

wwPDB X-ray Structure Validation Summary Report (i)

Nov 20, 2023 – 07:27 PM JST

PDB ID	:	7DRN
Title	:	Structure of ATP-grasp ligase PsnB complexed with precursor peptide PsnA2
		and AMPPNP
Authors	:	Song, I.; Yu, J.; Song, W.; Kim, S.
Deposited on		
Resolution	:	3.56 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:

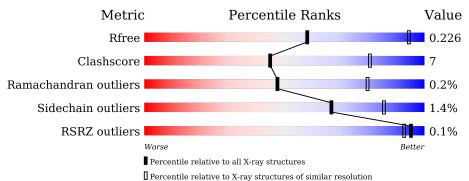
MolProbity Mogul Xtriage (Phenix) EDS	:	4.02b-467 1.8.5 (274361), CSD as541be (2020) 1.13 2.36
buster-report Percentile statistics Refmac	: : :	1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 3.56 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	$\begin{array}{l} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	$1020 \ (3.62-3.50)$
Clashscore	141614	1100 (3.62-3.50)
Ramachandran outliers	138981	1065 (3.62-3.50)
Sidechain outliers	138945	1066 (3.62-3.50)
RSRZ outliers	127900	1009 (3.64-3.48)

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	А	334	81%	12% 7%				
1	В	334	72%	16% 12%				
1	С	334	81%	12% 7%				
1	D	334	76%	12% • 11%				
2	Е	25	60% 8%	32%				
2	F	25	4% 68%	32%				



$7 \mathrm{DRN}$

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9425 atoms, of which 26 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	Δ	311	Total	С	Ν	0	\mathbf{S}	0	0	0
	А	311	2368	1484	423	450	11	0	0	0
1	В	295	Total	С	Ν	0	S	0	0	0
	D	295	2179	1361	388	419	11	0		0
1	С	311	Total	С	Ν	0	S	0	0	0
	C	311	2359	1480	422	446	11	0	0	0
1	Л	297	Total	С	Ν	0	S	0	0	0
	D	291	2203	1377	394	420	12	0	U	0

• Molecule 1 is a protein called ATP-grasp domain-containing protein.

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	-19	MET	-	expression tag	UNP A6G4D7
А	-18	GLY	-	expression tag	UNP A6G4D7
А	-17	SER	-	expression tag	UNP A6G4D7
А	-16	SER	-	expression tag	UNP A6G4D7
А	-15	HIS	-	expression tag	UNP A6G4D7
А	-14	HIS	-	expression tag	UNP A6G4D7
А	-13	HIS	-	expression tag	UNP A6G4D7
А	-12	HIS	-	expression tag	UNP A6G4D7
А	-11	HIS	-	expression tag	UNP A6G4D7
A	-10	HIS	-	expression tag	UNP A6G4D7
А	-9	SER	-	expression tag	UNP A6G4D7
А	-8	SER	-	expression tag	UNP A6G4D7
А	-7	GLY	-	expression tag	UNP A6G4D7
А	-6	LEU	-	expression tag	UNP A6G4D7
А	-5	VAL	-	expression tag	UNP A6G4D7
А	-4	PRO	-	expression tag	UNP A6G4D7
А	-3	ARG	-	expression tag	UNP A6G4D7
А	-2	GLY	-	expression tag	UNP A6G4D7
А	-1	SER	-	expression tag	UNP A6G4D7
А	0	HIS	-	expression tag	UNP A6G4D7
В	-19	MET	-	expression tag	UNP A6G4D7

Continued on next page...



