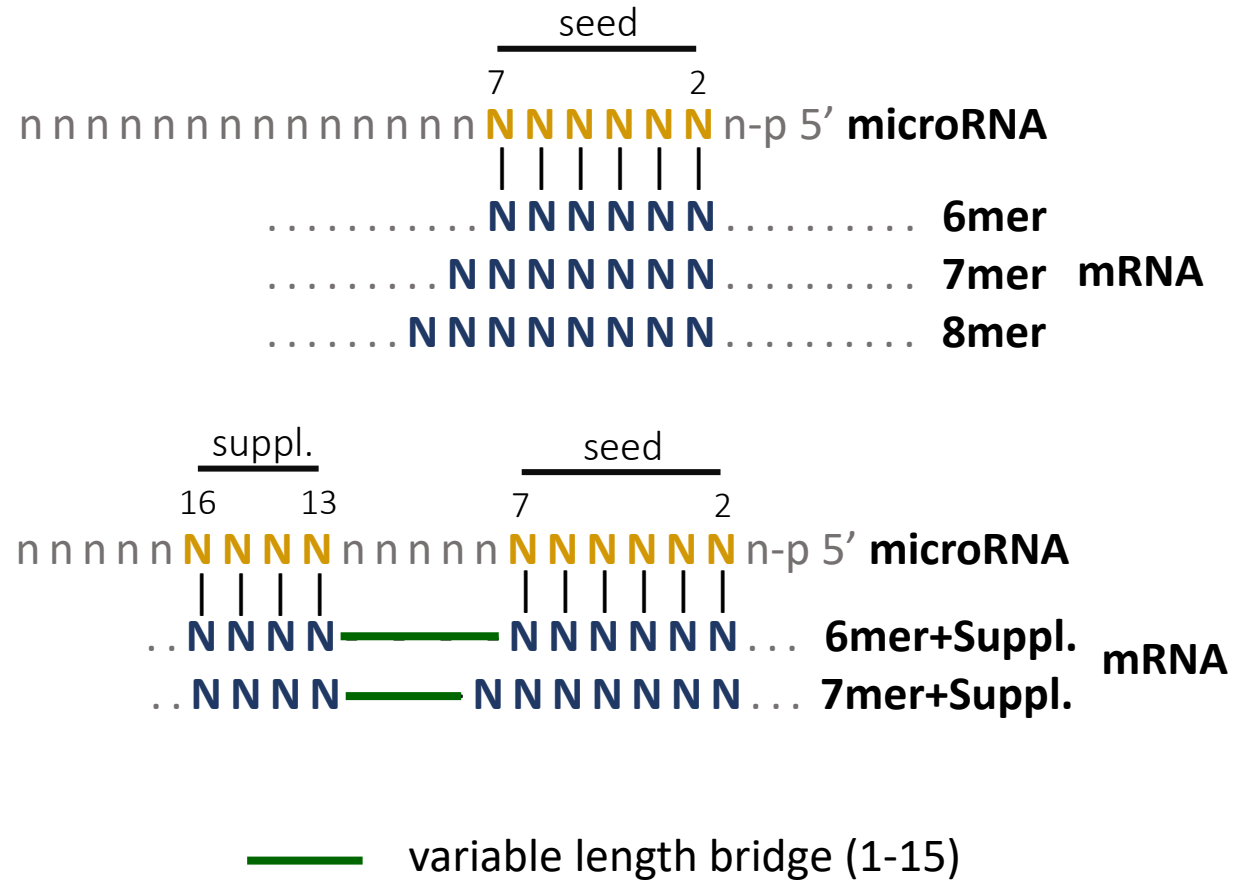














Readme



Firsts steps:

