

wwPDB X-ray Structure Validation Summary Report (i)

Aug 21, 2023 – 02:42 PM EDT

PDB ID	:	2OU7
Title	:	Structure of the Catalytic Domain of Human Polo-like Kinase 1
Authors	:	Ding, YH.; Kothe, M.; Kohls, D.; Low, S.
Deposited on		
Resolution	:	2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (1)) were used in the production of this report:

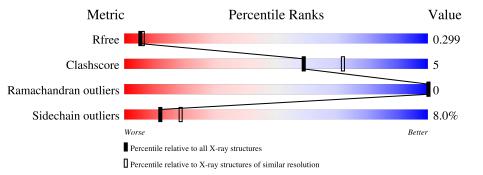
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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%

Mol	Chain	Length	Quality of chain			
1	А	335	73%	14%	•	13%

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
5	ANP	А	500[A]	Х	-	-	-
5	ANP	А	500[B]	Х	-	-	-



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2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2522 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 Serine/threonine-protein kinase PLK1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	292	Total 2370	C 1524	N 421	0 414	S 11	0	1	0

There are 3 discrepancies between the modelled and reference sequences:

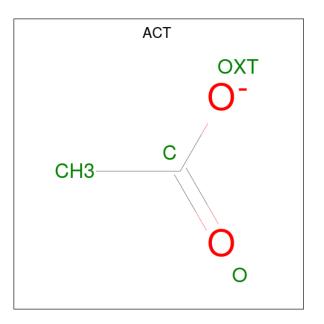
Chain	Residue	Modelled	Actual	Comment	Reference
А	11	GLY	-	cloning artifact	UNP P53350
А	12	PRO	-	cloning artifact	UNP P53350
А	210	VAL	THR	engineered mutation	UNP P53350

• Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Zn 1 1	0	0

• Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).





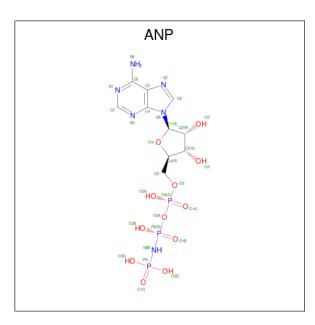
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	2	Total Mg 2 2	0	0

• Molecule 5 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).





Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf
5	Λ	1	Total	С	Ν	Ο	Р	0	1
5	A	1	44	10	7	21	6	0	1

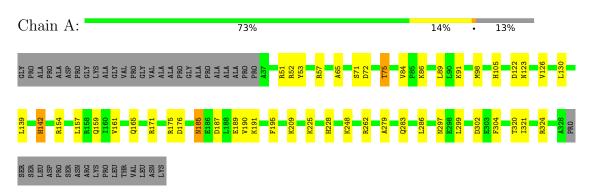
• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	97	Total O 97 97	0	0



3 Residue-property plots (i)

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.



• Molecule 1: Serine/threonine-protein kinase PLK1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants	65.96Å 65.96 Å 154.04 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.90 - 2.40	Depositor
nesolution (A)	45.88 - 2.40	EDS
% Data completeness	94.0 (45.90-2.40)	Depositor
(in resolution range)	$93.9 \ (45.88 - 2.40)$	EDS
R _{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) > 1$	$3.82 (at 2.39 \text{\AA})$	Xtriage
Refinement program	REFMAC $5.1.24$	Depositor
R, R_{free}	0.203 , 0.235	Depositor
$\mathbf{n}, \mathbf{n}_{free}$	0.292 , 0.299	DCC
R_{free} test set	758 reflections $(5.09%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	42.1	Xtriage
Anisotropy	0.773	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36, 33.6	EDS
L-test for twinning ²	$< L > = 0.48, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.048 for -h,-k,l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	2522	wwPDB-VP
Average B, all atoms $(Å^2)$	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.25% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ACT, ZN, ANP, 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	Bo	ond angles
	Mol Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.46	0/2429	0.69	3/3276~(0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	176	ASP	CB-CG-OD2	6.46	124.11	118.30
1	А	187	ASP	CB-CG-OD2	5.16	122.94	118.30
1	А	302	ASP	CB-CG-OD2	5.15	122.94	118.30

There are no chirality outliers.

