



SCHOLARLY PUBLICATIONS

School of Biotechnology

KIIT Deemed to be University

Journal Name: Plant Biotechnology Journal

IF: 12.8

Title: Unexpected Suppression of Tomato Fruit Cuticle Formation by Overexpression of a Key Cutin Biosynthetic Enzyme

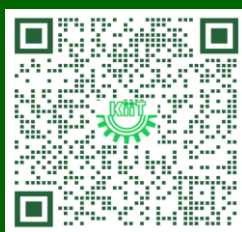
Author: Arya G.C.; Wassel E.; Mishra V.; Manasherova E.; Stark R.E.; Cohen H.

Details: August 2026

Abstract: Fruit cuticles regulate the diffusion of water, gases and solutes, functioning as essential protective interfaces against environmental and biotic stresses. Engineering cuticle structure and mechanics therefore represents a promising strategy for improving fruit quality and resilience. To enhance biosynthesis of cutin, the major structural component of the cuticle, we generated transgenic tomato lines expressing the Arabidopsis thaliana GLYCEROL-3-PHOSPHATE sn-2-ACYLTRANSFERASE 4 (AtGPAT4) gene specifically in exocarp tissues. AtGPAT4 is a key enzyme providing acylglycerol intermediates for cutin polymer assembly. We performed comprehensive phenotypic, microscopic, spectroscopic, transcriptional and surface nanomechanical analyses to monitor the structural consequences of AtGPAT4 overexpression and evaluated functional traits including water loss and susceptibility to the Botrytis cinerea fungus. Contrary to expectations, exocarp-targeted expression of AtGPAT4 generated fruits with cuticles that had diminished levels of cutin and epicuticular waxes, together with decreased cuticular stiffness and resistance to deformation, and whole fruit firmness. Evidently, these structural and chemical alterations did not affect thermal stability or water retention, but they increased susceptibility to fungal infection by B. cinerea. Although the engineering outcomes were unintended, they offered mechanistic insights into how manipulation of cutin biosynthesis pathways reshapes cuticle architecture, polymer composition and nanomechanical performance. This work underscores the complexity of engineering fruit surface traits and offers new perspectives for future biotechnological strategies aimed at improving cuticle robustness and pathogen resistance.



URL: <https://onlinelibrary.wiley.com/doi/10.1111/pbi.70742>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: International Journal of Biological Macromolecules

IF: 8.7

Title: Emerging roles of micropeptides in calcium cycling dysregulation and atrial fibrillation: A review

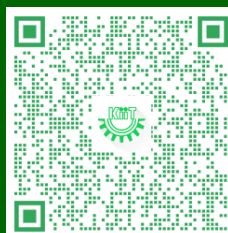
Author: Pani P.; Swalsingh G.; Sadayappan S.; Bal N.C.

Details: Volume 370, July 2026

Abstract: Atrial fibrillation (AF) is the most common sustained cardiac arrhythmia globally, marked by chaotic electrical impulses and irregular atrial contraction. At the cellular level, defective calcium (Ca^{2+}) handling plays a central role in AF pathogenesis, with the sarco/endoplasmic reticulum Ca^{2+} -ATPase (SERCA) pump being a critical determinant of intracellular Ca^{2+} reuptake and myocardial relaxation. Recent research has uncovered a class of small transmembrane micropeptides, phospholamban (PLB), sarcolipin (SLN), dwarf open reading frame (DWORF), myoregulin (MLN), endoregulin (ELN) and another-regulin (ALN), that directly modulate SERCA activity. Interestingly, these micropeptides exhibit chamber-specific expression and diverse regulatory mechanisms, functioning as inhibitors, uncouplers or facilitators of SERCA activity and are increasingly linked to atrial arrhythmogenesis. We explore evidence from genetically modified animal models and patient-derived data to elucidate how dysregulation of these peptides, particularly SLN and PLB, contributes to abnormal EC-coupling like Ca^{2+} cycling, delayed afterdepolarizations, oxidative stress and atrial remodeling. We also examine the influence of systemic metabolic regulators, such as thyroid hormones, catecholamines, dexamethasone and various exercise paradigms on micropeptide expression and function, offering insight into their intersection with AF progression. By dissecting the spatial, temporal and metabolic regulation of SERCA micropeptides, this review aims to offer current understanding about chamber-specific modulation of Ca^{2+} homeostasis and use these insights towards treatment of AF.



URL: <https://www.sciencedirect.com/science/article/abs/pii/S0141813026028503?via%3Dihub>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: Journal of Environmental Chemical Engineering

IF: 7.5

Title: Nano-biohybrid photocatalysts for sustainable wastewater treatment: Recent advances and future perspectives

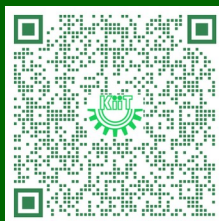
Author: Kumar M.; Sahoo P.C.; Pillai S.; Raut R.; Parida K.

