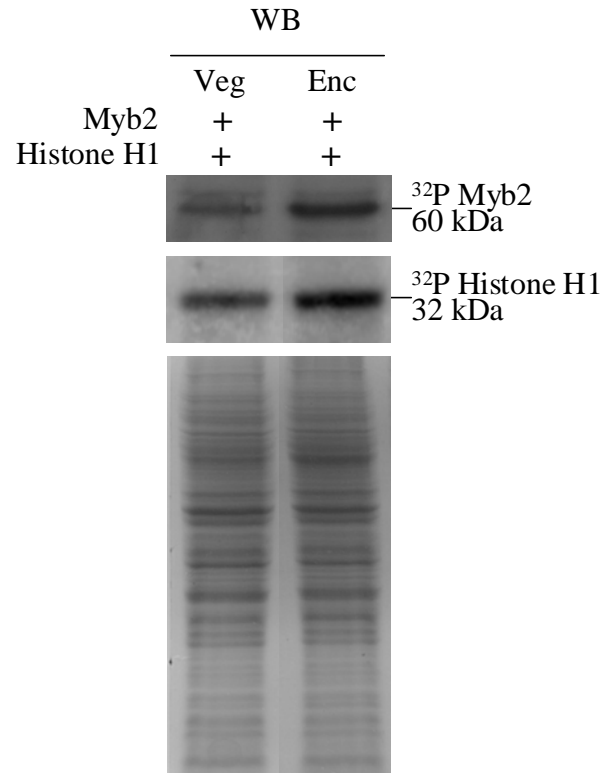


Figure S1



FIGUER S1. Phosphorylation of Myb2 by Cdks. The wild-type non-transfected WB cells were cultured in growth (Veg, vegetative growth) or encystation medium for 24 h (Enc, encystation). A p13^{SUC1}-associated fraction was prepared from each sample. Kinase activity was measured using purified recombinant Myb2 as a substrate. The bovine histone H1 protein was used as a positive control substrate. Equal amounts of total proteins were used for kinase assays for each sample as shown by Coomassie-staining.

