Characterization of Post-Translational Modifications Using Counting Approaches

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Introduction
There is an increasing interest in the identification and characterization of protein post-translational modifications (PTMs). The vast amount of information obtained within a typical differential proteomics study makes the measure of PTMs challenging. We have begun to explore counting methods for differential analysis of PTM changes in proteomes and have developed a software program to aid in this approach. The Software Tool for Rapid Annotation of Proteins: Post-Translation Modification edition (STRAP PTM) uses a new counting-based PTM scoring algorithm to facilitate multi-sample PTM comparison through collation and visualization. The application imports parsed protein data and ranks peptides based on differential PTMs. Here we show the utility of STRAP PTM across data sets with increasing complexity and compare the results with label-free analysis using Progenesis LC-MS (NonLinear Dynamics).

Results
System 1: Oxidation of CD40L

PTM Map
Legend: 1 µM 5 µM 20 µM 50 µM

METYQSTOP RSIATGFLPS KMKFMVLTVT FLTQMGSA
LAFVYLHRDKIREDNH EDVFMKTCQ RONTGERSLL
LLCIEKEKG FEGFXDNL NKEEKTICKEN FRMCKQGRDP
QIAHVISEA SSKSTTVLQG LKFQTRVTSKL NTSLQG
LYVKQGGLY IAQVTFCN REASSGKPI ASLCXKSPGR
FERRILRAAN THSSAKPCGQ OSNJLQGe LQPPMASVFN

System 2: PTM Peptides in Plasma

PTM Standards (PS) Proteins PTM Mix 1

Control EGF

125 82 25

PTM Map
Legend: A (125 nM) B (62 nM) C (25 nM)

PS_532

PTM Map
Legend: Control ATP EGF

System 3: EGFR Phosphorylation

PTM Map
Legend: Control ATP EGF

Label-Free Comparison
Progenesis LC-MS

Label-Free Comparison
Progenesis LC-MS

Conclusions
PTM counting is a powerful technique for rapid semi-quantitative integration of large MS-based proteomics data sets.
STRAP PTM is a novel counting approach with a new scoring algorithm to rank PTMs in differential proteomics experiments.
STRAP PTM software is easy to implement on a PC and provides fast turnaround for large data sets.
Select STRAP PTM results correlate well with label-free results from both simple and complex data sets.

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