**Frtfr5Table 1 miRNA based databases**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database / Tool** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | miRNET | Integrative platform for exploring miRNA–gene interactions, functional enrichment, and network-based analysis. | Hypergeometric enrichment tests, permutation-based statistics, and network topology measures (degree, betweenness, centrality). | [1] | [miRNet](https://www.mirnet.ca/) |
|  | miRTarBase | Curated database of experimentally validated miRNA–target interactions (MTIs). | Manual curation from literature and reporter assay/CLIP-seq validation data. | [2] | [miRTarBase: the experimentally validated microRNA-target interactions database](https://awi.cuhk.edu.cn/~miRTarBase/miRTarBase_2025/php/index.php) |
|  | TACCO | Tool for analyzing cancer-related omics data with focus on transcriptome, including miRNA expression. | Statistical modeling and integrative analysis pipelines for omics datasets (RNA-seq, microarray). | [3] | <https://tacco.life.nctu.edu.tw/> |
|  | CancerMIRNome | Comprehensive database of cancer-associated miRNA expression profiles and survival analysis. | Differential expression (limma/edgeR) and Kaplan–Meier survival analysis with Cox proportional hazards. | [4] | [CancerMIRNome](http://bioinfo.jialab-ucr.org/CancerMIRNome/) |
|  | ENCORI (StarBase) | Database for miRNA–RNA interactions, including lncRNAs, circRNAs, mRNAs, and protein–RNA binding data. | CLIP-seq supported interaction mapping, crosslinking-immunoprecipitation pipelines, and RNA–RNA interaction prediction models. | [5] | [starBase or ENCORI: Decoding the Encyclopedia of RNA Interactomes](https://rnasysu.com/encori/) |
|  | miRCarta | Repository of both known and candidate miRNAs, supporting miRNA discovery and annotation. | Sequence clustering, homology search, and deep sequencing re-analysis (alignment + miRNA prediction). | [6] | [miRCarta - miRBase overview](https://mircarta.cs.uni-saarland.de/) |
|  | miR-TV | Visualization platform for miRNA–target interactions, providing interactive exploration. | Network graph visualization algorithms and interactive query-based retrieval. | [7] | [miR-TV Introduction](https://mirtv.ibms.sinica.edu.tw/) |
|  | SM2miR | Database of small molecules affecting miRNA expression, linking drug–miRNA interactions. | Manual curation and text-mining of experimental studies (no predictive algorithm). | [8] | <http://www.jianglab.cn/SM2miR/> |
|  | ExplORRnet | Platform for exploring regulatory RNA networks, including miRNA-centered regulatory relationships. | Network inference and integration of validated RNA–RNA regulatory interactions. | [9] | [ExplORRnet](https://mirna.cs.ut.ee/) |
|  | miRWalk | Database providing predicted and validated miRNA binding sites across the complete sequence of genes (3′UTR, CDS, promoter). | Machine learning–based binding site prediction across whole gene regions; integration of validated data. | [10] | [Home - miRWalk](http://mirwalk.umm.uni-heidelberg.de/) |
|  | miRTargetLink 2.0 | Tool for constructing and visualizing miRNA–target gene interaction networks using validated and predicted data. | Network graph construction with validated MTIs (miRTarBase, TarBase) and predicted targets. | [11] | [miRTargetLink 2.0](https://ccb-compute.cs.uni-saarland.de/mirtargetlink2) |
|  | HumiR | Resource of human miRNAs with disease and function annotations. | Manual curation of experimentally supported associations and text-mining algorithms. | [12] | [HumiR](https://ccb-web.cs.uni-saarland.de/humir/) |
|  | miRDB | Database of predicted miRNA targets using machine learning models trained on experimental data. | MirTarget machine learning algorithm trained on high-throughput sequencing of RNA–RNA interaction (HITS-CLIP, PAR-CLIP). | [13] | [miRDB - MicroRNA Target Prediction Database](https://mirdb.org/) |
|  | miRactDB | Database linking miRNAs to functional activities and pathways inferred from activity profiles. | Activity inference models integrating differential expression and pathway enrichment analyses. | [14] | [miRactDB: a DataBase for miRNA-gene relation in pan-cancer](https://ccsm.uth.edu/miRactDB/) |
