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Architectures of whole-module and bimodular proteins from the 6-deoxyerythronolide B synthase

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The 6-deoxyerythronolide B synthase (DEBS) is a prototypical assembly line polyketide synthase (PKS) that synthesizes the macrocyclic core of the antibiotic erythromycin. We report small angle X-ray scattering (SAXS) analyses of a full module and bimodule from DEBS as well as a set of domains for which high-resolution structures are available. In all cases, the solution state was probed under previously established conditions that ensure each protein is catalytically active. Atomic-resolution structures of DEBS fragments are consistent with SAXS data collected for each protein. Therefore, we used the available high-resolution structures of DEBS domains to model the architectures of the larger protein assemblies using rigid body refinement. Our data supports a model in which, the third module of DEBS forms a disc-shaped structure which is capable of caging the acyl carrier protein domain proximal to each active site. The molecular envelop of DEBS3 is a thin, elongated ellipsoid, and the results of rigid body modeling suggest that modules 5 and 6 stack collinearly along the 2-fold axis of symmetry.

Biography

Andrea L Edwards has completed her Ph.D. at the age of 28 years from University of Colorado at Boulder and is a postdoctoral scholar at Stanford University. She is a 2012 recipient of the A.P. Giannini Foundation postdoctoral fellowship award. She has published more than 10 papers in reputed journals and is serving as an editorial board member of the journal Biochemical Engineering Research and Application.

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