SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

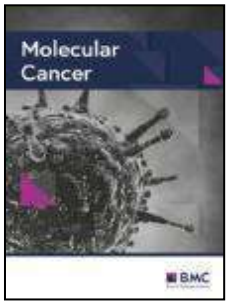
Journal Name: Molecular Cancer **IF: 33.9**

Title: Epithelial-to-mesenchymal transition (EMT) and cancer metastasis: the status quo of methods and experimental models 2025

Author: Allgayer H.; Mahapatra S.; Mishra B.; Swain B.; Saha S.; Khanra S.; Kumari K.; Panda V.K.; Malhotra D.; Patil N.S.; Leupold J.H.; Kundu G.C.

Details: Volume 24, Issue 1, December 2025, Article number 167

Abstract: Epithelial-to-mesenchymal transition (EMT) is a crucial cellular process for embryogenesis, wound healing, and cancer progression. It involves a shift in cell interactions, leading to the detachment of epithelial cells and activation of gene programs promoting a mesenchymal state. EMT plays a significant role in cancer metastasis triggering tumor initiation and stemness, and activates metastatic cascades resulting in resistance to therapy. Moreover, reversal of EMT contributes to the formation of metastatic lesions. Metastasis still needs to be better understood functionally in its major but complex steps of migration, invasion, intravasation, dissemination, which contributes to the establishment of minimal residual disease (MRD), extravasation, and successful seeding and growth of metastatic lesions at microenvironmentally heterogeneous sites. Therefore, the current review article intends to present, and discuss comprehensively, the status quo of experimental models able to investigate EMT and metastasis in vitro and in vivo, for researchers planning to enter the field. We emphasize various methods to understand EMT function and the major steps of metastasis, including diverse migration, invasion and matrix degradation assays, microfluidics, 3D co-culture models, spheroids, organoids, or latest spatial and imaging methods to analyze complex compartments. In vivo models such as the chorionallantoic membrane (CAM) assay, cell line-derived and patient-derived xenografts, syngeneic, genetically modified, and humanized mice, are presented as a promising arsenal of tools to analyze intravasation, site specific metastasis, and treatment response.



URL: https://molecular-cancer.biomedcentral.com/articles/10.1186/s12943-025-02338-2

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Journal of Hazardous Materials **IF: 11.3**

Title: Inactivation of Vaccinia Virus via Nitric Oxide-Plasma Activated Water: A Potential Way to Inactivate Mpox Virus

Author: Patel, P.; Acharya, T.R.; Lenka, S.S.; Ghosh, S.; Mukherjee, S.; Lamichhane, P.; Jaiswal, A.; Verma, S.K.; Kaushik, N.; Choi, E.H.; Kaushik, N.K.

Details: Volume 499 Issue 5 November 2025

Abstract: Mpox virus (*Poxviridae* family) an emerging environmental bio-contaminant caused a non-zoonotic human infection in 2022. The recent surge mirrors early COVID-19 trends, highlighting the need for effective viral inactivation to prevent outbreaks and reduce environmental risks. Our study explores an eco-friendly and non-toxic antiviral approach using nitric oxide (NO_x)-plasma activated water (PAW) for environmental decontamination. Vaccinia virus (VACV) chosen as a surrogate model due to their genetic similarities with Mpox virus (MPXV). Results demonstrated that NO_x-PAW was non-toxic to host cells and significantly reduced VACV infection in lung c ell cultures. Moreover, it induced structural alterations in viral attachment proteins A27 and H3, compromising their functionality resulting in reduced binding affinity towards heparan sulfate and lowering internalization via macropinocytosis. Sequence analysis between VACV and MPXV, including receptor-binding domains, confirmed high similarity, supporting VACV's utility as a model for MPXV inactivation studies. Furthermore, *in-silico* analysis revealed NO_x species (NO, NO_2, NO_3 and N_2O) played crucial role in modification of surface protein by interaction with the amino acids. Overall, the study demonstrated successful VACV inactivation highlighting NO_x-PAW as a promising environmentally safe antiviral strategy for mitigating the spread of DNA viruses like MPXV in contaminated settings, contributing to proactive outbreak prevention and environmental biosafety.

URL: https://www.sciencedirect.com/science/article/abs/pii/S0304389425028808

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

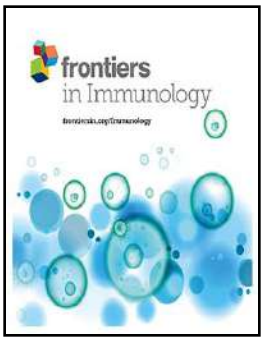
Journal Name: Frontiers in Immunology **IF: 5.9**

Title: Notch signalling in T cells: bridging tumour immunity and intratumoral cellular crosstalk

Author: Sultana, J.; Choudhury, P.R.; Bera, S.; Chakravarti, M.; Guha, A.; Das, P.; Das, J.; Iyer, G.S.; Sarkar, A.; Dhar, S.; Ganguly, N.; Baral, R.; Bose, A.; Banerjee, S.

