

# **A LARGE SCALE ANALYSIS OF GENE EXPRESSION IN THE MOUSE BRAIN**

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The mammalian brain contains several regions that have distinct anatomical and functional characteristics. A first step towards a complete understanding of the nervous system is the identification of the genes that are expressed in each sub region of the brain. In this work, using bioinformatics approaches, we searched for genes that are specifically or preferentially expressed in 10 sub regions of the mouse brain. Specifically for the selection of the candidate genes, we used data available from Massively Parallel Signature Sequencing (MPSS), a technique that measures gene expression and allows the analysis of rare messages in the transcriptome. We explored several characteristics of the selected genes, for example the Gene Ontology classification and the expression in male versus female brains. Our results show that ~3000 genes are specifically or preferentially expressed in different mouse brain regions. We identified 270 genes that are preferentially expressed in the olfactory bulb, an important region for olfaction. Gene ontology results show that the olfactory bulb contains a significant number of transcripts coding for genes involved in the regulation of gene transcription. Based on our results, we believe that a consistent large scale study of gene expression may contribute significantly to the understanding of the function of each brain region and may contribute to unveil the complexity of the nervous system.