

miRDB_McGuireSams_GradProjec-BIOL6860

Cierla McGuire Sams

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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”.

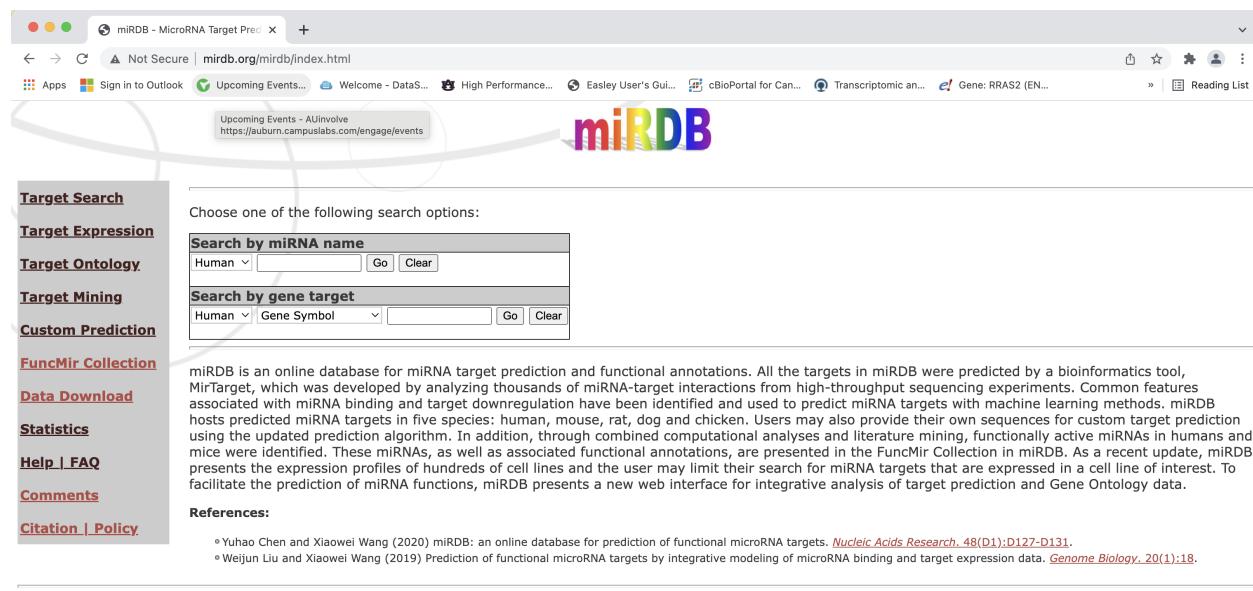


Figure 1: pic1

The screenshot shows a web browser window for the miRDB - Custom Prediction page. The URL is mirdb.org/mirdb/custom.html. The page features a large 'miRDB' logo at the top. On the left, a sidebar contains links: Target Search, Target Expression, Target Ontology, Target Mining, Custom Prediction, FuncMir Collection, Data Download, Statistics, Help | FAQ, Comments, and Citation | Policy. The main content area has two sections: '1) Target prediction with user-provided miRNA or gene target sequence' and '2) Search for unconventional target sites in the coding region or 5'-UTR'. Section 1 includes dropdowns for Species (Human), Submission type (miRNA Sequence), and checkboxes for Example miRNA submission and Example target mRNA submission. It also features a large text input field for sequence submission with 'Go' and 'Clear' buttons. A note below states: '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.' Section 2 contains two search boxes: 'Search by miRNA name' (Human dropdown, Coding Region dropdown, text input, Go, Clear) and 'Search by gene target' (Human dropdown, Gene Symbol dropdown, Coding Region dropdown, text input, Go, Clear). A note below these says: '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.' At the bottom, a link 'Click here' is provided for contact.

Figure 2: pic2

Select Custom Prediction from the list of functions on the left.

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.

