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From the protein-protein interactions analysis, we identified a list of drug targets which were central to this network. But as a case study, we have performed analysis with NadE protein only whereas; other drug targets can be analyzed in future studies.

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... the binding site residues are verified by using several benchmark systems where the topology of the unbound protein and the bound protein-ligand complex are known. Predictions are made on the

Identification and mapping of protein kinase A binding ...

... The muscle-specific protein, myospryn harbors a TRIM region located in the carboxy-terminal 550 amino acids of the full-length protein (3,739 amino acids) leaving well over 3,000 amino acids of the protein uncharacterized.

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An essential component of the goal to elucidate global biological function is the determination of protein-protein interaction networks. Current approaches for mapping protein-protein interactions include yeast two-hybrid system, affinity purification procedures based on immunoprecipitation (IP) 1 or a single (e.g.

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