



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 24, 2023 – 07:42 AM EDT

PDB ID : 5UGF
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 : 4.02b-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)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

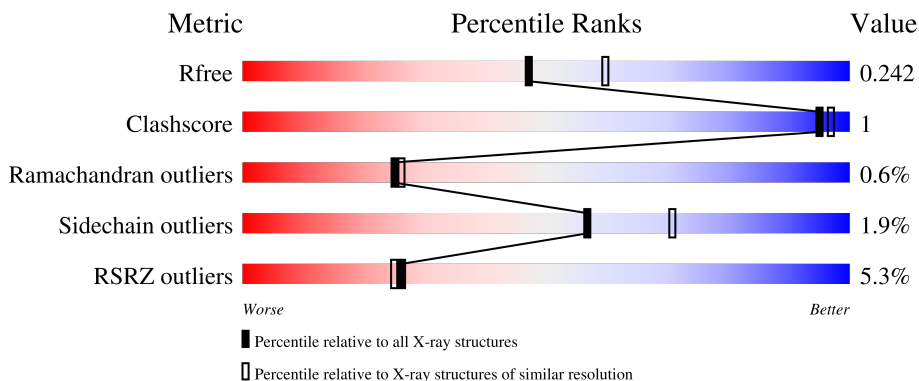
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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	 4% 86% 11%
1	B	320	 5% 84% 5% 10%
1	C	320	 4% 85% 5% 10%
1	D	320	 4% 86% 11%
1	E	320	 6% 86% 10%

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Mol	Chain	Length	Quality of chain
1	F	320	 A horizontal bar chart showing the quality of chain. The bar is divided into four segments: a small red segment at the beginning labeled '5%', a large green segment labeled '84%', a small yellow segment labeled '5%', and a grey segment at the end labeled '10%'.

2 Entry composition [i](#)

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

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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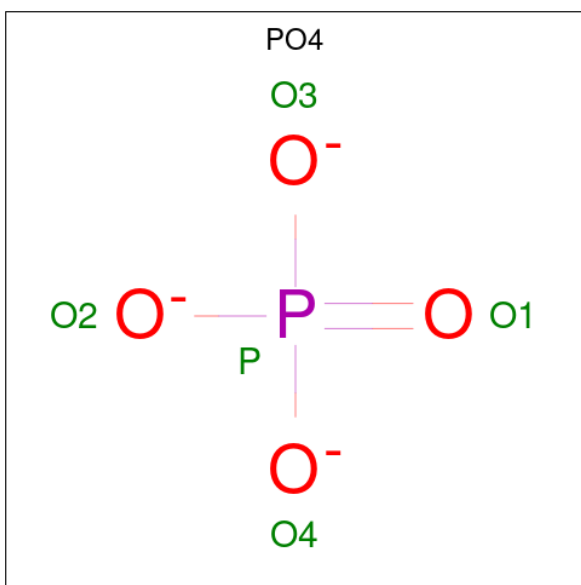
Chain	Residue	Modelled	Actual	Comment	Reference
E	-19	THR	-	expression tag	UNP P00491
E	-18	GLY	-	expression tag	UNP P00491
E	-17	GLY	-	expression tag	UNP P00491
E	-16	GLN	-	expression tag	UNP P00491
E	-15	GLN	-	expression tag	UNP P00491
E	-14	MET	-	expression tag	UNP P00491
E	-13	GLY	-	expression tag	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 (three-letter code: 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		

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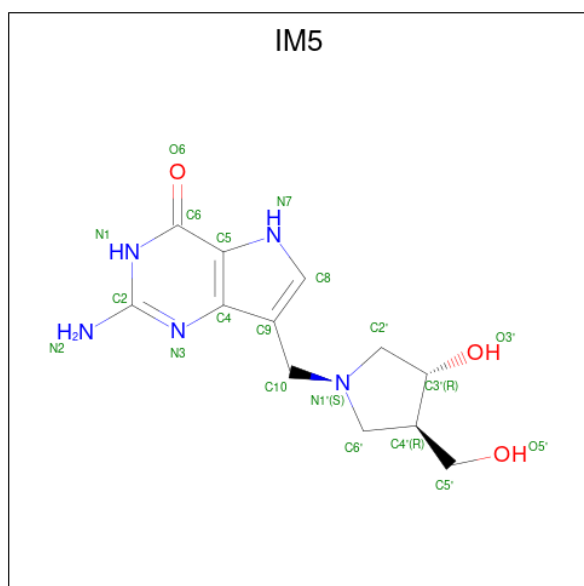
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	C	1	5	4	1	0	0
2	C	1	5	4	1	0	0
2	C	1	5	4	1	0	0
2	C	1	5	4	1	0	0
2	D	1	5	4	1	0	0
2	D	1	5	4	1	0	0
2	D	1	5	4	1	0	0
2	D	1	5	4	1	0	0
2	D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

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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 (three-letter code: 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		

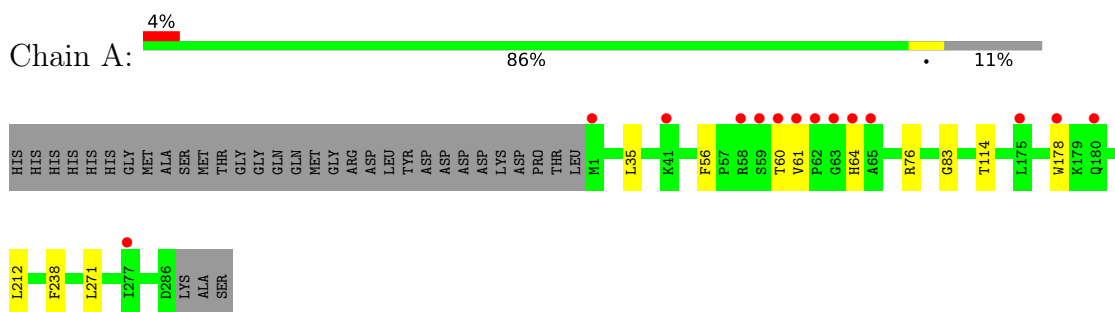
- Molecule 4 is water.

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

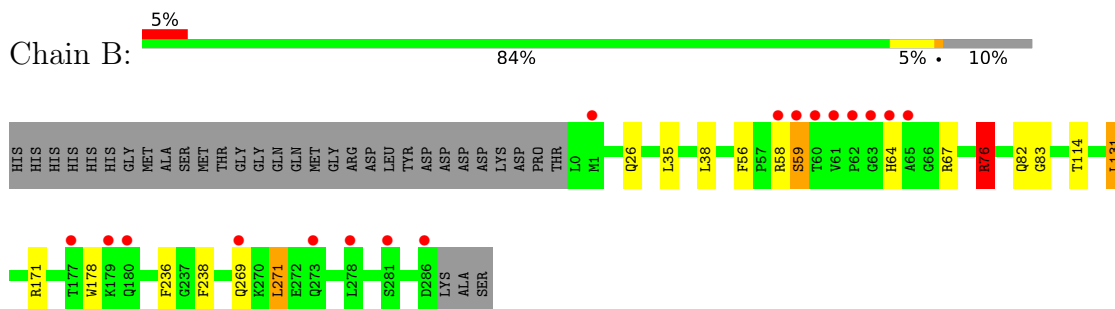
3 Residue-property plots [i](#)

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.

