IM5	C5-C6	2.11	1.48	1.41
3	A	308	IM5	C5-C6	2.09	1.48	1.41

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	303	IM5	C4-C5-C6	-7.40	114.90	121.41
3	A	308	IM5	C4-C5-C6	-7.17	115.10	121.41
3	E	306	IM5	C4-C5-C6	-6.96	115.28	121.41
3	D	307	IM5	C4-C5-C6	-6.96	115.29	121.41
3	B	306	IM5	C4-C5-C6	-6.82	115.42	121.41
3	C	305	IM5	C4-C5-C6	-6.31	115.86	121.41
3	F	303	IM5	C6-C5-N7	3.90	138.60	131.14
3	D	307	IM5	C6-C5-N7	3.62	138.07	131.14
3	A	308	IM5	C6-C5-N7	3.48	137.79	131.14
3	E	306	IM5	C6-C5-N7	3.47	137.76	131.14
3	B	306	IM5	C9-C10-N1'	3.30	117.99	113.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	305	IM5	C6-C5-N7	3.29	137.43	131.14
3	B	306	IM5	C6-C5-N7	3.05	136.98	131.14
3	B	306	IM5	O6-C6-C5	-3.03	119.95	127.26
3	A	308	IM5	O6-C6-C5	-2.72	120.69	127.26
3	C	305	IM5	C5-C4-N3	-2.69	122.40	124.86
3	E	306	IM5	C3'-C2'-N1'	-2.67	99.54	104.47
3	E	306	IM5	O6-C6-C5	-2.60	121.00	127.26
3	A	308	IM5	C5-C4-N3	-2.58	122.50	124.86
3	C	305	IM5	C9-C10-N1'	2.53	116.92	113.38
3	A	308	IM5	C6'-C4'-C5'	-2.51	109.26	112.71
3	C	305	IM5	O6-C6-C5	-2.46	121.33	127.26
3	D	307	IM5	O6-C6-C5	-2.32	121.67	127.26
3	F	303	IM5	C3'-C2'-N1'	-2.29	100.24	104.47
3	F	303	IM5	O6-C6-C5	-2.23	121.89	127.26
3	F	303	IM5	C5-C4-N3	-2.23	122.83	124.86
3	A	308	IM5	C9-C10-N1'	2.22	116.48	113.38
3	B	306	IM5	C6'-N1'-C2'	2.18	107.29	104.12
3	A	308	IM5	C6'-N1'-C2'	2.18	107.28	104.12
3	A	308	IM5	C5-C6-N1	2.16	118.05	112.13
3	D	307	IM5	C5-C4-N3	-2.15	122.89	124.86
3	F	303	IM5	N2-C2-N1	2.11	121.21	116.76
3	F	303	IM5	C5-C6-N1	2.11	117.92	112.13
3	B	306	IM5	C5-C4-N3	-2.10	122.95	124.86
3	E	306	IM5	C5-C4-N3	-2.09	122.95	124.86
3	D	307	IM5	N2-C2-N1	2.05	121.09	116.76
3	B	306	IM5	C3'-C2'-N1'	-2.02	100.73	104.47
3	B	306	IM5	N2-C2-N1	2.02	121.02	116.76

There are no chirality outliers.

All (2) torsion outliers are listed below:

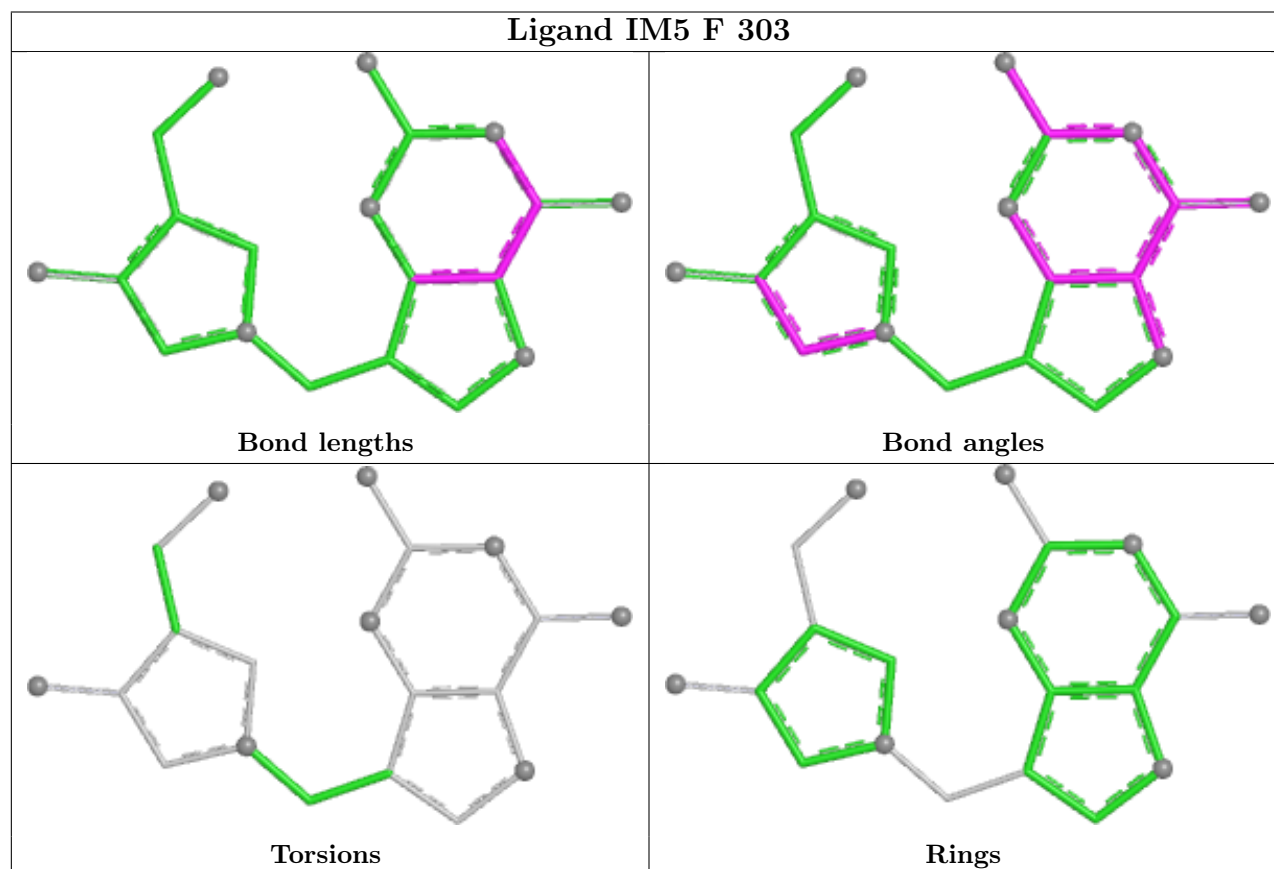
Mol	Chain	Res	Type	Atoms
3	D	307	IM5	C9-C10-N1'-C6'
3	E	306	IM5	C3'-C4'-C5'-O5'

