

wwPDB X-ray Structure Validation Summary Report (i)

Oct 5, 2023 – 05:49 AM EDT

PDB ID	:	6UPR
Title	:	Crystal Structure of GTPase Domain of Human Septin 2 $/$ Septin 8 Hetero-
		complex
Authors	:	Leonardo, D.A.; Pereira, H.M.; Brandao-Neto, J.; Araujo, A.P.U.; Garratt,
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Deposited on	:	2019-10-18
Resolution	:	2.30 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	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.30 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4475 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 Septin-2.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	267	Total 2160	C 1373	N 373	O 404	S 10	0	5	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	35	MET	-	initiating methionine	UNP Q15019

• Molecule 2 is a protein called Septin-8.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	В	270	Total 2167	C 1374	N 372	O 408	S 13	0	1	0

There are 16 discrepancies between the modelled and reference sequences:

Residue	Modelled	Actual	Comment	Reference
20	MET	-	initiating methionine	UNP Q92599
21	GLY	-	expression tag	UNP Q92599
22	SER	-	expression tag	UNP Q92599
23	SER	-	expression tag	UNP Q92599
24	HIS	-	expression tag	UNP Q92599
25	HIS	-	expression tag	UNP Q92599
26	HIS	-	expression tag	UNP Q92599
27	HIS	-	expression tag	UNP Q92599
28	HIS	-	expression tag	UNP Q92599
29	HIS	-	expression tag	UNP Q92599
30	SER	-	expression tag	UNP Q92599
31	GLN	-	expression tag	UNP Q92599
32	ASP	-	expression tag	UNP Q92599
33	PRO	-	expression tag	UNP Q92599
34	ASN	-	expression tag	UNP Q92599
	$\begin{array}{c} 20 \\ 21 \\ 22 \\ 23 \\ 24 \\ 25 \\ 26 \\ 27 \\ 28 \\ 29 \\ 30 \\ 31 \\ 32 \\ 33 \end{array}$	20 MET 21 GLY 22 SER 23 SER 24 HIS 25 HIS 26 HIS 27 HIS 28 HIS 30 SER 31 GLN 32 ASP 33 PRO	20 MET - 21 GLY - 22 SER - 23 SER - 23 SER - 24 HIS - 25 HIS - 26 HIS - 27 HIS - 28 HIS - 29 HIS - 30 SER - 31 GLN - 32 ASP - 33 PRO -	20MET-initiating methionine21GLY-expression tag22SER-expression tag23SER-expression tag24HIS-expression tag25HIS-expression tag26HIS-expression tag27HIS-expression tag28HIS-expression tag29HIS-expression tag30SER-expression tag31GLN-expression tag33PRO-expression tag

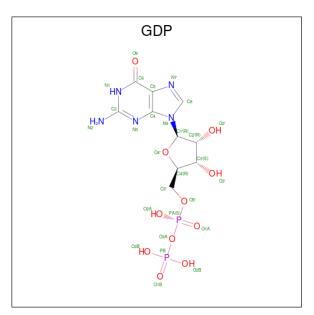
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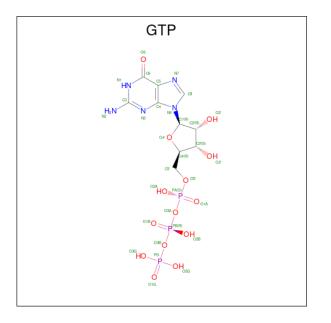
Chain	Residue	Modelled	Actual	Comment	Reference
В	35	SER	-	expression tag	UNP Q92599

• Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf
9	۸	1	Total	С	Ν	Ο	Р	0	0
0	A	1	28	10	5	11	2	0	0

• Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf
4	р	1	Total	С	Ν	Ο	Р	0	0
4	D	1	32	10	5	14	3	0	0

• Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	1	Total Mg 1 1	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	40	Total O 40 40	0	0
6	В	47	Total O 47 47	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.



