



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4KV9
Title : GTPase domain of Septin 10 from Schistosoma mansoni in complex with GDP
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Deposited on : 2013-05-22
Resolution : 1.93 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

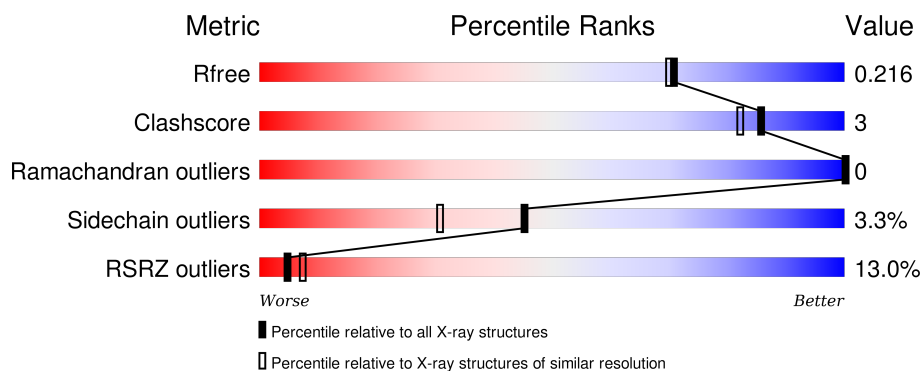
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.93 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}	91344	2910 (1.96-1.92)
Clashscore	102246	3095 (1.96-1.92)
Ramachandran outliers	100387	3062 (1.96-1.92)
Sidechain outliers	100360	3062 (1.96-1.92)
RSRZ outliers	91569	2915 (1.96-1.92)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	412	
1	B	412	

2 Entry composition [i](#)

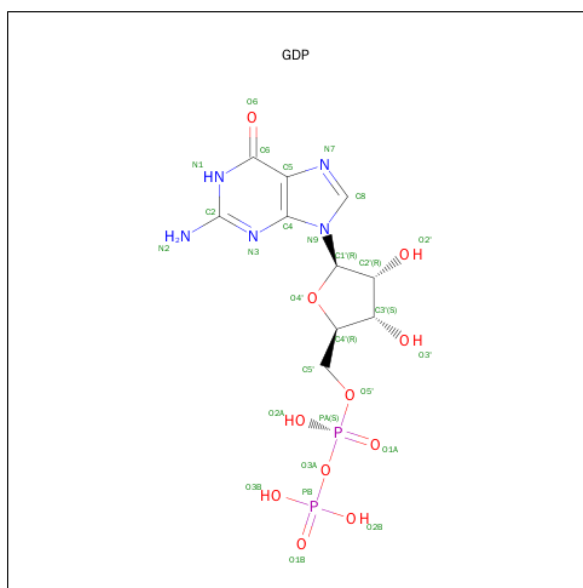
There are 3 unique types of molecules in this entry. The entry contains 4153 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	246	Total	C	N	O	S	0	2	0
			1976	1259	344	362	11			
1	B	253	Total	C	N	O	S	0	4	0
			1992	1268	348	365	11			

- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	70	Total 70	O 70	0	0
3	B	59	Total 59	O 59	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	160.90Å 45.05Å 95.49Å 90.00° 112.17° 90.00°	Depositor
Resolution (Å)	26.17 – 1.93 26.17 – 1.93	Depositor EDS
% Data completeness (in resolution range)	97.4 (26.17-1.93) 97.4 (26.17-1.93)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 1.93Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8.2_1309)	Depositor
R, R_{free}	0.184 , 0.217 0.180 , 0.216	Depositor DCC
R_{free} test set	2376 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	39.6	Xtriage
Anisotropy	0.496	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 46962 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4153	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

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: GDP

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	0.46	0/2013	0.57	0/2715
1	B	0.44	0/2036	0.54	0/2757
All	All	0.45	0/4049	0.56	0/5472

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	A	1976	0	1980	12	0
1	B	1992	0	1951	10	0
2	A	28	0	12	0	0
2	B	28	0	12	1	0
3	A	70	0	0	0	0
3	B	59	0	0	2	0
All	All	4153	0	3955	22	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 3.

All (22) 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:221:VAL:HG11	1:A:280:VAL:HG11	1.76	0.67
1:A:188:ILE:HG23	1:A:192:GLU:HG3	1.82	0.62
1:A:189:THR:OG1	1:A:192:GLU:HG2	2.00	0.61
1:B:80:LEU:HD12	1:B:99:VAL:HG22	1.83	0.60
1:A:80:LEU:HB2	1:A:99:VAL:HG22	1.85	0.57
1:A:188:ILE:CG2	1:A:192:GLU:HG3	2.36	0.56
1:A:241:GLU:HG3	1:A:252:VAL:O	2.08	0.52
1:B:253[B]:ARG:NH2	3:B:626:HOH:O	2.28	0.51
1:A:125:PHE:HB3	1:A:297:TYR:CD2	2.46	0.51
2:B:500:GDP:O2A	3:B:655:HOH:O	2.20	0.50
1:A:45:LEU:HD21	1:A:117:VAL:HG13	1.93	0.50
1:B:197:LYS:HE2	1:B:233:PRO:O	2.12	0.49
1:B:57[B]:LEU:HD13	1:B:153:PHE:CZ	2.51	0.46
1:A:68:PHE:HA	1:A:83:VAL:HG23	1.96	0.46
1:A:118:VAL:HG13	1:A:175:LYS:HE3	1.98	0.45
1:B:45:LEU:HD21	1:B:117:VAL:HG13	1.98	0.45
1:A:257:TRP:CE2	1:B:260:VAL:HG22	2.50	0.45
1:B:297:TYR:CE2	1:B:301:ARG:HG3	2.54	0.43
1:A:88:LYS:H	1:A:88:LYS:HG2	1.46	0.42
1:B:60:THR:HG23	1:B:251:ARG:HD2	2.02	0.42
1:B:279:ARG:HD3	1:B:279:ARG:HA	1.84	0.41
1:B:125:PHE:HB3	1:B:297:TYR:CD2	2.56	0.40

