Boxes framing the sequences represent the deduced different constitutive parts of the protein: the putative leader peptide (β), PSI domain (β/uniF020), spacer (hybrid domain) (β2/uniF020), β-like domain (β1/uniF020) with its MIDAS (α1), ADMIDAS (α2), and LIMBS (α3) sites, mid-region (hybrid domain) (α4/uniF020), four EGF domains (α5/uniF020), β-tail domain (α6), transmembrane region (α7), binding site of cytohesin (β3), Rack1 and α-actinin (β4), and potential cytoplasmatic-tail phosphorylation sites (+) are marked at the top of the sequences. Sequence data have been deposited at GenBank under accession no. EF585977.