3 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	52.75Å 82.77Å 78.14Å	Depositor
a, b, c, α , β , γ	90.00° 103.63° 90.00°	Depositor
Resolution (Å)	55.96 - 2.30	Depositor
% Data completeness	98.4 (55.96-2.30)	Depositor
(in resolution range)		-
R _{merge}	0.13	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.56 (at 2.29 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.208 , 0.255	Depositor
Wilson B-factor $(Å^2)$	43.8	Xtriage
Anisotropy	0.371	Xtriage
L-test for twinning ²	$ < L >=0.49, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4475	wwPDB-VP
Average B, all atoms $(Å^2)$	63.0	wwPDB-VP

EDS failed to run properly - this section is therefore incomplete.

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.98% 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.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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



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		
	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
4	GTP	В	401	5	26,34,34	1.14	2 (7%)	32,54,54	1.51	7 (21%)
3	GDP	А	1401	-	24,30,30	0.96	1 (4%)	30,47,47	1.10	3 (10%)

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. PMSZ is the rest mean square of all Z seeres of the hand 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
4	GTP	В	401	5	-	5/18/38/38	0/3/3/3
3	GDP	А	1401	-	-	1/12/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
4	В	401	GTP	C5-C6	-4.04	1.39	1.47
3	А	1401	GDP	C6-N1	-2.59	1.34	1.37
4	В	401	GTP	C2-N3	2.28	1.38	1.33

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^{o})$	$Ideal(^{o})$
4	В	401	GTP	PA-O3A-PB	-3.37	121.25	132.83
4	В	401	GTP	C8-N7-C5	3.09	108.87	102.99
4	В	401	GTP	C5-C6-N1	3.03	119.31	113.95
4	В	401	GTP	C2-N1-C6	-2.77	119.99	125.10
4	В	401	GTP	C3'-C2'-C1'	2.69	105.02	100.98

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

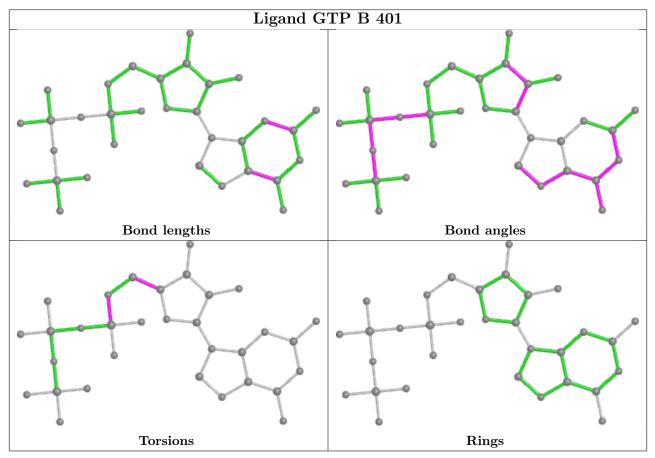
Mol	Chain	Res	Type	Atoms
4	В	401	GTP	C5'-O5'-PA-O3A
4	В	401	GTP	C5'-O5'-PA-O1A
4	В	401	GTP	C5'-O5'-PA-O2A
4	В	401	GTP	O4'-C4'-C5'-O5'
4	В	401	GTP	C3'-C4'-C5'-O5'



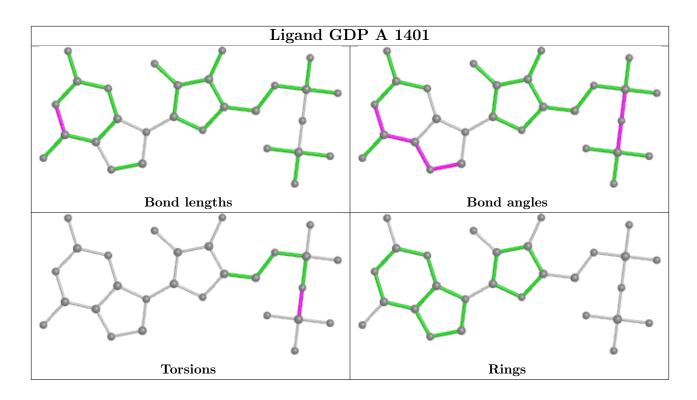
There are no ring outliers.

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.







4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

