



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 22, 2025 – 01:53 pm BST

PDB ID : 9GUC / pdb_00009guc
Title : Adhiron-mediated Identification of a Novel and Selective Allosteric Pocket in Aurora Kinase A
Authors : Roberts, J.P.; Miles, J.A.; Blinkhorne, F.; Gaule, T.G.; Bayliss, R.W.; Johnson, C.A.; Tomlinson, D.C.
Deposited on : 2024-09-19
Resolution : 2.10 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.46

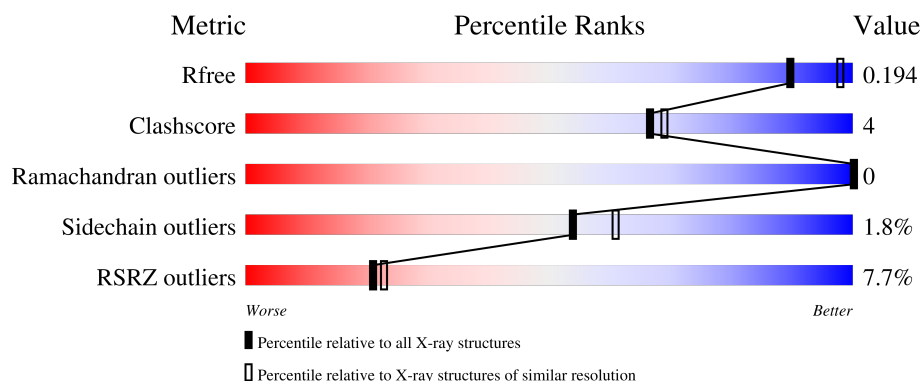
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.10 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}	164625	6234 (2.10-2.10)
Clashscore	180529	6893 (2.10-2.10)
Ramachandran outliers	177936	6839 (2.10-2.10)
Sidechain outliers	177891	6840 (2.10-2.10)
RSRZ outliers	164620	6234 (2.10-2.10)

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	285	
2	B	100	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5699 atoms, of which 2798 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 Aurora kinase A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	256	Total	C	H	N	O	S	66	1	0
			4216	1349	2123	368	371	5			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	119	GLY	-	expression tag	UNP O14965
A	120	ALA	-	expression tag	UNP O14965
A	121	MET	-	expression tag	UNP O14965
A	290	ALA	CYS	engineered mutation	UNP O14965
A	393	ALA	CYS	engineered mutation	UNP O14965

- Molecule 2 is a protein called Affimer (JR-Aff7).

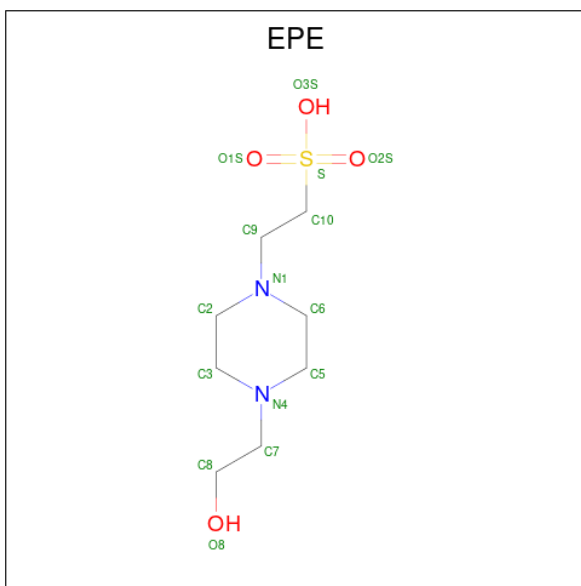
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	82	Total	C	H	N	O	S	31	0	0
			1280	424	633	106	115	2			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



