



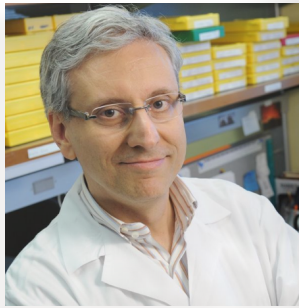
UNIVERSITÀ DEGLI STUDI  
DEL SANNIO Benevento

DST

DIPARTIMENTO DI SCIENZE E TECNOLOGIE

Dottorato di Ricerca in Scienze e Tecnologie per l'Ambiente e la Salute

## GIORNATE SCIENTIFICHE DEL DST



**Prof. Antonio Iavarone**

Institute for Cancer Genetics  
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# The drivers of oncogenesis of brain tumors: a model for precision medicine.

LUNEDÌ 23 SETTEMBRE 2019 ORE 11:00

Sala Riunioni del DST

Via F. de Sanctis, Benevento

### ABSTRACT

We use global and unbiased approaches to identify the genetic and transcriptional drivers of an obscure but incredibly important aberrant phenotype in brain tumors, the mesenchymal transformation of human high-grade glioma. This phenotype endows one of the most lethal types of human cancer (the glioblastoma multiforme, GBM) with extremely aggressive features such as the ability to invade the normal brain and form new blood vessels. In recent work we have identified and validated two transcription factors (Stat3 and C/EBP-beta) that, on their own, are necessary and sufficient to maintain the mesenchymal signature of high-grade glioma. We now exploit Stat3 and C/EBP-beta as promising therapeutic targets in glioblastoma. The availability of massively parallel sequencing technologies has revolutionized the field of cancer genetics. By analyzing the whole transcriptome of human glioblastoma, we recently discovered that a subgroup of GBM patients is defined by the presence of gene fusions of FGFR and TACC genes in their tumors. The identification of FGFR-TACC fusions in GBM patients and the elucidation of the mechanistic consequences triggered by the fusion proteins for development of brain tumors have allowed us to translate these findings to preclinical models of the disease and design clinical trials in GBM patients harboring FGFR-TACC fusions. This work provides the first example of an oncogenic and recurrent gene fusion in human GBM and leads our research towards the goal of personalized cancer translation.