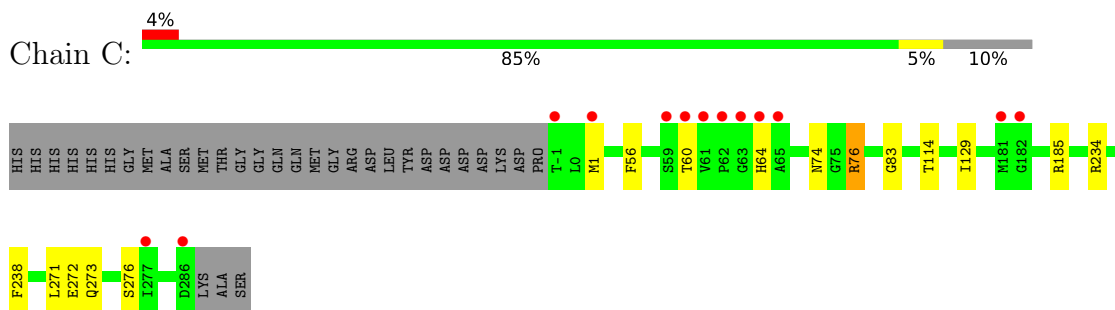
- Molecule 1: Purine nucleoside phosphorylase



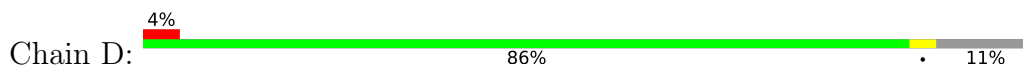
- Molecule 1: Purine nucleoside phosphorylase

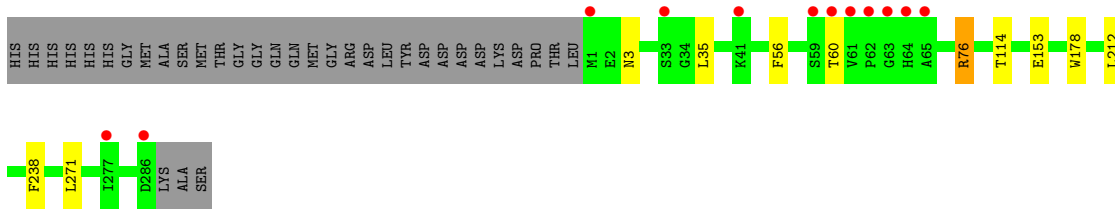


- Molecule 1: Purine nucleoside phosphorylase

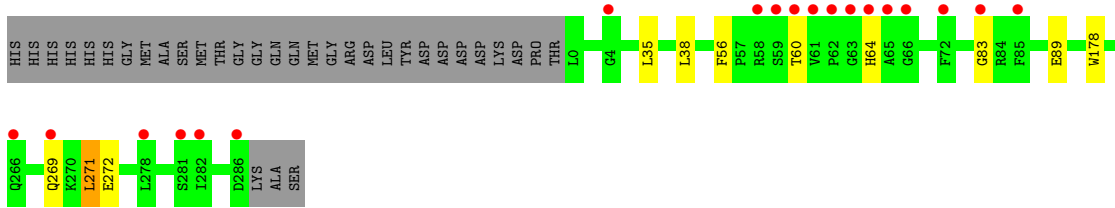
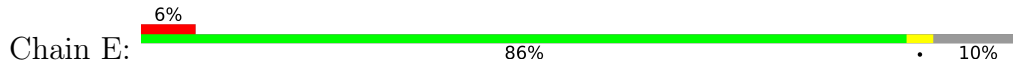


- Molecule 1: Purine nucleoside phosphorylase

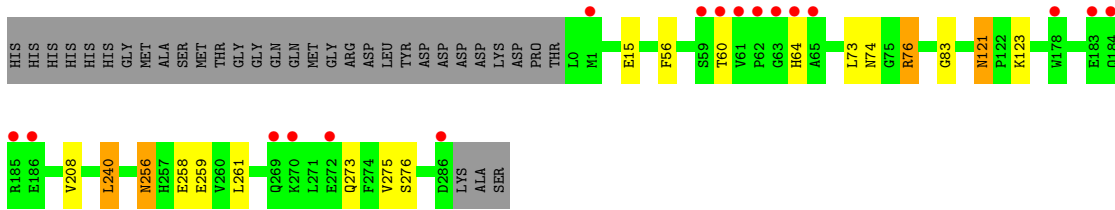
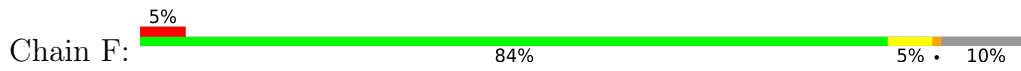




● Molecule 1: Purine nucleoside phosphorylase



● 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 69.17 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (69.26-2.20) 100.0 (69.17-2.20)	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 , 40.1	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	0.94	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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, IM5

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	0.45	0/2290	0.68	1/3102 (0.0%)
1	B	0.46	0/2296	0.68	2/3113 (0.1%)
1	C	0.47	0/2298	0.69	4/3113 (0.1%)
1	D	0.43	0/2271	0.65	1/3081 (0.0%)
1	E	0.44	2/2277 (0.1%)	0.65	0/3090
1	F	0.46	0/2272	0.72	4/3081 (0.1%)
All	All	0.45	2/13704 (0.0%)	0.68	12/18580 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	89[A]	GLU	CD-OE2	-5.09	1.20	1.25
1	E	89[B]	GLU	CD-OE2	-5.09	1.20	1.25

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	240	LEU	CB-CG-CD2	-9.39	95.03	111.00
1	F	240	LEU	CB-CG-CD1	9.08	126.44	111.00
1	B	76	ARG	NE-CZ-NH2	-8.79	115.90	120.30
1	C	185	ARG	NE-CZ-NH2	-7.71	116.44	120.30
1	F	76	ARG	NE-CZ-NH2	-7.17	116.72	120.30
1	C	76	ARG	NE-CZ-NH2	-6.89	116.85	120.30
1	C	76	ARG	NE-CZ-NH1	6.49	123.55	120.30
1	F	76	ARG	NE-CZ-NH1	6.29	123.44	120.30
1	A	60	THR	N-CA-C	5.51	125.87	111.00
1	D	76	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	B	76	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	C	234	ARG	NE-CZ-NH1	5.16	122.88	120.30

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
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 [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	285/320 (89%)	278 (98%)	5 (2%)	2 (1%)	22	22
1	B	287/320 (90%)	282 (98%)	3 (1%)	2 (1%)	22	22
1	C	286/320 (89%)	282 (99%)	3 (1%)	1 (0%)	41	46
1	D	285/320 (89%)	279 (98%)	3 (1%)	3 (1%)	14	12
1	E	286/320 (89%)	281 (98%)	3 (1%)	2 (1%)	22	22
1	F	285/320 (89%)	282 (99%)	2 (1%)	1 (0%)	34	37
All	All	1714/1920 (89%)	1684 (98%)	19 (1%)	11 (1%)	25	26

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 [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	236/266 (89%)	234 (99%)	2 (1%)	81	90
1	B	236/266 (89%)	231 (98%)	5 (2%)	53	67
1	C	238/266 (90%)	233 (98%)	5 (2%)	53	67
1	D	232/266 (87%)	229 (99%)	3 (1%)	69	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	233/266 (88%)	229 (98%)	4 (2%)	60	74
1	F	233/266 (88%)	225 (97%)	8 (3%)	37	47
All	All	1408/1596 (88%)	1381 (98%)	27 (2%)	57	71

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	PHE
1	A	212	LEU
1	B	56	PHE
1	B	76	ARG
1	B	131	LEU
1	B	269	GLN
1	B	271	LEU
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	153	GLU
1	E	56	PHE
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 (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	82	GLN
1	B	172	GLN

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Mol	Chain	Res	Type
1	B	269	GLN
1	C	74	ASN
1	C	172	GLN
1	C	273	GLN
1	E	266	GLN
1	E	269	GLN
1	F	74	ASN
1	F	121	ASN
1	F	256	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](#)

