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Eukaryotic Molecular Biology Databases: An Overview

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Abstract

A biological database is a big, structured body of continuous information, generally connected with computerized software intended to update, query, and recover information elements deposited within the framework. A straightforward database could be a single folder comprising several data, each carrying the same number of data. Such famous databases are GenBank from the National Center for Biotechnology Information, SwissProt from the Swiss Institute of Bioinformatics and PIR from the Protein Information Resource. Biological databases are bibliotheques of life science data, gathered from science studies, published literature, high-performance experimental technology, and computational analysis. Here we brefly described some recently published molecular databases.

Keywords: biological database, computational analysis, bioinformatics, software.

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Introduction

Bioinformatics is a steadily increasing area of studies fueled by the need to handle and evaluate the vast amounts of information produced by omics techniques. Decades of studies have produced several known multi-omics tools, including genome, proteome and transcriptome (1–3) with the sole objective of understanding every part of biology. Here we brefly described recent published database such as PhenomicDB, AAgMarker, CSCD, CR2Cancer, ActiveDriverDB, AmtDB, HEDD, DiseaseEnhancer, dreamBase, DASHR, MSDD, CancerSysDB, mirDIP, MeDReaders, LinkedOmics, Pancan-meQTL, PITDB, qPrimerDB, SEECancer, UniLectin3D, TranslatomeDB, Tiss-GDB, and TC3A Table (1).

Table 1. List of some recently published database.

Database name	Link	Reference	Database name	Link	Reference
PhenomicDB	http://www.phenomicDB.de	Kahraman et al. (4)	**mirDIP**	http://ophid.utoronto.ca /mirDIP/	Tokar et al. (16)
AAgMarker	http://bioinfo.wilmer.jhu.edu/ AAgMarker/	Pan et al. (5)	**MeDReaders**	http://medreader.org/	Wang et al. (17)
CSCD	http://gb.whu.edu.cn/CSCD	Xia et al. (6)	**LinkedOmics**	http://www.linkedomics.org	Vasaikar et al. (18)
CR2Cancer	http://cis.hku.hk/CR2Cancer	Ru et al. (7)	**Pancan-meQTL**	http://bioinfo.life.hust.edu.cn/ Pancan-meQTL/	Gong et al. (19)
ActiveDriverDB	https://www.ActiveDriverDB.org	Krassowski et al. (8)	**PITDB**	http://pitdb.org	Saha et al. (20)
AmtDB	https://amtdb.org	Ehler et al. (9)	**qPrimerDB**	http://biodb.swu.edu.cn/ qprimerdb	Lu et al. (21)
HEDD	http://zdzlab.einstein.yu.edu/1/ hedd.php	Wang et al. (10)	**SEECancer**	http://biocc.hrbmu.edu.cn/ SEECancer	Zhang et al. (22)
DiseaseEnhancer	http://biocc.hrbmu.edu.cn/ DiseaseEnhancer/	Zhang et al. (11)	**UniLectin3D**	https://www.unilectin.eu/ unilectin3D	Mariethoz et al. (23)
dreamBase	http://rna.sysu.edu.cn/dreamBase	Zheng et al. (12)	**TranslatomeDB**	http://www.translatomedb .net/	Liu et al. (24)
DASHR	http://lisanwanglab.org/DASHRv2	Kuksa et al. (13)	**Tiss-GDB**	http://zhaobioinfo.org/ TissGDB	Kim et al. (25)
MSDD	http://tdb.ccmb.res.in/msdb	Yue et al. (14)	**TC3A**	http://tc3a.org	Feng et al. (26)
CancerSysDB	https://cancersys.uni-koeln.de	Krempel et al. (15)			

PhenomicDB

By combining government genotype/phenotype information from a broad spectrum of model organisms and modern humans, Kahraman et al. (4) built a multi-species genotype / phenotype repository. They collected these riches of information into a single embedded database through coarse-grained semiconductor mapping of phenotypic information areas, including prevalent gene codes (NCBI Gene) and the use of related orthology. PhenomicDB enables researchers to concurrently compare and browse recognized phenotypes for a specified gene or a collection of genes from distinct species with its use-case-oriented interface. It can be found at http://www.phenomicDB.de.