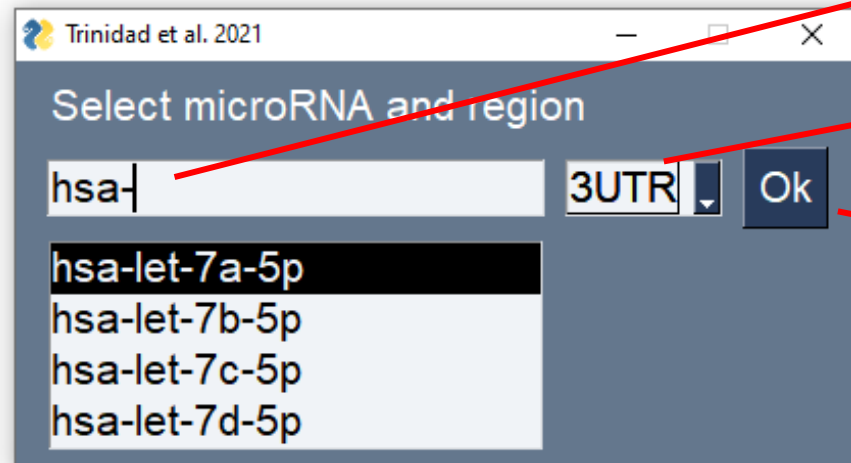
- Download the 2 executable files available on [github](#)
- Download the 4 files for human analysis on this [link](#)
- Executables and files must be downloaded in the same folder

The folder will look like this, 2 '.exe' files and 4 '.txt' files:

 searchByMicroRNA		7/2/2022 14:11	Aplicación	30.392 KB
 searchByMessengerRNA		7/2/2022 14:21	Aplicación	30.392 KB
 miR_Family_Info_targetScan_2016		9/7/2021 19:16	Normal text file	774 KB
 mart_export_CDS_2021_online		13/7/2021 14:15	Normal text file	145.433 KB
 mart_export_5UTRs_2021_online		13/7/2021 14:15	Normal text file	35.254 KB
 mart_export_3UTRs_2021_online		13/7/2021 14:15	Normal text file	116.218 KB

Search by microRNA

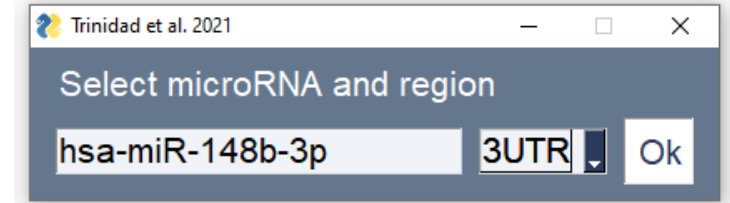
If you are interested in looking for all target mRNAs that have sequence complementarity with seeds and seed plus supplementary-region of certain microRNAs, you should open the **searchByMicroRNA** executable script:



- 1 Write or select microRNA name of interest
- 2 Select mRNA region in to look for
- 3 Press "OK" bottom to run the process

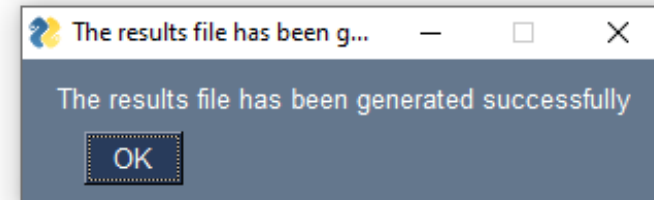
4

While process is running the “OK” bottom will be unavailable (white fill). This will take from few seconds to few minutes depending on the computer power.



5

When the file is ready this window will pop up.



6

Check for the **.csv** (comma separated) output in the folder where you run the **.exe**. The name must start with the microRNA name and finish with the region you search for.

	searchByMicroRNA	✓	7/2/2022 14:11	Aplicación	30.392 KB
	searchByMessengerRNA	✓	7/2/2022 14:21	Aplicación	30.392 KB
	miR_Family_Info_targetScan_2016	✓	9/7/2021 19:16	Normal text file	774 KB
	mart_export_CDS_2021_online	✓	13/7/2021 14:15	Normal text file	145.433 KB
	mart_export_5UTRs_2021_online	✓	13/7/2021 14:15	Normal text file	35.254 KB
	mart_export_3UTRs_2021_online	✓	13/7/2021 14:15	Normal text file	116.218 KB
	hsa-miR-148b-3p_finditer_microRNA_6mer_and_...	✓	7/2/2022 15:22	Archivo de valores...	3.304 KB



