




# Wizard2011

## Order

### Information

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You can edit the order of the arguments in an command line call of your tool here. At the bottom of the page you can see a preview of the resulting command line call. If this functionality depends on a certain order of arguments (e.g. a -f parameter has to be used before a -e parameter) please edit the order using the arrow buttons. You can also insert additional strings for calling the tool (like whitespaces) using the "+" button.

Type	Name	Value	
<b>Parameter</b>	<b>Nucleotide at 3'-End</b>		
Parameter	Minimal GC-Content		
Parameter	Maximal GC-Content		
Parameter	Number of Results		
Parameter	Minimal melting temperature		
Parameter	3'-Degeneracy		
Parameter	Maxmimal Primer Length		
Parameter	Minimal Primer Length		
Parameter	Maximal melting temperature		
Parameter	Primer Degeneracy		
Parameter	Minimal 3' GC-Content		
Parameter	Primer 3' Length		
Parameter	Tm of classic genefisher		
Parameter	Occurences in Sequence		
Parameter	Maximal 3' GC-Content		
Input	Input Sequence		
Output	GeneFisher Output		
  			

Example call: terminal1mingc0maxgc0limit8mintemp0max3degen0maxsize1minsize1maxtemp0maxdegen0min3gc0max3size3-oldtempuniq1max3gc0-tofile[FILE][FILE.RESULT]

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