Comprehensive List of Bioinformatics Tools and Databases

A complete collection of tools and databases utilized in the field of Bioinformatics, curated by COMBIGS, SASTRA Deemed to be University.

`Last update: 01/01/2024`

DDMut: predicting effects of mutations on protein stability using deep learning

ARMADiLLO: a web server for analyzing antibody mutation probabilities

DIANA-miRPath v4.0: expanding target-based miRNA functional analysis in cell-type and tissue contexts

PhD-SNPg: updating a webserver and lightweight tool for scoring nucleotide variants

CAID prediction portal: a comprehensive service for predicting intrinsic disorder and binding regions in proteins

sfkit: a web-based toolkit for secure and federated genomic analysis

GePI: large-scale text mining, customized retrieval and flexible filtering of gene/protein interactions

NBBC: a non-B DNA burden explorer in cancer

STellaris: a web server for accurate spatial mapping of single cells based on spatial transcriptomics data

FLUXestimator: a webserver for predicting metabolic flux and variations using transcriptomics data

Conserved unique peptide patterns (CUPP) online platform 2.0: implementation of +1000 JGI fungal genomes

SEPPA-mAb: spatial epitope prediction of protein antigens for mAbs

CRISPRimmunity: an interactive web server for CRISPR-associated Important Molecular events and Modulators Used in geNome edIting Tool identifYing

Human AGEs: an interactive spatio-temporal visualization and database of human archeogenomics

NORMSEQ: a tool for evaluation, selection and visualization of RNA-Seq normalization methods

The AnnotSV webserver in 2023: updated visualization and ranking

SMDB: a Spatial Multimodal Data Browser

ProAct: quantifying the differential activity of biological processes in tissues, cells, and user-defined contexts

Genome Context Viewer (GCV) version 2: enhanced visual exploration of multiple annotated genomes

PanDrugs2: prioritizing cancer therapies using integrated individual multi-omics data

GS-SMD server for steered molecular dynamics of peptide substrates in the active site of the γ-secretase complex:

PanDrugs2: prioritizing cancer therapies using integrated individual multi-omics data

FunARTS, the Fungal bioActive compound Resistant Target Seeker, an exploration engine for target-directed genome mining in fungi:

Abalign: a comprehensive multiple sequence alignment platform for B-cell receptor immune repertoires

ProAct: quantifying the differential activity of biological processes in tissues, cells, and user-defined contexts

Genome Context Viewer (GCV) version 2: enhanced visual exploration of multiple annotated genomes

ChemMaps.com v2.0: exploring the environmental chemical universe

SEanalysis 2.0: a comprehensive super-enhancer regulatory network analysis tool for human and mouse

PHASTEST: faster than PHASTER, better than PHAST

WebQUAST: online evaluation of genome assemblies

Mol* Volumes and Segmentations: visualization and interpretation of cell imaging data alongside macromolecular structure data and biological annotations

nCoVDock2: a docking server to predict the binding modes between COVID-19 targets and its potential ligands

MBROLE3: improved functional enrichment of chemical compounds for metabolomics data analysis

GenomeFLTR: filtering reads made easy

Breeze 2.0: an interactive web-tool for visual analysis and comparison of drug response data

miEAA 2023: updates, new functional microRNA sets and improved enrichment visualizations

MULocDeep web service for protein localization prediction and visualization at subcellular and suborganellar levels:

RNAincoder: a deep learning-based encoder for RNA and RNA-associated interaction

GeneRanger and TargetRanger: processed gene and protein expression levels across cells and tissues for target discovery

MicrobiomeAnalyst 2.0: comprehensive statistical, functional and integrative analysis of microbiome data

PEP-FOLD4: a pH-dependent force field for peptide structure prediction in aqueous solution

OnTarget: in silico design of MiniPromoters for targeted delivery of expression

MpoxRadar: a worldwide MPXV genomic surveillance dashboard

GeneRanger and TargetRanger: processed gene and protein expression levels across cells and tissues for target discovery

vissE.cloud: a webserver to visualise higher order molecular phenotypes from enrichment analysis

OpenXGR: a web-server update for genomic summary data interpretation

ACFIS 2.0: an improved web-server for fragment-based drug discovery via a dynamic screening strategy

IRSOM2: a web server for predicting bifunctional RNAs

WebTetrado: a webserver to explore quadruplexes in nucleic acid 3D structures

TransCRISPR–sgRNA design tool for CRISPR/Cas9 experiments targeting specific sequence motifs:

3D-GNOME 3.0: a three-dimensional genome modelling engine for analysing changes of promoter-enhancer contacts in the human genome

CAVE: a cloud-based platform for analysis and visualization of metabolic pathways

αCharges: partial atomic charges for AlphaFold structures in high quality

GPS 6.0: an updated server for prediction of kinase-specific phosphorylation sites in proteins

g:Profiler—interoperable web service for functional enrichment analysis and gene identifier mapping (2023 update):

ChroKit: a Shiny-based framework for interactive analysis, visualization and integration of genomic data

Tree Visualization By One Table (tvBOT): a web application for visualizing, modifying and annotating phylogenetic trees

antiSMASH 7.0: new and improved predictions for detection, regulation, chemical structures and visualisation

KVFinder-web: a web-based application for detecting and characterizing biomolecular cavities

Updated MS²PIP web server supports cutting-edge proteomics applications:

Proksee: in-depth characterization and visualization of bacterial genomes

DEPICTER2: a comprehensive webserver for intrinsic disorder and disorder function prediction

PAE viewer: a webserver for the interactive visualization of the predicted aligned error for multimer structure predictions and crosslinks

The LightDock Server: Artificial Intelligence-powered modeling of macromolecular interactions

TCRmodel2: high-resolution modeling of T cell receptor recognition using deep learning

PrismNet: predicting protein–RNA interaction using in vivo RNA structural information

dbCAN3: automated carbohydrate-active enzyme and substrate annotation

PANGEA: a new gene set enrichment tool for Drosophila and common research organisms

OrthoVenn3: an integrated platform for exploring and visualizing orthologous data across genomes

PASSer: fast and accurate prediction of protein allosteric sites

Prediction of protein structures, functions and interactions using the IntFOLD7, MultiFOLD and ModFOLDdock servers:

PlasMapper 3.0—a web server for generating, editing, annotating and visualizing publication quality plasmid maps:

e-RNA: a collection of web-servers for the prediction and visualisation of RNA secondary structure and their functional features

RNAcanvas: interactive drawing and exploration of nucleic acid structures

DIANA-microT 2023: including predicted targets of virally encoded miRNAs

DeepAlloDriver: a deep learning-based strategy to predict cancer driver mutations

DeepNeo: a webserver for predicting immunogenic neoantigens

Haplogrep 3 - an interactive haplogroup classification and analysis platform:

MyGeneset.info: an interactive and programmatic platform for community-curated and user-created collections of genes

AlloReverse: multiscale understanding among hierarchical allosteric regulations

FuzPred: a web server for the sequence-based prediction of the context-dependent binding modes of proteins

REVERSE: a user-friendly web server for analyzing next-generation sequencing data from in vitro selection/evolution experiments

The Ocean Gene Atlas v2.0: online exploration of the biogeography and phylogeny of plankton genes

Heml 2.0: an online service for heatmap illustration

iBIS2Analyzer: a web server for a phylogeny-driven coevolution analysis of protein families

