



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 02:41 AM BST

PDB ID : 5ORK  
Title : The crystal structure of CK2alpha in complex with compound 6  
Authors : Brear, P.; De Fusco, C.; Iegre, J.; Yoshida, M.; Mitchell, S.; Rossmann, M.; Carro, L.; Sore, H.; Hyvonen, M.; Spring, D.  
Deposited on : 2017-08-16  
Resolution : 2.14 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 : 2.13.1  
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) : 2.13.1

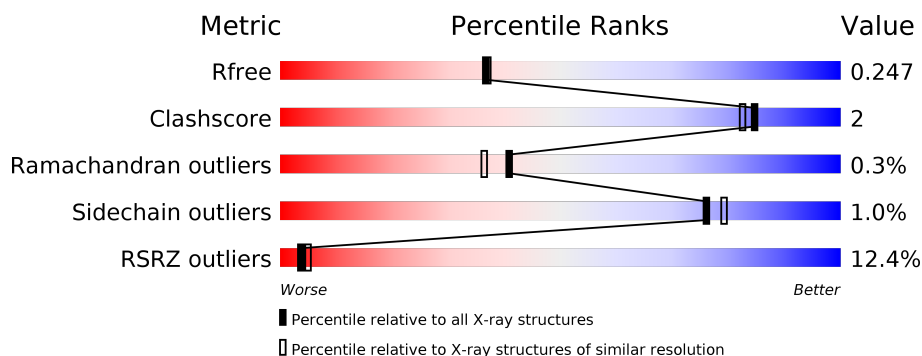
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.14 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	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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	352	<div> <div>4%</div> <div>84%</div> <div>8%</div> <div>8%</div> </div>
1	B	352	<div> <div>19%</div> <div>86%</div> <div>5%</div> <div>8%</div> </div>

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 5735 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 Casein kinase II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	323	Total	C	N	O	S	0	2	0
			2750	1762	483	494	11			
1	A	324	Total	C	N	O	S	0	2	0
			2757	1767	484	495	11			

There are 50 discrepancies between the modelled and reference sequences:

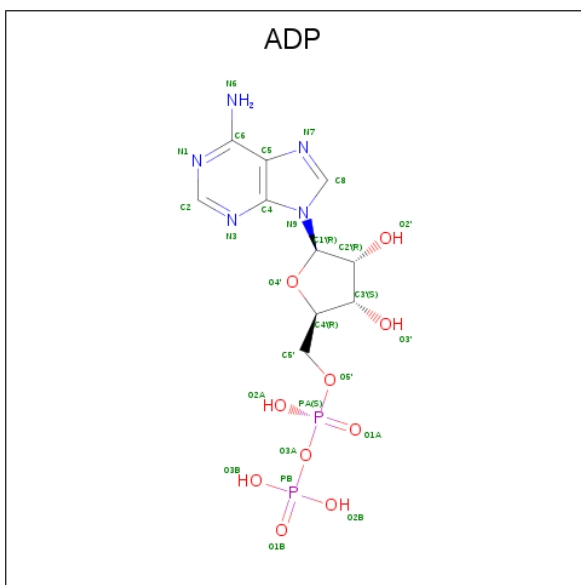
Chain	Residue	Modelled	Actual	Comment	Reference
B	-22	GLY	-	expression tag	UNP P68400
B	-21	SER	-	expression tag	UNP P68400
B	-20	MET	-	expression tag	UNP P68400
B	-19	ASP	-	expression tag	UNP P68400
B	-18	ILE	-	expression tag	UNP P68400
B	-17	GLU	-	expression tag	UNP P68400
B	-16	PHE	-	expression tag	UNP P68400
B	-15	ASP	-	expression tag	UNP P68400
B	-14	ASP	-	expression tag	UNP P68400
B	-13	ASP	-	expression tag	UNP P68400
B	-12	ALA	-	expression tag	UNP P68400
B	-11	ASP	-	expression tag	UNP P68400
B	-10	ASP	-	expression tag	UNP P68400
B	-9	ASP	-	expression tag	UNP P68400
B	-8	GLY	-	expression tag	UNP P68400
B	-7	SER	-	expression tag	UNP P68400
B	-6	GLY	-	expression tag	UNP P68400
B	-5	SER	-	expression tag	UNP P68400
B	-4	GLY	-	expression tag	UNP P68400
B	-3	SER	-	expression tag	UNP P68400
B	-2	GLY	-	expression tag	UNP P68400
B	-1	SER	-	expression tag	UNP P68400
B	0	GLY	-	expression tag	UNP P68400
B	1	SER	-	expression tag	UNP P68400
B	21	SER	ARG	engineered mutation	UNP P68400

