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EVOLUTIONARY AND GENOMIC MICROBIOLOGY

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Genome of the Epsilonproteobacterial Chemolithoautotroph *Sulfurimonas denitrificans*

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Cover photograph (Copyright © 2008, American Society for Microbiology. All Rights Reserved.): Structure of a hemp fiber-processing pectate lyase of *Xanthomonas* origin, illustrating a rare example of single-amino-acid substitution that results in a 6°C increase in the apparent melting temperature of the enzyme without compromising its catalytic efficiency. The overall right-handed β -helical structure is rendered as a yellow ribbon. Side chains at nine mutation positions are shown as CPK models and colored by mutation outcomes as follows: at residue R236 (blue), which is partially solvent exposed, a mutation to phenylalanine is stabilizing; at residue A31 (red), which is also solvent exposed, a mutation to glycine is activating; and mutations at other positions (green) have a marginal or detrimental effect on thermal stability. (See related article on page 1183.)