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PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Oct 30, 2023 – 09:15 PM JST

PDB ID	:	4ZKI
Title	:	The crystal structure of Histidine Kinase YycG with ADP
Authors	:	Cai, Y.
Deposited on	:	2015-04-30
Resolution	:	3.40 Å(reported)

The following versions of software and data (see references (i)) 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	:	2.36
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)	:	2.36

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 3.40 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.
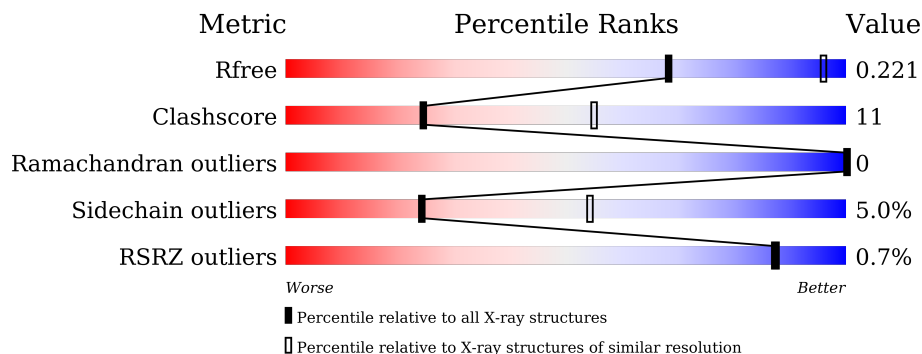
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% 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	277	.% 61% 22% • 16%
1	B	277	52% 22% • 25%

2 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 3582 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 Histidine kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	233	Total	C	N	O	S	0	0	0
			1871	1181	321	360	9			
1	B	209	Total	C	N	O	S	0	0	0
			1684	1072	285	319	8			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	348	MET	-	expression tag	UNP C6VIM1
A	349	GLY	-	expression tag	UNP C6VIM1
A	350	SER	-	expression tag	UNP C6VIM1
A	351	SER	-	expression tag	UNP C6VIM1
A	352	HIS	-	expression tag	UNP C6VIM1
A	353	HIS	-	expression tag	UNP C6VIM1
A	354	HIS	-	expression tag	UNP C6VIM1
A	355	HIS	-	expression tag	UNP C6VIM1
A	356	HIS	-	expression tag	UNP C6VIM1
A	357	HIS	-	expression tag	UNP C6VIM1
A	358	SER	-	expression tag	UNP C6VIM1
A	359	SER	-	expression tag	UNP C6VIM1
A	360	GLY	-	expression tag	UNP C6VIM1
A	361	LEU	-	expression tag	UNP C6VIM1
A	362	VAL	-	expression tag	UNP C6VIM1
A	363	PRO	-	expression tag	UNP C6VIM1
A	364	ARG	-	expression tag	UNP C6VIM1
A	365	GLY	-	expression tag	UNP C6VIM1
A	366	SER	-	expression tag	UNP C6VIM1
A	367	ALA	-	expression tag	UNP C6VIM1
A	368	GLU	-	expression tag	UNP C6VIM1
A	369	PHE	-	expression tag	UNP C6VIM1
B	348	MET	-	expression tag	UNP C6VIM1
B	349	GLY	-	expression tag	UNP C6VIM1
B	350	SER	-	expression tag	UNP C6VIM1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	351	SER	-	expression tag	UNP C6VIM1
B	352	HIS	-	expression tag	UNP C6VIM1
B	353	HIS	-	expression tag	UNP C6VIM1
B	354	HIS	-	expression tag	UNP C6VIM1
B	355	HIS	-	expression tag	UNP C6VIM1
B	356	HIS	-	expression tag	UNP C6VIM1
B	357	HIS	-	expression tag	UNP C6VIM1
B	358	SER	-	expression tag	UNP C6VIM1
B	359	SER	-	expression tag	UNP C6VIM1
B	360	GLY	-	expression tag	UNP C6VIM1
B	361	LEU	-	expression tag	UNP C6VIM1
B	362	VAL	-	expression tag	UNP C6VIM1
B	363	PRO	-	expression tag	UNP C6VIM1
B	364	ARG	-	expression tag	UNP C6VIM1
B	365	GLY	-	expression tag	UNP C6VIM1
B	366	SER	-	expression tag	UNP C6VIM1
B	367	ALA	-	expression tag	UNP C6VIM1
B	368	GLU	-	expression tag	UNP C6VIM1
B	369	PHE	-	expression tag	UNP C6VIM1

