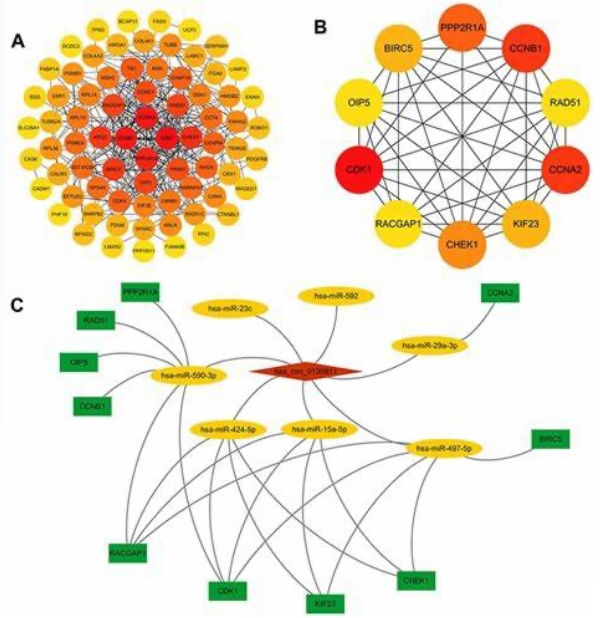
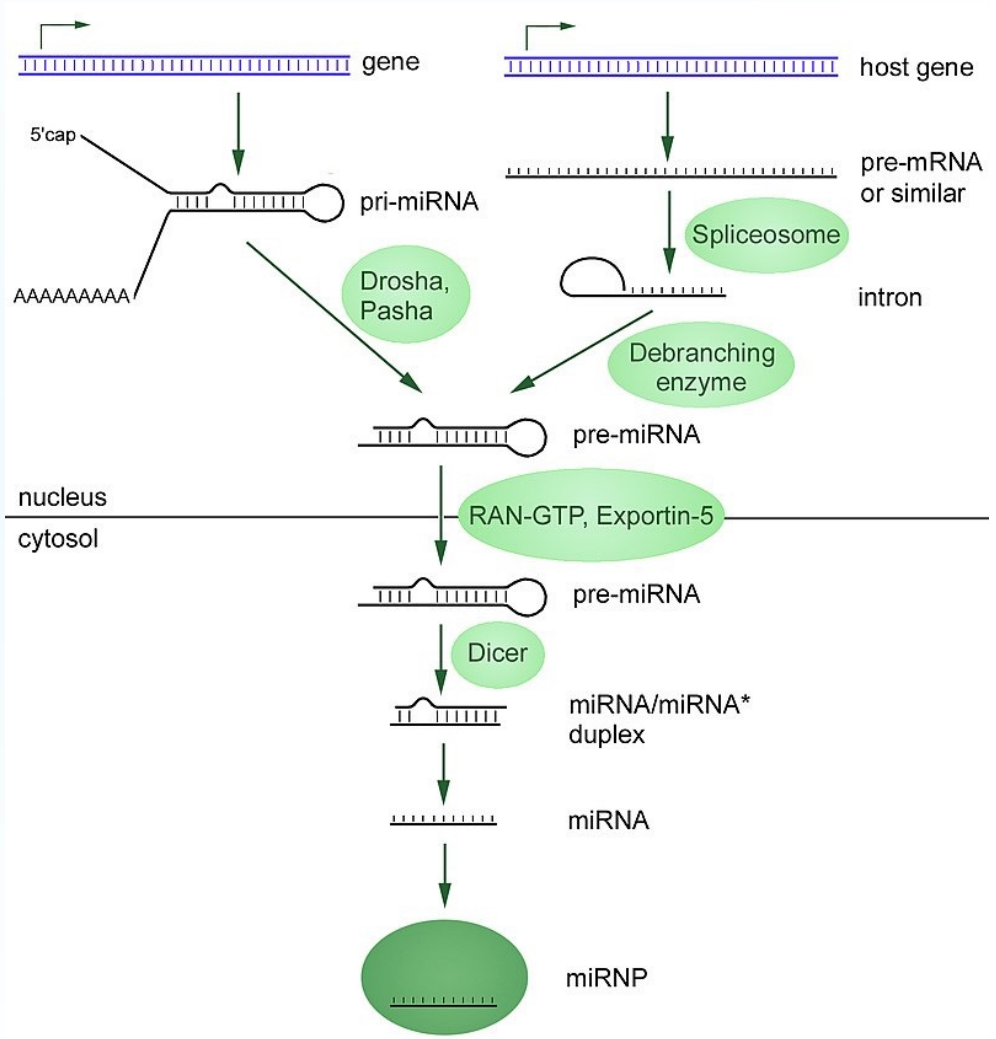
ceRNA网络


A
B
PPP2R1A
BIRC5
CCNB1
OIP5
RAD51
CDK1
CCNA2
RACGAP1
KIF23
CHEK1
C
hsa-miR-23c
hsa-miR-592
hsa-miR-29a-3p
hsa-miR-590-3p
hsa-miR-424-5p
hsa-miR-15a-5p
hsa-miR-497-5p

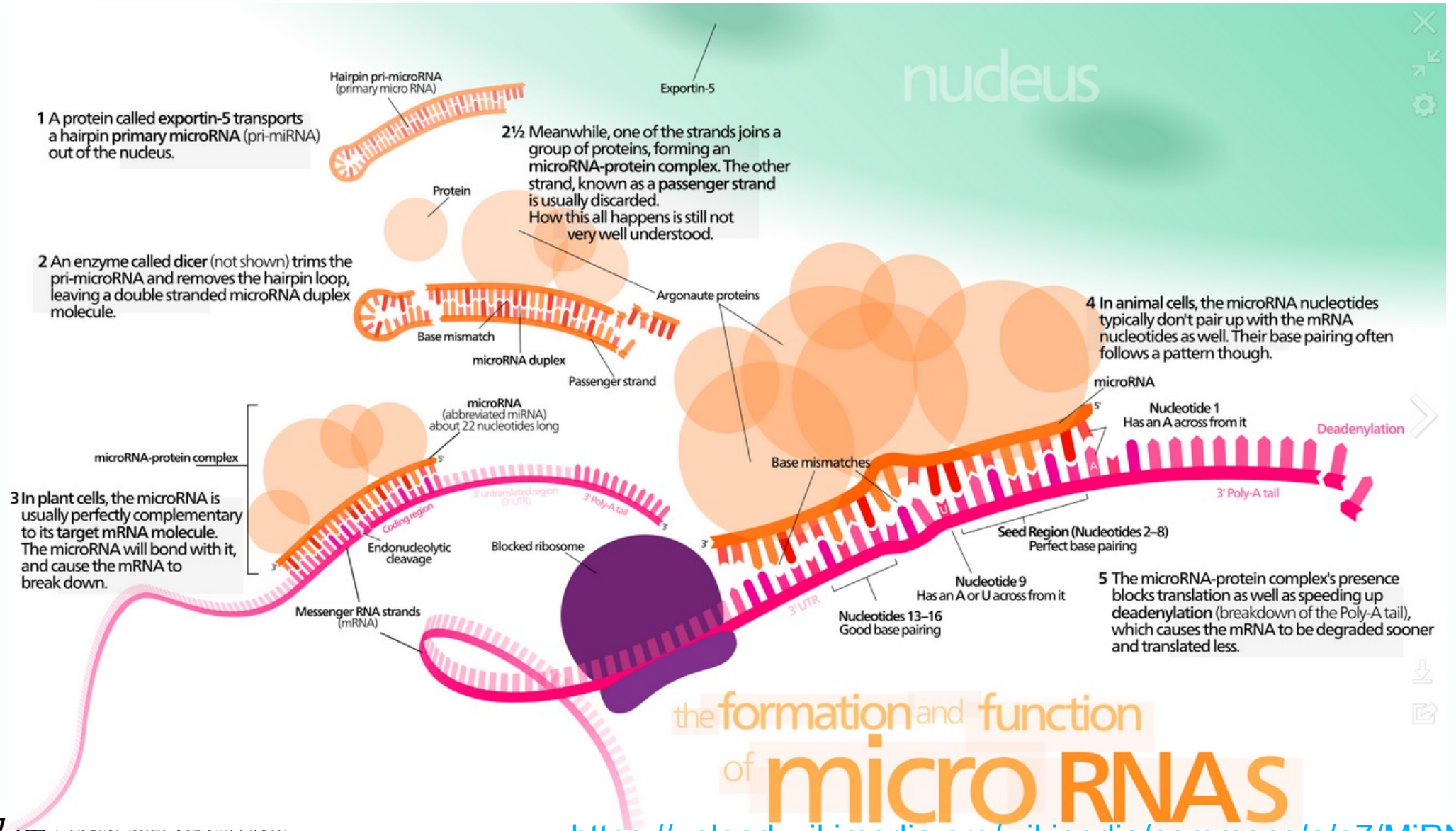
miRNA的产生

- 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.



