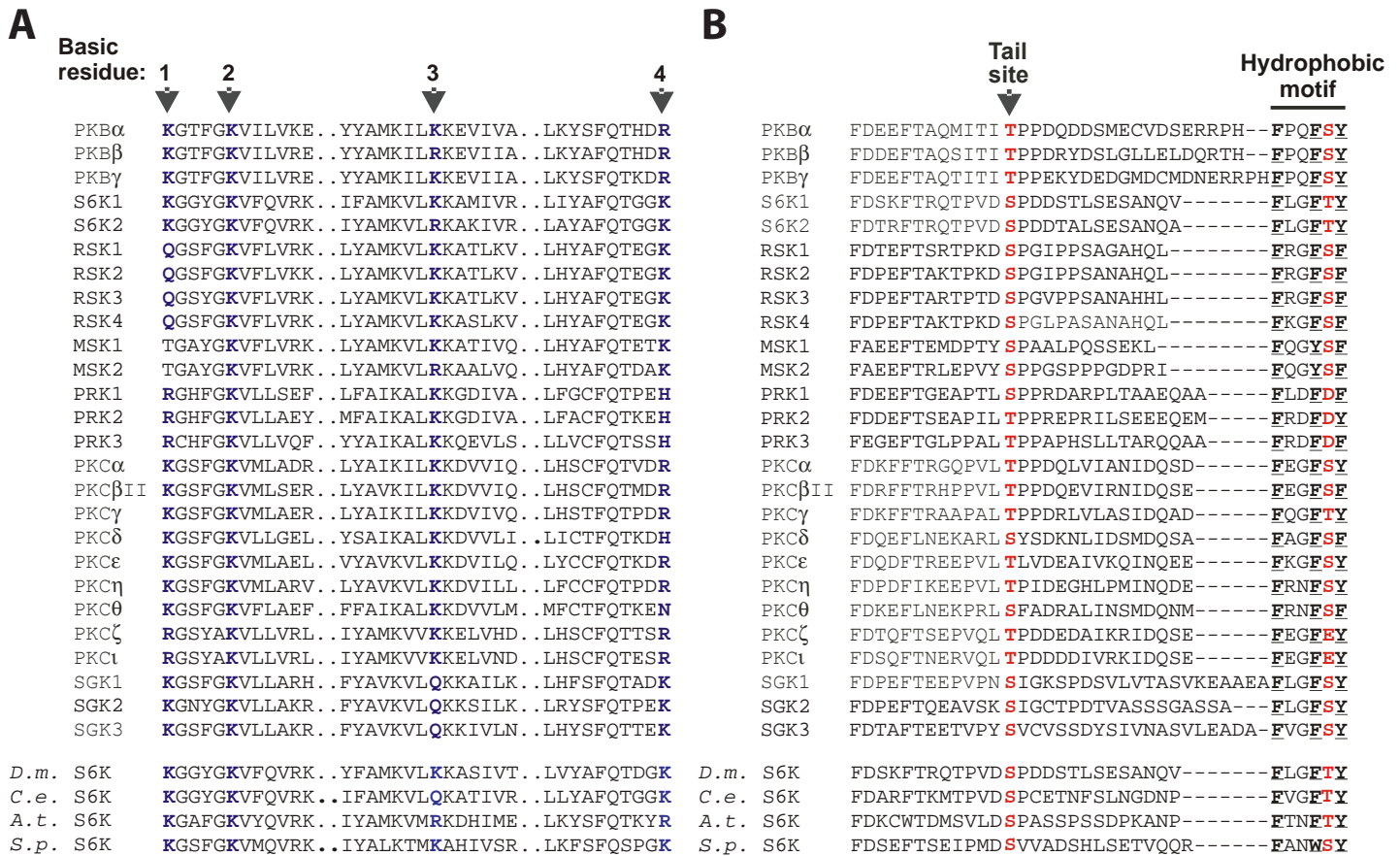


Supplementary Fig. 2



Supplementary Fig. 2. Conservation of the predicted binding site for the tail phosphoSer/Thr in 26 human growth factor-activated AGC kinases and in 4 orthologs of S6K. Partial amino acid sequence alignment of the kinase domain (A) and tail region (B) of various AGC kinases. Conserved basic residues that may bind the tail phosphoSer/Thr are shown in blue and labelled basic residue 1 to 4. Phosphorylation sites/phosphate-mimicking acidic residues are shown in red. The aromatic residues that define the HM are underlined. The sequence is human if nothing else is indicated.