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## Determination of Acetylated Residues in Mammalian Proteins in Silico

By Amna Naeem

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Bioinformatics is a helpful tool for experimental studies. It is less time consuming and may provide a platform for experimental work. Post translational modification is investigated in silico, with the help of the bioinformatics tool MAPRes. This tool mines association pattern around a modified residue and non-modified residue. In this work association rules were mined around acetylated Lys residues in proteins. For this purpose 393 proteins were collected from the dbPTM database. The rules showed by MAPRes are highest preference for Alanine, Histidine, Lysine and Glycine in modified proteins and Leucine, Alanine, Serine, Glutamic acid and Glycine in non-modified proteins. The comparison of MAPRes analysis results for predicted Lys and non-predicted Lys substrate sites with those of Pail, Ensemblepail and PredMod prediction methods show a high conformity level, ranging from 47% to 70%. This high rate of conformity points to the accuracy of the algorithm and the technique of data mining applied in MAPRes. This work will be helpful for determining acetyltransferases sequence specificity in proteins which will be helpful in diseases such as...



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