

# ACCELERATING QUANTUM-CHEMICAL MULTILIGAND SIMULTANEOUS DOCKING WITH DEEP REINFORCEMENT LEARNING

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This study employs quantum-chemical multiligand simultaneous docking (MLSD) to identify potent single or joint inhibitors of human acetylcholinesterase (hAChE), human butyrylcholinesterase (hBChE), and/or equine butyrylcholinesterase (eqBChE). Moving beyond traditional single-molecule docking, we adopted a fragment-based paradigm, docking multiple small molecular scaffolds designed for subsequent assembly *via* modular organic synthesis. To navigate the high-dimensional configurational space and the computational complexity associated with translational, rotational, and conformational degrees of freedom, we developed a parallelized Monte Carlo algorithm to enhance sampling efficiency.<sup>[1]</sup> This framework incorporates a smart structure generator for pre-screening and input optimization. Binding enthalpies were determined using the PM7 semiempirical Hamiltonian,<sup>[2]</sup> which has been shown to outperform other semiempirical methods for organic molecules.<sup>[3]</sup> To overcome the computational bottleneck of PM7 calculations, particularly in multiligand systems, we integrated deep neural networks (DNNs) trained on-the-fly *via* deep reinforcement learning.<sup>[4]</sup> These DNNs accurately approximate potential energy surfaces (PESs), substantially reducing the computational cost of energy determinations. Finally, active-site coverage was monitored dynamically throughout the simulations using probability density functions to ensure optimal ligand placement throughout the active site.

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## REFERENCES

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