CRISPRedict: a CRISPR-Cas9 web tool for interpretable efficiency predictions

CircadiOmics: circadian omic web portal

Web-based platform for analysis of RNA folding from high throughput chemical probing data:

NetSurfP-3.0: accurate and fast prediction of protein structural features by protein language models and deep learning

FUNAGE-Pro: comprehensive web server for gene set enrichment analysis of prokaryotes

AllerCatPro 2.0: a web server for predicting protein allergenicity potential

Identification of genome edited cells using CRISPRnano:

Annotation Query (AnnoQ): an integrated and interactive platform for large-scale genetic variant annotation

Shiny GATOM: omics-based identification of regulated metabolic modules in atom transition networks

FABIAN-variant: predicting the effects of DNA variants on transcription factor binding

PRECOGx: exploring GPCR signaling mechanisms with deep protein representations

MDsrv: visual sharing and analysis of molecular dynamics simulations

OmicsNet 2.0: a web-based platform for multi-omics integration and network visual analytics

GeCoViz: genomic context visualisation of prokaryotic genes from a functional and evolutionary perspective

AutoESD: a web tool for automatic editing sequence design for genetic manipulation of microorganisms

PCGA: a comprehensive web server for phenotype-cell-gene association analysis

BioExcel Building Blocks Workflows (BioBB-Wfs), an integrated web-based platform for biomolecular simulations:

EPIXplorer: A web server for prediction, analysis and visualization of enhancer-promoter interactions

GrAfSS: a webserver for substructure similarity searching and comparisons in the structures of proteins and RNA

5NosoAE: a web server for nosocomial bacterial antibiogram investigation and epidemiology survey

3DGenBench: a web-server to benchmark computational models for 3D Genomics

ExpressVis: a biologist-oriented interactive web server for exploring multi-omics data

PADLOC: a web server for the identification of antiviral defence systems in microbial genomes

Aquaculture Molecular Breeding Platform (AMBP): a comprehensive web server for genotype imputation and genetic analysis in aquaculture

RaacFold: a webserver for 3D visualization and analysis of protein structure by using reduced amino acid alphabets

CB-Dock2: improved protein–ligand blind docking by integrating cavity detection, docking and homologous template fitting

DrugVirus.info 2.0: an integrative data portal for broad-spectrum antivirals (BSA) and BSA-containing drug combinations (BCCs)

AlignMe: an update of the web server for alignment of membrane protein sequences

AlphaKnot: server to analyze entanglement in structures predicted by AlphaFold methods

PrankWeb 3: accelerated ligand-binding site predictions for experimental and modelled protein structures

PaintOmics 4: new tools for the integrative analysis of multi-omics datasets supported by multiple pathway databases

CSM-Potential: mapping protein interactions and biological ligands in 3D space using geometric deep learning

FuzDrop on AlphaFold: visualizing the sequence-dependent propensity of liquid–liquid phase separation and aggregation of proteins

Dali server: structural unification of protein families

CFM-ID 4.0 – a web server for accurate MS-based metabolite identification:

PiER: web-based facilities tailored for genetic target prioritisation harnessing human disease genetics, functional genomics and protein interactions

WebCSEA: web-based cell-type-specific enrichment analysis of genes

GEOexplorer: a webserver for gene expression analysis and visualisation

FuzDrop on AlphaFold: visualizing the sequence-dependent propensity of liquid–liquid phase separation and aggregation of proteins

Dali server: structural unification of protein families

CFM-ID 4.0 – a web server for accurate MS-based metabolite identification:

Cancer driver drug interaction explorer:

SynergyFinder 3.0: an interactive analysis and consensus interpretation of multi-drug synergies across multiple samples

CalFitter 2.0: Leveraging the power of singular value decomposition to analyse protein thermostability

IBS 2.0: an upgraded illustrator for the visualization of biological sequences

SWORD2: hierarchical analysis of protein 3D structures

GenePlexus: a web-server for gene discovery using network-based machine learning

Secondary Metabolite Transcriptomic Pipeline (SeMa-Trap), an expression-based exploration tool for increased secondary metabolite production in bacteria:

rna-tools.online: a Swiss army knife for RNA 3D structure modeling workflow

TIRSF: a web server for screening gene signatures to predict Tumor immunotherapy response

DLEB: a web application for building deep learning models in biological research

RING 3.0: fast generation of probabilistic residue interaction networks from structural ensembles

sRNAbench and sRNAtoolbox 2022 update: accurate miRNA and sncRNA profiling for model and non-model organisms

The Quest for Orthologs orthology benchmark service in 2022:

RSAT 2022: regulatory sequence analysis tools

BeStSel: webserver for secondary structure and fold prediction for protein CD spectroscopy

PhyloCloud: an online platform for making sense of phylogenomic data

CATANA: an online modelling environment for proteins and nucleic acid nanostructures

SubcellulaRVis: a web-based tool to simplify and visualise subcellular compartment enrichment

DEMO2: Assemble multi-domain protein structures by coupling analogous template alignments with deep-learning inter-domain restraint prediction

ICARUS, an interactive web server for single cell RNA-seq analysis:

BioUML—towards a universal research platform:

pubmedKB: an interactive web server for exploring biomedical entity relations in the biomedical literature

DEPCOD: a tool to detect and visualize co-evolution of protein domains

BioTransformer 3.0—a web server for accurately predicting metabolic transformation products:

SigCom LINCS: data and metadata search engine for a million gene expression signatures

VRprofile2: detection of antibiotic resistance-associated mobilome in bacterial pathogens

The mitoXplorer 2.0 update: integrating and interpreting mitochondrial expression dynamics within a cellular context

TADeus2: a web server facilitating the clinical diagnosis by pathogenicity assessment of structural variations disarranging 3D chromatin structure

MAPIYA contact map server for identification and visualization of molecular interactions in proteins and biological complexes:

TeachOpenCADD 2022: open source and FAIR Python pipelines to assist in structural bioinformatics and cheminformatics research

BioSimulators: a central registry of simulation engines and services for recommending specific tools

DDGun: an untrained predictor of protein stability changes upon amino acid variants

SuperPred 3.0: drug classification and target prediction—a machine learning approach

iFeatureOmega: an integrative platform for engineering, visualization and analysis of features from molecular sequences, structural and ligand data sets

GRaSP-web: a machine learning strategy to predict binding sites based on residue neighborhood graphs

Deep phenotyping: symptom annotation made simple with SAMS

Multi-CSAR: a web server for scaffolding contigs using multiple reference genomes

BusyBee Web: towards comprehensive and differential composition-based metagenomic binning

ProteinsPlus: a comprehensive collection of web-based molecular modeling tools

AutozygosityMapper: Identification of disease-mutations in consanguineous families

DeepLoc 2.0: multi-label subcellular localization prediction using protein language models

ERMer: a serverless platform for navigating, analyzing, and visualizing Escherichia coli regulatory landscape through graph database

ExPheWas: a platform for cis-Mendelian randomization and gene-based association scans

GraPES: The Granule Protein Enrichment Server for prediction of biological condensate constituents

KmerKeys: a web resource for searching indexed genome assemblies and variants

The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2022 update

DNAzymeBuilder, a web application for in situ generation of RNA/DNA-cleaving deoxyribozymes:

ANANASTRA: annotation and enrichment analysis of allele-specific transcription factor binding at SNPs

patcHwork: a user-friendly pH sensitivity analysis web server for protein sequences and structures

LoopGrafter: a web tool for transplanting dynamical loops for protein engineering