The screenshot shows the miRDB website interface. On the left, a sidebar lists various options: 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 'miRDB'. Below it, a section titled '1) Target prediction with user-provided miRNA or gene target sequence' contains fields for 'Species: Human' and 'Submission type: mRNA Target Sequence'. A large text input box contains a FASTA sequence:
GCCCTCCCTCGGGAAGCCCTCAGGAGGCCACACCAAGCTGTTCCACCTGCTGTGCAGTCACCTTAGATG
TTCAGAACGGCGTCTCTCCACTGAAAGGCTATGAGATAACGACAAATCTGCTTCAGCTTATGACTCT
ATGCAAGCAAAATACACAGTTTATTGCTGAATCTGTGTTCTTCAGCCCCACTTTATGCCCTTAACCT
AGTAAATGTTATTTGAAATTCTGAATTCTGTTCTGACCTAGAACGAAATTGATAATGAAAGTTCAGATGAGC
CCGTAAAGTCATAAGTAAATTCTGAATTGTTGTTCTGACCTAGAACGAAATTGATAATGAAAGTTCAGATGAGC
GAATATTGATAGAACCAATTGTTGTCATAAAACAGATTGGCATATATATATGATAAAAATAAAA
AATGGAAGTATGGTGTCTAGTAAAAAAA
The input box also includes 'Go' and 'Clear' buttons. Below this, a note states: '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.'

Below this, another section titled '2) Search for unconventional target sites in the coding region or 5'-UTR' 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 below says: '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.'

Figure 3: pic3

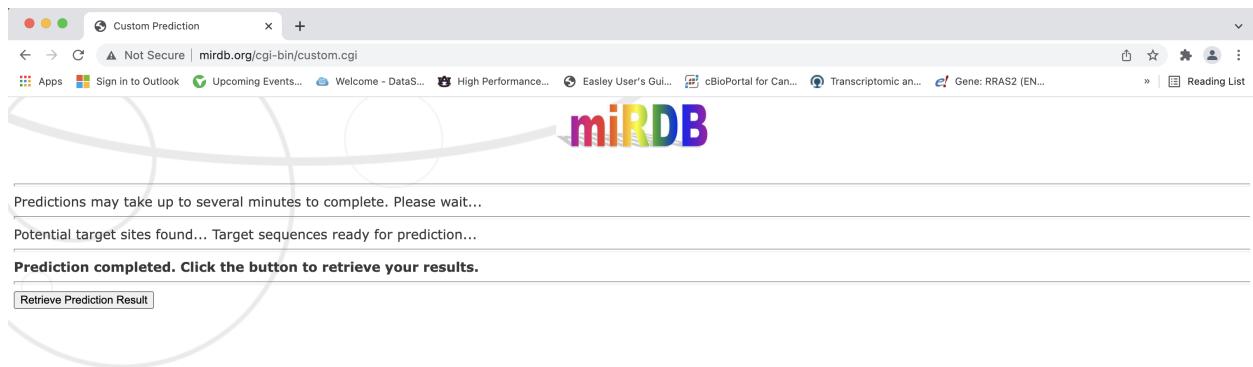


Figure 4: pic4

Custom Prediction

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

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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

Figure 5: 5
5

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.

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.

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.

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 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 nucleotide sequence.

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

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

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

13. From here, select ‘Human’ and select ‘Dec. 2013 GrCh38(hg38)’

Custom Prediction Result Detail + ▾

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

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

miRDB

MicroRNA and Target Gene Description:

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

Custom Target Sequence

```
1 gccctccctc ggcgaagcct ccagcaggcc acaccagctg tttcccaccc gctgtgcagt
 61 caccttagat gttcagaagc cgcttcctct ccactgaaga gctatgagat acgcacaata
 121 ctgcgtgttc acgttatgac tctcatgcaa gcaaaataca cagtttcatt gttctgaatc
 181 ctgtggtttc ttccagccca ctttatcgc cttaacctag ttaatgtata ttttgaattg
 241 tgtgtatgac ctcagaactg aaattgataa tgaagttgca agttttgata gcccgtgaag
 301 tgcataagta tctaattta cctgaattga tttgggggaa aattaccagt agaatgcctt
 361 ggtctgaata ttgtatagaa ccaattgttg tacataaaac agattgcgca tatataaaaa
 421 tgtataaaaa ataataaaat aatggaagat gatgggttcc tctagtaaaa aaaaaaaaaa
 481 aaaa
```

Figure 6: 6

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' - **uauauauacagccaugcacuc** - 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

---a	u	ua	c	c	gu	
ga	gg	ugagugga	uguu	uauauacagccaugcacu	ugua	u
cu	uc	acuuaccua	acaauauaua	ugucggua	acau	g
cga	u	--u	c	c	gg	

Figure 7: 7

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... Reading List

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	weety 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	GATAD2B	GATA zinc finger domain containing 2B
Details	9	100	hsa-miR-5011-5p	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 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 protein 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 CCCH-type containing 6
Details	35	100	hsa-miR-5011-5p	SMARCAD1	SWI/SNF-related, matrix-associated actin-dependent regulator of 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

Figure 8: 8

Figure 9: 9

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

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

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NCBI Resources How To

Nucleotide Nucleotide Search Help

Advanced

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

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 [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...

