



# MiRNA-ProtPred: Unlocking miRNA Secrets Against Pathogens

## HELP AND GUIDELINES

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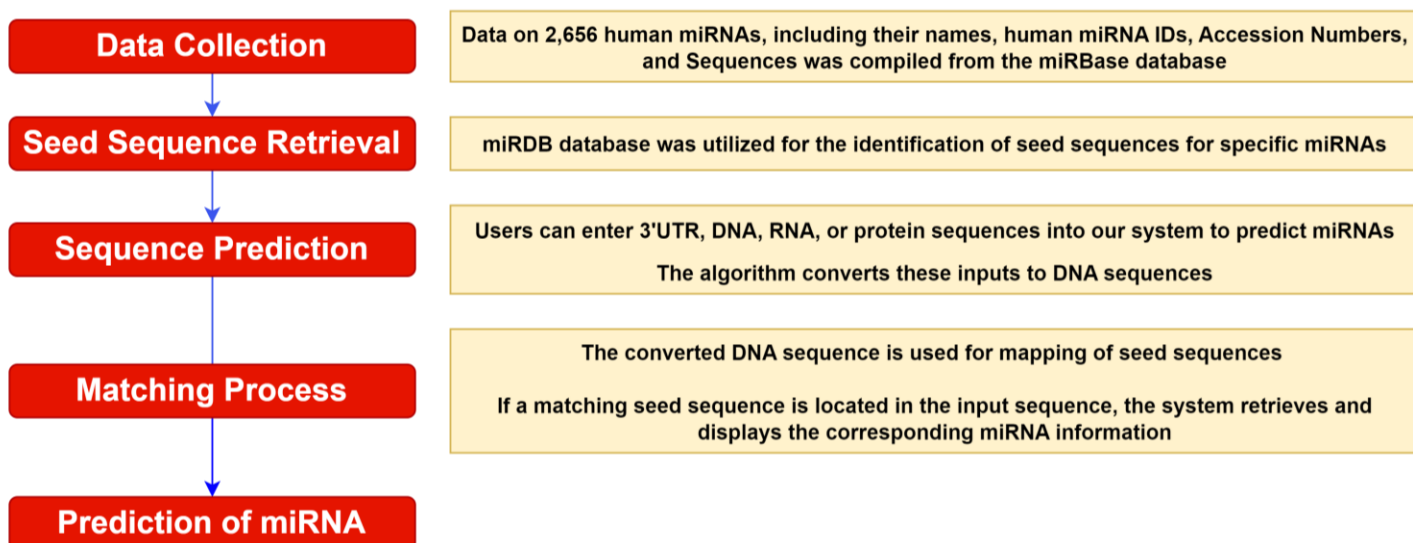
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## 1. OVERVIEW

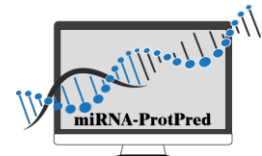
**miRNA-ProtPred** is the first online service that aids in the prediction and identification of the human miRNA with the potential to inhibit the expression of pathogen-specific genes and proteins.

## 2. BACKGROUND

Methodology used to train our model:



**Figure 1:** Flow chart of development of prediction tool.



### 3. 3'UTRmiRNA-Pred

Users with a 3'UTR of mRNA sequence from a pathogenic source can employ this tool to forecast potential human miRNAs capable of suppressing the expression of the corresponding protein or gene. Users are encouraged to input the 3'UTR of mRNA sequence of the relevant protein.

#### Procedure:

##### 3.1. Click on the “3'UTRmiRNA-Pred” option in the Menu Bar:

Home **3'UTRmiRNA-Pred** miRNA-SeqFinder miRNA-Validator Team Contact Us

## 3'UTRmiRNA-Pred

- If users have a 3'UTR sequence of mRNA of pathogen, they can use this tool for prediction of potential human miRNA that can inhibit the expression of respective protein or gene. Users can provide the 3'UTR sequence of mRNA of respective protein as input.
- It enables users to predict the binding position of the provided sequence at complementary site of miRNAs.
- After gathering this information, one may use it for further computational biology, bioinformatics, or wet lab experiments and analysis.
- The predicted miRNA or their miRNA mimic can be used as therapeutics against pathogens.

Job Id (Optional):

Enter Sequence (3'UTR of mRNA Sequence):

Search

##### 3.2. Enter a **Job Id**, although this step is not necessary, it is useful for systematic research purposes:

Home **3'UTRmiRNA-Pred** miRNA-SeqFinder miRNA-Validator Team Contact Us

## 3'UTRmiRNA-Pred

- If users have a 3'UTR sequence of mRNA of pathogen, they can use this tool for prediction of potential human miRNA that can inhibit the expression of respective protein or gene. Users can provide the 3'UTR sequence of mRNA of respective protein as input.
- It enables users to predict the binding position of the provided sequence at complementary site of miRNAs.
- After gathering this information, one may use it for further computational biology, bioinformatics, or wet lab experiments and analysis.
- The predicted miRNA or their miRNA mimic can be used as therapeutics against pathogens.