AAgMarker

Pan et al. (5) has collected many released raw information sets on proteome microarrays acquired from serum profiling assays and offers a toolbox for mining these information. AAgMarker's present edition includes 854 serum samples with 136 092 proteins. For 12 diseases, such as Alzheimer's disease, Bechet's disease, and Parkinson's disease, a total of 7803 (4470 non-redundant) candidate auto virus biomarkers were recognized and gathered. In order to quantitatively evaluate these biomarkers, seven statistical parameters were implemented. Users can use fundamental search, sophisticated search and browse to collect, analyze and compare the datasets. These biomarkers can also be downloaded in terms of disease. The AAgMarker can be found at http://bioinfo.wilmer.jhu.edu/AAgMarker/.

CSCD

Xia et al. (6) gathered 228 complete samples of RNA or polyA(-) RNA-seq from both cancer and ordinary cell lines and found 272,152 circR-NAs specific to cancer. In ordinary samples only a total of 950 962 circRNAs were recognized, and in both tumor and ordinary samples 170 909 circRNAs were detected, that could be even farther used as non-tumor context. A cancer-specific circRNA databases http://gb.whu.edu.cn/CSCD were built. They anticipated the microRNA response element locations and RNA binding protein positions for each circRNA in order to comprehend the functional impacts of circRNAs. In addition, prospective open reading frames were anticipated to show translatable circRNAs. They also identified the splicing occurrences in linear transcripts of each circRNA to comprehend the correlation between linear splicing and back splicing. As the first extensive circRNA database specific to cancer.

CR2Cancer

Ru et al. (7) introduced CR2Cancer, an extensive database for CRs in human cancer annotation and visualization built through high-throughput data analysis and mining literature. For more than 400 CRs across various kinds of cancer, they gathered and incorporated genomic, transcriptomic, proteomic, clinical and functional data. They also constructed various kinds of CR-related relationships, including dependent and autonomous cancer type relationships. In addition, about 6000 items of aberrant molecular alterations and CR interactions were manually curated from 5007 publications in the development of cancer. CR2Cancer offers an easy-to-use online interface to navigate,

search and download interesting information conveniently. http://cis.hku.hk/CR2Cancer, is readily accessible.

ActiveDriverDB

ActiveDriverDB is a comprehensive database of human proteogenomics which annotate disorder mutations and variants of the population via the PTM lens. More than 385,000 released PTM locations with 3.6 million replacements from the Cancer Genome Atlas (TCGA), the ClinVar disease gene database, and human genome mapping projects were incorporated (8). The database involves site-specific protein interaction networks, upstream enzymes like kinases, and those enzyme-targeted drugs. Also, by evaluating advantages and losses of kinase-bound gene motifs, anticipated network-rewiring effect of mutations. For researching PTM-associated mutations, ActiveDriverDB offers comprehensive visualization, processing, navigating, and search opportunities. Users can interactively submit mutation datasets and use the coding tool in pipelines. Integrative assessment of mutations and PTMs, as illustrated by case studies of TP53, BRCA2 and VHL, can assist decipher molecular processes of disease and phenotypes. It can be found at https://www.ActiveDriverDB.org.

AmtDB

AmtDB, the first database of ancient human mitochondrial genomes, is presented by Ehler et al. (9). Release edition includes 1107 hand-cured ancient samples, freely available for download, along with personal descriptors including geographic place, radiocarbon dating, and association to archeological culture. An interactive map for sample position visualization is also available in the database. On https://amtdb.org, AmtDB is a main platform for ancestral population genetic research.

HEDD

Wang et al. (10) founded the Human Enhancer Disease Database (HEDD) to promote enhancers research and their prospective functions in complicated human disorders. For some 2,8 million human enhancers recognized by EN-CODE, FANTOM5 and RoadMap, HEDD presently offers extensive genomic data with disease connection results based on enhancer-gene and gene-disease links. It also offers web-based analytical tools to conceptualize enhancer networks and rank enhancers in a particular gene network given a collection of targeted genes. At http://zdzlab.einstein.yu.edu/1/hedd.php, HEDD is readily available.

DiseaseEnhancer

Zhang et al. (11) developed DiseaseEnhancer for disease-associated enhancers, a manually curated database. As of July 2017, in 143 human illnesses, DiseaseEnhancer involves 847 disease-associated enhancers. Database attributes include fundamental data about enhancers; varieties of diseases; related variations of enhancers and their phenotypes mediated. They also include a website function for exporting any request outcomes to a folder and downloading the complete database. DiseaseEnhancer offers scientists with a successful opportunity for knowing enhancer deregulation in pathogenesis of disease and identifying new biomarkers for diagnosis and treatment of disorder. You can easily access DiseaseEnhancer at http://biocc.hrbmu.edu.cn/DiseaseEnhancer/.

