

About the DBI – BIM

The e-magazine delivers simple, concise, and relevant information of the happenings at Department of Bioinformatics. This is a periodical magazine published for June 2021 – May 2022.

The magazine is sent free of charge to all alumni of DBI, as well as to faculties, staffs, and students.

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Message From the Chief Editor

Dear all,

It is with immense delight that I write this editorial for the current issue of "e-Bioinformatics Magazine" (e-BIM). Our department was found in 2008, since then it has achieved exponential growth and stardom among the other departments of Alagappa University, Karaikudi as well as other institutions. The tireless efforts by the faculty members in research and teaching in various fields have paved way to attain greater heights. Our department is funded by several funding agencies like DST, DBT, CSIR, ICMR, UGC and TNSCST. It is also sponsored by UGC Innovative programme, DST-FIST and DST-PURSE. Our faculty members believe that teaching and research are like two eyes that look far into wider horizons with a view to broadening the frontiers of knowledge. Besides this, extension activities have become imperative today and the department cannot isolate themselves from this responsibility. It is these extension activities that carry the fruits of research and knowledge to the society at large. Research scholars and students have always been noteworthy in their contributions for our department e-BIM highlights various Departmental events, Invited talks by Eminent Scientists, Student activities, Publications, Achievements, Recognitions, Contributions, Conference related activities, etc., during Academic year of June 2021 to May 2022. It also highlights the Department of Biotechnology (DBT), New Delhi approved the Establishment of Bioinformatics and Computational Biology Centre at the Department of Bioinformatics, Alagappa University, Karaikudi.

e-BIM is believed to provide platform to look back our achievements and to bring our merits into limelight that would give us enormous passion and boost to scale the heights of Bioinformatics.

Chief Editor

(Mr. Lakshmanan L)

Department Events

(June 2021 to May 2022)

Orientation for First year M.Sc., Students

The Department of Bioinformatics, Alagappa University has organized an orientation programme for First Year Post Graduate Students on October 6, 2021 (2021 – 2022). Prof. J. Jeyakanthan, Professor and Head of the Department, elucidated the objectives of the programme that empower students by providing numerous resources like library, instrumentation, computational and student assistance facilities. He also presented a quick overview of the ongoing research projects and development prospects in the Department. Prof. Sanjeev Kumar Singh briefed the roles of each faculty member, responsibilities of students in contributing to research progress and significance of participating in research studies Dr. M. Karthikeyan introduced about the importance of the orientation programme. Dr. R M. Vidhyavathi, Dr. J. Joseph Sahayarayan, Dr. P. Boomi, and Dr. K. Langeswaran elucidated the infrastructure and resources available in the Department.







Ayutha Pooja and Saraswathi Pooja Celebrations

On 13thOctober, 2021, the Department of Bioinformatics celebrated Ayutha pooja. All the faculty members and students participated in this event to commemorate this devotional ceremony that serves as a reminder to all students in preserving our heritage and culture.









Mr. S. Arumugam, Office Assistant - Condolence Meeting

One of our office staff, Mr. S. Arumugam, started his carrier at our university on September 27, 1991, and has worked as an Office Assistant in the Department of Bioinformatics since 2011. Unfortunately, he suddenly passed away on 5thNovember, 2021. He was well-known among faculty, scholars, and students as a committed and honest worker during his tenure in the university. A condolence gathering was held in the Department of Bioinformatics on 11-11-2021, at 4 p.m. Dr. J. Jeyakanthan, Professor and Head, expressed his condolences for Mr. S. Arumugam and stated that Mr. Arumugam will be remember forever as a warm-hearted, *honest* and straightforward person. The Professors, Faculty Members, Office Staffs, Students, and Research Scholars participated in the condolence meet and prayed to rest Mr. S. Arumugam's *soul* in *peace*.









RUSA-Weekly Online Workshop- Cryptozens

RUSA sponsored weekly online Workshop (Cryptozens) was organized in the Conference Hall of Department of Bioinformatics on 16th November, 2021 at 3 p.m. (online). Mr. V. Nandakumar, IRS, Department of Revenue, Ministry of Finance, Government of India, delivered a special address about crypto currency, block chain and the ways people achieved prosperity by using digital currency. He also detailed about the government regulations in purchasing, selling, and transferring crypto currency.









Fresher's Day Celebration (Offline)

Second year M.Sc students (2020-2022) organized a Fresher's Day celebration to the fresher's (2021-23 Batch students) in the Conference Hall of Department of Bioinformatics on 19th November, 2021. Fresher's Day is intended to welcome newcomers with positive, accepting environment, encouraging them to show their creative potential, build confidence, and avoid ragging. It's a great day for seniors, juniors and research scholars to get-together and socialise with freshers. Dr. J. Jeyakanthan, Professor & Head, delivered the welcome address, and Prof. Dr. Sanjeev Kumar Singh offered the presidential address. Seniors shared the department activities and Fresher's discussed about their memorable experiences in UG as well as their course expectations in the Department for their future. Several cultural programmes and games were conducted to make freshers more comfortable.









Department of Biotechnology (DBT), New Delhi approved the Establishment of Bioinformatics and Computational Biology Centre at the Department of Bioinformatics, Alagappa University, Karaikudi.

Recently, DBT has approved Department of Bioinformatics, Alagappa University to establish Bioinformatics and Computational Biology (BIC) Centre with the objectives to create and maintain sophisticated Bioinformatics resources for the benefit of Researchers and aspiring students especially from rural backgrounds. This is a pride to Department of Bioinformatics as Alagappa University is the first University among the State Universities in Tamil Nadu to establish the BIC Centre. The credit goes to Dr. J. Jeyakanthan, Professor & Head with faculty members, Prof. Sanjeev Kumar Singh, and Asst. Prof. Dr. M. Karthikeyan who proposed in obtaining the BIC centre for research theme on "Identification of Potent Drug for Life-Threatening Diseases" to develop multivariate drugs through computational and experimental approaches.

Usually, a drug discovery process takes about 20 years to get expedited and approved. Bioinformatics tools applied in BIC Centre is a straight forward approach to decipher the Structural and Functional aspects of targeted proteins with respect to disease escalation through Structural Biology and Protein Crystallography techniques. Also, the Mechanism of Action (MoA) between the targeted proteins and the identified leads will be unravelled by Computer Aided Drug Discovery (CADD) approach that reduces the constraints of time, manpower and cost. The developed drugs will be targeted against several Life-Threatening diseases such as Cancer, Virus and Bacterial infectious diseases. In this current scenario where, effective drugs are the only requirement to completely curb the progression of diseases and facilitated by effective research collaboration originating from BIC Centre.

DBT-BIC has been granted to Department of Bioinformatics, Alagappa University for 5 years with a tune of Rs. 350 lakhs. The BIC and National Networking Project (NNP) is initiated under the stewardship of Prof. J. Jeyakanthan as the Project Coordinator & Principal

Investigator (PI) including Prof. Sanjeev Kumar Singh as PI and Dr. M. Karthikeyan as the Co-PI. Also, one of the outcomes of the BIC Centre is to produce highly skilled manpower trained in the area of Bioinformatics, Computational Biology and Computer Aided Drug Design.