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, Sharpen 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

Figure 10: 10

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

- Tab Bar:** 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
- Toolbar:** Apps, Sign in to Outlook, Upcoming Events..., Welcome - DataS..., High Performance..., Easley User's Gui..., Reading List.
- Header:** NCBI Resources, How To, Sign in to NCBI.
- Search Bar:** Nucleotide, Advanced, Search.
- COVID-19 Information Sidebar:** Public health information (CDC) | Research information (NIH) | SARS-CoV-2 data (NCBI) | Prevention and treatment information (HHS) | Español.
- Sequence View:** FASTA, 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).
- Sequence Content:** NCBI Reference Sequence: NM_025106.4. The sequence itself is a long string of nucleotide bases.

Figure 11: 11

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/>

miRDB Search Result Details | Homo sapiens sPLA/ryanodine | ucsc genome browser - Google | google.com/search?q=ucsc+genome+browser&oq=ucsc+genome+browser&aqs=chrome.0.69i59j0i512l4j69i60l3.2621j0j7&source...

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Google ucsc genome browser

All Books Videos News Images More Tools

About 10,700,000 results (1.24 seconds)

<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 ...

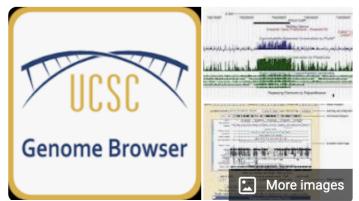
[More results from ucsc.edu »](#)

