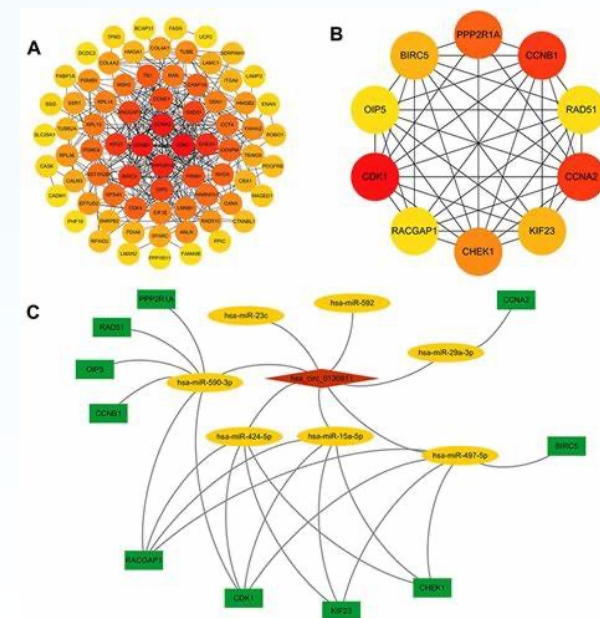




ceRNA网络

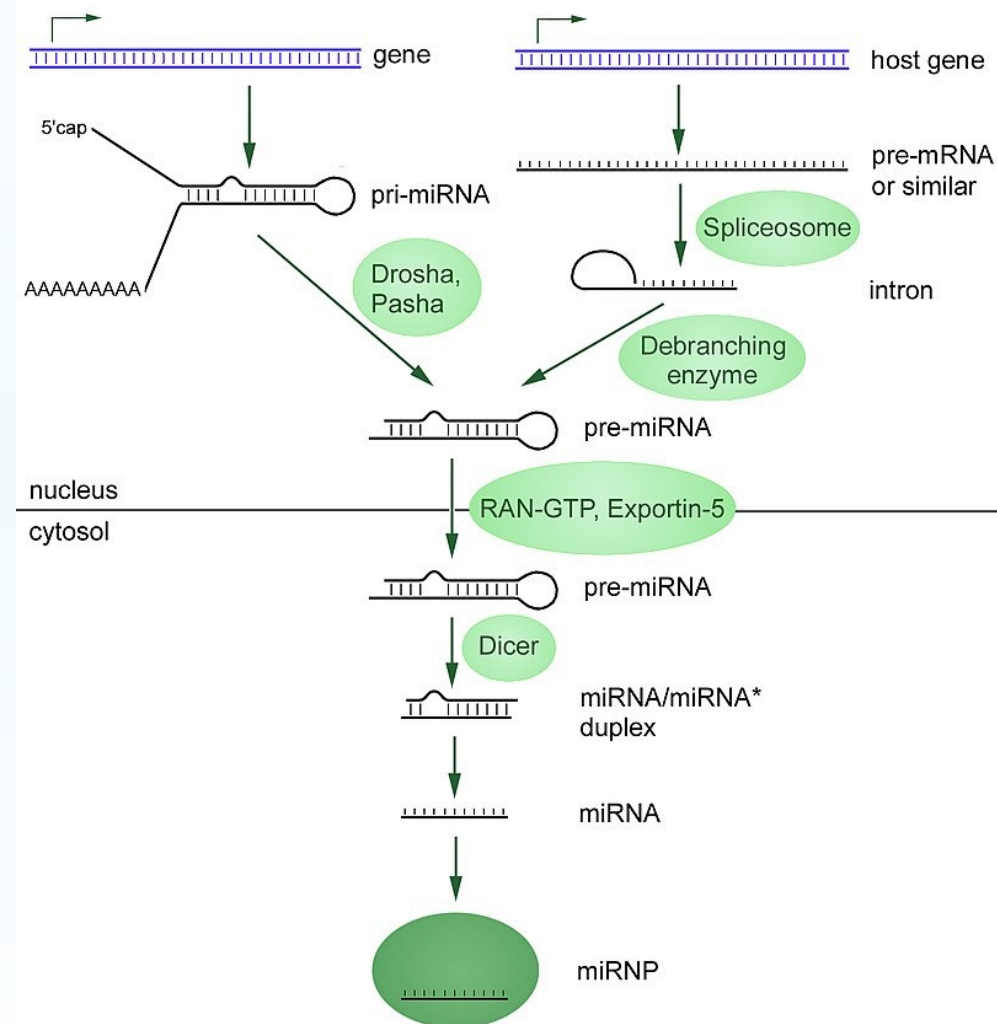


易汉博

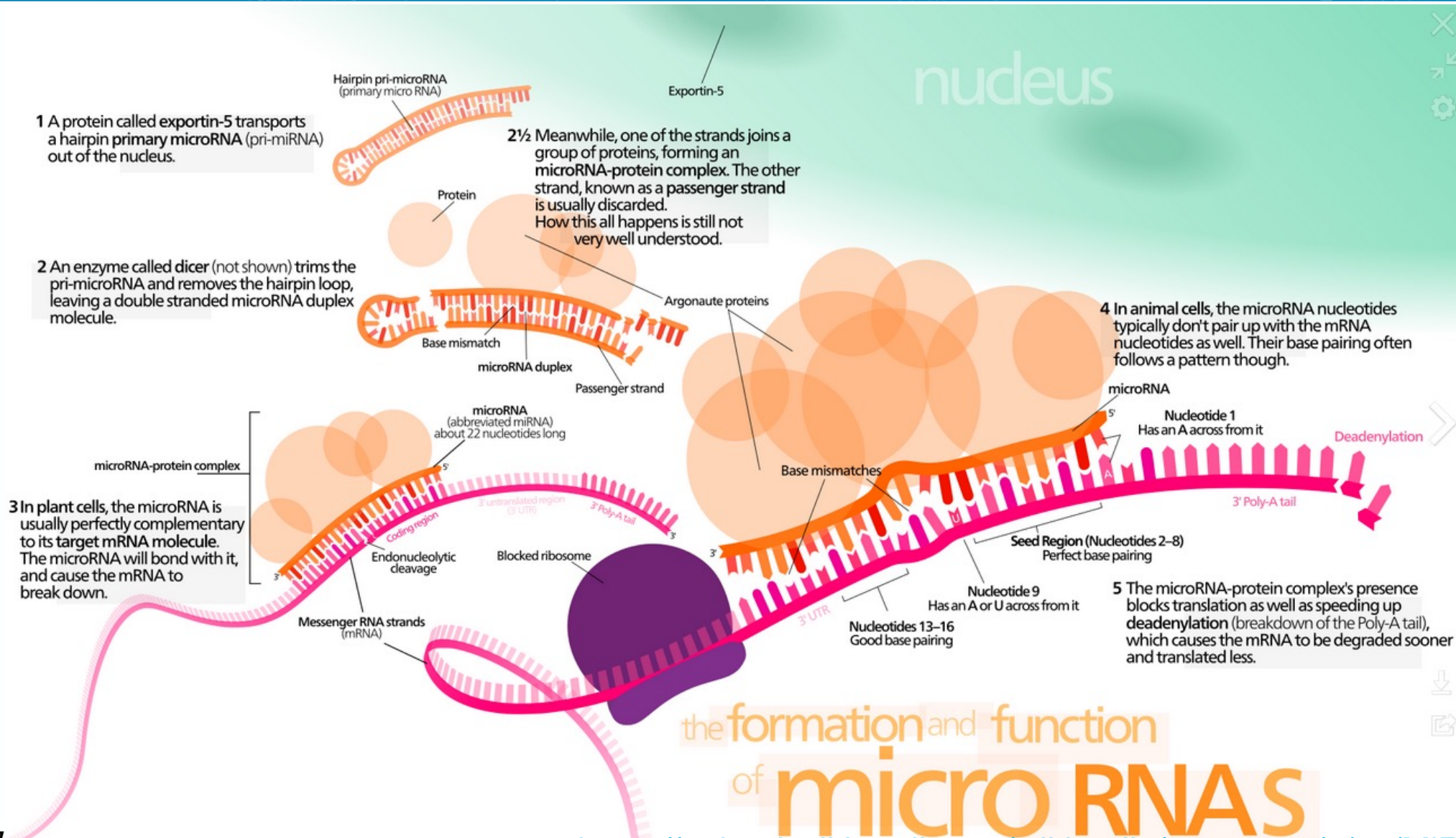
领先的大数据与健康解决方案
Leading solutions for big data and health