DreamBase

Zheng et al. (12) established dreamBase to enable research into DNA alteration, RNA regulation and protein interacting from multidimensional high-throughput sequencing information of probable expressed pseudogenes. Based on a series of data sets ChIP-seq and DNase-seq, genome-wide binding patterns of different transcription-associated variables were recognized around pseudo-gene loci. By incorporating some 18 000 RNA-seq information, they evaluated pseudogene expression profiles and examined their modelsof co-expressionin 32 cancers and 31 ordinary tissues with their parent genes.They revealed complicated post-transcription regulation networks comprising 275 microRNAs and 1201 pseudo-genes by connecting binding sites with microRNA. They researched transcriptome-wide relationships based on 458 CLIP-seq datasets between RNA binding enzymes (RBPs) and pseudo-genes. They also linked 1039 RNA alteration locations to 635 pseudo-genes in combination with epi-transcriptome sequencing information. This database would provide perspectives into pseudo-genes ' transcription regulating, expression, features and mechanisms as well as their functions in biological procedures and illnesses. At http://rna.sysu.edu.cn/dreamBase, DreamBase is readily available.

DASHR

Kuksa et al. (13) created a comprehensive catalog of annotation, expression, handling, conservation, tissue specificity and other biological characteristics for all human sncRNA genes and mature products obtained from all main RNA groups. The DASHR (Small Human Non-Coding RNAs Database) database is the first to incorporate human sncRNA gene as well as mature product profiles from numerous RNA-seq protocols. For both GRCh38/hg38 and GRCh37/hg19 assemblies, 185 tissue / cell forms and sncRNA annotations and > 800 curated tests from ENCODE and GEO / SRA are incorporated into DASHR. In addition, DASHR is the first to comprise both recognized and novel

sncRNA loci detected by unsupervised segmentation, earlier unnoted. DASHR also contains > 3,200,000 annotations for non-small genes of RNA and other genomic characteristics. In addition, an improved user interface, integrated experiment-by-locus table display, sncRNA locus sorting and biological feature processing is introduced. On http://lisanwanglab.org/DASHRv2, DASHR is readily accessible.

MSDD

Yue et al. (14) have been described as MSDD, presently documenting 525 associations among 182 human miRNAs, 197 SNPs, 153 genes, and 164 human illnesses through an analysis of over 2000 articles released. Each organization includes data on miRNAs, SNPs, miRNA target genes and disorder designations, SNP places and allies, miRNA dysfunctional model, experimental methods, a short functional description, initial reference and extra annotation. MSDD offers a user-friendly interface for browsing, retrieving, downloading and submitting new information conveniently. MSDD There is free access to http://tdb.ccmb.res.in/msdb.

CancerSysDB

The Cancer Systems Biology Database (CancerSysDB) was created by Krempel et al. (15), a tool for extremely flexible cancer queries and data analysis across various data types and various research. A CancerSysDB primary openly accessible instance can be used to achieve extremely versatile queries across various kinds of information as shown in extremely appropriate instances of use. They also show how the CancerSysDB can be used in the study network The Cancer Genome Atlas (TCGA) to classify predictive cancer based on all-exome information from 9091 individuals. CancerSysDB At https://cancersys.uni-koeln.de, it is publicly accessible.

mirDIP

Tokar et al. (16) provided mirDIP, providing practically 152 million predictions of human microRNA targets collected across 30 various resources. They also incorporated an interdisciplinary score, statistically implied from the predictions obtained and appointed to each unique microRNA-target activity to provide a unified measure of trust. They show that integration of predictions throughout various assets does not accumulate predictive bias towards biological procedures or pathways. mirDIP is accessible free of charge at http://ophid.utoronto.ca/mirDIP/.

MeDReaders

A total of 731 TFs that could attach to methylated DNA sequences in human and mouse research mentioned in the literature were individually selected by Wang et al. (17). Six human cell lines and one mouse cell line derived from the ENCODE and GEO database were used in silico approaches to anticipate methylated and un-methylated patterns of 292 TFs by incorporating whole genome bisulfite sequencing (WGBS) and ChIP-Seq data. The database of MeDReaders provides an extensive resource for further research and experiment plans to guide. The portal can be found at http://medreader.org/.

