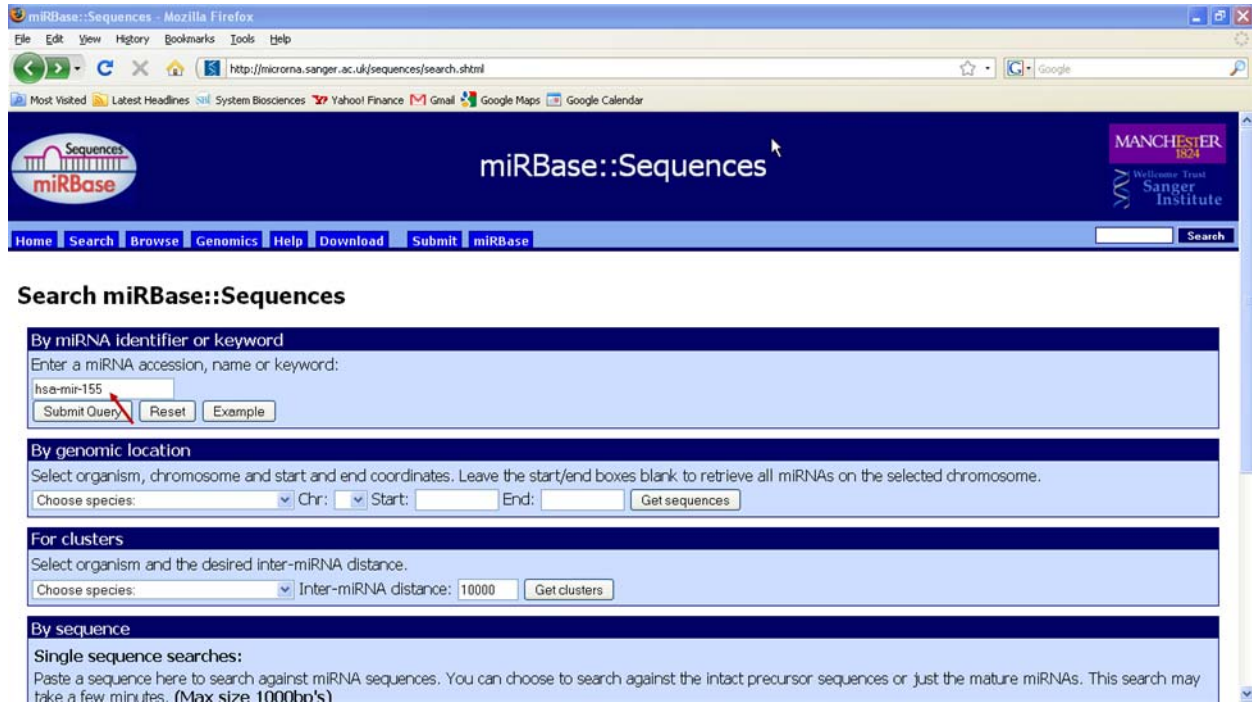


Searching for homology to mature human microRNA

1. Visit miRBase at: <http://microrna.sanger.ac.uk/sequences/>
2. Click on the Search tab at the top of the page:



3. Enter the microRNA of interest and click Submit [be sure to use the following format: xxx-miR-yyy; where xxx is species (hsa for human (Homo sapiens), mmu for mouse, rno for rat, ggo for gorilla, etc) and yyy is the microRNA of interest]:



