

Just in Time Semi-Automated Protein Production

The solution is a novel protocol for making and testing proteins called **Just in Time Semi-Automated Protein Production (JIT-SAPP)**, which allows a single user to produce up to 192 purified proteins in under a week.

What is the Problem?

Recent advances in designing new proteins using deep learning methods have enabled the creation of proteins with desired functions or properties that can be used in therapeutic, vaccine, and environmental sustainability applications. However, current standard laboratory methods to make proteins are labor intensive and low throughput. As a result, there is a need to develop high-throughput protein production methods.

What is the Solution?

The solution is a novel protocol for making and testing proteins called Just in Time Semi-Automated Protein Production (JIT-SAPP), which allows a single user to produce up to 192 purified proteins in under a week. This protocol makes four times more protein using less reagents and producing less waste than standard laboratory methods. JIT-SAPP uses a series of automated laboratory modules for DNA assembly, protein expression, and protein testing to reduce the time and effort required to generate new designer proteins.

What is the Competitive Advantage?

The competitive advantage of this technology lies in its ability to standardize and automate protein production methods, significantly increasing the throughput with which new proteins can be generated. JIT-SAPP is built with custom, end-to-end software for executing experiments and tracking data, enabling flexibility in protocol changes. This technology can be used to quickly bring a protein designed on the computer into the real world.

References

1. Watson, J.L., Juergens, D., Bennett, N.R., Trippe, B.L., Yim, J., Eisenach, H.E., Ahern, W., Borst, A.J., Ragotte, R.J., Milles, L.F., Wicky, B.I.M., Hanikel, N., Pellock, S.J., Courbet, A., Sheffler, W., Wang, J., Venkatesh, P., Sappington, I., Vázquez Torres, S., Lauko, A., De Bortoli, V., Mathieu, E., Ovchinnikov, S., Barzilay, R., Jaakkola, T.S., DiMaio, F., Baek, M., Baker, D.(2023) , <https://www.nature.com/articles/s41586-023-06415-8>, <https://www.nature.com/>, 620, 1089-1100

Technology ID

BDP 8637

Category

Software/Bioinformatics
Selection of Available
Technologies

Authors

David Baker

Learn more