There are no ring outliers.

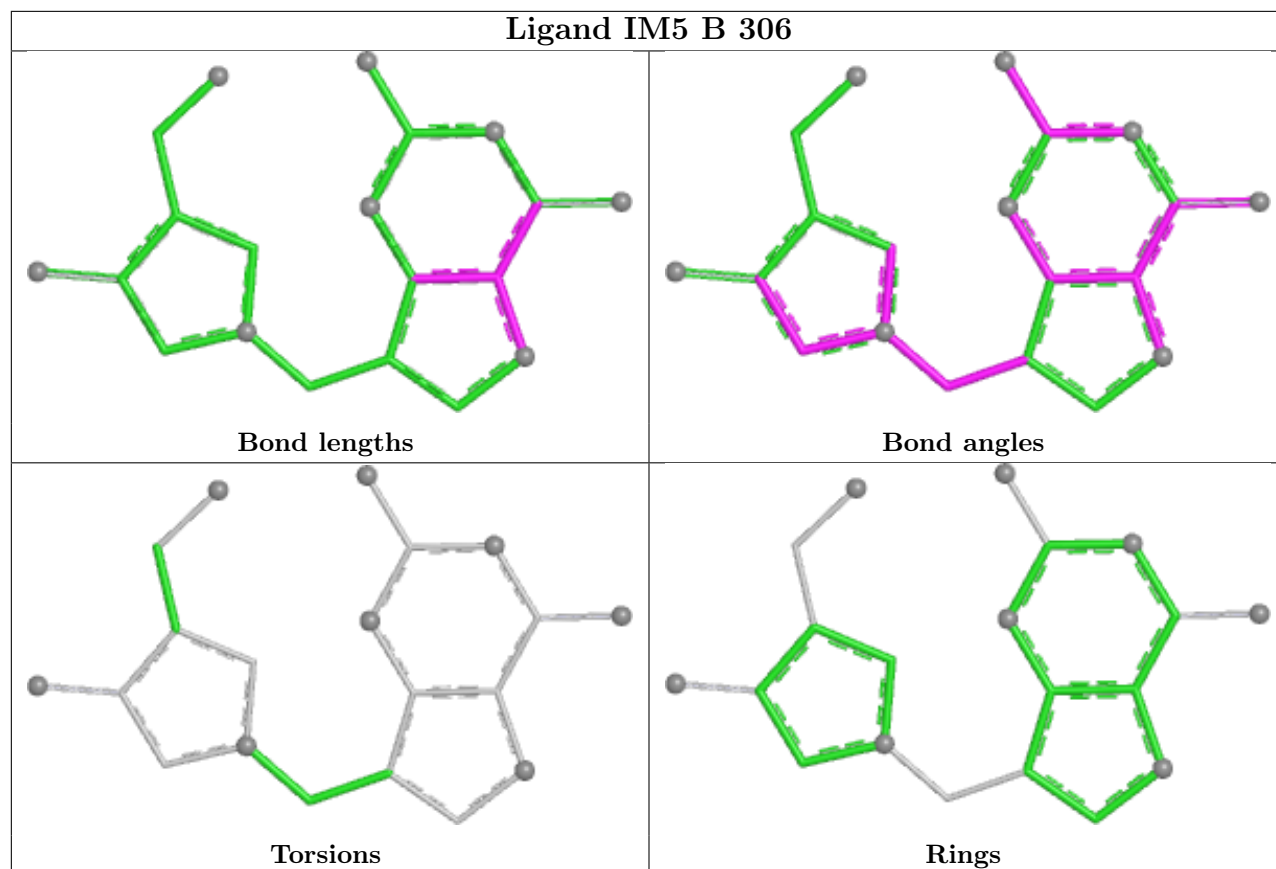
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

