A

rna|

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📖 tr**a**nscript/s**a**msa2

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📖 dianbaer/**a**nyupload

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📖 faressoft/termi**n**alizer

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9 code results in JhuangLab/BioInstaller or view all results on GitHub

inst/extdata/config/db/db_main.toml   TOML
Showing the top match   Last indexed 13 days ago

```
8      source_url = "http://srnanalyzer.systemsbiology.net/downloads/{{version}}.tar.gz"
9      version_available = ["sRNA_DBs", "MainDBs", "NCBI_NonHuman"]
10     version_description = ["small RNA Databases", "Human and Exogenous Databases", "NCBI
       Non-Human Databases"]
11
12     [db_cscd]
```

inst/extdata/config/github/github_meta.toml   TOML
Showing the top match   Last indexed on May 5

```
16     title = "a project-oriented pipeline for processing of RNA-seq data in high performance
       cluster environments"
17     description = "The wide range of RNA-seq applications and their high-computational needs
       require the development of pipelines orchestrating the entire workflow and optimizing
       usage of available computational resources. We present aRNApipe, a project-oriented
       pipeline for processing of RNA-seq data in high-performance cluster environments.
       aRNApipe is highly modular and can be easily migrated to any high-performance computing
       (HPC) environment. The current applications included in aRNApipe combine the essential
       RNA-seq primary analyses, including quality control metrics, transcript alignment, count
       generation, transcript fusion identification, alternative splicing and sequence variant
       calling. aRNApipe is project-oriented and dynamic so users can easily update analyses to
       include or exclude samples or enable additional processing modules. Workflow parameters
       are easily set using a single configuration file that provides centralized tracking of
       all analytical processes. Finally, aRNApipe incorporates interactive web reports for
       sample tracking and a tool for managing the genome assemblies available to perform an
       analysis."
```

C

Share bioinformatics database #12

[Edit] [New issue]

⊙ Open   **Miachol** opened this issue 8 days ago · 17 comments

Miachol commented 8 days ago · edited ▾   [Member]   +😊   ⋯

Configuration file: db_main.toml
Description: miRDB is an online database for miRNA target prediction and functional annotations.

```
[db_mirdb]
source_url = "http://mirdb.org/download/miRDB_v{{version}}_prediction_result.txt.gz"
version_avaliable = ["5.0", "4.0", "3.0", "2.0", "1.0"]
```

Miachol commented 8 days ago · edited ▾   [Member]   +😊   ⋯

Configuration file: db_main.toml
Description: As a database, miRTarBase has accumulated more than three hundred and sixty thousand miRNA-target interactions (MTIs), which are collected by manually surveying pertinent literature after NLP of the text systematically to filter research articles related to functional studies of miRNAs.

```
[db_mirtarbase]
source_url = "http://mirtarbase.mbc.nctu.edu.tw/cache/download/{{version}}/miRTarBase_MTI.x
version_avaliable = ["7.0"]
```

Hellenzz commented a minute ago   +😊   ⋯

Configuration file: db_main.toml
Description: HMDB is an online database of small molecule metabolites found in the human body, which facilitates human metabolomics research including the identification and characterization of human metabolites using NMR and MS.

```
[db_hmdb]
source_url = "http://www.hmdb.ca/system/downloads/current/{{version}}.zip"
avaliable_version = ["hmdb_proteins", "hmdb_metabolites", "structures"]
```

👍 2

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Projects ⚙
None yet

Milestone ⚙
No milestone

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1 participant