

Drug discovery of small molecule modulators for ubiquitin-proteasome system with *in silico* screening strategy, INTENDD

Hirotsugu Komatsu, Ken Ikeda, Takeshi Tanaka, Takao Matsuzaki

Interprotein Corporation

It is often mentioned that drug targets have been exhausted. However, large number of ubiquitin-proteasome system-related targets have not been examined yet and have a great potential as reservoir of drug targets. Although hit identification of protein degradation inhibitors and inducers including ubiquitin-proteasome system-targeting compounds are usually conducted by high throughput screening (HTS), literature-based compound synthesis evolution or binding energy-based standard *in-silico* screening, we have experienced that it is hard to identify good hit compounds for protein degradation inhibitors and inducers by these approaches. Based on these situations, Interprotein established INTerprotein's Engine for New Drug Design (INTENDD), a proprietary *in-silico* screening strategy that propose hit candidates by "binding mechanism"-based algorithm but not binding energy-based selection for final identification of hit candidates. Furthermore, utilizing INTENDD's knowhows, we also constructed AI-guided INTENDD, an artificial intelligence (AI)-introduced activity prediction system that is expected to accelerate lead generation/optimization of small molecules. In my presentation, I will introduce advantages of INTENDD and AI-guided INTENDD, and those applications for challenging drug targets including ubiquitin-proteasome system.