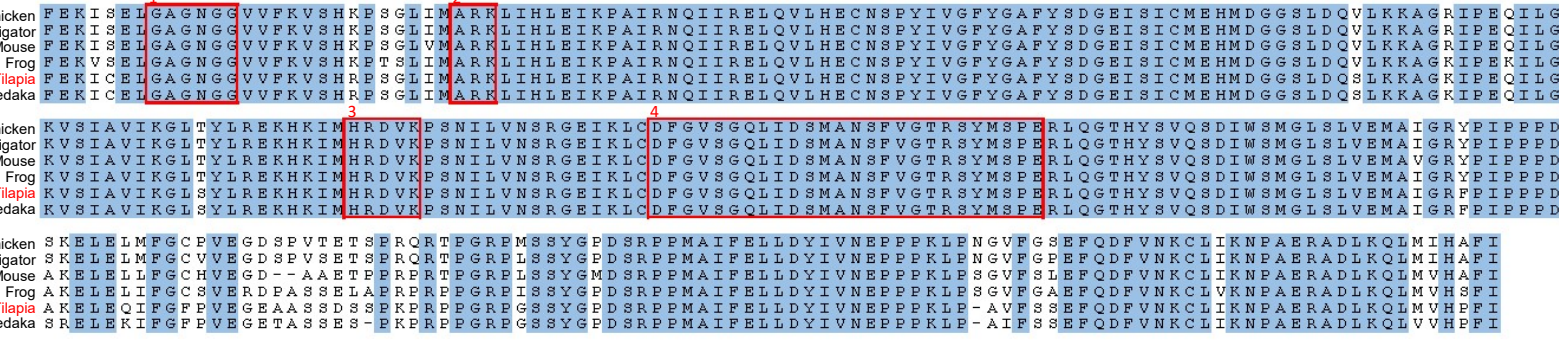


Figure S1

A



B



C

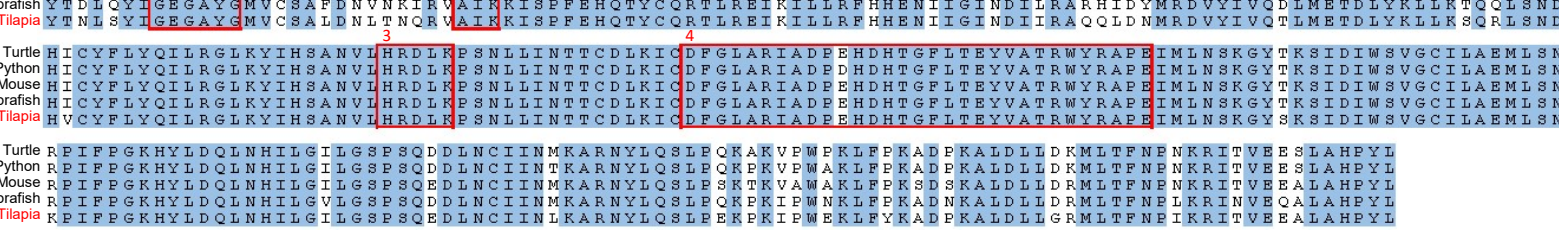


Figure S1. Multisequence alignment analysis of S/TKc domain in Mek1 (A), Mek2 (B) and Erk1 (C) from the indicated species. Amino acid residues with 100% identity are in blue, and similar amino acids are in white. The four conserved motifs are boxed: 1. Gly-rich region (GxGxxG) was an ATP binding loop; 2. AxK motif could couple with ATP phosphate group; 3. HRDxK motif is the catalytic loop; 4. Activation segment (starting with DFG, ending with APE or SPE) of almost all protein kinases. The accession numbers of selected sequences are listed in Table S1.