Robust in vitro affinity maturation strategy based on interface-focused high-throughput mutational scanning

Yasuhiro Fujino¹

Fujino.Yasuhiro@mb.mt-pharma.co.jp Risako Fujita²

Fujita.Risako@mv.mt-pharma.co.jp

Kouichi Wada³

Wada.Kouichi@me.mt-pharma.co.jp

Kotomi Fujishige⁴

Fujishige.Kotomi@mb.mt-pharma.co.jp

Takashi Kanamori⁵

kanamori@k.u-tokyo.ac.jp

Lindsey Hunt⁶

lhunt@sapidyne.com

Yoshihiro Shimizu⁷

yshimizu@riken.jp

Takuya Ueda⁸

ueda@k.u-tokyo.ac.jp

- 1-4 Advanced Medical Research Department, Mitsubishi Tanabe Pharma Corporation, 1000, Kamoshida-cho, Aoba-ku, Yokohama 227-0033 Japan
- ⁶ Sapidyne Instruments, 700 W. Diamond St. Boise, ID 83705 USA
- ⁷ Laboratory for Cell-Free Protein Synthesis, Quantitative Biology Center, RIKEN, 2-2-3, Minatojima-minamimachi, Chuo-ku, Kobe, Hyogo, 650-0047, Japan
- ^{5, 8} The Department of Medical Genome Sciences, Graduate School of Frontier Sciences, The University of Tokyo, FSB-401, 5-1-5, Kashiwanoha, Kashiwa, Chiba 277-8562, Japan

Keywords: Protein engineering; Affinity maturation; Mutation scanning; High-throughput sequencing; Ribosome display

Abstract

Development of protein therapeutics or biosensors often requires in vitro affinity maturation. Here we report a robust affinity engineering strategy using a custom designed library. The strategy consists of two steps beginning with identification of beneficial single amino acid substitutions then combination. A high quality combinatorial library specifically customized to a given binding-interface can be rapidly designed by high-throughput mutational scanning of single substitution scanning libraries. When applied to the optimization of a model antibody Fab fragment, the strategy created a diverse panel of high affinity variants. The most potent variant achieved a 2110-fold affinity improvement to an equilibrium dissociation constant (Kd) of 3.45 pM with only 7 amino acid substitutions. The method should facilitate affinity engineering of a wide variety of protein-protein interactions due to its context-dependent library design strategy.

[1] Fujino, Y., Fujita, R., Wada, K., Fujishige, K., Kanamori, T., Hunt, L., Yoshihiro, S., Takuya, U., Robust in vitro affinity maturation strategy based on interface-focused high-throughput mutational scanning. Biochem. Biophys. Res. Commun. 428:395-400, 2012