

miRBase-microRNA序列 数据库

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microRNA简介

“ microRNA (miRNA) 是一类长约22个核苷酸的非编码小RNA分子，最早在线虫中发现，并广泛存在于许多真核生物和细胞中，包括植物、动物、单细胞藻类、病毒等。miRNA主要通过与其靶mRNA的结合，在转录后水平介导mRNA降解（多见于植物）或翻译抑制（多见于动物）来调控基因表达。研究表明miRNA在动植物生长发育、动物细胞凋亡、癌症发生以及植物应答胁迫等方面发挥重要作用。

“ microRNA的命名规则：

1. 将物种缩写置于miRNA之前，成熟miRNA用miR表示，miRNA的基因或初级转录本中预测的茎环结构则用mir表示；
2. miRNA简写成miR，再根据其被克隆的先后顺序加上阿拉伯数字，并且编号是连续的；
3. 不同物种中同源的miRNA最好用同一个名字，同一物种中高度同源的miRNA在数字后加上英文小写字母；
4. 由不同染色体上的DNA序列转录加工而成的具有相同miRNA成熟序列而pre-miRNA序列不同的miRNA，则在后面加上阿拉伯数字以区分；
5. 如果一个前体的2个臂分别加工产生miRNA，则根据克隆试验，看看哪个是主要的成熟产物，次要的在后面加“*”号。

miRBase



miRBase

MANCHESTER
1824

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Latest miRBase blog posts

miRBase website "at risk", Thu 10th to Fri 18th Nov

Due to server room refurbishment, the miRBase website may experience time at either end of that period, but the website should be considered [miRBase 18 released](#)

After a little more pain than usual, miRBase 18 is finally released. The products, in 168 species. That represents 1488 new hairpin sequences have [...]

18226 hairpin precursor miRNAs
21643 mature miRNAs
168 species

miRBase: the microRNA database

miRBase provides the following services:

- The [miRBase database](#) is a searchable database of published miRNA sequences and annotation. Each entry in the miRBase Sequence database represents a predicted hairpin portion of a miRNA transcript (termed mir in the database), with information on the location and sequence of the mature miRNA sequence (termed miR). Both hairpin and mature sequences are available for [searching](#) and [browsing](#), and entries can also be retrieved by name, keyword, references and annotation. All sequence and annotation data are also [available for download](#).
- The [miRBase Registry](#) provides miRNA gene hunters with unique names for novel miRNA genes prior to publication of results. Visit the [help pages](#) for more information about the naming service.
- The miRBase Targets database and pipeline has been rebranded as [microCosm, and is now hosted at the FBI](#). The microCosm resource continues to be maintained by the [Enright group](#). miRBase currently links miRNAs to targets predicted by microCosm, [TargetScan](#) and [PicTar](#), and aims to provide a more extensive target prediction aggregation service in the future.

To receive email notification of data updates and feature changes please subscribe to the [miRBase announcements mailing list](#). Any queries about the website or naming service should be directed at mirbase@manchester.ac.uk.

miRBase is hosted and maintained in the [Faculty of Life Sciences](#) at the [University of Manchester](#) with funding from the [BBSRC](#), and was previously hosted and supported by the [Wellcome Trust Sanger Institute](#).

References

If you make use of the data presented here, please cite the following articles in addition to the primary data sources:

[miRBase: integrating microRNA annotation and deep-sequencing data.](#)

Kozomara A, Griffiths-Jones S.
NAR 2011 39(Database Issue):D152-D157

[miRBase: tools for microRNA genomics.](#)

Griffiths-Jones S, Saini HK, van Dongen S, Enright AJ.
NAR 2008 36(Database Issue):D154-D158

[miRBase: microRNA sequences, targets and gene nomenclature.](#)

Griffiths-Jones S, Grocock RJ, van Dongen S, Bateman A, Enright AJ.
NAR 2006 34(Database Issue):D140-D144

[The microRNA Registry.](#)

Griffiths-Jones S.
NAR 2004 32(Database Issue):D109-D111

The following publications provide guidelines on miRNA annotation:

[A uniform system for microRNA annotation.](#)

Ambros V, Bartel B, Bartel DP, Burge CB, Carrington JC, Chen X, Dreyfuss G, Eddy SR, Griffiths-Jones S, Marshall M, Matzke M, Ruvkun G, Tuschl T.
RNA 2003 9(3):277-279

[Criteria for annotation of plant MicroRNAs.](#)

Meyers BC, Axtell MJ, Bartel B, Bartel DP, Baulcombe D, Bowman JL, Cao X, Carrington JC, Chen X, Green PJ, Griffiths-Jones S, Jacobsen SE, Mallory AC, Martienssen RA, Poethig RS, Qi Y, Vaucheret H, Voinnet O, Watanabe Y, Weigel D, Zhu JK.
Plant Cell. 2008 20(12):3186-3190

miRNA count: 18226 entries

Release 18: November 2011

Search by miRNA name or keyword

Download published miRNA data

[Download page](#) | [FTP site](#)

This site is featured in:

[NetWatch - Science 303:1741 \(2004\)](#)
[Highlights, Web watch - Nature Reviews Genetics 5:244 \(2004\)](#)

miRBase

- “ miRBase序列数据库是一个提供包括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；库中所有数据都可以从首页Download page或直接进入FTP站点下载。
- “ miRBase主要由三部分组成：miRBase database、miRBase Registry和miRBase Targets database。而miRBase Targets database则已经更名为microcosm，并托管于EBI。

miRNA注册



提交所用的格式为**Fasta**格式。最终，提交的序列将会加入到
miRBase Sequence Database中。

miRNA搜索

Browse miRBase by species

Click taxa to expand and collapse the tree. Click species names to list microRNAs.
Jump to: [human](#), [mouse](#), [fly](#), [worm](#), [Arabidopsis](#).

