Supplemental Figures



Figure S1

Α

(1) Average sequence identity between full sequences

	REN2	REN3	mRNP1
REN1	16.25	16.76	16.00
REN2		23.12	18.23
REN3			16.97

(2) Average sequence identity between RNase III domains

REN2	REN3	mRNP1
28.47	31.16	35.04
	42.86	26.92
		27.27
	REN2 28.47	REN2 REN3 28.47 31.16 42.86

В

U1-like C2H2 ZnF

REN1	137 NLLETD	AAKNYCRLCMEEVQ.	. V. SP. KALI STPY	RGSHTNETCREV 179
REN2	111 VDLESD	FDGKRCKLCNESYM.	. Q W. HSES	SVI PHSGREA 146
REN3	49 TAPEYN	AGQRRCTLCDDRLE.	. T. SF. SALC	GYVGEVAEVG 85
mRPN1	52 NDFEFSR	SSASNCCRLCGEVSQ.	. T I . LSET	GSQALVTVEA 89
U1 50%		sssaaCcl Cssshs.	sssuh.csHh	pGK+Hpcplcch
		0 0	н	н

Putative dsRBD

REN1	365	GLEPQLYDSVCFVEINGVCEA RLAALVCHCLTEIYDLIVLSYVQELSGSAVPLAKQIAADRIWNSV 43	30
REN2	313	SSE TDACTTCYPLPFTCEMF. SLRALVVHVMEELAHVMFMYHVEHALAALQRVVRENQLQFI RADP 33	77
REN3	283	ASE LSCCSCQYPAFPTAEHR. YVRALVDHLLNELTHMVI MMRVGSTLENSKEYLAKYLLQGARQNG 34	47
mRPN1	303	SLQSSTNDEFTSI PSI HEAPYTI PUVSIVEECUDGI VELVI LALMARYAASLVPAVVDLVREKYLLD 3	70



REH2 downregulation does not affect the level of pre-gRNAs



Direct interaction of mRPN1 and TbRGG2 in yeast two-hybrids



Figure S5

Table S1

The mRPN1 associated proteins TbRGG2, 8170 and 4160 are also found in MRP-related complexes

	m	RPN1	R	EH2	MRB1	TbRGG1	GR	BC1/2	
Protein ID	ТАР		IP		IP	TAP	ТАР		Name (motif
T. brucei		NUase		NUase				NUase	Name/moth
Tb11.01.0150	6	4	n.d	n.d	n.d	n.d	n.d	n.d	mRPN1 RNaseIII
Tb10.406.0050	6	4	5	2	+	+	+	+	TbRGG2 RRM
Tb927.8.8170	5	5	14	4	+	+	n.d	n.d	none
Tb927.4.4160	5	3	12	3	+	+	+	+'/-	none