|  | ExomiRHub | Platform dedicated to exosomal miRNA expression and biomarker discovery in diseases. | Standard RNA-seq pipelines for differential expression; biomarker ranking via survival and ROC models. | [15] | [ExomiRHub](http://www.biomedical-web.com/exomirhub/home) |
|  | RNA22 v2 | Predictive tool for identifying miRNA binding sites and target genes using pattern recognition and folding energy. | Pattern recognition algorithm with dinucleotide word analysis and thermodynamic folding energy evaluation. | [16] | [RNA22 v2](https://cm.jefferson.edu/rna22/Interactive/) |

**Table 2 lncRNA based databases**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | LncTarD2.0 | Curated database of experimentally supported lncRNA–disease associations and mechanisms. | Manual literature curation, integration of functional assays (loss/gain-of-function, knockdown, reporter assays). | [17] | [LncTarD 2.0](https://lnctard.bio-database.com/) |
|  | LncPepAtlas | Resource for lncRNA-encoded peptides, integrating ribosome profiling and mass spectrometry evidence. | Ribosome profiling (Ribo-seq) footprinting, 6-frame translation, and MS/MS peptide-spectrum matching algorithms. | [18] | [Home](http://www.cnitbiotool.net/LncPepAtlas/) |
|  | lncHUB2/lncHUB | Knowledgebase of lncRNA functions, co-expression, and tissue-specific expression. | Co-expression network analysis (Pearson/Spearman correlation), functional enrichment, regression-based inference. | [19] | [lncHUB](https://maayanlab.cloud/lnchub/) |
|  | lncRNASNAP2-human | Provides subcellular localization and function predictions of human lncRNAs. | Machine learning classifiers (SVM, Random Forest) trained on sequence features, secondary structure, k-mers. | [20] | [lncRNASNP2-human](https://guolab.wchscu.cn/lncRNASNP/#!/) |
|  | LnCeCell2.0 | Updated version of LnCeCell, offering expanded ceRNA interaction data across more cell types. | ceRNA network construction using correlation analysis (Pearson), hypergeometric enrichment, and survival modeling. | [21] | <http://bio-bigdata.hrbmu.edu.cn/LnCeCell/LnCeCell_index.jsp> |
|  | AnnoLnc2 | Comprehensive annotation platform for human lncRNAs, including expression, function, structure, and conservation. | Integrative pipelines: sequence conservation (PhyloP/PhastCons), RNA structure prediction (RNAfold), and expression profiling (RNA-seq). | [22] | <https://annolnc.gao-lab.org/> |
|  | LncTOGeneN | Database for lncRNA–target gene associations. | Co-expression analysis (Pearson/Spearman), differential expression integration, survival regression models. |  |  |

**Table 3 non-coding RNA Databases**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database / Tool** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | RNAInter | Comprehensive RNA–RNA interaction database. | Integrates multiple predictive algorithms (IntaRNA, RNAplex, miRanda) with CLIP-seq and experimental datasets; network construction with statistical scoring. | [23] | [rnainter.org](http://www.rnainter.org/) |
|  | TarBase v9.0 | Curated experimentally validated miRNA–target interactions. | Manual curation from literature; high-throughput validation from CLIP-seq, degradome-seq, reporter assays (no predictive algorithm). | [24] | [TarBase v9.0](https://dianalab.e-ce.uth.gr/tarbasev9) |
|  | ctcRbase | Resource for circulating tumor cell (CTC)-related RNAs. | Manual curation of experimental data on CTC-derived RNAs; normalization pipelines for RNA-seq/microarray (no independent predictive algorithm). | [25] |  |
|  | EVAtlas | Database of extracellular vesicle RNA expression profiles. | Standard RNA-seq pipelines (alignment with STAR/Hisat2, quantification with RSEM/HTSeq); differential expression analysis using edgeR/DESeq2. | [26] |  |
|  | RNALocate | RNA subcellular localization database. | Machine learning classifiers (SVM, Random Forest) trained on sequence features, localization signals, and curated experimental evidence. | [27] | [RNALocate](https://www.rnalocate.org/) |