LinkedOmics

The database of LinkedOmics (18) includes information on multi-omics and clinical information for 32 kinds of cancer and a total of 11,158 clients from the TCGA initiative. It is also the first multi-omics repository to incorporate worldwide proteomics information from chosen TCGA tumor samples based on mass spectrometry (MS) produced by the Clinical Proteomic Tumor Analysis Consortium (CPTAC). Linked Omics has over a billion information points in total., To enable a extensive assessment of these data, the web application Linked Omics developed three analytical modules. The Link Finder module enables for flexible discovery of connections between a molecular or clinical trait of concern and all other characteristics, offering a chance to evaluate and visualize connections for each cancer cohort between billions of attribute pairs. They show that Linked Omics offers biologists and clinicians with a distinctive platform for accessing, analyzing and comparing multi-omics cancer information within and across tumor kinds. On http://www.linkedomics.org, Linked Omics is readily accessible.

Pancan-meQTL

Gong et al. (19) provided Pancan-meQTL, a repository that integrates genome-wide genotype and DNA methylation information to provide meQTLs across 23 cancer kinds from the Cancer Genome Atlas. In maximum, 8,028,964 cis-meQTLs and 965,050 trans-meQTLs were recognized. Overall patient survival rates are correlated with 23,432 meQTLs. In addition, 2,214 458 meQTLs were recognized that overlap with identified loci recognized by genome-wide correlation studies. Pancan-meQTL offers an easy-to-use web interface http://bioinfo.life.hust.edu.cn/Pancan-meQTL/ for browsing, scanning and accessing of interesting information.

PITDB

PITDB (20) is a free repository of translated genomic elements (TGEs) found in PIT (transcriptomics-informed proteomics) studies. In PIT, both RNA-seq transcriptomics as well as proteomic mass spectrometry are used to evaluate a

sample. Transcripts constructed from RNA-seq reads are being used to develop a library of sample-specific amino acid sequences that are searched for the obtained mass spectra, allowing the detection of any TGE, not just those in canonical proteome databases. PITDB includes more than 74 000 separate TGEs from four species at the moment of writing, backed by more than 600 000 matches in the peptide spectrum. The database, available at http://pitdb.org, offers guiding evidence for each TGE, often from multiple studies and an indicator of trust in the assessment and form of the TGE, varying from recognized protein to multiple protein component kinds including different splice isoforms, to a putative novel molecule.

qPrimerDB

Lu et al. (21) established the qPrimerDB repository based on the design of an automatic gene-specific qPCR primer and the verification workflow depending on thermodynamics. The qPrimerDB database is the most comprehensive qPCR primary database currently available, with a web front-end that provides gene-specific and pre-computed primary pairs across 147 major organisms including human, mouse, zebra fish, yeast, thale cress, rice, and corn. This database provides 3331426 of the best priming pairs for each gene, based on priming pair coverage, and 47760359 alternative gene-specific priming pairs, that can be easily downloaded in batch format. For qPCR priming pairs for 66 randomly chosen genes, the specificity and effectiveness was validated in six distinct species through qPCR assays and gel electrophoresis and it is open to the public via http://biodb.swu.edu.cn/qprimerdb.

SEECancer

Zhang et al. (22) has constructed a database on SEECancer, which serves to show an extensive developmental stage of cancer-specific somatic occurrences and their temporal orders. By manually curing more than 10 000 published papers, 1231 developmental stage-specific genomic occurrences and 5772 temporal orders containing 82 human cancers and 23 tissue origins were gathered and recorded in the SEECancer database. Each entry includes the somatic occurrence, the developmental phase, the sort of cancer, the identification strategy and the appropriate evidence. SEECancer offers an easy-to-use tool for browsing, finding and downloading developmental stage-specific somatic occurrences and temporal associations in multiple cancers.Increasing regard to the evolution of cancer genome, the required data in SEECancer has facilitated the knowledge of cancer etiology and the growth of developmental therapy, and has helped clinicians to find biomarkers for tumor progression surveillance. It is freely available via http://biocc.hrbmu.edu.cn/SEECancer.

UniLectin3D

Mariethoz et al. (23) has created a UniLectin3D database, a curated database that classifies source and fold lectins, cross-links to literature, many glycoscience databases and functional information such as recognized specificity. The database offers thorough data on lectins, their linked glycan ligands as well as their relationships using the Protein–Ligand Interaction Profiler (PLIP) server. Special attention was paid to the depiction of linked glycan ligands using easy graphical depiction and statistical format of cross-linking to other glycol scientific databases.They designed the layout of the database structure and navigation instruments to account for all species, and the search for oligosaccharide epitopes complexed inside selected binding regions. UniLectin3D is available link https://www.unilectin.eu/unilectin3D.

