



Access the GitHub for Download platform PmiRSelect:
<https://github.com/DeborahBambil/PmiRSelect>

DeborahBambil/PmiRSelect - Chromium

DeborahBambil/PmiRSele x +

github.com/DeborahBambil/PmiRSelect

Search or jump to... / Pull requests Issues Codespaces Marketplace Explore

DeborahBambil / PmiRSelect Public

Pin Unwatch 1 Fork 0 Star 0

<> Code Issues Pull requests Actions Projects Wiki Security Insights Settings

main 1 branch 0 tags

Go to file Add file <> Code

DeborahBambil Add files via upload f690bc4 2 hours ago 171 commits

CM100Threshold.rar	Add files via upload	2 hours ago
README.md	Update README.md	last week
data.rar	Add files via upload	2 hours ago
install.bin	Add files via upload	2 hours ago
run.bin	Add files via upload	2 hours ago

README.md

About

No description, website, or topics provided.

Readme Activity 0 stars 1 watching 0 forks

Releases

No releases published
[Create a new release](#)

Packages

No packages published
[Publish your first package](#)

Languages

Make Download



Search or jump to...

[Pull requests](#) [Issues](#) [Codespaces](#) [Marketplace](#) [Explore](#)[Notifications](#) [+](#) [Profile](#)[DeborahBambil / PmiRSelect](#) Public[Pin](#)[Unwatch](#) 1[Fork](#) 0[Star](#) 0[Code](#) [Issues](#) [Pull requests](#) [Actions](#) [Projects](#) [Wiki](#) [Security](#) [Insights](#) [Settings](#)[main](#) [1 branch](#) [0 tags](#)[Go to file](#)[Add file](#)[Code](#)**DeborahBambil** Add files via upload

f690bc4 2 hours ago 171 commits



CM100Threshold.rar

Add files via upload

2 hours ago



README.md

Update README.md

last week



data.rar

Add files via upload

2 hours ago



install.bin

Add files via upload

2 hours ago



run.bin

Add files via upload

2 hours ago



README.md



About

No description, website, or topics provided.

[Readme](#)[Activity](#)[0 stars](#)[1 watching](#)[0 forks](#)

