Alternative splicing is one of the mechanisms how to regulate gene expression. Under different conditions, different mRNAs encoding proteins with different function, localization or stability can be made from one cellular transcript. The human hSlu7 protein affects the alternative splicing of some genes through alternative 3´splice site (3´SS) selection. Although it was thought that alternative splicing is absent from Saccharomyces cerevisiae, recent results argue against such conclusion. We therefore decided to characterize the function of the yeast Slu7 protein, which participates in the second step of splicing and is closely associated with the 3´SS selection. We focused on a highly conserved uncharacterized motif in the essential part of the Slu7 protein named the RED motif. Mutations in this motif caused second step splicing defects with some substrates and altered the alternative 3´SS usage ratio of some splicing constructs. Our results implicate a role for the RED motif in selecting proper 3´splice sites, especially the distal ones. Genetic interactions of slu7 mutations with PRP22 and PRP45 mutant alleles add to the intricate interaction network of splicing factors and suggest a possible role of Slu7p in facilitating the Prp22p association with the spliceosome.