



DEPARTMENT OF BIOINFORMATICS  
ALAGAPPA UNIVERSITY



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14<sup>th</sup> – 17<sup>th</sup> February, 2017

**ABSTRACTS RECEIVED FOR POSTER PRESENTATION**

S. No	Title of Abstract	Status
1.	<b>Identification of Potent Angiotensin Converting Enzyme 2 Inhibitors through Virtual Screening and Structure-Based Pharmacophore Design</b> C. Zozimus Divya Lobo <sup>1</sup> , A. Syed Mohamed <sup>2*</sup> , C. Vedhi <sup>3</sup> <sup>1</sup> Department of Chemistry, St. Mary's College, Tuticorin, Tamil Nadu, India <sup>2</sup> Department of Chemistry, Sadakathullah Appa College, Tirunelveli, Tamil Nadu, India <sup>3</sup> Department of Chemistry, VOC College, Tuticorin, Tamil Nadu. (Email: asm2032@gmail.com)	Accepted
2.	<b>Specific Binding of RVV-V with Cleavage Site of FV Explored</b> Pradeep Kumar Yadav, A. Christian Bharathi and B. Syed Ibrahim Department of Bioinformatics, Pondicherry University, Pondicherry, India (Email: yadavpradeep755@gmail.com)	Accepted
3.	<b>Study of Intermolecular Recognition Mechanism Involved in C4 Activation through Serine Protease – an <i>In Silico</i> Approach</b> Vikrant Kumar Sinha, and Muthuvel Suresh Kumar* Centre for Bioinformatics, School of Life Sciences, Pondicherry University, Pondicherry, India. (E-mail: vik.nid13@gmail.com)	Accepted
4.	<b>Alleviating Autism Spectrum Disorder through a Traditional Approach</b> Vishnu Ranjit A <sup>1*</sup> and R. Sathishkumar <sup>2</sup> <sup>1</sup> Department of Physiology, PSG College of Arts and Science, Coimbatore, Tamil Nadu, India <sup>2</sup> Assistant Professor, Department of Botany, PSG College of Arts and Science, Coimbatore, Tamil Nadu, India	Accepted
5.	<b>E-Pharmacophore Based Design of Novel Protease Inhibitors for HIV-1</b> Ishwar Chandra, Chirasmita Nayak and Sanjeev Kumar Singh* Computer Aided Drug Design and Molecular Modeling lab, Department of Bioinformatics, Alagappa University, Karaikudi – 630 004, Tamil Nadu, India. (Email: skysanjeev@gmail.com)	Accepted
6.	<b>3D-QSAR Pharmacophore Based Studies of Ache Complexes, with Resveratrol similar Compounds: a new Insight for <i>Alzheimer's Diseases</i> Treatment</b> Mohd Babu Khan <sup>1</sup> , Bhagath Kumar P <sup>1</sup> , Tuleshwori Devi S <sup>1</sup> , Naidu Subbarao <sup>2</sup> , Dinakara Rao A <sup>1*</sup> <sup>1</sup> Centre for Bioinformatics, School of Life Sciences, Pondicherry University, Pondicherry, India <sup>2</sup> School of Computational and Integrative Sciences, Jawaharlal Nehru University, New Delhi, India (Email: mmbk.bioinfo@gmail.com, ampasaladr@gmail.com)	Accepted
7.	<b>Alpha Amyrin and Beta Amyrin- Anti Cancer Compounds from Methanolic Bark Extract of Shorea Robusta</b> V. Dhivya Jensi and P. Ananda Gopu* Department for Advanced Computing and Bioinformatics, PRIST University, Thanjavur	Accepted

	(*Email : panandagopu.crd@prist.ac.in)	
8.	<p><b>Screening of Potent Inhibitor against TNKS 2 Using <i>In Silico</i> Approaches</b></p> <p><b>Josephine Julia Balthasar</b>, John Marshal Jayaraj and Karthikeyan Muthusamy*  <sup>1</sup>Department of Bioinformatics, Alagappa University, Karaikudi – 630004, Tamil Nadu, India.  (*Email: mkbioinformatics@gmail.com)</p>	Accepted