Details: Volume-14, Issue-5, October 2026

Abstract: Currently, the rising discharge of industrial, agricultural and domestic effluents has severely contaminated the water bodies with a wide variety of organic and inorganic pollutants such as dyes, medicines, heavy metals and persistent organic compounds. Traditional wastewater treatment processes are often characterized by low efficiency, being costly to operate, secondary contamination, and weak elimination of the refractory pollutants. In that regard, it is possible to note that nano-biohybrid photocatalysts are becoming a prospective and viable alternative to advanced wastewater treatment. The mini-review will include a detailed account of the latest breakthroughs in designing, manufacturing and applications of nano- biohybrid photocatalysts with an accent on their prospects to alleviate the existing environmental issues. In detail, the synthesis strategies of nano-biohybrid systems (including incorporation of nanoparticles with enzymes, microbial cells or biomolecules), the importance of surface engineering, heterojunction formation and defect modulation in enhancing photocatalytic performance are reviewed. The mechanistic understanding of the pollutant degradation is established, where emphasis is made on the reactive oxygen species (ROS) formation, the efficiency of charge separation, and synergistic bio-nano interactions which enable the selective and quick degradation of a broad spectrum of pollutants. Recent studies have established that nano- biohybrid photocatalysts are more effective in degrading efficiencies, broad-spectrum pollutant removal, stability in operation, reuse and less energy is required as compared to traditional photocatalysts. These systems are special in that they incorporate biological specificity and catalytic activity with high surface area, tunable electronic structure, and light absorption characteristics of nanomaterials that lead to environmentally friendly, energy efficient, and long-term wastewater treatment. Lastly, the review mentions the current obstacles like material, scale-up, cost-effectiveness, and regulatory issues, and future trends including the creation of multifunctional, self-regenerative and scalable nano-biohybrid photocatalysts.



URL: <https://www.sciencedirect.com/science/article/abs/pii/S2213343726026175>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: Journal of Agriculture and Food Research

IF: 7.2

Title: Functional properties, health benefits, and biotechnological applications of the oyster mushroom (*Pleurotus ostreatus*): A comprehensive review

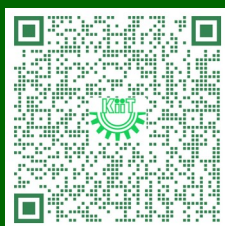
Author: Mukherjee K.; Panda S.K.; Samanta I.; Goswami L.; Maity P.J.; Love S.K.; Sasikumar R.; Chowdhary G.; T S.K.; Jaiswal A.K.

Details: Volume-29, July 2026

Abstract: *Pleurotus ostreatus*, commonly known as the “multi-purpose mushroom,” is an edible fungus distinguished by its unique convergence of nutritional, medicinal, and environmental attributes. In recent years, it has emerged as one of the most extensively studied and widely cultivated mushroom species, owing to its broad substrate adaptability and low input requirements. This review consolidates current knowledge of its nutritional composition and phytochemical profile, emphasising a diverse array of bioactive compounds with antimicrobial, anticancer, antioxidant, antidiabetic, anti-arthritis, and antiviral activities. The species is increasingly recognised as a functional food and a sustainable reservoir of bioactive molecules with significant potential for pharmaceutical applications. Emerging evidence also suggests its role in promoting mental health and overall well-being. The review further explores the interface between *P. ostreatus* and nanobiotechnology, as well as its potential applications. *P. ostreatus* secretes a spectrum of oxidative and ligninolytic enzymes, including lignin peroxidase, manganese peroxidase, laccases, and cellulases, enabling the degradation of pesticides, recalcitrant hydrocarbons, complex lignin polymers, and industrial pollutants. The multifaceted significance of *P. ostreatus* across functional foods, nutraceuticals, nanotechnology, therapeutics, and bioremediation positions it as an underexploited yet powerful platform for sustainable development, with strong potential to contribute to achieving the United Nations Sustainable Development Goals (2, 3, and 17).



URL: <https://www.sciencedirect.com/science/article/pii/S2666154326004734>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: LWT

IF: 7.1

Title: Development and characterisation of *Prunus nepalensis* fruit-aquafaba probiotic powder by vacuum freeze drying

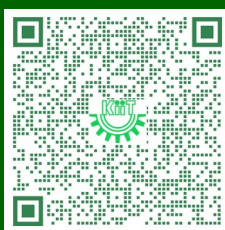
Author: Nongmaithem R.; Senthilkumar K.; Selva Kumar T.; Kaviarasu G.; Biswas S.; Panda S.K.; Rajarathinam R.; Sasikumar R.; Jaiswal A.K.

Details: Volume-253, 1st August, 2026

Abstract: Usage of probiotics in plant-based matrices has increased due to the addition of functional foods to the human diet. This work subjected to produce powdered probiotic sohiong juice to add value to a fruit rich in bioactives. *Lactobacillus plantarum* subsp. *lactis* (MCC 2974) inoculated into sohiong juice with different concentrations of aquafaba as a cryoprotectant and freeze dried. The freeze dried samples were characterized for the viable cell count, physicochemical properties, storage properties, and morphological characterisation. A formulation (F3) that contains probiotic juice and aquafaba at a 1:0.3 (v/v) ratio exhibits improved physicochemical properties, including lower hygroscopicity ($13.12 \pm 0.39\%$), indicating lower moisture absorption. This is followed by a wettability measurement of 38.15 ± 0.36 s, which indicates the time taken to sink the powder sample in water; it also retained colour parameters. The aquafaba mixed formulation shows increasing loose bulk density and reduction in porosity. Hausner Ratio and Carr's Index value prove that the formulated F3 sample passes the scale of flowability as per United States Pharmacopeia standards. Field Emission Scanning Electron Microscopy (FESEM) images confirmed proper particle formation of probiotics, followed by Fourier Transform Infrared (FTIR) Spectroscopy, which proved that the aquafaba formulation doesn't lose functional groups that present in the probiotic juice. Thermogravimetric Analysis (TGA) (30% residue at 800 °C) and Differential Scanning Calorimetry (DSC) (18.995 J/g) analysis results showed that aquafaba improved the thermal stability of sohiong fruit juice. It shows the potential of combining underutilized fruits with plant-based stabilizers to develop sustainable, health-promoting nutraceuticals.



URL: <https://www.sciencedirect.com/science/article/pii/S0023643826006869>





SCHOLARLY PUBLICATIONS
School of Biotechnology
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Journal Name: RSC Advances

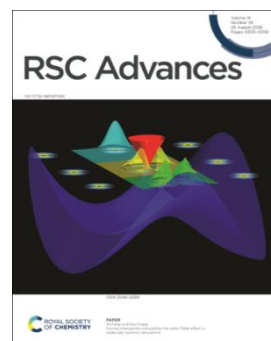
IF: 6.1

Title: Cu(ii) complex of a furoic acid-derived amide-imine conjugate for fluorescence detection of Th4+ with anticancer and molecular docking studies

Author: Changdar S.; Mitra P.; Chatterjee S.; Suryakanta U.; Mandal D.; Das D.

Details: Volume-16, Issue-39, August 2026

Abstract: A furoic acid derived amide based imine derivative has been employed to prepare a copper complex (C2) which is characterized by different analytical as well as spectroscopic techniques and, structurally authenticated by SC-XRD analysis. The C2 is explored for selective detection of Th4+ in ethyl acetate medium via 'turn-on' fluorescence, following the metal ion displacement protocol. The associated binding constant and detection limit for Th4+ are $3.03 \times 10^5 \text{ M}^{-1}$ and 7.58 nM respectively. ESI-MS spectrum and Job's plot confirm 1 : 1 (mole ratio) stoichiometric interaction. The C2 shows cytotoxicity against human colon cancer cell lines such as HCT 116 and a breast cancer cell line, MCF 7 having IC50 values of 2.07 μM and 1.72 μM , respectively. Moreover, molecular docking studies unveil drug-like behavior, along with the mode of action of C2 towards retrieved proteins.



URL: <https://pubs.rsc.org/ra/article/16/39/44490/1286220/Cu-ii-complex-of-a-furoic-acid-derived-amide-imine>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: International Journal of Pharmaceutics

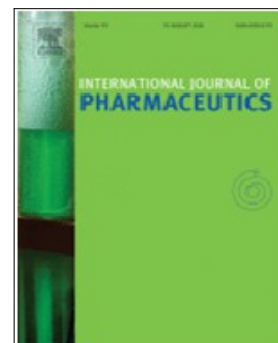
IF: 6.0

Title: Artificial intelligence and CRISPR-based approaches for targeted delivery of bacteriophages

Author: Pradhan R.R.; Pati S.; Samal S.K.

