

## BIOINFORMATICS SERVICE

### Centralised Service for transcriptome analysis of biological samples using an Agilent-based microarray system and bioinformatics analysis

At LTTA we have a transcriptome analysis service using microarray (Agilent platform) and a bioinformatics analysis service. The service can highlight the levels of expression of messenger RNA or microRNA or ultraconserved regions (UCRs) in biological samples of different species.

Using the service, users can obtain (1) quantification of the expression of the genes present in the genome under examination in the form of raw data, ready for analysis using bioinformatics approaches; (2) bioinformatics analysis to obtain information on the biological significance of the microarray data; (3) bioinformatics analysis of gene expression data, last generation sequencing, CGH, SNP, CNV supplied by the user.

The different types of service and relevant costs are shown below.

#### 1. Quantification using microarray for gene expression in a tested genome

Our Service offers:

Code no.	Type of service	Cost per sample (Eur)
	<b><u>COMPLETE ANALYSIS</u></b>	
B1001	<p><i>Gene Expression Analysis</i> (1 colour) for the entire genome on Agilent microarray platform (human, mouse or rat; please ask the Service about other species)</p> <p>The complete service <u>includes</u>:</p> <ul style="list-style-type: none"> <li>(i) qualitative and quantitative RNA analysis using Bioanalyzer</li> <li>(ii) RNA sample marking using fluorescent probe</li> <li>(iii) hybridisation of labelled sample on chip</li> <li>(iv) chip scan and data acquisition</li> <li>(v) sending raw data by computer (downloading via web or DVD)</li> <li>(vi) description of the procedure for scientific publishing purposes</li> </ul> <p>The complete service <u>does not include</u>:</p> <ul style="list-style-type: none"> <li>(i) data analysis</li> <li>(ii) submission of data to public databases</li> </ul> <p>Users are kindly requested to provide: 2 µg RNA at a concentration no lower than 200 ng/µl (Purification using Trizol Invitrogen produces RNA of a suitable quality for performing investigations)</p>	538.50
B1002	<p>Gene Expression Analysis on user-supplied microarray <b>(PLEASE NOTE: YOU MUST CONTACT THE SERVICE IN ADVANCE TO CHECK WHETHER THE USE OF MICROCHIPS PRODUCED BY COMPANIES OTHER THAN AGILENT!!!)</b></p> <p>Apart from supplying the slide containing the array, the service includes all the stages described previously (Type 1a), i.e.:</p> <ul style="list-style-type: none"> <li>(i) qualitative and quantitative RNA analysis using Bioanalyzer</li> <li>(ii) RNA sample marking using fluorescent probe</li> <li>(iii) hybridisation of labelled sample on chip</li> <li>(iv) chip scan and data acquisition</li> <li>(v) sending raw data by computer (downloading via web or DVD)</li> <li>(vi) description of the procedure for scientific publishing purposes</li> </ul> <p>The service <u>does not include</u>:</p>	323.10

Other services	(i) bioinformatic data analysis (ii) submission of data to public databases  Users are requested the slide containing the array supplied with a suitable file for recognising the samples on the grid (e.g. GAL file) and 2 µg RNA at a concentration of 200 ng/µl (Purification using Trizol Invitrogen produces RNA of a suitable quality for performing investigations)	
Code no.	<u>PARTIAL ANALYSIS</u>	Cost per sample (Eur)
<b>B1011</b>	RNA qualitative and quantitative analysis using Bioanalyzer (multiples of 12 samples)	32.30 (per 1-12 samples)
<b>B1021</b>	chip scan and data acquisition (user supplies the hybridised slide to be scanned)	21.10
<b>B1031</b>	Data storage (images and quantifications) for 1 year in dedicated hard drive.  N.B.: data are stored on the Service's computer for 1 month. After this time, the data will be deleted to recover space on the hard disk.	5.40

## 2. Agilent microarray bioinformatics analysis

In addition to the service above, it is possible to obtain support for data analysis.

Code no.	<u>DESCRIPTION</u>	Cost (Eur)
	Preliminary consultation for setting up the experimental design during which time an <u>estimate of the overall cost</u> of the analyses requested can be made	No charge
<b>B2001</b>	Setting-up of experiment: entering data for analysis using GeneSpring software (transcriptome software)	5.40/sample
<b>B2002</b>	Data analysis to identify genes differentially expressed between two classes (for example: treated vs. non-treated samples, or cancer vs. normal samples). The service includes: <ul style="list-style-type: none"> <li>a. data normalisation</li> <li>b. identification of differentially expressed genes by fold-change analysis</li> <li>c. where the number of samples allow it (&gt;=2 in each class for comparing) statistical analysis of the differentially expressed genes.</li> </ul>	161.60
<b>B2003</b>	Custom analyses by arrangement. This type of service requires active contribution from the user on hypotheses about the experiment in order to define the type of analysis to be performed. For example: <ul style="list-style-type: none"> <li>a. statistical analysis of samples (analysis of more than 2 classes)</li> <li>b. clustering analysis</li> <li>c. identification of predictive gene signatures;</li> <li>d. analysis of gene ontology and molecular pathways;</li> <li>e. kinetic analysis;</li> <li>f. preparation of images/tables for scientific publications</li> </ul>	86.10/hour

## 3. Bioinformatics analysis

Code no.	<u>BIOINFORMATICS ANALYSIS</u>	Cost (Eur)
<b>B3001</b>	Basic microarray experiment analysis: an experiment is understood to mean all the data relating to a biological sample. DAMA will perform the complete analysis of a 2-class experiment (for example, diseased and healthy samples), including quality	340.50

	control. Users will receive the results of the processing, including a list of the genes and significant values. N.B.: The analysis will only be performed once the data relating to all the samples in the experiment have been provided.	
<b>B3002</b>	Extended basic analysis to include additional sample data and extend the experiment to 2 classes, as referred to at BIO3001.	170.30
<b>B3003</b>	Multivariate analysis: the DAMA analyst will provide a thorough analysis of an experiment involving 2 or more classes (for example, clustering, multidimensional scaling, gene ontology, predictability, chromosome mapping, meta-analysis comparing different experiments, long-term scanning, etc).	79.50/hour
<b>B3004</b>	MIAME data bank: Submission of experiments to the Database (ArrayExpress or GEO).	33.30
<b>B3005</b>	Publication support Graphic processing of results, submission to public databases (EBI and NCBI), online publication of supplementary data, etc).	90.80/hour

Some of the services/products offered may be provided with the help of other services of the LTTA Laboratory.  
Each service includes a description of the procedure and supply of images of any scientific publication purposes.  
Prices are shown without VAT and are subject to change according to the cost of consumables necessary for the service (every 12 months).