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Estimation of caffeine in different beverages by ultraviolet spectroscopy

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This study was undertaken with the objective of estimation the concentration of caffeine in seven brands of soft drink with the use of an analytical method. Caffeine is a central nervous system (CNS) stimulant and a bitter white crystalline xanthine alkaloid. Preparation: The different brands of beverages were procured from different companies like Red Bull, Pepsi, Cola-Cola, Mountain dew, XXX, Power-X, and Thumps-up. The caffeine content in the different beverages was determined by dilution by water and then absorbance was measured by U.V Spectrophotometer Shimanzu1800 compact by absorption at λ max 271.2 nm. The amount of caffeine was determined against the absorbance from the standard curve of caffeine in distilled water at same λ max in the range of 5-30 µg/ml. The highest concentration of caffeine was found in Power-X (46µg/ml), and remaining was found to be containing 44µg/ml to 20.5µg/ml. So Power-X could be called as a strongest CNS stimulant among all samples and it could be harmful for health. And the lowest concentration of caffeine was found in XXX (19.5µg/ml) so it could be weaker CNS stimulant among all samples.

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Computational study of the human immunodeficiency virus Vpx2 protein

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Human immunodeficiency virus or HIV is a virus that needs to infect cells of living organism to grow and multiply. The fact that HIV attacks the immune system of the living organisms makes it the most perilous virus and it is the cause of AIDS. Millions of people are suffering from AIDS and millions who are living with this virus, in the process of development of AIDS. The genetic variability of HIV is the main obstacle for its treatment. HIV is mainly of two types HIV-I and HIV-II. There are many proteins that are associated with HIV and one of them is Vpx 2 that is, Virus Protein X. This protein is specifically associated in the expression of HIV-II and SIV (Simian Immunodeficiency Virus), which is closely related to Vpr it can be proved by considering their genetic sequences. As the studies reveal that Vpx is functionally related to Vpr which incorporates virions to the level of Gag proteins through the interaction of Gag p6. The role of Vpx protein is not clear especially in non-dividing cells such as macrophages, but it is known to be functionally involved in viral replication as it increases its efficiency. Hence, further effective understanding of this protein can be put into focus through computational modelling. Computational or homology modelling is the process of construction of a 3-dimensional structure of protein. 3-dimensional structure (the target) is created on the basis of a related homologous protein, which is the template. Therefore, homology modelling can effectively produce a structure model of high accuracy specially when the target and the template sequences are closely related. This paper deals with computational study of Vpx protein for the better understanding of its role in HIV replication.

Biography

S.Mounika has completed her graduation in Biotechnology and doing masters in Bioinformatics from Amity Institute of Biotechnology, Noida. She have attended one poster presentation and participated in national science congress and AP science congress, and won first prize in oral presentation.

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