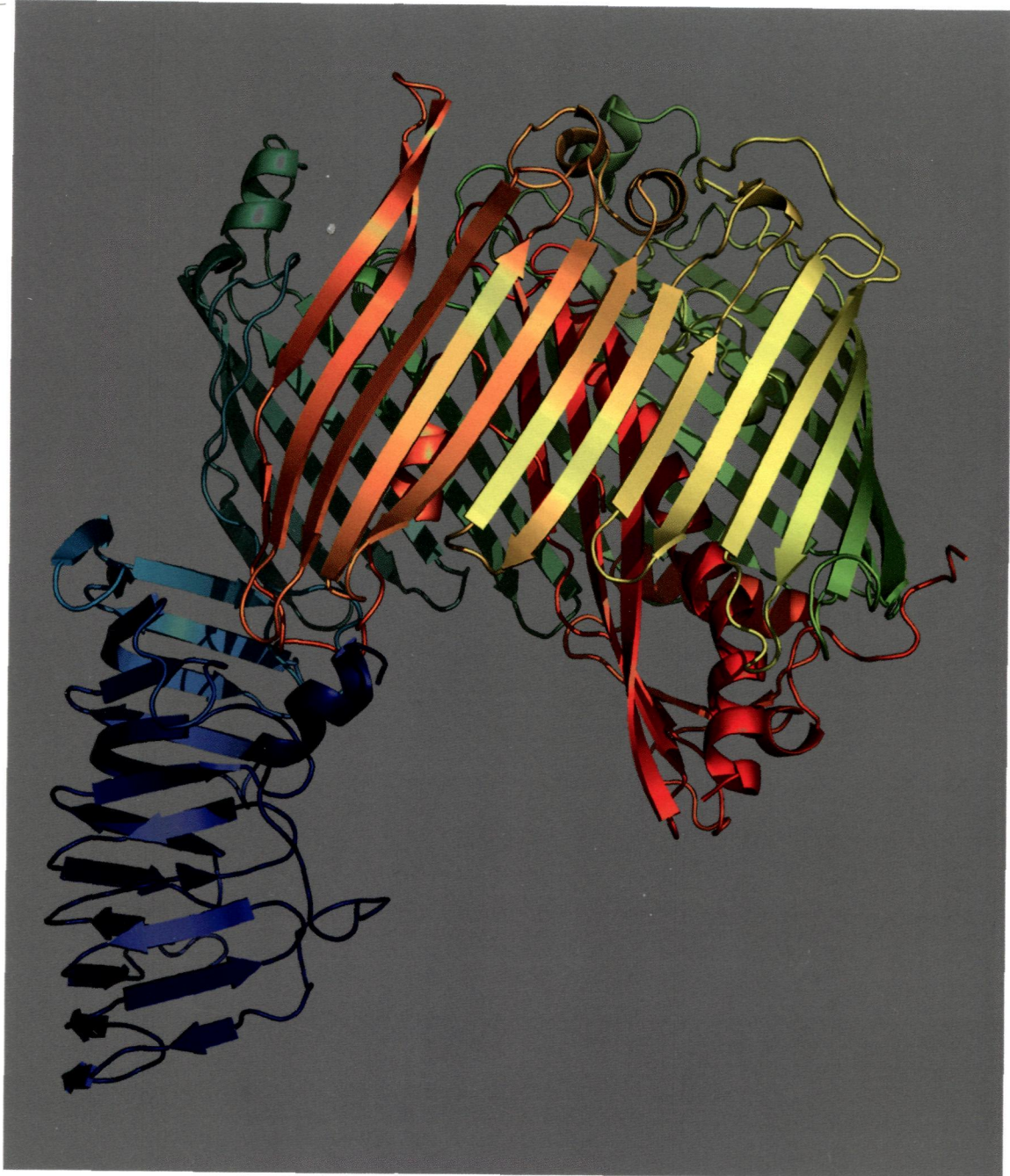


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AUTHOR CORRECTIONS

Correction for Anand et al., TprC/D (Tp0117/131), a Trimeric, Pore-Forming Rare Outer Membrane Protein of *Treponema pallidum*, Has a Bipartite Domain StructureArvind Anand, Amit Luthra, Star
Dunham-Ems, Melissa J. Caimano,
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Correction for Anand et al., The Major Outer Sheath Protein (Msp) of *Treponema denticola* Has a Bipartite Domain Architecture and Exists as Periplasmic and Outer Membrane-Spanning ConformersArvind Anand, Amit Luthra,
Maxwell E. Edmond, Morgan LeDoyt,
Melissa J. Caimano, Justin D. Radolf

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Cover photograph (Copyright © 2014, American Society for Microbiology. All Rights Reserved.): Model of the LptD/LptE complex from *Shigella flexneri* at 2.4-Å resolution. The structure reveals two domains in LptD: a β -jellyroll (in blue), for lipopolysaccharide delivery from the separate connected transperiplasmic filament subunits LptA/LptC, and the largest yet described 26-stranded transmembrane antiparallel β -barrel (in green-yellow-orange), for lipopolysaccharide insertion into the external leaflet of the outer membrane. LptE (in red) plugs the distal lobe of the β -barrel and functions to reorient the lipopolysaccharide into a vertical position, where it becomes bridged with magnesium ions to its nearest neighbors at the cell surface. Individual lipopolysaccharide molecules emerge laterally where the first and final LptD β -barrel strands merge. (See related article on page 3209.)