Output file

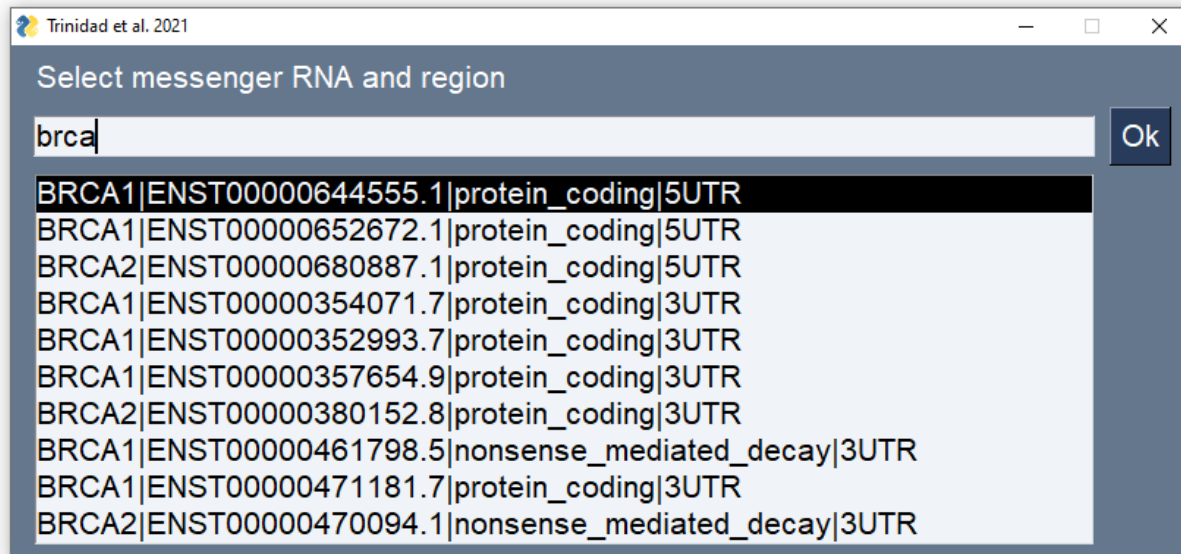
	A	B	C	D	E	F	G	H	I	J	K	L	M
	GeneName	TranscriptID	TranscriptType	mRNAregion	Interaction	microRNA	Type_of_Interaction	start	end	wholematch	BridgeSequence	BridgeLength	
2	CFTR	ENST00000003084.11	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	925	931	GCACTG	-	0	
3	PDK4	ENST000000005178.6	protein_coding	3UTR	seed	hsa-miR-148b-3p	8mer_site	759	767	TGCACTGA	-	0	
4	DBNDD1	ENST00000002501.11	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	1239	1245	GCACTG	-	0	
5	FKBP4	ENST00000001008.6	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	865	871	GCACTG	-	0	
6	FKBP4	ENST00000001008.6	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	1821	1827	GCACTG	-	0	
7	ESRRA	ENST00000000442.11	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	573	579	GCACTG	-	0	
8	CYP26B1	ENST00000001146.7	protein_coding	3UTR	seed	hsa-miR-148b-3p	7merm8_site	1117	1124	TGCACTG	-	0	
9	CYP26B1	ENST00000001146.7	protein_coding	3UTR	seed	hsa-miR-148b-3p	8mer_site	669	677	TGCACTGA	-	0	
10	HS3ST1	ENST00000002596.6	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	2476	2482	GCACTG	-	0	
11	NIPAL3	ENST00000003912.7	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	3194	3200	GCACTG	-	0	
12	NIPAL3	ENST00000003912.7	protein_coding	3UTR	seed	hsa-miR-148b-3p	7merA1_site	2531	2538	GCACTGA	-	0	
13	NDUFAF7	ENST00000002125.9	protein_coding	3UTR	seed	hsa-miR-148b-3p	7merA1_site	584	591	GCACTGA	-	0	
14	ARF5	ENST00000000233.10	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	363	369	GCACTG	-	0	
15	SLC7A2	ENST00000004531.14	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	805	811	GCACTG	-	0	
16	CX3CL1	ENST00000006053.7	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	553	559	GCACTG	-	0	
17	BAIAP2L1	ENST00000005260.9	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	961	967	GCACTG	-	0	
18	TRAPPC6A	ENST000000006275.8	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	23	29	GCACTG	-	0	
19	RPAP3	ENST00000005386.8	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	911	917	GCACTG	-	0	
20	CD4	ENST000000011653.9	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	1035	1041	GCACTG	-	0	
21	CD74	ENST00000009530.12	protein_coding	3UTR	seed	hsa-miR-148b-3p	7merm8_site	1319	1326	TGCACTG	-	0	
22	ITGA3	ENST00000007722.11	protein_coding	3UTR	seed	hsa-miR-148b-3p	7merm8_site	210	217	TGCACTG	-	0	
23	TSPAN9	ENST000000011898.10	protein_coding	3UTR	seed	hsa-miR-148b-3p	7merA1_site	289	296	GCACTGA	-	0	
24	VAMP3	ENST000000054666.11	protein_coding	3UTR	seed	hsa-miR-148b-3p	7merA1_site	1353	1360	GCACTGA	-	0	
25	FAM13B	ENST000000033079.7	protein_coding	3UTR	seed	hsa-miR-148b-3p	7merm8_site	1815	1822	TGCACTG	-	0	
26	RALBP1	ENST000000019317.8	protein_coding	3UTR	seed	hsa-miR-148b-3p	7merm8_site	1302	1309	TGCACTG	-	0	
27	PIGQ	ENST000000026218.9	protein_coding	3UTR	seed	hsa-miR-148b-3p	7merA1_site	237	244	GCACTGA	-	0	
28	SCTR	ENST000000019103.8	protein_coding	3UTR	seed	hsa-miR-148b-3p	6mer_site	57	63	GCACTG	-	0	