Job Id (Optional):

Enter Sequence (3'UTR of mRNA Sequence):

Search



### 3.3. Enter 3'UTR sequence of the mRNA of the pathogen of interest in the text box below “Enter Sequence (3'UTR)”:

Home 3'UTRmiRNA-Pred miRNA-SeqFinder miRNA-Validator Team Contact Us

## 3'UTRmiRNA-Pred

- If users have a 3'UTR sequence of mRNA of pathogen, they can use this tool for prediction of potential human miRNA that can inhibit the expression of respective protein or gene. Users can provide the 3'UTR sequence of mRNA of respective protein as input.
- It enables users to predict the binding position of the provided sequence at complementary site of miRNAs.
- After gathering this information, one may use it for further computational biology, bioinformatics, or wet lab experiments and analysis.
- The predicted miRNA or their miRNA mimic can be used as therapeutics against pathogens.

Job Id (Optional):  
Streptococcus pneumoniae

Enter Sequence (3'UTR of mRNA Sequence):

```
ATGAAATGAAGTTTCTATAACAAATTTGTTTCATGTCTTTTGCTAATCTGATTACAATCTTACAT
CAGTTATAGTTGACTAATTTACCAAAAATATGGGAGTAAC TGAGTATAGTTATTGGCAACTATATAT
TTTTTACCTAACATATATGGTTTTTTTCATCTGGGATGGATTGATGGAATTTATCTTAAATATGGCGGA
TTAGAGTACCAGAACCTAGATAAGAAACAGTTTTATTCTCAAATACTTCAATTTTCAGTTTTTAATTT
```

Search

### 3.4. Click the blue “Search” button located below the text box to obtain output:

Home 3'UTRmiRNA-Pred miRNA-SeqFinder miRNA-Validator Team Contact Us

## 3'UTRmiRNA-Pred

- If users have a 3'UTR sequence of mRNA of pathogen, they can use this tool for prediction of potential human miRNA that can inhibit the expression of respective protein or gene. Users can provide the 3'UTR sequence of mRNA of respective protein as input.
- It enables users to predict the binding position of the provided sequence at complementary site of miRNAs.
- After gathering this information, one may use it for further computational biology, bioinformatics, or wet lab experiments and analysis.
- The predicted miRNA or their miRNA mimic can be used as therapeutics against pathogens.

Job Id (Optional):  
Streptococcus pneumoniae

Enter Sequence (3'UTR of mRNA Sequence):

```
ATGAAATGAAGTTTCTATAACAAATTTGTTTCATGTCTTTTGCTAATCTGATTACAATCTTACAT
CAGTTATAGTTGACTAATTTACCAAAAATATGGGAGTAAC TGAGTATAGTTATTGGCAACTATATAT
TTTTTACCTAACATATATGGTTTTTTTCATCTGGGATGGATTGATGGAATTTATCTTAAATATGGCGGA
TTAGAGTACCAGAACCTAGATAAGAAACAGTTTTATTCTCAAATACTTCAATTTTCAGTTTTTAATTT
```

Search

### 3.5. The Output appears in the form of a table comprising of data on the following – Description, Human miRNA ID, Accession Number, Sequence, Seed, and Position:

Search

**Matching Rows: Streptococcus pneumoniae**

Description	Human miRNA ID	Accession Number	Sequence 5' to 3'	Seed	Position
HomosapiensmiR-494-3p	hsa-miR-494-3p	MIMAT0002816	UGAAACAUAACACGGGAAACCUC	tgtttca	29
HomosapiensmiR-3133	hsa-miR-3133	MIMAT0014998	UAAAGAACUCUAAAACCCAAU	gttcttt	37
HomosapiensmiR-10b-3p	hsa-miR-10b-3p	MIMAT0004556	ACAGAUUCGAUUCUAGGGGAU	aatctga	49
HomosapiensmiR-34a-3p	hsa-miR-34a-3p	MIMAT0004557	CAAUCAGCAAGUAUACUGCCCU	ctgatta	52

### 3.5.1 Description:

Description represents information on the microRNA molecule, these include – Organism name, the type of biomolecule, identifier or name (based on order of discovery), the strand from which it originates in its precursor molecule.

