

# ICRAMCS 2026

THE EIGHTH EDITION OF THE INTERNATIONAL CONFERENCE ON  
RESEARCH IN APPLIED MATHEMATICS AND COMPUTER SCIENCE

April 23-24-25, 2026 | Marrakech, Morocco



## AI-Assisted Virtual Screening and Molecular Docking for Rational Drug Discovery: A Systematic Review

### Communication Info

#### Authors:

Oumaima ELYAZYD<sup>1</sup>

Samir CHTITA<sup>3</sup>

Mohammed AIT DAOUD<sup>1,2</sup>

<sup>1</sup> Laboratory of Artificial Intelligences and Systems (LIAS), Faculty of Sciences Ben M'Sick, University Hassan II Casablanca, Morocco

<sup>2</sup> Moroccan Association for Artificial Intelligence and Innovation (AM2I), Faculty of Sciences Ben M'Sick, University Hassan II Casablanca, Morocco

<sup>3</sup> Laboratory of Analytical and Molecular Chemistry, Faculty of Sciences Ben M'Sick, University Hassan II of Casablanca, Morocco

#### Keywords:

- (1) Virtual Screening
- (2) Molecular Docking
- (3) Drug Discovery
- (4) Deep Learning

### Abstract

The discovery of novel therapeutics is a time-consuming and capital-intensive process and costs over \$2.6 billion per drug [1]. According to those limitations, the emergence of virtual screening (VS) and molecular docking were critical computational strategies to accelerate lead identification [2]. However, classical scoring functions suffer from limited accuracy [3].

The emergence of artificial intelligence (AI), specifically deep learning (DL), motivated by recent advances like AlphaFold [4], has revolutionized computer-aided drug design

This systematic review, conducted in accordance with the PRISMA 2020 guidelines [5], provides a comprehensive analysis of AI techniques in virtual screening. The review also highlights a critical gap in multi-target drug discovery strategies, which remain underrepresented despite their clinical importance for complex diseases.

© ICRAMCS 2026 Proceedings ISSN: 2605-7700

### References

- [1] J. A. DiMasi, H. G. Grabowski, and R. W. Hansen, 'Innovation in the pharmaceutical industry: new estimates of R&D costs', *J. Health Econ.*, vol. 47, 2016, pp. 20–33.
- [2] B. K. Shoichet, 'Virtual screening of chemical libraries', *Nature*, vol. 432, 2004, pp. 862–865.
- [3] S. F. Sousa, P. A. Fernandes, and M. J. Ramos, 'Protein-ligand docking: current status and future challenges', *Proteins*, vol. 65, 2006, pp. 15–26.
- [4] J. Jumper *et al.*, 'Highly accurate protein structure prediction with AlphaFold', *nature*, vol. 596, 2021, pp. 583–589.
- [5] M. J. Page *et al.*, 'The PRISMA 2020 statement: an updated guideline for reporting systematic reviews', *bmj*, vol. 372, 2021.