

wwPDB X-ray Structure Validation Summary Report (i)

Feb 3, 2024 – 11:05 AM EST

PDB ID : 1LIJ

Title : STRUCTURE OF T. GONDII ADENOSINE KINASE BOUND TO PRO-

DRUG 2 7-IODOTUBERCIDIN AND AMP-PCP

Authors: Schumacher, M.A.; Scott, D.M.; Mathews, I.I.; Ealick, S.E.; Roos, D.S.; Ull-

man, B.; Brennan, R.G.

Deposited on : 2002-04-17

Resolution : 1.86 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 (i) 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 (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED

EDS : NOT EXECUTED

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

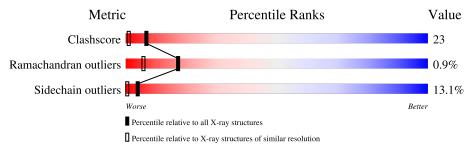
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 1.86 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain					
1	A	363	61%	21%	7% •	9%		

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	RPP	A	699	X	-	-	-



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2631 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 adenosine kinase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	330	Total	С	N	О	S	0	0	0
1	Α	330	2433	1546	415	457	15	0	U	U

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	126	THR	VAL	$\operatorname{conflict}$	UNP Q9TVW2
A	150	ILE	LEU	$\operatorname{conflict}$	UNP Q9TVW2
A	153	ASN	ASP	$\operatorname{conflict}$	UNP Q9TVW2
A	242	VAL	THR	conflict	UNP Q9TVW2
A	246	VAL	THR	$\operatorname{conflict}$	UNP Q9TVW2
A	327	GLY	ALA	conflict	UNP Q9TVW2

• Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

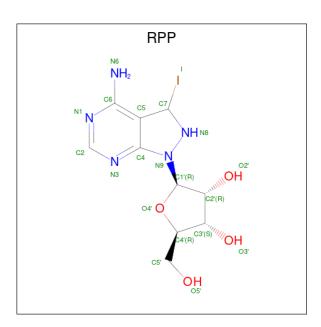
Mo	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0

• Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0

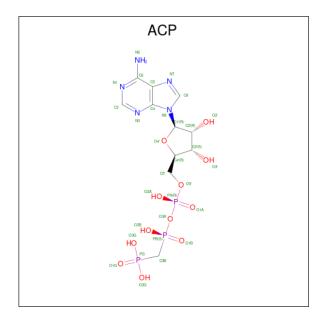
• Molecule 4 is 2-RIBOFURANOSYL-3-IODO-2,3-DIHYDRO-1H-PYRAZOLO[3,4-D]PYRI MIDIN-4-YLAMINE (three-letter code: RPP) (formula: C₁₀H₁₄IN₅O₄).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
4	Λ	1	Total	С	Ι	N	О	0	0
4	A	1	20	10	1	5	4	U	U

 \bullet Molecule 5 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3).$



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
5	A	1	Total 31			O 12	P 3	0	0

• Molecule 6 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	145	Total O 145 145	0	0

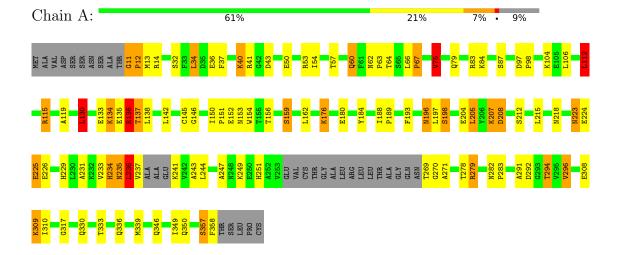


3 Residue-property plots (i)

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. 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 was not executed.

• Molecule 1: adenosine kinase





4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	P 21 21 2	Depositor	
Cell constants	167.70Å 46.97Å 44.09Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	10.00 - 1.86	Depositor	
% Data completeness	99.0 (10.00-1.86)	Depositor	
(in resolution range)	33.0 (10.00-1.00)	Depositor	
R_{merge}	0.09	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	TNT	Depositor	
R, R_{free}	0.185 , 0.239	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2631	wwPDB-VP	
Average B, all atoms (Å ²)	30.0	wwPDB-VP	



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: RPP, MG, ACP, CL

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

Mal	Chain	Bo	nd lengths	Во	ond angles
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.70	$2/2479 \ (0.1\%)$	1.15	$18/3369 \ (0.5\%)$

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
1	A	137	THR	C-N	-10.99	1.08	1.34
1	A	224	GLU	CD-OE2	-5.53	1.19	1.25

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
1	A	137	THR	O-C-N	-7.95	109.98	122.70
1	A	136	ARG	O-C-N	-7.55	110.62	122.70
1	A	11	GLY	C-N-CD	-7.13	104.92	120.60
1	A	249	LYS	CB-CA-C	6.73	123.85	110.40
1	A	130	LEU	CB-CA-C	6.67	122.88	110.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	241	LYS	CA



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	2433	0	2400	113	0
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	20	0	13	0	0
5	A	31	0	14	4	0
6	A	145	0	0	17	0
All	All	2631	0	2427	114	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 23.

