SRDHS
SOCIETY FOR RESEARCH DEVELOPMENT IN HEALTH SCIENCE

Society for Research Development in Health Sciences (RDHS),
Sponsored

2nd International Conference

Organized By
Ambe Durga Education Society's
Dadasaheb Balpande College of Pharmacy
(Degree and Diploma),
Near Swami Samarth Dham Mandir, Besa,
Nagpur-440037, Maharashtra, India.

on 14th and 15th February 2020

Theme:
"Invigorating Research in Pharmaceuticals: Reasonable Industrial Approach"

Venue: Hotel RE-GEN-TA, CENTRAL Nagpur. Jagnade Square, Nandanvan, Nagpur, Maharashtra, India.

Souvenir and Abstract Book

"An event that is full of potentials to learn the latest trends in the Pharma industry and to learn about the business culture."

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DEVELOPMENT AND VALIDATION OF UV-SPECTROPHOTOMETRIC METHOD FOR ESTIMATION OF RASAGILINE IN BULK AND PHAMRACEUTICAL FORMULATION

Chavan R.R , Dhandar A.G
Department of Pharmaceutics, Anuradha College of Pharmacy,
Chikhli, Buldana Ms, India- 443001
ranjitchavan492@gmail.com

ABSTRACT

The main objective was to develop and analyze the sensitive, accurate, rapid, precise and economical UV - Spectrophotometric method for the determination of Rasagiline in bulk and in pharmaceutical formulation. This method is based on generation of zero order equation for analysis by using water as a solvent. Absorption maxima of Rasagiline were found to be at 264 nm respectively. Beer's – lamberts law was obeyed in concentration range of 0.3- 1.8 µg/mL for Rasagiline with correlation coefficient value was near about R2 of 0.999. The percent R.S.D. was less than 2.0 as required by USP and ICH guidelines. The proposed method was applied to pharmaceutical formulation and percent amount of drug i.e. Rasagiline.

Keyword Rasagiline, UV-Spectrophotometer, zero order, Development and Validation.

COMPUTER ASSISTED MOLECULAR DRUG DOCKING IN NEW DRUG DISCOVERY

Himanshu M. Bhogekar
Dadasaheb Balpande College of Pharmacy, Besa, Nagpur, 440034, Maharashtra, India.
himanshubhogekar@yahoo.in

ABSTRACT

The field of computer aided drug design and discovery (CADDD) is a rapidly growing area that has seen much success in last few years. The explosion of structural informatics, genomics and proteomic plays a major role in leading the effort towards modern era of drug discovery and development. The newly developed drug molecule is tested for its activity inside of the body i.e. Mechanism of action. To make this study easy the molecular drug docking concept is incorporated. Molecular docking is a kind of computational modeling of the complexes, which is form from the interaction of two or more molecules. It predicts the three dimensional structure of adducts, based upon building properties of participating ligand and target molecules. The result of molecular drug docking predicts the optimized docked conformer based upon total energy of the system. In spite of all potential approaches, ligand chemistry (tautomerism and ionization), receptor flexibility (single conformation of rigid receptor) and scoring function (differentiate two binding mode) still remain the challenge.

Keywords Molecular Docking, Scoring function, Drug discovery, Computational Chemistry.