



Product Data Sheet

Product Name:	SeqIt™
Product Number:	AG-BT004-1
Description:	SeqIt™ is our web-based program for rapid database searching using amino acid sequences. SeqIt™ can find all proteins that contain a motif, no matter how variable it may be.

SeqIt™ is a protein database mining tool that uses specialized search engine technology to locate target sequence elements within a protein database. SeqIt™ can identify proteins containing similar or identical sequence elements corresponding to a user specified query sequence. The algorithm has been designed to emphasize database searching using relatively short query sequences (e.g., generally less than 20 residues in length). A major feature of the algorithm is that the query sequence can include a range of permutations such as unknown residues in a particular position, chemically conserved residues in a particular position, and a range of residues occurring between particular residues. The search can identify proteins having sequences that match exactly or with varying degrees of mismatch.

SeqIt™ can also find proteins that have your motif occurring within a defined number of residues from the amino or carboxy terminus. All identified proteins are aligned and have hypertext links to functional annotations. The program also colorizes specified residues in the alignments.

- SeqIt™ searches a database having approximately 200,000 protein sequences.
- SeqIt™ will format sequence alignments to colorize specific residues
- SeqIt will search for motifs in specific regions of all proteins (e.g., find proteins that have a certain motif)

occurring within a defined number of residues from the amino or carboxy terminus).

Terms of usage:

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