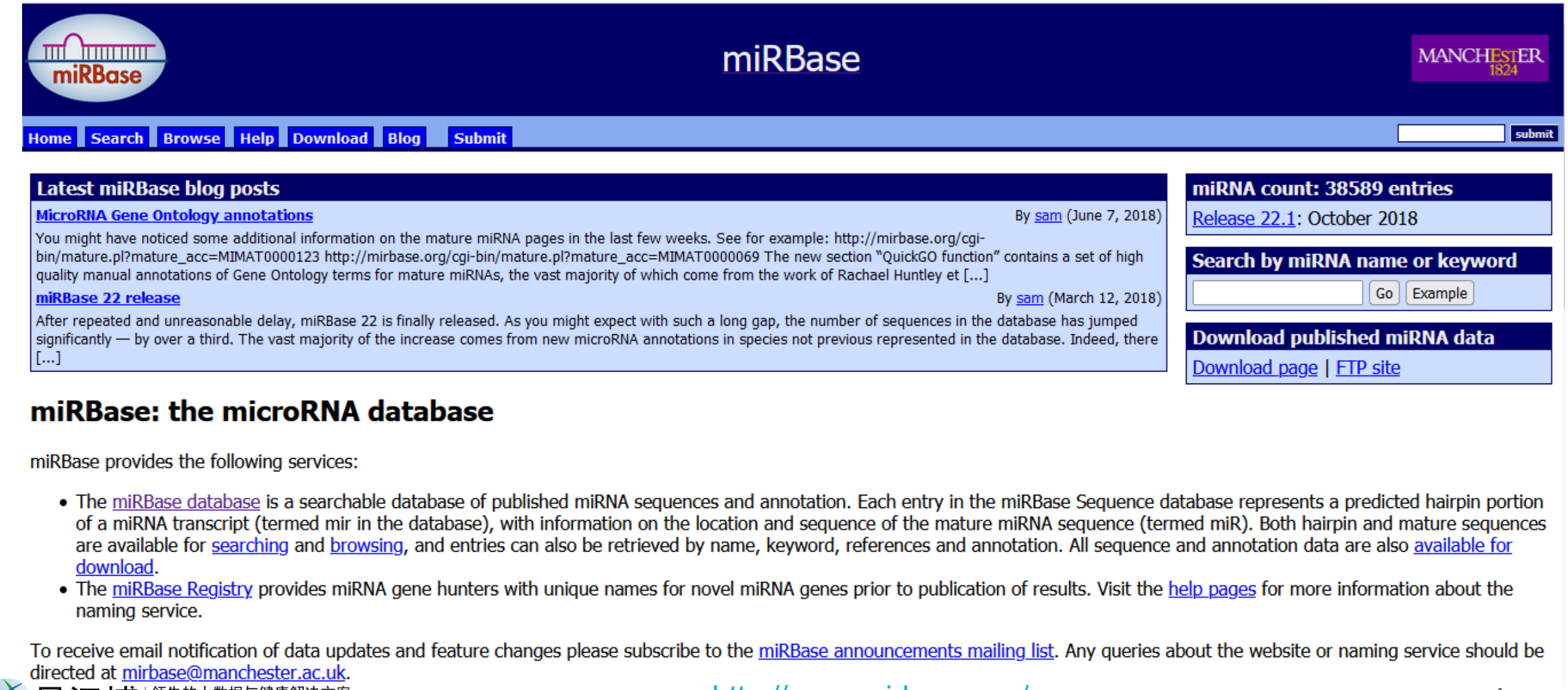
https://en.wikipedia.org/wiki/MicroRNA#Nomenclature

miRNA的生成和功能



https://upload.wikimedia.org/wikipedia/commons/a/a7/MiRNA.svg

miRBase：最全miRNA数据库



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.

miRNA count: 38589 entries

Release 22.1

Search by miRNA name or keyword

Go Example

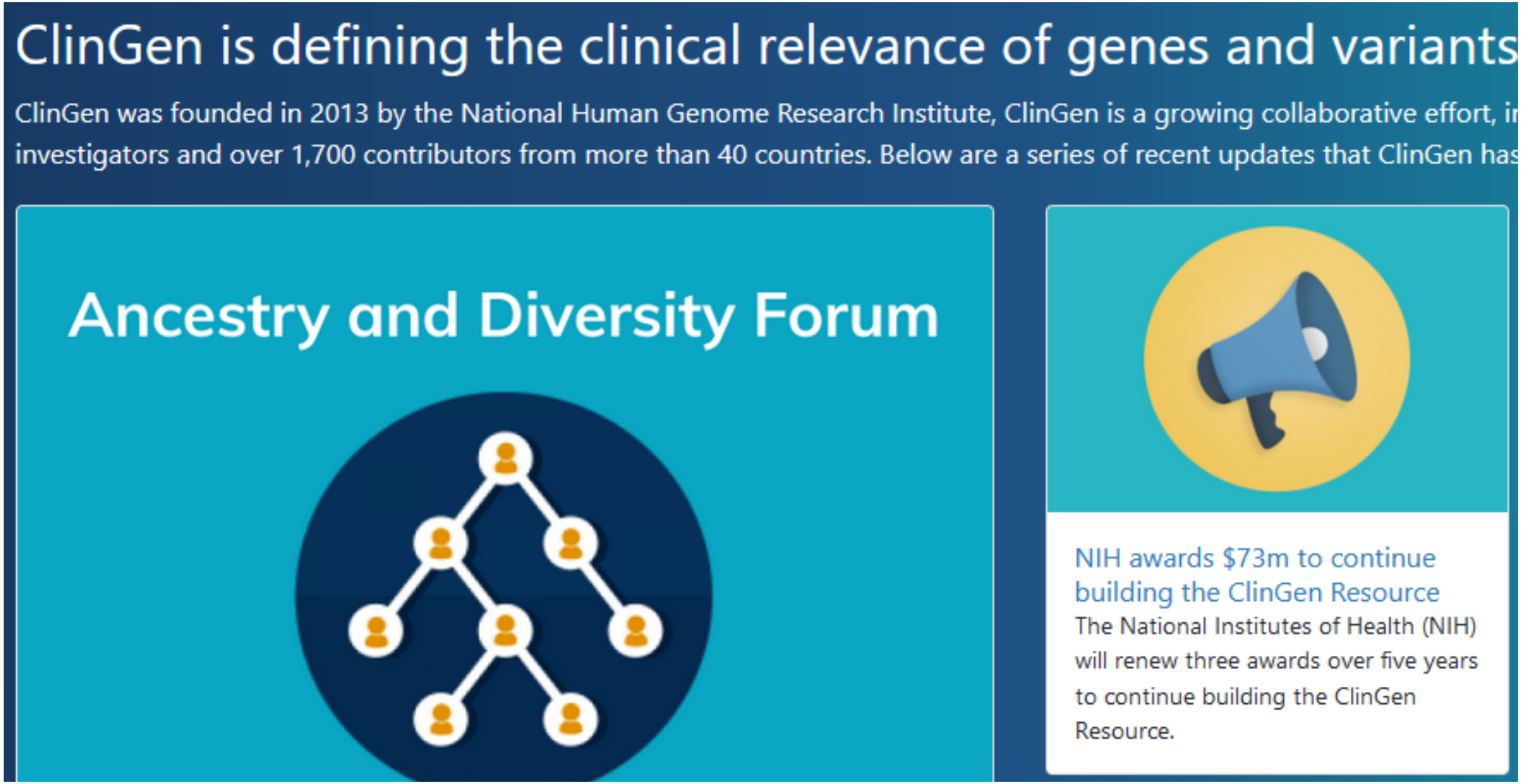
Download published miRNA data

Download page

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.

