

CircDesigNA is an easy-to-use application for designing DNA and RNA sequences. The program supports both conventional DNA and RNA sequences as well as circular DNA and RNA. Related Software Bacterial Circular Genome Browser is an easy-to-use application for visualizing all the nucleic acid sequences on a circularized genome. It allows you to view both linear and circular forms of sequences on a single or multiple genomes. CircBac19 is a Perl program for creating circular DNA sequences based on 2D tiling and word of mouth. In 2D tiling each number of nucleotides must be adjacent to its predecessor and successor along the circle. Riboscan is an application that helps to search for riboswitches in the input file. It searches for the hits in the input file and shows the distribution of the hits along the full sequence of the input file. NRGene is a Perl package designed to provide access to the NCBI non-redundant nucleotide sequences and RefSeq protein database. It allows to search for genes by their E-value, by the type of the gene (coding or noncoding), by chromosomal location, by the description of the gene, and by the presence of their isoforms. This software has a beautiful and intuitive graphical interface that supports several types of queries. Hiv plot is a tool for creating and plotting phylogenetic trees in the format of a plain text file. The text file must contain the concatenated sequence of several Viruses and therefore must be transferred between several software. RNA Structure software is an application for modeling RNA secondary structures. It allows you to create RNA structures with different thermodynamic energies. Its main features are: creation of RNA secondary structures with the possibility of specifying energetic energies weighting of the secondary structures highlight of binding regions in the sequences creation of dot-matrix plots generation of sequences given their secondary structures Counting transcriptions per coding region (FPKM or RPM) RNADB is a relational database of RNA-related data. RNA genes, their expression and splice variants, and microRNAs with their targets are currently the most integrated data in this database. It was developed and is maintained by Uppsala University, Sweden. AHFD: access to High-Throughput-Functional-DNA (database and

What's New in the CircDesigNA?

... bHRP is a Perl script to examine the sequence of a given DNA or RNA oligonucleotide and return the positions of all of its dHRPs. dHRPs are defined as the runs of consecutive dN's and dC's that break one of the four base-pairing symmetries (A-T, G-C, G-U, U-C). bHRP is still in beta-stage of development. Last updated... Srseq is a standalone graphical application for the analysis of sequencing data. Srseq is a part of the RepEncode project but it is not dependent on it. All the analysis done in Srseq is done in a separate application, Octave, developed in house at the EMBL Institute of molecular biology, Aachen. Structure and components of the Srseq algorithm Srseq is based... SUGPLINK is a Unix application that implements PERL5 and compatible notation of the SUGPLINK standard, to predict the relationship between nucleic acid sequences and their experimental results such as the degree of hybridization. SUGPLINK standard has been developed in order to provide useful information to experimentalists by analyzing the nucleic acid sequence and struct... Apache JMeter is an extensible framework for the development and testing of applications that send HTTP requests. Apache JMeter is a popular and free open-source performance measurement tool. It can load test servers, client side applications and services over the World Wide Web. JMeter can be used in a web-based or stand-alone mode, and runs on multiple platforms, from s... se-lib is the Library Package for Biorseq. SE-LIB is implemented to be used with Biorseq software in order to help the biorseq for the implementation of new features and for better quality of the results. The library class implements a set of functions that make the usage of the functions in biorseq easier. Example: - The library has functions that change the labels of genes i... USPyran-Seq uses a high-throughput sequencing technology (pyrosequencing) to measure pyrophosphate production in UTP-GTP exchange reactions catalyzed by various ribonucleotide-diphosphate (NDP) kinases in a temporal fashion. This analysis then allows the quantification of the kinetic parameters.

System Requirements For CircDesignNA:

Minimum: OS: Windows XP, Vista, or Windows 7 Processor: Intel i3 2.5GHz or AMD Athlon 2.5GHz Memory: 2GB RAM Graphics: Nvidia GeForce 4500/ATI Radeon 3650 DirectX: Version 9.0 Storage: 6GB available space Network: Broadband internet connection Additional Notes: Awards Won: Year-End Competition: Most People, Most Views, Most Subscribers End of Competition: October 31

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