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).
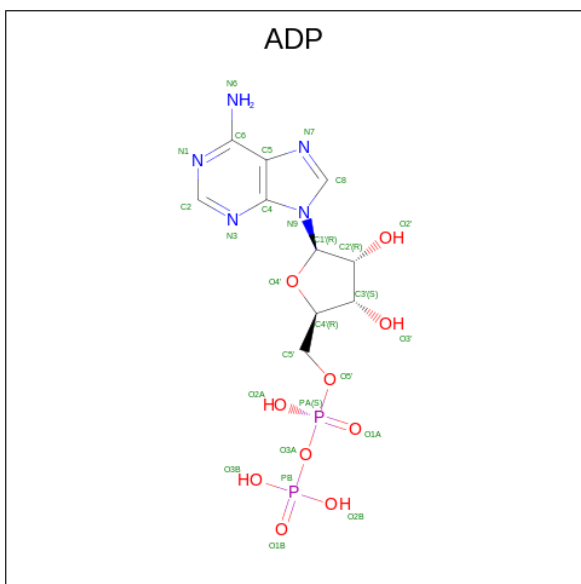
| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	B	1	27	10	5	10	2	0	0

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 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: Histidine kinase
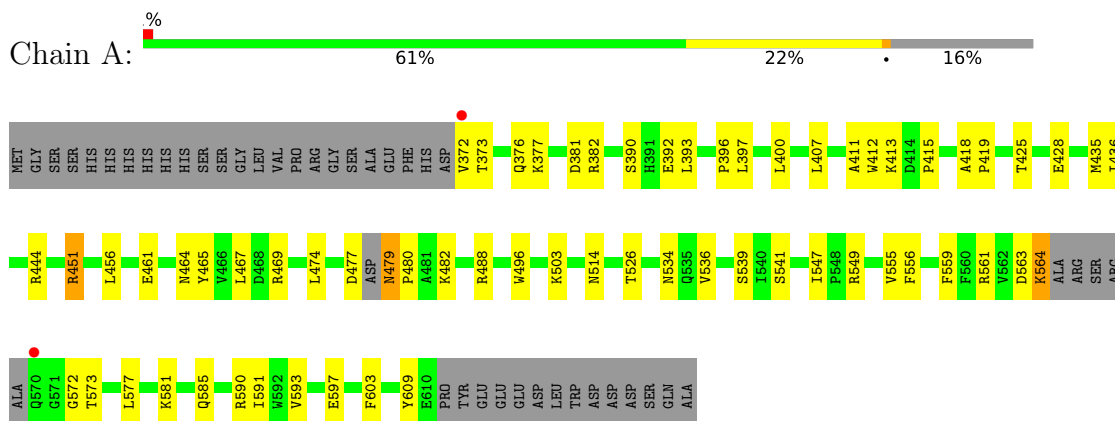
● Molecule 1: Histidine kinase
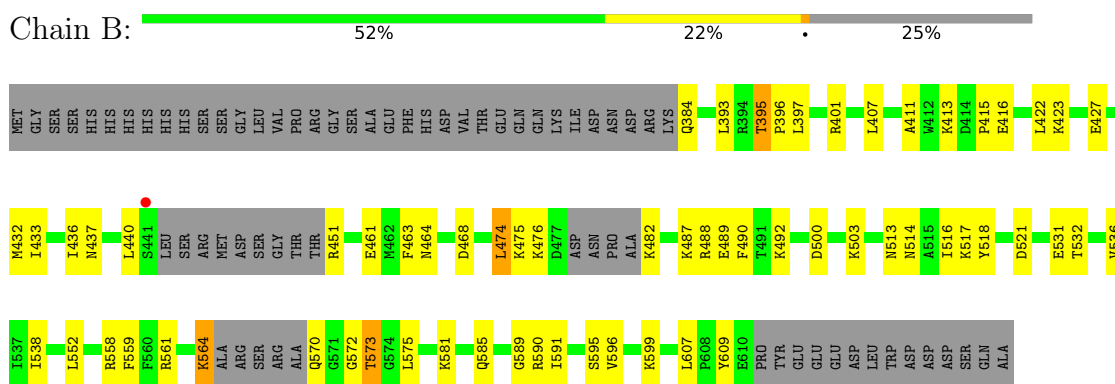
4   Data and refinement statistics   (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	53.50Å 96.03Å 119.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.82 – 3.40	Depositor
	48.82 – 3.40	EDS
% Data completeness	99.6 (48.82-3.40)	Depositor
(in resolution range)	99.6 (48.82-3.40)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.04 (at 3.40Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.201 , 0.222	Depositor
	0.205 , 0.221	DCC
R_{free} test set	450 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	77.7	Xtriage
Anisotropy	0.474	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 55.6	EDS
L-test for twinning[2]	$< \lvert L \rvert > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3582	wwPDB-VP
Average B, all atoms (Å^2)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.05% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< \lvert L \rvert >$, $< L^2 >$ 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