数据库的维护需要钱，很多钱



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：植物miRNA分析平台

psRobot: Plant Small RNA Analysis Toolbox

Home | Stem-loop Small RNA Prediction | Small RNA Target Predi

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

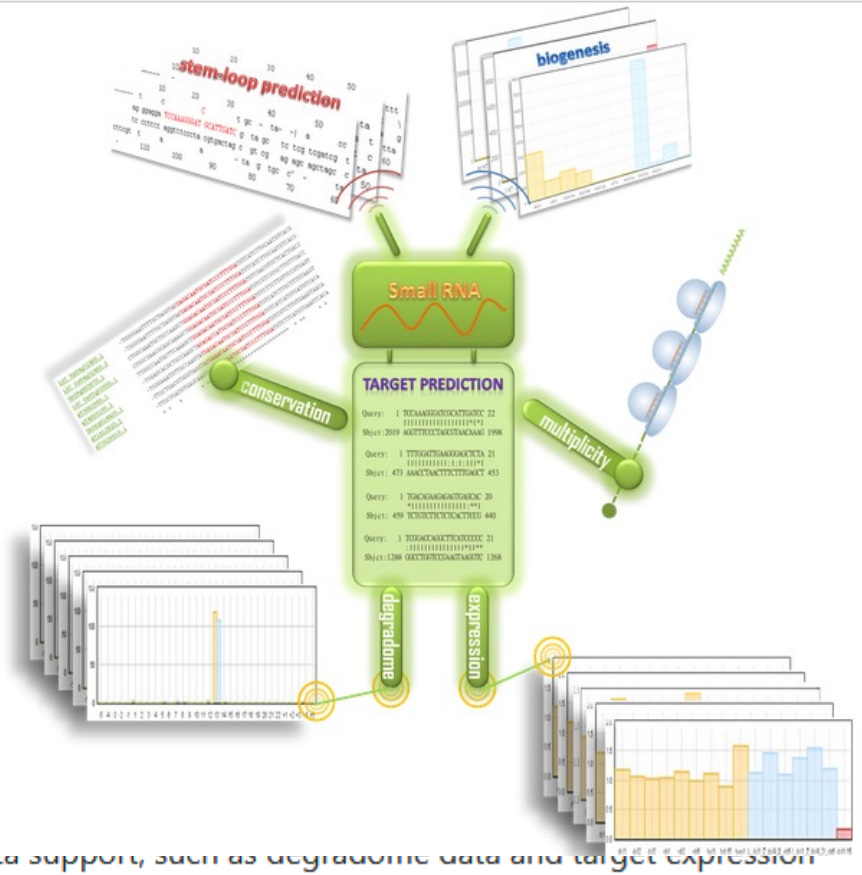
PsRobot is designed to analyz

The online version of psRobot

The stem-loop small RNA pre
smRNAs, including their expre
smRNA associated protein co
functional processes, their ge

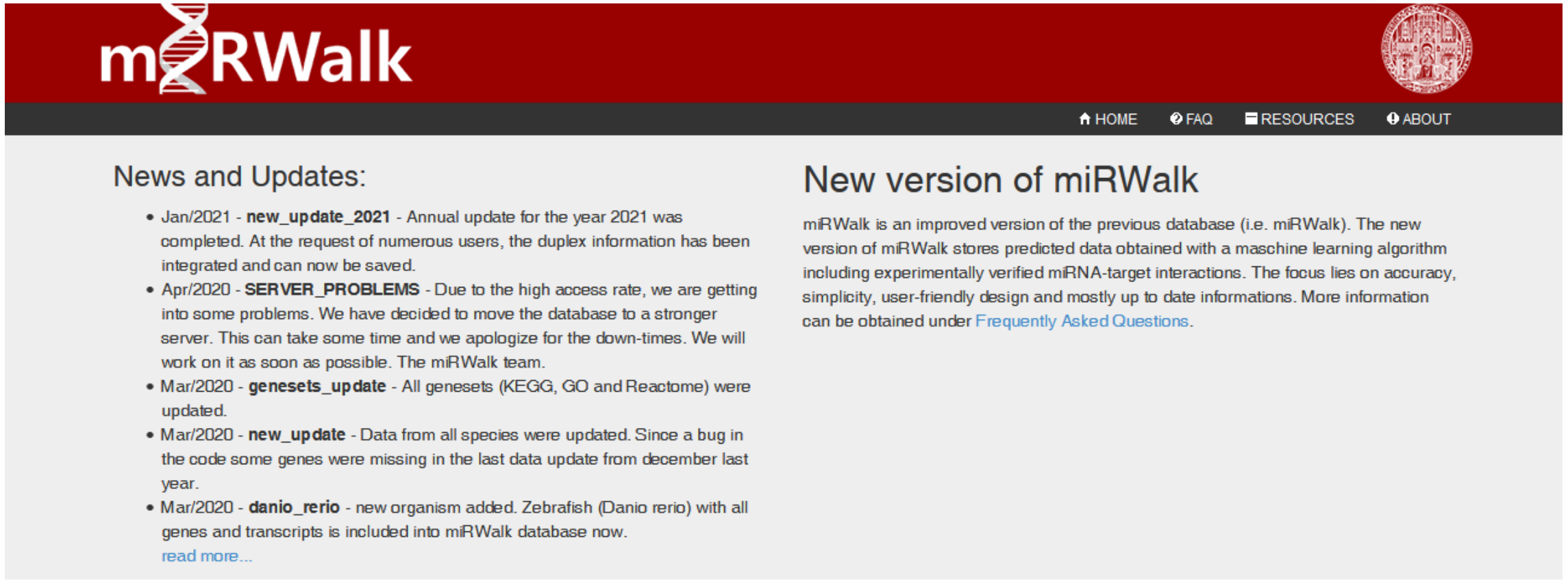
The second module, small RN
prediction results of smRNAs,
conservation and biological data support, such as degradome data and target expression
data in small RNA biogenesis mutants.