LOMETS3: integrating deep learning and profile alignment for advanced protein template recognition and function annotation

WashU Epigenome Browser update 2022:

3DLigandSite: structure-based prediction of protein–ligand binding sites

Search and sequence analysis tools services from EMBL-EBI in 2022:

RNAspider: a webserver to analyze entanglements in RNA 3D structures

ChIP-Atlas 2021 update: a data-mining suite for exploring epigenomic landscapes by fully integrating ChIP-seq, ATAC-seq and Bisulfite-seq data

DAVID: a web server for functional enrichment analysis and functional annotation of gene lists (2021 update)

CRISPRloci: comprehensive and accurate annotation of CRISPR–Cas systems

TIMEOR: a web-based tool to uncover temporal regulatory mechanisms from multi-omics data

DGLinker: flexible knowledge-graph prediction of disease–gene associations

eSkip-Finder: a machine learning-based web application and database to identify the optimal sequences of antisense oligonucleotides for exon skipping

Voronoia 4-ever:

catRAPID omics v2.0: going deeper and wider in the prediction of protein–RNA interactions

KOBAS-i: intelligent prioritization and exploratory visualization of biological functions for gene enrichment analysis

Mechnetor: a web server for exploring protein mechanism and the functional context of genetic variants

GPCRsignal: webserver for analysis of the interface between G-protein–coupled receptors and their effector proteins by dynamics and mutations

pegIT - a web-based design tool for prime editing:

DrugComb update: a more comprehensive drug sensitivity data repository and analysis portal

b2bTools: online predictions for protein biophysical features and their conservation

ncFANs v2.0: an integrative platform for functional annotation of non-coding RNAs

MTR3D: identifying regions within protein tertiary structures under purifying selection

GEPIA2021: integrating multiple deconvolution-based analysis into GEPIA

snpXplorer: a web application to explore human SNP-associations and annotate SNP-sets

GalaxyHeteromer: protein heterodimer structure prediction by template-based and ab initio docking

snpXplorer: a web application to explore human SNP-associations and annotate SNP-sets

DeepFun: a deep learning sequence-based model to decipher non-coding variant effect in a tissue- and cell type-specific manner

Mergeomics 2.0: a web server for multi-omics data integration to elucidate disease networks and predict therapeutics

LipidSig: a web-based tool for lipidomic data analysis

The COVID-19 Data Portal: accelerating SARS-CoV-2 and COVID-19 research through rapid open access data sharing

Aviator: a web service for monitoring the availability of web services

Estimage: a webserver hub for the computation of methylation age

NetGO 2.0: improving large-scale protein function prediction with massive sequence, text, domain, family and network information

Thunor: visualization and analysis of high-throughput dose–response datasets

ProLint: a web-based framework for the automated data analysis and visualization of lipid–protein interactions

BRIO: a web server for RNA sequence and structure motif scan

PlantDeepSEA, a deep learning-based web service to predict the regulatory effects of genomic variants in plants:

CPA: a web-based platform for consensus pathway analysis and interactive visualization

Graphery: interactive tutorials for biological network algorithms

G2PDeep: a web-based deep-learning framework for quantitative phenotype prediction and discovery of genomic markers

Preselector.uni-jena.de: optimize your cloning—a resource for identifying restriction enzymes for preselection reactions

DomainViz: intuitive visualization of consensus domain distributions across groups of proteins

LigAdvisor: a versatile and user-friendly web-platform for drug design

AnnotSV and knotAnnotSV: a web server for human structural variations annotations, ranking and analysis

MyCLADE: a multi-source domain annotation server for sequence functional exploration

RunBioSimulations: an extensible web application that simulates a wide range of computational modeling frameworks, algorithms, and formats

DeepGOWeb: fast and accurate protein function prediction on the (Semantic) Web

MetaboAnalyst 5.0: narrowing the gap between raw spectra and functional insights

KEA3: improved kinase enrichment analysis via data integration

The gutSMASH web server: automated identification of primary metabolic gene clusters from the gut microbiota

pLannotate: engineered plasmid annotation

ProteinTools: a toolkit to analyze protein structures

OmicsAnalyst: a comprehensive web-based platform for visual analytics of multi-omics data

Amino Acid Interactions (INTAA) web server v2.0: a single service for computation of energetics and conservation in biomolecular 3D structures

eVITTA: a web-based visualization and inference toolbox for transcriptome analysis

CNVxplorer: a web tool to assist clinical interpretation of CNVs in rare disease patients

SynLeGG: analysis and visualization of multiomics data for discovery of cancer ‘Achilles Heels’ and gene function relationships

PERCEPTRON: an open-source GPU-accelerated proteoform identification pipeline for top-down proteomics

DeepRefiner: high-accuracy protein structure refinement by deep network calibration

ProteoVision: web server for advanced visualization of ribosomal proteins

PredictProtein - Predicting Protein Structure and Function for 29 Years:

OpenAnnotate: a web server to annotate the chromatin accessibility of genomic regions

DoChaP: the domain change presenter

EDGAR3.0: comparative genomics and phylogenomics on a scalable infrastructure

The Dockstore: enhancing a community platform for sharing reproducible and accessible computational protocols

CoffeeProt: an online tool for correlation and functional enrichment of systems genetics data

InterEvDock3: a combined template-based and free docking server with increased performance through explicit modeling of complex homologs and integration of covariation-based contact maps

antiSMASH 6.0: improving cluster detection and comparison capabilities

The Dockstore: enhancing a community platform for sharing reproducible and accessible computational protocols

LZerD webserver for pairwise and multiple protein–protein docking:

ProteoSign v2: a faster and evolved user-friendly online tool for statistical analyses of differential proteomics

BENZ WS: the Bologna ENZyme Web Server for four-level EC number annotation

ModFOLD8: accurate global and local quality estimates for 3D protein models

Proteo3Dnet: a web server for the integration of structural information with interactomics data

Mol* Viewer: modern web app for 3D visualization and analysis of large biomolecular structures

CeLaVi: an interactive cell lineage visualization tool

LipidSuite: interactive web server for lipidomics differential and enrichment analysis

PLIP 2021: expanding the scope of the protein–ligand interaction profiler to DNA and RNA

Trips-Viz: an environment for the analysis of public and user-generated ribosome profiling data

LitSuggest: a web-based system for literature recommendation and curation using machine learning

PE-Designer and PE-Analyzer: web-based design and analysis tools for CRISPR prime editing

miRTargetLink 2.0—interactive miRNA target gene and target pathway networks:

OxDNA.org: a public webserver for coarse-grained simulations of DNA and RNA nanostructures

Vaxign2: the second generation of the first Web-based vaccine design program using reverse vaccinology and machine learning

ReFOLD3: refinement of 3D protein models with gradual restraints based on predicted local quality and residue contacts

VirtualTaste: a web server for the prediction of organoleptic properties of chemical compounds

IPC 2.0: prediction of isoelectric point and pKa dissociation constants

Recognizing and validating ligands with CheckMyBlob:

mmCSM-PPI: predicting the effects of multiple point mutations on protein–protein interactions

ADMETlab 2.0: an integrated online platform for accurate and comprehensive predictions of ADMET properties

MutationTaster2021:

Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation

Arena3Dweb: interactive 3D visualization of multilayered networks

miRMaster 2.0: multi-species non-coding RNA sequencing analyses at scale

Expasy, the Swiss Bioinformatics Resource Portal, as designed by its users:

iNetModels 2.0: an interactive visualization and database of multi-omics data

TISIGNER.com: web services for improving recombinant protein production

RNAProbe: a web server for normalization and analysis of RNA structure probing data

SNPnexus: a web server for functional annotation of human genome sequence variation (2020 update)

Tox21BodyMap: a webtool to map chemical effects on the human body

HomolWat: a web server tool to incorporate ‘homologous’ water molecules into GPCR structures

miRNet 2.0: network-based visual analytics for miRNA functional analysis and systems biology

mirnaQC: a webserver for comparative quality control of miRNA-seq data

CReSCENT: CanceR Single Cell ExpressioN Toolkit

TopMatch-web: pairwise matching of large assemblies of protein and nucleic acid chains in 3D

The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2020 update

FATCAT 2.0: towards a better understanding of the structural diversity of proteins

piNET: a versatile web platform for downstream analysis and visualization of proteomics data

mCSM-membrane: predicting the effects of mutations on transmembrane proteins

PaCRISPR: a server for predicting and visualizing anti-CRISPR proteins

ShiftCrypt: a web server to understand and biophysically align proteins through their NMR chemical shift values

EpiRegio: analysis and retrieval of regulatory elements linked to genes

ASAP 2020 update: an open, scalable and interactive web-based portal for (single-cell) omics analyses

PseudoChecker: an integrated online platform for gene inactivation inference

CVCDAP: an integrated platform for molecular and clinical analysis of cancer virtual cohorts

NanoSPC: a scalable, portable, cloud compatible viral nanopore metagenomic data processing pipeline

SYNERGxDB: an integrative pharmacogenomic portal to identify synergistic drug combinations for precision oncology

Fluxer: a web application to compute, analyze and visualize genome-scale metabolic flux networks

TIMER2.0 for analysis of tumor-infiltrating immune cells:

3D-GNOME 2.0: a three-dimensional genome modeling engine for predicting structural variation-driven alterations of chromatin spatial structure in the human genome

mmCSM-AB: guiding rational antibody engineering through multiple point mutations

ARTS 2.0: feature updates and expansion of the Antibiotic Resistant Target Seeker for comparative genome mining

webPSN v2.0: a webserver to infer fingerprints of structural communication in biomacromolecules

RiboToolkit: an integrated platform for analysis and annotation of ribosome profiling data to decode mRNA translation at codon resolution

mRNALoc: a novel machine-learning based in-silico tool to predict mRNA subcellular localization

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ToxicoDB: an integrated database to mine and visualize large-scale toxicogenomic datasets

PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins

InterPred: a webtool to predict chemical autofluorescence and luminescence interference

IRIS3: integrated cell-type-specific regulon inference server from single-cell RNA-Seq

AnnoLnc2: the one-stop portal to systematically annotate novel lncRNAs for human and mouse

Conserved unique peptide patterns (CUPP) online platform: peptide-based functional annotation of carbohydrate active enzymes

NetMHCpan-4.1 and NetMHCIIpan-4.0: improved predictions of MHC antigen presentation by concurrent motif deconvolution and integration of MS MHC eluted ligand data

AcrFinder: genome mining anti-CRISPR operons in prokaryotes and their viruses

InteractomeSeq: a web server for the identification and profiling of domains and epitopes from phage display and next generation sequencing data

PaccMann: a web service for interpretable anticancer compound sensitivity prediction

Atomic Charge Calculator II: web-based tool for the calculation of partial atomic charges

MISCAST: MIssense variant to protein StruCture Analysis web SuiTe

MutaRNA: analysis and visualization of mutation-induced changes in RNA structure

AlloSigMA 2: paving the way to designing allosteric effectors and to exploring allosteric effects of mutations

BIOMEX: an interactive workflow for (single cell) omics data interpretation and visualization

CoCoCoNet: conserved and comparative co-expression across a diverse set of species

CausalMGM: an interactive web-based causal discovery tool

EnzymeMiner: automated mining of soluble enzymes with diverse structures, catalytic properties and stabilities

Oviz-Bio: a web-based platform for interactive cancer genomics data visualization

ARIAweb: a server for automated NMR structure calculation

TeamTat: a collaborative text annotation tool

AWSEM-Suite: a protein structure prediction server based on template-guided, coevolutionary-enhanced optimized folding landscapes

SIB Literature Services: RESTful customizable search engines in biomedical literature, enriched with automatically mapped biomedical concepts

GeneTrail 3: advanced high-throughput enrichment analysis

The omics discovery REST interface:

COVTree: Coevolution in OVerlapped sequences by Tree analysis server

The Quest for Orthologs benchmark service and consensus calls in 2020:

miEAA 2.0: integrating multi-species microRNA enrichment analysis and workflow management systems

miRSwitch: detecting microRNA arm shift and switch events

LIST-S2: taxonomy based sorting of deleterious missense mutations across species

PDBMD2CD: providing predicted protein circular dichroism spectra from multiple molecular dynamics-generated protein structures

MetaPhOrs 2.0: integrative, phylogeny-based inference of orthology and paralogy across the tree of life

VarFish: comprehensive DNA variant analysis for diagnostics and research

MetagenoNets: comprehensive inference and meta-insights for microbial correlation networks

TFmotifView: a webserver for the visualization of transcription factor motifs in genomic regions

MusiteDeep: a deep-learning based webserver for protein post-translational modification site prediction and visualization

NOREVA: enhanced normalization and evaluation of time-course and multi-class metabolomic data

miRViz: a novel webserver application to visualize and interpret microRNA datasets

Zebra2: advanced and easy-to-use web-server for bioinformatic analysis of subfamily-specific and conserved positions in diverse protein superfamilies

SPEED2: inferring upstream pathway activity from differential gene expression

novoPathFinder: a webserver of designing novel-pathway with integrating GEM-model

OligoMinerApp: a web-server application for the design of genome-scale oligonucleotide in situ hybridization probes through the flexible OligoMiner environment

Galaxy HiCExplorer 3: a web server for reproducible Hi-C, capture Hi-C and single-cell Hi-C data analysis, quality control and visualization

ProteinsPlus: interactive analysis of protein–ligand binding interfaces

rMAPS2: an update of the RNA map analysis and plotting server for alternative splicing regulation

TREND: a platform for exploring protein function in prokaryotes based on phylogenetic, domain architecture and gene neighborhood analyses

Prediction of synonymous corrections by the BE-FF computational tool expands the targeting scope of base editing:

SynergyFinder 2.0: visual analytics of multi-drug combination synergies

LINbase: a web server for genome-based identification of prokaryotes as members of crowdsourced taxa

SuperCYPsPred—a web server for the prediction of cytochrome activity:

MTR-Viewer: identifying regions within genes under purifying selection

DNAvisualization.org: a serverless web tool for DNA sequence visualization

WashU Epigenome Browser update 2019:

LnCompare: gene set feature analysis for human long non-coding RNAs

CNIT: a fast and accurate web tool for identifying protein-coding and long non-coding transcripts based on intrinsic sequence composition

ORVAL: a novel platform for the prediction and exploration of disease-causing oligogenic variant combinations

RNAmod: an integrated system for the annotation of mRNA modifications

PRECOG: PREdicting COupling probabilities of G-protein coupled receptors

PatchSearch: a web server for off-target protein identification

BioUML: an integrated environment for systems biology and collaborative analysis of biomedical data