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	GLY	-	expression tag	UNP P68400
A	-21	SER	-	expression tag	UNP P68400
A	-20	MET	-	expression tag	UNP P68400
A	-19	ASP	-	expression tag	UNP P68400
A	-18	ILE	-	expression tag	UNP P68400
A	-17	GLU	-	expression tag	UNP P68400
A	-16	PHE	-	expression tag	UNP P68400
A	-15	ASP	-	expression tag	UNP P68400
A	-14	ASP	-	expression tag	UNP P68400
A	-13	ASP	-	expression tag	UNP P68400
A	-12	ALA	-	expression tag	UNP P68400
A	-11	ASP	-	expression tag	UNP P68400
A	-10	ASP	-	expression tag	UNP P68400
A	-9	ASP	-	expression tag	UNP P68400
A	-8	GLY	-	expression tag	UNP P68400
A	-7	SER	-	expression tag	UNP P68400
A	-6	GLY	-	expression tag	UNP P68400
A	-5	SER	-	expression tag	UNP P68400
A	-4	GLY	-	expression tag	UNP P68400
A	-3	SER	-	expression tag	UNP P68400
A	-2	GLY	-	expression tag	UNP P68400
A	-1	SER	-	expression tag	UNP P68400
A	0	GLY	-	expression tag	UNP P68400
A	1	SER	-	expression tag	UNP P68400
A	21	SER	ARG	engineered mutation	UNP P68400

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).

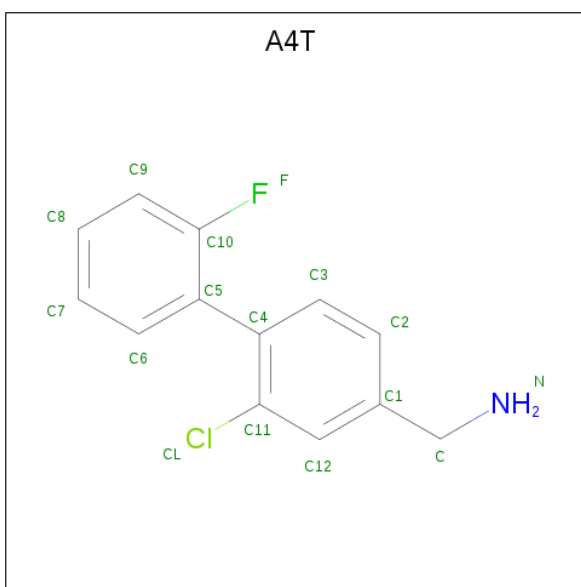


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

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

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

- Molecule 4 is [3-chloranyl-4-(2-fluorophenyl)phenyl]methanamine (three-letter code: A4T) (formula: C<sub>13</sub>H<sub>11</sub>ClFN) (labeled as "Ligand of Interest" by author).