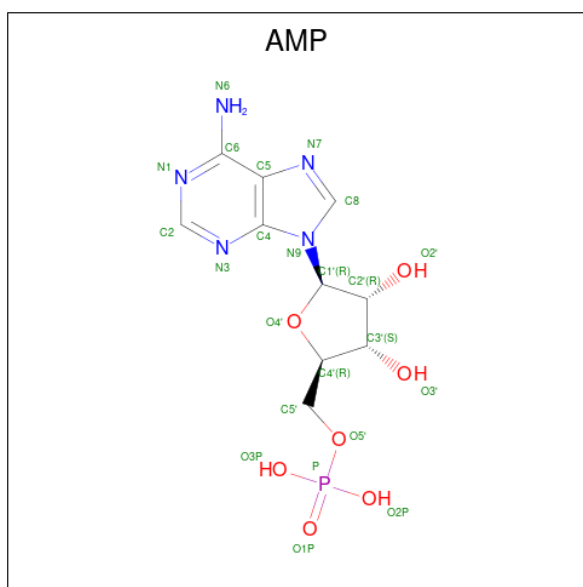
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	P	
			39	10	12	5	10	2	

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	S	
			33	8	18	2	4	1	

- Molecule 5 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	P	
			35	10	12	5	7	1	2
									0

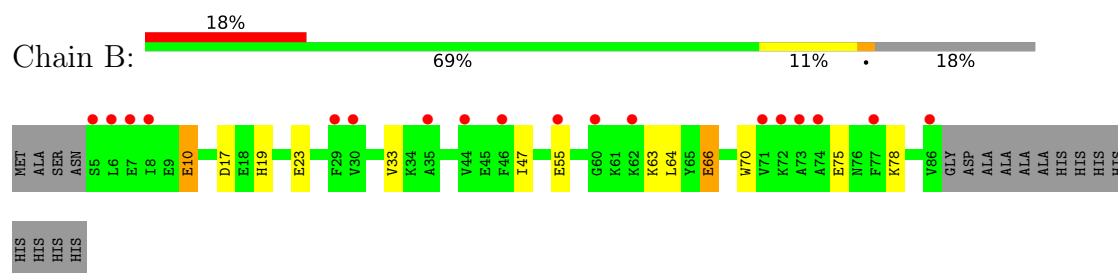
- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	88	Total	O		
			88	88	0	0
7	B	7	Total	O		
			7	7	0	0

- Molecule 1: Aurora kinase A



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	88.92Å 88.92Å 100.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.66 – 2.10 40.66 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.66-2.10) 99.8 (40.66-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.07 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.191 , 0.232 0.193 , 0.194	Depositor DCC
R_{free} test set	1307 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5699	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.18% 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

5.1 Standard geometry

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

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	0.64	0/2146	1.12	3/2898 (0.1%)
2	B	0.60	0/661	1.15	2/890 (0.2%)
All	All	0.63	0/2807	1.13	5/3788 (0.1%)

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	0	5

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	66	GLU	CB-CG-CD	6.63	123.86	112.60
1	A	389	LYS	CB-CA-C	5.92	117.22	108.87
1	A	337	THR	CA-CB-OG1	-5.61	101.18	109.60
2	B	17	ASP	CA-CB-CG	5.12	117.72	112.60
1	A	336	GLU	CB-CG-CD	5.06	121.21	112.60

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	251	ARG	Sidechain
1	A	343[A]	ARG	Sidechain
1	A	343[B]	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	371	ARG	Sidechain
1	A	375	ARG	Sidechain

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	2093	2123	2103	11	0
2	B	647	633	607	5	0
3	A	27	12	12	0	0
4	A	15	18	18	0	0
5	A	23	12	12	4	0
6	A	1	0	0	0	0
7	A	88	0	0	4	0
7	B	7	0	0	0	0
All	All	2901	2798	2752	20	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 4.

