miRBase



A Public Resource for miRNA Sequences, Predicted Targets, and Nomenclature

miRBase Agenda

- Introduction and Credits
- Basic Search & Results
- Deep Sequencing Report
- Advanced Search Options
- Additional Features
- Summary
- Exercises

miRBase: http://www.mirbase.org/

miRBase Homepage & Credits



Discovery of microRNA



C. elegans lin-4 (*Lee R et al. 1993*)
let-7 (*Reihhart et al. 2000*)



Victor Ambros

First miRNA - *C. elegans* lin-4 in 1993 by Victor Ambros & Lee

lin-4 causes temporal decreasing in LIN-14 protein expressed in the first larval stage (L1).

"The Caenorhabditis elegans heterochronic gene lin-4 encodes small RNAs with antisense complementarity to lin-14". CELL (1993)



Frank Slack

Second miRNA - *C. elegans* let-7 in 2000 by Frank Slack

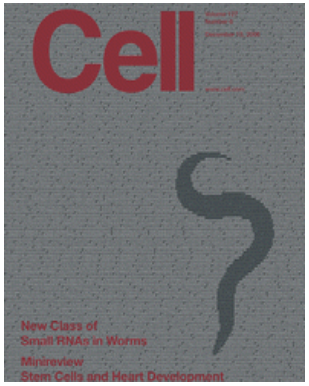
miRNA might be conservative in organic evolution and plays an important role in regulation of organic development.

"The 21-nucleotide let-7 RNA regulates developmental timing in Caenorhabditis elegans" . NATURE (2000)

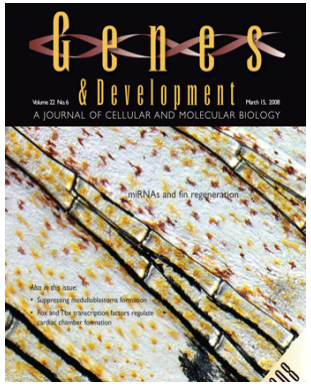




miRNAs host genes and transcription



New class of small RNAs in worms



miRNAs and fin development



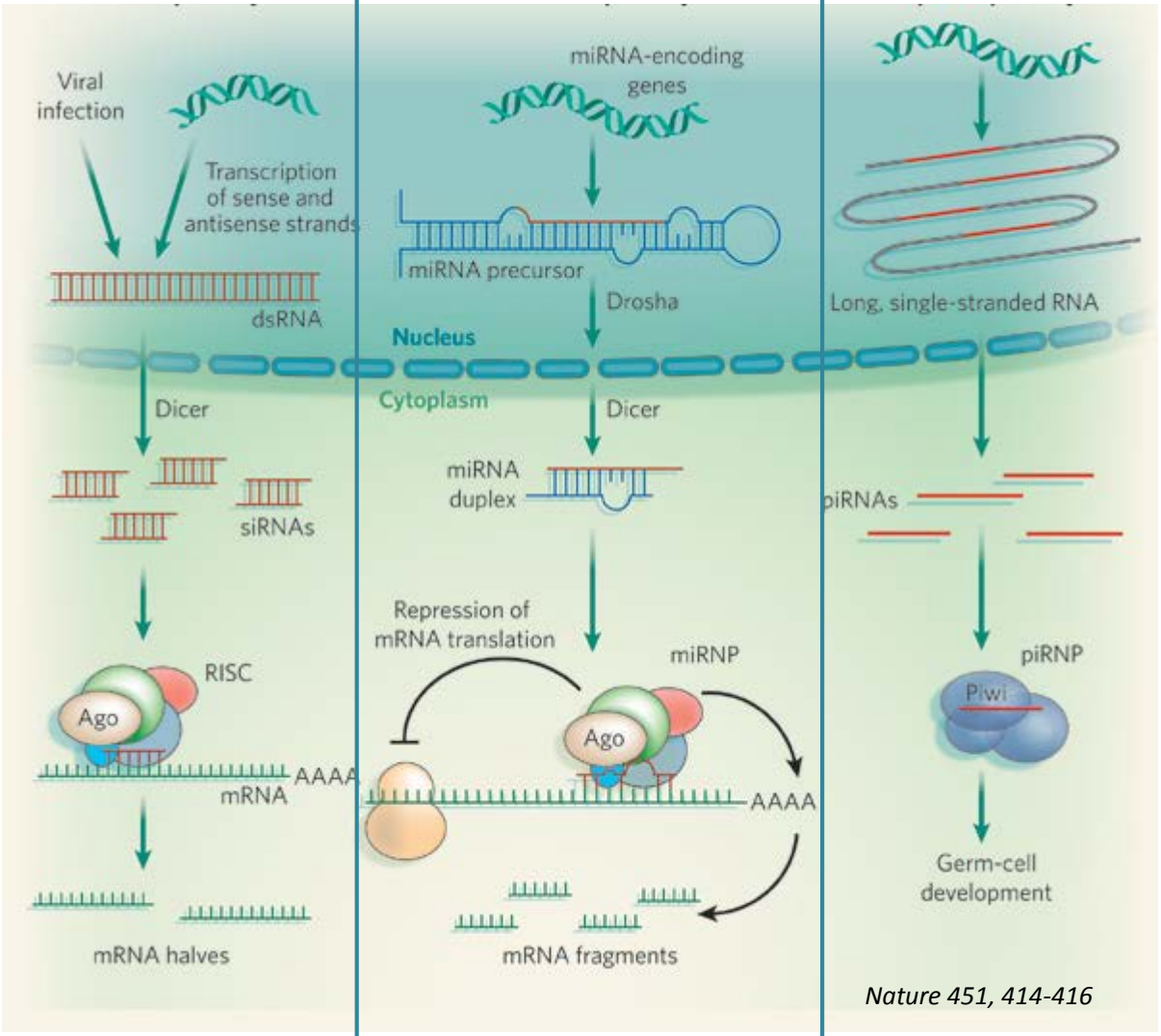
Stem cell division

Non-coding Regulatory RNAs

siRNA
Formed through cleavage of synthetic long double-stranded RNA molecules

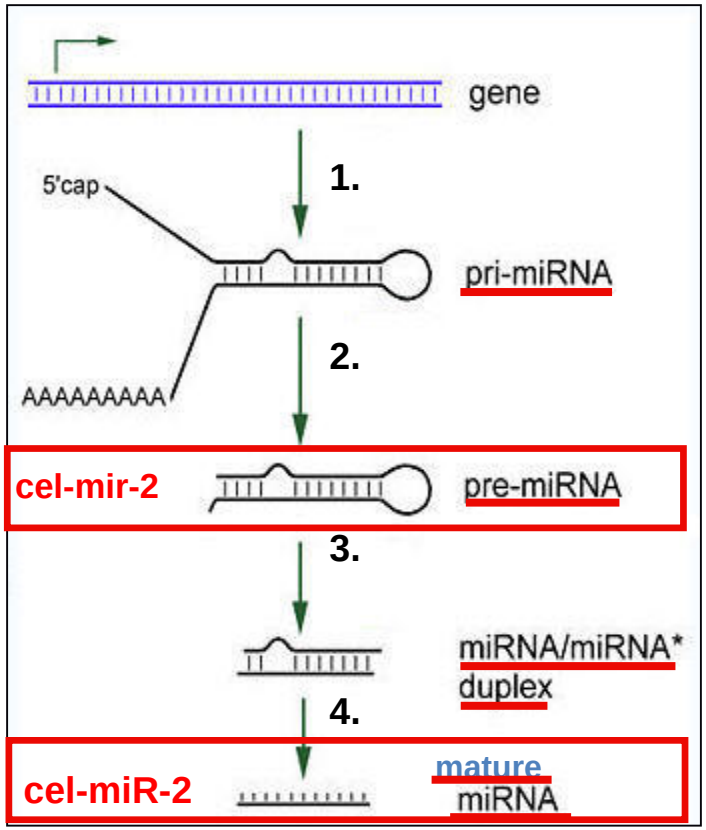
microRNA (miRNA)
Processed from long, single-stranded RNA sequences that fold into hairpin structures

Piwi-RNA (piRNA)
Generated from long single-stranded precursors.



Nature 451, 414-416

MicroRNA Biogenesis



1. Transcription of miRNA in the nucleus → pri-miRNA
2. Excision of stem-loop (a.k.a. hairpin) precursor that contains the microRNA sequence in one arm of the hairpin → pre-miRNA. Transport to cytoplasm
3. Processing of the stem-loop precursor into double-stranded RNA
4. Formation of mature miRNA

miRBase::Sequences stores pre-miRNA and mature miRNA sequences



From https://tools4mirs.org

microRNA – What is in the Name?

GENERAL FORM: species code – mir/miR – number-(suffix)
e.g. cel-mir-2

Orthologs → **identical number**

Accession	ID	
MI0000257	mmu-mir-143	mouse
MI0000459	hsa-mir-143	human
MI0000916	rno-mir-143	rat
MI0002007	dre-mir-143-1	*Danio rerio*
MI0002008	dre-mir-143-2	

Same mature sequence, different locus→ **numerical suffix**:

Accession	ID	
MI0001881	dre-mir-9-2	Chrom 10
MI0001883	dre-mir-9-3	Chrom 25
MI0001882	dre-mir-9-4	Chrom 22
MI0001884	dre-mir-9-5	Chrom 5

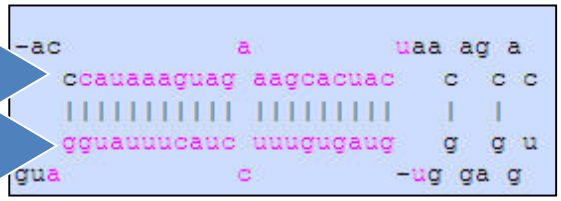
Related mature sequences → **lettered suffix**

```
dre-miR-27e UUCACAGUGGCUAAGUUCAGUG
dre-miR-27a UUCACAGUGGCUAAGUUCGCU
dre-miR-27d UUCACAGUGGCUAAGUUCUUCA
dre-miR-27b UUCACAGUGGCUAAGUUCUGCA
```

Mature miRNA from BOTH strands of hairpin→ **5p/3p suffix**

mmu-miR-142-5p

mmu-miR-142-3p



There are exceptions

miRBase References

References

If you make use of the data presented here, please cite the following articles in addition to the primary data sources:

miRBase: integrating microRNA annotation and deep-sequencing data.
Kozomara A, Griffiths-Jones S.
NAR 2011 39(Database Issue):D152-D157

miRBase: tools for microRNA genomics.
Griffiths-Jones S, Saini HK, va
NAR 2008 36(Database Issue

miRBase: microRNA sequenc
Griffiths-Jones S, Grocock RJ
NAR 2006 34(Database Issue

The microRNA Registry.
Griffiths-Jones S.
NAR 2004 32(Database Issue

The following publications

A uniform system for microR
Ambros V, Bartel B, Bartel DP
G, Tuschl T.
RNA 2003 9(3):277-279

Criteria for annotation of plan
Meyers BC, Axtell MJ, Bartel B
Jacobsen SE, Mallory AC, Mar
Plant Cell. 2008 20(12):3186

D152–D157 Nucleic Acids Research, 2011, Vol. 39, Database issue *Published online 30 October 2010*
doi:10.1093/nar/gkq1027

miRBase: integrating microRNA annotation and deep-sequencing data

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Faculty of Life Sciences, University of Manchester, Michael Smith Building, Oxford Road, Manchester, M13 9PT, UK

Received September 15, 2010; Accepted October 10, 2010

ABSTRACT

miRBase is the primary online repository for all microRNA sequences and annotation. The current release (miRBase 16) contains over 15 000 microRNA gene loci in over 140 species, and over 17 000 distinct mature microRNA sequences. Deep-sequencing technologies have delivered a sharp rise in the rate of novel microRNA discovery. We have mapped reads from short RNA deep-sequencing experiments to microRNAs in miRBase and developed web interfaces to view these mappings. The user

(5) to link to and aggregate microRNA target predictions and validations.

