Article of Significant Interest in This Issue

Structural Modeling of the *Treponema pallidum* Outer Membrane Protein Repertoire: a Road Map for Development of a Syphilis Vaccine

Syphilis, a sexually transmitted disease caused by *Treponema pallidum*, involves approximately 11 million new cases and 350,000 adverse pregnancy outcomes annually. Hawley et al. (e00082-21) performed advanced structural modeling of the Nichols strain’s repertoire of outer membrane proteins. The *T. pallidum* outer membrane protein repertoire (OMPeome) contains three transporter families, a multicomponent efflux system to extrude noxious molecules, and two “stand-alones” involved in outer membrane biogenesis. This work represents a major advance towards elucidating host-pathogen interactions during syphilis, understanding how *T. pallidum*, an extreme auxotroph, obtains a wide array of biomolecules from its obligate human host, and developing a vaccine with global efficacy.