

A

		CCCH motif	
Sc	1	MSGFHNVGNINMMAQQMQQNRRIKISVRNWQATMNDLINFISRNAVAV	50
		: . . . .   . . . . . : . . . . .   . . . . .	
Tb	1	-----MPNPNYRKNKDTSRIP <b>CVYF-KRGS</b> CANK	27
Sc	51	Y-DA-HVEGPLVIGYVNSKAEAESLMKWNGVRFAGSNLKFELLDNNGASA	98
		: . . . .   . . . . . : . . . . .   . . . . .   . . . . .	
Tb	28	<b>HCPFLH</b> VRGGEKVGH--EPGKAP-----GD--VGTNLLCTML-----	60
Sc	99	GTSDTISFLRGVLLKR-YDPQTKLLNLGALHSDPELIQKGVFSSISTQSK	147
		. . . . .   . . . . .   . . . . .   . . . . .   . . . . .	
Tb	61	----KLVFEK--QQQRVYNAETGVNLNTQFKEIPDL--TDVAGSINFNTQ	102
Sc	148	MFPAMMKLASTEKSLIV--ESVNLADNQLKDIS--AISTLAQTFP-NLK	191
		.   . . . .   . . . . .   . . . . .   . . . . .   . . . . .	
Tb	103	AF--CQALCSTIKSLIVPPPSAIQLKNGILSVSHLAMQLEKADLHLTLR	150
Sc	192	NLCLANNQIFRFRSLEVWKNKFKDLRELLMTNNPITTDKLYRTEMLRFP	241
		. . . . .   . . . . .   . . . . .   . . . . .   . . . . .	
Tb	151	AISLEANLIKSVESLQELK-KFTNLREIVLRDNP IANRSDYRTTIKKLMP	199
Sc	242	KLVVLD--N-----VIVRDEQKLQTVYSLP----MKIQQF--F--FENDA	276
		.   . . . .   . . . . .   . . . . .   . . . . .   . . . . .	
Tb	200	SLIGLDGESICVPPSLPWPQFSPTGYSEAQKHVLFQICGLLNPLEGD-	248
Sc	277	LGQSSTD <b>FATNFL-NLWDDNNREQLLNLYSPQSQFSVSDSTIPPSTVTD</b> S	325
		. . . . . : . . . . .   . . . . .   . . . . .   . . . . .	
Tb	249	-GASGVAHGVDVAVSDLYAANAVALTSLSSP--E--VAV-ST-PMRTMNGA	291
Sc	326	<b>DQTPAFGYMSSSRN-I---SKVSSEKS---IQQRL-SIGQESINSIF</b>	365
		. . . . .   . . . . .   . . . . .   . . . . .   . . . . .	
Tb	292	AGVPQ---QRNVIRDIVSLRLKQTESNHNLLHGKSTVVALGRTKVCSQM	338
Sc	366	<b>K--TLPKT--KHHLQEQPNEYSMETISY-----PQING--F-VITLHG--</b>	401
		: . . . .   . . . . .   . . . . .   . . . . .   . . . . .	
Tb	339	EHWLYPKTFRVHHYHSSASTVFLDNSYLTGSPSPAMKVPVTIVTLHGTM	388
Sc	402	<b>FFEETGKPELESNKKTGKNYQKNRRYNHGYNSTSNNKLSKKSFDRT-WV</b>	450
		. . . . .   . . . . .   . . . . .   . . . . .   . . . . .	
Tb	389	TWNNTGVP---GDATTIGPMTI-RR-----N--FTRVLSVTQGDAGRWL	426
Sc	451	IIVPMNSVVIASDLLTVRAYSTGAWKTA-S-IAIAQPPQQQAS--VL-PQ	495
		. . . . . : . . . . .   . . . . .   . . . . .   . . . . .	
Tb	427	I-----T---NDMVSlyLTPSGSSASSKSGNGVPETTQLSECRILLDPR	467
Sc	496	VASMNPNIITPPQ--PQPSVVP----GGMSIP-----GAPQGMVM	530
		. . . . .   . . . . .   . . . . .   . . . . .   . . . . .	
Tb	468	SDRSRAEVLRSRKKDVPVEVIMALCQHVGNDAELFTVLDLDIRGVPLSAFEH	517
Sc	531	APTLQLPPDVQSRNLNPVQL- <b>ELLNKLHLETKLNAEYTFMLAEQS-NWNYE</b>	578
		. . . . .   . . . . .   . . . . .   . . . . .   . . . . .	
Tb	518	<b>TAP-C</b> CANLA-GENIMES---IQMCRLVNLFGMAPQ-NA-LE-MLRHNNGNWSDT	560
Sc	579	<b>VAIKGFQSSMNGIPREAFVQF</b> 599	
		. . . . .   . . . . .   . . . . .   . . . . .	
Tb	561	VAAVAATAPVAAVPQ----- 575	

B

Dm	SGIPLVAIDDAFKEKMKVMTAKRYNIQTKALDLSRFHADPDLKQ--VFCPLFRQNVMGAA	245
	+ ++ + KRY+ QTK L+L H+DP+L Q VF + Q+ M A	
Sc	ASAGTSDTISFLRGVLL----KRYDPQTKLLNLGALHSDPELIQKGVFSSISTQSKMFPA	151
	GT+ + L+ V + Y+ +T +LNL P+L V SI+ ++ F	
Tb	GDVGTNLLCTMLKLVFEKQQQRVYNAETGVNLNTQFKEI PDLTD--VAGSINFNTQAF--	104
Dm	IDIMCDNIPDL-----EALNLDNSISSMEAFKG---VEKRLPNLKILYLGDNKIPSLAH	297
	+ + L E++NL DN + + A + + PNLK L L +N+I	
Sc	MMKLASTEKSLIV---ESVNLADNQLKDISAIST---LAQTFPNLKNLCLANNQIFRFRS	205
	L ST KSLIV ++ L N + +S ++ A L+ + L N I S	
Tb	CQALCSTIKSLIVPPPSAIQLKNGILSVSHLAMQLEKADLHLTLRAISLEANLIKSVES	164
Dm	LVVLRN--LSILELVLKNNPCRSRYKDSQQFISEVRRKFPKLVKLDG	342
	L V +N + EL++ NNP + + + +E+ R FPKLV LD	
Sc	LEVWKNKFKDLRELLMTNNPITPIT---DKLYRTEMLRFLFPKLVVLDN	248
	L+ K KF +LRE+++ +NPI YRT + +L P L+ LD	
Tb	LQELK-KFTNLRREIVLRDNPIAN---RSDYRTTIKKLMPSLIGLDG	206

## Figure S2: Alignment of the putative TbMex67 with homologues of other organisms.

**A)** Alignment of *S. cerevisiae* (Sc) Mex67 and *Trypanosoma brucei* (Tb) Tb11.22.0004 produced by Needle at <http://www.ebi.ac.uk/Tools/emboss/align/index.html> and using the blosum 40 matrix. There is 20.1% identity over the whole length of the two polypeptides. Domains recognized in the yeast Mex67 are indicated. The CCCH motif (only present in Tb Mex67) is framed and shown in the same colours as in Figure 1.

**B)** Alignments of the region of greatest identity between *S. cerevisiae* (Sc) Mex67 and *Trypanosoma brucei* (Tb) Tb11.22.0004 produced using NCBIblast2. A similar alignment of Mex67 and *Drosophila melanogaster* (Dm) NXF1 is shown for comparison.