

How to run:

TargetIdentifier.pl and Annotator.pl were implemented using the same algorithm, only the output formats are slightly different.

```
usage: perl ./TargetIdentifier.pl BlastOutputFile seqFastaFile aceFile  
lucy.info outputFile
```

Input:

- BlastOutputFile - BLAST output;
- seqFastaFile - sequences in FASTA format used for BLAST;
- aceFile (optional) - a file from PHRAP or CAP containing assembly data;
- lucy.info (optional) - a file containing the low quality sequence length trimmed by LUCY;

Output:

- outputFile - output with annotation

Warning: for optional files, file names must be inputted, empty files could be used

Please cite:

Min, X.J., Butler, G, Storms, R. and Tsang, A. TargetIdentifier: a web server for identifying full-length cDNAs from EST sequences. Nucleic Acids Res., 2005, Vol. 33, Web Server Issue W669-W672. Our server URL (<http://proteomics.ysu.edu/tools/TargetIdentifier.html>) can also be used as your reference.