Details: Volume-701, 10th August, 2026

Abstract: The rapid emergence of Multidrug-Resistant (MDR) bacteria has increased interest in bacteriophage therapy as a promising alternative to conventional antibiotics. Bacteriophages are host-specific bacterial viruses that selectively infect and destroy pathogenic bacterial strains. Recent developments in artificial intelligence (AI) and Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-based technologies offer innovative approaches to address challenges such as narrow host range, rapid immune clearance, phage instability, bacterial resistance, and biofilm penetration barriers. By integrating AI-driven structural modeling with CRISPR-mediated genome editing, these methods enable the targeted delivery of bacteriophages. This review focuses on next-generation approaches that combine AI-assisted phage identification, host prediction, and therapeutic optimization with CRISPR-based genome engineering for targeted phage delivery and improved safety. Overall, this review highlights the potential of AI- and CRISPR-assisted phage therapy for the treatment of MDR bacterial infections. It will also provide a systematic overview of bacteriophage biology, life cycle, and mechanisms of action, while focusing on the influence of phage morphology on therapeutic performance, recent advances, current clinical, preclinical studies, and future perspectives. Although phage therapy shows considerable potential against MDR bacterial infections, several challenges related to delivery, safety, and clinical translation remain. The integration of AI and CRISPR technologies has the potential to improve phage selection, targeting specificity, and therapeutic performance. However, continued research, clinical validation, and regulatory development will be essential for translating these advances into practical antimicrobial therapies.



URL: <https://www.sciencedirect.com/science/article/abs/pii/S0378517326006034>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: Materials Advances

IF: 5.8

Title: Correction: Hyperbranched poly(ethylene glycol)-trimesic acid polyesters as tunable scaffolds for modulating oxidative stress, calcium homeostasis, and neuro-keratinocyte interactions in tissue engineering

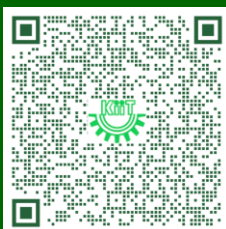
Author: Mukherjee A.; Kumar S.; Basak S.; Goswami L.; Goswami C.; Chanda J.; Ghosh P.; Mukhopadhyay R.; Bandyopadhyay A.

Details: Volume-7, Issue-15, August 2026

Abstract: Correction for 'Hyperbranched poly(ethylene glycol)-trimesic acid polyesters as tunable scaffolds for modulating oxidative stress, calcium homeostasis, and neuro-keratinocyte interactions in tissue engineering' by Aniruddha Mukherjee et al., Mater. Adv., 2025, 6, 6742-6754, <https://doi.org/10.1039/d5ma00216h>.



URL: <https://pubs.rsc.org/ma/article/7/15/7893/1282477/Correction-Hyperbranched-poly-ethylene-glycol>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: Materials Chemistry and Physics

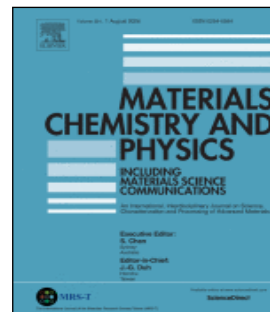
IF: 5.2

Title: Intraoral biocompatible mucoadhesive buccal patch imbued with bromelain for targeting oral fibrosis: Evaluation of functional activity, cytotoxicity, and safety

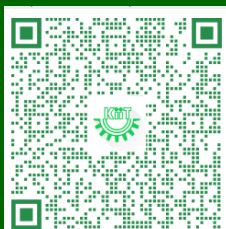
Author: Kokkanti R.R.; Bajoria A.A.; Parida N.; Viswanathan S.; Pritam P.; Kumar N.S.; Kushwaha G.S.; Panda A.K.; Veeraraghavan G.; Patnaik S.

Details: Volume 361, August 2026

Abstract: A bromelain-loaded mucoadhesive buccal patch was developed for enzymatic therapy in oral submucous fibrosis (OSF), a progressive fibrotic disorder characterized by excessive collagen deposition. The patch was analytically characterized for content, release kinetics, and enzymatic stability. HPLC and LC-MS/MS confirmed bromelain content and integrity, while in vitro release studies demonstrated near-complete release within 90 min in phosphate-buffered saline and artificial saliva. Zymography revealed 76.67 U/mL enzymatic activity at 2 h, even after 6 months of storage, confirming long-term stability. LC-MS peptide mapping validated collagen degradation. Ex vivo studies showed prolonged mucoadhesion (~137 min), supporting effective mucosal retention. HPLC confirmed drug purity. Biological assays including MTT, colony formation, wound healing, and live/dead staining indicated selective cytotoxicity and apoptosis in KB-3-1 oral cancer cells, with high viability of normal fibroblasts. Acute toxicity studies in rats revealed no systemic toxicity or organ damage. Together, these findings establish a robust analytical and biological profile for the patch, supporting its potential as a non-invasive, enzyme-based therapy for OSF. Future studies will focus on dose optimization, long-term in vivo efficacy, and translational potential.