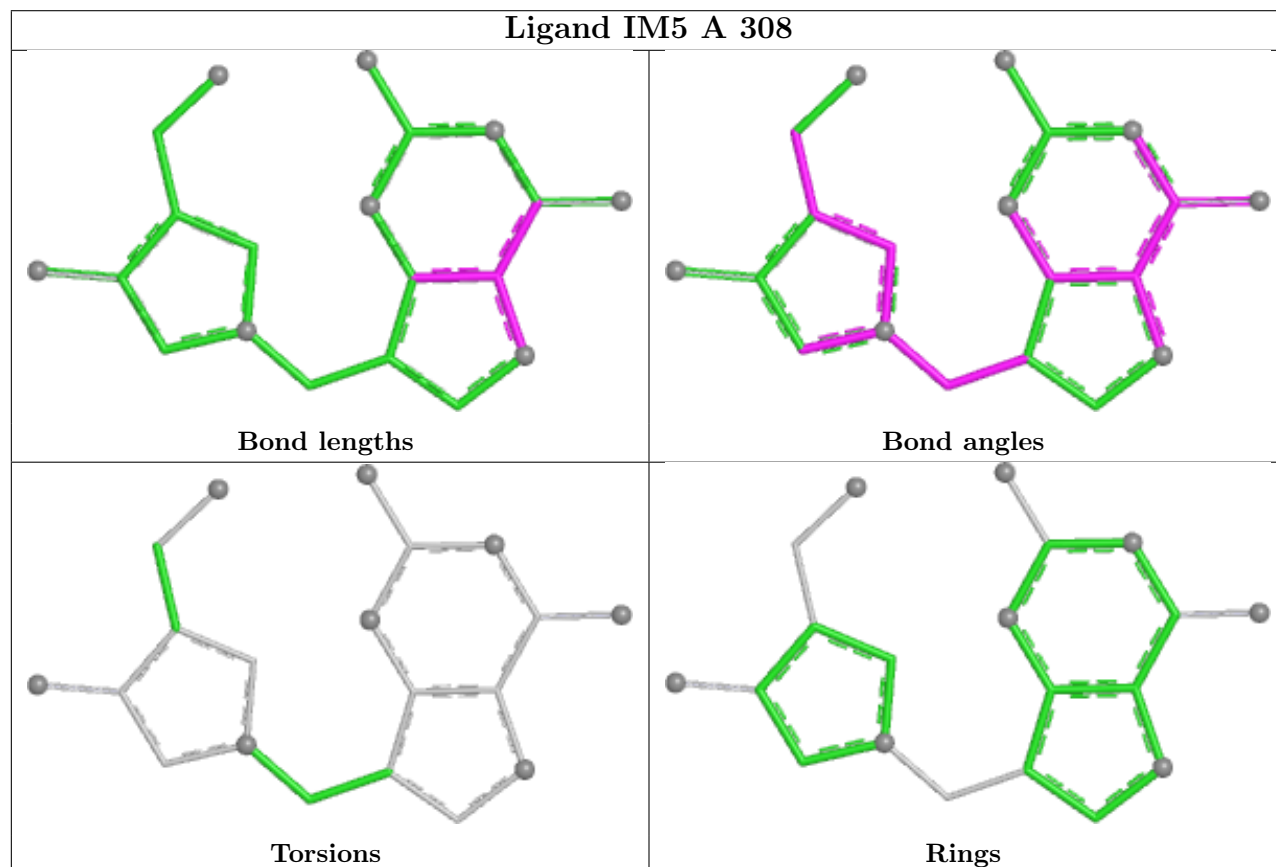
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



