List of 10 best papers with Highligtening the important discovers

1. Methicillin-resistant Vancomycin resistance and Staphylococcus aureus In both the hospital and community sectors, Enterococcus faecalis (VRE) are well-known pathogenic, multi-drug resistant (MDR) bacteria, and sulfamethoxazole, the first antibacterial medication, is no longer effective. Utilizing the dye-azo synthesis methodology, the monoterpene phenol thymol was conjugated with each of the seven sulfa drug derivatives independently. The conjugates were then examined utilizing spectral analysis methods like UV, FTIR, MS, HPLC, HNMR, 13C NMR, and SEM. The zone of inhibition, MIC, and MBC values of each conjugation were tested against isolated MRSA and VRE pathogens from clinical samples in vitro and in silico to determine their antibacterial efficacy. Since the protein database does not provide the 3-dimensional structures of the dihydropteroate synthases (DHPSs) of the targeted bacteria, homology models of the DHPS enzymes of both bacteria were created and validated by Ramachandran plots.MRSA-DHPS and VRE-DHPS were targeted by molecular docking using seven conjugates as ligands. To evaluate the standard drug-likeliness characteristics of conjugates, further bioinformatics tools, PASS prediction, Lipinski rules of five, computational LD50 value, toxicity class, HOMO, LUMO, and EPS plots were used. The lowest MIC and MBC values for the conjugate, 4b (thymol + sulfadiazine), against MRSA and VRE strains on agar plates were 20 and 40 mg/mL, whereas the reference antibiotic ampicillin had the lowest MIC and MBC values at 80 to 180 mg/mL. Using cultured human lymphocytes from umbilical cord blood, it was determined that 4b was generally non-toxic to human cells at a concentration of 15,000mg/L. In order to combat horrifying MDR bacteria, 4b could be marketed as a novel antibacterial. Cited by Swain, S.S., **Paidesetty, S.K.,** Padhy, R.N." Antibacterial activity, computational analysis, and host toxicity study of thymol-sulfonamide conjugates**"** ***Biomedicine and Pharmacotherapy***, **2017**, 88, pp. 181–193 10.1016/j.biopha.2017.01.036 Elsevier **SCI Impact factor 7.41**
2. Due to the rise of dapsone resistance, which affects the main medication in the current multidrug therapy, leprosy (cause, Mycobacterium leprae), continues to be a persistent public health issue with consistent incidence rates.Therefore, to develop additional dapsone derivatives (DDs), against the folic acid production route, structural modification through medicinal chemistry was applied to circumvent drug resistance. The strategy involved

theoretical modelling, molecular docking, molecular dynamic (MD) simulation, as well as determination of binding free energy for validation of newly developed seven DDs before synthesis.To comprehend the manner of binding and effectiveness of DDs against the wild-type and mutant dihydropteroate synthases (DHPS), docking, and MD simulation studies were employed. In order to comprehend the conformational dynamics of DHPS-DD complexes, principal component analysis was used. Furthermore, the Molecular Mechanics/Poisson Boltzmann Surface Area approach was used to determine the overall stability and negative binding free energy of DHPS-DD complexes. According to a study in molecular mechanics, DD3 has a larger binding free energy than dapsone when it comes to mutant DHPS. Van der Waals and electrostatic energy are shown to contribute significantly to the overall negative free energy, whereas polar solvation energy opposes the binding.Finally, DD3 was produced and studied utilising proton nuclear magnetic resonance, liquid chromatography, mass spectrometry, UV, and Fourier transform infrared spectroscopy methods. This study made the case for future promotion of DD3 as a new antileprosy drug. To save time and resources in the present drug development modules, effective therapies can be found with the aid of bioinformatics technologies and medicinal chemistry principles. Cited by Swain, S.S., **Paidesetty, S.K.**, Dehury, B., ...Hussain, T., Padhy, R.N. "Molecular docking and simulation study for synthesis of alternative dapsone derivative as a newer antileprosy drug in multidrug therapy***" Journal of Cellular Biochemistry***, **2018**, 119(12), 9838–985210.1002/jcb.27304Wiley pub **SCI Impact factor 4.48**

