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EMD Millipore introduces new kit

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EMD Millipore, the life sciences division of Merck of Germany, has introduced a rapid kit for bisulfite conversion, which is a critical first step in mapping the differences in genomic DNA methylation patterns. Aberrant DNA methylation can result in inappropriate activation or silencing of specific genes, and is associated with errors in embryonic development as well as the onset of diabetes, nd other diseases.

The new CpGenome Turbo kit reliably converts unmethylated cytosines to uracil in 90 minutes, which is twice as fast as commonly used bisulfite kits and reagents. By increasing throughput of bisulfite modification, CpGenome Turbo kit allows researchers to examine DNA from more samples in less time.

GE Healthcare launches ÄKTA avant 150

GE Healthcare, a global biosupplier company, has launched ÄKTA avant 150, the second system in the new generation of ÄKTA liquid chromatography systems. ÄKTA avant 150 complements the ÄKTA avant 25 system to fully exploit the advantages of modern bioprocess media, enabling calable chromatographic processes for biopharma production.

With flow rates up to 150 ml/min, the ÄKTA avant 150 is designed for process development and scale up. The UNICORN 6.1 control software enables seamless method transfer between ÄKTA avant 25 and ÄKTA avant 150. UNICORN 6.1 also comes with integrated Design of Experiments (DoE) functionality that provides time and cost savings, by capturing the information required for decision making in fewer experiments.

Agilent upgrades bioinformatics software

Agilent Technologies has introduced GeneSpring GX 11.5, an expansion of its popular bioinformatics software intovisualizing and analyzing multiple types of biological data. GeneSpring GX 11.5 interprets exon microarray, proteomics and metabolomics experiments together for the first time, using a familiar interface. These new capabilities join existing GeneSpring GX applications for gene expression analysis, genomic copy number analysis, genome-wide association analysis and transcriptomics data analysis.