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If clinicians could predict how a cancer patient would respond to specific chemotherapeutic drugs, they would be able to choose an individualized treatment protocol with greater chances of success and minimized side effects. In the September 11 [Proceedings of the National Academy of Sciences](#), Jane Staunton and colleagues from the [Whitehead Institute](#), Cambridge, Massachusetts describe a genomic approach for predicting chemosensitivity (*Proc Natl Acad Sci USA* 2001, **98**:10787-10792). They measured the expression levels of almost 7,000 genes in the sixty cancer cell lines of the NCI-60 panel from the National Cancer Institute's Developmental Therapeutics Program. They then used these [microarray data](#) to define sets of genes that could predict sensitivity to over 200 chemical compounds. Gene-drug relationships allowed the definition of a chemosensitivity classifier to predict the cytotoxicity of different compounds.

References

1. *Proceedings of the National Academy of Sciences* , [<http://www.pnas.org>]
2. Whitehead Institute , [<http://www.wi.mit.edu>]
3. Supplemental data for Staunton *et al.*, [<http://www.genome.wi.mit.edu/MPR/NCI60/NCI60.html>]