**Table 4 Gene expression and survival analysis**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database / Tool** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | GEPIA2 | TCGA/GTEx-based interactive platform for expression profiling and survival analysis. | Differential expression using ANOVA/limma; Kaplan–Meier survival with Cox proportional hazards. | [28] | [GEPIA 2](http://gepia2.cancer-pku.cn/#index) |
|  | UALCAN | TCGA-based resource for gene expression and survival correlations in cancers. | Statistical testing (t-test, ANOVA) with normalization pipelines for TCGA data; survival via Kaplan–Meier and Cox regression. | [29] | [UALCAN](https://ualcan.path.uab.edu/index.html) |
|  | Oncomine | Cancer microarray database for differential expression and co-expression analysis. | t-test and ANOVA for differential expression; clustering and co-expression algorithms; meta-analysis models. | [30] | [Oncomine Next-Generation Sequencing Solutions for Precision Oncology Research](https://www.oncomine.com/) |
|  | Oncopression | Database of cancer transcriptome expression profiles. | Linear models (limma) for expression differences; correlation-based clustering and survival models. | [31] | [Oncopression](http://oncopression.com/) |
|  | Lung Cancer Explorer | Portal for expression and clinical outcome analysis in lung cancer. | Cox regression, Kaplan–Meier plots, multivariate survival analysis; differential expression pipelines. | [32] | [lung cancer explorer | lung cancer database | lung cancer analysis | Quantitative Biomedical Research Center | UT Southwestern](https://lce.biohpc.swmed.edu/lungcancer/) |
|  | KM Plotter | Survival analysis tool linking gene expression with prognosis in cancers. | Kaplan–Meier with log-rank test; multivariate Cox regression with hazard ratio estimation. | [33] | [Kaplan-Meier plotter](https://kmplot.com/analysis/) |
|  | Survival ToPP | Multi-gene survival analysis in TCGA data. | Kaplan–Meier survival with permutation testing for multi-gene signatures. | [34] | [Survival](http://www.biostatistics.online/topp/index.php) |
|  | PrognoScan | Database for meta-analysis of prognostic gene expression data. | Cox proportional hazards and log-rank test integrated across GEO datasets; FDR-corrected meta-analysis. | [35] | [PrognoScan: A new database for meta-analysis of the prognostic value of genes.](https://dna00.bio.kyutech.ac.jp/PrognoScan/) |
|  | GENI | Gene Expression and Network integration database for cancer. | Gene set enrichment (GSEA), correlation analysis, and network-based prioritization. | [36] | [GENI - geni - gene enrichment identifier](https://yoavshaul-lab.shinyapps.io/gsea-geni/) |
|  | Correlation AnalyzeR | Tool for co-expression profiling and correlation analysis. | Pearson/Spearman correlation, differential correlation testing, and visualization algorithms. | [37] | [Correlation AnalyzeR](https://correlationanalyzer.bishop-lab.com/) |
|  | GeneFriends | Gene co-expression database based on RNA-seq. | Rank correlation across RNA-seq samples; network construction via co-expression matrices. | [38] | [GeneFriends](https://genefriends.org/) |
|  | bc-GenExMiner | Breast cancer gene expression mining tool. | Differential expression using ANOVA/limma; survival via Kaplan–Meier and Cox regression; correlation statistics. | [39] | [breast cancer gene expression database | bc-GenExMiner](https://bcgenex.ico.unicancer.fr/BC-GEM/GEM-Accueil.php?js=1) |
|  | GOBO | Gene expression-based outcome analysis tool for breast cancer. | Survival analysis (Kaplan–Meier, Cox regression); differential expression via t-test/ANOVA. | [40] | [GOBO: Gene Expression-Based Outcome for Breast Cancer Online | PLOS One](https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0017911) |
|  | TANRIC | TCGA-based platform for analyzing lncRNAs in cancer. | Co-expression analysis, survival modeling (Cox regression), and correlation-based network inference. | [41] | [TANRIC](https://bioinformatics.mdanderson.org/public-software/tanric/) |

**Table 5 Cancer Genomics & Mutations**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database / Tool** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | cBioPortal | Large-scale cancer genomics exploration (TCGA, ICGC, etc.). | Mutation analysis (MutSigCV), copy-number variation (GISTIC2), and co-occurrence/mutual exclusivity statistics. | [42] | [cBioPortal for Cancer Genomics](https://www.cbioportal.org/) |
|  | OncoMX | Integrated cancer mutation and biomarker database combining COSMIC, TCGA, and others. | Data harmonization and mapping across multiple repositories; mutation frequency and biomarker annotation pipelines. | [43] | [OncoMX](https://www.oncomx.org/) |