Remember this is a **comma separated file**, so, you must use Excel Data > Text to Columns or alternatively if you want the table to be formatted you can open excel, select Data and From Text/CSV and then select the file and load it. Here is an example:

<https://support.microsoft.com/en-us/office/split-text-into-different-columns-with-the-convert-text-to-columns-wizard-30b14928-5550-41f5-97ca-7a3e9c363ed7>

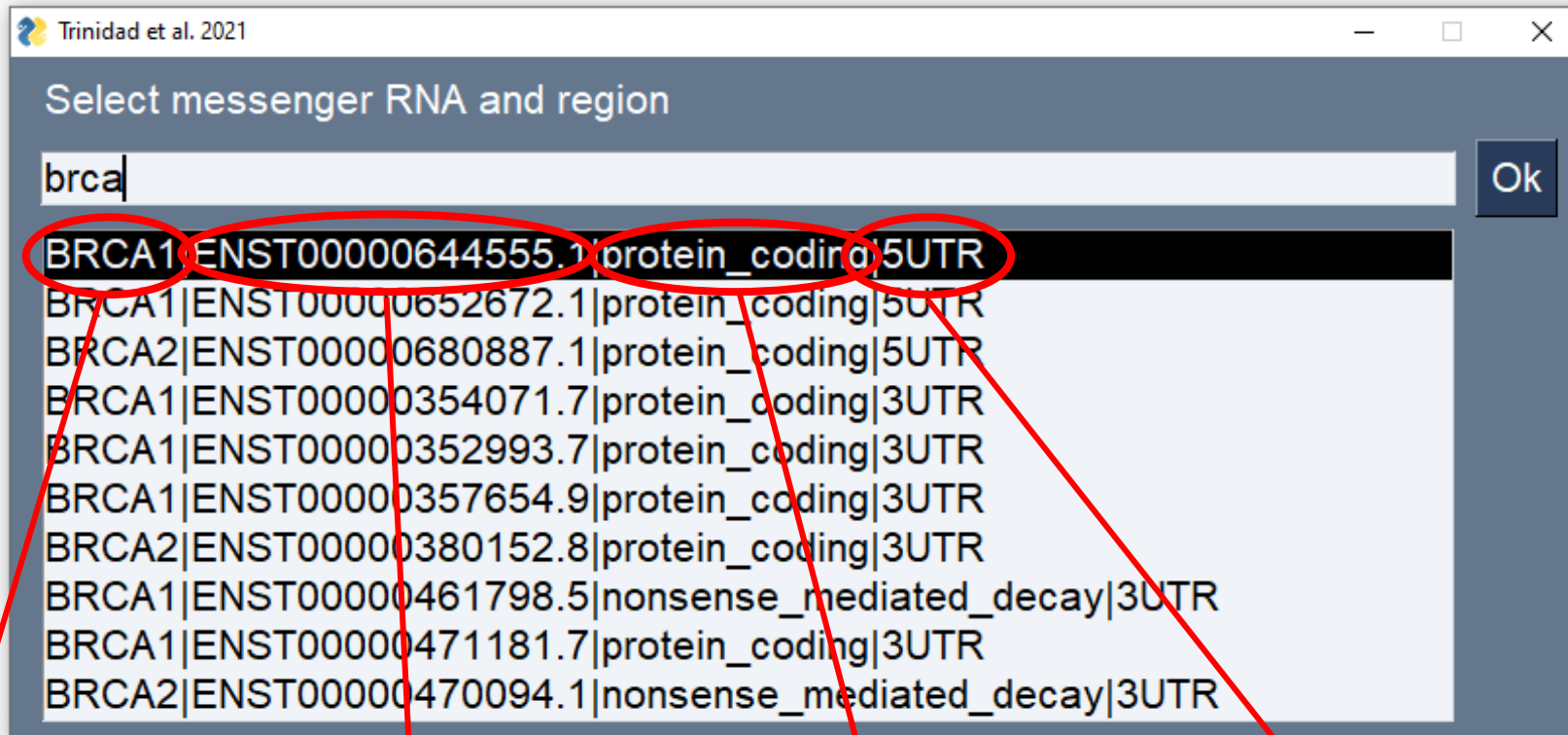
Search by mRNA

If you are interested in looking for with seeds and seed plus supplementary-region interactions of any