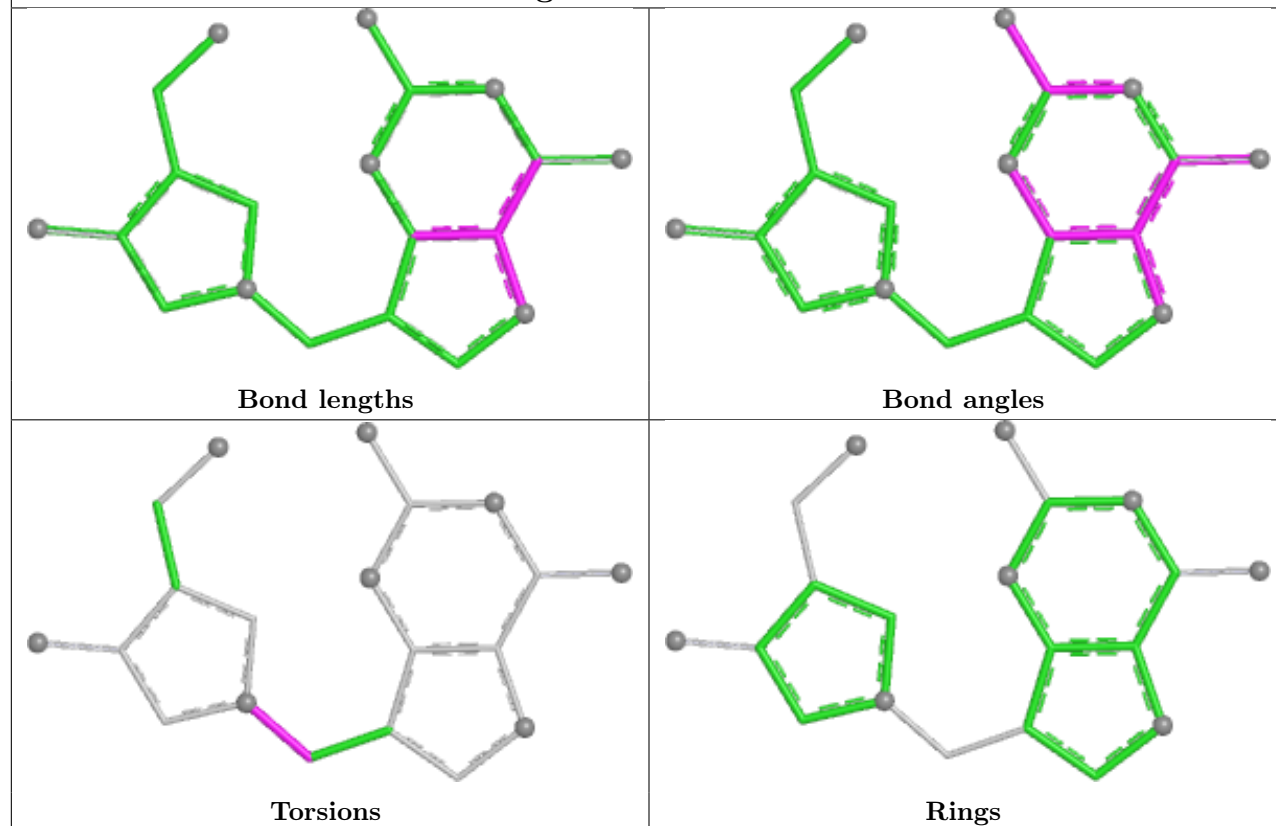
Ligand IM5 B 306



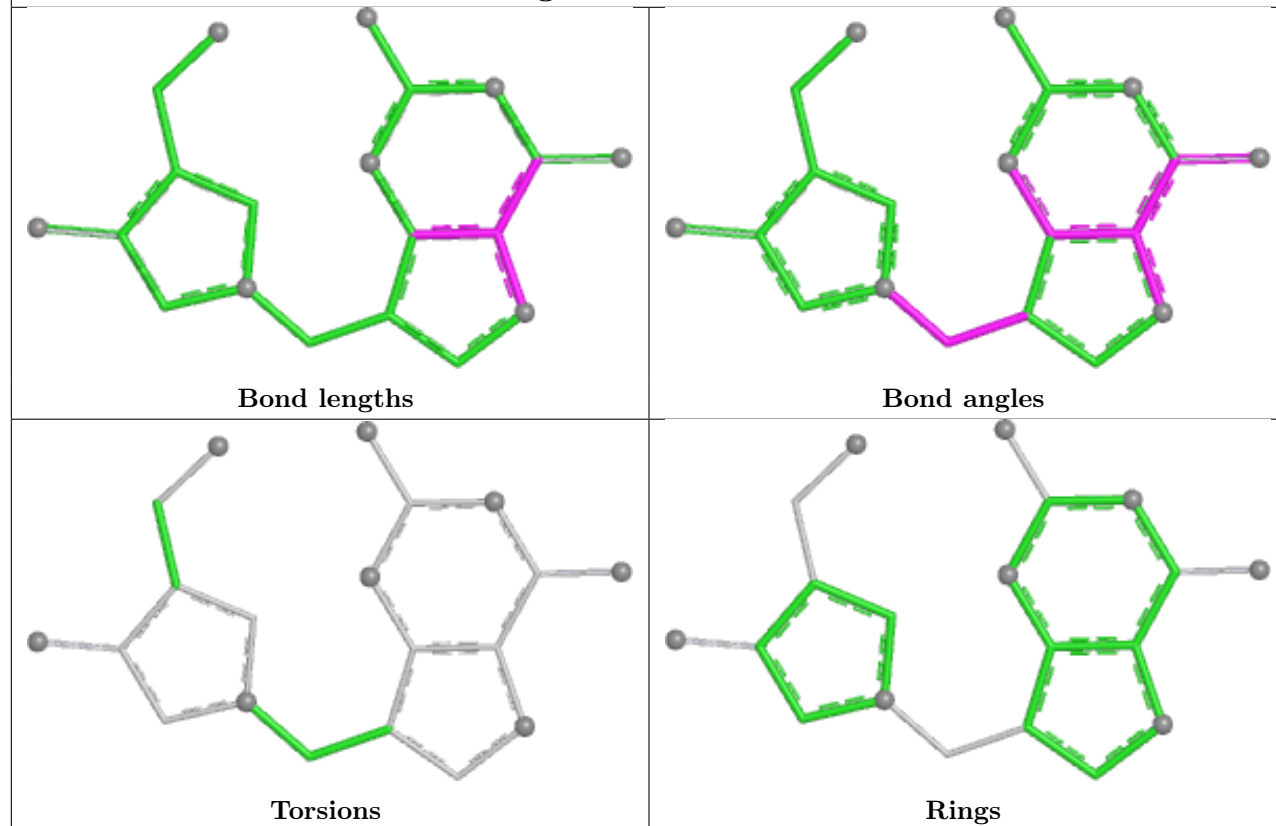
Ligand IM5 A 308

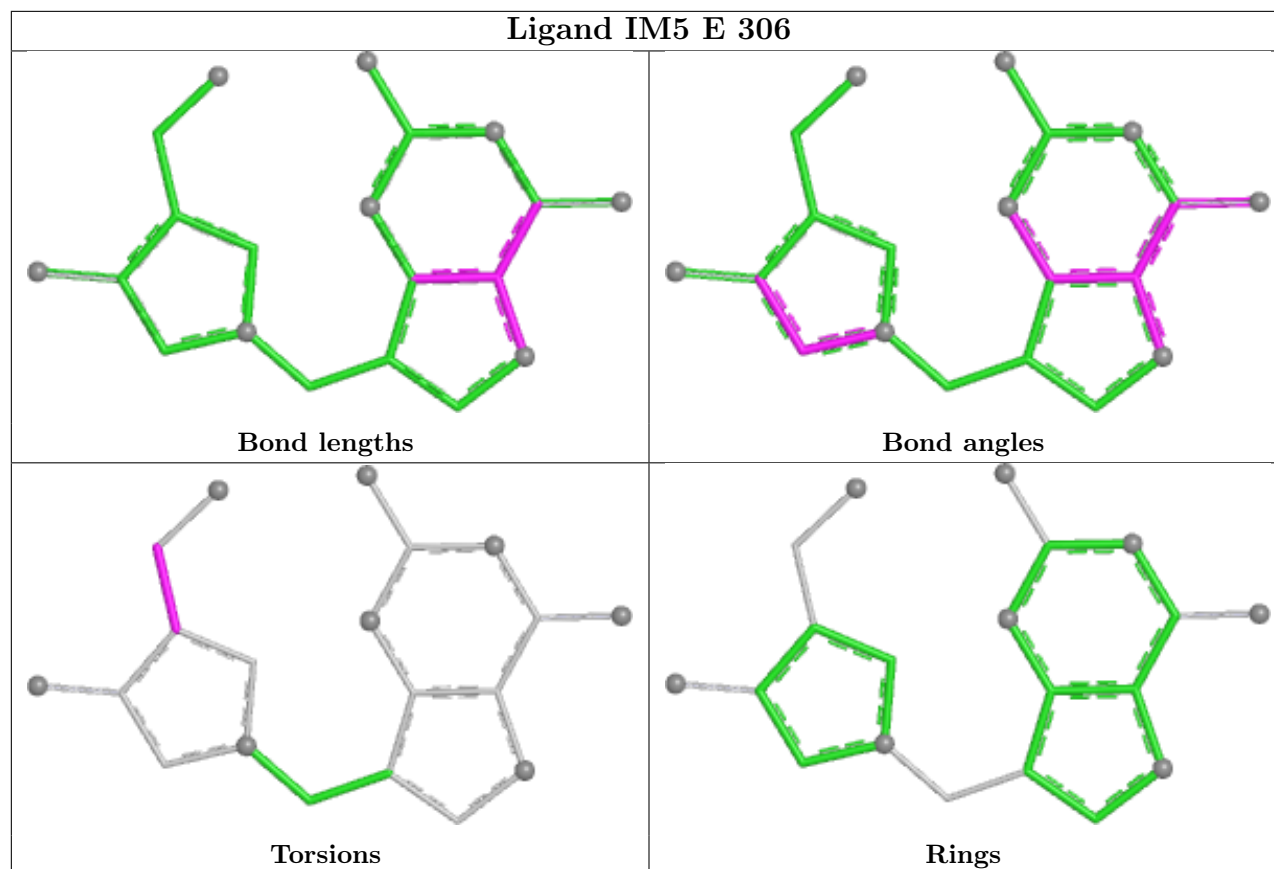


Ligand IM5 D 307



Ligand IM5 C 305





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, 95th 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	286/320 (89%)	0.34	22 (7%) 19 17	14, 27, 62, 148	1 (0%)
1	B	287/320 (89%)	0.57	42 (14%) 6 4	14, 28, 66, 134	2 (0%)
1	C	288/320 (90%)	0.26	24 (8%) 17 15	14, 25, 60, 113	0
1	D	286/320 (89%)	0.56	30 (10%) 11 9	18, 33, 66, 157	1 (0%)
1	E	287/320 (89%)	1.16	54 (18%) 3 2	18, 44, 74, 152	1 (0%)
1	F	287/320 (89%)	0.61	34 (11%) 9 7	18, 32, 81, 119	0
All	All	1721/1920 (89%)	0.58	206 (11%) 9 6	14, 31, 69, 157	5 (0%)

All (206) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	61	VAL	7.2
1	D	62	PRO	7.0
1	E	63	GLY	6.9
1	A	61	VAL	6.8
1	B	60	THR	6.7
1	D	61	VAL	6.6
1	A	1	MET	6.5
1	B	62	PRO	6.5
1	A	62	PRO	6.2
1	B	63	GLY	6.2
1	E	65	ALA	6.0
1	D	1	MET	6.0
1	C	63	GLY	5.9
1	C	62	PRO	5.8
1	E	61	VAL	5.7
1	D	65	ALA	5.7
1	E	278	LEU	5.6
1	F	62	PRO	5.6
1	E	64	HIS	5.5

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Mol	Chain	Res	Type	RSRZ
1	A	63	GLY	5.4
1	D	63	GLY	5.3
1	C	61	VAL	5.3
1	B	64	HIS	5.3
1	B	65	ALA	5.2
1	E	281	SER	5.2
1	A	60	THR	5.2