The miRBase database was established in 2002 (then called the microRNA Registry) to provide microRNA researchers with stable and unique gene names for their novel microRNA discoveries (aim 1) and an archive of all microRNA sequences (aim 2) (1–3). Official gene names assigned by miRBase should be used in the published version of articles that describe their identification; gene names are assigned in confidence for inpress manuscripts (1). The incorporation of short RNA deep-sequencing data into miRBase as evidence for

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News - release 16

We are mapping reads from deep sequencing experiments to miRNA annotations. These mappings can be viewed from links in the miRNA entry pages. We will be adding data over the coming weeks and months. As usual, please contact us (mirbase@manchester.ac.uk) with questions, comments or problems.

miRNA count: 15172 entries

Release 16: Sept 2010

Search by miRNA name or keyword

Go | Example

Download published miRNA data

Download page | FTP site

This site is featured in:

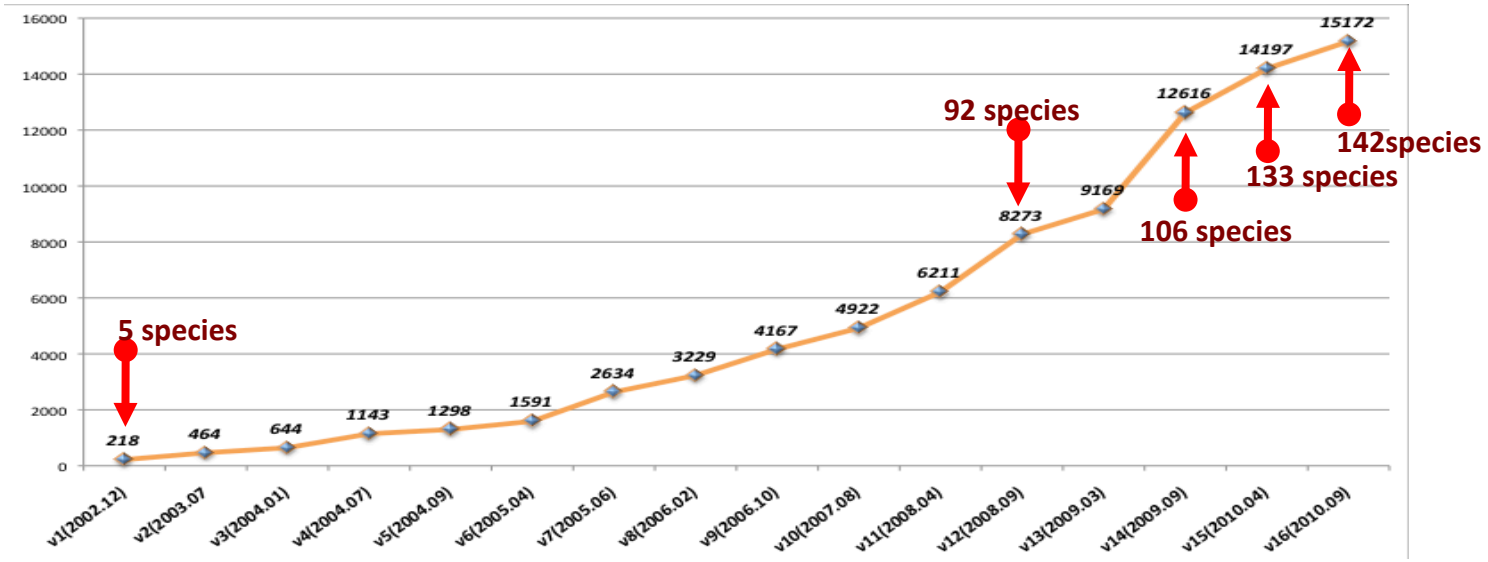
NetWatch - *Science* 303:1741 (2004)

Highlights, Web watch - *Nature Reviews Genetics* 5:244 (2004)

miRBase: the microRNA database

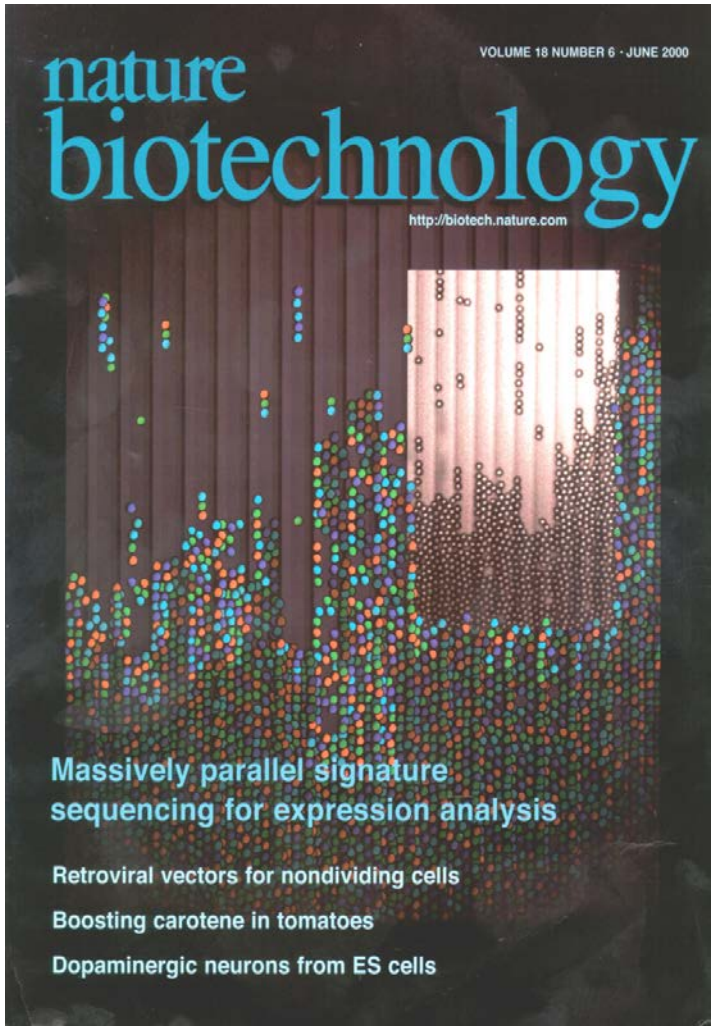
miRBase provides the following services:

- 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.
- The miRBase Targets database and pipeline has been rebranded as microCosm, and is now hosted at the EBI. The microCosm resource continues to be maintained by the Enright group. miRBase currently links miRNAs to targets predicted by microCosm, TargetScan and Pictar, and aims to provide a more extensive target prediction aggregation service in the future.

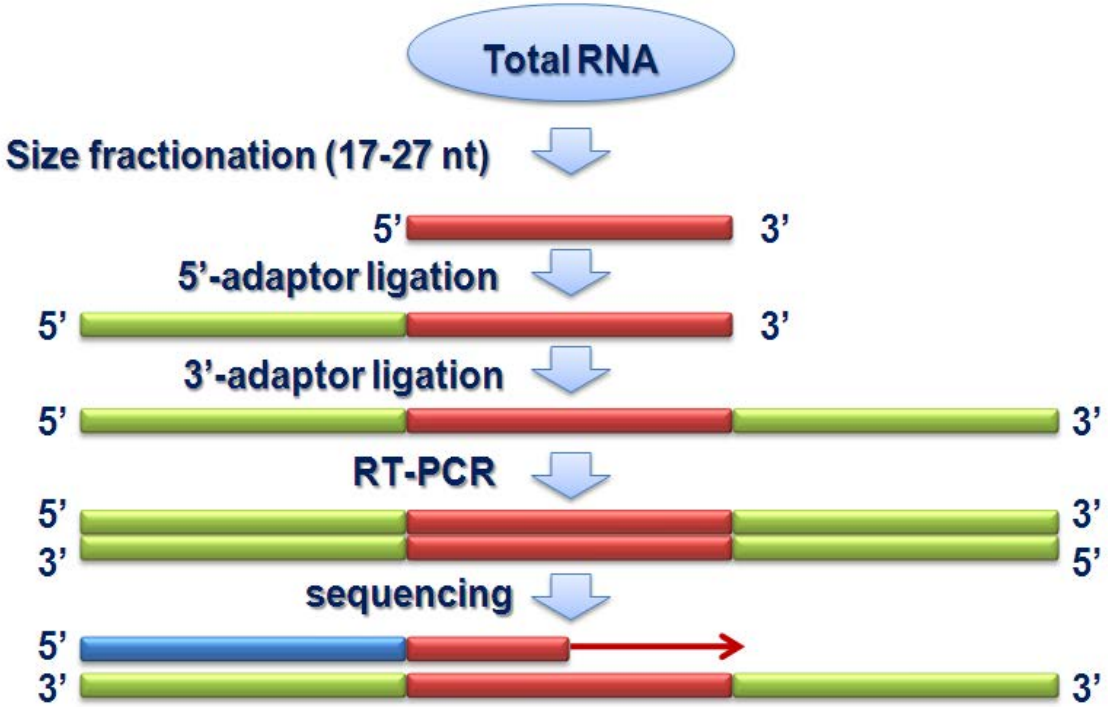


Next Generation Sequencing Technology

Roche illumina applied biosystems



Illumina SOLEXA sequencing by synthesis




```
@HWI-EAS82_3_FC204V1AAXX:6:1:886:345
AGAGTTCTACAGTCCGGACGATCTCGTATGCCGTC
+HWI-EAS82_3_FC204V1AAXX:6:1:886:345
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
```

40,000,000 reads of 35 bp long

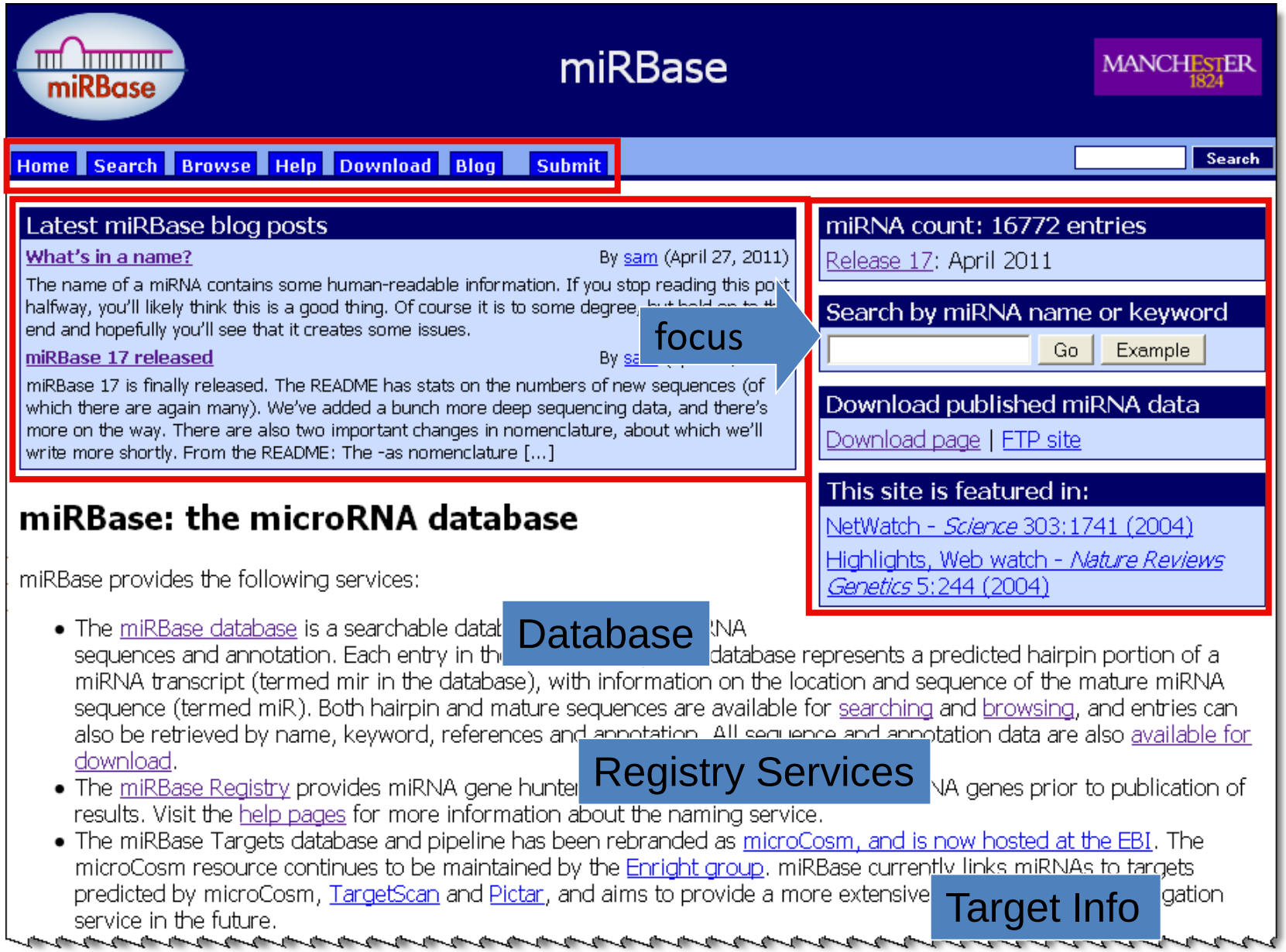
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miRBase Homepage: www.mirbase.org



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miRBase Basic Keyword Search



Search Results

We found **40** unique results for your query ("*mir-307*"), in **2** sections of the database.