B-18GLY-expression tagUNP A6G4D7B-17SER-expression tagUNP A6G4D7B-16SER-expression tagUNP A6G4D7B-15HIS-expression tagUNP A6G4D7B-13HIS-expression tagUNP A6G4D7B-11HIS-expression tagUNP A6G4D7B-11HIS-expression tagUNP A6G4D7B-10HIS-expression tagUNP A6G4D7B-10HIS-expression tagUNP A6G4D7B-9SER-expression tagUNP A6G4D7B-8SER-expression tagUNP A6G4D7B-6LEU-expression tagUNP A6G4D7B-6LEU-expression tagUNP A6G4D7B-5VAL-expression tagUNP A6G4D7B-2GLY-expression tagUNP A6G4D7B-1SER-expression tagUNP A6G4D7B-1SER-expression tagUNP A6G4D7B-1SER-expression tagUNP A6G4D7C-19MET-expression tagUNP A6G4D7C-19MET-expression tagUNP A6G4D7C-17SER-expression tagUNP A6G4D7C-18GLY- <td< th=""><th>Chain</th><th>Residue</th><th>Modelled</th><th>Actual</th><th>Comment</th><th>Reference</th></td<>	Chain	Residue	Modelled	Actual	Comment	Reference
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B -5 VAL $-$ expression tagUNP A6G4D7B -4 PRO $-$ expression tagUNP A6G4D7B -3 ARG $-$ expression tagUNP A6G4D7B -2 GLY $-$ expression tagUNP A6G4D7B -1 SER $-$ expression tagUNP A6G4D7B 0 HIS $-$ expression tagUNP A6G4D7C -19 MET $-$ expression tagUNP A6G4D7C -18 GLY $-$ expression tagUNP A6G4D7C -16 SER $-$ expression tagUNP A6G4D7C -13 HIS $-$ expression tagUNP A6G4D7C -14 HIS $-$ expression tagUNP A6G4D7C -13 HIS $-$ expression tagUNP A6G4D7C -12 HIS $-$ expression tagUNP A6G4D7C -10 HIS $-$ expressi	В	-6	LEU	-	expression tag	UNP A6G4D7
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B -2 GLY $-$ expression tagUNP A6G4D7B -1 SER $-$ expression tagUNP A6G4D7B0HIS $-$ expression tagUNP A6G4D7C -19 MET $-$ expression tagUNP A6G4D7C -18 GLY $-$ expression tagUNP A6G4D7C -16 SER $-$ expression tagUNP A6G4D7C -16 SER $-$ expression tagUNP A6G4D7C -16 SER $-$ expression tagUNP A6G4D7C -11 HIS $-$ expression tagUNP A6G4D7C -14 HIS $-$ expression tagUNP A6G4D7C -13 HIS $-$ expression tagUNP A6G4D7C -12 HIS $-$ expression tagUNP A6G4D7C -11 HIS $-$ expression tagUNP A6G4D7C -10 HIS $-$ expression tagUNP A6G4D7C -9 SER $-$ expression tagUNP A6G4D7C -7 GLY $-$ expression tagUNP A6G4D7C -6 LEU $-$ expression tagUNP A6G4D7C -6 LEU $-$ expression tagUNP A6G4D7C -3 ARG $-$ expression tagUNP A6G4D7C -3 ARG $-$ expression tagUNP A6G4D7C -3 ARG $-$ expression t	В	-4	PRO	-	expression tag	UNP A6G4D7
B-1SER-expression tagUNP A6G4D7B0HIS-expression tagUNP A6G4D7C-19MET-expression tagUNP A6G4D7C-18GLY-expression tagUNP A6G4D7C-16SER-expression tagUNP A6G4D7C-16SER-expression tagUNP A6G4D7C-16SER-expression tagUNP A6G4D7C-14HIS-expression tagUNP A6G4D7C-13HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-18GLY-e	В	-3	ARG	-	expression tag	UNP A6G4D7
B0HIS-expression tagUNP A6G4D7C-19MET-expression tagUNP A6G4D7C-18GLY-expression tagUNP A6G4D7C-17SER-expression tagUNP A6G4D7C-16SER-expression tagUNP A6G4D7C-15HIS-expression tagUNP A6G4D7C-13HIS-expression tagUNP A6G4D7C-13HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-3SER-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-18GLY-expression tagUNP A6G4D7D-19MET- <td< td=""><td>В</td><td>-2</td><td>GLY</td><td>-</td><td>expression tag</td><td>UNP A6G4D7</td></td<>	В	-2	GLY	-	expression tag	UNP A6G4D7
C-19MET-expression tagUNP A6G4D7C-18GLY-expression tagUNP A6G4D7C-17SER-expression tagUNP A6G4D7C-16SER-expression tagUNP A6G4D7C-16SER-expression tagUNP A6G4D7C-13HIS-expression tagUNP A6G4D7C-14HIS-expression tagUNP A6G4D7C-13HIS-expression tagUNP A6G4D7C-12HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-29SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-18GLY-<	В	-1	SER	-	expression tag	UNP A6G4D7
C-18 GLY -expression tagUNP A6G4D7C-17SER-expression tagUNP A6G4D7C-16SER-expression tagUNP A6G4D7C-15HIS-expression tagUNP A6G4D7C-14HIS-expression tagUNP A6G4D7C-13HIS-expression tagUNP A6G4D7C-13HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7D-18GLY-<	В	0	HIS	_	expression tag	UNP A6G4D7
C-17SER-expression tagUNP A6G4D7C-16SER-expression tagUNP A6G4D7C-15HIS-expression tagUNP A6G4D7C-14HIS-expression tagUNP A6G4D7C-14HIS-expression tagUNP A6G4D7C-13HIS-expression tagUNP A6G4D7C-12HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7	С	-19	MET	-	expression tag	UNP A6G4D7