Science Day

The science day was celebrated by Alagappa University on 28 Feb 2022. As a part it, Students and Teachers from various schools and colleges visited various labs in the Department of Bioinformatics and interacted with the faculties and Scholars. Teachers explained about the Bioinformatics and Computer Aided Drug Design to the students and also explained the ongoing research in Department of Bioinformatics.





Women's Day celebration

International Women's Day was celebrated in department of Bioinformatics on 8th March 2022 at Conference Hall. In this occasion, Dr. J. Jeyakanthan Professor & Head and all other faculties appreciated the roles and responsibilities of women. Women faculty, staff and students shared their views about the hurdles faced by women in daily life and how they overcome their struggles. The faculties have motivational speech to encourage and inspire the young minds to achieve higher as part of the celebration gifts and sweets were distributed.

Parents Teachers Alumni Meet (PTAM)

Parents-Teachers and Alumni Meet (PTAM) was conducted by Department of Bioinformatics, Alagappa University, Karaikudi on 06th March, 2022 through online (**Meeting ID: meet.google.com/xpm-sgja-osq**) at 11.00 am.

During the occasion Alumni shared their experiences and views about the Department. The occasion was graced by more than 15 Alumni across various batches and family members of the current batch students.

Speaking on the occasion, Prof. J. Jeyakanthan underlined and praised the achievements of Alumni in all walks/spheres of life. He felt that it was matter of great pride for Department of Bioinformatics, Alagappa University that its Alumni are holding prestigious positions in various Government organizations, Private sector and Academic Institutions. He praised the contribution of the Alumni towards the growth of the Department and emphasized on the need for further strengthening the linkage between the Alumni and current students of Alagappa University.

Alumni shared their experiences and views about the department in the gathering during the meeting. Many of the current students also interacted with the passed-out seniors and learned from their experiences. Parents gave very good feedback about the Department and the Faculty members. Parents were much satisfied on seeing the activities and facilities of the Department and assured their support to the growth and wellness of the Department.

The main purpose of this meet is to create a common platform, where teacher and parents come together to enrich the student's educational experiences and discuss variety of issues, regarding all round development of students.







Membership

Prof. Sanjeev Kumar Singh, Department of Bioinformatics was nominated by Honourable Governor of Tamil Nadu as Member of Planning Board Alagappa University 0n 25.03.2022 for the period of three years.

Invited Talks/Address

- Dr. J. Jeyakanthan delivered memorable lecture on "High-throughput crystallography and Biocomputing" as a Resource Person in the "Online Faculty Development Programme on Tools and technique in characterization of compounds" organized jointly by CSIR-Central Electro Chemical Research Institute and Dr. Umayal Ramanathan College for Women, Karaikudi (17th 21st, January 2022).
- **Dr. J. Jeyakanthan** gave outstanding lecture on "Structural and Functional Studies on Transcriptional Regulatory Protein from *Pyrococcus horikoshii* OT3 *In silico* and *in vitro* approach" in the International Virtual Conference on "Biological Innovations & Computational Exploration for Pandemic Challenges (BICPAC'22)" organized by Department of Biotechnology and Bioinformatics, Bishop Heber College (Autonomous), Trichy (24th -25th, February 2022).
- **Dr. J. Jeyakanthan** delivered a special lecture on "High–Throughput Structural Biology & Bio-Computing" in the "Theme based Activities (5D10TBA) Programme" organized by Department of Industrial Chemistry, Alagappa University, Karaikudi (24th, March 2022).
- **Dr. RM. Vidhyavathi** was invited as a Resource Person for one-day state level seminar on "Programming Aspects of Machine Learning and its Applications" at Vidhya Giri College of Arts and Science on 31st March 2022.

Recent and Key Publications



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RESEARCH ARTICLE



Molecular dynamics simulation of Toxin-Antitoxin (TA) system in Acinetobacter baumannii to explore the novel mechanism for inhibition of cell wall biosynthesis: Zeta Toxin as an effective therapeutic target

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The majority of bacteria and archaea contains Toxin-Antitoxin system (TA) that codes for the stable Toxin and unstable Antitoxin components forming a complex. The Antitoxin inhibits the catalytic activities of the Toxin. In general, the Antitoxin will be degraded by the proteases leading to the Toxin activation that subsequently targets essential cellular processes, including transcription, translation, replication, cell division, and cell wall biosynthesis. The Zeta Toxin-Epsilon Antitoxin system in ESKAPE pathogen stabilizes the resistance plasmid and promotes pathogenicity. The known TA system in Acinetobacter baumannii are known to be involved in the replication and translation, however, the mechanism of Zeta Toxin-Epsilon Antitoxin in cell wall biosynthesis remains unknown. In the present study, molecular docking and molecular dynamic (MD) simulations were employed to demonstrate whether Zeta Toxin can impair cell wall synthesis in A. baumannii. Further, the degradation mechanism of Antitoxin in the presence and absence of adenosine triphosphate (ATP) molecules are explained through MD simulation. The result reveals that the cleavage of Antitoxin could be possible with the presence of ATP by displaying its response from 20 ns, whereas the Zeta Toxin/ Epsilon was unstable after 90 ns. The obtained results demonstrate that Zeta Toxin is "temporarily favorable" for ATP to undergo phosphorylation at UNAG kinase through the substrate tunneling process. The study further evidenced that phosphorylated UNAG prevents the binding of MurA, the enzyme that catalyzes the initial step of bacterial peptidoglycan biosynthesis. Therefore, the present study explores the binding mechanism of Zeta Toxin/ Epsilon Antitoxin, which could be beneficial for preventing cell wall biosynthesis as well as for unveiling the alternative treatment options to antibiotics.

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RESEARCH ARTICLE

In silico identification of natural product inhibitors against Octamer-binding transcription factor 4 (Oct4) to impede the mechanism of glioma stem cells

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Abstract

Octamer-binding transcription factor 4 (Oct4) is a core regulator in the retention of stemness, invasive, and self-renewal properties in glioma initiating cells (GSCs) and its overexpression inhibits the differentiation of glioma cells promoting tumor cell proliferation. The Pit-Oct-Unc (POU) domain comprising POU-specific domain (POUs) and POU-type homeodomain (POU_{HD}) subdomains is the most critical part of the Oct4 for the generation of induced pluripotent stem cells from somatic cells that lead to tumor initiation, invasion, posttreatment relapse, and therapeutic resistance. Therefore, the present investigation hunts for natural product inhibitors (NPIs) against the POUHD domain of Oct4 by employing receptor-based virtual screening (RBVS) followed by binding free energy calculation and molecular dynamics simulation (MDS). RBVS provided 13 compounds with acceptable ranges of pharmacokinetic properties and good docking scores having key interactions with the POU_{HD} domain. More Specifically, conformational and interaction stability analysis of 13 compounds through MDS unveiled two compounds ZINC02145000 and ZINC32124203 which stabilized the backbone of protein even in the presence of linker and POUs domain. Additionally, ZINC02145000 and ZINC32124203 exhibited stable and strong interactions with key residues W277, R242, and R234 of the POUHD domain even in dynamic conditions. Interestingly, ZINC02145000 and ZINC32124203 established communication not only with the POUHD domain but also with the POUs domain indicating their incredible potency toward thwarting the function of Oct4. ZINC02145000 and ZINC32124203 also reduced the flexibility and escalated the correlations between the amino acid residues of Oct4 evidenced by PCA and DCCM analysis. Finally, our examination proposed two NPIs that can impede the Oct4 function and may help to improve overall survival, diminish tumor relapse, and achieve a cure not only in deadly disease GBM but also in other cancers with minimal side effects.