Section	Description	Number of hits
miRNA name	match the accession or ID of a hairpin precursor entry	40
Mature name	match the accession or ID of a mature miRNA sequence	58
Dead entry	match the accession or ID of a dead entry	0
Gene symbol	find miRNA entries based on gene symbols	0
Description	search miRNA entry description	0
Comments	search miRNA entry comments	0
PubMed ID	find miRNA entries based on literature reference PubMed ID	0
Literature reference	search title and authors of associated literature references	0

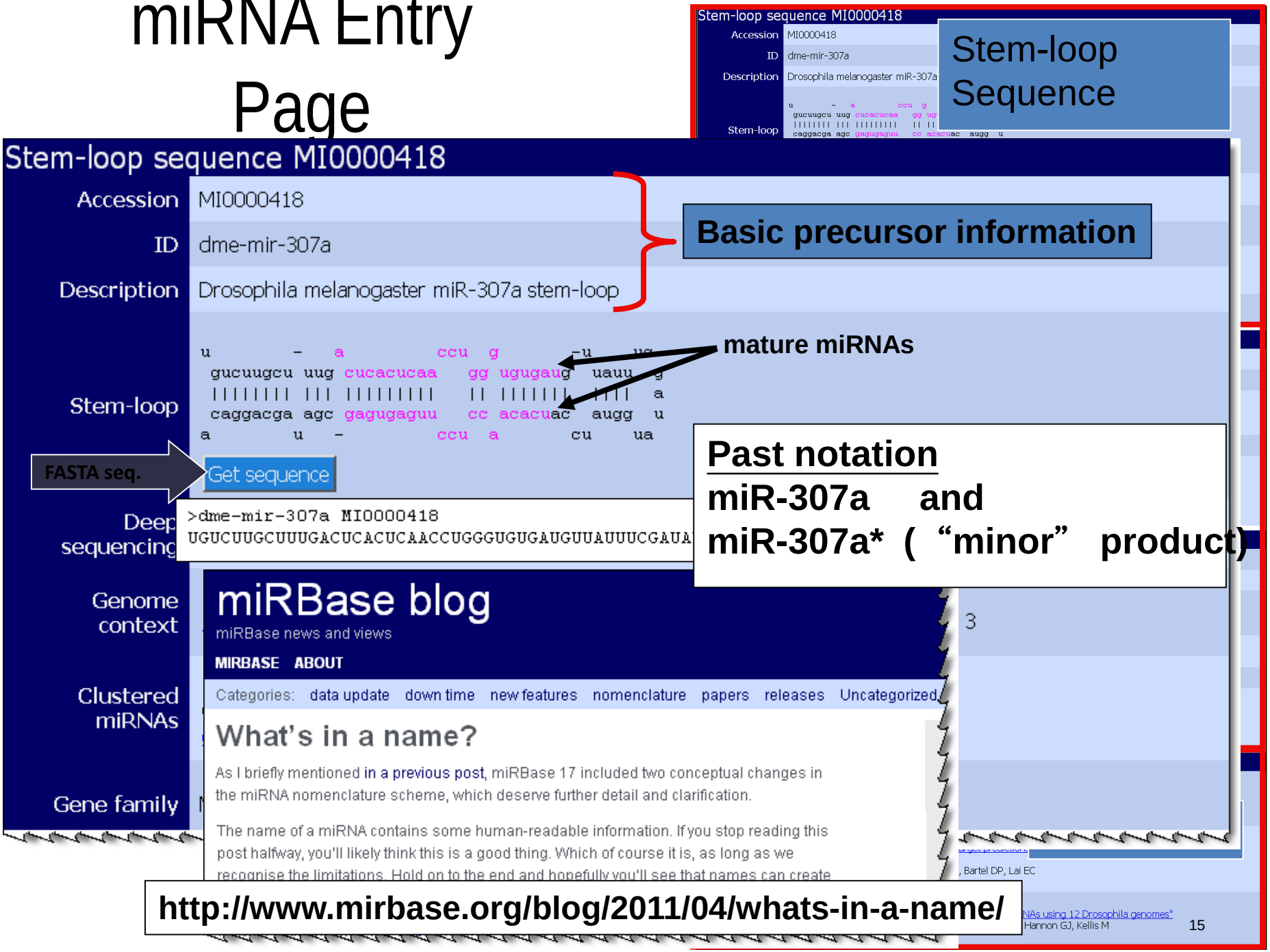
Unique miRNAs

The above key shows a brief description of each of the database sections, along with the number of hits found in each one. Only unique miRNA entries are shown in the results table below. Click the column headings to sort the results table, or restore to the original order .

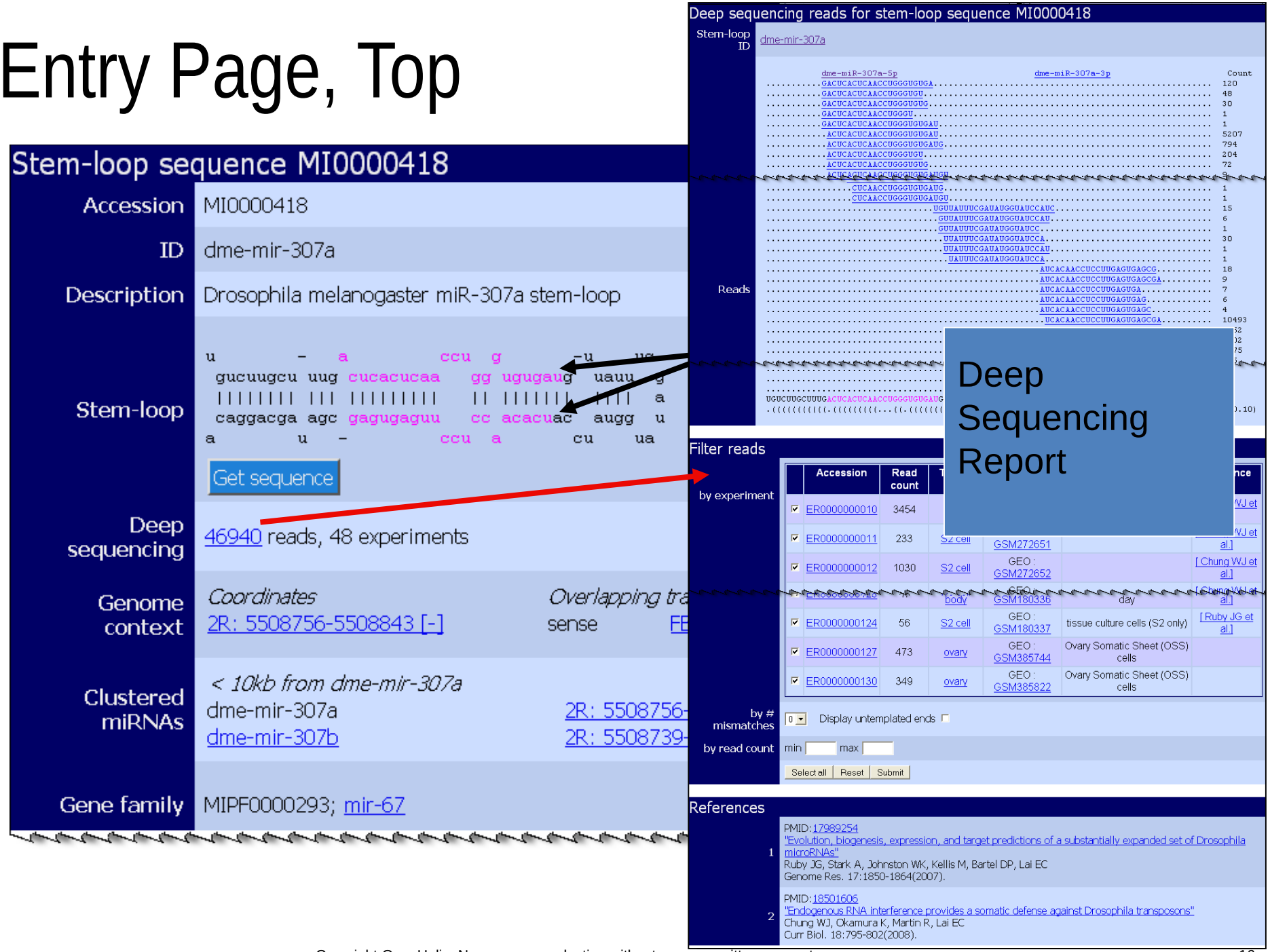
click

Accession	ID	miRNA name	Mature name
MI0000418	dme-mir-307a	✓	✓
MI0001352	dps-mir-307a	✓	✓
MI0001624	aga-mir-307	✓	✓

miRNA Entry Page

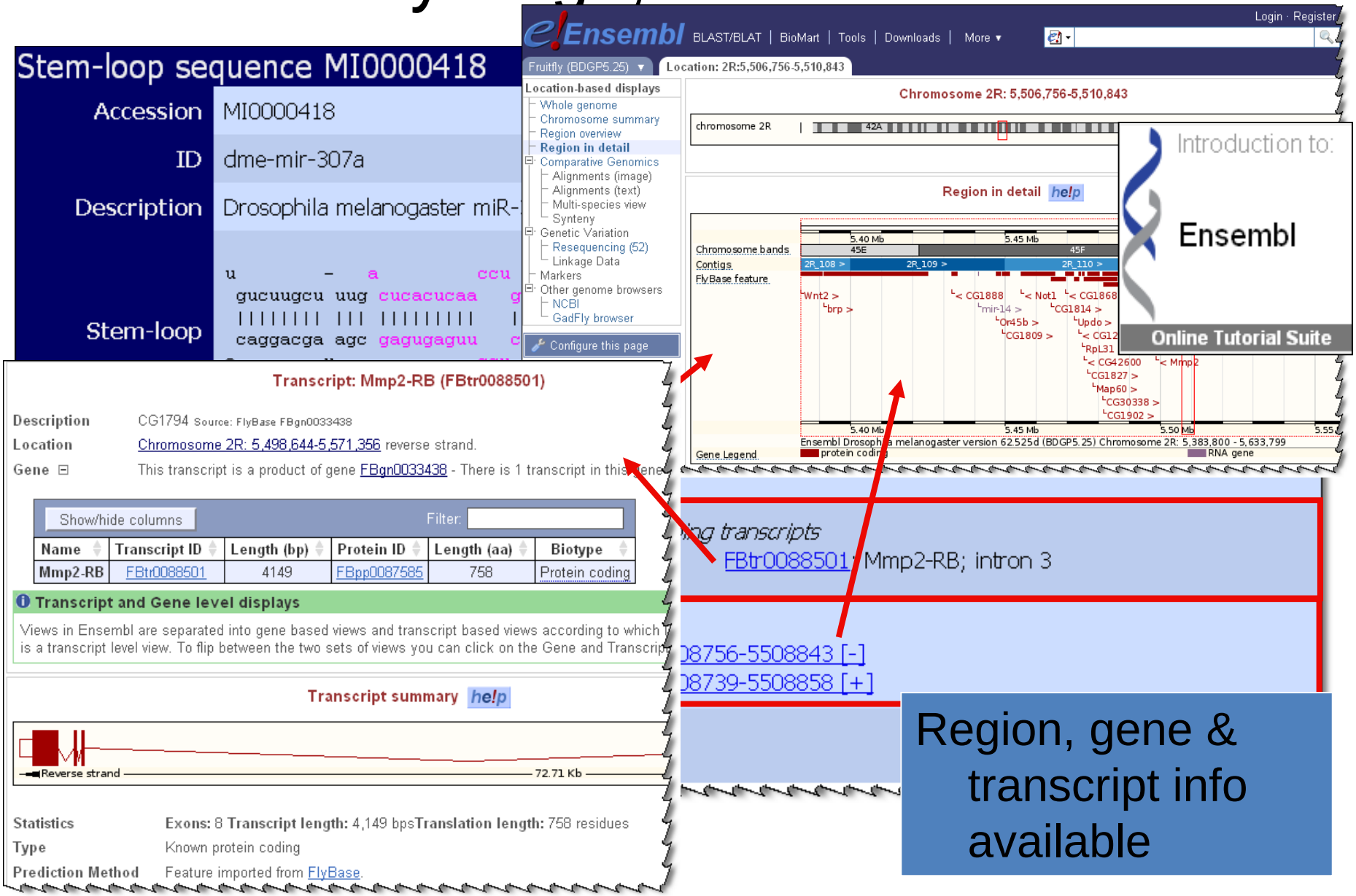


Entry Page, Top



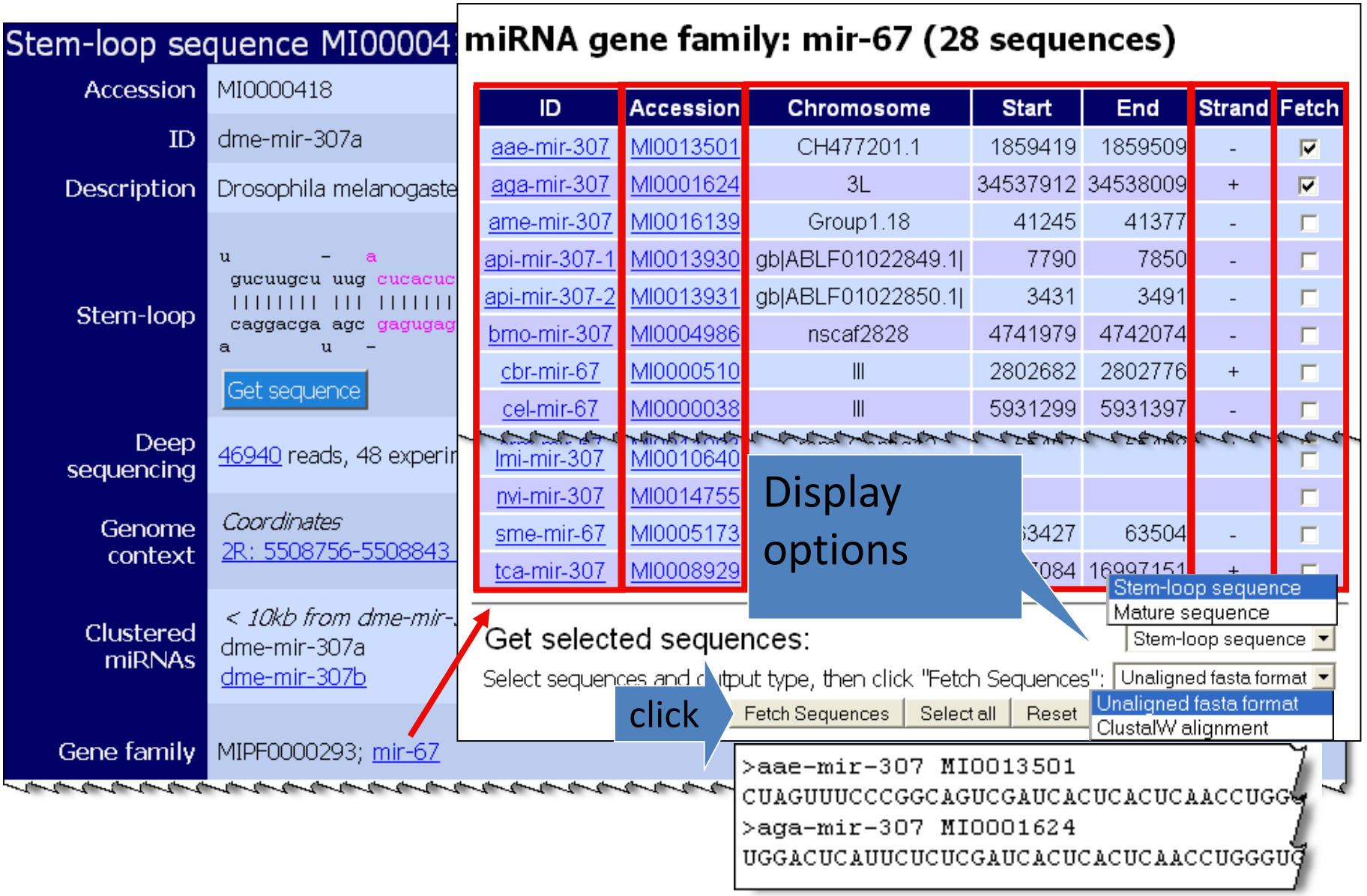
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Entry Page, Genome Context



