In silico analysis of the adenylation domains of the freestanding enzymes

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Motivation

This work presents a computational analysis of the molecular characteristics shared by the A domains from traditional nonribosomal peptide synthetases (NRPSs) and the group of the freestanding homologous enzymes: a-aminoadip ate semialdehyde dehydrogenase, a-aminoadipate reductase and the protein Ebony.

Results

The results of systematic sequence comparisons allow us to conclude that a specificity-conferring code, similar to that described for the NRPSs, can be recognized in such enzymes. The structural and functional roles of the residues involved in the substrate selection and binding are proposed through the analysis of the predicted interactions of the model active sites and their respective substrates. The indications deriving from this study can be useful for the programming of experiments aimed at a better characterization and at the engineering of this emerging group of single NRPS modules that are responsible for amino acid selection, activation and modification in the absence of other NRPS assembly line components.

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