

**NAME**

insilicut.bash – manual page for insilicut.bash 1.3.0

**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)
- fullh**  
use full fasta header (e.g. keep "chr1 Atha" instead of "chr1")
- 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

**AUTHOR**

Written by Timothée Flutre [cre,aut].

**REPORTING BUGS**

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

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