



# Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 05:03 am BST

PDB ID : 2HS0  
Title : T. maritima PurL complexed with ATP  
Authors : Ealick, S.E.; Morar, M.  
Deposited on : 2006-07-20  
Resolution : 2.52 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](mailto: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.

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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 : 2.11  
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) : 2.11

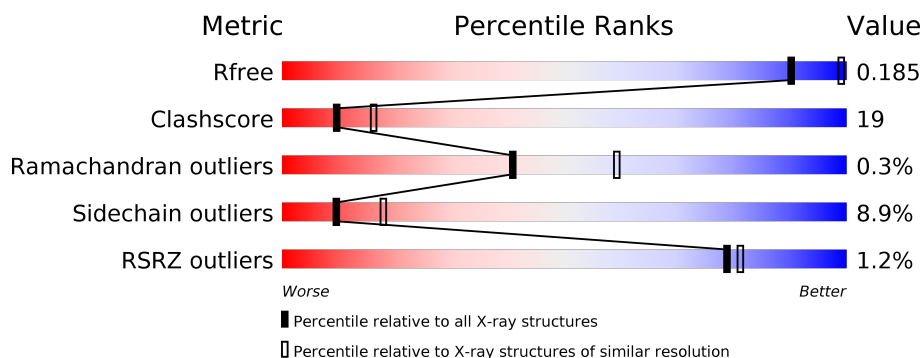
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.52 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	5743 (2.54-2.50)
Clashscore	141614	6463 (2.54-2.50)
Ramachandran outliers	138981	6335 (2.54-2.50)
Sidechain outliers	138945	6337 (2.54-2.50)
RSRZ outliers	127900	5630 (2.54-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	603	<div> <div></div> <div> <div></div> <div>65%</div> <div>25%</div> <div>5%</div> <div>• •</div> </div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4755 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 Phosphoribosylformylglycinamide synthase II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	580	Total	C	N	O	S	0	0	0
			4473	2849	764	842	18			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	A	1	Total	C	N	O	P	0	1
			45	11	5	23	6		

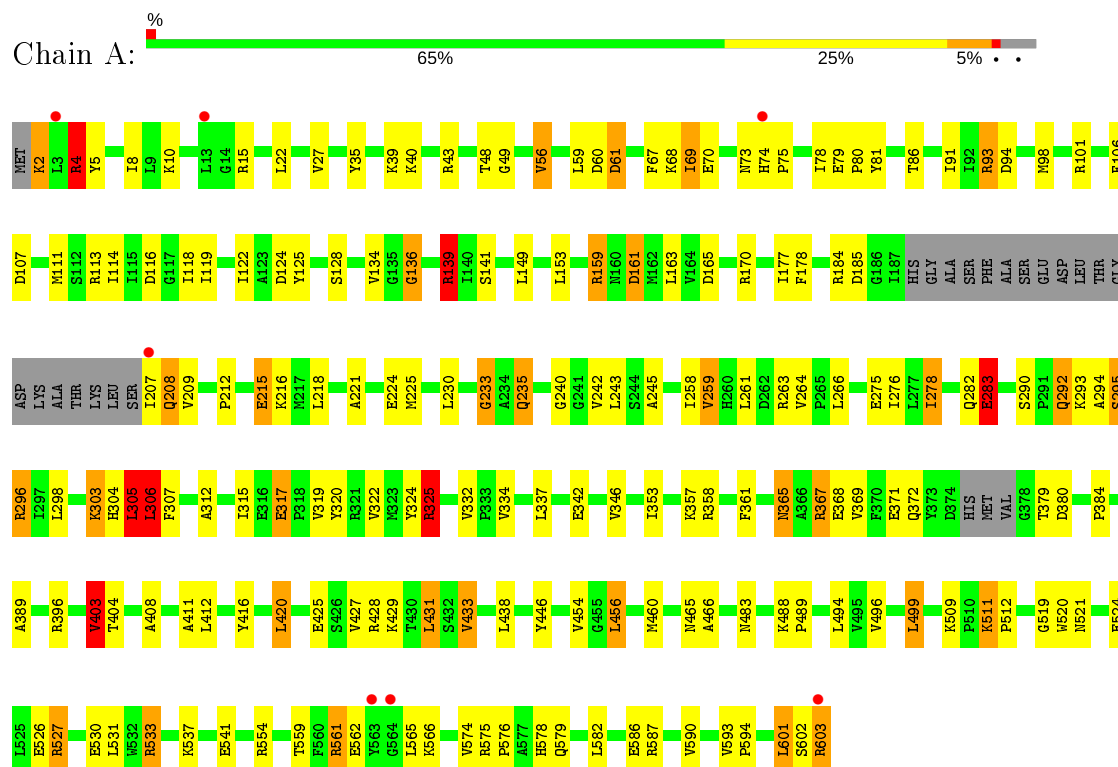
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	204	Total 204	O 204	0	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Phosphoribosylformylglycinamide synthase II



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.87Å 71.53Å 137.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.73 – 2.52 31.72 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (31.73-2.52) 92.7 (31.72-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.86 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.200 , 0.253 0.180 , 0.185	Depositor DCC
$R_{free}$ test set	940 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.6	Xtriage
Anisotropy	0.444	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 47.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4755	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.52% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.73	0/4562	1.34	43/6190 (0.7%)

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

There are no bond length outliers.

