

Resource Summary Report

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Starbase V2.0

RRID:SCR_016303

Type: Tool

Proper Citation

Starbase V2.0 (RRID:SCR_016303)

Resource Information

URL: <http://starbase.sysu.edu.cn/index.php>

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Description: Web based tool to visualize, analyze, discover and download of large-scale functional genomics data. Used for analysis of the CLIP-Seq and Degradome-Seq data sets, exploration of miRNA–target interactions and decoding RNA interaction networks from CLIP-Seq (HITS-CLIP, PAR-CLIP, iCLIP, CLASH) data. To show RNA-RNA and protein-RNA interaction networks in developmental, physiological and pathological processes.

Resource Type: software resource, web application

Defining Citation: [PMID:24297251](#)

Keywords: visualize, analyze, discover, download, large, genomic, data, set, miRNA, RNA-RNA, protein-RNA, interaction, network, decoding, CLIP-Seq, Degradome-Seq

Funding: Ministry of Science and Technology of China ;
National Basic Research Program No. 2011CB811300

Availability: Free, Freely available, Available for download

Resource Name: Starbase V2.0

Resource ID: SCR_016303

License: GNU

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260801T190530+0000

Ratings and Alerts

No rating or validation information has been found for Starbase V2.0.

No alerts have been found for Starbase V2.0.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 819 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Wen Q, et al. (2026) Identification and Validation of the Prognostic Value of PTTG1-Related Genes in Hepatocellular Carcinoma by Mendelian Randomization and Single-Cell Transcriptome Analysis. Iranian journal of biotechnology, 24(1), e4221.

Xu C, et al. (2025) An Exosome-Based Liquid Biopsy Predicts Depth of Response and Survival Outcomes to Cetuximab and Panitumumab in Metastatic Colorectal Cancer: The EXONERATE Study. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(6), 1002.

Wang A, et al. (2025) Endoplasmic reticulum stress-related CLIP4 plays a procarcinogenic role in hepatocellular carcinoma: an integrated analysis. BMC cancer, 25(1), 211.

Lv Y, et al. (2025) circDENND4C serves as a sponge for miR-200b to drive non-small cell lung cancer advancement by regulating MMP-9 expression. Frontiers in oncology, 15, 1441384.

Sun YK, et al. (2025) hnRNPA2B1 drives colorectal cancer progression via the circCDYL/EIF4A3/PHF8 axis. The Kaohsiung journal of medical sciences, 41(3), e12943.

Yang QH, et al. (2025) LncRNA-MALAT1 promotes triple-negative breast cancer progression and function as ceRNA to target REEP5 by sponging miR-106a-5p. European journal of medical research, 30(1), 159.

Hongyuan H, et al. (2025) Identification of mitochondria-related biomarkers for acute respiratory distress syndrome. Scientific reports, 15(1), 28221.

Zhang T, et al. (2025) Copper Metabolism-Related Genes as Biomarkers in Colon Adenoma and Cancer. International journal of general medicine, 18, 3021.

Zhen S, et al. (2025) Identification and validation of genes related to stem cells and telomere maintenance mechanisms as biomarkers for breast cancer. Frontiers in immunology, 16, 1618193.

Li R, et al. (2025) Regulatory Role of IGF2BP2 in Intestinal Mucosal Barrier Dysfunction in Ulcerative Colitis. The Turkish journal of gastroenterology : the official journal of Turkish Society of Gastroenterology, 36(4), 269.

Yang L, et al. (2025) METTL3 aggravates lung injury in neonatal mice with Streptococcus pneumoniae-induced pneumonia via the circ_0001239/KLF10 axis. Infection and immunity, 93(11), e0028825.

Wang J, et al. (2025) Expression patterns of serum miR-27a-3p and activating transcription factor 3 in children with bronchial asthma and their correlations with airway inflammation. The clinical respiratory journal, 19(3), e13631.

Zhang H, et al. (2025) Identification and characterization of mitochondrial autophagy-related genes in osteosarcoma and predicting clinical prognosis. Scientific reports, 15(1), 10158.

Ji L, et al. (2025) Circular RNA Circ_0002762 promotes cell migration and invasion in cervical squamous cell carcinoma via activating RelA/nuclear factor kappa B (Nf-kB) signalling pathway. RNA biology, 22(1), 1.

Bu T, et al. (2025) LncRNA of peripheral blood mononuclear cells: HYMAI acts as a potential diagnostic and therapeutic biomarker for female major depressive disorder. Frontiers in psychiatry, 16, 1241089.

Yu S, et al. (2025) Integrated bioinformatics decoding of the MASLD ceRNA network reveals novel therapeutic targets. Clinical and experimental medicine, 25(1), 354.

He L, et al. (2025) Cross-talk between mitophagy pathways in pre-eclampsia and gestational diabetes mellitus: a systematic analysis of shared molecular mechanisms. European journal of medical research, 30(1), 568.

Chen G, et al. (2025) The NEAT1/miR-124-3p/CCL2 axis in chronic kidney disease progression: integrated bioinformatics analysis and experimental validation. Epigenomics, 17(14), 935.

Mei K, et al. (2025) miR-221 is a prognostic marker and promotes the proliferation and migration of esophageal squamous cell carcinoma by inhibiting autophagy. Discover oncology, 16(1), 445.

Wang G, et al. (2025) miR-32-5p suppresses the progression of hepatocellular carcinoma by regulating the GSK3 β /NF- κ B signaling. Acta biochimica et biophysica Sinica, 57(7), 1125.