



Figure 7.10. Cluster image map (CIM) relating activity patterns of 118 drug compounds to the expression patterns of 1376 genes in 60 cell lines. See text for explanation. (Reproduced with permission from Scherf *et al.*, 2000 [10].)

These results of Scherf and his colleagues [10] clearly demonstrate the usefulness of unsupervised clustering algorithms for the analysis of large data sets. Nevertheless, it should be kept in mind that in most cases where small sets of data are examined unsupervised clustering methods do not perform as well. In these cases, attention must be paid to the experimental error and biological variance inherent in DNA microarray experiments, and statistical methods and supervised clustering procedures of the type described for the Lrp^+ vs. Lrp^- experiment described earlier in this chapter should be employed.

REFERENCES

1. Hung, S., Baldi, P. and Hatfield, G. W. Global gene expression profiling in *Escherichia coli* K12: The effects of leucine-responsive regulatory protein. 2002. *Journal of Biological Chemistry* 277(43):40309–40323.
2. Allison, D. B., Gadbury, G. L., Moonseong, H., Fernandez, J. R., Cheol-Koo, L., Prolla, T. A., and Weindruch, R. A mixture model approach for the