

miRDB_McGuireSams_GradProjec-BIOL6860

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miRDB: miRNA binding site prediction software

<http://mirdb.org/>

miRDB is a great tool for predicting the binding sites of miRNAs in a transcript, and especially in the 3' UTR.

All that is needed for using this tool is a computer with WiFi.

1. Go to <http://mirdb.org/>

Select the desired function. On the home page, one can search for a specific miRNA or Gene Target

For this tutorial we will focus on “Custom Prediction”.

The screenshot shows the miRDB home page. On the left, there is a sidebar with links: Target Search, Target Expression, Target Ontology, Target Mining, Custom Prediction (which is highlighted in red), FuncMir Collection, Data Download, Statistics, Help | FAQ, Comments, and Citation | Policy. The main content area has a heading "Choose one of the following search options:" followed by two sections: "Search by miRNA name" (with a dropdown set to "Human" and a text input field) and "Search by gene target" (with a dropdown set to "Human" and a text input field). Below these sections is a detailed description of miRDB's purpose and features. At the bottom, there are "References:" and two citations. A note at the very bottom encourages users to contact the website via email.

[Click here](#) to contact us with questions or comments about this website.

The screenshot shows the "Custom Prediction" page of miRDB. The left sidebar remains the same as the home page. The main content area has a heading "miRDB provides additional web interface below for more flexible miRNA target search can also be performed for unconventional sites in the coding region". It is divided into two sections: 1) Target prediction with user-provided miRNA or gene target sequence and 2) Search for unconventional target sites in the coding region. Section 1 contains fields for "Species" (Human), "Submission type" (miRNA Sequence), and checkboxes for "Example miRNA submission" and "Example target mRNA submission". Section 2 contains two search boxes: "Search by miRNA name" (Human, Coding Region, Go, Clear) and "Search by gene target" (Human, Gene Symbol, Coding Region, Go, Clear). A note at the bottom explains the requirements for custom miRNA sequences.

[Click here](#) to contact us with questions or comments about this website.

2. For this tutorial, we will select 'Human' for Species and the 'Sample target mRNA sequence' as an example, which will auto-populate when selected. ### Importantly, if you input your own sequence from UCSC or anywhere else, use FASTA format. ### This software is forgiving of spaces and numbers input with the FASTA sequence, however, this program does not allow you to utilise the carat '> NM_0000 Sample' format at the beginning, so leave this out. ### Select 'Go' to initiate the prediction.

Target Search

Target Expression

Target Ontology

Target Mining

Custom Prediction

FuncMir Collection

Data Download

Statistics

Help | FAQ

Comments

Citation | Policy

miRDB provides additional web interface below for more flexible miRNA target search. You may search targets by providing your own sequence. In addition, target search can also be performed for unconventional sites in the coding region or 5'-UTR.

1) Target prediction with user-provided miRNA or gene target sequence

Species: Human **Submission type:** mRNA Target Sequence

Example miRNA submission Example target mRNA submission

```
GCCTCCCTCGCGGAAGCTTCAGGAGGGCACACCAAGCTGTCCCCACCTGCTGTGCACTTAGATG  
TTCAAGAGCGCTTCTTCACAGTGAAAGCTATGAGATAGCGACAATACTTGCTTCACGTATGACTCTC  
ATGCAAGCAAATACACAGTTCATGTTGAATCTGTGTTCTTCAGCCCCACTTTATGCCCTAACCT  
AGTTAAATGATATTGAAATTGTTGATGACCTCAGAACTGAAATTGATAATGAAAGTTGCAAGTTGATAGC  
CCGTGAAGTGCAAGATCTAAATTAACTCCGAATTGATTGGGGGAAATTAACAGTGAAGATGCCCTGGCT  
GAATATTGATAGAACCAATTGTGTCACATAAAACAGATGGCGCATATATATATGATAAAAAAAATATAAA  
AATGGAAGATGGTGTCTCTAGTAAAAAAAAAAAAAAAAAA
```

2) Search for unconventional target sites in the coding region or 5'-UTR

Search by miRNA name
Human Coding Region Go

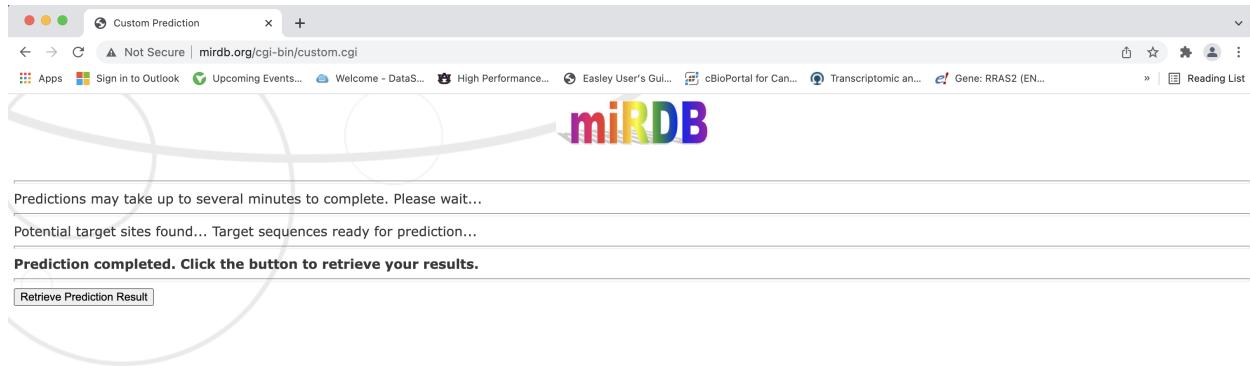
Search by gene target
Human Gene Symbol Coding Region Go

Custom miRNA sequences must be between 17 and 30 bases long; custom mRNA target sequences must be between 100 and 30,000 bases long. Please submit only one sequence at a time, consisting of A, T or U, C and G. Please note that all spaces, line breaks, and numbers within the submission will be removed, and multiple lines will be joined together to create a single sequence.

These options are provided for a database search for miRNA targets beyond the 3' UTR. Additional targets are accessible for the 5' UTR and the coding region.

[Click here](#) to contact us with questions or comments about this website.

3. When it is finished running, select 'Retrieve Prediction Results'



4. The output file will describe how many predicted miRNAs target the input region. ### THe predicted miRNAs will be ranked in order of Target Score. ### It is important to note that sometimes the outputs of similar sequences will vary a bit in the exact order of miRNAs listed for this reason--verify that the miRNA you compare is in both by examining the entire list—it may be in a different order and still be predicted to be present in the sequence.

Custom Prediction

Not Secure | mirdb.org/cgi-bin/custom.cgi

Apps Sign in to Outlook Upcoming Events... Reading List

miRDB

There are 33 predicted miRNAs targeting the submitted 484 nt long mRNA sequence.