microRNA in certain mRNAs, you should open the **searchByMessengerRNA** executable script :



→ 1 Write and select mRNA of interest.
Consider that selection include:

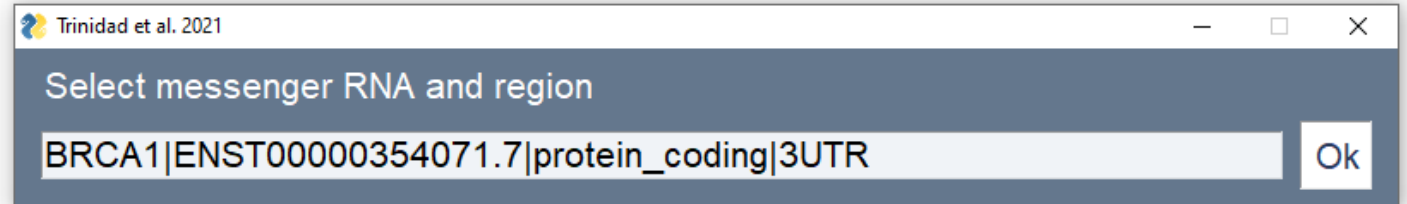
Gene Name | Transcript stable ID version | Gene type |
mRNA region to search for



Gene Name | Transcript stable ID version | Gene type | mRNA region to search for

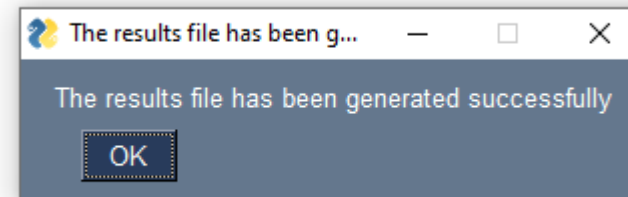
2

While process is running the “OK” bottom will be unavailable (white fill).
This will take from few seconds to few minutes depending on the computer speed.