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

NCE BLAST Galaxy Biocond... SAMtools

Feedback

Figure 12: 12

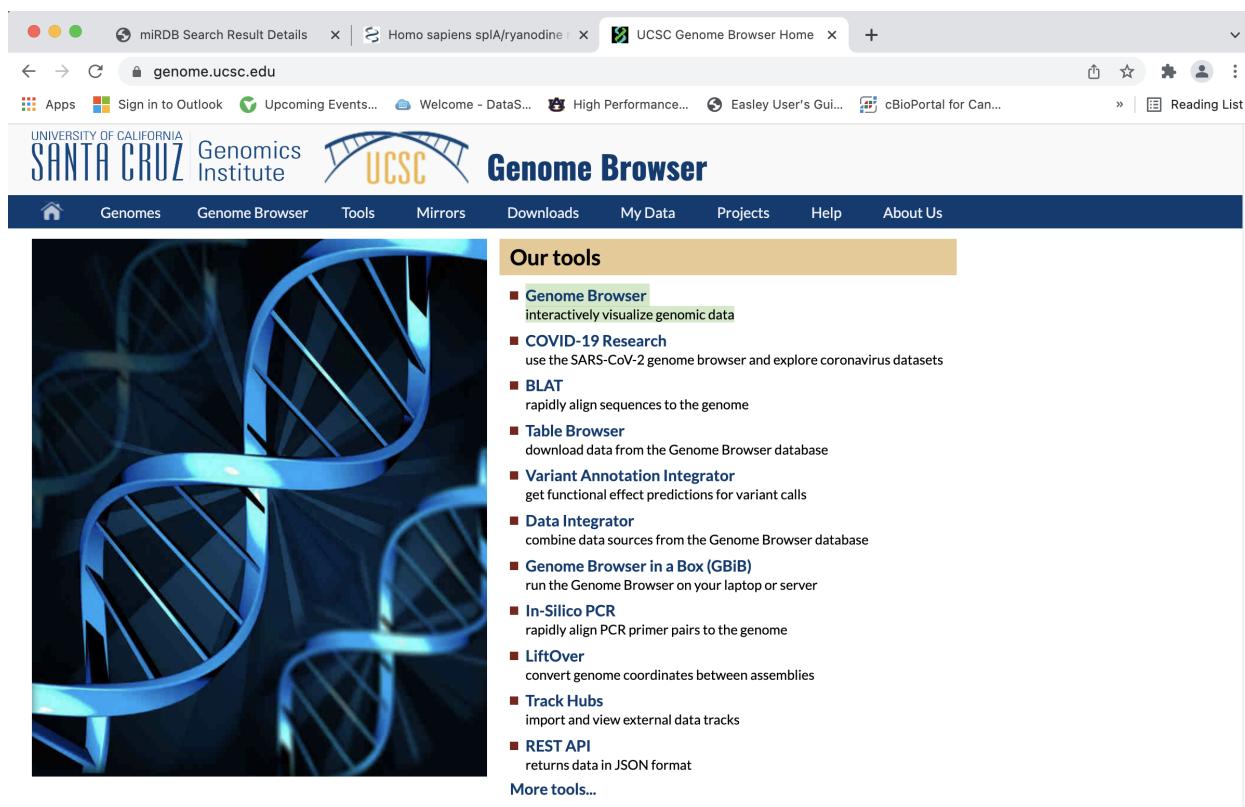


Figure 13: 13

miRDB Search Result Details | Homo sapiens sPLA/ryanodine | UCSC Genome Browser Gateway

genome.ucsc.edu/cgi-bin/hgGateway

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SANTA CRUZ Genomics Institute **UCSC Genome Browser Gateway**

Genomes Genome Browser Tools Mirrors Downloads My Data Projects Help About Us

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

Find Position

Human Assembly Dec. 2013 (GRCh38/hg38)

Position/Search Term NM_025106.4

Current position: chrX:15,560,138-15,602,945

GO

Human Genome Browser - hg38 assembly

view sequences

UCSC Genome Browser assembly ID: hg38
Sequencing/Assembly provider ID: Genome Reference Consortium Human GRCh38.p13 (GCA_000001405.28)
Assembly date: Dec. 2013 initial release; Dec. 2017 patch release 13
Assembly accession: GCA_000001405.28
NCBI Genome ID: 51 (Homo sapiens (human))
NCBI Assembly ID: GCF_000001405.39 (GRCh38.p13, GCA_000001405.28)
BioProject ID: PRJNA31257

Search the assembly:

- By position or search term: Use the "position or search term" box to find areas of the genome associated with many different attributes, such as a specific chromosomal coordinate range; mRNA, EST, or STS marker names; or keywords from the GenBank description of an mRNA. [More information](#), including sample queries.
- By gene name: Type a gene name into the "search term" box, choose your gene from the drop-down list, then press "submit" to go directly to the assembly location associated with that gene. [More information](#).
- By track type: Click the "track search" button to find Genome Browser tracks that match specific selection criteria. [More information](#).

Download sequence and annotation data:

- Using rsync (recommended)
- Using HTTP
- Using FTP
- Data use conditions and restrictions
- Acknowledgments

