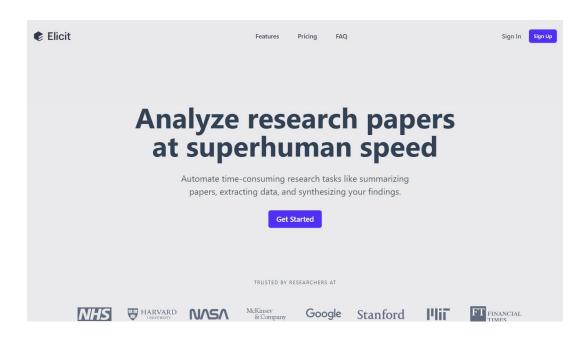
Elicit, ScholarGPT, ResearchRabbit, Connectpapers, SciSpace

Experimental Laboratory for Investigating Collaboration, Information-sharing, and Trust

¿Qué es ELICIT?

- Laboratorio experimental para investigar en colaboración, compartir información y confianza (Experimental Laboratory for Investigating Collaboration, Information-sharing, and Trust)
- El Programa de Investigación de Comando y Control (CCRP) del Departamento de Defensa de EE.
 UU. (OASD/NII) patrocinó el diseño y desarrollo de la plataforma ELICIT para la experimentación centrada en fenómenos de dominio informativo, cognitivo y social.



1. Crear cuenta

- Unlimited search across more than 125 million papers
- Unlimited summaries of 4 papers at once
- Unlimited chat with 4 papers at once
- Extract data from 10 uploaded
 PDFs per month
- Add 2 columns to your tables at a time
- View sources for answers
- ✓ Import from Zotero

Everything in Basic and...

- Unlimited summaries of 8 papers at once
- Unlimited chat with 8 full-text papers at once
- Export to RIS, CSV, BIB
- Extract data from 300 uploaded PDFs per year
- Add 5 columns to your tables at a time
- ✓ 1 high-accuracy column per table
- Extract data from tables inside research papers

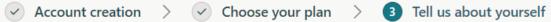
Everything in Plus and...

- Extract data from 1200 uploaded PDFs per year
- Unlimited high-accuracy columns
- Add 10 columns to your tables at a time