9.	<p><b>Genome-Wide Analysis of Secretory Proteins in <i>Trypanosoma Brucei</i>: Insights into Functional Characteristics of the Secretome</b></p> <p><b>Gowdham M</b>, Muruges Easwaran, Shanmughavel Piramanayagam*  Department of Bioinformatics, Bharathiar University, Coimbatore-641046, India  (*Email:gowdhamgct@gmail.com.)</p>	Accepted
10.	<p><b>Protein-Protein Interaction between <i>Vibrio Harveyi</i> Luxr and Phage Lysozyme using Molecular Docking and Molecular Dynamics Study</b></p> <p><b>Nattan Stalin<sup>a</sup></b>, Pappu Srinivasan<sup>b*</sup>  <sup>a</sup>Molecular Biology Laboratory, Department of Bioinformatics,  <sup>b</sup>Department of Animal Health and Management, Alagappa University, Karaikudi - 630 003, Tamil Nadu, India.</p>	Accepted
11.	<p><b>Identification of Pathogenesis associated Leptospiral Outer Membrane Proteins (OMPs) as Vaccine Candidates for Leptospirosis</b></p> <p><b>Muthu Prasad<sup>1</sup></b>, Paulsamy Chellapandi<sup>2</sup> and Kalimuthusamy Natarajaseenivasan<sup>1*</sup>  <sup>1</sup>Department of Microbiology, <sup>2</sup>Department of Bioinformatics, School of Life Sciences, Bharathidasan University, Tiruchirappalli, Tamil Nadu – 620024.  (*E-mail: natarajaseenivasan@gmail.com)</p>	Accepted
12.	<p><b>Synthesis and Characterization of <i>Capsicum Annuum</i> Fruitextract (Capsaicin) Coated Silver Nanoparticle (Ca-Agnps) and Their Toxicity Assessment on <i>Ceriodaphniacornuta</i> through <i>In Vivo</i> and <i>In Silico</i> Approaches</b></p> <p><b>Sekar Vijayakumar<sup>a</sup></b>, Venkatesan Suryanarayanan<sup>b</sup>, BalasubramanianMalaikozhundan<sup>a</sup>, Sanjeev Kumar Singh<sup>b</sup>,Baskaralingam Vaseeharan<sup>a*</sup>  <sup>a</sup>Nanobiosciences and Nanopharmacology Division, Biomaterials and Biotechnology in Animal Health Lab, Department of Animal Health and Management, Alagappa University, Karaikudi – 630 004,Tamil Nadu, India.  <sup>b</sup>Computer Aided Drug Design and Molecular Modelling Lab, Department of Bioinformatics,Alagappa University, Karaikudi-630004, Tamil Nadu, India  (*Email: vaseeharanb@gmail.com)</p>	Accepted
13.	<p><b>Anti-inflammatory and <i>in silico</i> studies of Loganic acid against COX-2</b></p> <p><b>Arumugam Sudha<sup>1</sup></b>, Jeyaraman Jeyakanthan<sup>1</sup> and Pappu Srinivasan<sup>2*</sup>  <sup>1</sup>Department of Bioinformatics,  <sup>2</sup>Department of Animal Health and Management, Alagappa University, Karaikudi -630 004, Tamil Nadu, India</p>	Accepted
14.	<p><b>Distant Phe345 Mutation Compromises the Stability and Activity of <i>Mycobacterium Tuberculosis</i> Isocitrate Lyase (Mtbicl) By Modulating Its Structural Flexibility</b></p> <p><b>Rohit Shukla</b>, Harish Shukla, Timir Tripathi*  Molecular and Structural Biophysics Laboratory, Department of Biochemistry, North-Eastern Hill University, Shillong 793022, India  (*Email:shuklarohit815@gmail.com)</p>	Accepted
15.	<p><b>In silico Screening of Marine Bioactive Compounds against Kaposi's Sarcoma-associated Herpes virus</b></p> <p><b>Nirmaladevi Ponnusamy<sup>a</sup></b>, Rajasree Odumpatta<sup>a</sup>, Sajitha Lulu<sup>a</sup>, Mohanapriya Arumugam<sup>a*</sup>  Department of Biotechnology, School of Biosciences and Technology, Vellore Institute of Technology University Vellore– 632014, Tamil Nadu, India  (*Email: mohanapriyaa@vit.ac.in)</p>	Accepted