RESEARCH ARTICLE



Structural and functional insights on vitamin D receptor and CYP24A1 deleterious single nucleotide polymorphisms: A computational and pharmacogenomics perpetual approach

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The development of chronic kidney disease (CKD) drugs remains a challenge due to the variations in the genes. The vitamin D receptor (VDR) and Cytochrome 24A1 (CYP24A1) genetic variants might affect the drug potency, efficacy and pathway. Here we have to analyse and determine the deleterious single-nucleotide polymorphisms (nsSNPs) of VDR and CYP24A1 genes and their different population's drug responses in different populations to understand the key role in CKD. Among that the large scale of nsSNP, we used certain computational tools that predicted six missense variants are observed to be significantly damaging effect and SNP variability with large differences in various populations. Molecular docking studies were carried out by clinical and our screened compounds to VDR and CYP24A1. Docking results revealed all the compounds have a good binding affinity (Score). The screened compounds (TCM_2868 and UNPD_141613) show good binding affinity when compared to known compounds. The QM/MM study revealed that the compounds have electron transfer ability and act as a donor/acceptor to mutated proteins. The structural and conformational changes of protein complexes were analysed by molecular dynamics study. Hence, this study helps to identify suitable drugs through drug discovery in CKD treatment. The abovementioned compounds have more binding affinity, efficacy, and potency of both wild and mutant of VDR and CYP24A1.

CYP24A1, molecular docking, nsSNPs, QM/MM and molecular dynamics, VDR

1 | INTRODUCTION

Chronic kidney disease (CKD) is recognized as a non-communicable disease that steadily increases mortality and morbidity around worldwide. The abnormalities in vitamin D metabolism and the gradual decline of vitamin D lead to the pathogenesis of CKD.2 Vitamin D is a secosteroid prohomone that biologically plays an important role in calcium and phosphate regulation, bone mineralization and a variety of physiological functions for instance immune response, immune inflammation, cell differentiation, growth and proliferation. The endocrine circulating level of 25-hydroxyvitamin D or 25(OH)D is a common biomarker to felicitate the vitamin D status.3 The metabolism of vitamin D is high up or downregulation of the expression disparity might cause by several key proteins activity which alters its effects or level.4 The key metabolic proteins comprise Cytochrome 24A1 (CYP24A1) enzyme is referred to as 25-hydroxyvitamin D3-24-hydroxylase which can catalyse the bi-functional conversion of 25-OH-D₃ and 1, 25-(OH) 2D₃ (Vitamin D₃) into 24 and 25 hydroxylated products and vitamin D receptor (VDR) is a nuclear receptor family, which acts as a vitamin D inducible factor exert calcium and phosphate homeostasis.⁵⁻⁹ Genetic factors such as single nucleotide polymorphisms (SNPs) or genetic variation play a crucial role in the

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Essential oils as an effective alternative for the treatment of COVID-19: Molecular interaction analysis of protease (M^{pro}) with pharmacokinetics and toxicological properties



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ABSTRACT

Background: The current health concern to the entire world is the chronic respiratory disease caused by coronavirus 2 (COVID-19). A specific treatment or proper therapy is still lacking, and the investigations from across the world for proper drug/vaccine development towards disease control are in progress. The Coronavirus replication takes place by the conversion of the polypeptide into functional protein and this occurs due to the key enzyme Main protease (M^{pro}). Therefore, identification of natural and effective M^{pro} inhibitors could be a safe and promising approach for COVID-19 control.

Methods: The present in silico study evaluates the effect of bioactive compounds found in Eucalyptus and

Corymbia species essential oil on M^{mo} by docking. Molecular docking of the major seven compounds of essential oil (citronellol, alpha-terpineol, eucalyptol, p-limonene, 3-carene, o-cymene, and alpha-pinene) with MPTO was studied by AutoDock 4.2, and the properties were analysed by PreADMET and Biovia Discovery Studio visualizer

Results: The calculated parameters such as binding energy, hydrophobic interactions, and hydrogen bond interactions of 6LU7 (Mpro) with Eucalyptus and Corymbia volatile secondary metabolites represented its scope as an effective therapy option against covid-19. Among the docked compounds, eucalyptol shows the least binding energy without toxicity.

Conclusions: The outcome of this study reported that the essential oil of Eucalyptus and Corymbia species. mainly eucalyptol can be utilized as a potential inhibitor against COVID-19 and also it can be used in its treatment. Hence, further analysis was required to explore its potential application in medicine.

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Introduction

Public health has always been a prime issue due to the continuous emerging of pandemics in last two decades. There were outbreaks of SARS-CoV-1, MERS-CoV, and now the current pandemic Coronavirus disease of 2019 (COVID-19) has become an extreme threat to human life, the livelihood, and also has brought about relentless social-economical along with political issues in the tainted countries [1]. The WHO has categorized COVID-19 as a pandemic [2]. The International Committee on Taxonomy of Viruses (ICTV) gave the name for this virus as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [3]. COVID-19 causes ARDS-Acute Respiratory Distress Syndrome, a condition in which

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In silico approach of naringin as potent phosphatase and tensin homolog (PTEN) protein against prostate cancer

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Communicated by Ramaswamy H. Sarma

ABSTRACT

Prostate cancer (PC) is one of the major impediments affecting men, which leads approximately 31,620 deaths in both developing and developed countries. Although some chemotherapy drugs have been reported for prostate cancer, they are not effective due to the lack of safety, efficacy and low selectivity. Hence, the novel alternative anticancer agents with remarkable effect are highly appreciable. Natural plants contain several bio-active compounds which have been traditionally used for the various medical treatments. Particularly, naringin is a natural bio-active compound commonly found in the citrus fruits, which have shown numerous biological activities. Phosphatase and tensin homolog (PTEN) is a tumor suppressor gene, which activates both lipid phosphates, this signaling pathway play an essential role in the cell survival, proliferation and migration. In the present *in silico* investigation, structure based virtual screening, molecular docking, molecular dynamics simulation and Adsorption, Distribution, Metabolism, Excretion (ADME) prediction were employed to determine the binding affinity, stability and drug likeness properties of top ranked screened compounds and naringin, respectively. The results revealed that the complex has good molecular interactions, binding stability (peak between 0.3 and 0.4 nm) and no violations in the Lipinski Rule of 5 in naringin, but the screened compounds violated the drug likeness properties. From the *in silico* analyses, it is identified that naringin compound might assist in the development of novel therapeutic candidate against prostate cancer.