miRNA的产生

- MicroRNAs (miRNAs) are a class of small noncoding RNAs of ~22nt in length which are involved in the regulation of gene expression at the posttranscriptional level by degrading their target mRNAs and/or inhibiting their translation.



miRNA的生成和功能



miRBase: 最全miRNA数据库



miRBase

MANCHESTER 1824

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Latest miRBase blog posts

[MicroRNA Gene Ontology annotations](#) By [sam](#) (June 7, 2018)
You might have noticed some additional information on the mature miRNA pages in the last few weeks. See for example: http://mirbase.org/cgi-bin/mature.pl?mature_acc=MIMAT0000123 http://mirbase.org/cgi-bin/mature.pl?mature_acc=MIMAT0000069 The new section "QuickGO function" contains a set of high quality manual annotations of Gene Ontology terms for mature miRNAs, the vast majority of which come from the work of Rachael Huntley et [...]

[miRBase 22 release](#) By [sam](#) (March 12, 2018)
After repeated and unreasonable delay, miRBase 22 is finally released. As you might expect with such a long gap, the number of sequences in the database has jumped significantly — by over a third. The vast majority of the increase comes from new microRNA annotations in species not previous represented in the database. Indeed, there [...]

miRNA count: 38589 entries
[Release 22.1](#): October 2018

Search by miRNA name or keyword

Download published miRNA data
[Download page](#) | [FTP site](#)

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.

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: 最全miRNA数据库



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.

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 managed by the [Griffiths-Jones lab](#) at the [Faculty of Biology, Medicine and Health, University of Manchester](#) with funding from the [BBSRC](#). miRBase was previously hosted and supported by the [Wellcome Trust Sanger Institute](#).

miRNA count: 38589 entries

[Release 22.1](#)

Search by miRNA name or keyword

Download published miRNA data

[Download page](#)



数据库的维护需要钱，很多钱



ClinGen is defining the clinical relevance of genes and variants

ClinGen was founded in 2013 by the National Human Genome Research Institute, ClinGen is a growing collaborative effort, in investigators and over 1,700 contributors from more than 40 countries. Below are a series of recent updates that ClinGen has

Ancestry and Diversity Forum



NIH awards \$73m to continue building the ClinGen Resource
The National Institutes of Health (NIH) will renew three awards over five years to continue building the ClinGen Resource.



下载miRNA前体和成熟的序列



miRBase Sequence Download

- ▶ [Go to the FTP site](#)
- ▶ [Previous releases](#)
- ▶ [README](#) Release notes - read these first!
- ▶ [miRNA.dat](#) all published miRNA data in EMBL format
- ▶ [hairpin.fa](#) Fasta format sequences of all miRNA hairpins
- ▶ [mature.fa](#) Fasta format sequences of all mature miRNA sequences
- ▶ [miRNA.diff](#) Changes between the last release and this
- ▶ [miRNA.dead](#) List of entries that have been removed from the database

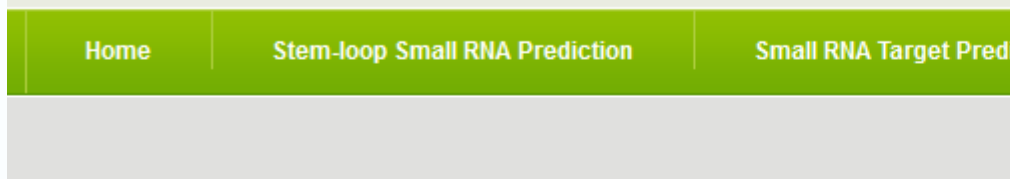
Genome coordinates

aae.gff3	ame.gff3	ath.gff3	bmo.gff3	bta.gff3	cbr.gff3	cel.gff3	cfa.gff3
cre.gff3	dme.gff3	dps.gff3	dre.gff3	ebv.gff3	fru.gff3	gga.gff3	hcmv.gff3
hsa.gff3	kshv.gff3	mdo.gff3	mghv.gff3	mml.gff3	mmu.gff3	osa.gff3	ptc.gff3
ptr.gff3	rno.gff3	sme.gff3	tni.gff3	vvi.gff3	xtr.gff3	zma.gff3	





psRobot: Plant Small RNA Analysis Toolbox



Visiting Statistics

Hits: 840467

Unique IPs: 20949

Executions: 610930

News And Updates

01-24-2013

Added wild tobacco (*Nicotiana benthamiana*) genome and annotated transcript library to the online version of psRobot.

