Software & DBs

Sequence Analysis

ASTRA	A database of elementary patterns of alternative splicing and transcription.	http://alterna.cbrc.jp/
ALN	Pairwise alignment of biological sequence supporting spliced alignment procedures.	http://www.cbrc.jp/ALN/
GeneDecoder	Gene finding system for eukaryotes, based on hidden Markov models .	http://www.genedecoder.org/
SOKOS/CAN	Software for Kernel computation over SCFG and SOKOS genome-scanning version.	http://www.cbrc.jp/sokos/
Scarna	Stem candidate aligner for RNA. A tool for sequence analyses of RNAs.	http://www.scarna.jp/
GUPPY	A Program to visualize sequence annotation data of the genetic sequence data with graphical layout.	http://www.cbrc.jp/GUPPY/
fRNA Database	fRNA DB to aim to support new functional RNA gene discovery is composed of fRNAdb and UCSC GenomeBrowser for Functional RNA.	http://www.ncrna.org/

Expression Informatics

CellMontage	A system for searching gene expression databases for cells or tissues similar to the query gene expression profile.	http://cellmontage.cbrc.jp/

Protein Structure / Function Prediction

GENIUS II	An automated database system, in which protein coding regions in complete genomes are asingned to known 3D structure.	http://genius.cbrc.jp/
EzCatDB	A database of enzyme catalytic mechanisms.	http://mbs.cbrc.jp/EzCatDB/
PDB-REPRDB	A database of representative protein chains from protein data bank.	http://mbs.cbrc.jp/pdbreprdb/
DB-SPIRE	A database for structure-based protein Interaction research.	http://mbs.cbrc.jp/DB-SPIRE/
ConfC	A database of conformation changes in protein structures.	http://mbs.cbrc.jp/ConfC/
FORTE	An algorithm used to accurately align a target protein profile against a protein profile of known structure.	http://www.cbrc.jp/forte/
PAPIA	Parallel protein information analysis system.	http://mbs.cbrc.jp/papia/
POODLE	Prediction of order and disorder by machine learning.	http://mbs.cbrc.jp/poodle/

Membrane Protein Informatics

SEVENS	Comprehensive collection of human 7TM receptors.	http://sevens.cbrc.jp/
GRIFFIN	G-protein and receptor interaction feature finding instrument.	http://griffin.cbrc.jp/
TMBETA-GENOME	Annotation of beta-barrel membrane proteins in genomic sequences.	http://psfs.cbrc.jp/tmbeta-genome/
WoLF PSORT	Protein sub-cellular localization system.	http://wolfpsort.cbrc.jp/

Cellular System Analysis

INOH	A pathway database of model organisms including human, mouse, rat and others.	http://www.inoh.org/
CoCoozo	Parallel high-speed engine for peptide MS/MS ions search.	http://www.cbrc.jp/cocoozo/
ASIAN	Network inference tool by the combination of hierarchical clustering and graphical Gaussian modeling (GGM)	http://eureka.cbrc.jp/asian/
SGCAL	Structural glycomics calculation.	http://sgcal.cbrc.jp/

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