URL: <https://www.sciencedirect.com/science/article/pii/S0254058426006814?via%3Dihub>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: ACS Omega

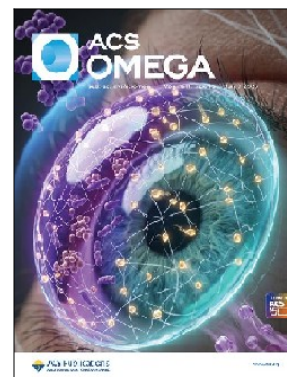
IF: 5.2

Title: Designing a Whole-Cell Biosensor for Detection of Toxic Metals Using Intein Splicing Inhibition of Mycobacterium tuberculosis SufB Protein

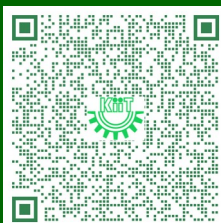
Author: Mehra A.; Nanda A.; Nayak S.

Details: Volume-11, Issue-26, 7th July, 2026

Abstract: Heavy metal contamination, driven by anthropogenic disruption of natural geochemical cycles, has led to widespread bioaccumulation, posing a serious global health threat. Addressing this crisis demands the development of simple and sensitive strategies capable of monitoring metal pollution in the environment. Leveraging nongenetically modified native organisms, this research offers a promising low-cost, eco-friendly screening approach for detecting heavy metals in contaminated samples. Current study uses post-translational splicing of the Mycobacterium tuberculosis (Mtb) SufB precursor protein to detect metals by linking metal-induced splicing inhibition to viability loss of native mycobacterial cells. Toxic metal ions like Cd^{2+} and Hg^{2+} blocked splicing activity of Mtb SufB precursor protein over a concentration range of 25 μM –2 mM, while Pb^{2+} and Cr^{3+} failed to do so. An innovative biosensor platform was designed to detect metals by a simple Alamar Blue assay using attenuated Mtb H37Ra as indicator cells. Qualitative metal detection was assessed via colorimetric variation relating to mycobacterial viability, while concurrent spectral absorbance measurement enabled metal ion quantification. Loss of H37Ra cell viability by metal ions over the 25 μM –2 mM concentration range highlighted the sensitivity of the designed biosensor, while the addition of metal-specific chelators reversed the effect. Multiplexing ability was evaluated by including known splicing inhibitors like Cu^{2+} , Zn^{2+} , and Pt^{4+} over various concentration ranges alongside Cd^{2+} and Hg^{2+} in a simple 96-well plate format. The designed intein-based biosensor offers a user-friendly platform, readily standardizable for high-throughput detection using native organisms harboring metal-sensing precursor proteins. As a proof-of-concept, this study demonstrates the applicability of intein-based biosensing for initial heavy metal screening in environmental and industrial effluents, serving as a rapid and accessible tool prior to targeted advanced analysis.



URL: <https://pubs.acs.org/acsodf/article/11/26/38663/5167004/Designing-a-Whole-Cell-Biosensor-for-Detection-of>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: Progress in Additive Manufacturing

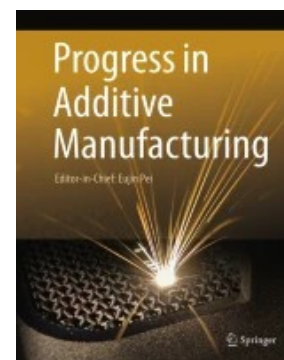
IF: 5.2

Title: Fabrication of cost-effective glass-bottom cell-culture device using fused deposition modeling: new avenue for bioimaging

Author: Swain S.; Shahul Hameed S.; Jain S.; Kumar S.S.; Pati F.; Unni H.N.; Suar M.; Giri L.

Details: 14th July, 2026

Abstract: Achieving high-resolution 4D imaging (XYZt) of larger areas is paramount for comprehensively characterizing engineered tissues and disease models. Yet the high cost and optical requirements of glass-bottom devices, which are essential for confocal microscopy, often hinder the use of such advanced imaging. This study presents an innovative method for crafting cost-effective microfluidic devices to overcome this challenge. Diverging from traditional soft lithography techniques, which require cleanroom facilities and costly materials, our approach harnesses fused deposition modeling (FDM) to fabricate glass-bottom polydimethylsiloxane (PDMS) devices that seamlessly incorporate a 0.17 mm glass coverslip optimized for laser scanning confocal microscopy (LSCM). Using glass-embedded acrylonitrile butadiene styrene (ABS) templates, we achieve precise fabrication of spiral channels in PDMS, thereby substantially reducing associated costs, including installation, infrastructure, and maintenance. The resultant device boasts numerous functionalities, facilitating diverse applications such as cell culture, reagent mixing, morphology monitoring, and on-chip immunoassays. Moreover, we showcase its versatility by demonstrating its efficacy for 4D calcium imaging with a resonance scanner in an LSCM, using HMC3 (human microglial) and MCF-7 (human breast cancer) cell lines. Beyond its cost-effectiveness, this biochip platform is suitable for applications such as toxicity analysis, drug screening, and real-time monitoring. This advancement promises new avenues for comprehensive bioimaging research, offering affordable and accessible solutions for studying complex biological systems. By democratizing access to high-resolution imaging, our method paves the way for a deeper understanding and characterization of diverse biological phenomena. Furthermore, its cost-effectiveness and ease of fabrication hold promise for adoption across various research fields, empowering researchers to further explore biological processes.