16.	<p><b>Computational Study on Tankyrase-Ankyrin Complex for the Identification of Potent Inhibitors for Colon Cancer</b></p> <p>Sheela Rani Rajendran, Lakshmanan Loganathan and Karthikeyan Muthusamy  Department of Bioinformatics, Alagappa University, Karaikudi – 630 004, Tamil Nadu, India  (*E-mail: <a href="mailto:mkbioinformatics@gmail.com">mkbioinformatics@gmail.com</a>)</p>	Accepted
17.	<p><b>Computational Screening and Investigation of Algal Bioactive Compounds against E6 Oncoprotein of Human Papilloma Virus-HPV16</b></p> <p>Pavithra Damodharan<sup>a</sup>, Sajitha Lulu<sup>a</sup> and Mohanapriya Arumugam<sup>a*</sup>  <sup>a</sup>Department of Biotechnology, School of Biosciences and Technology, Vellore Institute of Technology University  (Email: <a href="mailto:pavithradamodharan94@gmail.com">pavithradamodharan94@gmail.com</a>)</p>	Accepted
18.	<p><b>Identification of potent inhibitors for LuxS through Structure-Based Virtual screening, DFT and Molecular Dynamics Simulation study</b></p> <p>Dakshinamurthy Sasikala<sup>a</sup>, Jeyaraman Jeyakanthan<sup>a</sup> and Pappu Srinivasan<sup>b*</sup>  <sup>a</sup>Molecular Biology Laboratory, Department of Bioinformatics,  <sup>b</sup>Department of Animal Health and Management, Alagappa University, Karaikudi - 630 003, Tamil Nadu, India.</p>	Accepted
19.	<p><b><i>In Silico</i> Redesigning of Hgstm1 towards Suppression of Oxidative Stress in Rheumatoid Synovium</b></p> <p>R Kowshik Aravilli, Dr. V. Kohila*  Department of Biotechnology, National Institute of Technology, Warangal-506001  (E-mail: <a href="mailto:arkowshik228@gmail.com">arkowshik228@gmail.com</a>, <a href="mailto:kohilav@gmail.com">kohilav@gmail.com</a>)</p>	Accepted
20.	<p><b>Binding Mode Analysis of Viral Protein E7 and Retinoblastoma through <i>In Silico</i> Approaches</b></p> <p>Aarthy Murali and Sanjeev Kumar Singh*  Computer Aided Drug Design and Molecular Modelling Lab, Department of Bioinformatics, Alagappa University, Karaikudi-630004, Tamil Nadu, India  (*E-mail: <a href="mailto:skysanjeev@gmail.com">skysanjeev@gmail.com</a>)</p>	Accepted
21.	<p><b>Repurposing FDA Approved Drugs against Zika Virus Protease, a Computational Study</b></p> <p>Ankur Kumar<sup>1</sup>, Aarthy Murali<sup>2</sup>, Sanjeev Kumar Singh<sup>2</sup>, Rajanish Giri<sup>1</sup>  <sup>1</sup>School of Basic Science, Indian Institute of Technology Mandi, Kamand campus, Mandi – 175005  <sup>2</sup>Department of Bioinformatics, Alagappa University, Karaikudi- 630004  (Email : <a href="mailto:ankuranand89@gmail.com">ankuranand89@gmail.com</a>)</p>	Accepted
22.	<p><b>Molecular Modeling and Screening Studies for Finding new N<sup>5</sup>-CAIR Mutase Inhibitors from <i>Pyrococcus Horikoshii</i> OT3 – an <i>In Silico</i> Approach</b></p> <p>Guru Raj Rao R., Jayashree Biswal, Surekha Kanagarajan, Jeyaraman Jeyakanthan*  Structural Biology and Bio-Computing Lab, Department of Bioinformatics, Alagappa University, Karaikudi, 630 004, Tamil Nadu, India.  (*Email: <a href="mailto:jjkanthan@gmail.com">jjkanthan@gmail.com</a>)</p>	Accepted