Key: species name (miRNA count) [assembly version]



Browse



Expand all

Collapse all

- Chromalveolata
- Metazoa
- Mycetozoa
- Viridiplantae
- Viruses

Expand all

Collapse all

miRNA搜索

Homo sapiens miRNAs (1527 sequences)

ID	Accession	RPM	Chromosome	Start	End	Strand	Fetch
hsa-let-7a-1	MI0000060	1.33e+05	9	96938239	96938318	+	<input type="checkbox"/>
hsa-let-7a-2	MI0000061	1.18e+05	11	122017230	122017301	-	<input type="checkbox"/>
hsa-let-7a-3	MI0000062	1.6e+05	22	46508629	46508702	+	<input type="checkbox"/>
hsa-let-7b	MI0000063	8.54e+04	22	46509566	46509648	+	<input type="checkbox"/>
hsa-let-7c	MI0000064	1.19e+05	21	17912148	17912231	+	<input type="checkbox"/>
hsa-let-7d	MI0000065	1.11e+04	9	96941116	96941202	+	<input type="checkbox"/>
hsa-let-7e	MI0000066	5.3e+04	19	52196039	52196117	+	<input type="checkbox"/>
hsa-let-7f-1	MI0000067	1.15e+05	9	96938629	96938715	+	<input type="checkbox"/>
hsa-let-7f-2	MI0000068	1.19e+05	X	53584153	53584235	-	<input type="checkbox"/>
hsa-let-7g	MI0000433	1.16e+05	3	52302294	52302377	-	<input type="checkbox"/>
hsa-let-7i	MI0000434	1.49e+04	12	62997466	62997549	+	<input type="checkbox"/>
hsa-mir-1-1	MI0000651	2.2e+03	20	61151513	61151583	+	<input type="checkbox"/>
hsa-mir-1-2	MI0000437	2.17e+03	18	19408965	19409049	-	<input type="checkbox"/>
hsa-mir-7-1	MI0000263	2.34e+03	9	86584663	86584772	-	<input type="checkbox"/>
hsa-mir-7-2	MI0000264	1.59e+03	15	89155056	89155165	+	<input type="checkbox"/>
hsa-mir-7-3	MI0000265	2.3e+03	19	4770682	4770791	+	<input type="checkbox"/>
hsa-mir-9-1	MI0000466	3.16e+03	1	156390133	156390221	-	<input type="checkbox"/>

Homo sapiens



miRNA搜索



Search miRBase

By miRNA identifier or keyword

Enter a miRNA accession, name or keyword:

By genomic location

Select organism, chromosome and start and end coordinates. Leave the start/end boxes blank to retrieve all miRNAs on the selected chromosome.

Choose species: Chr: Start: End:

For clusters

Select organism and the desired inter-miRNA distance.

Choose species: Inter-miRNA distance:

By sequence

Single sequence searches:

Paste a sequence here to search against miRNA sequences. You can choose to search against the intact precursor sequences or just the mature miRNAs. This search may take a few minutes. (Max size 1000bp's)

Search sequences:

Search method:

Choose BLASTN to search for a miRNA in a longer sequence. SSEARCH is useful for finding a short sequence within the library of miRNAs (for instance, find a short motif in a miRNA or precursor stem-loop, or find mature sequences that are related to your query).

Or, select the sequence file you wish to

Submit file:

Search

By miRNA identifier or keyword

Enter a miRNA accession, name or keyword:

hsa-let-7a-1

提交查询内容

重置

Example

miRBase MANCHESTER 1824

Home Search Browse Genomics Help Download Submit **hsa-let-7a-1** Search

miRBase has moved to <http://www.mirbase.org/> - please update your links.

Stem-loop sequence MI0000060

Accession	MI0000060
ID	hsa-let-7a-1
Symbol	HGNC:MIRLET7A1
Description	Homo sapiens let-7a-1 stem-loop
Stem-loop	<pre> u gu uuagggucacac uggga gag aguagguuuguauaguu c auccu uuc ucaucuaacaaucuaa a u uuagggucacac</pre>
Comments	let-7a-1 cloned in [6] has a 1 nt 3' extension (U), which is incompatible with the genome sequence.
Genome context	<i>Coordinates (GRCh37)</i> 9: 96938239-96938318 [+] <i>Overlapping transcripts</i> intergenic View flanking features
Clustered miRNAs	< 10kb from <i>hsa-let-7a-1</i> hsa-let-7a-1 9: 96938239-96938318 [+] hsa-let-7a-1 9: 96938629-96938715 [+] hsa-let-7a-1 9: 96941116-96941202 [+]
Database links	EMBL: A421724 RFAM: RF00027 ; let-7 HGNC: 31476 ; MIRLET7A1 ENTREZGENE: 406881 ; MIRLET7A1
Gene family	MIPF0000002; let-7

Mature sequence MIMAT0000062

Accession	MIMAT0000062
ID	hsa-let-7a-1
Sequence	6 - u g e a g u a g u a g g u u g u a u a g u u - 27 Get sequence
Evidence	experimental; cloned [1-3,5-8], Northern [1]
Predicted targets	MICROCOSM: hsa-let-7a TARGETSCAN: hsa-let-7a PICTAR-VERT: hsa-let-7a

Minor miRBase copy: [hsa-let-7a-1](#) MIMAT0000062

>hsa-let-7a-1 MI0000060

UGGGAUGAGGUAGUAGGUCUUAAGUUUUAGGGUCACACCCACCACUGGGAGAUAAACUAUACAAUCUACUGUCUUUCCUA

以上内容仅为本文档的试下载部分，为可阅读页数的一半内容。如要下载或阅读全文，请访问：<https://d.book118.com/398141063006006052>