[Return to Custom Prediction](#)

| Target Detail | Target Rank | Target Score | miRNA Name | Gene Symbol |
|---------------|-------------|--------------|-----------------------------------|-------------|
| Details | 1 | 89 | hsa-miR-5011-5p | submission |
| Details | 2 | 89 | hsa-miR-8485 | submission |
| Details | 3 | 86 | hsa-miR-589-3p | submission |
| Details | 4 | 82 | hsa-miR-3529-3p | submission |
| Details | 5 | 81 | hsa-miR-190a-3p | submission |
| Details | 6 | 78 | hsa-miR-210-3p | submission |
| Details | 7 | 77 | hsa-miR-4795-3p | submission |
| Details | 8 | 74 | hsa-miR-4327 | submission |
| Details | 9 | 71 | hsa-miR-892c-5p | submission |
| Details | 10 | 70 | hsa-miR-3679-3p | submission |
| Details | 11 | 70 | hsa-miR-506-5p | submission |
| Details | 12 | 69 | hsa-miR-182-3p | submission |
| Details | 13 | 68 | hsa-miR-4656 | submission |
| Details | 14 | 65 | hsa-miR-892a | submission |
| Details | 15 | 65 | hsa-miR-10523-5p | submission |
| Details | 16 | 59 | hsa-miR-6885-3p | submission |
| Details | 17 | 58 | hsa-miR-891b | submission |
| Details | 18 | 58 | hsa-miR-1587 | submission |
| Details | 19 | 57 | hsa-miR-659-3p | submission |
| Details | 20 | 56 | hsa-miR-4738-3p | submission |
| Details | 21 | 56 | hsa-miR-12119 | submission |
| Details | 22 | 56 | hsa-miR-98-3p | submission |
| Details | 23 | 56 | hsa-miR-4789-5p | submission |
| Details | 24 | 56 | hsa-miR-1185-2-3p | submission |
| Details | 25 | 56 | hsa-miR-1185-1-3p | submission |
| Details | 26 | 56 | hsa-let-7f-2-3p | submission |
| Details | 27 | 56 | hsa-let-7f-1-3p | submission |
| Details | 28 | 56 | hsa-let-7b-3p | submission |
| Details | 29 | 56 | hsa-let-7a-3p | submission |
| Details | 30 | 54 | hsa-miR-4277 | submission |
| Details | 31 | 52 | hsa-miR-3941 | submission |
| Details | 32 | 52 | hsa-miR-7162-3p | submission |
| Details | 33 | 50 | hsa-miR-4787-3p | submission |

. ### 5. One can click on a

desired miRNA for information regarding the specific site locations by clicking the red hyperlink hsa-miR-5011-5p, for example. ### The higher the target score, the more one can trust the prediction. Prediction scores over 80 are thought to be valid. ### This also gives the exact miRNA Sequence, the Seed Location(s) and the input Target Length. ### When analyzing two separate inputs, such as a Wild-type sequence vs. a Mutant sequence with an introduced variation, one can easily compare the number of seed locations found in one vs. the other by comparing these side-by-side.

The screenshot shows a web browser window with the miRDB logo at the top. Below it, the title "MicroRNA and Target Gene Description:" is displayed. A table provides the following details:

| miRNA Name | hsa-miR-5011-5p | miRNA Sequence | UUAUAUAUACAGCCAUGCACUC |
|---------------|---------------------------------|----------------|------------------------|
| Target Score | 89 | Seed Location | 410, 411, 413, 415 |
| Target Length | 484 | | |

Custom Target Sequence

```

1 gcccctccctc ggcgaagcct ccaggcaggcc acaccagctg tttcccaccc gctgtgcagt
 61 caccttagat gttcagaagc cgcttcctct ccactgaaga gctatgagat acgcacaata
 121 ctgtctgttc acgttatgac tctcatgcaa gcaaaataca cagtttcatt gttctgaatc
 181 ctgtggtttc ttccagccca cttttatcgc cttaacctag ttaatgtata ttttgaattg
 241 tgtgtatgac ctcagaactg aaattgataa tgaagttgca agttttgata gcccgtgaag
 301 tgcataagta tctaattta cctgaattga tttgggggaa aattaccagt agaatgcctt
 361 ggtctgaata tttgatagaa ccaattgttg tacataaaac agattgcgca tatatatata
 421 tgtataaaaa ataataaaaat aatggaagat gatggtgttc tctagtaaaa aaaaaaaaaa
 481 aaaa

```

6. Going back to the original Prediction output table, one can instead select the 'Details' button to the left of the miRNA of interest. ### This will display useful information regarding both the mature and precursor miRNAs, their sequences, genomic location, and validated and predicted targets. ### It is also helpful to read the References on literature in which the miRNA of interest has been investigated.

hsa-miR-5011-5p Page

Not Secure | mirdb.org/cgi-bin/mature_mir.cgi?name=hsa-miR-5011-5p

Apps Sign in to Outlook Upcoming Events... Welcome - DataS... High Performance... Reading List

Mature miRNA: hsa-miR-5011-5p

Mature miRNA

| | |
|--------------------------|-------------------------------------------------------|
| miRNA Name | hsa-miR-5011-5p |
| miRNA Sequence | 5' - uaauauauacagccaugcacuc - 3' (length = 21) |
| Predicted Targets | miRDB |
| Validated Targets | TarBase |
| miRBase ID | MIMAT0021045 |

Precursor miRNA

| | |
|---------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Precursor Name | hsa-mir-5011 |
| Genomic Location | chr18:67081584-67081686 (+); nearby genomic features |
| NCBI GENE ID | 100847002 |
| miRBase ID | MI0017879 |
| Precursor Sequence | <pre>--a u uau c c gu ga gg ugaguggaug ugu<u>uaauauauacagccaugcacu</u> ugu<u>a</u> u cu uc acuuaccuuu acaaauauauaugucgguacguga acau g cga u --u c c gg</pre> |

References

- Enhancing miRNA annotation confidence in miRBase by continuous cross dataset analysis. Hansen TB, Kjems J, Bramsen JB. *RNA Biol.* 2011 May-Jun;8(3):378-83.
- miRBase: microRNA sequences, targets and gene nomenclature. Griffiths-Jones S, Grocock RJ, van Dongen S, Bateman A, Enright AJ. *Nucleic Acids Res.* 2006 Jan 1;34(Database issue):D140-4.

7. From the ‘Details’ page above, one can click on ‘Predicted Targets’ to see the full list that the miRNA of interest may target. ### Again, these are ranked and given a Target Score to help select those that are

miRDB Search Result

Not Secure | mirdb.org/cgi-bin/search.cgi?searchType=miRNA&searchBox=hsa-mi...

