

Assistant By Scite: The Power Of Language Models, Backed By Real, Up-To-Date Research

ChatGPT's universe is outdated, and it doesn't care about real references.

Scite Assistant does by:

- Augmenting language models by searching for **new** information in our system
- Adding guardrails for claims by language models to ensure they're grounded in real research
- Giving you observability into the search strategies used, and why references are being recommended

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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. 2021J Pep Sci

3 | 1 | 7 | 0

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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