LIST OF PUBLICATIONS

Refereed Journal Papers

- **Ritesh Sharma**, Sanjay Kumar Singh, et al. "Deep-AVPpred: Artificial intelligence driven discovery of peptide drugs for viral infections." IEEE Journal of Biomedical and Health Informatics 26.10 (2021): 5067-5074. **(SCIE, Q1, IF 7.021)**

- **Ritesh Sharma**, Sanjay Kumar Singh, et al. "Deep-AFPpred: identifying novel antifungal peptides using pretrained embeddings from seq2vec with 1DCNN-BiLSTM." Briefings in Bioinformatics 23.1 (2022): bbab422. **(SCIE, Q1, IF 13.994)**

- **Ritesh Sharma**, Sanjay Kumar Singh, et al. "EnDL-HemoLyt: Ensemble Deep Learning-based Tool for Identifying Therapeutic Peptides with Low Hemolytic Activity." IEEE Journal of Biomedical and Health Informatics (2023) : DOI-10.1109/JBHI.2023.3264941 **(SCIE, Q1, IF 7.021)**

- **Ritesh Sharma**, Sanjay Kumar Singh, et al. "Artificial intelligence-based model for predicting the minimum inhibitory concentration of antibacterial peptides against ESKAPEE pathogens" IEEE Journal of Biomedical and Health Informatics (2023) : Accepted for Publication **(SCIE, Q1, IF 7.021)**

- **Ritesh Sharma**, Sanjay Kumar Singh, et al. "XAI-INVENT: An explainable artificial intelligence based framework for rapid discovery of novel peptide antibiotics." Briefings in Bioinformatics (Under Review) **(SCIE, Q1, IF 13.994)**

Bibliography

[1] "Antibiotic Resistance (ABR) - PREVENT IT Project." [Online]. Available: https://preventit.in/about/antibiotic-resistance-prevention/

[2] "Ai machine learning in drug discovery development (2022)." [Online]. Available: https://www.insiderintelligence.com/insights/ai-machine-learning-in-drug-discovery-development/

[3] M. M. Hasan, N. Schaduangrat, S. Basith, G. Lee, W. Shoombuatong, and B. Manavalan, "Hlppred-fuse: improved and robust prediction of hemolytic peptide and its activity by fusing multiple feature representation," *Bioinformatics*, 2020, vol. 36, no. 11, pp. 3350–3356.

[4] T. S. Win, A. A. Malik, V. Prachayasittikul, J. E. S Wikberg, C. Nantasenamat, and W. Shoombuatong, "Hemopred: a web server for predicting the hemolytic activity of peptides," *Future medicinal chemistry*, 2017, vol. 9, no. 3, pp. 275–291.

[5] K. Chaudhary, R. Kumar, S. Singh, A. Tuknait, A. Gautam, D. Mathur, P. Anand, G. C. Varshney, and G. P. Raghava, "A web server and mobile app for computing hemolytic potency of peptides," *Scientific reports*, 2016, vol. 6, no. 1, p. 22843.

[6] C. Lea, R. Vidal, A. Reiter, and G. D. Hager, "Temporal convolutional networks: A unified approach to action segmentation," 2016.

[7] C. Lea, M. D. Flynn, R. Vidal, A. Reiter, and G. D. Hager, "Temporal convolutional networks for action segmentation and detection," in *proceedings of the IEEE Conference on Computer Vision and Pattern Recognition*, 2017, pp. 156–165.

[8] F. Yu and V. Koltun, "Multi-scale context aggregation by dilated convolutions," *arXiv preprint arXiv:1511.07122*, 2015.

[9] A. v. d. Oord, S. Dieleman, H. Zen, K. Simonyan, O. Vinyals, A. Graves, N. Kalchbrenner, A. Senior, and K. Kavukcuoglu, "Wavenet: A generative model for raw audio," *arXiv preprint arXiv:1609.03499*, 2016.

[10] R. Singh, V. Bharti, V. Purohit, A. Kumar, A. K. Singh, and S. K. Singh, "Metamed: Few-shot medical image classification using gradient-based meta-learning," *Pattern Recognition*, 2021, vol. 120, p. 108111. [Online]. Available: https://www.sciencedirect.com/science/article/pii/S0031320321002983

[11] E. S. Olivas, J. D. M. Guerrero, M. Martinez-Sober, J. R. Magdalena-Benedito, L. Serrano *et al.*, *Handbook of research on machine learning applications and trends: Algorithms, methods, and techniques.* IGI Global, 2009.