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	А	2370	0	2436	23	0
2	А	1	0	0	0	0
3	А	8	0	6	0	0
4	А	2	0	0	0	0
5	А	44	0	6	0	0
6	А	97	0	0	1	1
All	All	2522	0	2448	23	1



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 5.

The worst 5 of 23 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:142:HIS:ND1	6:A:509:HOH:O	2.28	0.61
1:A:159:GLN:NE2	1:A:190:VAL:H	2.00	0.60
1:A:185:ASN:ND2	1:A:189:GLU:H	2.06	0.53
1:A:84:VAL:HG22	1:A:126:VAL:HB	1.91	0.52
1:A:185:ASN:HD22	1:A:185:ASN:C	2.16	0.49

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:508:HOH:O	6:A:583:HOH:O[5_555]	2.15	0.05

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	А	291/335~(87%)	275~(94%)	16 (6%)	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 side chain 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	А	262/290~(90%)	241 (92%)	21 (8%)	12 18	

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	225	LYS
1	А	286	LEU
1	А	324	ARG
1	А	297	ASN
1	А	262	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	А	185	ASN
1	А	228	HIS
1	А	297	ASN
1	А	287	GLN
1	А	165	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



Mol	Type	Chain	Res	Link	Bo	ond leng	ths	B	ond ang	gles
1VIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
5	ANP	А	500[B]	4	29,33,33	2.02	4 (13%)	$31,\!52,\!52$	3.42	9 (29%)
5	ANP	А	500[A]	-	29,33,33	2.06	5 (17%)	31,52,52	3.27	10 (32%)
3	ACT	А	502	2	3,3,3	0.86	0	3,3,3	0.55	0
3	ACT	А	503	-	3,3,3	0.86	0	3,3,3	0.71	0

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).

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	ANP	А	500[B]	4	1/1/7/8	6/14/38/38	0/3/3/3
5	ANP	А	500[A]	-	1/1/7/8	5/14/38/38	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
5	А	500[A]	ANP	PB-O1B	7.15	1.57	1.46
5	А	500[B]	ANP	PB-O1B	7.04	1.57	1.46
5	А	500[A]	ANP	PG-01G	5.84	1.55	1.46
5	А	500[B]	ANP	PG-01G	5.20	1.54	1.46
5	А	500[B]	ANP	PB-N3B	3.71	1.73	1.63

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
5	А	500[B]	ANP	O1G-PG-N3B	-14.77	90.02	111.77
5	А	500[A]	ANP	O1G-PG-N3B	-13.29	92.20	111.77
5	А	500[A]	ANP	PB-O3A-PA	-5.63	112.78	132.62
5	А	500[A]	ANP	C3'-C2'-C1'	-5.41	92.84	100.98
5	А	500[B]	ANP	C3'-C2'-C1'	-5.41	92.84	100.98

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	А	500[A]	ANP	C1'
5	А	500[B]	ANP	C1'



Mol	Chain	Res	Type	Atoms
5	А	500[A]	ANP	PB-N3B-PG-O1G
5	А	500[A]	ANP	C5'-O5'-PA-O3A
5	А	500[B]	ANP	PB-N3B-PG-O1G
5	А	500[B]	ANP	PG-N3B-PB-O1B
5	А	500[B]	ANP	PG-N3B-PB-O3A

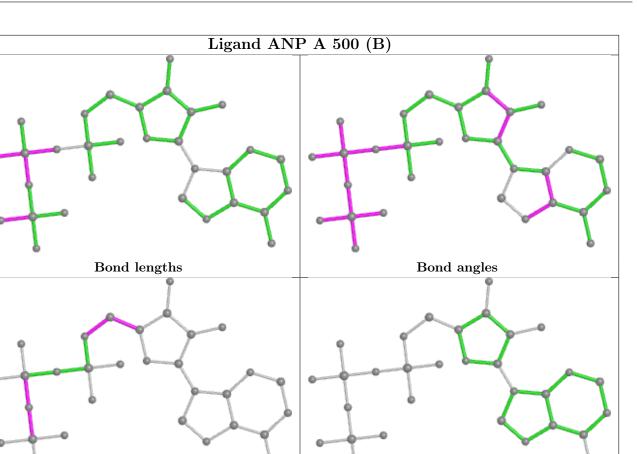
5 of 11 torsion outliers are listed below:

There are no ring outliers.

