

Departments of ¹Pediatrics; ²Medicine, ³Immunology, ⁴Molecular Biology and Biophysics, and ⁵Genetics and Genome Sciences, UConn Health, Farmington, CT 06030 USA; ⁶Computational Biology Core, University of Connecticut, Storrs, CT 06269 USA; ⁷Dermatology Hospital of Southern Medical University, Guangzhou, China; ⁸Department of Biology, Faculty of Medicine, Masaryk University, Brno, Czech Republic; ⁹Division of Infectious Diseases, Chapel Hill, NC 27599 USA; and ¹⁰Division of Infectious Diseases and Immunology, Connecticut Children's, Hartford, CT 06106 USA

Using a hand-operated pipeline, we inventoried the sequence variability on 3D models of 24 OMPs of 32 *T. pallidum* strains. Interestingly, we observed a broad variability spectrum between them; some OMPs (TP0859, a FadL ortholog; TP0126, TP0698 and TP0733, 8-stranded barrels; TP0969, a TolC ortholog) are fully conserved, and a few β -barrels (C-terminal domain of TprJ and TprC) are highly variable. It is worth mentioning that most of the variable residues were located in the ECLs of OMPs.