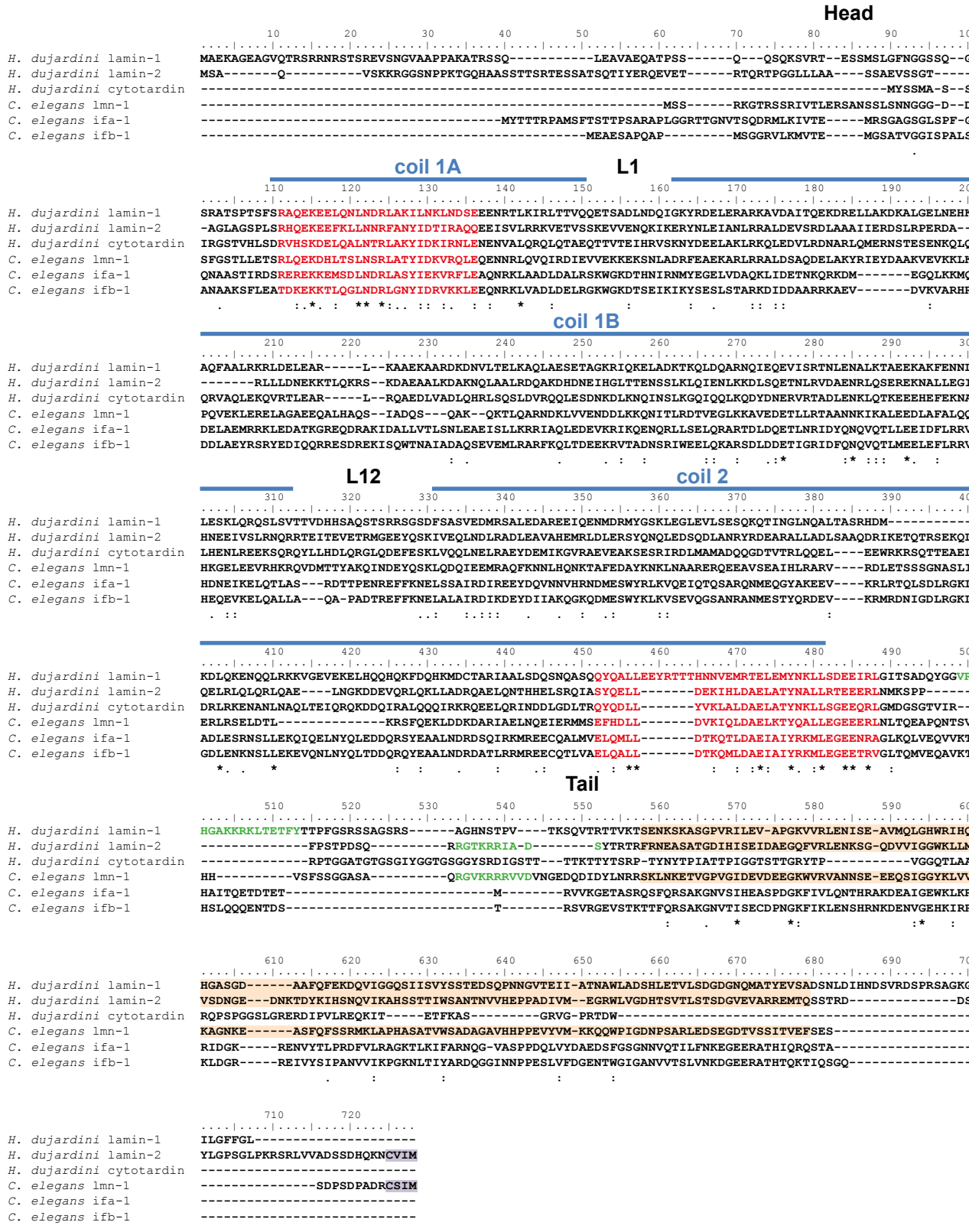

Figure 2—figure supplement 2. Protein sequence alignment of *H. dujardini* IF proteins with selected IF proteins from *Caenorhabditis elegans*. *C. elegans* ifa-1 and ifb-1 are epithelial cytoplasmic intermediate filament proteins, whereas lmn-1 represents the single lamin of *C. elegans*. The position 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. The intermediate filament consensus motifs are highlighted in red, the immunoglobulin fold (Ig fold) is marked in light orange, and the C-terminal prenylation motif of lamins (CaaX) is marked in purple. Note the presence of a prenylation motif in *H. dujardini* lamin-2 and *C. elegans* lmn-1 and its absence in the other proteins. 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.