



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:38 PM UTC

PDB ID : 1LIJ / pdb_00001lij
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 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
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

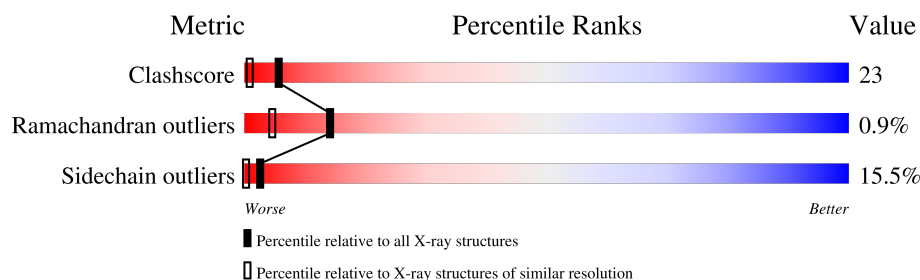
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.86 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	363	

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

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	A	330	Total	C	N	O	S	0	0	0
			2433	1546	415	457	15			

There are 6 discrepancies between the modelled and reference sequences:

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

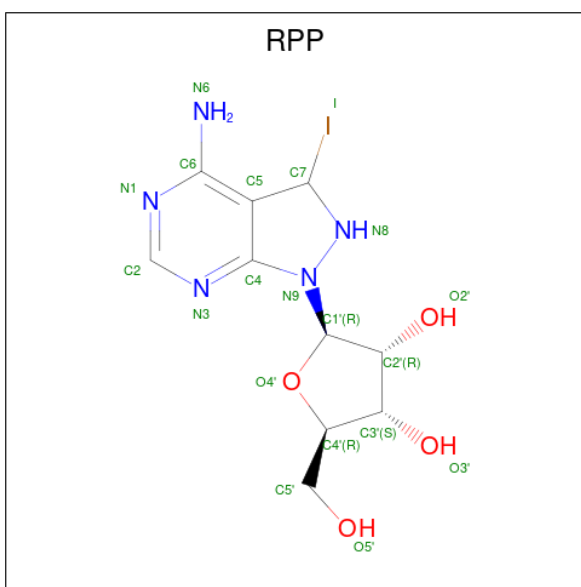
- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

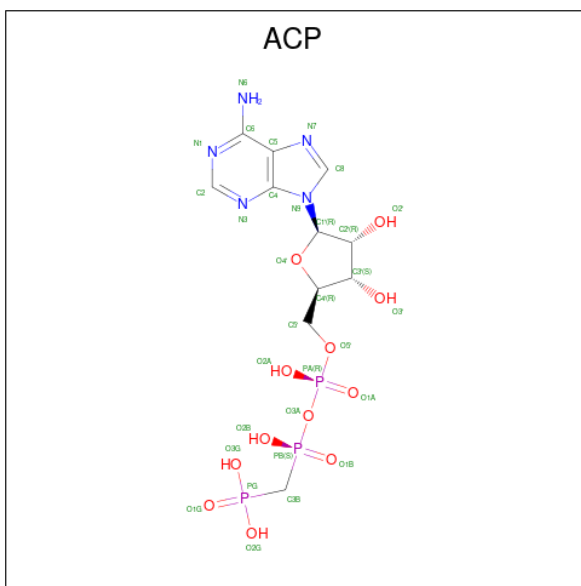
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 2-RIBOFURANOSYL-3-iodo-2,3-dihydro-1H-pyrazolo[3,4-d]pyrimidin-4-ylamine (CCD ID: RPP) (formula: C₁₀H₁₄IN₅O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	I	N	O	0	0
			20	10	1	5	4		

- Molecule 5 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

- Molecule 6 is water.

