DEPARTMENT OF BIOINFORMATICS
ALAGAPPA UNIVERSITY
(Reaccredited with 'A' Grade by NAAC)
KARAIKUDI-630 004, TAMIL NADU, INDIA

5th National Symposium cum Workshop on
"Recent Trends in Structural Bioinformatics and Computer Aided Drug Design" (SBCADD'2013)

19th - 22nd February, 2013

Abstract Status

S. No.	Title of the Abstract	Status
1.	Structural and functional insights into carbamoyl-phosphate synthase proteins of *Homo sapiens* and *Thermus thermophilus* HB8 - A comparative study **A. Devi Priyanka and J. Jeyakanthan*** Structural Biology and Biocomputing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
2.	MAGICdb – Mango Genetic stocks Identification and Characterization database **A. Dineshwaran[1], N. Senthil[1*], V. Vinothkumar[1], M. Raveendran[1], M. Kumar[2] and V. Ponnuswami[2]** [1]Department of Plant Molecular Biology & Bioinformatics, Tamil Nadu Agricultural University, Coimbatore – 641 003, Tamil Nadu [2]Horticulture College and Research Institute, Periyakulam – 625 604, Tamil Nadu	Accepted
3.	*In silico* design of novel synthetic small peptide inhibitor targeting the CDK2/cyclinA complex **A. Karthiga and Sanjeev Kumar Singh*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
4.	Pharmacophore-based virtual screening and atom-based 3D-QSAR studies on pyrrolo [3, 2-d] pyrimidine derivatives as EGFR inhibitors **A. Sudha and P. Srinivasan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
5.	Improving binding affinity of azide analogs of noscapine into α-β tublin dimer **AN. Kaarthik*, K. Vishnu Vandhana and Md. Afroz Alam** Department of Bioinformatics, Karunya University, Coimbatore-641 114, India	Accepted
6.	3D-QSAR and free energy analysis based lead identification of VEGFR-2 inhibitors **B. Sangeetha, R. Muthukumaran and R. Amutha*** Centre for Bioinformatics, School of Life Sciences, Pondicherry University, R.V. Nagar, Kalapet, Puducherry, India	Accepted
7.	Molecular modeling and docking of Rac1 and Rack1 proteins to induce the innate immunity in rice **B. Vinothini* and K. Sowmya** Department of Plant Molecular Biology & Bioinformatics, Tamilnadu Agricultural University, Coimbatore-641 003	Accepted

8.	Screening of potent lead molecules against phospholipase A2 - Virtual screening and molecular dynamics approach **C. Sathishkumar and M. Karthikeyan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi–630 004, Tamil Nadu, India	Accepted
9.	The molecular level energy calculation and molecular dynamics studies on structurally similar HTLV and HIV protease enzymes using HIV-PR inhibitors **C. Selvaraj and Sanjeev Kumar Singh*** Computer Aided Drug Design and Molecular Modeling Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
10.	The structural insights into interacting mechanism of wild type TPL-2 with P105 and ABIN-2 and onco-TPL-2 in MEK/ERK pathway: To understand TPL-2 mechanism in breast cancer **Chaten Kumar Meena, M. Kannan, P. Manivel, J. Muthukumar and R. Krishna*** Centre for Bioinformatics, Pondicherry University, Puducherry-605 014	Accepted
11.	Computational identification of potent immunodominant antigenic regions for DENV 2 **D. Nandhini, K. Gopinath and M. Karthikeyan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
12.	Functional prediction of hypothetical protein TTHA0731 from *Thermus thermophilus* HB8: A Computational Approach **D. Prabhu and J. Jeyakanthan*** Structural Biology and Biocomputing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
13.	Homology modeling and structure based virtual screening of wbpP virulence protein in *Vibrio vulnificus* **D. Sasikala and P. Srinivasan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
14.	Steps toward identification of novel antibacterial agents effective against virulence factor of *Clostridium difficile*: A computational perspective **E. Vijayalakshmi and Archana Pan*** Centre for Bioinformatics, School of Life Sciences, Pondicherry University, Pondicherry–605 014, India	Accepted
15.	Crystal structure analysis and docking studies of the compound (E)-2-({2-[(E)-(hydroxyimino)methyl]phenoxy}methyl)-3-p-tolylacrylonitrile **G. Suresh and S. Aravindhan*** Department of Physics, Presidency College, Chennai-600 005, Tamil Nadu, India	Accepted
16.	Pharmacophore modeling, molecular docking and electronic structure analysis on 2-aminopyrimidines as RAGE inhibitors **G. Nagalakshmi, V. Suryanarayanan and Sanjeev Kumar Singh*** Computer Aided Drug Design and Molecular Modeling Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
17.	Molecular modeling and docking of N-acetylneuraminic acid analogue-Cholera toxin complex	Accepted