No monomer is involved in short contacts.

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.



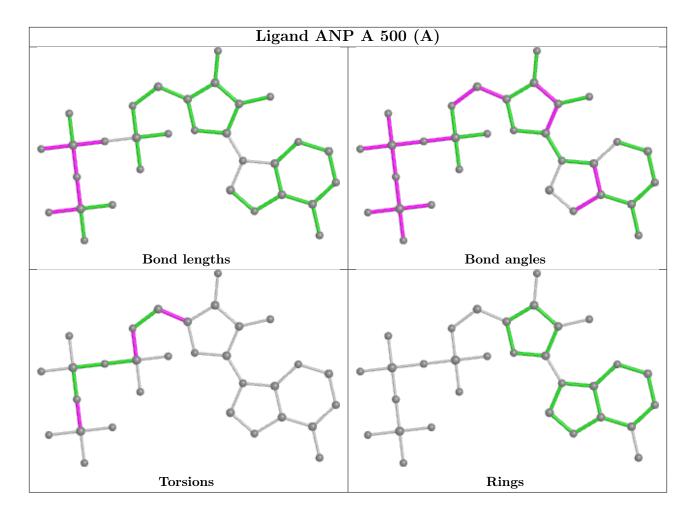


Torsions

Rings







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 (i)

6.1 Protein, DNA and RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

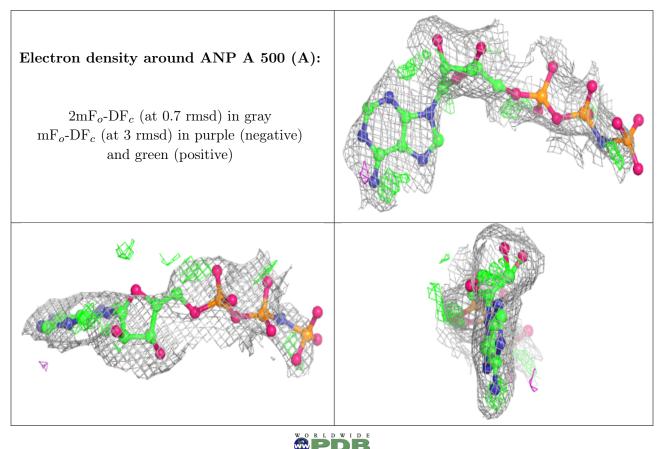
6.3 Carbohydrates (i)

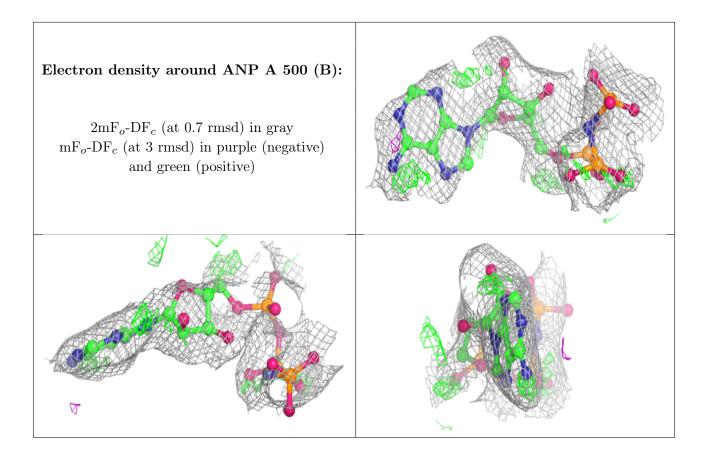
Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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.





6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

