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Computational study for designing peptide drugs based on statistical thermodynamics with sufficient accuracy and remarkably high speed

次世代ペプチド薬の物理理論に基づく高速デザイン法の開発

[Keywords]

Drug discovery and	Peptide	In silica	Free-energy	High-speed
development	therapeutics	screening	calculation	computation

■ Summary

Computational strategies are widely used to design the peptide drugs with high affinity to the target proteins. The rapid modeling of the native-like poses of a protein-peptide complex is difficult but crucial.

To overcome this issue, we have developed a physics-based free-energy function (FEF).^{1,2} For a protein-peptide complex possessing over 100 residues with a prescribed structure, the FEF calculation is finished in a few seconds on a standard workstation.

Next generation therapeutics Enzyme Receptor Protein-peptide interaction P53Pep Leugs Phe88

A peptide with only 10 amino acid residues

→ More than 10 trillion candidates!

■ Subject Details/Topic

Our strategy is as follows:

- (1) Complex structures with a wide variety of binding poses of a peptide are generated using the molecular dynamics simulation or the sampling algorithms employed in the protein-peptide docking programs
- (2) FEF is applied to the structures
- → The protein-peptide complex giving the lowest value to FEF is identified

Advantages over competing study

Physical insights into the stability of a protein-peptide complex can be obtained clearly in a few seconds. The calculation time is comparable to the AI based methods.

Possible applications

- Designing and in silico screening of various drug candidates
- Development of nanobiotechnologies and nanodevices

(1) S. Hikiri, T. Hayashi et al., J. Chem. Phys., 150:175101, 2019. (2) T. Yamada, T. Hayashi et al., J. Chem. Inf. Model., 59:3533, 2019.

■ We hope to collaborate with...

Companies and research institutes related to pharmaceuticals, biotechnology, life sciences, health care equipment & services, and software & services

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