	J. Jino Blessy* and Jeya Sundara Sharmila Department of Bioinformatics, Karunya Univesity, Karunya Nagar, Coimabtore-641 114	
18.	Virtual screening of potential drug analogs with their geometrical descriptors **J. Pradeep Kumar, K. Sumathi, N. Sharmila and T. V. Sundar*** P.G. and Research Department of Physics, National College (Autonomous), Tiruchirappalli-620 001, India	Accepted
19.	Role of PIN domain protein (TTHA0182) from *Thermus thermophilus* HB8 in DNA mismatch repair mechanism **J. Shivashankari[1], A. Devi Priyanka[2], D. Prabhu[2] and J. Jeyakanthan[2*]** [1]Department of Bioinformatics, School of Chemical and Biotechnology, SASTRA University, Thanjavur-613 401, Tamil Nadu, India [2]Structural Biology and Biocomputing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
20.	*In silico* mapping of genes and markers in public domain genome sequences **K. Deepika*, S. Gayathri, M. Mugilisai and V. Arunachalam** Department of Plant Molecular Biology and Bioinformatics, CPMB&B, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India	Accepted
21.	Structure based virtual screening and molecular dynamics for identification of 11β-HSD1 natural product inhibitors **K. Gopinath and M. Karthikeyan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
22.	A database revealing notch central signaling pathway cross talking to various cell signaling pathways an approach to deal with cancer **K. Lekharani, Sanjay Kumar Choubey and J. Jeyakanthan*** Structural Biology and Biocomputing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
23.	Biological interaction of β-lactam antibiotics with penicillin binding proteins and β-lactamases- A molecular docking and molecular simulation approach **K. M. Kumar*, P. Senthil, R. Sudha and A. Anand** Bioinformatics Division, School of Biosciences and Technology, VIT University, Vellore-632 014	Accepted
24.	*In silico* prediction of host-pathogen protein-protein interactions **K. Priya Dharshini and P. Srinivasan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
25.	*In silico* and structural bioinformatics approach to control cucumber anthracnose disease caused by *Colletotrichum lagenarium* **K. Priyadharshini, V. Sri Vidhya, N. Bharathi, P. Nagarajan and M. Azitha Begum*** Department of Plant Molecular Biology and bioinformatics, CPMB & B, Tamilnadu Agricultural University, Coimbatore-641 003,Tamil Nadu, India	Accepted
26.	Implicit the structural investigation of OPRTase from *Thermus thermophilus* HB8 using molecular docking and dynamics: Insights into conformational changes and ligand Binding **K. Sureka, D. Prabhu, M. Nachiappan and J. Jeyakanthan*** Structural Biology and Biocomputing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted

27.	Shape and pharmacophore-based virtual screening to identify potential cytochrome P450 sterol 14α-demethylase inhibitors **Karnati Konda Reddy and Sanjeev Kumar Singh*** Computer-Aided Drug Design and Molecular Modeling Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
28.	Molecular modeling and 3D-QSAR study on a large chemically diverse series of Angiotensin type 1 receptor (AT1R) antagonists **Kh. Dhanachandra Singh[1], M. Ranjini Shakthi[2] and M. Karthikeyan[1*]** [1]Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India [2]Department of Bioinformatics, School of Life Science, Bharathidasan University, Tiruchirappalli-24	Accepted
29.	Antibacterial activity of plant compounds against a wild and mutant autolysin protein of *Staphylococcus aureus* **L. Edel Usha, P. Vijayalakshmi and P. Daisy*** Bioinformatics centre (BIF), PG& Research Department of Biotechnology & Bioinformatics, Holy Cross College (Autonomous), Tiruchirapalli-620 002, Tamil Nadu	Accepted
30.	Virtual screening and molecular docking studies of marine bioactive compounds on *Staphylococcus hominis* **M. G. Karthih[1] and P. Srinivasan[2*]** [1]Department of Biotechnology, Sathyabama University, OMR road, Chennai-600 119 [2]Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
31.	Differential binding of diverse classes of inhibitors to inactive and active CDK2-CyclinA: An insight for structure-based drug design **M. Madhumathi, Sunil Kumar Tripathi and Sanjeev Kumar Singh*** Computer Aided Drug Designing and Molecular Modeling Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
32.	Phage protein-bacterial protein interaction study: an *in silico* approaches **M. Meenatchi, N. Stalin and P. Srinivasan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
33.	Crystal structure analysis of bis(6-chloro-4-phenyl-2-p-tolylquinolin-3-yl)sulfane **M. Nachiappan[1], J. Muthukumaran[2], R. Krishna[2], S. Chitra[3], P. Manisankar[3], Nidhin Paul[4], S. Muthusubramanian[4] and J. Jeyakanthan[1*]** [1]Structural Biology and Bio-Computing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India [2]Centre for Bioinformatics, Pondicherry University, Puducherry–605 014, India. [3]Department of Industrial Chemistry, Alagappa University, Karaikudi-630 003, Tamil Nadu, India [4]Department of Organic Chemistry, Madurai Kamaraj University, Madurai-625 021,Tamilnadu, India	Accepted
34.	Regulation of DNA damage checkpoint in human by TAO3 VIA p38/ MAPK14 kinase	Accepted