3. Even after being treated with ongoing multidrug therapy (MDT), leprosy remains a dangerous public health risk for the cause of severe impairment and final morbidity cases with stable prevalence rates. More unlucky individuals in some poor nations now fear leprosy as a result of dapsone (DDS) resistance. Here, using an azo-coupling procedure, DDS was chemically coupled with four different phytochemicals to create dapsone-phytochemical conjugates (DPCs). Before chemical synthesis and spectrum characterizations such as proton-HNMR, FTIR, UV, and LC-MS, possible biological activities were verified with computational chemistry and quantum mechanics via a molecular dynamics simulation programme. with the "mouse-foot-pad propagation method" and the active ingredient's host-toxicity testing, the in vivo antileprosy activity

was seen with the WHO-recommended concentration of 0.01% mg/kg each DPC for 12 weeks. The DPC4 reduced one-log bacilli cells in the footpads of DDS-resistant sick mice while leaving no bacilli in the hind pads of DDS-sensitive mice.Since a small percentage of dead cells were discovered under a fluorescent microscope to be red, the in vitro host toxicity investigation also confirmed that the DCP4 up to 5,000 mg/L level was safe for oral administration. Locating the prospective chemical entity could be aided by a number of cutting-edge bioinformatics techniques, saving time and resources for in vitro and in vitro studies. According to research on in vitro host toxicity and in vivo antileprosy activity, DPC4 could be employed in MDT in place of DDS. Cited by Swain, S.S., **Paidesetty, S.K.,** Dehury, B., ...Vedithi, S.C., Padhy, R.N. "Computer-aided synthesis of dapsone-phytochemical conjugates against dapsone-resistant Mycobacterium leprae" ***Scientific Reports***, **2020**, 10(1), 6839 10.1038/s41598-020-63913-9 **Springer nature SCI Impact factor 4.99**

4. The discovery of new UTI antibacterial agent(s) remains the order of the day given the prevalence of bacterial UTI (Urinary Tract Infection) around the world. Here, two series of 4-hydroxy coumarin derivatives based on Mannich, **7a-m** and **8a-m**, were created by condensing appropriate heterocyclic amines with aldehydes. In vitro antibacterial tests and 1H- and 13C-NMR spectrum analysis were used to analyse the synthesised compounds. With MIC values of 12.50 and 25 mM, respectively, the substance 4-hydroxy-3-((4-hydroxy-3-methoxyphenyl)(morpholino)methyl)-2H-chromen-2-one 8l was the major derivative against harmful bacteria *Staphylococcus aureus* and *Escherichia coli*..The analogues 7f, 7l, 8d, 8j, and 8k could be effective druggable compounds with considerable binding affinity towards bacterial tyrosine kinase, as target, according to computational assessments utilising the Lipinski's rule of five, ADMET characteristics, and molecular docking studies. Each system was subjected to molecular dynamics simulations for 100 ns in order to understand the manner of binding and intrinsic stabilities of powerful receptor-ligand complexes. The analogues 8l form a variety of non-bonded interactions, according to intermolecular contact studies and inherent hydrogen-bond stability, while the receptor tyrosine kinase is primarily dominated by electrostatic and hydrophobic contacts. The outcomes of the current structure-based designing technique may prove to be a useful tool in the near future for the discovery of new antibacterial medication candidate(s) against

UTI. Cited bySahoo, C.R., **Paidesetty, S.K.**, Dehury, B., Padhy, R.N. "Molecular dynamics and computational study of Mannich-based coumarin derivatives: potent tyrosine kinase inhibitor" ***Journal of Biomolecular Structure and Dynamics***, **2020**, 38(18), 5419. 5428, 10.1080/07391102.2019.1701554Taylor &Francis **SCIImpact factor 5.26**

5. Antibiotic resistance has been building for years and is finally manifesting itself as a major global public health problem. As a result, there is an urgent need for novel, more powerful medication candidates to combat the anticipated rise of antibiotic-resistant bacteria and fungi. The Mannich condensation synthesis of the corresponding cyclic amines 3a-3 g and N-heteroaryl- 4-amino benzenesulfonamide 3h-3l with thymol and formaldehyde in an acidic medium was devised and used to create a series of amino methylated sulfonamide congeners, 4a-4l, that contain thymol. By performing spectroscopic analyses, including $^{1}H/^{13}C$ NMR, FTIR, ESI-HRMS, and elemental analysis, the structures of the synthesised compounds were confirmed. XRD analysis was used to characterise the powder of the synthesised compounds. *Staphylococcus aureus, Streptococcus pyogenes*, and *Escherichia coli*, as well as *Candida*, were used to test the derived compounds' antibacterial and antifungal properties. All compounds' antimicrobial activities showed moderate to excellent bacterial inhibition, but 2-isopropyl-5-methyl-4-(pyrrolidin-1-ylmethyl)phenol, 4f, significantly inhibited S. aureus and *E. coli* with MICs of 3.12 g/ml and 12.5, respectively. With a MIC of 6.25 g/ml for *E. coli* and *S. aureus* and 3.12 g/ml for *T. rubrum*, the compound 4-((dimethylamino)methyl)-2-isopropyl-5-methylphenol, 4 g, showed good inhibition. The synthetic chemicals 4g and 4h inhibited the fungus *T. rubrum* with the maximum levels at 27 and 28 mm, respectively. As a result, the synthetic compounds containing methylated dimethylamino in thymol may be the best candidates for having antibacterial and antifungal effects. Cited by AK Bishoyi, M Mahapatra, **SK Paidesetty**, RN Padhy"Design, molecular docking, and antimicrobial assessment of newly synthesized phytochemical thymol Mannich base derivatives" ***Journal of Molecular Structure***, **2021**, 1244, 130908 10.1016/j.molstruc.2021.130908 Elsevier **SCI Impact factor 3.86**

