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The Bioinformatics Links Directory: a Compilation of Molecular Biology Web Servers

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ABSTRACT

The Bioinformatics Links Directory is an online community resource that contains a directory of freely available tools, databases, and resources for bioinformatics and molecular biology research. The listing of the servers published in this and previous issues of *Nucleic Acids Research* together with other useful tools and websites represents a rich repository of resources that are openly provided to the research community using internet technologies. The 166 servers highlighted in the 2005 Web Server Issue are included in the more than 700 links to useful online resources that are currently contained within the descriptive biological categories of the Bioinformatics Links Directory. This curated listing of bioinformatics resources is available online at the Bioinformatics Links Directory web site, http://bioinformatics.ubc.ca/resources/links_directory/. A complete listing of the 2005 *Nucleic Acids Research* Web Server Issue servers is available online at the Nucleic Acids web site, http://nar.oupjournals.org/, and on the Bioinformatics Links Directory web site, http://bioinformatics.ubc.ca/resources/links_directory/narweb2005/.

COMMENTARY

For the last two years, *Nucleic Acids Research* has published a special issue devoted to web servers. This Web Server Issue highlights bioinformatics servers that are provided to the research community using internet technologies. This issue represents a rich repository of resources that are freely accessible, ready to use, and have been subjected to rigorous peer review. In the 2005 Web Server issue, there are 160 articles that describe the utility and functionality of 166 servers. The scope of the server applications described in this issue covers diverse ground and is hosted on servers in many different locations around the world. Among the tools included are those for text mining (1,2), sequence feature detection (3,4), predicting aspects of protein 3D structure (5,6) and performing expression analyses (7,8). Combined with the annual Database Issue (9), these special issues at *Nucleic Acids Research* represent a valuable directory of resources for the global life sciences research community.

Starting in 2005, *Nucleic Acids Research* has teamed with the UBC Bioinformatics Centre at the University of British Columbia (UBC) to ensure that all of the URLs and a short description from the Web Server Issue are listed in the Bioinformatics Links Directory, a curated listing of bioinformatics resources. The Bioinformatics Links Directory (http://bioinformatics.ubc.ca/resources/links_directory/) is a community resource that contains a directory of freely available tools, databases and resources for bioinformatics research organized within categories familiar to a biologist. All servers from the Web Server Issue, as well as other selected resources, are categorized within the directory. Table 1 displays a summary of web servers from this issue organized within the Bioinformatics Links Directory classification scheme. This scheme organizes links under 11 top level categories (DNA, Protein, RNA, Other Molecules, Expression, Sequence Comparison, Model Organisms, Human Genome, Education, Literature and Computer Related) to enable quick and easy access to listings of relevant servers. For an online version of this listing of the 2005 *Nucleic Acids Research* Web Server Issue servers, please see http://bioinformatics.ubc.ca/resources/links_directory/narweb2005/.

The Bioinformatics Links Directory highlights web resources by providing a short synopsis for each link, placing links within descriptive biological categories, providing relevant PubMed citations, and identifying links as servers from the *Nucleic Acids Research* Web Server Issue. The Bioinformatics Links Directory is fully searchable and can be browsed through the biological categories. RSS feeds are available for recently added links and from within any biological category. All links are automatically checked to ensure that no broken links are presented.

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Table 1. Summary of servers from the Nucleic Acids Research 2005 Web Server Issue in the Bioinformatics Links Directory listed by category

Name	Description	URL[a]
Computer related		
Bio-programming tools		
CCT	CCT (Current Comparative Table) is a software package that you can install and set-up on your own system to help you to maintain and search databases.	http://orb.public.stolaf.edu/CCTdemo/
Statistics		
EVAcon	EVAcon automates the continuous evaluation of inter-residue contact prediction servers. Results can be viewed statically or dynamically generated.	http://www.pdg.cnb.uam.es/eva/con/index.html
DNA		
Annotations		
Babelomics	Babelomics is a suite of web tools for the functional annotation and analysis of groups of genes in high throughput experiments. Tools include: FatiGO, FatiWise, TransFAT, GenomeGO and TMT.	http://www.babelomics.org/
BASys	BASys (Bacterial Annotation System) is a tool for automated annotation of bacterial genomic (chromosomal and plasmid) sequences including gene/protein names, GO functions, COG functions, possible paralogues and orthologues, molecular weights, isoelectric points, operon structures, subcellular localization, signal peptides, transmembrane regions, secondary structures, 3-D structures, reactions and pathways.	http://wishart.biology.ualberta.ca/basys/
BRIGEP	The BRIDGE-based Genome-Transcriptome-Proteome Browser (BRIGEP) comprises three open-source web-based systems: GenDB, ProDB and EMMA. GenDB is a bacterial genome annotation system, ProDB is a storage and analysis system for mass spectrometry data, and EMMA is a storage and analysis system for transcriptome data.	https://www.cebitec.uni-bielefeld.de/groups/brf/software/brigep/
FeatureExtract	The FeatureExtract server extracts sequence and feature annotations, such as intron/exon structure, from GenBank entries and other GenBank format files.	http://www.cbs.dtu.dk/services/FeatureExtract/
MICheck	MICheck (Microbial Genome Checker) allows the user to verify gene annotations in previously published microbial genomes.	http://www.genoscope.cns.fr/agc/tools/micheck/
MutDB	MutDB is a database that associates protein structural information with mutations and polymorphisms in gene sequences. The data is derived from dbSNP and Swiss-Prot, and can be browsed by gene name or searched by keyword or by various identifiers.	http://www.mutdb.org/
SVC	SVC (Structured Visualization of Evolutionary Conserved Sequences) is a tool that can search for pairs of orthologous genes, align the protein coding sequences, and visualize the evolutionary sequence conservation mapped back onto the gene structure scaffold.	http://svc.molgen.mpg.de/
TargetIdentifier	TargetIdentifier is designed for identifying full-length EST cDNAs and functionally annotating EST cDNAs.	https://fungalgenome.concordia.ca/tools/TargetIdentifier.html
WebGestalt	WebGestalt (WEB-based GEne SeT AnaLysis Toolkit) is a system facilitating the analysis of sets of genes. Gene sets can be compared using set operations (intersection, union, etc.), different annotations can be selected and retrieved for the set, and sets can be visualized and organized by a user-selected method (Gene Ontology, chromosomal distribution, etc.). WebGestalt can also perform a statistical analysis to suggest areas of interest with respect to the set of genes selected.	http://genereg.ornl.gov/webgestalt/
Gene Prediction		
AUGUSTUS	AUGUSTUS is a eukaryotic gene prediction tool employing a more accurate method for modeling intron length distribution. It is particularly effective with larger sequences. It can be run through a web interface, or downloaded and run locally.	http://augustus.gobics.de/submission
GeneMark	The GeneMark family of programs employ Markov models and are specifically tuned for gene prediction for sequences from prokaryotes, viral genomes and eukaryotes.	http://opal.biology.gatech.edu/GeneMark/

Table 1. *Continued*

Name	Description	URL[a]
OrfPredictor	OrfPredictor is designed for prediction of Open Reading Frames (ORFs) and coding regions of a batch of EST or cDNA sequences.	https://fungalgenome.concordia.ca/tools/OrfPredictor.html
TargetIdentifier	TargetIdentifier is designed for identifying full-length EST cDNAs and functionally annotating EST cDNAs.	https://fungalgenome.concordia.ca/tools/TargetIdentifier.html
Mapping and assembly		
Projector 2	Projector 2 allows users to map completed portions of the genome sequence of an organism onto the finished (or unfinished) genome of a closely related species or strain. Using the related genome sequence as a template can facilitate sequence assembly and the sequencing of the remaining gaps.	http://molgen.biol.rug.nl/websoftware/projector2/
Phylogeny reconstruction		
Eclair	Éclair is a web service that implements the Eclat (EST CLAssification Tool) support vector machine (SVM) approach for the classification of species origin for, primarily, expressed sequence tags (ESTs).	http://eclair.btk.fi/
MLST	MLST (Multi Locus Sequence Typing) is a nucleotide sequence-based approach for the unambiguous characterization of isolates of bacteria and other organisms using the sequences of internal fragments of seven house-keeping genes.	http://www.mlst.net/
PHYML	Phyml is a program that constructs phylogenetic trees from sequence alignments using the maximum likelihood method.	http://atgc.lirmm.fr/phyml/
POWER	The Phylogenetic Web Repeater (POWER) allows users to perform phylogenetic analysis using the PHYLIP package. The POWER pipeline can start with processing either multiple sequence alignments (MSA) or can proceed directly with aligned sequences.	http://power.nhri.org.tw/
Sequence feature detection		
ARGO	ARGO is a tool for the detection and visualization of sets of region-specific degenerate oligonucleotide motifs in the regulatory regions of eukaryotic genes.	http://www.mgs2.bionet.nsc.ru/argo/
CisMols	CisMols (Cis-regulatory Modules) is a tool that identifies compositionally predicted *cis*-clusters that occur in groups of co-regulated genes within each of their ortholog-pair evolutionarily conserved *cis*-regulatory regions.	http://cismols.cchmc.org/
CONREAL	CONREAL (Conserved Regulatory Elements Anchored Alignment) allows identification of transcription factor binding sites (TFBS) that are conserved between two orthologous promoter sequences.	http://conreal.niob.knaw.nl/
Footer	Footer is a tool for identifying highly probable binding sites of known transcription factors using phylogenetic footprinting principles to analyse two homologous DNA sequences.	http://biodev.hgen.pitt.edu/Footer/
JCat	JCAT (Java Codon Adaptation Tool) is a tool that can adjust the codon usage of an input sequence to the selected organism. Useful for improving the expression of foreign genes in hosts with different codon usage.	http://www.prodoric.de/JCat/
OrfPredictor	OrfPredictor is designed for prediction of Open Reading Frames (ORFs) and coding regions of a batch of EST or cDNA sequences.	https://fungalgenome.concordia.ca/tools/OrfPredictor.html
P-Match	P-Match is a transcription factor binding site identification tool that increases its accuracy by combining weight matrix and pattern matching approaches. Registration at the site is free and is required to use P-Match.	http://www.gene-regulation.com/cgi-bin/pub/programs/pmatch/bin/p-match.cgi
PatMatch	PatMatch is a pattern matching tool that allows you to search for short (<20 residues) nucleotide or peptide sequences and can accomodate ambiguous/degenerate patterns.	http://www.arabidopsis.org/cgi-bin/patmatch/nph-patmatch.pl
POCO	POCO searches a set of promoters from co-expressed genes for nucleotide patterns that are over-represented.	http://ekhidna.biocenter.helsinki.fi/poco/
PromoterPlot	PromoterPlot takes the output from a TransFac search as input, and finds similarities between groups of promoters in an attempt to simplify the results of transcription factor searches. FASTA/Affymetrix IDs can also be used as input for a local installation of the tool.	http://promoterplot.fmi.ch/