Details: Volume 16. 2 October 2025

Abstract: Background**:** Notch receptor–ligand interaction is ubiquitous and fundamental for coordinating cellular differentiation and determining cell fate for the development of various tissues and organs. Aberrant mutations in the Notch cascade result in various pathophysiological disorders, including cancer. Diverse aspects of carcinogenesis regulated by Notch include the shaping of anti-tumour T-cell immunity through antigen-presenting cell (APC)–T cell interaction and effector functions. Chief content**:** Notch depends on juxtacrine and paracrine signalling to influence intercellular communications in the tumour microenvironment. Several preclinical and clinical studies have revealed Notch as a bi-effector molecule, which has a differential effect depending on the immune contexture of the tumour microenvironment. The Notch cascade serves as an effective therapeutic target in preventing off-target cell death and promoting tumour-specific T-cell priming. Conclusion**:** This review revolves around Notch crosstalk with respect to the interaction between T-cell populations and other intratumoral cellular components, including professional antigen-presenting cells like dendritic cells, macrophages, B cells, immunosuppressive myeloid-derived suppressor cells, and cancer stem cells. It also summarizes the impact of targeting Notch signalling within intratumoral T cells in combination with traditional oncotherapies.



URL: https://www.frontiersin.org/journals/immunology/articles/10.3389/fimmu.2025.1659614/full

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Food Bioscience **IF: 5.9**

Title: Synergistic control of Pseudomonas aeruginosa biofilms using Limosilactobacillus fermentum and preservation factors

Author: De, S.; Nayak, P.P.; Nayak, A.; Garnaik, S.; Kumar, S.; Das, S.; Paramasivan, S.S.; Sasikumar, R.; Panda, S.K.

Details: Volume 74, December, 2025

Abstract: Biofilms formed by Pseudomonas aeruginosa on food substrates and in processing environments are robust and difficult to penetrate or degrade, posing a significant challenge to current control strategies. The objective of the study was to develop and validate a safe strategy for controlling P. aeruginosa biofilm in the food industry. Limosilactobacillus fermentum GGS, isolated in our laboratory, exhibited excellent antimicrobial and antibiofilm activity against P. aeruginosa, a common foodborne opportunistic pathogen capable of forming biofilms. To ensure maximum control over the P. aeruginosa biofilm, the study considered the use of cell-free supernatant (CFS) from L. fermentum, in combination with common preservation factors, namely acetic acid (for lowering the pH), and salt (NaCl). Response surface methodology (RSM) employing Box-Behnken design (BBD) was used to optimize the control of biofilm formation with the three process variables (CFS, pH, and NaCl). Synergistic interactions among CFS (20.48 %), pH (5.29), and NaCl (3.23 %) were predicted to result in 88.71 % biofilm inhibition, according to the RSM model, a finding later confirmed in an in situ study. A quadratic model (R^2 = 0.975) was developed to predict the nonlinear interactions between the inhibitory agents and biofilm inhibition. This model was further validated using machine learning techniques. Among the models evaluated, Artificial Neural Network (ANN) (R^2 = 0.998) and Random Forest (RF) (R^2 = 0.989) showed strong agreement with the RSM predictions. Atomic force microscopy (AFM) analysis further revealed a reduction in mean roughness (Sa) and root mean square roughness (Sq), along with increased skewness, following treatment with the optimal combination of CFS, low pH, and NaCl.

URL: https://www.sciencedirect.com/science/article/abs/pii/S2212429225019741?via%3Dihub

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Biomass and Bioenergy **IF: 5.8**

Title: Fermentation of sugarcane bagasse for production of value-added phenolic compounds using potential bacterial strains: A comparative analysis

Author: Pattnaik B.; Preeti; Gupta D.; Deb D.; Selvaraj M.; Assiri M.A.; Mohapatra S.R.; Sahoo H.P.; Tapas S.; Sarangi P.K.

Details: Volume 202, November 2025

Abstract: The present study investigates the potential of bacterial strains, viz., Pseudomonas fragi, Lactobacillus plantarum, and Lactobacillus acidophilus, for the production of phenolic compounds from sugarcane bagasse (SCB). The important bio-transformed phenolic products isolated from the medium were ferulic acid (FA), vanillin and vanillic acid (VA), whose identification and quantification were done by high-performance thin-layer chromatography. Carbohydrate concentration from the de-starched bagasse was also assessed and compared with that of the original (control) bagasse. Results revealed that the utmost FA yield per kg of SCB was 275 mg from Lactobacillus acidophilus, 225 mg from Pseudomonas fragi on the 9th day, and 212 mg from Lactobacillus plantarum on the 12th day of incubation. Likewise, the peak vanillin and VA quantified per ml of fermented extract were 16 mg on 9th and 12th day of incubation, respectively, for Lactobacillus plantarum, 14 mg of vanillin and 13 mg of VA on 9th day for Pseudomonas fragi. However, in Lactobacillus acidophilus 15 mg of Vanillin and 18 mg of VA was recorded on 12th day of incubation. To compare enzymatic efficiency and structural integrity among ferulic acid esterases (FAEs), a 3D structural model was constructed. We first time demonstrated that the lid domain's structural integrity enhances enzyme efficiency which has been expressed in terms of yield. An ∼18 % higher yield of primary phenolic compound was obtained for L. acidophilus with compact FAE lid domain compared to PsfFAE. This finding highlights the metabolic potential of these strains for phenolics production and their relevance in biotransformation processes.

