The eukaryotic cell division cycle is a highly regulated process that consists of a complex series of events and involves thousands of proteins. Researchers have studied the regulation of the cell cycle in several organisms, employing a wide range of high-throughput technologies, such as microarray-based mRNA expression profiling and quantitative proteomics. Due to its complexity, the cell cycle can also fail or otherwise change in many different ways if important genes are knocked out, which has been studied in several microscopy-based knockdown screens. The data from these many large-scale efforts are not easily accessed, analyzed and combined due to their inherent heterogeneity. To address this, we have created Cyclebase-available at http://www.cyclebase.org-an online database that allows users to easily visualize and download results from genome-wide cell-cycle-related experiments. In Cyclebase version 3.0, we have updated the content of the database to reflect changes to genome annotation, added new mRNA and protein expression data, and integrated cell-cycle phenotype information from high-content screens and model-organism databases. The new version of Cyclebase also features a new web interface, designed around an overview figure that summarizes all the cell-cycle-related data for a gene.

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