

# CITATION REPORT

List of articles citing

## Genetic Algorithm inAb Initio Protein Structure Prediction Using Low Resolution Model: A Review

DOI: 10.1007/978-3-642-02193-0\_14  
Studies in Computational Intelligence, 2009, , 317-342.

**Source:** <https://exaly.com/paper-pdf/83748405/citation-report.pdf>

**Version:** 2024-04-25

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
18	Clustered memetic algorithm for protein structure prediction. <b>2010</b> ,		8
17	A hybrid genetic algorithm for the 3-D protein structure prediction problem using a path-relinking strategy. <b>2011</b> ,		5
16	Novel local improvement techniques in clustered memetic algorithm for protein structure prediction. <b>2011</b> ,		9
15	Protein structure prediction based on optimal hydrophobic core formation. <b>2012</b> ,		3
14	Protein Folding in the 2D HydrophobicHydrophilic (HP) Square Lattice Model is Chaotic. <i>Cognitive Computation</i> , <b>2012</b> , 4, 98-114	4.4	6
13	Computational approach for protein structure prediction. <i>Healthcare Informatics Research</i> , <b>2013</b> , 19, 137-47	3	13
12	Is protein folding problem really a NP-complete one? First investigations. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2014</b> , 12, 1350017	1	20
11	A Review of Evolutionary Algorithms for Computing Functional Conformations of Protein Molecules. <i>Methods in Pharmacology and Toxicology</i> , <b>2015</b> , 31-64	1.1	8
10	General overview on structure prediction of twilight-zone proteins. <i>Theoretical Biology and Medical Modelling</i> , <b>2015</b> , 12, 15	2.3	47
9	The study of unfoldable self-avoiding walks - Application to protein structure prediction software. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2015</b> , 13, 1550009	1	3
8	Finding the needle in the haystack: towards solving the protein-folding problem computationally. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , <b>2018</b> , 53, 1-28	8.7	23
7	A Novel Framework for Coarse Protein Structure Prediction. <i>Advances in Bioinformatics</i> , <b>2018</b> , 2018, 76073384	5.3	3
6	HPS_PSP: HIGH PERFORMANCE SYSTEM FOR PROTEIN STRUCTURE PREDICTION. <i>Journal of Biological Systems</i> , <b>2019</b> , 27, 487-502	1.6	1
5	Prediction of Native Protein Conformation by a Hybrid Algorithm of Clonal Selection and Differential Evolution. <i>Lecture Notes on Data Engineering and Communications Technologies</i> , <b>2022</b> , 314-330	0.4	
4	Principles and Overview of Sampling Methods for Modeling Macromolecular Structure and Dynamics. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1004619	5	124
3	Conflict Resolution Based Global Search Operators for Long Protein Structures Prediction. <i>Lecture Notes in Computer Science</i> , <b>2011</b> , 636-645	0.9	
2	A Knowledge-Based Initial Population Generation in Memetic Algorithm for Protein Structure Prediction. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 546-553	0.9	

- 1 Computational Coarse Protein Modeling of HIV-1 Sequences Using Evolutionary Search Algorithm. **2019**, 97-115