12-03-2012

领先的解决方案
Leading solutions for big data and health

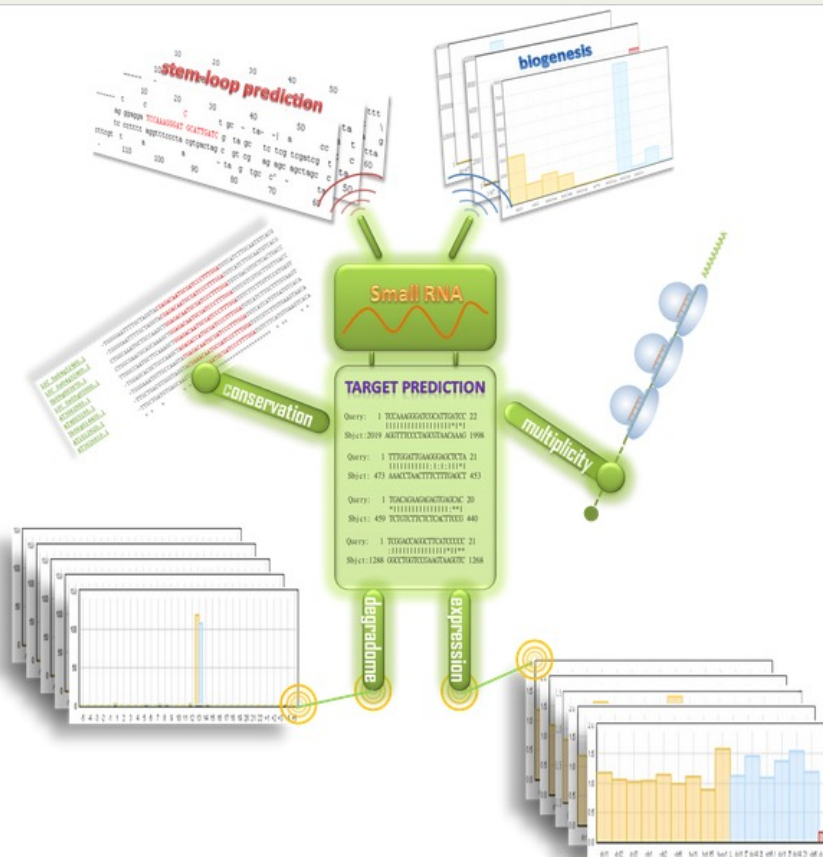
PsRobot is designed to analyze

The online version of psRobot

The **stem-loop small RNA prediction** module, including their expression, smRNA associated protein coding, and functional processes, their genomic location, and



The second module, **small RNA target prediction**, provides prediction results of smRNAs, conservation and biological data support, such as degradome data and target expression data in small RNA biogenesis mutants.

PsRobot also features a **local version**. The local programs offer a larger capacity for input



<http://omicslab.genetics.ac.cn/psRobot/>





HOMEFAQRESOURCESABOUT

News and Updates:

- Jan/2021 - **new_update_2021** - Annual update for the year 2021 was completed. At the request of numerous users, the duplex information has been integrated and can now be saved.
- Apr/2020 - **SERVER PROBLEMS** - Due to the high access rate, we are getting into some problems. We have decided to move the database to a stronger server. This can take some time and we apologize for the down-times. We will work on it as soon as possible. The miRWalk team.
- Mar/2020 - **genesets_update** - All genesets (KEGG, GO and Reactome) were updated.
- Mar/2020 - **new_update** - Data from all species were updated. Since a bug in the code some genes were missing in the last data update from december last year.
- Mar/2020 - **danio_rerio** - new organism added. Zebrafish (Danio rerio) with all genes and transcripts is included into miRWalk database now.
[read more...](#)

New version of miRWalk

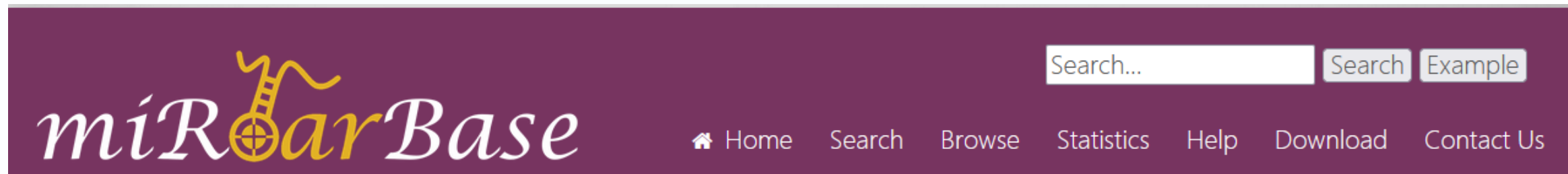
miRWalk is an improved version of the previous database (i.e. miRWalk). The new version of miRWalk stores predicted data obtained with a machine learning algorithm including experimentally verified miRNA-target interactions. The focus lies on accuracy, simplicity, user-friendly design and mostly up to date informations. More information can be obtained under [Frequently Asked Questions](#).

Search for a single gene or miRNA

miRNAs: miRNA names (e.g. hsa-miR-214-3p) or Accession numbers (e.g. MIMAT0000271) based on current miRBase. While searching single miRNAs, also short names or family miRNA (e.g. let-7) belongs to several miRNAs are also acceptable. A list of miRNAs will be shown. mRNAs: Official Genesymbols (e.g. GAS2), EntrezIDs (e.g. 10608), EnsemblIDs (e.g.

