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## Prostate markers

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Prostate cancer is the most commonly diagnosed cancer in men. In the August 23 *Nature*, Saravana Dhanasekaran and colleagues from the [University of Michigan Medical School](#) describe the use of cDNA microarrays to define 'signature' gene-expression profiles for human prostate cancer (*Nature* 2001, **412**:822-826). They compared the expression levels of almost ten thousand genes in benign and malignant prostate cancer samples, compared with normal adjacent prostate tissue. Clustering analysis revealed differences between normal and malignant samples, and between metastatic and localized prostate tumours. Dhanasekaran *et al.* used tissue microarrays to confirm the upregulation in neoplastic samples of the cell-surface serine protease hepsin and the proto-oncogene kinase PIM1. Thus, the combination of DNA microarrays and tissue microarrays with clinical data offers a powerful strategy to define prognostic markers for prostate cancer.

## References

1. Molecular genetics of prostate cancer
2. *Nature* , [<http://www.nature.com>]
3. University of Michigan Medical School , [<http://www.umich.edu>]