



## Md Adnan Karim

**Nationality:** Bangladeshi **Date of birth:** 13/10/1997 **Phone number:** (+49) 1744027333

**Email address:** [mdka00001@stud.uni-saarland.de](mailto:mdka00001@stud.uni-saarland.de)

**LinkedIn:** <https://www.linkedin.com/in/md-adnan-rahin-214905162/>

**Home:** Richard-wagner-str. 91, 66125 Saarbrücken (Germany)

### ABOUT ME

I am a dedicated Bioinformatics researcher with over three years of experience in managing workflows for processing transcriptomic and epigenomic next-generation sequencing (NGS) data, multi-omics research and developing ML classifiers for protein classification.

### WORK-RELATED SKILLS

#### Languages and frameworks

Python, R, C++, Bash, MySQL/PostgreSQL, Django, Flask, SQLAlchemy, Rshiny, Docker, HTML-CSS, Git.

#### Sequencing data analysis

High-throughput sequencing data analysis (NGS) RNAVATAC\ChIP-seq data, metagenome analysis (16S and ITS rRNA Sequencing), Non-coding RNA analysis (miRNA).

#### Statistical learning

Machine and Deep learning (Scikitlearn, PyTorch, Keras, Tensor-Flow).

#### Workflow management

ETL workflow management (Apache Airflow, Kafka), SnakeMake, NextFlow.

### WORK EXPERIENCE

#### Bioinformatician

**KIST Europe** [ 01/12/2021 – Current ]

City: Saarbrücken | Country: Germany

Developed laboratory information management software system for research data management.  
Development of OpenCV and CNN-based real-time cardiomyocyte and cardiac organoid contractility detection application.  
Maintained workflow pipelines for RNA & ATAC-seq processing with SnakeMake and NextFlow.

#### Bioinformatics researcher

**BioSol Centre** [ 01/07/2019 – 31/12/2021 ]

City: Jashore | Country: Bangladesh

Performed systematic studies on Microarray datasets to correlate molecular functions of genes with cancer prognosis,  
Facilitated numerous training sessions on OMICs data analysis.

#### University research assistant

**Jashore University of Science and Technology** [ 01/07/2018 – 01/04/2020 ]

City: Jashore | Country: Bangladesh

Performed 16 rRNA sequencing based characterization of cellulolytic strains of Mangrove forest region of Bangladesh,  
Performed evaluation of bioactivity and phytochemical screening of endophytic fungi isolated from selective Mangrove plant species.  
Report writing and manuscript publication.

### PROJECTS

[ 02/2024 – Current ]

**KIST-LIMS System Frameworks:** API: Kotlin, Springboot-JPA, PSQl; Flask-Sqlalchemy, UI: Typescript,React, MinIO, Docker.

Designed and implemented application architecture, data models, usecases, for the API-endpoints.  
Integrated microscopic image analysis API-clients dedicated to organoid-based toxicity screening platforms.

[ 12/2022 – 06/2023 ]

**MixTox Web Frameworks:** Rshiny, MySQL

Employs sigmoid functions to predict the cytotoxicity of a mixture of chemicals from the concentration-dependent effects of the individual chemicals.

Link: <https://mdka00001.shinyapps.io/mixtox/>

[ 08/2021 – 08/2021 ]

**Computational Epigenetics** Utilized the cloud infrastructure of German Network for Bioinformatics Infrastructure de.NBI to identify DEGs from RNA-seq data of human kidney and liver samples and integrate with ATAC-seq and ChIP-seq data.

## EDUCATION AND TRAINING

---

### Master of Science in Bioinformatics

**Saarland University** [ 01/04/2020 – 30/06/2024 ]

**City:** Saarbrücken | **Country:** Germany | **Thesis:** Identification and characterization of membrane transporter protein pores using AlphaFold proteins

Analyzed protein engineering on pore characteristics, membrane embedding properties and substrate transportation properties of transmembrane transporter protein structures and used ML classifiers to predict transporters by substrate type.

## PUBLICATIONS

---

### A combined in vitro-in silico method for assessing the androgenic activities of bisphenol A and its analogues

Park CG, Adnan KM, Cho H, Ryu CS, Yoon J, Kim YJ., Toxicology in Vitro. 2024 May 4:105838.

### Prediction of potential inhibitors for RNA-dependent RNA polymerase of SARS-CoV-2 using comprehensive drug repurposing and molecular docking approach

Parvez MS, Karim MA, Hasan M, Jaman J, Karim Z, Tahsin T, Hasan MN, Hosen MJ., International journal of biological macromolecules. 2020 Nov 15;163:1787-97.

### multi-omics analysis of bone morphogenetic protein 5 (BMP5) mRNA expression and clinical prognostic outcomes in different cancers using bioinformatics approaches

Karim MA, Samad A, Adhikari UK, Kader MA, Kabir MM, Islam MA, Hasan MN., Biomedicines. 2020 Jan 21;8(2):19.

## CONFERENCES AND SEMINARS

---

[ 02/2024 – 02/2024 ] Rome, Italy

**15th International Conference on Bioinformatics Models, Methods and Algorithms Poster presentation:** A Comparative Study of in silico Modeling Approaches for the Ligand-Binding Domain of Zebrafish Androgen Receptor and Empirical Evaluation.

[\[Poster link\]](#)

## RECOMMENDATIONS

---

**Name: Prof. Dr. Volkhard Helms** | Chair of Bioinformatics, Universität des Saarlandes

Thesis Supervisor

Email: [volkhard.helms@bioinformatik.uni-saarland.de](mailto:volkhard.helms@bioinformatik.uni-saarland.de) | Phone number: (+49) 68130270701

**Name: Dr. Michael Hutter** | Senior lecturer, Universität des Saarlandes

Thesis Co-supervisor

Email: [michael.hutter@bioinformatik.uni-saarland.de](mailto:michael.hutter@bioinformatik.uni-saarland.de) | Phone number: (+49) 68130270703