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Tumor genomic sequencing to guide treatment

Identification of key genetic mutations in tumors can be exploited to prescribe treatments specifically targeted to those mutations. Tumors harbor many mutations/rearrangements, and it is not clear which mutation or combination of mutations is most critical. We have developed an integrated approach that combines genomic analytics and experimental validation to provide precise treatment options to patients that fail standard of care. Tumors are interrogated by a combination of MPseq, RNAseq and WES. MPseq is a process that provides a detailed description of all DNA rearrangements at a resolution that can show how individual genes are disturbed thus providing necessary novel insight for correct clinical interpretation. The potential detection of targetable rearrangements and mutations cross-validated by RNAseq provides relatively robust evidence that the associated pathways are targetable. Related drugs can then be validated experimentally in 3D-culture model systems, termed microtumors. The combination of the above processes could provide reasonable indication to oncologists to act.

Biography

George Vasmatzis, PhD, is the Co-Director of the Biomarker Discovery Program within the Center for Individualized Medicine. In addition to earning a Doctorate in Biomedical Engineering, he has acquired experience in diverse disciplines, including bioinformatics, molecular biology and computational biology. His research team consists of bioinformatics specialists, molecular biologists, epidemiologists and pathologists.

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