

microRNA靶基因的预测

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所用软件和网站:

1、 psRNATarget

(<http://plantgrn.noble.org/psRNATarget/?dowhat=Citation>)

2、 blastx

(<http://blast.ncbi.nlm.nih.gov/Blast.cgi>)

3、 KEGG (Kyoto Encyclopedia of Genes and Genomes)

(http://www.genome.jp/kegg/tool/color_pathway.html)

To cite psRNATarget, please check out from [here](#).

Location: Citation

To Reference psRNATarget, Please Cite:

Xinbin Dai and Patrick X. Zhao, psRNATarget: A Plant Small RNA Target Analysis Server, *Nucleic Acids Research*, 2011, doi: 10.1093/nar/GKR319. ([Link](#)).

List of Papers Citing the psRNATarget Server(as of February 2011 per [Google Scholar](#)):

1. Ruan,M., Zhao,Y., Meng,Z., Wang,X., Yang,W. (2009) Conserved miRNA analysis in *Gossypium hirsutum* through small RNA sequencing. *Genomics*, 94:263-268.
2. Naqvi,A.R., Choudhury,N.R., Mukherjee,S.K., Haq,Q.M. (2011) *In silico* analysis reveals that several tomato microRNA/microRNA* sequences exhibit propensity to bind to tomato leaf curl virus (ToLCV) associated genomes and most of their encoded open reading frames (ORFs). *Plant Physiol Biochem*, 49:13-17.
3. Zhang,Z., Yu,J., Li,D., Zhang,Z., Liu,F., Zhou,X., Wang,T., Ling,Y., Su,Z. (2010) PMRD: plant microRNA database. *Nucleic Acids Res.*, 38:806-813.
4. Trap-Gentil MV, Hébrard C, Lafon-Placette C, Delaunay A, Hagège D, Joseph C, Brignolas F, Lefebvre M, Barnes S, Maury S. (2011) Time course and amplitude of DNA methylation in the shoot apical meristem are critical points for bolting induction in sugar beet and bolting tolerance between genotypes. *J Exp Bot* 62. 2011 Jan 12. doi:

To cite psRNATarget, please check out from [here](#).

Location: Analysis

User-submitted small RNAs / preloaded transcripts

Preloaded small RNAs / user-submitted transcripts

User-submitted small RNAs / user-submitted transcripts

Upload small RNA sequence(s) in FASTA format:

[\[Load demo data\]](#)



浏览...

or paste sequences below:

```
UCGCUUGGUGCAGGUCGGGAC
```

UCGCUUGGUGCAGGUCGGGAC

- file / input sequence size limit: 20M.

- invalid small RNAs will be ignored during analysis. 

Select a preloaded transcript/genomic library for target search:

- Solanum lycopersicum (tomato) DFCI Gene Index Release 13
- Solanum melongena (Eggplant) DFCI Gene Index (SOMEGI) Release 1
- Solanum tuberosum (potato) DFCI Gene Index (STGI) Release 13**
- Solanum tuberosum Group Phureja DM1-3 516R44 (CIP801092) Genome 3.4 transcripts, potatogenomics.plantbiology.msu.edu/data/PGSC_DM_.....
- Sorghum_bicolor (Sorghum) DFCI Gene Index (SBGI) Release 9
- Striga_hermonthica (Purple_witchweed) DFCI (SHGI) Release 1
- Thellungiella_halophila ESTContig on PlantGDB, Thellungiella_halophila.mRNA.PUT.fasta, Jan-16-2009
- Theobroma_cacao (Cocoa) DFCI Gene Index (TCAGI) Release 3
- Triphysaria DFCI Gene Index (TRIPHGI) Release 1
- Triphysaria_versicolor DFCI Gene Index (TVERGI) Release 2

- Request to add / update a transcript library.

Maximum expectation (* Prefer lower false positive prediction rate? Please set a

>PGSC0003DMT400079716

CGATTTTCTCTCTACAAATCACAGTCTTCACCCCTCACTCGTTTTCTCTCTATCTCTCTTAGTACTTTTTCTGCCCTTTTTTTTTATTTTCTGTGTACGTTTTGGGTGCTGTGG

blastx

Choose a BLAST program to run.