23.	<p><b>Kinase-Substrate Interplay and Proteome-Wide Phosphorylation Dynamics</b></p> <p>R. Shyama Prasad Rao<sup>1,*</sup>, and Nagib Ahsan<sup>2</sup>  <sup>1</sup>Biostatistics and Bioinformatics Division, Yenepoya Research Center, Yenepoya University, Mangalore –575018, India  <sup>2</sup>Division of Biology and Medicine, Alpert Medical School, Brown University; and Center for Cancer Research and Development, Proteomics Core Facility, Rhode Island Hospital, Providence, RI 02903, USA  (*Email: <a href="mailto:drsprao@gmail.com">drsprao@gmail.com</a>)</p>	Accepted
24.	<p><b><i>In Silico</i> and <i>In Vivo</i> Studies on Predicted Kanamycin Resistance Protein from <i>Thermus Thermophilus</i> HB8</b></p> <p>Arindam Ghosh, Dhamodharan Prabhu, Mutharasappan Nachiappan, Jeyaraman Jeyakanthan*</p>	Accepted

	Structural Biology and Bio-Computing Lab, Dept. of Bioinformatics, Alagappa University, Karaikudi- 630 004, Tamil Nadu, India. (*Email: jkkanthan@gmail.com)	
25.	<b>Structural and Functional Prediction of Hypothetical Protein TTHA0983 from <i>Thermus thermophilus</i> HB8: a Combined Experimental and Computational Approach</b> Poopandi Saritha <sup>1</sup> , Mutharasappan Nachiappan <sup>2</sup> , Guru Raj Rao <sup>2</sup> , Dhamodharan Prabhu <sup>2</sup> and Jeyaraman Jeyakanthan <sup>2*</sup> <sup>1</sup> Department of Biotechnology, Rajalakshmi Engineering College, Thandalam, Chennai -602105. Structural Biology and Biocomputing Lab, Department of Bioinformatics, Alagappa University, Karaikudi - 630 004, Tamil Nadu, India. (*Email: jkkanthan@gmail.com)	Accepted
26.	<b>Crystal Structure of Asparaginyl tRNA Synthetase from <i>Thermus Thermophilus</i> HB8 and its Complexes</b> Nachiappan Mutharasappan <sup>1</sup> , Vitul Jain <sup>2</sup> , Yogavel Manickam <sup>2</sup> , Amit Sharma <sup>2</sup> , and Jeyakanthan Jeyaraman <sup>1*</sup> <sup>1</sup> Structural Biology and Bio-Computing Laboratory, Department of Bioinformatics, Alagappa University, Karaikudi, Tamil Nadu, India - 630 004. <sup>2</sup> Structural Parasitology Lab, International Centre for Genetic Engineering and Biotechnology, Aruna Asaf Ali Marg, New Delhi - 110 067. (*E-mail: jkkanthan@gmail.com)	Accepted
27.	<b>Cloning, Expression and Preliminary Purification of Hypothetical Protein E3 Binding Protein (E3BP) from <i>Thermus Thermophilus</i> HB8.</b> Malaisamy Veerapandiyan, Mutharasappan Nachiappan, Dhamodharan Prabhu and Jeyaraman Jeyakanthan* Structural Biology and Biocomputing Lab, Department of Bioinformatics, Alagappa University, Karaikudi - 630 004, Tamil Nadu, India. (Email: jkkanthan@gmail.com)*	Accepted
28.	<b>Modeling and Molecular Dynamics Simulation Studies on Aspartokinase (Wbm0441) Enzyme from <i>Wolbachia</i> Endosymbiont <i>Brugia Malayi</i></b> Mathimaran Amala, Sanjay Kumar Choubey, Dhamodharan Prabhu, Surekha Kanagarajan, Mutharasappan Nachiappan and Jeyaraman Jeyakanthan* Structural Biology and Bio-Computing Lab, Department of Bioinformatics, Alagappa University, Karaikudi – 630 004, Tamil Nadu, India. (*Email: jkkanthan@gmail.com)	Accepted
