

# Navigating the Cyp2 Gene Family Research Landscape: A Comprehensive Bibliometric Analysis

Kristiadi Priambodo<sup>1</sup>, Jefman Efendi Marzuki HY<sup>2</sup>, Risma Ikawaty<sup>2,\*</sup>,  
Baharuddin<sup>2</sup> and Salsa Bella Destri Syafika<sup>1</sup>

<sup>1</sup>Bachelor of Medicine Program, Medical Faculty, University of Surabaya, Surabaya, 60293, Indonesia

<sup>2</sup>Faculty of Medicine, University of Surabaya, Surabaya, 60293, Indonesia

**Keywords:** Mapping of Science, CYP2 Gene, Precision Medicine, Bibliometrik.

**Abstract:** This study elucidates the role of the CYP2 gene family in the pharmacokinetics and pharmacodynamics of drugs. The variability in these genes significantly influences drug efficacy and individual response. With the increasing volume of scientific publications, a comprehensive understanding of the current research on the CYP2 gene family is crucial. Numerous studies have examined these genetic variations, yet a thorough assessment of this research landscape and the identification of unexplored areas are still needed. Through bibliometric analysis and global mapping, this study enables a more systematic interpretation of publication data, offering new insights. The aim is to perform scientific mapping and interpretation of the CYP2 gene family research corpus. Utilizing literature review methods and bibliometric analysis based on PRISMA guidelines, a search in the Scopus database with the keyword cyp2\* yielded 11,867 articles. After cleaning and preparation, 9,439 articles remained for analysis. The results indicate a significant increase in CYP2 gene research, particularly between 2012-2023. Mapping reveals five main clusters, with CYP2E1 and CYP2D6 as the largest. CYP2C9 stands out for its polarization with three other clusters, indicating strong research collaboration. Identified strategic areas include opioids, atrial fibrillation, PCI, DNA methylation, hepatocellular carcinoma, and bile acid. Key genes in polymorphism studies include CYP2C19 and CYP2C8, while CYP2D6 is crucial in drug monitoring. This science mapping provides essential insights for research development in precision medicine.

## 1 INTRODUCTION

The CYP2 gene family holds significant importance in the field of medicine, particularly in the study of pharmacokinetics and pharmacodynamics of drugs. Genes such as CYP2C9, CYP2C19, and CYP2C16 influence how drugs are metabolized in the body (pharmacokinetics), which can affect the effectiveness of how drugs interact with their biological targets (pharmacodynamics) (Gong et al., 2023). For example, variations in these genes can impact the efficacy of drugs like warfarin, with certain genetic variants increasing the risk of side effects. Although research has deepened our understanding of these genes, there is a need to assess the entire research landscape and identify areas that are not yet fully explored. With the growing number of scientific publications, it is essential to have a

comprehensive understanding of how research related to the CYP2 gene family has evolved. Understanding the "mapping of science" in this field will not only reveal current trends but also identify knowledge gaps that may not have been recognized. This is crucial for maximizing the efficiency of research efforts and directing resources to the most needy or strategic areas. Bibliometric analysis, with its ability to map and interpret publication data systematically, offers a solution to this challenge. In analyzing trends in the medical field, this tool has been effectively used, such as in orthopedic therapy studies (Jin et al., 2023). Although reviews on the CYP2 family are still scarce, utilizing this analytical approach makes exploration easier. Therefore, this study aims to delve deeper into the research landscape between topics, and highlight opportunities for future research related to precision medicine.

\* Corresponding author