3

When the file is ready this window will pop up.



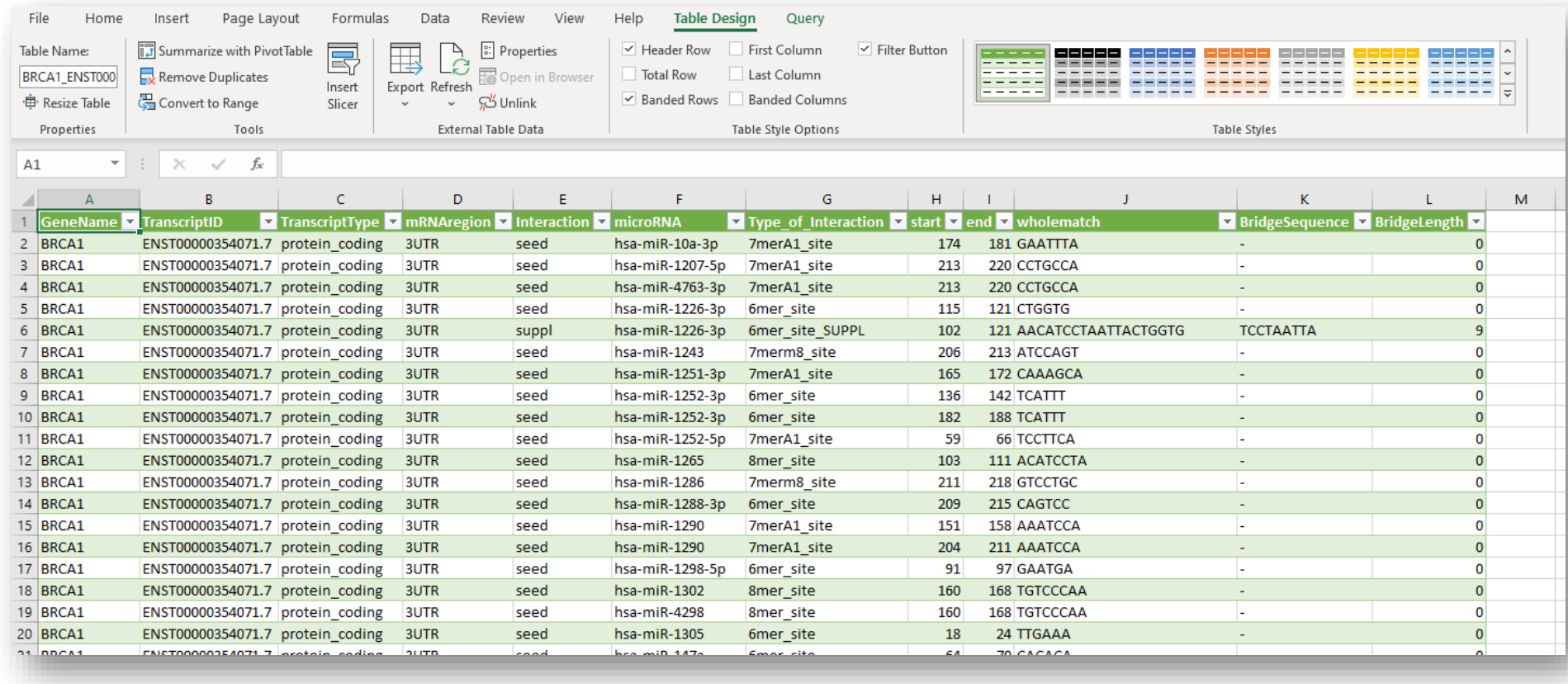
4

Check for the **.csv** (comma separated) output in the folder where you run the **.exe**
The name must start with the mRNA name and include all information selected in the first window.

