



## Meta-analysis of differentially expressed genes in autism based on gene expression data

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**ABSTRACT.** The purpose of this study was to identify differentially expressed (DE) genes and biological processes associated with changes in gene expression in autism. We performed a meta-analysis using new publicly available Gene Expression Omnibus (GEO) datasets of autism. We performed Gene Ontology (GO) enrichment analyses and pathway analysis using the Kyoto Encyclopedia of Genes and Genomes (KEGG). Ten GEO datasets, including 364 cases and 248 controls, were available for the meta-analysis. We identified 3105 genes that were consistently DE in autism (1425 upregulated and 1680 downregulated genes). We also found that 7 genes were associated with phospholipase A2 (PLA2), including *LYPLA2P1*, *PLA2G4D*, *PNPLA2*, *LYPLA2*, *PLA2G6*, *PLA2G7*, and *PLA2G5*. We found GO terms for molecular functions significantly enriched in structural constituent of ribosome (GO: 0003735, P = 1.87E-06) and transcription regulator activity (GO: 0030528, P = 8.86E-04), while for biological processes, the enriched GO terms were involved in translational elongation (GO: 0006414, P = 1.74E-12) and the response to cytokine stimuli (GO: 0034097, P = 2.76E-05). The most significant pathway in our KEGG analysis was the ribosome pathway (P = 7.90E-

12). Our meta-analysis identified genes that were consistently DE and biological pathways associated with gene expression changes in autism.

**Key words:** Autism; Differentially expressed genes; Expression data; Meta-analysis; Microarray