Apps Sign in to Outlook Upcoming Events... Welcome - DataS... High Performance... »

miRDB

There are 2622 predicted targets for hsa-miR-5011-5p in miRDB.

| Target Detail | Target Rank | Target Score | miRNA Name | Gene Symbol | Gene Description |
|-------------------------|-------------|--------------|-----------------|--------------------------|----------------------------------------------------------------------------------------------------|
| Details | 1 | 100 | hsa-miR-5011-5p | SPSB1 | splA/ryanodine receptor domain and SOCS box containing 1 |
| Details | 2 | 100 | hsa-miR-5011-5p | SMAD2 | SMAD family member 2 |
| Details | 3 | 100 | hsa-miR-5011-5p | STARD13 | StAR related lipid transfer domain containing 13 |
| Details | 4 | 100 | hsa-miR-5011-5p | NMT1 | N-myristoyltransferase 1 |
| Details | 5 | 100 | hsa-miR-5011-5p | TTYH3 | tweety family member 3 |
| Details | 6 | 100 | hsa-miR-5011-5p | FIGN | fidgetin, microtubule severing factor |
| Details | 7 | 100 | hsa-miR-5011-5p | SCN11A | sodium voltage-gated channel alpha subunit 11 |
| Details | 8 | 100 | hsa-miR-5011-5p | GATA2B | GATA zinc finger domain containing 2B |
| Details | 9 | 100 | hsa-miR-5011-5p | RAPH1 | Ras association (RalGDS/AF-6) and pleckstrin homology domain containing 1 |
| Details | 10 | 100 | hsa-miR-5011-5p | NDUFB3 | NADH:ubiquinone oxidoreductase subunit B3 |
| Details | 11 | 100 | hsa-miR-5011-5p | HCN1 | hyperpolarization activated cyclic nucleotide gated potassium channel 1 |
| Details | 12 | 100 | hsa-miR-5011-5p | BAG1 | BCL2 associated athanogene 1 |
| Details | 13 | 100 | hsa-miR-5011-5p | PLAG1 | PLAG1 zinc finger |
| Details | 14 | 100 | hsa-miR-5011-5p | MARCH7 | membrane associated ring-CH-type finger 7 |
| Details | 15 | 100 | hsa-miR-5011-5p | HUWE1 | HECT, UBA and WWE domain containing 1, E3 ubiquitin ligase |
| Details | 16 | 100 | hsa-miR-5011-5p | ST8SIA2 | ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 2 |
| Details | 17 | 100 | hsa-miR-5011-5p | LZTS3 | leucine zipper tumor suppressor family member 3 |
| Details | 18 | 100 | hsa-miR-5011-5p | CACNA1G | calcium voltage-gated channel subunit alpha1 G |
| Details | 19 | 100 | hsa-miR-5011-5p | ENSA | endosulfine alpha |
| Details | 20 | 100 | hsa-miR-5011-5p | FAM19A1 | family with sequence similarity 19 member A1, C-C motif chemokine like |
| Details | 21 | 100 | hsa-miR-5011-5p | ZMYM2 | zinc finger MYM-type containing 2 |
| Details | 22 | 100 | hsa-miR-5011-5p | RYBP | RING1 and YY1 binding protein |
| Details | 23 | 100 | hsa-miR-5011-5p | PBRM1 | polybromo 1 |
| Details | 24 | 100 | hsa-miR-5011-5p | SLC35E3 | solute carrier family 35 member E3 |
| Details | 25 | 100 | hsa-miR-5011-5p | CBX8 | chromobox 8 |
| Details | 26 | 100 | hsa-miR-5011-5p | DDX6 | DEAD-box helicase 6 |
| Details | 27 | 100 | hsa-miR-5011-5p | MYCN | MYCN proto-oncogene, bHLH transcription factor |
| Details | 28 | 100 | hsa-miR-5011-5p | PTP4A2 | protein tyrosine phosphatase type IVA, member 2 |
| Details | 29 | 100 | hsa-miR-5011-5p | GIMAP7 | GTPase, IMAP family member 7 |
| Details | 30 | 100 | hsa-miR-5011-5p | ZDHHC5 | zinc finger DHHC-type containing 5 |
| Details | 31 | 100 | hsa-miR-5011-5p | VGLL2 | vestigial like family member 2 |
| Details | 32 | 100 | hsa-miR-5011-5p | PTPRJ | protein tyrosine phosphatase, receptor type J |
| Details | 33 | 100 | hsa-miR-5011-5p | NCSTN | nicastrin |
| Details | 34 | 100 | hsa-miR-5011-5p | ZC3H6 | zinc finger CCHC-type containing 6 |
| Details | 35 | 100 | hsa-miR-5011-5p | SMARCAD1 | SWI/SNF-related, matrix-associated actin-dependent chromatin, subfamily a, containing DEAD/H box 1 |
| Details | 36 | 100 | hsa-miR-5011-5p | BTAF1 | B-TFIID TATA-box binding protein associated factor 1 |
| Details | 37 | 100 | hsa-miR-5011-5p | HIPK3 | homeodomain interacting protein kinase 3 |
| Details | 38 | 100 | hsa-miR-5011-5p | EFHC1 | EF-hand domain containing 1 |
| Details | 39 | 100 | hsa-miR-5011-5p | GRIA4 | glutamate ionotropic receptor AMPA type subunit 4 |
| Details | 40 | 100 | hsa-miR-5011-5p | PIAS2 | protein inhibitor of activated STAT 2 |
| Details | 41 | 100 | hsa-miR-5011-5p | ATXN3 | ataxin 3 |
| Details | 42 | 100 | hsa-miR-5011-5p | MFAP5 | microfibril associated protein 5 |
| Details | 43 | 100 | hsa-miR-5011-5p | MSR1 | macrophage scavenger receptor 1 |
| Details | 44 | 100 | hsa-miR-5011-5p | GSR | glutathione-disulfide reductase |

most likely to be valid targets.

8. For this example, we will select the first Predicted Target by selecting 'Target Gene'. ### This

details all of the Seed Locations within its 3' UTR, length of the 3' UTR, the exact miRNA sequence and Target Score. #### It also includes a Gene Description and a helpful 'NCBI Gene ID' hyperlink to further investigate the targeted gene.

9. Clicking on the ‘NCBI Gene ID’ hyperlink will open a new window with the gene page in the NCBI database. ### From here, one can select ‘FASTA’ directly under the bold heading in order to view the nu-

miRDB Search Result Details × Homo sapiens splA/ryanodine receptor domain and SOCS box containing 1 (SPSB1), mRNA × +

← → ⌂ ncbi.nlm.nih.gov/nuccore/NM_025106

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NCBI Resources How To

Nucleotide Nucleotide Advanced Search Help

COVID-19 Information

Public health information (CDC) | Research information (NIH) | SARS-CoV-2 data (NCBI) | Prevention and treatment information (HHS) | Español

GenBank ▾ Send to: ▾ Change region shown

Homo sapiens splA/ryanodine receptor domain and SOCS box containing 1 (SPSB1), mRNA

NCBI Reference Sequence: NM_025106.4

FASTA Graphics

Go to: ▾

LOCUS NM_025106 3106 bp mRNA linear PRI 17-OCT-2021

DEFINITION Homo sapiens splA/ryanodine receptor domain and SOCS box containing 1 (SPSB1), mRNA.

