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The AmiGO database [14] provides a set of commands and interfaces to automate all database operations. Recent work also showed how to use AmiGO to solve some of the most common uses and problems. For instance, AmiGO can provide a list of all database and project-specific settings (e.g., database location, configuration settings, etc.), generating the appropriate URLs for dataset access in the JBrowse genome browser. To automatically identify the project-specific settings, the user simply has to configure a few options (e.g., organism species, project name) and the rest of the settings will be automatically applied. The AmiGO REST interface [15] is freely available in both batch and URL forms and provides an XML- and JSON-based document format. Using this interface, AMIGO can query GO terms in the current database, download subsets or subsets with particular identifiers, and download annotations for different species. More details are given in the AmiGO manual. This interface also makes it possible to download GO terms, their definitions, and their annotations in a set of tab-delimited files [16]. Accurate integration of gene/protein sequences into the GO is a complex and active area of GO and functional annotation research. Many different techniques have been used in the past, and the first tools, such as InterProScan [17] and Pfam [18], provided the ability to identify domains, including those in proteins with unknown function. More recently, tools such as CDD [19], HORIZON [20], and NetPhos [21], designed for various data types, have been developed. However, based on experience, it is not feasible to try all of these tools, given their complexity, time requirements, and the amount of data that they process. It is, however, possible to identify domains through sequence-based analysis. In fact, this is the approach used by AmiGO to map sequences to their GO terms and annotations.

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