[12] I. Goodfellow, Y. Bengio, and A. Courville, *Deep learning.* MIT Press, 2016.

[13] J. Brownlee, *Deep learning for computer vision: image classification, object detection, and face recognition in python.* Machine Learning Mastery, 2019.

[14] M. Heinzinger, A. Elnaggar, Y. Wang, C. Dallago, D. Nechaev, F. Matthes, and B. Rost, "Modeling aspects of the language of life through transfer-learning protein sequences," *BMC bioinformatics*, 2019, vol. 20, no. 1, pp. 1–17.

[15] A. Rives, J. Meier *et al.*, "Biological structure and function emerge from scaling unsupervised learning to 250 million protein sequences," *Proceedings of the National Academy of Sciences*, 2021, vol. 118, no. 15.

[16] D. P. Kingma and J. Ba, "Adam: A method for stochastic optimization," *arXiv preprint arXiv:1412.6980*, 2014.

[17] P. K. Meher, T. K. Sahu, V. Saini, and A. R. Rao, "Predicting antimicrobial peptides with improved accuracy by incorporating the compositional, physico-chemical and structural features into chou's general pseaac," *Scientific reports*, 2017, vol. 7, no. 1, pp. 1–12.

[18] P. Agrawal, S. Bhalla, K. Chaudhary, R. Kumar, M. Sharma, and G. P. Raghava, "In silico approach for prediction of antifungal peptides," *Frontiers in microbiology*, 2018, vol. 9, p. 323.

[19] A. Tyagi, S. Roy, S. Singh, M. Semwal, A. K. Shasany, A. Sharma, and I. Provazník, "Phytoafp: In silico approaches for designing plant-derived antifungal peptides," *Antibiotics*, 2021, vol. 10, no. 7, p. 815.

[20] N. Thakur, A. Qureshi *et al.*, "Avppred: collection and prediction of highly effective antiviral peptides," *Nucleic acids research*, 2012, vol. 40, no. W1, pp. W199–W204.

[21] N. Schaduangrat, C. Nantasenamat *et al.*, "Meta-iavp: a sequence-based meta-predictor for improving the prediction of antiviral peptides using effective feature representation," *International journal of molecular sciences*, 2019, vol. 20, no. 22, p. 5743.

[22] Y. Pang, L. Yao *et al.*, "Avpiden: a new scheme for identification and functional prediction of antiviral peptides based on machine learning approaches," *Briefings in Bioinformatics*, 2021.

[23] P. B. Timmons and C. M. Hewage, "Ennavia is a novel method which employs neural networks for antiviral and anti-coronavirus activity prediction for therapeutic peptides," *Briefings in Bioinformatics*, 2021.

[24] C. J. Bartel, "Data-centric approach to improve machine learning models for inorganic materials," *Patterns*, 2021, vol. 2, no. 11, p. 100382.

[25] L. Xu, J. Liu *et al.*, "Dataclue: A benchmark suite for data-centric nlp," *arXiv preprint arXiv:2111.08647*, 2021.

[26] A. Ng, "Data-centric ai competition." [Online]. Available: https://https-deeplearning-ai.github.io/data-centric-comp

[27] ——, "Mlops: From model-centric to data-centric ai." [Online]. Available: www.deeplearning.ai/wp-content/uploads/2021/06/MLOps-From-Model-centric-to-Data-centric-AI.pdf

[28] G. Campbell-Platt and P. Cook, "Fungi in the production of foods and food ingredients," *Journal of applied bacteriology*, 1989, vol. 67, pp. 117s–131s.

[29] N. P. Money, "Chapter 12 - fungi and biotechnology," in *The Fungi (Third Edition)*, third edition ed., S. C. Watkinson, L. Boddy, and N. P. Money, Eds. Boston: Academic Press, 2016, pp. 401–424. [Online]. Available: https://www.sciencedirect.com/science/article/pii/B9780123820341000128

[30] D. Mukherjee, S. Singh, M. Kumar, V. Kumar, S. Datta, and D. S. Dhanjal, "Fungal biotechnology: Role and aspects," in *Fungi and their Role in Sustainable Development: Current Perspectives*, P. Gehlot and J. Singh,

Eds. Singapore: Springer Singapore, 2018, pp. 91–103. [Online]. Available: https://doi.org/10.1007/978-981-13-0393-7$_6$

[31] M. Fernández de Ullivarri, S. Arbulu, E. Garcia-Gutierrez, and P. D. Cotter, "Antifungal peptides as therapeutic agents," *Frontiers in Cellular and Infection Microbiology*, 2020, vol. 10, p. 105.

