

Parasitology

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Front Cover illustration: The rapidly expanding gene datasets for parasitic helminths provide the impetus for the development of tools such as RNAi (right-hand panel; Xhang and Hunter, this issue) and genetic transformation as well as methods to determine phenotypic outcomes (centre and left-hand panels; Zawadzki *et al.* and Selkirk *et al.*, both this issue) with the aim of defining gene function with the expectancy that these approaches will lead to novel control targets.

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