



SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Molecular Cancer

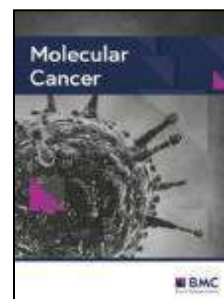
IF: 33.9

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

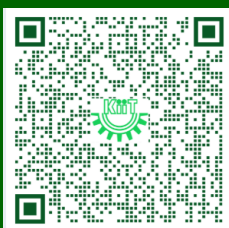
Author: Patel, P.; Acharya, T.R.; Lenka, S.S.; Ghosh, S.; Mukherjee, S.; Lamichhane, P.; Jaiswal, A.; Verma, S.K.; Kaushik, N.; Choi, E.H.; Kaushik, N.K.

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 cell 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, NO₂, NO₃ and N₂O) 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: Journal of Environmental Management

IF: 8.4

Title: Algae-based nanoparticles for enhancing sustainable applications in integrated food-water ecosystem

Author: Nayak S.; Behera B.; Newmei K.; S. M.S.; Kumar V.; Lalnunmawii E.; Senthil Kumar N.; Das B.; Rathinavel L.

Details: Volume 392, September 2025

Abstract: Over the past decade with the ever-increasing population growth, the concurrent demands for food and water have risen, thus significantly affecting sustainability. Recently, biogenic nanoparticles produced from algal biomass inherently rich in secondary metabolites have garnered huge attention to sort the complexities related to food-water nexus. This critical review aims to explore recent advancements in the synthesis, characterization, and functional properties of algae-based nanoparticles (ANPs), highlighting their role in supporting sustainable solutions across the food and water sectors. Interactions of ANPs with various components present in water and soil are discussed to comprehend the potential challenges and seek solutions for improving their real-time applicability. Further, the underlying mechanisms have been correlated with potential applications linked to environmental bioremediation, agricultural applications and food supply chain management. The morphology and physicochemical characteristics of ANPs depend on the algae type, procedure used, and other factors such as the concentration of algal extract and metal, incubation time, temperature, and pH levels. ANPs depending on their surface and functional properties have been reported to have a higher remediation efficiency for heavy metals, dyes, and nutrients from wastewater. High antimicrobial and antioxidant activity also makes them a good candidate for active food packaging to extend shelf-life. Challenges in scalability, stability, and environmental risk are also elaboratively discussed. Overall, this review provides a foundational framework for future interdisciplinary research aimed at optimizing algae-based nanotechnologies for sustainable development



URL: <https://www.sciencedirect.com/science/article/abs/pii/S0301479725027537?via%3Dihub>





SCHOLARLY PUBLICATIONS

School of Biotechnology

KIIT Deemed to be University

Journal Name: British Journal of Cancer

IF: 6.8

Title: NEK9-mediated Wnt signalling repressor TLE3 rewires Docetaxel resistance in cancer cells by inducing pyroptosis

Author: S.A., Ansari, Shamima Azma; S., Mohanty, Sibasish; P., Mohapatra, Pallavi; S., Datta, Sudeshna; M., Swain, Mamuni; R., Rath, Rachna; D.K., Muduly, Dillip Kumar; S.K.D., Majumdar, Saroj Kumar Das; R.K., Swain, Rajeeb Kumar; S.K., Raghav, Sunil Kumar

Details: September, 2025

Abstract: Background: Docetaxel is the most common chemotherapy regimen for several neoplasms, including advanced OSCC (Oral Squamous Cell Carcinoma). Unfortunately, chemoresistance leads to relapse and adverse disease outcomes. Methods: We performed CRISPR-based kinome screening to identify potential players of Docetaxel resistance. Immunohistochemistry was performed to examine the expression profile of the target gene across tumour tissues. Global transcriptome analysis was performed to determine the molecular mechanism underlying Docetaxel resistance. NEK9 kinase assay was performed to identify a putative kinase inhibitor. Results: Upon conducting CRISPR-based kinome screening, Never In Mitosis Gene-A Related Kinase-9 (NEK9) was identified as a major player of Docetaxel resistance in OSCC, prostate, and pancreatic cancer lines. NEK9 ablation restores Docetaxel-induced cell death in chemoresistant cells. Mechanistically, we found that NEK9 deletion upregulates Transducin-like enhancer protein 3 (TLE3), which in turn represses Wnt signalling. Fostamatinib was identified as a potent NEK9 inhibitor that overcomes Docetaxel resistance. Conclusions: Our study demonstrated that NEK9 plays an important role in Docetaxel resistance. The novel combination of NEK9 inhibitor Fostamatinib and Docetaxel needs further clinical investigation in advanced OSCC.



URL: <https://www.nature.com/articles/s41416-025-03148-5>





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: 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: Biomaterials Science

IF: 5.7

Title: Mimicking the osteosarcoma surfaceome on nanoparticles for targeted gene therapy

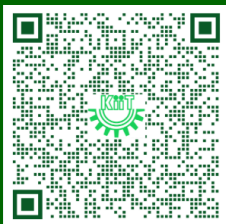
Author: Dash, P.; Das, K.; Dash, M.

