

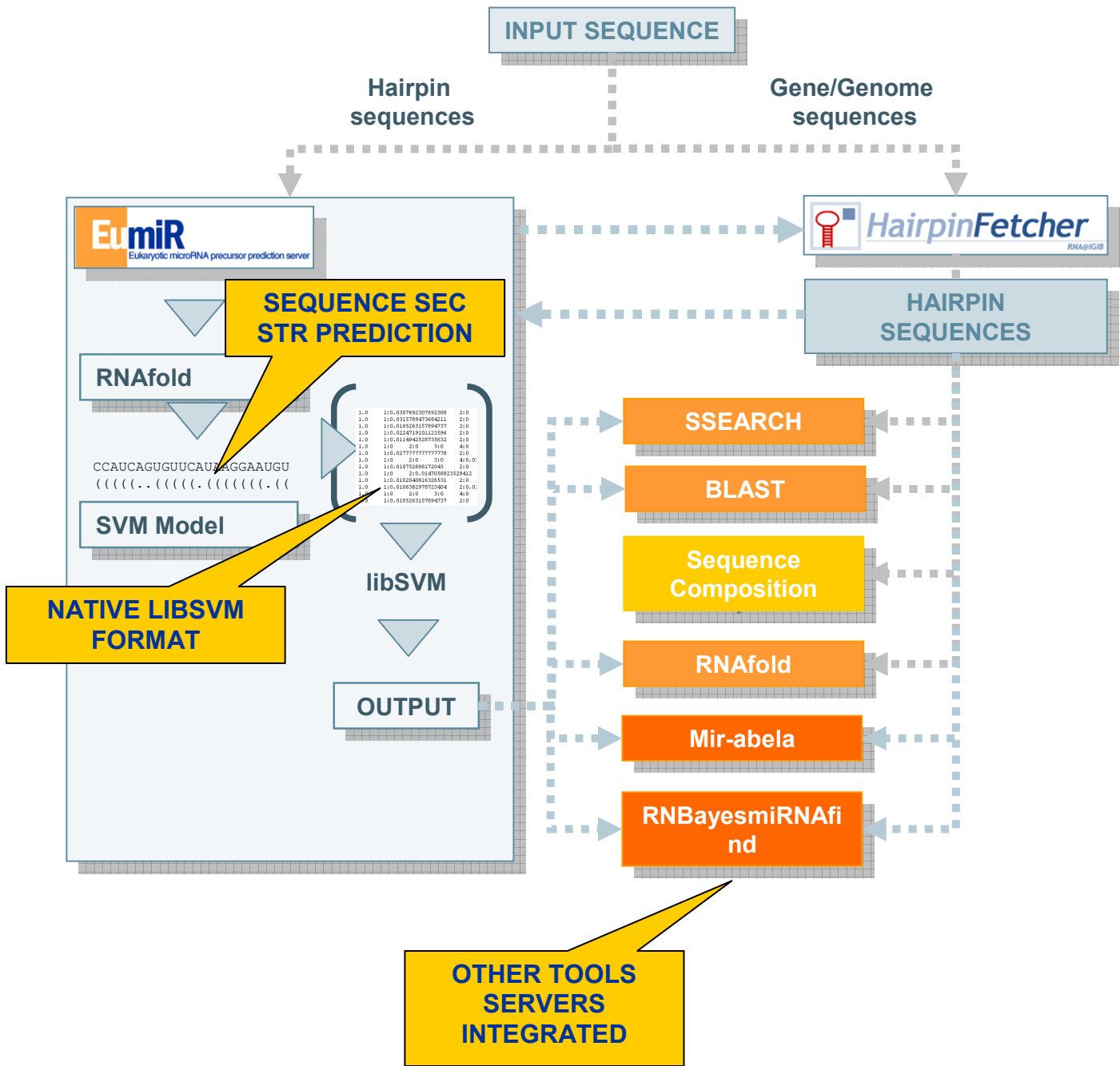
# HELP DOCUMENT



[ [bugs](#) | [suggestions](#) | [accessibility](#) ]

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# LAYOUT AND FUNCTIONALITY OF EUMIR



# EumiR QUERY INTERFACE

URL: <http://miracle.igib.res.in/eumir/>

The screenshot shows the EumiR query interface in a Microsoft Internet Explorer browser. The page title is "Eumir | Eukaryotic microRNA prediction server | Prediction of Eukaryotic microRNA precursors base". The browser address bar shows "http://miracle.igib.res.in/eumir/". The page features a search form with a text area containing multiple lines of nucleotide sequences. A "SEARCH AND FIND RESULTS" button is located below the text area. To the right, there is a "Hairpin Fetcher" section with a "SUBMIT" button and a "Reset" button. A "HELP DOCUMENT" link is also visible. The page includes a logo for "EumiR Eukaryotic microRNA precursor prediction server" and a "Contact" section at the bottom right.