Abbreviations: ADME: adsorption, distribution, metabolism, excretion; BOILED: Brain or intestinal EstimateD; GROMACS: GROningen MAchine for Chemical Simulation; MDS: molecular dynamics simulation; MM-GBSA: molecular mechanics-generalized born surface area; OPLS: optimized potentials for liquid simulations; PC: prostate cancer; PTEN: phosphatase and tensin homolog; PDB: Protein Data Bank; RMSD: root mean square deviation; RMSF: root mean square fluctuation

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1. Introduction

Prostate cancer (PC) is the most common non-cutaneous cancer and fifth leading cause of cancer related death affecting men globally (Ishizuya et al., 2020; Naveed et al., 2016). In 2019, approximately 174,650 new cases were identified and 31,620 people were died (Chen et al., 2019; Kohaar et al., 2019). The PC of metastatic behaviors has promoted by the voltage-gated sodium channel, which stimulates the various cellular processes (Gumushan Aktas & Akgun, 2018). It is a hereditary disease and genetic risk factor of PC may be passed from parent to child (Osanyinpeju et al., 2018). Currently, several significant treatments such as androgen deprivation therapy (Ferroni et al., 2017), surgery (Hensbergen et al., 2020),

radio ligand therapy (Wang et al., 2018) and hormonal therapy (Tonry et al., 2015;) have been undertaken to improve the patient outcomes. Due to adverse side effects such as peripheral neuropathy, high-frequency hearing loss and affecting normal healthy cell, it is very difficult to eradicate. Hence, it is evident that there is a need to develop new anticancer agent that hinder the metastatic potential and cause the cell death response of prostate cancer cells.

PTEN is a lipid phosphatase of PI 3-Kinase and directly opposing the activation of the PI3K signaling by converting the PIP3 produced by PI3K back to PIP2 (Álvarez-Garcia et al., 2019). Accordingly, loss of PTEN tumor suppressor gene result in the deficiency of regulation of PIP3 levels leads to promote prostate cancer development (Zhou et al., 2019).

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Press Release



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கொரோனா வைரசை அழிக்கும் மருந்து சேர்மங்கள் கண்டுபிடிப்பு

காரைக்குடி, ஜன. 6: கொரோனா வைரஸின் முக்கிய மூலக்கூறுகளை அழிக்கும் மருந்துகள் மற் றும் அதற்கான சாத்தியக் கூறுகள்கணினி முறையில் கண்டுபிடிக்கப்பட்டுள் னது என அழகப்பா பல்க லைக்கழக பேராசிரியர் ஜெயகாந்தன் தெறிவித் துள்ளார்.

துள்ளார். வைகுறிவைத்து கிவகங்கை மாவட் அழிப் பதற்கு டம். காரைக்குடி அழ தேவை யான கப்பா பல்கலைக்கழக மருந்து கன் உயிர் தகவலியல் பேராசி கணினி முறை ரியர் ஜெயகாந்தன் கூறிய யில் கண்டுபி

தாவது: ஸ்வீடன் ஸ்டாக் ஸ் விடன் ஸடாக ஹோம் கே.டி. எச். ராயல் இன்ஸ்டியட் ஆப் டெக் னாலதி வேதியியல் மற் றும் உயிரியியல் துறையின் டாக்டர் அருள் முருகனு டன் இணைந்து, மருந்து சேர் மங்கள் கணினி முறையில் கண்டுபிடிக் முறையில் கண்டுபடிக் கப்பட்டுள்ளது. வைரஸ் புரத மூலக்கூறு களை பொறுத்தவரை அதிகள் வில் பல மூலக்கூறுகள் வில் படி புகாகது என நடக்கும். இருக்கும். இதற்கு ஒரு டும். மருந்து அளிக்கும்பட்சத் பாலோக்சாவீர் மார் என ஆராய்ச்சியில் கண் தில் அனைத்தையும் சரி பாக்சில், நடமைசின், டுபிடிக்கப்பட்டுள்ளது செய்யாது. மீதம் உள்ள ஆர்யூ 85053 ஆகிய மருந் இவ்வாறு அவர்கூறினார்.

அழகப்பா – ஸ்வீடன் பல்கலை. பேராசிரியர்கள் வடிவமைப்பு

வைரஸ் மூலக் கூறு களை கண்டுபிடித்து உரு மா றும் வைரஸ்களின் பல புரதங்க ளை குறிவைத்து டிக்கப்பட்டுள்

on Al.



பேராசிரியர் ஜெயகாந்தன்

ளது இம் மருந்து வைர வின் உருமாற்றங்களை சுற்றி செயல்பட உதவும். கொரோனா வைரஸ் அதன் புரதங்களை மாற் றியமைத்து விரைவாக உருமாறுகிறது பல புரதங் களை குறிவைத்து தாக்கக் கூடிய மருந்து இருந்தால். ஒன்று உருமாறினாலும் மற்றவைகளுக்கும் அது பயனுள்ளதாக செயல்ப

துகள் முன்று வைரஸ் புர வைரஸ் புர தங் களை குறிவைத்து தரக்கு வது தாக்கு வது டெஸ். வைரஸ் மூலம் பரவும் நோய்களுக்கு சிவச்சையளிப் சுக்கதையின் பதில் இறம் பட செயல்ப டுதிறது. தவிர நந்தன் இவரன் மு விப், ஓவரப ரிப், சோலிப்னோட்கின்,

கோல்வாடினிப், சோனி டேகிப், ரெகோராபெ னிப் மற்றும் பி.சி.ஒ. 371 ஆகியவைகளும் சோத னைக்குப் பரிந்துரைக் சுப்பட்டுள்ளன. தவிர பைதாலோசையனின், பைதாலோ சையனை, டாடாலாப்பில் போன்ற மருத்துகள் விரைவாக உருமாலும் கொரோனா வைரணை எதிர்ப்பதில்

Published in Scientific Reports

scientific reports

OPEN Searching for target-specif and multi-targeting organi for Covid-19 in the Drugba database with a double scc approach

Natarajao And Munigan²— Sanjir Kumari, Jeparaman Jepakanthami, The current outless of Covid-29 Polection due to 6ARS CoV-Z, a vilous from his become a major threat to human healthorns. This virus has a leady infect of medicine. This tedificial discovery of production than a life discovery of medicine. This tedificial discovery of production of the covid-ce development and demand for a high policy test restrict which can not be adopted infection. Rather we need a south and care-flexible apprecases to inhibits and with the field of commissional coversion agreed some one for choosing agent.