URL: <https://link.springer.com/article/10.1007/s40964-026-01837-y>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: Expert Opinion on Therapeutic Targets

IF: 5.1

Title: 5-FU in combination with PARP inhibitor ABT-888 deregulates MGMT-dependent mismatch repair (MMR) pathway in MMR-proficient colorectal cancer stem cells by modulating MGMT/PARP1/MSH6 complex

Author: Paul S.; Das C.; Bhal S.; Sinha S.; Dash S.R.; Acharya S.S.; Goswami A.; Goutam K.; Kundu C.N.; Parija T.

Details: Volume-30, Issue-7, July 2026

Abstract: Background: Previous study showed the PARP inhibitor ABT-888 potentiates the cytotoxicity of 5-fluorouracil (5-FU) by inhibiting PARP1-mediated mismatch repair (MMR) pathway via MSH6 deregulation in MMR-proficient colorectal cancer stem cells (CRC-CSCs). Emerging evidence indicates 5-FU regulates O6 -methylguanine-DNA-methyltransferase (MGMT) activity, but the mechanistic basis of MGMT involvement in PARP1-mediated MMR pathway following 5-FU treatment remains complex and poorly defined. Research design and methods: This study delineates the role of MGMT in 5-FU-induced MMR pathway activation and evaluates 5-FU+ABT-888 combination effects on MGMT modulation in CRC-CSCs. The molecular mechanism has been studied by using colocalization, western blot, co-immunoprecipitation, MGMT gene-knockdown, and molecular docking in in vitro, in silico, and ex vivo preclinical models. Results: 5-FU treatment induced PARylated-PARP1 in CRC-CSCs, promoting PARP1-MGMT-MSH6 interactions that activated MMR. ABT-888 inhibited PARylation in 5-FU-pre-exposed CSCs. Therefore, PARP1 could not physically interact with both MGMT and MSH6, and complete abolishment of MGMT and MSH6, and MMR protein downregulation were observed in combination treatment. MGMT silencing confirmed its critical role in PARP1-mediated MMR activation. Similar findings were obtained in in silico and ex vivo models. Conclusions: 5-FU+ABT-888 enhanced CRC-CSCs death by inhibiting the PARP1-MGMT-MSH6 interaction and simultaneously inhibiting the MGMT-dependent PARP1-mediated MMR pathway in MMR-proficient CRC-CSCs.



URL: <https://www.tandfonline.com/doi/full/10.1080/14728222.2026.2706483>





SCHOLARLY PUBLICATIONS
School of Biotechnology
KIIT Deemed to be University

Journal Name: Journal of Molecular Structure

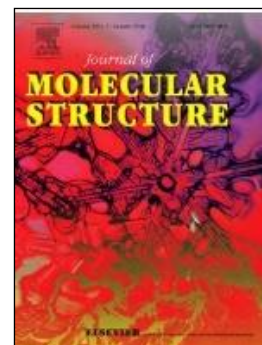
IF: 4.9

Title: Tetranuclear defective dicubanes of vanadium complexes: Synthesis, characterization and their potential biological activities

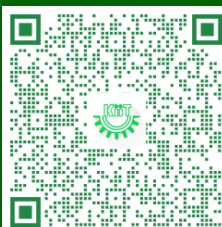
Author: Singh A.R.; Rajpurohit A.S.; Khongsai L.; Singh S.A.; Chingakham B.S.; Jaccob M.; Lonibala R.

Details: Volume 1373, October 2026

Abstract: Four tetranuclear V(V) complexes 1-4 with unique $\{V_4O_8\}$ defective dicubane cores were synthesized through novel route under methanolic condition using bis(acetylacetonato) oxovanadium(IV) precursor along with 2,2'-bipyridine and substituted 2,2'-bipyridine ligands i.e. 2,2'-bipyridine in (1), 4,4'-dimethyl-2,2'-bipyridine (2), 5,5'-dimethyl-2,2'-bipyridine (3) and 4,4'-dimethoxy-2,2'-bipyridine (4). The complexes are characterized on the basis of CHN, UV-visible, IR and SC-XRD analysis data. Single-crystal X-ray diffraction analysis revealed the solid-state structures of all complexes (1-4) with distorted octahedral geometries for the four V(V) ions. The electronic nature of the complexes and their molecular surfaces were investigated using density functional theory (DFT) and Hirshfeld surface analysis. In vitro antidiabetic studies indicated that the complexes possess good antidiabetic activities against α -glucosidase and in vitro studies of anticancer activities against A549 cells, complex 3 shows better activity with $IC_{50} = 2.5 \pm 1.07 \mu M$.



