

Dr. Farman Ali

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Research gate:

<https://www.researchgate.net/profile/Farman-Ali-20/publications>

Google Scholar:

<https://scholar.google.co.uk/citations?user=GzlaocQAAAAJ&hl=en>

Scopus ID:

<https://www.scopus.com/authid/detail.uri?authorId=57224837156>

GitHub link: <https://github.com/farmanphd>

- HEC Approved PhD supervisor
- Total Published papers: **52**
- First author: **14**
- Corresponding author: **19**
- Co-author: **19**
- HEC **W** category journals: **38**
- HEC **X** category journals: **09**
- HEC **Y** category journals: **04**
- Conference papers: **01**
- Google citations: **2474**

Academic Information

Postdoctoral Computer Science

University of Jeddah, Saudi Arabia
Sep, 2021 – Aug, 2022

Ph.D. Computer Science & Technology

Nanjing University of Science & Technology, Nanjing, China
Oct, 2017 – Jun, 2021

M.S. Computer Science

Abdul Wali Khan University, Mardan, Pakistan
Dec, 2012 – Apr, 2015

M.Sc. Computer Science (2 years)

University of Peshawar, Pakistan
Nov, 2006 – Sep, 2008

B.Sc. Computer Science (2 years)

University of Peshawar, Pakistan
Sep, 2004 – Aug, 2006

Research Thesis

Ph.D. Thesis Title

Research on Prediction of DNA-binding Proteins Based on Efficient Computational Models

M.S. Thesis Title

Classification of Membrane Protein Types using Voting Feature Interval and Chou's Pseudo Amino Acid Composition

Professional Teaching Courses

Bachelor of Education (B.ED)

Abdul Wali Khan University Mardan, Pakistan
Apr, 2010 – Jun, 2011 (1 year)

Certificate of Teaching (C.T)

Allama Iqbal Open University, Islamabad, Pakistan
Aug, 2007 – Dec, 2008 (1 year)

Teaching Experience

A. Designation: **Assistant Professor**

Institute: Department of Computer Science, Bahria University Islamabad, Pakistan
Work from: since 01-04-2024 to still date

B. Designation: **Assistant Professor**

Institute: Department of Software Engineering, Sarhad University of Science and Information Technology Peshawar Mardan Campus, KPK, Pakistan
Work From: June, 2021 to 30-03-2024

Research Areas	Artificial Intelligence, Machine Learning, Bioinformatics, Deep Learning
Research Tools	Matlab, Python, Weka
Research experience	<p>I worked in Bioinformatics, Machine Learning, and Deep Learning research projects related to DNA, Peptides, Proteins, and medical images and published 51 research articles mostly in high impact factor and SCI journals with 2474 citations.</p> <p>In these projects, we developed novel computational methods using machine learning or deep learning algorithms for prediction of diverse biological problems including DNA/RNA (i.e., enhancers, and recombination spots, piwiRNA), Peptides (i.e., antifungal peptides, antitubercular peptides, neuropeptide, antifungal peptides, cell-penetrating peptides, and anticancer peptides), Proteins (i.e., growth hormone-binding proteins, DNA-binding proteins, druggable proteins, immunoglobulin proteins, amyloid proteins, antifreeze proteins, SARS CoV-2 Coronavirus proteins, bacteriophage virion proteins, angiogenic protein, antioxidant proteins, membrane protein types, mycobacterium tuberculosis, and extracellular Matrix proteins), and medical images (i.e., MR images).</p>
Editorial Board Member	<ul style="list-style-type: none"> Intelligence and Applications (https://ojs.bonviewpress.com/index.php/AIA/index)
Reviewer Services	<ol style="list-style-type: none"> Computer in Biology and Medicine IEEE Access Artificial Intelligence in Medicine Chemometrics and Intelligent Laboratory Systems Scientific Reports ACM Transactions on Intelligent Systems and Technology Neural Processing Letters
Research Paper Publications	<p><u>Paper publication in 2024</u></p> <p>[52] F. Ali, M Khalid, A. Almuhaimeed, A. Masmoudi, W. Alghamdi, A. Yafoz, "IP-GCN: A Deep Learning Model for Prediction of Insulin using Graph Convolutional Network for Diabetes Drug Design", <i>Journal of Computational Science</i> (2024), (SCIE, Q2, I.F=3.1)</p> <p>[51] F. Ali, A. Almuhaimeed, M Khalid, H. Alshanbari, A Masmoudi, R Alsini, "DEEP-EP: Identification of epigenetic protein by ensemble residual convolutional neural network for drug discovery", <i>Methods</i> (2024), (SCIE, Q2, I.F=4.8)</p> <p>[50] M Khalid, F. Ali, W Alghamdi, A Alzahrani, R Alsini, A Alzahrani, "An ensemble computational model for prediction of clathrin protein by coupling machine learning with discrete cosine transform", <i>Journal of Molecular Structure and Dynamics</i> (2024), (SCIE, Q2, I.F=4.4)</p>