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	139	ARG	NE-CZ-NH2	-19.83	110.39	120.30
1	A	139	ARG	NE-CZ-NH1	13.40	127.00	120.30
1	A	59	LEU	CB-CG-CD2	-9.82	94.31	111.00
1	A	304	HIS	C-N-CA	9.27	144.87	121.70
1	A	403	VAL	CB-CA-C	-8.59	95.08	111.40
1	A	601	LEU	CB-CG-CD2	-8.48	96.59	111.00
1	A	304	HIS	CA-C-N	8.22	135.29	117.20
1	A	94	ASP	CB-CG-OD1	8.18	125.66	118.30
1	A	499	LEU	CA-CB-CG	8.05	133.81	115.30
1	A	98	MET	CG-SD-CE	7.92	112.87	100.20
1	A	325	ARG	NE-CZ-NH1	7.92	124.26	120.30
1	A	304	HIS	O-C-N	-7.59	110.56	122.70
1	A	304	HIS	N-CA-C	7.32	130.75	111.00
1	A	305	LEU	N-CA-CB	-7.24	95.93	110.40
1	A	428	ARG	NE-CZ-NH2	-7.13	116.74	120.30
1	A	60	ASP	CB-CG-OD1	7.11	124.70	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	412	LEU	CB-CG-CD2	-6.74	99.55	111.00
1	A	61	ASP	N-CA-CB	6.17	121.71	110.60
1	A	420	LEU	CB-CG-CD1	-6.17	100.51	111.00
1	A	296	ARG	NE-CZ-NH2	6.05	123.33	120.30
1	A	420	LEU	CB-CG-CD2	-5.90	100.97	111.00
1	A	283	GLU	CA-CB-CG	5.84	126.24	113.40
1	A	494	LEU	CB-CG-CD2	-5.79	101.16	111.00
1	A	161	ASP	CB-CG-OD1	5.75	123.48	118.30
1	A	431	LEU	CB-CG-CD2	-5.71	101.29	111.00
1	A	565	LEU	CB-CG-CD2	-5.67	101.35	111.00
1	A	159	ARG	NE-CZ-NH1	-5.67	117.47	120.30
1	A	403	VAL	CG1-CB-CG2	5.56	119.80	110.90
1	A	305	LEU	CB-CG-CD1	5.54	120.42	111.00
1	A	43	ARG	NE-CZ-NH2	-5.49	117.55	120.30
1	A	216	LYS	CD-CE-NZ	5.47	124.27	111.70
1	A	306	LEU	N-CA-C	5.41	125.61	111.00
1	A	337	LEU	CA-CB-CG	5.39	127.70	115.30
1	A	136	GLY	N-CA-C	-5.34	99.74	113.10
1	A	125	TYR	CB-CG-CD1	5.28	124.17	121.00
1	A	49	GLY	N-CA-C	-5.25	99.98	113.10
1	A	101	ARG	NE-CZ-NH1	5.23	122.92	120.30
1	A	185	ASP	CB-CG-OD1	5.21	122.99	118.30
1	A	4	ARG	NE-CZ-NH1	-5.20	117.70	120.30
1	A	56	VAL	CG1-CB-CG2	-5.19	102.60	110.90
1	A	263	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	A	233	GLY	N-CA-C	-5.11	100.33	113.10
1	A	61	ASP	CB-CG-OD1	-5.02	113.78	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	61	ASP	CA

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	4473	0	4510	176	0
2	A	2	0	0	0	0
3	A	76	0	18	2	0
4	A	204	0	0	8	0
All	All	4755	0	4528	176	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 19.

