

SCIENTIFIC SEMINAR

Host: Arkaitz Carracedo

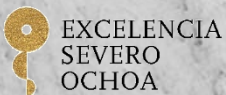


Prof. Xosé Antón Suárez Puente
*Biochemistry and Molecular Biology Department
University of Oviedo*

Cancer genomes: driver mutations beyond protein-coding genes

Friday,
January 17
Atrio 800.
12.00H

CIC bioGUNE



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RESEARCH &
TECHNOLOGY
ALLIANCE

Genomic analysis of cancer genomes has been instrumental in defining the set of driver alterations present in these pathologies. The analysis of more than 500 cases of chronic lymphocytic leukemia (CLL) by whole genome or whole exome sequencing revealed the presence of at least 60 driver genes. However, integration of whole genome sequencing, RNA-sequencing and chromatin conformation data, has revealed the presence of driver mutations outside of protein-coding regions in different types of cancer. These include mutations in enhancers, or mutations altering RNA maturation. Despite being located in non-coding regions, these mutations are able to alter protein-coding regions by different mechanisms. Additionally, these mutations define a set of patients with worse prognosis, showing their utility as clinical markers.