



Computational protocol for the identification and *in silico* analysis of protein tyrosine phosphatases (PTPs)

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Abstract: Tyrosine phosphorylation is one of the most studied and extensively used signaling mechanisms, controlled by a family of protein tyrosine phosphatases (PTPs). PTPs cooperate with protein tyrosine kinases to regulate signal transduction pathways. The regulation of this type of phosphorylation is reversible, dynamic and multifaceted. Here we present a computational approach for the identification and analysis of PTPs; can be used to support the hypothesis-oriented experimental research through the elaboration of online databases related to the concerned area. We present a protocol and schema for the identification of ortholog candidates and novel isoforms. Here we use sequence similarity searches and their utilization in the classification based on alignments and phylogenetic analysis.

Keywords: Tyrosine phosphorylation, orthologs, signal pathways, PTPs.

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