



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 28, 2026 – 02:26 AM UTC

PDB ID : 1QK4 / pdb_00001qk4
Title : TOXOPLASMA GONDII HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE IMP COMPLEX
Authors : Heroux, A.; White, E.L.; Ross, L.J.; Borhani, D.W.
Deposited on : 1999-07-09
Resolution : 1.90 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ 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	:	FAILED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

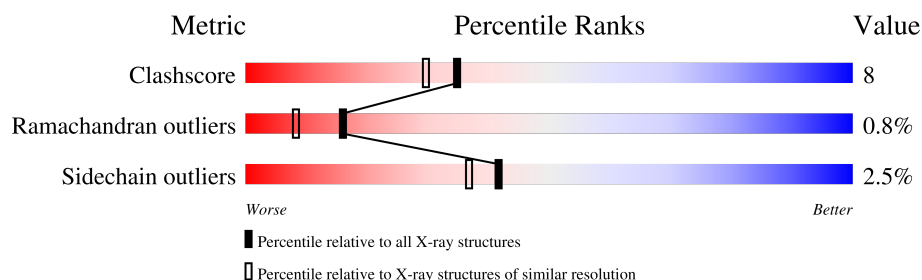
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)

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 $\leq 5\%$

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	233	
1	B	233	
1	C	233	
1	D	233	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7683 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.

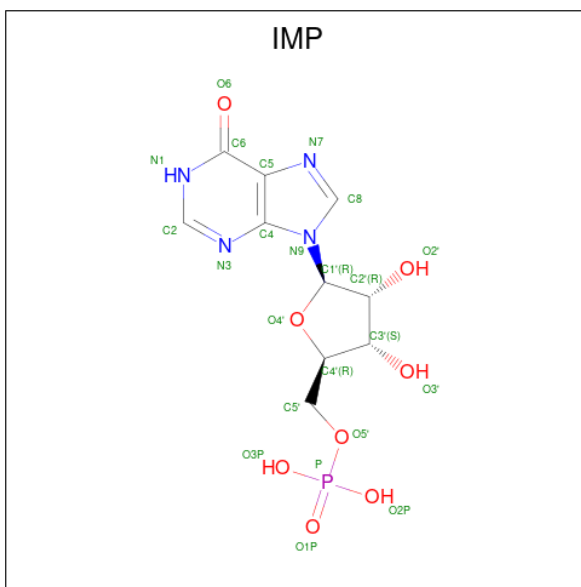
- Molecule 1 is a protein called HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	0	0
			1815	1173	301	333	8			
1	B	224	Total	C	N	O	S	0	2	0
			1807	1168	300	330	9			
1	C	213	Total	C	N	O	S	0	5	0
			1725	1117	282	319	7			
1	D	219	Total	C	N	O	S	0	3	0
			1759	1144	286	320	9			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0A	GLY	-	cloning artifact	UNP Q26997
A	0B	SER	-	cloning artifact	UNP Q26997
A	0C	HIS	-	cloning artifact	UNP Q26997
B	0A	GLY	-	cloning artifact	UNP Q26997
B	0B	SER	-	cloning artifact	UNP Q26997
B	0C	HIS	-	cloning artifact	UNP Q26997
C	0A	GLY	-	cloning artifact	UNP Q26997
C	0B	SER	-	cloning artifact	UNP Q26997
C	0C	HIS	-	cloning artifact	UNP Q26997
D	0A	GLY	-	cloning artifact	UNP Q26997
D	0B	SER	-	cloning artifact	UNP Q26997
D	0C	HIS	-	cloning artifact	UNP Q26997

- Molecule 2 is INOSINIC ACID (CCD ID: IMP) (formula: C₁₀H₁₃N₄O₈P).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	124	Total	O	0	0
			124	124		
3	B	105	Total	O	0	0
			105	105		
3	C	135	Total	O	0	0
			135	135		
3	D	121	Total	O	0	0
			121	121		

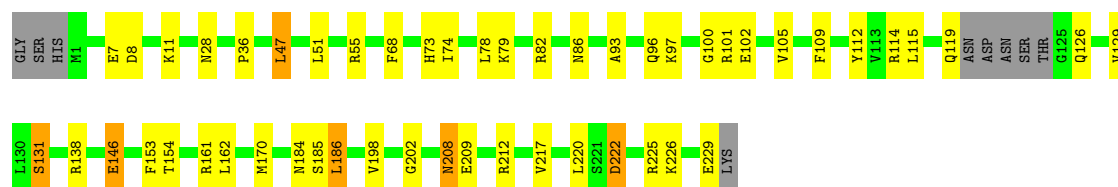
3 Residue-property plots [i](#)

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. 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. 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.