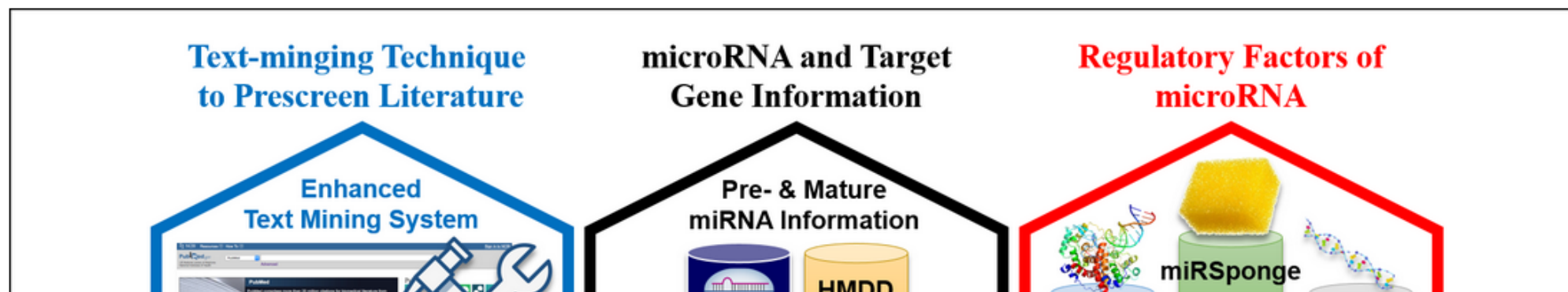


实验验证的miRNA-靶点数据库

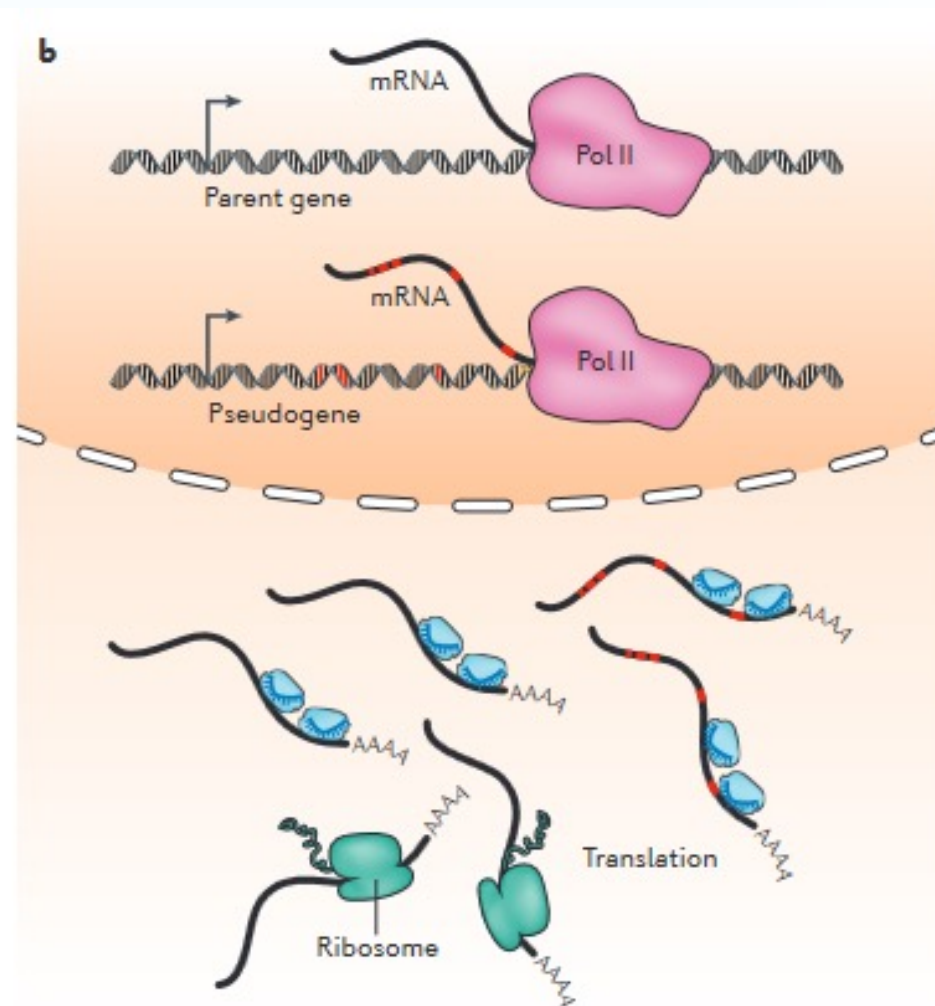
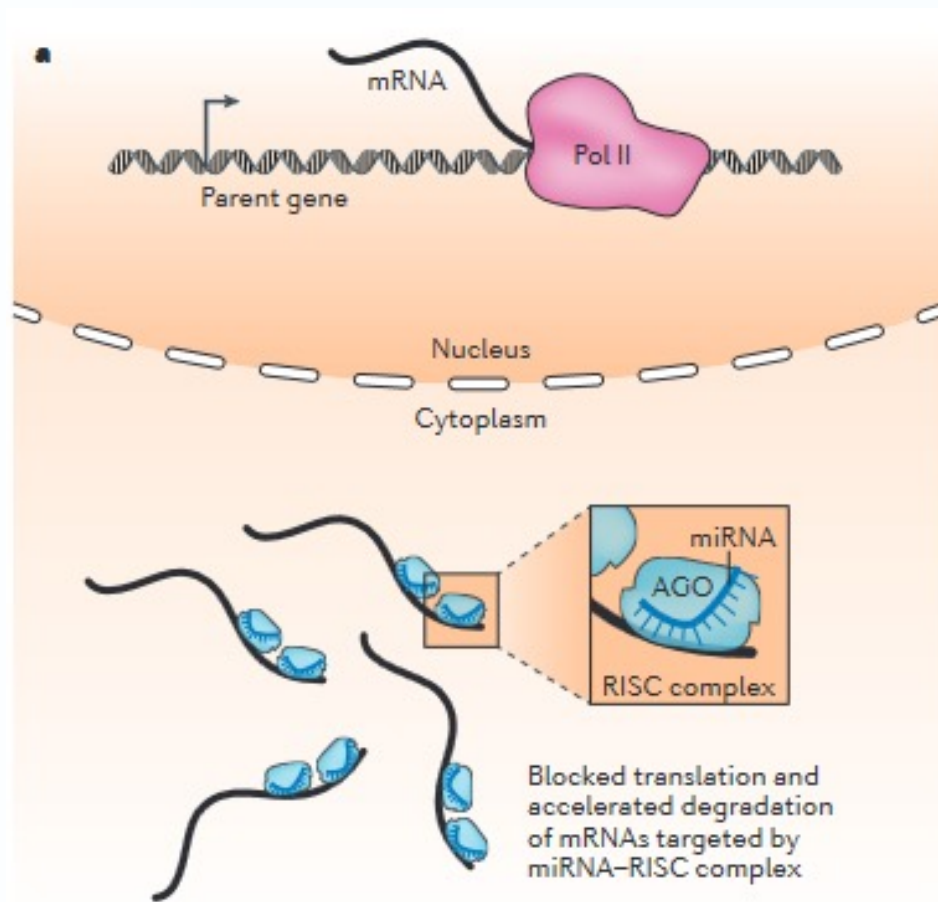


miRTarBase: The experimentally validated microRNA-target interactions database

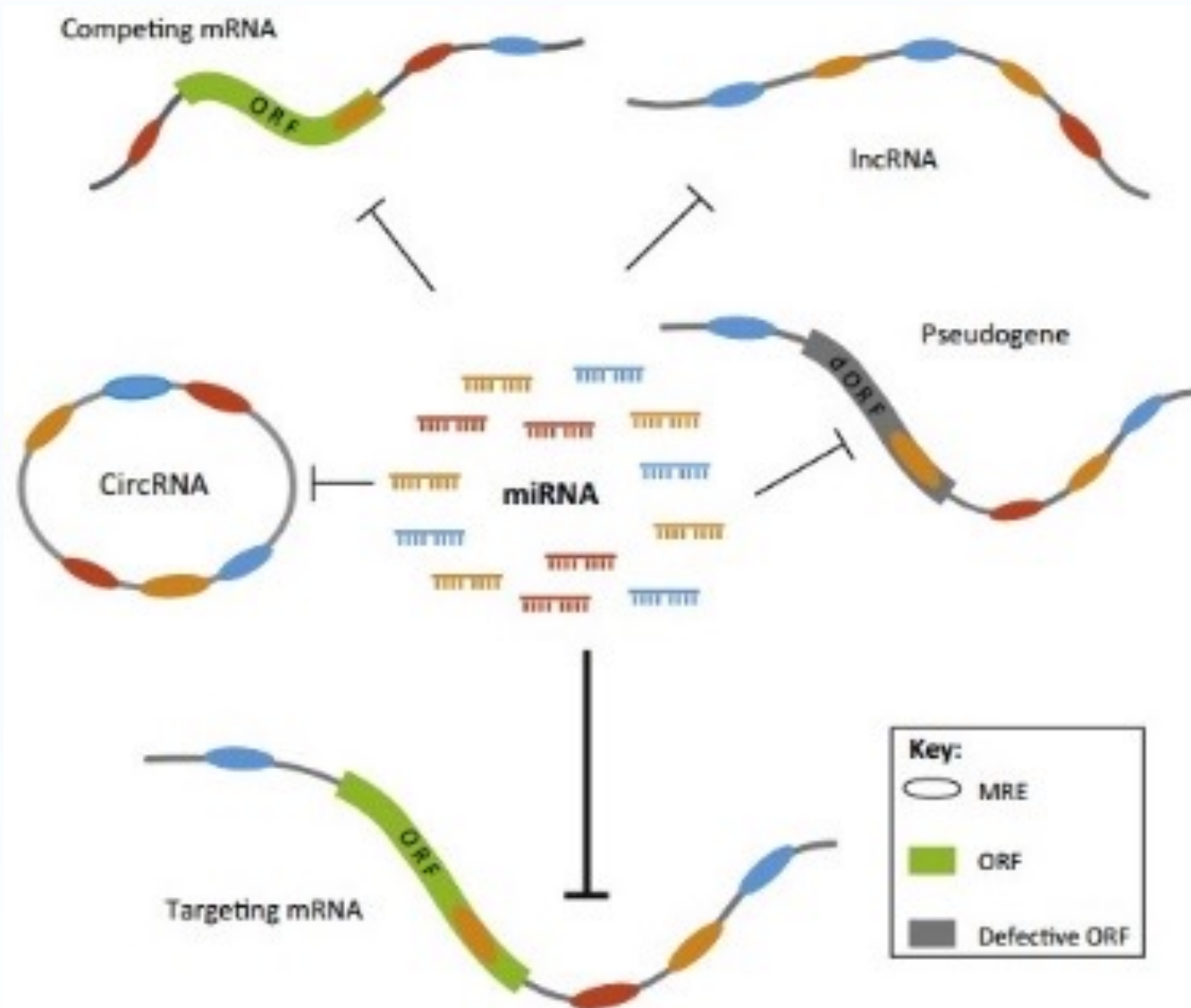
As a database, **miRTarBase** has accumulated more than three hundred and sixty thousand miRNA-target interactions (MTIs), which are collected by manually surveying pertinent literature after NLP of the text systematically to filter research articles related to functional studies of miRNAs. Generally, the collected MTIs are validated experimentally by reporter assay, western blot, microarray and next-generation sequencing experiments. While containing the largest amount of validated MTIs, the miRTarBase provides the most updated collection by comparing with other similar, previously developed databases.