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- [49] R. Alsini, A Almuhaimeed, **F. Ali**, M Khalid, M Farrash, A Masmoudi, "Deep-VEGF: deep stacked ensemble model for prediction of vascular endothelial growth factor by concatenating gated recurrent unit with two-dimensional convolutional neural network", *Journal of Molecular Structure and Dynamics* (2024), (**SCIE, Q2, I.F=4.4**)

Paper publication in 2023

- [48] O. Alghushairy, F. Ali, W. Alghamdi, M. Khalid, R. Alsini, O. Asiry, "Machine learning-based model for accurate identification of druggable proteins using light extreme gradient boosting", *Journal of Molecular Structure and Dynamics* (2023), (**SCIE, Q2, I.F=4.4**)
- [47] A. Adnan, W. Hongya, **F. Ali**, M. Khalid, O. Alghushairy, R. Alsini, "A bi-layer model for identification of piwiRNA using deep neural learning", *Journal of Molecular Structure and Dynamics* (2023), (**SCIE, Q2, I.F=4.4, Citations:1**)
- [46] **F. Ali**, W. Alghamdi, A. Almagrabi, O. Alghushairy, A. Banjar, M. Khalid, "Deep-AGP: Prediction of angiogenic protein by integrating two-dimensional convolutional neural network with discrete cosine transform", *International Journal of Biological Macromolecules* (2023), (**SCIE, Q1, I.F=8.02, Citations:2**)
- [45] S. Akbar, H. Mohamed, H. Ali, A. Saeed, A. Ahmed, S. Gul, A. Ahmed, **F. Ali** "Identifying Neuropeptides via Evolutionary and Sequential based Multi-perspective Descriptors by Incorporation with Ensemble Classification Strategy", *IEEE Access*, (2023), (**SCIE, Q2, I.F=3.47, Citations:9**)
- [44] **F. Ali**, H. Kumar, W. Alghamdi, F. Kateb, F. Alarfaj, "Recent Advances in Machine Learning-Based Models for Prediction of Antiviral Peptides", *Archives of Computational Methods in Engineering*, (2023), (**SCIE, Q1, I.F=9.7, Citations:4**)
- [43] S. Akbar, H. Ali, A. Ahmad, M. Sarker, A. Saeed, E. Salwana, S. Gul, A. Khan, **F. Ali** "Prediction of Amyloid Proteins Using Embedded Evolutionary & Ensemble Feature Selection Based Descriptors With eXtreme Gradient Boosting Model", *IEEE Access*, (2023), (**SCIE, Q2, I.F=3.47, Citations:6**)
- [42] G. Ali, Z. Swati, **F. Ali**, S. Tunio, N. Jabeen, N. Iqbal, "DeepImmuno-PSSM: Identification of Immunoglobulin based on Deep learning and PSSM-Profiles" *VAWKUM Transactions on Computer Sciences*, (2023), (**I.F=0, Citations:4**)
- [41] A. Khan, J. Uddin, **F. Ali**, H. Kumar, W. Alghushairy, A. Ahmad, "AFP-SPTS: Accurate Prediction of Antifreeze Proteins using Sequential and Pseudo Tri-Slicing Evolutionary Features with Extremely Randomized Tree", *Journal of Chemical Information and Modeling*, (2023), (**SCIE, Q1, I.F=6.06, Citations:6**)