6. We are currently using the Debus-Radziszewski multicomponent synthesis reaction to synthesize two sets of 2,4,5-tri- and 1,2,4,5-tetra-substituted (4a–4d) and 6a–6d) imidazole derivatives in our cascading effort to create new, powerful compounds. The obtained

compounds confirm their structures were interpreted by 1H/13C NMR, FT-IR, elemental analysis, purity, and HPLC examination of the retention time. We have synthesized various imidazole derivatives based on the molecular docking studies for their binding affinities, wherein chemical 6c has demonstrated greater anti-proliferative action by producing higher rate of apoptosis than the other chemicals, supporting the *in-silico* prediction. By a single XRD study, the crystalline of compound 4d has been established. The triple negative breast cancer cell line (MDA-MB-221) was used to test the synthesized compounds for their *in vitro* anti-cancer effects. Results from oral squamous cell carcinoma cell line (H357) and pancreatic cancer cell lines (MIA PaCa-2) suggested that each substance, at different times, suppressed cell growth in a concentration-dependent manner. The *S. aureus* bacterial strain was found to be susceptible to compounds 4b and 6d, but only with a MIC of 12.5 µg/mL, compound 4d fairly inhibited the fungus *T. rubrum*. Research of molecular docking demonstrates effective interaction of the synthetic chemicals with the oncogenesis-related target known as MELK elevated binding profiles. The thorough molecular dynamics analysis was used to further examine the lead molecule 6c make sure the system is stable. Cited by Monalisa Mahapatra, Priyanka Mohapatra, Kakarla Pakeeraiah, Ravi Kumar Bandaru, ..., **Sudhir Kumar Paidesetty** "*In-vitro* anticancer evaluation of newly designed and characterized tri/tetra-substituted imidazole congeners- Maternal Embryonic Leucine Zipper Kinase inhibitors: molecular docking and MD Simulation approaches" ***International Journal of Biological Macromolecules*** **249 (2023) 126084 SCI Impact factor 8.87** **https://doi.org/10.1016/j.ijbiomac.2023.126084**

7. A series of *N*-heteroaryl- 4-(1-(2-oxo-2 H -chromen-3-yl) ethylideneamino) benzenesulfonamide (5a- 5h) have been produced by the condensation reaction of suitable N -heteroaryl- 4-amino benzenesul- fonamide (4a-4f) with derivatives of 3-acetyl coumarin (3a-3b) in ethanol. By using techniques like $^{1}H/^{13}C$NMR, FTIR, HRMS, and elemental analysis, as well as XRD, the structures of these congeners were verified. Additionally, the antimicrobial assay findings for compounds 5a, 5d, and 5f showed that they were effective against the terbinafine-resistant *Trichophyton rubrum* when compared to ketoconazole, with an acceptable MIC value of 12.5 µg/ mL. Additionally, as compared to Gentamicin, compound 5f had the largest zone of inhibition against *Staphylococcus aureus*. Prior to molecular docking utilizing AutoDock4.2 and other concomitant settings, the generated

hybrid molecules were examined and adjusted. The docking results of compounds 5d, 5e, 5f, and 5h with the cancer-causing protein showed binding energies in an ascending series of -9.28, -10.08, -11.88, and -12.4 Kcal/mol, which further motivated the evaluation of in vitro anticancer activity. The findings of screening the synthesized molecules against the MDA-MB-231, MIA PaCa-2, and H357 cancer cell lines showed that all of the compounds suppressed the proliferation of the cancer cells in a concentration-dependent way at various time points. Cited by Monalisa Mahapatra, Priyanka Mohapatra, ..., **Sudhir Kumar Paidesetty** "Design, synthesis, and in-silico study of chromen-sulfonamide congeners as potent anticancer and antimicrobial agents" ***Journal of Molecular Structure***, 1283, (2023), 135190 **SCI Impact factor 3.86** https://doi.org/10.1016/j.molstruc.2023.135190

