

How to Run OrfPredictor

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The perl script is easy to run in Linux, Mac or Window with Perl installed:

```
> perl ./OrfPredictor.pl
```

Usage: OrfPredictor.pl fastaFile BLASTX bFlag strand E-value output

fastaFile: a multiple-sequence file in fasta format

BLASTX: optional, blastx output of submitted sequences – a file must be provided (can be an empty file)

bFlag: 1 or 0

strand: +, - or both

E-value: used in blastx, if no blx, put a value of 1

output: predicted peptide after removing 5' and 3' -UTR in fasta format with frame, start and stop values

Note: if you have a blx file, the bFlag value should be 1. If no blx output, you still need to provide a file name (a file has no contents), with bFlag value as 0.

extractCDS.pl is used to extract cds from original EST sequences.

Usage: extractCDS.pl estFile orfPredictor.out output

If you have other questions, please carefully read the document at http://proteomics.ysu.edu/tools/docs/OrfPredictor_faq.html

If the problems still exist, pls contact me at xmin@ysu.edu.

Please cite our paper when you publish your result.

Min, X.J., Butler, G., Storms, R. and Tsang, A. OrfPredictor: predicting protein-coding regions in EST-derived sequences. Nucleic Acids Res., 2005, Web Server Issue W677-W680