

技術創新重新定義引文索引

目前的引文索引平台依然侷限於展示科學論文之間的關聯性，而未能提供如引用動機等深入的背景資訊。由於缺乏此類背景資料，當前的引文分析僅限於統計論文的被引用次數，而無法系統性地探討論文被引用的具體情境和方式。現實中有很多被引量高、品質低的文章。例如，1998年《柳葉刀》上Wakefield文章“*Ileal-Lymphoid-nodular hyperplasia, non-specific colitis, and pervasive developmental disorder in Children*”（已撤稿，被引量超過3000次，但大多數是批判性引用）。

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。

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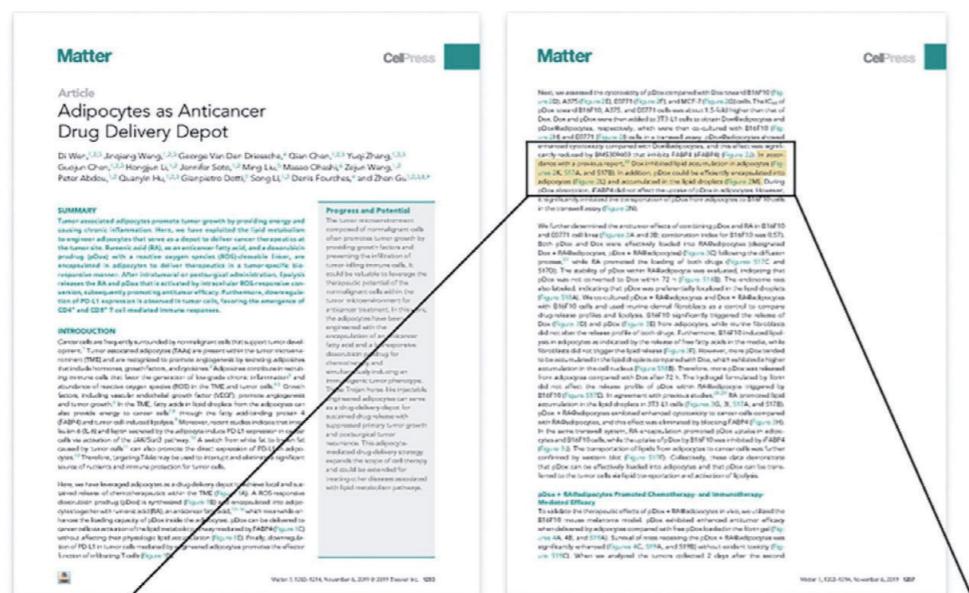
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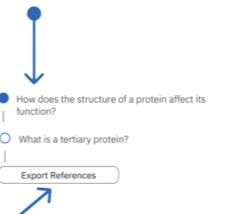


辨識論文中所引用之文獻，並提取引用敘述

“...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

對話中的提問清單



匯出 scite 參考文獻的列表

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 (Rozbesky et al., 2018). Factors like the type of cross-linker, protein concentration, and cross-linker concentration can influence protein structure and function (Rozbesky 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 these properties (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.

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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 organization is often used to describe the overall fold of a protein. It is distinct from primary, secondary, and quaternary structures. Tertiary structures are stabilized by various interactions between the different elements, including hydrophobic interactions, hydrogen bonding, and van der Waals forces.

Ask a question... (type '?' for menu)

繼續提問

How does the structure of a protein affect its function?

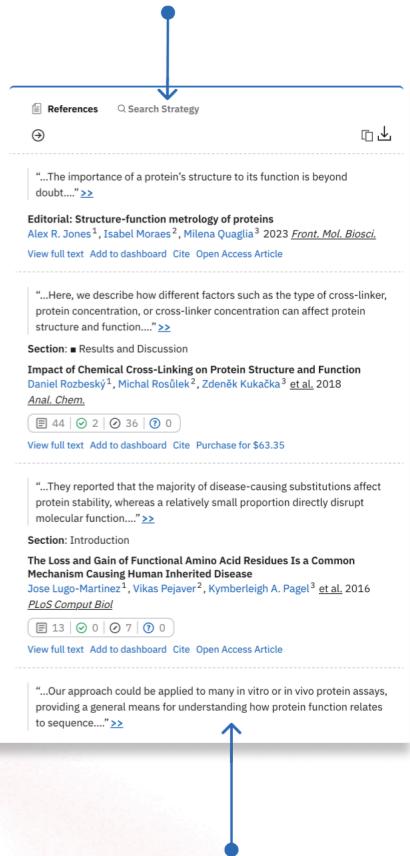
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以學術論文內容，解答學術問題

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 幫助研究。

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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 3-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-Zhi Li³ et al. 2021 *J. Pep Sci.*

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Reference #2

Understanding protein non-folding

Vladimir N. Uversky⁴, A. Keith Dunker² 2010 *Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics*

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