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Abstract

The Cysteine Synthase (CS) enzyme, which is responsible for the synthesis of cysteine, plays non-canonical regulatory roles by binding to and altering the functions of various proteins. By binding to a small number of other proteins that have a C-terminal “CS-binding motif” that ends in a terminal ILE, it performs its moonlighting function in addition to its catalytic and regulatory functions in the cysteine biosynthesis pathway. As a result, we hypothesized that the “CS-binding motif” of numerous other distinct proteins could be controlled by CS. In this study, we validated our prediction using analytical and structural methods and developed an iterative sequence matching method for mapping CS's moonlighting biochemistry. We demonstrate, employing a minimal protein-peptide interaction system that five previously unknown CS-binder proteins involved in various metabolic processes interact species-specifically with CS. In addition, the findings demonstrate that the well-known CS-Binder, serine acetyltransferase (SAT), closely matches protein–protein interactions, including thermodynamic, competitive-inhibition, and structural characteristics.

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We tried to come up with a “protein-specific” strategy for looking