|  | OncoDB | Cancer genomics portal for gene expression, mutation, and survival analysis. | Differential expression (limma), survival analysis (Kaplan–Meier, Cox regression), and mutation frequency analysis. | [44] | [oncodb.org/version2/](https://oncodb.org/version2/) |
|  | DriverDBv4 | Database of cancer driver genes with multi-omics annotations. | Driver gene identification using MutSigCV, OncodriveFM, ActiveDriver; integration with TCGA multi-omics. | [45] | [DriverDBv4](http://driverdb.bioinfomics.org/) |
|  | TumorPortal | Cancer driver mutations and oncogene analysis portal. | MutSigCV, OncodriveCLUST, and other driver prioritization algorithms. |  |  |
|  | Broad GDAC Firehose | TCGA data processing and analysis pipelines (Broad Institute). | Standardized pipelines (MutSigCV, GISTIC2, Firehose pipeline for expression and methylation analysis). | [46] | [Broad GDAC Firehose](https://gdac.broadinstitute.org/) |
|  | TCGAnalyzeR | Web-based TCGA visualization and integrative analysis tool. | Differential expression via DESeq2/edgeR; survival via Cox regression; mutational burden scoring. | [47] | [tcganalyzer.mu.edu.tr](http://tcganalyzer.mu.edu.tr/) |
|  | CR2Cancer | Database of cancer-related chromatin regulators. | Integration of expression profiling, mutation frequency analysis, and correlation with survival (Cox regression). | [48] | [CR2Cancer](http://cis.hku.hk/CR2Cancer/) |
|  | DegronMD | Database of degron motifs involved in protein degradation. | Motif prediction algorithms, sequence conservation analysis, and degron-mutation mapping. | [49] | [DegronMD](https://bioinfo.uth.edu/degronmd/) |
|  | ClinVar | Archive of human genetic variants and their relationship to disease, including cancer. | Expert/manual curation of variant classifications; aggregation of submitter interpretations (no predictive algorithm). |  |  |

**Table 6 Immune-related / Tumor Microenvironment**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database / Tool** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | TIMER2.0 | Immune infiltration analysis across cancer types using TCGA data. | Deconvolution algorithms including TIMER, CIBERSORT, quanTIseq, xCell, MCP-counter, and EPIC to estimate immune cell abundance; correlation and Cox regression for survival analysis. | [50] | <http://timer.cistrome.org/> |
|  | TISIDB | Cancer immunology database for tumor–immune system interactions. | Integration of high-throughput immune expression data with statistical association analyses (Spearman/Pearson), survival modeling, and immunomodulator scoring. | [51] | [TISIDB](http://cis.hku.hk/TISIDB/) |
|  | TIDE | Tumor Immune Dysfunction and Exclusion tool for immunotherapy response prediction. | Machine learning–based predictive framework modeling T-cell dysfunction (in tumors with high cytotoxic T lymphocytes) and T-cell exclusion (in tumors with low infiltration); integrates gene expression signatures with regression scoring. |  | [Tumor Immune Dysfunction and Exclusion (TIDE)](http://tide.dfci.harvard.edu/login/) |
|  | DrCAF | Cancer-associated fibroblast gene expression and function database. | Differential expression pipelines (limma/edgeR) for CAF marker identification; survival correlation using Cox regression and Kaplan–Meier models. | [52] | [GYP - Welcome to DrCAF](http://caf.zbiolab.cn/) |
|  | TIGER |  | Integrates bulk RNA-seq with single-cell RNA-seq; immune deconvolution pipelines (CIBERSORT, TIMER, quanTIseq) plus survival and response prediction models for immunotherapy. | [53] | <http://tiger.canceromics.org/#/> |

