SSE1 and SSE2 encode chaperonins that are in the Hsp110 subclass of HSP70 proteins. HSP70 is a large family of proteins that has been evolutionarily conserved from bacteriato humans. HSP70 proteins were originally classified based upon their induction by heat shock and their size of ~70kDa. The main function of these proteins is to serve as molecular chaperones, binding newly-translated proteins to assist in proper folding and prevent aggregation/misfolding. SSE1 and SSE2 are two of nine cytosolic forms of HSP70 found in S. cerevisiae.SSE is the yeast homolog of mammlian HSP110; the SSE/HSP110 subclass is only found in eukaryotic cells. It appears that the main function of these proteins is to act as nucleotide exchange factorsfor HSP70 chaperones during protein refolding. Additionally, independent of their NEF activity, these proteins can bind unfolded peptides and act as a 'holdase', maintaining their substrates in a folding-competent state by preventing misfolding/aggregation. Sse protein function has also been implicated in PKA signaling and HSP90 chaperone complex activity.SSE1 and SSE2 are 76% identical to each other and share 70% similarity with the HSP70 subfamily SSA. Like all other Hsp70 proteins, Sse1p and Sse2p contain an N-terminal ATPase domain and a C-terminal peptide-binding domain, but unlike other HSP70s, these domains have been shown to function and interact in trans. ATPase activity of Sse1p is stimulated by the DnaJ/HSP40 co-chaperone Sis1p. The Sse ATPase domain is also required for Sse1p to interact with Ssa1p and Ssb1p. Expression of SSE1 and SSE2 is induced by heat shock via the transcriptional factor Hsf1p, which binds to a heat shock element in the SSE gene promoter. Deletion of SSE1 derepresses Hsf1p activity and also decreases cell growth rate, while sse2 null mutations have no discernable phenotype, and loss of both gene products results in lethality.