Details: 16 September 2025

Abstract: This study developed biomimetic nanoparticles by coating poly(lactic-co-glycolic acid) (PLGA) nanoparticles with membranes derived from osteosarcoma cells, forming cell membrane-coated nanoparticles (CMCNPs). The CMCNPs showed specific binding to their source cancer cells (homotypic targeting) while evading detection by macrophages and degradation in lysosomes. The stealth property of CMCNPs was demonstrated by reduced protein adsorption and minimal liver retention *in vivo*. The work highlights the role of Disabled Homolog-2 (Dab2) in mediating the internalization of CMCNPs. Through mass spectrometry based label-free quantitative proteomics and inhibitor studies, this study reveals the contribution of Dab2 to enhancing the cytosolic delivery of nanoparticles. Building on this mechanistic insight, the therapeutic potential of CMCNPs was evaluated by encapsulating an siRNA payload targeting the oncogenic mRNA survivin. The release of siRNA from the nanoparticles demonstrated significant tumor penetration and regression activity, with no off-target effects observed on major organs *in vivo*, enabling precise survivin gene targeting with enhanced specificity and therapeutic efficacy for osteosarcoma management.



URL: <https://pubs.rsc.org/en/content/articlelanding/2025/bm/d5bm01104c>





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

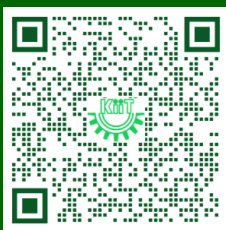
Author: Suryakanta, U.; Panigrahi, B.; Das, S.; Mandal, D.

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 internalization 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, Iqar; 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 μ M, 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: 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 $\sim 41.91\%$ reduction, while plastic-stored samples showed a $\sim 36.29\%$ increase. Mid-IR spectra revealed a blue shift ($\sim 4\text{--}14\text{ cm}^{-1}$) in O–H stretching and a red shift ($\sim 2\text{--}3\text{ cm}^{-1}$) 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 ($\sim 2\text{--}17\text{ cm}^{-1}$), 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 ($\sim 45.34\%$) in glass-stored medicines, while plastic-stored samples showed an enthalpic loss ($\sim 56.60\%$), 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: FEBS Journal

IF: 4.2

Title: Fractalkine is a key player in skeletal muscle metabolism and pathophysiology

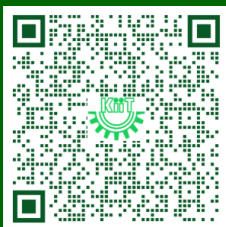
Author: Swalsingh, G; Pani, P; Sadayappan, S; Bal, NC

Details: 25 September 2025

Abstract: Fractalkine (CX3CL1) is increasingly recognised for its role in regulating the metabolism of various tissues, including skeletal muscle. The circulating level of CX3CL1 is influenced by multiple organs including the brain, adipose tissue and immune cells, with skeletal muscles emerging as a significant source. Growing evidence shows that CX3CL1 modulates muscle metabolism through autocrine and paracrine mechanisms as well as influencing properties (i.e. migration, secretion, cellular communication) of local immune cells. Within skeletal muscle, CX3CL1-signaling is involved in the regulation of fibre-type composition, mitochondrial remodeling, local inflammation, and regenerative capacity. These actions affect muscle plasticity and adaptability in both resting and active states. CX3CL1 also facilitates substrate uptake, particularly glucose and lipids, by interacting synergistically with insulin-signaling pathways, especially during metabolic stress or exercise. Furthermore, CX3CL1 contributes to the coordination of skeletal muscle function with other key metabolic organs such as adipose tissue, liver and brain. Notably, CX3CL1 appears to play a role in the pathogenesis of several chronic diseases, including type 2 diabetes (T2D), obesity, cardiovascular disease (CVD), insulin resistance (IR) and arthritis. These findings underscore the relevance of CX3CL1 in both health and disease. Here, we critically assess recent advances in CX3CL1 research, including its mechanism of action, and explore its potential implications in physiological and pathological scenarios.



URL: <https://febs.onlinelibrary.wiley.com/doi/10.1111/febs.70267>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: Journal of Molecular Structure

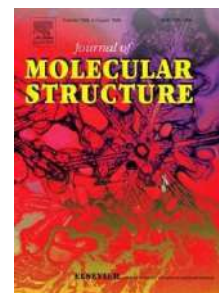
IF: 4.0

Title: Antimicrobial activities of novel substituted spiropyrrolidine based heterocycles synthesized by multicomponent reaction against *Bacillus subtilis* and *Pseudomonas aeruginosa*

Author: Suresh Babu A.R.; Rani S.; Singh S.P.; Khera A.; Alajangi H.K.; Parandaman S.; Raj A.R.N.; Gavaskar D.; Gartia J.; Pandey A.; Yadav V.K.; Singh G.; Barnwal R.P.

