

The *SSB1* heat shock cognate gene of the yeast *Saccharomyces cerevisiae*

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The *SSB1* gene (formerly called YG101) of *Saccharomyces cerevisiae* encodes a 66,601 molecular weight protein related to the hsp70 heat shock protein of other eucaryotes (1,2). The *SSB1* protein is 28% divergent from either of the yeast *SSA1* or *SSA2* hsp70-related proteins and is 39% divergent from the *Drosophila* hsp70 protein (2,3). In contrast to the expression of the heat-induced *SSA1* gene, *SSB1* transcript levels decline upon heat shock (2,3,4). Limited sequence analysis of another heat shock cognate gene, *SSB2* (formerly called YG103), shows less than 6% divergence in the amino termini of the *SSB1* and *SSB2* proteins, whereas the 5' non-protein coding regions are very dissimilar (3; L.S. Stinson and E.A. Craig, unpublished data), suggesting a possible functional difference between *SSB1* and *SSB2* proteins. A functional difference has also been postulated to explain a similar abrupt divergence in non-protein coding regions between the *SSA1* and *SSA2* genes (5). Interestingly, a *ssb1 ssb2* double mutant strain is cold-sensitive for growth (6) while a *ssa1 ssa2* double mutant is heat-sensitive (7), indicating a functional difference between the *SSA* and *SSB* subfamilies of hsp70-related genes (1,6).

The *SSB1* nucleotide sequence was determined on both DNA strands by the chemical cleavage method and all overlaps were obtained. The 613 amino acid protein coding region for *SSB1* extends from nucleotide 210 to 2051 and the 5' end of the *SSB1* message maps to nucleotide 181 (± 5 bases) (2,4).

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CTTTTTTT 9
TTTTTTTTATAGCACGCACTGAAAAAAGAAAAAATTTTCATCTTCGCTCGACGTTTCTTTTGTAGTACTCATCTTTTTATATAAAGATT 109
AATTAGTTATTGTCGCTTTGCTTTTCCTCTTTAAAAAATGTTCTTGCTTTGGATTTTCAGATGTCCCAAGATCATTACAGTATTTTAAATGAACAAA 209
ATGGCTGAAGGTGTTTCCAAGGTGCTATCGGTATCGAATTAGGTACAACCTACTCTTGTTGCTACTTACGAAATCCCGTGAATATTATGCCAACG 309
AACAAAGTAAACAGAGTCAACCCATCTTTCGTTGCTTCACTCCAGAAGAAAGATTGATTGGTATGCTGCCAAGAACCAAGCTGTTTGAACCCAAGAAA 409
CACTGCTTCGATGCTAAGCGTTTGTATGGTAGAAGATCGACGACGAATCTGTTCAAAGGACATGAAGACCTGGCCCTTCAAGGTTATCGACGTCGAT 509
GGTAACCCAGTCATCGAAGTCCAATACTTGAAGAACAAGACATTTCTCCCAAGAAGAAATTCGCTATGGTTTTGACCAAGATGAAGAAATTGCTG 609
AAGCTAAGATTGGTAAAGAGTTGAAAGGCCGTCATTACTGTCCAGCTTACTTTAACGACGCTCAAAGACAAGTACCAAGGATGCCGGTGCATTTC 709
TGTTTTGAAGCTTTGGGTATCATCAACGAACCTACTGCGCGTCTATTGCTTACGGTCTAGGTGCTGGTAAAGTCCGAAAAGGAAAGACATGTTTGATT 809
TTCGATTTGGGTGGTGGTATCTTGAACACTTCAAGGCTGAATTCAGAAGAAGACTGGTTGGACATCTCCGACGATCCGACAGCTTTGAGAAGATTGAG 909
AAGATTTGACACCAACTTGTGGAACTTCAAGGCTGAATTCAGAAGAAGACTGGTTGGACATCTCCGACGATCCGACAGCTTTGAGAAGATTGAG 1009
AACTGCTGCTGAAAAGCTTAGAAGACTTATCTCTGTCACTCAAACCTACCGTTGAAGTGTACTTTGGTTGACGGTGAAGATTTCGAATCTCTTTG 1109
ACTAAGCTAGATTGAAAGACTTGAAGCGCCGATTTGTTCAAGTCTACTTTGGAACCTGTTGAACAACTTTTGAAGGATGCTTAAGATCTCTAAGTCTCAA 1209
TCGACGAAGTTGCTTGGTTGGTGGTTCCACAGAATTCAAAGGTCCAAAGTGGTTGCTGACTTCTTTGACGGTGAAGCAATGGAAGAAATCTATTA 1309
CCAGATGAAGCTGTTGCTTACGCTGCTGCTTTCAAGTGTCTACTTCCGCGCAATCCACTCTGACGAACCAAGCACTTTGTTGTTAGATGTT 1409
GCTCCATATCTCTAGTGTGGTATGCAAGGTGACATGTCGGTATCTGTTCCAGAACAACACTACTGTTCCAAACATCAAGAGAAGAACTTTACTA 1509
CATGTGCTGACAACCAACCCTTCAATTCAGTCTACCAAGGTGAAGTGTAACTGTAAGAAAACACTTTGTTGGGTGAATTCGACTTGAAGAA 1609
CATCCCAATGATGCCACTGGTGAACAGCTTGGAAAGTATCTTCGAAGTGTGATCTTAACGATATCTGAAGTGTACTGCCCTCGAAAAGTCTACCGGT 1709
AAGTCTTCAACTACTACTTCTAAGCGTGTGGTAGATTGCTCTGAAGAAATGAAAAGATGGTTAACCAAGCTGAAGATTTCAAGGCTGCCGATG 1809
AAGCTTTGCCAGAAGCAGAGCTAGACAAAGATTGGAATCCTACGTTGCTCCATCGAACCAACTGTCACTGACCCAGTCTGTCTTCTAAATGAA 1909
GAGAGGTTCCAAAGTCAAAGTGAAGCTGCTTTGTCGCGATGTTGGCTGCTTTCGAAATCGAAGACCACTCTGCTGATGAATGAGAAGGCTGAAGTT 2009
GTTTTGAAGAGGTTGTCACCAAGCCATGCTTTCTCGATTAA 2051
    
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