

## **REVIEW of Ocimum Biosolutions iRNAWiz** **By Peter Azmi**

### **Initial Impressions:**

Ocimum has made yet another great looking program. *iRNAWiz* is a visually appealing program with a clean, unencumbered interface. The neatness of the interface should be a great bonus for those who are not computer savvy.

### **Intuitiveness and Ease of Use:**

*iRNAWiz* is fairly intuitive to use. Operational order (importing new sequences and analyzing existing sequences) follows a logical format that should be intuitive for any user. Importing new sequences is as simple as copy and pasting text sequences into the new sequence window, or selecting a saved raw text sequence file (".txt"). Analyzing imported sequences for siRNA design is as easy as double clicking on the sequence that the user wishes to analyze. Search patterns for competent siRNA species are available as well as filters for outcomes which would not produce useful siRNAs.

Once the appropriate search patterns and filters are selected, the program generates a list of possible siRNA species. The user is then able to employ advanced analysis tools to further judge the value of generated siRNAs.

A basic to intermediate understanding of siRNA (RNAi) theory is helpful in making the best use of the various tools and settings offered in this program. There is a lot of information in this regard on the internet - this should be sufficient for the novice user.

### **Functionality and Features:**

A great number of options and optimization tools are offered in order to facilitate the choice of competent siRNA sequences. Furthermore, a great deal of flexibility has been incorporated into this program. Users can design and edit search and filter parameters to meet personal needs or to incorporate new advances in siRNA selection criteria. After the program generates a list of possible siRNAs, the user can very quickly identify competent sequences by sequentially using the tools and filters offered in the "analyze" window.

Filters and analysis tools include: open reading frame analysis (ORF analysis), a domain/ motif search, a secondary structure search (stem loop search) and a BLAST search for est alignments. Indeed, one of the most problematic issues in the design of siRNAs has been the tendency for RNAi species to silence more than

just the intended gene. In order to increase the specificity of siRNA species, the BLAST est alignment search will probably prove to be one of the most useful tools offered by *iRNAWiz*.

Other useful features include the ability to establish a local database for BLAST searches and to view details about selected siRNA species. This program's greatest asset however, might be the flexibility that it offers in creating unique siRNA search patterns and filters – thereby allowing users from many different biological interests to make best use of the program.

Problems encountered were few. However, I was unable to view all statistical information about selected siRNAs – perhaps due to a potential bug in the program. Also, even though *iRNAWiz* allows for a user to input search parameters and filter patterns, the novice or casual user would probably not know what to “search for” and as such it might be useful to include more pre-set search parameters.

#### **Value and Overall Impressions:**

*iRNAWiz* is an impressive program! The software seems to offer a fully integrated and flexible software solution for siRNA design. As the interest and demands for conducting siRNA knockdown experiments grow, *iRNAWiz* should be an indispensable tool for designing competent siRNAs.

The ease by which a user can tailor the program with advanced pattern searches will make using *iRNAWiz* very effective over the long run.

The time a user saves in design and optimization (as well as in trial and error resulting from non-optimal siRNA design) should quickly pay for the program. This product would be highly recommended for any laboratories interested in conducting siRNA-based gene knockdown experiments.