

THE *SCHISTOSOMA MANSONI* GENOME SEQUENCE DRAFT: PROSPECTS FOR BIOLOGY AND POST-GENOMICS.

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Over the past 2-3 years, a draft genome sequence has been produced by the Wellcome Trust Sanger Institute in collaboration with The Institute for Genomic Research, using a whole genome shotgun sequencing strategy http://www.sanger.ac.uk/Projects/S_mansoni/. Approximately 3.8 million pooled reads have been produced by the two genome centres and have been assembled using the Phusion assembly algorithm. The estimated coverage is 7-fold. Despite a large body of publicly available EST resources, gene prediction for *S. mansoni* is proving quite challenging. Genes are typically large, with numerous small exons. Suffice to say, gene models are being continually refined, thanks to input from members of the research community. The current genome dataset, v4.0, complete with annotation as it currently stands, is available via GeneDB <http://www.schistodb.org>. This evolving dataset provides an applied resource for the research community, aspects of which I shall discuss.