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PROTAC Design based on Bioinformatics

boc.protac [1]

[1]BOC Sciences

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dx.doi.org/10.17504/protocols.io.dm6gpbox1lzp/v1

PROTAC

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In order to simplify and accelerate the discovery of PROTAC, it is necessary to grasp the design rules of PROTAC, which is helpful to establish a reliable PROTAC evaluation platform. To date, most reported PROTAC designs are based on target protein-binding ligands (usually inhibitors). Because the crystal complex structure of the target protein and its binding ligand and the structure-activity relationship information of the ligand have been used to guide PROTAC design, such as determining the Linker binding site of the target protein binding ligand. Recent research uses bioinformatics to guide PROTAC optimization. Bioinformatics methods play an irreplaceable role in the process of drug discovery, especially for the analysis of large-scale multi-group data. at present, many disease-related database resources have emerged, and a variety of bioinformatics methods have been established to discover potential drug targets based on biological network characteristics, multi-gene chip, proteome, metabolome data and so on. The target drug availability and drug side effects were predicted.

As a leading service provider in drug discovery and research, BOC Sciences is fully capable and committed to providing one-stop proteolysis targeting molecular drug discovery based on chimeric (PROTAC®). With a comp rehensive and advanced platform, we provides PROTAC design based on bioinformaticsservices to customers around the world to meet new drug discovery goals.

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https://ptc.bocsci.com/services/protac-design-based-on-bioinformatics.html

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