

## METHYLATION STATE ASSESSMENT OF DAP-kinase GENE PROMOTER

**AMPLI-SET-DAP-kinase**

**Cat. n. 1.422**

The methylation of the residues of cytosine in the “CpG islands” is very important for the regulation of the genic expression. The hypermethylation of the “CpG islands” in the promoter region of a gene suppress the transcription of the same gene. In many tumours the hypermethylation of the promoter of the suppressor genes, as p16, p15, E-cadherine and other genes as “DAP-kinase”, inhibitor gene of the metastatic progression, O<sup>6</sup>-methylguanine DNA methyltransferase (MGMT), gene involved in the repair of DNA, Glutathione-S-transferasi (GSTP1) involved in the prevention of the oxidative damage of DNA, etc has been showed.

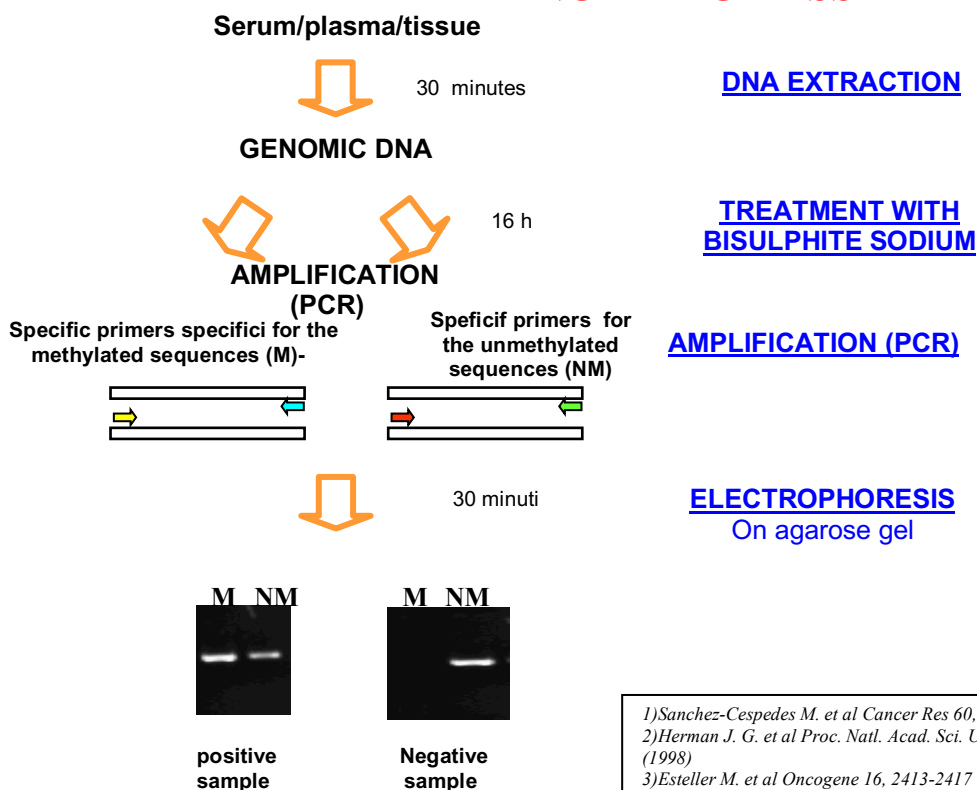
The detection of the gene promoter methylation can be performed on genomic DNA. Plasma and serum of patients carrier of malignant neoplasia contains much genomic DNA than the control subjects (up to 4 times as much) The assessment of the state of hyper-methylation of a gene is an appreciable molecular marker of the risk, and allows a precocious diagnosis and a prognosis of neoplastic diseases.

The principle of the assay is the extraction of genomic DNA from serum, or plasma or tissue, the treatment with bisulphite sodium in order to convert the unmethylate residue of cytosine in uracil, the PCR amplification with specific oligonucleotides for the methylate sequences and unmethylated sequences using the Real Time PCR technique and revelation on agarose gel.

The gene hyper-methylation state assesment can be considered as a sensitive molecular marker of the risk state, allowing to have an early diagnosis and to give a prognosis in neoplastic diseases.

The kit allows the identification of the methylation state in the gene DAP-kinase promoter.

### PRINCIPLE OF ASSAY



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