[32] T. Roemer and D. J. Krysan, "Antifungal drug development: challenges, unmet clinical needs, and new approaches," *Cold Spring Harbor perspectives in medicine*, 2014, vol. 4, no. 5, p. a019703.

[33] F. Bongomin, G. S. O. RO, and D. Denning, "Hiv–associated cryptococcal disease in resource-limited setting: A case for prevention is better than cure," *Global and Multi-National Prevalence of Fungal Diseases—Estimate Precision. J Fungi*, 2017, vol. 3, p. 57.

[34] M. H. Miceli, J. A. Díaz, and S. A. Lee, "Emerging opportunistic yeast infections," *The Lancet infectious diseases*, 2011, vol. 11, no. 2, pp. 142–151.

[35] T. Chen and C. Guestrin, "Xgboost: A scalable tree boosting system," in *Proceedings of the 22nd acm sigkdd international conference on knowledge discovery and data mining*, 2016, pp. 785–794.

[36] C. Cortes and V. Vapnik, "Support-vector networks," *Machine learning*, 1995, vol. 20, no. 3, pp. 273–297.

[37] L. Breiman, "Random forests," *Machine learning*, 2001, vol. 45, no. 1, pp. 5–32.

[38] D. G. Kleinbaum and M. Klein, *Logistic regression: a self-learning text.* Boston, MA: Springer Science & Business Media, 2010.

[39] I. Rish *et al.*, "An empirical study of the naive bayes classifier," in *IJCAI 2001 workshop on empirical methods in artificial intelligence*, vol. 3, no. 22, 2001, pp. 41–46.

[40] T. Cover and P. Hart, "Nearest neighbor pattern classification," *IEEE transactions on information theory*, 1967, vol. 13, no. 1, pp. 21–27.

[41] F. H. Waghu, R. S. Barai, P. Gurung, and S. Idicula-Thomas, "Campr3: a database on sequences, structures and signatures of antimicrobial peptides," *Nucleic acids research*, 2016, vol. 44, no. D1, pp. D1094–D1097.

[42] X. Kang, F. Dong, C. Shi, S. Liu, J. Sun, J. Chen, H. Li, H. Xu, X. Lao, and H. Zheng, "Dramp 2.0, an updated data repository of antimicrobial peptides," *Scientific data*, 2019, vol. 6, no. 1, pp. 1–10.

[43] L. Aguilera-Mendoza, Y. Marrero-Ponce, J. A. Beltran, R. Tellez Ibarra, H. A. Guillen-Ramirez, and C. A. Brizuela, "Graph-based data integration from bioactive peptide databases of pharmaceutical interest: toward an organized collection enabling visual network analysis," *Bioinformatics*, 04 2019, vol. 35, no. 22, pp. 4739–4747.

[44] L. Aguilera-Mendoza, Y. Marrero-Ponce, C. R. García-Jacas, E. Chavez, J. A. Beltran, H. A. Guillen-Ramirez, and C. A. Brizuela, "Automatic construction of molecular similarity networks for visual graph mining in chemical space of bioactive peptides: an unsupervised learning approach," *Scientific reports*, 2020, vol. 10, no. 1, pp. 1–23.

[45] U. Consortium, "Uniprot: a worldwide hub of protein knowledge," *Nucleic acids research*, 2019, vol. 47, no. D1, pp. D506–D515.

[46] G. Chen, P. Chen, Y. Shi, C.-Y. Hsieh, B. Liao, and S. Zhang, "Rethinking the usage of batch normalization and dropout in the training of deep neural networks," *arXiv preprint arXiv:1905.05928*, 2019.

[47] M. Ward, C.-H. Min, H. Salamy, and K. Nepal, "Dilated temporal convolutional neural network architecture with independent component layer for human activity recognition," 11 2019, pp. 49–52.

[48] F. Chollet, "Keras," https://github.com/fchollet/keras, 2015.

[49] F. Pedregosa, G. Varoquaux, A. Gramfort, V. Michel, B. Thirion, O. Grisel, M. Blondel, P. Prettenhofer, R. Weiss, V. Dubourg, J. Vanderplas, A. Passos, D. Cournapeau, M. Brucher, M. Perrot, and E. Duchesnay, "Scikit-learn: Machine learning in Python," *Journal of Machine Learning Research*, 2011, vol. 12, pp. 2825–2830.

