

Supplemental Data

The EF-G-like GTPase Snu114p Regulates Spliceosome Dynamics Mediated

by Brr2p, a DExD/H Box ATPase

Eliza C. Small, Stephanie R. Leggett, Adrienne A. Winans, and Jonathan P. Staley

Supplemental Experimental Procedures

Strains and Plasmids. (See Tables S1 and S2 below.) yJPS762 and yJPS1004 were made by TAP-tagging (Rigaut et al., 1999) *PRP43* or *PRP28*, respectively, through integrative transformation of BY4741 (Open Biosystems) with DNA amplified from pKG810 (Tasto et al., 2001) using primers Prp43-TAPF and Prp43-TAPR or Prp28-TAPF and Prp28-TAPR, respectively. The plasmid shuffle strains yJPS996, yJPS997 and yJPS998 were created by transforming yJPS762 with the wild-type, *URA3*-marked plasmids pSN123, pJPS1492 and pTB1, respectively, after which *BRR2* was replaced (Brachmann et al., 1998) with *LEU2* and *PRP22* and *SNU114* were replaced with *HIS3*, respectively. The plasmid shuffle strains yJPS1114 and yJPS1107 were created by transforming yJPS1004 with the wild-type, *URA3*-marked plasmid pSN123 and pTB1, respectively, after which *BRR2* was replaced with *LEU2* and *SNU114* was replaced with *HIS3*, respectively. The final, experimental strains were generated by first transforming yJPS996, yJPS997, yJPS998, yJPS1107, or yJPS1114 with plasmids encoding wild-type or mutant *BRR2*, *PRP22* or *SNU114* plasmids and then selecting against strains that maintained the corresponding *URA3*-marked plasmid by growth on 5-fluoroorotic acid (Boeke et al., 1984). pJPS1492, pJPS1518, and pJPS1521 were made by subcloning the inserts in p358-PRP22 and p358-G810A (Schwer and Meszaros, 2000) into the appropriate vector (see Table S2) by restriction enzyme digest using SacI and Sall. pJPS1346 and pJPS1347 were made by subcloning the inserts in pJPS298 and pJPS643 (Leeds et al., 2006) into pRS313 by restriction enzyme digest using SacI and XhoI. pJPS654 was made by introducing the point mutation into pPR130 by QuickChange mutagenesis (Stratagene).

Oligonucleotides. Oligonucleotides for snRNA primer extensions were previously described (Staley and Guthrie, 1999; Leeds et al., 2006). For detection of psoralen-crosslinked species by Northern analysis, templates for random-primed probes were generated for U2, U5 and U6 by PCR of genomic DNA using the following primers.

U2F, 5'ACGAATCTCTTTGCCCTTTTGGCTTAGATCA

U2R, 5'CGCGAGAATAACAACCTAAAGAAGCGAGCA

U5F, 5'AAGCAGCTTTACAGATCAATGGCGGAGGGA

U5R, 5'TTGAGAAAAAGGGCAGAAAAGTTCCAAAA

U6F, 5'GTTCGCGAAGTAACCCTTCGTGGACATTTGGTCAA

U6R, 5'AAAACGAAATAAATCTCTTTGTAAAACGGTTCATC

Oligonucleotides for Northern analysis for U3A precursors, intermediates and products were as follows.

U3A intron, 5'AGCTGCTGCAATGGTTG

U3A mRNA, 5'TTCCTATAGAAATGATCCTATGAAG

Oligonucleotides for Northern analysis of snRNAs were previously described (Noble and Guthrie, 1996).

