Boxes framing the sequences represent the deduced different constitutive parts of the protein: the putative leader peptide (.), the seven repeats that surround the αf-domain (.), and the central divalent cation-binding motifs of the three COOH-terminal repeats (.), the αf-domain (.), with its MIDAS (.), the thydin (.), the genu (.), the CALF-1 (.) and CALF-2 (.) domains, the transmembrane region (.) and the highly conserved “GFFKR” motif (.)

The important “IαKGN” motif, P345-E353, K1125, are framed in black boxes. Cysteine residues (.), potential N-glycosylation sites (#), potential cytoplasmic-tail phosphorylation sites (+) and alleles E168D (D) and D621E (E) are marked at the top of the sequences. Sequence data have been deposited at GenBank under accession no. EF585976.