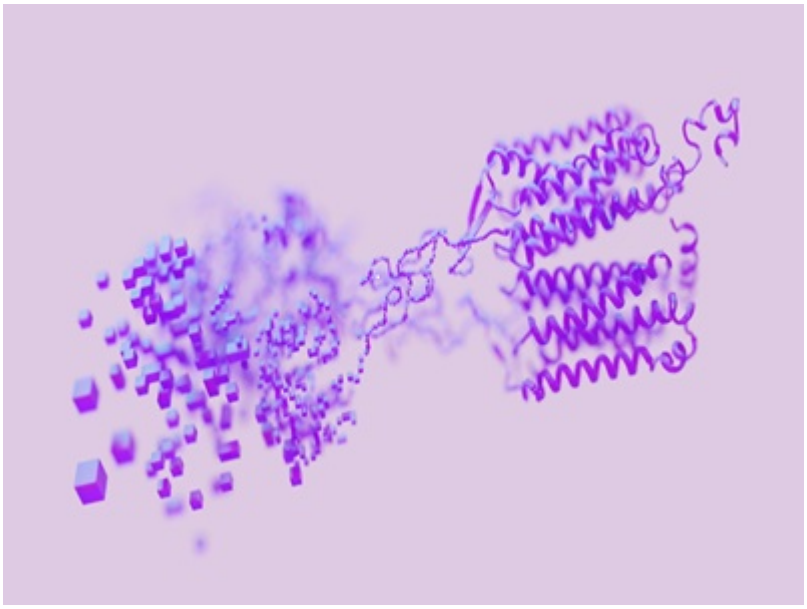
Protein Homodimers with Tunable Symmetric Pockets: A Novel Approach to Binding Symmetric Molecules

This technology offers de novo designed protein homodimers with tunable symmetric pockets, enabling the binding of symmetric molecules for diverse applications.



Technology ID

BDP 8497

Category

Selection of Available Technologies

Therapeutics/Other

Authors

David Baker

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What is the Problem?

The design of proteins capable of binding arbitrary small molecules is a significant challenge in biotechnology. The binding of small molecules requires the design of proteins with pockets that match the shape of the ligand. Despite progress in designing proteins to bind asymmetric molecules, there is a gap in the ability to facilitate the binding of symmetric molecules, which could unlock new possibilities in biosensors and medicine.

What is the Solution?

The technology involves de novo designed protein homodimers that contain tunable symmetric pockets. To bind symmetric ligands, protein homo-oligomers are designed with matching symmetry so that each protein subunit can make identical interactions with the ligand. These symmetric proteins are designed to form hyperstable structures with pockets of diverse size

and shape. The approach allows for the creation of thousands of unique protein structures, providing a solution to the need for customizable proteins in various applications.

What is the Competitive Advantage?

This technology enables the ability to create a vast array of protein structures with tunable features. The de novo designed protein homodimers can bind a wide range of symmetric compounds, which could enable the creation of new enzymes, therapeutics, and light harvesting proteins. This technology provides a solution to the need for proteins that can bind symmetric molecules, opening up new applications such as ligand controllable cell engineering.

Patent Information:

US20230114825A1

References

1. Hicks, D. R., Kennedy, M. A., Thompson, K. A., DeWitt, M., Coventry, B., Kang, A., Bera, A. K., Brunette, T. J., Sankaran, B., Stoddard, B., Baker, D.(2022) , https://www.pnas.org/doi/full/10.1073/pnas.2113400119, https://www.pnas.org/, 119, e2113400119