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



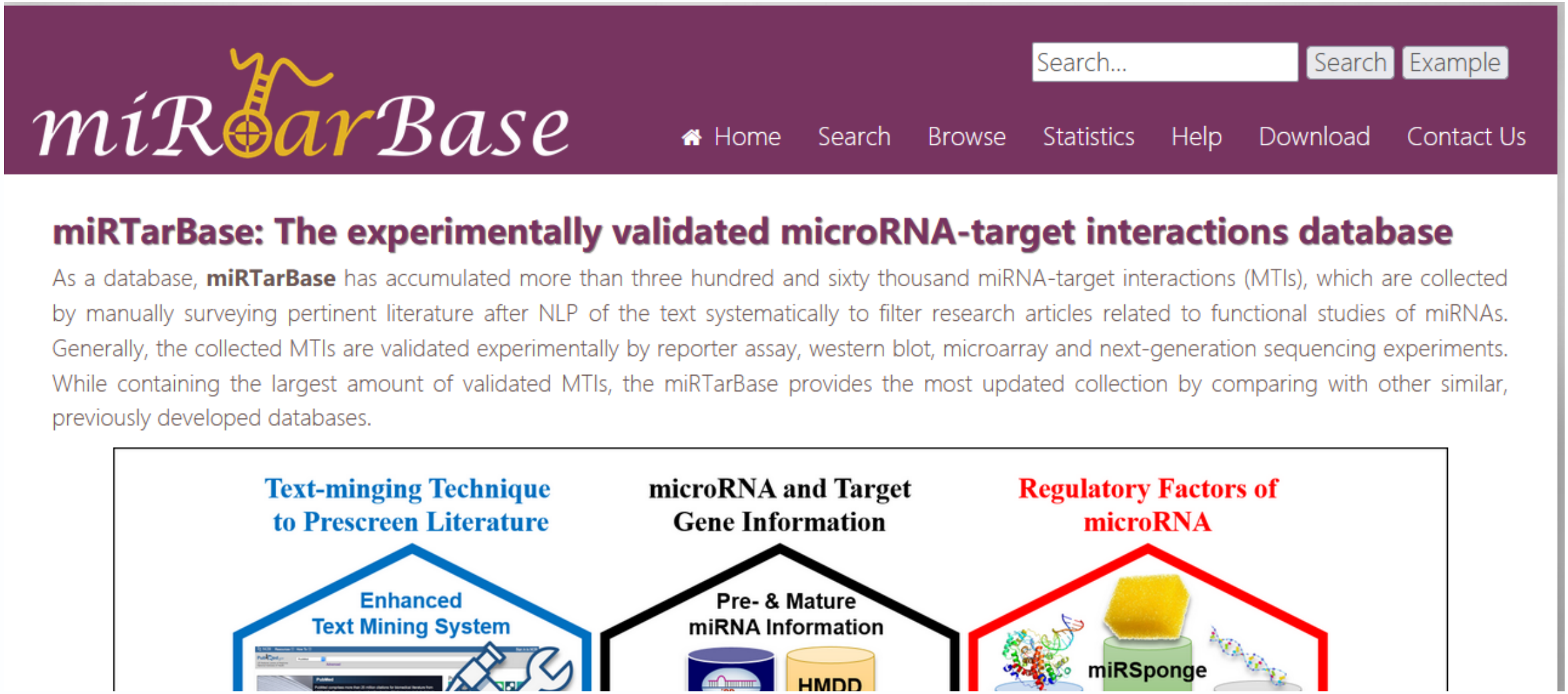
http://omicslab.genetics.ac.cn/psRobot/

miRNA靶点数据库



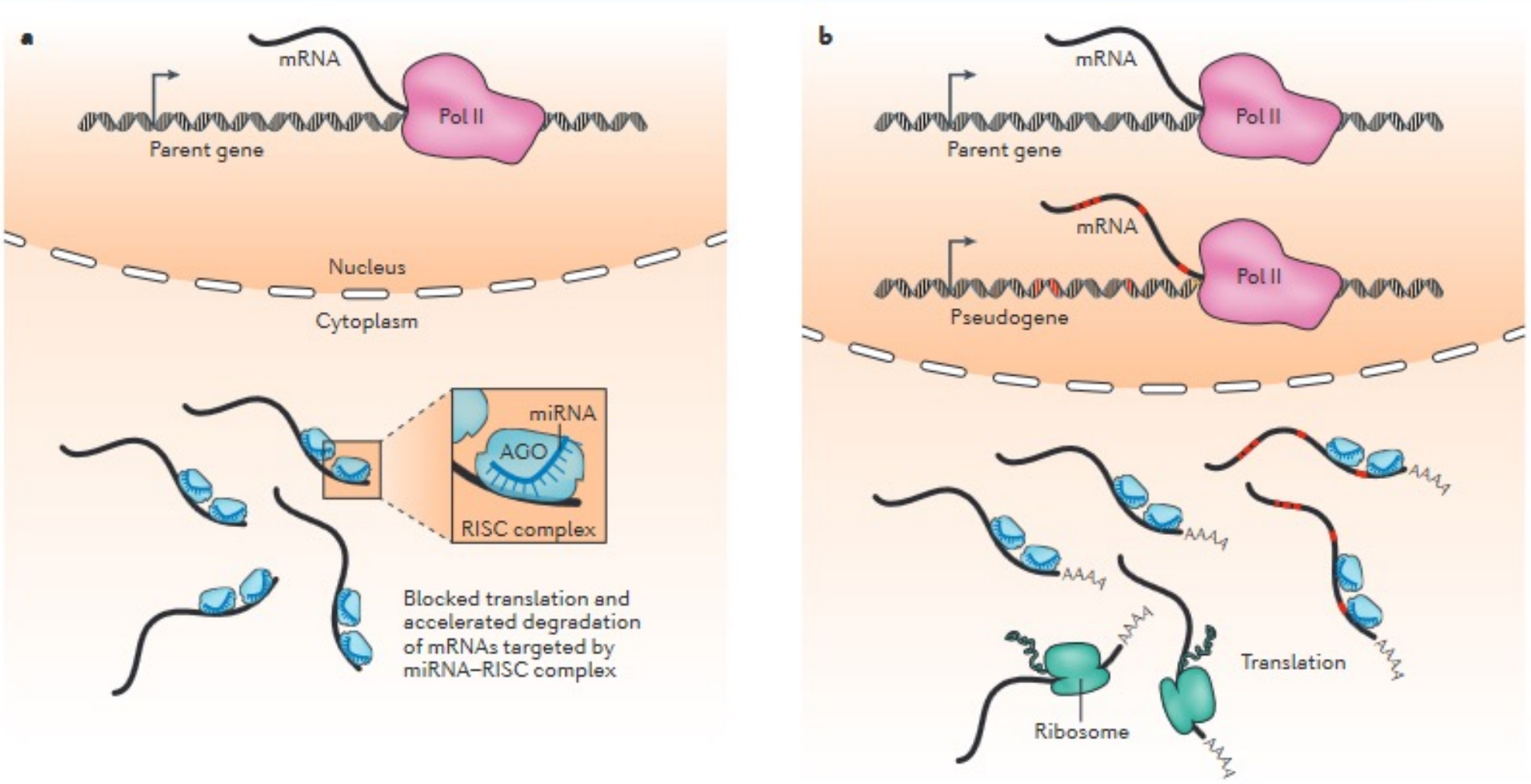
http://mirwalk.umm.uni-heidelberg.de/resources/

实验验证的miRNA-靶点数据库



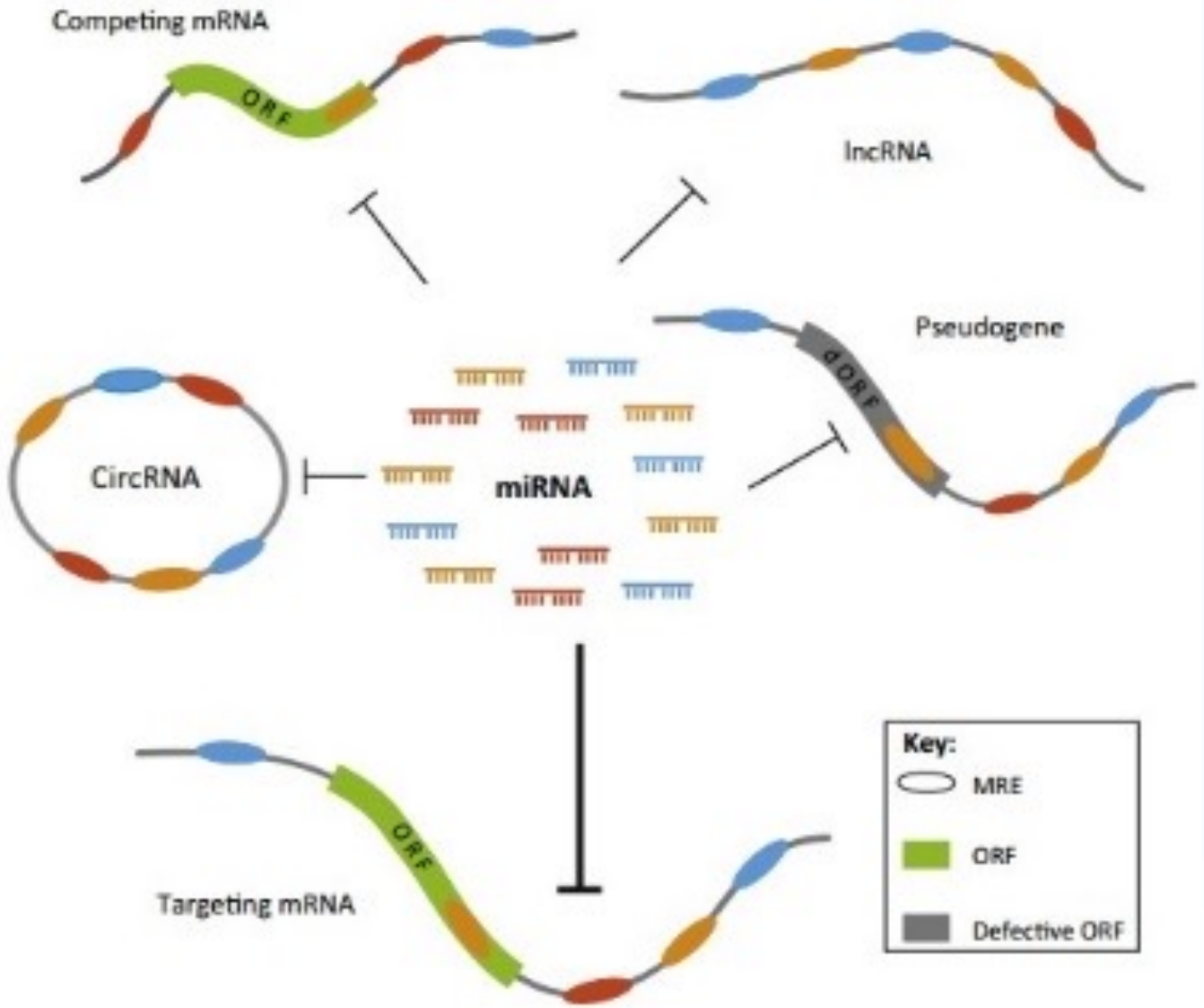
https://mirtarbase.cuhk.edu.cn/~miRTarBase/miRTarBase_2019/php/index.php