Básico Plus Pro







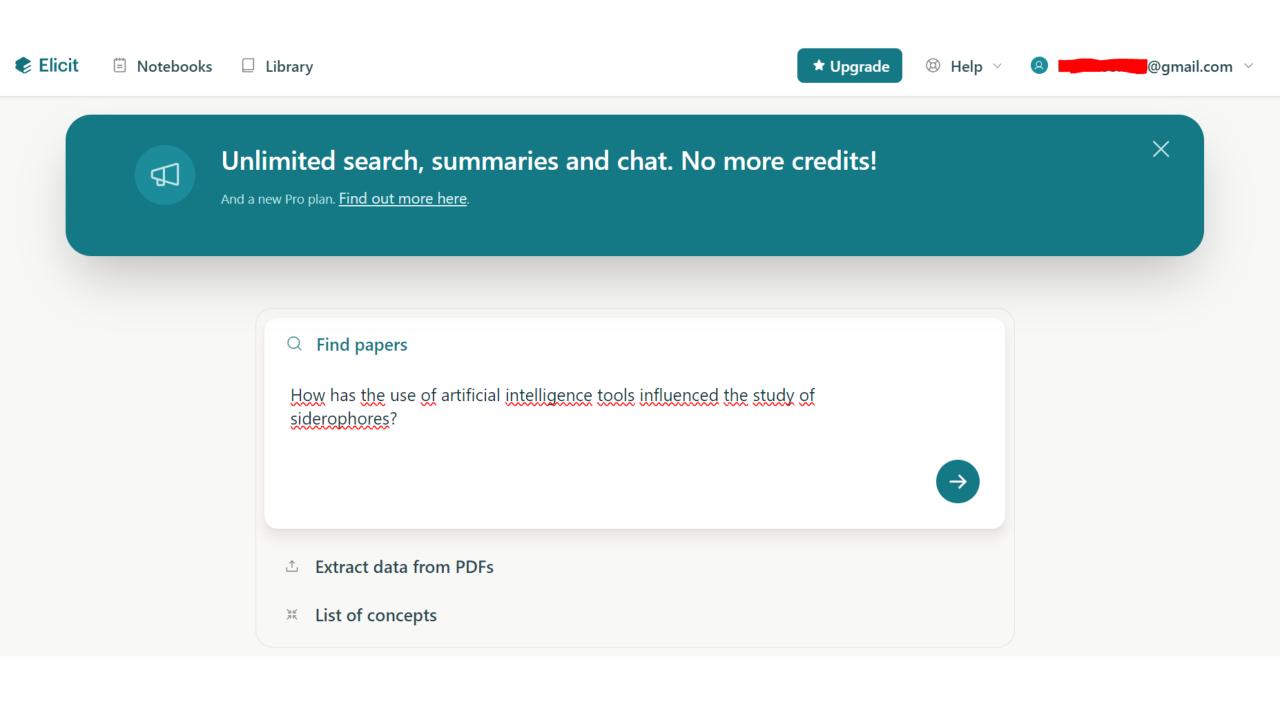


Tell us about yourself

1→ What's your name?*

Type your answer here...





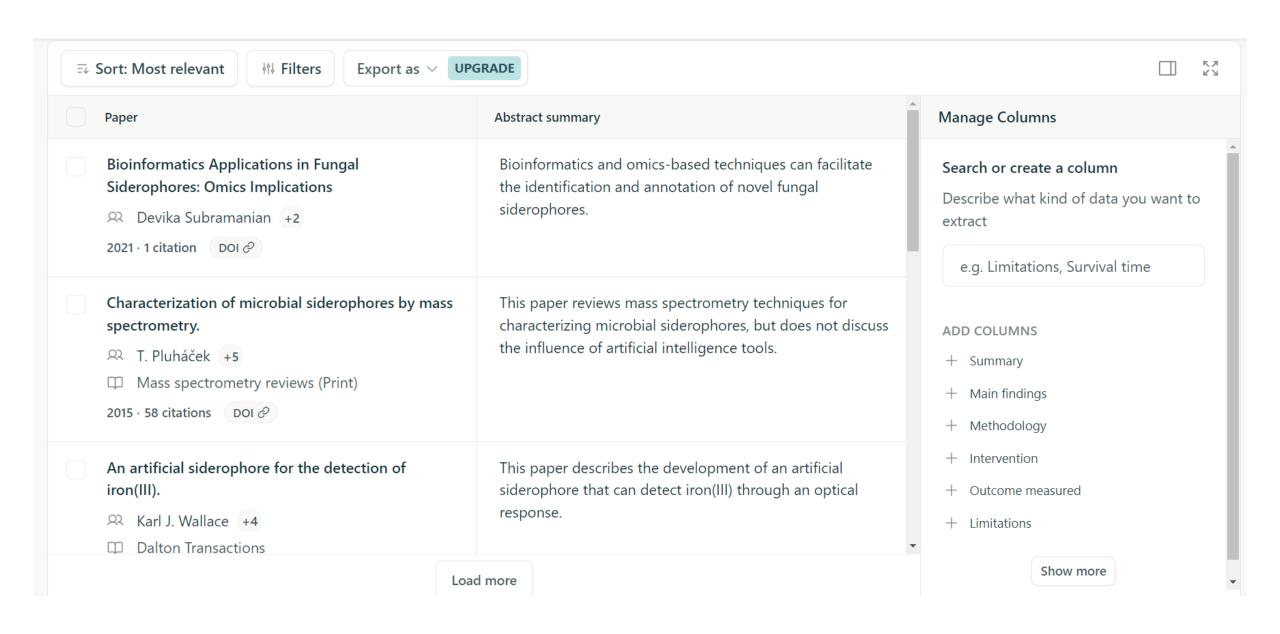
Impact of AI on Siderophore Research

Q How has the use of artificial intelligence tools influenced the study of siderophores?