All (20) 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)
5:A:503:AMP:H3'	5:A:503:AMP:P	2.13	0.88
5:A:503:AMP:H3'	5:A:503:AMP:O2P	1.86	0.76
1:A:221:GLU:HG2	1:A:232:ARG:NH2	2.08	0.69
5:A:503:AMP:P	5:A:503:AMP:C3'	2.81	0.68
1:A:275:PHE:HD2	7:A:618:HOH:O	1.89	0.56
2:B:33:VAL:HG21	2:B:64:LEU:HD11	1.88	0.55
1:A:275:PHE:CD2	7:A:618:HOH:O	2.53	0.55
2:B:10:GLU:C	2:B:10:GLU:OE2	2.50	0.55
1:A:339:LYS:HE2	1:A:343[A]:ARG:NH1	2.23	0.53
5:A:503:AMP:H3'	5:A:503:AMP:O1P	2.11	0.51
2:B:55:GLU:HA	2:B:63:LYS:O	2.11	0.51
2:B:70:TRP:O	2:B:78:LYS:HA	2.12	0.49
2:B:19:HIS:CE1	2:B:23:GLU:HG3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:GLU:HG2	1:A:232:ARG:HH21	1.82	0.44
1:A:339:LYS:CE	1:A:343[A]:ARG:NH1	2.81	0.44
1:A:195:ARG:HD2	7:A:661:HOH:O	2.18	0.44
1:A:183:GLU:O	1:A:187:HIS:ND1	2.43	0.43
1:A:254:HIS:NE2	1:A:274:ASP:O	2.53	0.42
1:A:220:ARG:HD2	7:A:675:HOH:O	2.20	0.41
1:A:166:LYS:HA	1:A:169:LEU:HD12	2.03	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	253/285 (89%)	246 (97%)	7 (3%)	0	100	100
2	B	80/100 (80%)	77 (96%)	3 (4%)	0	100	100
All	All	333/385 (86%)	323 (97%)	10 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	221/249 (89%)	220 (100%)	1 (0%)	86	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	60/84 (71%)	56 (93%)	4 (7%)	13	11
All	All	281/333 (84%)	276 (98%)	5 (2%)	54	61

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	127	GLN
2	B	10	GLU
2	B	47	ILE
2	B	66	GLU
2	B	75	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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, 1 is 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	ADP	A	501	6	24,29,29	0.64	0	29,45,45	0.93	1 (3%)
4	EPE	A	502	-	15,15,15	0.55	0	18,20,20	0.85	1 (5%)
5	AMP	A	503	-	22,25,25	0.72	0	25,38,38	1.37	4 (16%)

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	ADP	A	501	6	-	4/12/32/32	0/3/3/3
4	EPE	A	502	-	-	4/9/19/19	0/1/1/1
5	AMP	A	503	-	-	6/6/26/26	0/3/3/3

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	503	AMP	C3'-C2'-C1'	-3.51	95.70	100.98
5	A	503	AMP	C2'-C3'-C4'	-2.49	97.81	102.64
3	A	501	ADP	C5-C6-N6	2.34	123.90	120.35
5	A	503	AMP	C5-C6-N6	2.31	123.86	120.35
4	A	502	EPE	O3S-S-C10	-2.21	102.20	105.77
5	A	503	AMP	C1'-N9-C4	-2.18	122.82	126.64

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	502	EPE	C9-C10-S-O1S
4	A	502	EPE	C9-C10-S-O2S
5	A	503	AMP	C5'-O5'-P-O1P
5	A	503	AMP	C5'-O5'-P-O2P
5	A	503	AMP	C5'-O5'-P-O3P
5	A	503	AMP	C4'-C5'-O5'-P
3	A	501	ADP	O4'-C4'-C5'-O5'
5	A	503	AMP	C3'-C4'-C5'-O5'
5	A	503	AMP	O4'-C4'-C5'-O5'
4	A	502	EPE	C9-C10-S-O3S
3	A	501	ADP	PB-O3A-PA-O1A