1	F	268	ALA	5.2
1	F	61	VAL	5.1
1	F	183	GLU	5.0
1	E	0	LEU	5.0
1	B	281	SER	5.0
1	F	60	THR	4.9
1	F	184	GLN	4.9
1	C	60	THR	4.9
1	A	65	ALA	4.8
1	F	63	GLY	4.8
1	C	65	ALA	4.6
1	E	58	ARG	4.6
1	D	60	THR	4.5
1	E	60	THR	4.5
1	E	62	PRO	4.4
1	A	178	TRP	4.4
1	A	59	SER	4.4
1	E	59	SER	4.3
1	E	280	ALA	4.3
1	F	181	MET	4.2
1	C	182	GLY	4.2
1	B	278	LEU	4.1
1	A	64	HIS	4.0
1	B	59	SER	3.9
1	B	58	ARG	3.9
1	F	185	ARG	3.9
1	B	180	GLN	3.9
1	F	182	GLY	3.9
1	F	65	ALA	3.9
1	E	282	ILE	3.9
1	B	179	LYS	3.9
1	D	59	SER	3.8
1	C	59	SER	3.8
1	F	178	TRP	3.8
1	B	168	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
1	D	64	HIS	3.7
1	F	271	LEU	3.7
1	F	270	LYS	3.7
1	D	252	LEU	3.7
1	C	64	HIS	3.6
1	B	177	THR	3.6
1	B	268	ALA	3.6
1	F	267	ALA	3.6
1	C	181	MET	3.6
1	D	277	ILE	3.6
1	F	59	SER	3.5
1	A	277	ILE	3.5
1	B	286	ASP	3.5
1	A	180	GLN	3.5
1	B	274	PHE	3.5
1	E	267	ALA	3.4
1	A	58	ARG	3.4
1	F	286	ASP	3.3
1	F	64	HIS	3.3
1	E	285	PRO	3.2
1	C	277	ILE	3.2
1	E	266	GLN	3.2
1	B	271	LEU	3.2
1	B	277	ILE	3.2
1	D	66	GLY	3.1
1	B	269	GLN	3.1
1	B	284	LEU	3.1
1	F	1	MET	3.1
1	F	186	GLU	3.1
1	D	176	SER	3.1
1	E	57	PRO	3.1
1	F	265	LYS	3.0
1	F	58	ARG	3.0
1	D	286	ASP	3.0
1	F	272	GLU	3.0
1	A	182	GLY	3.0
1	B	182	GLY	3.0
1	D	58	ARG	2.9
1	E	269	GLN	2.9
1	E	83	GLY	2.9
1	E	279	MET	2.9
1	E	177	THR	2.9

