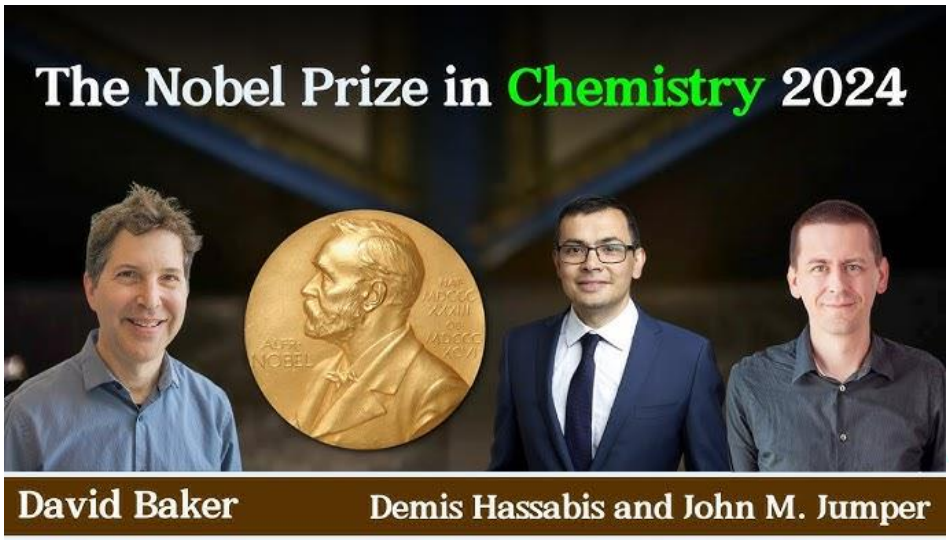
Nobel Prize 2024 For Chemistry

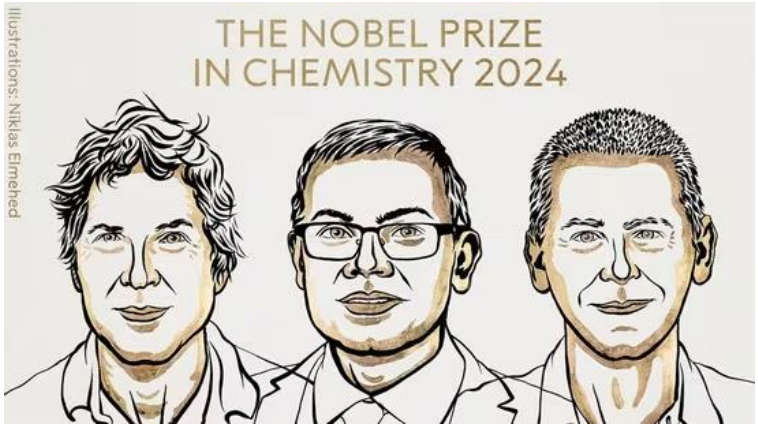
Why In News

- **2024 Nobel Prize in Chemistry**: The Nobel Prize in Chemistry 2024 has been awarded to **David Baker, Demis Hassabis and John M Jumper. While Baker** (62), who works at the University of Washington, Seattle, won “for computational protein **design the American Jumper** (39) and Briton Hassabis (48), who both work at Google DeepMind, were honoured for “protein structure prediction”.



Why Is Work On Proteins Important

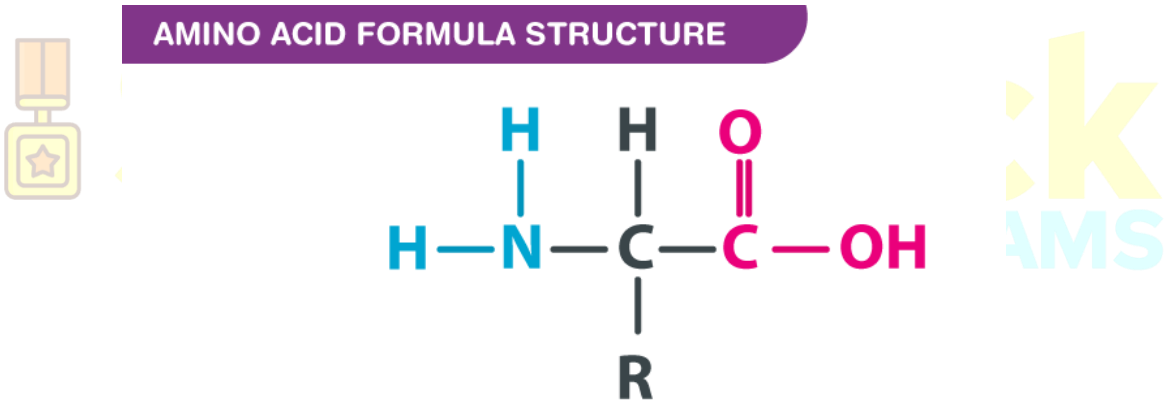
- **Proteins are fundamental to almost all biological processes**, or as the Nobel Prize website poetically says, to “the exuberant chemistry of life”.