Releases

No releases published

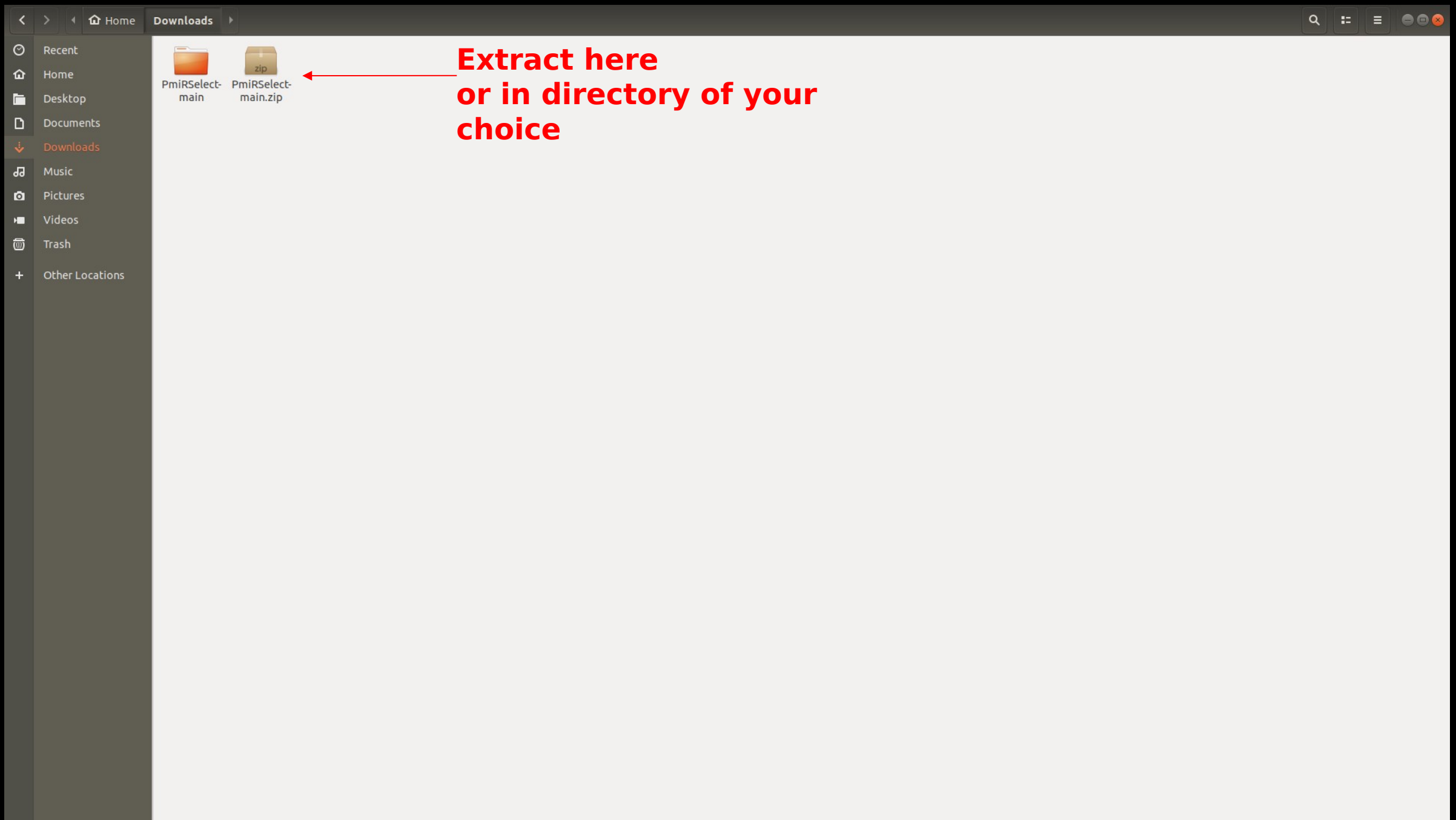
[Create a new release](#)

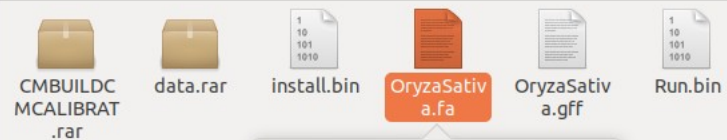
Packages

No packages published

[Publish your first package](#)