All (176) 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:208:GLN:HA	1:A:208:GLN:HE21	1.12	1.13
1:A:427:VAL:O	1:A:431:LEU:HD23	1.49	1.10
1:A:561:ARG:HH11	1:A:561:ARG:HG2	0.98	1.09
1:A:593:VAL:HG13	1:A:594:PRO:HD2	1.31	1.08
1:A:561:ARG:NH1	1:A:561:ARG:HG2	1.56	1.06
1:A:365:ASN:HD21	1:A:367:ARG:CB	1.71	1.01
1:A:40:LYS:HE3	1:A:342:GLU:OE1	1.62	0.98
1:A:602:SER:HB2	1:A:603:ARG:HD2	1.46	0.97
1:A:561:ARG:HH11	1:A:561:ARG:CG	1.76	0.97
1:A:365:ASN:HD21	1:A:367:ARG:HB2	1.30	0.97
1:A:601:LEU:N	1:A:601:LEU:HD23	1.81	0.94
1:A:208:GLN:HE21	1:A:208:GLN:CA	1.81	0.93
1:A:431:LEU:N	1:A:431:LEU:HD22	1.79	0.93
1:A:208:GLN:HA	1:A:208:GLN:NE2	1.86	0.90
1:A:601:LEU:H	1:A:601:LEU:HD23	1.33	0.90
1:A:593:VAL:HG13	1:A:594:PRO:CD	2.03	0.88
1:A:431:LEU:CD2	1:A:431:LEU:N	2.39	0.86
1:A:261:LEU:HD21	1:A:322:VAL:HG13	1.58	0.84
1:A:420:LEU:HD12	1:A:466:ALA:HB2	1.60	0.82
1:A:243:LEU:HD22	1:A:278:ILE:HD11	1.62	0.82
1:A:170:ARG:HD2	4:A:1120:HOH:O	1.80	0.81
1:A:379:THR:HG22	1:A:380:ASP:H	1.45	0.81
1:A:79:GLU:OE2	1:A:207:ILE:HG12	1.80	0.80
1:A:208:GLN:NE2	1:A:209:VAL:H	1.79	0.80
1:A:243:LEU:CD2	1:A:278:ILE:HD11	2.12	0.80
1:A:379:THR:HG22	1:A:380:ASP:N	1.97	0.80
1:A:261:LEU:CD2	1:A:322:VAL:HG13	2.14	0.77
1:A:488:LYS:HD3	1:A:489:PRO:HD2	1.68	0.75
1:A:358:ARG:NH2	1:A:576:PRO:HA	2.03	0.73
1:A:384:PRO:HD3	4:A:1111:HOH:O	1.87	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:320:TYR:HB2	1:A:334:VAL:HG23	1.70	0.72
1:A:261:LEU:HD12	1:A:276:ILE:HG22	1.71	0.71
1:A:431:LEU:CD2	1:A:431:LEU:H	2.03	0.71
1:A:379:THR:CG2	1:A:380:ASP:H	2.04	0.70
1:A:165:ASP:O	1:A:233:GLY:HA2	1.90	0.70
1:A:365:ASN:HD21	1:A:367:ARG:HB3	1.55	0.69
1:A:524:GLU:H	1:A:579:GLN:NE2	1.91	0.69
1:A:527:ARG:HE	1:A:579:GLN:NE2	1.92	0.67
1:A:294:ALA:O	1:A:298:LEU:HG	1.95	0.67
1:A:365:ASN:ND2	1:A:367:ARG:CB	2.52	0.67
1:A:184:ARG:NH1	1:A:275:GLU:OE1	2.27	0.66
1:A:365:ASN:HD22	1:A:365:ASN:C	1.98	0.66
1:A:520:TRP:CH2	1:A:593:VAL:HG22	2.30	0.66
1:A:367:ARG:HG3	1:A:367:ARG:HH11	1.60	0.66
1:A:601:LEU:CD2	1:A:601:LEU:N	2.58	0.65
1:A:379:THR:CG2	1:A:380:ASP:N	2.62	0.61
1:A:425:GLU:O	1:A:429:LYS:HG3	1.99	0.61
1:A:431:LEU:H	1:A:431:LEU:HD23	1.65	0.61
1:A:574:VAL:HG22	1:A:578:HIS:HB3	1.82	0.61
1:A:139:ARG:HG3	1:A:361:PHE:CD2	2.37	0.60
1:A:208:GLN:HE21	1:A:209:VAL:H	1.49	0.59
1:A:159:ARG:NH2	1:A:161:ASP:OD2	2.32	0.59
1:A:416:TYR:OH	1:A:465:ASN:ND2	2.24	0.59
1:A:4:ARG:HE	1:A:5:TYR:HE2	1.50	0.59
1:A:404:THR:HA	1:A:496:VAL:O	2.04	0.58
1:A:295:SER:HB3	4:A:1253:HOH:O	2.04	0.57
1:A:320:TYR:HB2	1:A:334:VAL:CG2	2.34	0.57
1:A:488:LYS:HD3	1:A:489:PRO:CD	2.33	0.57
1:A:367:ARG:NH1	1:A:367:ARG:HG3	2.18	0.57
1:A:208:GLN:HE21	1:A:209:VAL:N	2.01	0.57
1:A:511:LYS:NZ	1:A:586:GLU:HG3	2.19	0.57
1:A:106:PHE:HB2	1:A:153:LEU:HB3	1.87	0.56
1:A:264:VAL:O	1:A:266:LEU:CD1	2.53	0.56
1:A:208:GLN:NE2	1:A:209:VAL:N	2.50	0.56
1:A:365:ASN:ND2	1:A:365:ASN:C	2.57	0.56
1:A:561:ARG:CG	1:A:561:ARG:NH1	2.40	0.56
1:A:221:ALA:O	1:A:225:MET:HG3	2.06	0.55
1:A:389:ALA:HA	1:A:403:VAL:HG13	1.88	0.55
1:A:139:ARG:HG2	1:A:361:PHE:HE2	1.71	0.55
1:A:243:LEU:HD22	1:A:278:ILE:CD1	2.32	0.55
1:A:261:LEU:HD12	1:A:276:ILE:CG2	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:GLU:OE2	1:A:303:LYS:NZ	2.38	0.55
1:A:139:ARG:HG2	1:A:361:PHE:CE2	2.42	0.55
1:A:521:ASN:HA	1:A:574:VAL:HG23	1.88	0.55
1:A:593:VAL:CG1	1:A:594:PRO:CD	2.81	0.54
1:A:80:PRO:HB3	1:A:118:ILE:HG13	1.87	0.54
1:A:264:VAL:O	1:A:266:LEU:HD12	2.08	0.54
1:A:35:TYR:O	1:A:39:LYS:HG2	2.07	0.54
1:A:527:ARG:HE	1:A:579:GLN:HE22	1.55	0.54
1:A:139:ARG:HD3	4:A:1067:HOH:O	2.07	0.54
1:A:15:ARG:HH11	1:A:15:ARG:HG2	1.74	0.53
1:A:261:LEU:HD21	1:A:322:VAL:CG1	2.36	0.53
1:A:603:ARG:NE	4:A:1127:HOH:O	2.42	0.53
1:A:290:SER:HB3	1:A:292:GLN:OE1	2.08	0.53
1:A:261:LEU:CD2	1:A:322:VAL:CG1	2.87	0.52
1:A:524:GLU:H	1:A:579:GLN:HE22	1.57	0.52
1:A:56:VAL:HG11	1:A:163:LEU:HD22	1.92	0.52
1:A:118:ILE:O	1:A:122:ILE:HG12	2.10	0.52
1:A:177:ILE:HD13	1:A:242:VAL:HG22	1.91	0.52