Figure 14: 14

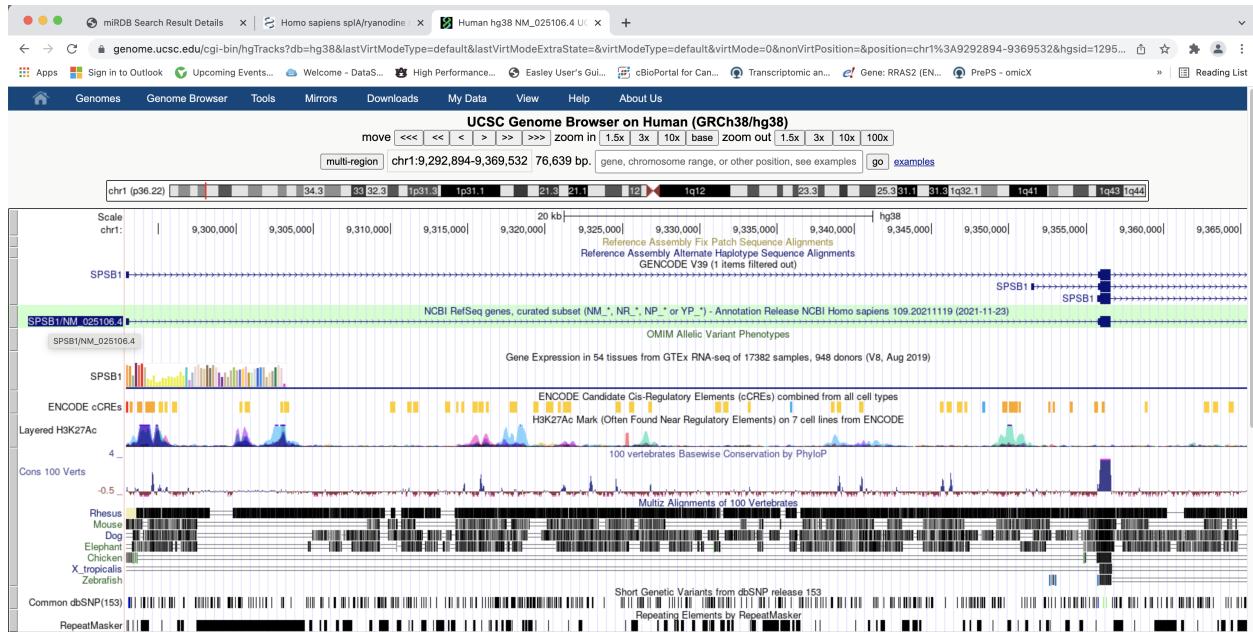


Figure 15: 15

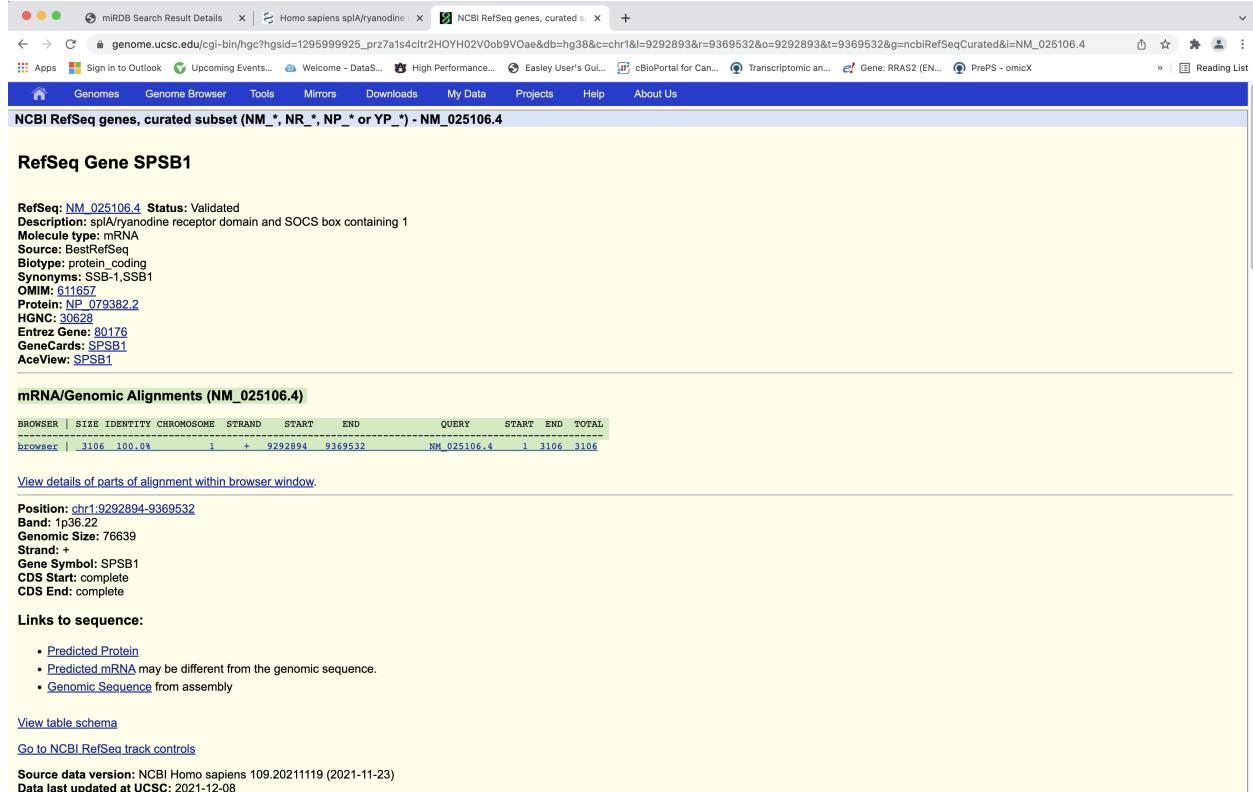


Figure 16: 16

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

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

```

GCACAGAAAGT CGCGCTCGGG CAGCCTGCGC GCTCGCAGCA GGAACCAGGC 50
TCCAGGGCCC GGCGCCGGGG CGGGGGCCCG GGGGAGGAGG CGACTTCGCT 100
CCCTGGGGCG GGCGCGGCCG GGGCGCCCGA GCCTCCTCGG CCTTGGAGAG 150
CAGCGGGCGG GGC CGCACCC CGGGCGCGC AATACTGAAC ACTCGCAGC 200
TTGCGAGAGT CTCTTGCCAG CCCTCATTTAG GAATTCTCTC TGCCCCCGAT 250
CAAGATACTG GAGACGAGAC CACCGAGATTG ATGAGTTTGC CTTGGAGTC 300
GGTAAGAAGG TGAAGCCAGG GGC GAACATG GGT CAGAAGG TCACTGGAGG 350
GATCAAGACT GTGGACATGA GGGGACCCAC GTACAGGCC C TGAAGCAGG 400
AGCTCTCAGGG TCTGGATTAC T GCAAGGCCA CCCGGCTGGA TCTGCTACTG 450
GACATGCCCG CTGTGTCTTA TGATGTCCAG CTGCTGCATT CATGGAACAA 500
CAACAGCCAGG TC GCGCTCAATG TCTTTGTGA GGAGGACAGC AA GCTCATCT 550
TTCACCGGCA TCCGGTGGCC CAAGAGCACCG AC GCTATCAG GGGCAAAGTC 600
GGGTATAACCGT CTGGGCTGCA CGTGTGGAG ATCACGTGGG CCATGAGACA 650
GGCGGGCAC A CAGCCGTGG TGGGGGTGGC GACGGCAGAC GCCCCCTCGC 700
ACTCTGTCTGG T GACACACACC CTCGTGGGG A TAAACCGCA GTCTGGGGC 750
TGGGACTCTGG GGC GCAACCG GCTCTACAC GATGGAAGA ACCAGCCAAG 800
CAAACACATCA CCAGCCCTTTC T GGAACAGCA TGAGACATTC ATTGTCCTCG 850
ACTCCCTCTCCTGGTACCGGCA GACATGGAGC AGGGACTCT GACCTTCATT 900
