Phosphoproteomics is a branch of proteomics that identifies, catalogs, and characterizes proteins containing a phosphate group as a post-translational modification. Phosphorylation is a key reversible modification that regulates protein function, subcellular localization, complex formation, degradation of proteins and therefore cell signalling networks. With all of these modification results, it is estimated that between 30% - 65% of all proteins may be phosphorylated, some multiple times.

Based on statistical estimates from many datasets, 230,000, 156,000 and 40,000 phosphorylation sites should exist in human, mouse, and yeast, respectively.

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