Paper publication in 2022

- [40] A. Khan, J. Uddin, **F. Ali**, A. Ahmad, O. Alghushairy, A. Banjar, A. Daud, "Prediction of antifreeze proteins using machine learning", *Scientific Reports*. 12(1), 1-10, (**SCIE, Q2, I. F=5, Citations:7**)
- [39] A. Khan, J. Uddin, **F. Ali**, A. Banjar, A. Daud, "Comparative analysis of the existing methods for prediction of antifreeze proteins", *Chemometrics and Intelligent Laboratory Systems*, (2022), 104729. (**SCIE, Q2, I. F=4.17, Citations:7**)
- [38] S. Rahu, A. Ghulam, **F. Ali**, "Ubi-Xgb: Identification Of Ubiquitin Proteins Using Machine Learning Model" *Journal of Mountain Area Research*, (2022), 8, 14-26. (**Citations:6**)
- [37] A. Banjar, **F. Ali**, O. Alghushairy, A. Daud, "iDBP-PBMD: A machine learning model for detection of DNA-binding proteins by extending compression techniques into evolutionary profile" *Chemometrics and Intelligent Laboratory Systems*, (2022), 231, 104697. (**SCIE, Q2, I. F=4.17, Citations:6**)
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- [36] S. Akbar, **F. Ali**, M. Hayat, A. Ahmad, S. Khan, S. Gul "Prediction of Antiviral peptides using transform evolutionary & SHAP analysis based descriptors by incorporation with ensemble learning strategy", *Chemometrics and Intelligent Laboratory Systems*, (2022), 104682. (**SCIE, Q2, I. F=4.17, Citations:18**)
 - [35] **F. Ali**, O. Barukab, A.B. Gadicha, S. Patil, O. Alghushairy, A.Y. Sarhan " DBP-iDWT: Improving DNA-Binding Proteins Prediction Using Multi-Perspective Evolutionary Profile and Discrete Wavelet Transform" *Computational Intelligence and Neuroscience* (2022), 2987407. (**SCIE, Q2, I. F=3.01, Citations:7**)
 - [34] **F. Ali**, H. Kumar, S. Patil, A. Ahmad, A. Babour, A. Daud "Deep-GHBP: Improving prediction of Growth Hormone-binding proteins using deep learning model", *Biomedical Signal Processing and Control*, (2022), 78, 103856. (**SCIE, Q2, I. F=5.076, Citations:13**)
 - [33] **F. Ali**, H. Kumar, S. Patil, A. Ahmed, A. Banjar, A. Daud, "DBP-DeepCNN: Prediction of DNA-binding proteins using wavelet-based denoising and deep learning" *Chemometrics and Intelligent Laboratory Systems*, (2022), 229, 104639, (**SCIE, Q2, Elsevier Journal, I. F=4.17**)
 - [32] A. Ghulam, R. Sikandar, **F. Ali**, "AI and Machine Learning-based practices in various domains: A Survey", *VAWKUM Transactions on Computer Sciences*, (2022) (**Citations:5**)
 - [31] A. Ghulam, **F. Ali**, R. Sikandar, A. Ahmad, A. Ahmed, S. Patil "ACP-2DCNN: Deep learning-based model for improving prediction of anticancer peptides using two-dimensional convolutional neural network", *Chemometrics and Intelligent Laboratory Systems*, (2022), 226, 104589. (**SCIE, Q2, I. F=4.17, Citations:25**)
 - [30] **F. Ali**, H. Kumar, S. Patil, K. Kotecha, A. Banjar, A. Daud "Target-DBPPred: An intelligent model for prediction of DNA-binding proteins using discrete wavelet transform based compression and light eXtreme gradient boosting", *Computers in Biology and Medicine*, (2022), 145, 105533 (**SCIE, Q1, I. F=6.698, Citations:13**)
 - [29] S. Rahu, A. Ghulam, **F. Ali** "XGB-DrugPred: computational prediction of druggable proteins using eXtreme gradient boosting and optimized features set", *Scientific Reports*, (2022), 12 (1), 1-9. (**SCIE, Q2, I.F=5, Citations:33**)
 - [28] O. Barukab, **F. Ali**, W. Alghamdi, Y. Bassam, S.A. Khan, " DBP-CNN: Deep Learning-based Prediction of DNA-binding Proteins by Coupling Discrete Cosine Transform with Two-dimensional Convolutional Neural Network", *Expert Systems with Applications*, (2022), 116729. (**SCIE, Q1, I. F=8.665, Citations:24**)
 - [27] A. Ghulam, S. Rahu, **F. Ali**, Z.N.K. Swati, A. Unar, D.B. Talpur " Accurate prediction of immunoglobulin proteins using machine learning model", *Informatics in Medicine Unlocked*, (2022), 29, 100885. (**I. F= 3.37, Citations:20**)
 - [26] A. Ahmad, S. Akbar, M.Tahir, M. Hayat, **F. Ali**, " iAFPs-EnC-GA: Identifying antifungal peptides using sequential and evolutionary descriptors based multi-information fusion and ensemble learning approach" *Chemometrics and Intelligent Laboratory Systems*, (2022), 222, 104516. (**SCIE, Q2, I. F=4.17, Citations:39**)