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அரசின் விதிமுறைகளை கடைபிடிப்பதே பாதுகாப்பானது

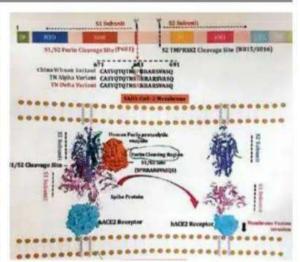
கொரோனா வைரஸ் பரவல் நீண்ட காலத்திற்கு இருக்கும்

அழகப்பா பல்கலைக்கழக பேராசிரியர் தகவல்

காரைக்குடி, அக். 7: கொரோனா வைரசின் முக்கிய புரதங்களை அழிக் கும் மருந்துகள் மற்றும் சாத்தியக்கூறுகள் குறித்து சிவகங்கை மாவட்டம், காரைக்குடி அழகப்பா பல்கலைக்கழக உயிரி தகவலியல் துறை தலை வர் ஜெயகாந்தன் தலை மையில் அராய்ச்சி மாண வர்கள் ரிசாட் மரியதாஸ், ராஜூ ஆகியோர் ஸ்பைக் புரதங்களை அடிப்படை யாககொண்டு ஆராய்ச்சி மேற்கொண்டனர்.

இதுகுறித்து பேராசி ரியர் ஜெயகாந்தன் கூறு கையில், "இந்தியாவில் பரவும் டெல்டா வகை கொரோனா வைரஸின் நோய்த்தொற்று தொடர் பான புரதங்களையும் அதன் மாறும் தன்மை யையும் கணினி முறை யில் கண்டுபிடிக்கும் ஆராய்ச்சி மேற்கொள் ளப்பட்டது. இந்நோய் பரவலுக்கு முக்கிய பங் காற்றும் ஸ்பைக் புரதம் 1,273 அமினோ அமிலங் களை கொண்டது. மற்ற வைரஸ்களை போன்றே கோவிட் 19 வைரஸ் பல் வேறு வகையான மரபணு மாற்றங்களுக்கு உட்படும் தன்மை கொண்டவை. ஸ்பைக் புரதத்தில் ஏற்ப டும் மாற்றங்கள் நோயின் தீவிரம் மற்றும் தொற்று பரவுதலை அதிகரிக்கும்.

உலகளவில் பல்வேறு அராய்ச்சி ஆய்வகங்களில் 3,60,009 கோவிட் தரவுகள் பதிவேற்றம் செய்யப்பட் டுள்ளது. அவற்றிலிருந்து



🕨 ஸ்பைக் புரத அமைப்பு மற்றும் பிளவு ஏற்படுத்தும் பகுதியை பற்றி கணினி மூலம் கண்டறியப்பட்ட படம்.

47 ஆயிரம் இந் திய ஸ்பைக் புர தங்களை மட்டும் எடுத்துக்கொண்டு ஆராய்ச்சி மேற் கொள்ளப்பட் டது. ஒவ்வொரு புரத மூலக்கூறுக ளும் ஒவ்வொரு விதமான வேலை செய்யும். இதில்

கோவிட் வைரஸ் தாக்குத லுக்கு முக்கியமான புரத மாகும். இதில் உள்ள 1,273 அமினோ அமிலங்களில் 681வது அமினோஅமில மாக புரோலின் உள்ளது. இந்த அமினோ அமிலம், அரிஜினைன் அமினோ *அமிலமாகமாறி டெல்டா* வைரஸ் என பெயரி டப்பட்டுள்ளது. இதில் வேறுவிதமான அமினோ



பேராசிரியர் ஜெயகாந்தன்

அமில மாற்றங் கள் ஏற்பட**ல**ாம். அவ்வாறு ஏற்ப டும்போது டெல் டாவை விட அதி தீவிர பாதிப்பை ஏற்படுத்தும் என கணினியின் மூலம் மேற்கொள்ளப் பட்ட ஆய்வின் முடிவில் அறியப்

ஸ்பைக் புரத மூலக்கூறு பட்டுள்ளது. சரியான தடுப்பு மருந்து கண்டு பிடிக்காத வரையில் கோவிட் 19 என்பது முற்று பெறாமல் மாற்றங் கள் நடந்துகொண்டே இருக்கும். எனவே அரசு அறிவித்துள்ள அனைத்து வழிகாட்டு விதிமுறைக ளையும் கடைபிடிப்பதே நம்மை பாதுகாத்துக் கொள்ள சரியான தீர்வு" என்றார்.



Geschi'Gungand yandung Geschung Kong dipun wansi meerlungga di urijah pebhasij.

கணினி பகுப்பாய்வு ஆராய்ச்சியில் உறுதி

கீழாநெல்லி, வெற்றிலை, கபசுர குடிநீர் நோய் எதிர்ப்பாற்றலை அதிகரிக்கிறது

காரைக்குடி, நடி 3: இநா நெல்லி வெற்றிகையற்றும் கடன் குடிதி நோய் எதிர்ப பாற்றலை அடுகரித்து சிறத்தமுறையில் செயல்ப Dasks month of Line Harrison ஆராய்ச்சியில் உறுகு செய் பியாட்டுள்ளது என. அழ கப்பா பல்கணைக்கழக உலிரி நகவலியல் துறை தலைவர் தெரிவித்தார்.

சிவைவர் தேருவத்தார். சிவன்னை மாவட்டம், காணக்குடி அழகப்பர் பன்கவைக்கழக உறிரி தவைவேல் துறை தலைவர் Currentifiers Oppositions M. DUBTERNE

Gardgrann moon வின் கைபக் புரத்தில் எந் படும் மாத்தங்கள் மற்றும் தோய் தொடர்பு புரதங் களை அழிக்கும் மருதுகள் ans and an analysis of the control o ores appendes comes som argumen species தாவரங்களை கொள்டு

அழகப்பா பல்கலைக்கழக போசிரியர் தகவல்

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தொடர்ந்து ஆய் வுகள் » பேராகிரியர் ஆராங்கியில் சுறுடு மேற்கொள்ளப் நேறுகாந்தன், செவ்வப்பட்டுள்ளது ஜெயகாந்தன். un Dangson Arman and Arman டிரு அல்கேறிக்கப்பட்ட டேக்கார பித்தாணோன் அகாலாப்பட்டினிப், நபா Charles ne co specience muric comité, maisse mair பரித்துரைக்கப்பட்ட இழர தெல்ல், வெற்றினை மற்றும்

នបទរ ក្នុយុទ្ធវ មិត្តបល់ន និងបស់បន្តិទិត្តវ Degasila ema

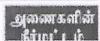
கள் சேர்ந்த கல்லை. வைர சுக்கு ராக ஆன்பு வைர வாகவும், தோய் எதிர்ப் பாற்றமை அதிகரிந்து சிறந்த முறையில் செயல்ப டுவது கணினி பகுப்

நப்ரசன் மற்றும் அனைத்து விறுமான நோயாளிகளும் பலன்படுத்தனைம் இந்த பான படுத்தனர். இத் முகை ஆசியில் கன் செபுறைக் ஆசிய இது வின் மற்றும் செபான் நீ சினிக் ஆசிய ஆகெவை வைரசுத்த எடுராக சிறப் பாக செயல்படுகிறது.