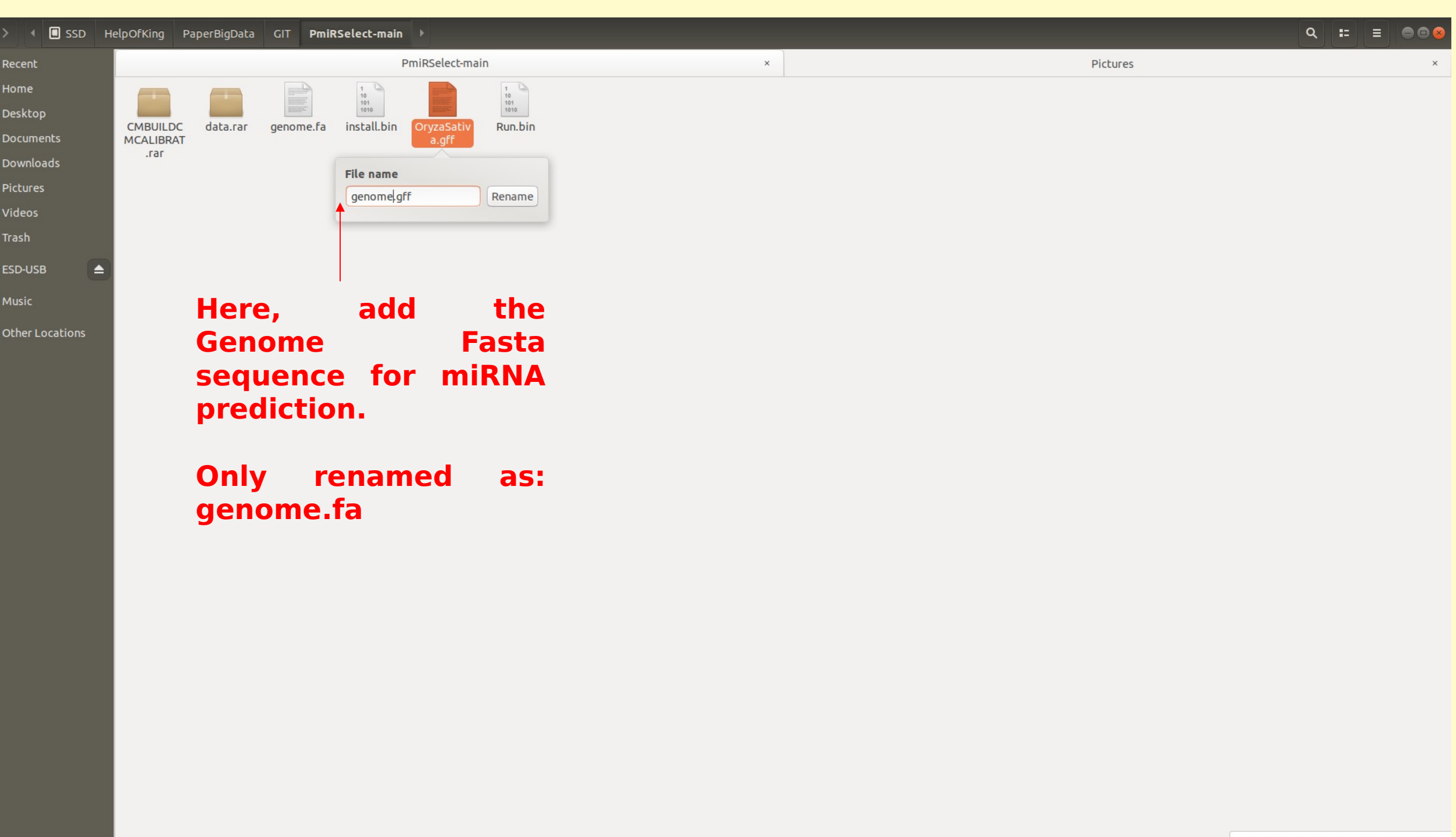
Languages





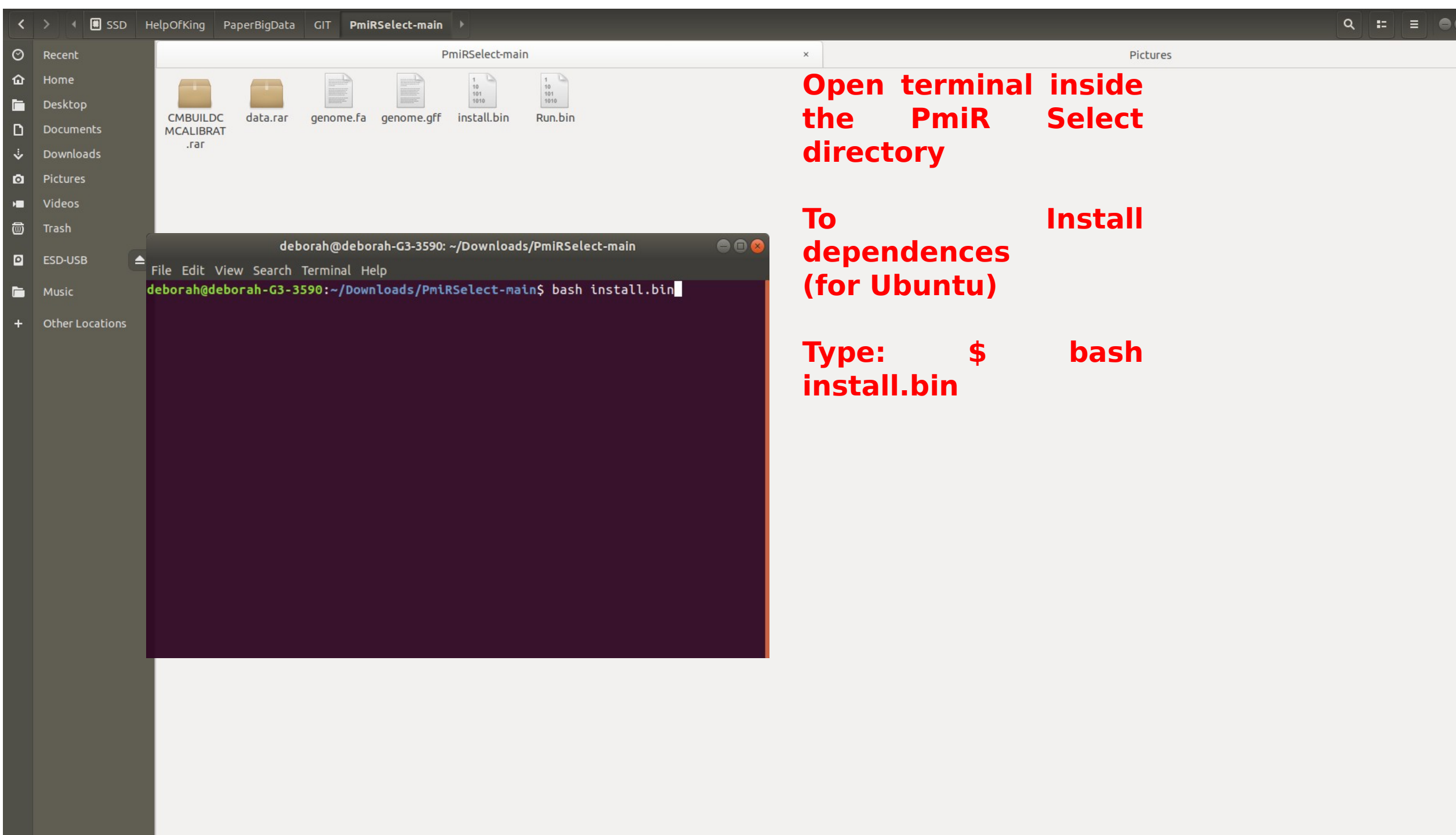
Here, add the Genome Fasta sequence for miRNA prediction.

