

scite_

在學術研究和知識探索中，引用（Citation）是構建知識體系和學術誠信的重要環節。scite是一個引文分析工具，它透過分析學術論文中的引用情況，說明研究人員和讀者理解引用的上下文和意義。以下是結合不同應用場景說明scite引文重要性的幾個例子：



學術研究

研究人員在撰寫論文時，需要引用先前的研究作為自己研究的基石。scite可以幫助他們找到相關領域的權威文獻，並經由分析引用的上下文，瞭解這些文獻是如何被其他研究者所使用。

文獻探討

在準備文獻探討時，scite可以展示特定主題或理論的引用趨勢，幫助研究人員快速把握該領域的研究動態和主流觀點。



學術評價

scite可以揭示論文的影响力，透過分析引用的正面或負面評價，幫助學術機構和研究人員評估論文的學術價值。

知識發現

scite的分析可以幫助研究人員發現被低估或未被充分探索的研究領域，促進知識的創新和拓展。



教育

在教育領域，scite可以作為教學工具，幫助學生理解如何正確引用文獻，並經由引用來建構具說服力的論證。

出版決策

出版社和期刊編輯可以使用scite來評估提交稿件的引用品質，作為決定是否接受論文稿件的一個參考。



政策制定

政策制定者可以利用scite分析特定政策或研究領域的引用情況，以瞭解其在學術界的影響力和接受度。

專利和創新

企業研發部門可以經由scite分析技術領域的引用模式，來指導新產品的研發方向或專利策略。



合作夥伴



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基於引文分類的智慧引文索引

scite.ai 於 2018 年成立，是一家位於美國布魯克林的科技創新公司。scite.ai 致力於協助研究人員發現被驗證過的研究論文及領域內的頂級專家。此外，scite 還為企業決策者驗證研究規劃，分析競爭對手，並精準地識別出戰略性的合作夥伴和關鍵行業意見領袖。scite 是第一個透過對海量學術全文進行資料探勘，運用 AI 分析論文引用性質的智慧型引文索引。借助於 scite，研究人員可以大幅減少文獻篩選與閱讀的時間，並確保研究及研發工作不會因建立在有爭議或遭拒的研究基礎上，而面臨損失。

分析超過 3,450 萬
篇學術全文

標記、索引、分類超過
13 億個引用敘述

篩選引文類型，
快速發掘研究脈絡

智能AI 助手

個人化服務

存取控制
IP/EzProxy/Email Domain

引文檢索
引文敘述檢索

引用文獻查驗

提供即時使用統計資料

利用深度學習技術提取引文上下文，並進行分類



支持

Supporting



提及

Mentioning



不支持

Contrasting



智能引文

supporting

Confidence: 93%

"...pDox@adipocytes showed enhanced cytotoxicity compared with Dox@adipocytes, and this effect was significantly reduced by BMS309403 that inhibits FABP4 (Figure 2J). In accordance with a previous report, 26 Dox inhibited lipid accumulation in adipocytes (Figures 2K, S17A, and S17B). In addition, pDox could be efficiently encapsulated into adipocytes (Figure 2L) and accumulated in the lipid droplets (Figure 2M)."

Adipocytes as Anticancer Drug Delivery Depot Wen, et al. 2019 Matter Section: RA@adipocytes
Loaded with Dox Prodrug Promoted Tumor Cell Death



scite 透過與全球出版社合作，同時運用 OA 資源，獲得跨學科的學術文章，並對論文全文進行資料探勘，建立 scite 獨有的 Citation Statement 資料庫，並對其進行索引分類，幫助師生、研發人員、編輯等獲取相關學術出版物的資訊，快速瞭解領域內的學術討論資訊，更客觀地評價研究品質。

對話中的提問清單

您輸入的問題

scite Assistant
的回覆

繼續提問

scite_ 智能AI助手

以學術論文內容，解答學術問題

scite 智能 AI 助手運用所分析之學術內容，藉著 ChatGPT 技術，能協助解答學術問題、生成論述，並列出引用文獻。scite 智能 AI 助手可依使用者需求設定搜尋內容來源、並顯示檢索策略，過程透明，確保使用者以負責任的方式使用 AI 協助研究。

參考文獻中檢附來自摘要/全文
的片段，供讀者審核確認

辨識論文中所引用之文獻，並提取引用敘述

"...pDox@adipocytes showed enhanced cytotoxicity compared with Dox@adipocytes, and this effect was significantly reduced by BMS309403 that inhibits FABP4 (iFABP4) (Figure 2J). In accordance with a previous report, **26** Dox inhibited lipid accumulation in adipocytes (Figures 2K, S17A, and S17B). In addition, pDox could be efficiently encapsulated into adipocytes (Figure 2L) and accumulated in the lipid droplets (Figure 2M)...."

