EXECUTIVE SUMMARY

Title : Azo (-N=N-) and imine (-C=N-) functionalized sulfamethoxazole and their metal complexes: Spectral, structural, photophysical, redox characterization and biochemical activities

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Sulfonamides are useful antibiotic and prevent bacterial growth by acting as a competitive inhibitor to *p*-aminobenzoic acid (PABA) of the key enzyme in folate synthesis, the dihydropteroate synthase (DHPS). However, prolong use of sulfonamides causes fever, skin rashes, breathing trouble, abdomen pain, nausea, headache, vomiting, diarrhea, loss of appetite, kidney damage etc. Research is going on to improve drug activity and reduce toxicity by designing new derivatives to explore the drug-protein interaction of functionalized sulfonamides and their complexes. In this research work a series of functionalized sulfonamides have been characterized and their transition metal complexes are also structurally established. Antimicrobial activities of these hitherto unknown compounds have been examined and have been interpreted by Molecular Docking and DNA interaction studies.

Azo-Sulfonamides

Sulphamethoxazolyl azo and imine functionalized molecules are characterized by spectroscopic (UV-Vis, IR, Mass, ^{1}H NMR, ^{13}C NMR) and also structures are confirmed by single crystal X-ray diffraction measurements. Biological activities such as antimicrobial and molecular docking have been studied. DFT and TDDFT computations of ligands and metal complexes have been carried out to determine the composition and energy of the molecular levels.

Sulfonamide Schiff bases

Sulfonamide Schiff bases containing phenolic group have been prepared in this work. Imine (-C=N-) derivatives are obtained from Suffamethoxazole, Sulfathiazole, Sulfapyridine, Sulfadiazine, Sulfamerazine and Sulfaguanidine upon condensation with different aromatic aldehydes. The derivatives are characterized by spectroscopic techniques (IR, Mass, NMR) and the crystal structures of some of them have been established. Chemical, anti-bacterial activities as well as chemo-sensing property of the ligands have been investigated.

Drug design and Docking Studies

Molecular docking is useful tool for drug discovery. Basic Local Alignment Search Tool, or BLAST, is used for primary biological sequence information. After completion of identifying target, validating a target, finding three dimensional structure of target and then using their structural information a new compound may be searched from ZINC database. The molecules with the binding energy better than the natural docked molecule are reported for further analysis. QSAR is also done for all the proposed molecules. Molecular dynamics simulations (MDS) have been done to observe the effect of explicit solvent molecules on the drug-protein complex and stability to achieve time-averaged attributes of the bimolecular system, along with diverse thermodynamic parameters. Drug likeness has been examined following Lipinski's rule of five filter. The molecular orbitals are used to calculate the electronic configuration, molecular reactivity and stability of the compounds by Density Functional Theory (DFT). Pharmacophore map generation has also done to observe steric and electronic features of best docked molecules that ensured the optimal interactions with a receptor and to block its biological response. Finally filtration was done for evaluation of druglikeness of the target molecules by ADMET properties. A series of designed drugs for Tuberculosis, diabetic and prostate cancer treatment are added from this research.

Achievements

So far we have published ten original articles in peer reviewed internationally reputed journals and five are submitted for publications. Three students have pursued their Ph. D. work and one of them received Ph. D. Degree and two are preparing their Thesis for submission.