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Release notes for EpiQuest version 4.0.0.1

Your EpiQuest experience is improving as we work to release new features. Here is an account of the main improvements you will find in the latest release.

What is new?

- **EpiQuest IM** - a tool for predicting the actual immunogenicity of a protein's linear epitopes and sequence domains. The algorithm combines the relative antigenicity of the domain with its exposure to the immune system and allows you to define the epitopes that will be immunogenic when the organism is exposed to the native antigen's molecule. It is highly useful in defining epitopes that will elicit humoral immune response and will perform as immunodominant epitopes.
- **EpiQuest-H** - a tool to create a hydrophobicity profile of the proteins using up to 7 individual matrixes simultaneously.
- **EpiQuest-M** - a tool allowing you to view more stable regions of the molecule and the domains prone to mutations.
- **EpiStat** - a program to analyse the amino acid content of a molecule or group of molecules.
- New group of **Scanner** programs, that allow you to range according to the selected feature of a large group (database) of epitopes: by antigenicity for humoral response (**B-Scanner**), by functional strength in CTL epitope assays (**T-Scanner**), or by the epitope's immunological complexity/uniqueness (**C-scanner**).

What is fixed or improved?

- Detailed new **Manuals** were added for each individual program
- The option for creating multiple individual graphs for various types of analysis for a single sequence was added to **EpiQuest-B**.
- New **colour coding** was introduced for histograms obtained in different EpiQuest Programs.
- Many **new Demo/Test sequences** were introduced to individual programs. Now we are releasing presentations showing details of analysing and interpreting the results for these Demo sequences.

Overall, all programs were significantly improved with respect to ease of use, viewing and analysing the results. You will also likely the appreciate new layouts and new skin of the programs.