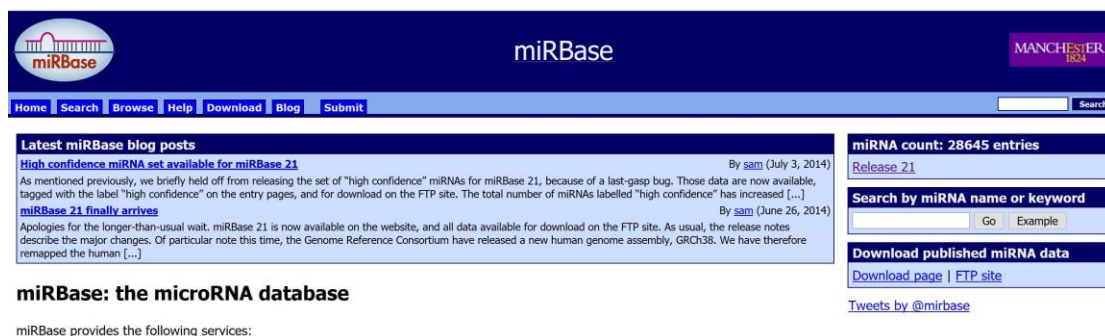




miRBase

<http://www.mirbase.org>

miRBase 数据库是一个提供包括已发表的 miRNA 序列数据、注释、预测基因靶标等信息的全方位数据库，是存储 miRNA 信息最主要的公共数据库之一。该数据库于 2014 年 6 月更新为最新版本 V21.0，包含 223 个物种的 35828 个成熟的 miRNA 序列。该数据库提供便捷的网上查询服务，允许用户使用关键词或序列在线搜索已知的 miRNA 和靶标信息（仅包含已有的靶标信息，所以会出现部分 miRNA 靶标信息无的现象）。该数据库用于 miRNA 信息查询较多，靶关系预测较少。



TargetScan

<http://www.targetscan.org>

TargetScan 数据库是大家比较常用的预测 miRNA 靶基因数据库，主要通过搜索和每条 miRNA 种子区域匹配的保守的 8mer 和 7mer 位点来预测靶基因。该数据库提供人、小鼠、大鼠、奶牛、狗、猩猩、恒河猴、负鼠、鸡和青蛙等动物信息。最新更新时间为 2015 年 8 月，版本为 V7.0。



Search for predicted microRNA targets in mammals

[\[Go to TargetScanMouse\]](#)

[\[Go to TargetScanWorm\]](#)

[\[Go to TargetScanFly\]](#)

[\[Go to TargetScanFish\]](#)

1. Select a species

AND

2. Enter a human gene symbol (e.g. "Hmga2")
or an Ensembl gene (ENSG00000149948) or transcript (ENST00000403681) ID

AND/OR

3. Do one of the following:

• Select a broadly conserved* microRNA family

• Select a conserved* microRNA family

• Select a poorly conserved but confidently annotated microRNA family

• Select another miRBase annotation

Note that most of these families are star miRNAs or RNA fragments misannotated as miRNAs.

• Enter a microRNA name (e.g. "miR-9-5p")

PicTar

<http://www.pictar.org/>

PicTar 是通过一定计算法则来鉴定 microRNA 的靶目标的。该可搜索的网站可以提供以下物种的关于 microRNA 靶目标的预测详细信息，包括：脊椎动物、七个果蝇种类、三个线虫种类和人类的非保守但共表达的 microRNA 的靶目标（例如：表达在同一组织的 microRNA 和 mRNA）。



Welcome To PicTar

PicTar is an algorithm for the identification of microRNA targets. This searchable website provides details (3' UTR alignments with predicted sites, links to various public databases etc) regarding:

(1) microRNA target predictions in vertebrates ([Krek et al, Nature Genetics 37:495-500 \(2005\)](#))

(2) microRNA target predictions in seven *Drosophila* species ([Grün et al, PLoS Comp. Biol. 1:e13 \(2005\)](#))

(3) microRNA targets in three nematode species ([Lall et al, Current Biology 16, 1-12 \(2006\)](#))

(4) human microRNA targets that are not conserved but co-expressed (i.e. the microRNA and mRNA are expressed in the same tissue) ([Chen and Rajewsky, Nat Genet 38, 1452-1456 \(2006\)](#)) [co-expressed targets](#)

starBase v2.0

<http://starbase.sysu.edu.cn/>

该数据库采集了 6000 多份样本, 14 种癌症来自于 37 个独立研究的 108 份 CLIP-seq 数据, 同时辅助降解组实验数据搜寻 miRNA 的靶标, 提供了各式各样的可视化界面去探讨 miRNA 靶标。除了 miRNA 和靶标 mRNA 之间关系, 该数据库还进行 lncRNA、circRNA、protein 与 mRNA 之间的相互作用分析, 并分析了 ceRNA 机制。该数据库主要包含人、小鼠、线虫 3 个物种信息。



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Home miRNA-lncRNA miRNA-mRNA ceRNA Network Pan-Cancer Protein-RNA Function Prediction Download Contact Us

Welcome to starBase

starBase is designed for decoding **Pan-Cancer** and **Interaction Networks** of lncRNAs, miRNAs, competing endogenous RNAs (ceRNAs), RNA-binding proteins (RBPs) and mRNAs from large-scale **CLIP-Seq (HITS-CLIP, PAR-CLIP, iCLIP, CLASH)** data and **tumor samples (14 cancer types, >6000 samples)**.

starBase is also developed for deciphering **Protein-RNA** and **miRNA-target interactions**, such as protein-lncRNA, protein-sncRNA, protein-mRNA, protein-pseudogene, miRNA-lncRNA, miRNA-mRNA, miRNA-circRNA, miRNA-pseudogene, miRNA-sncRNA interactions and ceRNA networks from **108 CLIP-Seq (HITS-CLIP, PAR-CLIP, iCLIP, CLASH)** datasets.

starBase provides **miRFunction** and **ceRNAFunction** web tools to **predict the function** of ncRNAs (miRNAs, lncRNAs, pseudogenes) and protein-coding genes from the **miRNA-mediated (ceRNA) regulatory networks**.

How to Cite: **NEW** [Li et al. Nucleic Acids Res. 2014](#) & [Yang et al. Nucleic Acids Res. 2011](#).

What's New

starBase v2.0 release at Sept. 2013

- **NEW Pan-Cancer Analysis**
- **starBase v2.0 paper in Nucleic Acids Res.**
- 14 Cancer Types
- > 6000 tumor samples
- 111 CLIP-Seq data

NEW [starBase Pan-Cancer Tutorial](#)
[starBase v2.0 Tutorial](#)

Data Sets

starBase contains **108** CLIP-Seq data from **37** studies. [Details](#)

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