

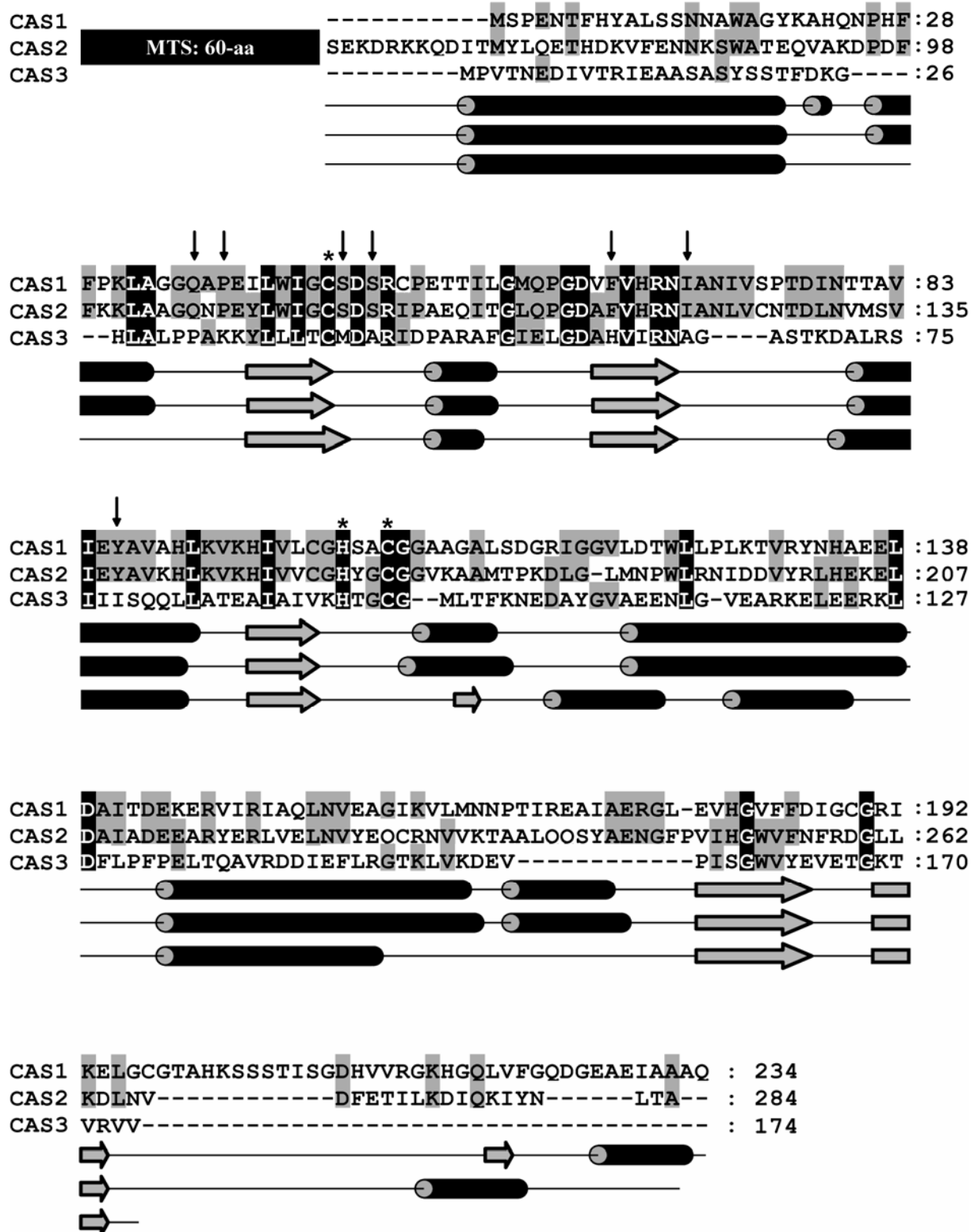


Figure S2: Amino acid sequence comparison of the three β -class CAs from *S. macrospora* with secondary structure predictions. Sequences of CAS1, CAS2 and CAS3 were aligned to maximized similarities using clustalX (Thompson et al. 2002). Conserved amino acids that are predicted to be important for zinc-coordination are marked by an asterisk. Amino acid

residues that are indicative to differentiate between plant-type and cab-type β -CAs are marked by arrows. Residues, which are conserved in all three sequences are indicated in white and boxed in black, identical amino acids in two sequences are boxed in grey. Secondary structures (barrels indicate α -helices and arrows denote β -strands) were predicted using the PSIPRED Protein Structure Prediction Server (McGuffin et al. 2000) are given below the amino acid sequence alignment. Amino acid positions are given as numbers at the side of the alignment.