Note EDS failed to run properly.

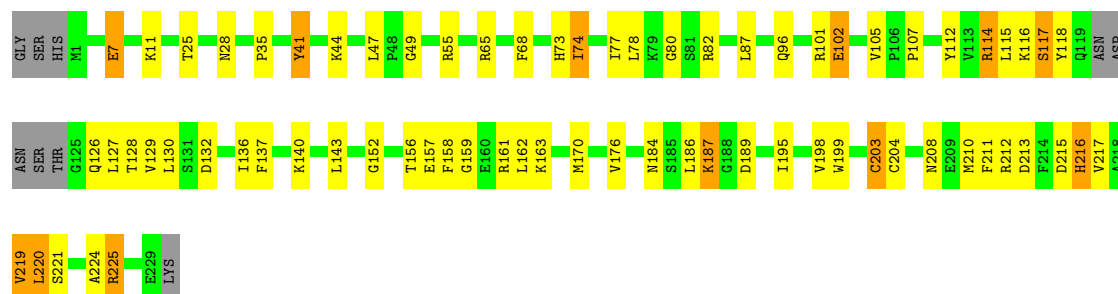
• Molecule 1: HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE

Chain A: 



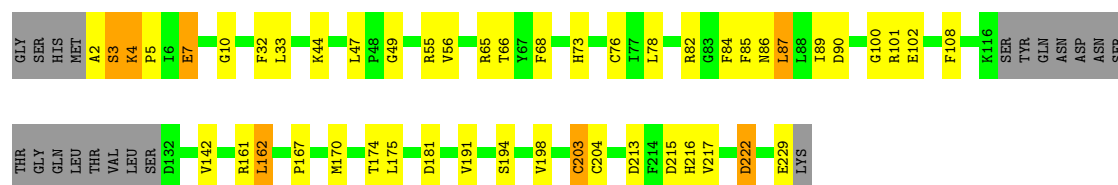
• Molecule 1: HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE

Chain B: 



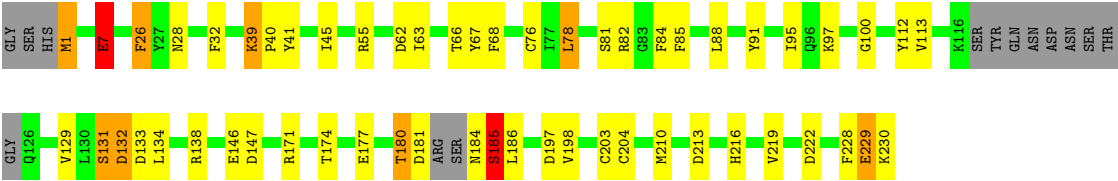
• Molecule 1: HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE

Chain C: 



• Molecule 1: HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE

Chain D: 



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.54Å 102.44Å 108.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.50 – 1.90	Depositor
% Data completeness (in resolution range)	99.6 (12.50-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 1.90Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.189 , 0.238	Depositor
Wilson B-factor (Å ²)	19.6	Xtriage
Anisotropy	0.396	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7683	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% of the height of the origin peak. No significant pseudotranslation is detected.*

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: IMP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.92	0/1858	1.71	27/2505 (1.1%)
1	B	0.86	0/1860	1.81	40/2510 (1.6%)
1	C	0.95	0/1792	1.77	35/2422 (1.4%)
1	D	0.90	0/1818	1.76	30/2453 (1.2%)
All	All	0.91	0/7328	1.76	132/9890 (1.3%)

There are no bond length outliers.

