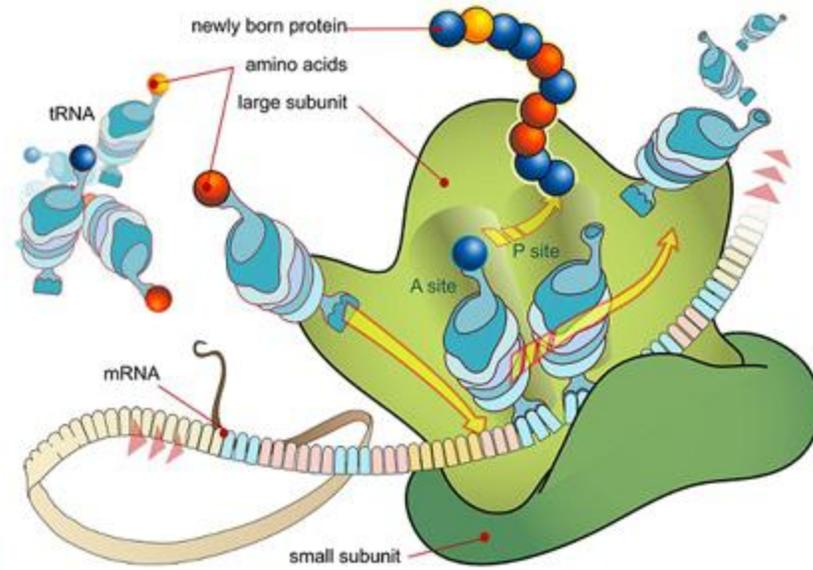
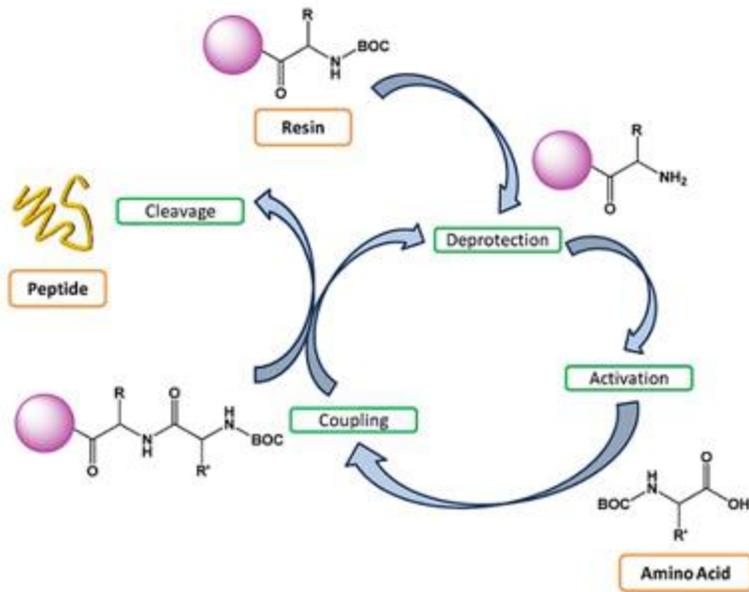




Creative
Proteomics

Custom peptide synthesis

In the quantitative proteomics research, several MS-based methodologies for relative quantification have been introduced for comparison of different proteomes from collected biological samples. Meanwhile, MS-based methods for absolute quantification of specific proteins have been developed to accurately determine the protein concentrations. According to the guidelines for bioanalytical methods, the establishment and validation of accurate analytic proposals require standard compounds of high purity for calibrating and quality controls. Currently the dominant quantitative strategy is usually a combination of shotgun method and isotope dilution strategy. The targeted proteins in the complicated biological samples would release free peptide fragments induced by specific enzymatic cleavage, and the stable peptides with unique primary sequences in the digest mixture would be utilized as surrogates for corresponding parent proteins, so the small-molecular peptides can be quantified to estimate the protein concentration.



Contact

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