GTGAGATGGAC AGTACATGG AGTGGCTTT CCGGGACTCA AGGGCAAAA 950
ACTGTATCTCTG T GAGTGTAGT CCGCTGTGGG CCACTGTGAG ATCCGAATGC 1000
GCTACTTGAAC CGGAGCTCGAT CCGGAGCCG T GCGCTCAT GGATTGTGC 1050
CGTCTGTGGG T GCGCTCTGG C CTGGGGAGG GAGGCCCTGG GGGAGATCCA 1100
CACGCTGCCG CTGCGGCTT C CTCAGCAAGG C TACCTCTC T ACCAGTGAC 1150
GTTGCCCATC ATACCGCCAG CCGGAGACGG ACCTGCTGCC AACTCACTGA 1200
GCCGCTCTGG GCTGGGGCCG CCGCACCCCTG CACCTTGAC CGGCATCCGT 1250
AGCCATGGAC AGAGGTCTCCCT GGTCTTCCCT CATCCTCGGT GGCTGCCTCC 1300
ATGGGACAAAG GACCGATTCC AACACAGGT C CTCTTCCC C CTTCCCGAC 1350
ATCAGGAGAA GGCAGCATCC CTGCACTGGC TCCGTATACA ACCCCCTCTT 1400
GAAAAAAAGAC ACAGAGAATA AACTCTAACG AAAGCCCTAC ATTGAGCTCC 1450
AAATCTGCTGG GGGTGGGAGC GGTGCTTCCC ACACCTCTGG GAGAAGCTG 1500
CAGCCACCTG GGGTCTCCAGG GGTGGTGGGG GTGGCAGGTG GTACCAACAGC 1550
TCTGAGAGCA GATACCAGGG GTACTAAGAG GTGCTTAGAC AAGGGCTGGT 1600
GCCCGGCCCA GGTGCCCCAG CGGGGCCATG CCATGGAGA TAAAGCTCAG 1650
GACGTCAAAA ACTCACCATG GACCCCAAGG CAGAAACCAA GAAC TGTCTG 1700
CAGGCAAAATA AGCAGCCAG ACCCATCTCG GCTGCCGGTG CCCGTACCC 1750
TGTATTATTAT CTTTTAACAA TAACAAAAGC CATT TATT TA TTCCATCTAG 1800
AAAGGAAACCTG CTGTTTCACTG CCCCCTCTCTC TGGCTGTCT GTTACTCTTC 1850
TTCCACCTGT GCCCCTCCCTG GGATATGTAT G C CTCGCCCG C CTCCTCTGG 1900
GCACATGTGC ACACGTGCCG AGGCACAAAGT ATGCTCTGG GTCTCTGGC 1950
CTGCACTTTC CAGGGGCTC T GCTCCAAAGT T C C T C A G G G G G C C C C T C A G G 2000
