

## NIT Rourkela decodes sugar molecules and bone protein complex to boost bone regeneration technology

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**To aid in optimising drug delivery during treatment and reducing side effects for patients**



Scientists at National Institute of Technology (NIT) Rourkela, Odisha have uncovered how natural sugar-like molecules in the human body can alter the behaviour of Bone Morphogenetic Protein-2 (BMP-2), a protein responsible for bone formation and repair.

Published in the journal *Biochemistry*, the findings of this research can be used for advanced treatments in bone and cartilage regeneration, improved implants, and more effective protein-based medicines.

BMP-2 plays a crucial role in forming bones and cartilage, healing injuries, and guiding stem cells to become bone-forming cells. However, in the human body, this protein interacts with different Glycosaminoglycans (GAGs), special sugar-like molecules found in connective tissues and joint fluids.

The NIT Rourkela research team investigated how these different GAGs affect BMP-2 when it is exposed to “stress” in the form of urea-induced chemical denaturation.

The team observed that BMP-2 unfolded faster in the presence of Sulfated Hyaluronic Acid (SHA), a type of GAG, compared to regular Hyaluronic Acid or without additives. The researchers found that SHA binds directly to BMP-2 protein, gently

altering its structure and making it unfold in a more controlled manner.

Speaking about the findings and potential real-world impact of this research, Prof. Harekrushna Sahoo, said. “BMP-2 is a critical protein in humans that plays a fundamental role in osteogenesis and bone regeneration, residing within the glycosaminoglycan-rich extracellular matrix environment of bone tissue. Our study reveals how specific GAG–BMP-2 interactions influence unfolding dynamics and structural stability. These insights allow scaffold designs to actively preserve BMP-2’s functional conformation, prolong bioactivity, lower dosage needs, and reduce side effects. Furthermore, the work offers a mechanistic basis for tailoring GAG functional group modifications to modulate protein structure and activity, guiding next-generation pharmaceutical formulation.”