C-16SER-expression tagUNP A6G4D7C-15HIS-expression tagUNP A6G4D7C-14HIS-expression tagUNP A6G4D7C-13HIS-expression tagUNP A6G4D7C-12HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7	С	-18	GLY	-	expression tag	UNP A6G4D7
C-15HIS-expression tagUNP A6G4D7C-14HIS-expression tagUNP A6G4D7C-13HIS-expression tagUNP A6G4D7C-12HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-8SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7	С	-17	SER	-	expression tag	UNP A6G4D7
C-14HIS-expression tagUNP A6G4D7C-13HIS-expression tagUNP A6G4D7C-12HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7		-16	SER	-	expression tag	UNP A6G4D7
C-13HIS-expression tagUNP A6G4D7C-12HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-8SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7		-15	HIS	-	expression tag	UNP A6G4D7
C-12HIS-expression tagUNP A6G4D7C-11HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-8SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7	С	-14	HIS	-	expression tag	UNP A6G4D7
C-11HIS-expression tagUNP A6G4D7C-10HIS-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-8SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-2GLY-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7		-13	HIS	-	expression tag	UNP A6G4D7
C-10HIS-expression tagUNP A6G4D7C-9SER-expression tagUNP A6G4D7C-8SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-4PRO-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-2GLY-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7		-12	HIS	-	expression tag	
C-9SER-expression tagUNP A6G4D7C-8SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-4PRO-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-2GLY-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7				-		
C-8SER-expression tagUNP A6G4D7C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-4PRO-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-2GLY-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7		-10		-	expression tag	
C-7GLY-expression tagUNP A6G4D7C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-4PRO-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-2GLY-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7		-9	SER	-	expression tag	
C-6LEU-expression tagUNP A6G4D7C-5VAL-expression tagUNP A6G4D7C-4PRO-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-2GLY-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7				-	<u> </u>	
C-5VAL-expression tagUNP A6G4D7C-4PRO-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-2GLY-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7				-	expression tag	
C-4PRO-expression tagUNP A6G4D7C-3ARG-expression tagUNP A6G4D7C-2GLY-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7				-	<u> </u>	
C-3ARG-expression tagUNP A6G4D7C-2GLY-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7		-5		-	- 0	
C-2GLY-expression tagUNP A6G4D7C-1SER-expression tagUNP A6G4D7C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7				-		
C-1SER-expression tagUNP A6G4D7C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7				-		
C0HIS-expression tagUNP A6G4D7D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7				-		
D-19MET-expression tagUNP A6G4D7D-18GLY-expression tagUNP A6G4D7				-		
D -18 GLY - expression tag UNP A6G4D7				-	- 0	
				-		
D -17 SER - expression tag UNP A6G4D7				-	- 0	
	D	-17	SER	-	expression tag	UNP A6G4D7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP A6G4D7
D	-15	HIS	-	expression tag	UNP A6G4D7
D	-14	HIS	-	expression tag	UNP A6G4D7
D	-13	HIS	-	expression tag	UNP A6G4D7
D	-12	HIS	-	expression tag	UNP A6G4D7
D	-11	HIS	-	expression tag	UNP A6G4D7
D	-10	HIS	-	expression tag	UNP A6G4D7
D	-9	SER	-	expression tag	UNP A6G4D7
D	-8	SER	-	expression tag	UNP A6G4D7
D	-7	GLY	-	expression tag	UNP A6G4D7
D	-6	LEU	-	expression tag	UNP A6G4D7
D	-5	VAL	-	expression tag	UNP A6G4D7
D	-4	PRO	-	expression tag	UNP A6G4D7
D	-3	ARG	-	expression tag	UNP A6G4D7
D	-2	GLY	-	expression tag	UNP A6G4D7
D	-1	SER	-	expression tag	UNP A6G4D7
D	0	HIS	-	expression tag	UNP A6G4D7