The worst 5 of 132 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	4	LYS	N-CA-C	15.13	130.06	110.39
1	B	65	ARG	CD-NE-CZ	12.46	141.84	124.40
1	D	78	LEU	O-C-N	-11.65	109.80	122.96
1	B	78	LEU	O-C-N	-11.42	109.83	122.85
1	B	212	ARG	NE-CZ-NH2	10.81	128.93	119.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1815	0	1802	27	0
1	B	1807	0	1789	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1725	0	1690	18	0
1	D	1759	0	1726	30	0
2	A	23	0	11	0	0
2	B	23	0	11	0	0
2	C	23	0	11	0	0
2	D	23	0	11	0	0
3	A	124	0	0	2	0
3	B	105	0	0	2	0
3	C	135	0	0	0	0
3	D	121	0	0	2	0
All	All	7683	0	7051	107	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 8.

The worst 5 of 107 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:49:GLY:H	1:C:216:HIS:HD2	1.07	0.98
1:B:156[A]:THR:HG21	1:B:184:ASN:HD21	1.25	0.97
1:B:49:GLY:H	1:B:216:HIS:HD2	1.16	0.91
1:D:184:ASN:O	1:D:185:SER:HB2	1.72	0.90
1:B:220:LEU:HD23	1:B:225:ARG:HG2	1.55	0.86

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	220/233 (94%)	212 (96%)	7 (3%)	1 (0%)	24	16
1	B	222/233 (95%)	213 (96%)	7 (3%)	2 (1%)	14	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	214/233 (92%)	211 (99%)	2 (1%)	1 (0%)	24	16
1	D	216/233 (93%)	210 (97%)	3 (1%)	3 (1%)	9	3
All	All	872/932 (94%)	846 (97%)	19 (2%)	7 (1%)	16	8

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	220	LEU
1	B	221	SER
1	C	3	SER
1	D	132	ASP
1	D	133	ASP

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	199/207 (96%)	196 (98%)	3 (2%)	57	56
1	B	198/207 (96%)	194 (98%)	4 (2%)	48	46
1	C	190/207 (92%)	182 (96%)	8 (4%)	26	19
1	D	191/207 (92%)	186 (97%)	5 (3%)	40	35
All	All	778/828 (94%)	758 (97%)	20 (3%)	42	35

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	222	ASP
1	D	39	LYS
1	D	229	GLU
1	D	185	SER
1	B	187	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	184	ASN
1	C	216	HIS
1	D	86	ASN
1	B	216	HIS
1	A	86	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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	IMP	C	300	-	25,25,25	0.92	2 (8%)	37,38,38	1.31	4 (10%)
2	IMP	A	300	-	25,25,25	0.84	1 (4%)	37,38,38	1.11	2 (5%)
2	IMP	D	300	-	25,25,25	0.81	0	37,38,38	1.22	5 (13%)
2	IMP	B	300	-	25,25,25	1.02	2 (8%)	37,38,38	1.23	3 (8%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	IMP	C	300	-	-	0/10/26/26	0/3/3/3
2	IMP	A	300	-	-	3/10/26/26	0/3/3/3
2	IMP	D	300	-	-	5/10/26/26	0/3/3/3
2	IMP	B	300	-	-	2/10/26/26	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	300	IMP	C2-N1	3.20	1.41	1.35
2	C	300	IMP	C2-N1	2.37	1.39	1.35
2	A	300	IMP	C2-N3	2.25	1.34	1.30
2	B	300	IMP	C2-N3	2.22	1.34	1.30
2	C	300	IMP	P-O2P	-2.07	1.47	1.54

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	300	IMP	O3P-P-O5'	-3.09	98.62	106.67
2	D	300	IMP	O2'-C2'-C1'	2.90	120.08	110.10
2	B	300	IMP	O3'-C3'-C2'	2.70	120.48	111.82
2	D	300	IMP	C2'-C1'-N9	-2.70	105.73	113.25
2	C	300	IMP	O2'-C2'-C1'	2.59	119.03	110.10