TranslatomeDB

Liu et al. (24) has developed an extensive TranslatomeDB database that offers a set and embedded assessment of published and client-generated translatom sequencing information. The present edition involves 2453 Ribo-seq, 10 RNC-seq and 1394 associated mRNA-seq datasets for 13 species. In relation to dataset sets, the database emphasizes the evaluation tasks. All datasets were evaluated using a unified, reliable, precise and experimentally verifiable pipeline centered on the FANSe3 mapping algorithm and edgeR for DGE analysis. TranslatomeDB also enables clients to upload their own datasets and use the same unified pipeline to evaluate their information. Accessible at http://www.translatomedb.net/.

TissGDB

Kim et al. (25) constructed Tiss-GDB (Tissue Specific Gene DataBase for Cancer) by collecting and manually curated 2461 tissue-specific genes (TissGenes) across 22 tissue classes corresponding to 28 cancers of the Cancer Genome Atlas (TCGA) from three different tissue-specific gene cell assets: the Human Protein Atlas (HPA), the Tissue-specific Gene Expression and Regulation (TiGER) and the Genoty map. These 2461 TissGenes also conducted gene expression, somatic mutation, and prognostic marker-based analyzes of 28 kinds of cancer using TCGA information. TissGDB sets out seven types of annotations: TissGene-Exp,TissGene Summary, TissGeneMut, and TissGene-miRNA. It is freely via http://zhaobioinfo.org/TissGDB.

TC3A

Feng et al. (26) proved that CFIm25-mediated 3 UTR reducing through APA encourages in vitro and in vivo development of glioblastoma tumors and further underscores its importance for tumorgenesis. Cancer 3 UTR Atlas (TC3A), an extensive APA use tool for 10,537 tumors across 32 kinds of cancer, is reported. These APA occurrences are possibly novel prognostic biomarkers and may uncover novel processes for the regulation of cancer-causing genes. TC3A is constructed on top of the current cBioPortal de facto standard. A big group of current cBioPortal consumers and clinical researchers will therefore discover TC3A acquainted and immediately available at http://tc3a.org.

Referances

1. Mokhtar MM, Adawy SS, El-Assal SE-DS, Hussein EHA. Genic and Intergenic SSR Database Generation, SNPs Determination and Pathway Annotations, in Date Palm (Phoenix dactylifera L.). PLoS One. Public Library of Science; 2016;11(7):e0159268.

2. Adawy SS, Mokhtar MM, Alsamman AM, Sakr MM. Development of annotated EST-SSR database in olive (Olea europaea). Int J Sci Res. 2015;4(9):1063–73.

3. Zhang Y, Zhang X, Wang Y, Shen S. De Novo Assembly of Transcriptome and Development of Novel EST-SSR Markers in Rhododendron rex Lévl . through Illumina Sequencing. 2017;8(September):1–12.

4. Kahraman A, Avramov A, Nashev LG. PhenomicDB : a multi-species genotype / phenotype database for comparative phenomics. Bioinformatics. 2018; 21(3): 418–20.

5. Pan J, Liu S, Zhu H, Qian J. AAgMarker 1 . 0 : a resource of serological autoantigen biomarkers for clinical diagnosis and prognosis of various human diseases. Nucleic Acids Res. Oxford University Press; 2018;46(August 2017):886–93.

6. Xia S, Feng J, Chen K, Ma Y, Gong J, Cai F, et al. CSCD : a database for cancer-specific circular RNAs. Nucleic Acids Res. Oxford University Press; 2018;46(September 2017):925–9.

7. Ru B, Sun J, Tong Y, Wong CN, Chandra A, Tsz A, et al. CR2Cancer : a database for chromatin regulators in human cancer. Nucleic Acids Res. Oxford University Press; 2018;46(October 2017):918–24.

8. Krassowski M, Paczkowska M, Cullion K, Huang T, Dzneladze I, Ouellette BFF, et al. ActiveDriverDB : human disease mutations and genome variation in post-translational modification sites of proteins. Nucleic Acids Res. 2018;46(November 2017):901–10.