1:A:365:ASN:ND2	1:A:367:ARG:HB3	2.21	0.52
1:A:86:THR:O	1:A:86:THR:HG22	2.11	0.51
1:A:317:GLU:O	1:A:319:VAL:N	2.43	0.51
1:A:603:ARG:HA	1:A:603:ARG:NE	2.26	0.51
1:A:243:LEU:HD23	1:A:278:ILE:HD11	1.88	0.51
1:A:139:ARG:HG2	4:A:1069:HOH:O	2.12	0.50
1:A:40:LYS:HG3	4:A:1113:HOH:O	2.12	0.50
1:A:128:SER:CB	1:A:212:PRO:HB2	2.42	0.50
1:A:68:LYS:HE2	3:A:1066[A]:ATP:O1B	2.11	0.49
1:A:114:ILE:HG23	1:A:119:ILE:HD12	1.93	0.49
1:A:208:GLN:CA	1:A:208:GLN:NE2	2.55	0.49
1:A:389:ALA:HB2	1:A:403:VAL:HG13	1.93	0.49
1:A:74:HIS:HB3	1:A:75:PRO:HD3	1.94	0.49
1:A:27:VAL:HG11	1:A:240:GLY:HA2	1.94	0.49
1:A:78:ILE:HG22	1:A:79:GLU:HG3	1.94	0.49
1:A:367:ARG:CG	1:A:367:ARG:HH11	2.26	0.48
1:A:114:ILE:CG2	1:A:119:ILE:HD12	2.43	0.48
1:A:2:LYS:O	1:A:2:LYS:HG3	2.14	0.48
1:A:533:ARG:HH11	1:A:533:ARG:HG2	1.77	0.48
1:A:258:ILE:CD1	1:A:315:ILE:HG21	2.44	0.48
1:A:10:LYS:HE2	1:A:10:LYS:HB2	1.79	0.48
1:A:70:GLU:OE2	3:A:1066[A]:ATP:O1G	2.31	0.48
1:A:365:ASN:ND2	1:A:367:ARG:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:SER:HB2	1:A:212:PRO:HB2	1.94	0.47
1:A:389:ALA:CA	1:A:403:VAL:HG13	2.44	0.47
1:A:259:VAL:HB	1:A:312:ALA:HB2	1.96	0.47
1:A:69:ILE:O	1:A:69:ILE:HG23	2.14	0.47
1:A:365:ASN:ND2	1:A:367:ARG:H	2.12	0.47
1:A:70:GLU:HB2	1:A:91:ILE:HD13	1.95	0.47
1:A:530:GLU:OE2	1:A:533:ARG:HD3	2.15	0.47
1:A:521:ASN:ND2	4:A:1201:HOH:O	2.47	0.47
1:A:365:ASN:ND2	1:A:367:ARG:N	2.63	0.46
1:A:389:ALA:CB	1:A:403:VAL:HG13	2.44	0.46
1:A:93:ARG:HD3	1:A:215:GLU:OE1	2.16	0.46
1:A:139:ARG:CG	1:A:361:PHE:CE2	2.98	0.46
1:A:261:LEU:HD23	1:A:322:VAL:HG13	1.97	0.46
1:A:353:ILE:O	1:A:353:ILE:HG23	2.15	0.46
1:A:561:ARG:HH22	1:A:566:LYS:HG2	1.82	0.45
1:A:559:THR:O	1:A:562:GLU:HB2	2.17	0.45
1:A:119:ILE:HD13	1:A:369:VAL:CG1	2.47	0.45
1:A:81:TYR:OH	1:A:124:ASP:OD2	2.27	0.45
1:A:139:ARG:HG3	1:A:361:PHE:HD2	1.81	0.45
1:A:128:SER:HB2	1:A:212:PRO:CB	2.46	0.45
1:A:159:ARG:HH21	1:A:161:ASP:CG	2.19	0.45
1:A:230:LEU:HA	1:A:293:LYS:HD3	1.99	0.45
1:A:134:VAL:CG1	1:A:134:VAL:O	2.65	0.45
1:A:533:ARG:HH11	1:A:533:ARG:CG	2.30	0.44
1:A:511:LYS:HZ1	1:A:586:GLU:HG3	1.83	0.44
1:A:114:ILE:HG23	1:A:119:ILE:CD1	2.47	0.44
1:A:368:GLU:OE2	1:A:554:ARG:NH2	2.51	0.44
1:A:111:MET:HB3	1:A:113:ARG:O	2.17	0.44
1:A:324:TYR:O	1:A:325:ARG:HB2	2.18	0.44
1:A:446:TYR:O	1:A:483:ASN:HB2	2.17	0.44
1:A:537:LYS:NZ	1:A:541:GLU:OE2	2.31	0.44
1:A:574:VAL:HG22	1:A:578:HIS:CB	2.47	0.44
1:A:433:VAL:HG13	1:A:433:VAL:O	2.18	0.44
1:A:531:LEU:HD22	1:A:579:GLN:HB3	1.98	0.43
1:A:261:LEU:N	1:A:261:LEU:HD22	2.32	0.43
1:A:91:ILE:HD12	1:A:91:ILE:HA	1.81	0.43
1:A:235:GLN:HG2	1:A:245:ALA:HA	2.00	0.43
1:A:511:LYS:HZ3	1:A:586:GLU:HG3	1.84	0.43
1:A:15:ARG:HG2	1:A:15:ARG:NH1	2.34	0.43
1:A:527:ARG:HH21	1:A:579:GLN:HE21	1.67	0.42
1:A:178:PHE:CE2	1:A:218:LEU:HD12	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:GLY:O	1:A:243:LEU:HB3	2.20	0.42
1:A:456:LEU:HD22	1:A:460:MET:HG2	2.01	0.42
1:A:184:ARG:HH11	1:A:275:GLU:CD	2.22	0.42
1:A:298:LEU:HA	1:A:298:LEU:HD23	1.78	0.42
1:A:282:GLN:HB2	1:A:283:GLU:OE2	2.20	0.41
1:A:346:VAL:HG11	1:A:454:VAL:HG22	2.02	0.41
1:A:519:GLY:HA2	1:A:593:VAL:CG1	2.50	0.41
1:A:306:LEU:H	1:A:306:LEU:HG	1.56	0.41
1:A:4:ARG:O	1:A:8:ILE:HG13	2.19	0.41
1:A:69:ILE:HA	1:A:153:LEU:HA	2.02	0.41
1:A:73:ASN:OD1	1:A:149:LEU:HA	2.20	0.41
1:A:107:ASP:O	1:A:136:GLY:HA3	2.21	0.41
1:A:305:LEU:CD1	1:A:305:LEU:N	2.83	0.41
1:A:27:VAL:HG11	1:A:240:GLY:CA	2.51	0.41
1:A:208:GLN:HE21	1:A:208:GLN:C	2.24	0.41
1:A:590:VAL:HG12	1:A:590:VAL:O	2.21	0.41
1:A:178:PHE:HA	1:A:307:PHE:O	2.21	0.41
1:A:511:LYS:HB2	1:A:512:PRO:HD2	2.02	0.41
1:A:582:LEU:HA	1:A:582:LEU:HD23	1.80	0.41
1:A:367:ARG:NH2	1:A:562:GLU:OE2	2.55	0.40
1:A:134:VAL:HG12	1:A:134:VAL:O	2.22	0.40
1:A:575:ARG:O	1:A:576:PRO:C	2.60	0.40
1:A:408:ALA:HA	1:A:411:ALA:HB3	2.04	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	574/603 (95%)	541 (94%)	31 (5%)	2 (0%)	41 59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	306	LEU
1	A	325	ARG