29.	<b>Identification of Potent PAK1 Antagonists Using E-Pharmacophore Based Mapping and Screening– an <i>In Silico</i> Approach.</b> Jayashree Biswal <sup>1</sup> , Suresh Kumar Rayala <sup>2</sup> , Ganesh Venkatraman <sup>3</sup> and Jeyaraman Jeyakanthan <sup>1*</sup> <sup>1</sup> Structural Biology and Bio-Computing Lab, Department of Bioinformatics, Alagappa University, Karaikudi - 630 004, Tamil Nadu, India <sup>2</sup> Department of Biotechnology, Indian Institute of Technology Madras, Chennai-600 036, Tamil Nadu <sup>3</sup> Department of Human Genetics, College of Biomedical Sciences, Sri Ramachandra University, Porur, Chennai-600 116, Tamil Nadu, INDIA. (* Email: jkkanthan@gmail.com)	Accepted
30.	<b>Computational Identification of Potent Inhibitors for Streptomycin 3''-Adenylyltransferase of <i>Serratia Marcescens</i></b> Dhamodharan Prabhu, Ramasamy Vidhyavathi, Jeyaraman Jeyakanthan* <sup>1</sup> Structural Biology and Bio-Computing Laboratory, Department of Bioinformatics, Alagappa University, Karaikudi - 630 004, Tamil Nadu, India (* Email: jkkanthan@gmail.com)	Accepted
31.	<b>Exploration of Plant Bioflavonoids as Potential Matrix Metalloproteinase-9(MMP-9) Inhibitors for the Management of Rheumatoid Arthritis- a Computational Approach</b>	Accepted

	<p><b>Pradiba D<sup>1</sup>, Shunmuga Priya V<sup>1</sup>, Aarthi M<sup>2</sup>, Sanjeev Kumar Singh<sup>2</sup> and Vasanthi M<sup>*1</sup></b>  <sup>1</sup>Department of Biotechnology, Kamaraj College of Engineering and Technology, Virudhunagar 626 001  <sup>2</sup>Computer Aided Drug Design and Molecular Modelling Lab, Department of Bioinformatics, Alagappa University, Karaikudi 630 004  <i>(*E-mail: vasanthimadurai@gmail.com)</i></p>	
32.	<p><b>Energy based Pharmacophore screening and molecular dynamics simulation studies in the discovery of potent inhibitors for Type II Diabetes</b>  <b>J. Prajisha</b> and Jeyaraman Jeyakanthan*  Structural Biology and Bio-Computing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi - 630 004, Tamil Nadu, India  <i>(* Email: jjkanthan@gmail.com)</i></p>	Accepted
33.	<p><b>Structural Insights on Binding mechanism of CAD Complexes (CPSase, ATCase and DHOase)</b>  <b>Kanagarajan Surekha,</b> Dhamodharan Prabhu, Mutharasappan Nachiappan and Jeyaraman Jeyakanthan*  Structural Biology and Biocomputing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi - 630 004, Tamil Nadu, India  <i>(* Email: jjkanthan@gmail.com)</i></p>	Accepted
34.	<p><b>In Silico Based Network Pharmacology Approaches to Evaluate the Anti-Diabetic Potential of Poly-Herbal Formulation</b>  <b>Vaishali. K,</b> Pradiba.D, Soundaryalakshmi.M and Vasanthi.M  Department of Biotechnology, Kamaraj College of Engineering and Technology, Virudhunagar- 626 001  <i>(Email:kvs.vaishu@gmail.com)</i></p>	Accepted
35.	<p><b>Unraveling the Transcriptional Activation/Deactivation Mechanism of TRP-DNA Complex in Response to Exogenous Amino Acids Using Computational Approach</b>  <b>Richard Mariadasse</b> and Jeyaraman Jeyakanthan*  Structural Biology and Bio-Computing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi - 630 004, Tamil Nadu, India  <i>(* Email: jjkanthan@gmail.com)</i></p>	Accepted