URL: https://www.sciencedirect.com/science/article/abs/pii/S0961953425005720?via%3Dihub

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

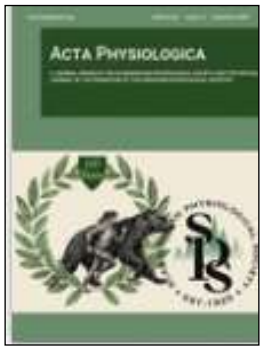
Journal Name: Acta Physiologica **IF: 5.6**

Title: Is Predisposition to T2D Impacted by Polymorphisms in Genes Involved in Insulin Signaling and Cellular Bioenergetics?

Author: Pati, B.; Jastroch, M.; Bal, N.C.

Details: Volume 241, Issue 12, December, 2025

Abstract: Background: Type 2 diabetes (T2D) represents a growing global health challenge, with its prevalence and associated metabolic complications rising sharply over the past two decades. Although the pathogenesis of T2D is complex and influenced by lifestyle and (micro)environmental factors, genetic constituents have been considered major predisposing factors. Recent literature shows significant individual variations in both the progression of T2D and the efficacy of antidiabetic drugs. These individual variations are expected to emanate from the inherent genetic make-up and potential epigenetic modifications by environmental factors. Hypothesis: It has been proposed that altered metabolism (including cellular bioenergetic mechanisms) provides protection from T2D. Moreover, several researchers have proposed that proteins regulating cellular bioenergetics, for example, involved in adaptive thermogenesis, represent good targets to counter T2D. Therefore, we thoroughly searched the literature on genetic variability associated with T2D in this review. Results: We could only find genes involved in (1) insulin secretion (INS, PDX1, ABCC8, KCNJ11, KCNQ1, CDKAL1, IGFBP2) and (2) cellular bioenergetics in insulin-responsive tissues (INSR, IRS, AKT, SLC2A4, TBC1D4, PPP1R3A, LEP, LEPR, ADIPOQ, TCF7L2, PPAR-γ, SLC30A8). Specific attention is given to diverse ethnic populations, in particular Indian subgroups where these genetic factors may display clearer association to T2D. Conclusion: By emphasizing genetic predispositions, this review highlights the lack of studies on the genetic association of cellular bioenergetics proteins in T2D pathogenesis. It also underscores the potential for early detection, personalized management, and the development of targeted therapies for individuals with T2D across different genetic profiles.



URL: https://onlinelibrary.wiley.com/doi/10.1111/apha.70122

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

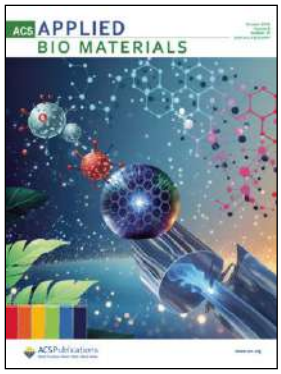
Journal Name: ACS Applied Bio Materials **IF: 4.7**

Title: Peptide-Functionalized Selenium Nanoparticle-Based Effective Delivery System for Src-Targeting siRNA in Triple-Negative Breast Cancer Cells

Author: Suryakanta, U.; Panigrahi, B.; Das, S.; Mandal, D.

Details: Volume 8, Issue 10, October 2, 2025

Abstract: siRNA technology represents a promising approach in RNAi-based gene therapy due to its unique ability to silence target-specific genes implicated in life-threatening diseases, such as cancer. However, developing an effective nucleic acid delivery system remains challenging due to its limitations, such as enzymatic degradation, poor cellular internalizatio n of nucleic acids, and cytotoxicity of the delivery vehicles, which are considered to be critical factors for clinical translation. Herein, we developed peptide-functionalized selenium nanoparticles to address this issue. In this study, eight short linear peptides (LP) primarily composed of tryptophan and arginine residues were designed for the one-pot synthesis of peptide-capped selenium nanoparticles (LP-SeNPs). The synthesized LP-SeNPs were characterized using field emission scanning electron microscopy (FE-SEM), energy-dispersive X-ray spectroscopy (EDX), and the dynamic light scattering (DLS) technique. Among the SeNPs, LP5-SeNP showed the highest siRNA loading capacity and protection against 25% serum. Flow cytometry analysis indicated significant cellular uptake of FAM-siRNA with 23–24% of the cell population when delivered using LP1-SeNP and LP5-SeNP, respectively, compared to control FAM-siRNA. Fluorescence microscopy confirmed the cytosolic localization of SeNP/siRNA complexes. Further, Western blotting analysis exhibited that the LP5-SeNP/Src siRNA complex could efficiently down-regulate ∼70% Src protein expression in triple-negative breast cancer cells, MDA-MB-231. The cellular uptake mechanism revealed that LP5-SeNP/siRNA most probably followed the macropinocytosis pathway for successful internalization of the complex into TNBC cells. In summary, the designed peptides can generate stable peptide-coated SeNPs, which may unveil a new therapeutic strategy for siRNA therapy.



URL: https://pubs.acs.org/doi/10.1021/acsabm.5c01486

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Bioorganic Chemistry **IF: 4.7**

Title: Quinazoline-based fourth-generation EGFR tyrosine kinase inhibitors to overcome C797S-mediated resistance in non-small cell lung Cancer (NSCLC)

Author: B.R., Patil, Bhatu R.; K., Pawara, K.; M., Shaikh, Matin; F., Ahmed, Faizan; C.R., Patil, Chandragouda Raosaheb; C.S., Gawli, Chandrakant S.; C.N., Kundu, Chanakya Nath; B., Das, Biswajit; I., Ahmad, Iqrar; H.M., Patel, Harun M.