GAGAAATAGC CTCACGTCA ATCTGGGTGT CTT CGGGGGC CCGTCTGAA 2050
GGGGCTGCAGC AAT T C C C T G T G T C T C A G G A A C A G C C C C A G T T C A 2100
TCAGGCAACCCCTTGGCACAGG TTGCACTTTCTT TTAGTCTCT GTGGGTCTTT 2150
TGATGTGGGT TTGATTCTGG TTTTGTCTT CTAGCTGAGA TT T C C C A A G T 2200
GCATCCTCG AAGCTCTGGG TGTGCCAGAG GACCCCTAGA ACTAAGAAGG 2250
GAGGGCAGACT GGGTCTCCAT T C C C C G A G A G A G C C C C G G G G G A G T 2300
GGGAAGACCA GAGCAGAGT CGAGCCTCAC AGAAGCAGC GCGGGCTCT 2350
GCTCAGCACC CCAGCCGGG CTCTGGACCC AGGGTAACAG CCCCAGTTCA 2400
TCCCAACCCCTTGGCACAGG TCAAGAGGGG TAGCTCGCT GCGGGAAAGAG 2450
AGGGGTGCCCTATCCCTGCA AACCCCTCCA CCTAGCGTAC CCCAGCACCT 2500
GCCACCGCCCTTGCACTTTC TTTGAGCTTG AAGTAACTC TCTTAGAGTC 2550
TAACATTGCTGTCACAGGTACAA TAGATGACTT TTTTGTCTTA 2600
AAATGTAAAT TATATATACA TACATATATA TATATTTGTC TGTAAGAATT 2650
ATGTTTAAAGCAGCTGCTGT AGAGTACCTT TTTTAAGTA AATCTTACAG 2700
TGGAGTATAT TTTTTAAAGC ACAAATTTGG TGCAAGACT GGGTGAAGAAA 2750
TGTCATTTAC CCCCCTATTA TTTTGACGGT TTTTTTTTC GGGGCAGGG 2800
ACCTTACCTGTAAGACTTTTAAAGATTTTCCTCCCTCTGTTTCAGGTGG 2850
GTCACATTTGCTGATGAATGTT TCCCTTGACAGATCCAGC TTATGGCTT 2900
GACCCAGCCCTCCTCAGA TGCGGGGTGA CCCTCTAGCT CTCTCTGCT 2950
CTCCCAACCCCTCGACACCCCTGGGACCCCTCG ACCCCACCCCT TCTTCTCTAC 3000
CAGCCCAAGAGCTTGTGGCT TGACAGTTTGAAACTCCC GTTCTTATTTT 3050
ATGATGGTTGATAATAGTCAGTAACCTAAT AAAGGAACGT TTGTTAAAT 3100
ATCAA