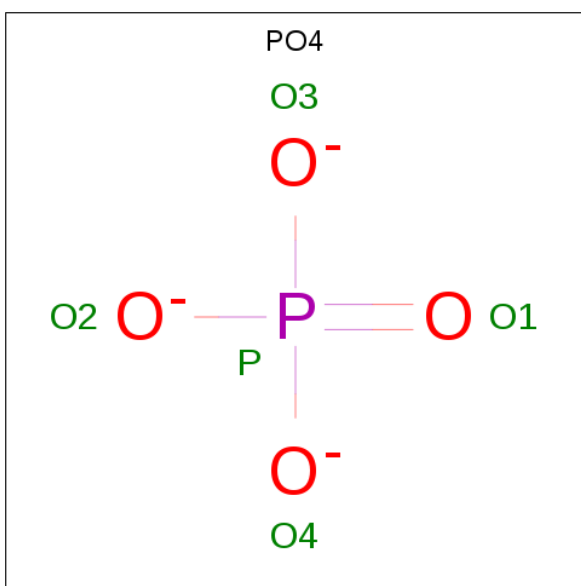


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Cl	F	N	0	0
			16	13	1	1	1		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	49	Total	O	0	0
			49	49		
7	A	101	Total	O	0	0
			101	101		





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.98 Å 68.74 Å 332.07 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	166.04 – 2.14 166.04 – 2.14	Depositor EDS
% Data completeness (in resolution range)	99.1 (166.04-2.14) 99.6 (166.04-2.14)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.41 (at 2.14 Å)	Xtriage
Refinement program	BUSTER 2.10.1	Depositor
R, $R_{free}$	0.216 , 0.243 0.216 , 0.247	Depositor DCC
$R_{free}$ test set	2099 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.0	Xtriage
Anisotropy	0.513	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 60.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5735	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.72% 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, A4T, PO4, ADP, 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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.60	0/2832	0.65	0/3831
1	B	0.50	0/2825	0.63	0/3821
All	All	0.56	0/5657	0.64	0/7652

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

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	2757	0	2698	15	0
1	B	2750	0	2689	11	0
2	A	27	0	12	0	0
2	B	27	0	12	0	0
3	A	2	0	0	0	0
4	A	16	0	0	1	0
5	A	1	0	0	0	0
6	A	5	0	0	0	0
7	A	101	0	0	0	0
7	B	49	0	0	0	0
All	All	5735	0	5411	25	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 2.

All (25) 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:B:224:SER:HB2	1:B:230:GLU:HG2	1.74	0.67
1:A:224:SER:HB2	1:A:230:GLU:HG2	1.76	0.67
1:A:73:VAL:HG22	1:A:74:LYS:H	1.68	0.58
1:B:258:ILE:HA	1:B:263:ILE:HD12	1.88	0.55
1:A:120:ASP:HB3	1:A:123:GLN:HB2	1.90	0.54
1:A:134:ARG:HG2	1:A:323:TYR:CZ	2.44	0.53
1:A:165:ASP:HB3	1:A:170:LYS:HB3	1.91	0.52
1:B:165:ASP:HB3	1:B:170:LYS:HB3	1.92	0.51
1:B:73:VAL:HG22	1:B:74:LYS:H	1.76	0.51
1:B:20:PRO:HG2	1:A:105:VAL:HG11	1.95	0.49
1:A:33:TRP:CH2	1:A:109:PRO:HB3	2.47	0.49
1:A:162:VAL:HG11	4:A:404:A4T:CL	2.52	0.46
1:B:303:LYS:HB3	1:B:313:LEU:HG	2.00	0.43
1:A:258:ILE:HA	1:A:263:ILE:HD12	2.00	0.42
1:B:251:THR:O	1:B:255:TYR:HD2	2.02	0.42
1:A:303:LYS:HB3	1:A:313:LEU:HG	2.00	0.42
1:B:224:SER:CB	1:B:230:GLU:HG2	2.47	0.42
1:B:128:LEU:HD22	1:B:132:ASP:HB3	2.01	0.42
1:A:285:VAL:HG22	1:A:293:VAL:HG11	2.02	0.41
1:A:322:PRO:O	1:A:325:TYR:HD2	2.03	0.41
1:B:47:ARG:HG3	1:B:52:GLU:HG3	2.02	0.41
1:A:33:TRP:CZ3	1:A:109:PRO:HB3	2.56	0.41
1:A:47:ARG:HG3	1:A:52:GLU:HG3	2.03	0.40
1:A:31:VAL:HG11	1:A:82:ILE:HD13	2.02	0.40
1:B:246:ALA:HA	1:B:307:TYR:OH	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	324/352 (92%)	313 (97%)	10 (3%)	1 (0%)	41	36
1	B	323/352 (92%)	309 (96%)	13 (4%)	1 (0%)	41	36
All	All	647/704 (92%)	622 (96%)	23 (4%)	2 (0%)	41	36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	73	VAL
1	A	73	VAL