[nucleotide blast](#)

Search a **nucleotide** database using a **nucleotide** query
Algorithms: blastn, megablast, discontinuous megablast

[protein blast](#)

Search **protein** database using a **protein** query
Algorithms: blastp, psi-blast, phi-blast, delta-blast

[blastx](#)

Search **protein** database using a **translated nucleotide** query

[tblastn](#)

Search **translated nucleotide** database using a **protein** query

[tblastx](#)

Search **translated nucleotide** database using a **translated nucleotide** query

[search pages.](#)

So you have made a few BLAST searches and after adjusting the database, organism limits and maybe a few Algorithm Parameters you arrive at what you think is a good search strategy.

 [More tips...](#)

Specialized BLAST

Choose a type of specialized search (or database name in parentheses.)

- Make specific primers with [Primer-BLAST](#)
- Search [trace archives](#)
- Find [conserved domains](#) in your sequence (cds)



Translated BLAST: blastx

[blastn](#) [blastp](#) **[blastx](#)** [tblastn](#) [tblastx](#)

BLASTX search protein databases using a translated nucleotide query. [more...](#)

[Reset page](#) [Bookmark](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

[Clear](#)

Query subrange

```
CAAGGAGGGCGTTGAAGTTGGAGGATCGTCGTCGTTTGACCAAGATAGAGAGGCCAAGGTTGTCACG
CCCCGAAGCTACCCCCAGGGCGTAAACATGAGACCTAAGATCACGAGTGACCCCAAGCTAACCCCTCA
GCTGGCATATCATAGCATACTAGACAAATTGAAATGAGAAATACTGTGCAGAAGCTTAAACATGAT
GTAAACTAAAAT
```

From

To

Or, upload file

浏览...

Genetic code

Standard (1)

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Job Title

Enter a descriptive title for your BLAST search 

Align two or more sequences 

Choose Search Set

Database

Non-redundant protein sequences (nr) 

Organism

potato

Exclude 

Optional

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. 

Exclude

Models (XM/XP) Uncultured/environmental sample sequences

Optional

Entrez Query

Optional

Enter an Entrez query to limit search 

BLAST

Search database Non-redundant protein sequences (nr) using Blastx (search protein databases using a translated nucleotide query)

Show results in a new window

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Ma ide
Q43644.1	RecName: Full=NADH dehydrogenase [ubiquinone] iron-sulfur protein	25.4	25.4	11%	4.7	39%

Alignments

Select All [Get selected sequences](#)

> [sp|Q43644.1|NDUS1_SOLTU](#) RecName: Full=NADH dehydrogenase [ubiquinone] iron-sulfur protein
1, mitochondrial; AltName: Full=76 kDa mitochondrial complex
I subunit; AltName: Full=Complex I-76kD; Short=CI-76kD;
AltName: Full=NADH-ubiquinone oxidoreductase 76 kDa subunit;
Flags: Precursor
[emb|CAA59818.1|](#) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]
Length=738

Score = 25.4 bits (54), Expect = 4.7, Method: Compositional matrix adjust.
Identities = 13/33 (39%), Positives = 20/33 (61%), Gaps = 0/33 (0%)
Frame = +3

Query 315 I.LD.I.TP.SE.A.I.T.S.H.P.P.S.T.T.E.S.S.D.D.E.I.G.D.E.A.I.D.V.T 413

KEGG



KEGG Mapper – Search&Color Pathway

KEGG Mapper

Search Pathway
Search&Color Pathway
Color Pathway

Search Brite
Search&Color Brite
Join Brite

Search Module

Search against: Homo sapiens (human) 

Primary ID: KEGG identifiers (NCBI and UniProt IDs may be used for organism-specific pathways)

Enter objects one per line followed by bgcolor, fgcolor:

PPP3R1 blue

Examples:

(Reference pathway (KO))

K01803 red,blue

C00118 pink 

(Homo sapiens pathway)

7167 red,blue

C00118 pink

Alternatively, enter the file name containing the data:

If necessary, change default bgcolor:

Include aliases

Use uncolored diagrams

Display objects not found in the search

Search&Color Pathway is an advanced version of the KEGG pathway mapping tool, where given objects (genes, proteins, compounds, glycans, reactions, drugs, etc.) are searched against KEGG pathway maps and found objects are marked in any background and foreground colors (bgcolor and fgcolor). The objects in different types of [pathway maps](#) are specified by the following [KEGG identifiers](#) and aliases.

Prefix	Type	KEGG identifier	Alias
map	Reference pathway - metabolic	K/R/EC numbers, C/G/D numbers	KO alias

B CELL RECEPTOR SIGNALING PATHWAY