Details: Volume 165, October 2025

Abstract: The emergence of resistance mutations, particularly C797S, in epidermal growth factor receptor tyrosine kinase (EGFR-TK) has significantly limited the long-term efficacy of Osimertinib in non-small cell lung cancer (NSCLC). In this study, we designed and evaluated a series of quinazoline derivatives targeting the triple mutant EGFR (L858R/T790M/C797S). Among them, compound **8d** exhibited the highest potency against EGFR L858R/T790M/C797S, with an IC_{50} of 0.068 μM, demonstrating strong binding affinity and effective suppression of kinase activity compared to Osimertinib. Molecular docking studies revealed key interactions with catalytic Lys745. Molecular dynamics (MD) simulations over 100 ns confirmed ligand stability, with an average root-mean-square deviation (RMSD) below 2.0 Å and a binding free energy of −44 kcal/mol (MM/GBSA). Structure-activity relationship (SAR) analysis highlighted the critical role of a bulkier hydrophobic substituent at the C2 position of the quinazoline ring in combination with a sulfonyl group, which improved affinity and potency. These findings establish quinazoline derivatives, particularly compound **8d**, as promising fourth-generation EGFR inhibitors for overcoming C797S-mediated resistance in NSCLC therapy.

URL: https://www.sciencedirect.com/science/article/abs/pii/S0045206825008715?via%3Dihub

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

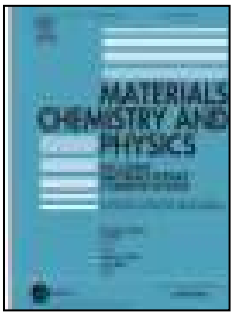
Journal Name: Materials Chemistry and Physics **IF: 4.7**

Title: Deciphering biosurfactant-salt interaction and its influence on biosurfactant activity in muga silk fibroin extraction

Author: Biswal B.; Das M.; Das D.; Prusty D.; Dan A.K.

Details: Volume 344, October 2025

Abstract: Degumming of silk cocoons is the initial technique employed to separate two silk proteins (fibroin and sericin), which further leads to the formulation of diverse silk-based biomaterials for biomedical applications. In this study, a novel approach has been implemented in a mixed system. Specifically, this paper emphasizes the impact of degumming on fibroin fiber, which was carried out using varying concentrations of sodium carbonate (Na_2CO_3) and crude biosurfactant extracted from Acacia concinna (Willd.) Dc. The study investigated the effectiveness of the degumming process under a specific concentration of Na_2CO_3 with crude biosurfactant extract, examining the influence of reaction time, temperature, and mixed reagent concentration. The results of the degumming process show that approximately 24.8 % degumming occurred when using 0.012 g/mL of biosurfactant extract with 3×10^{-4} g/mL of Na_2CO_3 as degumming reagents. Furthermore, SEM, XRD, TGA, and mechanical strength analyses suggest that the quality of fibers extracted using the crude biosurfactant (BSE) and Na_2CO_3 mixture in the degumming process yielded significant results. This innovative approach of degumming can extract the silk fibroin from the cocoons in the fastest and most effective way. Moreover, this strategy may significantly diminish the harmful contamination of sericin and degumming chemicals in the effluent.



URL: https://www.sciencedirect.com/science/article/pii/S0254058425008107?via%3Dihub

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

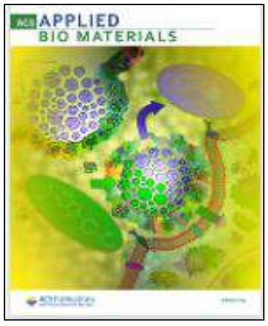
Journal Name: **ACS Bio Applied Materials** **IF: 4.7**

Title: Adhesive and Wound Healing, Dual Active Hydrogel with Snail Mucus Proteins

Author: Das, O; Newar, J; Verma, S; Swalsingh, G; Das, A; Reddy, KS; Bal, NC; Ghatak, A

Details: November, 2025

Abstract: Many gastropods secrete mucus, which is more viscous and adhesive than the common trail mucus. The primary biochemical distinction between the two types of mucus is the higher protein content of the adhesive mucus. Not enough is known about the function of each of these proteins. In the current study, two of such mucus proteins were isolated from the adhesive mucus of the land snail *Macrochlamys indica*. In an attempt to imitate the structure of the mucus, these proteins were mixed with commercial hyaluronic acid (HA). The resultant hydrogel was found to have adhesive properties. A cell viability assay revealed that each of the hydrogel components and their mixtures were biologically safe and compatible. The *in vitro* cell migration assay showed better wound closure in case of the mucus protein as compared to HA, which is already known for its wound healing properties. The hydrogel was used for incision wound healing in mice, followed by histological staining. The result showed faster healing when compared to that of commercial wound healing ointment. In conclusion, this study presents a wound repair material, formulated from snail protein and HA and useful as an adhesive wound dressing with healing effects.