### 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	301/319 (94%)	298 (99%)	3 (1%)	76	79
1	B	300/319 (94%)	297 (99%)	3 (1%)	76	79
All	All	601/638 (94%)	595 (99%)	6 (1%)	76	79

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	21	SER
1	B	258	ILE
1	B	288	GLU
1	A	21	SER
1	A	288	GLU
1	A	327	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	118	ASN

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Mol	Chain	Res	Type
1	B	186	GLN
1	A	118	ASN
1	A	186	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	$\# Z  > 2$
4	A4T	A	404	-	17,17,17	0.13	0	23,23,23	0.37	0
6	PO4	A	406	-	4,4,4	2.50	2 (50%)	6,6,6	0.66	0
2	ADP	A	401	3	24,29,29	0.74	0	29,45,45	0.86	1 (3%)
2	ADP	B	401	-	24,29,29	0.64	0	29,45,45	0.92	2 (6%)

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
4	A4T	A	404	-	-	2/6/6/6	0/2/2/2
2	ADP	B	401	-	-	1/12/32/32	0/3/3/3
2	ADP	A	401	3	-	1/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	406	PO4	P-O1	4.12	1.60	1.50
6	A	406	PO4	P-O2	2.00	1.60	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	ADP	O3B-PB-O3A	2.36	112.55	104.64
2	B	401	ADP	C5-C6-N6	2.22	123.72	120.35
2	A	401	ADP	C5-C6-N6	2.15	123.62	120.35

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	ADP	PB-O3A-PA-O1A
4	A	404	A4T	N-C-C1-C2
2	A	401	ADP	PB-O3A-PA-O1A
4	A	404	A4T	N-C-C1-C12