Paper publication in 2021

- [25] Adnan, **F. Ali**, A. Ghulam, Z. A. Maher, M.A.Khan, and W.Hongya, "Deep-PCL: A deep learning model for prediction of cancerlectins and non cancerlectins using optimized integrated features". *Chemometrics and Intelligent Laboratory Systems*, (2021), 221, 104484 (**SCIE, Q2, I. F=4.17, Citations:15**)
 - [24] **F. Ali**, S. Akbar, A. Ghulam, Z. A. Maher, A. Unar, and D. B. Talpur, "AFP-CMBPred: Computational identification of antifreeze proteins by extending consensus sequences into multi-blocks evolutionary information," *Computers in Biology and Medicine*, (2021),139, 105006. (**SCIE, Q1, I. F=6.69, Citations:34**)
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- [23] O. Barukab, **F. Ali**, and S. A. Khan, "DBP-GAPred: An intelligent method for prediction of DNA-binding proteins types by enhanced evolutionary profile features with ensemble learning," *Journal of Bioinformatics and Computational Biology*, (2021), 19, 2150018. **(SCIE, Q4, I. F=1.20, Citations:24)**
- [22] S. Akbar, A. Ahmad, M. Hayat, A. U. Rehman, S. Khan, and **F. Ali**, "iAtbP-Hyb-EnC: Prediction of Antitubercular peptides Via Heterogeneous Feature Representation and Genetic Algorithm based Ensemble Learning Model," *Computers in Biology and Medicine*, (2021), 137, 104778. **(SCIE, Q1, I. F=6.69, Citations:49)**
- [21] Z. U. Khan, D. Pi, S. Yao, A. Nawaz, **F. Ali**, and S. Ali, " piEnPred: a bi-layered discriminative model for enhancers and their subtypes via novel cascade multi-level subset feature selection algorithm", *Frontiers of Computer Science*, (2021), 15, 1-11. **(SCIE, Q2, I. F=2.56, Citations:28)**
- [20] A. Ghulam, M. Memon, **F. Ali**, Identification of Novel Protein Sequencing SARS CoV-2 Coronavirus Using Machine Learning, *Bioscience Research*, (2021), 18(SI-1): 47-58. **(I. F=0.737, Citations:6)**
- [19] I.A Khan, D. Pi, N. Khan, A. Nawaz, **F. Ali**, A privacy-conserving framework based intrusion detection method for detecting and recognizing malicious behaviours in cyber-physical power networks, *Applied Intelligence*, (2021), 51, 7306–7321. **(SCIE, Q2, I. F=5.01, Citations:49)**
- [18] A. Ahmad, S. Akbar, S. Khan, M. Hayat, **F. Ali**, A. Ahmed, M. Tahir, Deep-AntiFP: Prediction of antifungal peptides using discriminative multi-informative features incorporating with deep neural networks, *Chemometrics and Intelligent Laboratory Systems*, (2020), 208, 104214. **(SCIE, Q2, I. F=4.17, Citations:57)**

