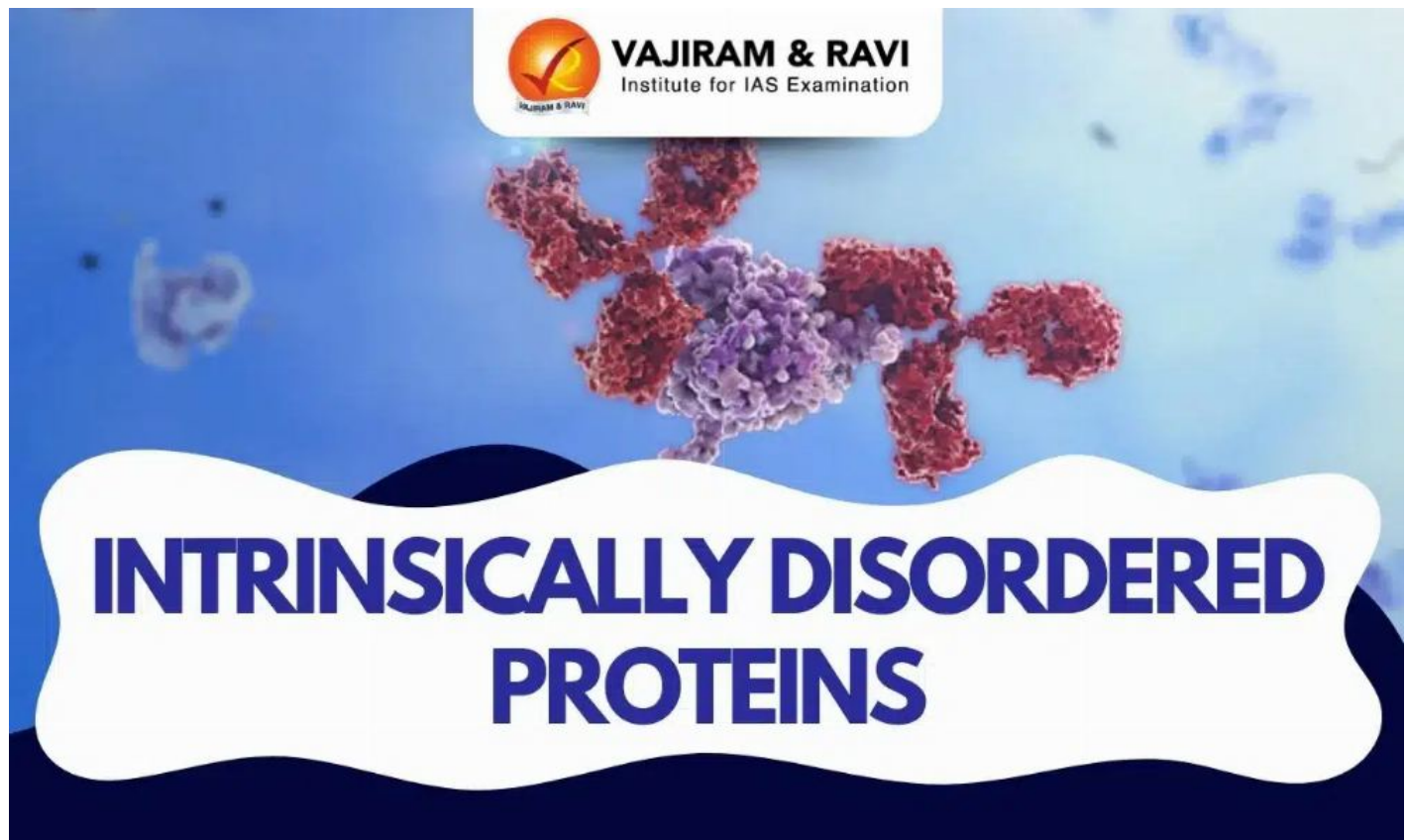


Intrinsically Disordered Proteins

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Intrinsically Disordered Proteins Latest News

Researchers have developed a deep-learning tool named Disobind that can predict how intrinsically disordered proteins (IDP) latch on to their binding partners.

About Intrinsically Disordered Proteins

- Intrinsically disordered proteins are **defined as proteins or regions of proteins** that **lack a fixed** or ordered three-**dimensional structure** under biological conditions.
- **Other Names:** Also called natively unfolded or **intrinsically unstructured proteins**.
- These are important for **cellular signaling and regulation**.

Functions of Intrinsically Disordered Proteins

- They are shape shifting molecules **vital to cellular communication**.
- They don't **form a fixed structure**.
- They guide **signalling networks**.

- They help proteins **move and find partners within the cell**, regulate which genes are switched on or off,
- IDP supports **protein folding and quality control**, and assembles flexible cellular **hubs called condensates**.

Key Facts about Disobind Tool

- It is developed by the researchers of **National Centre for Biological Sciences (NCBS), Tata Institute of Fundamental Research, Bengaluru**.

Features of Disobind Tool

- It is **open-source** and freely available for researchers worldwide.
- It **analyses the protein sequences** and uses **protein language models** (a form of AI trained on millions of known protein sequences).
- **No structural info needed:** It does **not require any structural information** or sequence alignments, making it super convenient.
- **High accuracy:** Disobind outperformed popular tools like AlphaFold-multimer and AlphaFold3 in tests on new protein pairs.
- Disobind delivered consistently higher accuracy when tested on new protein pairs it had not seen before.
- Applications of the tool could span from **disease biology to drug design**.

Source: **TH**

Source: <https://vajiramandravi.com/current-affairs/intrinsically-disordered-proteins/>

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