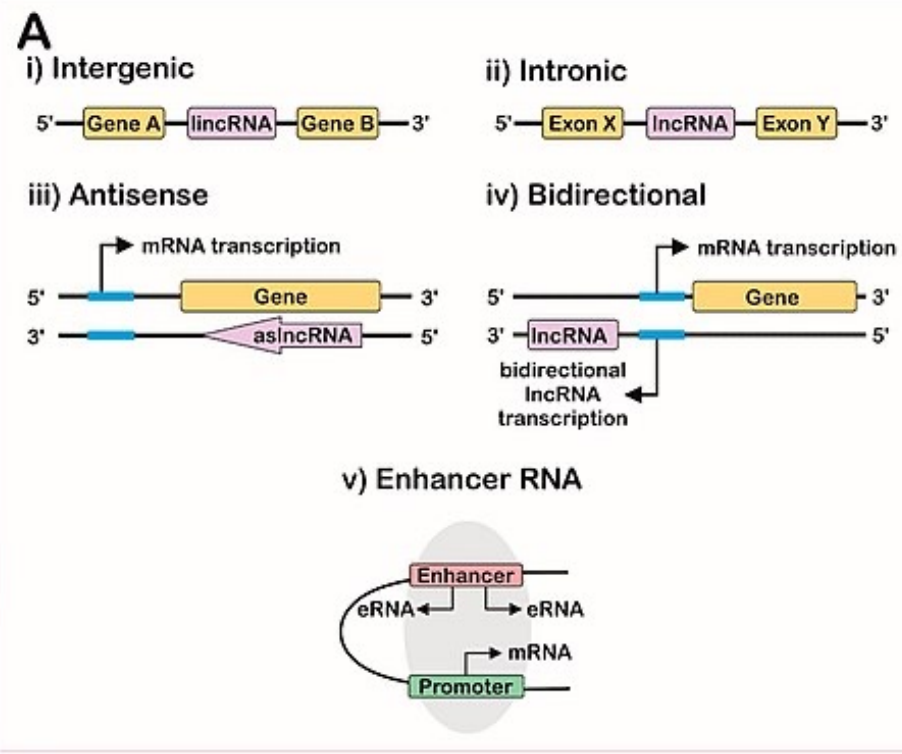
ceRNA竞争机制



Sponge可以有多种

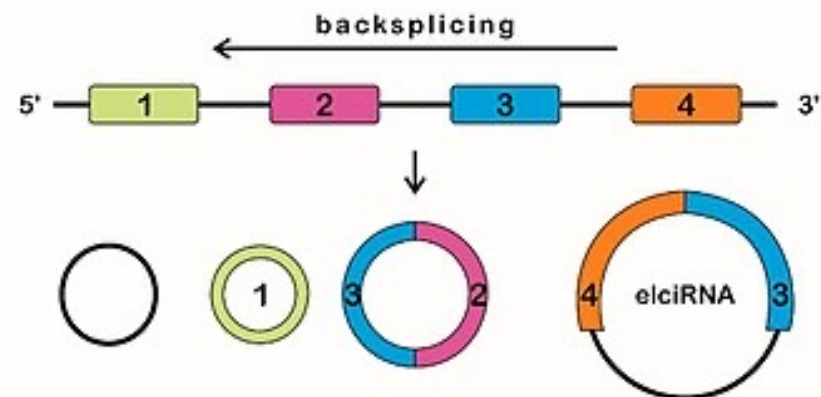


不同类型RNA的产生方式

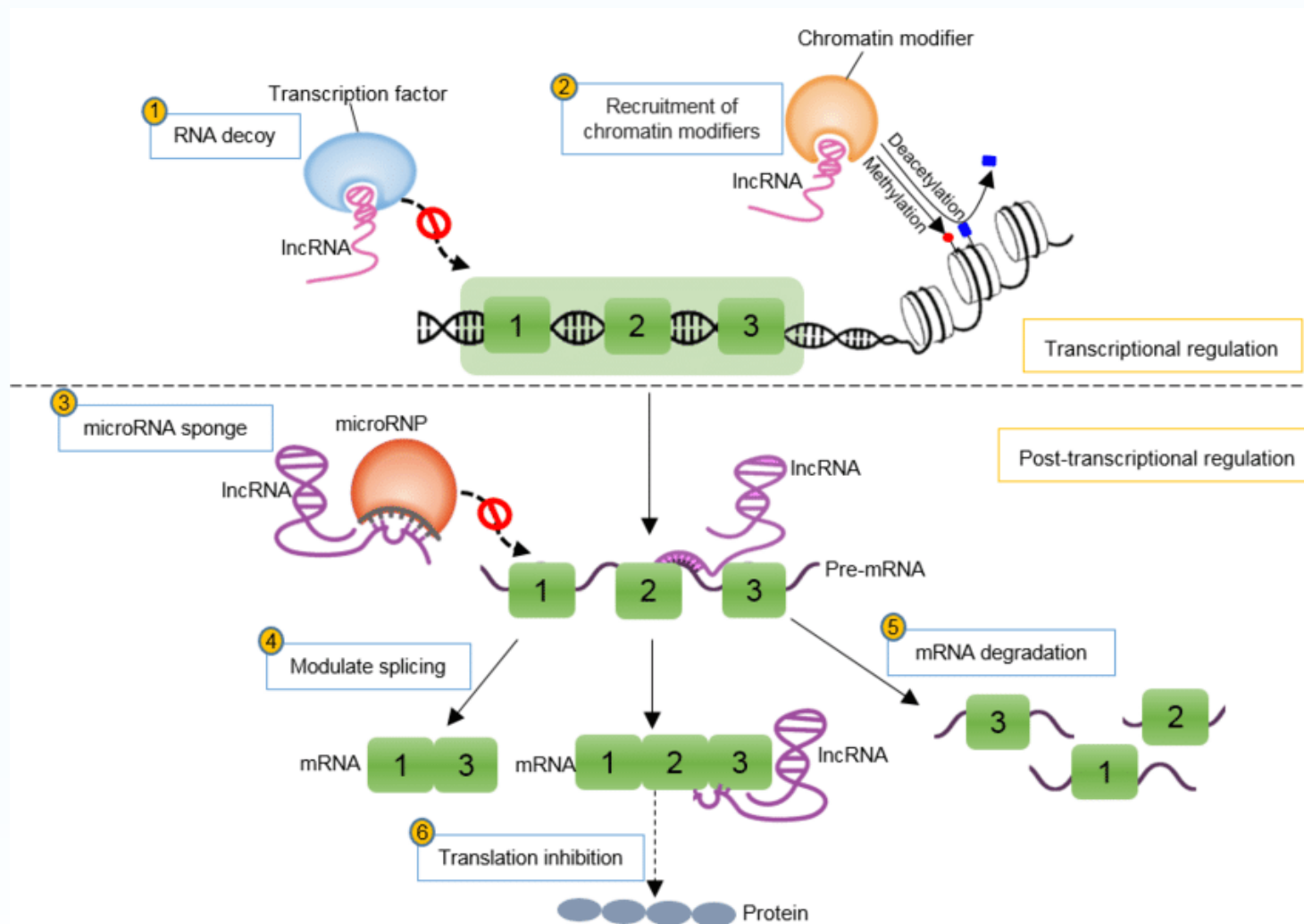


B

General formation of circRNAs



lncRNA的作用模式



lncRNA预测工具 – CPC2



CPC 2.0

Home

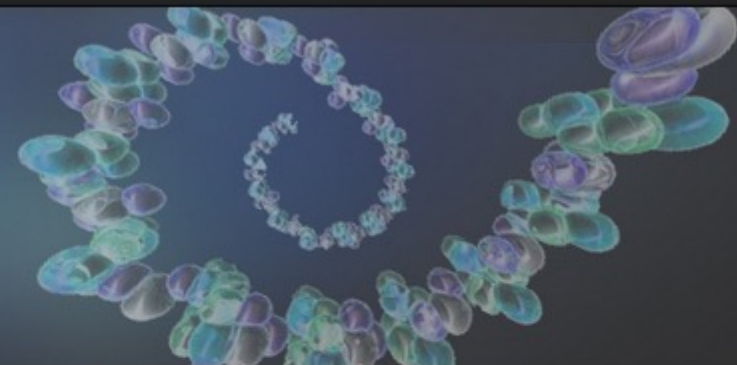
Batch

Download

Help

About

Coding Potential Calculator 2



NEW Are you working with Human Long Noncoding RNAs? Also try the **AnnoLnc** for an integrative annotation of your lncRNAs.

NEW CPC 2.0 beta is online now, please report to cpc@mail.cbi.pku.edu.cn for any questions or comments.

Paste your sequences (in FASTA format) here.

<http://cpc2.gao-lab.org/>



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领先的大数据与健康解决方案
Leading solutions for big data and health

RNAsamba评估转录本编码潜能



Documentation



GitHub

About

