DISTILLER: microarray compendium

If you use our microarray compendium in your research, please cite the following publication:
Lemmens *et al.* (2009) DISTILLER: a data integration framework to reveal condition dependency of complex regulons in *Escherichia coli.* Genome Biology, 10:R27

Please direct comments and questions to kathleen.marchal@biw.kuleuven.be.

The following files are available:

- Compendium.txt. The Compendium.txt file contains all expression values. The first rows indicates the array_ids, whereas the first column consists of the gene_ids.

- Genes.txt. The first column of this file consists of the gene_ids used in the Compendium.txt file. The second column represents the Blattner number, while the last column contains the gene names. The Blattner number of genes can sometimes change because of reannotation of the gene. As a result, the newest microarrays will refer to the new Blattner number, while older microarrays might still use the old Blattner number. If a gene has multiple Blattner numbers, these are separated by a "| ".

- Arrays.txt. The Arrays.txt file consists of two columns. The first column contains the array_ids as used in the Compendium.txt file, while the second column shows the array names.

- Arrayinfo.txt. This file contains additional information on the arrays, such as the experiments from which the arrays were obtained and the functional category to which the arrays were assigned.