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	0.53	0/1901	0.68	0/2563
1	B	0.50	0/1712	0.72	0/2307
All	All	0.52	0/3613	0.70	0/4870

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	1871	0	1864	42	0
1	B	1684	0	1679	40	0
2	B	27	0	12	2	0
All	All	3582	0	3555	78	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 11.

The worst 5 of 78 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:451:ARG:O	1:A:503:LYS:NZ	2.09	0.85
1:B:474:LEU:HD11	1:B:516:ILE:HD13	1.65	0.78
1:B:393:LEU:HD11	1:B:436:ILE:HD11	1.66	0.77
1:A:561:ARG:NH2	1:A:572:GLY:O	2.18	0.76
1:B:407:LEU:HA	1:B:411:ALA:HB3	1.71	0.73

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	227/277 (82%)	217 (96%)	10 (4%)	0	100	100
1	B	201/277 (73%)	192 (96%)	9 (4%)	0	100	100
All	All	428/554 (77%)	409 (96%)	19 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	210/247 (85%)	203 (97%)	7 (3%)	38	66
1	B	188/247 (76%)	175 (93%)	13 (7%)	15	45
All	All	398/494 (81%)	378 (95%)	20 (5%)	24	54

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	532	THR
1	B	570	GLN
1	B	590	ARG
1	B	573	THR
1	A	590	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	479	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is modelled in this entry.

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	#$|Z| > 2$
2	ADP	B	701	-	24,29,29	4.97	7 (29%)	29,45,45	3.33	8 (27%)

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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
2	ADP	B	701	-	-	7/12/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	ADP	C2'-C1'	-17.26	1.27	1.53
2	B	701	ADP	O4'-C1'	10.82	1.56	1.41
2	B	701	ADP	C3'-C4'	-9.99	1.27	1.53
2	B	701	ADP	O4'-C4'	4.96	1.56	1.45
2	B	701	ADP	C2'-C3'	4.60	1.65	1.53

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	701	ADP	C5-C6-N6	12.26	138.98	120.35
2	B	701	ADP	N6-C6-N1	-8.65	100.62	118.57
2	B	701	ADP	C3'-C2'-C1'	5.20	108.81	100.98
2	B	701	ADP	N3-C2-N1	-5.08	120.74	128.68
2	B	701	ADP	O2B-PB-O3A	3.21	115.39	104.64