The worst 5 of 114 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:333:THR:H	1:A:336:GLN:NE2	1.44	1.12
1:A:310:ILE:HD12	1:A:349:ILE:HD12	1.35	1.04
1:A:193:PHE:H	1:A:218:ASN:HD22	1.17	0.92
1:A:333:THR:N	1:A:336:GLN:HE21	1.66	0.91
1:A:196:ASN:HD22	1:A:198:SER:H	1.20	0.87

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	324/363 (89%)	306 (94%)	15 (5%)	3 (1%)	17 6	

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	236	LEU
1	A	12	PRO
1	A	198	SER

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	252/287 (88%)	219 (87%)	33 (13%)	4 0

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	279	ARG
1	A	294	THR
1	A	357	SER
1	A	130	LEU
1	A	115	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	234	HIS
1	A	336	GLN
1	A	351	HIS
1	A	342	ASN
1	A	218	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)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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

Mol Type	Chain Res	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Pag	Link	Bo	ond leng	ths	В	ond ang	les
MIOI	Mol Type Chain F	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2											
5	ACP	A	799	3	27,33,33	2.16	3 (11%)	32,52,52	1.93	6 (18%)										
4	RPP	A	699	-	19,22,22	3.20	2 (10%)	22,33,33	0.81	1 (4%)										

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.

\mathbf{Mol}	\mathbf{Type}	Chain	Res	Link	Chirals	Torsions	Rings
5	ACP	A	799	3	-	3/15/38/38	0/3/3/3
4	RPP	A	699	-	1/1/6/7	0/6/34/34	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
4	A	699	RPP	C5-C7	-12.33	1.39	1.50

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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
5	A	799	ACP	PB-O3A	9.95	1.69	1.58
4	A	699	RPP	N8-N9	-6.21	1.36	1.43
5	A	799	ACP	PB-O1B	-2.22	1.46	1.51
5	A	799	ACP	PA-O5'	-2.15	1.50	1.59

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
5	A	799	ACP	C1'-N9-C4	-6.22	115.72	126.64
5	A	799	ACP	O1B-PB-C3B	-4.51	97.17	109.07
5	A	799	ACP	O1G-PG-C3B	-4.38	101.80	111.24
5	A	799	ACP	O2B-PB-O1B	4.33	124.54	110.07
5	A	799	ACP	O3G-PG-O2G	2.75	116.11	108.08

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	699	RPP	C7

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	799	ACP	C5'-O5'-PA-O1A
5	A	799	ACP	C5'-O5'-PA-O2A
5	A	799	ACP	C5'-O5'-PA-O3A

There are no ring outliers.

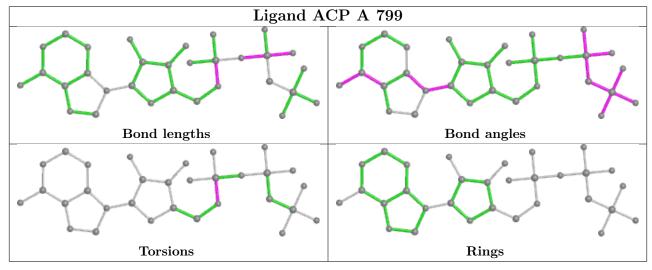
1 monomer is involved in 4 short contacts:

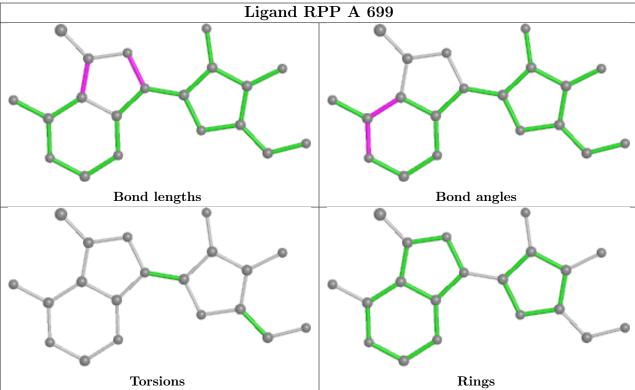
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	799	ACP	4	0

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	137:THR	С	138:LEU	N	1.08



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