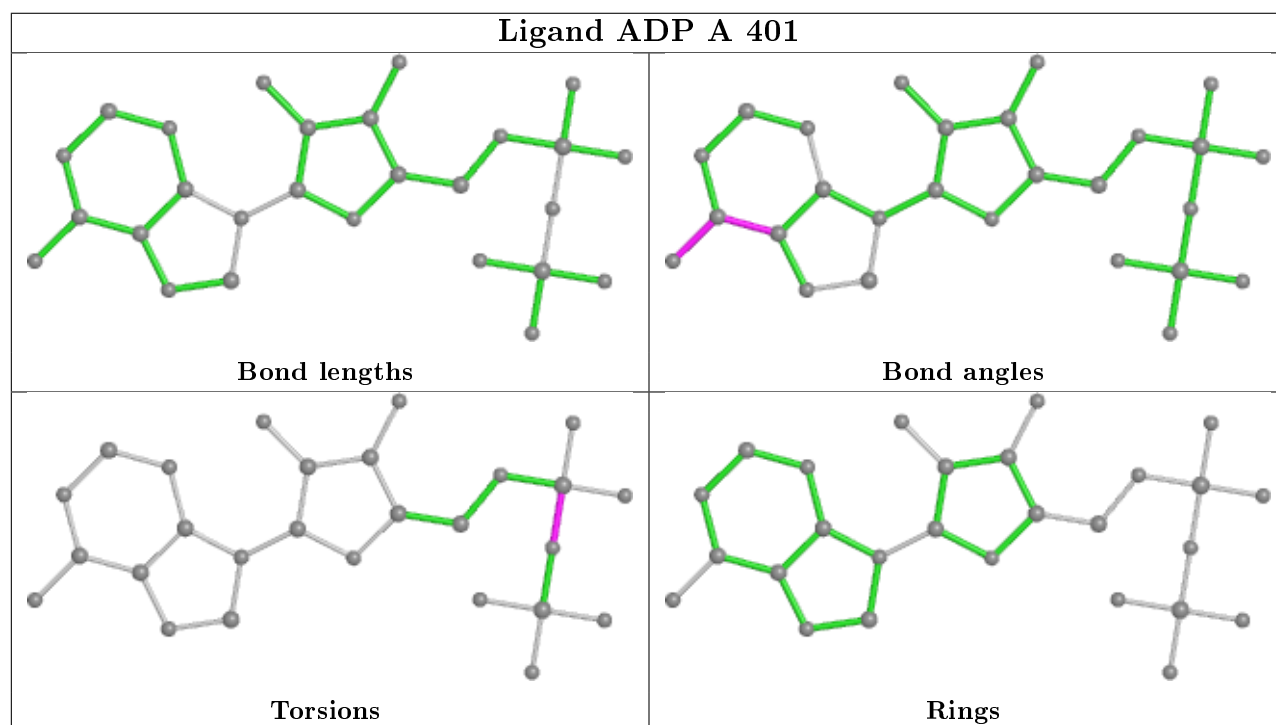
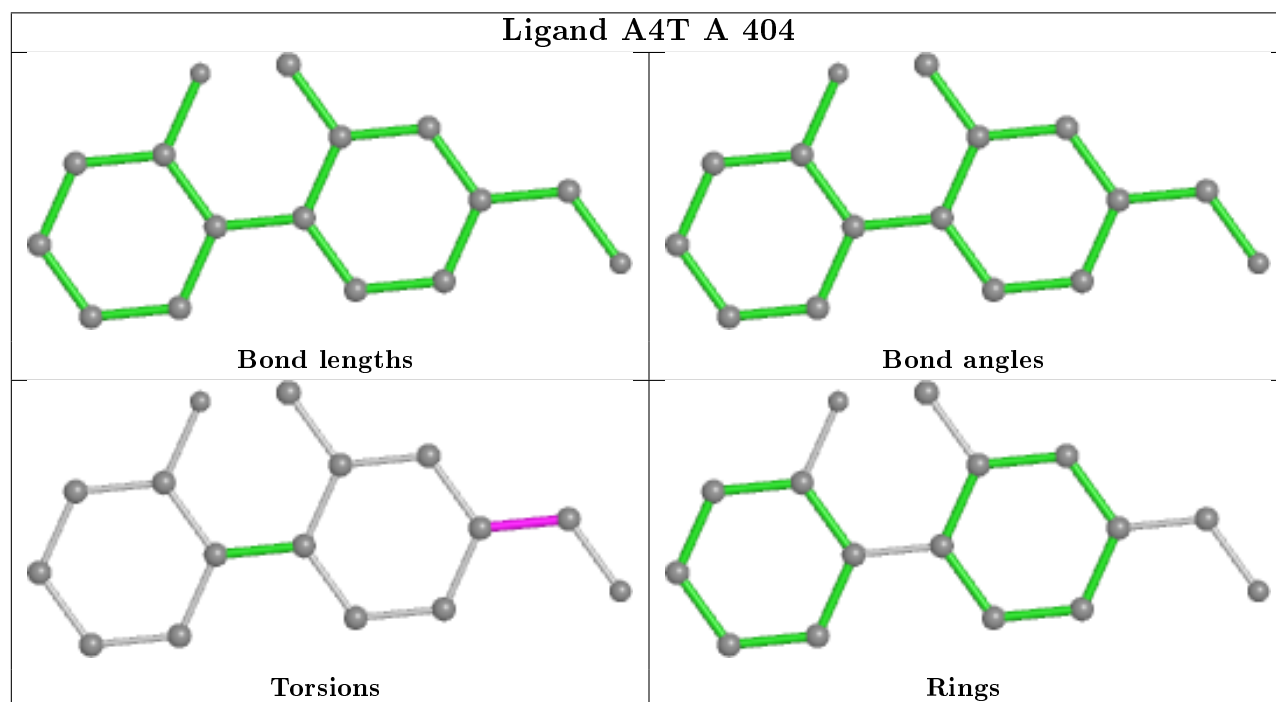
There are no ring outliers.