URL: <https://www.sciencedirect.com/science/article/abs/pii/S0022286026013293?via%3Dihub>





SCHOLARLY PUBLICATIONS
School of Biotechnology
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Journal Name: Scientific Reports

IF: 4.9

Title: Structure-based virtual screening and molecular dynamics elucidate novel inhibitors of HIV-1 TAR RNA from enamine library

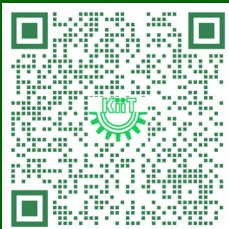
Author: Mundlia P.; Singh S.P.; Gartia J.; Ranawat P.; Singh G.; Barnwal R.P.

Details: Volume-16, Issue-1, December 2026

Abstract: The HIV-1 trans-activation response (TAR) RNA is a key regulatory element necessary for viral replication, presenting a high-value target for anti-HIV therapeutics. Recent advances in RNA-targeted drug discovery have leveraged large, diverse compound libraries, such as the Enamine collection, using structure-based virtual screening to uncover novel modulators of RNA structure and function. In this study, we employed an integrative in silico approach combining high-throughput virtual screening of the Enamine library against the central bulge region of HIV-1 TAR RNA with molecular dynamics (MD) simulations to assess binding stability and conformational adaptability of lead molecules. Virtual screening pinpointed multiple candidate ligands predicted to disrupt the critical Tat-TAR interaction interface, with subsequent MD simulations over 500-nanosecond timescales revealing ligand-induced stabilization of druggable RNA conformations and dynamic remodelling of key binding pockets. Notably, some top-scoring compounds featured strong and persistent contacts within the U23-C25 bulge and the adjacent major groove, recapitulating pharmacologically relevant mechanistic disruption. These findings reinforce the synergy of structure-based screening and MD for identifying and validating RNA-targeted small molecules and provide promising new scaffolds for further experimental testing as selective HIV-1 replication inhibitors.



URL: <https://www.nature.com/articles/s41598-026-50156-3>





SCHOLARLY PUBLICATIONS

School of Biotechnology

KIIT Deemed to be University

Journal Name: Biology

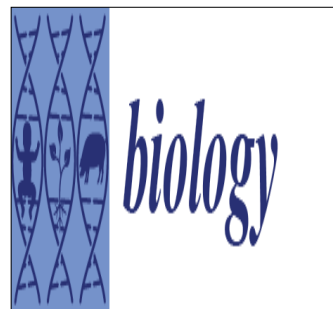
IF: 4.3

Title: Scaling Across Environments: Distinct Genetic Architectures Underlie Thermal and Nutritional Plasticity of Size and Morphological Scaling in *Drosophila melanogaster*

Author: Ghosh S.M.; Vea I.M.; Wilcox A.S.; Frankino W.A.; Shingleton A.W.

Details: Volume-15, Issue-14, July 2026

Abstract: Across animals, variation in adult body size is accompanied by coordinated variation in the size of individual morphological traits. However, the same morphological trait can scale differently with body size depending on what drives the size variation. In *Drosophila melanogaster*, for example, wing size scales differently from body size when size varies because of developmental nutrition versus developmental temperature. Whether the genetic basis of size plasticity and scaling is shared across different environmental regulators of size remains unclear, but it is central to predicting how selection acts on the developmental mechanisms that regulate trait size, plasticity, and morphological scaling. Using ~100 isogenic *D. melanogaster* lineages, we measured wing and leg size across nutritional and thermal treatments. For each lineage, we estimated nutritional and thermal plasticity for both traits, as well as the wing–leg individual-level scaling relationship, or ILSR, generated by each environmental source of size variation. We found extensive genetic variation in both thermal and nutritional plasticity for wings and legs and in the slope of the ILSR between them. However, a lineage’s thermal plasticity was genetically uncorrelated with its nutritional plasticity for either trait, and we detected no genetic correlation between the slopes of thermal and nutritional wing–leg ILSRs. We also found no genetic correlation in the slope of nutritional wing–leg ILSRs between temperatures. Thus, the slope of a lineage’s nutritional ILSR at 17 °C was not predictive of its slope at 25 °C or 28 °C. Nevertheless, the overall pattern of nutritional ILSRs was conserved across temperatures. These results suggest that the genetic architecture of size plasticity and scaling depends on the environmental source of size variation. Consequently, the evolutionary response of scaling to selection in heterogeneous environments may not be predictable from genetic variation measured in any single environment.