ACCESSION NM_025106

VERSION NM_025106.4

KEYWORDS RefSeq; MANE Select.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3106)

AUTHORS Haenig C, Atias N, Taylor AK, Mazza A, Schaefer MH, Russ J, Riechers SP, Jain S, Coughlin M, Fontaine JF, Freibaum BD, Brusendorf L, Zenkner M, Porras P, Stroedicke M, Schnoegl S, Arnsburg K, Boeddrich A, Pigazzini L, Heutink P, Taylor JP, Kirstein J, Andrade-Navarro MA, Sharan R and Wanker EE.

TITLE Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains

JOURNAL Cell Rep 32 (7), 108050 (2020)

PUBMED 32814053

REFERENCE 2 (bases 1 to 3106)

AUTHORS Zhou L, Zheng L, Hu K, Wang X, Zhang R, Zou Y, Zhong L, Wang S, Wu Y and Kang T.

TITLE SUMOylation stabilizes hSSB1 and enhances the recruitment of NBS1 to DNA damage sites

JOURNAL Signal Transduct Target Ther 5 (1), 80 (2020)

PUBMED 32576812

REMARK GeneRIF: SUMOylation stabilizes hSSB1 and enhances the recruitment of NBS1 to DNA damage sites.

Publication Status: Online-Only

Send to: ▾ Change region shown

Customize view

Analyze this sequence

Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

Show in Genome Data Viewer

Articles about the SPSB1 gene

Dual proteome-scale networks reveal cell-specific remodeling of the human proteome [Cell. 2021]

Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains [Cell Rep. 2020]

SUMOylation stabilizes hSSB1 and enhances its recruitment to DNA damage sites [Signal Transduct Target Ther. ...]

See all...

Pathways for the SPSB1 gene

Antigen processing: Ubiquitination & Proteasome degradation

Class I MHC mediated antigen processing & presentation

Adaptive Immune System

See all...

cleotide sequence.

10. After selecting the FASTA sequence, the accession number for the target gene can be copied.

The screenshot shows a web browser window with the following details:

- Header:** miRDB Search Result Details, Homo sapiens splA/ryanodine receptor domain and SOCS box containing 1 (SPSB1), mRNA
- Address Bar:** ncbi.nlm.nih.gov/nuccore/NM_025106.4?report=fasta
- Navigation:** Back, Forward, Stop, Refresh, Home, Favorites, Help, Sign in to NCBI
- Toolbar:** Apps, Sign in to Outlook, Upcoming Events..., Welcome - DataS..., High Performance..., Easley User's Guide, Reading List
- NCBI Header:** NCBI Resources, How To, Sign in to NCBI, Help
- Banner:** COVID-19 Information (with links to CDC, NIH, SARS-CoV-2 data, Prevention and treatment information, and Español)
- Section:** FASTA -
- Sequence ID:** NCBI Reference Sequence: NM_025106.4
- Sequence Content:**

```
>NM_025106.4 Homo sapiens splA/ryanodine receptor domain and SOCS box containing 1 (SPSB1), mRNA
GCACAGAACGTCGGCTCGGGCAGCCCTGCGCCTCGCAGCAGGAACCAGGCCAGGTCCAGGCAGGCCGGCGCCGG
CGGGGGCGCGGGAGGGAGGGGACTTCCGCTCCCTGCGCGGGCGGCCGGCGCCGGCGCCGGCGCCGGCGCCGGCGCCGG
CCTTGGAGAGCAGCGGGCGGGCGGCCGGCACCCGGGGCGCGCAATACTGAACACTGCGCAGCTTGAGAGGT
CTCCGGCAGCCCCCTCATTAAGAAATTCTGTCGGCCCCGATCAGAATACTGGAGAGCAGAGACCCACGAGATTG
ATGAGTTGCTTGGGAGTCGTTAAGGAAGGTGAAGCCAGGGCGAACATGGGTCAAAGGTCACTGGAG
GATCAAGACTGTGGACATGAGGGACCCACGTACAGGCCCTGAAGCAGGAGCTCCAGGGTCGTGATTAC
```
- Options:** Send to: Change region shown, Customize view, Analyze this sequence (Run BLAST, Pick Primers, Highlight Sequence Features, Find in this Sequence, Show in Genome Data Viewer)

11. In a new browser window, search for ‘UCSC Genome Browser’ and select ‘UCSC Genome Browser Home’

miRDB Search Result Details | Homo sapiens spIa/ryanodine | ucsc genome browser - Google Search

<https://genome.ucsc.edu>

UCSC Genome Browser Home

The UCSC Genome Browser is developed and maintained by the Genome Bioinformatics Group, a cross-departmental team within the UCSC Genomics Institute.

Genome Browser
move start, Click on a feature for details. Click+shift+drag to ...

Gateway
GRCh38/hg38 - View sequences - FTP - ...

In-Silico PCR
In-Silico PCR searches a sequence database with a pair ...

Human BLAT Search
Only DNA sequences of 25,000 or fewer bases and protein or ...

Table Browser
Use this tool to retrieve and export data from the Genome Browser ...

hg19/GRCh37
Use drop-down controls below and press refresh to alter tracks ...

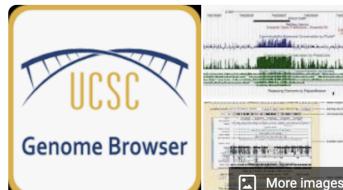
[More results from ucsc.edu >](#)

People also ask :

What is UCSC Genome Browser used for?

How do I read UCSC Genome Browser?

UCSC Genome Browser



The UCSC Genome Browser is an online and downloadable genome browser hosted by the University of California, Santa Cruz. [Wikipedia](#)

Developer: Jim Kent

Description: The UCSC Genome Browser

Primary citation: Navarro Gonzalez & al. (2021)

Research center: University of California Santa Cruz

People also search for

 BLAST
 Galaxy
 Bioconda
 SAMtools

[Feedback](#)



12. Then, select ‘Genome Browser’ option (highlighted in green).

13. From here, select ‘Human’ and select ‘Dec. 2013 GrCh38(hg38)’ ### Past the accession number

Santa Cruz Genomics Institute | UCSC | Genome Browser Gateway

Genomes | Genome Browser | Tools | Mirrors | Downloads | My Data | Projects | Help

Browse>Select Species

POPULAR SPECIES

Human Mouse Rat Zebrafish Fruitfly Worm Yeast

Enter species, common name or assembly ID

Can't find a genome assembly?