### 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	484/502 (96%)	441 (91%)	43 (9%)	9 18

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	4	ARG
1	A	22	LEU
1	A	48	THR
1	A	61	ASP
1	A	67	PHE
1	A	69	ILE
1	A	93	ARG
1	A	116	ASP
1	A	139	ARG
1	A	141	SER
1	A	208	GLN
1	A	215	GLU
1	A	235	GLN
1	A	259	VAL
1	A	278	ILE
1	A	283	GLU
1	A	292	GLN
1	A	295	SER
1	A	296	ARG
1	A	303	LYS
1	A	305	LEU
1	A	317	GLU
1	A	332	VAL
1	A	357	LYS

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Mol	Chain	Res	Type
1	A	365	ASN
1	A	367	ARG
1	A	371	GLU
1	A	372	GLN
1	A	396	ARG
1	A	403	VAL
1	A	433	VAL
1	A	438	LEU
1	A	456	LEU
1	A	499	LEU
1	A	509	LYS
1	A	511	LYS
1	A	526	GLU
1	A	527	ARG
1	A	533	ARG
1	A	561	ARG
1	A	587	ARG
1	A	603	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	HIS
1	A	127	ASN
1	A	208	GLN
1	A	339	ASN
1	A	365	ASN
1	A	465	ASN
1	A	486	GLN
1	A	579	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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$
3	ATP	A	1066[B]	2	26,33,33	0.94	2 (7%)	31,52,52	2.10	10 (32%)
3	ATP	A	1066[A]	-	26,33,33	0.93	2 (7%)	31,52,52	1.78	4 (12%)
3	ATP	A	1065	2	26,33,33	0.93	1 (3%)	31,52,52	1.64	7 (22%)

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	ATP	A	1066[B]	2	-	2/18/38/38	0/3/3/3
3	ATP	A	1066[A]	-	-	7/18/38/38	0/3/3/3
3	ATP	A	1065	2	-	3/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1066[B]	ATP	C5-C4	2.53	1.47	1.40
3	A	1066[A]	ATP	C5-C4	2.53	1.47	1.40
3	A	1065	ATP	C5-C4	2.36	1.47	1.40
3	A	1066[B]	ATP	O4'-C1'	2.06	1.43	1.41
3	A	1066[A]	ATP	O4'-C1'	2.06	1.43	1.41

All (21) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1066[B]	ATP	C4-C5-N7	-6.75	102.36	109.40
3	A	1066[A]	ATP	C4-C5-N7	-6.75	102.36	109.40
3	A	1066[B]	ATP	PA-O3A-PB	-4.96	115.81	132.83
3	A	1065	ATP	C2-N1-C6	3.94	125.50	118.75
3	A	1065	ATP	N3-C2-N1	-3.49	123.22	128.68
3	A	1065	ATP	N6-C6-N1	3.28	125.38	118.57
3	A	1066[B]	ATP	C5-C6-N6	3.13	125.11	120.35
3	A	1066[A]	ATP	C5-C6-N6	3.13	125.11	120.35
3	A	1066[A]	ATP	PB-O3B-PG	-2.90	122.89	132.83
3	A	1065	ATP	C5-C6-N1	-2.86	113.86	120.35
3	A	1066[B]	ATP	O5'-C5'-C4'	-2.78	99.42	108.99
3	A	1066[B]	ATP	O2G-PG-O3B	-2.72	95.53	104.64
3	A	1065	ATP	O2B-PB-O1B	2.57	124.95	112.24
3	A	1066[B]	ATP	O3G-PG-O2G	2.48	117.12	107.64
3	A	1065	ATP	O4'-C1'-C2'	-2.37	103.46	106.93
3	A	1066[B]	ATP	O4'-C1'-C2'	-2.13	103.81	106.93
3	A	1066[A]	ATP	O4'-C1'-C2'	-2.13	103.81	106.93
3	A	1065	ATP	O2'-C2'-C1'	2.11	118.66	110.85
3	A	1066[B]	ATP	O2A-PA-O1A	2.03	122.29	112.24
3	A	1066[B]	ATP	O2B-PB-O1B	2.01	122.20	112.24
3	A	1066[B]	ATP	PB-O3B-PG	-2.01	125.92	132.83

There are no chirality outliers.

All (12) torsion outliers are listed below:

