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## Amygdala arrays

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The complex anatomical organization and cellular heterogeneity of the mammalian brain may complicate the interpretation of transcriptome analysis of brain tissues. In the April 24 [Proceedings of the National Academy of Sciences](#), Zirlinger *et al.* describe how *in situ* hybridization studies can improve microarray analysis of the brain (*Proc Natl Acad Sci USA* 2001, **98**:5270-5275). The authors compared the expression of over 34,000 genes using Affymetrix GeneChip oligonucleotide arrays with RNA from five different anatomical regions dissected from mice brains. About 1.3% of the genes analysed were enriched in only one of the five regions. Subsequent *in situ* hybridization was used to confirm the microarray results. About 60% of genes were consistent with microarray analysis, 20% gave no signal, and 20% were not enriched or inconsistent with microarray results. The [amygdala](#) region is involved in emotional behaviours and has been anatomically divided into 13 [subregions](#). When Zirlinger *et al.* examined some of the 33 amygdala-enriched genes, they found that 75% were expressed in restricted subregions. This report highlights the benefits of using *in situ* hybridization to validate microarray results.

## References

1. *Proceedings of the National Academy of Sciences*, [<http://www.pnas.org>]
2. Emotion: clues from the brain.
3. Organization of intra-amygdaloid circuitries in the rat: an emerging framework for understanding functions of the amygdala.