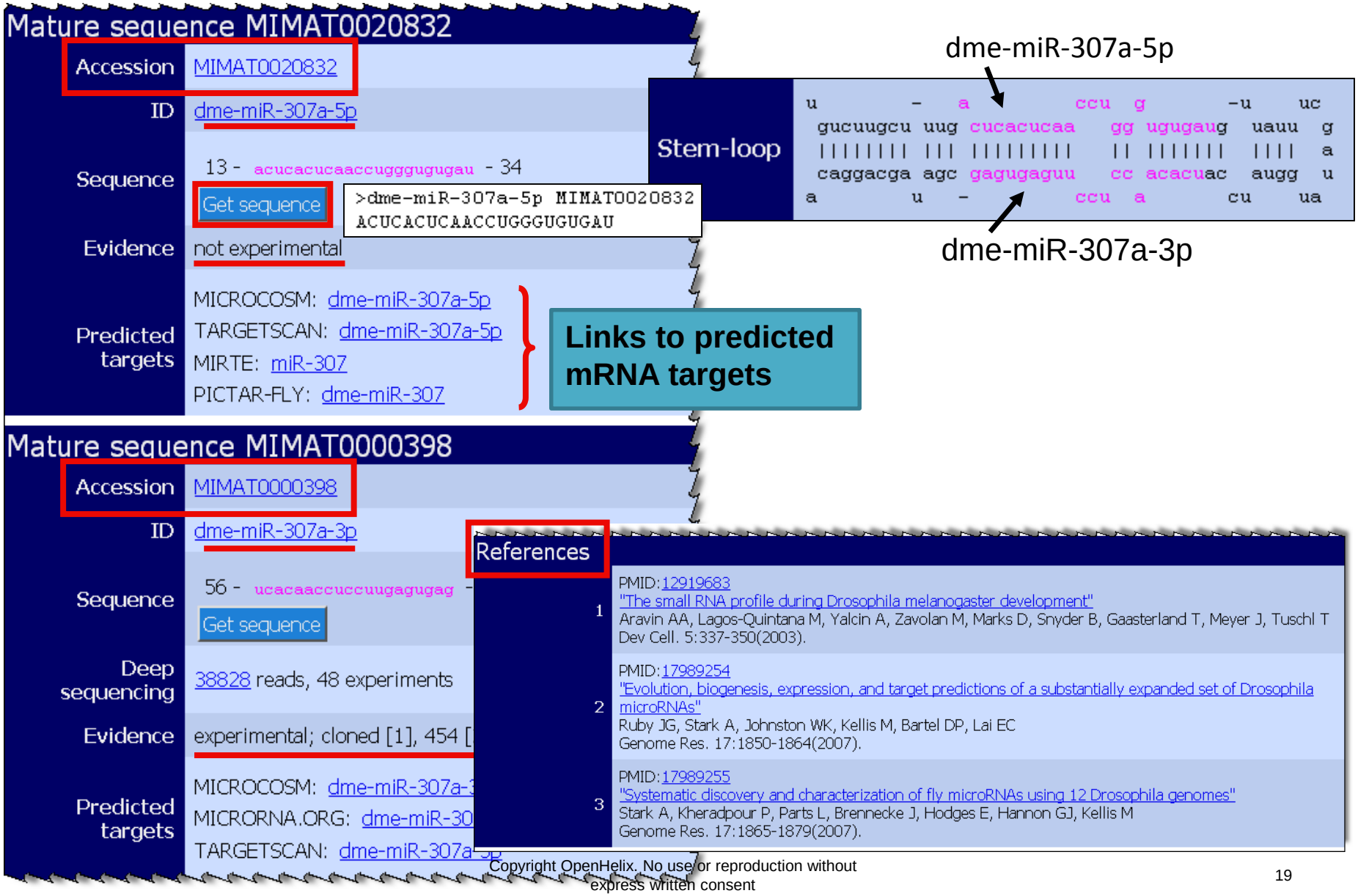
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Entry Page, Related Sequences



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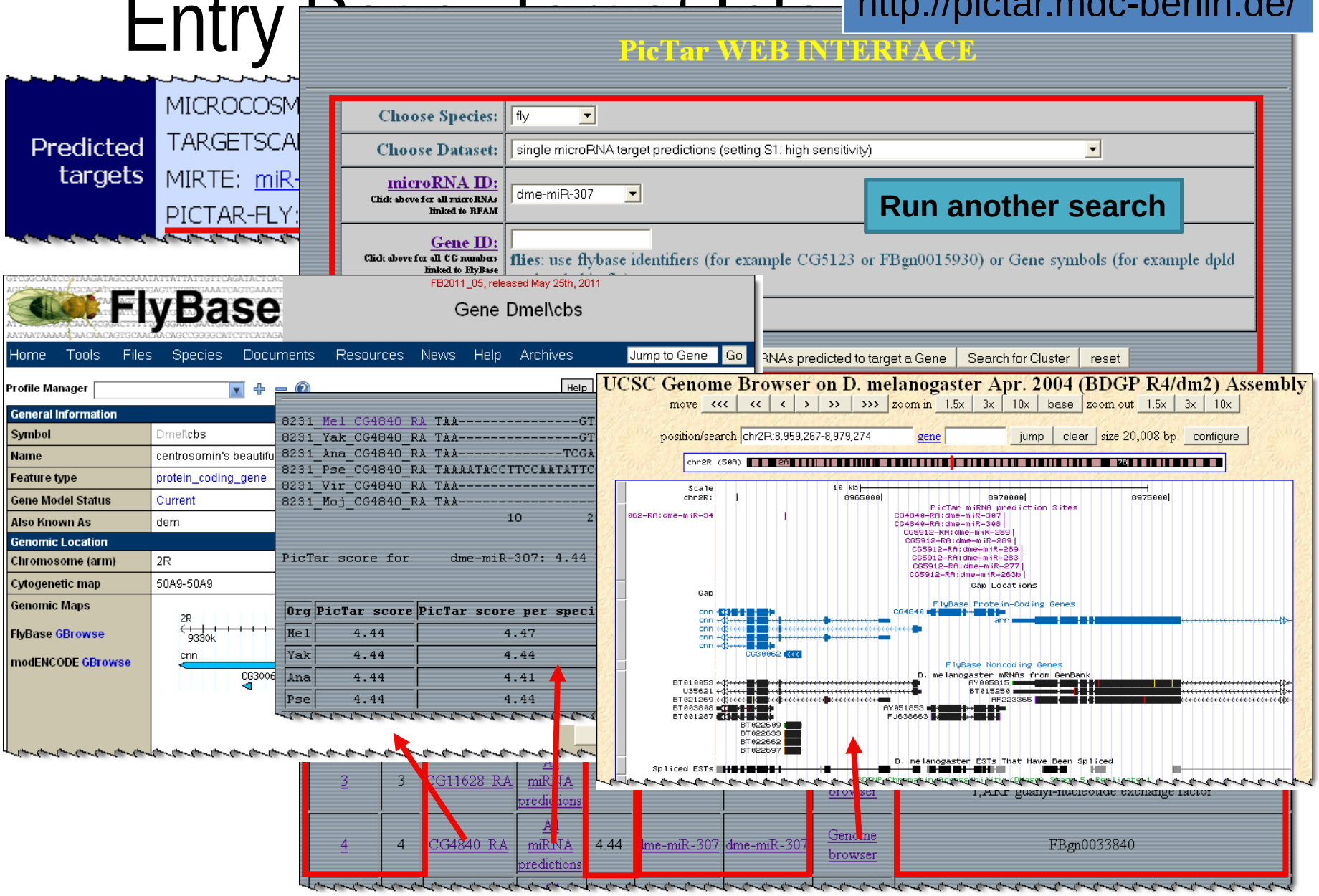
Entry Page, Mature MicroRNA



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Entry

http://pictar.mdc-berlin.de/



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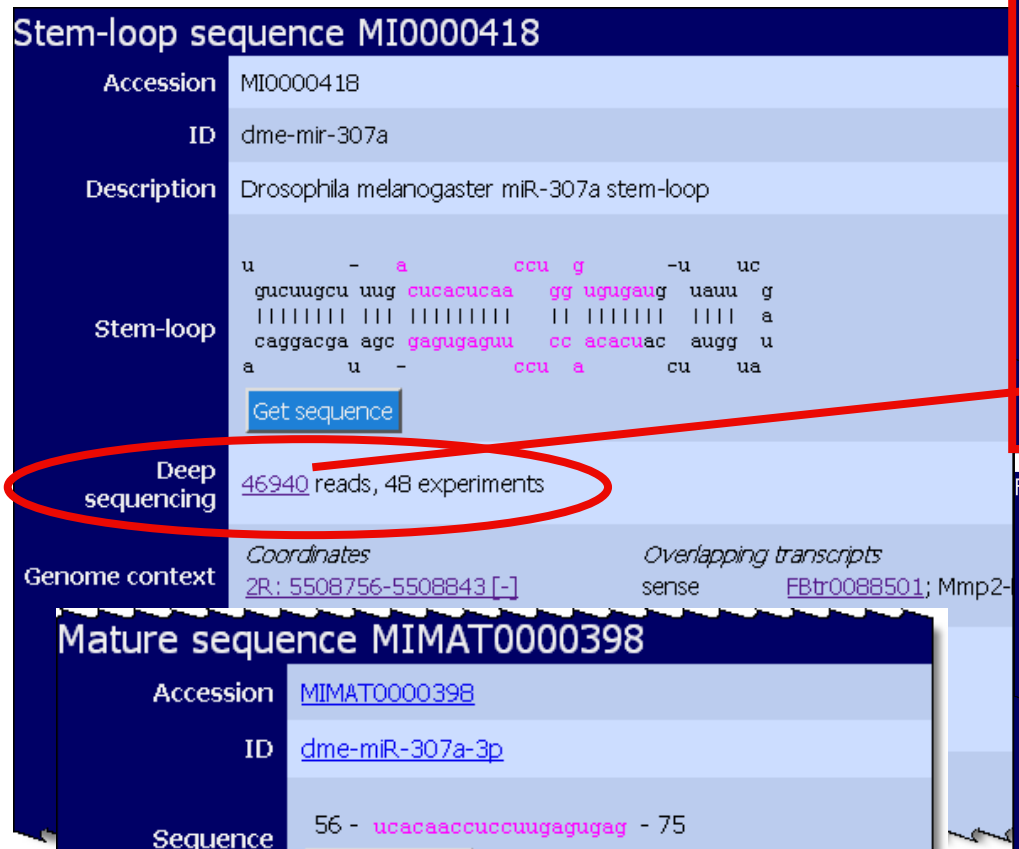
miRBase Agenda