Details: Volume 1339, 5 September 2025, Article number 142373

Abstract: The growing resistance of bacteria to antimicrobial agents has intensified the need for novel strategies to combat bacterial infections, particularly those associated with biofilm formation. Biofilms enhance bacterial resilience against hostile environments, immune responses, and antimicrobial treatments. The ability of biofilms to influence bacterial pathogenesis underscores the critical need for new antibacterial agents with anti-biofilm activity. This research aims to synthesize cost-effective, structurally diverse, chemical compounds with the biological significance of disrupting biofilm formation. Here, we report a facile sequential reaction for one-pot, four-component synthesis of spiropyrrolidine heterocycles with 1,3-dipolar cycloaddition of azomethine ylide. The multicomponent reaction (MCR) provides high yield and regioselectivity of the desired product, under mild reaction conditions. Preliminary screening for these novel compounds involves biofilm assays, which assess the developmental processes of biofilms, providing insights into the compounds' biological potential. Subsequent in vitro experiments assessed their antibacterial potential against *B. subtilis* and *P. aeruginosa* using the minimum inhibitory concentration (MIC) assay. A cell culture assay evaluated toxicity of these compounds in MDA-MB-231 cell lines. All these investigations cumulatively highlight the potential of these molecules as antibacterial agents for *B. subtilis* and *P. aeruginosa*.



URL: <https://www.sciencedirect.com/science/article/pii/S0022286025010531?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: Microbiology Spectrum

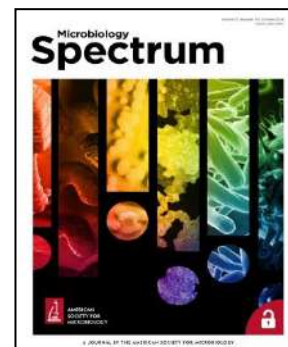
IF: 3.8

Title: Telmisartan, an anti-hypertensive drug, impedes JEV infection, possibly via the AT1/PPAR γ 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 PPAR γ) 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 IC₅₀ of 24.68 μ M and a CC₅₀ of >350 μ M (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 (PPAR γ antagonist) and AG (AT1 agonist), viral infection was increased remarkably, while AT1 was upregulated and PPAR γ was downregulated. TM treatment reversed these levels during infection. In addition, siRNA knockdowns of AT1 and PPAR γ showed an insignificant change in infection upon TM treatment. Furthermore, reduction of inflammatory markers like p-IRF-3, COX-2, and p-NF- κ B was observed after TM treatment in RAW264.7 cells, suggesting its immunomodulation through the AT1/PPAR γ 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: Plant Signaling and Behavior

IF: 3.6

Title: Genome-wide identification and expression analysis of NPR1-like genes in pearl millet under diverse biotic and abiotic stresses and phytohormone treatments

Author: J., Nayak, Jagatjeet; C., Jeky, Chanwala; B., Saha, Baisista; N., Dey, Nrisingha; S.R., Mahapatra, Soumya Ranjan; N., Misra, Namrata; M.K., Giri, Mrunmay Kumar

Details: Volume 20, Issue 1, September 2025

Abstract: Nonexpressor of pathogenesis-related genes 1 (NPR1) is a master regulator of salicylic acid (SA)- facilitated plant hormone signaling and plays a crucial role in plant defense through the activation of systemic acquired resistance (SAR). Although *NPR1*-like genes are associated with stress responses in a variety of plant species, no thorough genome-wide investigation of these genes has been undertaken in pearl millet (*Pennisetum glaucum*). This study discovered seven *PgNPR1*-like genes on four pearl millet chromosomes (Chr1, Chr2, Chr4, and Chr6), which exhibit close affinity to NPRs from other plants and have common gene structures, conserved motifs, and domains. The promoter regions of *PgNPR1*-like genes have numerous cis-acting elements connected with biotic and abiotic stresses, natural plant growth, and development. The qPCR results showed that *PgNPR1*-like genes were differentially expressed in distinct tissues, developmental stages, and under various biotic and abiotic stresses. *In silico* expression study of the *PgNPR1*-like genes after *Sclerospora graminicola* infection, causing downy-mildew disease, revealed that *Pgl_GLEAN_10029279* and *Pgl_GLEAN_10004489* were significantly upregulated. In addition, the docking results also showed that *Pgl_GLEAN_10029279* and *Pgl_GLEAN_10007810* out of all seven *PgNPRs* have strong interactions with the ligand SA, which proves their potential involvement in SA signaling and hence plant defense. These results offer a firm framework for comprehending the roles and development of *PgNPR1*-like genes in pearl millet.



URL: <https://www.tandfonline.com/doi/full/10.1080/15592324.2025.2552895#abstract>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: Biochimie

IF: 3.0

Title: Small molecule based targeting of the CsaA 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 CsaA 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 CsaA RNA thermometer.



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