IAMBEE: a web-service for the identification of adaptive pathways from parallel evolved clonal populations

tRNAviz: explore and visualize tRNA sequence features

PSICA: a fast and accurate web service for protein model quality analysis

The Gene Sculpt Suite: a set of tools for genome editing

Web 3DNA 2.0 for the analysis, visualization, and modeling of 3D nucleic acid structures:

mCSM-PPI2: predicting the effects of mutations on protein–protein interactions

Evolview v3: a webserver for visualization, annotation, and management of phylogenetic trees

PubTator central: automated concept annotation for biomedical full text articles

WebGestalt 2019: gene set analysis toolkit with revamped UIs and APIs

Interactive web-based visualization and sharing of phylogenetic trees using phylogeny.IO:

ChEA3: transcription factor enrichment analysis by orthogonal omics integration

DaReUS-Loop: a web server to model multiple loops in homology models

Protein Interaction Z Score Assessment (PIZSA): an empirical scoring scheme for evaluation of protein–protein interactions

Prophage Hunter: an integrative hunting tool for active prophages

MEXPRESS update 2019:

web-rMKL: a web server for dimensionality reduction and sample clustering of multi-view data based on unsupervised multiple kernel learning

BEERE: a web server for biomedical entity expansion, ranking and explorations

HNADOCK: a nucleic acid docking server for modeling RNA/DNA–RNA/DNA 3D complex structures

Simple ClinVar: an interactive web server to explore and retrieve gene and disease variants aggregated in ClinVar database

WebGestalt 2019: gene set analysis toolkit with revamped UIs and APIs

Interactive web-based visualization and sharing of phylogenetic trees using phylogeny.IO:

ChEA3: transcription factor enrichment analysis by orthogonal omics integration

GEPIA2: an enhanced web server for large-scale expression profiling and interactive analysis

ImmuneRegulation: a web-based tool for identifying human immune regulatory elements

IEDB-AR: immune epitope database—analysis resource in 2019

Geneshot: search engine for ranking genes from arbitrary text queries

VOLPES: an interactive web-based tool for visualizing and comparing physicochemical properties of biological sequences

sRNAbench and sRNAtoolbox 2019: intuitive fast small RNA profiling and differential expression

Fido-SNP: the first webserver for scoring the impact of single nucleotide variants in the dog genome

ResponseNet v.3: revealing signaling and regulatory pathways connecting your proteins and genes across human tissues

ProSNEx: a web-based application for exploration and analysis of protein structures using network formalism

SEPPA 3.0—enhanced spatial epitope prediction enabling glycoprotein antigens:

EpiAlignment: alignment with both DNA sequence and epigenomic data

Caver Web 1.0: identification of tunnels and channels in proteins and analysis of ligand transport

QBiC-Pred: quantitative predictions of transcription factor binding changes due to sequence variants

Doc2Hpo: a web application for efficient and accurate HPO concept curation

HawkDock: a web server to predict and analyze the protein–protein complex based on computational docking and MM/GBSA

Drug ReposER: a web server for predicting similar amino acid arrangements to known drug binding interfaces for potential drug repositioning

Pergola-web: a web server for the visualization and analysis of longitudinal behavioral data using repurposed genomics tools and standards

EPIC-TABSAT: analysis tool for targeted bisulfite sequencing experiments and array-based methylation studies

Yvis: antibody high-density alignment visualization and analysis platform with an integrated database

NAPS update: network analysis of molecular dynamics data and protein–nucleic acid complexes

SwissTargetPrediction: updated data and new features for efficient prediction of protein targets of small molecules

RegulationSpotter: annotation and interpretation of extratranscriptic DNA variants

Yosshi: a web-server for disulfide engineering by bioinformatic analysis of diverse protein families

MutationDistiller: user-driven identification of pathogenic DNA variants

MERMAID: dedicated web server to prepare and run coarse-grained membrane protein dynamics

CHOPCHOP v3: expanding the CRISPR web toolbox beyond genome editing

NetGO: improving large-scale protein function prediction with massive network information

iMKT: the integrative McDonald and Kreitman test

LOMETS2: improved meta-threading server for fold-recognition and structure-based function annotation for distant-homology proteins

DOGMA: a web server for proteome and transcriptome quality assessment

VoroMQA web server for assessing three-dimensional structures of proteins and protein complexes:

INGA 2.0: improving protein function prediction for the dark proteome

The RNA workbench 2.0: next generation RNA data analysis

AppA: a web server for analysis, comparison, and visualization of contact residues and interfacial waters of antibody–antigen structures and models

modEnrichr: a suite of gene set enrichment analysis tools for model organisms

MISIM v2.0: a web server for inferring microRNA functional similarity based on microRNA-disease associations

AlloDriver: a method for the identification and analysis of cancer driver targets

SPADE web service for prediction of allergen IgE epitopes:

MFEprimer-3.0: quality control for PCR primers

g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019 update)

DrugComb: an integrative cancer drug combination data portal

CPGAVAS2, an integrated plastome sequence annotator and analyzer:

MAFFT-DASH: integrated protein sequence and structural alignment

OrthoVenn2: a web server for whole-genome comparison and annotation of orthologous clusters across multiple species

Cistrome-GO: a web server for functional enrichment analysis of transcription factor ChIP-seq peaks

Aggrescan3D (A3D) 2.0: prediction and engineering of protein solubility

MyDGR: a server for identification and characterization of diversity-generating retroelements

SeqTailor: a user-friendly webserver for the extraction of DNA or protein sequences from next-generation sequencing data

MRPrimerW2: an enhanced tool for rapid design of valid high-quality primers with multiple search modes for qPCR experiments

IntFOLD: an integrated web resource for high performance protein structure and function prediction

antiSMASH 5.0: updates to the secondary metabolite genome mining pipeline

NGPhylogeny.fr: new generation phylogenetic services for non-specialists

SEanalysis: a web tool for super-enhancer associated regulatory analysis

Updated MS²PIP web server delivers fast and accurate MS² peak intensity prediction for multiple fragmentation methods, instruments and labeling techniques:

The PSIPRED Protein Analysis Workbench: 20 years on

LitSense: making sense of biomedical literature at sentence level

GalaxyRefine2: simultaneous refinement of inaccurate local regions and overall protein structure

AutoMLST: an automated web server for generating multi-locus species trees highlighting natural product potential

The EMBL-EBI search and sequence analysis tools APIs in 2019:

OrganellarGenomeDRAW (OGDRAW) version 1.3.1: expanded toolkit for the graphical visualization of organellar genomes

NetworkAnalyst 3.0: a visual analytics platform for comprehensive gene expression profiling and meta-analysis

Interactive Tree Of Life (iTOL) v4: recent updates and new developments

CircadiOmics: circadian omic web portal

GeneMANIA update 2018:

KnotGenome: a server to analyze entanglements of chromosomes

Identification and visualization of protein binding regions with the ArDock server:

MISTIC2: comprehensive server to study coevolution in protein families

HMMER web server: 2018 update

cgDNAweb: a web interface to the cgDNA sequence-dependent coarse-grain model of double-stranded DNA

The Microbial Genomes Atlas (MiGA) webserver: taxonomic and gene diversity analysis of Archaea and Bacteria at the whole genome level

EasyFRAP-web: a web-based tool for the analysis of fluorescence recovery after photobleaching data

Galaxy HiCExplorer: a web server for reproducible Hi-C data analysis, quality control and visualization