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	E	301	-	4,4,4	0.99	0	6,6,6	0.53	0
2	PO4	E	305	-	4,4,4	0.88	0	6,6,6	0.49	0
2	PO4	B	301	-	4,4,4	0.99	0	6,6,6	0.73	0
2	PO4	C	304	-	4,4,4	0.80	0	6,6,6	0.58	0
2	PO4	B	305	-	4,4,4	0.83	0	6,6,6	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PO4	D	304	-	4,4,4	0.94	0	6,6,6	0.53	0
3	IM5	E	306	-	18,22,22	0.81	0	18,32,32	1.30	2 (11%)
2	PO4	A	307	-	4,4,4	0.85	0	6,6,6	0.49	0
2	PO4	A	301	-	4,4,4	0.95	0	6,6,6	0.44	0
2	PO4	A	306	-	4,4,4	0.83	0	6,6,6	0.59	0
2	PO4	A	304	-	4,4,4	0.83	0	6,6,6	0.47	0
2	PO4	E	304	-	4,4,4	0.87	0	6,6,6	0.43	0
2	PO4	F	302	-	4,4,4	0.87	0	6,6,6	0.40	0
2	PO4	C	301	-	4,4,4	1.09	0	6,6,6	0.53	0
2	PO4	E	302	-	4,4,4	0.99	0	6,6,6	0.53	0
2	PO4	A	302	-	4,4,4	1.06	0	6,6,6	0.50	0
2	PO4	B	303	-	4,4,4	0.88	0	6,6,6	0.39	0
2	PO4	D	306	-	4,4,4	0.94	0	6,6,6	0.47	0
3	IM5	B	306	-	18,22,22	0.82	0	18,32,32	1.52	4 (22%)
2	PO4	D	303	-	4,4,4	0.98	0	6,6,6	0.36	0
2	PO4	E	303	-	4,4,4	0.92	0	6,6,6	0.37	0
2	PO4	B	304	-	4,4,4	0.83	0	6,6,6	0.72	0
3	IM5	F	303	-	18,22,22	0.86	1 (5%)	18,32,32	1.30	3 (16%)
2	PO4	D	305	-	4,4,4	0.86	0	6,6,6	0.52	0
3	IM5	A	308	-	18,22,22	0.74	0	18,32,32	1.44	3 (16%)
3	IM5	D	307	-	18,22,22	0.84	0	18,32,32	1.28	2 (11%)
2	PO4	C	303	-	4,4,4	0.91	0	6,6,6	0.52	0
2	PO4	D	302	-	4,4,4	1.01	0	6,6,6	0.41	0
2	PO4	D	301	-	4,4,4	1.03	0	6,6,6	0.68	0
2	PO4	A	303	-	4,4,4	0.93	0	6,6,6	0.54	0
2	PO4	A	305	-	4,4,4	0.89	0	6,6,6	0.50	0
3	IM5	C	305	-	18,22,22	0.85	0	18,32,32	1.31	1 (5%)
2	PO4	B	302	-	4,4,4	0.99	0	6,6,6	0.51	0
2	PO4	F	301	-	4,4,4	0.95	0	6,6,6	0.60	0
2	PO4	C	302	-	4,4,4	0.95	0	6,6,6	0.60	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	F	303	-	-	0/5/18/18	0/3/3/3
3	IM5	E	306	-	-	0/5/18/18	0/3/3/3
3	IM5	A	308	-	-	0/5/18/18	0/3/3/3
3	IM5	D	307	-	-	0/5/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	IM5	B	306	-	-	0/5/18/18	0/3/3/3
3	IM5	C	305	-	-	0/5/18/18	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	303	IM5	C6-N1	-2.22	1.34	1.37

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	306	IM5	C9-C10-N1'	3.00	117.99	112.75
3	E	306	IM5	C3'-C2'-N1'	-2.56	99.54	104.44
3	C	305	IM5	C9-C10-N1'	2.39	116.92	112.75
3	A	308	IM5	C5-C6-N1	2.32	118.05	113.95
3	B	306	IM5	O6-C6-C5	-2.27	119.95	124.37
3	F	303	IM5	C5-C6-N1	2.25	117.92	113.95
3	F	303	IM5	C3'-C2'-N1'	-2.20	100.24	104.44
3	A	308	IM5	C9-C10-N1'	2.13	116.48	112.75
3	F	303	IM5	N2-C2-N1	2.11	121.21	116.71
3	B	306	IM5	C6'-N1'-C2'	2.08	107.29	104.19
3	A	308	IM5	C6'-N1'-C2'	2.08	107.28	104.19
3	D	307	IM5	N2-C2-N1	2.05	121.09	116.71
3	D	307	IM5	C5-C6-N1	2.05	117.57	113.95
3	B	306	IM5	N2-C2-N1	2.02	121.02	116.71
3	E	306	IM5	C5-C6-N1	2.01	117.50	113.95

There are no chirality outliers.

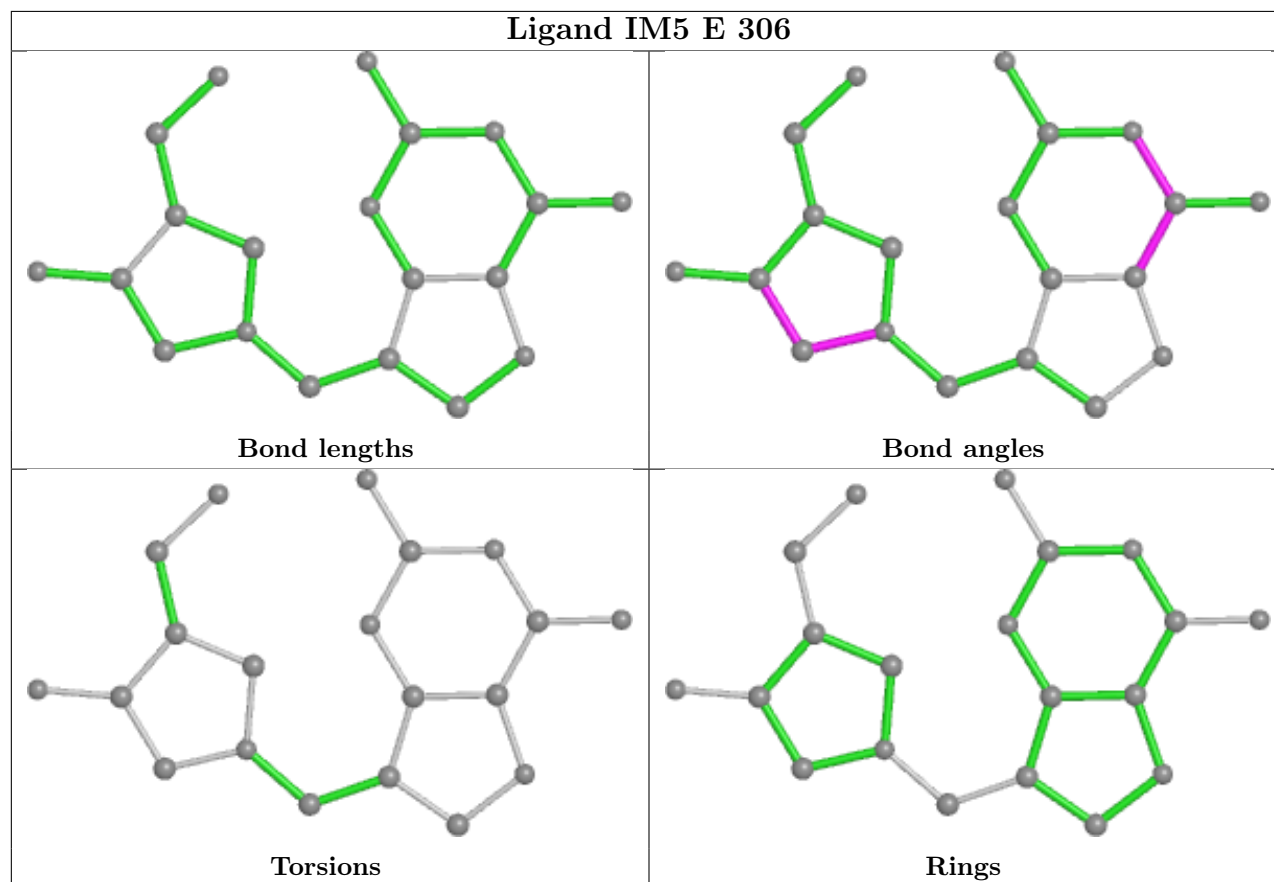
There are no torsion outliers.