Table 1. *Continued*

Name	Description	URL[a]
RibEx	Riboswitch Explorer (RibEx) searches sequences for known riboswitches and also for predicted bacterial regulatory elements that are highly conserved	http://www.ibt.unam.mx/biocomputo/RibEx.html
SynoR	SynoR searches vertebrate genomes for synonymous regulatory elements.	http://synor.dcode.org/
T-Reg Comparator	T-Reg Comparator is a tool for the analysis of transcriptional regulation that allows you to compare a set of position weight matrices (PWMs) against the T-Reg database (a collection of PWMs built from Transfac and Jaspar).	http://treg.molgen.mpg.de/
TargetIdentifier	TargetIdentifier is designed for identifying full-length EST cDNAs and functionally annotating EST cDNAs.	https://fungalgenome.concordia.ca/tools/TargetIdentifier.html
TOUCAN 2	TOUCAN 2 is a regulatory sequence analysis workbench for Metazoan sequences, directly linked with the Ensembl database and implementing SOAP clients for diverse alignment and motif detection algorithms.	http://www.esat.kuleuven.ac.be/~saerts/software/toucan.php
WordSpy	WordSpy allows the user to search for over-represented words in a set of sequences and to search for discriminative words using negative sequence data. WordSpy employs this functionality as a means to search for transcription factor binding motifs.	http://cic.cs.wustl.edu/wordspy/
Sequence polymorphisms		
ARTS	ARTS (Advanced Retrieval Tool for SNPs) can be used to retrieve SNP that are polymorphic between several different mouse strains to aid in the design of genome-wide SNP marker panels.	http://andromeda.gsf.de/arts
ISTECH SNPAnalyzer	ISTECH SNPAnalyzer is a tool for the statistical analysis of SNP data that includes Hardy Weinberg equilibrium (HWE), haplotype estimation, linkage disequilibrium (LD) and QTL analyses. Registration required; some browser requirements and set-up necessary.	http://www.istech.info/istech/board/login_form.jsp
MuPlex	Multi-Objective Multiplex PCR Assay Design (MuPlex) is a tool to assist in the design of multiplex PCR assays. MuPlex takes a set of DNA sequences and other experimental information as input and provides a set of multiplex PCR assays intended to cover as many of the user-supplied sequences as possible.	http://genomics14.bu.edu:8080/MuPlex/MuPlex.html
MutDB	MutDB is a database that associates protein structural information with mutations and polymorphisms in gene sequences. The data is derived from dbSNP and Swiss-Prot, and can be browsed by gene name or searched by keyword or by various identifiers.	http://www.mutdb.org/
nsSNPAnalyzer	nsSNPAnalyzer is a tool to predict whether a nonsynonymous single nucleotide polymorphism (nsSNP) is phenotypically neutral or disease associated.	http://snpanalyzer.utmem.edu/
PupasView	PupasView takes a single gene identifier as input and reports SNPs that have the potential to affect phenotype. In addition to looking for potential amino acid changes, PupaSNP also searches for SNPs with the potential to affect proper transcription, such as those in intron/exon boundaries, predicted transcription factor binding sites, and exonic splicing enhancers.	http://pupasview.bioinfo.cnio.es/
SNP Cutter	SNP Cutter is a tool that automates PCR-RFLP assay design for SNP genotyping.	http://bioinfo.bsd.uchicago.edu/SNP_cutter.htm
SNPserver	SNPServer combines BLAST, cap3 and a SNP discovery module into a single pipeline for the discovery of SNPs in user submitted files or dynamically created assemblies.	http://hornbill.cspp.latrobe.edu.au/snpdiscovery.html
Sequence retrieval and submission		
EBI Tools	EBI Tools is a project that aims to provide programmatic access to the various databases and retrieval and analysis services EBI provides through Simple Object Access Protocol (SOAP) and other related web service technologies.	http://www.ebi.ac.uk/Tools/webservices/
FeatureExtract	The FeatureExtract server extracts sequence and feature annotations, such as intron/exon structure, from GenBank entries and other GenBank format files.	http://www.cbs.dtu.dk/services/FeatureExtract/
MRS	MRS is a biological data retrieval system that can be accessed over the web, or installed and used locally. MRS indexes several flat-file data sets for searching, including EMBL nucleotide, UniProt, PDB and KEGG. Searches can be performed globally, or on one or more flat file fields per data set.	http://mrs.cmbi.ru.nl/

Table 1. *Continued*

Name	Description	URL[a]
Tools for the bench		
AMOD	AMOD (Assisted Morpholino Design) is a tool for designing antisense morpholino oligonucleotides (reagents to modulate gene expression) for an input sequence.	http://www.secretomes.umn.edu/AMOD/
ASePCR	ASePCR (Alternative Splicing electronic PCR) is a tool for carrying out e-PCR to detect differences in amplicon sizes in transcripts from different tissues and organs.	http://genome.ewha.ac.kr/ASePCR/
Assembly PCR Oligo Maker	Assembly PCR Oligo Maker is a tool for designing oligodeoxynucleotides for the PCR-based construction of long DNA molecules.	http://publish.yorku.ca/~pjohnson/AssemblyPCRoligomaker.html
DINAMelt	DINAMelt is a tool for predicting hybridization and folding (secondary structure) of DNA and RNA using equilibrium thermodynamic methods.	http://www.bioinfo.rpi.edu/applications/hybrid/
dnaMATE	dnaMATE calculates a consensus melting temperature ($_{Tm}$) for any given short DNA sequence (16–30 nt) based on three independent thermodynamic data tables. Stand-alone version available; list of other melting temperature calculation servers also provided.	http://dna.bio.puc.cl/tm.html
dsCheck	dsCheck takes a nucleotide sequence as input and estimates off-target effects caused by dsRNA (double-stranded RNA) employed in RNAi studies. dsCheck can be used either to verify previously designed dsRNA sequences, or to design off-target minimized dsRNAs.	http://dscheck.rnai.jp/
E-RNAi	E-RNAi is a tool for designing and evaluating dsRNA constructs suitable for RNAi experiments in *Drosophila* and *Caenorhabditis elegans*; can also be used for the design of enzymatically digested long dsRNA (esiRNAs) for mammalian cells.	http://e-rnai.dkfz.de/
MuPlex	Multi-Objective Multiplex PCR Assay Design (MuPlex) is a tool to assist in the design of multiplex PCR assays. MuPlex takes a set of DNA sequences and other experimental information as input and provides a set of multiplex PCR assays intended to cover as many of the user-supplied sequences as possible.	http://genomics14.bu.edu:8080/MuPlex/MuPlex.html
OligoWiz	OligoWiz 2.0 is a client for microarray probe design that allows for the integration of sequence annotations, probe quality parameters and the placement of multiple probes per transcript.	http://www.cbs.dtu.dk/services/OligoWiz2/
PriFi	PriFi is a tool for designing and evaluating primer pairs based on the input of a DNA sequence alignment; useful for the PCR amplification of homologs.	http://cgi-www.daimi.au.dk/cgi-chili/PriFi/main
SOP3v2	SOP3v2 takes a list of gene names, a list of reference sequence IDs or a chromosomal location as input and provides a set of PCR and sequencing primers as output. These primers are optimized for sequence-based genotyping assays.	http://imgen.ccbb.pitt.edu/sop3v2/
Stitchprofiles.uio.no	Stitchprofiles.uio.no is a server that performs web-based computations on DNA melting. In addition to creating stitch profile diagrams representing the alternative conformations that partly melted DNA can adopt, the server can also plot the classical melting curves, probability profiles and temperature profiles.	http://stitchprofiles.uio.no/
Education		
Directories and portals		
EBI Tools	EBI Tools is a project that aims to provide programmatic access to the various databases and retrieval and analysis services EBI provides through Simple Object Access Protocol (SOAP) and other related web service technologies.	http://www.ebi.ac.uk/Tools/webservices/
Expression		
cDNA, EST, SAGE		
AntiHunter 2.0	AntiHunter 2.0 is a tool to detect potential EST antisense transcripts within a given genomic region from the analysis of BLAST output.	http://bioinfo.crs4.it/AH2.0/
Babelomics	Babelomics is a suite of web tools for the functional annotation and analysis of groups of genes in high throughput experiments. Tools include: FatiGO, FatiWise, TransFAT, GenomeGO and TMT.	http://www.babelomics.org/
Eclair	Éclair is a web service that implements the Eclat (EST CLAssification Tool) support vector machine (SVM) approach for the classification of species origin for, primarily, expressed sequence tags (ESTs)	http://eclair.btk.fi/