[50] D. Wheeler, "Selecting the right protein-scoring matrix," 2002.

[51] R. Agarwala, T. Barrett, and et al., "Database resources of the National Center for Biotechnology Information," *Nucleic Acids Research*, jan 2018, vol. 46, no. D1, pp. D8–D13.

[52] C. Vens, M.-N. Rosso, and E. G. Danchin, "Identifying discriminative classification-based motifs in biological sequences," *Bioinformatics*, 2011, vol. 27, no. 9, pp. 1231–1238.

[53] P. Gogoi, S. Shrivastava, P. Shah, S. Saxena, S. Srivastava, and G. K. Gaur, "Linear and branched forms of short antimicrobial peptide-irk inhibit growth of multi drug resistant staphylococcus aureus isolates from mastitic cow milk," *International Journal of Peptide Research and Therapeutics*, 2021, pp. 1–11.

[54] P. Shah, S. Shrivastava, R. James Singh, P. Gogoi, S. Saxena, S. Srivastava, N. Kumar, and G. K. Gaur, "Synthetic antimicrobial peptide polybia mp-1 (mastoparan) inhibits growth of antibiotic resistant pseudomonas aeruginosa isolates from mastitic cow milk," *International Journal of Peptide Research and Therapeutics.*

[55] S. Gupta, S. Shrivastava, R. J. Singh, P. Gogoi, B. Kumar *et al.*, "Evaluation of antibacterial activity of magainin and mastoparan and its novel hybrid against mdr e. coli isolates of neonatal calves," *International Journal of Peptide Research and Therapeutics*, 2021, vol. 27, no. 2, pp. 1111–1119.

[56] M. Cascella, M. Rajnik *et al.*, "Features, evaluation, and treatment of coronavirus (covid-19)," *StatPearls*, 2021.

[57] D. E. Bloom and D. Cadarette, "Infectious disease threats in the twenty-first century: strengthening the global response," *Frontiers in immunology*, 2019, vol. 10, p. 549.

[58] N. D. Grubaugh and o. Ladner, "Tracking virus outbreaks in the twenty-first century," *Nature microbiology*, 2019, vol. 4, no. 1, pp. 10–19.

[59] A. Zappa, A. Amendola *et al.*, "Emerging and re-emerging viruses in the era of globalisation," *Blood transfusion*, 2009, vol. 7, no. 3, p. 167.

[60] T. S. Torres, S. W. Cardoso *et al.*, "Incidence rate of modifying or discontinuing first combined antiretroviral therapy regimen due to toxicity during the first year of treatment stratified by age," *Brazilian Journal of Infectious Diseases*, 2014, vol. 18, pp. 34–41.

[61] Z. Sthoeger and K. Mahlab-Guri, "Aids-an old disease with new challenges," *Harefuah*, 2013, vol. 152, no. 4, pp. 194–5.

[62] H. Madanchi, M. Shoushtari *et al.*, "Antimicrobial peptides of the vaginal innate immunity and their role in the fight against sexually transmitted diseases," *New microbes and new infections*, 2020, vol. 34, p. 100627.

[63] G. Castel, M. Chtéoui *et al.*, "Phage display of combinatorial peptide libraries: application to antiviral research," *Molecules*, 2011, vol. 16, no. 5, pp. 3499–3518.

[64] M. Pirtskhalava, A. Gabrielian *et al.*, “Dbaasp v. 2: an enhanced database of structure and antimicrobial/cytotoxic activity of natural and synthetic peptides,” *Nucleic acids research*, 2016, vol. 44, no. D1, pp. D1104–D1112.

[65] G. Shi, X. Kang *et al.*, “Dramp 3.0: an enhanced comprehensive data repository of antimicrobial peptides,” *Nucleic Acids Research*, 2021.

[66] S. Singh, K. Chaudhary *et al.*, “Satpdb: a database of structurally annotated therapeutic peptides,” *Nucleic acids research*, 2016, vol. 44, no. D1, pp. D1119–D1126.

[67] L. Aguilera-Mendoza, Y. Marrero-Ponce *et al.*, “Graph-based data integration from bioactive peptide databases of pharmaceutical interest: toward an organized collection enabling visual network analysis,” *Bioinformatics*, 2019, vol. 35, no. 22, pp. 4739–4747.

[68] T. U. Consortium, “UniProt: the universal protein knowledgebase in 2021,” *Nucleic Acids Research*, 11 2020, vol. 49, no. D1, pp. D480–D489.