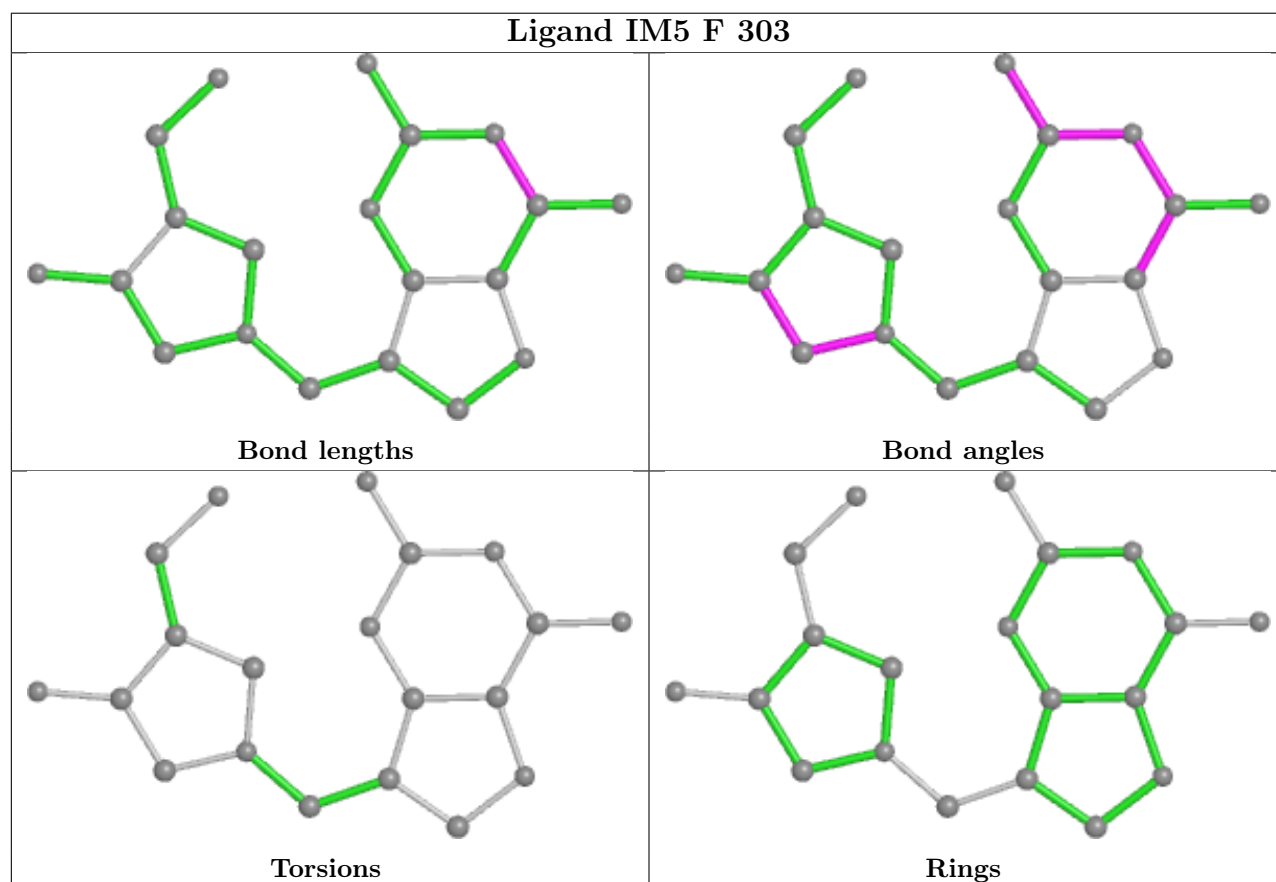
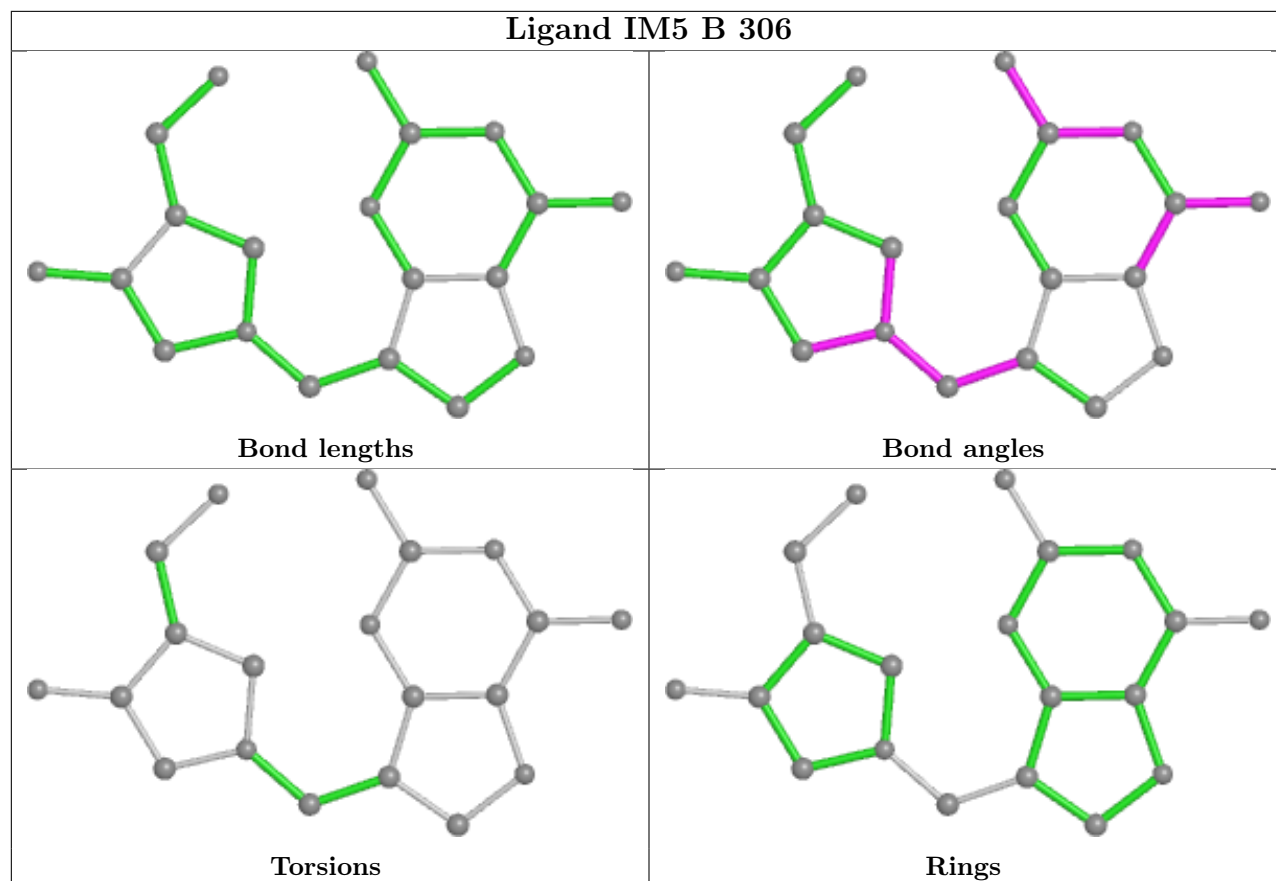
There are no ring outliers.

