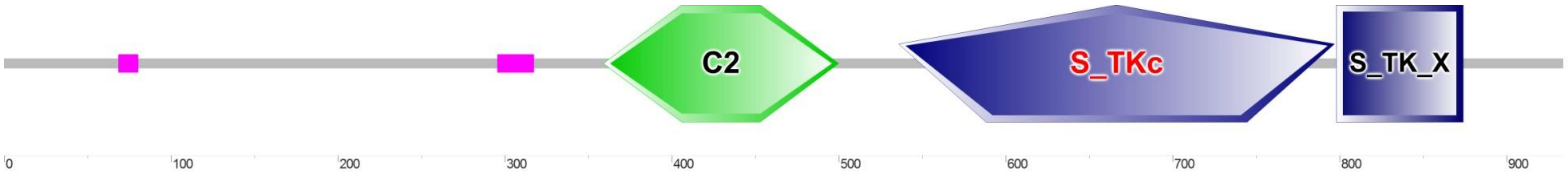
A.



B.

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Sch9: 305 SKRSSNSSS--GSSNGPKNDSSHPIWHHKTTF---DVLGSHSELDISVYDAAHDHMFLGQ 359
          S++SSN+S+  G     K+  + P W+H+ T    DVLG  SE+D+SVYD  +   FLG
SchA: 424 SRQSSNNSAMEGHDFRGKSPVTDPHWNHEATLYNSDVLGEESEIDVSVYDRNNQEAFLGH 483

Sch9: 360 VRLYPMIHNLAHASQHQWHSLKPR-VIDEVVSGDILIKWTYKQTKKRHYGPQDFEVLRLL 418
          VRL   +    H+    W  L  R   D  +SG+I ++  +++T+K+  GP DF++L+L+
SchA: 484 VRLSLNLKE-DHSRLEGWFPLSARGAGDSQISGEIHLEMLFEKTEKKQVGPNDFQILKLI 542

Sch9: 419 GKGTFGQVYQVKKKDTQRIYAMKVLSKKVIVKKNEIAHTIGERNILVTTASKSSPFIVGL 478
          GKGTFGQVYQV KKDT RIYAMKVLSKKVI++K E+AHT+GERNILV TA  +SPFIVGL
SchA: 543 GKGTFGQVYQVMKKDTHRIYAMKVLSKKVIIQKKEVAHTLGERNILVRTAMAASPFIVGL 602

Sch9: 479 KFSFQTPTDLYLVTDYMSGGELFWHLQKEGRFSEDRAKFYIAELVLALEHLHDNDIVYRD 538
          KFSFQTPTDLYLVTDYMSGGELFWHLQKEGRF E RAKFYIAEL+LAL+HLHD+DIVYRD
SchA: 603 KFSFQTPTDLYLVTDYMSGGELFWHLQKEGRFQEARAKFYIAELILALQHLHDHDIVYRD 662

Sch9: 539 LKPENILLDANGNIALCDFGLSKADLK--DRTNTFCGTTEYLAPELLLDETGYTKMVDFW 596
          LKPENILLDANG+IALCDFGLSKA+L   D TNTFCGTTEYLAPE+LLDE GYTKMVDFW
SchA: 663 LKPENILLDANGHIALCDFGLSKANLTQNDTTNTFCGTTEYLAPEVLLDEQGYTKMVDFW 722

Sch9: 597 SLGVLIFEMCCGWSPFFAENNQKMYQKIAFGKVKFPRDVLSQEGRSFVKGLLNRNPKHRL 656
          SLGVL+FEMCCGWSPF+AE+ Q+MY+ IAFGKV+FPRD LS EGR+FVKGLLNRNPKHRL
SchA: 723 SLGVLVFEMCCGWSPFYAEDTQQMYKNIAFGKVRFPRDALSTEGRNFVKGLLNRNPKHRL 782

Sch9: 657 GAIDDGRELRAHPFFADIDWEALKQKKIPPPFKPHLVSETDTSNFDPEFTTA--STSYMN 714
          GA  D +EL AHPFF DIDWEAL +K + PPFKP L S+TDTSNFDPEFT A  +++ +N
SchA: 783 GAKGDAKELMAHPFFHDIDWEALARKDVIPPFKPKLKSDTDTSNFDPEFTNALDNSASLN 842

Sch9: 715 KHQP------MMTATPLSPAMQAKFAGFTFVDESAIDEHVNNN 751
                    M  +TPLSP MQA F GFTFV+E++ID H+ ++
SchA: 843 DRAAALANGFMPASTPLSPGMQANFKGFTFVNENSIDHHMKHD 885
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S1 Figure – (A) Protein organization of the *A. fumigatus* SchA.
(B) Alignment betwen *S. cerevisiae* Sch9 and *A. fumigatus* SchA. Aminoacids labeled in red are those conserved residues phosphorylated by TOR.