

One more conserved sequence motif in helicases

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Recently 6 conserved sequence stretches were identified in bacterial, yeast and viral proteins constituting a superfamily of (putative) helicases (1-3). An additional conserved segment has been observed in DNA helicases (2,3). Here we identify a similar motif in a number of other DNA and (putative) RNA helicases. Its secondary structure prediction suggests that it may be an element of the β/α core of these proteins (3) involved in some conserved activity other than DNA binding.

Secondary structure			bbbbtttttaaaaaaa???	
Herpes-	VZV	gp55	GKS-11-CIITGSTRVAA-QNVHAKL	(4)
viruses	HSV	UL5	GKS-11-CVVTGATRIAA-QNMYAKL	(4)
Fungi	<i>S.cerevisiae</i>	PIF	GKS-18-VAVTASTGLAAC-NIGGIT	(5)
Eubacteria	<i>E.coli</i>	rep	GKT-20-IAAVTFTNKAAR-EMKERV	(3)
		uvrD	GKT-20-IMAVTFTNKAAR-EMRHRI	(3)
		recB	GKT-28-LLVVFTEAATA-ELRGRI	(3)
		recD	GKT-20-IRLAAPTGKAAA-RLTESL	(3)
		uvrB	GKT-13-TMVLAPNKTLAA-QLYGM	(6)
	<i>S.typhimurium</i>	mutS	GKS-27-PIDRIFTRVGAADDLASGR	(7)
	<i>S.pneumoniae</i>	HexA	GKS-27-IFDAIFTRIGAADDLVSGQ	(7)
Mammals	man	p68	GKT-24-CLVLAPTRELA-QOVQVA	(8)
	mouse	eIF-4A	GKT-19-ALVLAPTRELA-QOIQKV	(8)
Flavi-	Dengue 2	NS3	GKT-17-TLILAPTRVVAA-EMEEAL	(9)
viruses	YFV	NS3	GKT-17-TLVLAPTRVVLS-EMKEAF	(9)
Poty-	TEV	CI	GKS-12-VLMLEPTRPLT-DNMHKQL	(10)
viruses	TVMV	CI	GKS-12-VLLLEPTRPLA-ENVTKQM	(10)
Tobravirus	TRV	p130	GKS-10-VDVVLSTGAAATDDLIERF	(11)
Potex-	WCIMV	p147	GKS-15-VTIILPTTDLDR-NDWTTKV	(12)
viruses	PVX	p180	GKS-15-ITVVLPTNELR-LDWSKKV	(13)
CONSENSUS		0.9	T	!* Reference
Frequencies of		0.8	* * * * *	
respective		0.7	* * * * *	
residues		0.6	* * * * *	
		0.5	* * * * *	

*= hydrophobic residue; &=small residue; != D,E,N or Q. GKS/T is the C-terminal part of the "A" site of the NTP-binding motif (14). The new motif resides between "A" and "B" sites of the NTP-motif (10,14). Secondary structure predicted by Chou-Fasman rules; b=strand, t=turn, a=helix, ?= no prediction.

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