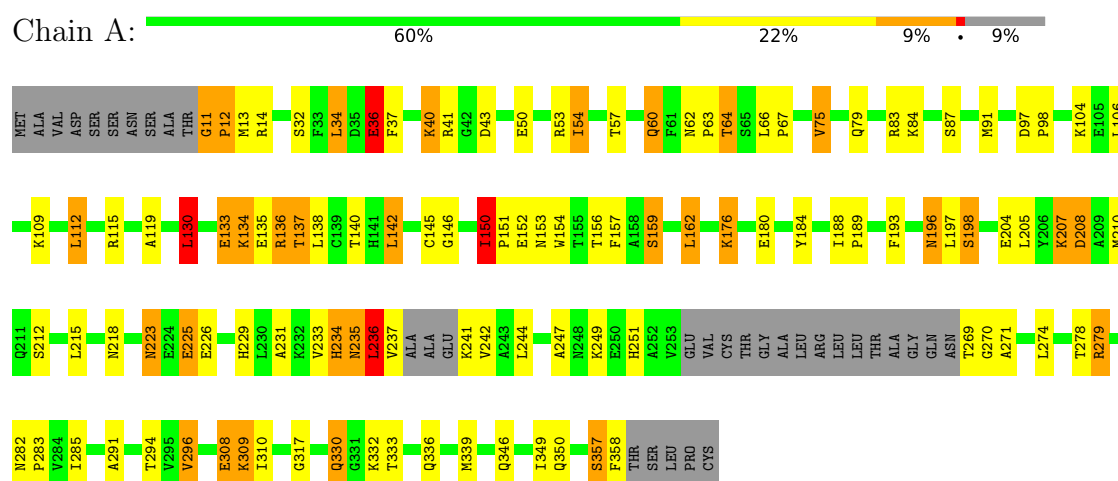
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	145	Total 145	O 145	0	0

3 Residue-property plots

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

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	167.70 Å 46.97 Å 44.09 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.86	Depositor
% Data completeness (in resolution range)	99.0 (10.00-1.86)	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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACP, CL, MG, RPP

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	0.88	2/2479 (0.1%)	1.42	27/3369 (0.8%)

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

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	137	THR	C-N	-18.66	1.08	1.33
1	A	241	LYS	CA-CB	-5.16	1.43	1.53

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	THR	O-C-N	-11.20	109.98	123.30
1	A	136	ARG	O-C-N	-9.91	110.62	123.21
1	A	137	THR	CA-C-N	9.45	136.04	123.00
1	A	137	THR	C-N-CA	9.45	136.04	123.00
1	A	130	LEU	CB-CA-C	7.83	122.88	110.19
1	A	54	ILE	CB-CA-C	-7.28	102.31	112.14
1	A	136	ARG	CA-C-N	7.28	133.26	122.99
1	A	136	ARG	C-N-CA	7.28	133.26	122.99
1	A	249	LYS	CB-CA-C	6.41	123.85	110.32
1	A	308	GLU	N-CA-CB	6.12	120.55	110.39
1	A	234	HIS	CB-CA-C	6.12	122.60	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	296	VAL	N-CA-CB	5.72	119.03	111.25
1	A	251	HIS	CB-CA-C	-5.65	99.49	110.46
1	A	64	THR	N-CA-CB	-5.65	101.42	111.08
1	A	36	GLU	N-CA-CB	5.63	118.89	110.22
1	A	140	THR	N-CA-CB	-5.60	101.50	111.08
1	A	133	GLU	N-CA-C	-5.52	99.05	110.80
1	A	241	LYS	N-CA-CB	5.44	119.75	110.50
1	A	150	ILE	CB-CA-C	-5.43	104.43	110.68
1	A	274	LEU	N-CA-CB	-5.40	101.47	111.13
1	A	242	VAL	N-CA-C	5.37	115.99	110.36
1	A	43	ASP	CB-CA-C	-5.29	99.45	110.40
1	A	142	LEU	N-CA-C	5.17	116.91	111.28
1	A	133	GLU	N-CA-CB	5.15	119.19	110.49
1	A	241	LYS	CB-CA-C	5.07	119.74	110.10
1	A	11	GLY	CA-C-N	5.00	126.09	119.84
1	A	11	GLY	C-N-CA	5.00	126.09	119.84

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	114	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	115	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.