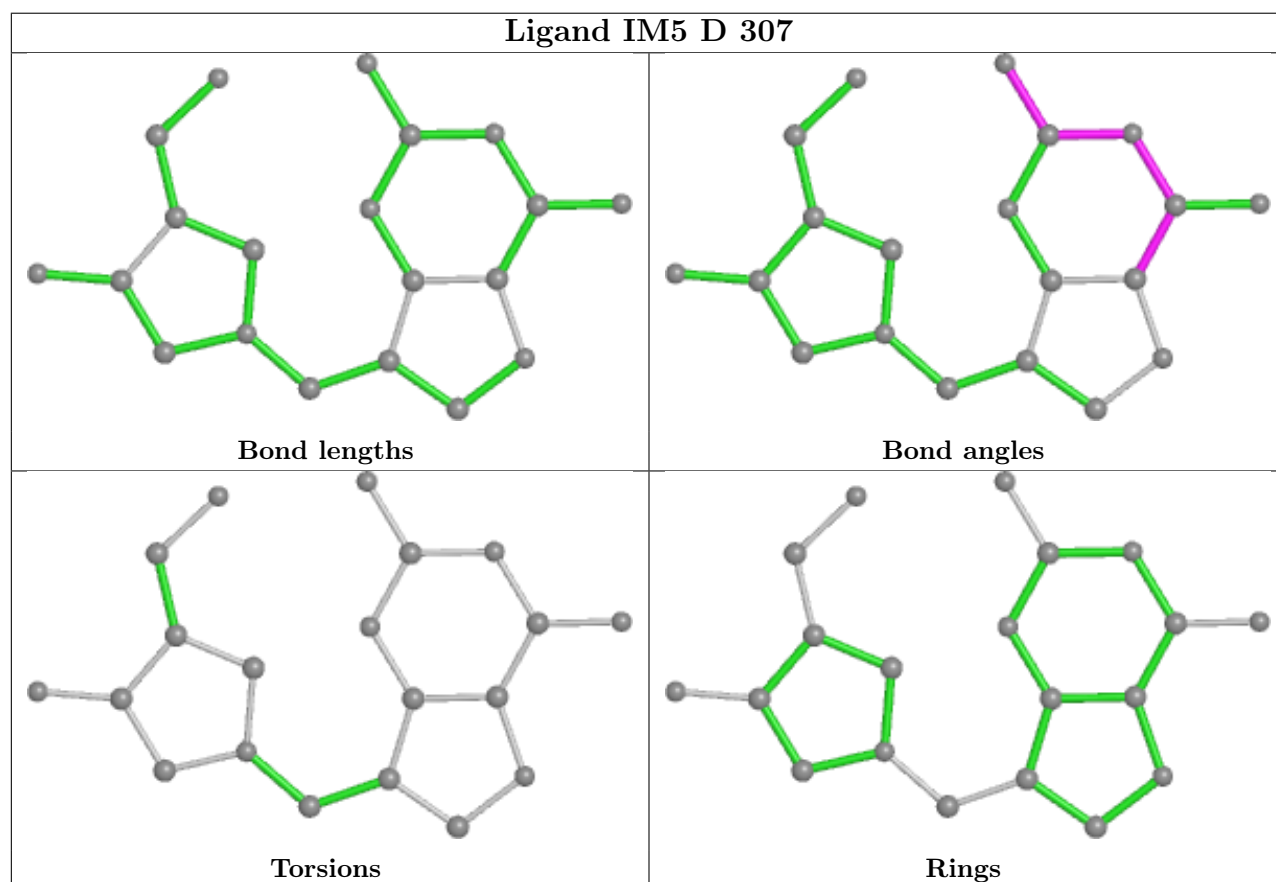
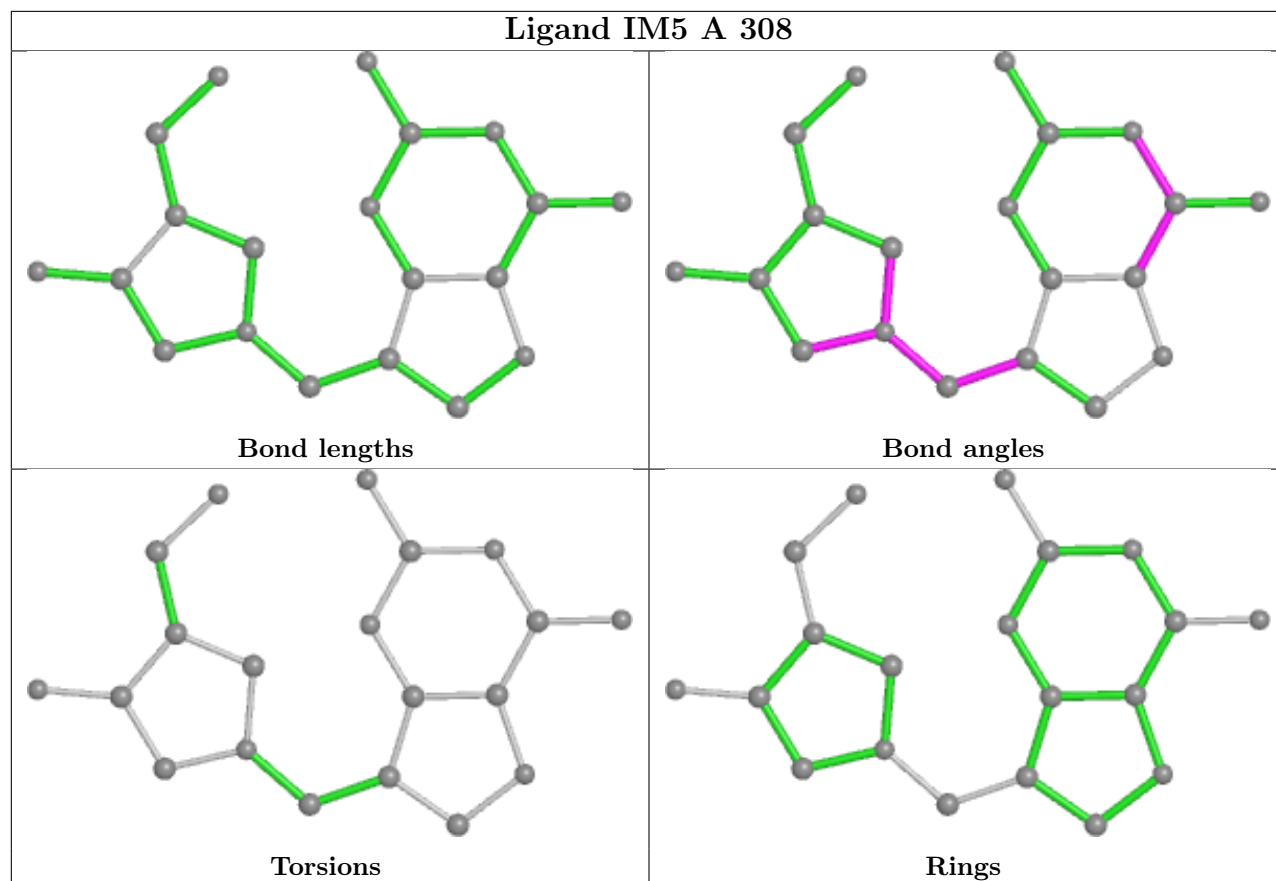
No monomer is involved in short contacts.