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	701	ADP	PA-O3A-PB-O2B
2	B	701	ADP	C5'-O5'-PA-O1A
2	B	701	ADP	C5'-O5'-PA-O3A
2	B	701	ADP	O4'-C4'-C5'-O5'
2	B	701	ADP	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	ADP	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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand ADP B 701

Bond lengths

Bond angles

Torsions

Rings
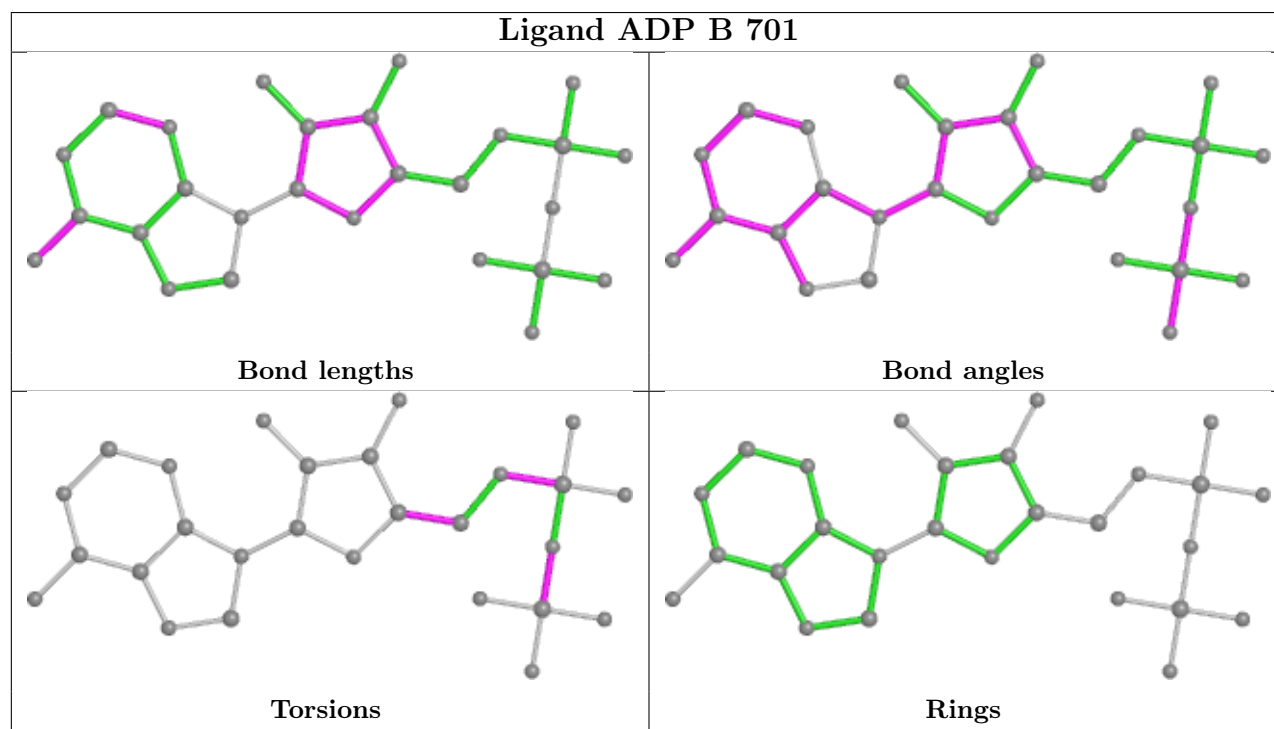
5.7 Other polymers ⓘ

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	233/277 (84%)	0.13	2 (0%)	84	83	45, 64, 103, 130	0
1	B	209/277 (75%)	0.29	1 (0%)	91	90	49, 75, 115, 150	0
All	All	442/554 (79%)	0.20	3 (0%)	87	87	45, 70, 112, 150	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	372	VAL	4.7
1	A	570	GLN	2.0
1	B	441	SER	2.0