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12 சிறிய மூலைக்குற் கிகரிக்கப்பட்ட நடைமு கள் சேர்த்த கல்லை, கூறவில் உள்ள மருந்து களுடன் ஒப்பிடுவகமில் இந்த முகைக்குழகள் புரத் சீன்னர்க்கை பக்களின்றப டுத்தி வைரஸ், மனித செல்விலுள் தழைவதை தடுக்கிறது சுபகர் குடிதீர். வீழாகேல்லி மற்றும் வெற் றிவை அகியவற்றில் மகுத் துவக் குணங்கள் குறித்து தொடர்ந்து பல்வேறு monachten gyrtuideach amhadhgpaneGingeach னப்பட்டு வகுகிறது.

இவ்வாறு கூறினர்.



காணக்கள்கள் காண்கள் கண்ணக்கில் ச

டங்களாக கோர்க்கை பூழம் நாறும் முதல்வர். ட்

அழகப்பா பல்கலைக் கழகத்தில்

्राग्रीवंदिकारोठी दिवासी एक हें हा கண்டறிய ஆரப்ப்ச்சி மையம்

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DINAKARAN - 21.01.2022

பரவும் தன்மை அதிகமாக இருந்தாலும்

ஓமிக்ரானால் உயிர்ப்பலி ஏற்படும் வாய்ப்பு குறைவு

காளுக்குடி, ஐன். 21: பர அம் தன்மை அடுகமாக இந்த தாலும் ஒமிக்கா காஸ் உலில்பாசி ஏற்பட கால்ப்புகள் குறைவு என அநகப்பா பல்வைக்கும் உலிர் தகைவில் நுறை தலைவர் தெரிவித்துள் னார். இவல்கை மாலட்டம்

சுவகங்கையாவட்டம். காரைக்குடி அழகப்பா பங்கலைக்கழக உவிரித கவனியல் துறை தலைவர் ஜெயகாத்தன் உறியதா தொரோனா வைர

தொட்கு நொட்க வருக்கு மீர் குர்ப்பட்ட பட்டி முற்றில் கால்க் நெட்கி வருக்கு நிறைக்கு மற்றில் கால்க்கு நிறிக்க கடித்த கூற்றில் காற்றில் காற்

Bound Frt. 21 Jacuary 2022 https://epoper.dinakaran.com/c/65730228

அழகப்பா பல்கலை. பேராசிரியர் தகவல்





expansed by the State Misseiters. Union Committee Mrs. Kamatchi, attended the function

President of the Maydadarbara and students from various colleges

DBT sanctions Rs. 350 lakh to Algappa University to set up BIC

The Department of Biotechnology (DBT), New Delhi has approved and sauctioned some of Rs. 350 lakhs to the Department of Bioinformatics, Alagappa University, Katakuda, to evtablish a Riconformatics, and Computational Biology Centre (BIC) for a period of 5 years. The objectives of the BIC country is to create and maintain sophisticated Bioinformatics resources and conduct workshops / hands-on mining programmes for the benefit of resourchers and aspering students and teachers, especially

from stand background. It is the first state University in Tamiloudu to establish this BIC centre Both, the BIC Centre and National Nesworking Project (NNP), were proposed and initiated by the Project Condition and Principal Investigator

世報

Prof De Jayakanthan. HOD of Bounformatics Prof. Sanjery Kumar Singh and Asst Prof Dr M Karthakeyan are he other Co-Principal inversity-softer

The main work of the BEC Centre is to produce highly skilled gaugeower trained in the avea of Bioinformatics, Computational Biology and Computer Aided Drug Design. The BIC Centre will also develop multi drugs through computational and experimental approaches



on the research theme of "Identification of Potent Dorg for Life-Threatening Diseases A typical drug

discovery cycle takes about 15 years with an approximate cost of 500 nullson to get approval for marketing However, the BIC Centre in the Department of Biometormatics, Alagraph University, will employ rapid and cost-effective Bioinformatic methods to decipher the Structural and Functional aspects of therapeutic protein targets in various infections disease and furnish disorders and famous descrives using various Structural Baclogy and Protein Crystallography techniques Besides, the

Mechanism of Action

of the torreted interactions with the identified leads can also be unaveiled by Computer-Aided Drag Discovery (CADD)

approach The developed drugs will be targeted against several life-disestening diseases such as Cancer. Virus and Bacterial Infectious diseases Especially the research in BIC will focus on identifying potent leads for viral fever caused by mesquito bome diseases as Dengue, Malasia and Chikangenya. In addation, Crystallography studies on major druggable proteum

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responsible for human life-threatening diseases such as Cancer. Hypertension and Diabetes will also be decimbered besides identifying movel therapeutics against the targets. The convence of the Vice-Chancellos Officiating Committee of Alagappa University DeD Karthikeyau IAS, Principal Secretary Department of Highes Education, Government of Tamilanda, and

tembers De R.Swammathan Prof.S.Karappachamy. Syndicate Members Prof. K. Sankaramarayanan, Or K. Gunaseksent, Dr M. L. Raja and the Registrar tle Prof. 5. Raja Mohan congratulated the Professors and research students on their richly deserved innour for doing outstanding resourch for many years that contributed to this noteworthy achievement

MISSING

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Department Profile

DEPARTMENT PROFILE

Objectives

Department of Bioinformatics established in the year 2008 is one of the pioneer Departments in India facilitates learning in the interdisciplinary area of Structural Bioinformatics, Computational Genomics and Proteomics as well as to make the learners competent in Computational and Experimental aspects of their research interests.

Special Features

- Focusing on multidisciplinary areas to converge at a point of bringing out an effective drug using Computational sources against dreadful diseases.
- Unique blend of fundamental sciences, practical application with computational programs and insight into medicinal perspective.

Programs Offered

- **M.Sc.** Bioinformatics (Two year)
- **M.Phil.** Bioinformatics (One year)
- **Ph.D.** Full-time/Part-time
- **P.G. Diploma** in Structural Pharmacogenomics (One Year) UGC Innovative Program
- **P.G. Diploma** in Bioinformatics (One Year)

Faculty Members

Name	Qualification	Area of Research
Dr. J. Jeyakanthan	M.Sc., M.Phil.,	Structural Biology and Bio-Computing
Professor & Head	Ph.D.	
9	M.Sc., Ph.D.	Structural Bioinformatics and Computer Aided Drug
Professor		Design
Dr. M. Karthikeyan	M.Sc., Ph.D.	Pharmacogenomics and Computer Aided Drug Design
Assistant Professor		
Dr. RM. Vidhyavathi	M.Sc., M.Phil.,	Data Mining and Data Warehousing, Database
Assistant Professor	M.Tech., Ph.D	Management System
Dr. J. Joseph Sahayarayan	M.Sc., Ph.D.	Plant Bioinformatics and Biotechnology
Assistant Professor		
Dr. P. Boomi	M.Sc., Ph.D.	Nanoparticles synthesis and Nano drug delivery
Assistant Professor		
Dr. V. K. Langeswaran	M.Sc., Ph.D.	Molecular Oncology and Environmental Toxicology
Assistant Professor		