All (115) 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: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
1:A:137:THR:HB	6:A:1132:HOH:O	1.79	0.82
1:A:333:THR:H	1:A:336:GLN:HE21	0.84	0.81
1:A:231:ALA:HA	1:A:236:LEU:CD1	2.11	0.81
1:A:333:THR:HG23	1:A:336:GLN:NE2	1.96	0.78
1:A:119:ALA:HB1	6:A:1121:HOH:O	1.83	0.78
1:A:223:ASN:ND2	1:A:226:GLU:H	1.82	0.77
1:A:225:GLU:HG2	1:A:226:GLU:N	1.97	0.77
1:A:196:ASN:ND2	1:A:198:SER:H	1.84	0.75
1:A:142:LEU:HB3	6:A:1119:HOH:O	1.89	0.72
1:A:231:ALA:HA	1:A:236:LEU:HD12	1.71	0.72
1:A:310:ILE:CD1	1:A:349:ILE:HD12	2.19	0.71
1:A:333:THR:N	1:A:336:GLN:NE2	2.30	0.68
1:A:12:PRO:HG2	1:A:13:MET:H	1.58	0.68
1:A:236:LEU:CB	1:A:247:ALA:HB1	2.24	0.68
1:A:317:GLY:H	5:A:799:ACP:H3B2	1.58	0.68
1:A:235:ASN:O	1:A:237:VAL:N	2.27	0.67
1:A:41:ARG:HG2	1:A:135:GLU:OE2	1.95	0.67
1:A:207:LYS:HD3	1:A:207:LYS:H	1.60	0.67
1:A:235:ASN:N	1:A:235:ASN:OD1	2.29	0.66
1:A:309:LYS:HZ2	1:A:309:LYS:HB2	1.60	0.66
1:A:207:LYS:HD3	1:A:207:LYS:N	2.10	0.65
5:A:799:ACP:N7	6:A:1000:HOH:O	2.29	0.65
1:A:330:GLN:NE2	6:A:1039:HOH:O	2.30	0.64
1:A:357:SER:OG	1:A:358:PHE:N	2.30	0.64
1:A:133:GLU:CD	1:A:134:LYS:HG2	2.23	0.63
1:A:104:LYS:NZ	6:A:1117:HOH:O	2.29	0.63
1:A:40:LYS:HE3	1:A:40:LYS:HA	1.81	0.62
1:A:40:LYS:HB3	6:A:1087:HOH:O	2.00	0.62
1:A:184:TYR:CZ	1:A:188:ILE:HD11	2.34	0.62
1:A:130:LEU:HB2	6:A:1132:HOH:O	1.97	0.62
1:A:223:ASN:C	1:A:223:ASN:HD22	2.08	0.61
1:A:146:GLY:N	6:A:1119:HOH:O	2.25	0.61
1:A:231:ALA:HA	1:A:236:LEU:HD11	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:GLY:O	1:A:14:ARG:HD2	2.00	0.61
1:A:136:ARG:NE	5:A:799:ACP:O3G	2.31	0.60
1:A:66:LEU:HB2	1:A:67:PRO:HD2	1.82	0.60
1:A:309:LYS:HG3	1:A:309:LYS:O	2.00	0.59
1:A:207:LYS:HG2	1:A:208:ASP:N	2.18	0.59
1:A:207:LYS:HG2	1:A:208:ASP:H	1.68	0.59
1:A:235:ASN:C	1:A:236:LEU:HG	2.28	0.59
1:A:204:GLU:OE1	1:A:229:HIS:HD2	1.87	0.58
1:A:271:ALA:N	6:A:1126:HOH:O	2.25	0.58
1:A:278:THR:C	1:A:279:ARG:HG2	2.28	0.58
1:A:57:THR:O	1:A:60:GLN:HG3	2.03	0.56
1:A:223:ASN:HD22	1:A:226:GLU:H	1.53	0.56
1:A:189:PRO:HA	6:A:1019:HOH:O	2.06	0.56
1:A:236:LEU:HB3	1:A:247:ALA:HB1	1.87	0.56
1:A:97:ASP:HB2	1:A:98:PRO:HD2	1.88	0.55
1:A:193:PHE:H	1:A:218:ASN:ND2	1.97	0.55
1:A:236:LEU:HB2	1:A:247:ALA:HB1	1.88	0.55
1:A:133:GLU:OE2	1:A:134:LYS:HG2	2.07	0.55
1:A:153:ASN:ND2	6:A:1136:HOH:O	2.39	0.55
1:A:196:ASN:HD22	1:A:197:LEU:N	2.05	0.54
1:A:40:LYS:HE2	1:A:41:ARG:N	2.23	0.54
1:A:223:ASN:HD21	1:A:225:GLU:CD	2.16	0.54
1:A:346:GLN:HE21	5:A:799:ACP:H2	1.73	0.54
1:A:207:LYS:HE2	1:A:208:ASP:OD1	2.09	0.52
1:A:346:GLN:O	1:A:350:GLN:NE2	2.43	0.52
1:A:145:CYS:HB2	6:A:1119:HOH:O	2.09	0.52
1:A:150:ILE:HG21	1:A:154:TRP:CD1	2.46	0.50
1:A:156:THR:O	1:A:159:SER:HB2	2.11	0.50
1:A:50:GLU:HB2	6:A:1007:HOH:O	2.11	0.50
1:A:115:ARG:NH1	6:A:1028:HOH:O	2.29	0.50
1:A:330:GLN:HG2	6:A:1039:HOH:O	2.11	0.49
1:A:244:LEU:O	1:A:247:ALA:HB3	2.13	0.49
1:A:207:LYS:H	1:A:207:LYS:CD	2.26	0.49
1:A:196:ASN:HD22	1:A:196:ASN:C	2.21	0.49
1:A:151:PRO:HB2	1:A:153:ASN:OD1	2.13	0.48
1:A:184:TYR:CE2	1:A:188:ILE:HD11	2.48	0.48
1:A:231:ALA:HB1	1:A:237:VAL:HA	1.94	0.48
1:A:12:PRO:CG	1:A:13:MET:H	2.25	0.48
1:A:176:LYS:O	1:A:180:GLU:HG3	2.13	0.48
1:A:225:GLU:HG2	1:A:226:GLU:HG3	1.94	0.48
1:A:269:THR:O	1:A:269:THR:OG1	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:GLN:HE22	1:A:87:SER:N	2.12	0.47
1:A:57:THR:O	1:A:57:THR:HG22	2.15	0.46
1:A:309:LYS:HB2	1:A:309:LYS:NZ	2.29	0.46
1:A:32:SER:O	1:A:36:GLU:HG2	2.15	0.46
1:A:336:GLN:HA	1:A:339:MET:HE2	1.98	0.46
1:A:115:ARG:HH22	1:A:153:ASN:ND2	2.13	0.45
1:A:91:MET:HE2	1:A:115:ARG:HB3	1.98	0.45
1:A:188:ILE:HG23	1:A:189:PRO:HD2	1.99	0.45
1:A:270:GLY:HA3	1:A:291:ALA:HB2	1.98	0.45
1:A:223:ASN:OD1	1:A:225:GLU:OE2	2.34	0.45
1:A:75:VAL:HG13	1:A:112:LEU:HD21	1.98	0.45
1:A:150:ILE:CG2	1:A:154:TRP:CD1	3.00	0.45
1:A:79:GLN:HE22	1:A:87:SER:H	1.63	0.44
1:A:91:MET:HE3	1:A:157:PHE:CD2	2.52	0.44
1:A:97:ASP:HB2	1:A:98:PRO:CD	2.47	0.44
1:A:223:ASN:HD21	1:A:225:GLU:CG	2.31	0.44
1:A:150:ILE:HG22	1:A:151:PRO:O	2.18	0.43
1:A:134:LYS:HE3	1:A:134:LYS:HB3	1.59	0.43
1:A:40:LYS:HA	1:A:40:LYS:CE	2.48	0.43
1:A:229:HIS:O	1:A:233:VAL:HG23	2.18	0.43
1:A:34:LEU:HD12	1:A:34:LEU:HA	1.81	0.42
1:A:37:PHE:HE2	1:A:53:ARG:HB3	1.85	0.42
1:A:279:ARG:HB2	1:A:282:ASN:HB2	2.01	0.42
1:A:14:ARG:HG2	6:A:1131:HOH:O	2.20	0.42
1:A:205:LEU:N	1:A:205:LEU:CD1	2.83	0.42
1:A:233:VAL:HG12	1:A:234:HIS:CD2	2.55	0.42
1:A:193:PHE:N	1:A:218:ASN:HD22	2.00	0.41
1:A:282:ASN:HB3	1:A:283:PRO:HD2	2.02	0.41
1:A:223:ASN:HD21	1:A:226:GLU:HG3	1.85	0.41
1:A:223:ASN:HD21	1:A:226:GLU:H	1.62	0.41
1:A:333:THR:OG1	1:A:336:GLN:HG3	2.20	0.41
1:A:162:LEU:HD13	1:A:162:LEU:HA	1.81	0.41
1:A:235:ASN:HB2	1:A:236:LEU:H	1.61	0.40
1:A:309:LYS:NZ	1:A:309:LYS:CB	2.80	0.40
1:A:62:ASN:N	1:A:63:PRO:HD3	2.36	0.40
1:A:333:THR:HG23	1:A:336:GLN:HE21	1.84	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	324/363 (89%)	306 (94%)	15 (5%)	3 (1%)	14 4