miRBase::Sequences

Home Search Browse Genomics Help Download Submit miRBase

Search miRBase::Sequences

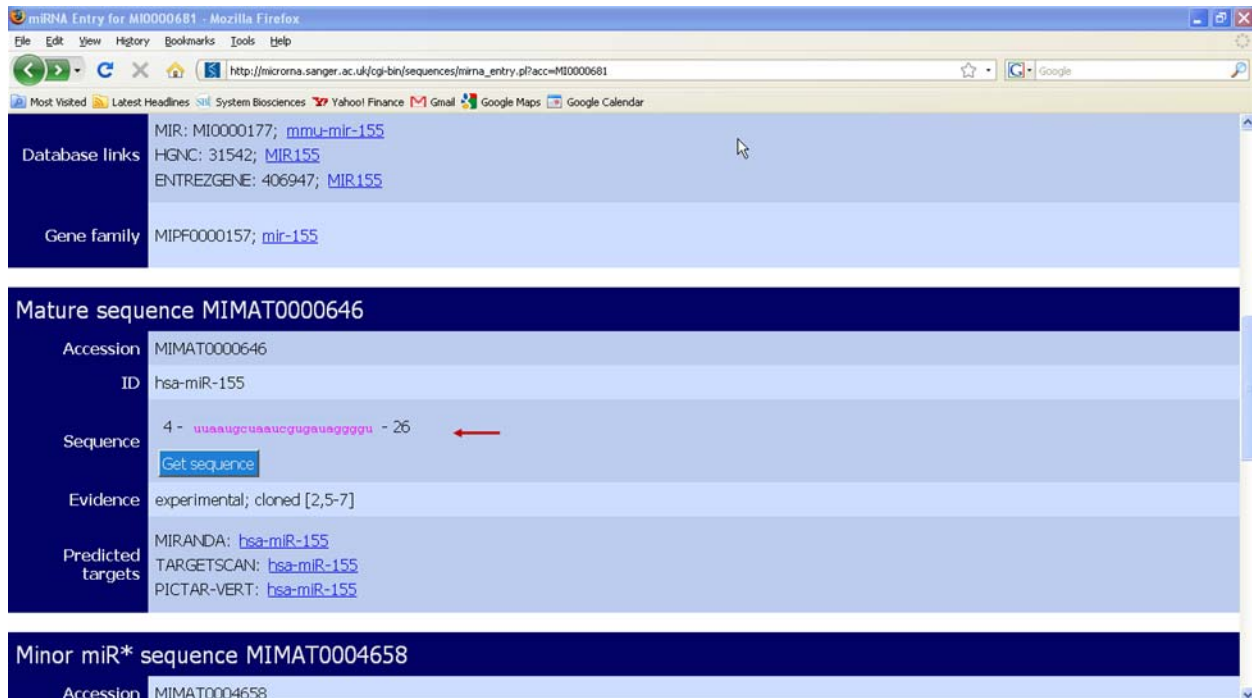
By miRNA identifier or keyword
Enter a miRNA accession, name or keyword:
hsa-mir-155
Submit Query Reset Example

By genomic location
Select organism, chromosome and start and end coordinates. Leave the start/end boxes blank to retrieve all miRNAs on the selected chromosome.
Choose species: Chr: Start: End: Get sequences


For clusters
Select organism and the desired inter-miRNA distance.
Choose species: Inter-miRNA distance: 10000 Get clusters

By sequence
Single sequence searches:
Paste a sequence here to search against miRNA sequences. You can choose to search against the intact precursor sequences or just the mature miRNAs. This search may take a few minutes. (Max size 1000bp's)

4. Once the microRNA page has loaded, scroll down to the Mature Sequence section:




The screenshot shows a web browser window with the URL http://microma.sanger.ac.uk/cgi-bin/sequences/mirna_entry.pl?acc=MIM000681. The page content is as follows:

Database links	MIR: MIM000177; mmu-mir-155 HGNC: 31542; MIR155 ENTREZGENE: 406947; MIR155
Gene family	MIPF0000157; mir-155
Mature sequence MIMAT000646	
Accession	MIMAT000646
ID	hsa-miR-155
Sequence	4 - uuuuugcuuaaucgugauaggggu - 26 
Evidence	experimental; cloned [2,5-7]
Predicted targets	MIRANDA: hsa-miR-155 TARGETSCAN: hsa-miR-155 PICTAR-VERT: hsa-miR-155
Minor miR* sequence MIMAT0004658	
Accession	MIMAT0004658