Table 1. *Continued*

Name	Description	URL[a]
GBA Server	The GBA Server is an EST-based gene expression profiling and analysis platform. It implements the GBA (Guilt-by-Association) algorithm and, given a UniGene cluster, can be used to find genes with similar expression patterns.	http://gba.cbi.pku.edu.cn
PatMatch	PatMatch is a pattern matching tool that allows you to search for short (<20 residues) nucleotide or peptide sequences and can accomodate ambiguous/degenerate patterns.	http://www.arabidopsis.org/cgi-bin/patmatch/nph-patmatch.pl
T-STAG	Tissue-Specific Transcripts And Genes (T-STAG) is a system integrating EST, gene expression, alternative splicing and human–mouse orthology information for the analysis of tissue-specific gene and transcript expression patterns.	http://tstag.molgen.mpg.de/
TargetIdentifier	TargetIdentifier is designed for identifying full-length EST cDNAs and functionally annotating EST cDNAs.	https://fungalgenome.concordia.ca/tools/TargetIdentifier.html
WebSage	WebSage is a tool that performs statistical analysis of SAGE data.	http://bioserv.rpbs.jussieu.fr/websage/
Gene regulation		
AMOD	AMOD (Assisted Morpholino Design) is a tool for designing antisense morpholino oligonucleotides (reagents to modulate gene expression) for an input sequence.	http://www.secretomes.umn.edu/AMOD/
AntiHunter 2.0	AntiHunter 2.0 is a tool to detect potential EST antisense transcripts within a given genomic region from the analysis of BLAST output.	http://bioinfo.crs4.it/AH2.0/
ARGO	ARGO is a tool for the detection and visualization of sets of region-specific degenerate oligonucleotide motifs in the regulatory regions of eukaryotic genes.	http://www.mgs2.bionet.nsc.ru/argo/
AthaMap	AthaMap is a genome-wide map of putative transcription factor binding sites in *Arabidopsis thaliana*.	http://www.athamap.de/
Babelomics	Babelomics is a suite of web tools for the functional annotation and analysis of groups of genes in high throughput experiments. Tools include: FatiGO, FatiWise, TransFAT, GenomeGO and TMT.	http://www.babelomics.org/
CisMols	CisMols (*Cis*-regulatory Modules) is a tool that identifies compositionally predicted *cis*-clusters that occur in groups of co-regulated genes within each of their ortholog-pair evolutionarily conserved *cis*-regulatory regions.	http://cismols.cchmc.org/
CONREAL	CONREAL (Conserved Regulatory Elements Anchored Alignment) allows identification of transcription factor binding sites (TFBS) that are conserved between two orthologous promoter sequences.	http://conreal.niob.knaw.nl/
dsCheck	dsCheck takes a nucleotide sequence as input and estimates off-target effects caused by dsRNA (double-stranded RNA) employed in RNAi studies. dsCheck can be used either to verify previously designed dsRNA sequences, or to design off-target minimized dsRNAs.	http://dscheck.rnai.jp/
E-RNAi	E-RNAi is a tool for designing and evaluating dsRNA constructs suitable for RNAi experiments in *Drosophila* and *C.elegans*; can also be used for the design of enzymatically digested long dsRNA (esiRNAs) for mammalian cells.	http://e-rnai.dkfz.de/
Footer	Footer is a tool for identifying highly probable binding sites of known transcription factors using phylogenetic footprinting principles to analyze two homologous DNA sequences.	http://biodev.hgen.pitt.edu/Footer/
JCat	JCAT (Java Codon Adaptation Tool) is a tool that can adjust the codon usage of an input sequence to the selected organism. Useful for improving the expression of foreign genes in hosts with different codon usage.	http://www.prodoric.de/JCat/
MicroInspector	MicroInspector is a tool that detects miRNA (microRNA) binding sites in your input sequence by searching against databases of known miRNA binding sites.	http://147.52.170.155/
miRU	miRU is a tool that takes as an input a small miRNA sequence and then searches for complementary matches in TIGR plant-specific gene data sets to predict potential target genes.	http://bioinfo3.noble.org/miRU.htm
P-Match	P-Match is a transcription factor binding site identification tool that increases its accuracy by combining weight matrix and pattern matching approaches. Registration at the site is free and is required to use P-Match.	http://www.gene-regulation.com/cgi-bin/pub/programs/pmatch/bin/p-match.cgi
PatMatch	PatMatch is a pattern matching tool that allows you to search for short (<20 residues) nucleotide or peptide sequences and can accomodate ambiguous/degenerate patterns.	http://www.arabidopsis.org/cgi-bin/patmatch/nph-patmatch.pl

Table 1. *Continued*

Name	Description	URL[a]
POCO	POCO searches a set of promoters from co-expressed genes for nucleotide patterns that are over-represented.	http://ekhidna.biocenter.helsinki.fi/poco/
PromoterPlot	PromoterPlot takes the output from a TransFac search as input, and finds similarities between groups of promoters in an attempt to simplify the results of transcription factor searches. FASTA/Affymetrix IDs can also be used as input for a local installation of the tool.	http://promoterplot.fmi.ch/
RibEx	Riboswitch Explorer (RibEx) searches sequences for known riboswitches and also for predicted bacterial regulatory elements that are highly conserved.	http://www.ibt.unam.mx/biocomputo/RibEx.html
SynoR	SynoR searches vertebrate genomes for synonymous regulatory elements.	http://synor.dcode.org/
T-Reg Comparator	T-Reg Comparator is a tool for the analysis of transcriptional regulation that allows you to compare a set of position weight matrices (PWMs) against the T-Reg database (a collection of PWMs built from Transfac and Jaspar).	http://treg.molgen.mpg.de/
TOUCAN 2	TOUCAN 2 is a regulatory sequence analysis workbench for Metazoan sequences, directly linked with the Ensembl database and implementing SOAP clients for diverse alignment and motif detection algorithms.	http://www.esat.kuleuven.ac.be/~saerts/software/toucan.php
WordSpy	WordSpy allows the user to search for over-represented words in a set of sequences and to search for discriminative words using negative sequence data. WordSpy employs this functionality as a means to search for transcription factor binding motifs.	http://cic.cs.wustl.edu/wordspy/
Microarrays		
ArrayXPath	ArrayXPath is a web-based service for matching microarray gene-expression profiles with known biological pathways. Input is a clustered gene-expression profile in a tab-delimited text format. Output includes pathway diagrams.	http://www.snubi.org/software/ArrayXPath/
ASIAN	ASIAN (Automatic System for Inferring a Network) is a server for inferring regulatory networks from gene expression profiles that combines cluster analysis, regression analysis and graphical Gaussian modeling.	http://eureka.ims.u-tokyo.ac.jp/asian/
Babelomics	Babelomics is a suite of web tools for the functional annotation and analysis of groups of genes in high throughput experiments. Tools include: FatiGO, FatiWise, TransFAT, GenomeGO and TMT.	http://www.babelomics.org/
BRIGEP	The BRIDGE-based Genome-Transcriptome-Proteome Browser (BRIGEP) comprises three open-source web-based systems: GenDB, ProDB and EMMA. GenDB is a bacterial genome annotation system, ProDB is a storage and analysis system for mass spectrometry data, and EMMA is a storage and analysis system for transcriptome data.	https://www.cebitec.uni-bielefeld.de/groups/brf/software/brigep/
BROP	The Bioinformatics Resource for Oral Pathogens (BROP) contains tools for genomics of oral pathogens including Genome Viewer, GOAL (genome wide ORF alignment), an oral pathogen microarray database, an entrez counter, oral pathogen-specific BLAST, and a codon usage database.	http://brop.org/
Expression Profiler	Expression Profiler is a web-based platform for microarray data analysis developed at the EBI. This resource is integrated with the ArrayExpress database, a public repository for microarray data.	http://www.ebi.ac.uk/expressionprofiler/
GEMS	GEMS (Gene Expression Mining Server) is a tool for biclustering microarray data. It is available as a web tool and as a stand-alone command-line program.	http://genomics10.bu.edu/terrence/gems/
GEPAS	The Gene Expression Pattern Analysis Suite (GEPAS) is a collection of tools for the analysis of microarray data including data pre-processing, clustering, sample comparison, data mining based on GO terms (FatiGO) and annnotation. Also included are tools for the analysis of CGH-arrays (InSilicoCGH).	http://www.gepas.org/
GFINDer	Genome Functional INtegrated Discoverer (GFINDer) takes a list of gene/clone IDs with classification information as input, and allows the user to characterize the different gene classes in the list using annotations of various types from several different sources.	http://www.medinfopoli.polimi.it/GFINDer/
MIDAW	MIDAW (MIcroarray Data Analysis Web tool) is a data normalization and analysis tool for microarray data.	http://muscle.cribi.unipd.it:2701/

Table 1. *Continued*

Name	Description	URL[a]
OligoWiz	OligoWiz 2.0 is a client for microarray probe design that allows for the integration of sequence annotations, probe quality parameters and the placement of multiple probes per transcript.	http://www.cbs.dtu.dk/services/OligoWiz2/
Onto-Tools	Onto-Tools is a suite of tools for data mining based on information from Gene Ontology (GO). Functional groupings of lists of differentially expressed genes can be created using Onto-Express. Contains tools for assessing the functional bias for sets of genes (Onto-Design and Onto-Compare). Tools to convert lists of identifiers (Onto-Translate), to query for more information about lists of genes (Onto-Miner), and to provide graphical representations of gene interactions (Pathway-Express) also exist.	http://vortex.cs.wayne.edu/Projects.html
Pathway Explorer	Pathway Explorer is a tool for visualizing high throughput expression data simultaneously with biological pathway data available from KEGG, BioCarta and GenMAPP.	https://pathwayexplorer.genome.tugraz.at/
RACE	RACE (Remote Analysis Computation for gene Expression data) is a collection of web tools designed to assist with the analysis of DNA microarray data and results.	http://race.unil.ch/
T-profiler	T-profiler is a tool for the analysis of gene expression data from yeast that uses the *t*-test to score changes in the average activity of pre-defined groups of genes.	http://www.t-profiler.org/
VAMPIRE	VAMPIRE is a collection of Java tools designed to perform Bayesian statistical analysis of gene expression array data.	http://genome.ucsd.edu/VAMPIRE/
Splicing		
ASePCR	ASePCR (Alternative Splicing electronic PCR) is a tool for carrying out e-PCR to detect differences in amplicon sizes in transcripts from different tissues and organs.	http://genome.ewha.ac.kr/ASePCR/
T-STAG	Tissue-Specific Transcripts And Genes (T-STAG) is a system integrating EST, gene expression, alternative splicing and human–mouse orthology information for the analysis of tissue-specific gene and transcript expression patterns.	http://tstag.molgen.mpg.de/
Human genome		
Annotations		
Babelomics	Babelomics is a suite of web tools for the functional annotation and analysis of groups of genes in high throughput experiments. Tools include: FatiGO, FatiWise, TransFAT, GenomeGO and TMT.	http://www.babelomics.org/
CBS DAS protein viewer	The CBS DAS protein viewer uses the distributed annotation system (DAS) to integrate and present annotation data from multiple sources for a protein sequence.	http://www.cbs.dtu.dk/cgi-bin/das
FeatureExtract	The FeatureExtract server extracts sequence and feature annotations, such as intron/exon structure, from GenBank entries and other GenBank format files.	http://www.cbs.dtu.dk/services/FeatureExtract/
Health and disease		
GeneSeeker	GeneSeeker allows you to generate a list of candidate genes related to a human genetic disorder by searching against localization and expression databases.	http://www.cmbi.ru.nl/GeneSeeker/
PEPVAC	PEPVAC is a tool to assist in the development of multi-epitope vaccines. It is optimized for this task by predicting peptides with the ability to bind to several human leukocyte antigens that have similar peptide binding specificity.	http://immunax.dfci.harvard.edu/PEPVAC/
T-STAG	Tissue-Specific Transcripts And Genes (T-STAG) is a system integrating EST, gene expression, alternative splicing and human–mouse orthology information for the analysis of tissue-specific gene and transcript expression patterns.	http://tstag.molgen.mpg.de/