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%)	213 (84%)	39 (16%)	2 0

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LEU
1	A	36	GLU
1	A	40	LYS
1	A	54	ILE
1	A	60	GLN
1	A	64	THR
1	A	75	VAL
1	A	83	ARG

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Mol	Chain	Res	Type
1	A	84	LYS
1	A	106	LEU
1	A	109	LYS
1	A	112	LEU
1	A	130	LEU
1	A	134	LYS
1	A	138	LEU
1	A	150	ILE
1	A	152	GLU
1	A	159	SER
1	A	162	LEU
1	A	176	LYS
1	A	196	ASN
1	A	207	LYS
1	A	208	ASP
1	A	210	MET
1	A	212	SER
1	A	215	LEU
1	A	223	ASN
1	A	225	GLU
1	A	235	ASN
1	A	236	LEU
1	A	279	ARG
1	A	285	ILE
1	A	294	THR
1	A	296	VAL
1	A	308	GLU
1	A	309	LYS
1	A	330	GLN
1	A	332	LYS
1	A	357	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	79	GLN
1	A	132	ASN
1	A	190	ASN
1	A	196	ASN
1	A	218	ASN
1	A	223	ASN

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Mol	Chain	Res	Type
1	A	229	HIS
1	A	234	HIS
1	A	330	GLN
1	A	336	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](#)

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	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	ACP	A	799	3	31,33,33	2.55	4 (12%)	47,52,52	1.68	7 (14%)
4	RPP	A	699	-	17,22,22	3.05	1 (5%)	19,33,33	0.72	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
5	ACP	A	799	3	-	3/19/38/38	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	Observed(Å)	Ideal(Å)
4	A	699	RPP	C5-C7	-12.42	1.39	1.50
5	A	799	ACP	PB-O3A	9.95	1.69	1.58
5	A	799	ACP	PA-O3A	8.95	1.69	1.59
5	A	799	ACP	PA-O5'	-2.25	1.50	1.59
5	A	799	ACP	PB-O1B	-2.24	1.46	1.51

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	799	ACP	C1'-N9-C8	4.97	138.13	127.09
5	A	799	ACP	C4-N9-C1'	-4.67	115.72	126.63
5	A	799	ACP	O1B-PB-C3B	-4.51	97.17	109.05
5	A	799	ACP	O2B-PB-O1B	4.48	124.54	109.95
5	A	799	ACP	O1G-PG-C3B	-4.39	101.80	111.37
5	A	799	ACP	O3G-PG-O2G	2.86	116.11	107.96
5	A	799	ACP	O3A-PA-O1A	2.58	118.46	110.70

