# Article information:

Comparative Meta-Analysis of Transcriptomics Data during Cellular Senescence and In Vivo Tissue Ageing - PMC
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4419258/>

# Article summary:

1. A meta-analysis of transcriptomics data from human cell and biopsy-based microarrays experiments was conducted to identify gene expression signatures that mark human ageing.

2. Pathways involved in cancer, focal adhesion, actin cytoskeleton, MAPK signalling, and metabolism regulation were identified as coregulated genes in postmitotic muscle and nervous tissues.

3. Genes and pathways related to neurodegeneration, focal adhesion, actin cytoskeleton, proteasome, cell cycle, DNA replication, oxidative phosphorylation and metabolic signalling were found to be differentially regulated during cellular senescence and in vivo tissue ageing.

# Article rating:

Appears moderately imbalanced: The article provides some useful information, but is missing several important points or pieces of evidence that would be required to present the discussed topics in a balanced and reliable way. You are encouraged to seek a more balanced perspective on the presented issues by exploring the provided research topics and looking at different information sources.

# Article analysis:

The article is generally reliable as it provides a comprehensive overview of the findings from a meta-analysis of transcriptomics data from human cell and biopsy-based microarrays experiments studying cellular senescence or in vivo tissue ageing. The authors provide detailed descriptions of the pathways involved in cancer, focal adhesion, actin cytoskeleton, MAPK signalling, metabolism regulation etc., which are coregulated genes in postmitotic muscle and nervous tissues. Furthermore, they also discuss genes and pathways related to neurodegeneration, focal adhesion, actin cytoskeleton etc., which are differentially regulated during cellular senescence and in vivo tissue ageing.

However there are some potential biases that should be noted when assessing the trustworthiness of this article. Firstly, the authors do not provide any evidence for their claims regarding the pathways involved in cellular senescence or tissue ageing; instead they rely solely on their own analysis of transcriptomics data without providing any external sources for validation or further exploration into these topics. Additionally there is no discussion about possible risks associated with these findings or any counterarguments presented to challenge their conclusions. Finally there is a lack of impartiality as only one side (the authors’ own) is presented without exploring alternative perspectives or opinions on this topic.

# Topics for further research:

* Cellular senescence pathways
* In vivo tissue ageing pathways
* Cancer pathways
* Focal adhesion pathways
* MAPK signalling pathways
* Metabolism regulation pathways

# Report location:

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