5. Copy the mature sequence.

6. Click on Search at the top of the page again:



miRNA Entry for MI0000681 - Mozilla Firefox

http://microrna.sanger.ac.uk/cgi-bin/sequences/mirna_entry.pl?acc=MI0000681

Sequences
miRBase

miRBase::Sequences

MANCHESTER 1854
Wellcome Trust
Sanger
Institute

Home Search Browse Genomics Help Download Submit miRBase hsa-mir-155 Search

Stem-loop sequence MI0000681

Accession MI0000681

ID hsa-mir-155

Symbol [HGNC:MIR155](#)

Description Homo sapiens miR-155 stem-loop

Stem-loop

```

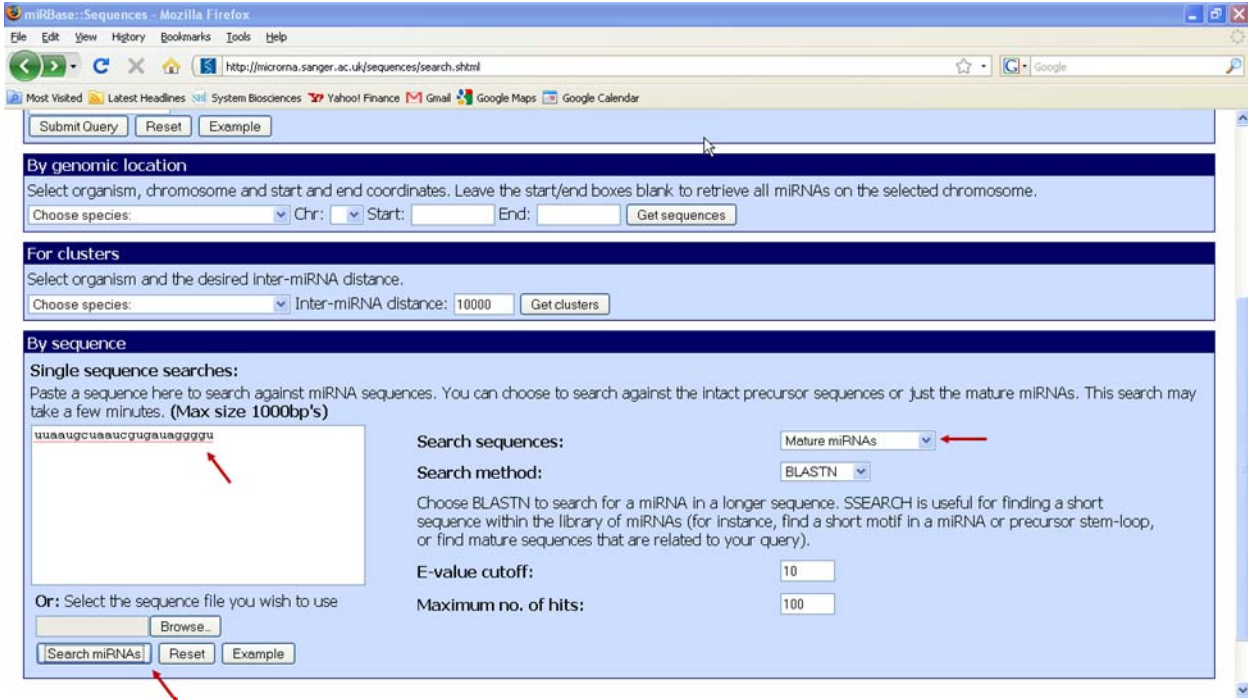
      c   a           -u   c
cuguaaaugcuaau  gug  uagggguu  uug  c
|||||
gacaauuacgaua  uac  auccuag  aac  u
      -   -           uc   c
  
```

[Get sequence](#)

Comments

Human mir-155 is predicted based on homology to a cloned miR from mouse ([MI0000177](#)) [1], and later experimentally validated in human HL-60 leukemia cells [2]. Like the mouse miRNA, human mir-155 resides in the non-coding BIC transcript (EMBL:AF402776), located on chromosome 21 [3]. The mature form differs from that in mouse at a single position. Eis et al. confirm that miR-155 is processed from the BIC transcript in human, and demonstrate elevated expression of miR-155 in lymphoma samples [4]. The mature sequence shown here represents the most commonly cloned form from large-scale cloning studies [5].

