PatMatch Notes

TAIR's PatMatch software allows you to search for short nucleotide or peptide sequences, or ambiguous/degenerate patterns. It uses the same Arabidopsis datasets as TAIR's BLAST implementation.

Features

- Set the minimum number of hits per sequence.
- Set the maximum number of hits per sequence.
- The maximum number of hits retrieved is increased to 250,000.
- The minimum number of the input pattern is 3 residues.
- Select the number of total mismatches and types of mismatches allowed.
- Improved checking of input pattern syntax.
- Modified pattern syntax for peptide searches to conform to standard one-letter codes for amino acids.
- Patterns containing regular expressions now support mismatch options.
- Patterns containing wildcards now support mismatch options.