Oligonucleotides for strain construction:

Prp43-TAPF,

5'TTGAAACAAGGTAAAAACAAAAAGAAGAGTAAGCACTCCAAGAAAATGAAGCGACGATGG
AAAAAGAATTTC

Prp43-TAPR,

5'AAATTTATATAAATCTATTTTTTTTTTTTTTTTCGACACAAAATGTTACGACTCACTATAGGGA

Prp28-TAPF,

5'AACAAATATAACGTCGGCAAACAGCTCAGTAATGAGATTATATATATGAAGCGACGATGGA
AAAAAGAATTTC

Prp28-TAPR,

5'TGAGATCTTGGGTCCATCAAAAAAAAAAGAAAGAAAATAATATAACTTACGACTCACTATAG

Supplemental References

- Boeke, J.D., LaCroute, F., and Fink, G.R. (1984). A positive selection for mutants lacking orotidine-5'-phosphate decarboxylase activity in yeast: 5-fluoro-orotic acid resistance. *Mol. Gen. Genet.* *197*, 345-346.
- Brachmann, C.B., Davies, A., Cost, G.J., Caputo, E., Li, J., Hieter, P., and Boeke, J.D. (1998). Designer deletion strains derived from *Saccharomyces cerevisiae* S288C: a useful set of strains and plasmids for PCR-mediated gene disruption and other applications. *Yeast* *14*, 115-132.
- Brenner, T.J., and Guthrie, C. (2005). Genetic analysis reveals a role for the C-terminus of the *Saccharomyces cerevisiae* GTPase Snu114 during spliceosome activation. *Genetics* *170*, 1063-1080.
- Leeds, N.B., Small, E.C., Hiley, S.L., Hughes, T.R., and Staley, J.P. (2006). The splicing factor Prp43p, a DEAH box ATPase, functions in ribosome biogenesis. *Mol. Cell. Biol.* *26*, 513-522.
- Noble, S.M., and Guthrie, C. (1996). Transcriptional pulse-chase analysis reveals a role for a novel snRNP-associated protein in the manufacture of spliceosomal snRNPs. *EMBO J.* *15*, 4368-4379.
- Ragunathan, P.L., and Guthrie, C. (1998). RNA unwinding in U4/U6 snRNPs requires ATP hydrolysis and the DEIH-box splicing factor Brr2. *Curr. Biol.* *8*, 847-855.
- Rigaut, G., Shevchenko, A., Rutz, B., Wilm, M., Mann, M., and Séraphin, B. (1999). A generic protein purification method for protein complex characterization and proteome exploration. *Nat. Biotechnol.* *17*, 1030-1032.
- Schwer, B., and Meszaros, T. (2000). RNA helicase dynamics in pre-mRNA splicing. *EMBO J.* *19*, 6582-6591.

- Staley, J.P., and Guthrie, C. (1999). An RNA switch at the 5' splice site requires ATP and the DEAD box protein Prp28p. *Mol. Cell* 3, 55-64.
- Tasto, J.J., Carnahan, R.H., McDonald, W.H., and Gould, K.L. (2001). Vectors and gene targeting modules for tandem affinity purification in *Schizosaccharomyces pombe*. *Yeast* 18, 657-662.