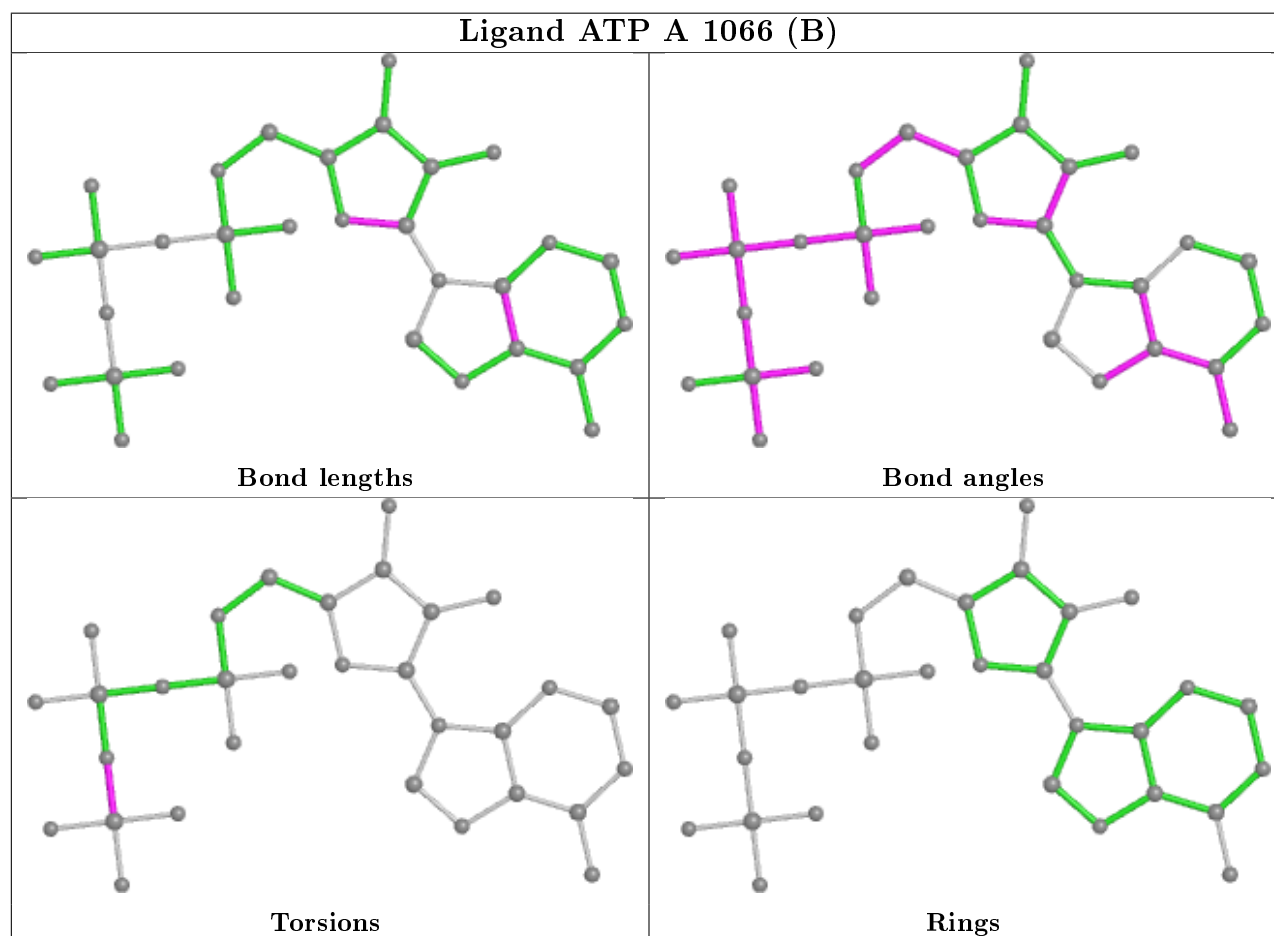
Mol	Chain	Res	Type	Atoms
3	A	1066[B]	ATP	PB-O3B-PG-O3G
3	A	1066[A]	ATP	PB-O3B-PG-O3G
3	A	1066[A]	ATP	C5'-O5'-PA-O1A
3	A	1065	ATP	PB-O3B-PG-O2G
3	A	1066[A]	ATP	C3'-C4'-C5'-O5'
3	A	1066[A]	ATP	O4'-C4'-C5'-O5'
3	A	1066[A]	ATP	PB-O3A-PA-O5'
3	A	1065	ATP	PB-O3B-PG-O3G
3	A	1066[B]	ATP	PB-O3B-PG-O1G
3	A	1066[A]	ATP	PB-O3A-PA-O2A
3	A	1065	ATP	PB-O3B-PG-O1G
3	A	1066[A]	ATP	C5'-O5'-PA-O3A

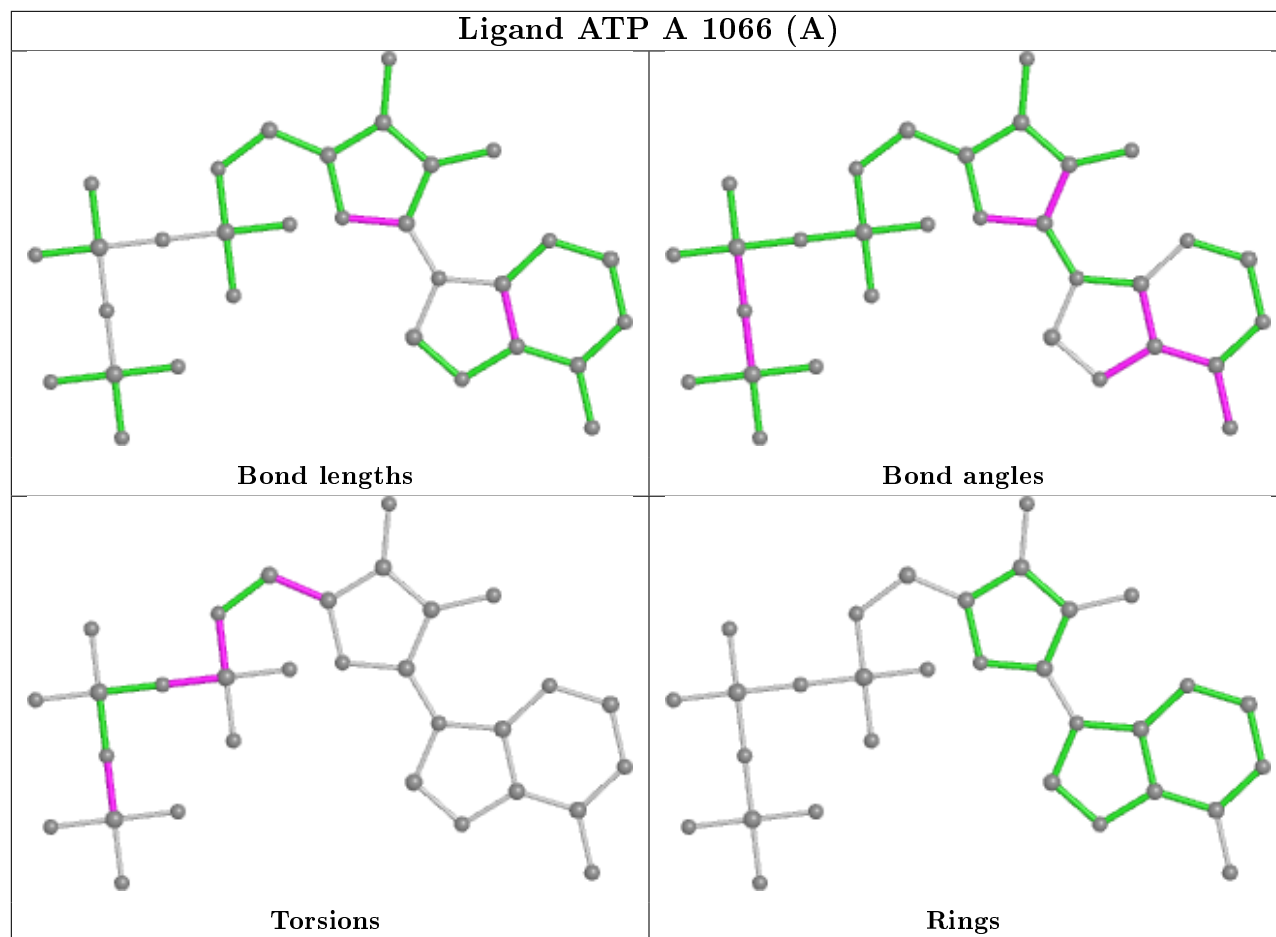
There are no ring outliers.