ceRNA竞争机制

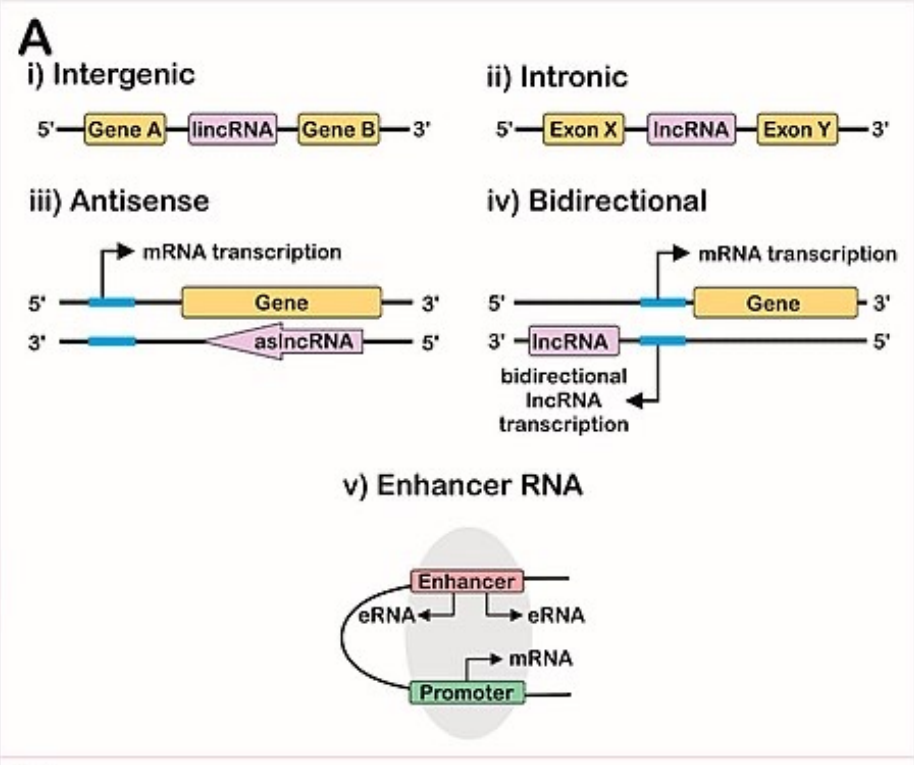


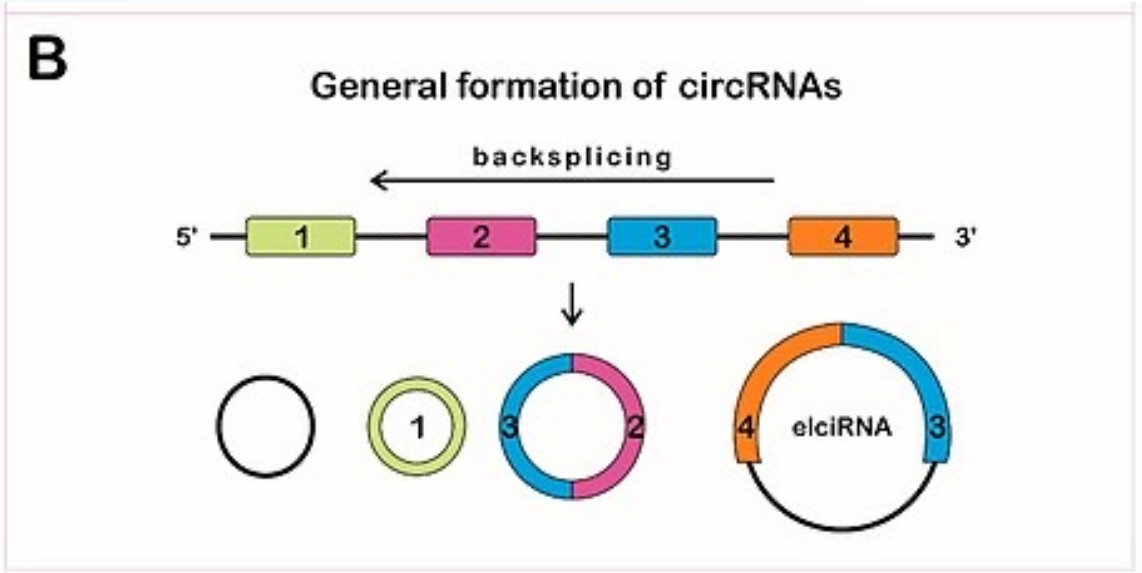
https://www.nature.com/articles/nrg.2016.20

