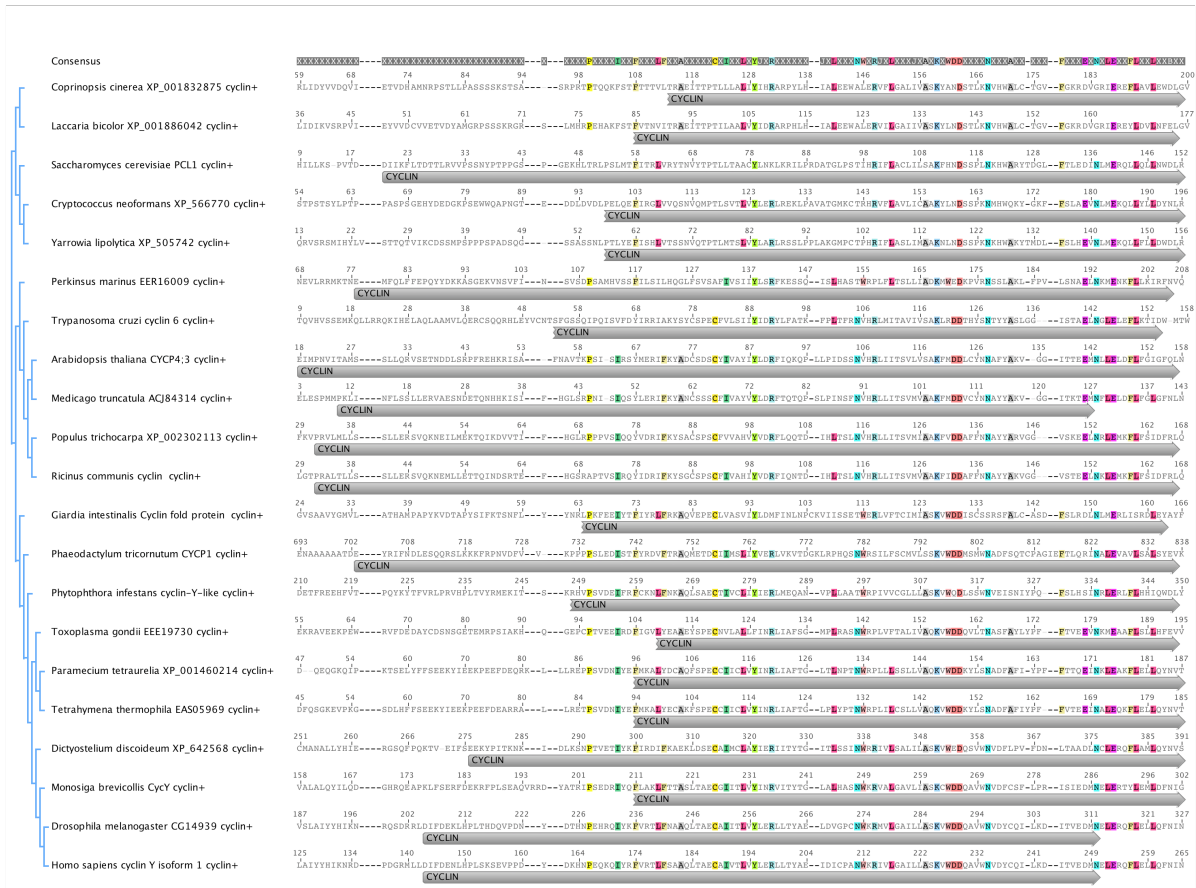


A. Alignment of the cyclin domains from human, *Drosophila*, and *Monosiga* cyclin Y and the most related protein from many distantly related species.



B. The Y-type cyclin domain is only distantly related to other cyclin domains.

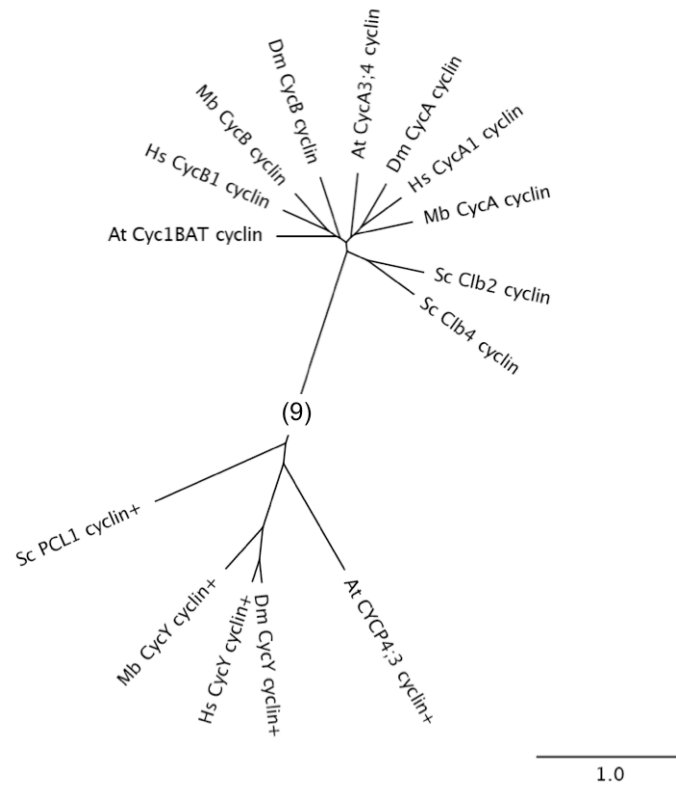


FIGURE S2.—The cyclin domain of Y-type cyclins is novel and conserved throughout the eukaryotic kingdom. (A) Alignment of the cyclin domains from the proteins that are reciprocal best-match BLAST hits of *Drosophila* CycY in many non-metazoan species. These proteins are also reciprocal best-match BLAST hits of human CycY. Alignments include the cyclin domains (arrows) as annotated by the Conserved Domain Database (MARCHLER-BAUER *et al.* 2009) along with the indicated flanking region of each protein. A consensus sequence was obtained as 31 residues that are identical in at least 50% of the proteins (colored); the *Drosophila* and human proteins each share 27 of these consensus residues. Only the top related protein from each species is shown. (B) Dendrogram showing sequence similarity among the cyclin domains from several distant species. Cyclin domains from *Drosophila melanogaster* (Dm) CycA, CycB, and CycY and their reciprocal best-match BLAST hits in human (Hs), *Monosiga brevicollis* (Mb), *Arabidopsis thaliana* (At), and *Saccharomyces cerevisiae* (Sc) were aligned. The cyclin domains from the Y-type cyclins included the annotated cyclin domain and small flanking regions as shown in Figure S2A (cyclin+). Only the top related protein from each species is shown. The length of the lines is proportional to sequence similarity. The lower cluster of Y-type cyclin domains and the upper cluster of A and B-type cyclin domains are separated by a relative distance of 9 (see scale bar for relative distances).