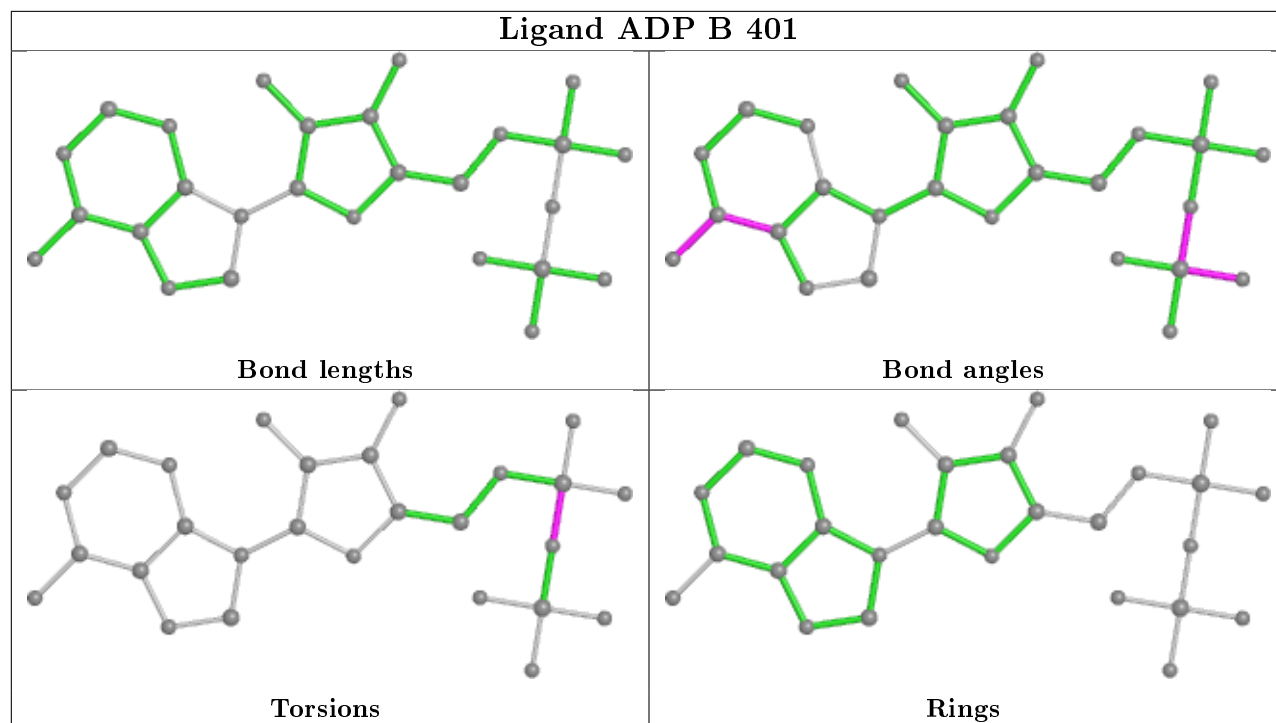
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	404	A4T	1	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	324/352 (92%)	0.48	14 (4%) 35 43	29, 46, 81, 101	0
1	B	323/352 (91%)	1.13	66 (20%) 1 1	42, 72, 108, 138	0
All	All	647/704 (91%)	0.80	80 (12%) 4 5	29, 59, 100, 138	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	50	TYR	12.9
1	B	50	TYR	9.2
1	B	5	VAL	6.1
1	A	33	TRP	6.0
1	B	73	VAL	5.9
1	B	125	TYR	5.8
1	B	49	LYS	5.7
1	B	72	PRO	5.2
1	A	325	TYR	5.1
1	B	307	TYR	4.9
1	B	288	GLU	4.8
1	B	77	LYS	4.6
1	B	325	TYR	4.6
1	B	271	ASP	4.5
1	B	29	HIS	4.3
1	B	305	LEU	4.2
1	B	292	LEU	4.2
1	B	227	PHE	4.1
1	B	298	LEU	4.1
1	B	122	LYS	4.0
1	B	75	LYS	4.0
1	A	71	LYS	4.0
1	B	269	PHE	4.0
1	B	33	TRP	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	72	PRO	3.8
1	A	49	LYS	3.8
1	B	273	LEU	3.8
1	B	267	PRO	3.7
1	A	70	LEU	3.6
1	B	257	TYR	3.6
1	B	278	ARG	3.6
1	B	280	ARG	3.6
1	A	122	LYS	3.5
1	B	166	HIS	3.5
1	B	47	ARG	3.5
1	B	167	GLU	3.4
1	A	326	THR	3.4
1	B	119	THR	3.3
1	B	74	LYS	3.3
1	B	270	ASN	3.0
1	B	124	LEU	3.0
1	B	108	THR	2.9
1	B	71	LYS	2.9
1	B	268	ARG	2.9
1	B	286	HIS	2.9
1	A	268	ARG	2.7
1	B	168	HIS	2.7
1	B	284	PHE	2.7
1	B	70	LEU	2.7
1	A	73	VAL	2.7
1	A	271	ASP	2.6
1	A	104	PRO	2.6
1	B	123	GLN	2.6
1	B	322	PRO	2.6
1	B	120	ASP	2.6
1	B	326	THR	2.5
1	B	254	LEU	2.5
1	B	249	LEU	2.4
1	B	126	GLN	2.4
1	B	283	ARG	2.4
1	B	45	LEU	2.4
1	B	30	VAL	2.4
1	B	301	LEU	2.4
1	B	76	LYS	2.4
1	B	117	ASN	2.4
1	B	250	GLY	2.4