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Mol	Chain	Res	Type	RSRZ
1	F	269	GLN	2.9
1	D	35	LEU	2.9
1	B	282	ILE	2.9
1	A	177	THR	2.8
1	D	184	GLN	2.8
1	F	0	LEU	2.8
1	E	274	PHE	2.8
1	B	172	GLN	2.8
1	B	0	LEU	2.8
1	C	184	GLN	2.7
1	B	276	SER	2.7
1	F	83	GLY	2.7
1	C	58	ARG	2.7
1	E	277	ILE	2.7
1	B	173	ARG	2.7
1	B	175	LEU	2.7
1	B	273	GLN	2.6
1	E	72	PHE	2.6
1	E	179	LYS	2.6
1	E	85	PHE	2.6
1	A	83	GLY	2.6
1	E	284	LEU	2.6
1	D	36	GLY	2.6
1	B	174	ALA	2.6
1	A	181	MET	2.6
1	C	1	MET	2.6
1	F	264	GLY	2.6
1	B	170	MET	2.5
1	F	180	GLN	2.5
1	C	187	LEU	2.5
1	E	42	LEU	2.5
1	D	285	PRO	2.5
1	B	169	THR	2.5
1	D	177	THR	2.5
1	B	176	SER	2.5
1	E	14	ALA	2.5
1	D	182	GLY	2.5
1	A	66	GLY	2.5
1	E	182	GLY	2.5
1	B	236	PHE	2.4
1	A	175	LEU	2.4
1	D	38	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	40	ASP	2.4
1	E	8	GLU	2.4
1	D	178	TRP	2.4
1	E	178	TRP	2.4
1	E	184	GLN	2.4
1	A	57	PRO	2.4
1	E	66	GLY	2.4
1	C	-1	THR	2.4
1	B	1	MET	2.4
1	B	185	ARG	2.4
1	E	268	ALA	2.4
1	C	19	SER	2.4
1	D	44	GLN	2.4
1	E	276	SER	2.3
1	C	286	ASP	2.3
1	E	7	TYR	2.3
1	F	263	ALA	2.3
1	E	53	ILE	2.3
1	E	56	PHE	2.3
1	F	187	LEU	2.3
1	E	40	ASP	2.3
1	C	186	GLU	2.3
1	D	2	GLU	2.3
1	F	273	GLN	2.3
1	D	179	LYS	2.3
1	E	78	CYS	2.3
1	E	16	TRP	2.3
1	C	0	LEU	2.2
1	C	185	ARG	2.2
1	E	10	TYR	2.2
1	E	94	TRP	2.2
1	E	37	GLY	2.2
1	A	109	ASP	2.2
1	A	286	ASP	2.2
1	E	286	ASP	2.2
1	B	66	GLY	2.2
1	B	272	GLU	2.2
1	C	250	GLU	2.2
1	E	262	ALA	2.2
1	E	271	LEU	2.2
1	C	179	LYS	2.2
1	F	15	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	176	SER	2.2
1	D	19	SER	2.2
1	E	51	SER	2.2
1	F	277	ILE	2.1
1	B	178	TRP	2.1
1	E	11	LYS	2.1
1	D	186	GLU	2.1
1	B	275	VAL	2.1
1	F	4	GLY	2.1
1	D	276	SER	2.1
1	E	74	ASN	2.1
1	E	275	VAL	2.1
1	E	75	GLY	2.1
1	B	181	MET	2.0
1	C	268	ALA	2.0
1	E	1	MET	2.0
1	D	37	GLY	2.0
1	D	33	SER	2.0
1	C	252	LEU	2.0

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 oligosaccharides 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, 95th 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
2	PO4	E	303	5/5	0.58	0.12	90,90,92,93	0
2	PO4	E	304	5/5	0.59	0.21	103,106,107,109	0
2	PO4	F	302	5/5	0.59	0.20	88,90,91,92	0
2	PO4	B	305	5/5	0.67	0.16	77,77,82,83	0

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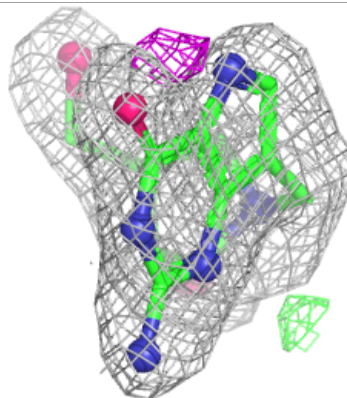
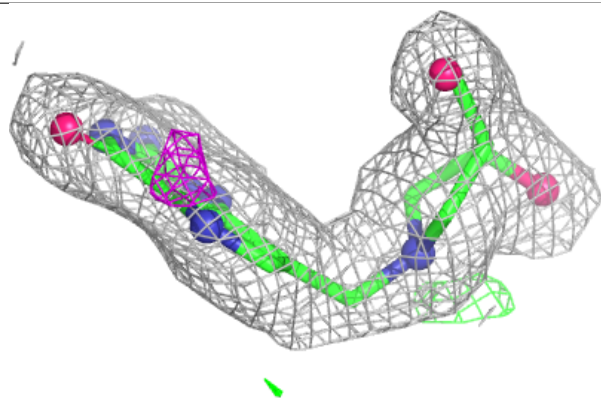
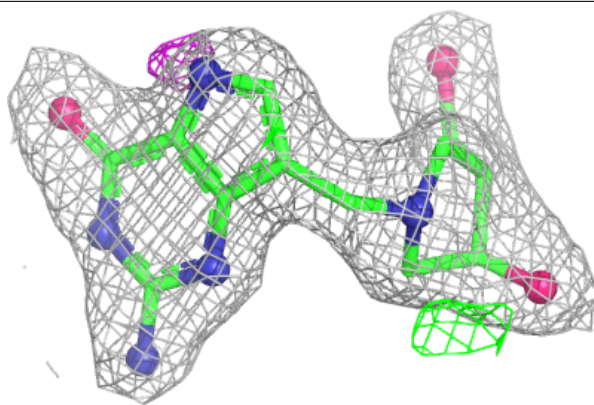
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PO4	C	304	5/5	0.67	0.16	67,70,75,76	0
2	PO4	D	306	5/5	0.67	0.16	77,77,81,82	0
2	PO4	A	306	5/5	0.74	0.17	63,64,66,67	0
2	PO4	A	304	5/5	0.76	0.12	67,70,72,74	0
2	PO4	E	305	5/5	0.80	0.11	67,70,72,74	0
2	PO4	A	305	5/5	0.80	0.11	77,78,80,81	0
2	PO4	C	303	5/5	0.81	0.13	68,69,69,71	0
2	PO4	B	304	5/5	0.83	0.12	63,64,65,66	0
2	PO4	D	304	5/5	0.84	0.10	68,70,72,76	0
2	PO4	A	307	5/5	0.85	0.20	58,61,63,63	0
2	PO4	D	305	5/5	0.86	0.10	64,66,67,68	0
2	PO4	A	303	5/5	0.87	0.14	42,44,44,45	0
2	PO4	B	303	5/5	0.91	0.15	58,59,60,62	0
2	PO4	D	303	5/5	0.92	0.12	49,50,51,53	0
2	PO4	E	302	5/5	0.92	0.17	56,56,58,60	0
2	PO4	D	302	5/5	0.93	0.17	46,47,47,48	0
2	PO4	C	302	5/5	0.94	0.14	38,40,42,43	0
3	IM5	D	307	20/20	0.94	0.07	27,29,30,30	0
3	IM5	E	306	20/20	0.94	0.07	23,24,24,24	0
3	IM5	A	308	20/20	0.95	0.06	17,18,18,19	0
2	PO4	A	302	5/5	0.96	0.08	39,40,41,42	0
3	IM5	B	306	20/20	0.96	0.05	15,16,19,19	0
3	IM5	F	303	20/20	0.96	0.06	16,18,21,21	0
2	PO4	B	302	5/5	0.97	0.08	34,34,36,36	0
2	PO4	D	301	5/5	0.97	0.06	32,32,34,34	0
3	IM5	C	305	20/20	0.97	0.04	12,13,14,14	0
2	PO4	E	301	5/5	0.98	0.06	29,29,31,31	0
2	PO4	F	301	5/5	0.99	0.06	20,20,21,22	0
2	PO4	C	301	5/5	0.99	0.05	15,15,15,16	0
2	PO4	A	301	5/5	0.99	0.04	20,20,21,21	0
2	PO4	B	301	5/5	0.99	0.05	17,17,18,19	0