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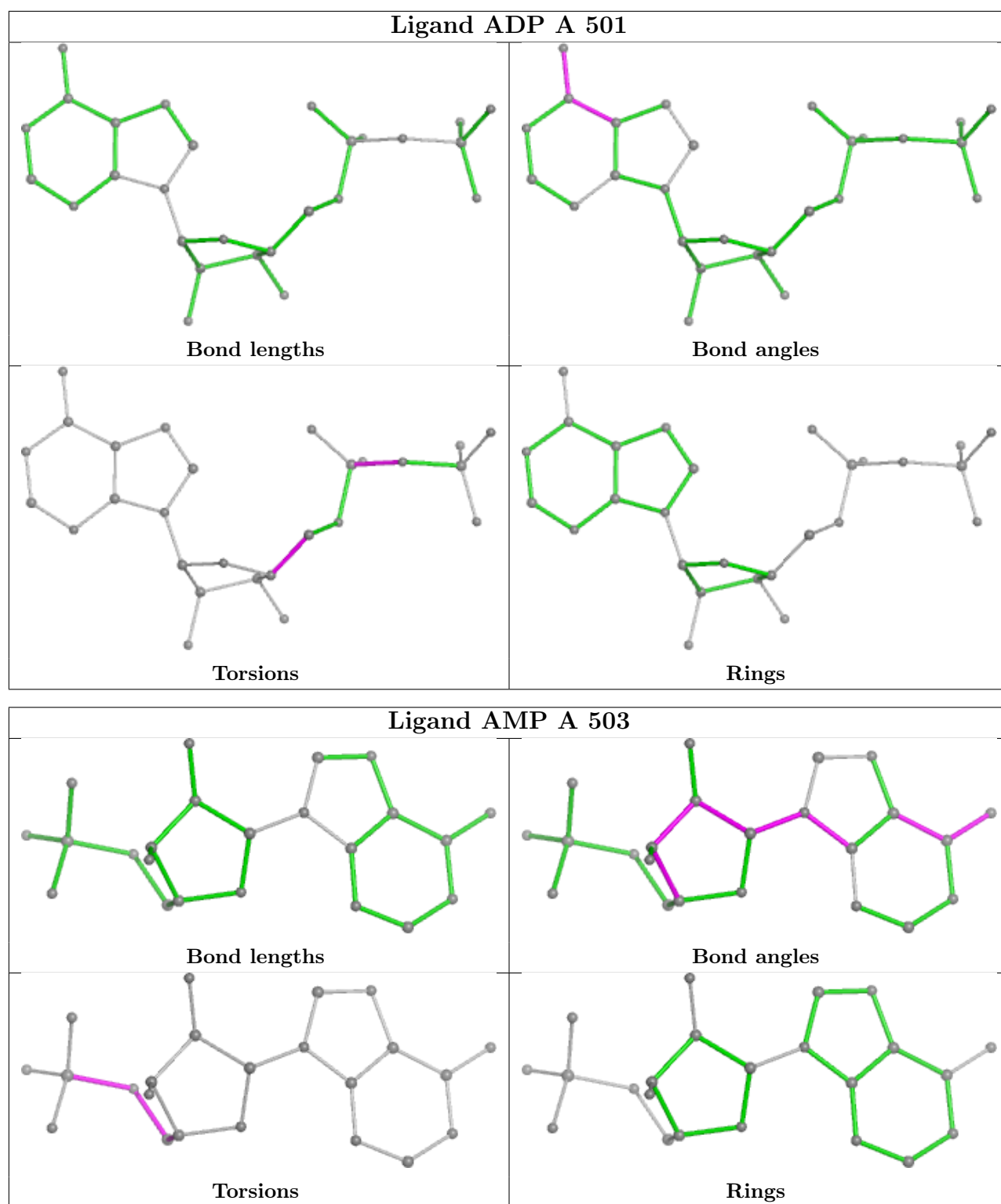
Mol	Chain	Res	Type	Atoms
3	A	501	ADP	C3'-C4'-C5'-O5'
4	A	502	EPE	S-C10-C9-N1
3	A	501	ADP	PB-O3A-PA-O2A

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	503	AMP	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	256/285 (89%)	-0.12	8 (3%) 51 53	17, 33, 76, 93	1 (0%)
2	B	82/100 (82%)	1.09	18 (21%) 3 3	30, 49, 64, 87	0
All	All	338/385 (87%)	0.17	26 (7%) 21 23	17, 38, 75, 93	1 (0%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	5	SER	5.1
2	B	73	ALA	4.3
2	B	74	ALA	4.0
1	A	275	PHE	3.3
1	A	288	THR	3.3
2	B	29	PHE	3.2
2	B	55	GLU	3.2
2	B	60	GLY	3.2
1	A	174	VAL	3.1
2	B	72	LYS	2.8
2	B	7	GLU	2.7
2	B	62	LYS	2.7
2	B	86	VAL	2.7
2	B	8	ILE	2.7
2	B	44	VAL	2.6
2	B	77	PHE	2.6
1	A	274	ASP	2.4
2	B	6	LEU	2.3
2	B	46	PHE	2.3
1	A	255	ARG	2.2
2	B	71	VAL	2.2
2	B	30	VAL	2.2
1	A	289	LEU	2.1
1	A	178	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	35	ALA	2.1
1	A	142	GLY	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