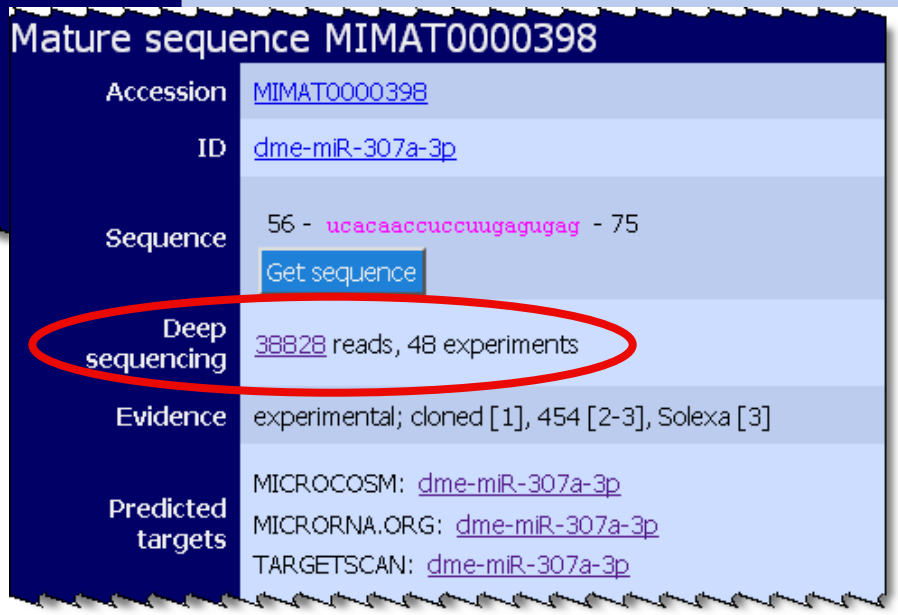
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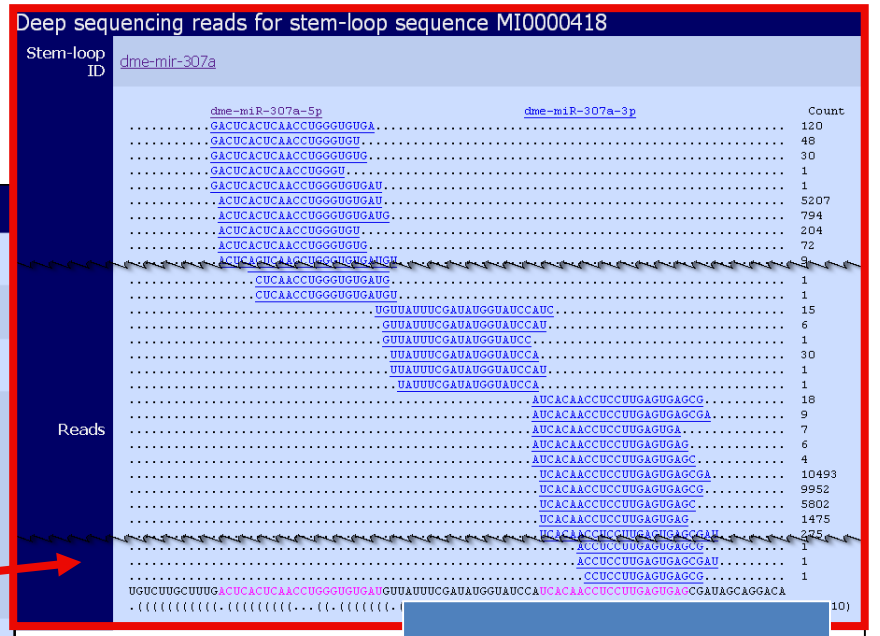
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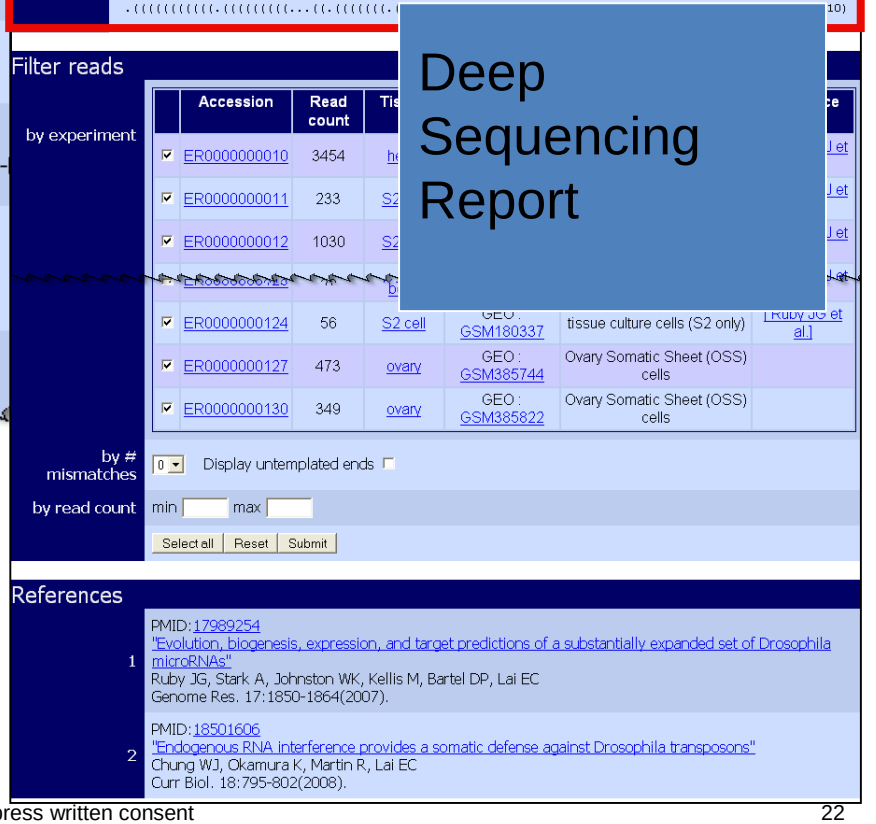
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Entry Page, Top





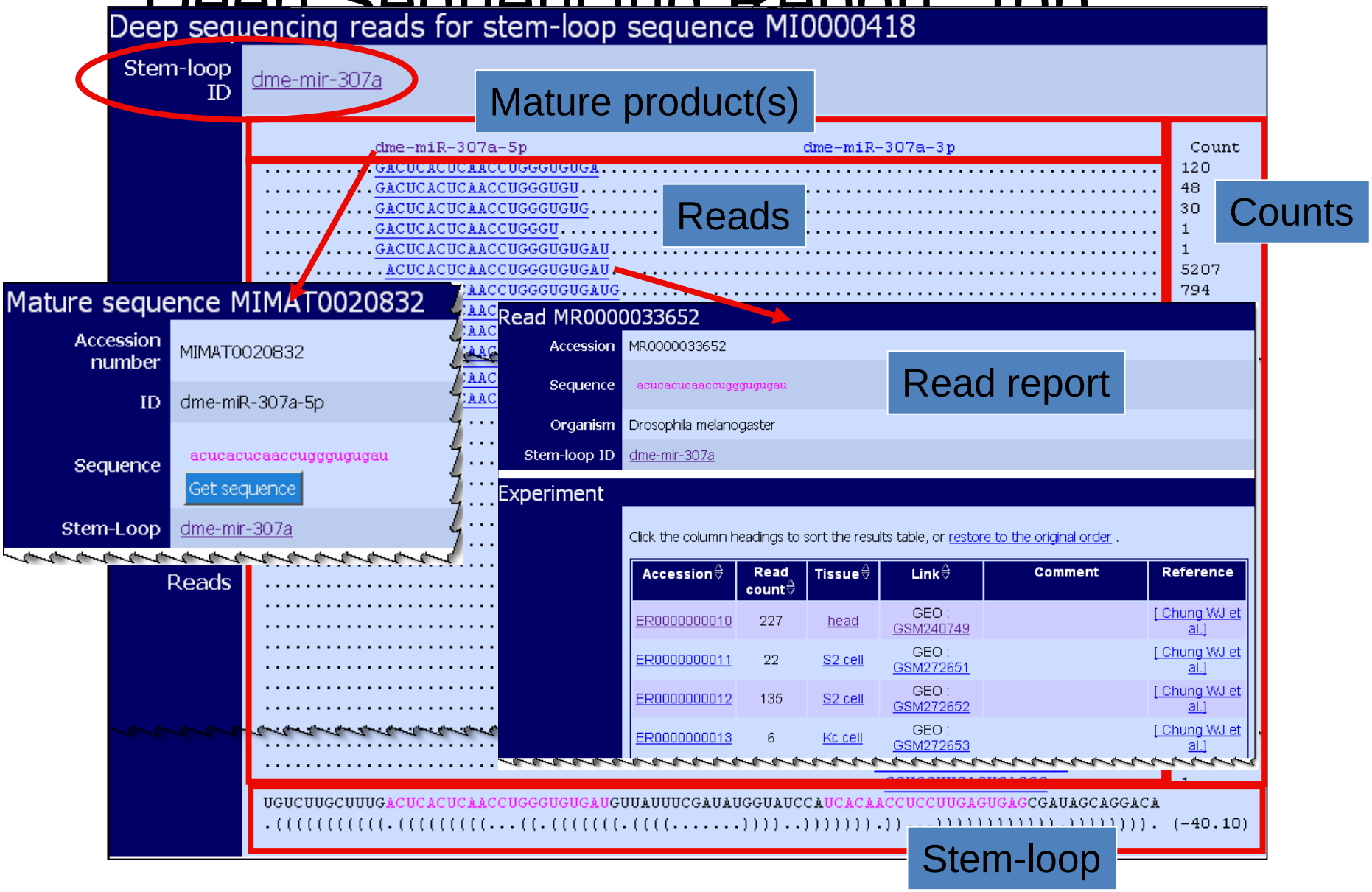




Deep Sequencing Report

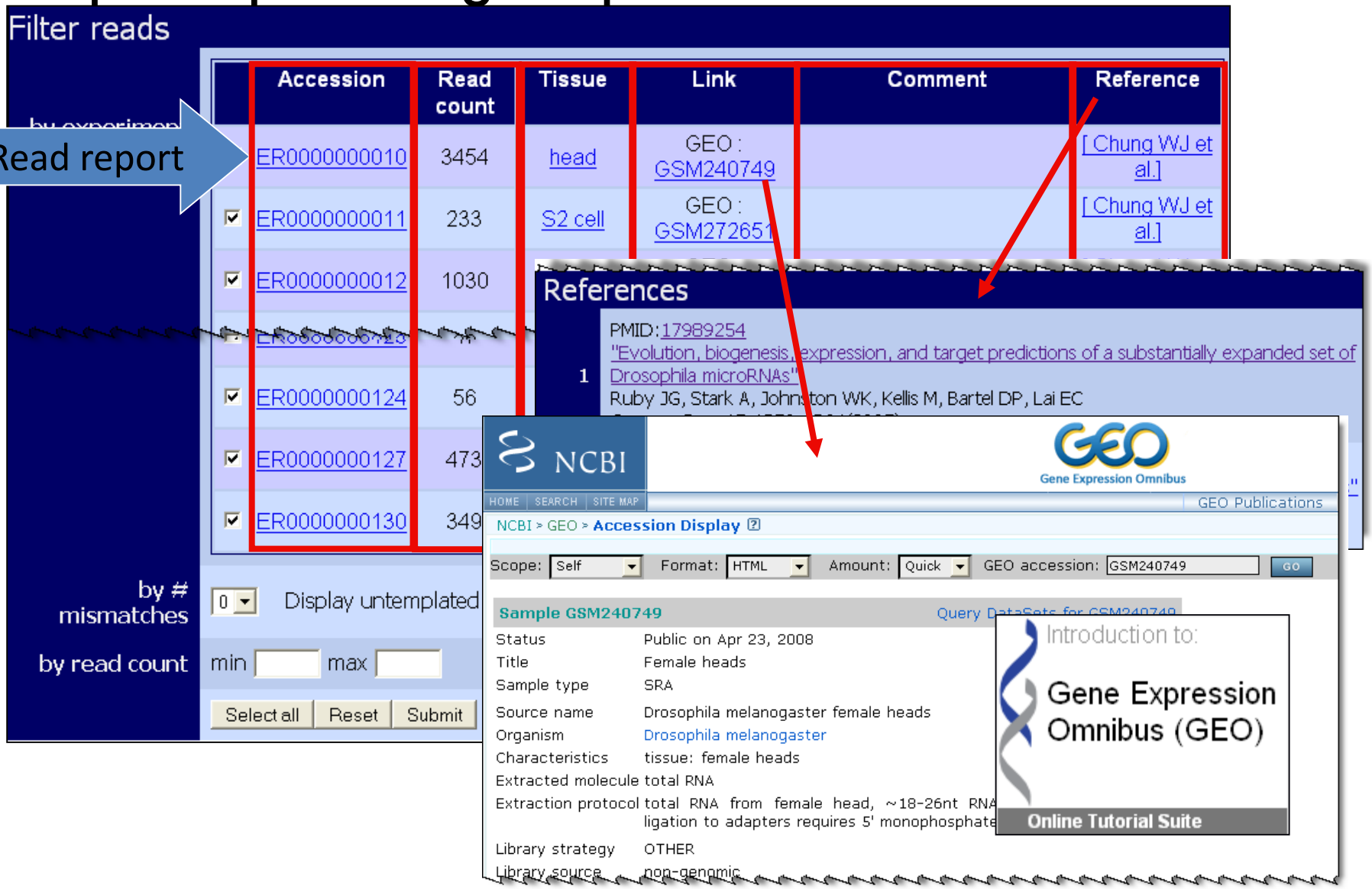
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Deep Sequencing Report: Top



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Deep Sequencing Report: Middle & Bottom