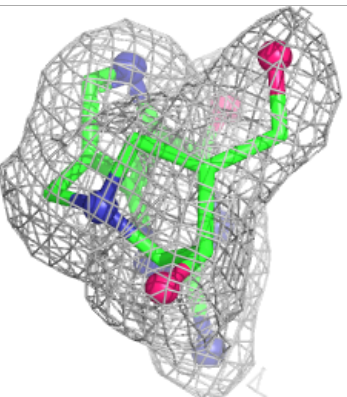
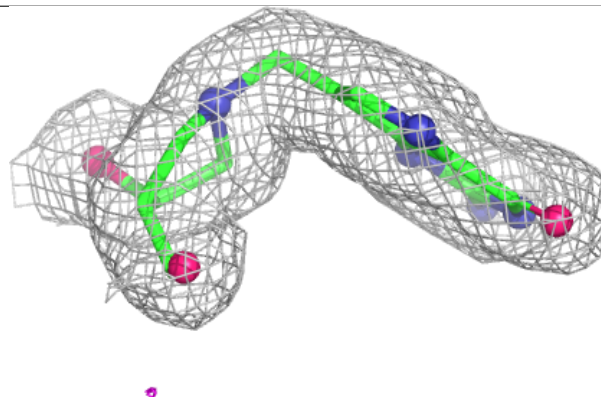
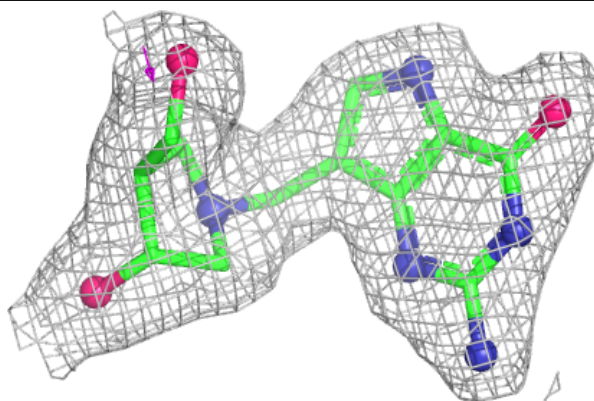
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around IM5 D 307:

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

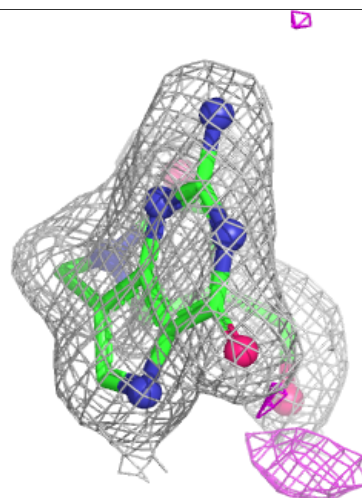
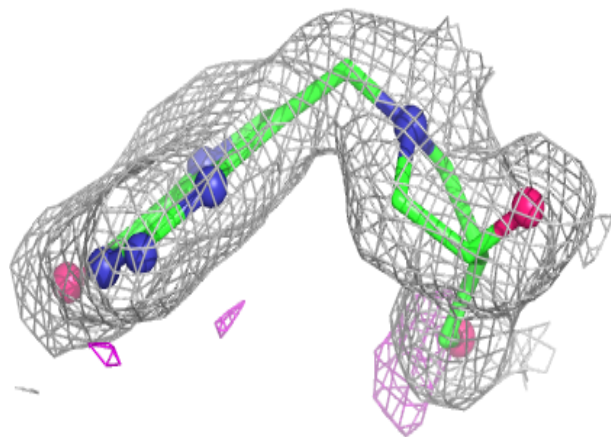
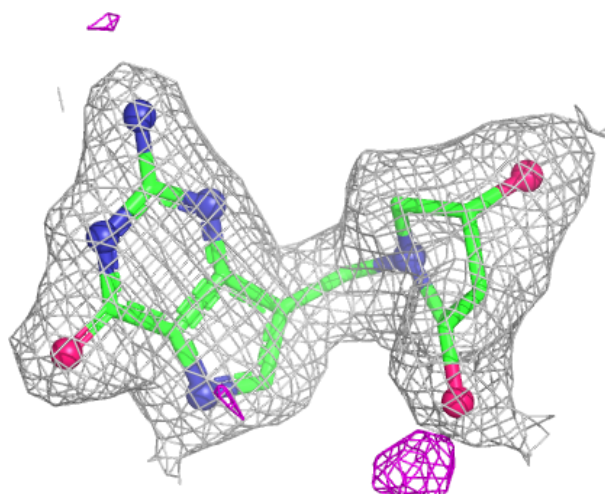
**Electron density around IM5 E 306:**