Table 1. *Continued*

Name	Description	URL[a]
Other resources		
DCODE.ORG	The dcode.org website provides access to tools for comparative genomic analyses developed by the Comparative Genomics Center at the Lawerence Livermore National Laboratory. Tools include: zPicture, Mulan, eShadow, rVista, CREME and the ECR Browser.	http://www.dcode.org/
WikiGene	WikiGene is a scientific project that follows a community-based approach to collect data about genes and gene regulatory events.	http://andromeda.gsf.de/wiki
Sequence polymorphisms		
ISTECH SNPAnalyzer	ISTECH SNPAnalyzer is a tool for the statistical analysis of SNP data that includes Hardy Weinberg equilibrium (HWE), haplotype estimation, linkage disequilibrium (LD) and QTL analyses. Registration required; some browser requirements and set-up necessary.	http://www.istech.info/istech/board/login_form.jsp
nsSNPAnalyzer	nsSNPAnalyzer is a tool to predict whether a nonsynonymous single nucleotide polymorphism (nsSNP) is phenotypically neutral or disease associated.	http://snpanalyzer.utmem.edu/
PupasView	PupasView takes a single gene identifier as input and reports SNPs that have the potential to affect phenotype. In addition to looking for potential amino acid changes, PupaSNP also searches for SNPs with the potential to affect proper transcription, such as those in intron/exon boundaries, predicted transcription factor binding sites and exonic splicing enhancers.	http://pupasview.bioinfo.cnio.es/
SNP Cutter	SNP Cutter is a tool that automates PCR–RFLP assay design for SNP genotyping.	http://bioinfo.bsd.uchicago.edu/SNP_cutter.htm
SNPserver	SNPServer combines BLAST, cap3 and a SNP discovery module into a single pipeline for the discovery of SNPs in user submitted files or dynamically created assemblies.	http://hornbill.cspp.latrobe.edu.au/snpdiscovery.html
Literature		
Search tools		
EBI Tools	EBI Tools is a project that aims to provide programmatic access to the various databases and retrieval and analysis services EBI provides through Simple Object Access Protocol (SOAP) and other related web service technologies.	http://www.ebi.ac.uk/Tools/webservices/
GoPubMed	GoPubMed is a tool that allows users to explore the results of PubMed queries in the context of Gene Ontology (GO) terms.	http://www.gopubmed.org/
PubFinder	PubFinder is a tool to facilitate searching through PubMed abstracts. The user chooses a set of abstracts that are representative of the subject area of their search. PubFinder then uses words from the selected abstracts to search for other papers belonging to the same subject area.	http://www.glycosciences.de/tools/PubFinder/
Text mining		
LitMiner	LitMiner is a literature data mining tool that is based on the annotation of key terms in article abstracts followed by statistical co-citation analysis of annotated key terms in order to predict relationships between genes, compounds, diseases and phenotypes, and tissues and organs.	http://andromeda.gsf.de/litminer
PubFinder	PubFinder is a tool to facilitate searching through PubMed abstracts. The user chooses a set of abstracts that are representative of the subject area of their search. PubFinder then uses words from the selected abstracts to search for other papers belonging to the same subject area.	http://www.glycosciences.de/tools/PubFinder/
Model organisms		
Microbes		
BASys	BASys (Bacterial Annotation System) is a tool for automated annotation of bacterial genomic (chromosomal and plasmid) sequences including gene/protein names, GO functions, COG functions, possible paralogues and orthologues, molecular weights, isoelectric points, operon structures, subcellular localization, signal peptides, transmembrane regions, secondary structures, 3-D structures, reactions and pathways.	http://wishart.biology.ualberta.ca/basys/

Table 1. *Continued*

Name	Description	URL[a]
BROP	The Bioinformatics Resource for Oral Pathogens (BROP) contains tools for genomics of oral pathogens including Genome Viewer, GOAL (genome wide ORF alignment), an oral pathogen microarray database, an entrez counter, oral pathogen-specific BLAST and a codon usage database.	http://brop.org/
MLST	MLST (Multi Locus Sequence Typing) is a nucleotide sequence-based approach for the unambiguous characterization of isolates of bacteria and other organisms using the sequences of internal fragments of seven house-keeping genes.	http://www.mlst.net/
Projector 2	Projector 2 allows users to map completed portions of the genome sequence of an organism onto the finished (or unfinished) genome of a closely related species or strain. Using the related genome sequence as a template can facilitate sequence assembly and the sequencing of the remaining gaps.	http://molgen.biol.rug.nl/websoftware/projector2/
Mouse and rat		
ARTS	ARTS (Advanced Retrieval Tool for SNPs) can be used to retrieve SNP that are polymorphic between several different mouse strains to aid in the design of genome-wide SNP marker panels.	http://andromeda.gsf.de/arts
PredBALB/c	PredBALB/c is a tool that will predict MHC binding peptides in your protein sequence of interest for the H2d haplotype of the BALB/c mouse.	http://antigen.i2r.a-star.edu.sg/predBalbc/
Plants		
AthaMap	AthaMap is a genome-wide map of putative transcription factor binding sites in *Arabidopsis thaliana*	http://www.athamap.de/
Yeast		
SCMD	The Sacharomyces Cerevisiae Morphological Database (SCMD) is a collection of micrographs of budding yeast mutants; visualization and data mining tools are provided.	http://scmd.gi.k.u-tokyo.ac.jp/
T-profiler	T-profiler is a tool for the analysis of gene expression data from yeast that uses the t-test to score changes in the average activity of pre-defined groups of genes.	http://www.t-profiler.org/
Other molecules		
Carbohydrates		
Glyprot	Glyprot is a tool for predicting and modelling all potential N-glycosylation sites in a given 3D structure.	http://www.glycosciences.de/glyprot/
SEARCHGTr	SEARCHGTr is a tool for the analysis of glycosyltransferases (GTrs) that allows you to compare a query sequence with the sequences of characterized GTrs.	http://www.nii.res.in/searchgtr.html
Protein		
2-D Structure prediction		
BhairPred	BhairPred is a tool for predicting beta-hairpins in protein sequences using a support vector machine.	http://www.imtech.res.in/raghava/bhairpred/
Bioverse	Bioverse is a system that uses computational techniques to facilitate exploring the relationships between molecular, genomic, proteomic, systems and organismal information.	http://bioverse.compbio.washington.edu/
CBS DAS protein viewer	The CBS DAS protein viewer uses the distributed annotation system (DAS) to integrate and present annotation data from multiple sources for a protein sequence.	http://www.cbs.dtu.dk/cgi-bin/das
PRALINE	Praline is a multiple sequence alignment program that can integrate information from sequence similarity searches and secondary structure prediction.	http://ibivu.cs.vu.nl/programs/pralinewww/
SCRATCH	SCRATCH is a suite of protein structure software and servers for the prediction of secondary structure, solvent accessibility, disulphide bridges, stability effects of single amino acid mutations, disordered regions, domains, beta-residue and beta-strand pairings, amino acid contact maps, and tertiary structure.	http://www.igb.uci.edu/servers/psss.html