BeStSel: a web server for accurate protein secondary structure prediction and fold recognition from the circular dichroism spectra

EviNet: a web platform for network enrichment analysis with flexible definition of gene sets

OmicsNet: a web-based tool for creation and visual analysis of biological networks in 3D space

TAM 2.0: tool for MicroRNA set analysis

LOLAweb: a containerized web server for interactive genomic locus overlap enrichment analysis

PSSMSearch: a server for modeling, visualization, proteome-wide discovery and annotation of protein motif specificity determinants

Coloc-stats: a unified web interface to perform colocalization analysis of genomic features

IUPred2A: context-dependent prediction of protein disorder as a function of redox state and protein binding

CASTp 3.0: computed atlas of surface topography of proteins

VarAFT: a variant annotation and filtration system for human next generation sequencing data

COACH-D: improved protein–ligand binding sites prediction with refined ligand-binding poses through molecular docking

The BaMM web server for de-novo motif discovery and regulatory sequence analysis:

HSYMDOCK: a docking web server for predicting the structure of protein homo-oligomers with Cn or Dn symmetry

GDA, a web-based tool for Genomics and Drugs integrated analysis:

gRINN: a tool for calculation of residue interaction energies and protein energy network analysis of molecular dynamics simulations

GIANT 2.0: genome-scale integrated analysis of gene networks in tissues

PaintOmics 3: a web resource for the pathway analysis and visualization of multi-omics data

SMARTIV: combined sequence and structure de-novo motif discovery for in-vivo RNA binding data

eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks

HotSpot Wizard 3.0: web server for automated design of mutations and smart libraries based on sequence input information

ComplexContact: a web server for inter-protein contact prediction using deep learning

CRISPRCasFinder, an update of CRISRFinder, includes a portable version, enhanced performance and integrates search for Cas proteins:

TCRmodel: high resolution modeling of T cell receptors from sequence

Mutalisk: a web-based somatic MUTation AnaLyIS toolKit for genomic, transcriptional and epigenomic signatures

The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update

Kinact: a computational approach for predicting activating missense mutations in protein kinases

CellAtlasSearch: a scalable search engine for single cells

SWISS-MODEL: homology modelling of protein structures and complexes

GPCRM: a homology modeling web service with triple membrane-fitted quality assessment of GPCR models

mTM-align: a server for fast protein structure database search and multiple protein structure alignment

Freiburg RNA tools: a central online resource for RNA-focused research and teaching

BAGEL4: a user-friendly web server to thoroughly mine RiPPs and bacteriocins

FragFit: a web-application for interactive modeling of protein segments into cryo-EM density maps

The Ocean Gene Atlas: exploring the biogeography of plankton genes online

WEGO 2.0: a web tool for analyzing and plotting GO annotations, 2018 update

ezTag: tagging biomedical concepts via interactive learning

GlobAI Distribution of GEnetic Traits (GADGET) web server: polygenic trait scores worldwide

dbCAN2: a meta server for automated carbohydrate-active enzyme annotation

GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits

MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis

CRISPOR: intuitive guide selection for CRISPR/Cas9 genome editing experiments and screens

CalFitter: a web server for analysis of protein thermal denaturation data

LitVar: a semantic search engine for linking genomic variant data in PubMed and PMC

CABS-flex 2.0: a web server for fast simulations of flexibility of protein structures

AAI-profiler: fast proteome-wide exploratory analysis reveals taxonomic identity, misclassification and contamination

AlloFinder: a strategy for allosteric modulator discovery and allosterome analyses

SNPnexus: assessing the functional relevance of genetic variation to facilitate the promise of precision medicine

CavityPlus: a web server for protein cavity detection with pharmacophore modelling, allosteric site identification and covalent ligand binding ability prediction

RepeatsDB-lite: a web server for unit annotation of tandem repeat proteins

INTERSPIA: a web application for exploring the dynamics of protein-protein interactions among multiple species

HPEPDOCK: a web server for blind peptide–protein docking based on a hierarchical algorithm

PANNZER2: a rapid functional annotation web server

xiSPEC: web-based visualization, analysis and sharing of proteomics data

InterEvDock2: an expanded server for protein docking using evolutionary and biological information from homology models and multimeric inputs

SPAR: small RNA-seq portal for analysis of sequencing experiments

CSAR-web: a web server of contig scaffolding using algebraic rearrangements

oriTfinder: a web-based tool for the identification of origin of transfers in DNA sequences of bacterial mobile genetic elements

Patscanui: an intuitive web interface for searching patterns in DNA and protein data

RSAT 2018: regulatory sequence analysis tools 20th anniversary

CoNekT: an open-source framework for comparative genomic and transcriptomic network analyses

geno2pheno[ngs-freq]: a genotypic interpretation system for identifying viral drug resistance using next-generation sequencing data

DynaMut: predicting the impact of mutations on protein conformation, flexibility and stability

ProTox-II: a webserver for the prediction of toxicity of chemicals

Oli2go: an automated multiplex oligonucleotide design tool

RNApdbee 2.0: multifunctional tool for RNA structure annotation

BUSCA: an integrative web server to predict subcellular localization of proteins

RNApdbee 2.0: multifunctional tool for RNA structure annotation

PhytoNet: comparative co-expression network analyses across phytoplankton and land plants

iPath3.0: interactive pathways explorer v3

MetExplore: collaborative edition and exploration of metabolic networks

Oli2go: an automated multiplex oligonucleotide design tool

DynaMut: predicting the impact of mutations on protein conformation, flexibility and stability

ProTox-II: a webserver for the prediction of toxicity of chemicals

pirScan: a webserver to predict piRNA targeting sites and to avoid transgene silencing in C. elegans

BRepertoire: a user-friendly web server for analysing antibody repertoire data

GPCR-SSFE 2.0—a fragment-based molecular modeling web tool for Class A G-protein coupled receptors:

The RNA workbench: best practices for RNA and high-throughput sequencing bioinformatics in Galaxy

HGVA: the Human Genome Variation Archive

LimTox: a web tool for applied text mining of adverse event and toxicity associations of compounds, drugs and genes

SDM: a server for predicting effects of mutations on protein stability

NOREVA: normalization and evaluation of MS-based metabolomics data

SCENERY: a web application for (causal) network reconstruction from cytometry data

RNA-MoIP: prediction of RNA secondary structure and local 3D motifs from sequence data

GeMSTONE: orchestrated prioritization of human germline mutations in the cloud

CPC2: a fast and accurate coding potential calculator based on sequence intrinsic features

VCF.Filter: interactive prioritization of disease-linked genetic variants from sequencing data

ProteoSign: an end-user online differential proteomics statistical analysis platform

HDOCK: a web server for protein–protein and protein–DNA/RNA docking based on a hybrid strategy

XSuLT: a web server for structural annotation and representation of sequence-structure alignments

SODA: prediction of protein solubility from disorder and aggregation propensity

DEOGEN2: prediction and interactive visualization of single amino acid variant deleteriousness in human proteins

RiPPMiner: a bioinformatics resource for deciphering chemical structures of RiPPs based on prediction of cleavage and cross-links

compleXView: a server for the interpretation of protein abundance and connectivity information to identify protein complexes

GenProBiS: web server for mapping of sequence variants to protein binding sites

ThreaDomEx: a unified platform for predicting continuous and discontinuous protein domains by multiple-threading and segment assembly

AMMOS2: a web server for protein–ligand–water complexes refinement via molecular mechanics