Research Focus on

- Small and Macro Molecule X-ray crystallography, Biological and Macromolecular Database Development, Computer Aided Drug Design.
- Computer Aided Drug Designing, Molecular Modelling, Structural Bioinformatics, Quantum Mechanics, QSAR Studies, Database and Tool Development
- Human Molecular Genetics, Pharmacogenomics and Computer Aided Drug Discovery, Cell Signaling, Database Creation & Management.
- Data Mining and Data Warehousing, Database Management System, Networking and Image Processing

- Antimicrobial and anticancer activity studies, Quantification and Purification of Bioactive compounds, Structural Elucidation of Compounds, Genotoxicity studies, Transgenic Tissue Engineering and *In silico* studies
- Polymer synthesis, Nanoparticles synthesis, Bioinorganic chemistry, Nano drug delivery, Electrochemistry, Biomedical applications (Antimicrobial, Anticancer activities) using nano, micro and macromolecules
- Molecular Oncology, Environmental Toxicology and Reproductive Toxicity

Funding Agencies

DBT	UGC	DST	CSIR	AURF	TNSCST	ICMR	BRNS	UGC-	DST	MHRD	DST-
								Innovative	INDO-	-RUSA	FIST
								Program#	TAIWAN	2.0	Level-I
296.90	92.15	160.75	32.00	07.44	01.89	54.59	30.33	54.00	227.29	69.39	62.00
								Total	1088.73		

[#] Plus, two assistant professor's salary for a period of five years

Award/ Recognition

- The Department of Bioinformatics has been recognized for its innovation programme under UGC scheme of Innovation and DST-FIST for the Improvement of S & T Infrastructure
- Faculty members have been conferred with the UGC-Research and ICMR Lala Ram Khandhari Award(s) for their contribution towards drug development for Diabetes and Sexually transmitted diseases.

Research Collaborating Organizations/ Institutes

	Ongoing		
National			
N. Rama Varier Ayurveda Foundation (NRAF), Madurai 2			
Bishop Heber College (Autonomus), Tiruchirap	ppalli	2018-23	
GE Healthcare Pvt. Ltd., Karnataka		2017-19	
Indian Institute of Technology- Madras, Chenna	ai	2017-22	
Sri Ramachandra University, Chennai		2016-21	
		2014-17	
International			
National Synchrotron Radiation Research Center, Taiwan 2017-20			
University of Manchester, Manchester, United Kingdom 2016-2		2016-21	
,		2016-21	
1 , 1		2016-21	
School of Science, Osaka University, Japan 2010-		2010-15	
RIKEN, Kanagawa, Japan 2010-		2010-15	
Institute of Protein Research, Osaka University, Japan 2010-		2010-15	
Bio-Metal Science Lab, RIKEN, Harima Institute, SPring-8, Japan 2010-1		2010-15	
National Collaboration			
Anna University, Tiruchirappalli	Bharathiar University, Coimbator	e	
Bharathidasan University, Tiruchirappalli	Chhatrapati Shahu Ji Maharaj Un	iversity, Kanpur	
CSIR - Central Drug Research Institute, Lucknow CSIR - Central Electrochemical Chemical Research Institute, Karaikudi		Chemical Research	

CSIR - Centre for Cellular and Molecular	CSIR-National Chemical Laboratory, Pune
Biology, Hyderabad	•
Indian Institute of Technology, BHU, Varanasi	Indian Institute of Technology-Delhi
Indian Institute of Technology-Kanpur, Uttar Pradesh	Indian Institute of Technology-Madras, Chennai
Indian Institute of Technology-Mandi, Himachal Pradesh	Indian Institute of Technology-Guwahati, Assam
Indian Institute of Science, Bangalore	Indian Institute of Science Education and Research, Bhopal
Indian Institute of Science, Education and Research, Pune	Institute of Life Sciences, Bhubaneswar
Integral University, Lucknow	International Centre for Genetic Engineering and Biotechnology, New Delhi
Jawaharlal Nehru Tropical Botanic Garden and Research Institute, Kerala	Jawaharlal Nehru University, New Delhi
King George Medical University, Lucknow	Madurai Kamaraj University, Madurai
National Institute of Immunology, New Delhi	North-Eastern Hill University, Shillong
Noorul Islam University, Nagercoil	Pondicherry University, Puducherry
SASTRA University, Thanjavur	Sri Ramachandra University, Chennai
University of Madras, Chennai	University of Mysore, Mysuru
VIT University, Vellore	
International Collaboration	
Konkuk University, South Korea	Loma Linda University, USA
Nanyang Technological University, Singapore	National Synchrotron Radiation Research Center, Taiwan
Osaka University, Japan	RIKEN, Harima Institute, SPring-8, Japan
Other Collaboration	
Eminent Biosciences, Indore	Schrödinger, USA
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Infrastructure Facilities in the Department

- Total area of the Department: 28.38 x 40.88 mts
- Smart Classrooms
- Well-equipped laboratory facilities for Practical and Research works
- Good stock of Library books and Journals
- INFLIBNET facility to access e-journals
- E-Library facility to access e-books

Resources

- AKTA TM protein purification system with cold cabinet
- AMBER & Geneious Pro
- Bio safety cabinets
- Bio photometer Plus
- Cambridge Structural Database
- Cold Room
- Deep Freezers (-80°C and -20°C)
- ELISA Reader and Washer
- Electrophoresis and Western Blot Units

- Ice Flakers
- In-house protein database
- Kinetics Spectrophotometer
- Microscope
- Milli-Q Integral Water Purification System
- Multiplate Reader
- Nano Spectrophotometer
- Orbital Shaker
- Power backup (20, 10 and 5 KVA UPSs)

- Gel Documentation system
- **Gradient PCRs**
- High End Servers and workstations
 High Performance Computing cluster system
 High Speed Cooling Centrifuges
- Protein Crystallization Facility Smart Class Room Facilities
- Ultra Sonicator
- UV VIS Spectrophotometer



















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Web: www.alagappauniversity.ac.in, www.bioinfoau.org

ALAGAPPA UNIVERSITY PLACEMENT CELL

Alagappa University, Karaikudi 630 003

1.1 Details required the preparation of department profile for the Academic Year 2021-22

CORE COMPETENCY

The **Department of Bioinformatics** have been focusing to develop novel and potent drug candidates against human disorders (Cancer, Diabetes, Hypertension and Chronic Kidney disease) and infectious diseases including bacterial infections (Malaria, Filariasis, TB and Nosocomial infections namely ESKAPE pathogens) and viral infections (Influenza, Dengue, Chikungunya, HIV, ZIKA and COVID-19) through streamlining of both computational and experimental techniques to hasten the discovery of novel drug candidates against various human diseases. The generated data are compiled, stored and maintained in the form of user-friendly databases which can be retrieved easily and will be resourceful for the Scientific Community. The industry-academia collaboration brought about in the DBT approved BIC Centre and National Network Projects (NNP) will certainly enhance the training opportunities for the students, research scholars and faculty members. Apart from the training, the Centre will also refine and take lead molecules to the next phase of clinical evaluations leading to product-oriented outcomes and Patents.