Sponge可以有很多种

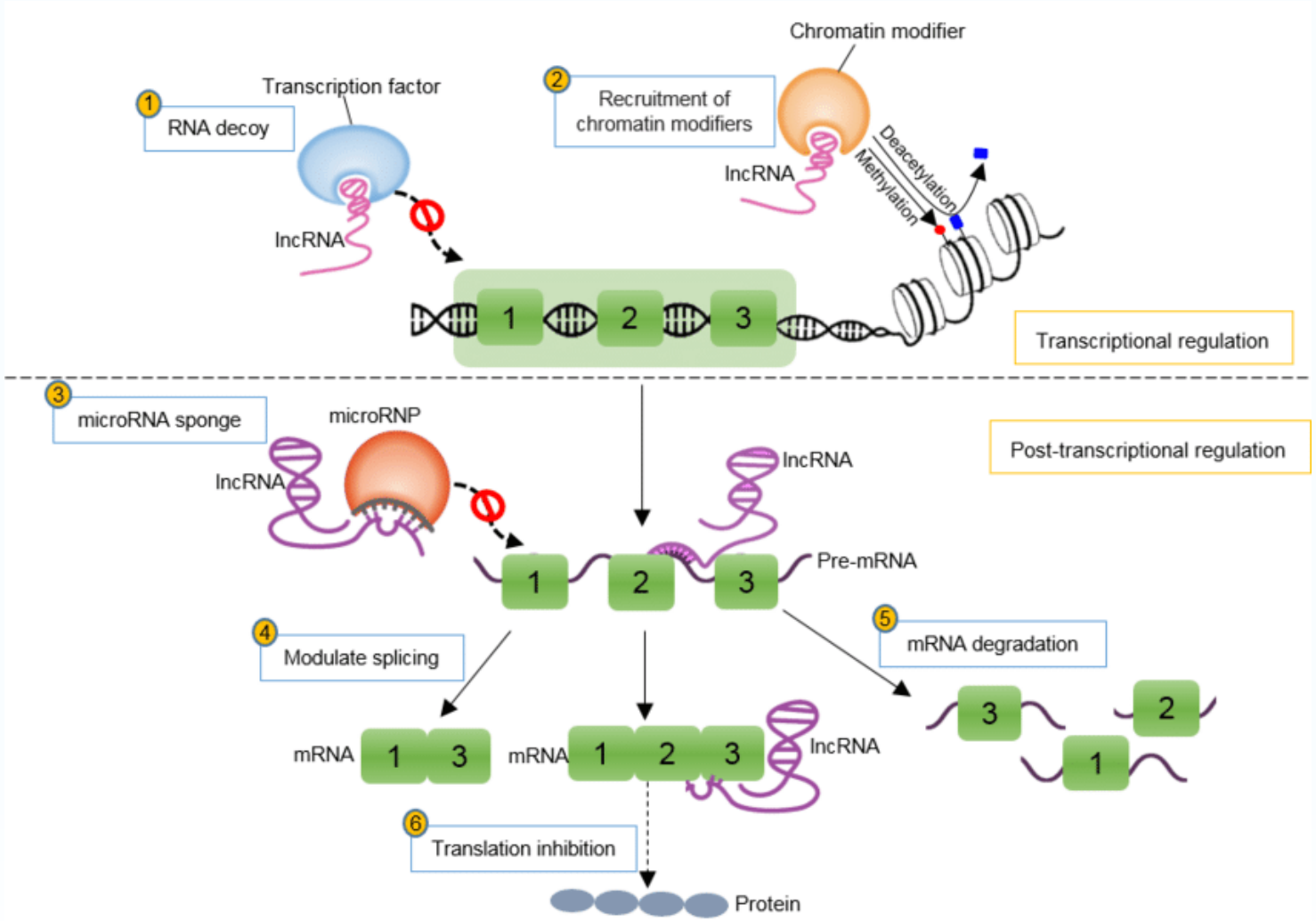


不同类型RNA的产生方式





lncRNA的作用模式



https://www.researchgate.net/publication/316286339

lncRNA预测工具 – CPC2

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

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.

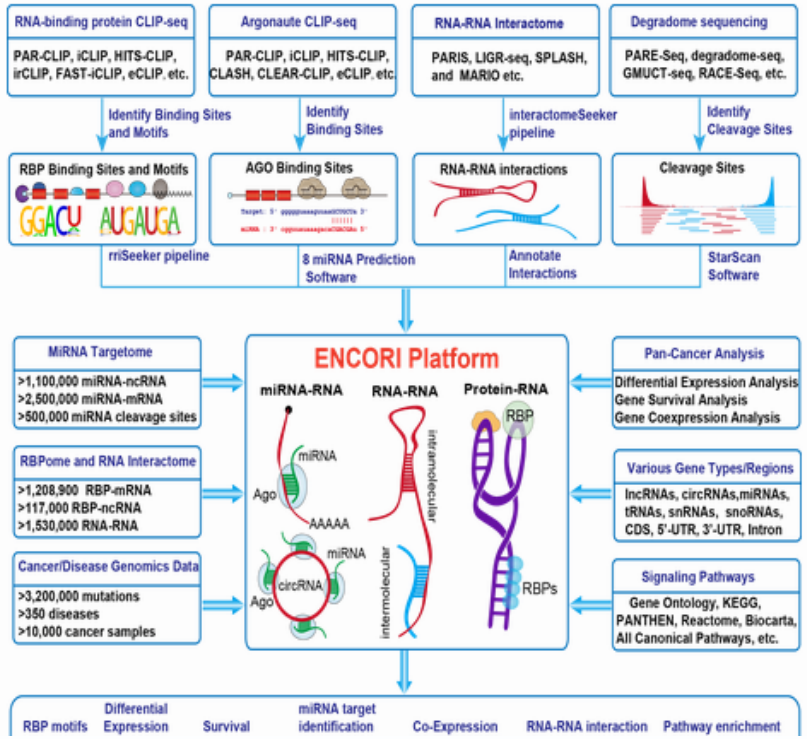
Choose a FASTA file (Max.: 50 MB or 50,000 sequences) Browse Submit

https://rnasamba.lge.ibi.unicamp.br/

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

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

Welcome to ENCORI!

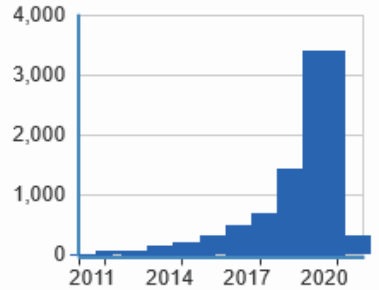


Previous version (starBase,Cite Our Paper) of ENCORI (The Encyclopedia of RNA Interactomes) is mainly focus on miRNA-target interactions. ENCORI is an open-source platform for studying the miRNA-ncRNA, miRNA-mRNA, ncRNA-RNA, RNA-RNA, RBP-ncRNA and RBP-mRNA interactions from CLIP-seq, degradome-seq and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

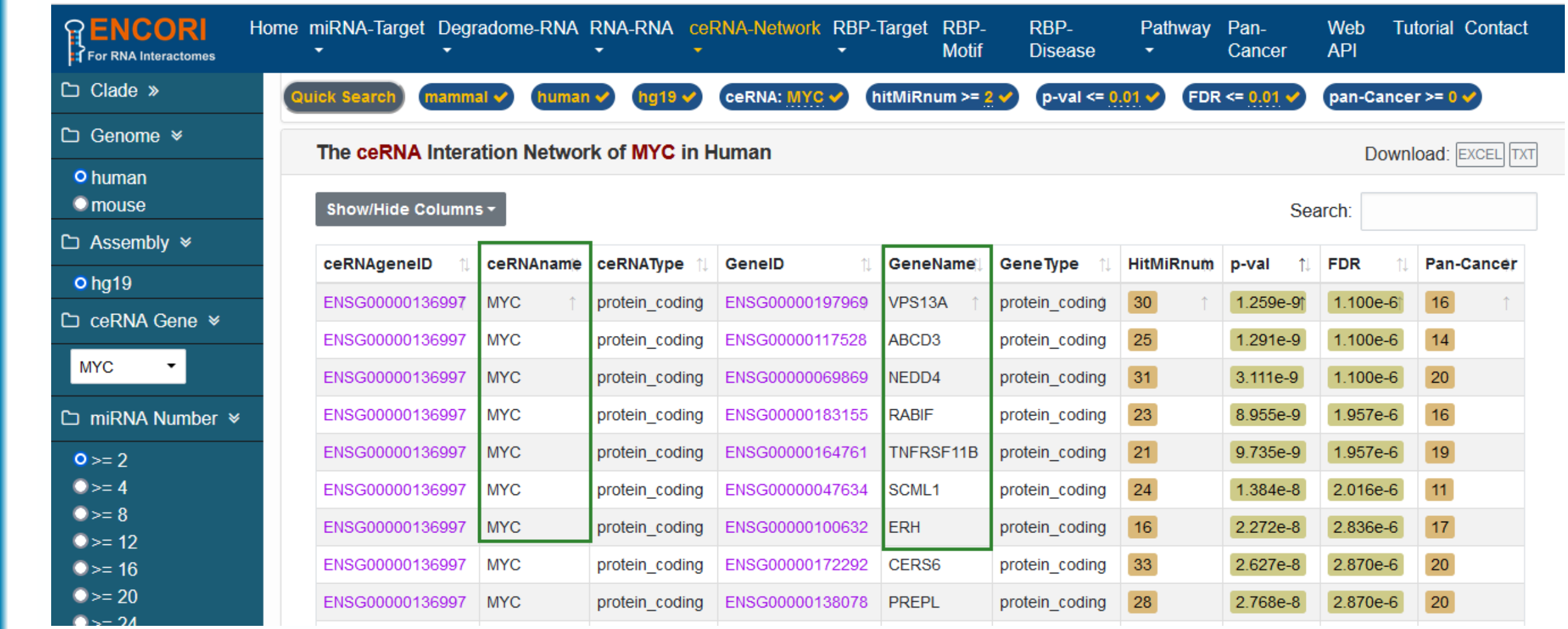


- **Average Daily Usage:** ~5000 visits from ~500 unique researchers
- **Average Annual Usage:** >1,000,000 visits from >100 countries