[69] R. Sharma, S. Shrivastava *et al.*, “Deep-ABPpred: identifying antibacterial peptides in protein sequences using bidirectional LSTM with word2vec,” *Briefings in Bioinformatics*, 03 2021, vol. 22, no. 5.

[70] ——, “AniAMPpred: artificial intelligence guided discovery of novel antimicrobial peptides in animal kingdom,” *Briefings in Bioinformatics*, 07 2021. [Online]. Available: https://doi.org/10.1093/bib/bbab242

[71] V. Singh, S. Shrivastava *et al.*, “StaBle-ABPpred: a stacked ensemble predictor based on biLSTM and attention mechanism for accelerated discovery of antibacterial peptides,” *Briefings in Bioinformatics*, 11 2021, bbab439. [Online]. Available: https://doi.org/10.1093/bib/bbab439

[72] Y. Huang, B. Niu *et al.*, “Cd-hit suite: a web server for clustering and comparing biological sequences,” *Bioinformatics*, 2010, vol. 26, no. 5, pp. 680–682.

[73] N. Xiao, D.-S. Cao, M.-F. Zhu, and Q.-S. Xu, “protr/protrweb: R package and web server for generating various numerical representation schemes of protein sequences,” *Bioinformatics*, 2015, vol. 31, no. 11, pp. 1857–1859.

[74] A. T. Müller, G. Gabernet, J. A. Hiss, and G. Schneider, “modlamp: Python for antimicrobial peptides,” *Bioinformatics*, 2017, vol. 33, no. 17, pp. 2753–2755.

[75] A. Isaacs, J. Lindenmann *et al.*, “Virus interference. ii. some properties of interferon,” *Proceedings of the Royal Society of London. Series B-Biological Sciences*, 1957, vol. 147, no. 927, pp. 268–273.

[76] F.-c. Lin and H. A. Young, “Interferons: success in anti-viral immunotherapy,” *Cytokine & growth factor reviews*, 2014, vol. 25, no. 4, pp. 369–376.

[77] H. Zhou, S. Chen *et al.*, “Interferons and their receptors in birds: a comparison of gene structure, phylogenetic analysis, and cross modulation,” *International Journal of Molecular Sciences*, 2014, vol. 15, no. 11, pp. 21 045–21 068.

[78] L.-J. Zhao, S.-F. He *et al.*, “Inhibition of stat pathway impairs anti-hepatitis c virus effect of interferon alpha,” *Cellular Physiology and Biochemistry*, 2016, vol. 40, no. 1-2, pp. 77–90.

[79] K. Gibbert, J. Schlaak *et al.*, “Ifn-α subtypes: distinct biological activities in anti-viral therapy,” *British journal of pharmacology*, 2013, vol. 168, no. 5, pp. 1048–1058.

[80] L. A. Pinto, V. Blazevic *et al.*, “Inhibition of human immunodeficiency virus type 1 replication prior to reverse transcription by influenza virus stimulation,” *Journal of virology*, 2000, vol. 74, no. 10, pp. 4505–4511.

[81] H. Jenssen, P. Hamill, and R. E. Hancock, “Peptide antimicrobial agents,” *Clinical microbiology reviews*, 2006, vol. 19, no. 3, pp. 491–511.

[82] M. R. Yeaman and N. Y. Yount, “Mechanisms of antimicrobial peptide action and resistance,” *Pharmacological reviews*, 2003, vol. 55, no. 1, pp. 27–55.

[83] K. A. Brogden, “Antimicrobial peptides: pore formers or metabolic inhibitors in bacteria?” *Nature reviews microbiology*, 2005, vol. 3, no. 3, pp. 238–250.

[84] F. H. Waghu, R. S. Barai, P. Gurung, and S. Idicula-Thomas, “Campr3: a database on sequences, structures and signatures of antimicrobial peptides,” *Nucleic acids research*, 2016, vol. 44, no. D1, pp. D1094–D1097.

[85] B. G. D. L. Torre and F. Albericio, “Peptide therapeutics 2.0,” *Molecules*, May 2020, vol. 25, no. 10. [Online]. Available: https://europepmc.org/articles/PMC7287585

[86] S. Datta and A. Roy, “Antimicrobial peptides as potential therapeutic agents: A review,” 2020.

