A bioinformatics approach to the structural and functional analysis of the glycogen phosphorylase protein family

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The enzyme glycogen phosphorylase plays a major role in carbohydrate metabolism by catalyzing the breakdown of glycogen into glucose subunits. In this study, we utilized computational methods to examine 282 sequences in the glycogen phosphorylase protein family. Specifically, we integrated multiple sequence alignments obtained from a variety of different algorithms into a single refined alignment using the GeneDoc program and identified twenty highly conserved motifs in the set of sequences using MEME. A phylogenetic tree, constructed using the PHYLIP suite software, SeqSpace, and GEnt, provided insight into the patterns of evolutionary descent for the protein family and organized sequences in the family into various subfamilies based on distinctive sequence characteristics. Preliminary analysis of the tree identified twelve major subfamilies as well as brain (B), liver (L) and muscle (M) isozymes within mammals in the Metazoan subfamily. Visualization of the conserved and variable features among subfamily members through Rasmol and VMD revealed their structural and functional significance to protein activity.