Summary of top (4 papers ∨

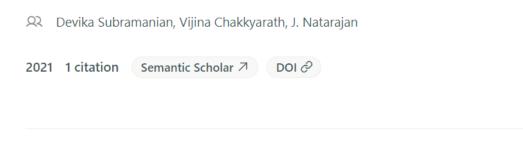
□ Сору

Artificial intelligence tools have significantly advanced the study of siderophores, microbial iron chelators crucial for pathogenicity. Bioinformatics applications, particularly in-silico genome mining, have revolutionized the discovery and annotation of fungal siderophores produced by non-ribosomal peptide synthetases (Subramanian et al., 2021). Mass spectrometry techniques, including ICP-MS and high-resolution separations, enable characterization of siderophores in complex samples, facilitating their use as disease biomarkers and potential drugs (Pluháček et al., 2015). Al-driven approaches have also contributed to the development of artificial siderophores, such as squaraine dyes, for iron(III) detection (Wallace et al., 2005). These advancements have expanded the potential applications of siderophores in various fields, including medicine, biochemistry, and agriculture. Furthermore, the synthesis of siderophore-drug conjugates shows promise in developing species-selective active drug transport systems to combat drug-resistant microbial infections (Roosenberg et al., 2000).



Seleccioné la primera de la lista

Bioinformatics Applications in Fungal Siderophores: Omics Implications



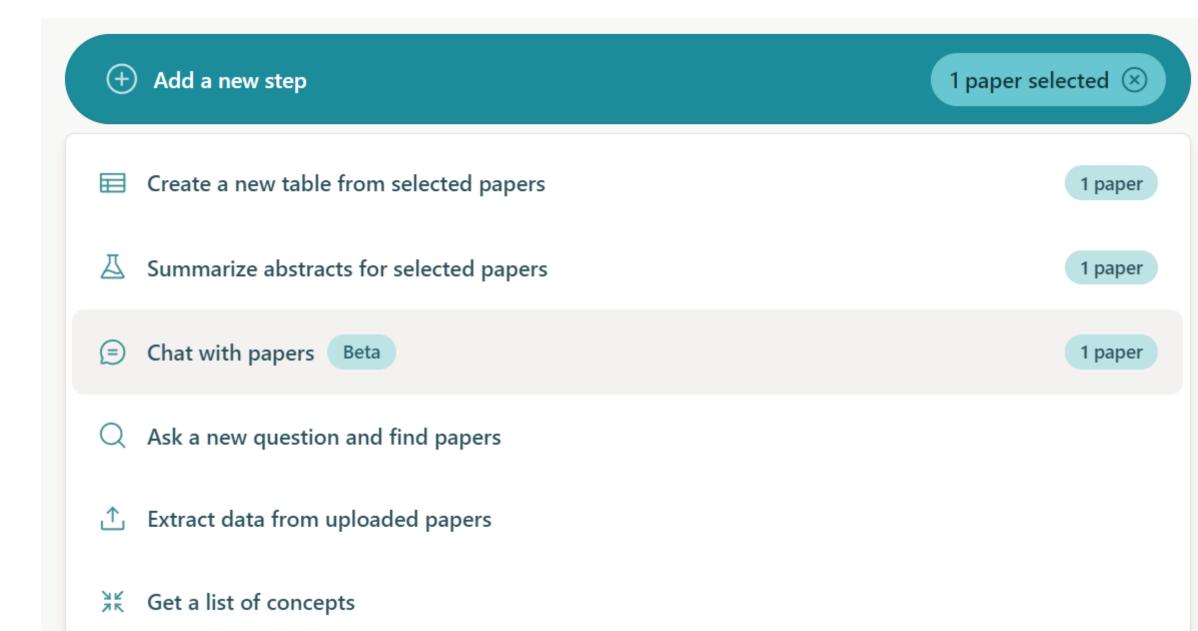
Abstract summary

Bioinformatics and omics-based techniques can facilitate the identification and annotation of novel fungal siderophores.

