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In Silico Determination of Methylated Residues in Mammalian Proteins

By Anila Saeed

LAP Lambert Academic Publishing Mai 2012, 2012.

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Bioinformatics is a helpful tool to 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. In this work association rules were mined around methylated Lys/Arg residues in protein. These rules show highest preference for Gly in modified protein Arg and Ser and Gln in modified protein Lys. 75% data support the preference of Gly in methylated Arg with 100% confidence level. 25% data support the preference of Ser and Gln in methylated Lys with 100% confidence level. The comparison of MAPRes analysis results for predicted Lys and predicted Arg substrate sites with those of MeMo, MASA and BPB-MMS prediction methods show a high conformity level, ranging from 13% to 72%. 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 methyltransferases sequence specificity in protein which will...



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