

ΔS2-G17

Sequence: ALAGLKEVEGHLQYHCNRIVNRKNSKRM~~DKIFINGSFCLS~~ΔI320-S340
 Prediction: -----+-----+-----+-----+-----+-----+-----
 Confidence: 75878447363545236373558998984378695836773

ΔS2-G17

T.brucei_Trm140	-----MSFSSDEKK-----	9
T.brucei_MTase37	-----	0
S.cerevisiae_Trm140	DSTKTGENDDTTGDTTSSTTSIAIQEVNDLEVVDSDCLGIDQQHNREHLKALTQDVKEETL	300
H.sapiens_METTL6	-----	0
M.musculus_METTL6	-----	0
T.brucei_Trm140	-PTRTRGGGAL-TDPHAV-----KL---HGNDFSLDEKLGGLA-----PEER	46
T.brucei_MTase37	-----MPDKIENNTRKRPRELPPFVEDYRPYT-----	26
S.cerevisiae_Trm140	ENIAHEGRGDNTGDQNAVEKSDFEKSDTEGSRIGRDLPFEFGKRNLTEESDVWDHNAWDN	360
H.sapiens_METTL6	-----MASLQR	6
M.musculus_METTL6	-----MASFOR	6

T.brucei_Trm140	K-VVAEYIEKCEETLLQLSKRGCNTPII-----PFNSENHSWDSLYKVNKRHF-PLKNY	98
T.brucei_MTase37	-----GGQLA--QLKVRKTTTHKEHWDQYYRNNTLNGYDRHY	61
S.cerevisiae_Trm140	VEWGEEQVQQAEEKIKE---QFKHPVPEFDKKLYENPARYWDIFYKNKNENFFKDRKW	416
H.sapiens_METTL6	KGLQARILTSEEEEEKLK---RDQTLVSDFKQKLEQEAQKNWDLFYKRNSTNFFKDRHW	62
M.musculus_METTL6	KGLQARILSTEEEEKLK---RDQALVSFAFKOOKLEKEAOKNWDLFYKRNSTNFFKDRHW	62

T.brucei_Trm140	IILAFPLKSIICG-----PKRESKYIVECGCGTGSTLLPIMNQF--KDGVFHIGFDVS	150
T.brucei_MTase37	ILREFSELREALERLKKNNEATLEECVWMEAGCGVGNVAFPIPKDYGDVSGWRVVGFDIS	121
S.cerevisiae_Trm140	LQIEFPILYASTRK-----DAEPVTIFEIGCGGAGNTFFFPILKDNNEN-LRIIADFA	468
H.sapiens_METTL6	TTREFEELRSCREF-----EDQKLTMLEAGCGVGNCLFPLLEED--PN-IFAYACDFS	112
M.musculus_METTL6	TTREFEELRSCREY-----EGOKLTMLEAGCGVGNCLFPLLEED--LN-LFAYACDFS	112

T.brucei_Trm140	TAAVSALLEHPIASDFSAGRLTVFPYDLCYGRVSASEDCRRTKFKTECGTLKTTLLEKV	210
T.brucei_MTase37	TVAIKLLREKQNTLPHVEQEKFTAQVVLNPVEQDIAPIT-----ASVARQSR	168
S.cerevisiae_Trm140	PRAVELVKNSE--QFNPKYGHATVWDLANPDGNLPDG-----	503
H.sapiens_METTL6	PRAIEYVKQNP--LYDTERC--KVFQCDLTKDDLLDH-----	145
M.musculus_METTL6	PRAVDYVKQHP--LYNAERC--KVFQCDLTRDLDLH-----	145

T.brucei_Trm140	PGCSKGVDAAILVFLVSSLPTIECMLYALTEIKSILHNDGILLFRDYAVDPDHNLFREFVRQ	270
T.brucei_MTase37	PRGDGLVDFVSMIFVLCSIPVEE-HAVVLRRRIAACMKEGGVFFFRDYCVDDHAEKRFSAH	227
S.cerevisiae_Trm140	-VEPHSVDIAVMVIFVFSALAPNQ-WDQAMDNLHKILKPGGKIIFRDYAGYDLTQVRFFKN	561
H.sapiens_METTL6	-VPPESVDVVMILIFVLSAVHPDK-MHLVLQNIYKVLKPGKSVLFRDYGLDHAMLRFKAS	203
M.musculus_METTL6	-VPPESVDAVTLIFVLSAVHPEK-MRLVLLNVYKVLKPGRSVLFRDYGLDHAMLRFKAG	203

T.brucei_Trm140	QNKKHNDLSFCKGDGTLQMFFFELNFTKRKLFALAGLKEVEGHGLQYHCNR	TVNRKNSKRM	330
T.brucei_MTase37	CR--VEANTFSRTNGTLSHFFSVSELRLDFCSVGFELIN--VEVVEREVVNRREGMNLQ		282
S.cerevisiae_Trm140	RI--LEENFYVRQDGTGRVYFFSEKLEIFFTKKYFLENK---IGTDRLLLVNRKRLQKMY		616
H.sapiens_METTL6	SK--LGENFYVRQDGTGRSYFFTTDFLAQLFMDTGYYEEVV---NEYVRFRETVNKKEGL---		255
M.musculus_METTL6	SK--LGENFYVRQDGTGRSYFFTDEFLAQLFVDAGYEEVV---NEYVRFRETVNKKEGLCVP		258

T.brucei_Trml140	KIFINGSFCLS-----	341
T.brucei_MTase37	RRFLQGRFRKIRRIGDNGIDIAGNGNLSRNMPQK	316
S.cerevisiae_Trml140	RCWVQAVFDVPQ-----	628
H.sapiens_METTL6	-----	255
M.musculus_METTL6	RVFLQSKFRKPPKDPAPTSDSASL-----	282

Supplementary Figure 2. Predicted RNA-binding residues of TbTrm140. (A) Output from BindN predicting RNA-binding residues in the 341 amino acid sequence of Trm140 (Wang and Brown 2006). The + symbols denote likely RNA binding residues. (B) Clustal 2.1 multiple sequence alignment of *S. cerevisiae* and *T. brucei* Trm140. Putative motifs (I-VI) characteristic of class 1 Rossmann-fold methyltransferases are indicated above the sequence and key conserved residues are highlighted in black. Gray highlighted regions in both the BindN and alignment correspond to the N-terminal and C-terminal deletion mutants, Δ S2-G17 and Δ I320-S340, respectively.