For example, in the first output generated above i.e., **HomosapiensmiR-494-3p**:

Organism name – *Homo sapiens*

Type of biomolecule – miR (micro-RNA)

Identifier - 494

The strand from which it originates in its precursor molecule – 3p

**Matching Rows: Streptococcus pneumoniae**

Description	Human miRNA ID	Accession Number	Sequence 5' to 3'	Seed	Position
HomosapiensmiR-494-3p	hsa-miR-494-3p	MIMAT0002816	UGAAACAUAACACGGGAAACCUC	tgtttca	29
HomosapiensmiR-3133	hsa-miR-3133	MIMAT0014998	UAAAGAACUCUAAAACCCAAU	gttcttt	37
HomosapiensmiR-10b-3p	hsa-miR-10b-3p	MIMAT0004556	ACAGAUUCGAUUCUAGGGGAU	aatctga	49
HomosapiensmiR-34a-3p	hsa-miR-34a-3p	MIMAT0004557	CAAUCAGCAAGUAUACUGCCCU	ctgatta	52

### 3.5.2 Human miRNA ID:

The miRNA IDs are frequently utilized in publications, databases, and bioinformatics tools to guarantee coherence and precision in research pertaining to miRNAs, it can be seen as a simplified version of the **Description**.

### Matching Rows: Streptococcus pneumoniae

Description	Human miRNA ID	Accession Number	Sequence 5' to 3'	Seed	Position
HomosapiensmiR-494-3p	hsa-miR-494-3p	MIMAT0002816	UGAAACAUACACGGGAAACCUC	tgtttca	29
HomosapiensmiR-3133	hsa-miR-3133	MIMAT0014998	UAAAGAACUCUAAAAACCCAAU	gttcttt	37
HomosapiensmiR-10b-3p	hsa-miR-10b-3p	MIMAT0004556	ACAGAUUCGAUUCUAGGGGAAU	aatctga	49
HomosapiensmiR-34a-3p	hsa-miR-34a-3p	MIMAT0004557	CAAUCAGCAAGUAUACUGCCCU	ctgatta	52

### 3.5.3 Accession Number:

Accession numbers standardise miRNA sequence and information access for researchers.

miRBase is a notable miRNA database. MiRBase assigns accession numbers like "MI0000XXX" for mature miRNAs and "MI0000XXX.1" for precursor miRNAs. Each miRNA entry has a unique numerical identification "XXX".

### Matching Rows: Streptococcus pneumoniae

Description	Human miRNA ID	Accession Number	Sequence 5' to 3'	Seed	Position
HomosapiensmiR-494-3p	hsa-miR-494-3p	MIMAT0002816	UGAAACAUACACGGGAAACCUC	tgtttca	29
HomosapiensmiR-3133	hsa-miR-3133	MIMAT0014998	UAAAGAACUCUAAAAACCCAAU	gttcttt	37
HomosapiensmiR-10b-3p	hsa-miR-10b-3p	MIMAT0004556	ACAGAUUCGAUUCUAGGGGAAU	aatctga	49
HomosapiensmiR-34a-3p	hsa-miR-34a-3p	MIMAT0004557	CAAUCAGCAAGUAUACUGCCCU	ctgatta	52

### 3.5.4 Sequence 5' to 3':

Unique nucleotide sequence of the microRNA comprising of Adenine(A), Guanine(G), Uracil(U) and Cytosine(C).

### Matching Rows: Streptococcus pneumoniae

Description	Human miRNA ID	Accession Number	Sequence 5' to 3'	Seed	Position
HomosapiensmiR-494-3p	hsa-miR-494-3p	MIMAT0002816	UGAAACAUACACGGGAAACCUC	tgtttca	29
HomosapiensmiR-3133	hsa-miR-3133	MIMAT0014998	UAAAGAACUCUAAAAACCCAAU	gttcttt	37
HomosapiensmiR-10b-3p	hsa-miR-10b-3p	MIMAT0004556	ACAGAUUCGAUUCUAGGGGAAU	aatctga	49
HomosapiensmiR-34a-3p	hsa-miR-34a-3p	MIMAT0004557	CAAUCAGCAAGUAUACUGCCCU	ctgatta	52

### 3.5.5 Seed:

Seed Sequence refers to the heptametrical sequence located primarily at positions 2-7 from the miRNA 3' end.

### Matching Rows: Streptococcus pneumoniae

Description	Human miRNA ID	Accession Number	Sequence 5' to 3'	Seed	Position
HomosapiensmiR-494-3p	hsa-miR-494-3p	MIMAT0002816	UGAAACAUACACGGGAAACCUC	tgtttca	29
HomosapiensmiR-3133	hsa-miR-3133	MIMAT0014998	UAAAGAACUCUAAAACCCAAU	gttcttt	37
HomosapiensmiR-10b-3p	hsa-miR-10b-3p	MIMAT0004556	ACAGAUUCGAUUCUAGGGGAAU	aatctga	49
HomosapiensmiR-34a-3p	hsa-miR-34a-3p	MIMAT0004557	CAAUCAGCAAGUAUCUGCCCU	ctgatta	52

### 3.5.6 Position:


Position is based on DNA sequence of provided input data (3'UTR, DNA, RNA and Protein).

