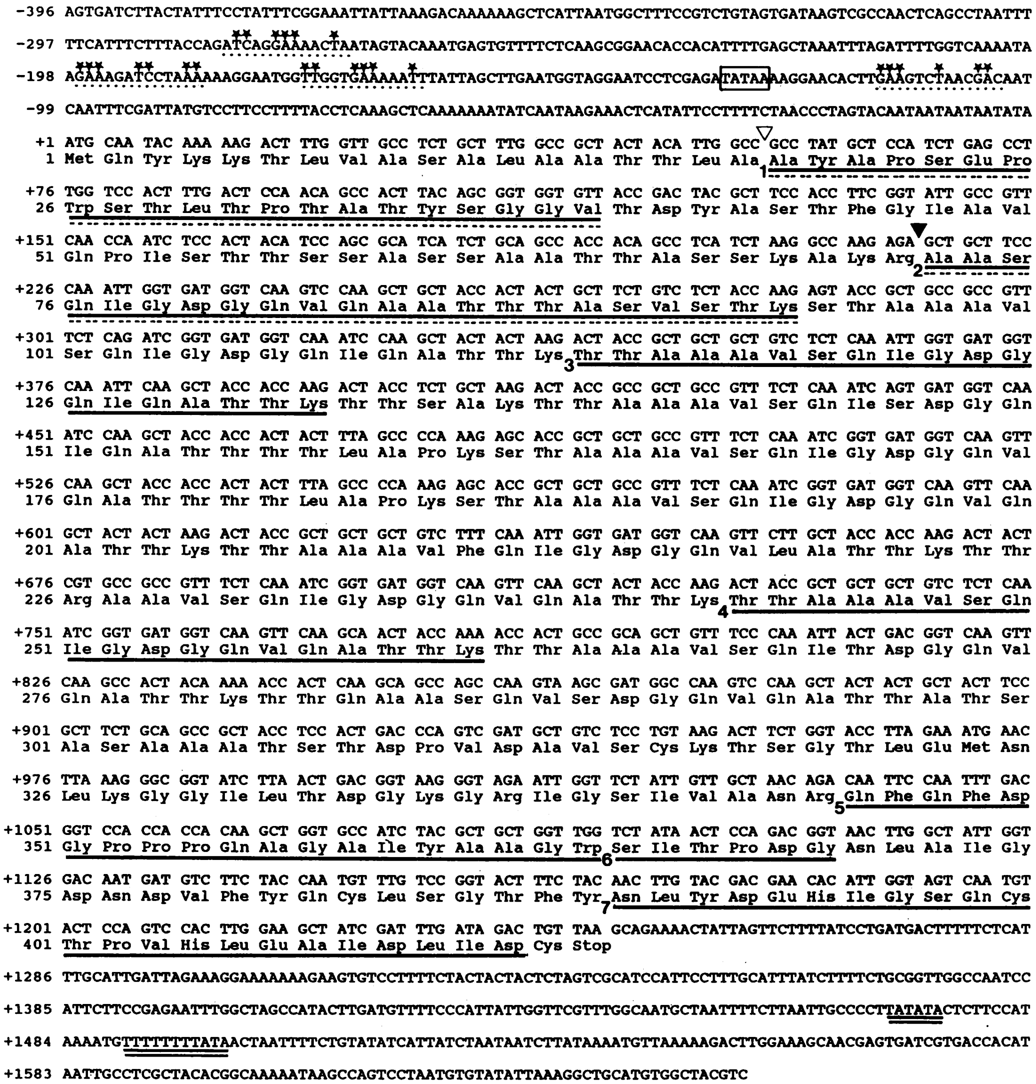
Biochemistry. In the article "A heat shock gene from *Saccharomyces cerevisiae* encoding a secretory glycoprotein" by Patrick Russo, Nisse Kalkkinen, Hannele Sareneva, Juha Paakkola, and Marja Makarow, which appeared in number 9, May 1, 1992, of *Proc. Natl. Acad. Sci. USA* (**89**, 3671–3675), the authors wish that the following correction be noted. The nucleotide sequence of the coding region of *HSP150* shown in Fig. 2 lacks A^{133}, C^{134}, and C^{189}, which are included in the corrected Fig. 2 shown here. This changes amino acids 45–62 in the original figure to amino acids 45–63 in the corrected figure. Thus, subunit I of the HSP150 protein has 54 amino acids instead of 53.



