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format2fasta.exe

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Format2fasta

Manual installation:

- 1) Download "format2fasta.exe" to a folder on your computer.

Automatic installation on the C: drive depending on your browser:

With Chrome:

- 1) Click on the document called "format2fasta installer".
- 2) Double click on the downloaded file called "format2fasta_installer.exe" at the bottom of the browser window.
- 3) Allow the program to make changes to your computer.
- 4) Follow the instructions.

With Firefox:

- 1) Click on the document called "format2fasta installer".
- 2) Save the file.
- 3) Double click on the downloaded file called "format2fasta_installer.exe" in the "Downloads" window.
- 4) Allow the program to make changes to your computer.
- 5) Follow the instructions.

With Internet Explorer:

- 1) Click on the document called "format2fasta installer".
- 2) Click on "Run" at the bottom of the browser window.
- 3) Click on "Run" once more at the bottom of the browser window or, if your computer comes up with some security warnings, grant the necessary permissions to run the installer.
- 4) Follow the instructions.

About fasta format and format2fasta

Fasta format is sequence format used by many bioinformatic tools including Peptide Pattern Recognition. A sequence in Fasta format consist of a line starting with ">" followed by the name, accession number and other information about the sequence and a second line containing the sequence without any additional information, "carriage returns" or other signs and symbols. Sequences in Fasta format are normally stored as text (".txt") files.

Strict fasta format looks like this:

```
>name of sequence  
sequence
```

Format2fasta was designed for formatting sequence data that are almost in fasta format to strict fasta format.

Moreover, format2fasta will remove redundant sequences.

The tool was written for Windows and has been tested under Windows XP and Windows7.

An example of an input could be a text file generated by copy-paste of a Blast search made at NCBI and formatted to FASTA(text) into a text editor. Such a file has a lot of "carriage returns" inserted in the sequence. It takes a lot of work to remove all these "carriage returns" manually but "format2fasta.exe" can do it for you!

To use format2fasta:

- 1) Place the file you want to format in the same folder as "format2fasta.exe".
- 2) Double click the icon of "format2fasta.exe". - This will open a small dos window.
- 3) Enter the name of the file you want to format and press "enter".
- 4) Format2fasta will format the sequences to strict fasta format, remove redundant sequences and store the result in the input file.

If the dos window disappears it means that format2fasta could not find a file with the specified name. Control the file name and try again.

- 5) Press "enter" to close the dos window.

Good luck!

Peter Busk, 25.February.2013

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