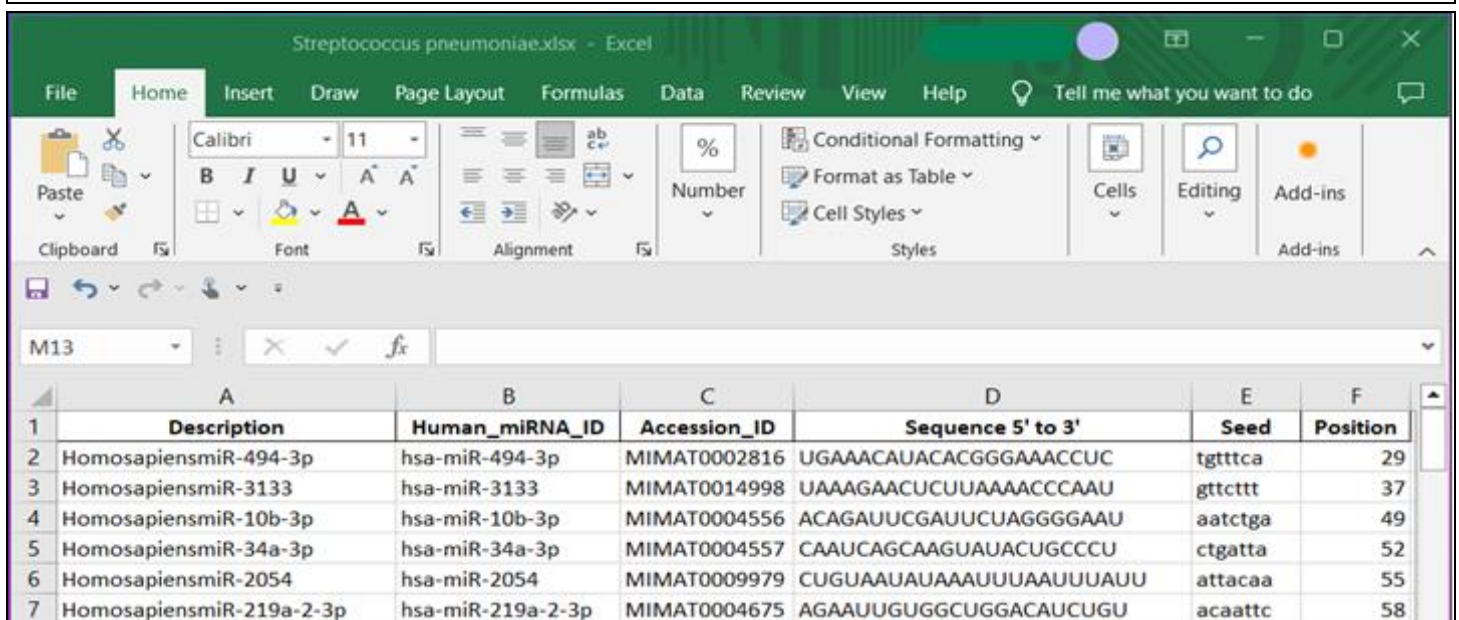
### Matching Rows: Streptococcus pneumoniae

Description	Human miRNA ID	Accession Number	Sequence 5' to 3'	Seed	Position
HomosapiensmiR-494-3p	hsa-miR-494-3p	MIMAT0002816	UGAAACAUACACGGGAAACCUC	tgtttca	29
HomosapiensmiR-3133	hsa-miR-3133	MIMAT0014998	UAAAGAACUCUAAAACCCAAU	gttcttt	37
HomosapiensmiR-10b-3p	hsa-miR-10b-3p	MIMAT0004556	ACAGAUUCGAUUCUAGGGGAAU	aatctga	49
HomosapiensmiR-34a-3p	hsa-miR-34a-3p	MIMAT0004557	CAAUCAGCAAGUAUCUGCCCU	ctgatta	52

**3.5.6.** You can select the “Download Complete Data” option below the table to obtain the output in the form of an excel sheet (.xls file format).

HomosapiensmiR-3185	hsa-miR-3185	MIMAT0015065	AGAAGAAGCGGUGCGUCUGCGG	ttcttca	1281
HomosapiensmiR-4709-3p	hsa-miR-4709-3p	MIMAT0019812	UUGAAGAGGAGGUGCUCUGUAGC	tcttcaa	1282
HomosapiensmiR-4635	hsa-miR-4635	MIMAT0019692	UCUUGAAGUCAGAACCCGCAA	cttcaag	1283
HomosapiensmiR-624-5p	hsa-miR-624-5p	MIMAT0003293	UAGUACCAGUACCUUGUGUUCA	tggtact	1291

[Download Complete Data](#) 