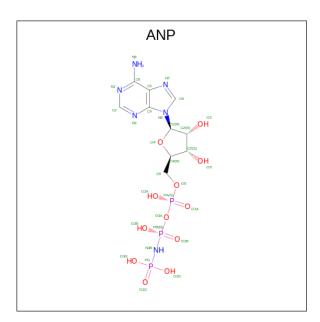
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• Molecule 2 is a protein called PsnA214-38, Precursor peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	Е	17	Total				0	0	0
			116	75	18	23		Ũ	Ŭ
2	F	17	Total	С	Ν	0	0	0	0
	Ľ	11	112	72	17	23	0	0	0

• Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$) (labeled as "Ligand of Interest" by depositor).





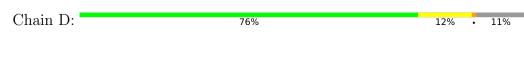
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
9	Δ	1	Total	С	Η	Ν	Ο	Р	0	0
0	A	1	44	10	13	6	12	3	0	0
2	C	1	Total	С	Η	Ν	Ο	Р	0	0
5	U	1	44	10	13	6	12	3	0	0



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 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.

- Chain A: 81% 12% 7% • Molecule 1: ATP-grasp domain-containing protein Chain B: 72% 16% 12% MET GLY SERV HISSER HISSER HISS HISSER HISS SERV CUV LEU VAL CUV VAL CUV VAL CUV VAL MISSER SERV MISSER MIS • Molecule 1: ATP-grasp domain-containing protein Chain C: 81% 12% 7% • Molecule 1: ATP-grasp domain-containing protein
- Molecule 1: ATP-grasp domain-containing protein





GLN SER PRO GLY ALA ALA TYR GLY VAL THR ASP GLU ILE ASP PHE PHE GLN ALA GLN GLN

K313 ARG

• Molecule 2: PsnA214-38, Precursor peptide

Chain E: 60% 8% 32% THR GLY GLY GLY GLY GLY PRO TYR Ξ

• Molecule 2: PsnA214-38, Precursor peptide

~	4%			
Ch	nain F:	68%	32%	
3	G7 K8 V9 CLY GLY GLY GLY GLY FRO GLY FRO FRO FRO			



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	92.29Å 92.65Å 99.57Å	Depositor
a, b, c, α , β , γ	90.00° 100.90° 90.00°	Depositor
Resolution (Å)	32.95 - 3.56	Depositor
Resolution (A)	39.23 - 3.56	EDS
% Data completeness	99.2 (32.95-3.56)	Depositor
(in resolution range)	99.2 (39.23-3.56)	EDS
R _{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$4.91 (at 3.57 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
D D.	0.224 , 0.228	Depositor
R, R_{free}	0.223 , 0.226	DCC
R_{free} test set	1007 reflections (5.07%)	wwPDB-VP
Wilson B-factor $(Å^2)$	72.4	Xtriage
Anisotropy	0.532	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.27, 22.6	EDS
L-test for twinning ²	$ \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	0.90	EDS
Total number of atoms	9425	wwPDB-VP
Average B, all atoms $(Å^2)$	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.48% 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: ANP

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		
WIOI	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.36	0/2408	0.54	0/3271	
1	В	0.39	0/2213	0.54	0/3012	
1	С	0.35	0/2399	0.53	0/3260	
1	D	0.38	0/2238	0.53	0/3044	
2	Е	0.56	0/115	0.60	0/152	
2	F	0.50	0/111	0.68	0/148	
All	All	0.38	0/9484	0.54	0/12887	

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 (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	2368	0	2322	29	0
1	В	2179	0	2062	36	0
1	С	2359	0	2313	29	0
1	D	2203	0	2103	31	0
2	Е	116	0	104	2	0
2	F	112	0	93	0	0
3	А	31	13	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	С	31	13	13	0	0
All	All	9399	26	9023	120	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 7.

The worst 5 of 120 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:D:133:LYS:HB2	1:D:134:PRO:HD3	1.59	0.82
1:B:41:PHE:HB3	1:B:42:PRO:HD3	1.65	0.77
1:B:65:ARG:O	1:B:65:ARG:HG3	1.83	0.75
1:A:187:ASP:HA	1:A:192:ARG:HD3	1.69	0.75
1:C:172:LYS:HB3	1:C:180:THR:HG22	1.70	0.72