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



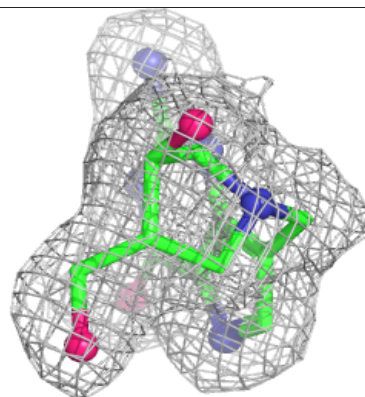
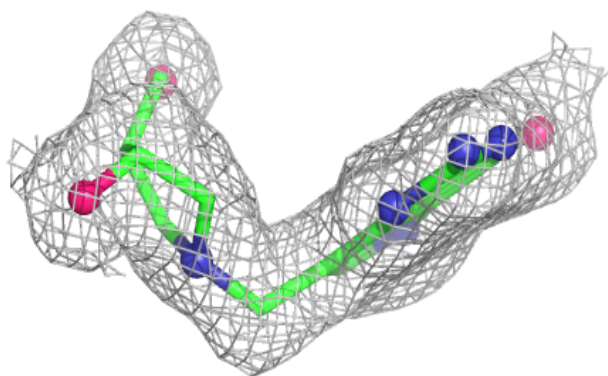
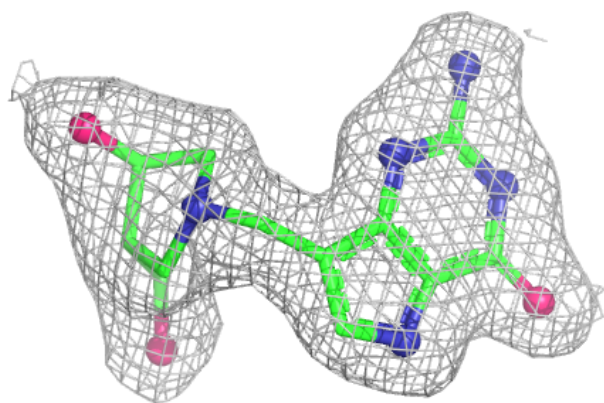
Electron density around IM5 A 308:

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

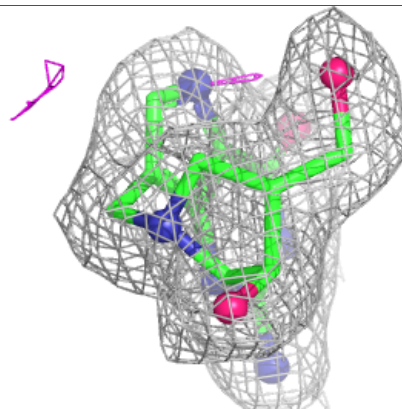
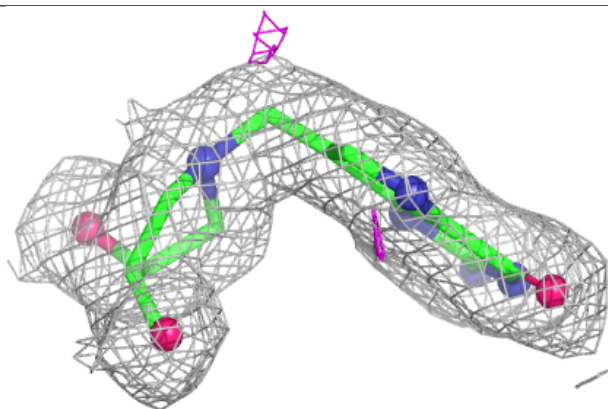
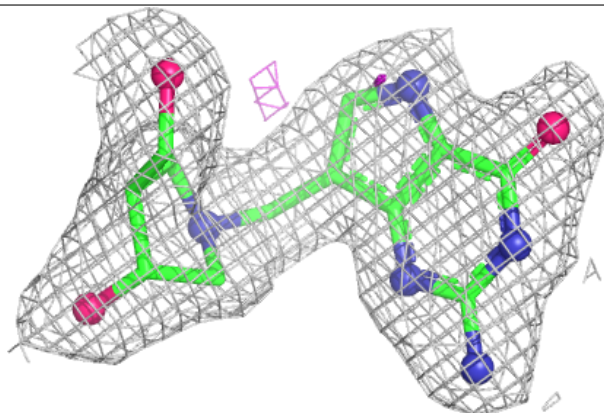


Electron density around IM5 B 306:

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

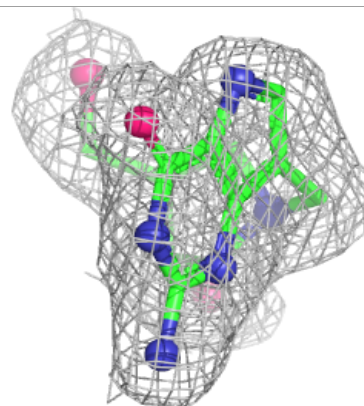
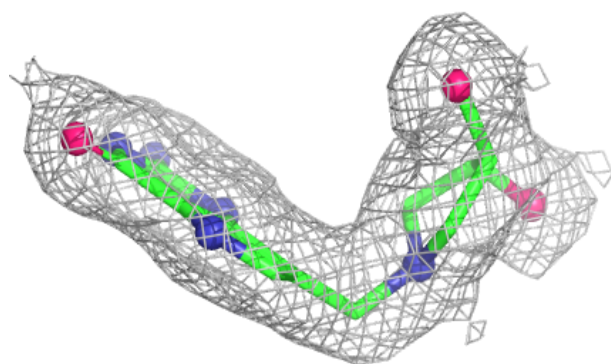
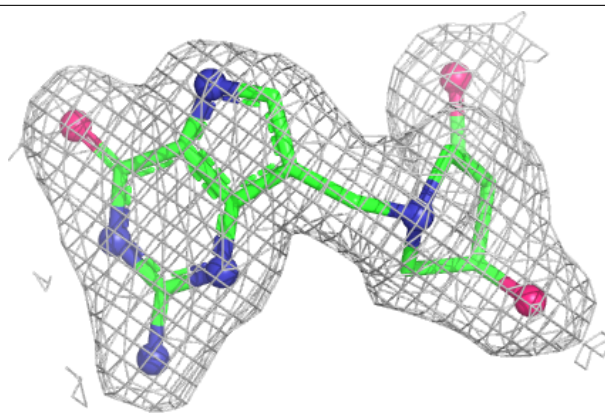
**Electron density around IM5 F 303:**

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



Electron density around IM5 C 305:

$2mF_o-DF_c$ (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.