	A	B	C	D	E	F
	Description	Human_miRNA_ID	Accession_ID	Sequence 5' to 3'	Seed	Position
1	HomosapiensmiR-494-3p	hsa-miR-494-3p	MIMAT0002816	UGAAACAUACACGGGAAACCUC	tgtttca	29
2	HomosapiensmiR-3133	hsa-miR-3133	MIMAT0014998	UAAAGAACUCUAAAACCCAAU	gttcttt	37
3	HomosapiensmiR-10b-3p	hsa-miR-10b-3p	MIMAT0004556	ACAGAUUCGAUUCUAGGGGAAU	aatctga	49
4	HomosapiensmiR-34a-3p	hsa-miR-34a-3p	MIMAT0004557	CAAUCAGCAAGUAUCUGCCCU	ctgatta	52
5	HomosapiensmiR-2054	hsa-miR-2054	MIMAT0009979	CUGUAAUAUAAAUUUAUUUAUU	attacaa	55
6	HomosapiensmiR-219a-2-3p	hsa-miR-219a-2-3p	MIMAT0004675	AGAAUUGUGGUGGACAUCUGU	acaattc	58



## 4. miRNA-SeqFinder

For prediction of potential human miRNA binding within coding sequence (CDS), user can use **miRNA-SeqFinder**.

The **miRNA-SeqFinder** allows users to predict human miRNA using DNA, RNA, or protein sequences as input.

### Procedure:

#### 4.1. Click on the “miRNA-SeqFinder” option in the Menu Bar:

The screenshot shows the top navigation bar with links: Home, 3'UTRmiRNA-Pred, **miRNA-SeqFinder**, miRNA-Validator, Team, and Contact Us. The main heading is "miRNA-SeqFinder". Below the heading, there are several bullet points providing information about the tool's capabilities and usage. At the bottom of the form area, there is a "Job Id (Optional):" label followed by an empty text input field, and an "Enter Sequence (DNA, RNA, or Protein):" label followed by a larger empty text input field. A blue "Search" button is located at the bottom left of the form area.

#### 4.2. Enter a **Job Id**, although this step is not necessary, it is useful for systematic research purposes:

This screenshot is similar to the previous one, but the "Job Id (Optional):" text input field is highlighted in yellow and contains the text "Streptococcus pneumoniae - Pneumococcal Surface Proteins". The "Enter Sequence (DNA, RNA, or Protein):" field remains empty. The "Search" button is still present at the bottom left.



### 4.3. Enter DNA, RNA or Protein sequence of the target protein of the pathogen of interest in the text box below “Enter Sequence (DNA, RNA, or Protein)”:

Home 3'UTRmiRNA-Pred **miRNA-SeqFinder** miRNA-Validator Team Contact Us

## miRNA-SeqFinder

- If the users have no data of 3'UTR of mRNA of pathogen. They can provide DNA, RNA, or protein sequences of target protein of pathogen for prediction of potential human miRNA.
- We have observed that in most of the cases, human miRNA that can interact with 3'UTR of pathogen mRNA or inhibit the protein/gene expression of pathogen, have also shown presence of seed sequence of miRNA in the cDNA sequence of respective protein.
- The predicted human miRNA can be further used for computational biology, bioinformatics, or wet lab experiments and analysis as well as a therapeutic agent against that specific pathogen.
- If we upregulate the predicted human miRNA or use miRNA mimic against pathogens, it will significantly diminish their growth. Ultimately, it may help to control the pathogenic disease.
- Before clinical trials, the predicted human miRNA must be experimentally validated.

Job Id (Optional):

Streptococcus pneumoniae - Pneumococcal Surface Proteins

**Enter Sequence (DNA, RNA, or Protein):**

GACGACGACAAGATGGAGAAGTCAGCAGATCAACAAGCTGAAGAAGACTATGCTCGTAGATCAGAAGAAG  
AATATAATCGCTTGACCCAACAGCAACCGTAAACCGGGCTTCTCCTC

**Search**

### 4.4. Click the blue “Search” button located below the text box to obtain output:

Home 3'UTRmiRNA-Pred **miRNA-SeqFinder** miRNA-Validator Team Contact Us

## miRNA-SeqFinder

- If the users have no data of 3'UTR of mRNA of pathogen. They can provide DNA, RNA, or protein sequences of target protein of pathogen for prediction of potential human miRNA.
- We have observed that in most of the cases, human miRNA that can interact with 3'UTR of pathogen mRNA or inhibit the protein/gene expression of pathogen, have also shown presence of seed sequence of miRNA in the cDNA sequence of respective protein.
- The predicted human miRNA can be further used for computational biology, bioinformatics, or wet lab experiments and analysis as well as a therapeutic agent against that specific pathogen.
- If we upregulate the predicted human miRNA or use miRNA mimic against pathogens, it will significantly diminish their growth. Ultimately, it may help to control the pathogenic disease.
- Before clinical trials, the predicted human miRNA must be experimentally validated.