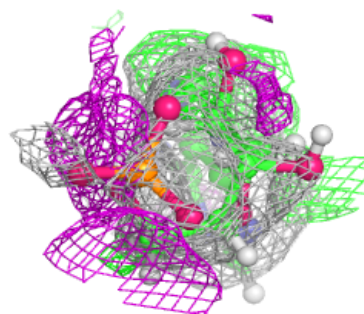
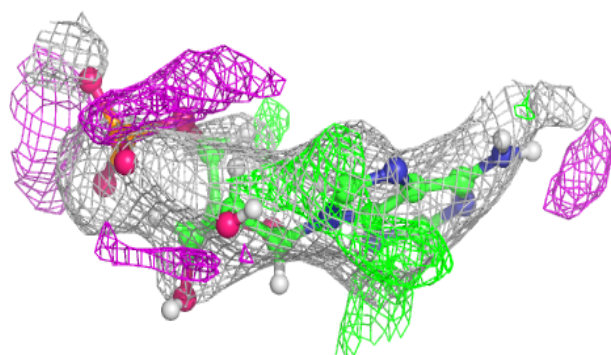
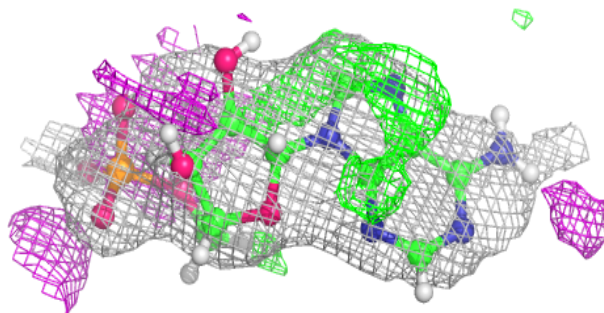
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	AMP	A	503	23/23	0.70	0.22	63,78,103,115	2
4	EPE	A	502	15/15	0.89	0.19	37,89,108,115	2
6	MG	A	504	1/1	0.91	0.10	66,66,66,66	0
3	ADP	A	501	27/27	0.92	0.08	28,46,81,84	2

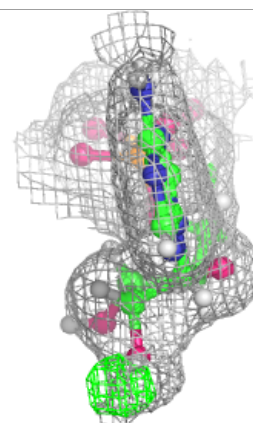
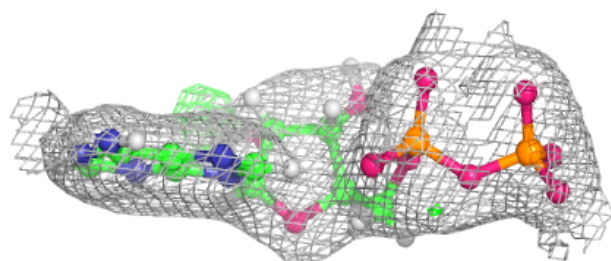
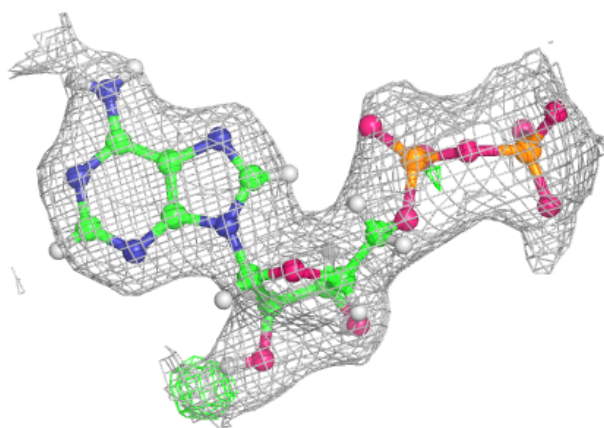
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around AMP A 503:

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

**Electron density around ADP A 501:**

$2mF_o-DF_c$ (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.