[87] H.-K. Kang, C. Kim, C. H. Seo, and Y. Park, "The therapeutic applications of antimicrobial peptides (amps): a patent review," *Journal of microbiology*, 2017, vol. 55, no. 1, pp. 1–12.

[88] A. K. Marr, W. J. Gooderham, and R. E. Hancock, "Antibacterial peptides for therapeutic use: obstacles and realistic outlook," *Current opinion in pharmacology*, 2006, vol. 6, no. 5, pp. 468–472.

[89] C. H. Chen and T. K. Lu, "Development and challenges of antimicrobial peptides for therapeutic applications," *Antibiotics*, 2020, vol. 9, no. 1.

[90] M. T. Ribeiro, S. Singh, and C. Guestrin, "" why should i trust you?" explaining the predictions of any classifier," in *Proceedings of the 22nd ACM SIGKDD international conference on knowledge discovery and data mining*, 2016, pp. 1135–1144.

[91] Z. Yu, J. Tang, T. Khare, and V. Kumar, "The alarming antimicrobial resistance in eskapee pathogens: Can essential oils come to the rescue?" *Fitoterapia*, 2020, vol. 140, p. 104433.

[92] A. Reza, J. M. Sutton, and K. M. Rahman, "Effectiveness of efflux pump inhibitors as biofilm disruptors and resistance breakers in gram-negative (eskapee) bacteria," *Antibiotics*, 2019, vol. 8, no. 4, p. 229.

[93] M. Pirtskhalava, A. A. Amstrong, M. Grigolava, M. Chubinidze, E. Alimbarashvili, B. Vishnepolsky, A. Gabrielian, A. Rosenthal, D. E. Hurt, and M. Tartakovsky, "Dbaasp v3: database of antimicrobial/cytotoxic activity and structure of peptides as a resource for development of new therapeutics," *Nucleic acids research*, 2021, vol. 49, no. D1, pp. D288–D297.

[94] R. Sharma, S. Shrivastava, S. Kumar Singh, A. Kumar, S. Saxena, and R. Kumar Singh, "Deep-ABPpred: identifying antibacterial peptides in protein sequences using bidirectional LSTM with word2vec," *Briefings in Bioinformatics*, 03 2021. [Online]. Available: https://doi.org/10.1093/bib/bbab065

[95] V. Singh, S. Shrivastava, S. Kumar Singh, A. Kumar, and S. Saxena, "Accelerating the discovery of antifungal peptides using deep temporal convolutional networks," *Briefings in Bioinformatics*, 2022, vol. 23, no. 2.

[96] R. Sharma, S. Shrivastava *et al.*, "Deep-AFPpred: identifying novel antifungal peptides using pretrained embeddings from seq2vec with 1DCNN-BiLSTM," *Briefings in Bioinformatics*, 10 2021. [Online]. Available: https://doi.org/10.1093/bib/bbab422

[97] R. Sharma, S. Shrivastava, S. K. Singh, A. Kumar, A. K. Singh, and S. Saxena, "Deep-avppred: Artificial intelligence driven discovery of peptide drugs for viral infections," *IEEE Journal of Biomedical and Health Informatics*, 2021, pp. 1–1.

[98] R. Gautier, D. Douguet, B. Antonny, and G. Drin, "Heliquest: A web server to screen sequences with specific -helical properties," *Bioinformatics (Oxford, England)*, 10 2008, vol. 24, pp. 2101–2.

[99] A. Lamiable, P. Thévenet, J. Rey, M. Vavrusa, P. Derreumaux, and P. Tufféry, "PEP-FOLD3: faster de novo structure prediction for linear peptides in solution and in complex," *Nucleic Acids Research*, 04 2016, vol. 44, no. W1, pp. W449–W454. [Online]. Available: https://doi.org/10.1093/nar/gkw329

[100] D. M. De Oliveira *et al.*, "Antimicrobial resistance in eskape pathogens," *Clinical microbiology reviews*, 2020, vol. 33, no. 3, pp. e00 181–19.

[101] V. Hamers *et al.*, "Antibacterial compounds from mushrooms: A lead to fight eskapee pathogenic bacteria?" *Planta Medica*, 2021, vol. 87, no. 05, pp. 351–367.

[102] E. I. Kritsotakis *et al.*, "Burden of multidrug and extensively drug-resistant eskapee pathogens in a secondary hospital care setting in greece," *Epidemiology & Infection*, 2022, vol. 150, p. e170.

