The genetic information for life is stored in the nucleic acids (i.e. DNA) while proteins are the workhorses that are responsible for transforming this information into physical reality. Proteins are the macromolecules that perform most important tasks in organisms, such as the catalysis of biochemical reactions, transport of nutrients, recognition and transmission of signals. Experimental determination of the function of a protein is a complex and laborious task requiring several months and the dedicated efforts of an entire lab. Due to large-scale sequencing projects, we currently know the genome (DNA) sequences of over 5000 organisms. This translates to over 5 million protein sequences. However, some degree of experimental annotation of function is available for only around 100,000 proteins. In this scenario development of computational methods for predicting protein function are of vital importance. During the course of this dissertation, I have developed the most accurate set of tools currently available for predicting the subcellular localization of a protein. These tools will significantly enhance our understanding of protein function.

Computational prediction of subcellular localization. - Abstract   Motivation: Protein subcellular localization is pivotal in understanding a proteins function. Computational prediction of subcellular localization h. Going from where to why—interpretable prediction of protein   MOTIVATION: Protein subcellular localization is pivotal in understanding a proteins function. Computational prediction of subcellular LOCALIZER: subcellular localization prediction of both plant and   During the last decade, there have been many efforts to develop computational methods to predict protein subcellular localization. Early studies Computational Prediction of Subcellular Localization - Springer Figure 4: Flow chart of the computational prediction for subcellular localization of E. coli B genome. Protein sequence of E. coli B genome (4205 ORFs) were Computational Prediction of Subcellular Localization SpringerLink Computational methods for predicting protein The CELLO method enables prediction of five subcellular Computational Prediction of Candidate Proteins for S-Nitrosylation Title: Computational Prediction of Protein Subcellular Localization from Amino Acid Sequence Using Soft Computing Techniques. Researcher: Betsy Sheena BUSCA: an integrative web server to predict subcellular localization It is widely recognized that much of the information for determining the final subcellular localization of proteins is found in their amino acid sequences. Thus the Computational prediction and analysis of subcellular localization of Automated prediction of bacterial protein subcellular localization is an important tool In addition, neither PSORT nor any of the other computational methods Computational Prediction of Subcellular Localization - ResearchGate Computational prediction of subcellular localization. Thus the prediction of protein localization sites is of both theoretical and practical interest. In most cases Bioinformatics predictions of localization and targeting. - NCBI - NIH Meinken and Min, 2012, Computational Prediction of Protein Subcellular Eukaryotes Protein subcellular location Secretome Computational prediction Validating subcellular localization prediction tools with - NCBI - NIH Computational predictions of subcellular localization are an important step of the most recent methods for the prediction of subcellular localization and protein   The structure and the subcellular localization of acyl-coA binding proteins (ACBP) in Brassica napus were computationally predicted in this study. Earlier, the