Paper publication in 2020

- [17] S. Akbar, S. Khan, **F. Ali**, M. Hayat, M. Qasim, S. Gul, iHBP-DeepPSSM: Identifying hormone binding proteins using PsePSSM based evolutionary features and deep learning approach, *Chemometrics and Intelligent Laboratory Systems*, (2020) 204,104103. **(SCIE, Q2, I. F=4.17, Citations:58)**
- [16] M. Arif, **F. Ali**, S. Ahmad, M. Kabir, Z. Ali, M. Hayat, Pred-BVP-Unb: Fast prediction of bacteriophage Virion proteins using un-biased multi-perspective properties with recursive feature elimination, *Genomics*, 112 (2020) 1565-1574. **(SCIE, Q2, I. F=4.31, Citations:42)**
- [15] M. Arif, S. Ahmad, **F. Ali**, G. Fang, M. Li, D.-J. Yu, TargetCPP: accurate prediction of cell-penetrating peptides from optimized multi-scale features using gradient boost decision tree, *Journal of Computer-Aided Molecular Design*, (2020) 34, 841–856. **(SCIE, Q2, I. F=4.13, Citations:46)**
- [14] A. Ahmad, S. Akbar, M. Hayat, **F. Ali**, M Sohail, Identification of antioxidant proteins using a discriminative intelligent model of k-spaced amino acid pairs based descriptors incorporating with ensemble feature selection, *Biocybernetics and Biomedical Engineering*, (2020), 42, 727-735. **(SCIE, Q2, I. F=5.68, Citations:26)**

Paper publication in 2019

- [13] **F. Ali**, M. Arif, Z.U. Khan, M. Kabir, S. Ahmed, D.-J. Yu, SDBP-Pred: Prediction of single-stranded and double-stranded DNA-binding proteins by extending consensus sequence and K-segmentation strategies into PSSM, *Analytical biochemistry*, 589, (2019) 113494. **(SCIE, Q3, I. F=3.19, Citations:31)**
- [12] **F. Ali**, S. Ahmed, Z.N.K. Swati, S. Akbar, DP-BINDER: machine learning model for prediction of DNA-binding proteins by fusing evolutionary and physicochemical information, *Journal of Computer-Aided Molecular Design*, 33, 645–658 **(SCIE, Q2, I. F=4.13, Citations:52)**
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- [11] Z.U. Khan, **F. Ali**, I.A. Khan, Y. Hussain, D. Pi, iRSpot-SPI: Deep learning-based recombination spots prediction by incorporating secondary sequence information coupled with physio-chemical properties via Chou's 5-step rule and pseudo components, *Chemometrics and Intelligent Laboratory Systems*, 189 169-180 (**SCIE, Q2, I. F=4.17, Citations:65**)
 - [10] Z.U. Khan, **F. Ali**, I. Ahmad, M. Hayat, D. Pi, iPredCNC: Computational prediction model for cancerlectins and non-cancerlectins using novel cascade features subset selection, *Chemometrics and Intelligent Laboratory Systems*, 195 (2019) 103876. (**SCIE, Q2, I. F=4.17, Citations:28**)
 - [9] M. Kabir, M. Arif, **F. Ali**, S. Ahmad, Z.N.K. Swati, D.-J. Yu, Prediction of membrane protein types by exploring local discriminative information from evolutionary profiles, *Analytical biochemistry*, 564 (2019) 123-132. (**SCIE, Q3, I. F=3.19, Citations:22**)
 - [8] Z.N.K. Swati, Q. Zhao, M. Kabir, **F. Ali**, Z. Ali, S. Ahmed, J. Lu, Content-Based Brain Tumor Retrieval for MR Images Using Transfer Learning, *IEEE Access*, 7 (2019) 17809-17822. (**SCIE, Q2, I. F=3.47, Citations:180**)
 - [7] Z.N.K. Swati, Q. Zhao, M. Kabir, **F. Ali**, Z. Ali, S. Ahmed, J. Lu, Brain tumor classification for MR images using transfer learning and fine-tuning, *Computerized Medical Imaging and Graphics*, 75 (2019), 34-46. (**SCIE, Q1, I. F=7.42, Citations:523**)