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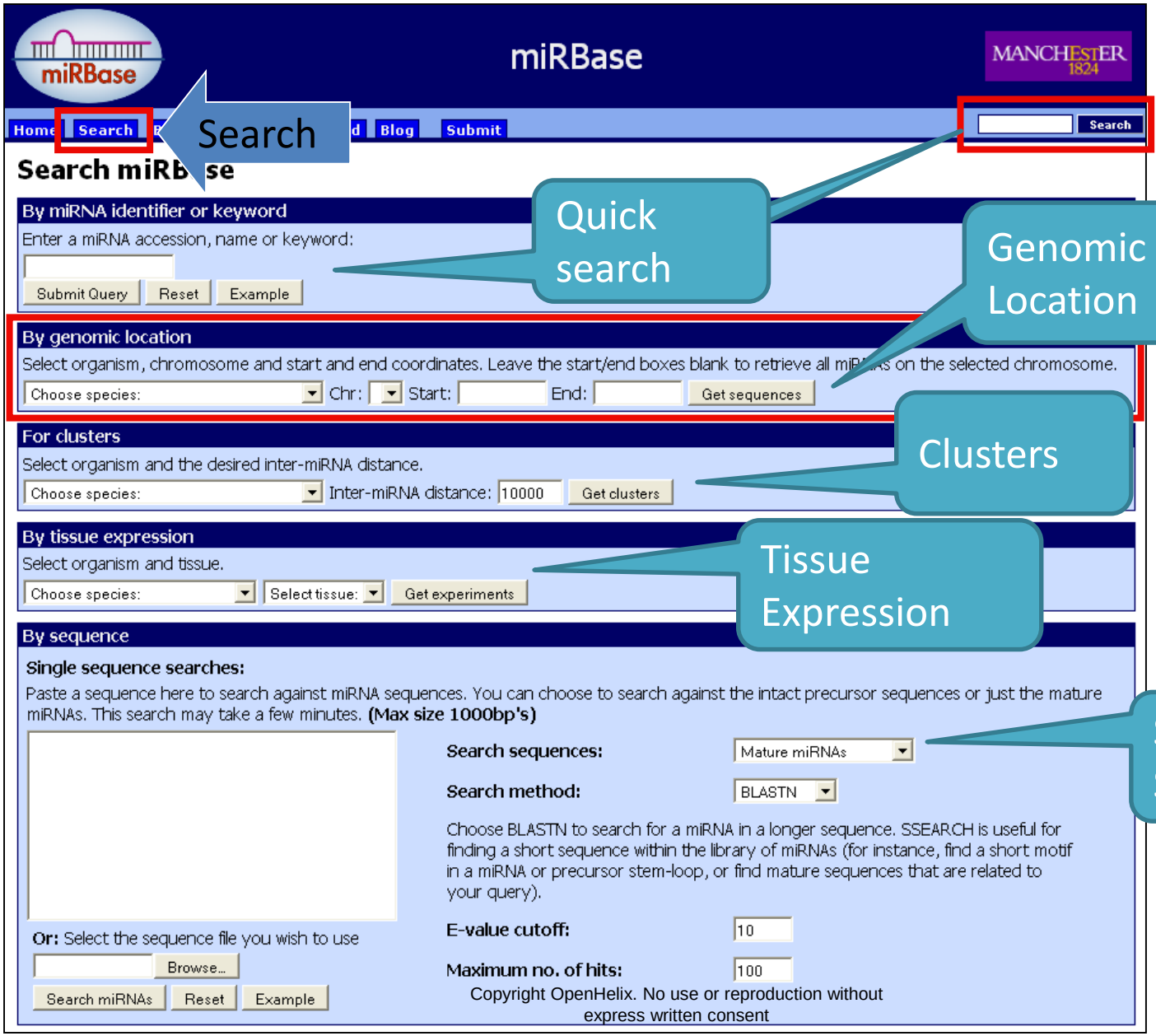
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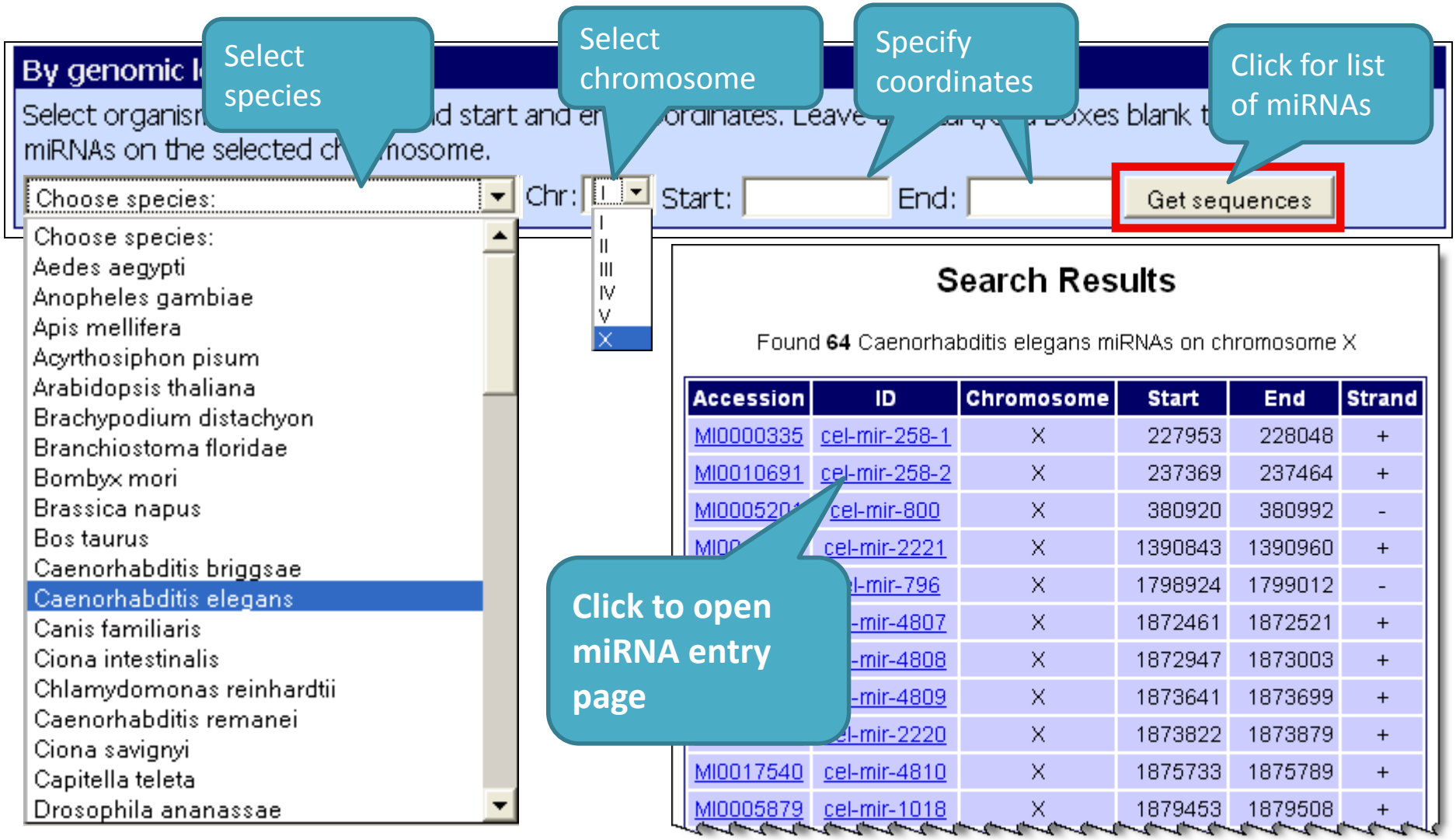
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Advanced Search Tab



Search by Genomic Location

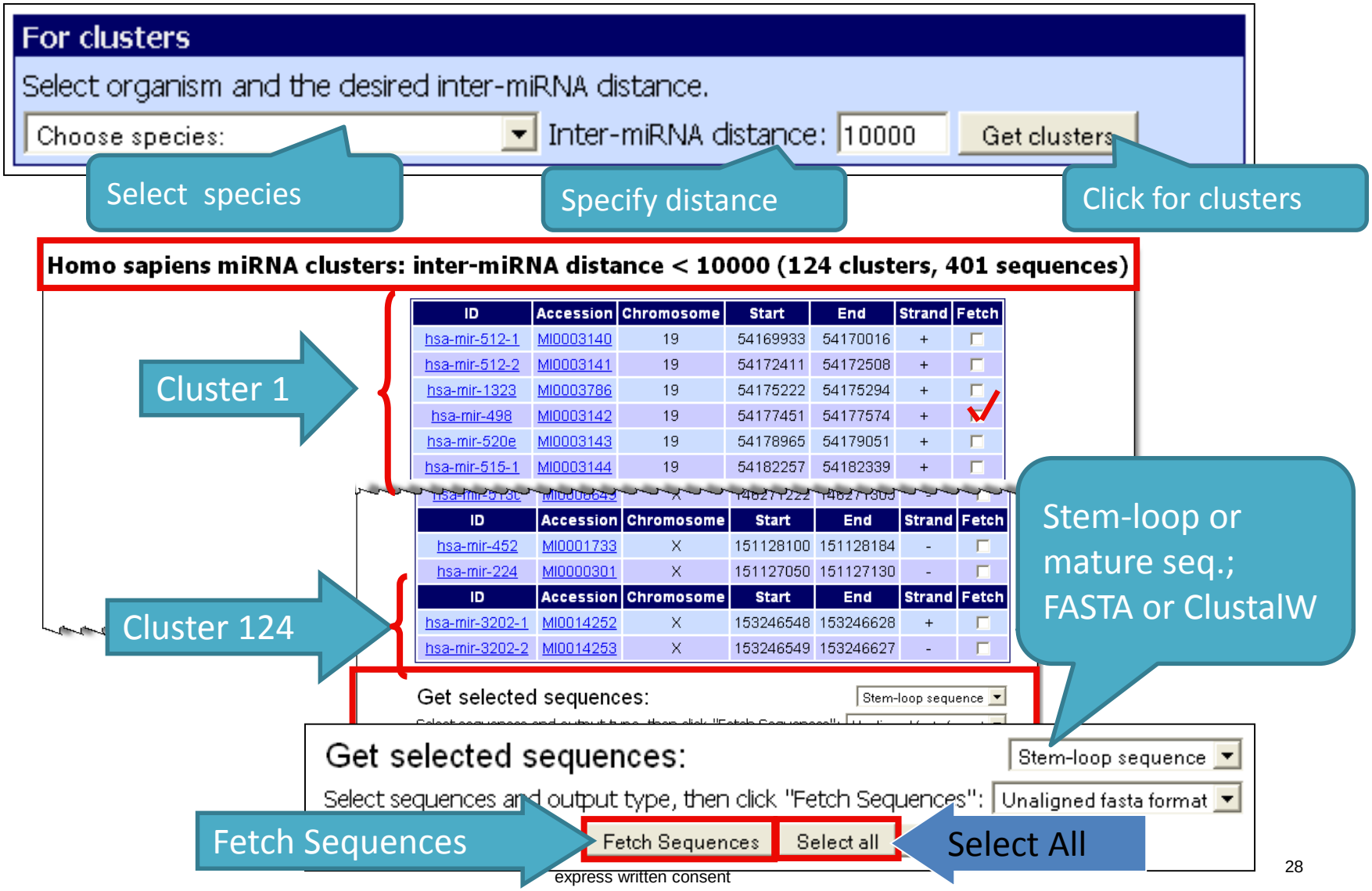
Select species →Select Chromosome →Specify coordinates →Get miRNA list



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Search for MicroRNA Clusters

Select species → Specify inter-microRNA distance → Get clusters



ID	Accession	Chromosome	Start	End	Strand	Fetch
hsa-mir-512-1	MI0003140	19	54169933	54170016	+	
hsa-mir-512-2	MI0003141	19	54172411	54172508	+	
hsa-mir-1323	MI0003786	19	54175222	54175294	+	
hsa-mir-498	MI0003142	19	54177451	54177574	+	✓
hsa-mir-520e	MI0003143	19	54178965	54179051	+	
hsa-mir-515-1	MI0003144	19	54182257	54182339	+	

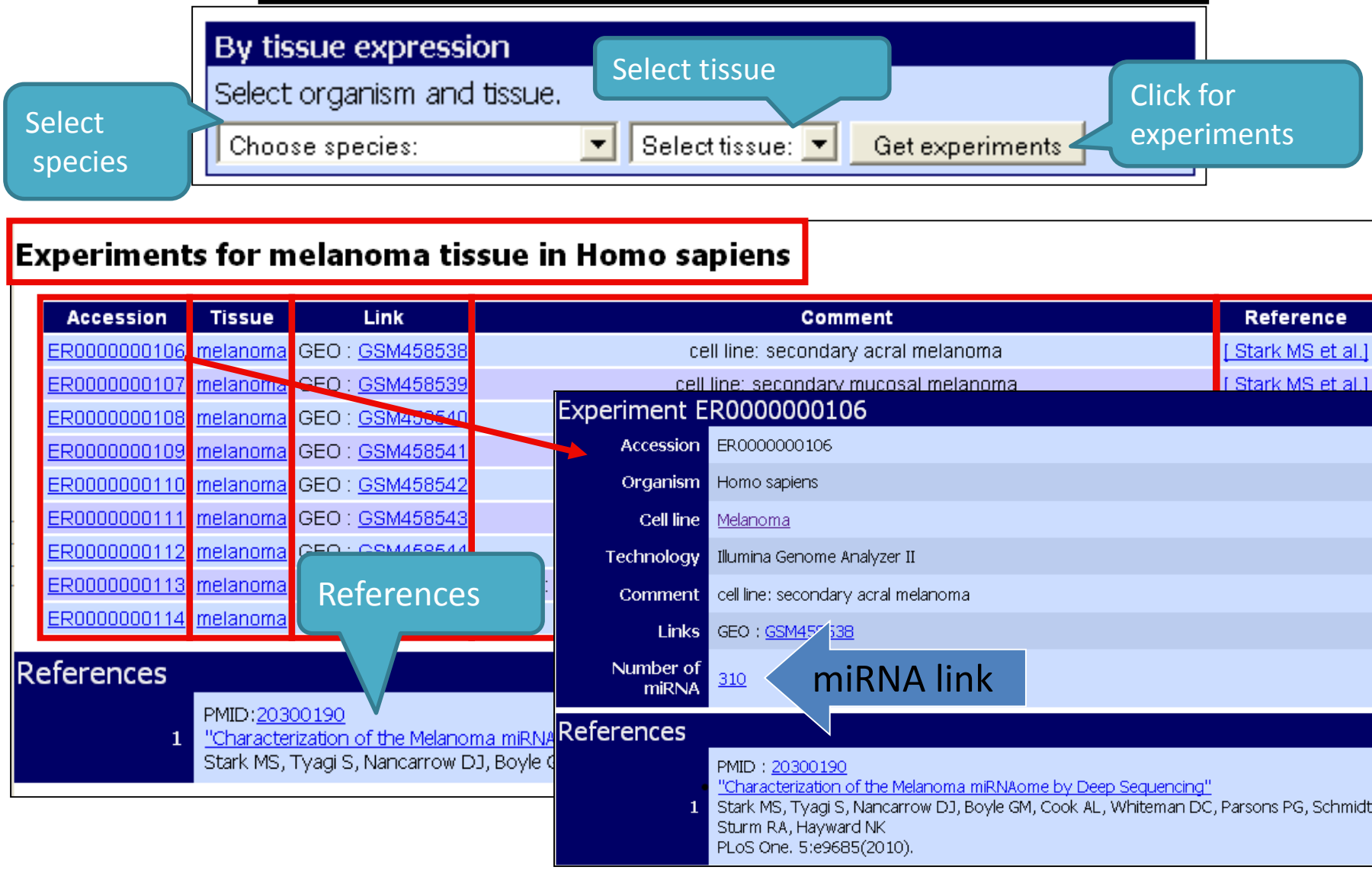
ID	Accession	Chromosome	Start	End	Strand	Fetch
hsa-mir-452	MI0001733	X	151128100	151128184	-	
hsa-mir-224	MI0000301	X	151127050	151127130	-	

