



**ampli set COLON<sup>CE IVD</sup> 24 tests (144 reactions) cat 1413**  
detection of methylation of promoter of genes involved in colorectal cancer.

The methylation of the residues of cytosine in the "CpG islands" is very important for the regulation of the genic expression. The hyper- methylation of the "CpG islands" in the promoter region of a gene suppresses the transcription of the same gene. In many tumors the hyper-methylation of the promoter of the suppressor genes, as p16, p15, E-cadherine and other genes as "DAP-kinase", inhibitor gene of the metastatic progression, 06-metilguanina DNA methyltransferase (MGMT), gene involved in the repair of DNA, Glutathione-S-transferasi (GSPT1) etc.

Plasma and serum of patients carrier of malignant neoplasia contains much genomic DNA than the control subjects.

The principle of the assay is the extraction of genomic DNA from plasma or serum, the treatment with bisulfite sodium in order to transform the unmethylated residue of cytosine in uracil, the PCR amplification with specific oligonucleotides for the methylated sequences and unmethylated (MSP:methylation specific PCR) followed by detection on agarose gel.

The assessment of the state of hypermethylation of a gene is an appreciable marker of the risk, and allows a precocious diagnosis and a prognosis of a neoplastic diseases .

The kit allows the detection of the methylation of the promoter of the tumor suppressor gene p16 , of the 06-methylguanina DNA methyltransferase gene (MGMT), and of the hMLH1 gene, involved in the repair of "DNA mismatch", which show respectively a hypermethylation state of the 25-35%, of 40% and of 20-30% in sporadic colorectal cancer .

### Principle of assay

Extraction from: serum, tissue.

Conversion: treatment with sodium bisulfite.

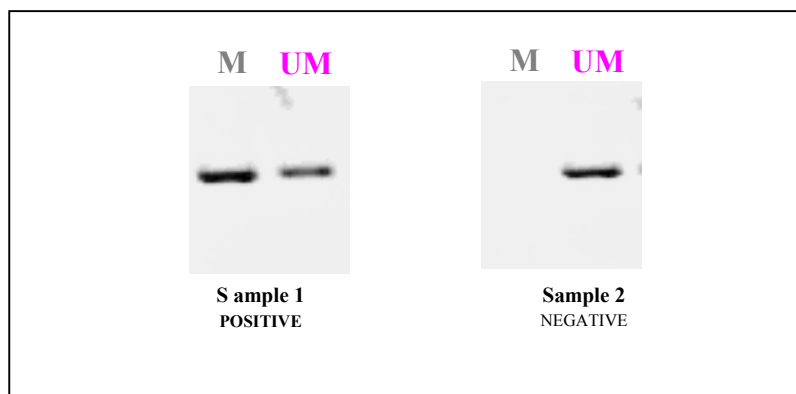
Amplification with specific primers for methylated and unmethylated sequences of the promoter of the genes:

**p16- MGMT- hMLH1**

Detection on agarose gel

### Applicability

Serum, tissue.



### REFERENCES:

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