

P02-04

Amino acid preference mapping on protein-protein interaction surface using mixed-solvent molecular dynamics

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P01-01

Cyclosporin A: Conquering
Conformational Complexity and
Chameleonicity

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P01-05

QM/MM simulations of artificial ion channel in membrane-water system

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P03-12

Protein-ligand complex structure generation with diffusion-based generative models

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P04-01

Computational search for compounds exhibiting the same activity from database by molecular fingerprints and 3D pseudo-atom methods

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P06-03

Application of Deep Learning to the Evaluation of Seizure-like Behavior Using Zebrafish

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AI-AAM. Downsizing and scaffold hopping from a peptide to small-molecule inhibitors

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Estimation of Interaction
Mechanism in CompoundProtein Interaction Prediction
Using Interpretable Deep
Learning

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Understanding Molecular
Mechanism of Drug Off-Target
Effect in Tyrosine-Protein
Kinase LCK Using Molecular
Dynamics Simulation

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Automated hetero shuffling combined with FMO calculations

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