The use of Artemis for the analysis and annotation of *Schizosaccharomyces pombe*

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Artemis is a DNA sequence viewer and annotation tool written in Java. It can read EMBL-format feature tables and display these within the context of the sequence and its six frame translation. The package can also display the results of external analyses, or plot the results of statistical calculations, performed on the sequence or CDS features. Artemis is used routinely for annotation of sequences up to 4 Mb.
Artemis is now the main annotation tool used for analysis of the genome of the fission yeast *Schizosaccharomyces pombe*. Currently 80% of the 12.8 Mb S. pombe genome is publicly available with the remainder of the genome sequence scheduled for completion by the millennium.
Artemis is being used to integrate the reanalysis and annotation of large S. pombe contiguous sequences, and should provide additional insights into structure and organisation of complex genomes.
The use of Artemis for the analysis and annotation of S. pombe will be presented.

Artemis is available to download from the Artemis Web site at
`http://www.sanger.ac.uk/Software/Artemis/`

The European S. pombe genome sequencing project can be accessed at
`http://www.sanger.ac.uk/Projects/S_pombe/`