URL: https://pubs.acs.org/doi/10.1021/acsabm.5c01923

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy **IF:4.6**

Title: Spectroscopic investigation of hydrogen bond network stability and microplastic leaching in ethanol-based potentised medicines at extreme dilutions during prolonged plastic storage

Author: Chakraborty S.; Ghosh K.; Biswas S.; Roy Chaudhuri C.; Roy Chowdhury A.; Chakravarty R.; Nayak D.; Kaushik S.; Barui A.; Kundu S.

Details: Vol. 343, Dec 2025

Abstract: The quality and efficacy of pharmaceutical products stored under proper conditions are critical. This study examined the effects of long-term plastic storage on extremely diluted ethanol-based potentised (EP) medicines using advanced spectroscopic techniques. Four medicines, Arnica montana, Rhus toxicodendron, Conium maculatum, and Belladonna, at ultra-high (200C, 1 M) and moderate-high (30C, 200C) potencies, were stored in glass and plastic containers for one month. Glass-stored medicines showed increased antioxidant activity and zeta potential with higher potency, while plastic-stored samples showed a decreasing trend. Conductivity was inversely correlated with zeta potential, with glass-stored medicines showing a ~ 41.91 % reduction, while plastic-stored samples showed a ~ 36.29 % increase. Mid-IR spectra revealed a blue shift (~4–14 cm^{-1}) in O–H stretching and a red shift (~2–3 cm^{-1}) in H–O–H bending for glass-stored medicines, showing weaker inter-molecular H-bonds at higher potencies. In contrast, plastic-stored medicines showed opposite shifts (~2–17 cm^{-1}), implying more constrained H-bonding due to carbonyl-water interaction in presence of microplastics, disrupting the native ethanol-water H-Bond network. Far-IR spectra showed an enthalpic gain (~45.34 %) in glass-stored medicines, while plastic-stored samples showed an enthalpic loss (~56.60 %), confirming structural destabilisation of native water-network due to microplastic leaching. Our findings show that plastic containers compromised the efficacy of studied medicines by altering H-bond network stability and electrical properties. Further studies on different plastic grades and storage durations are needed to validate these findings and explore cost-effective alternatives for long-term storage of such medicines.

URL: https://www.sciencedirect.com/science/article/abs/pii/S1386142525009229?via%3Dihub

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Results in Surfaces and Interfaces **IF: 4.4**

Title: Smart stimuli responsive pNIPAM-co-AAc@Ag/Au bimetallic hybrids: Tunable catalytic activity by varying Ag/Au molar ratio

Author: Majumdar A.G.; Mohanty M.; Pany B.; Mukherjee D.; Singh H.D.; Majumdar S.; Si S.; Mohanty P.S.

Details: Volume 21, October 2025

Abstract: We report synthesis of Ag/Au bimetallic nanoparticles within a stimuli-responsive pNIPAM-co-AAc microgel matrix using seed-mediated growth strategy. By systematically varying the Au^{3+} precursor, we obtained a series of nanohybrids (MG-Ag/Au 1–9) with tunable Ag/Au molar ratios. The COO^- groups of the microgel facilitated stabilization of Ag/Au bimetallic NPs, enabling colloidal stability of the nanohybrids. Our UV–vis and XRD analysis confirmed formation of heterostructured Ag and Au domains rather than homogeneous alloys. Catalytic activity of these bimetallic nanocomposites was evaluated with a borohydride mediated (BH_4^-) model reduction of 4-nitrophenol (4-NP) to 4-aminophenol (4-AP) which shows a significant trend of gradual increase and then rapid decrease in K_{app} while gradually decreasing Ag/Au molar ratio. pNIPAM-co-AAc @Ag/Au 6 showed a remarkable K_{app} of 4.519 min^{-1}, outperforming many previously reported similar bimetallic systems. Furthermore, it showcased increased catalytic efficiency compared to their monometallic counterparts i.e. ~8.5-fold higher than pNIPAM-co-AAc@Ag and ~27-fold higher than pNIPAM-co-AAc@Au. In-silico molecular docking studies demonstrated binding energy of −0.57, −0.94 and −1.55 kcal/mol for BH_4^--NIPAM, 4-NP-COO^- and 4-NP-NIPAM. This work highlights the importance of bimetallic compositional tuning inside microgel matrix in developing efficient nanocatalysts for future applications.

URL: https://www.sciencedirect.com/science/article/pii/S2666845925002260?via%3Dihub

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: FASEB Journal **IF: 4.2**

Title: CRISPR-Induced Mutations of mk2b and mk3 Host Proteins Enhance Chikungunya Virus Susceptibility and Modulate Host Immune Responses in Zebrafish

Author: Keshry, S.S.; Nayak, U.; Mamidi, P.; Mohanty, S.; Ghorai, U.; Swain, R.K.; Chattopadhyay, S.

