

CzeekD: Fragment-based *de novo* Drug Design System for Drug Discovery

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For early stages in drug development, it is a critical issue to find lead compounds with novel scaffolds. However, the set of all possible small organic molecules has been estimated to consist of more than 10^{60} compounds, it is difficult to figure out the best scaffolds from among the vast chemical space through experimental synthetic approaches.

We have developed a computational approach to efficiently generate lead compounds with novel scaffolds using fragment chemical library. The fragment-based drug *de novo* design system with a fast stochastic optimization algorithm, called “CzeekD”, has following functions:

- Generation of novel scaffolds in vast chemical space is achieved by combination of building blocks in fragment library.
- It is easy to synthesize the designed chemical structures because of using basic chemical reactions, i.e. RECAP rule.
- Chemical Genomics-Based Virtual Screening (CGBVS) is implemented as a scoring function, which can efficiently estimate the possibility of molecular interactions between the generated compounds and the target proteins.
- Particle Swarm Optimization (PSO) algorithm was newly developed to swiftly explore druggable molecular seeds and to efficiently find out diverse structures among the vast chemical space.

As a result of bioactivity evaluation of the designed compounds through organic synthesis and *in vitro* assay, we successfully identified novel active compounds with highly hit rate (20–40%) for GPCR proteins. This result suggested that CzeekD provides a powerful solution to guide medicinal chemists into the discovery of novel bioactive molecules.

- [1] Hartenfeller M, Proschak E, Schüller A, and Schneider G., Concept of combinatorial *de novo* design of drug-like molecules by particle swarm optimization, *Chem Biol Drug Des*, 72:16-26. 2008.
- [2] Lewell XQ, Judd DB, Watson SP, and Hann MM., RECAP–retrosynthetic combinatorial analysis procedure: a powerful new technique for identifying privileged molecular fragments with useful applications in combinatorial chemistry, *J Chem Inf Comput Sci*, 38:511-22, 1998.
- [3] Yabuuchi H, Nijima S, Takematsu H, Ida T, Hirokawa T, Hara T, Ogawa T, Minowa Y, Tsujimoto G, and Okuno Y., Analysis of multiple compound-protein interactions reveals novel bioactive molecules, *Mol Syst Biol*, 7:1-12, 2011.
- [4] J. Kennedy and R. C. Eberhart, Particle swarm optimization, *Proc. IEEE International Conference on Neural Networks*, 1942-1948, 1995.