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

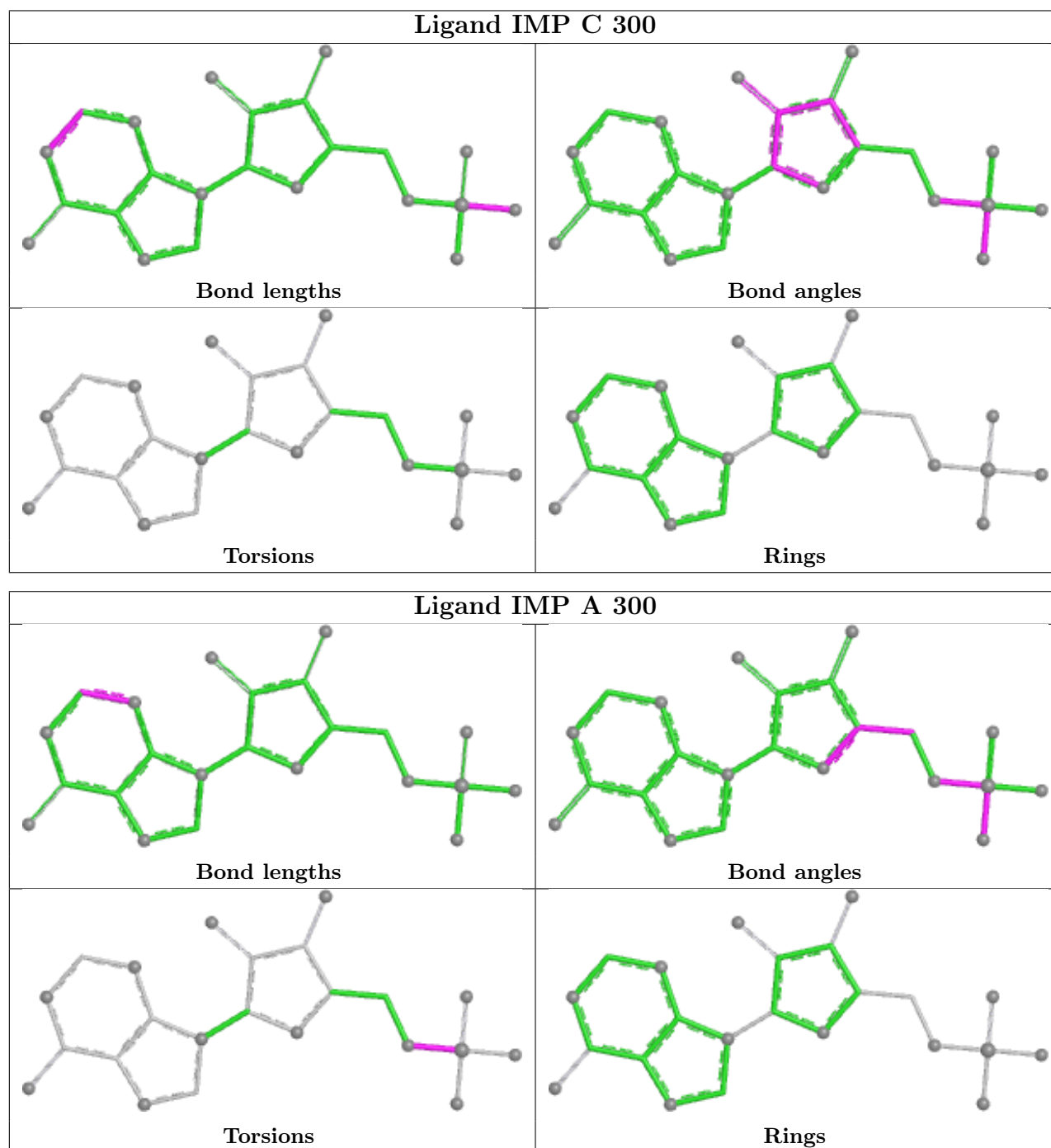
Mol	Chain	Res	Type	Atoms
2	A	300	IMP	C5'-O5'-P-O2P
2	A	300	IMP	C5'-O5'-P-O3P
2	B	300	IMP	O4'-C4'-C5'-O5'
2	D	300	IMP	C5'-O5'-P-O2P
2	D	300	IMP	C5'-O5'-P-O3P