REPRESENTED SPECIES

Human
Chimp
Bonobo
Gorilla
Orangutan
Gibbon
Green monkey
Crab-eating macaque
Rhesus
Baboon (anubis)
Baboon (hamadryas)
Proboscis monkey
Golden snub-nosed monkey
Marmoset
Squirrel monkey
Tarsier
Mouse lemur
Bushbaby
Mouse
Rat
Chinese hamster
Kangaroo rat
Naked mole-rat
Opossum

Find Position

Human Assembly
Dec. 2013 (GRCh38/hg38)

Position/Search Term
NM_025106.4
Current position: chrX:15,560,138-15,602,945

Human Genome Browser - hg38 assembly

UCSC Genome Browser assembly ID: hg38
Sequencing/Assembly provider ID: Genome Reference Consortium GRCh38.p13 (GCA_000001405.28)
Assembly date: Dec. 2013 initial release; Dec. 2013 update
Assembly accession: GCA_000001405.28
NCBI Genome ID: 51 (Homo sapiens (human))
NCBI Assembly ID: GCF_000001405.39 (GRCh38)
BioProject ID: PRJNA31257

Search the assembly:

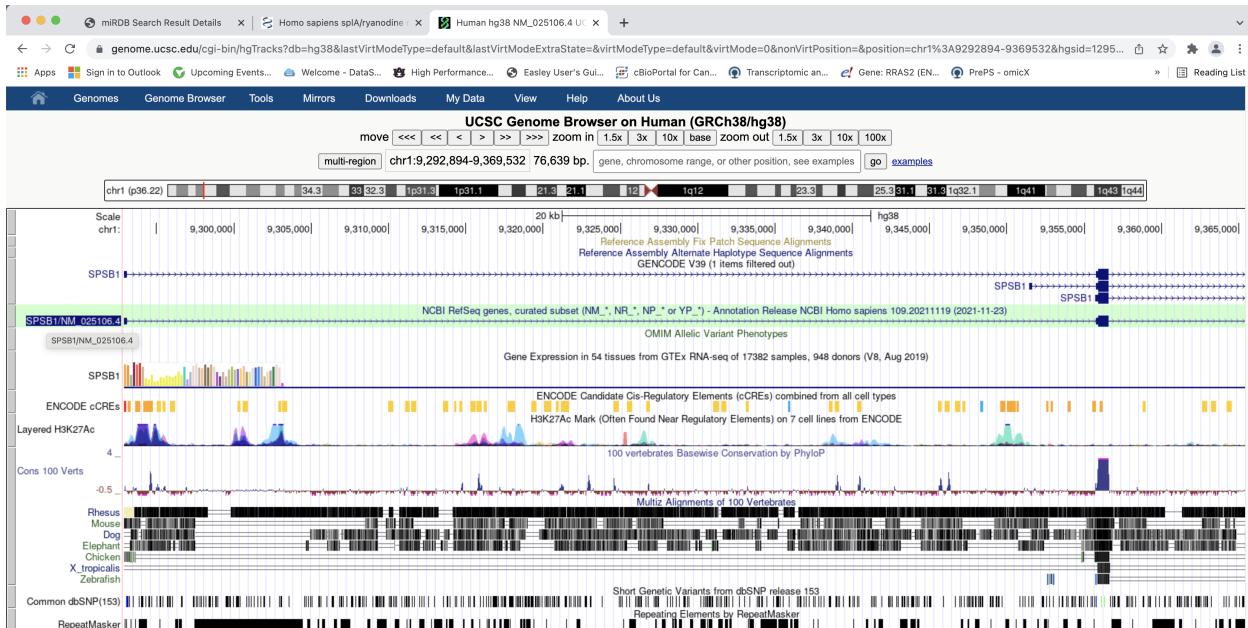
- **By position or search term:** Use the "position" or "search term" input fields associated with many different attributes, such as genomic coordinates, EST, or STS marker names; or keywords related to the assembly, including sample queries.
- **By gene name:** Type a gene name into the "gene name" input field and press "submit" to go directly to the gene's page.
- **By track type:** Click the "track search" button to search for tracks based on specific selection criteria. [More information](#).

Download sequence and annotation data:

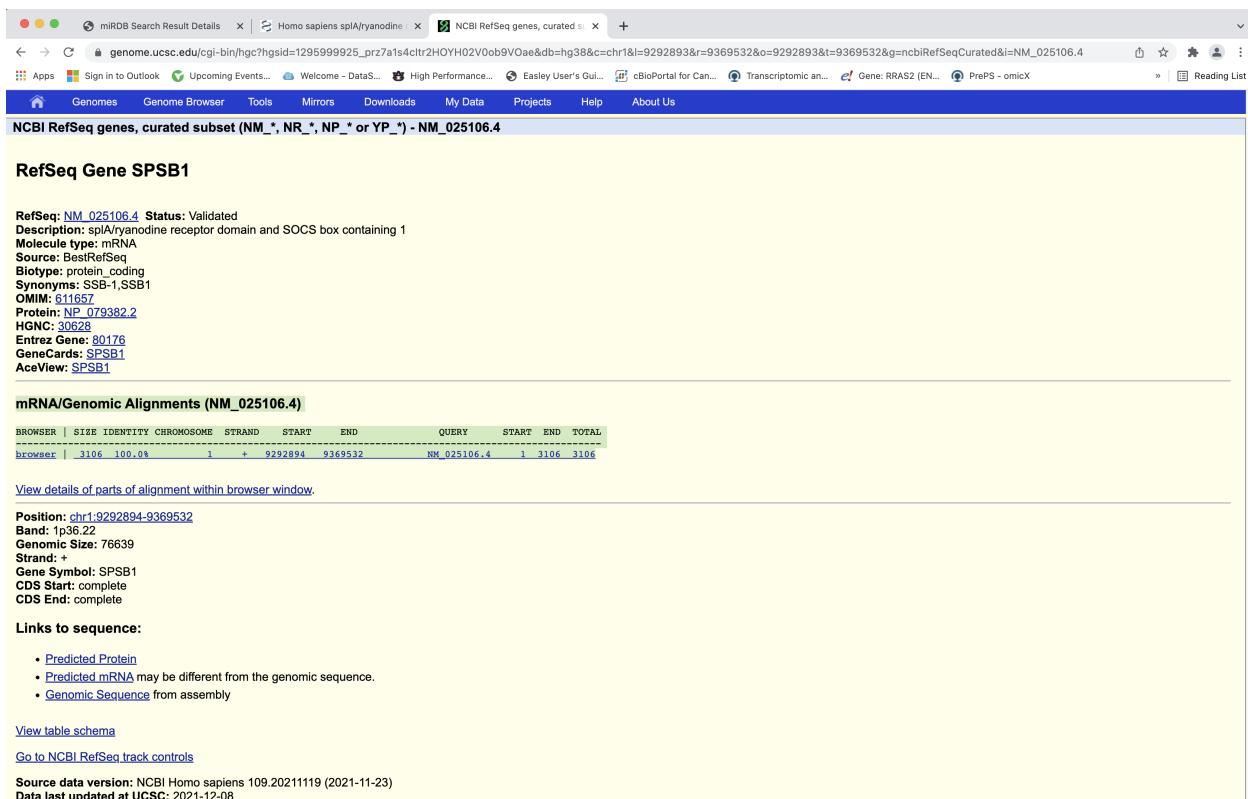
- [Using rsync \(recommended\)](#)
- [Using HTTP](#)
- [Using FTP](#)
- [Data use conditions and restrictions](#)
- [Acknowledgments](#)

obtained from the NCBI FASTA page, and select 'Go'.

14. Select the Dark blue 'NCBI RefSeq genes' track (highlighted in green).



15. This will display the RefSeq gene information for the target gene. ### Select the ‘mRNA/Genomic Alignment’ (highlighted in green).