**Table 7 Protein / Proteomics / PTMs**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database / Tool** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | STRING | Protein–protein interaction (PPI) network database with functional associations. | Bayesian integration of multiple evidence channels (experimental, text-mining, co-expression, co-occurrence, gene fusion, databases); network confidence scoring. | [54] | [STRING: functional protein association networks](https://string-db.org/) |
|  | The Human Protein Atlas | Tissue-based protein expression and localization atlas. | Immunohistochemistry-based scoring, antibody validation pipelines, RNA-seq quantification, and image-based localization algorithms. | [55] | [The Human Protein Atlas](https://www.proteinatlas.org/) |
|  | Cancer Proteome | Proteomics resource for cancer-associated proteins. | Mass spectrometry–based protein identification and quantification; spectral counting and label-free quantification pipelines. | [56] | [CancerProteome](http://bio-bigdata.hrbmu.edu.cn/CancerProteome/index.jsp) |
|  | ProteomicsDB | Human proteome and quantitative proteomics resource. | Mass spectrometry data processing (MaxQuant, Andromeda search engine), peptide-spectrum matching, FDR correction, and quantitative profiling. | [57] | [Drug | ProteomicsDB](https://www.proteomicsdb.org/drug) |
|  | DbPTM | Post-translational modification (PTM) database. | Integration of experimental PTM sites with sequence-based prediction algorithms (support vector machines, motif scanning, and conservation scoring). | [58] | [dbPTM](https://biomics.lab.nycu.edu.tw/dbPTM/) |
|  | SMART | Database for conserved protein domains and motifs. | Hidden Markov Models (HMMs) via HMMER for domain detection; multiple sequence alignment and evolutionary conservation scoring. | [59] | [SMART: About](https://smart.embl.de/help/smart_about.shtml) |
|  | SubCELL | Database of protein subcellular localization. | Integration of mass spectrometry, fluorescent imaging, and biochemical fractionation data; machine learning models (SVM, Random Forest) for localization prediction. | [60] | [SubCELL: the landscape of subcellular compartment-specific molecular interactions](https://subcell.idrblab.cn/) |

**Table 8 Epigenetics & Methylation**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database / Tool** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | DNMIVD | DNA methylation interactive visualization database. | TCGA/ICGC methylation array data processed via normalization (β-values); integration with expression using correlation and survival analysis (Cox regression, Kaplan–Meier). | [61] | [DNMIVD | Home](http://119.3.41.228/dnmivd/) |
|  | dbDMEC | Database of differentially methylated and expressed genes in cancer. | Differential methylation analysis using statistical testing (t-test, Wilcoxon); integration with RNA-seq expression profiles for methylation–expression correlation. | [62] | [dbDEMC](https://www.biosino.org/dbDEMC/index) |
|  | Wanderer | Tool for exploring DNA methylation and gene expression across TCGA cancers. | TCGA Illumina 450K array methylation processed to β-values; comparisons using non-parametric tests (Wilcoxon/Mann–Whitney); visualization pipelines. | [63] |  |
|  | EPD | Experimentally validated promoters and transcription start sites. | Promoter annotation based on experimentally validated TSS from CAGE, 5′ RACE, and high-throughput sequencing; motif discovery using PWM scanning. |  |  |
|  | MethMotif | Database of DNA methylation and transcription factor binding motifs. | Integration of bisulfite sequencing (WGBS), ChIP-seq, and motif scanning with position weight matrices (PWM); correlation of methylation with TF binding activity. | [64] | [MethMotif](https://methmotif.org/) |

**Table 9 Pathway & Network Analysis**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database / Tool** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | Enrichr | Gene set enrichment analysis across multiple biological categories (GO, pathways, etc.). | Fisher’s exact test and rank-based enrichment; combined score = log(p-value) × z-score; integrated with curated libraries. | [65] | [Enrichr](https://maayanlab.cloud/Enrichr/) |
|  | GSEA | Gene Set Enrichment Analysis (Broad Institute). | Rank-based, non-parametric enrichment score (ES) across gene lists; significance via permutation testing; normalized enrichment score (NES) and false discovery rate (FDR). | [66] | [GSEA | MSigDB](https://www.gsea-msigdb.org/gsea/msigdb/index.jsp) |