The query interface has the form for querying multiple sequences which have potential to form hairpin secondary structures, each delimited by a line break.

## NOTE

Each sequence should not have length more than 150 nucleotides or less than 50 nucleotides.

## NOTE

The server will accept only 5000 nucleotides in a single submission. If you need a standalone version or need to mirror the server for large scale predictions, please contact the **Business Development Management Group** at [rchat@igib.res.in](mailto:rchat@igib.res.in)

## NOTE

Sequences should have only nucleotide characters [ATUGC]

# EumiR RESULTS INTERFACE

The screenshot shows the EumiR RESULTS INTERFACE with several callout boxes highlighting key features:

- RESULT DOWNLOADS**: Points to the DOWNLOADS section, which includes links for Input Sequence, RNAfold Output, Result File, and Log File.
- ANALYSIS OPTIONS**: Points to the ANALYSIS TOOLKIT section, which includes BLAST sequences at miRBase and SSEARCH sequences at miRBase.
- RNA SECONDARY STRUCTURE**: Points to the RNA secondary structure prediction results, showing sequence and structure diagrams.
- TOOLKIT LEGENDS**: Points to the legend for the analysis toolkit, showing icons for BLAST (B), SSEARCH (S), RNAfold (R), BayesmiRNAfind (BF), and mir-abela (M).
- PREDICTION POS/NEG**: Points to the PREDICTION column, which shows the prediction status (POSITIVE) and the prediction method used.
- CHECKBOX FOR BLAST**: Points to the checkbox in the PREDICTION column, which allows users to select or deselect specific results for BLAST.
- BLAST OPTIONS**: Points to the BLAST options section, which includes a dropdown menu for Blast (selected), a dropdown menu for Blast\_Selected, an E-value input field (set to 10), a dropdown menu for Database (selected as nr), and a Submit button.

## ANALYSIS OPTIONS AVAILABLE

- BLAST miRbase
- BLAST NCBI (**this may be slow at times**)
- SSEARCH miRbase
- Secondary Structure-> RNAfold
- Predict using BayesmiRNAfind
- Predict using mir-abela

# HAIRPINFETCHER QUERY INTERFACE

URL: <http://miracle.igib.res.in/hfinder/>

The screenshot shows the HairpinFetcher web interface in a Microsoft Internet Explorer browser window. The browser's address bar displays <http://miracle.igib.res.in/hfinder/>. The page header includes the logo for HairpinFetcher (RNA@IGIB) and a gear icon labeled 'LINK TO EUMIR'. The main content area features an 'INPUT SEQUENCE' section with a text input field and a 'SEQUENCE INPUT' callout box. Below the input field, there are two numeric input fields: 'Hairpin Length' set to 20 (with a 'MINIMUM HAIRPIN LENGTH' callout) and 'Free Energy' set to -15 (with a 'FREE ENERGY CUTOFF FOR HAIRPIN' callout). 'Submit' and 'Reset' buttons are positioned to the right of these fields. On the right side of the page, there is a diagram of the Eumir server workflow and a 'HELP DOCUMENT' callout box. At the bottom, a blue banner states: 'HairpinFetcher is an integral part of Eumir and VimiR programs for microRNA precursor prediction.' The browser's status bar at the bottom shows 'Done' and 'Internet'.

# HAIRPINFETCHER RESULTS INTERFACE

The screenshot displays the HairpinFetcher results interface. At the top, the 'Project Information' section shows the project name, submission date (Tue Jan 30 17:30:15 2007), and HairpinFetcher ID (1170158415). Below this, the 'Sequence' section shows the input sequence with positions 10, 20, 30, 40, 50, 60, 70, 80, and 90 marked. The 'Length of Sequence' is 375, 'Hairpin Length' is 20, 'Minimum Free energy' is -15, 'Total No of Sequenc' is 1, and 'Total Number of Hairpin' is 5.

