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A Prediction System for Protein Interaction (PreSPI) and Its Validation Dong Soo Han

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Since protein-protein interaction prediction techniques can give considerable benefits to biologists in terms of reducing time and efforts, many protein-protein interaction prediction techniques have been developed. Specially, PreSPI (http://prespi.icu.ac.kr) has adopted the domain combination based protein-protein interaction prediction method and provides protein-protein interaction prediction services to the public. However the usefulness of the prediction techniques is still unclear. A validation of the domain combination based protein-protein interaction prediction method is conducted focused on Androgen Receptor (AR). According to the validation, 60 proteins are predicted to be interacting with AR and 39 proteins are predicted to be non-interacting with AR. 21 out of 60 protein interactions were confirmed as true positive by DIP, HPRD, Medline literature search, whereas 39 predicted proteins are revealed to be validated in vivo. This indicates that if the prediction results from PreSPI are judiciously filtered and interpreted, biologists can obtain valuable information from the results.