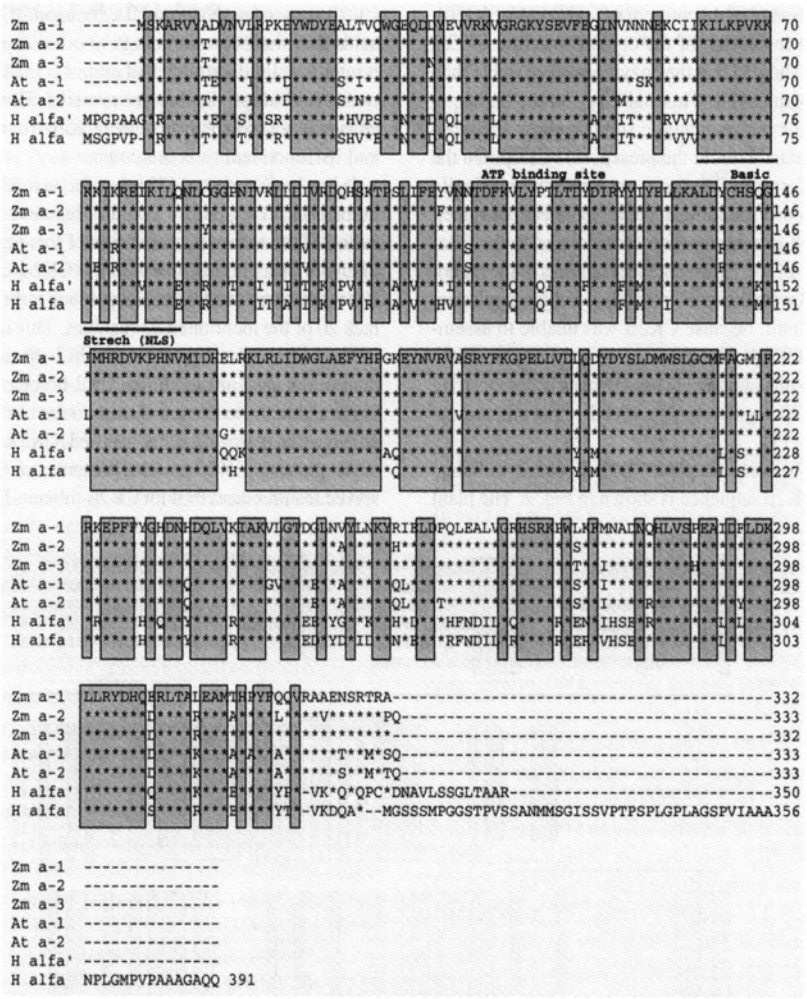

Fig. 1. Alignment of the plant CK2α catalytic subunits with the human CK2α and CK2α′ sequences. The amino acid sequence of the three maize CK2α subunits, Zm a-1 (CAA43659), Zm a-2 (CAA72290), Zm a-3 (AAG36872) and the two Arabidopsis CK2α subunits At a-1 (Q08467) and At a-2 (Q08466) has been aligned with human CK2α′ , H alfa′ (AAA51548) and CK2α, H alfa (AAA355503). Invariant residues are indicated by asterisks and by shaded boxes, and dash indicates a gap introduced to maximize alignment. Characteristics domains of CK2α catalytic subunits, ATP binding site and the basic stretch (NLS) are underlined.

activity [23], it confers stability to the enzyme [24] and it provides specificity for the interaction with substrates and inhibitors [25]. Whereas in most organisms only one gene for CK2β has been described, two genes (*CKB1* and *CKB2*) have been identified in *Saccharomyces cerevisiae* [26]. At least two genes exist in *Drosophila melanogaster* [27, 28], plus the β-like protein *Stellate* [22]. In contrast to the catalytic subunits, deletion of *CKB1* and/or *CKB2* genes coding for regulatory subunits is not lethal for the yeast cells; it does not affect yeast growth under normal conditions but results in a phenotype of hypersensitivity to Na^+ and Li^+ cations [29].

The level of identity between plant, yeast and human CK2β regulatory subunits is not as high as in the case of CK2α subunits; for this reason complementation assays were needed in order to isolate CK2β regulatory subunits (CK2β1 and CK2β2) in *Arabidopsis thaliana* [10]. Recently, a third CK2β regulatory subunit (CK2β3) has been identified in *Arabidopsis* [11]. Data from the computational analysis of the Arabidopsis genome indicates the existence of a fourth CK2β subunit. During several years, there was controversy about the existence of CK2β subunits in maize. For instance, antibodies raised against chicken CK2β failed to