The main results table lists five hairpins, each with a checkbox, a 'B S E B R B F M' analysis options button, and a 'Send to Eumir Option' button. The first hairpin has a 'Stop: 71' and 'Length: 71'. The second has 'Start: 74', 'Stop: 141', and 'Length: 69'. The third has 'Start: 142', 'Stop: 218', and 'Length: 78'. The fourth has 'Stop: 283' and 'Length: 63'. The fifth has 'Length: 91'. Each row also displays the sequence and its secondary structure.

At the bottom, the 'Eumir' and 'Blast' sections are visible. The 'Eumir' section has a 'Submit' button. The 'Blast' section has a 'Blast\_Selected' dropdown, an 'E-value' field set to 10, and a 'Database' dropdown set to 'nr'. Below these are 'SEQUENCE PROFILE' and 'RESULT DOWNLOADS' sections. The 'RESULT DOWNLOADS' section has three options: 'Input Sequence', 'Folding Output', and 'Hairpin', each with a download icon.

Callouts in yellow boxes point to various features: 'INPUT SEQUENCE' points to the sequence text; 'SEQUENCE INFORMATION' points to the project information; 'ANALYSIS OPTIONS' points to the 'B S E B R B F M' buttons; 'SEND TO EUMIR OPTION' points to the 'Send to Eumir Option' buttons; 'BLAST OPTIONS' points to the 'Blast' section; 'SEQUENCE PROFILE' points to the 'SEQUENCE PROFILE' section; and 'RESULT DOWNLOADS' points to the 'RESULT DOWNLOADS' section.

## ANALYSIS OPTIONS AVAILABLE

- BLAST miRbase
- BLAST NCBI (this may be slow at times)
- SSEARCH miRbase
- Secondary Structure-> RNAfold
- Predict using BayesmiRNAfind
- Predict using mir-abela
- Predict using EumiR

# PREDICTION ACCURACIES

	TRUE miRNA hairpins	PSEUDO miRNA hairpins
Predicted +ve	462 TP	88 FP
Predicted -ve	80 FN	414 TN

**Sensitivity** = 85.24

**Specificity** = 82.47

**Accuracy** = 83.91

**Positive Predictive Value** = 84

**Negative Predictive Value** = 83.8

The calculations were undertaken on the randomly derived half of the total set, which contained total of 542 true precursor miRNA hairpins and 502 pseudo microRNA hairpins.

## COMPARISON OF PREDICTION EFFICACIES

Virus	PREDICTIONS		
	Bayes miRNAfind	Mir-abela	EumiR
Epstein-Barr Virus (23)	21 <b>91.30%</b>	18 <b>78.26%</b>	23 <b>100%</b>
Cytomegalovirus (11)	10 <b>90.91%</b>	5 <b>-45.45%</b>	10 <b>90.91%</b>
Kaposi Sarcoma Herpesvirus (13)	9 <b>69.23%</b>	5 <b>38.46%</b>	9 <b>69.23%</b>
Rhesus Lympho-cryptovirus (16)	16 <b>100%</b>	11 <b>68.75</b>	16 <b>100%</b>
Mouse gamma herpesvirus (9)	5 <b>55.5%</b>	2 <b>22.2%</b>	9 <b>100%</b>
Mareks disease virus (8)	4 <b>50%</b>	7 <b>87.5%</b>	5 <b>62.5%</b>
<b>TOTAL (80)</b>	<b>65</b> <b>81.25%</b>	<b>48</b> <b>60%</b>	<b>72</b> <b>90%</b>

Comparison of the prediction efficiency of the mir-abela, BayesmiRNAfind and EumiR on viral microRNA precursors from miRbase. The numbers in brackets that follow the organism name denote the total number of sequences and the numbers in bold denote the percentage true predictions.

The dataset of viral microRNA precursors were taken because it formed an independent unbiased set which had little homology to human or other eukaryotic microRNA precursors. Error! No index entries found.

## COMPARISON WITH OTHER WEB SERVERS\*

	SENSITIVITY	SPECIFICITY	ACCURACY
EumiR	<b>85.24</b>	82.47	<b>83.91</b>
Mir-abela	65.49	99.20	81.70
BayesmiRNAfind	77.49	91.43	<b>84.10</b>

\*The calculations were undertaken on the randomly derived half of the total set (the testing set for the SVM model), which contained total of 542 true precursor miRNA hairpins and 502 pseudo microRNA hairpins.

The evaluation has not been undertaken on an unbiased set of true negatives as there is no independent dataset of experimentally validated pseudo-microRNA forming hairpins reported in literature