ID	Accession	Chromosome	Start	End	Strand	Fetch
hsa-mir-3202-1	MI0014252	X	153246548	153246628	+	
hsa-mir-3202-2	MI0014253	X	153246549	153246627	-	

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Search by Tissue Expression

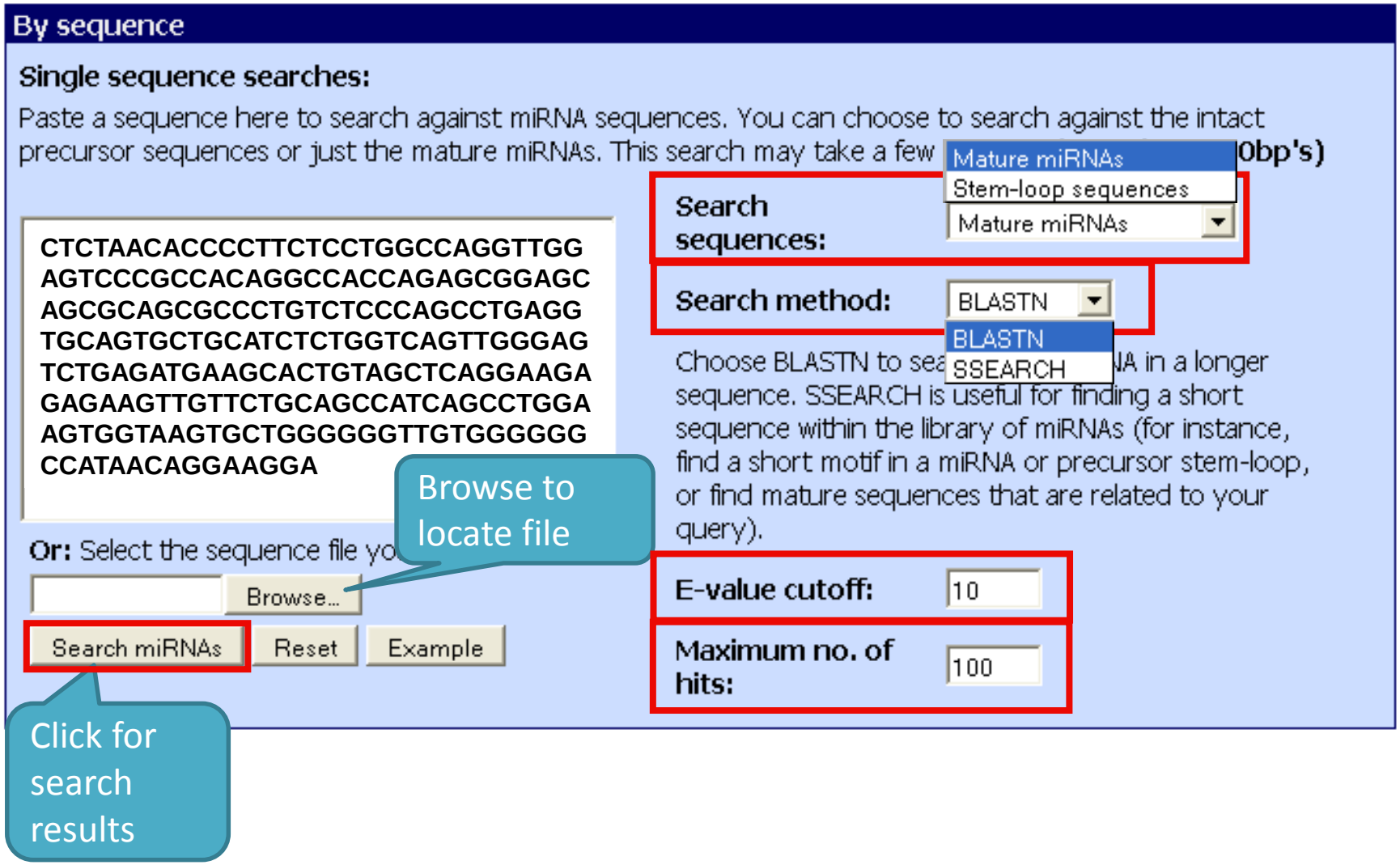
Select species → Select tissue → Get experiments



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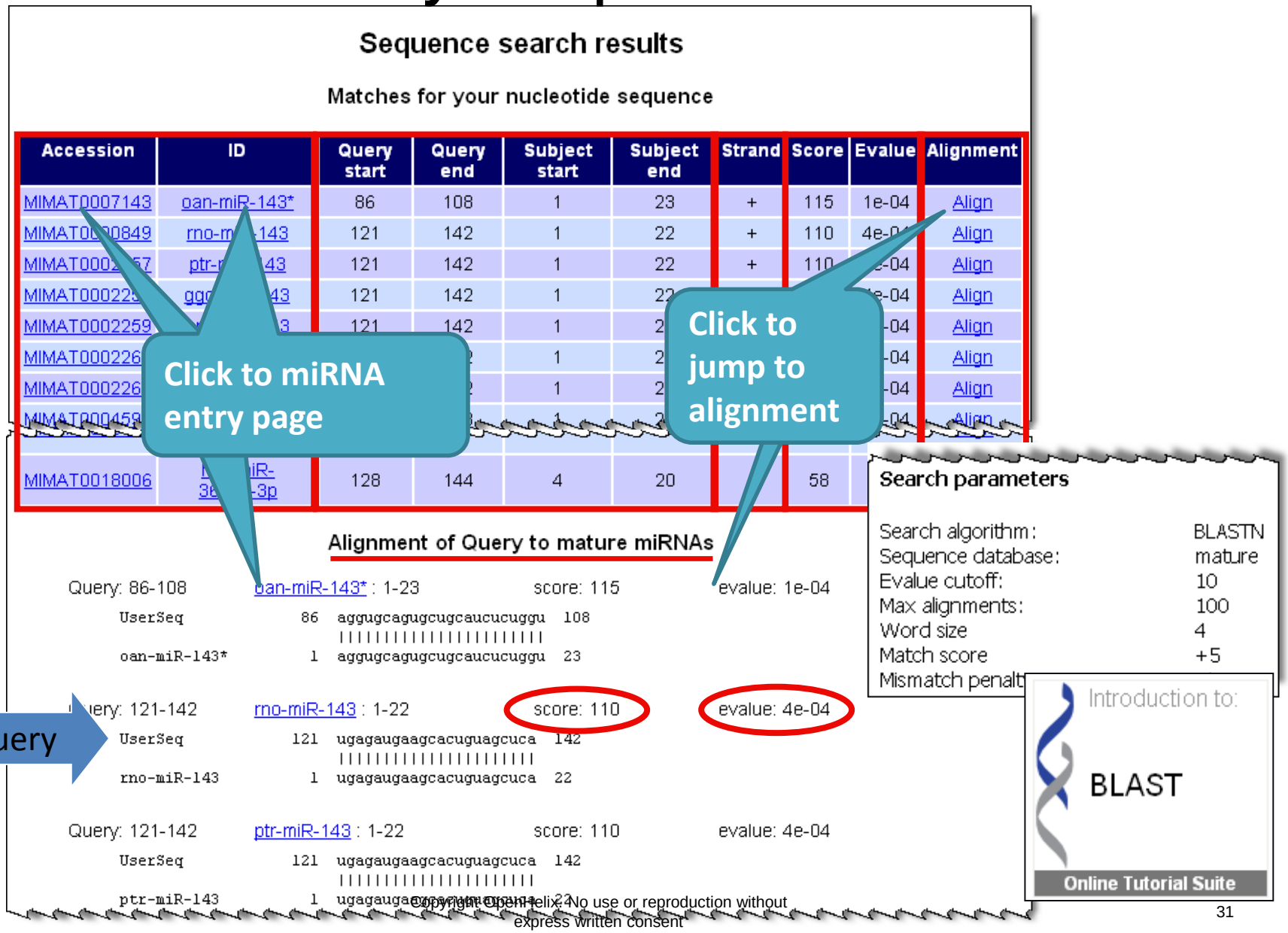
Search by Sequence

Enter sequence → Set search parameters → Click "Search miRNAs"



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Search by Sequence – Results



query

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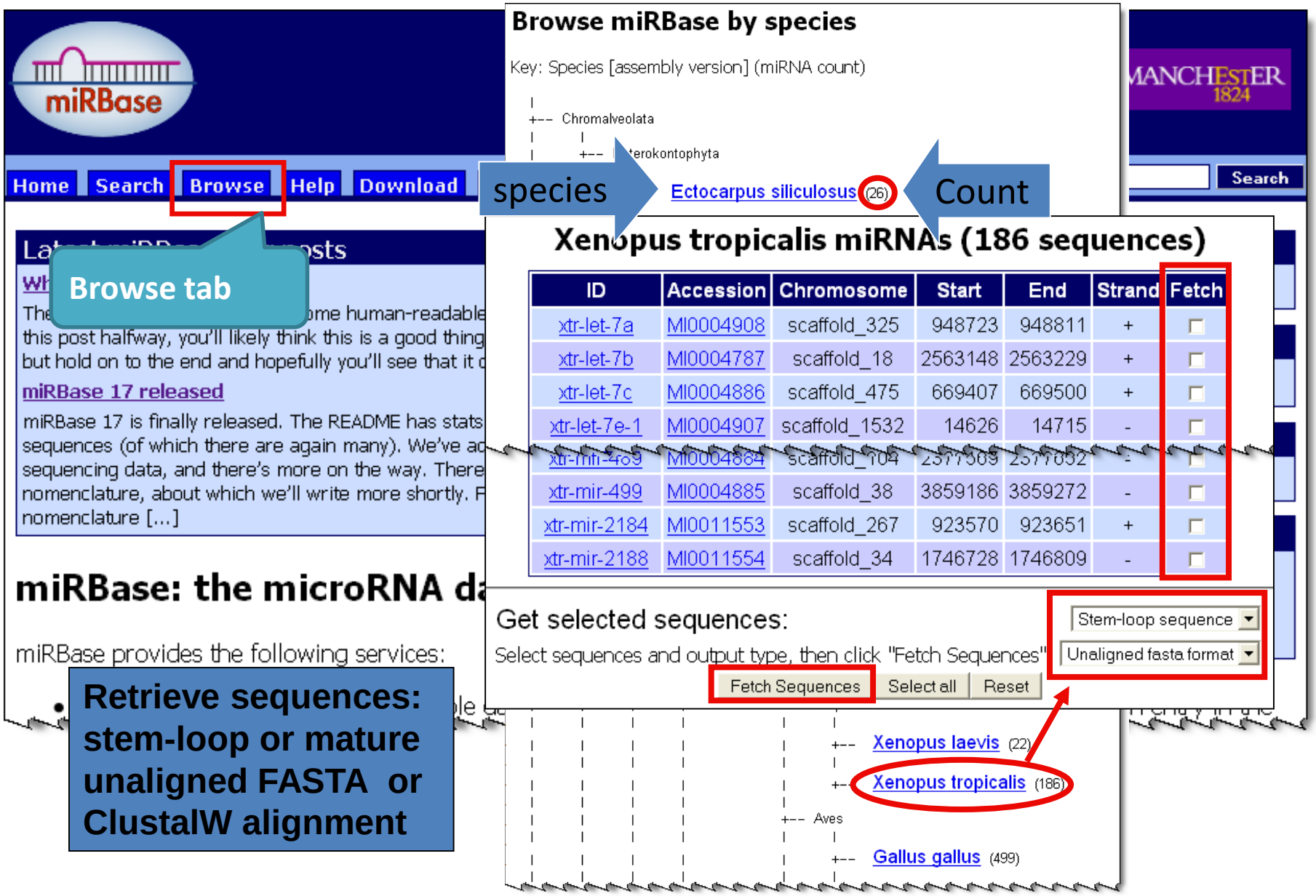
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Browse miRBase by Species