*Continued on next page...*

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Mol	Chain	Res	Type	RSRZ
1	B	105	VAL	2.3
1	B	272	ILE	2.3
1	B	233	PHE	2.3
1	B	48	GLY	2.3
1	A	131	TYR	2.3
1	B	46	GLY	2.3
1	B	51	SER	2.2
1	B	121	PHE	2.2
1	B	135	PHE	2.2
1	B	232	PHE	2.1
1	B	264	GLU	2.1
1	B	281	TRP	2.1
1	B	263	ILE	2.1
1	B	110	ALA	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 monosaccharides 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.

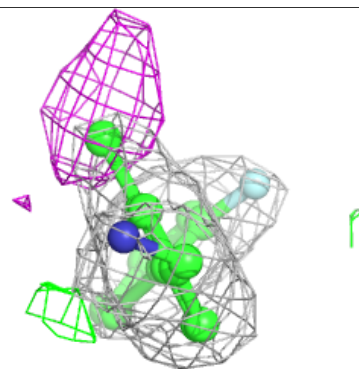
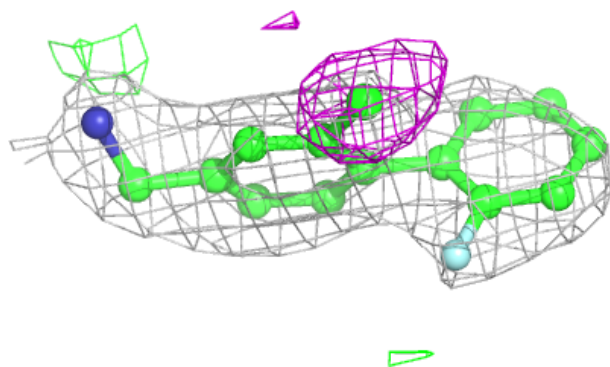
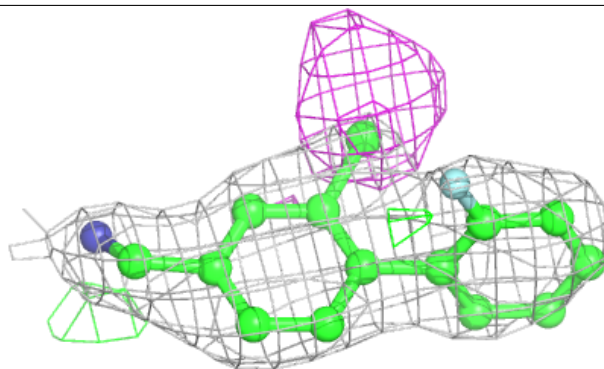
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	A4T	A	404	16/16	0.82	0.23	51,63,71,72	0
2	ADP	B	401	27/27	0.85	0.26	75,94,103,104	0
3	MG	A	403	1/1	0.91	0.12	52,52,52,52	0
2	ADP	A	401	27/27	0.93	0.14	41,55,72,74	0
6	PO4	A	406	5/5	0.93	0.14	72,74,81,82	0
3	MG	A	402	1/1	0.94	0.08	49,49,49,49	0
5	CL	A	405	1/1	0.96	0.27	69,69,69,69	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.