Summary

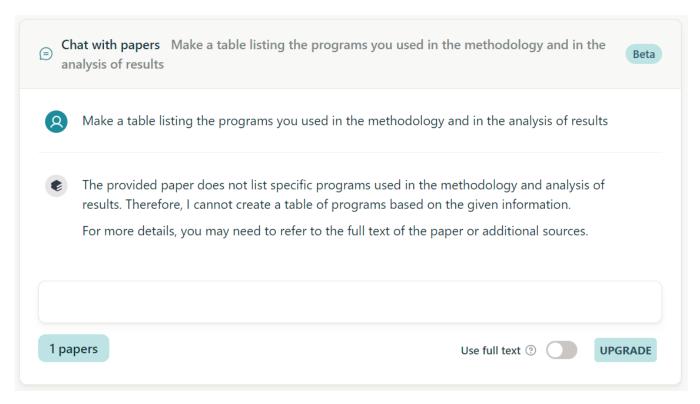
The summary of this paper is that it provides an overview of current methodologies and recent progress in the areas of bioinformatics related to omics-based discovery and analysis of fungal siderophores.

The 'omics' era driven by advanced genomic and metabolomic analysis has revolutionized the discovery and annotation of secondary metabolites and their pre-cursors. Some of the most important organisms that produce secondary metabolites belong to the eukaryotic kingdom of fungi. Fungal siderophores are secondary metabolites synthesized by nonribosomal peptide synthetases (NRPSs) in fungi and play an important role in iron uptake. In-silico genome mining is an efficient high-throughput approach to reveal potential NRPS genes. Analytical pipelines that link genomics with other omics such as proteomics and metabolomics data are under development and can facilitate the study of such natural products. Yet, siderophore analysis using computational tools tend to be focused on prokaryotes leading to an obvious bias in data availability as well as algorithm development for fungal research. Hence, it is important to review the differences and test the applicability of available tools on fungal data. Generation, curation and organization of siderophore-producing fungal NRPS data are essential to develop and train prediction/classification models for fungal siderophores. Existing algorithms for the identification of NRPS integrated with high-throughput omics-based techniques can lead to the identification and annotation of novel siderophores with novel biological significances. The current chapter provides an overview of current methodologies and recent progress in the areas of bioinformatics related to omics-based discovery and analysis of fungal siderophores.



Chatea con el paper

The 'omics' era driven by advanced genomic and metabolomic analysis has revolutionized the discovery and annotation of secondary metabolites and their precursors. Some of the most important organisms that produce secondary metabolites belong to the eukaryotic kingdom of fungi. Fungal siderophores are secondary metabolites synthesized by non-ribosomal peptide synthetases (NRPSs) in fungi and play an important role in iron uptake. In-silico genome mining is an efficient highthroughput approach to reveal potential NRPS genes. Analytical pipelines that link genomics with other omics such as proteomics and metabolomics data are under development and can facilitate the study of such natural products. Yet, siderophore analysis using computational tools tend to be focused on prokaryotes leading to an obvious bias in data availability as well as algorithm development for fungal research. Hence, it is important to review the differences and test the applicability of available tools on fungal data. Generation, curation and organization of siderophore-producing fungal NRPS data are essential to develop and train prediction/classification models for fungal siderophores. Existing algorithms for the identification of NRPS integrated with high-throughput omics-based techniques can lead to the identification and annotation of novel siderophores with novel biological significances. The current chapter provides an overview of current methodologies and recent progress in the areas of bioinformatics related to omics-based discovery and analysis of fungal siderophores.



- which is the What is the main contribution to knowledge in this area?
- The main contribution to knowledge in this area is the emphasis on the need to develop and test computational tools specifically for fungal siderophores, as current tools are biased towards prokaryotic data. The paper highlights the importance of generating, curating, and organizing siderophore-producing fungal NRPS data to develop and train prediction/classification models for fungal siderophores. It also underscores the potential of integrating existing algorithms for NRPS identification with high-throughput omics-based techniques to discover and annotate novel siderophores with significant biological implications (Subramanian, 2021).

