# Article information:

双RNASeq揭示细胞内持久性过程中NTHi-巨噬细胞转录组学变化 - PubMed
<https://pubmed.ncbi.nlm.nih.gov/34497778/>

# Article summary:

1. This study used dual RNA sequencing to investigate the transcriptomic changes of NTHi-macrophage interactions during intracellular persistence.

2. Analysis of macrophage responses to NTHi identified a time-regulated transcriptome with a “core” profile, showing conserved expression across time points.

3. Gene list enrichment analysis identified an enrichment of immune response pathways in the core gene set, and KEGG pathway analysis revealed specific enrichment of intracellular immune response pathways.

# Article rating:

Appears well balanced: The article presents the information in a reliable and balanced way, without biases and prejudices. The claims made in the article are well supported and, where applicable, all sides of the argument are given opportunity to present their point of view. The article appears trustworthy and reliable.

# Article analysis:

This article provides an in-depth look at the transcriptomic changes that occur during NTHi-macrophage interactions during intracellular persistence. The authors use dual RNA sequencing to analyze the data and provide detailed results on their findings. The article is well written and provides clear explanations for each step taken in the research process, as well as providing evidence for their claims through figures and tables.

The article does not appear to have any biases or one-sided reporting, as it presents both sides equally and does not make any unsupported claims or omit any points of consideration. All evidence presented is supported by figures and tables, which are clearly labeled and explained in detail. Furthermore, all potential risks are noted throughout the article, such as the use of antibiotics which can lead to antibiotic resistance if used incorrectly or excessively.

In conclusion, this article appears to be trustworthy and reliable due to its thoroughness in presenting evidence for its claims and noting potential risks associated with its research methods.

# Topics for further research:

* NTHi-macrophage interactions
* Intracellular persistence
* Dual RNA sequencing
* Antibiotic resistance
* Transcriptomic changes
* RNA sequencing data analysis

# Report location:

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