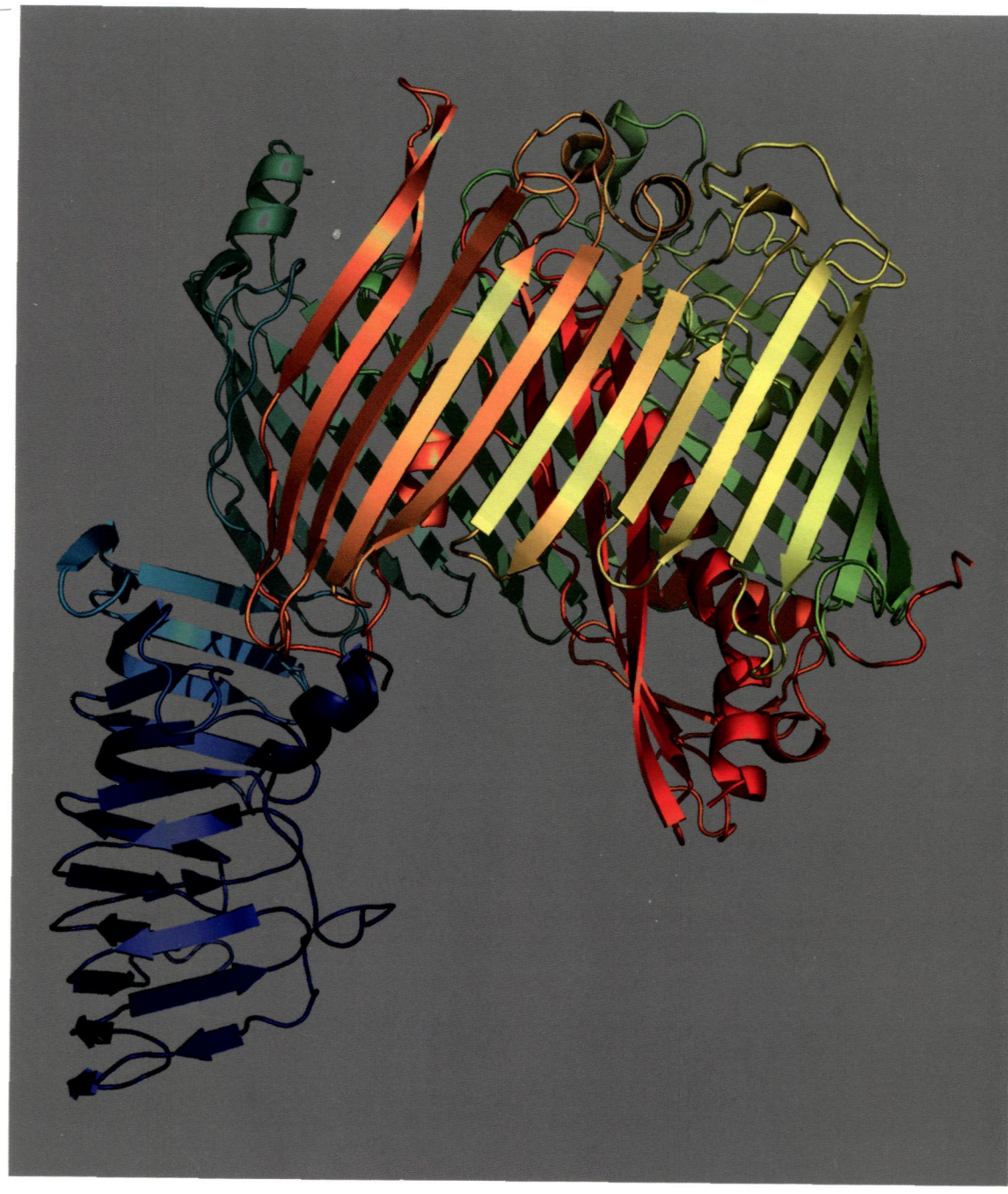

September 2014
Volume 196
Number 18
Published Twice Monthly

AMERICAN
SOCIETY FOR
MICROBIOLOGY

JB

Journal of Bacteriology

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Journals.ASM.org

SEPTEMBER 2014 • VOLUME 196 • NO. 18

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AUTHOR CORRECTIONS

Cover photograph (): 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.*)