	M. Ramamurthi, M. Nachiappan, A. Devi Priyanka, D. Prabhu and J. Jeyakanthan* Structural Biology and Bio-computing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	
35.	*In silico* and hairy root induction studies for anticancer in *Tephrosia tinctoria* Pers **M. Sobana*, K. Rajaram and P. Suresh Kumar** Department of Biotechnology, BIT Campus, Anna University, Tiruchirappalli-620 024	Accepted
36.	Three-dimensional quantitative structure-activity relationship analysis and molecular docking of inhibitors of HIV-1 integrase **R. S. Monisha Ilakkia, Karnati Konda Reddy and Sanjeev Kumar Singh*** Computer-Aided Drug Design and Molecular Modeling Lab, Department of Bioinformatics, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
37.	A computer aided drug design: Discovery of a new drug for *Xanthinuria* **N. Ramesh Kannan, B. Muthukumar and E. Natarajan*** PG & Research Department of Botany, National College (Autonomous), Tiruchirappalli-620 001	Accepted
38.	Exploring the role of cation-π interactions in metalloproteins **P. Anitha*, R. G. Swetha, A. Anand and R. Sudha** Bioinformatics Division, School of Bioscience and Technology, VIT University, Vellore-632 014	Accepted
39.	Molecular mechanism of the interaction between selective inhibitors of PARP and Tankyrase enzymes **P. Kirubakaran and M. Karthikeyan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
40.	Exploring anti-TB leads from *Justicia adhatoda*: An in vitro and in silico study **P. Lavanya*, A. Anand and R. Sudha** Bioinformatics Division, School of Biosciences & Technology, VIT University, Vellore-632 014	Accepted
41.	SNP analysis of Tetra Amelia Syndrome: A computational biological approach **P. Likith Reddy* and Manoj** Department of Bioinformatics, Sathyabama University, Chennai-600 009	Accepted
42.	*In silico* characterization of cyanobacterial fur antisense RNA's as CRISPR RNA's and assessment of interaction with HOX operon **P. Manivannan[1], V. Vasanthan[2], S. Revathi[2] and G. Muralitharan[1*]** [1]Division of Molecular Evolution, Department of Microbiology, Bharathidasan University, Tiruchirappalli–620 024, Tamilnadu, India [2]Department of Bioinformatics, Bharathidasan University, Bharathidasan University, Tiruchirappalli–620 024, Tamilnadu, India	Accepted
43.	Insight into the structural mechanism involved in inducing resistance against taxol in cancer cells through molecular docking and dynamic studies **P. Manivel, M. Kannan, J. Muthukumaran, S. Upasana and R. Krishna*** Centre for Bioinformatics, Pondicherry University, Puducherry-605 014	Accepted
44.	*In silico* analysis of phage endolysin protein against *Pseudomonas aeruginosa* **PK. Malarvizhi, S. Rajamanikandan, T. Sindhu and P. Srinivasan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted

