

This research article from the peer-reviewed journal “Cell Press” is a primary article as the text discusses the various cell types that make up the human genome and how those cells may be involved in certain immune responses by gene expression. The authors in the study primarily report their own empirical findings as well as statistically and conceptually analyzing their own data. For instance, the article provides different figures that quantify data involving RNA-seq data graphs, pie charts, line graphs, bar graphs, and Venn diagrams based on the research they conducted themselves. The format also follows a similar structure to other primary articles: Abstract (the article presents the abstract through a graphic), Summary, Introduction, Results, Discussion, and References. Overall, the article attempts to measure how many human cell types are involved in gene expression within the human immune system.

The relevance of the article to genetics is largely significant. The text goes in-depth on various methods that analyze the human genome of a certain population sample through RNA sequence analysis, which determines what genes are activated in a certain area, and fluorescence-activated cell sorting (FACS) analysis, where the technique sorts different cell types and can evaluate possible genetic disorders.

References

Schmiedel, B. J., et al. Impact of Genetic Polymorphisms on Human Immune Cell Gene Expression. Cell; <https://doi.org/10.1016/j.cell.2018.10.022> (2018).