Job Id (Optional):

Streptococcus pneumoniae - Pneumococcal Surface Proteins

**Enter Sequence (DNA, RNA, or Protein):**

GACGACGACAAGATGGAGAAGTCAGCAGATCAACAAGCTGAAGAAGACTATGCTCGTAGATCAGAAGAAG  
AATATAATCGCTTGACCCAACAGCAACCGTAAACCGGGCTTCTCCTC


**Search** ←



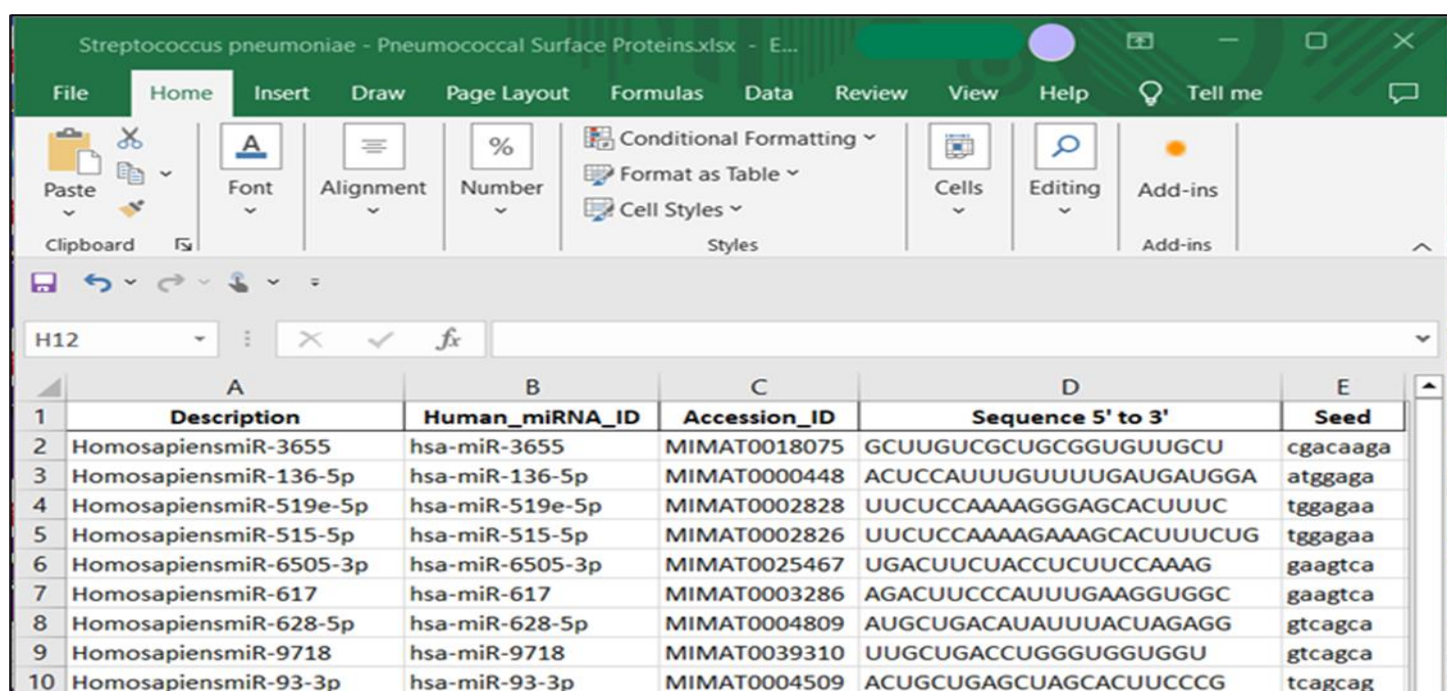
4.5. The Output appears in the form of a table comprising of data on the following – **Description, Human miRNA ID, Accession Number, Sequence, Seed, and Position:**

**Matching Rows:**

Description	Human miRNA ID	Accession Number	Sequence 5' to 3'	Seed	Position
HomosapiensmiR-3147	hsa-miR-3147	MIMAT0015019	GGUUGGGCAGUCAGGAGGGUGUGA	cccaaca	83
HomosapiensmiR-4425	hsa-miR-4425	MIMAT0018940	UGUUGGGAUUCAGCAGGACCAU	cccaaca	83
HomosapiensmiR-3192-3p	hsa-miR-3192-3p	MIMAT0027027	CUCUGAUCGCCUCUCAGCUC	gatcagaa	56
HomosapiensmiR-3655	hsa-miR-3655	MIMAT0018075	GCUUGUCGCUGCGGUGUUGCU	cgacaaga	6
HomosapiensmiR-3940-3p	hsa-miR-3940-3p	MIMAT0018356	CAGCCCCGAUCCAGCCCACUU	ccgggct	101
HomosapiensmiR-4778-3p	hsa-miR-4778-3p	MIMAT0019937	UCUUCUCCUUUCAGAGUUGA	gaagaag	40

[Download Complete Data](#) 

4.6. You may select the “**Download Complete Data**” option below the table to obtain the output in the form of an excel sheet (.xlsx file format).