ScholarGPT



ScholarGPT

Por Eimen Hamedat ♣

I answer your research questions.

haz una tabla con 10 articulos que abordan cómo el uso de inteligencia artificial puede potenciar el estudio de sideróforos

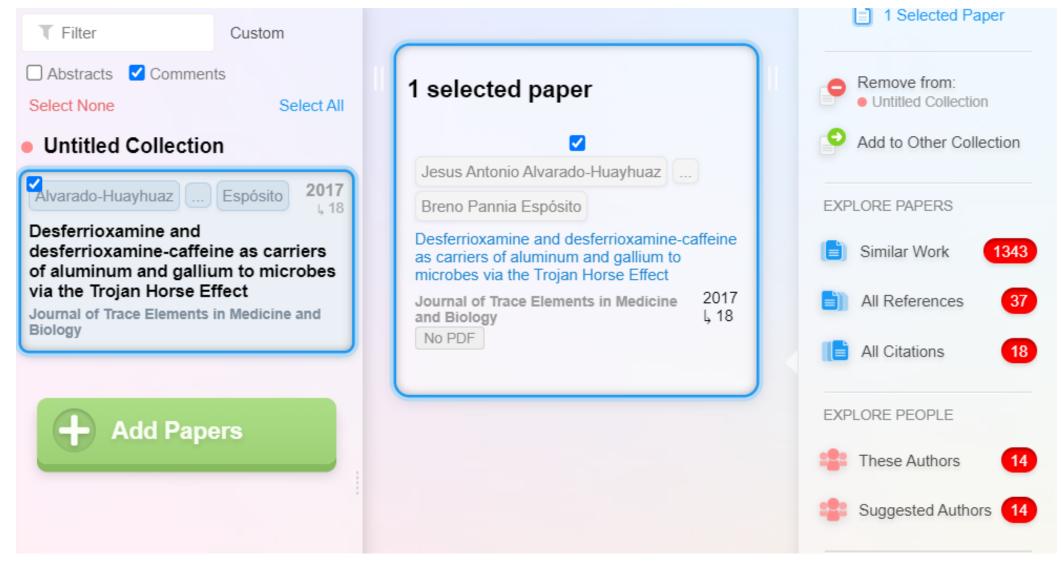


Aquí tienes una tabla con 10 artículos que abordan cómo el uso de la inteligencia artificial (IA) puede potenciar el estudio de sideróforos:

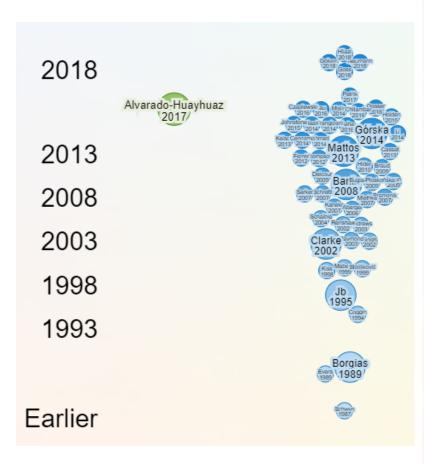
Título del Artículo	Autores	Año	Revista	Resumen	Enlace
Al-Based Screening of Siderophore-Producing Bacteria	Li et al.	2022	Journal of Microbial Biotechnology	Aplicación de algoritmos de IA para identificar bacterias productoras de sideróforos.	Link
Application of Machine Learning in Siderophore Prediction	Smith et al.	2021	Computational Biology Journal	Uso de aprendizaje automático para predecir la producción de sideróforos en diferentes condiciones ambientales.	Link
Enhancing Siderophore Research through Al- Driven Metabolic Pathway Analysis	Johnson et al.	2020	Biochemical Engineering Journal	Análisis de vías metabólicas mediante IA para optimizar la producción de sideróforos.	Link
AI-Powered High- Throughput Screening for Siderophore - ·	Wang et al.	2019	Applied Trobiology and Biotechnology	Implementación de IA en procesos de cribado de alto rendimiento para descubrir	Link