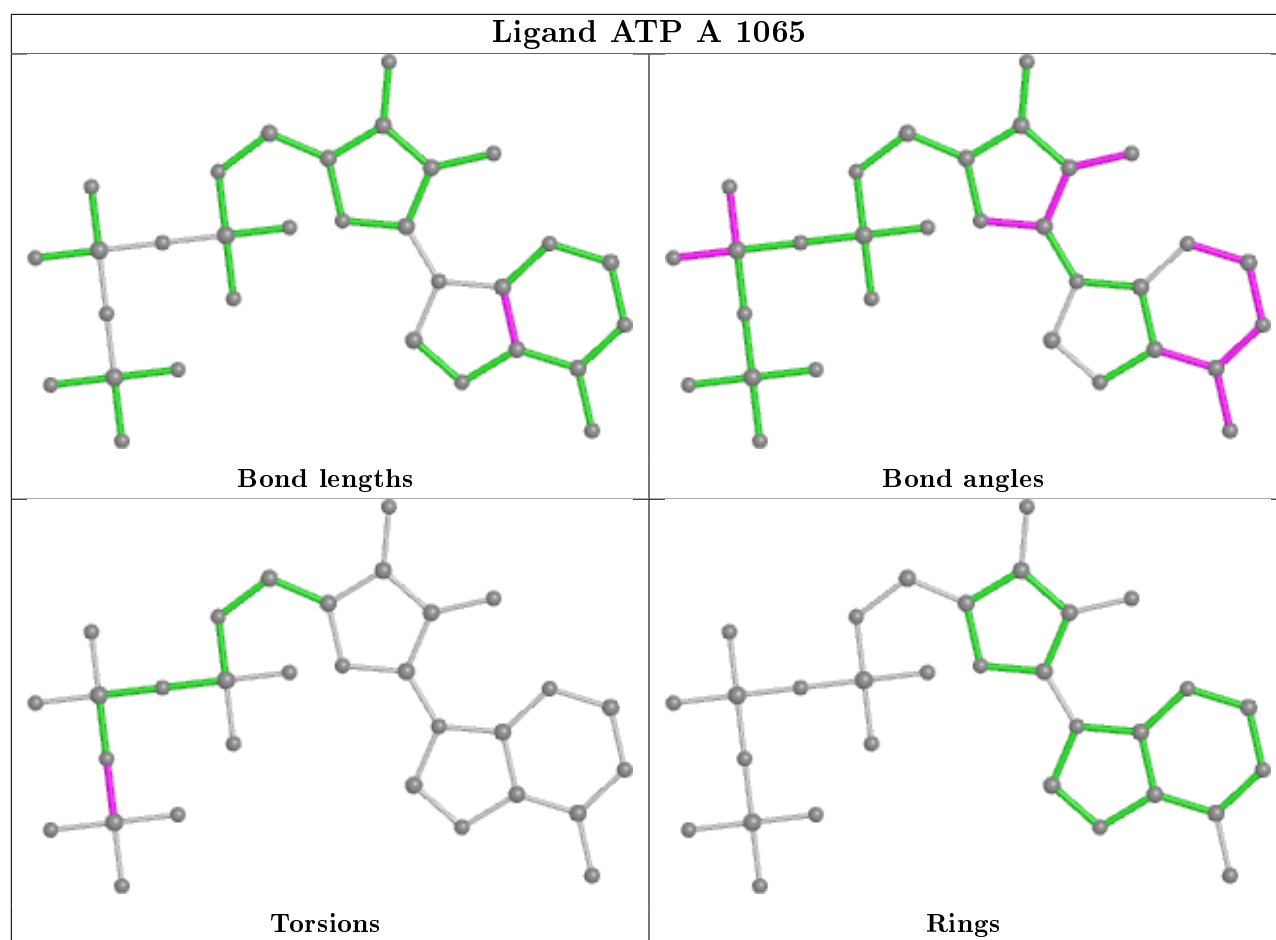
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1066[A]	ATP	2	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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	580/603 (96%)	-0.38	7 (1%) 79 81	21, 38, 62, 89	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	207	ILE	2.8
1	A	74	HIS	2.6
1	A	603	ARG	2.4
1	A	3	LEU	2.2
1	A	563	TYR	2.2
1	A	13	LEU	2.1
1	A	564	GLY	2.0

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

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

### 6.3 Carbohydrates ⓘ

There are no carbohydrates 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	MG	A	903	1/1	0.85	0.23	29,29,29,29	0

