

Prepare input files in  
.fa or .fasta format  
under ../input



Run the code under the correct  
repository



View the results at  
../output

```
ENST00000493797.1|ENSG00000239906.1|OTTHUMG00000002481.1|
OTTHUMT00000007038.1|AL627309.2-201|AL627309.2|323|
TTGGTTTCCCAGGGGCGAGTGCTGAGCTCTTTGCCAGTGGGAAATGGGATGCTGGTGATT
TCCAGTAGGTGACCTCACAGTGACTCAAGCTACCACTTACTGTTGATTGTGACGAAATGC
CAGCTGAGGCACATGCCTTGGGAGCTAAGTGGTTGCTGCCCTTGACCACTGTGAAGACTG
GTGTGGGAAGGGTCGTTTTGGATGCACTTGAGCAGGGGTCCCAACCCCTGAGCCATGGA
GCCGCAAGGAGCCACACAGCAGGAGGTGGGAACATCCAGTTGCAGGAAAACAAGCTTAAC
ACGCCCCTGATTCTACATTATG
>ENST00000491962.1|ENSG00000241860.7|OTTHUMG00000002480.4|
OTTHUMT00000007168.1|AL627309.5-204|AL627309.5|278|
TGAGGTGGAGTCTTGCTCTGTCATCCAGGCTGGCAGTGGCGTGATCTTGGCTCACTGCAA
TGTCTGCCTCCTGGGTTTCAGGTGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGACTAC
```

```
python code/csv_RNA.py -input inputfile -output output_file_name
```

1	ENST00000653898.1	lncRNA
2	ENST00000667139.1	lncRNA
3	ENST00000656152.1	lncRNA
4	gi 1908918805 ref NM_001387165.1	mRNA
5	gi 1908918771 ref NM_001387166.1	mRNA
6	gi 1908918752 ref NM_001387167.1	mRNA