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Tissue transcriptomes

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In the Early Edition of the [Proceedings of the National Academy of Sciences](#), Su *et al.* describe high-throughput gene-expression analysis of the mouse and human transcriptomes in different tissues ([Proc Natl Acad Sci USA, 10.1073/pnas.012025199](#)). They performed oligonucleotide hybridization experiments on samples from 46 human and 45 mouse tissues of diverse origin. They found that 6% of genes are ubiquitously expressed, and individual samples express 30-40% of genes; almost 80% of genes are differentially expressed. The authors show that comparative gene-expression profiling might be used to gain insights into gene function. Expression in specific tissues also gives clues about possible physiological function or regulation. For example, they were able to find pituitary-specific genes that may be regulated by the [Pit1 transcription factor](#); they also found genes implicated in disease states, such as prostate cancer. The mouse and human transcriptomes can be compared on the authors' [website](#).

References

1. *Proceedings of the National Academy of Sciences*, [<http://www.pnas.org>]
2. Large-scale analysis of the human and mouse transcriptomes, [<http://www.pnas.org/cgi/content/abstract/012025199v1>]
3. Allosteric effects of Pit-1 DNA sites on long-term repression in cell type specification.
4. Gene expression atlas: Text query, [<http://expression.gnf.org>]