Only renamed as: genome.fa



**Here, add the
Genome Fasta
sequence for miRNA
prediction.**

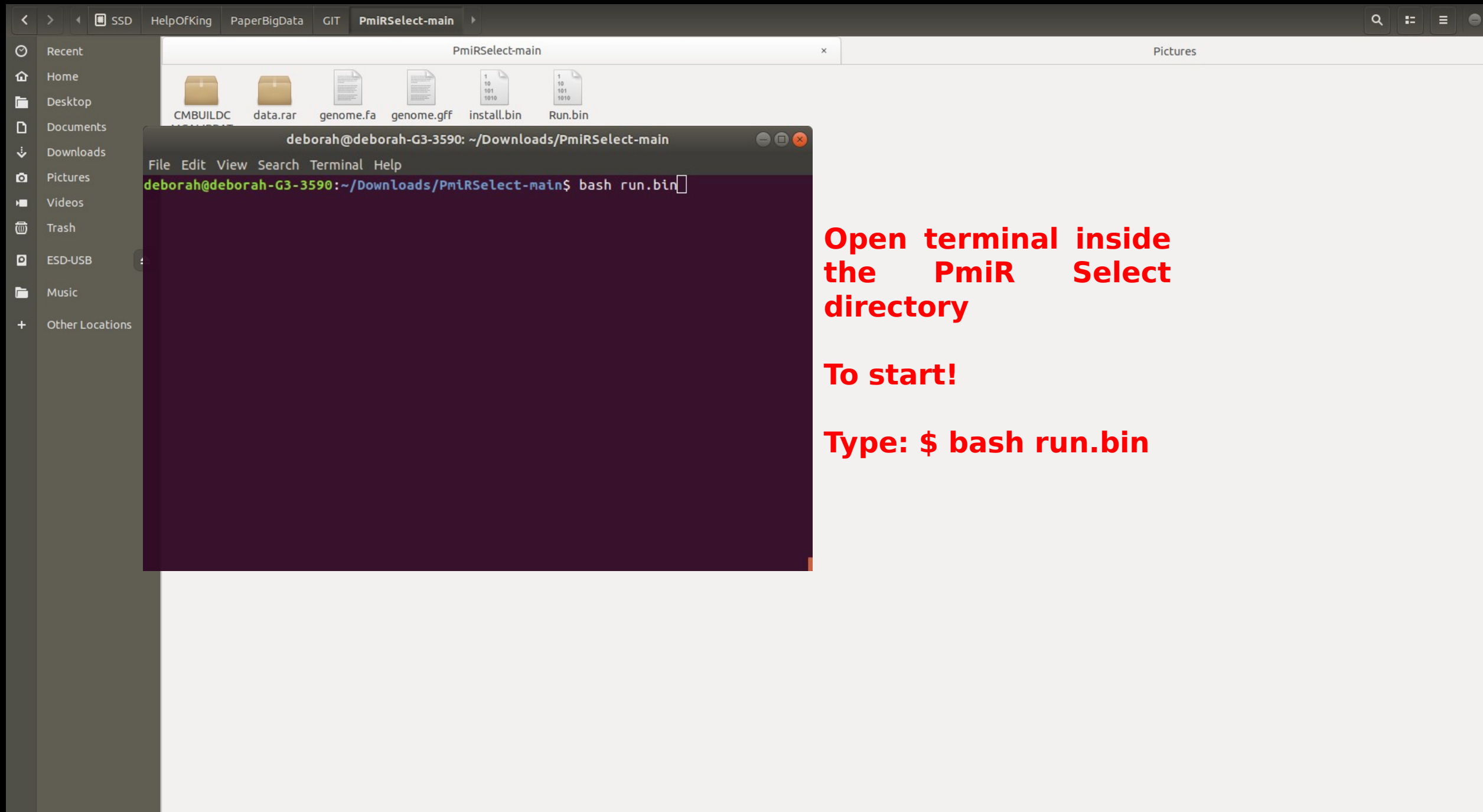
**Only renamed as:
genome.fa**



**Open terminal inside
the PmiR Select
directory**

**To Install
dependencies
(for Ubuntu)**

**Type: \$ bash
install.bin**



**Open terminal inside
the PmiR Select
directory**

To start!

Type: \$ bash run.bin


```
deborah@deborah-G3-3590: /media/deborah/SSD/HelpOfKing/PaperBigData/GIT/PmiRSelec...
File Edit View Search Terminal Help
Extracting CMBUILDCMCALIBRAT/MIR9780.cm OK
Extracting CMBUILDCMCALIBRAT/MIR9781.cm OK
Extracting CMBUILDCMCALIBRAT/MIR9782.cm OK
Extracting CMBUILDCMCALIBRAT/MIR9783.cm OK
Extracting CMBUILDCMCALIBRAT/MIR9863.cm OK
Extracting CMBUILDCMCALIBRAT/MIR9897.cm OK
All OK

UNRAR 5.50 freeware      Copyright (c) 1993-2017 Alexander Roshal

Extracting from data.rar

Creating    data                                OK
Extracting data/PlantHairpin.fa                OK
Extracting data/PlantHairpinBlast.nhr          OK
Extracting data/PlantHairpinBlast.nin          OK
Extracting data/PlantHairpinBlast.nsq          OK
Extracting data/PlantMature.fa                 OK
Extracting data/PlantMatureBlast.nhr           OK
Extracting data/PlantMatureBlast.nin           OK
Extracting data/PlantMatureBlast.nsq           OK
All OK
```

