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# Leishmania After The Genome

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*Leishmania* is a vector-borne pathogenic parasite found in 88 countries worldwide and is the causative agent of leishmaniasis. The different *Leishmania* species infect macrophages and dendritic cells of the host immune system, causing symptoms that range from disfiguring cutaneous and mucocutaneous lesions, widespread destruction of mucous membranes, or visceral disease affecting the haemopoetic organs. The recent publication of the complete genome sequences of three different *Leishmania* species provides new insights into this leading pathogen and presents scientists with an exciting resource to improve the understanding of its complex molecular and cellular biology. In this book, internationally recognised Leishmania experts critically review the most important aspects of current *Leishmania* research, providing the first coherent picture of the organism's molecular and cellular biology since the publication of the genome sequence. Chapters are written from a molecular and genomic perspective and discuss in depth Leishmania-specific aspects of trypanosomatid biology and pathology. Topics include: diagnosis and epidemiology, genome structure and content, regulation of gene expression, the *Leishmania* metabolome, *Leishmania* differentiation, interaction with the sand fly vector, drug discovery, drug resistance, and much more. Essential reading for all researchers working with *Leishmania*, trypanosomes and protozoa. A recommended book for all biology and medical libraries.

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