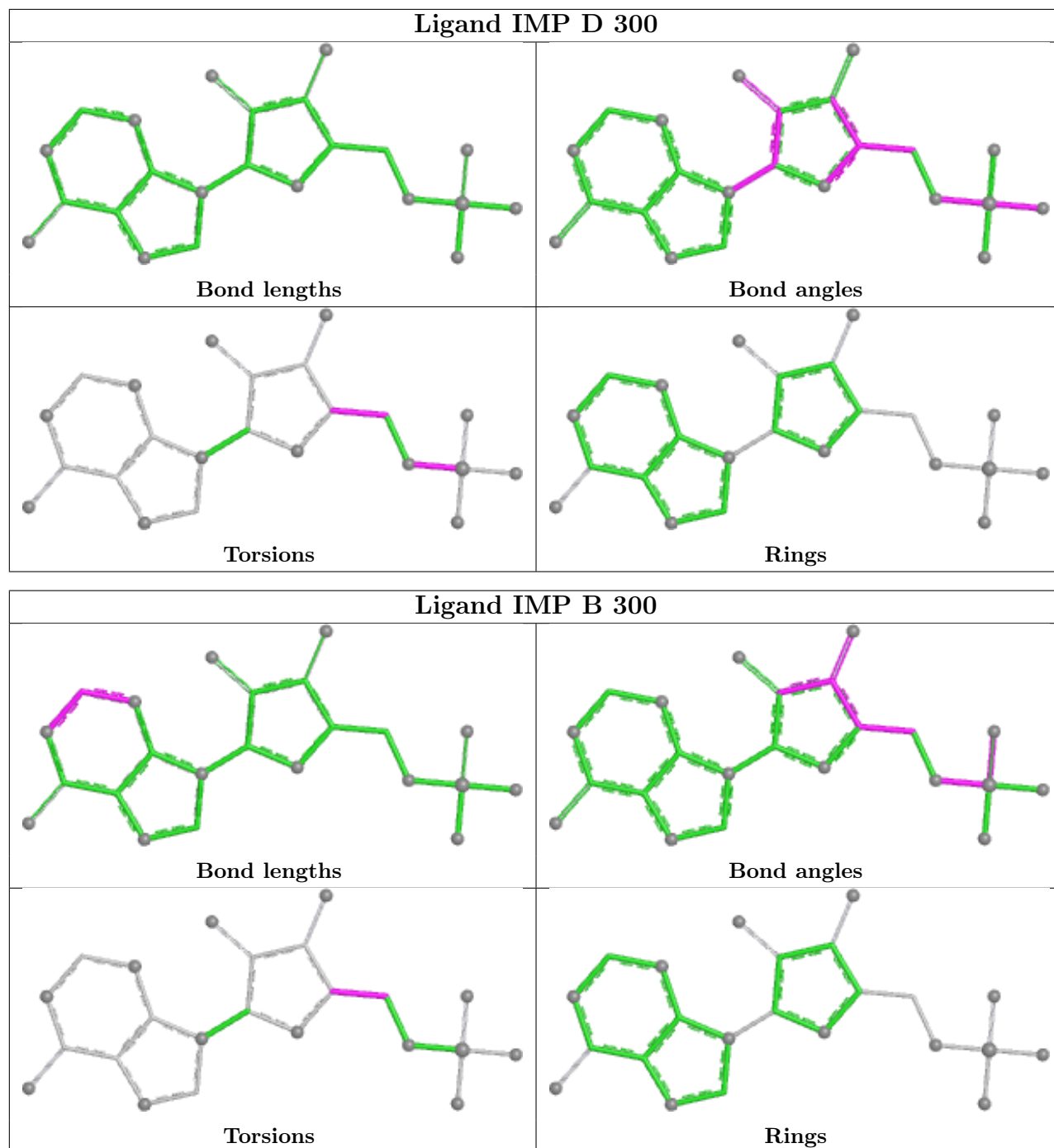
There are no ring outliers.

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

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.