



*Your Optimized Protein.
Just A Few Clicks Away.*

At Dezyme, we are on a mission to help scientists to rapidly identify and select the right protein for their specific applications.

Based on the combination of a highly intuitive web software and substantial expertise in bioinformatics, we can support you to optimize your screening and experimental efforts.

In a performing, reliable and cost-effective manner.

Our Software

A powerful platform for rapid rational design of mutant proteins

We have designed our software keeping simplicity in mind. Operated through a highly intuitive interface, the online platform is the solution for the rapid rational design of mutant proteins and ensures a straight and optimal user experience.



With 15 years of academic research and already more than 500 users,

Dezyme software has demonstrated to offer a significantly greater predictive power compared with classical methods, consequently limiting the number of experimental tests.

By allowing the systematic in-silico screening of mutant proteins, even the most complex, Dezyme is an efficient solution to improve the stability and the thermal resistance.

Currently available, for any mutation in any protein:

- **PoPMuSiC™** : to predict Thermodynamic stability
- **HoTMuSiC™** : to predict Thermal stability

www.dezyme.com





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Our Services

From *in silico* prediction to experimental validation

We work every day to be your privileged partner for the optimization of your proteins. Our goal is to control modification of specific physical, chemical and biological features, such as stability, thermal resistance, docking and solubility, without affecting the protein's activity.

We exploit for that purpose newly developed energy functions derived from known protein structures. An original functionality is the estimation of the optimality of each amino acid in the sequence with respect to the stability. Clusters of non-optimal residues represent particularly interesting sites for introducing targeted mutations.

To adapt to your specific needs, we offer:

- Protein audits
- *In silico* prediction of stable mutants
- Experimental validation of stable mutants
- Support in the integration of our web software



Contact Us

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