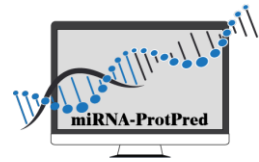


The screenshot shows an Excel spreadsheet with the following data:

	A	B	C	D	E
1	Description	Human_miRNA_ID	Accession_ID	Sequence 5' to 3'	Seed
2	HomosapiensmiR-3655	hsa-miR-3655	MIMAT0018075	GCUUGUCGCUGCGGUGUUGCU	cgacaaga
3	HomosapiensmiR-136-5p	hsa-miR-136-5p	MIMAT0000448	ACUCCAUUUGUUUGAUGAUGGA	atggaga
4	HomosapiensmiR-519e-5p	hsa-miR-519e-5p	MIMAT0002828	UUCUCCAAAAGGGAGCACUUUC	tggagaa
5	HomosapiensmiR-515-5p	hsa-miR-515-5p	MIMAT0002826	UUCUCCAAAAGAAAGCACUUUCUG	tggagaa
6	HomosapiensmiR-6505-3p	hsa-miR-6505-3p	MIMAT0025467	UGACUUCUACCUCUCCAAAG	gaagtca
7	HomosapiensmiR-617	hsa-miR-617	MIMAT0003286	AGACUCCCAUUUGAAGGUGGC	gaagtca
8	HomosapiensmiR-628-5p	hsa-miR-628-5p	MIMAT0004809	AUGCUGACAUUUUACUAGAGG	gtcagca
9	HomosapiensmiR-9718	hsa-miR-9718	MIMAT0039310	UUGCUGACCUGGGUGGUGGU	gtcagca
10	HomosapiensmiR-93-3p	hsa-miR-93-3p	MIMAT0004509	ACUGCUGAGCUAGCACUCCCCG	tcagcag

## 5. miRNA-Validator

The **miRNA-Validator** can be utilized to validate the predicted human miRNA by using experimentally reported downregulated miRNA (ERD miRNA) during pathogenic infection. Sometimes, ERD miRNA and predicted miRNA have similar seeds. Users can provide list of ERD miRNA and sequences (Protein/mRNA/DNA/3'UTR) for validation. If given ERD miRNA is positive, user can match positive miRNA with predicted miRNA and perform *in silico* validation of predicted miRNA.



## Procedure:

### 5.1. Click on the “miRNA-Validator” option in the Menu Bar:

Home 3'UTRmiRNA-Pred miRNA-SeqFinder **miRNA-Validator** Team Contact Us

## miRNA-Validator

- For in silico validation of predicted human miRNA, user can use miRNA-Validator tool.
- If users have details of downregulated miRNA during the specific pathogenic infection (Such as HIV, influenzas, etc.), they can use this tool. Users can provide the list of downregulated miRNAs as input along with the 3'UTR sequence of mRNA or protein/DNA/mRNA sequence as input. This will help to identify and in silico validation of more potential human miRNA that can be further used as potential therapeutics.
- To obtain the results, the user must submit -
  - Sequence of 3'UTR of mRNA or DNA/RNA/protein sequence of surface protein/pathogenesis-associated protein of pathogen.
  - List of human miRNAs that are reported as downregulated during pathogenic disease.

Enter Sequence (DNA, RNA, or Protein):

Enter Human miRNA IDs (comma-separated):

Search

### 5.2. Enter either the **3'UTR sequence of the mRNA** or the **DNA, RNA or Protein sequence of the target protein of the pathogen of interest** in the text box below “Enter Sequence (DNA, RNA, or Protein)”:

Home 3'UTRmiRNA-Pred miRNA-SeqFinder **miRNA-Validator** Team Contact Us

## miRNA-Validator

- For in silico validation of predicted human miRNA, user can use miRNA-Validator tool.
- If users have details of downregulated miRNA during the specific pathogenic infection (Such as HIV, influenzas, etc.), they can use this tool. Users can provide the list of downregulated miRNAs as input along with the 3'UTR sequence of mRNA or protein/DNA/mRNA sequence as input. This will help to identify and in silico validation of more potential human miRNA that can be further used as potential therapeutics.
- To obtain the results, the user must submit -
  - Sequence of 3'UTR of mRNA or DNA/RNA/protein sequence of surface protein/pathogenesis-associated protein of pathogen.
  - List of human miRNAs that are reported as downregulated during pathogenic disease.