Supplemental Tables

Table S1. Yeast Strains Used in this Study

Strain	Relevant Gene(s)	Genotype	Source/Reference
yJPS797	PRP43-TAP-KanMX	<i>MATa his3Δ leu2Δ met15Δ ura3Δ prp43::HIS3 pJPS1162</i>	Leeds et al., 2006
yJPS773	PRP22-TAP-KanMX	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i>	Leeds et al., 2006
yJPS798	<i>prp43-Q423N-TAP-KanMX</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ prp43::HIS3 pJPS1163</i>	Leeds et al., 2006
yJPS762	PRP43-TAP-KanMX	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i>	This study
yJPS997	PRP43-TAP-KanMX PRP22	<i>MATa his3Δ leu2Δ met15Δ ura3Δ prp22::HIS3 pJPS1492</i>	This study
yJPS1049	PRP43-TAP-KanMX PRP22	<i>MATa his3Δ leu2Δ met15Δ ura3Δ prp22::HIS3 pJPS1518</i>	This study
yJPS1052	PRP43-TAP-KanMX <i>prp22-G810A</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ prp22::HIS3 pJPS1521</i>	This study
yJPS996	PRP43-TAP-KanMX BRR2	<i>MATa his3Δ leu2Δ met15Δ ura3Δ brr2::LEU2 pSN123</i>	This study
yJPS999	PRP43-TAP-KanMX BRR2	<i>MATa his3Δ leu2Δ met15Δ ura3Δ brr2::LEU2 pPR130</i>	This study
yJPS1000	PRP43-TAP-KanMX <i>brr2-1</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ brr2::LEU2 pPR133</i>	This study
yJPS1001	PRP43-TAP-KanMX <i>brr2-RI107A</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ brr2::LEU2 pJPS654</i>	This study
yTB135	PRP43 SNU114	<i>MATa his3Δ leu2Δ ura3Δ trp1Δ lys2Δ prp43::KanMX snu114::KanMX pTB1 pTB123</i>	Brenner et al., 2005
yJPS998	PRP43-TAP-KanMX SNU114	<i>MATa his3Δ leu2Δ met15Δ ura3Δ snu114::HIS3 pTB1</i>	This study
yJPS1053	PRP43-TAP-KanMX SNU114	<i>MATa his3Δ leu2Δ met15Δ ura3Δ snu114::HIS3 pTB106</i>	This study
yJPS1120	PRP43-TAP-KanMX <i>snu114-14</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ snu114::HIS3 pTB108</i>	This study
yJPS1056	PRP43-TAP-KanMX <i>snu114-60</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ snu114::HIS3 pTB113</i>	This study
yJPS1054	PRP43-TAP-KanMX <i>snu114-D271N</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ snu114::HIS3 pTB114</i>	This study
yJPS1004	PRP28-TAP-KanMX	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i>	This study
yJPS1107	PRP28-TAP-KanMX SNU114	<i>MATa his3Δ leu2Δ met15Δ ura3Δ snu114::HIS3 pTB1</i>	This study
yJPS1108	PRP28-TAP-KanMX SNU114	<i>MATa his3Δ leu2Δ met15Δ ura3Δ snu114::HIS3 pTB106</i>	This study
yJPS1111	PRP28-TAP-KanMX <i>snu114-D271N</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ snu114::HIS3 pTB114</i>	This study
yJPS1114	PRP28-TAP-KanMX BRR2	<i>MATa his3Δ leu2Δ met15Δ ura3Δ brr2::LEU2 pSN123</i>	This study
yJPS1115	PRP28-TAP-KanMX BRR2	<i>MATa his3Δ leu2Δ met15Δ ura3Δ brr2::LEU2 pPR130</i>	This study
yJPS1117	PRP28-TAP-KanMX <i>brr2-RI107A</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ brr2::LEU2 pJPS654</i>	This study

Table S2. Plasmids Used in this Study

Plasmid	Genotype	Vector Backbone	Source or Reference
pJPS1162	<i>PRP43-TAP</i>	pRS316	(Leeds et al., 2006)
pJPS1163	<i>prp43-Q423N-TAP</i>	pRS316	(Leeds et al., 2006)
pJPS1492	<i>PRP22</i>	pRS316	This lab
pJPS1518	<i>PRP22</i>	pRS315	This lab
pJPS1521	<i>prp22-G810A</i>	pRS315	This lab
pSN123	<i>BRR2</i>	pRS426	(Ragunathan and Guthrie, 1998)
pPR130	<i>BRR2</i>	pSE362	(Ragunathan and Guthrie, 1998)
pPR133	<i>brr2-1</i>	pSE362	(Ragunathan and Guthrie, 1998)
pJPS654	<i>brr2-R1107A</i>	pSE362	This study
pJPS298	<i>PRP43</i>	pRS315	(Leeds et al., 2006)
pJPS643	<i>prp43-Q423N</i>	pRS315	(Leeds et al., 2006)
pJPS1346	<i>PRP43</i>	pRS313	This lab
pJPS1347	<i>prp43-Q423N</i>	pRS313	This lab
pTB123	<i>PRP43</i>	pSE360	(Brenner and Guthrie, 2005)
pTB1	<i>SNU114</i>	pRS316	(Brenner and Guthrie, 2005)
pTB106	<i>SNU114</i>	pRS315	C. Guthrie
pTB108	<i>snu114-14</i>	pRS315	C. Guthrie
pTB113	<i>snu114-60</i>	pRS315	C. Guthrie
pTB114	<i>snu114-D271N</i>	pRS315	C. Guthrie