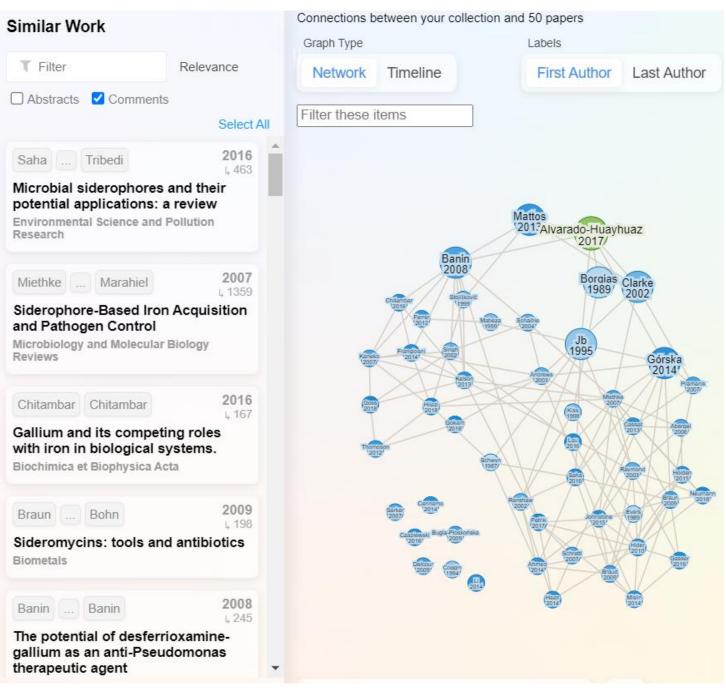


https://doi.org/10.1016/j.jtemb.2017.01.006

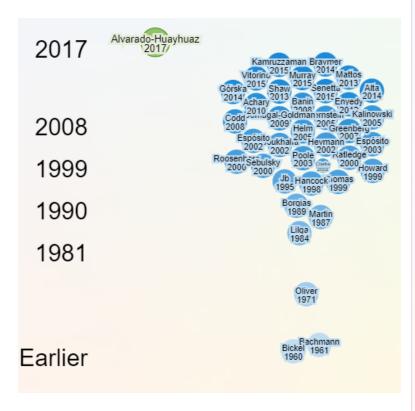


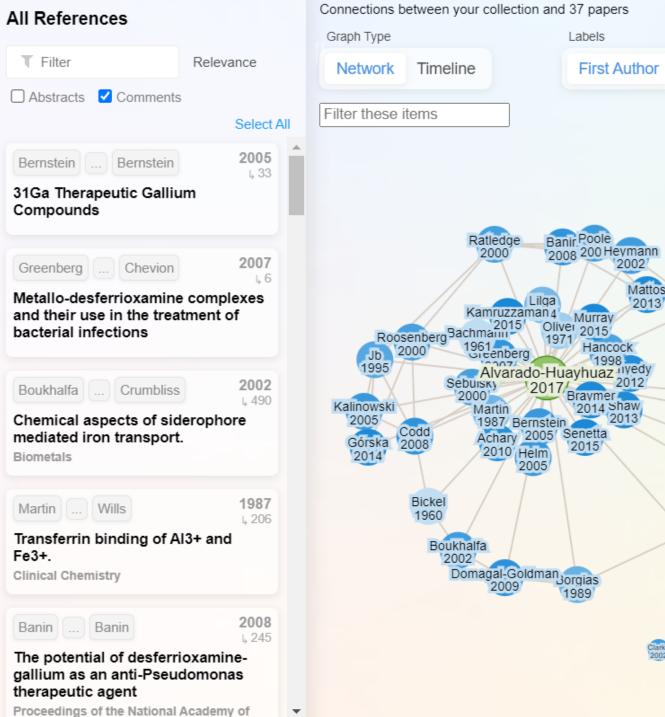












Last Author

Howard

Thomas

1999

Alta 2014 Vitorino

2015

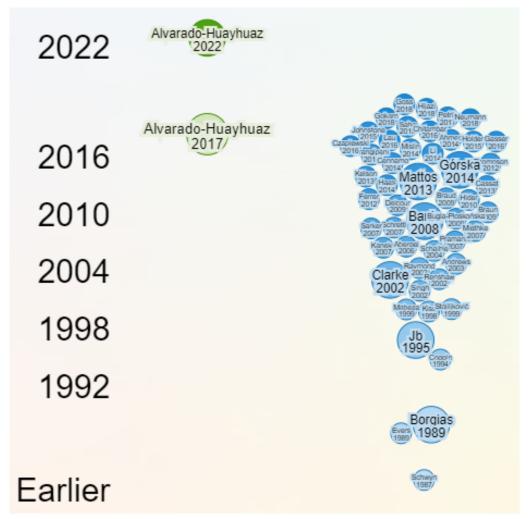
Espósito

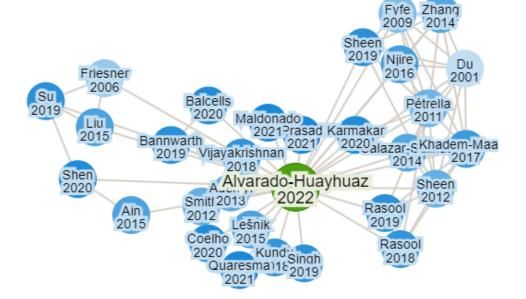
2002

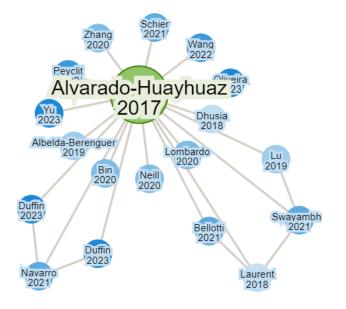
Espósito

2003









Scispace

Entra al siguiente enlace y participa comentando en uno de los 3 campos. También puedes crear una pregunta para que los demás aporte:

https://padlet.com/m4teosolano/scispace_sqp



Caso de aplicación

Revista da Associação Medica Brasileira • Open Access • Volume 69, Issue 9 • 2023 • Article number e20230560

Document type

Article . Gold Open Access

Source type

Journal

ISSN

01044230

DOI

10.1590/1806-9282.20230560