RNAsamba is a tool for computing the coding potential of RNA sequences using a neural network classification model. It can be used to identify mRNAs and lncRNAs without relying on database searches.

Use RNAsamba online

Upload a FASTA file containing transcript sequences ([example](#)). We allow the following file extensions: *fasta*, *fa* and *fna*. After submitting your data, you will be redirected to a page where you can view and download your results as soon as they are ready.

Choose a FASTA file (Max.: 50 MB or 50,000 sequences)

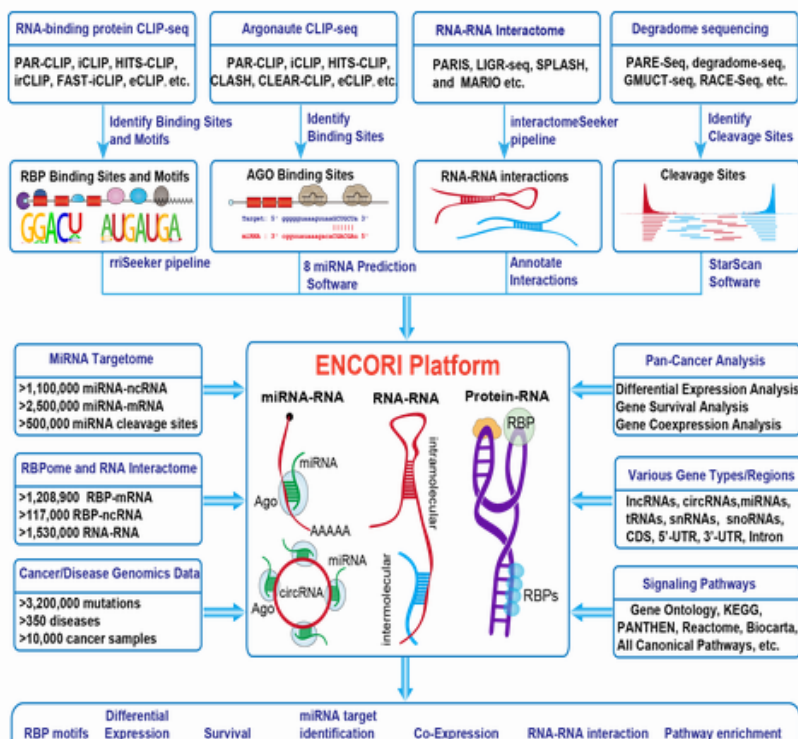
Browse

Submit





Welcome to ENCORI!

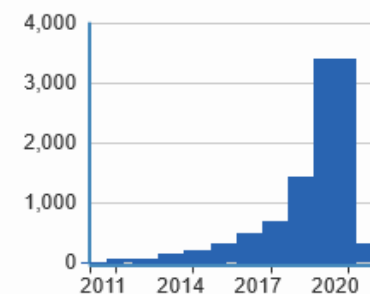


Previous version (starBase, [Cite Our Paper](#)) of ENCORI (The [Encyclopedia of RNA Interactomes](#)) is mainly focus on miRNA-target interactions. ENCORI is an open-source platform for studying the miRNA-ncRNA, miRNA-mRNA, ncRNA-RNA, RNA-RNA, RBP-ncRNA and RBP-mRNA interactions from CLIP-seq, degradome-seq and RNA-RNA interactome data.