Table 1. *Continued*

Name	Description	URL[a]
Servers at University College London	A suite of tools that includes: PSIPRED, a protein structure prediction server; GenTHREADER, for genomic protein fold recognition; MEMSAT2, for transmembrane protein structure prediction; GTD, the genomic threading database; DISOPRED, a dynamic disorder prediction server; DomPred, a domain prediction server; and COPS, for the comparison of protein structure classifications.	http://bioinf.cs.ucl.ac.uk/software.html
Services from Zhou Laboratory	Tools from the Zhou laboratory including predictors of transmembrane topology (THUMBUP, UMDHMM-TMHP, TUPS); prediction/analysis tools for tertiary structure (SPARKS2, SP3); and, prediction/analysis tools for interactions (DMONOMER, DLOOP, DMUTANT, DCOMPLEX, DDNA, TCD, DOGMA).	http://theory.med.buffalo.edu/
TMB-Hunt	TMB-Hunt (Transmembrane Barrel—Hunt) classifies protein sequences as transmembrane B-barrel (TMB) or non-TMB based on amino acid composition.	http://www.bioinformatics.leeds.ac.uk/betaBarrel/
TMBETA-NET	Tool that predicts transmembrane beta strands in an outer membrane protein from its amino acid sequence.	http://psfs.cbrc.jp/tmbeta-net/
TRAMPLE	TRAMPLE is a tool for the prediction of transmembrane helices, transmembrane strands, secondary structure and signal peptides.	http://gpcr.biocomp.unibo.it/biodec/
3D structure prediction, comparison		
AS2TS	The AS2TS (Amino acid Sequence to Tertiary Structure) system consists of servers for protein structure analysis and modelling.	http://as2ts.llnl.gov/
BhairPred	BhairPred is a tool for predicting beta-hairpins in protein sequences using a support vector machine.	http://www.imtech.res.in/raghava/bhairpred/
Bioverse	Bioverse is a system that uses computational techniques to facilitate exploring the relationships between molecular, genomic, proteomic, systems and organismal information.	http://bioverse.compbio.washington.edu/
CBS DAS protein viewer	The CBS DAS protein viewer uses the distributed annotation system (DAS) to integrate and present annotation data from multiple sources for a protein sequence.	http://www.cbs.dtu.dk/cgi-bin/das
CHC_FIND	CHC_FIND is a tool to analyze conserved hydrophobic contacts (CHC) from multiple structural alignments. In addition to a multiple sequence alignment, a structural alignment which provides the superposition of structurally conserved regions (SCRs) (i.e. results from SCR_FIND) needs to be provided.	http://schubert.bio.uniroma1.it/CHC_FIND/index.html
ConSurf	The ConSurf server allows one to map levels of amino acid conservation to known protein structures in order to study areas of potential functional importance on the surface of the protein. A PDB file is required as input, and a multiple sequence alignment is optional. If an alignment is not provided, ConSurf will build one by performing a search for homologous sequences and then aligning them.	http://consurf.tau.ac.il/
DIAL	DIAL (Domain Identification Algorithm) is a web server for the automatic identification of structural domains given the three-dimensional coordinates of a protein.	http://caps.ncbs.res.in/DIAL/home.html
Diamond STING	Diamond STING is a suite of tools for the analysis of protein sequence, structure, stability and function—and the relationship between them.	http://trantor.bioc.columbia.edu/SMS/
EVAcon	EVAcon automates the continuous evaluation of inter-residue contact prediction servers. Results can be viewed statically or dynamically generated.	http://www.pdg.cnb.uam.es/eva/con/index.html
FF—Fragment Finder	FF (Fragment Finder) takes a PDB ID, a structure coordinate file or a list of phi and psi angles as input and searches for matches to a specified structural fragment. Users can tailor the search based on sequence similarity and vary the dataset searched against.	http://cluster.physics.iisc.ernet.in/ff/

Table 1. *Continued*

Name	Description	URL[a]
FFAS03	The Fold & Function Assignment System (FFAS03) takes an amino-acid sequence as input and generates a profile which is compared to several sets of sequence profiles including SCOP and PFAM.	http://ffas.burnham.org/
FoldX	FOLD-X is a program for calculating the folding energies of proteins and for calculating the effect of a point mutation on the stability of a protein.	http://foldx.embl.de/
Fragnostic	Fragnostic is a tool for exploring common structural elements, or fragments, between proteins which have different folds.	http://ffas.burnham.org/Fragnostic
Glyprot	Glyprot is a tool for predicting and modelling all potential N-glycosylation sites in a given 3D structure.	http://www.glycosciences.de/glyprot/
H++	H++ is a tool for the prediction of protonation states and p*K* of ionizable groups in macromolecular structures.	http://biophysics.cs.vt.edu/H++
HHpred	Based on the comparison of profile HMMs, HHpred takes a protein sequence or multiple sequence alignment as input and searches for remote homologues in an assortment of databases such as PDB, SMART and Pfam. The user can select either a local or global alignment method, and the search results can be used to generate 3D structural models.	http://protevo.eb.tuebingen.mpg.de/hhpred
I-Mutant2.0	I-Mutant2.0 is a tool that can predict the effect of a single point mutation on protein stability from protein sequences or protein structures.	http://gpcr2.biocomp.unibo.it/cgi/predictors/I-Mutant2.0/I-Mutant2.0.cgi
I2I-SiteEngine	Interface-to-Interface (I2I)-SiteEngine compares pairs of interacting protein binding sites by recognizing similarity of physico-chemical properties and shapes in the protein–protein interfaces.	http://bioinfo3d.cs.tau.ac.il/I2I-SiteEngine/
ICGEBnet Protein Tools	ICGEBnet Protein Tools is a resource for analysis of 3D protein structures including domain predictors, a protein fold similiarity server (PRIDE), and tools for calculating atom protusion (CX) and/or depth (DPX) indexes in 3D models.	http://www.icgeb.org/protein/
PatchDock	PatchDock is an algorithm for molecular docking. The input is two molecules of any type: proteins, DNA, peptides, drugs. The output is a list of potential complexes sorted by shape complementarity criteria.	http://bioinfo3d.cs.tau.ac.il/PatchDock/
pdbFun	pdbFun allows the user to search the PDB as a database of annotated residues. One can limit the search by annotations such as domains, binding sites, active sites, solvent exposure and residue type.	http://pdbfun.uniroma2.it/
PISCES	PISCES (Protein Sequence Culling Server) allows the user to weed out sequences from a set in order to obtain a subset of relatively high PDB structure quality and/or mutual sequence identity.	http://dunbrack.fccc.edu/pisces/
ProFunc	ProFunc takes a PDB-format structure as input and predicts the likely function of the protein based on various sequence and structural analysis methods.	http://www.ebi.ac.uk/thornton-srv/databases/ProFunc/
ProTarget	ProTarget offers a method for the prediction of novel structural superfamilies by assessing the relationship of input protein sequences to previously solved 3D structures.	http://www.protarget.cs.huji.ac.il/index.php
Protinfo	Protinfo takes a protein sequence as input and returns the atomic coordinates for a prediction of tertiary structure for that protein. Predictions can be made by comparative or *de novo* modelling.	http://protinfo.compbio.washington.edu/
RPBS	Ressource Parisienne en Bioinformatique Structurale (RPBS) is a structural bioinformatics resource with several types of specific services including tools for searching sequence (AUTOMAT) and structure (YAKUSA) databases and for homology modelling (WLOOP).	http://bioserv.rpbs.jussieu.fr/
SCRATCH	SCRATCH is a suite of protein structure software and servers for the prediction of secondary structure, solvent accessibility, disulphide bridges, stability effects of single amino acid mutations, disordered regions, domains, beta-residue and beta-strand pairings, amino acid contact maps and tertiary structure.	http://www.igb.uci.edu/servers/psss.html
SCR_FIND	SCR_FIND is a tool to analyze structurally conserved regions (SCRs) from superimposed structures and multiple sequence alignments.	http://schubert.bio.uniroma1.it/SCR_FIND/

Table 1. *Continued*

Name	Description	URL[a]
Servers at University College London	A suite of tools that includes: PSIPRED, a protein structure prediction server; GenTHREADER, for genomic protein fold recognition; MEMSAT2, for transmembrane protein structure prediction; GTD, the genomic threading database; DISOPRED, a dynamic disorder prediction server; DomPred, a domain prediction server; and COPS, for the comparison of protein structure classifications.	http://bioinf.cs.ucl.ac.uk/software.html
Services from Zhou Laboratory	Tools from the Zhou laboratory including predictors of transmembrane topology (THUMBUP, UMDHMM-TMHP, TUPS); prediction/analysis tools for tertiary structure (SPARKS2, SP3); and, prediction/analysis tools for interactions (DMONOMER, DLOOP, DMUTANT, DCOMPLEX, DDNA, TCD, DOGMA).	http://theory.med.buffalo.edu/
SiteEngine	SiteEngine is a server that searches protein structures for regions that can potentially function as binding sites by scanning for regions on the surface of one protein structure that resemble a specific binding site on the other.	http://bioinfo3d.cs.tau.ac.il/SiteEngine/
SPACE	SPACE (Structure Prediction and Analysis based on Complementarity with Environment) is a suite of tools for predicting and analyzing structures of biomolecules and their complexes.	http://ligin.weizmann.ac.il/space/
Sride	Sride is a tool for identifying the stabilizing residues in protein structure.	http://sride.enzim.hu/
SymmDock	SymmDock is a server for prediction of complexes with cyclical symmetry by geometry-based molecular docking.	http://bioinfo3d.cs.tau.ac.il/SymmDock/
3D Structure retrieval, viewing		
AISMIG	AISMIG (An Interactive Server-side Molecule Image Generator) is a tool for generating and visualizing high resolution 3D images from PDB structure files.	http://www.dkfz-heidelberg.de/spec/aismig
MINER	MINER is a tool for the identification and visualization of phylogenetic motifs (regions within a multiple sequence alignment (MSA) that conserve the overall phylogeny of the complete family).	http://www.pmap.csupomona.edu/MINER/
MovieMaker	MovieMaker is a web server that accepts PDB files or PDB accession numbers as input and allows short (~10 s) downloadable movies to be generated of protein motions and interactions.	http://wishart.biology.ualberta.ca/moviemaker/
MRS	MRS is a biological data retrieval system that can be accessed over the web, or installed and used locally. MRS indexes several flat-file data sets for searching, including EMBL nucleotide, UniProt, PDB and KEGG. Searches can be performed globally, or on one or more flat file fields per data set.	http://mrs.cmbi.ru.nl/
PPG	The Protein Picture Generator (PPG) is a tool for making pictures (and animations) of protein structures from PDB files.	http://bioserv.rpbs.jussieu.fr/cgi-bin/PPG
RPBS	Ressource Parisienne en Bioinformatique Structurale (RPBS) is a structural bioinformatics resource with several types of specific services including tools for searching sequence (AUTOMAT) and structure (YAKUSA) databases and for homology modelling (WLOOP).	http://bioserv.rpbs.jussieu.fr/
Biochemical features		
Bioverse	Bioverse is a system that uses computational techniques to facilitate exploring the relationships between molecular, genomic, proteomic, systems and organismal information.	http://bioverse.compbio.washington.edu/
CBS DAS protein viewer	The CBS DAS protein viewer uses the distributed annotation system (DAS) to integrate and present annotation data from multiple sources for a protein sequence.	http://www.cbs.dtu.dk/cgi-bin/das
Diamond STING	Diamond STING is a suite of tools for the analysis of protein sequence, structure, stability and function—and the relationship between them.	http://trantor.bioc.columbia.edu/SMS/
DiANNA	DiANNA (DiAminoacid Neural Network Application) includes tools for cysteine state and disulfide Bond partner prediction	http://clavius.bc.edu/~clotelab/DiANNA/