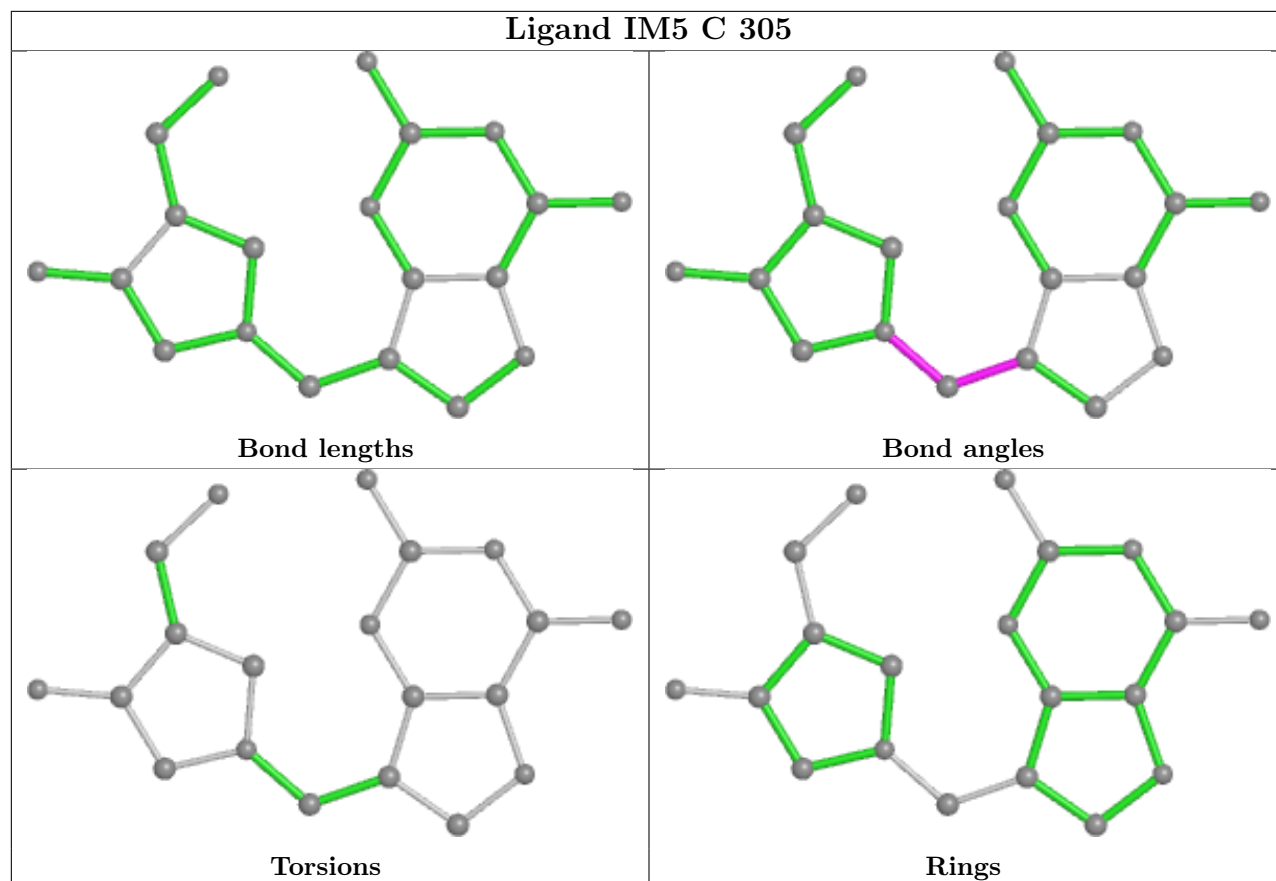
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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









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%)	-0.02	14 (4%) 29 28	14, 27, 62, 148	0
1	B	287/320 (89%)	0.10	17 (5%) 22 21	14, 28, 66, 134	0
1	C	288/320 (90%)	-0.12	13 (4%) 33 32	14, 25, 60, 113	0
1	D	286/320 (89%)	0.08	12 (4%) 36 34	18, 33, 66, 157	0
1	E	287/320 (89%)	0.39	19 (6%) 18 17	20, 44, 74, 152	0
1	F	287/320 (89%)	0.10	17 (5%) 22 21	18, 32, 81, 119	0
All	All	1721/1920 (89%)	0.09	92 (5%) 26 25	14, 31, 69, 157	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	63	GLY	12.1
1	F	60	THR	11.2
1	D	63	GLY	11.2
1	D	62	PRO	11.1
1	A	62	PRO	10.2
1	D	61	VAL	9.6
1	E	61	VAL	9.5
1	A	1	MET	9.2
1	B	60	THR	8.7
1	E	60	THR	8.0
1	A	61	VAL	7.6
1	E	64	HIS	7.0
1	D	64	HIS	6.8
1	B	62	PRO	6.8
1	C	60	THR	6.8
1	A	64	HIS	6.5
1	A	63	GLY	6.3
1	F	62	PRO	6.1
1	A	60	THR	6.0

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Mol	Chain	Res	Type	RSRZ
1	E	281	SER	5.8
1	E	278	LEU	5.7
1	D	1	MET	5.7
1	B	61	VAL	5.4
1	B	286	ASP	5.4
1	B	64	HIS	5.1
1	E	65	ALA	4.9
1	B	63	GLY	4.9
1	C	63	GLY	4.9
1	B	65	ALA	4.7
1	F	64	HIS	4.6
1	E	62	PRO	4.5
1	E	59	SER	4.4
1	D	60	THR	4.4
1	B	281	SER	4.2
1	C	64	HIS	4.1
1	C	286	ASP	4.1
1	F	184	GLN	4.1
1	F	65	ALA	4.0
1	F	183	GLU	3.9
1	F	63	GLY	3.9
1	D	286	ASP	3.7
1	B	278	LEU	3.7
1	D	65	ALA	3.7
1	F	269	GLN	3.6
1	A	59	SER	3.5
1	A	65	ALA	3.2
1	F	286	ASP	3.2
1	A	58	ARG	3.2
1	C	-1	THR	3.2
1	F	59	SER	3.2
1	E	286	ASP	3.1
1	E	269	GLN	3.1
1	B	180	GLN	3.0
1	B	177	THR	3.0
1	B	59	SER	2.9
1	C	61	VAL	2.9
1	F	185	ARG	2.9
1	B	1	MET	2.9
1	F	1	MET	2.8
1	B	269	GLN	2.8
1	B	179	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	178	TRP	2.7
1	C	65	ALA	2.7
1	B	58	ARG	2.7
1	C	59	SER	2.6
1	C	62	PRO	2.6
1	C	182	GLY	2.6
1	E	58	ARG	2.5
1	F	186	GLU	2.5
1	D	59	SER	2.4
1	E	266	GLN	2.4
1	E	83	GLY	2.3
1	C	277	ILE	2.3
1	A	180	GLN	2.3
1	F	270	LYS	2.3
1	E	72	PHE	2.3
1	F	272	GLU	2.3
1	F	61	VAL	2.3
1	C	1	MET	2.2
1	C	181	MET	2.2
1	E	282	ILE	2.2
1	A	277	ILE	2.1
1	A	41	LYS	2.1
1	E	4	GLY	2.1
1	B	273	GLN	2.1
1	F	178	TRP	2.1
1	A	175	LEU	2.1
1	D	33	SER	2.1
1	D	277	ILE	2.1
1	E	66	GLY	2.1
1	E	85	PHE	2.0
1	D	41	LYS	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 monosaccharides in this entry.

