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**Protein Crystallization by Surface Entropy Reduction: Novel Crystal Structures Showcase its Utility.** Y. Surendranath, I. Janda, Y. Devedjiev, U. Derewenda, M. Chruszcz, W. Minor, A. Joachimiak, Z.S. Derewenda, Dept. of Molecular Physiology and Biological Physics, Univ. of Virginia, Charlottesville, VA 22908.

One of the primary challenges in solving difficult structures is obtaining crystals of high diffraction quality. Surface entropy reduction (SER) is a novel method of inducing crystallization based on surface protein engineering, replacing residues with high conformational entropy with small amino acids conducive to forming intermolecular, lattice-forming contacts. Here, we report the application of this technique to selected targets of the *B. subtilis* structural genomics program, which failed to crystallize in the high-throughput pipeline. The *YkoF* gene product was crystallized after lysines 33 and 34 were replaced with alanines. A SeMet-labeled crystal was used to solve the structure by MAD at 1.6 Å. The refined model reveals a novel fold. A Ca<sup>2+</sup> ion forms crystal contacts with mutated residues from both symmetry related molecules. The structure suggested that the protein may function by binding thiamin. Structure solution of a complex of YkoF with a thiamin ligand confirmed that it is the first in a new class of bacterial thiamin binding proteins. The *YdeN* gene product was crystallized using a double mutant, K88A/Q89A. A SeMet-labeled crystal was used to solve the structure by SAD, and the model was refined at 1.8 Å resolution. Finally, the *HsIa* gene product was crystallized using a double mutant, E100A/Q101A, and the structure was solved at 1.9 Å resolution.