Table 1. *Continued*

Name	Description	URL[a]
H++	H++ is a tool for the prediction of protonation states and p*K* of ionizable groups in macromolecular structures.	http://biophysics.cs.vt.edu/H++
PCE	PCE (Protein Continuum Electrostatics) is an interface to electrostatic potentials and p*K*a calculations using the MEAD package.	http://bioserv.rpbs.jussieu.fr/Help/PCE.html
RPBS	Ressource Parisienne en Bioinformatique Structurale (RPBS) is a structural bioinformatics resource with several types of specific services including tools for searching sequence (AUTOMAT) and structure (YAKUSA) databases and for homology modelling (WLOOP).	http://bioserv.rpbs.jussieu.fr/
WebProAnalyst	WebProAnalyst is a tool for searching for residues whose substitutions are correlated with variations in protein activity. Key physicochemical characteristics of these sites can be calculated.	http://www.mgs.bionet.nsc.ru/mgs/programs/panalyst/
Domains and motifs		
CBS DAS protein viewer	The CBS DAS protein viewer uses the distributed annotation system (DAS) to integrate and present annotation data from multiple sources for a protein sequence.	http://www.cbs.dtu.dk/cgi-bin/das
CEP	CEP (Conformational Epitope Prediction) is a server for the prediction of probable antibody binding sites of protein antigens.	http://bioinfo.ernet.in/cep.htm
DIAL	DIAL (Domain Identification Algorithm) is a web server for the automatic identification of structural domains given the three-dimensional coordinates of a protein.	http://caps.ncbs.res.in/DIAL/home.html
EBI Tools	EBI Tools is a project that aims to provide programmatic access to the various databases and retrieval and analysis services EBI provides through Simple Object Access Protocol (SOAP) and other related web service technologies.	http://www.ebi.ac.uk/Tools/webservices/
FF—Fragment Finder	FF (Fragment Finder) takes a PDB ID, a structure coordinate file or a list of phi and psi angles as input and searches for matches to a specified structural fragment. Users can tailor the search based on sequence similarity and vary the dataset searched against.	http://cluster.physics.iisc.ernet.in/ff/
FFAS03	The Fold & Function Assignment System (FFAS03) takes an amino-acid sequence as input and generates a profile which is compared to several sets of sequence profiles including SCOP and PFAM.	http://ffas.burnham.org/
GPS	Using datasets of known phosphorylation sites, the Group based Phosphorylation Scoring method (GPS) allows the prediction of kinase-specific phosphorylation sites from primary protein sequences.	http://973-proteinweb.ustc.edu.cn/gps/gps_web/predict.php
GraBCas	GraBCas is a tool for predicting granzyme B and caspase cleavage sites.	http://wwwalt.med-rz.uniklinik-saarland.de/med_fak/humangenetik/software/index.html
InterProScan	InterProScan allows you to query using different protein signature recognition methods to look up InterPro annotations for your sequence.	http://www.ebi.ac.uk/InterProScan/
KinasePhos	KinasePhos is a tool for identifying kinase-specific phosphorylation sites in protein sequences.	http://kinasephos.mbc.nctu.edu.tw/
MULTIPRED	MULTIPRED is a tool for mapping T-cell epitopes by prediction peptides that bind to human leukocyte antigen (HLA) class I A2, A3 and class II DR supertypes.	http://antigen.i2r.a-star.edu.sg/multipred/
One-Block CYRCA	One-Block CYRCA is a program for identifying blocks (local ungapped profiles of the most conserved regions of protein families and domains) in a multiple sequence alignment based on the LAMA and CYRCA block-to-block alignment methods.	http://bioinformatics.weizmann.ac.il/~milana/OneCYRCA/
PatMatch	PatMatch is a pattern matching tool that allows you to search for short (<20 residues) nucleotide or peptide sequences and can accomodate ambiguous/degenerate patterns.	http://www.arabidopsis.org/cgi-bin/patmatch/nph-patmatch.pl
pdbFun	pdbFun allows the user to search the PDB as a database of annotated residues. One can limit the search by annotations such as domains, binding sites, active sites, solvent exposure and residue type.	http://pdbfun.uniroma2.it/

Table 1. *Continued*

Name	Description	URL[a]
PhyloDome	PhyloDome is a tool with which you can visualize and analyze the phylogenetic distribution of one or more eukaryotic domains.	http://mendel.imp.univie.ac.at/PhyloDome/
PredBALB/c	PredBALB/c is a tool that will predict MHC binding peptides in your protein sequence of interest for the H2d haplotype of the BALB/c mouse.	http://antigen.i2r.a-star.edu.sg/predBalbc/
PRODOC	PRODOC is a repository of domain assignments from Pfam for proteins encoded in different complete genomes and a tool for querying this information.	http://hodgkin.mbu.iisc.ernet.in/~prodoc/
ProFunc	ProFunc takes a PDB-format structure as input and predicts the likely function of the protein based on various sequence and structural analysis methods.	http://www.ebi.ac.uk/thornton-srv/databases/ProFunc/
ProTeus	ProTeus (Protein Terminus) is an archive of functional signatures in protein termini	http://www.proteus.cs.huji.ac.il/index.php
QuasiMotiFinder	QuasiMotiFinder uses physicochemical similarity to PROSITE motifs and evolutionary conservation to predict sequence locations with possible function (pseudo-motifs).	http://quasimotifinder.tau.ac.il/
SCANMOT	SCANMOT is a sequence similarity searching tool that adds the additional constraints of simultaneous matching of multiple motifs.	http://www.ncbs.res.in/~faculty/mini/scanmot/scanmot.html
Scooby-domain	Scooby-domain (sequence hydrophobicity predicts domains) is a method to identify globular domains in protein sequence, based on the observed lengths and hydrophobicities of domains from proteins with known tertiary structure.	http://ibivu.cs.vu.nl/programs/scoobywww/
SCRATCH	SCRATCH is a suite of protein structure software and servers for the prediction of secondary structure, solvent accessibility, disulphide bridges, stability effects of single amino acid mutations, disordered regions, domains, beta-residue and beta-strand pairings, amino acid contact maps, and tertiary structure.	http://www.igb.uci.edu/servers/psss.html
SEARCHGTr	SEARCHGTr is a tool for the analysis of glycosyltransferases (GTrs) that allows you to compare a query sequence with the sequences of characterized GTrs.	http://www.nii.res.in/searchgtr.html
Servers at University College London	A suite of tools that includes: PSIPRED, a protein structure prediction server; GenTHREADER, for genomic protein fold recognition; MEMSAT2, for transmembrane protein structure prediction; GTD, the genomic threading database; DISOPRED, a dynamic disorder prediction server; DomPred, a domain prediction server; and COPS, for the comparison of protein structure classifications.	http://bioinf.cs.ucl.ac.uk/software.html
Function		
Bioverse	Bioverse is a system that uses computational techniques to facilitate exploring the relationships between molecular, genomic, proteomic, systems and organismal information.	http://bioverse.compbio.washington.edu/
CBS DAS protein viewer	The CBS DAS protein viewer uses the distributed annotation system (DAS) to integrate and present annotation data from multiple sources for a protein sequence.	http://www.cbs.dtu.dk/cgi-bin/das
Diamond STING	Diamond STING is a suite of tools for the analysis of protein sequence, structure, stability and function—and the relationship between them.	http://trantor.bioc.columbia.edu/SMS/
GPCRsclass	GPCRsclass is a tool for predicting amine-binding receptors based on a protein sequence provided by the user.	http://www.imtech.res.in/raghava/gpcrsclass/
GRIFFIN	GRIFFIN (G-protein-Receptor Interacting Feature Finding INstrument) uses a support vector machine and hidden markov model to predict G-protein coupled receptors (GPCRs) and G-protein coupling selectivity.	http://griffin.cbrc.jp/
MEDock	MEDock (Maximum-Entropy based Docking) is a tool for predicting ligand binding sites.	http://medock.csie.ntu.edu.tw/
MINER	MINER is a tool for the identification and visualization of phylogenetic motifs (regions within a multiple sequence alignment (MSA) that conserve the overall phylogeny of the complete family).	http://www.pmap.csupomona.edu/MINER/