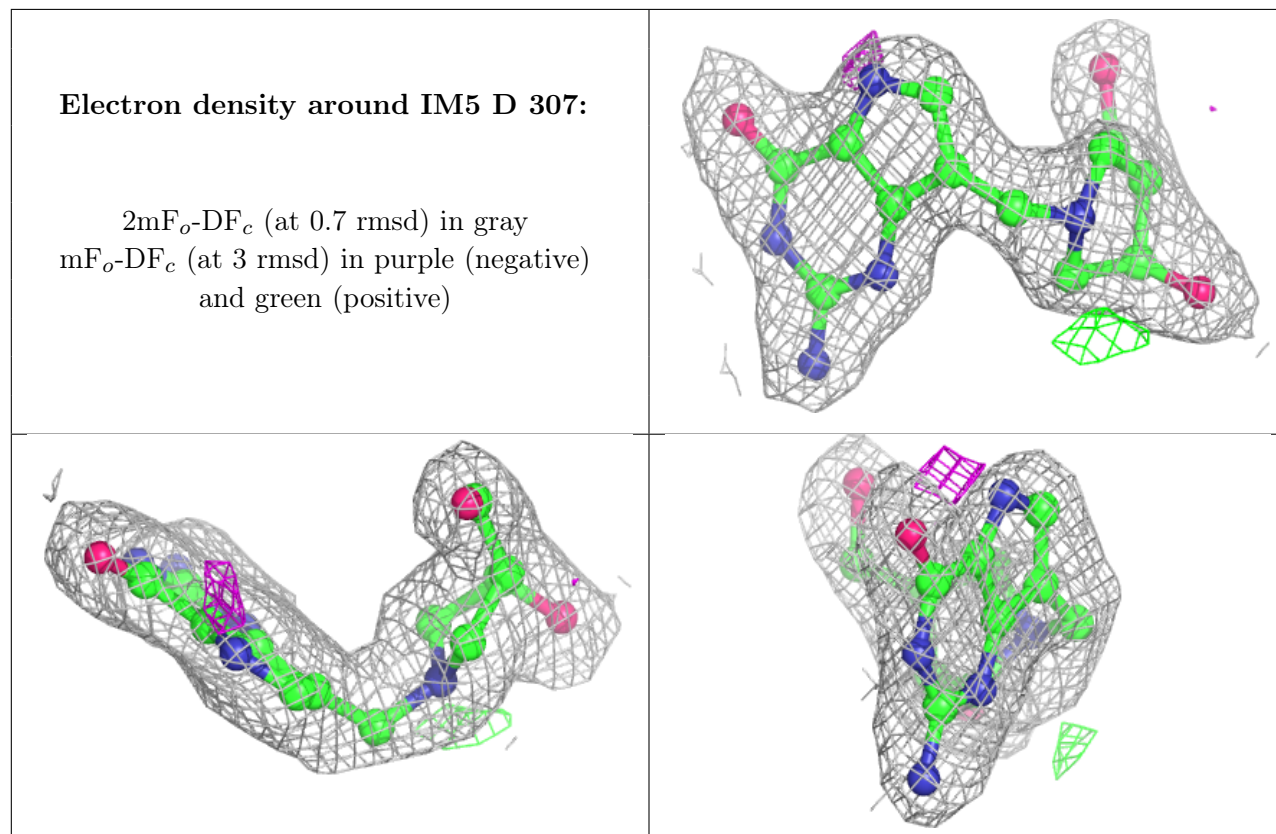
6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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(Å ²)	Q<0.9
2	PO4	E	304	5/5	0.54	0.26	103,106,107,109	0
2	PO4	C	304	5/5	0.69	0.24	67,70,75,76	0
2	PO4	B	305	5/5	0.76	0.24	77,77,82,83	0
2	PO4	F	302	5/5	0.78	0.20	88,90,91,92	0
2	PO4	E	303	5/5	0.81	0.20	90,90,92,93	0
2	PO4	A	304	5/5	0.87	0.17	67,70,72,74	0
2	PO4	A	307	5/5	0.88	0.23	58,61,63,63	0
2	PO4	E	305	5/5	0.88	0.21	67,70,72,74	0
2	PO4	A	306	5/5	0.88	0.23	63,64,66,67	0
2	PO4	D	306	5/5	0.90	0.25	77,77,81,82	0
2	PO4	B	303	5/5	0.91	0.15	58,59,60,62	0
2	PO4	B	304	5/5	0.91	0.15	63,64,65,66	0
2	PO4	A	303	5/5	0.91	0.15	42,44,44,45	0
2	PO4	D	304	5/5	0.93	0.16	68,70,72,76	0
2	PO4	C	303	5/5	0.93	0.18	68,69,69,71	0
2	PO4	A	305	5/5	0.94	0.14	77,78,80,81	0
2	PO4	D	305	5/5	0.95	0.13	64,66,67,68	0
3	IM5	D	307	20/20	0.95	0.14	27,29,30,30	0
3	IM5	E	306	20/20	0.95	0.10	23,24,24,24	0
3	IM5	B	306	20/20	0.96	0.10	15,16,19,19	0
2	PO4	D	303	5/5	0.96	0.15	49,50,51,53	0
3	IM5	A	308	20/20	0.96	0.09	17,18,18,19	0
3	IM5	F	303	20/20	0.96	0.10	16,18,21,21	0
3	IM5	C	305	20/20	0.97	0.10	12,13,14,14	0
2	PO4	C	302	5/5	0.97	0.17	38,40,42,43	0
2	PO4	D	302	5/5	0.97	0.19	46,47,47,48	0
2	PO4	E	302	5/5	0.97	0.24	56,56,58,60	0
2	PO4	E	301	5/5	0.98	0.09	29,29,31,31	0
2	PO4	B	302	5/5	0.98	0.12	34,34,36,36	0
2	PO4	A	302	5/5	0.98	0.13	39,40,41,42	0
2	PO4	B	301	5/5	0.99	0.11	17,17,18,19	0
2	PO4	C	301	5/5	0.99	0.10	15,15,15,16	0
2	PO4	D	301	5/5	0.99	0.09	32,32,34,34	0
2	PO4	A	301	5/5	0.99	0.10	20,20,21,21	0
2	PO4	F	301	5/5	1.00	0.09	20,20,21,22	0

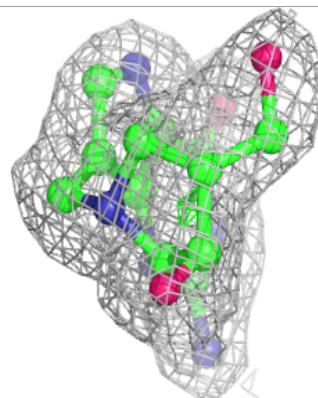
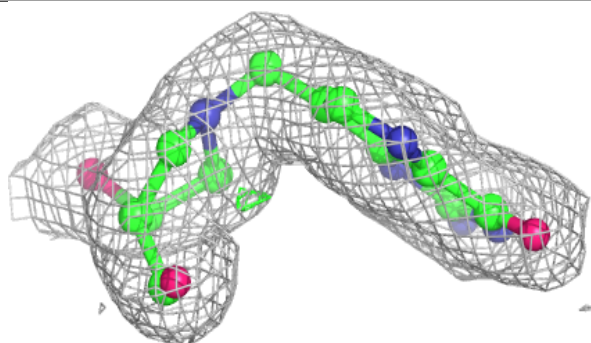
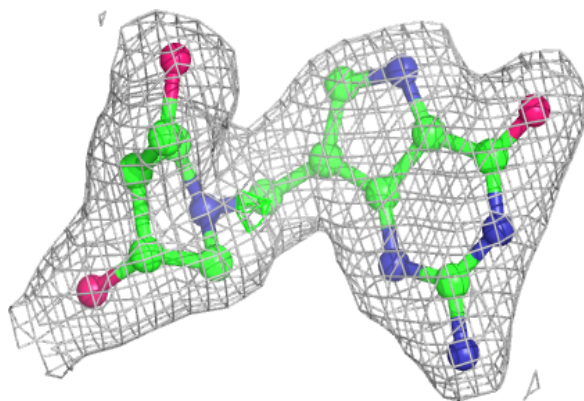
The following is a graphical depiction of the model fit to experimental electron density of all

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.