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

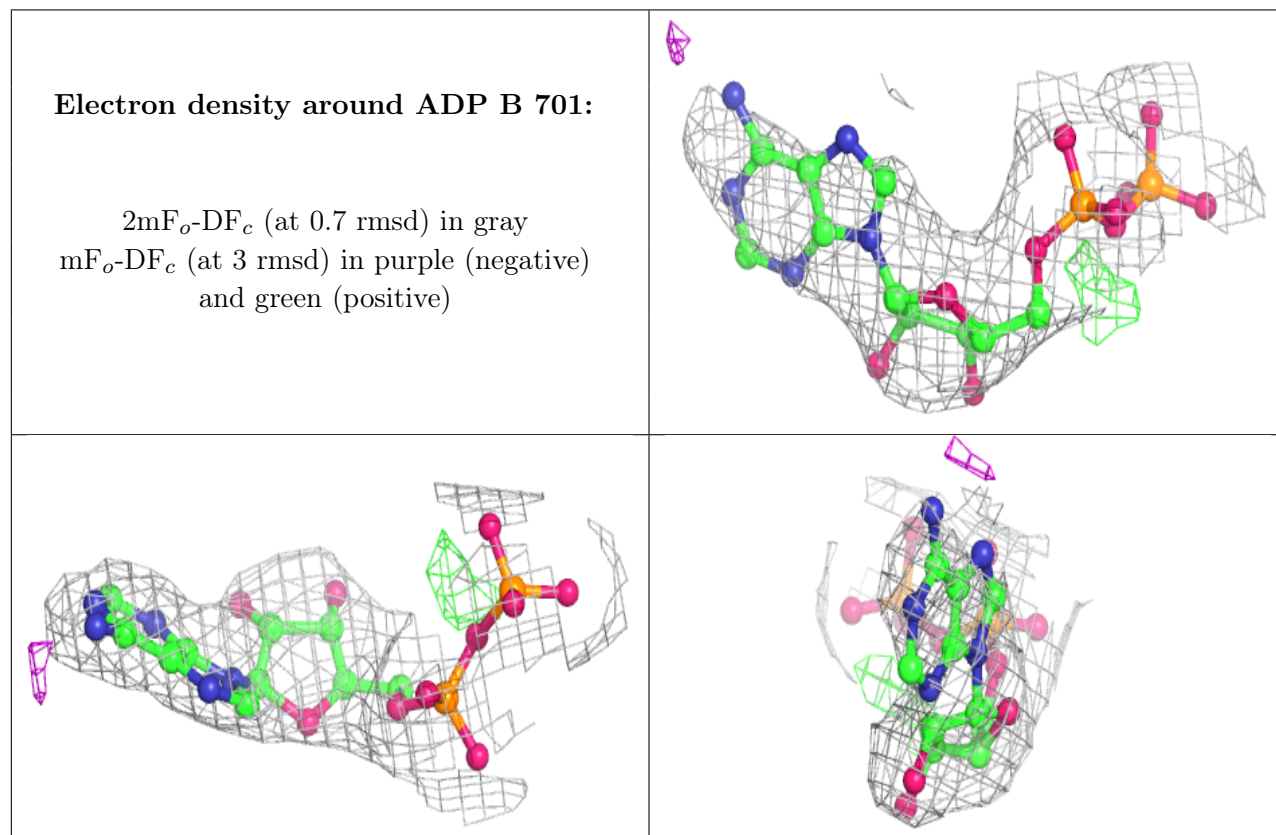There are no non-standard protein/DNA/RNA residues in this entry.

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, 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(Å^2)	Q<0.9
2	ADP	B	701	27/27	0.89	0.25	90,90,90,90	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 ADP B 701:

$2mF_o$-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.