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	Perce	ntiles
1	А	309/334~(92%)	291 (94%)	18 (6%)	0	100	100
1	В	289/334~(86%)	269~(93%)	20 (7%)	0	100	100
1	С	309/334~(92%)	294 (95%)	14 (4%)	1 (0%)	41	74
1	D	291/334~(87%)	276 (95%)	14 (5%)	1 (0%)	41	74
2	Е	13/25~(52%)	11 (85%)	2(15%)	0	100	100
2	F	13/25~(52%)	10 (77%)	3(23%)	0	100	100
All	All	1224/1386~(88%)	1151 (94%)	71 (6%)	2(0%)	47	80

All (2) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	D	41	PHE
1	С	123	ASN

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	242/274~(88%)	238~(98%)	4 (2%)	60 83
1	В	212/274~(77%)	209~(99%)	3~(1%)	67 85
1	С	240/274~(88%)	238~(99%)	2(1%)	81 92
1	D	217/274~(79%)	213~(98%)	4(2%)	59 81
2	Е	9/18~(50%)	9 (100%)	0	100 100
2	F	8/18 (44%)	8 (100%)	0	100 100
All	All	928/1132~(82%)	915~(99%)	13 (1%)	67 85

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	235	ARG
1	С	282	GLU
1	D	290	ARG
1	D	40	ARG
1	D	211	ASP

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. There are no such side chains 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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands are 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).

Mal	Mol Type	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Dec	Link	Bo	Bond lengths			Bond angles		
	туре	Chain	\mathbf{Res}	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2											
3	ANP	С	401	-	29,33,33	1.74	7 (24%)	31,52,52	1.95	8 (25%)											
3	ANP	А	401	-	29,33,33	1.80	7 (24%)	31,52,52	1.81	8 (25%)											

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	ANP	С	401	-	-	6/14/38/38	0/3/3/3
3	ANP	А	401	-	-	3/14/38/38	0/3/3/3

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(A)	Ideal(Å)
3	А	401	ANP	PG-N3B	4.58	1.75	1.63
3	А	401	ANP	PB-N3B	4.49	1.75	1.63
3	С	401	ANP	PG-N3B	4.30	1.74	1.63
3	С	401	ANP	PB-N3B	4.21	1.74	1.63
3	С	401	ANP	PG-01G	3.03	1.51	1.46

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	С	401	ANP	O1G-PG-N3B	-5.67	103.42	111.77

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Mol	Chain	Res	Type	Atoms		$Observed(^{o})$	$Ideal(^{o})$
3	А	401	ANP	O2B-PB-O1B	4.12	118.55	109.92
3	А	401	ANP	C3'-C2'-C1'	3.67	106.51	100.98
3	С	401	ANP	O1B-PB-N3B	-3.53	106.58	111.77
3	А	401	ANP	O1G-PG-N3B	-3.52	106.59	111.77

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There are no chirality outliers.

5 of 9 torsion outliers are listed below:

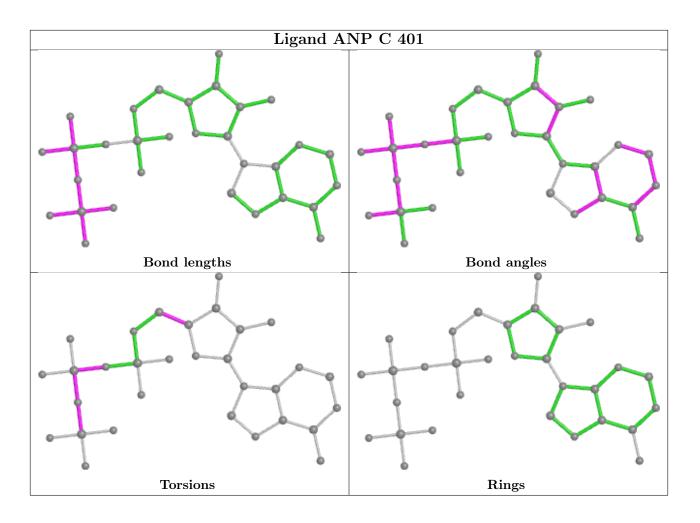
Mol	Chain	Res	Type	Atoms
3	А	401	ANP	PG-N3B-PB-O1B
3	А	401	ANP	PG-N3B-PB-O3A
3	С	401	ANP	PB-N3B-PG-O1G
3	С	401	ANP	PA-O3A-PB-O1B
3	С	401	ANP	PA-O3A-PB-O2B

There are no ring outliers.