Enter Sequence (DNA, RNA, or Protein):

Enter Human miRNA IDs (comma-separated):

Search



**5.3. Enter the list of human miRNAs that are downregulated during pathogenic disease in the text box below “Enter Human miRNA IDs (comma-spaced)”:**

Home 3'UTRmiRNA-Pred miRNA-SeqFinder **miRNA-Validator** Team Contact Us

## miRNA-Validator

- For in silico validation of predicted human miRNA, user can use miRNA-Validator tool.
- If users have details of downregulated miRNA during the specific pathogenic infection (Such as HIV, influenzas, etc.), they can use this tool. Users can provide the list of downregulated miRNAs as input along with the 3'UTR sequence of mRNA or protein/DNA/mRNA sequence as input. This will help to identify and in silico validation of more potential human miRNA that can be further used as potential therapeutics.
- To obtain the results, the user must submit -
  - o Sequence of 3'UTR of mRNA or DNA/RNA/protein sequence of surface protein/pathogenesis-associated protein of pathogen.
  - o List of human miRNAs that are reported as downregulated during pathogenic disease.

Enter Sequence (DNA, RNA, or Protein):

```
atgggcgcaaatggagcaaaagcagcattgtggctggccgaggtgcgcaacgattccgcccgcgcccggcgccgcccggcgccgctggggccgggtgagccaggatctggataaatggcgcggtgaccagcagcaacaccgcg  
cgaacaacgcgattgcccgtgctggaagcgcaggaagaagaagtggtcttccgggtgcccgcaggtgcccgtgcccgatgacctataaaggcgctttgatctgagcattttctgaaagaaaaaggcgccctggatgctgatt  
atagcaaaaaacgcccaggaattctggtatcaccagggctatttccggattggcagccgggcattcgcttccgctgaccttggctggtgctataaactggtgcccgggtggatccggcggaagtgaagaagcgaccgaaggc  
gaaaacaacagcctgctcctcatttccagcatggatgatgaagaaaaagaagtgctgatgtgaaatttgatagccgctggcgctgacctatcgccgcaactgcatccggaatttataaagattgc
```

Enter Human miRNA IDs (comma-separated):

miR-1253, miR-29a-3p, miR-133a-3p

Search

**5.4. Click the blue “Search” button located below the text box to obtain output:**

Home 3'UTRmiRNA-Pred miRNA-SeqFinder **miRNA-Validator** Team Contact Us

## miRNA-Validator

- For in silico validation of predicted human miRNA, user can use miRNA-Validator tool.
- If users have details of downregulated miRNA during the specific pathogenic infection (Such as HIV, influenzas, etc.), they can use this tool. Users can provide the list of downregulated miRNAs as input along with the 3'UTR sequence of mRNA or protein/DNA/mRNA sequence as input. This will help to identify and in silico validation of more potential human miRNA that can be further used as potential therapeutics.
- To obtain the results, the user must submit -
  - o Sequence of 3'UTR of mRNA or DNA/RNA/protein sequence of surface protein/pathogenesis-associated protein of pathogen.
  - o List of human miRNAs that are reported as downregulated during pathogenic disease.

Enter Sequence (DNA, RNA, or Protein):

```
atgggcgcaaatggagcaaaagcagcattgtggctggccgaggtgcgcaacgattccgcccgcgcccggcgccgcccggcgccgctggggccgggtgagccaggatctggataaatggcgcggtgaccagcagcaacaccgcg  
cgaacaacgcgattgcccgtgctggaagcgcaggaagaagaagtggtcttccgggtgcccgcaggtgcccgtgcccgatgacctataaaggcgctttgatctgagcattttctgaaagaaaaaggcgccctggatgctgatt  
atagcaaaaaacgcccaggaattctggtatcaccagggctatttccggattggcagccgggcattcgcttccgctgaccttggctggtgctataaactggtgcccgggtggatccggcggaagtgaagaagcgaccgaaggc  
gaaaacaacagcctgctcctcatttccagcatggatgatgaagaaaaagaagtgctgatgtgaaatttgatagccgctggcgctgacctatcgccgcaactgcatccggaatttataaagattgc
```

Enter Human miRNA IDs (comma-separated):

miR-1253, miR-29a-3p, miR-133a-3p

Search

**5.5.** The output obtained suggests whether each of the given miRNA corresponding to their respective IDs are potential binder (**Positive**) or non-binder (**Negative**) to the given sequences:

Search	
<b>Results:</b>	
miRNA ID: hsa-miR-1253 -----	Negative
miRNA ID: hsa-miR-29a-3p -----	Positive
miRNA ID: hsa-miR-133a-3p -----	Negative

**Final search:** User can use the positive miRNA (predicted as positive) for further analysis. If user will search for positive miRNA in the list of predicted miRNAs, they can find some common miRNA. This will ultimately validate that the current approach is a promising strategy for identification of potential human miRNA for development of therapeutics against pathogens.

#### **Future study:**

- Users can use the finally selected miRNA for bioinformatics analysis or experimental validation.
- Bioinformatics can include miRNA-mRNA docking, MD simulation, pathway analysis, and so on.
- Wet lab experimental validation can include binding assay, pathogenic protein expression inhibition test, pathogen growth inhibition assay (GIA), and so on.
- For experimental analysis, users can order miRNA mimics from authorized vendors.