

The Fleishman lab is developing methods for computational protein design that have become widely used among protein engineers and biochemists. For example, the lab developed web servers for automated design of stable variants of therapeutic proteins, including enzymes and vaccine immunogens[1,2] and a server for dramatically increasing the catalytic efficiency of therapeutic enzymes[3].

The lab is now developing a new strategy for designing vast repertoires of antibodies for therapeutic targets and is seeking a part-time programmer with experience in bioinformatics and web server development. The successful applicant will have experience working on a project in bioinformatics or a related field and will work in a highly collaborative environment of biochemists and programmers at the Department of Biomolecular Sciences in the Weizmann Institute of Science.

Please email a CV to sarel@weizmann.ac.il

Lab website: <http://www.fleishmanlab.org>

[1] Goldenzweig, A.; Goldsmith, M.; Hill, S. E.; Gertman, O.; Laurino, P.; Ashani, Y.; Dym, O.; Unger, T.; Albeck, S.; Prilusky, J.; Lieberman, R. L.; Aharoni, A.; Silman, I.; Sussman, J. L.; Tawfik, D. S.; Fleishman, S. J. Automated Structure- and Sequence-Based Design of Proteins for High Bacterial Expression and Stability. *Mol. Cell* **2016**, *63* (2), 337–346.

[2] Campeotto, I.; Goldenzweig, A.; Davey, J.; Barfod, L.; Marshall, J. M.; Silk, S. E.; Wright, K. E.; Draper, S. J.; Higgins, M. K.; Fleishman, S. J. One-Step Design of a Stable Variant of the Malaria Invasion Protein RH5 for Use as a Vaccine Immunogen. *Proc. Natl. Acad. Sci. U. S. A.* **2017**, *114* (5), 998–1002.

[3] Khersonsky, O.; Lipsh, R.; Avizemer, Z.; Ashani, Y.; Goldsmith, M.; Leader, H.; Dym, O.; Rogotner, S.; Trudeau, D. L.; Prilusky, J.; Amengual-Rigo, P.; Guallar, V.; Tawfik, D. S.; Fleishman, S. J. Automated Design of Efficient and Functionally Diverse Enzyme Repertoires. *Mol. Cell* **2018**, *72* (1), 178–186.e5.

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