

recognize the presence of this protein in maize extracts [30]. Furthermore, the resolution of the crystal structure of *Zea mays* CK2 α [12] showed that the enzyme is more stable than recombinant human CK2 α . This stability and the high specific activity of the maize catalytic subunit allow speculating that it could exist without the presence of CK2 β . On the other hand, two forms of the maize enzyme were originally purified: CK2A, corresponding to the typical heterotetramer, and CK2B, which is a monomeric form related to the catalytic subunit CK2 α [30]. However, the properties of the monomeric form CK2B were different from those of the recombinant maize CK2 α subunit, because CK2B was unable to assemble with human CK2 β , whereas recombinant maize CK2 α does [31, 21]. Results obtained in our lab clearly demonstrate that multiple CK2 β regulatory subunits do exist and are expressed in maize [13].

The alignment between the plant CK2 β regulatory subunits and the human CK2 β sequence is shown in Fig. 2. The plant

CK2 β present an N-terminal extension of about 90 amino acids that shares no homology to other known proteins but it retains a significant level of amino acid identity (55%) between *Arabidopsis* and maize proteins. This N-terminal extension is not present in any other CK2 β from other organisms and its functionality is unknown.

It has been reported [32] that the last 33 residues of the human CK2 β regulatory subunit are relevant for oligomerization of the tetramer, as deletion of this region reduced the intensity of its interaction with the CK2 α catalytic subunit. It is noteworthy that all *Arabidopsis* and maize CK2 β subunits lack 20 of the mentioned 33 residues. This might imply that, in plants, the interaction between CK2 α / β subunits is weaker than in the case of the human CK2 holoenzyme, thus making possible the existence of the two forms of the maize CK2 enzyme that were originally purified, CK2A and CK2B [30].

All the plant CK2 β proteins present each of the major conserved features described for CK2 β subunits from other organ-

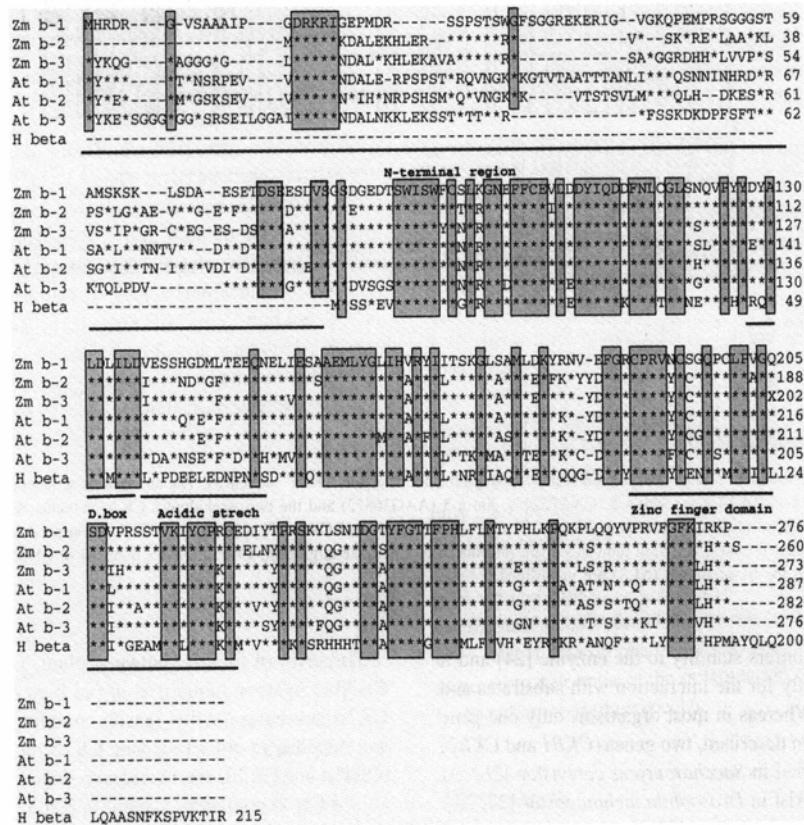


Fig. 2. Alignment of the plant CK2 β regulatory subunits with the human CK2 β sequence. The amino acid sequence of the three maize CK2 β subunits Zm b-1 (AAG36869), Zm b-2 (AAG36870), Zm b-3 (AAG36871) and the three *Arabidopsis* CK2 β subunits, At b-1 (AAA36869), At b-2 (AAA36870) and At b-3 (AF068318) as been aligned with human CK2 β , H beta (CAA34379). Invariant residues are indicated by asterisks and by shaded boxes, and dash indicates a gap introduced to maximize alignment. Characteristics domains of CK2 β regulatory subunits, the N-terminal region, the destruction box, the acidic stretch and the zinc finger domain are underlined.