Figure S2

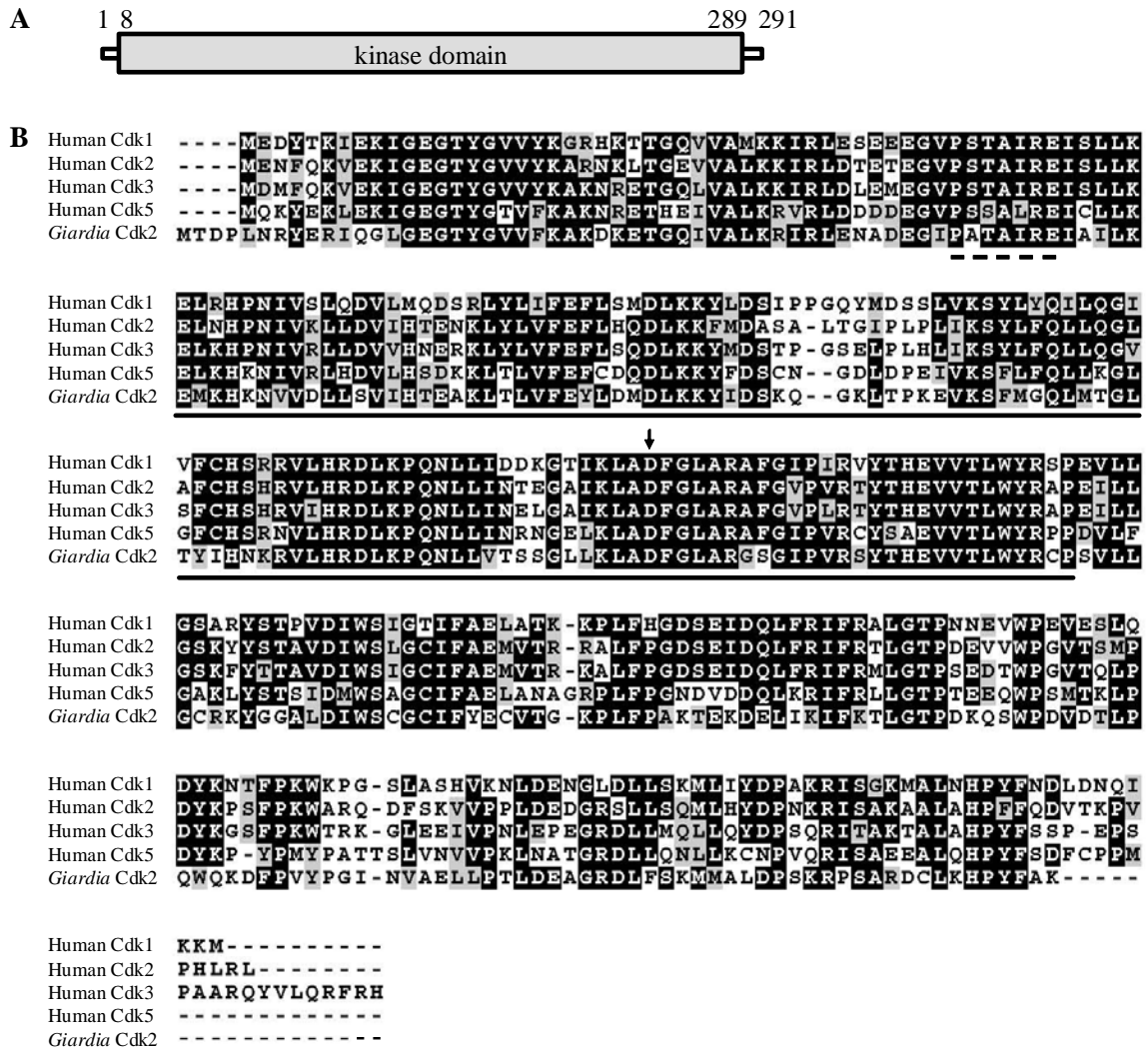


FIGURE S2. Domain architecture of Cdk2 protein and alignment of the Cdks. (A) Schematic representation of the giardial Cdk2 protein. The gray box indicates the kinase domain. (B) Alignment of amino acid sequences of the Cdk proteins. The full-length amino acid sequences of the Cdk proteins from human and *Giardia* were aligned by ClustalW 1.82 (90). GenBank accession numbers for human Cdk1, 2, 3, 5, and *Giardia* Cdk2 are [NP_001777](#), [NP_001789](#), [NP_001249](#), [NP_004926](#), and [XP_001709931.1](#), respectively. Letters in black boxes, letters in gray boxes, and hyphens indicate identical amino acids, similar amino acids, and gaps in the respective proteins, respectively. The conserved PSTAIRE motif (54) is indicated by a dotted line. A conserved Asp (residue 145) important for ATP-binding in human Cdk2 (74) is indicated by an arrow. A region (residues 49-174) deleted for analysis of the giardial Cdk2 function (Fig. 3A) is underlined.

Figure S3

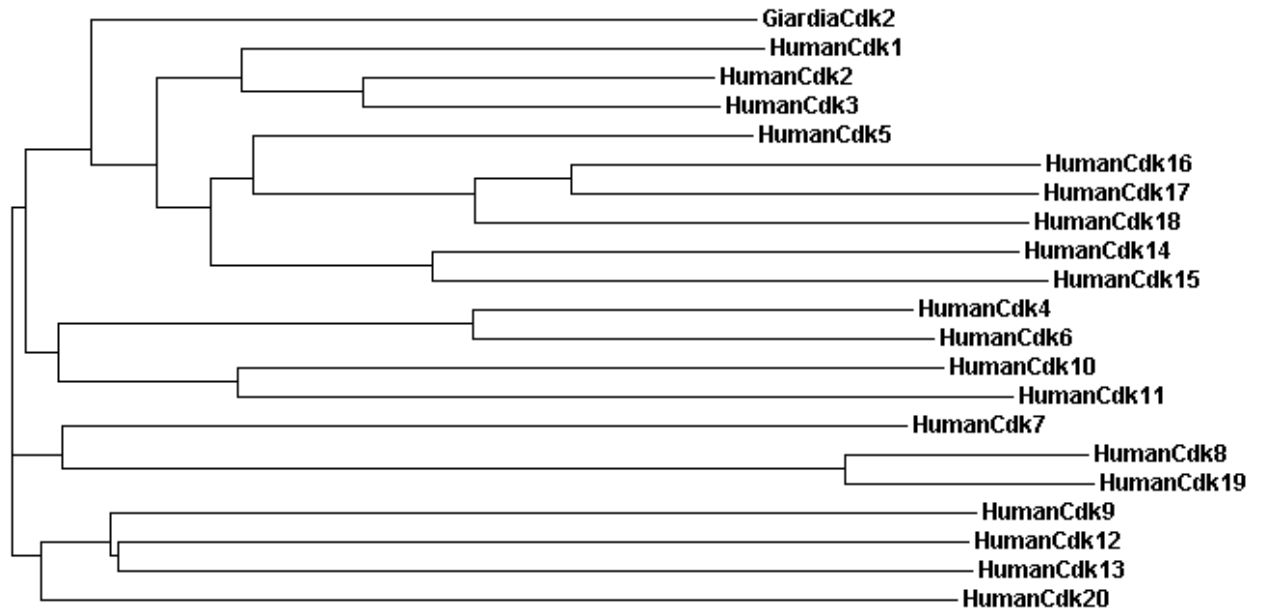


FIGURE S3. Phylogenetic analysis of giardial Cdk2 and human Cdk1-13. The sequences of giardial Cdk2 and human Cdk1-20 were subjected to multiple sequence alignment using Clustal W 1.82 with all default settings (Chenna *et al.*, 2003). The tree type was neighbor-joining. GenBank accession numbers for human Cdk1-20 and *Giardia* Cdk2 are NP_001777, NP_001789, NP_001249, NP_000066, NP_004926, NP_001250, NP_001790, NP_001251, NP_001252, NP_443714, NP_277027, NP_057591, NP_003709, NP_036527.1, NP_631897.1, NP_001163931.1, NP_001181692.1, NP_997668.1, NP_055891.1, NP_001034892.1, and XP_001709931.1, respectively.