Table 1. *Continued*

Name	Description	URL[a]
PEPVAC	PEPVAC is a tool to assist in the development of multi-epitope vaccines. It is optimized for this task by predicting peptides with the ability to bind to several human leukocyte antigens that have similar peptide binding specificity.	http://immunax.dfci.harvard.edu/PEPVAC/
ProFunc	ProFunc takes a PDB-format structure as input and predicts the likely function of the protein based on various sequence and structural analysis methods.	http://www.ebi.ac.uk/thornton-srv/databases/ProFunc/
ProTeus	ProTeus (Protein Terminus) is an archive of functional signatures in protein termini	http://www.proteus.cs.huji.ac.il/index.php
Interactions, pathways and enzymes		
ArrayXPath	ArrayXPath is a web-based service for matching microarray gene-expression profiles with known biological pathways. Input is a clustered gene-expression profile in a tab-delimited text format. Output includes pathway diagrams.	http://www.snubi.org/software/ArrayXPath/
Babelomics	Babelomics is a suite of web tools for the functional annotation and analysis of groups of genes in high throughput experiments. Tools include: FatiGO, FatiWise, TransFAT, GenomeGO and TMT.	http://www.babelomics.org/
GenePath	GenePath is a tool for automated construction of genetic networks and proposal of genetic experiments from mutant data.	http://www.genepath.org/genepath2
I2I-SiteEngine	Interface-to-Interface (I2I)-SiteEngine compares pairs of interacting protein binding sites by recognizing similarity of physico-chemical properties and shapes in the protein–protein interfaces.	http://bioinfo3d.cs.tau.ac.il/I2I-SiteEngine/
Metabolic PathFinding	The Metabolic PathFinding website takes a source and a target metabolic node as input and finds the shortest path between them in a graph based on the reactions and compounds from the KEGG LIGAND database. Various types of input can be provided, including LIGAND database identifiers and EC numbers. The web tool employs two selectable methods to filter out pathways going through highly connected compounds such as water.	http://www.scmbb.ulb.ac.be/pathfinding/
PatchDock	PatchDock is an algorithm for molecular docking. The input is two molecules of any type: proteins, DNA, peptides, drugs. The output is a list of potential complexes sorted by shape complementarity criteria.	http://bioinfo3d.cs.tau.ac.il/PatchDock/
Pathway Explorer	Pathway Explorer is a tool for visualizing high throughput expression data simultaneously with biological pathway data available from KEGG, BioCarta, and GenMAPP.	https://pathwayexplorer.genome.tugraz.at/
PEPVAC	PEPVAC is a tool to assist in the development of multi-epitope vaccines. It is optimized for this task by predicting peptides with the ability to bind to several human leukocyte antigens that have similar peptide binding specificity.	http://immunax.dfci.harvard.edu/PEPVAC/
POPSCOMP	POPSCOMP is a system for analyzing the interaction between components of complexes based on calculations of the accessible surface that is buried when the complex is formed.	http://ibivu.cs.vu.nl/programs/popscompwww/
PRISM	PRISM (PRotein Interactions by Structural Matching) is a tool for analyzing protein interfaces and predicting protein–protein interactions.	http://gordion.hpc.eng.ku.edu.tr/prism/
Services from Zhou Laboratory	Tools from the Zhou laboratory including predictors of transmembrane topology (THUMBUP, UMDHMM-TMHP, TUPS); prediction/analysis tools for tertiary structure (SPARKS2, SP3); and, prediction/analysis tools for interactions (DMONOMER, DLOOP, DMUTANT, DCOMPLEX, DDNA, TCD, DOGMA).	http://theory.med.buffalo.edu/
SymmDock	SymmDock is a server for prediction of complexes with cyclical symmetry by geometry-based molecular docking.	http://bioinfo3d.cs.tau.ac.il/SymmDock/
VisANT	VisANT is a system allowing different types of networks of biological associations and interactions to be visualized and analyzed. VisANT is java-based, and can be run as a java applet, as a java web application, or downloaded and run locally.	http://visant.bu.edu/

Table 1. *Continued*

Name	Description	URL[a]
Localization and targeting		
CBS DAS protein viewer	The CBS DAS protein viewer uses the distributed annotation system (DAS) to integrate and present annotation data from multiple sources for a protein sequence.	http://www.cbs.dtu.dk/cgi-bin/das
GPCRsclass	GPCRsclass is a tool for predicting amine-binding receptors based on a protein sequence provided by the user.	http://www.imtech.res.in/raghava/gpcrsclass/
LOCSVMpsi	LOCSVMpsi is a tool for prediction of eukaryotic protein subcellular localization based on support vector machines (SVMs) and PSI-BLAST.	http://bioinformatics.ustc.edu.cn/LOCSVMPSI/LOCSVMPSI.php
Servers at University College London	A suite of tools that includes PSIPRED, a protein structure prediction server; GenTHREADER, for genomic protein fold recognition; MEMSAT2, for transmembrane protein structure prediction; GTD, the genomic threading database; DISOPRED, a dynamic disorder prediction server; DomPred, a domain prediction server; and COPS, for the comparison of protein structure classifications.	http://bioinf.cs.ucl.ac.uk/software.html
TMB-Hunt	TMB-Hunt (Transmembrane Barrel—Hunt) classifies protein sequences as transmembrane B-barrel (TMB) or non-TMB based on amino acid composition.	http://www.bioinformatics.leeds.ac.uk/betaBarrel/
TMBETA-NET	Tool that predicts transmembrane beta strands in an outer membrane protein from its amino acid sequence.	http://psfs.cbrc.jp/tmbeta-net/
TRAMPLE	TRAMPLE is a tool for the prediction of transmembrane helices, transmembrane strands, secondary structure and signal peptides.	http://gpcr.biocomp.unibo.it/biodec/
Phylogeny reconstruction		
Diamond STING	Diamond STING is a suite of tools for the analysis of protein sequence, structure, stability and function—and the relationship between them.	http://trantor.bioc.columbia.edu/SMS/
MINER	MINER is a tool for the identification and visualization of phylogenetic motifs (regions within a multiple sequence alignment (MSA) that conserve the overall phylogeny of the complete family).	http://www.pmap.csupomona.edu/MINER/
PhyloDome	PhyloDome is a tool with which you can visualize and analyze the phylogenetic distribution of one or more eukaryotic domains.	http://mendel.imp.univie.ac.at/PhyloDome/
PHYML	Phyml is a program that constructs phylogenetic trees from sequence alignments using the maximum likelihood method.	http://atgc.lirmm.fr/phyml/
POWER	The Phylogenetic Web Repeater (POWER) allows users to perform phylogenetic analysis using the PHYLIP package. The POWER pipeline can start with processing either multiple sequence alignments (MSA) or can proceed directly with aligned sequences.	http://power.nhri.org.tw/
Proteomics		
BRIGEP	The BRIDGE-based Genome-Transcriptome-Proteome Browser (BRIGEP) comprises three open-source web-based systems: GenDB, ProDB and EMMA. GenDB is a bacterial genome annotation system, ProDB is a storage and analysis system for mass spectrometry data, and EMMA is a storage and analysis system for transcriptome data.	https://www.cebitec.uni-bielefeld.de/groups/brf/software/brigep/
DeNovoID	DeNovoID is a tool for protein identification using *de novo* peptide sequence data from mass spectrometry experiments.	http://proteomics.mcw.edu/denovoid/
Sequence features		
CBS DAS protein viewer	The CBS DAS protein viewer uses the distributed annotation system (DAS) to integrate and present annotation data from multiple sources for a protein sequence.	http://www.cbs.dtu.dk/cgi-bin/das
DiANNA	DiANNA (DiAminoacid Neural Network Application) includes tools for cysteine state and disulfide Bond partner prediction	http://clavius.bc.edu/~clotelab/DiANNA/
I-Mutant2.0	I-Mutant2.0 is a tool that can predict the effect of a single point mutation on protein stability from protein sequences or protein structures.	http://gpcr2.biocomp.unibo.it/cgi/predictors/I-Mutant2.0/I-Mutant2.0.cgi
Pcleavage	Pcleavage is a tool that uses a support vector machine to predict immunoproteasome and constitutive proteasome cleavage sites in antigenic sequences.	http://www.imtech.res.in/raghava/pcleavage/

Table 1. *Continued*

Name	Description	URL[a]
REPPER	REPPER (REPeats and their PERiodicities) is a tool for detecting and analyzing regions in protein sequences or sequence alignments that have short gapless repeats.	http://protevo.eb.tuebingen.mpg.de/repper
RPBS	Ressource Parisienne en Bioinformatique Structurale (RPBS) is a structural bioinformatics resource with several types of specific services including tools for searching sequence (AUTOMAT) and structure (YAKUSA) databases and for homology modelling (WLOOP).	http://bioserv.rpbs.jussieu.fr/
Sequence retrieval		
Bioverse	Bioverse is a system that uses computational techniques to facilitate exploring the relationships between molecular, genomic, proteomic, systems and organismal information.	http://bioverse.compbio.washington.edu/
EBI Tools	EBI Tools is a project that aims to provide programmatic access to the various databases and retrieval and analysis services EBI provides through Simple Object Access Protocol (SOAP) and other related web service technologies.	http://www.ebi.ac.uk/Tools/webservices/
FeatureExtract	The FeatureExtract server extracts sequence and feature annotations, such as intron/exon structure, from GenBank entries and other GenBank format files.	http://www.cbs.dtu.dk/services/FeatureExtract/
MRS	MRS is a biological data retrieval system that can be accessed over the web, or installed and used locally. MRS indexes several flat-file data sets for searching, including EMBL nucleotide, UniProt, PDB and KEGG. Searches can be performed globally, or on one or more flat-file fields per data set.	http://mrs.cmbi.ru.nl/
PISCES	PISCES (Protein Sequence Culling Server) allows the user to weed out sequences from a set in order to obtain a subset of relatively high PDB structure quality and/or mutual sequence identity.	http://dunbrack.fccc.edu/pisces/
RNA		
Functional RNAs		
MicroInspector	MicroInspector is a tool that detects miRNA (microRNA) binding sites in your input sequence by searching against databases of known miRNA binding sites.	http://147.52.170.155/
miRU	miRU is a tool that takes as an input a small miRNA sequence and then searches for complementary matches in TIGR plant-specific gene data sets to predict potential target genes.	http://bioinfo3.noble.org/miRU.htm
snoGPS	snoGPS allows you to search for H/ACA snoRNA (small nucleolar RNA) genes in a genomic sequence	http://lowelab.ucsc.edu/snoGPS/
snoscan	Snoscan allows you to search for C/D box methylation guide snoRNA (small nucleolar RNA) genes in a genomic sequence	http://lowelab.ucsc.edu/snoscan/
tRNAscan-SE	tRNAscan-SE allows you to search for tRNA genes in genomic sequence. (site hosted by Lowe Lab at UCSC)	http://lowelab.ucsc.edu/tRNAscan-SE/
Motifs		
FOLDALIGN	FOLDALIGN is an algorithm for local simultaneous folding and aligning two or more RNA sequences.	http://foldalign.kvl.dk/
MicroInspector	MicroInspector is a tool that detects miRNA (microRNA) binding sites in your input sequence by searching against databases of known miRNA binding sites.	http://147.52.170.155/
PatMatch	PatMatch is a pattern matching tool that allows you to search for short (<20 residues) nucleotide or peptide sequences and can accomodate ambiguous/degenerate patterns.	http://www.arabidopsis.org/cgi-bin/patmatch/nph-patmatch.pl
Sequence retrieval		
EBI Tools	EBI Tools is a project that aims to provide programmatic access to the various databases and retrieval and analysis services EBI provides through Simple Object Access Protocol (SOAP) and other related web service technologies.	http://www.ebi.ac.uk/Tools/webservices/
FeatureExtract	The FeatureExtract server extracts sequence and feature annotations, such as intron/exon structure, from GenBank entries and other GenBank format files.	http://www.cbs.dtu.dk/services/FeatureExtract/
Structure prediction, visualization and design		
DINAMelt	DINAMelt is a tool for predicting hybridization and folding (secondary structure) of DNA and RNA using equilibrium thermodynamic methods.	http://www.bioinfo.rpi.edu/applications/hybrid/