	searchByMicroRNA	✓	7/2/2022 14:11	Aplicación	30.392 KB
	searchByMessengerRNA	✓	7/2/2022 14:21	Aplicación	30.392 KB
	miR_Family_Info_targetScan_2016	✓	9/7/2021 19:16	Normal text file	774 KB
	mart_export_CDS_2021_online	✓	13/7/2021 14:15	Normal text file	145.433 KB
	mart_export_5UTRs_2021_online	✓	13/7/2021 14:15	Normal text file	35.254 KB
	mart_export_3UTRs_2021_online	✓	13/7/2021 14:15	Normal text file	116.218 KB
	BRCA1_ENST00000354071.7_protein_coding_3UT...	✓	7/2/2022 15:38	Archivo de valores...	15 KB



Output file



GeneName	TranscriptID	TranscriptType	mRNARegion	Interaction	microRNA	Type_of_Interaction	start	end	wholematch	BridgeSequence	BridgeLength
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-10a-3p	7merA1_site	174	181	GAATTTA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1207-5p	7merA1_site	213	220	CCTGCCA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-4763-3p	7merA1_site	213	220	CCTGCCA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1226-3p	6mer_site	115	121	CTGGTG	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	suppl	hsa-miR-1226-3p	6mer_site_SUPPL	102	121	AACATCCTAATTACTGGTG	TCCTAATTA	9
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1243	7merm8_site	206	213	ATCCAGT	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1251-3p	7merA1_site	165	172	CAAAGCA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1252-3p	6mer_site	136	142	TCATTT	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1252-3p	6mer_site	182	188	TCATTT	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1252-5p	7merA1_site	59	66	TCCTTCA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1265	8mer_site	103	111	ACATCTCA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1286	7merm8_site	211	218	GTCCTGC	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1288-3p	6mer_site	209	215	CAGTCC	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1290	7merA1_site	151	158	AAATCCA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1290	7merA1_site	204	211	AAATCCA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1298-5p	6mer_site	91	97	GAATGA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1302	8mer_site	160	168	TGTCCCAA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-4298	8mer_site	160	168	TGTCCCAA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-1305	6mer_site	18	24	TTGAAA	-	0
BRCA1	ENST00000354071.7	protein_coding	3UTR	seed	hsa-miR-147a	6mer_site	64	70	CACACA	-	0

Remember this is a **comma separated file**, so, you must use Excel Data > Text to Columns or alternatively if you want the table to be formatted you can open excel, select Data and From Text/CSV and then select the file and load it. Here is an example:

<https://support.microsoft.com/en-us/office/split-text-into-different-columns-with-the-convert-text-to-columns-wizard-30b14928-5550-41f5-97ca-7a3e9c363ed7>

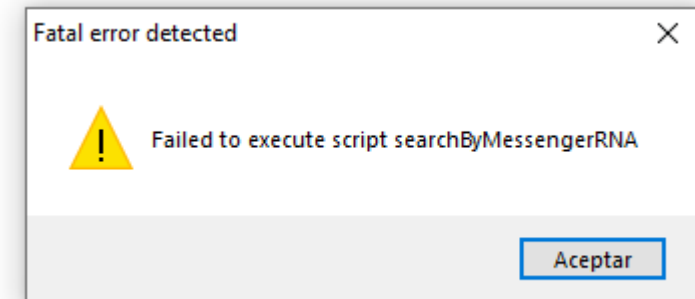
Troubleshooting

Contact jtrinidad@fcien.edu.uy

Most common problem:

Not running program. Check if **texts files (.txt)** are in the same folder than **.exe files**.

To run the programs, you need these .txt files in the same folder.



Interested in running the program for any other specie?

Do not hesitate to contact us, we will be happy to help!

Contact: jtrinidad@fcien.edu.uy