Details: Volume 39, Issue 20, October2025

Abstract: Host factors are essential at every stage of the viral life cycle and therefore represent attractive and potentially effective targets for the development of antiviral therapeutics. This study highlights the crucial roles of host factors, specifically mitogen-activated protein kinase 2 (mk2) and mitogen-activated protein kinase 3 (mk3), both of which are stress-stimulated serine/threonine kinases. The roles of mk2 and mk3 were investigated by generating single (mk2b−/− and mk3−/−) and double knockouts (mk2b−/−mk3−/−) in a zebrafish model using the CRISPR-Cas9 technique, followed by chikungunya virus (CHIKV) infection. All knockout lines exhibited significantly higher CHIKV titers and severe phenotypes compared to the WT control, with mk3^{-}/$^{-}$ showing the greatest susceptibility. After CHIKV infection, expression levels of TNF-α changed across all knockout models. Notably, mk2b^{-}/$^{-}$ and mk2b^{-}/$^{-}$mk3^{-}/$^{-}$ double knockout larvae exhibited reduced TNF-α expression, suggesting that higher levels of TNF-α may be associated with viral clearance via the p38-MK2-TNF-α signaling axis. In contrast, mk3−/− zebrafish exhibited increased vulnerability to CHIKV through alternative, yet unidentified, pathways. Furthermore, an increase in viral titer corresponded with an enhanced host immune response, as indicated by significantly higher expression levels of ifnϕ1 and rsad2 in all knockout groups. In conclusion, this study confirms that the mk2b and mk3 host proteins are essential in controlling CHIKV infection at the organism level. These findings might have implications towards designing strategies for future antiviral therapeutics. Furthermore, the knockout model of mk2b and mk3 in zebrafish could serve as a valuable tool for studying their roles in other viral infections.

URL: https://faseb.onlinelibrary.wiley.com/doi/10.1096/fj.202501236RR

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Plant Science **IF: 4.1**

Title: Unearthing the secrets of drought-driven root system architecture: Nutrient acquisition and rhizosphere microbe interplay

Author: Nayak, J.; Chattopadhyay, D.; Giri, M.K.; Singh, N.

Details: Volume 363, February 2026

Abstract: Drought, a climatic occurrence that cyclically affects all climatic regions, is more prevalent in tropical and subtropical areas. This phenomenon inflicts physiological harm upon plants within ecosystems and agroecosystems. Apart from the direct scarcity of water, which severely impairs plant development and productivity, there can be consequential issues related to mineral nutrition. These secondary effects can arise and further impact plant development. Amidst drought conditions, roots play a critical role in shaping the growth and development of plants. During these circumstances, our understanding of the molecular mechanisms governing critical responses and interactions between plant roots and their surrounding rhizosphere is less comprehensive in comparison to other studies with well-characterized model species like Arabidopsis. This article examines the molecular mechanisms governing the adaptability of root system architecture (RSA) to drought stress in plants. It also explores how soil nutrients and microorganisms are regulated in response to these adaptive processes. We first give a general description of how plant hormones control RSA under water-scarce conditions. Additionally, we explore how nutrients, particularly phosphorus and nitrogen, affect the developmental responses of RSA to low water status. Additionally, this article delves into the existing understanding of the interactions between RSA and soil microbial niches under drought. Based on these understandings, our conclusion emphasizes that to achieve a more comprehensive grasp of the mechanisms underlying drought adaptation in plant roots, future research should adopt a holistic network perspective.

URL: https://www.sciencedirect.com/science/article/abs/pii/S016894522500473X?via%3Dihub

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Scientific Reports **IF: 3.9**

Title: Novel endophytic actinomycetes species Streptomyces panacea of Panax sokpayensis produce antimicrobial compounds against multidrug resistant Staphylococcus aureus

Author: Rai S.; Singh L.S.; Liriina K.; Jeyaram K.; Parija T.; Sahoo D.

Details: Volume 15, Issue 1, December 2025, Article number 19863

Abstract: Endophytic actinomycetes of medicinal plants have recently been in focus for developing novel antimicrobial compounds to combat multidrug-resistant pathogens. In this study, we isolated and characterised endophytic actinomycetes of Panax sokpayensis rhizome traditionally used as medicine in Sikkim-Himalayan region and assessed their antimicrobial activity against multidrug-resistant (MDR) clinical isolates of Staphylococcus aureus. Saccharopolyspora dominated as the endophytic actinomycetes of P. sokpayensis rhizome. However, a novel actinomycete strain PSRA5^T belongs to the genus Streptomyces, with the highest genome sequence similarity of 91.54% with its closest relative Streptomyces niveus NCIMB 11891 has shown an effective inhibition of six clinical isolates of MDR S. aureus during disc diffusion assay. Further comparative analysis of cellular fatty acids composition and phenotypic and biochemical characteristics of strain PSRA5^T with its phylogenetically closely related strain of S. niveus, classified as representing a novel species of the genus Streptomyces, for which the name Streptomyces panacea sp. nov. is proposed here with type strain PSRA5^T (= MCC5238^T). The minimum inhibition concentration of ethyl acetate crude extract of PSRA5^T culture supernatant against MDR S. aureus isolates was 5.5 to 13.5 µg/mL. Further correlation between biosynthetic gene clusters identified by genome search with LC-MS analysis-based chemical profiling of PSRA5^T culture extract and antibacterial activity of the representative compounds detected several compounds of aminoglycosides and polyketides with antimicrobial activity against MDR S. aureus isolates.

