

Abstract

Post-translational modifications are an important form of cellular regulation, including metabolism, growth, differentiation, transcription activation, membrane transport and cell death. Experimental identification of post-translational modifications (PTMs), especially phosphorylation, is still time consuming and expensive. Progress *in silico* PTM prediction tools was influenced an enormous growth of known sequences which are suitable for training set, processing and final result's interpretation. *In silico* prediction may facilitate the identification of potential phosphorylation sites and it may speed up in future research.