# Article information:

Frontiers | Single-Cell RNA-Seq Technologies and Related Computational Data Analysis  
<https://www.frontiersin.org/articles/10.3389/fgene.2019.00317/full>

# Article summary:

1. Single-cell RNA sequencing (scRNA-seq) provides opportunities to explore gene expression profiles at the single-cell level.

2. Different scRNA-seq protocols have been proposed in recent years, including full-length transcript sequencing approaches and 3’/5’ end transcript sequencing technologies.

3. Quality control is essential for identifying and removing low-quality scRNA-seq data, and various tools have been designed to analyze scRNA-seq data.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article “Single-Cell RNA-Seq Technologies and Related Computational Data Analysis” provides a comprehensive overview of the current state of single cell RNA sequencing technologies and related computational data analysis methods. The article is well written and provides a clear explanation of the different types of single cell RNA sequencing protocols available, as well as the challenges associated with analyzing this type of data due to its high technical noise and complexity. The article also provides recommendations on selecting appropriate analytical approaches for effectively handling the high variability of scRNA-seq data.

The article is generally reliable, however there are some potential biases that should be noted. For example, the article does not provide any information on potential risks associated with using these technologies or any counterarguments that could be made against their use. Additionally, while the article does provide an overview of different types of single cell RNA sequencing protocols available, it does not provide any detailed information on how they differ from one another or which protocol may be best suited for a particular application. Furthermore, while the article does mention quality control as an important step in analyzing scRNA-seq data, it does not provide any specific details on how this should be done or what metrics should be used to assess quality control results.

In conclusion, while this article provides a comprehensive overview of single cell RNA sequencing technologies and related computational data analysis methods, there are some potential biases that should be noted when evaluating its trustworthiness and reliability.

# Topics for further research:

* Single cell RNA sequencing protocols comparison
* Quality control for scRNA-seq data
* Risks associated with single cell RNA sequencing
* Analytical approaches for scRNA-seq data
* Metrics for assessing quality control results
* Counterarguments against single cell RNA sequencing

# Report location:

<https://www.fullpicture.app/item/a540f7a4c614ce434727b5cdc39da4c8>