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Dickens to DNA: Introduction to de novo sequence assembly, Michael Schatz, Ph.D. Yzing Amino Acid Sequences Lab
Researchers have been investigating whether silent mutations have a biological impact. We know that proteins are made of amino acids. A gene's sequence | Cell And Molecular Biology ...

Silent Genetic Substitutions Can Affect Protein Function
A new artificial intelligence program readily predicts the structure of protein complexes, such as the immune signal interleukin-12 (blue) bound to its receptor. Proteins are the minions of life, ...

Protein structure prediction now easier, faster
Accurate protein structure prediction now accessible to all. Scientists have waited months for access to highly accurate protein structure prediction since DeepMind presented remarkable progress in ...

Advanced New Artificial Intelligence Software Can Compute Protein Structures in 10 Minutes
The COVID-19 lab leak theory is considered "bogus" by a report published in The Times of India on Wednesday. The report cited multiple pieces of evidence and scientific theories to refute the claim.

Evidence proves COVID-19 lab leak theory is 'bogus': Report Evidence proves COVID-19 lab leak theory is 'bogus': Report
Scientists have dreamed of simply predicting a protein's shape from its amino acid sequence—an ability that would open a world of insights into the workings of life. "This problem has been around for ...

Researchers unveil 'phenomenal' new AI for predicting protein structures
Scientists have waited months for access to high-accuracy protein structure prediction since DeepMind presented remarkable progress in this area at the 2020 Critical Assessment of Structure Prediction ...

AI Can Compute Protein Structures in 10 Minutes
The lab of David Baker at the University of Washington's Institute for Protein Design has released findings solving one of the toughest problems in the life sciences: how to quickly and ...

New protein folding technology from UW lab rivals DeepMind, promises to accelerate research
Protein design researchers have created a freely available method, RoseTTAFold, to provide access to highly accurate protein structure prediction. Scientists around the world are using it to build ...

Accurate protein structure prediction now accessible to all
The theory that the COVID-19 pandemic was triggered by the Sars-CoV-2 virus being leaked from the Wuhan Institute of Virology in China was recently given new life following an explosive article in the ...

Wuhan Lab-Leak Theory: "Rare" Genetic Sequence Doesn't Mean the COVID Virus Was Engineered
Machine-learning systems from the company and from a rival academic group are now open source and freely accessible.

DeepMind's AI for protein structure is coming to the masses
Your body synthesizes insulin from the amino acids it gets from the proteins you eat. Peptides and small proteins can be synthesized in a lab as well ... acid in your sequence is already attached ...

How Peptides Are Made
Cross-species comparisons can help make sense of subtle genetic variants in people with autism and identify hundreds of new genes that may contribute to the condition.

Evolutionary approach reveals impact of missense variants in autism
Delta's prevalence rose from around 10% of all samples sequenced in February 2021 to around 90% by the end of May 2021 ...

Dawn of Delta: How a New Variant Makes SARS-CoV-2 a Moving Target
New research has shown that the mutations arising in the COVID-19-causing SARS-CoV-2 virus seem to run in the family—or at least the genus of coronaviruses most dangerous to humans.

SARS-CoV-2 Following Predictable Mutational Footsteps
Scientists have waited months for access to highly accurate protein structure prediction since DeepMind presented remarkable progress in this area at the 2020 Critical Assessment of Structure ...

New artificial intelligence software can compute protein structures in 10 minutes
They say that the presence of a particular genetic sequence ... cell to add the amino acid arginine. The authors of the WSJ article argue that Sars-CoV-2 originated in a lab based on the presence ...