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

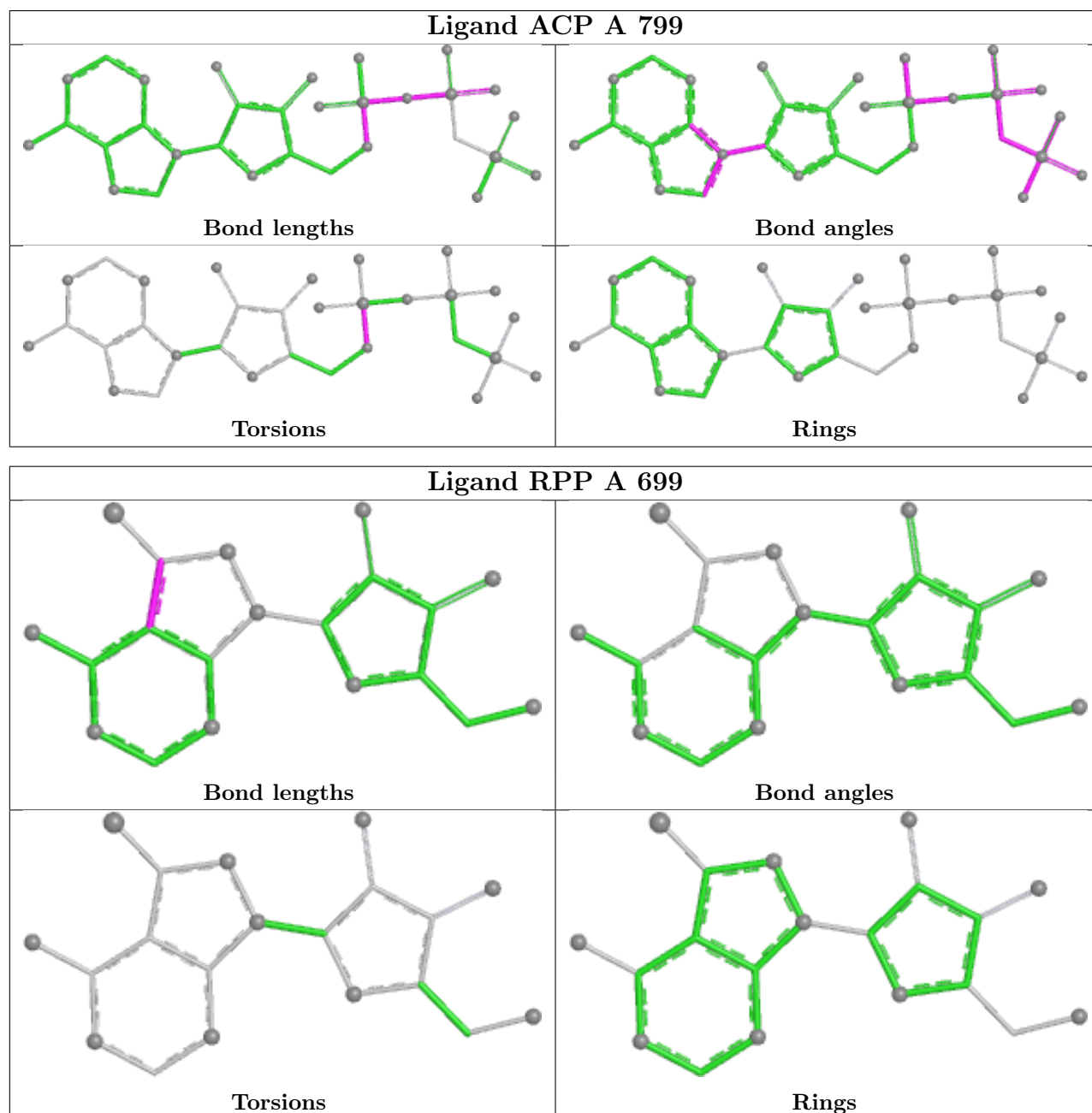
There are no ring outliers.

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 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](#)

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	C	138:LEU	N	1.08

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.