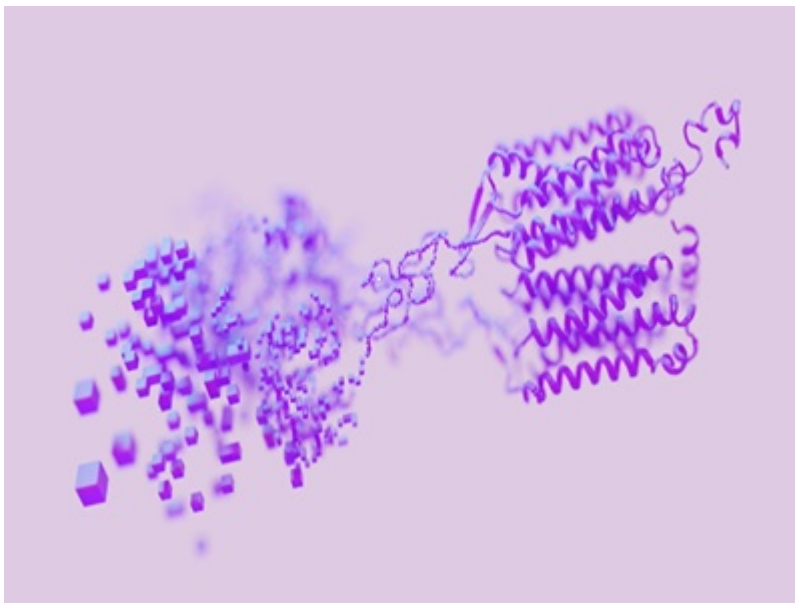


Design of Customizable Immunoglobulin-like Domains

This technology is a novel approach to design highly stable immunoglobulin-like domains, offering tailored structures with superior biophysical properties.



Technology ID

BDP 8566

Category

Research Tools
Selection of Available
Technologies

Authors

David Baker

Learn more



What is the Problem?

The current market for antibody-based drugs, which are primarily built on immunoglobulin (Ig) β -sandwich scaffolds, is rapidly growing. However, the design and production of these drugs often face challenges in terms of stability and customization. Different diseases require different therapeutic approaches, and the ability to tailor these drugs to specific needs is crucial.

What is the Solution?

The solution is the design of immunoglobulin-like domains using a set of design rules developed specifically for the Ig fold architecture. This approach allows for the creation of highly stable Ig domains de novo. These domains can correctly scaffold functional loops, which are crucial for the drug's ability to bind to its target. This opens the door to the design of antibody-like scaffolds with tailored structures, which can be customized to meet specific therapeutic needs.

What is the Competitive Advantage?

This technology offers a significant advantage over current alternatives in the market by enabling the design of antibody-like scaffolds with superior biophysical properties. This could potentially enhance the efficacy of antibody-based drugs. Furthermore, the ability to design these domains de novo provides an unprecedented level of customization, enabling the development of more targeted and effective therapeutic solutions. The technology is based on a set of design rules, making it a systematic and reproducible approach. This could potentially streamline the drug design process, making it more efficient and cost-effective.

Patent Information:

[US20230279055A1](#)

References

1. Chidyausiku, T. M., Mendes, S. R., Klima, J. C., Nadal, M., Eckhard, U., Roel-Touris, J., Houliston, S., Guevara, T., Haddox, H. K., Moyer, A., Arrowsmith, C. H., Gomis-Rüth, F. X., Baker, D., Marcos, E.(2022), <https://www.nature.com/articles/s41467-022-33004-6>, <https://www.nature.com/ncomms/>, 13, 5661