[103] A. Kumar, S. K. Singh, S. Saxena, A. K. Singh, S. Shrivastava, K. Lakshmanan, N. Kumar, and R. K. Singh, "Comhisp: A novel feature extractor for histopathological image classification based on fuzzy svm with within-class relative density," *IEEE Transactions on Fuzzy Systems*, 2021, vol. 29, no. 1, pp. 103–117.

[104] A. Kumar, S. K. Singh, S. Saxena, K. Lakshmanan, A. K. Sangaiah, H. Chauhan, S. Shrivastava, and R. K. Singh, "Deep feature learning for histopathological image classification of canine mammary tumors and human breast cancer," *Information Sciences*, 2020, vol. 508, pp. 405–421.

[105] A. Kumar, V. Purohit *et al.*, "Medisecfed: Private and secure medical image classification in the presence of malicious clients," *IEEE Transactions on Industrial Informatics*, 2021, pp. 1–1.

[106] R. Singh, T. Ahmed, A. Kumar, A. K. Singh, A. K. Pandey, and S. K. Singh, "Imbalanced breast cancer classification using transfer learning," *IEEE/ACM transactions on computational biology and bioinformatics*, 2020, vol. 18, no. 1, pp. 83–93.

[107] V. Bharti, B. Biswas, and K. K. Shukla, "Emocgan: a novel evolutionary multiobjective cyclic generative adversarial network and its application to unpaired image translation," *Neural Computing and Applications*, 2021, pp. 1–15.

[108] N. A. O'Leary *et al.*, "Reference sequence (refseq) database at ncbi: current status, taxonomic expansion, and functional annotation," *Nucleic acids research*, 2016, vol. 44, no. D1, pp. D733–D745.

[109] V. Singh *et al.*, "Multi-scale temporal convolutional networks and continual learning based in silico discovery of alternative antibiotics to combat multi-drug resistance," *Expert Systems with Applications*, 2022, p. 119295.

[110] J. C. Kimmel *et al.*, "Deep convolutional and recurrent neural networks for cell motility discrimination and prediction," *IEEE/ACM transactions on Computational Biology and Bioinformatics*, 2019, vol. 18, no. 2, pp. 562–574.

[111] V. Singh *et al.*, "Accelerating the discovery of antifungal peptides using deep temporal convolutional networks," *Briefings in Bioinformatics*, 2022, vol. 23, no. 2.

[112] M. Youmans *et al.*, "Classification of antibacterial peptides using long short-term memory recurrent neural networks," *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2019, vol. 17, no. 4, pp. 1134–1140.

[113] M. Mathur *et al.*, "Nfeature: A platform for computing features of nucleotide sequences," *bioRxiv*, 2021.

[114] C.-R. Chung, T.-R. Kuo, L.-C. Wu, T.-Y. Lee, and J.-T. Horng, "Characterization and identification of antimicrobial peptides with different functional activities," *Briefings in bioinformatics*, 2020, vol. 21, no. 3, pp. 1098–1114.

[115] V. Singh, S. Shrivastava, S. K. Singh, A. Kumar, and S. Saxena, "Multi-scale temporal convolutional networks and continual learning based in silico discovery of alternative antibiotics to combat multi-drug resistance," *Expert Systems with Applications*, 2023, vol. 215, p. 119295.

[116] D. Veltri, U. Kamath, and A. Shehu, "Deep learning improves antimicrobial peptide recognition," *Bioinformatics*, 2018, vol. 34, no. 16, pp. 2740–2747.

[117] H. Nogusa, H. Hamana *et al.*, "Improved in vivo antitumor efficacy and reduced systemic toxicity of carboxymethylpullulan-peptide-doxorubicin conjugates," *Japanese journal of cancer research*, 2000, vol. 91, no. 12, pp. 1333–1338.

[118] D. J. Craik, D. P. Fairlie *et al.*, "The future of peptide-based drugs," *Chemical biology & drug design*, 2013, vol. 81, no. 1, pp. 136–147.

[119] C. Oo and S. S. Kalbag, "Leveraging the attributes of biologics and small molecules, and releasing the bottlenecks: a new wave of revolution in drug development," *Expert Review of Clinical Pharmacology*, 2016, vol. 9, no. 6, pp. 747–749.

[120] T. Uhlig, T. Kyprianou *et al.*, "The emergence of peptides in the pharmaceutical business: From exploration to exploitation," *EuPA Open Proteomics*, 2014, vol. 4, pp. 58–69.