Start!

deborah@deborah-G3-3590: ~/Downloads/PmiRSelect-main

File Edit View Search Terminal Help

```
# sequence reporting threshold:      E-value <= 0.05
# number of worker threads:         8
# - - - - -
```

Error: no E-value parameters were read for CM: MIR12176

```
# cmsearch :: search CM(s) against a sequence database
# INFERNAL 1.1.2 (July 2016)
# Copyright (C) 2016 Howard Hughes Medical Institute.
# Freely distributed under a BSD open source license.
```

```
# - - - - -
# query CM file:                    CMBUILD_CMCALIBRAT_Part1/MIR12177.cm
# target sequence database:         organism.fa
# MSA of significant hits saved to file: CMSEARCH/MIR12177
# sequence reporting threshold:     E-value <= 0.05
# number of worker threads:         8
# - - - - -
```

Error: no E-value parameters were read for CM: MIR12177

Extract regions from a sequence alignment

Regions to extract (eg: 4-57,78-94) [1-262]:

Here, press Enter!

```
deborah@deborah-G3-3590: ~/Downloads/PmiRSelect-main
File Edit View Search Terminal Help
Error: Unable to read sequence 'CMSEARCH/MIR5214'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5215'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5216'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5217'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5218'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5219'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5221'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
Extract regions from a sequence alignment
Error: Unable to read sequence 'CMSEARCH/MIR5222'
Died: extractalign terminated: Bad value for '-sequence' and no prompt
```

```
deborah@deborah-G3-3590: ~/Downloads/PmiRSelect-main
File Edit View Search Terminal Help
Error: Unable to read sequence 'Curated/MIR1080'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1081'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1082'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1083'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1084'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1085'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1086'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
Remove redundant sequences from an input set
Error: Unable to read sequence 'Curated/MIR1087'
Died: skipredundant terminated: Bad value for '-sequences' and no prompt
```

```
deborah@deborah-G3-3590: ~/Downloads/PmiRSelect-main
File Edit View Search Terminal Help
ed/MIR1439'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1440'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1441'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1442'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1444'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1445'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1446'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1447'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1448'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1449'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1450'
Command line argument error: Argument "query". File is not accessible: `Predict
ed/MIR1507'
```

If these "errors" screens showed.

Do not worry!

It's just the families that didn't find homologs.

Keep Calm, wait, the predicts are already being selected!

```
deborah@deborah-G3-3590: /media/deborah/SSD/HelpOfKing/PaperBigData/GIT/PmiRSelec...  
File Edit View Search Terminal Help  
Curated/MIR12161  
Curated/MIR12162  
Curated/MIR12163  
Curated/MIR12164  
Curated/MIR12165  
Curated/MIR12166  
Curated/MIR12167  
Curated/MIR12168  
Curated/MIR12169  
Curated/MIR1217  
Curated/MIR12170  
Curated/MIR12171  
Curated/MIR12172  
Curated/MIR12173  
Curated/MIR12174  
Curated/MIR12175  
Curated/MIR12176  
Curated/MIR12177  
Curated/MIR1218  
Curated/MIR1219  
Curated/MIR1220  
Curated/MIR1221  
deborah@deborah-G3-3590: /media/deborah/SSD/HelpOfKing/PaperBigData/GIT/PmiRSelec  
t-main$
```

Finish!

**Go to the directory to see
the predicts and analyze
the data!**