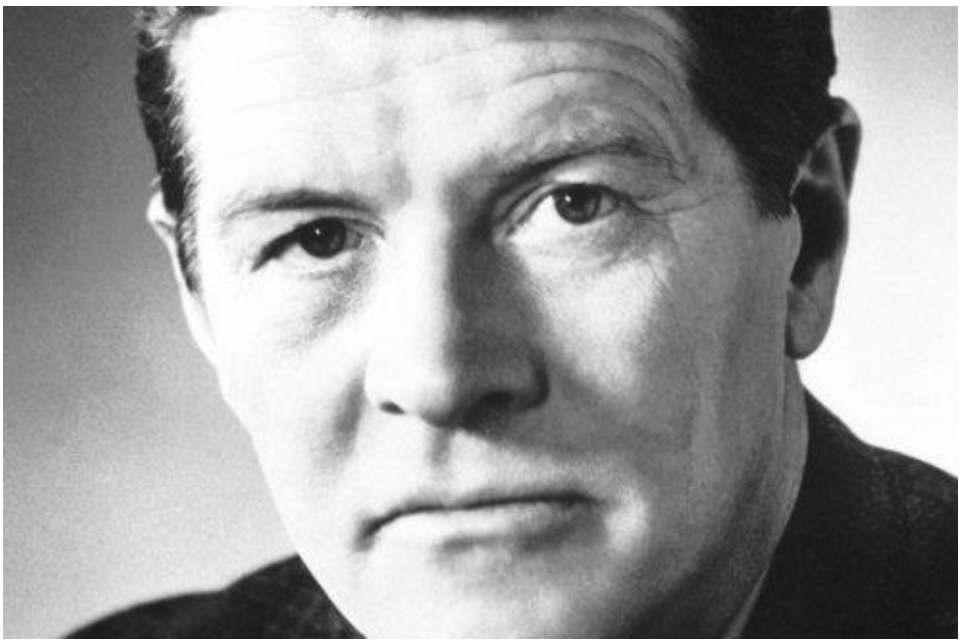
- In human bodies, for example, the protein **haemoglobin transports oxygen,** insulin helps absorption of glucose from blood, etc. Thus, anything that impacts protein production can have consequences for human health.
- **Given their central importance, proteins** have been extensively studied for a long time. There was even a competition about predicting protein structures running from 1994 (**called Critical Assessment of Protein Structure Prediction**, or CASP), which ended only after Jumper's contributions to Hassabis's work helped them win it decisively in 2020. **Baker, separately, had participated** in the competition in 1998.

What Did Jumper And Hassabis Do

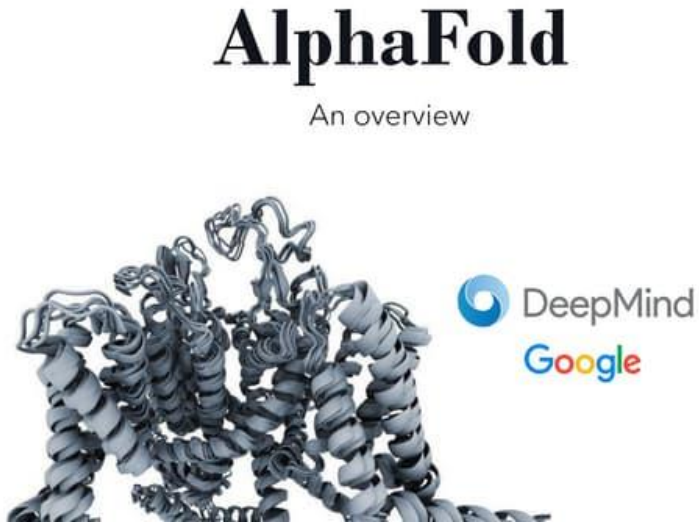
- **Proteins are built from 20 amino acids**, joined into long strings.As the Nobel Prize website explains, the "**string of amino acids twists and folds** into a distinct – sometimes unique – three-dimensional structure. This structure is what gives proteins their function."



