

Editorial for Journal of Proteomics and Genomics Research

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The application of proteomic and genomic methods has risen exponentially in the past few years. This inaugural issue of the open access Journal of Proteomics and Genomics Research presents a variety of such applications. Han and Collins use in silico methods to determine an updated profile of ESPs, eukaryotic signature proteins. Their method was applied to the genome of *Giardia lamblia* and they identified 274 ESPs. The protocol can be applied to any eukaryote and can incorporate new data easily. Ayme-Southgate, et al., used a combination of techniques to provide a comprehensive, cross-species analysis of the NH2-terminal Ig domains of insect projectin. By RT-PCR with degenerative primers, they amplified cDNAs encoding this region from dragonfly, cricket, and moth. They also applied in silico techniques, in this case for prediction of intrinsically disordered regions (IDRs). They propose that a combination of alternative splicing and disordered sequences contribute to the elasticity of this protein in the flight muscles of insects. The authors Li and Dorf used the approach of affinity purification followed by tandem mass spectrometry (AP-MS) to identify sets of interacting proteins in mammalian cells. They carefully optimized the purification method and developed an analytical tool, Z-score plus prey occurrence and reproducibility (ZSPORE) for data analysis. As an example, they investigated the GRB2 complex and identified 26 new GRB2 binding partners in addition to 24 known binding partners. The approach of AP-MS is becoming widely used and the difficulty is finding a way to verify the increased number of binding partners detected by the sensitive technique of mass spectrometry. Such an analytical tool could help researchers in narrowing their hits to the ones most likely to be physiologically significant.

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