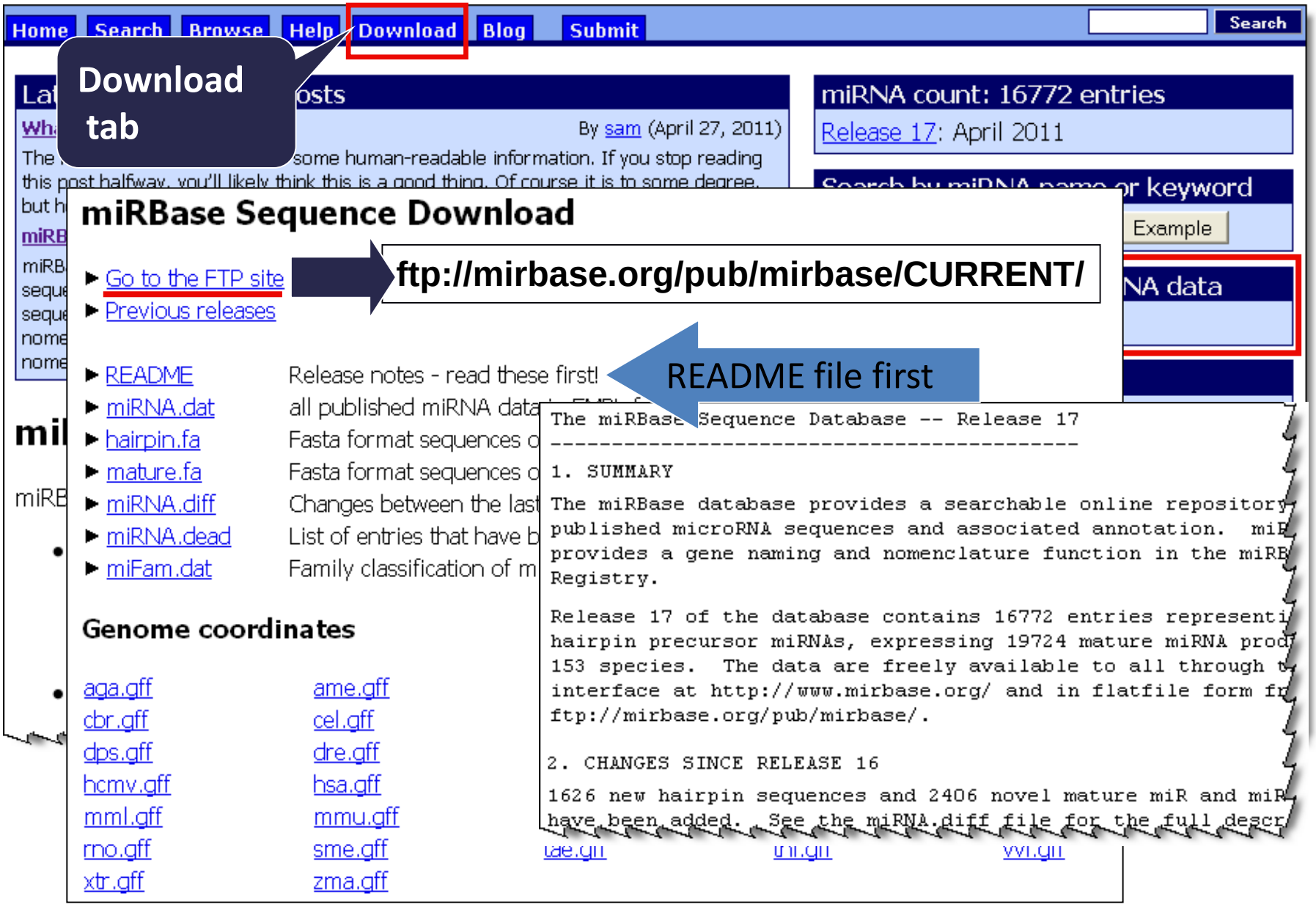
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miRBase Help and Registry



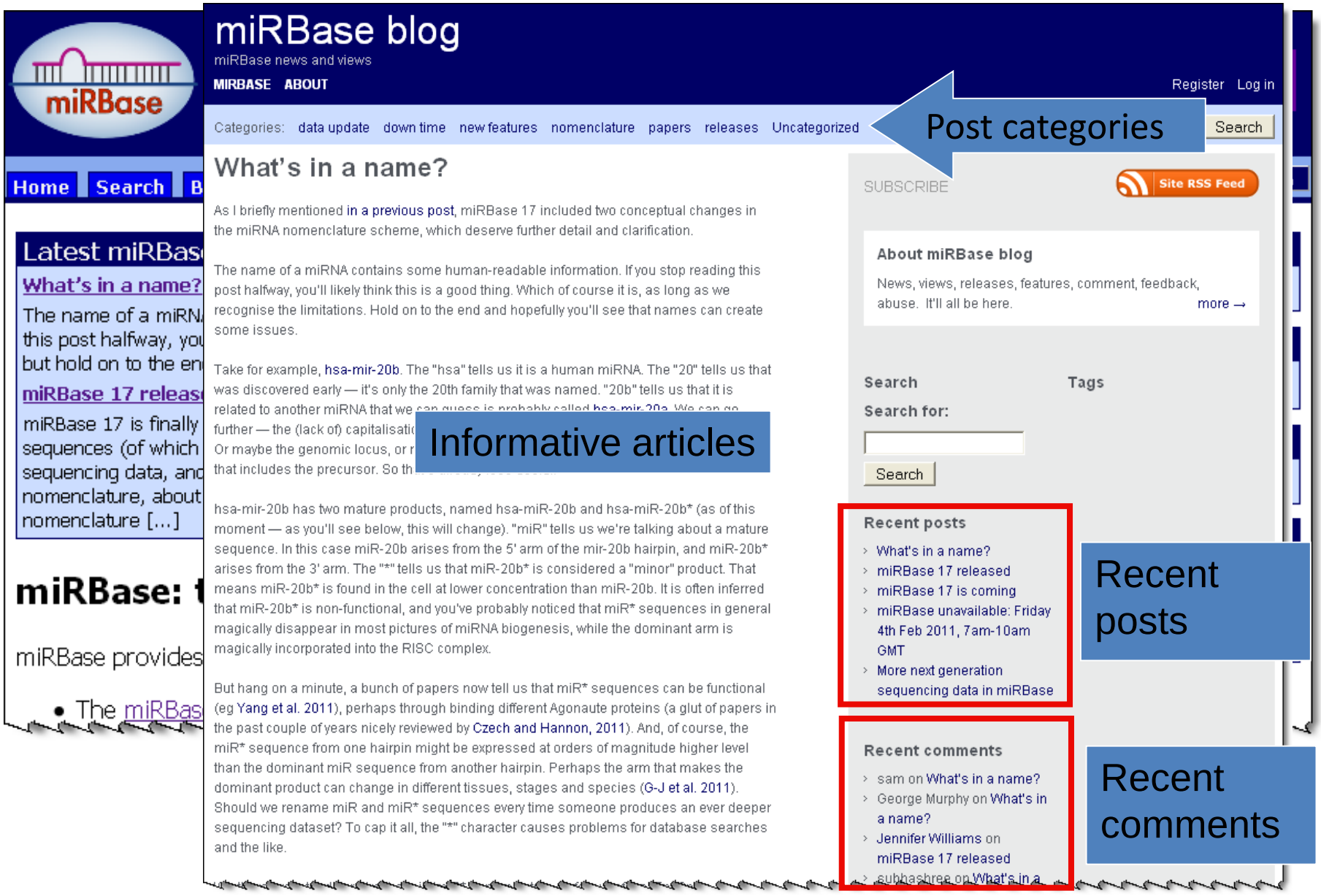
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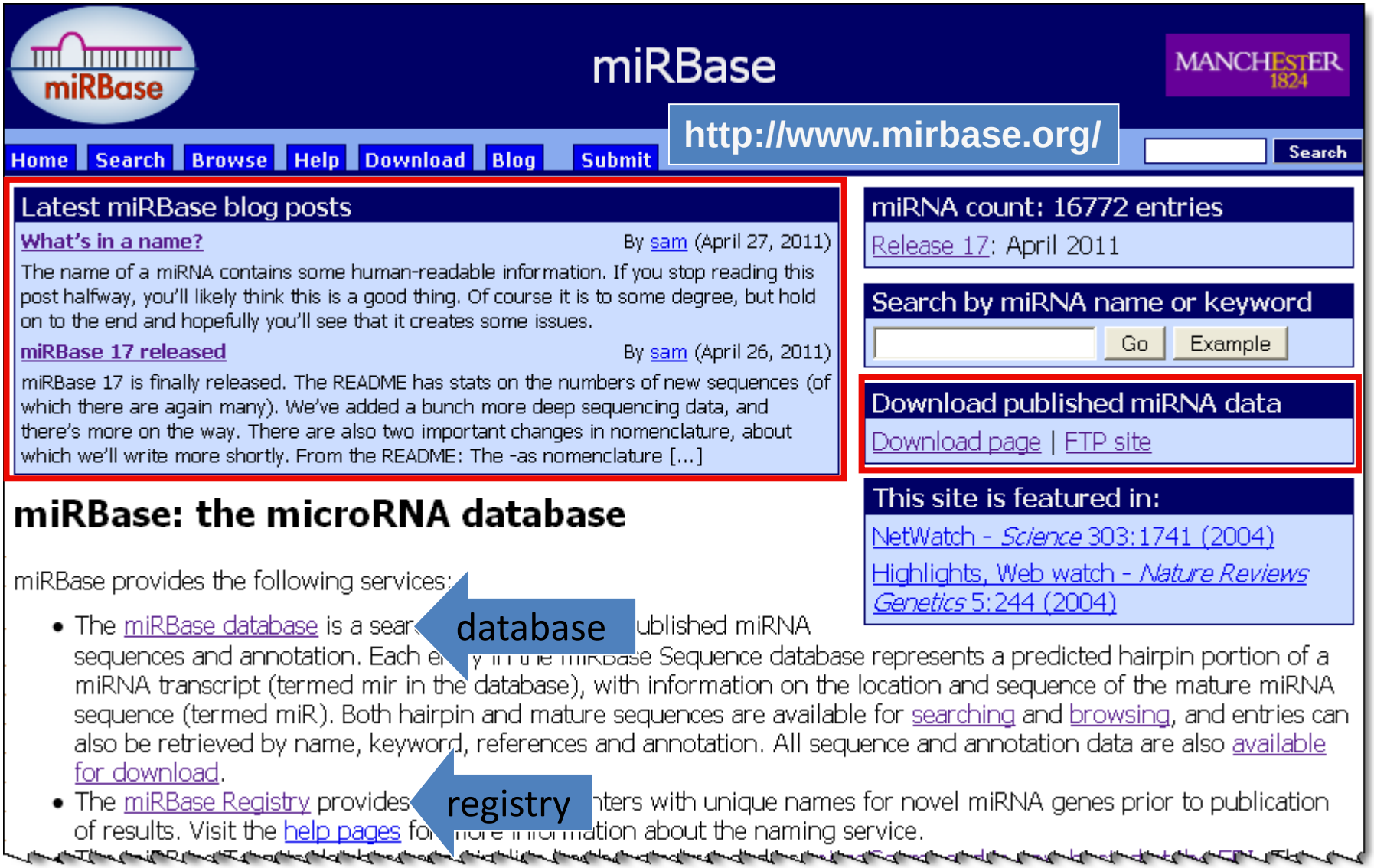
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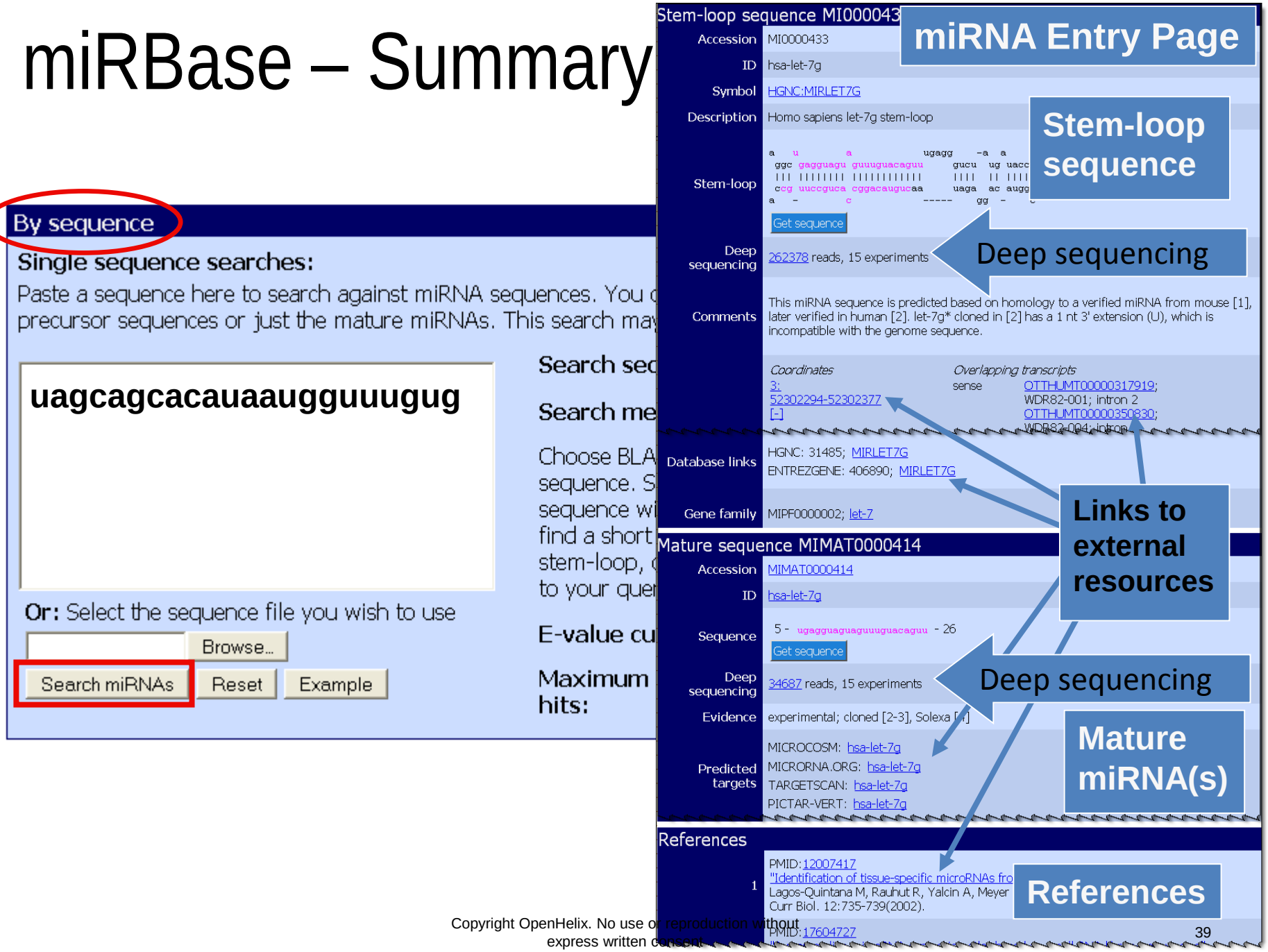
miRBase – Summary



miRBase team at the University of Manchester

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miRBase – Summary



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