7. Scroll down to the By Sequence section and paste the mature human sequence.
8. Once it is pasted, be sure to set the Search Sequences to Mature miRNAs, then click Search miRNAs.



miRBase::Sequences - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://microrna.sanger.ac.uk/sequences/search.shtml

Submit Query Reset Example

By genomic location

Select organism, chromosome and start and end coordinates. Leave the start/end boxes blank to retrieve all miRNAs on the selected chromosome.

Choose species: Chr: Start: End: Get sequences

For clusters

Select organism and the desired inter-miRNA distance.

Choose species: Inter-miRNA distance: 10000 Get clusters

By sequence

Single sequence searches:

Paste a sequence here to search against miRNA sequences. You can choose to search against the intact precursor sequences or just the mature miRNAs. This search may take a few minutes. (Max size 1000bp's)

uuuuugcuaaucguguaaggggu

Search sequences: Mature miRNAs

Search method: BLASTN

Choose BLASTN to search for a miRNA in a longer sequence. SSEARCH is useful for finding a short sequence within the library of miRNAs (for instance, find a short motif in a miRNA or precursor stem-loop, or find mature sequences that are related to your query).

E-value cutoff: 10

Maximum no. of hits: 100

Or: Select the sequence file you wish to use

Browse...

Search miRNAs Reset Example

9. From the results page, click Align for the species of interest (mouse in this example):

Sequence search results

Matches for your nucleotide sequence

Accession	ID	Query start	Query end	Subject start	Subject end	Strand	Score	Evalue	Alignment
MIMAT0000646	hsa-miR-155	1	23	1	23	+	115	0.24	Align
MIMAT0006988	oan-miR-155	1	23	1	23	+	115	0.24	Align
MIMAT0006216	mml-miR-155	1	23	1	23	+	115	0.24	Align
MIMAT0006671	cfa-miR-155	1	23	1	23	+	115	0.24	Align
MIMAT0008048	ptr-miR-155	1	23	1	23	+	115	0.24	Align
MIMAT0009241	bta-miR-155	1	23	1	23	+	115	0.24	Align
MIMAT0001106	gga-miR-155	1	22	1	22	+	110	0.43	Align
MIMAT0001851	dre-miR-155	1	22	1	22	+	110	0.43	Align
MIMAT0003608	xtr-miR-155	1	22	1	22	+	110	0.43	Align
MIMAT0000165	mmu-miR-155	1	23	1	23	+	106	0.62	Align
MIMAT0006105	cin-miR-155	1	21	1	21	+	96	1.9	Align

Alignment of Query to mature miRNAs

10. In this particular example, it appears as if the mature sequence of the human miR-155 and mouse miR-155 differ by 1 nucleotide.

miRNA Search Results - Mozilla Firefox

http://micro.smith.man.ac.uk/cgi-bin/mirbase/blast.pl?mmu-miR-155

UserSeq 1 UUA AUGCUAAUCGUGAUAGGGG 22

dre-miR-155 1 UUA AUGCUAAUCGUGAUAGGGG 22

Query: 1-22 [xtr-miR-155](#): 1-22 score: 110 evalue: 0.43

UserSeq 1 UUA AUGCUAAUCGUGAUAGGGG 22

xtr-miR-155 1 UUA AUGCUAAUCGUGAUAGGGG 22

Query: 1-23 [mmu-miR-155](#): 1-23 score: 106 evalue: 0.62

UserSeq 1 UUA AUGCUAAUCGUGAUAGGGG 23

mmu-miR-155 1 UUA AUGCUAAUUGGGAUAGGGG 23

Query: 1-21 [cin-miR-155](#): 1-21 score: 96 evalue: 1.9

UserSeq 1 UUA AUGCUAAUCGUGAUAGGGG 21

cin-miR-155 1 UUA AUGCUAAUAGUGAUAGGGG 21

Search parameters

Search Method: Blastn
Sequence database: mature
Evalue cutoff: 10
Max alignments: 100

Comments or questions? Send a mail to microma@sanger.ac.uk