

Fig. 1 Amino acid sequence comparison of RPA2 homologs from rice (*Oryza sativa*; OsRPA2), *Arabidopsis thaliana* (At3g02920 and At2g24490), *Homo sapiens* (HsRPA32), *Rattus norvegicus* (RnRPA30), *Mus musculus* (MmRPA30), *Schizosaccharomyces pombe* (SpRPA30) and *Saccharomyces cerevisiae* (ScRPA30). Sequences were aligned by the GeneDoc program. Conserved amino acids are highlighted: black highlighting indicate at least 6 out of 8 and gray highlighting at least 3 out of 8 similar sequences. Amino acid similarity groups are: D, N; E, Q; S, T; K, R; F, Y, W; and L, I, V, M. Two phosphorylation sites at conserved serine residues are indicated by an arrowhead above the respective amino acid. The bar above the sequences marks the deduced OB-folds that confer DNA-binding activity. The box highlights the XPA- and UDG-binding region that was identified in human HsRPA32

