**NAME**
>   insilicut.bash − manual page for insilicut.bash 1.0

**SYNOPSIS**
>   **insilicut.bash** [*OPTIONS*] ...

**DESCRIPTION**
>   'insilicut.bash' reports fragments when cutting genomic DNA with a restriction enzyme.

**OPTIONS**
>   **−h**, **−−help**
>   >   display the help and exit
>
>   **−V**, **−−version** output version information and exit
>
>   **−v**, **−−verbose** verbosity level (0/default=1/2/3)
>
>   **−−gf**     path to the file containing the genomic DNA (fasta format)
>
>   **−−gn**     name of the genomic DNA (e.g. 'Athaliana')
>
>   **−−ef**     path to the file containing the restriction enzyme (fasta format)
>
>   **−−en**     name of the enzyme (e.g. 'ApeKI')
>
>   **−−ls**     lower bound on fragments size (default=100)
>
>   **−−us**     upper bound on fragments size (default=300)
>
>   **−−clean**
>   >   remove temporary files
>
>   **−−p2i**    absolute path to the insilicut directory (default=) used for testing purposes only (e.g. in 'make check')

**EXAMPLES**
>   insilicut.bash −−gf Athaliana_genome.fa −−gn Athaliana −−ef ApeKI.fa −−en ApeKI

>   **Remarks:**
>   >   if R is installed, a histogram of fragments size is also produced

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**REPORTING BUGS**
>   Report bugs to <timothee.flutre@supagro.inra.fr>.

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