Statistics of ENCORI

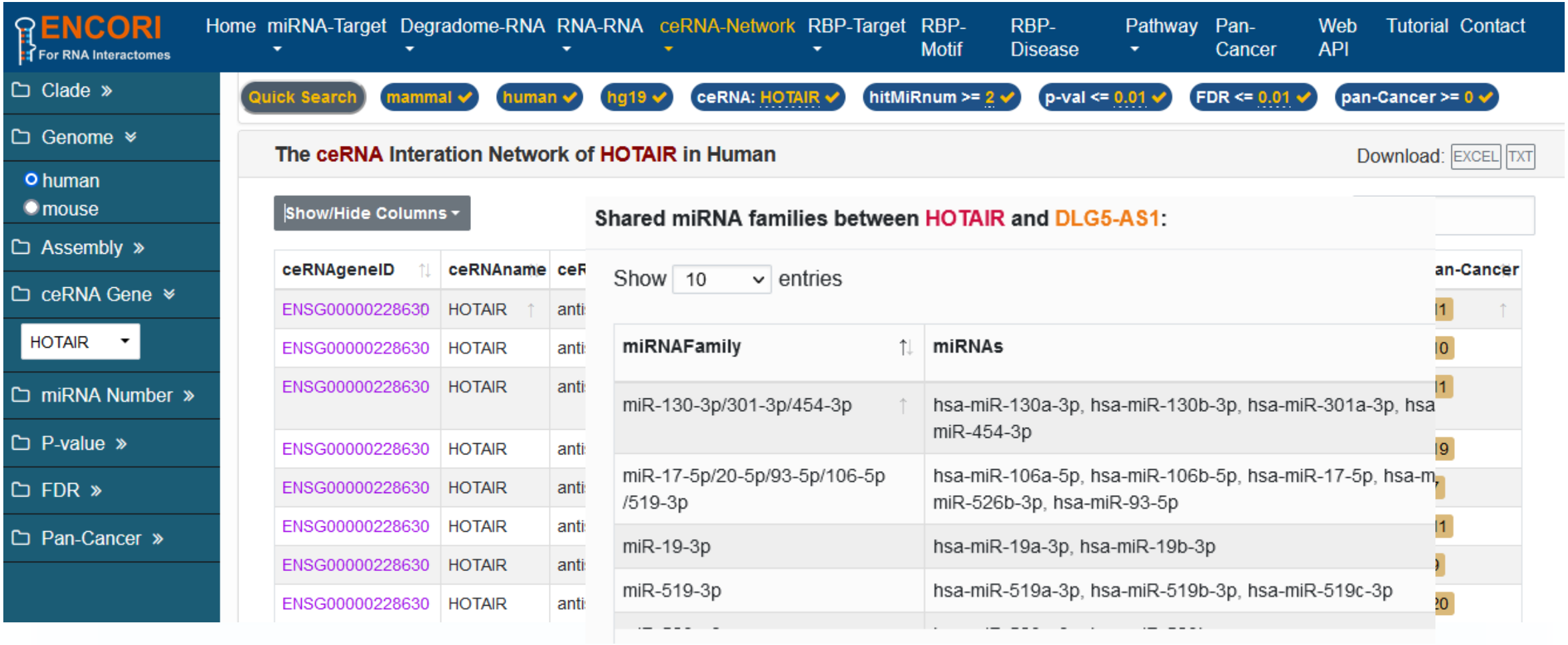
- **Species:** 23 Species

Gene-gene的ceRNA关系

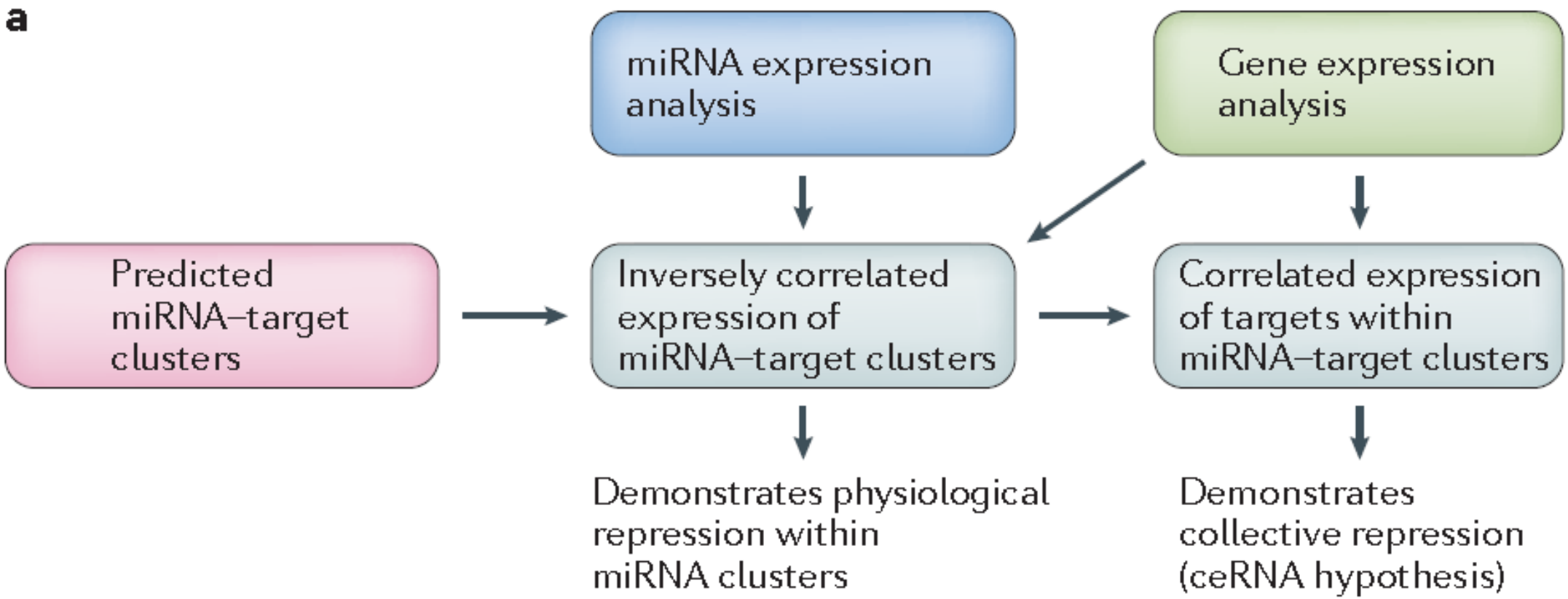


ceRNAgeneID	ceRNAname	ceRNAType	GeneID	GeneName	GeneType	HitMiRnum	p-val	FDR	Pan-Cancer
ENSG00000136997	MYC	protein_coding	ENSG00000197969	VPS13A	protein_coding	30	1.259e-9	1.100e-6	16
ENSG00000136997	MYC	protein_coding	ENSG00000117528	ABCD3	protein_coding	25	1.291e-9	1.100e-6	14
ENSG00000136997	MYC	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