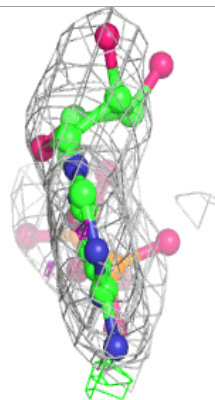
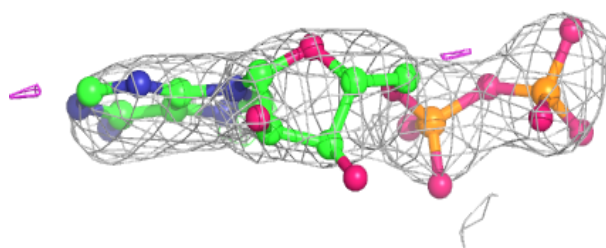
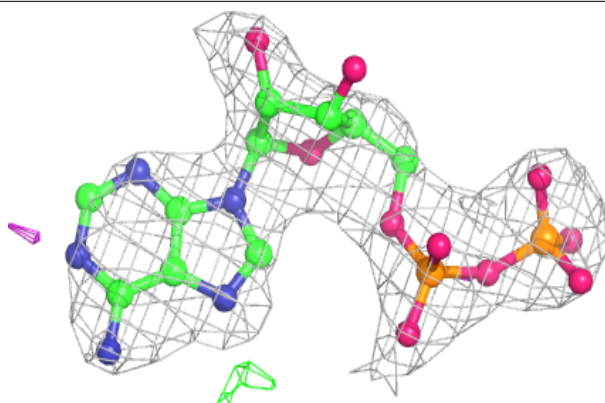
**Electron density around A4T A 404:**

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

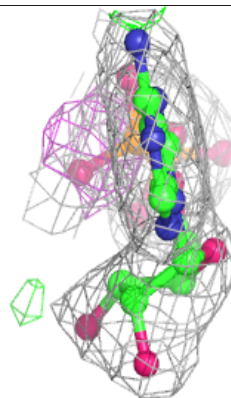
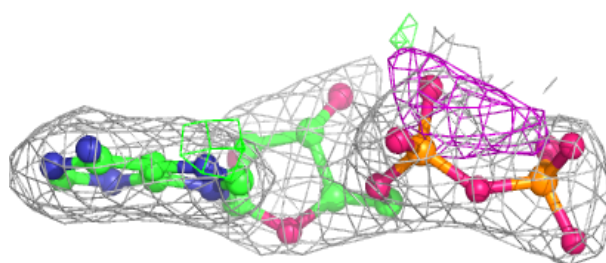
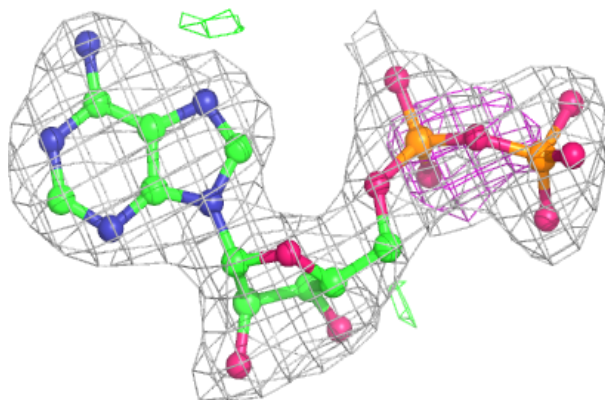


**Electron density around ADP B 401:**

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

**Electron density around ADP A 401:**

$2mF_o-DF_c$  (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.