

PROSITE

PROSITE consists of documentation entries describing protein domains, families and functional sites as well as associated patterns and profiles to identify them **PROSITE** is complemented by **ProRule**, a collection of rules based on profiles and patterns, which increases the discriminatory power of profiles and patterns by providing additional information about functionally and/or structurally critical amino acids.

(in sequence analysis) a database that houses diagnostic patterns, or signatures, usually derived from conserved regions of multiple sequence alignments of protein families or domains. Areas of conservation are encoded, for example, in the form of regular expressions, fingerprints, blocks, or *hidden Markov models* (HMMs). Examples of such databases include PROSITE, PRINTS, Blocks, and Pfam. They tend to include varying levels of annotation describing the protein families they encode and technical details concerning how the pattern was derived.