URL: https://www.nature.com/articles/s41598-025-05333-1

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

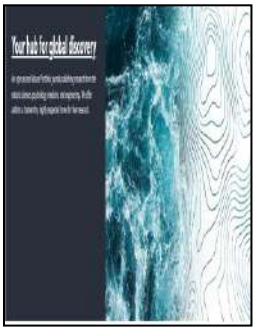
Journal Name: Scientific Reports **IF: 3.9**

Title: Association of intermediate monocytes with dengue severity among the pediatric population of Odisha, India

Author: Dash, M.K.; Samal, S.; Rout, S.; Bhola, R.K.; Gartia, J.; Saha, I.; Behera, C.K.; Hamdi, H.; Sahu, M.C.; Das, B.

Details: Volume 15, Issue 1, December, 2025

Abstract: Dengue virus (DENV) infection in children exhibits varied clinical presentations, wherein the role of monocytes is important in the innate immune response. In this study, laboratory-confirmed DENV pediatric patients (n = 120), with DENV-2 infection, were categorized into dengue fever (DF), dengue with warning signs (DWS) and severe dengue (SD) were assessed for monocyte subpopulation analysis using immunophenotyping involving CD14 and CD16 host-surface markers. Molecular docking was performed using HADDOCK 2.4 to analyze the interactions between CD14, CD16 and DENV envelope and capsid proteins. Among the cases, 84 (70%) were classified as DF and 36 (30%) as DWS & SD. Hematological and biochemical parameters indicated that thrombocytopenia and elevated hematocrit (> 40%) were significantly more common in DWS & SD, with markedly elevated liver enzymes (ALT and AST) in severe cases. Classical monocytes (CM-CD14++ CD16−) constituted 72.51% and 66.25% of the monocyte population in DF and DWS & SD cases, respectively. Intermediate monocytes (IM-CD14+ CD16+) comprised 9.89% and 30.86% in DF and DWS & SD cases, respectively. Non-classical monocytes (NCM-CD14+ CD16++) comprised 5.75% and 8.12% in DWS & SD and DF cases, respectively. In silico analysis revealed host CD16 and CD14 exhibited potential interactions with DENV capsid and envelope proteins, with binding energies − 8.9, − 10.1, − 8.6, and − 11.1 kcal/mol, respectively. IM was significantly increased in DWS & SD compared to DF ($p < 0.05$). These findings suggest that IM could act as host markers of DENV severity in children.



URL: https://www.nature.com/articles/s41598-025-21089-0

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

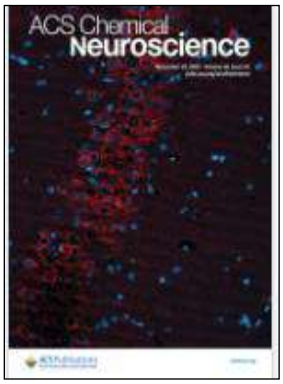
Journal Name: ACS Chemical Neuroscience **IF: 3.9**

Title: Identifying Novel Spiro-Indenoquinoxaline-Pyrrolidine-Based Amyloid Beta Inhibitors in Alzheimer's Disease from In Silico to In Vitro

Author: Rani, S.; Kaur, M.; Pothal, P.; Rajput, K.; Khera, A.; Sharma, A.; Thombare, V.; Sethi, A.; Paul, B.; Gartia, J.; Yadav, V.K.; Patil, N.A.; Ranawat, P.; Suresh Babu, A.R.; Singh, G.; Barnwal, R.P.

Details: Volume 16, Issue 22, November, 2025

Abstract: Alzheimer's disease (AD) is the most prevalent neurodegenerative disease characterized by memory loss and other cognitive functions. The key hallmarks of AD include extracellular beta-amyloid clumps and intracellular neurofibrillary tau tangles in the neurons. Cholinesterase inhibitors and NMDA-receptor antagonists and their combination are already approved treatments; however, these only give short-term symptom relief. Therefore, new therapeutic techniques and novel drugs are required to combat the century-old AD. This study includes the screening of nine novel small compounds (spiro-indenoquinoxaline-pyrrolidines) via in silico approaches; these compounds have been scrutinized to explore their potential as antiamyloidogenic drugs. Computational tools, including ADMET analysis, molecular docking, and molecular dynamics (MD) simulations, have been used for screening the selected compounds against monomeric peptides of Aβ ($A\beta_{1-40}$and $A\beta_{1-42}$) and their oligomeric counterparts, i.e., $6A\beta_{9-40}$and $6A\beta_{1-42}$. Among the nine molecules screened for this study, ADPR-d reflected the best drug-likeness and negligible toxicity. Further, ADPR-d has the highest binding affinity for all the peptides selected for this study. Additionally, MD simulations of Aβ peptide–ADPR-d complexes confirmed a stable complex formation. In vitro aggregation assay and cell culture studies for $A\beta_{1-42}$also support our in silico findings. The positive findings of the presented study highlight that the ADPR-d molecule may prove to be a potential therapeutic molecule against AD. However, these results would require further in vitro and in vivo analysis before proceeding to clinical settings with these compounds against AD.