HALLMARKS

- ★ More than 58 Publications, 12 books and 1 monograph were published during this year.
- ★ 2 Patents were filled and published.
- ★ Completed **DAE-BRNS** Projects (**Rs.30.33 lakhs** 2018-2021)
- ★ Ongoing research projects during this year include **DST INDO-TAIWAN**, **TANSCHE** Govt. of Tamil Nadu and **ICMR**.
- ★ Research Competency of the department was further enhanced with generous funding by National and International agencies.
- ★ Organized Hands-on Training (Workshop) has been conducted for the students and other participant's to get familiar with the recent developments in the area of Computer Aided Drug Design.
- ★ Conducted Career guidance for the M.Sc students to enlighten them of various job prospects and opportunities available at different sectors.
- ★ Outstanding scholars were given opportunity to visit sophisticated laboratories to carry out their research work at premier institutes.

Collaborative research work with the following leading Institutions:

- ➤ Department of Biology, College of Science in **Zulfi, Majmaah University**, Majmaah, Saudi Arabia.
- ➤ IIT Madras-69.38, NSRRC, Taiwan-73.72,
- **DST INDO-TAIWAN** collaborative research project, Taiwan.
- Nanyang Technological University, Singapore.
- ➤ University of Manchester, U.K National Institute of Health, USA and Institute of Experimental Medicine, Czech Republic.
- > International Centre for Genetic Engineering and Biotechnology, Delhi.

- ➤ IISC Bangalore, IIT –Madras, Guwahati, Delhi and Mandi University of Madras, and Chhatrapati Shahuji Maharaj University, Kanpur, CSIR-NCL, Pune, CSIR-CDRI, Lucknow and CSIR-CECRI, Karaikudi.
- ➤ OrbitO Asia Diagnostics, Coimbatore, Sree Balaji Medical College and Hospital, Chennai, Sastra Deemed University, Thanjavur, KTH Royal Institute of Technology, Sweden and Indian Institute of Food Processing Technology(NIFTEN T), Thanjavur.

DEEDS & DEVELOPMENTS

- ♦ Five days International Conference cum Workshop on "Recent Trends in Structural Bioinformatics and Computer Aided Drug Design" ICSBCADD'2022 from 21st November to 25th November 2022
- ❖ 38 distinguished scientists and eminent academicians from across India and countries like the USA, Singapore, Taiwan, and Japan participated
- ♦ More than 200 participants from various countries across the world
- It helped participants to develop technical Proficiency in handling computational tools to respond to biological issues
- ❖ **DBT-BIC** has been granted BIC and National Networking Project (NNP) to Department of Bioinformatics, Alagappa University for **5 years** with a tune of **Rs. 350 lakhs**.
- ❖ The Broad-Based Board of Studies (BBBOS) was held on July 28th, 2022 at 11.00 am through hybrid mode in the Department of Bioinformatics, Alagappa University
- ❖ RUSA-Weekly online workshop- Cryptozens was conducted on November 16, 2021.
- Special address on crypto currency and block chain was organized in the department for efficient use of digital currency.

AWARDS & ACHIEVEMENTS

Faculty Achievements/Awards:

- ♣ Patent was received during the year 2021-22.
- Faculties delivered invited lectures in National and International conferences.

Students/Scholars:

- Five research scholars got Post-Doctoral Fellow positions in world class universities.
- ↓ 17 Research scholars received prestigious fellowships [ICMR,ICMR-SRF, JRF, DST-INDO
 -TAIWAN and TANSCHE].
- Research scholars also won prizes for Best Presentation of papers at various National and International conferences.



An Academic Society for Connecting People Worldwide (Registered under Tamil Nadu Act 27 of 1975 with St. No. 42/2017)

MHO WE SERVE

Academicians
 Research Scholars
 Industrialists

· Students

WHAT WE DO &

- · Conference's
- · Symposium & Workshop
- · Awards
- · Recognizing scientific contributions

WHAT WE CAN DO

- Provide an opportunity to develop scientific network
- Foster and conduct collaborative research
 - Platform to bring out research ideas

Promote research training

WHAT YOU GET 🏡

Knowledge from Eminent Scientists

Discussion with Experts

Recognition of research works

WHO WE ARE

Bioinformatics and Drug Discovery Society (BIDDS) is an Indian academic society for the development of Bioinformatics and Computational Biology with a mission to develop the application of Bioinformatics in India.

Serve as a platform for dissemination of scientific knowledge and function as a central hub between Bioinformatics, Biological sciences and other allied Life Sciences.

Helps in discovering the scientific and academic efforts throughout the globe and recognizes the researchers and scientist bestowed with the awards and credits.

JOIN US Web link: http://www.bidds.org/ Google form link: https://rb.qy/bxwed

- 1.Registration Fee for BIDDS Life membership for Faculties/PDF/- INR. 3000/-.
- 2.Registration Fee for BIDDS Life membership for Students - INR. 500/-.
- 3.Registration Fee for Corporate Individuals INR. 10,000/-

Bank Name	:	State Bank of India (581), Karaikudi
Account name	4	Bioinformatics and Drug Discovery Society
Account number	*	36993002251
IFSC Code	:	58IN00000855



President

Prof. D. Velmurugan, SRMIST, Chennai

Secretary General

Prof. Sanjeev Kumar Singh Email: secretary.bidds@qmail.com Ph: +91-4565-223342



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BIDDS REGISTRATION



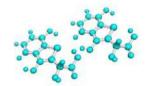
Membership Details

· Eligibility for Membership:

B.Sc., M.Sc., Ph.D. or equivalent degree in science and actively engaged in research or teaching in the field of Life science.

•Registration Fee:

Registration Fee for BIDDS Life membership for Faculties - INR. 3000/-Registration Fee for Student Membership - INR. 500/-Registration Fee for Corporate Individuals - INR. 10,000/-



· Online Electronic Transfer Details:

Name of the Bank	:	State Bank of India (SBI)
Branch	:	Karaikudi
Branch Code	:	855
Address	:	Subramaniapuram 1 st Street, Sekkalai Karaikudi-630002, Tamil Nadu
Account name	:	Bioinformatics and Drug Discovery Society
Account number	:	36993002251
IFSC Code	:	SBIN0000855
CIF	:	89869362836



The Demand Draft : "Bioinformatics and Drug Discovery Society" should be in favour of

Payable at : Karaikudi



Contact Prof. Sanjeev Kumar Singh Secretary General - BIDDS

Department of Bioinformatics Science Campus, Alagappa University Karaikudi - 630004 Tamil Nadu, India. Phone: +91-04565-223342

Email: secretary.bidds@gmail.com Web link: http://www.bidds.org