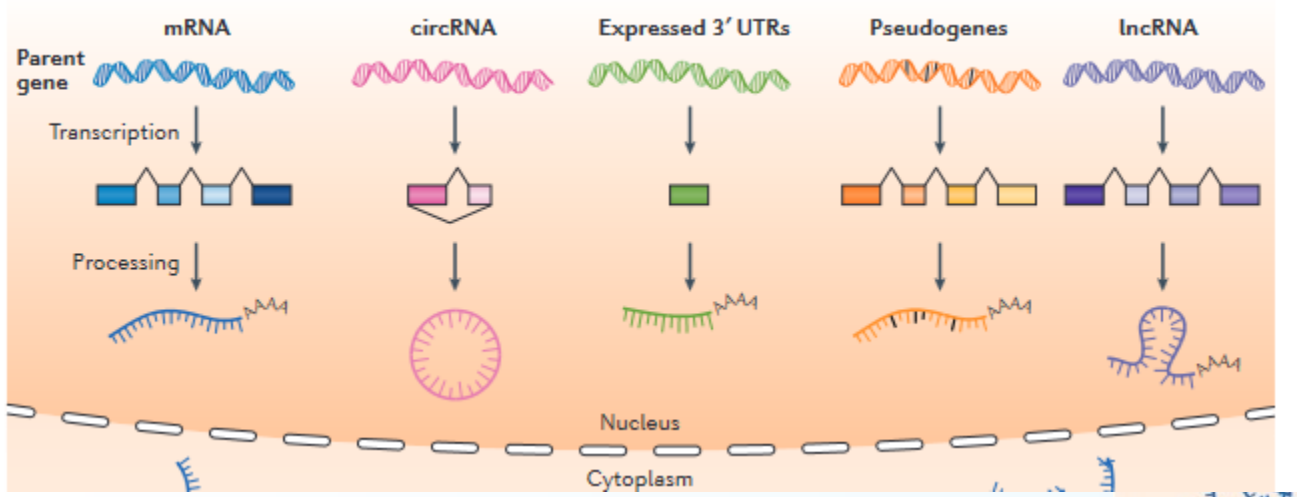
lncRNA-gene直接的ceRNA关系

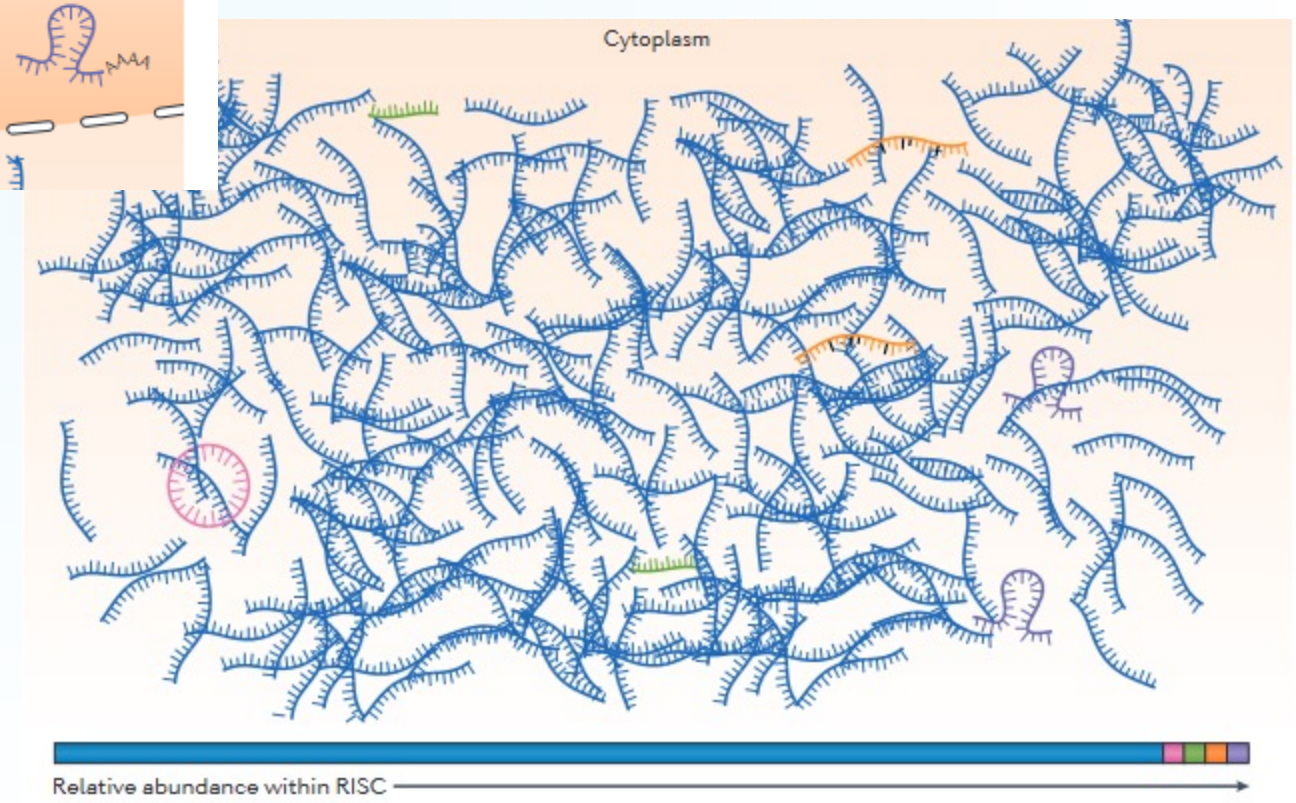


ceRNA的计算思路


a
miRNA expression analysis
Gene expression analysis
Predicted miRNA–target clusters
Inversely correlated expression of miRNA–target clusters
Correlated expression of targets within miRNA–target clusters
Demonstrates physiological repression within miRNA clusters
Demonstrates collective repression (ceRNA hypothesis)

内源性的sponge是否有足够的量发挥这个作用

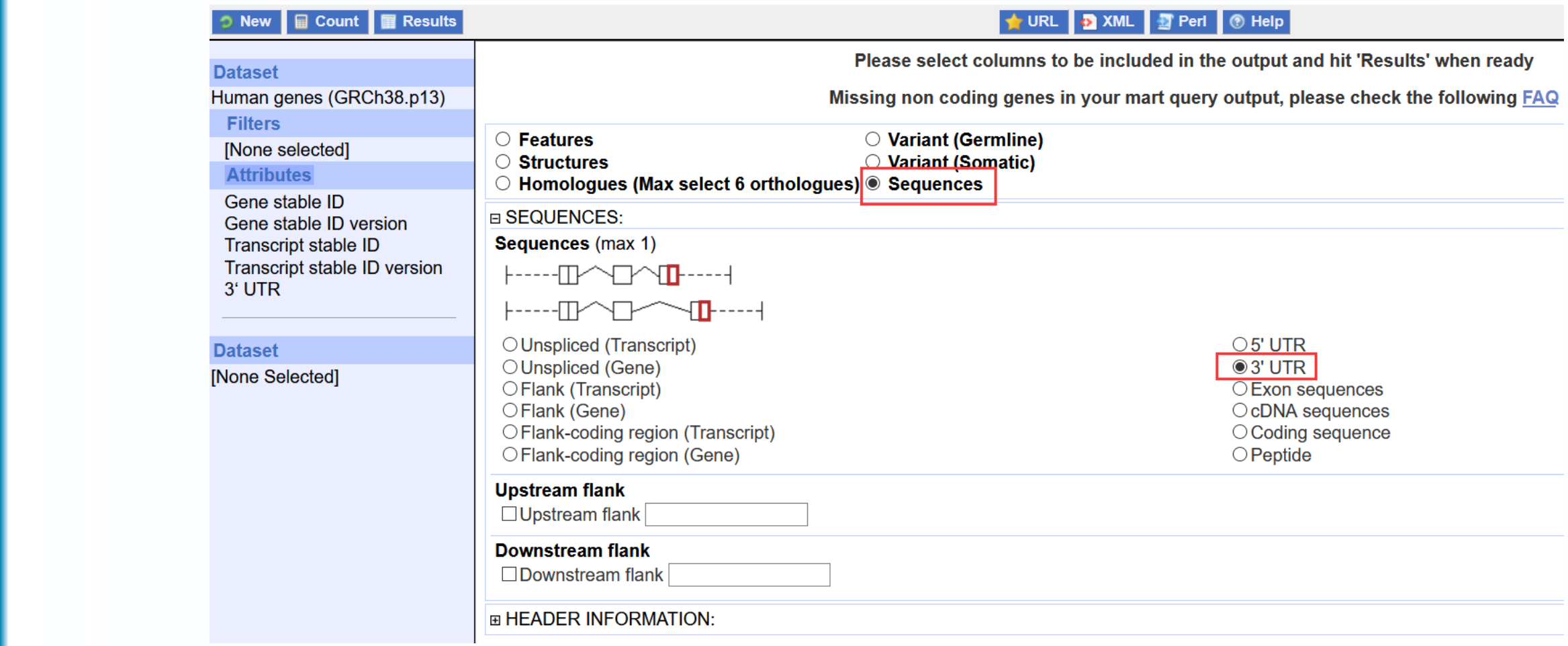




https://www.nature.com/articles/nrg.2016.20

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

如何获得3’UTR的序列 - ensembl biomart



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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