URL: https://pubs.acs.org/doi/10.1021/acschemneuro.5c00728

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

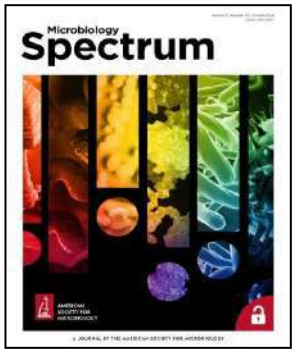
Journal Name: **Microbiology Spectrum** **IF: 3.8**

Title: Telmisartan, an anti-hypertensive drug, impedes JEV infection, possibly via the AT1/PPARγ axis

Author: Datey, A; Chatterjee, S; Ghosh, S; Kumar, PS; De, S; Ghorai, U; Hota, D; Subudhi, BB; Chattopadhyay, S

Details: Volume 13, Issue 10, October 2025

Abstract: Japanese encephalitis, caused by Japanese encephalitis virus (JEV), is a vector-borne disease with no specific therapeutics available yet. Binding of angiotensin II (Ang II) to angiotensin II type 1 (AT1) receptor induces the release of inflammatory cytokines associated with viral encephalitis. Accordingly, Ang II receptor blockers (ARBs) have been proposed to manage encephalitis. Since telmisartan (TM, antagonist of AT1 and agonist of PPARγ) has relatively better brain access than other ARBs, this investigation aims to evaluate its anti-JEV efficacy *in vitro* and *in vivo*. TM reduced JEV titer, RNA, and protein (NS3) significantly in the BHK-21 cells with an IC_{50} of 24.68 µM and a CC_{50} of >350 µM (Selectivity Index >14.18), indicating its potential for repurposing against JEV. The anti-JEV efficacy of TM was further observed in other physiologically relevant cells. Interestingly, the viral load was reduced significantly in pre-, co-, and post-treatment conditions of TM. In the presence of GW (PPARγ antagonist) and AG (AT1 agonist), viral infection was increased remarkably, while AT1 was upregulated and PPARγ was downregulated. TM treatment reversed these levels during infection. In addition, siRNA knockdowns of AT1 and PPARγ showed an insignificant change in infection upon TM treatment. Furthermore, reduction of inflammatory markers like p-IRF-3, COX-2, and p-NF-κB was observed after TM treatment in RAW264.7 cells, suggesting its immunomodulation through the AT1/PPARγ axis. Finally, the anti-JEV potential of TM was validated in a mouse model through the reduction of disease score, viral protein, and histological changes. Thus, the preclinical efficacy of TM suggests its suitability for repurposing against JEV.



URL: https://journals.asm.org/doi/10.1128/spectrum.03003-24

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Biochimie **IF: 3.0**

Title: Small molecule based targeting of the CssA RNA thermometer: insights from computational and biophysical approaches

Author: Sharma A.; Gopi P.; Trivedi R.; Kumar D.; Gartia J.; Suresh Babu A.R.; Pandya P.; Singh G.; Barnwal R.P.

Details: Volume 237, October 2025

Abstract: The exploration of RNA as a therapeutic target is relatively recent. The field of RNA targeting with small molecules remains elusive despite significant advances via approaches such as the development of bioinformatics tools and strategies facilitating improved modes of action. Non-coding RNAs like RNA thermometers reported in many bacterial pathogens are exciting targets due to the translational control exerted by these RNA elements. The current work involves virtual screening of an in house library of small molecules against CssA RNA thermometer from Neisseria meningitidis via docking and molecular dynamics (MD) simulations followed by in vitro experiments to affirm the binding of small molecules to the target RNA. Fluorescence binding assay and NMR provide evidence for RNA thermometer-small molecule binding. The present study would open new avenues in the domain of small molecule-based targeting of RNA. Interestingly, an RNA thermometer has never been exploited as a drug target. Targeting such RNA elements with small molecules would facilitate structure-based small molecule design with better affinity for the target RNA. From among spiro-pyrrolidine based heterocycles that showed the best binding affinity with the RNAs, a small molecule was identified as the top lead with the potential for targeting the CssA RNA thermometer.

URL: https://www.sciencedirect.com/science/article/abs/pii/S0300908425001580?via%3Dihub

SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Journal of Material Cycles and Waste Management **IF: 3.0**

Title: Harnessing the untapped value of food waste: A review of integrated valorization technologies

Author: Lenka, B.; El Fels, L.; Acharya, R.; Raklami, A.

Details: November 2025

Abstract: The continuous growth of the global population has led to a market rise in food waste (FW) generation, posing serious environmental and economic challenges. Improper and inadequate FW management negatively impact soil, water, and air quality, contributing to environmental degradation, and hampering economic progress. The conventional methods of managing FW, such incineration and landfilling, remain widely practiced, however, these practices often result in the release of harmful by-products, such as greenhouse gas emissions which undermine environmental sustainability. While current standalone conversion technologies, including gasification, pyrolysis, anaerobic digestion, hydrothermal carbonization, composting, and fermentation, have shown potential for energy recovery and resource valorization, they often lack integration and scalability. Nevertheless, these technologies still face limitations, such as incomplete waste conversion, low process efficiency, and the generation of toxic intermediates or inhibitors. To address these limitations, integrated valorization approaches should be adopted to enable the production of high-energy-yielding products, including solid biofuels (hydrochar), liquid biofuels (biodiesel), biogas (methane), and hydrogen-rich syngas. The successful implementation of advanced and sustainable food waste valorization strategies can play a pivotal role in realizing a circular bioeconomy and mitigating the global food waste crisis. Achieving this requires interdisciplinary collaboration among researchers, stakeholders, and policymakers to ensure strong alignment with the sustainable development goals.

URL: https://link.springer.com/article/10.1007/s10163-025-02423-0