45.	Structural view on hypothetical protein (TTHA0427) from *Thermus thermophilus* HB8 - A bioinformatics approach **R. Maharaja, D. Prabhu, A. Devi Priyanka and J. Jeyakanthan*** Structural Biology and Biocomputing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
46.	Identification of novel drug targets using network analysis **R. Mohana Priya[1]*, R. Revathi[1], S. Sherlie Miriam[1], Tina Mathew[1], P. Renuka Devi[2], D. Velmurugan[3]** [1]Department of Bioinformatics, Karunya University, Coimbatore [2]Department of Biotechnology, Anna University Regional Centre, Coimbatore [3]CAS in Crystallography and Biophysics, University of Madras, Chennai	Accepted
47.	Structural and dynamics studies of PH0702 protein of *Pyrococcus horikoshii* OT3 **R. Naga Soundarya, S. G. Rethinamaliga and J. Jeyakanthan*** Structural Biology and Biocomputing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
48.	Molecular modeling, docking and dynamics studies of lipoprotein lipase- a potential target for the development of anticancer drugs **R. Vanajothi and P. Srinivasan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
49.	Optimal descriptor set selection for anti-cancer compounds using genetic programming based methods **Renu Vyas*[1], Chandan Dipke[2] and Sanjeev S. Tambe[1]** [1]National Chemical Laboratory Pune-411 008, India [2]Dr. D. Y. Patil Biotechnology and Bioinformatics Institute, Pune - 411 033, India	Accepted
50.	TargetMab: A novel screening approach to prioritize and characterize potential therapeutic candidates **S. Buvaneswari and Archana Pan*** Centre for Bioinformatics, School of Life Sciences, Pondicherry University, Pondicherry-605 014	Accepted
51.	*In silico* studies on the protein PHO140 from *Pyrococcus horikoshii* OT3 to reveal the global functioning and regulations of leucine regulatory protein **S. G. Rethina Malliga and J. Jeyakanthan*** Structural Biology and Biocomputing Lab, Department of Bioinformatics, Alagappa University, Science Block, Karaikudi–630 004, Tamil Nadu, India	Accepted
52.	PPIRDB - Phage protein informative resource database **S. Gokila Vani, C. Selvaraj and Sanjeev Kumar Singh*** Computer Aided Drug Design and Molecular Modeling Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
53.	Tamil Nadu Agricultural University Proteome DataBase (TNAU PDB) **S. Jeyarekha*, N. Senthil, V. Vinoth Kumar, N. Jagadeesh Selvam and M. Raveendran** Department of Plant Molecular Biology and Bioinformatics, CPMB&B, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India	Accepted
54.	Molecular dynamics and virtual screening analysis of Fla A protein in *Vibrio anguillarum*	Accepted

	S. Rajamanikandan and P. Srinivasan* Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	
55.	*In silico* screening of flavonoids for breast cancer specific histone deacetylase (HDAC) 1 and 3 inhibitors **S. Sangeetha[1*], S. Ranjitha[2], Sunil Kumar Tripathi[3], Sanjeev Kumar Singh[3], J. Sridhar[4] and R. Gopal[1]** [1]Bioinformatics Lab, AU-KBC Research Centre, Anna University, M.I.T Campus, Chennai, India [2]Centre for Biotechnology, Anna University, Chennai, India. [3]Computer Aided Drug Designing and Molecular Modeling Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India [4]UGC-NRCBS, School of Biological Sciences, Madurai Kamaraj University, Madurai, India	Accepted
56.	Exploring the association of NOTCH signaling and various anti- tumor suppression mechanism in progression of germ cell cancer-seminoma **Sanjay Kumar Choubey and J. Jeyakanthan*** Structural Biology & Biocomputing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
57.	Identification of multidrug efflux receptor proteins in Salmonella typhi: MD simulation and docking based approach **Sarika Prem, P. Perumal, T. Jebastin* and N. Sundara Baalaji** Structural Biology Lab, Department of Bioinformatics, Bharathiar University, Coimbatore-46, India	Accepted
58.	Multiple docking assessment of 3, 5 diaminoindazole series of CDK2 inhibitors **Sunil Kumar Tripathi and Sanjeev Kumar Singh*** Computer Aided Drug Designing and Molecular Modeling Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
59.	Docking study of laccase from *Pycnoporus cinnabarinus* with ABTS (2, 2'-azino-bis (3-ethylbenzothiazoline-6-sulfunic acid)) **Surya Narayan Rath*, Badri Narayan Sahu, Hrudayanath Thatoi and Sukanta Kumar Pradhan** *Department of Bioinformatics, Centre for Post Graduate Studies, Orissa University of Agriculture & Technology, Bhubaneswar, Odisha, India Department of Bioinformatics, BJB (A) College, Bhubaneswar, Odisha, India Department of Biotechnology, College of Engineering and Technology, Bhubaneswar, Odisha, India	Accepted
60.	*In silico* investigation of gene-gene interaction in PPAR-γ network **Susmita Bag*, A. Anand and R. Sudha** Bioinformatics división, School of Biosciences and Technology, VIT University, Vellore-632 014	Accepted
61.	A web-based database for buffer molecule bound into the proteins **T. Divya[1], R. Santhosh[1], M. Kirti Vaishnavi[2], K. Sekar[2] and J. Jeyakanthan[1*]** [1]Structural Biology and Biocomputing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India [2]Supercomputer Education and Research Centre, Indian Institute of Science, Bangalore-560 012, India	Accepted