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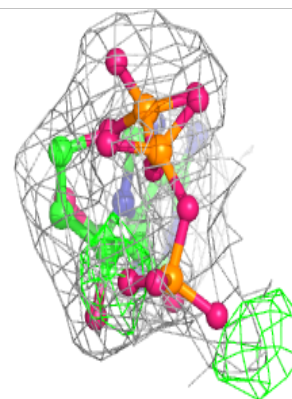
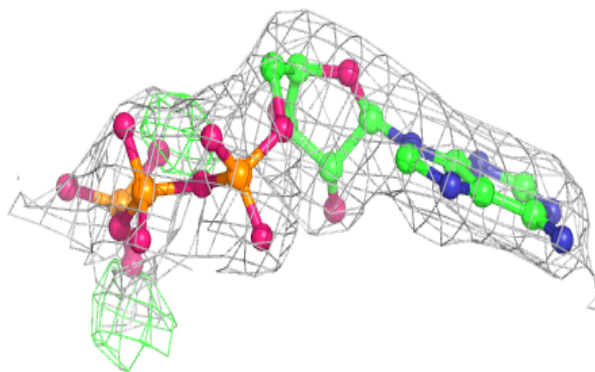
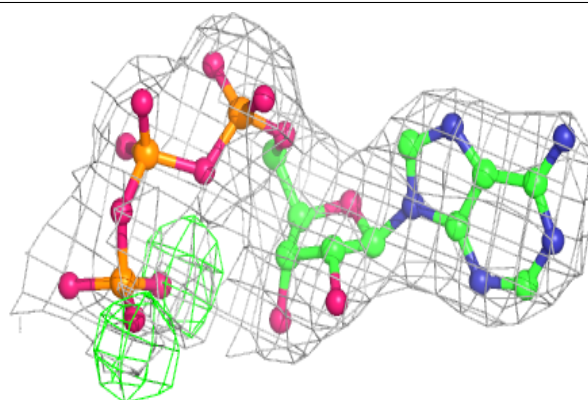
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MG	A	904	1/1	0.86	0.34	54,54,54,54	0
3	ATP	A	1066[B]	31/31	0.90	0.20	34,49,56,57	14
3	ATP	A	1066[A]	31/31	0.90	0.20	34,49,67,68	14
3	ATP	A	1065	31/31	0.98	0.15	26,30,33,34	0

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.

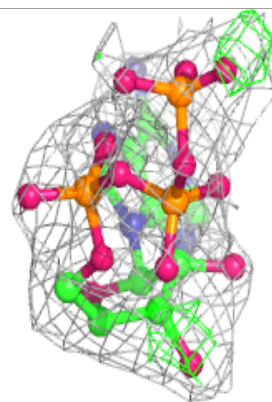
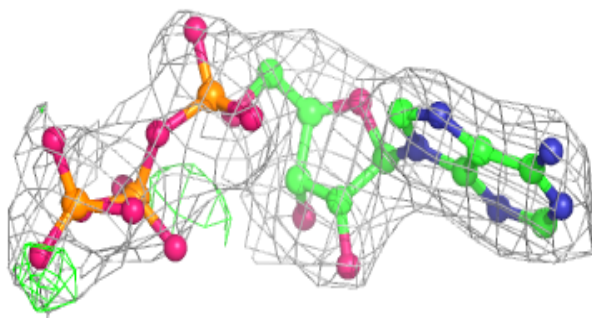
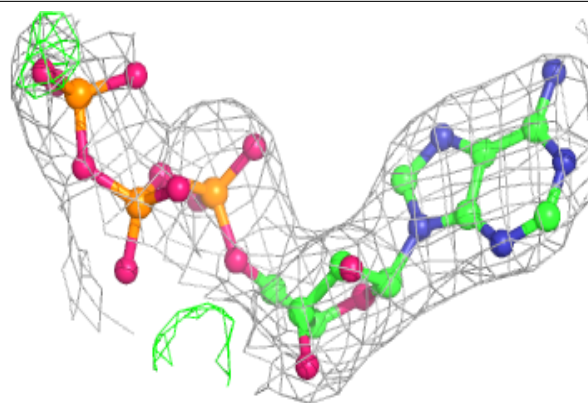
**Electron density around ATP A 1066 (B):**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

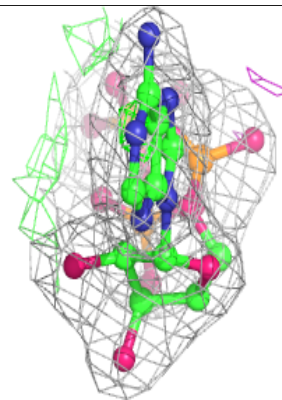
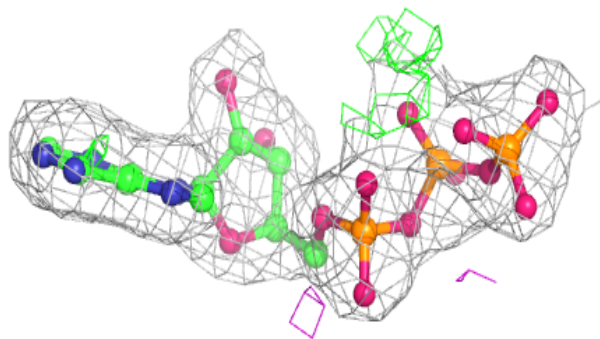
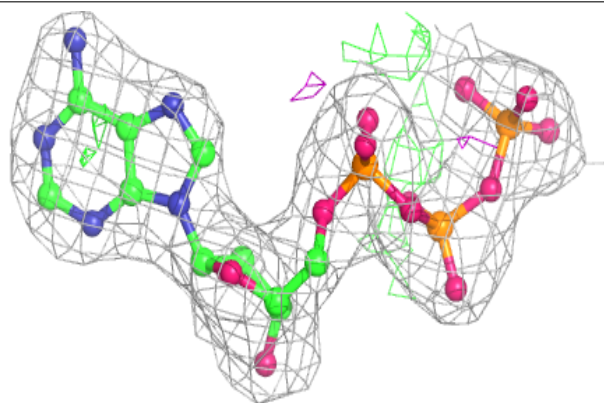


**Electron density around ATP A 1066 (A):**

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

**Electron density around ATP A 1065:**

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



## 6.5 Other polymers ⓘ

There are no such residues in this entry.