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Proteome-wide Detection of Abl1 SH3-binding Peptides by Integrating Computational Prediction and Peptide Microarrays

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Abstract:
Protein-protein interactions are essential for regulating almost all aspects of cellular functions. Many of these interactions are mediated by weak and transient protein domain-peptide binding, but they are often under-represented in high throughput screening of protein-protein interactions using techniques such as yeast two-hybrid and mass spectrometry. On the other hand, computational predictions and *in vitro* binding assays are valuable in providing clues of *in vivo* interactions. We present here a systematic approach that integrates computer modeling and a peptide microarray technology to identify binding peptides of the SH3 domain of the tyrosine kinase Abl1 in the human proteome. Our study provides a comprehensive list of candidate interacting partners for the Abl1 protein, among which the presence of numerous methyltransferases and RNA splicing proteins may suggest a novel function of Abl1 in chromatin remodeling and RNA processing. This study illustrates a powerful approach for integrating computational and experimental methods to detect protein interactions mediated by domain-peptide recognition.

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