|  | Metascape | Functional enrichment, clustering, and biological pathway annotation tool. | Hypergeometric test for enrichment; hierarchical clustering of enriched terms; PPI network construction with MCODE algorithm. | [67] | [Metascape](https://metascape.org/gp/index.html#/main/step1) |
|  | GeneMANIA | Functional association network tool for gene-gene predictions. | Label propagation algorithm across heterogeneous networks (PPI, co-expression, pathways); weighting via Gaussian normalization. | [68] | [GeneMANIA](https://genemania.org/) |
|  | TRRUST | Database of transcriptional regulatory relationships. | Manual curation of TF–target pairs; inference via text-mining and literature validation (no predictive algorithm). | [69] | [TRRUST - Transcriptional Regulatory Relationships Unraveled by Sentence-based Text mining](https://www.grnpedia.org/trrust/) |
|  | GSCA | Gene set cancer analysis platform integrating expression, mutation, and drug response. | Differential expression (limma/DESeq2), survival analysis (Cox regression, Kaplan–Meier), immune infiltration (CIBERSORT, TIMER), drug sensitivity via GDSC/CTRP correlation. | [70] | <https://guolab.wchscu.cn/GSCA/#/> |
|  | NetworkAnalyst 3.0 | Web-based tool for network-based multi-omics analysis. | Statistical enrichment tests (Fisher’s, hypergeometric), network topology measures (degree, betweenness, centrality), meta-analysis models. | [71] | [NetworkAnalyst](https://www.networkanalyst.ca/) |
|  | OmicsNet 2.0 | 3D multi-omics network visualization and integration tool. | Network inference using graph algorithms; clustering via modularity optimization; 3D network visualization. | [72] | [OmicsNet](https://www.omicsnet.ca/) |
|  | Harmonizome 3.0 | Collection of gene–attribute associations across omics datasets. | Standardized processing pipelines: z-score normalization, gene–attribute matrix construction; cosine similarity for functional associations. | [73] | [Harmonizome](https://maayanlab.cloud/Harmonizome/) |
|  | ShinyGO 0.80 | Web-based GO enrichment analysis tool with visualization. | Hypergeometric/Fisher’s exact test for enrichment; visualization via hierarchical clustering, KEGG/GO mapping. | [74] | [ShinyGO 0.80](https://bioinformatics.sdstate.edu/go80/) |

**Table 10 Single-Cell Resources**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database / Tool** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | scRNASeqDB | Database of human single-cell RNA sequencing expression profiles. | Standard single-cell RNA-seq pipelines: quality control, normalization, dimensionality reduction (PCA, t-SNE, UMAP), and clustering (k-means/graph-based). | [75] | [scRNASeqDB](https://bioinfo.uth.edu/scrnaseqdb/) |
|  | scCancerExplorer | Single-cell RNA-seq database focused on cancer cells. | scRNA-seq preprocessing via Seurat, cell type annotation using marker-based classifiers, differential expression testing (Wilcoxon rank-sum), and pathway enrichment analysis. | [76] | <https://bianlab.cn/scCancerExplorer> |
|  | DISCO | Multi-omics cancer atlas for single-cell and bulk RNA-seq integration. | Large-scale data harmonization using batch-effect correction (Harmony, Seurat CCA); clustering (Louvain/Leiden algorithms); cell–cell communication via CellPhoneDB and ligand–receptor scoring. | [77] | [DISCO](https://disco.bii.a-star.edu.sg/) |
|  | CellTracer | Single-cell lineage tracing and dynamic trajectory analysis tool. | Pseudotime and trajectory inference using Monocle/Slingshot; RNA velocity estimation (Velocyto, scVelo); clustering-based lineage reconstruction. | [78] | [CellTracer: Home](http://bio-bigdata.hrbmu.edu.cn/CellTracer/) |

**Table 11 Drug Response & Therapeutics**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database / Tool** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | DepMap | Cancer dependency map showing gene essentiality across cell lines (CRISPR/RNAi). | CERES algorithm for CRISPR-Cas9 gene dependency scores; DEMETER2 for RNAi; PRISM drug response profiling with viability scoring. |  | [DepMap: The Cancer Dependency Map Project at Broad Institute](https://depmap.org/portal/) |
|  | GDSC | Genomics of Drug Sensitivity in Cancer database. | IC50/area-under-curve (AUC) estimation; ANOVA to identify genomic markers of drug response; machine learning models for drug sensitivity prediction. | [79] | [Home page - Cancerrxgene - Genomics of Drug Sensitivity in Cancer](https://www.cancerrxgene.org/) |
