



**Figure 2—figure supplement 1.** Protein sequence alignment of *H. dujardini* cytotardin with selected human (*Homo sapiens*) cytoplasmic IF proteins. Human type I keratins K14 (epidermis) and K18 (simple epithelia) are forming IFs from obligatory heterodimers with type II keratins K5 (epidermis) and K8, respectively. The type III IF protein vimentin is able to form homopolymeric IFs. The position of the cytotardin rod domain, containing the coiled-coil and linkers (coil 1A, L1, coil 1B, L12, coil 2; predicted from the protein sequence alignment in Figure 2), is indicated by blue lines. Note the sequence similarities of the rod domain, especially at the rod domain-flanking intermediate filament consensus motifs (highlighted in red). Note also 42 amino acids in the coil 1B of cytotardin, which have been deleted from the ancestral cytoplasmic IF protein gene in chordates. The alignment (Clustal Omega) has been performed using Analysis Tool Web Services from the EMBL-EBI (McWilliam et al. 2013, Nucleic Acids Res. 41, W597–W600). (\*) indicates positions which have a single, fully conserved residue. (:) Indicates conservation between groups of strongly similar properties — scoring > 0.5 in the Gonnet PAM 250 matrix. (.) Indicates conservation between groups of weakly similar properties — scoring ≤ 0.5 in the Gonnet PAM 250 matrix.