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-396 AGTGATCTTACTATTTCCTATTTCGGAAATTATTAAAGACAAAAAAGCTCATTAATGGCTTTCCGTCTGTAGTGATAAGTCGCCAACTCAGCCTAATTT
-297 TTCATTTCTTTACCAGATCAGGAAAACTAATAGTACAAATGAGTGTTTTCTCAAGCGGAACACCACATTTTGAGCTAAATTTAGATTTTGGTCAAAATA
-198 AGAAAGATCCTAAAAAAGGAATGGTTGGTGAAAAATTTATTAGCTTGAATGGTAGGAATCCTCGAGATATAAAAGGAACACTTGAAGTCTAACGACAAT
 -99 CAATTTCGATTATGTCCTTCCTTTTACCTCAAAGCTCAAAAAAATATCAATAAGAAACTCATATTCCTTTTCTAACCCTAGTACAATAATAATAATATA

  +1 ATG CAA TAC AAA AAG ACT TTG GTT GCC TCT GCT TTG GCC GCT ACT ACA TTG GCC GCC TAT GCT CCA TCT GAG CCT
   1 Met Gln Tyr Lys Lys Thr Leu Val Ala Ser Ala Leu Ala Ala Thr Thr Leu Ala Ala Tyr Ala Pro Ser Glu Pro
 +76 TGG TCC ACT TTG ACT CCA ACA GCC ACT TAC AGC GGT GGT GTT ACC GAC TAC GCT TCC ACC TTC GGT ATT GCC GTT
  26 Trp Ser Thr Leu Thr Pro Thr Ala Thr Tyr Ser Gly Gly Val Thr Asp Tyr Ala Ser Thr Phe Gly Ile Ala Val
+151 CAA CCA ATC TCC ACT ACA TCC AGC GCA TCA TCT GCA GCC ACC ACA GCC TCA TCT AAG GCC AAG AGA GCT GCT TCC
  51 Gln Pro Ile Ser Thr Thr Ser Ser Ala Ser Ser Ala Ala Thr Thr Ala Ser Ser Lys Ala Lys Arg Ala Ala Ser
+226 CAA ATT GGT GAT GGT CAA GTC CAA GCT GCT ACC ACT ACT GCT TCT GTC TCT ACC AAG AGT ACC GCT GCC GCC GTT
  76 Gln Ile Gly Asp Gly Gln Val Gln Ala Ala Thr Thr Thr Ala Ser Val Ser Thr Lys Ser Thr Ala Ala Ala Val
+301 TCT CAG ATC GGT GAT GGT CAA ATC CAA GCT ACT ACT AAG ACT ACC GCT GCT GCT GTC TCT CAA ATT GGT GAT GGT
 101 Ser Gln Ile Gly Asp Gly Gln Ile Gln Ala Thr Thr Lys Thr Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly
+376 CAA ATT CAA GCT ACC ACC AAG ACT ACC TCT GCT AAG ACT ACC GCC GCT GCC GTT TCT CAA ATC AGT GAT GGT CAA
 126 Gln Ile Gln Ala Thr Thr Lys Thr Thr Ser Ala Lys Thr Thr Ala Ala Ala Val Ser Gln Ile Ser Asp Gly Gln
+451 ATC CAA GCT ACC ACC ACT ACT TTA GCC CCA AAG AGC ACC GCT GCT GCC GTT TCT CAA ATC GGT GAT GGT CAA GTT
 151 Ile Gln Ala Thr Thr Thr Thr Leu Ala Pro Lys Ser Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Val
+526 CAA GCT ACC ACC ACT ACT TTA GCC CCA AAG AGC ACC GCT GCT GCC GTT TCT CAA ATC GGT GAT GGT CAA GTT CAA
 176 Gln Ala Thr Thr Thr Thr Leu Ala Pro Lys Ser Thr Ala Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Val Gln
+601 GCT ACT ACT AAG ACT ACC GCT GCT GCT GTC TTT CAA ATT GGT GAT GGT CAA GTT CTT GCT ACC ACC AAG ACT ACT
 201 Ala Thr Thr Lys Thr Thr Ala Ala Ala Val Phe Gln Ile Gly Asp Gly Gln Val Leu Ala Thr Thr Lys Thr Thr
+676 CGT GCC GCC GTT TCT CAA ATC GGT GAT GGT CAA GTT CAA GCT ACT ACC AAG ACT ACC GCT GCT GCT GTC TCT CAA
 226 Arg Ala Ala Val Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Thr Lys Thr Thr Ala Ala Ala Val Ser Gln