|  | canSAR.ai | Integrated cancer drug discovery resource (targets, drugs, models). | AI-driven target prioritization models; chemoinformatics algorithms for ligand–target interactions; network-based druggability scoring. | [80] | [canSAR.ai | the Cancer Drug Discovery Platform | canSAR.ai](https://cansar.ai/) |
|  | My Cancer Genome | Clinical resource linking cancer mutations to targeted therapies. | Expert/manual curation of published clinical trials and FDA/EMA drug–mutation evidence (no predictive algorithm). | [81] | [Home - My Cancer Genome](https://www.mycancergenome.org/) |
|  | PerturbDB | Resource for perturbation-response gene expression profiles. | Normalization of high-throughput perturbation screens; regression-based scoring of gene essentiality; integration with viability assays. | [82] | [perturbdb](http://research.gzsys.org.cn/perturbdb/) |
|  | IMPPAT | Database of phytochemicals from Indian medicinal plants with pharmacological properties. | Computational chemoinformatics pipelines: drug-likeness scoring, ADMET prediction, and network pharmacology mapping. | [82] | [IMPPAT | IMPPAT: Indian Medicinal Plants, Phytochemistry And Therapeutics](https://cb.imsc.res.in/imppat/) |
|  | Lung Cancer Explorer | Portal for expression and clinical outcome analysis in lung cancer. | Survival analysis via Cox regression/Kaplan–Meier; differential expression (limma/edgeR); pathway enrichment. | [83] | [lung cancer explorer | lung cancer database | lung cancer analysis | Quantitative Biomedical Research Center | UT Southwestern](https://lce.biohpc.swmed.edu/lungcancer/) |
|  | bc-GenExMiner | Breast cancer gene expression mining tool. | ANOVA/limma for differential expression; Kaplan–Meier and Cox regression for survival; correlation-based co-expression. | [84] | [breast cancer gene expression database | bc-GenExMiner](https://bcgenex.ico.unicancer.fr/BC-GEM/GEM-Accueil.php?js=1) |
|  | GOBO | Gene expression-based outcome analysis tool for breast cancer. | Survival analysis (Kaplan–Meier, Cox regression); differential expression (t-test, ANOVA); clustering of gene expression patterns. | [85] | [GOBO - Gene expression-based Outcome for Breast cancer Online](https://co.bmc.lu.se/gobo/) |

**Table 12 General Genomic Resources**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Database / Tool** | **Function / Application** | **Algorithm used** | **References** | **Link** |
|  | UCSC Xena | Visualization and analysis platform for TCGA and functional genomics data. | Standardized pipelines for expression normalization (FPKM, TPM), survival modeling (Cox regression, Kaplan–Meier), and integrative visualization. | [86] | [UCSC Xena](https://xena.ucsc.edu/) |
|  | UCSC Genome Browser | Genome-wide visualization and annotation platform. | Genome alignment and visualization using BLAT (BLAST-like alignment tool); coordinate-based genome annotation; track-based integration (no predictive algorithm). |  |  |
|  | GEO2R (GEO) | NCBI tool for comparing groups of samples in GEO datasets. | limma (linear models for microarray and RNA-seq), empirical Bayes moderation, and multiple testing correction (FDR, Benjamini–Hochberg). |  | [GEO2R - GEO - NCBI](https://www.ncbi.nlm.nih.gov/geo/geo2r/) |
|  | OMIM | Online Mendelian Inheritance in Man: human genetic disorders and phenotypes. | Expert/manual curation of literature-based associations (no predictive algorithm). | [87] | [Home - OMIM - (OMIM.ORG)](https://www.omim.org/) |
|  | GeneOptimizer Process | Tool for optimizing synthetic gene design (codon usage, expression). | Proprietary multi-parameter optimization: codon usage, GC content, mRNA structure minimization, motif removal, and translation efficiency scoring. | [88] |  |
|  | OGEE | Online Gene Essentiality database. | Integration of experimental essentiality screens (CRISPR, RNAi); computational annotation using gene network centrality and evolutionary conservation metrics. | [89] | [OGEE](https://v3.ogee.info/#/home) |