Paper publication in 2018

- [6] **F. Ali**, M. Kabir, M. Arif, Z.N.K. Swati, Z.U. Khan, M. Ullah, D.-J. Yu, DBPPred-PDSD: Machine Learning Approach for Prediction of DNA-binding Proteins using Discrete Wavelet Transform and Optimized Integrated Features Space, *Chemometrics and Intelligent Laboratory Systems*, 182 (2018), 21-30. (**SCIE, Q2, I. F=4.17, Citations:50**)
- [5] M. Ullah, A. Iltaf, Q. Hou, **F. Ali**, C. Liu, A Foreground Extraction Approach Using Convolutional Neural Network with Graph Cut, *2018 IEEE 3rd International Conference on Image, Vision and Computing (ICIVC)*, IEEE, 2018, pp. 40-44. (**Citations:18**)
- [4] S. Ahmed, M. Kabir, Z. Ali, M. Arif, **F. Ali**, D.-J. Yu, An Integrated Feature Selection Algorithm for Cancer Classification using Gene Expression Data, *Combinatorial chemistry & high throughput screening*, 21 (2018), 631-645. (**SCIE, Q3, I. F=1.71, Citations:20**)
- [3] S. Ahmed, M. Kabir, M. Arif, Z. Ali, **F. Ali**, Z.N.K. Swati, Improving secretory proteins prediction in Mycobacterium tuberculosis using the unbiased dipeptide composition with support vector machine, *International Journal of Data Mining and Bioinformatics*, 21 (2018) 212-229. (**SCIE, Q4, I. F=0.66, Citations:16**)

Paper publication in 2016

- [2] **F. Ali**, M. Hayat, Machine learning approaches for discrimination of Extracellular Matrix proteins using hybrid feature space, *Journal of theoretical biology*, 403 (2016), 30-37. (**SCIE, Q3, I. F=2.40, Citations:40**)

Paper publication in 2015

- [1] **F. Ali**, M. Hayat, Classification of membrane protein types using voting feature interval in combination with Chou' s pseudo amino acid composition, *Journal of theoretical biology*, 384 (2015) 78-83. (**SCIE, Q3, I. F=2.40, Citations:151**)

Students supervised	PhD students: 01
	MS students: 02

List of Projects Participated	[1] National Natural Science Foundation of China (No. 61772273, 61373062). [2] Natural Science Foundation of Jiangsu (No. BK20141403). [3] Fundamental Research Funds for the Central Universities (No. 30916011327) [4] Deanship of Scientific Research at King Khalid University (No. RGP.1/85/42)
Awards	Achieved Chinese Govt. Scholarship for PhD study in 2017
Language	English (Good) , Urdu (Excellent) , Pashto (Excellent)