Redox Proteomics of Arabidopsis thaliana

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It becomes increasingly clear that many important cellular processes are controlled by redox state of the cell. In general the activities of redox-controlled proteins are modulated by thiol-disulfide exchange between cysteines in proteins or between glutathione and a cysteine residue in a protein. Therefore, it will be interesting to see what proteins are in disulfide bond in a particular condition. We developed an affinity chromatography which specifically capture proteins with disulfide bond. The captured proteins were separated by polyacrylamide gel electrophoresis and identified by MALDI-TOF MS and Nanoelectrospray tandom mass spectrometry. We applied this method to A. thaliana and were able to isolate most proteins whose activities were known to be controlled by cellular redox state.

Protein interaction prediction system, PreDIN (prediction-oriented database of interaction network): a new tool for functional profiling

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The post-genomic view is expanding the protein's role as an element in a network of protein-protein interactions as well, in which it has a contextual or cellular function within functional modules. In this context, we developed a prediction system for protein-protein interaction by using a computational algorithm based on the weighted scoring system for domain interactions between interacting protein pairs. A statistical scoring system, named \"PID matrix score\" was designed and applied as a measure of interaction probability between domains. The prediction system gives about 50% sensitivity and 98% specificity. We applied this system to yeast genome and constructed a virtual protein interaction map for yeast. This predicted map covers 44% of known interactions. Based on the PID matrix, we develop a system providing several interaction information-finding services in the Internet. The system, named PreDIN (Prediction-oriented Database of Interaction Network) provides interacting domain-finding services and interacting protein-finding services. It is demonstrated that mapping of the genome-wide interaction network can be achieved by using the PreDIN system.