URL: <https://www.mdpi.com/2079-7737/15/14/1157>





SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: Biochimie

IF: 3.4

Title: Sedentariness disrupts, while exercise restores, thermogenic and metabolic plasticity in inguinal adipose tissue of mice

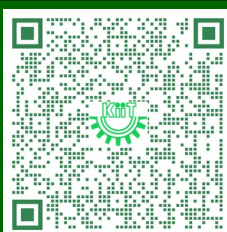
Author: Sahu B.; Senapati U.; Pani P.; Pani S.; Swalsingh G.; Pati B.; Tikoo O.; Giri S.; Kar B.P.; Trivedi R.; Bahadi C.K.; Nikhil K.; Kumar D.; Bal N.C.

Details: Volume-249, October 2026

Abstract: Inguinal WAT (IngWAT) quickly adapts its metabolism to body energy status variations, including uncoupling protein 1 (UCP1) expression. However, its long-term metabolic response to long-term sedentary and exercise training has not been fully characterized. This study investigated IngWAT's long-term response to sedentary (SED, restricted cage) vs. exercise (EXER, treadmill running with a defined protocol) conditions in mice. EXER mice showed increased expression of Sarcoendoplasmic Reticulum Calcium ATPase (SERCA)2b and UCP1, along with a reduction in adipocyte size, indicating activation of thermogenesis. Fascinatingly, exercise elevated the expression of CIDEA in tiny adipocytes and promoted a beiging effect in mice. Elevated OXPHOS complex proteins expression and NMR-based metabolite profiling in IngWAT revealed that exercise profoundly reprogrammed energy metabolism by strengthening phosphocreatine-creatine buffering, regulating TCA cycle metabolite cycling (citrate and succinate), and increasing ketone body formation (3-hydroxybutyrate and acetone). Elevated glycerol level, a higher glycerol-lactate ratio, and reduced carnitine in IngWAT of EXER mice reflected improved fatty acid uptake and β -oxidation, in contrast to the metabolic inefficiency observed during sedentariness. Moreover, increased vascularization was accomplished by upregulated expression of vascular endothelial growth factor 1a (VEGF1a), angiopoietins (ANG)1&2, supports elevated metabolic state in exercise. Conversely, SED mice showed larger adipocytes with uniform CIDEA expression, but a downregulation of thermogenic proteins. Interestingly, a significant downregulation of mitochondrial complex III was also observed, which indicates altered mitochondrial physiology in SED mice. Data presented here suggest that IngWAT is metabolically flexible and can undergo both structural and metabolic adaptations in accordance with physical activity level.



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SCHOLARLY PUBLICATIONS School of Biotechnology KIIT Deemed to be University

Journal Name: Chemical Biology & Drug Design

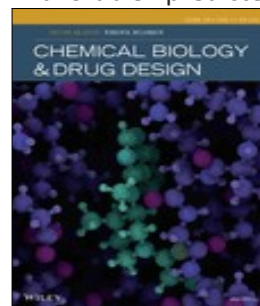
IF: 3.3

Title: Discovery of Potent Antimalarial Agents Targeting Plasmodium falciparum DNA Gyrase B by Integrating Computational and Experimental Approaches

Author: Naik, B; Sahu, W; Sethi, G; Prashar, C; Baldodiya, GM; Poswal, J; Mandal, CC; Hwang, JH; Panday, KC; Reddy, KS; Prusty, D

Details: Volume 108, Issue 1, 21st July, 2026

Abstract: The global spread of drug-resistant Plasmodium falciparum, particularly artemisinin-resistant strains, underscores the urgent need for novel antimalarial agents with distinct mechanisms of action and improved therapeutic potential. In this study, we employed an integrated in silico and in vitro strategy to identify compounds with inhibitory activity against P. falciparum apicoplast Gyrase B (PfGyrB). High-throughput virtual screening identified hit compounds with favorable predicted interactions against the target protein, which were subsequently evaluated using biochemical ATPase inhibition and parasite growth inhibition assays. UNC8153 and Fexofenadine hydrochloride demonstrated time-dependent antiplasmodial activity, with lower IC₅₀ values at 96 h than at 48 h under prolonged exposure conditions. UNC8153 exhibited greater antiplasmodial activity (~25-fold) than the reference compound novobiocin during the second intraerythrocytic cycle. Morphological analysis indicated impaired parasite development during the second intraerythrocytic cycle under prolonged exposure conditions. Importantly, UNC8153 retained inhibitory activity against the artemisinin-resistant C580Y strain and exhibited minimal cytotoxicity toward HEK-293 cells under the tested experimental conditions. Structural similarity analysis indicated that the identified compounds are chemically distinct from currently used antimalarial drugs, supporting their structural novelty. Collectively, these findings identify UNC8153 as a structurally distinct new antiplasmodial scaffold warranting further mechanistic, pharmacological, and in vivo evaluation.



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