16. This displays both the cDNA and genomic DNA sequences. This is where one can obtain the exact sequence regions of interest for the target gene.

miRDB Search Result Details | Homo sapiens splA/ryanodine receptor 1 | NM_025106.4 vs Genomic [incl] | genome.ucsc.edu/cgi-bin/hg?hgSID=1295999925_prz7a1s4cltr2HOYH02V0ob9VOae&g=htcCdnaAli... | + | | Apps | Sign in to Outlook | Upcoming Events... | Welcome - DataS... | High Performance... | Easley User's Gui... | Reading List

Alignment of NM_025106.4

Alignment of NM_025106.4 and chr1:9292894-9369532

Click on links in the frame to the left to navigate through the alignment. Matching bases in coding regions of cDNA and genomic sequences are colored blue and capitalized. Matching bases in UTR regions of cDNA and genomic sequences are colored red and capitalized. Light blue (coding) or orange (UTR) bases mark the boundaries of gaps in either sequence (often splice sites).

cDNA NM_025106.4

```

GCACAGAAAGT CGCGCTCGGG CAGCCTGCGC GCTCGCAGCA GGAACCAAGGC 50
TCCAGGCCGG CGCGCCGGGG CGCGGCCCGC GGGGAGGAGG CGACTTCGCT 100
CCCTGCGGGC GGCGCGGCCG GGGCGCCCGA GCCTCCTCGG CCTTGGAGAG 150
CAGCGGCACC CGGGCGCAGG AATACTGAAAC ACTGCCAGC 200
TTGCAGAGGT CTCTTGCCAG CCCCATTAG GAATTCCTGTC TGCCCCCGAT 250
CAGAACATCTG GAGACGAGAC CACGAGATTG ATGAGTTTC CTTGGGAGTC 300
GGTAAGAAGG TGAAGGCCAGG GGGGAACATG GGTCAGAAAGG TCACCTGGAG 350
GATCAAGACT GTGGACATGA GGGACCCAC GTACAGGCC CTGAAGCAGG 400
AGCTCCAGGG TCTGGATTAC TGAAGGCCA CCCGGCTGGA TCTGCTACTG 450
GACATGGCCC CTGATGTCCTA TGATGTCAGG CTGCTGCAATT CATGGAAACA 500
CAACGACCGA TCGCTCATAG TCTTTGTGA GGAGGACGAC AACCTCATCT 550
TTCACCGGCA TCCGGTGGCC CAGAGCACGG ACGGTATCAG GGGCAAAGTC 600
GGGTATACCC GTGGGCTGCA CGTGTGGCAG ATCAGTGGG CCATGAGACA 650
GGGGGGCACA CACCCCTGGG TGGGGTGGC GACGGCAGAC GCCCCCCCTGC 700
ACTCTGTCGG CTACACAAAC CTGCTGGGG ATAACCACGA GTCTGGGGC 750
TGGGACTTGG GGCACAAACG GCTCTACAC GATGGCAAGA ACCAGCCAAG 800
CAAACACATAC CAACGCTTTC TGGAAACCGA TGAGACATTC ATTGTCCTG 850
ACTCTTCTCT GTAGACCCCTG GACATGGACG ACGGGACTCT GAGCTTCATT 900
GTGGATGGAC AGTACATGGG AGTGGCTTT CGGGGACTCA AGGGCAAAAAA 950
ACTGTATCTT GTAGTGAGT CGCTCTGGGG CCACTGTGAG ATCCGAATGC 1000
GCTACTTGA CGGACTCGAT CGCGAGCCGC TGCCGCTCAT GGATTGTGTC 1050
CGTGCCTGG CGTGCCTGGC CCTGGGGAGG GAGCGCCTGG GGGAGATCCA 1100
CACGGCTGGC CTGGCGCTT CACCTCAAGGC TAACCTCTTC TACCACTGAC 1150
GTTGCGCATC ATACCGGACG CGGGACAGCC ACCTGTTGCC AACTCTACTG 1200
GCCGCCTGCC GGGTGGCCCG CGGCACCCCTG CACCTTGGAC CGGCATCCGT 1250
AGCCATGGAC AGAGGTTCCC GGTCCTCCCT CATCCCTCGT GGCTGCCCTC 1300
ATGGACACAG GACGGATTCC AACACAGGG CCTCTTTCCC CCTTTCCGAC 1350
ATCAGCAGAA GGCAGCATCC CTGCACTGCC TCCGTATACAA ACCCTCTTT 1400
GAAAAGAAC ACAGAGAAATA AACTCTAG AAACCCCTAC ATTGAGCTCC 1450
AATCTGCTCG GGGTGGGACG GTTGGCTTCCC ACACCTCTGG GAGAAGGCTG 1500
CAGGGCACCTG GGGTGGCCCG GGTGGTGGGG GTGGCAGGTG GTACCAACAGC 1550
TCTGAGAGCA GATACCAAGG GTACTAAAGAG GTGCTTAGAC AAGGGCTGGT 1600
GCCGAGCCCA GGGTGGCCCG CGGGGCCATG CCATGGCAGA TAAAGCTCAG 1650
GACGTCAAAA ACTCACCATG GACCCCAAGG CAGAAACCAA GAACGTCTG 1700
CAGGCAAATA AGCACCCAGC ACCCATCTTG GCTGCCGGT CCCGGTACCC 1750
TGTATTATG CTTTTAACAA TAACAAAAGC CATTATTATTA TTCCCATCTAG 1800
AAAGGAAACCC CTGTTTCAGT CCCCTCTCTC TGCTGTCTCT GTTACTTTCC 1850
TTCCACCTGT GCCCCTCCCT GGATATGTAT GCCTGCCCG CCCTCCCTGG 1900
GCACATGTCCC ACACGTCGCC AGGCACAAGT ATGTCCTGG GTCCCTTGGC 1950
CTGCAGTTTC CAGGGGGCTC TGCTCCAAGT TCCCTAGGG GCCCCTCAGG 2000
GAGAAATAGC CTCACAGTGA ATCTGGGTG CTTGGGGGC CCGTCTGGAA 2050
GGGCTGCACG AATCCCCCTG TGCTCTCAGG TAACAGCTA ACTCTTGGCC 2100
TCAGGCACCC TTGACAGGG TTGCAATTCT TTAGTCTCT GTGGGCTTT 2150
TGATGTGGG TTGATTTTC TTTTGCTTT CTAGCTGAGA TTTCCAAGT 2200
GCATCTCTAG AAGCTCTGGG TGTCGAGAG GACCCCCAGA ACTAAGAAGG 2250
GAGGGCAGT GGGTCTCCAT TCCCCGAGAA CGCCGGGCA GGGTGGGATG 2300
GGGAAGACCA GGAGCAGAGT CGAGCCTCAC AGAAGCCAGC CGGGTCTCT 2350
GCTCAGCACCC CGACCCGGG CTCAGGACCC AGGGTAACAG CCCCACTTC 2400
TCCCAACCCCCC TCTCAGAGCC TCAAGAGGGG TAGTCGGCT GCCGGAAGAG 2450
AGGGGTGCCCT TATCCCTGCC AACCCCTCCA CGTAGCGTAC CCCAGCACCT 2500
GCCACCCGCCCT TTGCCATTTC TTGAGCTTGG AAGGTTAACCT TCTTAGAGTC 2550
TAACTTTGCT CTCATTTCTGC ACAGGTACAA TAGATGACTT TATTTGTTA 2600
AAATGTTAA TATATATACA TACATATATA TATATTGTC TGTAAGAATT 2650
ATGTTTTAA CAGCTGCTG AGAGTACCTT TTGTTAAAGT AATCTTACAG 2700
TGGAGTATAAT TTTTTAAAGC ACAAAATTGG TGCAAGACT GGGTGAAGAAA 2750
TGTACATTAC CCCCTTATTA TTTTGACGGT TTTTTTTTC GGGGCAGGGG 2800
ACCTTACCTG TAAGACTTTT AAAGATTTTC CTCCCTCTGG TTTCAAGGTGG 2850
GTCACATTCT GATGAATGTT TCCCTTGTAC AGATCCAGC TTATGCCCTT 2900
GACCCAGCCG TCCCTCACAGA TGCGGGGTGA CCCTCTAGCT CTCTCTGCAT 2950
CTCCCAACCCC CGGACACCCCT GGGACCCCTCG ACCCCACCCCT TTCTTCCCTAC 3000
CAGCCCCAGG CCTTGTGGCT TGACAGTT TGAAACTCC GTTCTATTIT 3050
ATGATGGTTG ATAATAGTC GTAACCTAAT AAAGAACGT TTGTTAAAAT 3100
ATCAA