```

Figure 17: 17

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

[genome.ucsc.edu/cgi-bin/hgc?hgsid=1295999925_prz7a1s4cltr2HOYH02V0ob9VOae&g=htcCdnaAli...](#)

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Alignment of NM_025106.4

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cDNA NM_025106.4

CACAGAAAGT	CGCGCTCGGG	CAGCCTGC	GCTCGCAGCA	GGAACCAAGGC	50
TCCAGGCC	GGCGCCGGG	CCGGGGCC	GGGGAGGAGG	CGACTTCGCT	100
CCCTGGGG	GGCGCGGCC	GGCGGCCG	GCTCTCTCGG	CCTTGGAGAG	150
CAGCGGCC	GGCGCACCC	GGGGCGC	AATACTGAAC	ACTGCCAGC	200
TTTCAGAGGT	CTCTTGGCAG	CCCTCATTA	GAATTCTGTC	TGGCCCCGAT	250
CAGAATACTG	GAGACGAGAC	CACGAGATTG	ATGAGTTTGC	CTTGGGAGTC	300
GGTAAGAAGG	TGAAGGCCAGG	GGCGAACATG	GGTCAGAAGG	TCACTGGAGG	350
GATCAAGACT	GTGGACATGA	GGGACCCAC	GTACAGGCC	CTAACAGCAGG	400
AGCTCCAGGG	TCTGGATTAC	TGCAAGCCC	CCCGCTGGA	TCTGCTACTG	450
GACATGCC	CTGCTGCC	TGATGTCC	CTGCTGCATT	CATGGAAACAA	500
CAAACACCGA	TCCGCTCAATG	TCTTTGTGA	GGAGGACGAC	AAGCTCATCT	550
TTCACCGGA	TCCGGTGGCC	CAGAGCACGG	ACGGTATCAG	GGGCAAAGTC	600
GGGTATACCC	GTGGGCTGCA	CCTGTGGCAG	ATCACGTGGG	CCATGAGACA	650
GGGGGGCACA	CACGCCGTG	TGGGGTGGC	GACGGCAGAC	GCCCCCTG	700
ACTCTGTGG	CTACACAAAC	CTGGTGGGA	ATAACCCACGA	GTCTGGGGC	750
TGGGACTTGG	GGCGCAACCG	GCTCTACCAC	GATGGCAAGA	ACCAGCCAAG	800
CAAACATAC	CCAGCCTTC	TGGAACCCAGA	TGAGACATTC	ATTGTCCTG	850
ACTCTTCTT	GGTAGCCCTG	GACATGGACG	ACGGGACTCT	GAGCTTCATT	900
GTGGATGGAC	AGTACATGGG	AGTGGCTTT	CGGGGACTCA	AGGGCAAAAA	950
ACTGTATCTT	GTAGTGAGT	CCCTCTGGGG	CCACTGTGAG	ATCCGAATGC	1000
GCTACTTGAA	CGGACTCGAT	CCCGAGCCGC	TGCCGCTCAT	GGATTTGTGC	1050
CGTCGCTGG	TGCGCCTGGC	CCTGGGGAGG	GAGCGCCTGG	GGGAGATCCA	1100
CACGCTGGG	CTGGCGCTT	CCCTCAAGGC	CTACCTCTT	TACCACTGAC	1150
GTTCGCCATC	ATACCGCCAG	CGGGACAGCC	ACCTGGTGC	AACTCACTGA	1200
GCCGCTGGC	GCTGGGGCCG	CCGCACCCCTG	CACCTTGAC	GGGCATCCGT	1250
AGCCATGGAC	AGAGGTCCTC	GGTCTTCC	CATCTCCGT	GGCTGCCCTC	1300

Figure 18: 18

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

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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 CAGCCTGCGC GCTGCCAGCA GGAACCAGGC 50
TCCAGGCGCC GGCGCCGGGG CCAGGGGCCG GGGGAGGAGG CGACTTCGCT 100
CCCTGCGGCG GGCGCGCCC GGGCGCCCGA GCCTCTCGG CCTTGAGAG 150
CAGCGGCGGC GGCGGCCACCC CGGGCGCGGC AATACTGAAC ACTGCGCAGC 200
TTGCAGAGGT CTCTGGAG CCCTCATTA GAATTCTGTC TGGCCCCGAT 250
CAGAATACTG GAGACGAGAC CACGAGATTG ATGAGTTGC CTTGGGAGTC 300
GGTAAGAAGG TGAAGCCAGG GGCGAAC
```

Go **Clear**

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="text"/> Go Clear
Search by gene target
Human <input type="button" value="Gene Symbol"/> <input type="button" value="Coding Region"/> <input type="text"/> Go 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.

Figure 19: 19

Custom Prediction

Homo sapiens splA/ryanodine... | NM_025106.4 vs Genomic [nc]

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miRDB

There are 2 predicted miRNAs targeting the submitted 327 nt long mRNA sequence.

Return to Custom Prediction

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

Figure 20: 20