[121] I. Cree and P. Andreotti, "Measurement of cytotoxicity by atp-based luminescence assay in primary cell cultures and cell lines," *Toxicology in vitro*, 1997, vol. 11, no. 5, pp. 553–556.

[122] N. Uchide, K. Ohyama *et al.*, "Lactate dehydrogenase leakage as a marker for apoptotic cell degradation induced by influenza virus infection in human fetal membrane cells," *Intervirology*, 2009, vol. 52, no. 3, pp. 164–173.

[123] G. Fotakis and J. A. Timbrell, "In vitro cytotoxicity assays: comparison of ldh, neutral red, mtt and protein assay in hepatoma cell lines following exposure to cadmium chloride," *Toxicology letters*, 2006, vol. 160, no. 2, pp. 171–177.

[124] B. C. Evans, C. E. Nelson *et al.*, "Ex vivo red blood cell hemolysis assay for the evaluation of ph-responsive endosomolytic agents for cytosolic delivery of biomacromolecular drugs," *JoVE (Journal of Visualized Experiments)*, 2013, no. 73, p. e50166.

[125] S. Gupta, P. Kapoor *et al.*, *Peptide Toxicity Prediction*. New York, NY: Springer New York, 2015, pp. 143–157.

[126] M. Pirtskhalava, A. A. Amstrong, M. Grigolava, M. Chubinidze, E. Alimbarashvili, B. Vishnepolsky, A. Gabrielian, A. Rosenthal, D. E. Hurt, and M. Tartakovsky, "Dbaasp v3: database of antimicrobial/cytotoxic activity and structure of peptides as a resource for development of new therapeutics," *Nucleic acids research*, 2021, vol. 49, no. D1, pp. D288–D297.

[127] H. Moriwaki, Y.-S. Tian *et al.*, "Mordred: a molecular descriptor calculator," *Journal of cheminformatics*, 2018, vol. 10, no. 1, pp. 1–14.

[128] L. Quan, J. Mei *et al.*, "Quantifying intensities of transcription factor-dna binding by learning from an ensemble of protein binding microarrays," *IEEE Journal of Biomedical and Health Informatics*, 2021, vol. 25, no. 7, pp. 2811–2819.

[129] S. Wang, Y. He *et al.*, "Fcngru: locating transcription factor binding sites by combing fully convolutional neural network with gated recurrent unit," *IEEE Journal of Biomedical and Health Informatics*, 2021, vol. 26, no. 4, pp. 1883–1890.

[130] W. Xie, Z. Zheng *et al.*, "Srg-vote: Predicting mirna-gene relationships via embedding and lstm ensemble," *IEEE Journal of Biomedical and Health Informatics*, 2022.

[131] J. Luo, W. Ouyang *et al.*, "Multi-relation graph embedding for predicting mirna-target gene interactions by integrating gene sequence information," *IEEE Journal of Biomedical and Health Informatics*, 2022.

[132] A. Manna, R. Kundu *et al.*, "A fuzzy rank-based ensemble of cnn models for classification of cervical cytology," *Scientific Reports*, 2021, vol. 11, no. 1, pp. 1–18.

[133] R. Kundu, H. Basak, P. K. Singh, A. Ahmadian, M. Ferrara, and R. Sarkar, "Fuzzy rank-based fusion of cnn models using gompertz function for screening covid-19 ct-scans," *Scientific reports*, 2021, vol. 11, no. 1, pp. 1–12.

[134] R. Pramanik, M. Biswas, S. Sen, L. A. de Souza Júnior, J. P. Papa, and R. Sarkar, "A fuzzy distance-based ensemble of deep models for cervical cancer detection," *Computer Methods and Programs in Biomedicine*, 2022, vol. 219, p. 106776.

[135] A. E. Kavur, L. I. Kuncheva, and M. A. Selver, "Basic ensembles of vanilla-style deep learning models improve liver segmentation from ct images," in *Convolutional Neural Networks for Medical Image Processing Applications.* CRC Press, 2020, pp. 52–74.

[136] L. I. Kuncheva, *Combining pattern classifiers: methods and algorithms.* John Wiley & Sons, 2014.

[137] A. E. Kavur, N. S. Gezer *et al.*, "Chaos challenge-combined (ct-mr) healthy abdominal organ segmentation," *Medical Image Analysis*, 2021, vol. 69, p. 101950.

[138] D. Chicco and G. Jurman, "The advantages of the matthews correlation coefficient (mcc) over f1 score and accuracy in binary classification evaluation," *BMC genomics*, 2020, vol. 21, pp. 1–13.