# Article information:

HPA RNA-seq normal tissues (ID 231263) - BioProject - NCBI
<https://www.ncbi.nlm.nih.gov/bioproject/PRJEB4337/>

# Article summary:

1. RNA-seq was performed on tissue samples from 95 human individuals representing 27 different tissues.

2. The purpose of the study was to determine tissue-specificity of all protein-coding genes.

3. The data was published in a paper titled "Analysis of the human tissue-specific expression by genome-wide integration of transcriptomics and antibody-based proteomics" in Mol Cell Proteomics in 2014.

# 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 titled "HPA RNA-seq normal tissues" provides information on a transcriptome or gene expression study that was conducted on tissue samples from 95 human individuals representing 27 different tissues. The aim of the study was to determine the tissue-specificity of all protein-coding genes.

The article is based on a BioProject submission to NCBI and provides details about the project's scope, data type, and publications. The project was registered on December 12, 2013, at the Science for Life Laboratory in Stockholm, Sweden.

One potential bias in this article is that it only focuses on normal tissues and does not consider any abnormal or diseased tissues. This could limit the generalizability of the findings to other contexts where abnormal tissues are present.

Another potential bias is that the study only includes samples from human individuals and does not consider other species. This could limit the applicability of the findings to other organisms.

The article reports that RNA-seq was performed on tissue samples from 95 human individuals representing 27 different tissues. However, it does not provide any information about how these individuals were selected or whether they were representative of the broader population. This missing information could affect the generalizability of the findings.

The article cites a publication by Fagerberg et al., which analyzed human tissue-specific expression by integrating transcriptomics and antibody-based proteomics. However, it does not provide any evidence to support its claim that this study is relevant to its own findings.

Overall, while this article provides some useful information about a transcriptome study conducted on normal human tissues, it has several limitations and biases that should be considered when interpreting its findings.

# Topics for further research:

* Transcriptome studies on abnormal or diseased tissues
* Comparative transcriptomics across different species
* Sample selection criteria for transcriptome studies
* Limitations of RNA-seq technology for gene expression analysis
* Integration of transcriptomics and proteomics for tissue-specific expression analysis
* Applications of tissue-specific gene expression in disease diagnosis and treatment

# Report location:

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