GeSeq – versatile and accurate annotation of organelle genomes:

CSTEA: a webserver for the Cell State Transition Expression Atlas

PhD-SNPg: a webserver and lightweight tool for scoring single nucleotide variants

Web3DMol: interactive protein structure visualization based on WebGL

mTCTScan: a comprehensive platform for annotation and prioritization of mutations affecting drug sensitivity in cancers

Pathview Web: user friendly pathway visualization and data integration

P4P: a peptidome-based strain-level genome comparison web tool

C-SPADE: a web-tool for interactive analysis and visualization of drug screening experiments through compound-specific bioactivity dendrograms

IntaRNA 2.0: enhanced and customizable prediction of RNA–RNA interactions

ConTra v3: a tool to identify transcription factor binding sites across species, update 2017

PIGSPro: prediction of immunoGlobulin structures v2

Exploring background mutational processes to decipher cancer genetic heterogeneity:

agriGO v2.0: a GO analysis toolkit for the agricultural community, 2017 update

DSSR-enhanced visualization of nucleic acid structures in Jmol:

WebGestalt 2017: a more comprehensive, powerful, flexible and interactive gene set enrichment analysis toolkit

Olelo: a web application for intuitive exploration of biomedical literature

CAFE: aCcelerated Alignment-FrEe sequence analysis

PharmMapper 2017 update: a web server for potential drug target identification with a comprehensive target pharmacophore database

DynOmics: dynamics of structural proteome and beyond

The EBI search engine: EBI search as a service—making biological data accessible for all

The Antibiotic Resistant Target Seeker (ARTS), an exploration engine for antibiotic cluster prioritization and novel drug target discovery:

I-TASSER-MR: automated molecular replacement for distant-homology proteins using iterative fragment assembly and progressive sequence truncation

ProteinsPlus: a web portal for structure analysis of macromolecules

BusyBee Web: metagenomic data analysis by bootstrapped supervised binning and annotation

COFACTOR: improved protein function prediction by combining structure, sequence and protein–protein interaction information

BIS2Analyzer: a server for co-evolution analysis of conserved protein families

IslandViewer 4: expanded prediction of genomic islands for larger-scale datasets

BepiPred-2.0: improving sequence-based B-cell epitope prediction using conformational epitopes

RegulatorTrail: a web service for the identification of key transcriptional regulators

COFACTOR: improved protein function prediction by combining structure, sequence and protein–protein interaction information

Interactive microbial distribution analysis using BioAtlas:

The pepATTRACT web server for blind, large-scale peptide–protein docking:

HH-MOTiF: de novo detection of short linear motifs in proteins by Hidden Markov Model comparisons

SpartaABC: a web server to simulate sequences with indel parameters inferred using an approximate Bayesian computation algorithm

kpLogo: positional k-mer analysis reveals hidden specificity in biological sequences

WoPPER: Web server for Position Related data analysis of gene Expression in Prokaryotes

ModFOLD6: an accurate web server for the global and local quality estimation of 3D protein models

GASS-WEB: a web server for identifying enzyme active sites based on genetic algorithms

SBSPKSv2: structure-based sequence analysis of polyketide synthases and non-ribosomal peptide synthetases

antiSMASH 4.0—improvements in chemistry prediction and gene cluster boundary identification:

PRISM 3: expanded prediction of natural product chemical structures from microbial genomes

SeMPI: a genome-based secondary metabolite prediction and identification web server

plantiSMASH: automated identification, annotation and expression analysis of plant biosynthetic gene clusters

PMut: a web-based tool for the annotation of pathological variants on proteins, 2017 update

TraitRateProp: a web server for the detection of trait-dependent evolutionary rate shifts in sequence sites

A PanorOmic view of personal cancer genomes:

The Bologna Annotation Resource (BAR 3.0): improving protein functional annotation

FireProt: web server for automated design of thermostable proteins

MicrobiomeAnalyst: a web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data

GWAB: a web server for the network-based boosting of human genome-wide association data

LigParGen web server: an automatic OPLS-AA parameter generator for organic ligands

Gene ORGANizer: linking genes to the organs they affect

Programmatic access to bioinformatics tools from EMBL-EBI update: 2017

TRAPP webserver: predicting protein binding site flexibility and detecting transient binding pockets

DNAproDB: an interactive tool for structural analysis of DNA–protein complexes

minepath.org: a free interactive pathway analysis web server

NNAlign: a platform to construct and evaluate artificial neural network models of receptor–ligand interactions

GEPIA: a web server for cancer and normal gene expression profiling and interactive analyses

GibbsCluster: unsupervised clustering and alignment of peptide sequences

ReFOLD: a server for the refinement of 3D protein models guided by accurate quality estimates

Omicseq: a web-based search engine for exploring omics datasets

GalaxyHomomer: a web server for protein homo-oligomer structure prediction from a monomer sequence or structure

SLiMSearch: a framework for proteome-wide discovery and annotation of functional modules in intrinsically disordered regions

The Proteins API: accessing key integrated protein and genome information

mCSM–NA: predicting the effects of mutations on protein–nucleic acids interactions

The RING 2.0 web server for high quality residue interaction networks:

Heatmapper: web-enabled heat mapping for all

QuadBase2: web server for multiplexed guanine quadruplex mining and visualization

3D-GNOME: an integrated web service for structural modeling of the 3D genome

incaRNAfbinv: a web server for the fragment-based design of RNA sequences

MoRFchibi SYSTEM: software tools for the identification of MoRFs in protein sequences

tRNAscan-SE On-line: integrating search and context for analysis of transfer RNA genes

PSSweb: protein structural statistics web server

PASMet: a web-based platform for prediction, modelling and analyses of metabolic systems

Breaking-Cas—interactive design of guide RNAs for CRISPR-Cas experiments for ENSEMBL genomes:

MutaBind estimates and interprets the effects of sequence variants on protein–protein interactions:

BetaSCPWeb: side-chain prediction for protein structures using Voronoi diagrams and geometry prioritization

KeyPathwayMinerWeb: online multi-omics network enrichment

NAPS: Network Analysis of Protein Structures

PathwAX: a web server for network crosstalk based pathway annotation

GREAT: a web portal for Genome Regulatory Architecture Tools

PHASTER: a better, faster version of the PHAST phage search tool

The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update

Actionable pathways: interactive discovery of therapeutic targets using signaling pathway models

Evolview v2: an online visualization and management tool for customized and annotated phylogenetic trees

Protein Frustratometer 2: a tool to localize energetic frustration in protein molecules, now with electrostatics

3Drefine: an interactive web server for efficient protein structure refinement

Rtools: a web server for various secondary structural analyses on single RNA sequences

Dali server update:

MRE: a web tool to suggest foreign enzymes for the biosynthesis pathway design with competing endogenous reactions in mind

The MPI bioinformatics Toolkit as an integrative platform for advanced protein sequence and structure analysis:

PHYLOViZ Online: web-based tool for visualization, phylogenetic inference, analysis and sharing of minimum spanning trees

CoinFold: a web server for protein contact prediction and contact-assisted protein folding

PSI/TM-Coffee: a web server for fast and accurate multiple sequence alignments of regular and transmembrane proteins using homology extension on reduced databases

USR-VS: a web server for large-scale prospective virtual screening using ultrafast shape recognition techniques