In summary, ENCORI identifies more than 1.1 million miRNA-ncRNA, 2.5 million miRNA-mRNA, 2.1 million RBP-RNA and 1.5 million RNA-RNA interactions from multi-dimensional

ENCORI Citations (2011-2021) [Cite Our Paper](#)

>7000 Citations in Google Scholar (starBase)



- **Average Daily Usage:** ~5000 visits from ~500 unique researchers
- **Average Annual Usage:** >1,000,000 visits from >100 countries

Statistics of ENCORI

- **Species:** 23 Species



Gene-gene的ceRNA关系



ENCORI
For RNA Interactomes

Home miRNA-Target Degradome-RNA RNA-RNA **ceRNA-Network** RBP-Target RBP-Motif RBP-Disease Pathway Pan-Cancer Web API Tutorial Contact

Clade »

Genome ▾

☒ human
☐ mouse

Assembly ▾

☒ hg19

ceRNA Gene ▾
MYC

miRNA Number ▾
☒ >= 2
☐ >= 4
☐ >= 8
☐ >= 12
☐ >= 16
☐ >= 20
☐ >= 24

Quick Search mammal ✓ human ✓ hg19 ✓ ceRNA: MYC ✓ hitMiRnum >= 2 ✓ p-val <= 0.01 ✓ FDR <= 0.01 ✓ pan-Cancer >= 0 ✓

The **ceRNA** Interaction Network of **MYC** in Human

Download:

Show/Hide Columns ▾

Search:

ceRNAgeneID	ceRNAname	ceRNAType	GeneID	GeneName	GeneType	HitMiRnum	p-val	FDR	Pan-Cancer
ENSG00000136997	MYC	protein_coding	ENSG00000197969	VPS13A	protein_coding	30	1.259e-9	1.100e-6	16
ENSG00000136997	MYC	protein_coding	ENSG00000117528	ABCD3	protein_coding	25	1.291e-9	1.100e-6	14
ENSG00000136997	MYC	protein_coding	ENSG00000069869	NEDD4	protein_coding	31	3.111e-9	1.100e-6	20
ENSG00000136997	MYC	protein_coding	ENSG00000183155	RABIF	protein_coding	23	8.955e-9	1.957e-6	16
ENSG00000136997	MYC	protein_coding	ENSG00000164761	TNFRSF11B	protein_coding	21	9.735e-9	1.957e-6	19
ENSG00000136997	MYC	protein_coding	ENSG00000047634	SCML1	protein_coding	24	1.384e-8	2.016e-6	11
ENSG00000136997	MYC	protein_coding	ENSG00000100632	ERH	protein_coding	16	2.272e-8	2.836e-6	17
ENSG00000136997	MYC	protein_coding	ENSG00000172292	CERS6	protein_coding	33	2.627e-8	2.870e-6	20
ENSG00000136997	MYC	protein_coding	ENSG00000138078	PREPL	protein_coding	28	2.768e-8	2.870e-6	20



lncRNA-gene直接的ceRNA关系



ENCORI
For RNA Interactomes

Home miRNA-Target Degradome-RNA RNA-RNA **ceRNA-Network** RBP-Target RBP-Motif RBP-Disease Pathway Pan-Cancer Web API Tutorial Contact

Clade »
Genome »
human
mouse
Assembly »
ceRNA Gene »
HOTAIR
miRNA Number »
P-value »
FDR »
Pan-Cancer »

Quick Search mammal human hg19 ceRNA: HOTAIR hitMiRnum >= 2 p-val <= 0.01 FDR <= 0.01 pan-Cancer >= 0

The **ceRNA** Interaction Network of **HOTAIR** in Human Download: EXCEL TXT

Show/Hide Columns

Shared miRNA families between HOTAIR and DLG5-AS1:

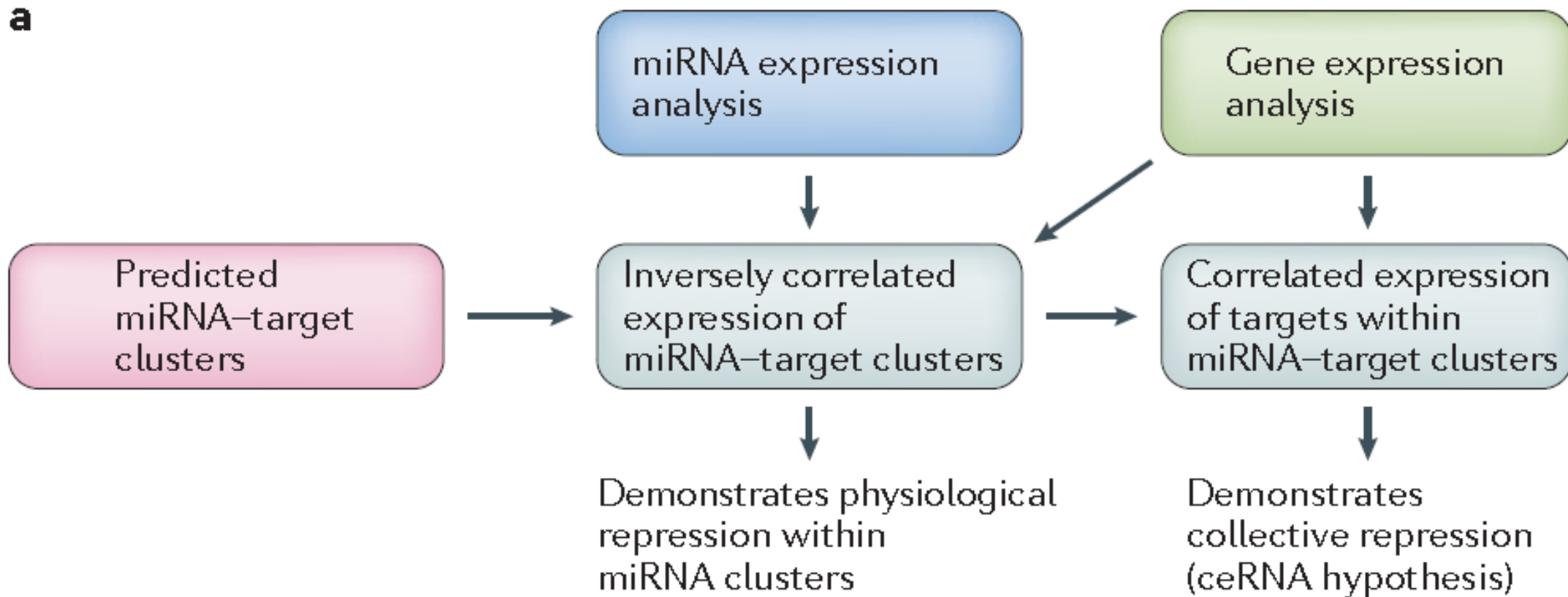
ceRNAgeneID	ceRNAname	ceRNAtype	miRNAFamily	miRNAs	Pan-Cancer
ENSG00000228630	HOTAIR	antisense			1
ENSG00000228630	HOTAIR	antisense			0
ENSG00000228630	HOTAIR	antisense	miR-130-3p/301-3p/454-3p	hsa-miR-130a-3p, hsa-miR-130b-3p, hsa-miR-301a-3p, hsa-miR-454-3p	1
ENSG00000228630	HOTAIR	antisense	miR-17-5p/20-5p/93-5p/106-5p/519-3p	hsa-miR-106a-5p, hsa-miR-106b-5p, hsa-miR-17-5p, hsa-miR-526b-3p, hsa-miR-93-5p	9
ENSG00000228630	HOTAIR	antisense	miR-19-3p	hsa-miR-19a-3p, hsa-miR-19b-3p	1
ENSG00000228630	HOTAIR	antisense	miR-519-3p	hsa-miR-519a-3p, hsa-miR-519b-3p, hsa-miR-519c-3p	20



