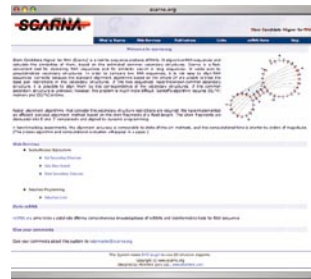


Scarna

Stem candidate aligner for RNA. A tool for sequence analyses of RNAs.

<http://www.scarna.org/>



SOCOS/CAN

Software for Kernel computation over SCFG and SOKOS genome-scanning version.

<http://www.cbrc.jp/sokos/>



INOH

A pathway database of model organisms including human, mouse, rat and others.

<http://www.inoh.org/>



ASTRA

A database of elementary patterns of alternative splicing and transcription.

<http://alterna.cbrc.jp/>



Wolf PSORT

Software to predict sub-cellular localization sites of proteins based on their amino acid sequences.

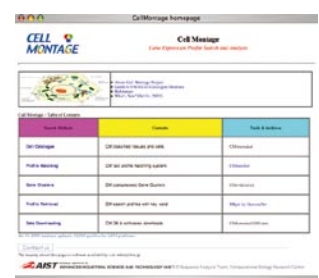
<http://wolfsort.seq.cbrc.jp/>



CellMontage

A system for searching gene expression databases for cells or tissues similar to the query gene expression profile.

<http://cellmontage.cbrc.jp/>



SEVENS

A database including seven transmembrane helix receptor candidates predicted from the complete genomes of several eukaryotes.

<http://sevencbrc.jp/>



GRIFFIN

A system for predicting GPCR — G-protein coupling selectivity using SVM and HMM.

<http://griffin.cbrc.jp/>



FORTE

A profile-profile comparison tool for protein fold recognition.

<http://www.cbrc.jp/forte/>



EzCatDB

A database of enzyme catalytic mechanisms.

<http://mbs.cbrc.jp/EzCatDB/>



CoCoozo

Parallel high-speed engine for peptide MS/MS ions search.

<http://www.cbrc.jp/cocoozo/>



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