62.	Pharmacophore modeling and atom based 3D-QSAR studies on H1N1 inhibitors **T. Raja Rajeshwari, P. Kirubakaran and M. Karthikeyan *** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
63.	Pharmacophore modeling, 3D QSAR and molecular docking studies of benzimidazole derivatives as potential FXR agonists **T. Sindhu and P. Srinivasan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
64.	Evolution of non-coding DNA in eukaryotic genome **V. Pavithra* and S. Arul Mugilan** Department of Bioinformatics, Karunya Univesity, Karunya Nagar, Coimabtore-641 114	Accepted
65.	3D QSAR studies and evaluation of dual inhibitor strategies of isothiazolone derivatives as PCAF inhibitors **V. Suryanarayanan and Sanjeev Kumar Singh*** Computer Aided Drug Design and Molecular Modeling Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
66.	Cytochrome P450 3A4-mediated drug interaction studies on anti-HIV and anti-tuberculosis drugs **M. Jayakanthan*, J. Pranitha and P. P. Mathur** Centre for Bioinformatics, School of Life Sciences, Pondicherry University, Pondicherry – 605014	Accepted
67.	Pharmacophore mapping and atom based 3D-QSAR studies on VDR agonists **S. Nagamani[1], C. Kesavan[2,3], M. Karthikeyan[1*]** [1]Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India [2]Musculoskeletal Disease Center, JLP VA Medical Center, Loma Linda, USA [3]Dept of Medicine, Loma Linda University, Loma Linda, USA	Accepted
68.	Insights into the interacting mechanism of MARK4 and its inhibition by kinase inhibitors, a computational approach to understand the role of MARK4 in prostate cancer progression **J. Pranitha*, M. Jayakanthan and P. P. Mathur** Centre for Bioinformatics, School of Life Sciences, Pondicherry University, Pondicherry – 605 014	Accepted
69.	*In silico* analysis of antiviral proteins in *Clerodendrum inerme* **R. Sathya, N. Bharathi and R. Renuka** Department of Plant Molecular Biology and bioinformatics, CPMB & B, Tamilnadu Agricultural University, Coimbatore-641 003,Tamil Nadu, India	Accepted
70.	Pharmacophore modeling and 3D-QSAR study of macrocycle 11-(2-pyrrolidin-1-yl-ethoxy)-14,19-dioxa-5,7,26-triaza-tetracyclo [19.3.1.1 (2,6).1 (8,12)] heptacosa-1(25),2(26),3,5,8,10,12(27),16,21,23- decaene derivatives as Jak2 kinase inhibitors **E. Queen Naveena, Kh Dhanachandra Singh and M. Karthikeyan*** Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted
71.	A Study on homology modeling of reverse transcriptase of Rous Sarcoma Virus **B. Sivasankari, M. Anandharaj* and S. Vimalarani**	Accepted

	Department Of Biology, Gandhigram Rural Institute- Deemed University, Gandhigram-624302	
72.	Functional annotation of hypothetical proteins to identify the metal involving proteins from *Thermus Thermophilus* HB8 **B. Dhivya[1], S. Yogapriya[1], A. Devi Priyanka[2], D. Prabhu[2] and J. Jeyakanthan[2*]** [1]Department of Bioinformatics, Bharathidasan University, Trichy-620024 [2]Structural Biology and Biocomputing Laboratory, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi-630 004, Tamil Nadu, India	Accepted

Sponsored by

Alagappa University, Tamilnadu
Department of Biotechnology (DBT), New Delhi
Department of Science & Technology (DST), New Delhi