```

17. We originally saw that the miRNA had binding sites in the 3' UTR of the target gene, but using this cDNA sequence, we can also determine if it binds in the 3' UTR (or the entire transcript– we will focus on the 5' UTR for now in this tutorial). ### Copy the entire 5' UTR (highlighted in green). ### Red letters at the beginning of the sequence denote non-coding regions; blue denote coding regions.

miRDB Search Result Details | Homo sapiens splA/ryanodine | NM_025106.4 vs Genomic [incl] | +

genome.ucsc.edu/cgi-bin/hgc?hgSID=1295999925_prz7a1s4cltr2HOYH02V0ob9VOae&g=htcCdnaAli... | Apps | Sign in to Outlook | Upcoming Events... | Welcome - DataS... | High Performance... | Easley User's Gui... | Reading List

Alignment of NM_025106.4

Alignment of NM_025106.4 and chr1:9292894-9369532

Click on links in the frame to the left to navigate through the alignment. Matching bases in coding regions of cDNA and genomic sequences are colored blue and capitalized. Matching bases in UTR regions of cDNA and genomic sequences are colored red and capitalized. Light blue (coding) or orange (UTR) bases mark the boundaries of gaps in either sequence (often splice sites).

cDNA NM_025106.4

| | | | | | |
|-------------|-------------|-------------|-------------|-------------|------|
| CACAGAAAGT | CGCGCTCGGG | CAGCCTGCC | GCTCGCAGCA | GGAAACCAGGC | 50 |
| TCCAGGCGCC | GGGCCGGGG | CCGGGGCCGC | GGGGAGGAGG | CGACTTCGGCT | 100 |
| CCCTGCGGC | GGCGCGGCC | GGGGCAGCCGA | GCCTCCTCGG | CCTTGGAGAG | 150 |
| CAGCGCGGC | GGCGGCACCC | GGGGCGCCGC | AATACTGAAC | ACTGCCAGC | 200 |
| TTTCAGAGGT | CTCTCTGGAG | CCCTCATTA | GAATTCCTTC | TGGCCCCGAT | 250 |
| CAGAACATCG | GAGACGAGAC | CACGAGATTG | ATGAGTTTGC | CTTGGGAGTC | 300 |
| GTTAAGAAGG | TGAAGCCAGG | GGGGAAACATG | GCTCAGAAAGG | TCACTGGAGG | 350 |
| GATCAAGACT | GTGGACATGA | GGGACCCAC | GTACAGGCC | CTGAAGCAGG | 400 |
| AGCTCCAGGG | TCTGGATTAC | TGCAAGCCA | CCCGGCTGGA | TCTGCTACTG | 450 |
| GACATGCCCC | CTGTGTCCTTA | TGATGTCCAG | CTGCTGCATT | CATGGAAACAA | 500 |
| CAACGACCGA | TCGCTCAATG | TCTTTGTA | GGAGGACGAC | AAGCTCATCT | 550 |
| TTCACCGGCA | TCCGGTGGCC | CAGAGCACGG | ACGCTATCAG | GGGAAAGTC | 600 |
| GGGTATACCC | GTGGGCTGCA | CGTGTGCGAG | ATCACGTTGG | CCATGAGACA | 650 |
| GGGGGGCACA | CACCGCGTGG | TGGGGGTGCG | GACGGCAGAC | GCCCCCTGTC | 700 |
| ACTCTGTCGG | GTACACAACC | CTCGTGGGA | ATAACCACGA | GTCCTGGGC | 750 |
| TGGGACTTGG | GGGCCAACCCG | GCTCTACAC | GATGCAAGA | ACCAGCCAAG | 800 |
| CAAAACATAC | CCAGCCCTTC | TGGAACCCAGA | TGAGACATTC | ATTGTCCTG | 850 |
| ACTCCTTCTT | GGTAGCCCTG | GACATGGACG | ACGGGACTCT | GAGCTTATT | 900 |
| GTGGATGGAC | AGTACATGGG | AGTGGCTTTT | CGGGGACTCA | AGGGCAAAAA | 950 |
| ACTGTATCTT | GTAGTGAGT | CCCTCTGGGG | CCACTGTGAG | ATCCGAATGC | 1000 |
| GCTACTTGAA | CGGACTCGAT | CCCGAGCCGC | TGCCGCTCAT | GGATTGTGC | 1050 |
| CGTCGCTCGG | TGCCGCTCGG | CCCTGGGGAGG | GAGGCCCTGG | GGGAGATCCA | 1100 |
| CACGCTGCCG | CTGCCGGCTT | CCCTCAAGGC | CTACCTCTC | TACCAAGTC | 1150 |
| GTTCGCGCAT | ATACCGCCAG | CGCGACAGCC | ACCTGGTGCC | AACTCACTGA | 1200 |
| GCCGCCCTGCC | GCTGGGGCCCG | CCGCACCCCTG | CACCTTGAC | CGGCATCCGT | 1250 |
| AGCCATGGAC | AGAGGTCCCT | GGTCTCCCT | CATCCCTCGT | GGCTGCCCTCC | 1300 |

18. Open a new browser window with <http://mirdb.org/> ### Paste the entire copied sequence into the text box. Select ‘Human’ for Species. This time, do NOT select Sample target mRNA input. Select ‘Go’.

miRDB - Custom Prediction | Homo sapiens splA/ryanodine receptor 2 | NM_025106.4 vs Genomic [nc] | +

Not Secure | mirdb.org/mirdb/custom.html

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miRDB

Target Search

Target Expression

Target Ontology

Target Mining

Custom Prediction

FuncMir Collection

Data Download

Statistics

Help | FAQ

Comments

Citation | Policy

miRDB provides additional web interface below for more flexible miRNA target search. You may search targets by providing your own sequence. In addition, target search can also be performed for unconventional sites in the coding region or 5'-UTR.

