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On the Cover: *Leishmania* parasite infections are the 9th largest infectious disease burden. The lifecycle requires precise adaptation to survive shifts between sandfly and mammalian hosts. Constitutive transcription in these parasites means gene regulation is reliant on *Leishmania* trans-regulators. We present a comprehensive analysis of mRNA binding proteins (mRBPs) and whole cell proteomes from the three main *Leishmania* lifecycle stages. For details, see the article by De Pablos *et al.*, pages 1271–1284.

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