The use of artificial intelligence to improve the scientific writing of non-native english speakers

Giglio, Auro Dela;

da Costa, Mateus Uerlei Pereira^b



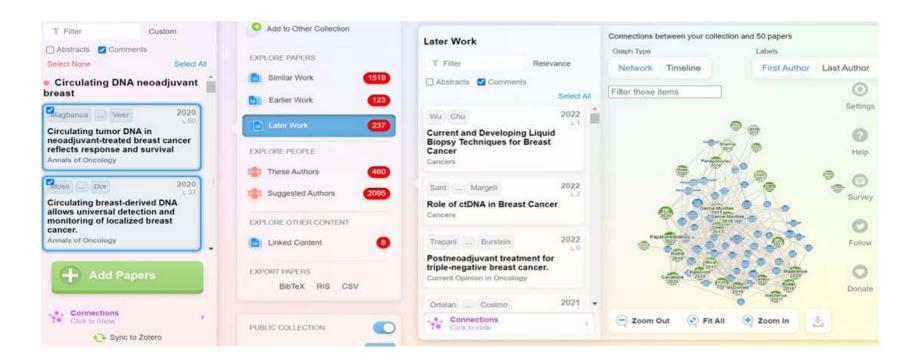
Save all to author list

Uso en revisión no sistemática

MÉTODOS

Debido al acceso generalizado y reciente a programas basados en IA como ChatGPT, no había evidencia suficiente en la literatura médica para realizar una revisión sistemática. Por lo tanto, optamos por realizar una revisión no sistemática de la literatura más reciente utilizando los términos "inteligencia artificial", "escritura científica" y "hablantes no angloparlantes" para crear una revisión narrativa utilizando Google Scholar, Google y programas de recuperación de referencias basados en IA como Elicit (www.elicit.org) y ResearchRabbit (https://www.researchrabbit.ai/).

lr a: ▶



Actividad

 Adjunta dos artículos científicos donde utilizaron algunas de estas IA's.