9. Ehler E, Juras A, Chyle M. AmtDB : a database of ancient human mitochondrial genomes. Nucleic Acids Res. 2018;46:4–7.

10. Wang Z, Zhang Q, Zhang W, Lin J, Cai Y, Mitra J, et al. HEDD : Human Enhancer Disease Database. Nucleic Acids Res. Oxford University Press; 2018;46(October 2017):113–20.

11. Zhang G, Shi J, Zhu S, Lan Y, Xu L, Yuan H, et al. DiseaseEnhancer : a resource of human disease-associated enhancer catalog. Nucleic Acids Res. Oxford University Press; 2018;46(October 2017):78–84.

12. Zheng L, Zhou K, Liu S, Zhang D, Wang Z, Chen Z, et al. dreamBase : DNA modification , RNA regulation and protein binding of expressed pseudogenes in human health and disease. Nucleic Acids Res. Oxford University Press; 2018;46(October 2017):85–91.

13. Kuksa PP, Amlie-wolf A, Katanić Ž, Val- O, Wang L, Leung YY. DASHR 2 . 0 : integrated database of human small non-coding RNA genes and mature products. Bioinformatics. 2018;(August).

14. Yue M, Zhou D, Zhi H, Wang P, Zhang Y, Gao Y, et al. MSDD : a manually curated database of experimentally supported associations among miRNAs , SNPs and human diseases. Nucleic Acids Res. Oxford University Press; 2018;46(November 2017):181–5.

15. Krempel R, Kulkarni P, Yim A, Lang U, Habermann B, Frommolt P. Integrative analysis and machine learning on cancer genomics data using the Cancer Systems Biology Database (CancerSysDB). BMC Bioinformatics. BMC Bioinformatics; 2018;19:1–10.

16. Tokar T, Pastrello C, Rossos AEM, Abovsky M, Hauschild A, Tsay M, et al. mirDIP 4 . 1 — integrative database of human microRNA target predictions. Nucleic Acids Res. Oxford University Press; 2018;46(November 2017):360–70.

17. Wang G, Luo X, Wang J, Wan J, Xia S, Zhu H, et al. MeDReaders : a database for transcription factors that bind to methylated DNA. Nucleic Acids Res. Oxford University Press; 2018;46(November 2017):146–51.

18. Vasaikar S V, Straub P, Wang J, Zhang B. LinkedOmics : analyzing multi-omics data within and across 32 cancer types. Nucleic Acids Res. Oxford University Press; 2018;46(November 2017):956–63.

19. Gong J, Wan H, Mei S, Ruan H, Zhang Z, Liu C, et al. Pancan-meQTL : a database to systematically evaluate the effects of genetic variants on methylation in human cancer. Nucleic Acids Res. Oxford University Press; 2018;46:1–7.

20. Saha S, Chatzimichali EA, Matthews DA, Bessant C. PITDB : a database of translated genomic elements. Nucleic Acids Res. Oxford University Press; 2018;46(October 2017):1223–8.

21. Lu K, Li T, He J, Chang W, Zhang R, Liu M, et al. qPrimerDB : a thermodynamics-based gene-specific qPCR primer database for 147 organisms. Nucleic Acids Res. Oxford University Press; 2018;46(August 2017):1229–36.

22. Zhang H, Luo S, Zhang X, Liao J, Quan F, Zhao E, et al. SEECancer : a resource for somatic events in evolution of cancer genome. Nucleic Acids Res. Oxford University Press; 2018;46(October 2017):1018–26.

23. Mariethoz J, Salentin S, Robin X, Imberty A, Schroeder M, Perez S. UniLectin3D , a database of carbohydrate binding proteins with curated information on 3D structures and interacting ligands Franc. Nucleic Acids Res. 2018;46:1–9.

24. Liu W, Xiang L, Zheng T, Jin J, Zhang G. TranslatomeDB : a comprehensive database and cloud-based analysis platform for translatome sequencing data. Nucleic Acids Res. Oxford University Press; 2018;46(November 2017):206–12.

25. Kim P, Park A, Han G, Sun H, Jia P, Zhao Z. TissGDB : tissue-specific gene database in cancer. Nucleic Acids Res. Oxford University Press; 2018;46(September 2017):1031–8.

26. Feng X, Li L, Wagner EJ, Li W. TC3A : The Cancer 3 UTR Atlas. Nucleic Acids Res. Oxford University Press; 2018;46(October 2017):1027–30.