One position is available for a **student in Bioinformatics** at the IRCCS Regina Elena National Cancer Institute under the supervision of Dr.Giacomo Corleone. The project is **1 year long** and focused on understanding the molecular factors driving therapeutic resistance in Multiple Myeloma.

Recent evidence demonstrates that epigenetic shifts contribute to acquiring drug resistance. Indeed, epigenetic aberration can profoundly affect the chromatin organization and, subsequently the gene expression, resulting in activation and/or, repression of phenotypic drivers such as enhancer RNA (eRNA) or transcription factors (TFs). This project aims to 1) map chromatin asset variegation sustaining MM drug resistance, 2) define the epigenetic events leading to the arising of therapeutic resistance in a longitudinal cohort of matched pre-post therapy MM patients, and 3) translate the findings in two unique primary cell lines model recently developed in our lab. The critical questions remain unanswered: what is the extent of non-genetic alteration occurring on MM cells exposed to the treatments? Would it be possible to monitor and predict the evolution acquisition of therapy-resistant clones by investigating regulatory plasticity?

The candidate will work on genomics data such as ATAC-seq, ChIP-seq, WES, and more from bulk and single cell. The ideal candidate should have a keen interest in cancer biology and gene regulation. Candidates are expected to have a strong will to work in a highly multidisciplinary environment. Keen interest in the field of genomics and willingness to pursue a Ph.D. is a plus.