Adipocytes as Anticancer Drug Delivery Depot Wen, et al. 2019 Matter Section: RA@adipocytes
Loaded with Dox Prodrug Promoted Tumor Cell Death

↳ How does the structure of a protein affect its function?

The structure of a protein is fundamental in determining its function. Proteins consist of amino acids arranged in specific sequences that fold into intricate three-dimensional structures, essential for their proper function (Jones et al., 2023). Protein structure can impact stability, activity, and interactions with other molecules (Rozbeský et al., 2018). Factors like the type of cross-linker, protein concentration, and cross-linker concentration can influence protein structure and function (Rozbeský et al., 2018).

Understanding the effects of mutations on protein structure and function is crucial. Missense mutations for instance, can impact protein stability and disrupt molecular function [Lugo-Martinez *et al.*, 2016]. High-resolution mapping of protein sequence-function relationships has been instrumental in revealing how protein function correlates with its sequence [Fowler *et al.*, 2010]. Computational methods have been developed to pinpoint functional residues in protein structures, underscoring the significance of structure-based approaches in predicting protein function [Xin & Radivojac, 2011].

Moreover, the binding of ions to proteins can significantly alter their structure and function (Kuhn et al., 2018). Studies on uranyl-protein interactions have shed light on the structural features of these complexes and their functional implications (Lin, 2020). The influence of genetic variation on protein structure and function has also been explored, with tools like SIFT utilized to forecast how substitutions may impact protein function (Bhattacharya et al., 2017).

In summary, a protein's structure is intricately tied to its function. Changes in protein structure induced by mutations, cross-linking, or interactions with other molecules can have substantial effects on protein stability, activity, and overall function. Understanding these relationships is vital for the advancement of fields such as structural biology, bioinformatics, and drug discovery.

↳ What is a tertiary protein?

A tertiary protein structure refers to the three-dimensional arrangement of a protein's secondary structural elements, such as alpha-helices, beta-sheets, and loops (Deka & Sarma, 2012). This level of

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Classification, and Billing sites | Peer Review #2 of "Image-based effective"

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 How does the structure of a protein affect its function?

Proteins are essential for the proper functioning of living organisms, and their structure plays a crucial role in their function. The structure of a protein is determined by its amino acid sequence, which in turn affects its folding and stability [6]. The interactions between charged amino acids significantly influence the structure and function of proteins [1]. The number of hydrophobic methylenes linking the backbone to the charged functionality of amino acids affects protein structure stability [1]. Protein secondary structures, such as β -sheet structures, are the fundamental three-dimensional building blocks of protein structures [1]. Intrinsically disordered proteins (IDPs) are a family of proteins that fail to form rigid α -D structures under physiological conditions, either along their entire lengths or only in localized regions [2]. IDPs exist as dynamic ensembles within which atom positions and backbone Ramachandran angles exhibit extreme temporal fluctuations without specific equilibrium values [2].

What do you need help with?

References

Reference #1

Longer charged amino acids favor β -strand formation in hairpin peptides

Jingyuan Chang¹, Jing-Yuan Chang², Nian-Zh
Li³ et al. 2021J Pep Sci

Interactions between charged amino acids significantly influence the structure and function of proteins. The encoded charged amino acids Asp, Glu, Arg, and Lys have different number of hydrophobic methylenes linking the backbone to the charged functionality...

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Reference #2

Understanding protein non-folding
Vladimir N. Uversky¹, A. Keith Dunker² 2010
*Biochimica et Biophysica Acta (BBA) - Proteins
and Proteomics*

1017 24 1112 0

This review describes the family of intrinsically disordered proteins, members of which fail to form rigid 3-D structures under physiological conditions, either along their entire lengths or only in localized regions...

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