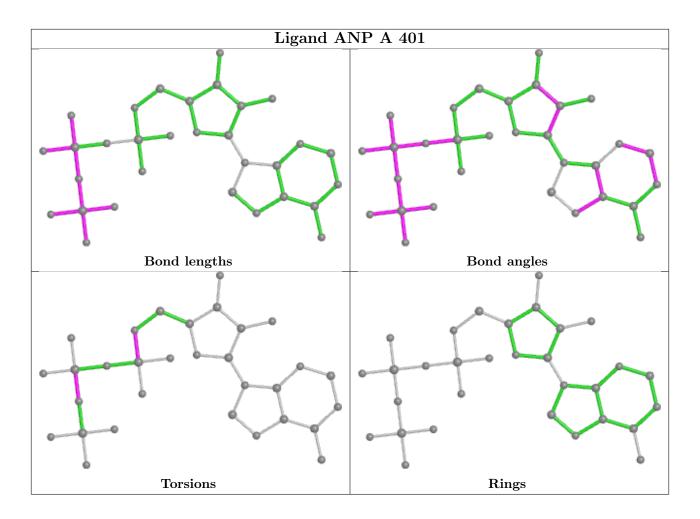
No monomer is involved in short contacts.

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.









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)

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^{th} 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	$\langle RSRZ \rangle$	# RSRZ > 2	$OWAB(Å^2)$	Q < 0.9
1	А	311/334~(93%)	-0.54	0 100 100	49, 62, 79, 91	0
1	В	295/334~(88%)	-0.38	0 100 100	49, 76, 97, 109	0
1	С	311/334~(93%)	-0.51	0 100 100	47,65,83,94	0
1	D	297/334~(88%)	-0.36	0 100 100	45, 74, 94, 115	0
2	Ε	17/25~(68%)	0.18	0 100 100	64, 72, 87, 88	0
2	F	17/25~(68%)	-0.02	1 (5%) 22 13	63, 72, 90, 100	0
All	All	1248/1386~(90%)	-0.44	1 (0%) 95 93	45, 68, 91, 115	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	7	GLY	2.5

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 monosaccharides in this entry.

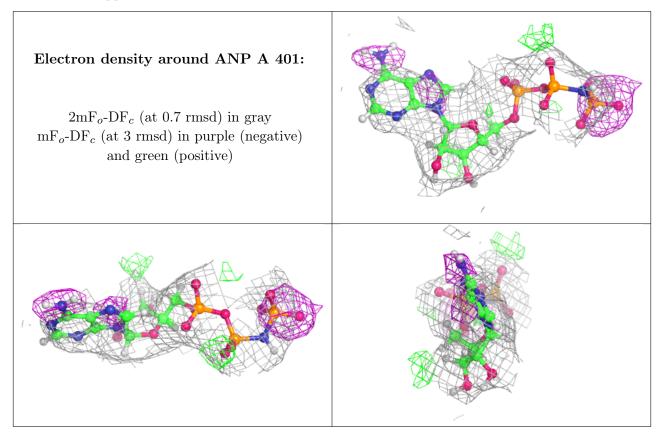
6.4 Ligands (i)

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, 95^{th} 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.

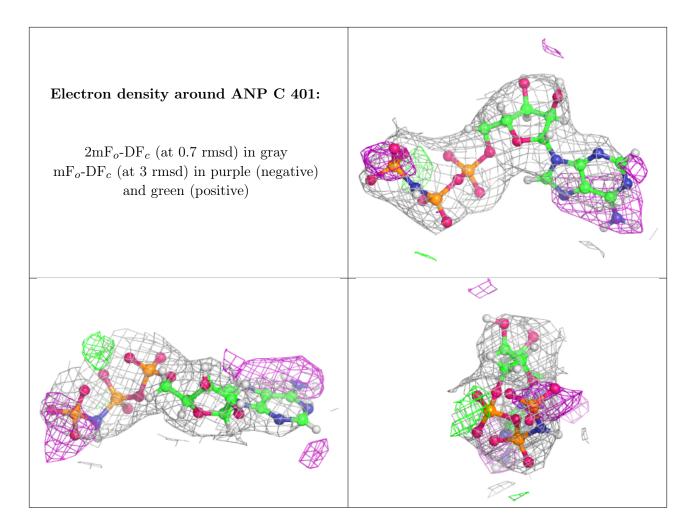


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9
3	ANP	А	401	31/31	0.85	0.27	44,70,79,99	0
3	ANP	С	401	31/31	0.87	0.29	43,69,80,111	0

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.







6.5 Other polymers (i)

There are no such residues in this entry.