1) Target prediction with user-provided miRNA or gene target sequence

Species: Human

Submission type: mRNA Target Sequence

Example miRNA submission Example target mRNA submission

```
GCACAGAAAGT CGCGCTCGGG CAGCTTGCAGCA GGAACCAGGC 50
TCCAGGCCGC GGCGCCGGGG CGGGGCCGC GGGGAGGAGG CGACTTCGCT 100
CCCTGCGCGC GGCGCGGCC CGGGGCCGC GA CCTCTTCGG CCTTGAGAG 150
CAGCGGGGC GGCGGACCC CGGGCGCGGC AATACTGAAC ACTGCGCAGC 200
TTGAGAGGT CTCTGGCAG CCCTATTAG GA ATTCTGTC TGGCCCGAT 250
CAGAATACTG GAGACGAGAC CACGAGATTG ATGAGTTGC CTTGGAGTC 300
GGTAAGAAGG TGAAGCCAGG GGCGAAC
```

Custom miRNA sequences must be between 17 and 30 bases long; custom mRNA target sequences must be between 100 and 30,000 bases long. Please submit only one sequence at a time, consisting of A, T or U, C and G. Please note that all spaces, line breaks, and numbers within the submission will be removed, and multiple lines will be joined together to create a single sequence.

2) Search for unconventional target sites in the coding region or 5'-UTR

| |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Search by miRNA name |
| Human <input type="button" value="▼"/> Coding Region <input type="button" value="▼"/> <input type="text"/> <input type="button" value="Go"/> <input type="button" value="Clear"/> |
| Search by gene target |
| Human <input type="button" value="▼"/> Gene Symbol <input type="button" value="▼"/> Coding Region <input type="button" value="▼"/> <input type="text"/> <input type="button" value="Go"/> <input type="button" value="Clear"/> |

These options are provided for a database search for miRNA targets beyond the 3' UTR. Additional targets are accessible for the 5' UTR and the coding region.

[Click here](#) to contact us with questions or comments about this website.

19. Again, select the Predicted Sequences output link. ### Now, one can see that there are two predicted miRNAs binding to the 5' UTR of the target gene, and its nucleotide length.

The screenshot shows a web browser window with the miRDB website loaded. The title bar includes tabs for "Custom Prediction", "Homo sapiens splA/ryanodine", and "NM_025106.4 vs Genomic [nc]". Below the title bar, the URL is "Not Secure | mirdb.org/cgi-bin/custom.cgi". The miRDB logo is prominently displayed. A message states "There are 2 predicted miRNAs targeting the submitted 327 nt long mRNA sequence." A "Return to Custom Prediction" button is visible. A table lists the predicted miRNAs:

| Target Detail | Target Rank | Target Score | miRNA Name | Gene Symbol |
|---------------|-------------|--------------|---------------------------------|-------------|
| Details | 1 | 68 | hsa-miR-3925-3p | submission |
| Details | 2 | 52 | hsa-miR-6869-3p | submission |

20. From here, one can further investigate the miRNAs by both clicking on the red hyperlink with its name and/or selecting 'Details' to view the References and locations as we did before at the beginning of this tutorial.

This tutorial is meant to guide one through the steps of obtaining miRNA binding site predictions for a sequence of interest—this could be an entire cDNA (mRNA) sequence, or even simply a gene's 3' UTR (a common binding site for miRNAs). It is important to investigate the potential interaction of various miRNAs with target genes. For example, some miRNAs can have oncogenic properties when they bind and disrupt the localization of a DNA repair gene and cause aberrant protein expression to occur, promoting oncogenesis. (Si et al. citation below) miRDB is an excellent tool for guiding this investigation as it has an extensive database of miRNAs and target genes. It also has a good amount of references populated for each miRNA, which is very useful when amassing literature for a review or academic research.

Although not covered in this tutorial, miRDB has other functions (as seen in Step 1 on the left side of the webpage) such as:

Target Search <http://mirdb.org/index.html> (Search by miRNA name or by gene target)

Target Expression <http://mirdb.org/expression.html> (Identify a miRNA of interest and select a cell line of interest for target prediction.)

Target Ontology <http://mirdb.org/ontology.html> (Identify a miRNA of interest and select a Gene Ontology category for target functional analysis in PANTHER.)

Target Mining <http://mirdb.org/mining.html> (When searching for miRNA gene targets, full mature miRNA names are required. When searching for miRNAs, you may provide either NCBI gene IDs or official gene symbols.)

FuncMir Collection <http://mirdb.org/FuncMir.html> (FuncMir is a collection of functional miRNAs in humans and mice. Currently, FuncMir includes 568 human precursor miRNAs, 654 human mature miRNAs, 452 mouse precursor miRNAs and 442 mouse mature miRNAs.)

Data Download (miRDB Data Download set of Target Prediction Files)

Statistics pages (miRDB statistics on predicted miRNA gene targets in human, mouse, rat, dog and chicken.)

for extra resources when investigating both genes and miRNAs of interest. It also has a very useful ‘Help | FAQ’ page for further information on how the software functions and how they evaluated that a target score of >80 was predicted to be valid, for example. <http://mirdb.org/faq.html>

Next steps for the savvy researcher include using the information in this tutorial to obtain FASTA sequences for their own gene or miRNA of interest and utilizing not only the ‘Custom Prediction’ feature, but the others listed above to help understand the relationships between miRNAs and their targets and how they translate into disease or prevention of disease, etc.

Overall, miRDB is an essential tool for predicting miRNA binding and gene targets. It is a great resource for not only making predictions, but also learning more about the literature behind each component.

References:

Si W, Shen J, Zheng H, Fan W. The role and mechanisms of action of microRNAs in cancer drug resistance. Clin Epigenetics. 2019;11(1):25. Published 2019 Feb 11. doi:10.1186/s13148-

018-0587-8 <https://pubmed.ncbi.nlm.nih.gov/30744689/>

Chen Y, Wang X. miRDB: an online database for prediction of functional microRNA targets. Nucleic Acids Res. 2020;48(D1):D127-D131. doi:10.1093/nar/gkz757 <https://pubmed.ncbi.nlm.nih.gov/31504780/>

Liu W, Wang X. Prediction of functional microRNA targets by integrative modeling of microRNA binding and target expression data. Genome Biol. 2019;20(1):18. Published 2019 Jan 22. doi:10.1186/s13059-019-1629-z <https://pubmed.ncbi.nlm.nih.gov/30670076/>