ALLEGATOB

Curriculumformativo,didattico,scientificoeprofessionaledelcandidato

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Dichiarazionesostitutivadicertificazioni

(Art.46,D.P.R.28 dicembre2000n. 445)

Dichiarazionesostitutivadell'attodinotorietà

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(Art.47,D.P.R.28 dicembre2000n. 445)

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Estremidelbandodi selezione	CALL FOR RESEARCH FELLOWSHIP N. 13/2025 – REP.303 /2025 July 8, 2025
Informazioniaggiornateal	July 16, 2025
NomeeCognome	IZAZMONIRKAMAL
Datadinascita	

Siraccomandadiindicareconprecisionetuttiglielementivalutabiliaisensidelbandodi selezione (aggiungere o togliere righe secondo necessità).

Esperienzaprofessionale

Periodo	Ente	Principaliattivitàeresponsabilità
2019-2024	CSIR-Indian Institute of Chemical Biology	Ph.D.ResearchinComputationalBiologyandDrugDesign under Dr. Saikat Chakrabarti. Developed MetaDOCK, MLDoV, and DbNSP platforms. Published 8 research papers. Research focus on protein-ligand interactions, moleculardocking,machinelearningapplicationsindrug discovery.
2024-Present	CSIR-Indian Institute of Chemical Biology	Continued research in computational drug discovery and machinelearningapplicationsinbiology.Developmentof web-based computational platforms using Python, PHP, JavaScript,and Flask.

Istruzione,formazione(es.titolidistudio,certificazioni professionali/linguistiche/informatiche)

Data	Titolo/Principali tematiche	Ente
2019-2025	Ph.D. in Computational Biology and Drug Design - Thesis:"Meta-DockingApproachforProtein-Ligand ComplexesandValidationUsingMachineLearning Techniques"	CSIR-IndianInstitute of Chemical Biology (AcSIR)
2016-2018	M.Sc.inLifeScience(FirstClass)-Specializationin MolecularBiologyandBiochemistry	PresidencyUniversity
2013-2016	B.Sc.inZoology(FirstClass)-FoundationinBiological Sciences	SripatSinghCollege, UniversityofKalyani
2019	DBTJRF, ICMRJRF,GATEXL,GATEBT,SET Qualified-Nationallevelcompetitiveexaminations	VariousNational Agencies

Pubblicazioni / Convegni

1. Kamal IM, Chakrabarti S. MetaDOCK: A Combinatorial Molecular Docking Approach. ACS Omega. 2023 Jan 31;8(6):5850-5860.
2. Kamal IM, et al. A Novel spice-antioxidant-based nano-vehicle as alternative AChE inhibitor. J Biomol Struct Dyn. 2023 Aug 28:1-18.
3. Das R, Kamal IM, Das S, Chakrabarti S, Chakrabarti O. MITOL-mediated DRP1 ubiquitylation and degradation promotes mitochondrial hyperfusion in a CMT2A-linked MFN2 mutant. J Cell Sci. 2022 Jan 15;135(2): jcs257808.
4. Maity S, Kamal IM, Das S, Chakraborty J, Chakrabarti S, Chakrabarti O. Endoplasmic reticulum protein FAM134B interacts with DRP1 to maintain mitochondrial morphology. Cell Death and Disease. 2024 Dec 15.
5. Bandopadhyay S, Kamal IM, Padmanaban E, Ghosh DD, Chakrabarti S, Roy SS. Oncogene-mediated nuclear accumulation of lactate promotes epigenetic alterations to induce cancer cell proliferation. J Cell Biochem. 2023 Apr;124(4):495-519.
6. Das R, Maity S, Das P, Kamal IM, Chakrabarti S, Chakrabarti O. CMT2A-linked MFN2 mutation, T206I promotes mitochondrial hyperfusion and predisposes cells towards mitophagy. Mitochondrion. 2024 Jan;74:101825.
7. Kulavi S, Dhar D, Kamal IM, Chakrabarti S, Bandyopadhyay J. EIF4A3 Targeted Therapeutic Intervention in Glioblastoma Multiforme Using Phytochemicals from Indian Medicinal Plants – An Integration of Phytotherapy into Precision Onco-medicine. J Biomol Struct Dyn. 2024 Jan.
8. Biswas N, Kumar K, Mallick P, Das S, Kamal IM, Bose S, Choudhury A, Chakrabarti S. Structural and drug screening analysis of the non-structural proteins of SARS-CoV-2 virus extracted from Indian COVID-19 patients. Frontiers in Genetics. 2021; 12:171.
9. Garg A, Goel N, Abhinav N, Varma T, Achari A, Bhattacharjee P, Kamal IM, Chakrabarti S, Ravichandiran V, Reddy AM, Gupta S, Jaisankar P. Virtual screening of natural products inspired in-house library to discover potential lead molecules against the SARS-CoV-2 main protease. J Biomol Struct Dyn. 2023
10. Patent: MLDoV - Machine Learning based Protein-Ligand complex validation (Final Patent Submitted)

Altre attività scientifiche

Development of MetaDOCK web platform (http://www.hpppi.iicb.res.in/metadock/index.html) - Full-stack web application for molecular docking integrating AutoDock4.2, LeDock, and rDOCK algorithms with >90% accuracy in binding pose prediction

Development of MLDoV machine learning pipeline for docking validation using Python, scikit-learn, TensorFlow with integrated SVM, Random Forest, and XGBoost models

Development of DbNSP database and analysis platform for viral protein analysis (http://www.hpppi.iicb.res.in/covid19/index.php) built with PHP, MySQL, and Python

Training of 250+ M.Sc. and Ph.D. students in computational drug design and bioinformatics

Expertise in molecular modeling software: SCHRODINGER, GROMACS, NAMD, DS, GLIDE, GOLD, VMD, CHIMERA, PYMOL

Proficiency in AlphaFold, BindCraft, Rfdiffusion, Protein and Ligand MPNN for protein structure prediction and design

Ulteriori informazioni pertinenti

Programming & Development Skills:

Core Languages: Python, PHP, Perl, Java
Web Development: HTML/CSS/JavaScript, PHP
Machine Learning: TensorFlow, PyTorch, scikit-learn, NumPy, Pandas
Database: MySQL
Version Control: Git, GitHub, Zenodo

High Performance Computing Experience:

Experience with HPC clusters and parallel computing
Job scheduling (SLURM, PBS)
GPU acceleration for ML applications

Research Profiles:

Google Scholar: https://scholar.google.com/citations?user=JqB6-RcAAAAJ
ResearchGate: https://www.researchgate.net/profile/Izaz-Kamal

Awards & Recognition:

DBT Research Fellowship (2019-2024)
Qualified multiple national-level examinations (DBT JRF, ICMR JRF, GATE, SET)

Additional Technical Expertise:

Statistical analysis (ANOVA, PCA, Regression, multivariate analysis)
Experimental techniques: Western Blotting, UV Spectroscopy, X-ray Crystallography
Custom script development for automation and pipeline optimization

Luogo, data: Kolkata, July 16, 2025   Firma digitale: