

1. Job title

Posizione da Bioinformatico (Bioinformatics Analyst, Scientist) al San Raffaele Telethon Institute for Gene Therapy (SR-Tiget), Milan, Italy

2. Unit and SR-Tiget description

We are looking for a highly motivated bioinformatician to work at the San Raffaele Telethon Institute for Gene Therapy (SR-Tiget) in Milan, Italy, at the interface with the following research groups:

Alessio Cantore Unit (shorturl.at/fsHL4)

Luigi Naldini Unit (cancerbiotechnology.com)

SR-Tiget has given a pioneering contribution to the field of gene and cell therapy with relevant discoveries in vector design, gene transfer and editing, stem cell biology, identity and mechanism of action of innate immune cells. SR-Tiget has also established the framework for translating these advances into experimental therapies and has implemented several successful gene therapy clinical trials which have already treated >130 patients and have led, through collaboration with industrial partners, to the filing and approval of advanced gene therapy medicines. SR-Tiget now comprises 15 Research Units, 5 Development Cores, 2 Clinical Units embedded within the San Raffaele hospital, with a total staff of >230 people from 10 different countries.

3. Main Activities

The successful applicant will apply bioinformatic approaches to different types of NGS data, such as RNA-Seq, scRNA-Seq, ChIP-seq, and WGS, produced by the above SR-Tiget labs or already available in public databases. Moreover, the applicant will contribute to shared bioinformatic activities ongoing at the SR-Tiget bioinformatic core and the Center for Omic Sciences (COSR) of the San Raffaele Scientific Institute. She/He will be based in a dynamic, multidisciplinary and internationally renowned research center, benefiting from daily close interactions and supervision from PIs of the SR-Tiget and peers at the SR-Tiget bioinformatic core and COSR.

4. Who we are looking for

The candidate should hold a scientific degree and expertise in areas related to Bioinformatics, Biotechnology, Computer science, Computer systems engineering, Biomedical engineering. A PhD in related areas is a plus. The candidate should have a solid background in Next-Generation Sequencing (NGS) data analysis, the capacity of using well established bioinformatic and biostatistical approaches (R, Bioconductor), a proficiency in programming (Python, Bash) and interest in developing novel computational methods to study both biological and translational aspects of gene and cell therapy in genetic diseases and cancer. Experience in single cell and spatial single cell data analysis is considered a plus.

5. Details

We offer 1-year renewable contract, competitive salary, based on qualification and experience. The position is immediately available.

6. Contact and selection procedure

Applications, including a CV, a cover letter and the names and contact details of at least one referent should be sent by e-mail to squadrito.mario@hsr.it. Evaluation of applications/interviews will begin immediately and continue until the position is filled.