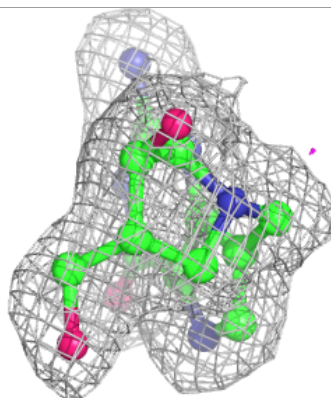
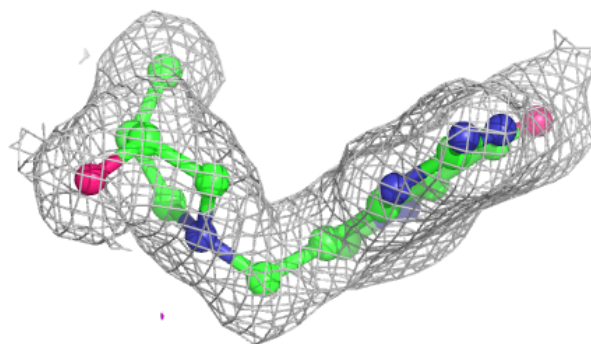
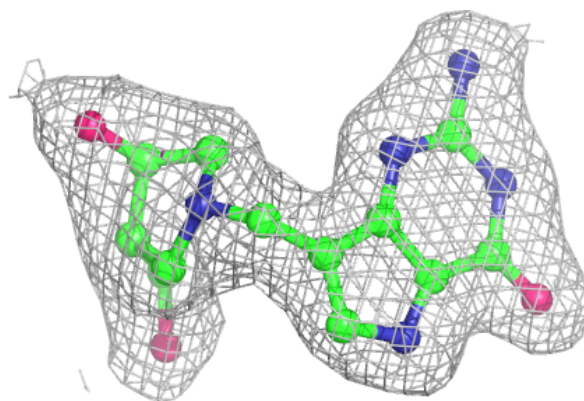


Electron density around IM5 E 306:

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

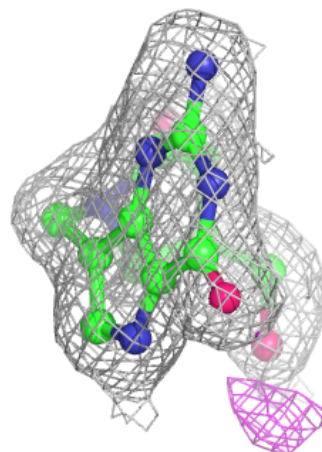
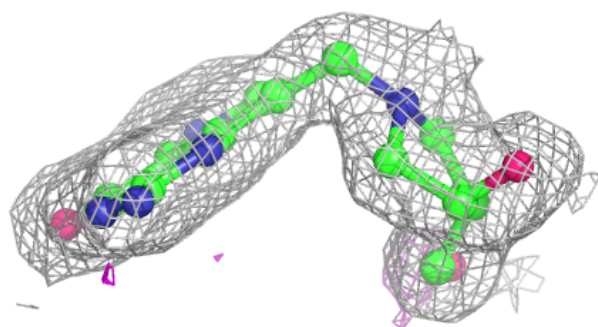
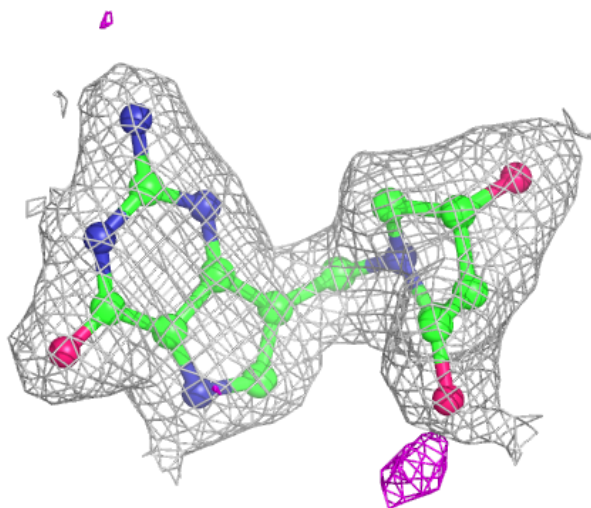
**Electron density around IM5 B 306:**

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



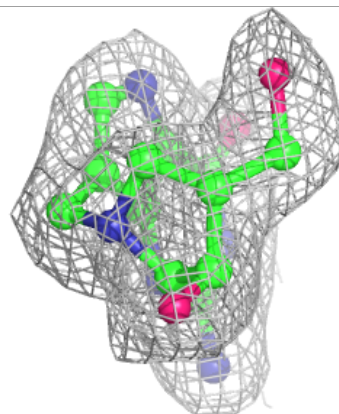
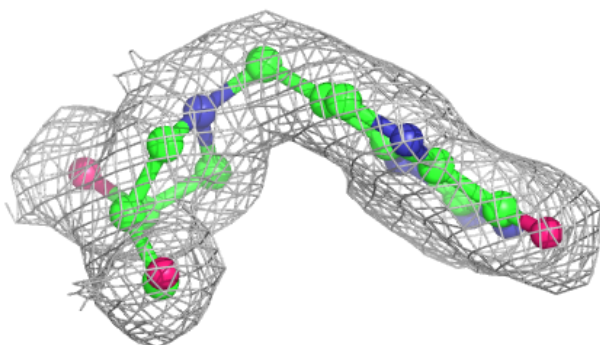
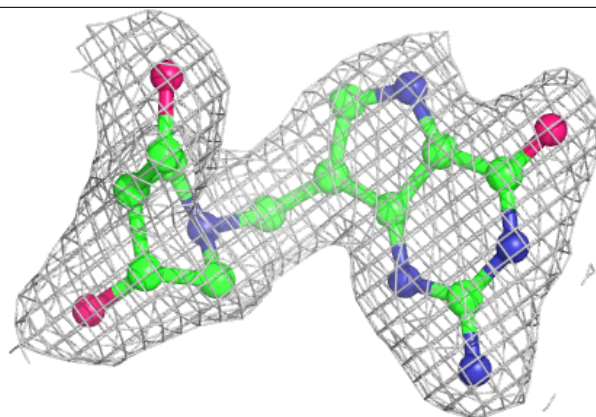
Electron density around IM5 A 308:

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

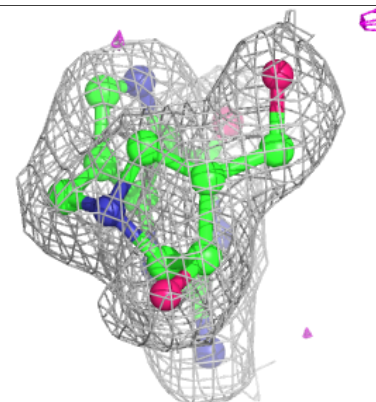
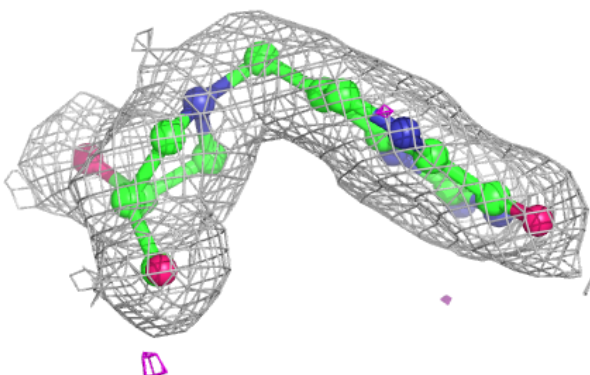
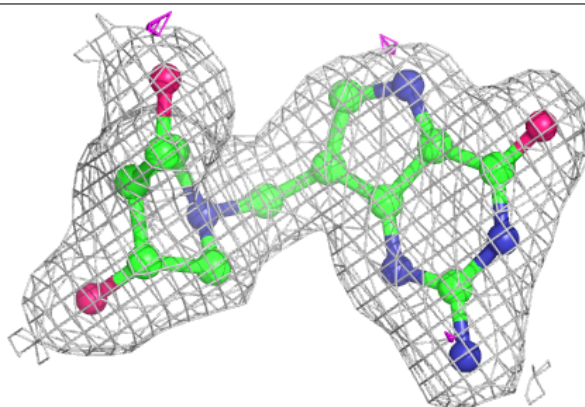


Electron density around IM5 F 303:

$2mF_o-DF_c$ (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.