



The ExoGene program is a Mac OSX and Windows app that retrieves gene sequences from Ensembl and annotates them with information about exons, coding sequence, UTR's and even the option to include a file with primers that can be used to annotate custom features to the sequence. This program integrates with the ApE.app program so make sure that is installed and the default program to open “.ape” files.

Software Requirements

MacOS 10.13.1+ : OSX High Sierra or above (may work on others but not tested)

OR

Windows 10 (may work on Windows 7 but not tested)

Access to Ensembl website (<https://www.ensembl.org>)

Annotated genome on Ensembl website

ApE program installed (<http://jorgensen.biology.utah.edu/wayned/apel/>)

ExoGene Information

ExoGene 1.0.1

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License

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Using the ExoGene Program

Click on the ExoGene icon and wait for the program to load.

When the program is open you may enter the name of gene (1) and select species (2). Multiple genes may be entered if the Batch input option (3) is selected and genes are separated by a comma.

By default the program will annotate the gene transcript/cDNA (4) and genomic DNA/gDNA (5). Unclick either option if you do not want to download that sequence. For cDNA you can select which isoform(s) to download (6), a single transcript that makes either the longest protein (Longest ORF) or the longest transcript sequence (Longest cDNA), or download all isoforms. For gDNA you download additional bases upstream of the transcription start site and downstream of the transcript end (7). Enter the number of extra bases to add on both sides, up to 100000. There is also the option to download a text FASTA file of the protein sequence (8).

To add your primers to the ApE files, click the “Import primers” option (9) and select the your primer file (10), either an Excel or text file. For Excel, the primers should be on the first worksheet with primer names in the first column and primer sequences in the second column. For text files, use comma separated name and sequences with each primer on a new line. You can allow for mismatches between your primers and the gene sequence (11). Files can also include sequences other than primers that you want to add to your gene, just use the same format used for primers in the file. Select the folder you want the annotated gene files to be saved to (12) and select if you want the ExoGene to automatically open the genes files in ApE after annotation is complete (13). In order for files to open, ApE must be downloaded on your computer and set to be the default program to open ApE files or select where ApE program is located (14). Click “OK” (15) and the annotation will begin.

The screenshot shows the ExoGene 1.0.1 application window. It contains the following elements:

- Gene name:** (1) [text field]
- Species:** [dropdown menu showing 'danio rerio'] (2)
- Batch input genes (comma separated):** (3) ☐
- get cDNA sequence:** (4) ☒ (5) **get gDNA sequence:** ☒
- Longest ORF:** (6) ☒ (8) **Longest cDNA:** ☐ **All isoforms:** ☐
- bp flanking gene:** (7) [text field with '0']
- get protein as FASTA:** (8) ☐
- Import primers from file:** (9) ☒
- Select primer file:** [text field with '/Users/MATT/Shared/primers.xlsx'] (10)
- Allow up to:** [text field with '0'] **mismatches in primers:** (11)
- Select destination folder:** [text field with '/Users/MATT/Documents/code/Science/sequence'] (12)
- Automatically open files after annotation complete:** (13) ☒
- Select ApE program:** [text field with '/Applications/ApE.app'] (14)
- Buttons:** (15) OK, Reset, Cancel