- **In the 1960s, Christian Anfinsen**, an American scientist, got a protein structure to unfold and fold itself. He found that the protein assumed exactly the same shape every time, and realised that this shape is determined by its sequence of amino acids.
- This created an exciting possibility: "if chemists know a protein's amino acid sequence, they should be able to predict the protein's three-dimensional structure," the Nobel website says.



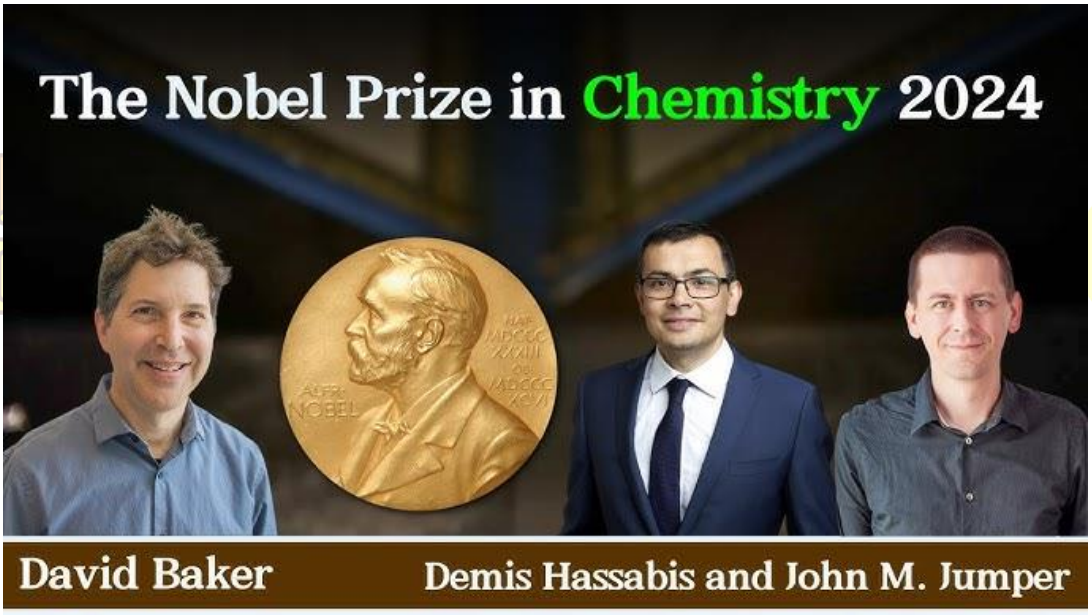
- This prediction eluded scientists for a long time.
- **Hassabis, meanwhile, had been working in the field of AI, and had** co-founded DeepMind, which built AI models for boardgames and was later sold to Google. In 2018, he entered the CASP.
- **His team built an AI model called AlphaFold**, which displayed around 60 per cent accuracy in predicting protein structures.



- **While impressive at the time, this accuracy rate** was not good enough. Research on AlphaFold continued, but saw a breakthrough only after Jumper joined Google DeepMind.

What Did Baker Do

- **Baker developed Rosetta, a** software to predict protein structures.
- "Baker made his debut in the CASP competition in 1998 using Rosetta and, in comparison to other participants, it did really well.
- This success led to a new idea – that **David Baker's team could use the software in reverse**.
- **Instead of entering amino acid sequences in Rosetta and getting protein** structures out, they should be able to enter a desired protein structure and obtain suggestions for its amino acid sequence, which would allow them to create entirely new proteins," the Nobel website says.
- Baker and his team succeeded, and today, a variety of new proteins with various functions can be created in labs.



Conclusion

- As the Nobel website says, "That we can now so **easily visualise the structure of these small molecular machines** is mind boggling; it allows us to better understand how life functions, including why some diseases develop, how antibiotic resistance occurs or why some microbes can decompose plastic."
- "The ability to create proteins that are loaded with new functions is just as astounding. This can lead to **new nanomaterials, targeted pharmaceuticals**, more rapid development of vaccines, minimal sensors and a greener chemical industry – to name just a few applications that are for the greatest benefit of humankind," the website adds.