SensiPath: computer-aided design of sensing-enabling metabolic pathways

EXPLoRA-web: linkage analysis of quantitative trait loci using bulk segregant analysis

miRNet - dissecting miRNA-target interactions and functional associations through network-based visual analysis:

SL2: an interactive webtool for modeling of missing segments in proteins

GIANT API: an application programming interface for functional genomics

Pharmit: interactive exploration of chemical space

Interactive tree of life (iTOL) v3: an online tool for the display and annotation of phylogenetic and other trees

SimRNAweb: a web server for RNA 3D structure modeling with optional restraints

W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis

RBscore&NBench: a high-level web server for nucleic acid binding residues prediction with a large-scale benchmarking database

DeepBlue epigenomic data server: programmatic data retrieval and analysis of epigenome region sets

MBROLE 2.0—functional enrichment of chemical compounds:

deepTools2: a next generation web server for deep-sequencing data analysis

RNAssess—a web server for quality assessment of RNA 3D structures:

R3D-2-MSA: the RNA 3D structure-to-multiple sequence alignment server

CATNAP: a tool to compile, analyze and tally neutralizing antibody panels

SNiPlay3: a web-based application for exploration and large scale analyses of genomic variations

I-COMS: Interprotein-COrrelated Mutations Server

RNAiFold 2.0: a web server and software to design custom and Rfam-based RNA molecules

INGA: protein function prediction combining interaction networks, domain assignments and sequence similarity

sRNAtoolbox: an integrated collection of small RNA research tools

DeAnnCNV: a tool for online detection and annotation of copy number variations from whole-exome sequencing data

PatternQuery: web application for fast detection of biomacromolecular structural patterns in the entire Protein Data Bank

StemChecker: a web-based tool to discover and explore stemness signatures in gene sets

LYRA, a webserver for lymphocyte receptor structural modeling:

Primerize: automated primer assembly for transcribing non-coding RNA domains

Multidimensional gene search with Genehopper:

StarScan: a web server for scanning small RNA targets from degradome sequencing data

MS2PIP prediction server: compute and visualize MS2 peak intensity predictions for CID and HCD fragmentation

APPRIS WebServer and WebServices:

MyProteinNet: build up-to-date protein interaction networks for organisms, tissues and user-defined contexts

SIFTER search: a web server for accurate phylogeny-based protein function prediction

CSI 3.0: a web server for identifying secondary and super-secondary structure in proteins using NMR chemical shifts

PrionW: a server to identify proteins containing glutamine/asparagine rich prion-like domains and their amyloid cores

Web-Beagle: a web server for the alignment of RNA secondary structures

PrionW: a server to identify proteins containing glutamine/asparagine rich prion-like domains and their amyloid cores

ZCURVE 3.0: identify prokaryotic genes with higher accuracy as well as automatically and accurately select essential genes

DIANA-miRPath v3.0: deciphering microRNA function with experimental support

NPDock: a web server for protein–nucleic acid docking

ClustVis: a web tool for visualizing clustering of multivariate data using Principal Component Analysis and heatmap

The TOPCONS web server for consensus prediction of membrane protein topology and signal peptides:

IMP 2.0: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks

GalaxyPepDock: a protein–peptide docking tool based on interaction similarity and energy optimization

CATH FunFHMMer web server: protein functional annotations using functional family assignments

RNA-Redesign: a web server for fixed-backbone 3D design of RNA

OrthoVenn: a web server for genome wide comparison and annotation of orthologous clusters across multiple species

SCUDO: a tool for signature-based clustering of expression profiles

Pse-in-One: a web server for generating various modes of pseudo components of DNA, RNA, and protein sequences

PhyloGene server for identification and visualization of co-evolving proteins using normalized phylogenetic profiles:

NaviCell Web Service for network-based data visualization:

xVis: a web server for the schematic visualization and interpretation of crosslink-derived spatial restraints

PockDrug-Server: a new web server for predicting pocket druggability on holo and apo proteins

ProtPhylo: identification of protein–phenotype and protein–protein functional associations via phylogenetic profiling

The MEME Suite:

SELPHI: correlation-based identification of kinase-associated networks from global phospho-proteomics data sets

antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters:

PACCMIT/PACCMIT-CDS: identifying microRNA targets in 3′ UTRs and coding sequences

CCTOP: a Consensus Constrained TOPology prediction web server

FlyNet: a versatile network prioritization server for the Drosophila community

CABS-dock web server for the flexible docking of peptides to proteins without prior knowledge of the binding site:

HMMER web server: 2015 update

(PS)2: protein structure prediction server version 3.0

TFmiR: a web server for constructing and analyzing disease-specific transcription factor and miRNA co-regulatory networks

MapMyFlu: visualizing spatio-temporal relationships between related influenza sequences

FNTM: a server for predicting functional networks of tissues in mouse

NFFinder: an online bioinformatics tool for searching similar transcriptomics experiments in the context of drug repositioning

RNAPattMatch: a web server for RNA sequence/structure motif detection based on pattern matching with flexible gaps

Galahad: a web server for drug effect analysis from gene expression

Pathways with PathWhiz:

Localize.pytom: a modern webserver for cryo-electron tomography

PUG-SOAP and PUG-REST: web services for programmatic access to chemical information in PubChem

NGL Viewer: a web application for molecular visualization

PolySearch2: a significantly improved text-mining system for discovering associations between human diseases, genes, drugs, metabolites, toxins and more

i-cisTarget 2015 update: generalized cis-regulatory enrichment analysis in human, mouse and fly

IslandViewer 3: more flexible, interactive genomic island discovery, visualization and analysis

ChIP-Array 2: integrating multiple omics data to construct gene regulatory networks

Stock-based detection of protein oligomeric states in jsPISA:

Introducing the PRIDE Archive RESTful web services:

BetaCavityWeb: a webserver for molecular voids and channels

RSAT 2015: Regulatory Sequence Analysis Tools

Babelomics 5.0: functional interpretation for new generations of genomic data

The BioMart community portal: an innovative alternative to large, centralized data repositories

MetaboAnalyst 3.0—making metabolomics more meaningful:

miRiadne: a web tool for consistent integration of miRNA nomenclature

RBO Aleph: leveraging novel information sources for protein structure prediction

pyDockSAXS: protein–protein complex structure by SAXS and computational docking

The iceLogo web server and SOAP service for determining protein consensus sequences:

Assessing the impact of mutations found in next generation sequencing data over human signaling pathways:

webSDA: a web server to simulate macromolecular diffusional association

I-TASSER server: new development for protein structure and function predictions

ChEMBL web services: streamlining access to drug discovery data and utilities

FAF-Drugs3: a web server for compound property calculation and chemical library design

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ChEMBL web services: streamlining access to drug discovery data and utilities

NGS-eval: NGS Error analysis and novel sequence VAriant detection tooL

PheNetic: network-based interpretation of molecular profiling data

PLIP: fully automated protein–ligand interaction profiler

MTiOpenScreen: a web server for structure-based virtual screening

SANSparallel: interactive homology search against Uniprot

TCS: a web server for multiple sequence alignment evaluation and phylogenetic reconstruction

The EBI Search engine: providing search and retrieval functionality for biological data from EMBL-EBI

WAXSiS: a web server for the calculation of SAXS/WAXS curves based on explicit-solvent molecular dynamics

The EMBL-EBI bioinformatics web and programmatic tools framework:

IntFOLD: an integrated server for modelling protein structures and functions from amino acid sequences

RiceNet v2: an improved network prioritization server for rice genes