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Housekeeping clusters

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Operons, clustered groups of co-expressed genes, are well known in prokaryotes, but few examples exist in [eukaryotic organisms](#). The availability of extensive transcriptome and genomic data for many eukaryotes is encouraging researchers to look more closely for clusters of co-regulated genes in higher organisms. In an Advanced Online Publication in [Nature Genetics](#) Martin Lercher and colleagues at the [University of Bath](#), UK, report the existence of clusters of housekeeping genes in the human genome (6 May 2002, *Nature Genetics* DOI:10.1038/ng887). A [recent study](#) suggested that highly expressed human genes are located in clustered domains. Lercher *et al.* took a similar approach, examining SAGE expression profiles of over 11,000 genes in 14 different tissues. They found a high correlation between expression rate and the breadth of expression, even when they removed tandem-duplicated regions. Further analysis led them to conclude that the clusters (upto 350 kilobases long) can be accounted for by housekeeping genes (expressed in multiple tissues) rather than tissue-specific genes. The authors speculate that clustering of housekeeping genes in regions of 'open' chromatin may allow them to be co-regulated in multiple cell types.

References

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