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	Percentiles	
1	A	240/412 (58%)	233 (97%)	7 (3%)	0	100	100
1	B	251/412 (61%)	243 (97%)	8 (3%)	0	100	100
All	All	491/824 (60%)	476 (97%)	15 (3%)	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	219/378 (58%)	211 (96%)	8 (4%)	41	26
1	B	213/378 (56%)	205 (96%)	8 (4%)	40	24
All	All	432/756 (57%)	416 (96%)	16 (4%)	45	26

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	LEU
1	A	88	LYS
1	A	160	SER
1	A	164	ILE
1	A	191	SER
1	A	253	ARG
1	A	272[A]	ARG
1	A	272[B]	ARG
1	B	80	LEU
1	B	100	GLU
1	B	123	ASN
1	B	206	SER
1	B	217	ASP
1	B	253[A]	ARG
1	B	253[B]	ARG
1	B	276	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GDP	A	500	-	23,30,30	1.24	2 (8%)	30,47,47	1.68	6 (20%)
2	GDP	B	500	-	23,30,30	1.08	2 (8%)	30,47,47	1.81	6 (20%)

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	GDP	A	500	-	-	0/12/32/32	0/3/3/3
2	GDP	B	500	-	-	0/12/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	GDP	C5-C4	2.82	1.46	1.40
2	B	500	GDP	C6-C5	3.14	1.47	1.41
2	A	500	GDP	C5-C4	3.27	1.47	1.40
2	A	500	GDP	C6-C5	3.90	1.49	1.41

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	GDP	C5-C6-N1	-4.24	117.79	123.59
2	A	500	GDP	C5-C6-N1	-3.99	118.13	123.59
2	B	500	GDP	C2'-C1'-N9	-3.60	108.79	114.29
2	A	500	GDP	C4-C5-N7	-3.50	106.25	109.48
2	A	500	GDP	C6-C5-C4	-3.09	117.21	120.90
2	B	500	GDP	C6-C5-C4	-3.06	117.23	120.90
2	B	500	GDP	N3-C2-N1	-2.95	122.95	127.44
2	B	500	GDP	C4-C5-N7	-2.86	106.84	109.48
2	A	500	GDP	N3-C2-N1	-2.58	123.52	127.44
2	A	500	GDP	C2'-C1'-N9	-2.41	110.61	114.29
2	A	500	GDP	C6-N1-C2	4.01	121.51	115.94
2	B	500	GDP	C6-N1-C2	4.54	122.24	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	500	GDP	1	0

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, 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	246/412 (59%)	0.34	29 (11%) 6 9	33, 48, 82, 98	0
1	B	253/412 (61%)	0.65	36 (14%) 4 5	31, 53, 87, 124	0
All	All	499/824 (60%)	0.50	65 (13%) 5 7	31, 51, 87, 124	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	220	ALA	8.2
1	B	221	VAL	7.2
1	B	219	GLU	5.5
1	A	243	VAL	4.7
1	B	151	LEU	4.5
1	B	141	ALA	4.4
1	B	153	PHE	4.4
1	B	89	GLU	4.3
1	B	216	THR	4.2
1	A	236	VAL	4.2
1	B	149	VAL	4.1
1	B	181	VAL	4.1
1	B	217	ASP	4.1
1	B	218	ASP	3.8
1	A	102	CYS	3.8
1	B	102	CYS	3.8
1	A	57[A]	LEU	3.8
1	B	45	LEU	3.6
1	A	151	LEU	3.5
1	A	249	THR	3.5
1	A	90	ALA	3.4
1	B	140	GLN	3.4
1	B	236	VAL	3.3
1	B	306	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	273	LEU	3.2
1	A	181	VAL	3.1
1	A	245	ILE	3.1
1	B	46	CYS	3.1
1	B	182	ILE	3.0
1	B	57[A]	LEU	2.9
1	A	87	LEU	2.9
1	B	91	ASN	2.8
1	A	182	ILE	2.8
1	A	88	LYS	2.8
1	B	179	ILE	2.8
1	A	91	ASN	2.8
1	B	85	TYR	2.7
1	B	237	VAL	2.6
1	B	245	ILE	2.6
1	B	235	ALA	2.6
1	B	150	CYS	2.6
1	A	150	CYS	2.6
1	A	153	PHE	2.5
1	B	152	TYR	2.5
1	B	47	VAL	2.4
1	B	70	PRO	2.4
1	A	244	LYS	2.3
1	B	234	PHE	2.3
1	A	149	VAL	2.3
1	B	68	PHE	2.3
1	A	235	ALA	2.3
1	A	45	LEU	2.2
1	B	208	GLU	2.2
1	A	234	PHE	2.2
1	A	178	VAL	2.2
1	A	179	ILE	2.2
1	A	159	HIS	2.2
1	A	44	ILE	2.1
1	B	44	ILE	2.1
1	A	237	VAL	2.1
1	B	88	LYS	2.0
1	A	183	ALA	2.0
1	A	46	CYS	2.0
1	A	250	VAL	2.0
1	A	89	GLU	2.0

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	GDP	A	500	28/28	0.97	0.09	-1.18	32,38,45,47	0
2	GDP	B	500	28/28	0.97	0.10	-1.24	30,38,43,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.