



## POSITION

### Project Title/ Job position title

Bioinformatic tools to obtain complete information about the epigenetic machinery / Pre-doctoral position

### Area of Knowledge (choose only one)

Life Science Panel

Medicine, Public Health, Sports Science, Nutrition, Clinical Psychology, Healthcare Management

Plant, Animal and Environmental Biology, Physiology, Ecology and Conservation

Human Biology, Microbiology, Genetics, Cell Biology, Genomics and Proteomics, Biochemistry

Agriculture, Veterinary Studies, Animal Production, Forest Sciences

Biotechnology, Bioinformatics, Pharmaceuticals, Food Technology

### Research Project/Research Group Description

The use of experimental techniques that allow the massive study of both targeted regions and complete genomes from an epigenetic point of view makes it necessary to approach them also from the bioinformatic and computational field.

In the search and characterization of future epigenetic biomarkers, it is necessary to study the epigenome in different contexts, which entails correlating a very varied omic information, including, among others, the analysis of transcript expression, non-coding RNAs such as miRNAs and lncRNAs, or methylation levels both in the classical promoter regions and in regulatory regions determined by the study of binding sites for transcription factors or enhancers.

All this information obtained firstly in laboratory samples of both cell lines and patients allows us to characterize the possible epigenetic regulation to which certain phenotypes are subjected in the different experimental contexts. However, this entails a significant limitation in number of samples and extrapolation of results. It is at this point that the public databases created and maintained by international consortia come into play, in which a large number of well-characterized samples are available to validate our hypotheses arising from the previous laboratory approach with a smaller number of samples.

The large amount of data obtained, its diverse origin, as well as the correct assembly and analysis of them, makes necessary the use of bioinformatic tools that allow us to obtain complete information about what happens in the epigenetic machinery. In fact, this is a very



innovative area that is in progress, being necessary the continuous experimental validation of candidates as well as to gain insight into their biological roles through functional assays.

The pre-doctoral researcher will be integrated in the experimental therapies and biomarkers in cancer group , led by Inmaculada Ibañez, Senior Researcher of IdiPAZ, and Javier de Castro, Head of Lung Cancer Unit of the HULP. The group is focused in two different areas:

- Genetic and epigenetic mechanisms involved in the resistance to chemotherapeutic drugs,
- Novel molecular approaches to improve the clinical management in NSCLC patients.

### **Job position description**

#### Skills:

Candidates should have a degree in biology, chemistry, medicine or pharmacy and expertise in bioinformatics preferentially through a master degree.

#### Role:

Participation in the design and of the screening pannels for NGS determinations: RNA-seq, miRNA-seq, Methyl-seq, DNA variants, expression arrays.

Analysis and correlation between obtained metadata and clinical parameters to get insight into the mechanisms involved in cancer progression and therapeutic response.

### **GROUP LEADER**

**Title:** PhD

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**Research project/Research group website:**

<http://idipaz.es/PaginaDinamica.aspx?IdPag=258&Lang=EN>