+751 ATC GGT GAT GGT CAA GTT CAA GCA ACT ACC AAA ACC ACT GCC GCA GCT GTT TCC CAA ATT ACT GAC GGT CAA GTT
 251 Ile Gly Asp Gly Gln Val Gln Ala Thr Thr Lys Thr Thr Ala Ala Ala Val Ser Gln Ile Thr Asp Gly Gln Val
+826 CAA GCC ACT ACA AAA ACC ACT CAA GCA GCC AGC CAA GTA AGC GAT GGC CAA GTC CAA GCT ACT ACT GCT ACT TCC
 276 Gln Ala Thr Thr Lys Thr Thr Gln Ala Ala Ser Gln Val Ser Asp Gly Gln Val Gln Ala Thr Thr Ala Thr Ser
+901 GCT TCT GCA GCC GCT ACC TCC ACT GAC CCA GTC GAT GCT GTC TCC TGT AAG ACT TCT GGT ACC TTA GAA ATG AAC
 301 Ala Ser Ala Ala Ala Thr Ser Thr Asp Pro Val Asp Ala Val Ser Cys Lys Thr Ser Gly Thr Leu Glu Met Asn
+976 TTA AAG GGC GGT ATC TTA ACT GAC GGT AAG GGT AGA ATT GGT TCT ATT GTT GCT AAC AGA CAA TTC CAA TTT GAC
 326 Leu Lys Gly Gly Ile Leu Thr Asp Gly Lys Gly Arg Ile Gly Ser Ile Val Ala Asn Arg Gln Phe Gln Phe Asp
+1051 GGT CCA CCA CCA CAA GCT GGT GCC ATC TAC GCT GCT GGT TGG TCT ATA ACT CCA GAC GGT AAC TTG GCT ATT GGT
 351 Gly Pro Pro Pro Gln Ala Gly Ala Ile Tyr Ala Ala Gly Trp Ser Ile Thr Pro Asp Gly Asn Leu Ala Ile Gly
+1126 GAC AAT GAT GTC TTC TAC CAA TGT TTG TCC GGT ACT TTC TAC AAC TTG TAC GAC GAA CAC ATT GGT AGT CAA TGT
 375 Asp Asn Asp Val Phe Tyr Gln Cys Leu Ser Gly Thr Phe Tyr Asn Leu Tyr Asp Glu His Ile Gly Ser Gln Cys
+1201 ACT CCA GTC CAC TTG GAA GCT ATC GAT TTG ATA GAC TGT TAA GCAGAAAACTATTAGTTCTTTTATCCTGATGACTTTTTCTCAT
 401 Thr Pro Val His Leu Glu Ala Ile Asp Leu Ile Asp Cys Stop

+1286 TTGCATTGATTAGAAAGGAAAAAAAGAAGTGTCCTTTTCTACTACTACTCTAGTCGCATCCATTCCTTTGCATTTATCTTTTCTGCGGTTGGCCAATCC
+1385 ATTCTTCCGAGAATTTGGCTAGCCATACTTGATGTTTTCCCATTATTGGTTCGTTTGGCAATGCTAATTTTCTTAATTGCCCCTTATATACTCTTCCAT
+1484 AAAATGTTTTTTTTATAACTAATTTTCTGTATATCATTATCTAATAATCTTATAAAATGTTAAAAAGACTTGGAAAGCAACGAGTGATCGTGACCACAT
+1583 AATTGCCTCGCTACACGGCAAAAATAAGCCAGTCCTAATGTGTATATTAAAGGCTGCATGTGGCTACGTC
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FIG. 2. Nucleotide sequence of *HSP150* and predicted amino acid sequence of the HSP150 protein. Three putative regulatory elements are indicated in the flanking sequences of the coding region: the TATA element (box), heat shock element (HSE)-like sequences (dotted underline), and two transcription termination signals (double underline). Nucleotides matching the HSE consensus are indicated by asterisks. The open and full arrowheads show the signal sequence and the KEX2 protease-specific cleavage sites, respectively. The underlined and numbered amino acid sequences were confirmed by direct amino acid sequencing of tryptic peptides of mature secreted HSP150. The sequences of peptides 1 and 2 (dashed underline) were obtained by direct N-terminal sequence analysis and thus represent the N termini of subunits I and II.