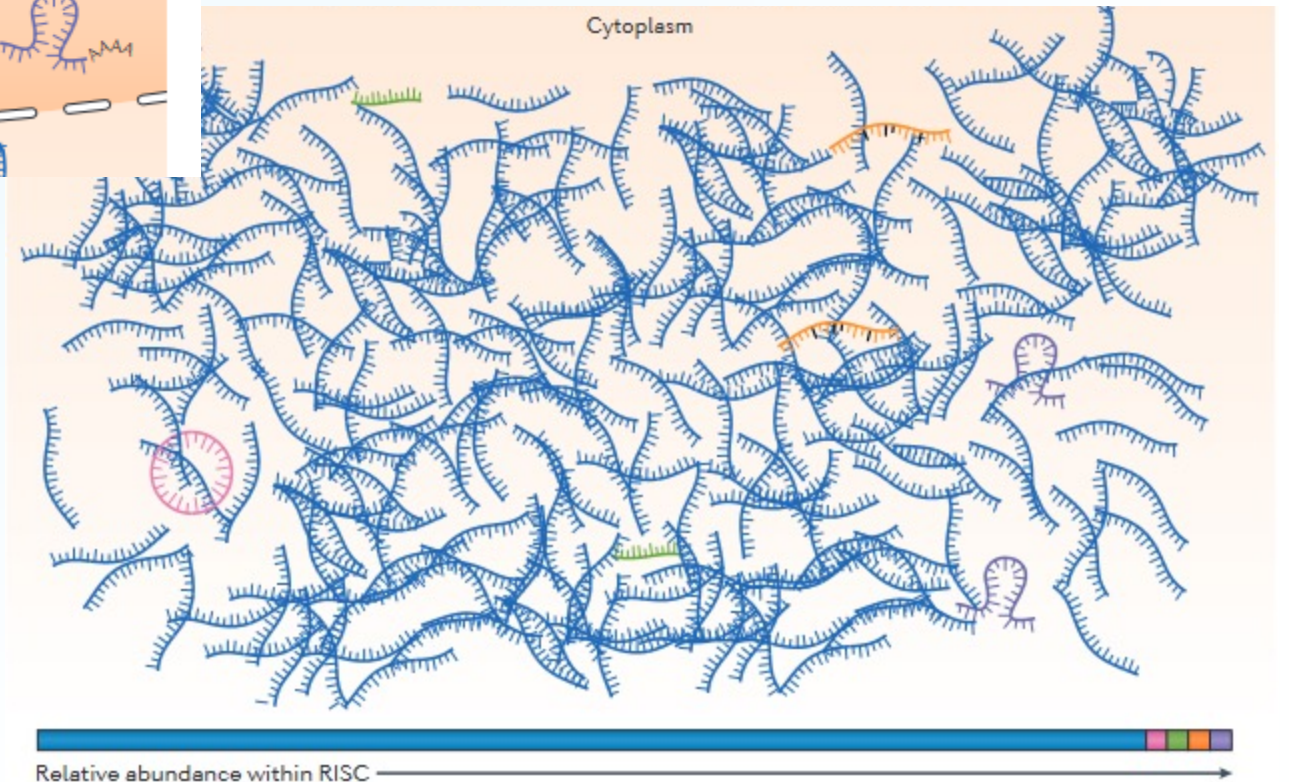
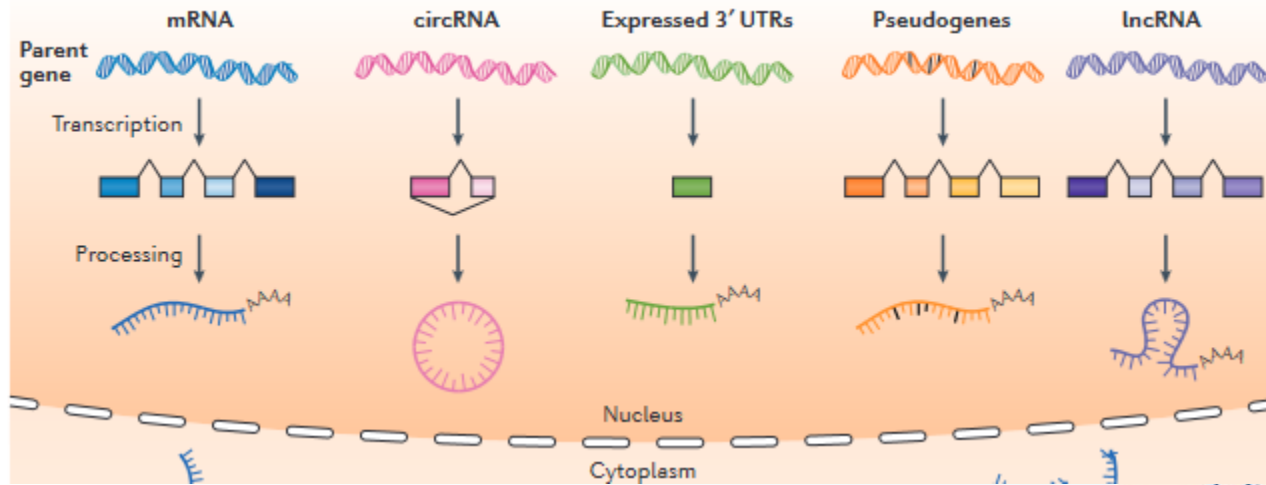
ceRNA的计算思路



a



内源性的sponge是否有足够的量发挥这个作用



如何获得3'UTR的序列 - ensembl biomart



New Count Results URL XML Perl Help

Dataset

Human genes (GRCh38.p13)

Filters

[None selected]

Attributes

Gene stable ID
Gene stable ID version
Transcript stable ID
Transcript stable ID version
3' UTR

Dataset

[None Selected]

Please select columns to be included in the output and hit 'Results' when ready

Missing non coding genes in your mart query output, please check the following [FAQ](#)

☐ Features

☐ Structures

☐ Homologues (Max select 6 orthologues)

☐ Variant (Germline)

☐ Variant (Somatic)

☒ Sequences

SEQUENCES:

Sequences (max 1)

☐ Unspliced (Transcript)

☐ Unspliced (Gene)

☐ Flank (Transcript)

☐ Flank (Gene)

☐ Flank-coding region (Transcript)

☐ Flank-coding region (Gene)

☐ 5' UTR

☒ 3' UTR

☐ Exon sequences

☐ cDNA sequences

☐ Coding sequence

☐ Peptide

Upstream flank

☐ Upstream flank

Downstream flank

☐ Downstream flank

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Leading solutions for big data and health

22



扫码关注生信宝典，学习更多生信知识



扫码关注宏基因组，获取专业学习资料

易生信，没有难学的生信知识



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