8. Due to a number of intrinsic factors, including resistance to antibacterials acquired through bacterial consortia, and extrinsic factors, including non-uniform antibacterial policy and the migration of resistant bacteria through human and other routes, bacterial multidrug resistance has recently become a common issue in clinics. Clinics are eagerly awaiting the creation of newer, more potent anti-mycobacterial candidates. Hybrid molecules might be more effective than conventional molecules in fighting invasive bacterial strains, but newer antibiotics are always being developed. Here, two series of Schiff-based salicylaldehyde S1–S7 and furfuraldehyde F1–F7 molecules, each having a sulfonamide group, are designed and developed. These compounds were synthesized, and their structures were validated by spectrum characterization. Simulated molecular dynamics of all atoms had been carried out concurrently to understand the mechanism of action with these leading complexes. These data imply that the synthesized Schiff-based salicylaldehyde hybrids would be promising anti-tubercular compounds, which further need potent pharmacological evaluations. Cited by Chita Ranjan Sahoo , **Sudhir Kumar Paidesetty** , Budheswar Dehury , Rabindra Nath Padhy "Computational study on schiff base derived salicylaldehyde and furfuraldehyde derivatives as potent anti-tubercular agents: Prospect to dihydropteroate synthase inhibitors" ***Journal of Biomolecular Structure and Dynamics***,2023, **SCI Impact factor 5.23** 10.1080/07391102.2023.2217918
9. It has been decades in the making, but antibiotic-resistant bacteria and fungus are suddenly becoming a potential worldwide public health emergency. In order to combat incidents of antibiotic resistance, fresh, more effective medication options are urgently needed. A new

series of p-cuminal sulfonamide Schiff base congeners 3a-3h were devised, synthesized, and had their structures verified by numerous spectral analyses in an effort to combat the issues with antimicrobial multi-drug resistance. *Staphylococcus aureus*, *Streptococcus pyogenes*, Methicillin-resistant *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella pneumoniae*, and pathogenic fungi *Candida tropicalis* and *Trichophyton rubrum* were tested for the antimicrobial activities of the obtained products. With a MIC of 3.12 µg/mL, compound 3b significantly inhibited all strains of bacteria, and compound 3e showed the greatest amount of inhibition. In comparison to Ketoconazole, compound 3e showed the most promising control of both C. *tropicalis* and *T. rubrum* (MIC 6.25 µg/mL), as well as good inhibition of both *S. aureus* and MRSA at MIC 6.25 µg/mL. Sulfamoyl, azomethine, and certain heteroaryl rings in specific compounds may have enhanced their antibacterial effects, while the presence of guanyl and acetyl groups in the chemical structure may have contributed to their antifungal effects. Furthermore, biological targets have been determined for in silico research and drug-likeness. Cited by A K Bishoyi, M Mahapatra, **SK Paidesetty**, RN Padhy" Design, molecular docking and antimicrobial assessment of newly synthesized p-cuminal-sulfonamide Schiff base derivatives" ***Journal of Molecular Structure***, 2022, 1250 131824, 10.1016/j.molstruc.2021.131824 **,** Elsevier. **SCI Impact factor 3.86**

10. According to the World Health Organisation, breast cancer is currently the most common type of cancer. The most lethal subtype of breast cancer is triple negative, which is characterised by a high rate of metastasis and a dismal prognosis due to the absence of progesterone, oestrogen, and HER-2 receptors, three crucial therapeutic targets. In 45-70% of infected patients, this lethal variety shows overexpression of the epidermal growth factor receptor. The current study investigates a method to produce gold nanoparticles conjugated to flavonoids (luteolin) that may be easily and quickly synthesised with the aid of ultrasonication. The TEM measurements of the synthesised nanoparticles revealed a diameter of 30.23 9.96 nm and good stability, as shown by zeta potential of 38.1 1.49 mV. In UV-Vis spectroscopy, the particles displayed a distinctive plasmonic resonance at 541 nm. sphere-shaped particles. Spherical particles with face centered cubic crystalline structure were observed through HR-TEM, SAED and XRD analysis. In MDA-MB-231 TNBC cells, synthesised nanoparticles significantly increased cytotoxicity (IC50 value of

2 g/mL). Confocal imaging demonstrated that targeted nanoparticles quickly localised in the nucleus of cancer cells, improving its effectiveness. Evaluations of the cell cycle and apoptosis revealed that after an increase of MDA-MB-231 cells in the sub-G1 phase, both necrotic and apoptotic cell death occurred. It's interesting to note that NIH-3T3 cells, which are not cancerous, were cytocompatible with nanoparticles, confirming their therapeutic promise as a biosafe formulation. The study presents the first report of targeted therapies for triple-negative breast cancer using biosafe gold nanoparticles conjugated to luteolin. Cited by Suvadeep Mal, Tiyasa Saha, Asim Halder, **Sudhir Kumar Paidesetty**, ..., Partha Roy "EGF-conjugated bio-safe luteolin gold nanoparticles induce cellular toxicity and cell death mediated by site-specific rapid uptake in human triple negative breast cancer cells" ***Journal of drug and delivery system and technology*** 80 (2023), 104148 **SCI Impact factor 5.26** https://doi.org/10.1016/j.jddst.2022.104148