Table 1. *Continued*

Name	Description	URL[a]
E-RNAi	E-RNAi is a tool for designing and evaluating dsRNA constructs suitable for RNAi experiments in *Drosophila* and *C.elegans*; can also be used for the design of enzymatically digested long dsRNA (esiRNAs) for mammalian cells.	http://e-rnai.dkfz.de/
FOLDALIGN	FOLDALIGN is an algorithm for local simultaneous folding and aligning two or more RNA sequences.	http://foldalign.kvl.dk/
Kinefold	Kinefold calculates (and animates) the folding kinetics of RNA sequences including pseudoknots.	http://kinefold.u-strasbg.fr/
RNALOSS	RNALOSS (RNA locally optimal secondary structure) is a tool for the computation of locally optimal secondary structures.	http://clavius.bc.edu/~clotelab/RNALOSS/
Sequence comparison		
Alignment editing and visualization		
CHAOS/DIALIGN WWW server	The CHAOS/DIALIGN WWW server is a multiple sequence alignment site which passes input sequences through CHAOS to create a list of local similarities. These similarities serve as anchor points, allowing DIALIGN to conduct global alignments faster. ABC can then be used for the interactive visualization of the alignment.	http://dialign.gobics.de/chaos-dialign-submission
enoLOGOS	enoLOGOS creates sequence logos based on a variety of input, including sequence alignments, probability and alignment matrices and energy measurements.	http://biodev.hgen.pitt.edu/enologos/
Analysis of aligned sequences		
CAMPO	CAMPO is a tool to analyze conserved regions from a multiple sequence alignment	http://schubert.bio.uniroma1.it/CAMPO/index.html
CHC_FIND	CHC_FIND is a tool to analyze conserved hydrophobic contacts (CHC) from multiple structural alignments. In addition to a multiple sequence alignment, a structural alignment which provides the superposition of structurally conserved regions (SCRs) (i.e. results from SCR_FIND) needs to be provided.	http://schubert.bio.uniroma1.it/CHC_FIND/index.html
ConSurf	The ConSurf server allows one to map levels of amino acid conservation to known protein structures in order to study areas of potential functional importance on the surface of the protein. A PDB file is required as input, and a multiple sequence alignment is optional. If an alignment is not provided, ConSurf will build one by performing a search for homologous sequences and then aligning them.	http://consurf.tau.ac.il/
FFAS03	The Fold & Function Assignment System (FFAS03) takes an amino-acid sequence as input and generates a profile which is compared to several sets of sequence profiles including SCOP and PFAM.	http://ffas.burnham.org/
MaM	The Multiple alignment Manipulator (MaM) takes a multiple alignment of genomic sequences as input and calculates the locations of exons, common repeat elements and unique regions based on user-selected programs/information. The graphical display also allows users to focus an assessment of sequence variation on the identified regions.	http://compbio.cs.sfu.ca/MAM.htm
MINER	MINER is a tool for the identification and visualization of phylogenetic motifs (regions within a multiple sequence alignment (MSA) that conserve the overall phylogeny of the complete family).	http://www.pmap.csupomona.edu/MINER/
One-Block CYRCA	One-Block CYRCA is a program for identifying blocks (local ungapped profiles of the most conserved regions of protein families and domains) in a multiple sequence alignment based on the LAMA and CYRCA block-to-block alignment methods.	http://bioinformatics.weizmann.ac.il/~milana/OneCYRCA/
PriFi	PriFi is a tool for designing and evaluating primer pairs based on the input of a DNA sequence alignment; useful for the PCR amplification of homologs.	http://cgi-www.daimi.au.dk/cgi-chili/PriFi/main

Table 1. *Continued*

Name	Description	URL[a]
SCR_FIND	SCR_FIND is a tool to analyze structurally conserved regions (SCRs) from superimposed structures and multiple sequence alignments.	http://schubert.bio.uniroma1.it/SCR_FIND/
SVC	SVC (Structured Visualization of Evolutionary Conserved Sequences) is a tool that can search for pairs of orthologous genes, align the protein coding sequences, and visualize the evolutionary sequence conservation mapped back onto the gene structure scaffold.	http://svc.molgen.mpg.de/
WebMAM	This is the web version of the Multiple alignment Manipulator (MaM), which takes a multiple alignment of genomic sequences as input and calculates the locations of exons, common repeat elements and unique regions based on user-selected programs/information. The graphical display also allows users to focus an assessment of sequence variation on the identified regions.	http://atgc.lirmm.fr/mam/
WebProAnalyst	WebProAnalyst is a tool for searching for residues whose substitutions are correlated with variations in protein activity. Key physicochemical characteristics of these sites can be calculated.	http://www.mgs.bionet.nsc.ru/mgs/programs/panalyst/
Comparative genomics		
CisMols	CisMols (*Cis*-regulatory Modules) is a tool that identifies compositionally predicted *cis*-clusters that occur in groups of co-regulated genes within each of their ortholog-pair evolutionarily conserved *cis*-regulatory regions.	http://cismols.cchmc.org/
DCODE.ORG	The dcode.org website provides access to tools for comparative genomic analyses developed by the Comparative Genomics Center at the Lawerence Livermore National Laboratory. Tools include: zPicture, Mulan, eShadow, rVista, CREME and the ECR Browser.	http://www.dcode.org/
GENSTYLE	GENSTYLE is based on the genomic signature paradigm and allows the user to classify and characterize nucleotide sequences using oligonucleotide frequencies.	http://genstyle.imed.jussieu.fr/
MLST	MLST (Multi Locus Sequence Typing) is a nucleotide sequence-based approach for the unambiguous characterization of isolates of bacteria and other organisms using the sequences of internal fragments of seven house-keeping genes.	http://www.mlst.net/
Projector 2	Projector 2 allows users to map completed portions of the genome sequence of an organism onto the finished (or unfinished) genome of a closely related species or strain. Using the related genome sequence as a template can facilitate sequence assembly and the sequencing of the remaining gaps.	http://molgen.biol.rug.nl/websoftware/projector2/
SVC	SVC (Structured Visualization of Evolutionary Conserved Sequences) is a tool that can search for pairs of orthologous genes, align the protein coding sequences and visualize the evolutionary sequence conservation mapped back onto the gene structure scaffold.	http://svc.molgen.mpg.de/
T-STAG	Tissue-Specific Transcripts And Genes (T-STAG) is a system integrating EST, gene expression, alternative splicing and human–mouse orthology information for the analysis of tissue-specific gene and transcript expression patterns.	http://tstag.molgen.mpg.de/
Multiple sequence alignments		
CHAOS/DIALIGN WWW server	The CHAOS/DIALIGN WWW server is a multiple sequence alignment site which passes input sequences through CHAOS to create a list of local similarities. These similarities serve as anchor points, allowing DIALIGN to conduct global alignments faster. ABC can then be used for the interactive visualization of the alignment.	http://dialign.gobics.de/chaos-dialign-submission
PRALINE	Praline is a multiple sequence alignment program that can integrate information from sequence similarity searches and secondary structure prediction.	http://ibivu.cs.vu.nl/programs/pralinewww/

Table 1. *Continued*

Name	Description	URL[a]
Pairwise sequence alignments		
ParAlign	ParAlign provides a service for sequence similarity searching powered by parallel computing technology. The two comparison algorithms used are Smith–Waterman and ParAlign (a heuristic method for sequence alignment).	http://www.paralign.org/
YASS	YASS performs local alignments of DNA sequences. It is available through a web interface and as a stand-alone command-line tool.	http://www.loria.fr/projects/YASS/
Similarity searching		
EBI Tools	EBI Tools is a project that aims to provide programmatic access to the various databases and retrieval and analysis services EBI provides through Simple Object Access Protocol (SOAP) and other related web service technologies.	http://www.ebi.ac.uk/Tools/webservices/
HHpred	Based on the comparison of profile HMMs, HHpred takes a protein sequence or multiple sequence alignment as input and searches for remote homologues in an assortment of databases such as PDB, SMART and Pfam. The user can select either a local or global alignment method, and the search results can be used to generate 3D structural models.	http://protevo.eb.tuebingen.mpg.de/hhpred
ParAlign	ParAlign provides a service for sequence similarity searching powered by parallel computing technology. The two comparison algorithms used are Smith–Waterman and ParAlign (a heuristic method for sequence alignment).	http://www.paralign.org/
SCANMOT	SCANMOT is a sequence similarity searching tool that adds the additional constraints of simultaneous matching of multiple motifs.	http://www.ncbs.res.in/~faculty/mini/scanmot/scanmot.html

[a]A complete listing of these URLs can be accessed online at http://bioinformatics.ubc.ca/resources/links_directory/narweb2005/.

The Bioinformatics Links Directory is a community-driven resource and aims to offer a useful resource that is more than just a search engine. Therefore, the sites listed in the directory are suggested by the research community, are carefully selected and are curated by experts. Individuals who know of a resource that should be listed in the Bioinformatics Links Directory should suggest the URL here: http://bioinformatics.ubc.ca/resources/links_directory/add.php

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