36.	<p><b>Molecular modeling, Dynamics Studies and Density Functional Theory Approaches to Identify Potential Inhibitors of SIRT4 protein from Homo sapiens: a Novel Target for the Treatment of Type 2 Diabetes</b>  <b>Sanjay K Choubey,</b> Dhamodharan Prabhu, Mutharasappan Nachiappan, Jayshree Biswal and Jeyaraman Jeyakanthan*  Structural Biology and Bio-Computing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi - 630 004, Tamil Nadu, India  <i>(* Email: jjkanthan@gmail.com)</i></p>	Accepted
37.	<p><b>A Web-Based Database on the Fatty Acid Compound and Their Interactions in Protein Structures</b>  <b>Santhosh Rajendran<sup>1</sup>,</b> Sekar Kanagaraj<sup>2</sup> and Jeyakanthan Jeyaraman<sup>1*</sup>  <sup>1</sup> Structural Biology and Bio Computing Lab, Department of Bioinformatics, Alagappa University, Karaikudi - 630 004, Tamil Nadu, India  <sup>2</sup> Department of Computational and Data Sciences, Indian Institute of Science, Bangalore - 560 012, Karnataka India  <i>(*E-mail: jjkanthan@gmail.com)</i></p>	Accepted
38.	<p><b>Computational Analysis for Drug Target Identification in Nautella Italica: Modelling, Docking and Simulation Studies of Target Protein, Rpob</b>  <b>Rajasree Odumpatta<sup>a</sup>,</b> Mohanapriya Arumugam<sup>a*</sup>  Department of Biotechnology, School of Biosciences and Technology, Vellore Institute of Technology University</p>	Accepted
39.	<p><b>Molecular Docking and Dynamic Studies of Bioactive Compounds from Clematis gouriana Roxb. ex DC Against Snake Venom</b></p>	Accepted

	<p><b>Phospholipase (PLA<sub>2</sub>) Protein</b></p> <p>Sathishkumar Chinnasamy and Karthikeyan Muthusamy*  Department of Bioinformatics, Alagappa University, Science Block, Karaikudi – 630 004  (*Email: <a href="mailto:mkbioinformatics@gmail.com">mkbioinformatics@gmail.com</a>)</p>	
40.	<p><b>Molecular Docking and Molecular Dynamic Studies to Screen Inhibitors for Tissue transglutaminase: a Potential Drug Target to Combat Renal Fibrosis</b></p> <p>Lakshmi Prasanna, Arpita Devi, Madhava Reddy B A, PrakashPrabhu, A K Pasupulati*  School of Life Sciences, University of Hyderabad  (*Email: <a href="mailto:pakumarsl@uohyd.ernet.in">pakumarsl@uohyd.ernet.in</a>)</p>	Accepted
41.	<p><b>SCN5A Gene SNP's in Irritable Bowel Syndrome and Its Influence in Structural Variance</b></p> <p>Fathima Shifana S, Aameena N and Vidhyavathi RM*  Department of Bioinformatics, Alagappa University, Science Block, Karaikudi – 630 004.  (* Email: <a href="mailto:vidhyamiss@gmail.com">vidhyamiss@gmail.com</a>)</p>	Accepted
42.	<p><b>Combined Structure and Ligand Based Virtual Screening to Identify New Potent Negative Allosteric Modulators of Mglur5 against CNS Disorders</b></p> <p>Sitrarasu Vijaya Prabhu and Sanjeev Kumar Singh*  Computer Aided Drug Design and Molecular Modelling Lab, Department of Bioinformatics, Alagappa University, Karaikudi-630004, Tamil Nadu, India  (*E-mail: <a href="mailto:skysanjeev@gmail.com">skysanjeev@gmail.com</a>)</p>	Accepted
43.	<p><b>Deciphering the Binding Mode of Pyridine 1-Oxide Derivatives as PCAF BRD Inhibitors: a Docking And MM/PB(GB)SA Based Approach</b></p> <p>Venkatesan Suryanarayanan and Sanjeev Kumar Singh*  Computer Aided Drug Design and Molecular Modelling Lab, Department of Bioinformatics, Alagappa University, Karaikudi-630004, Tamil Nadu, India  (*Email: <a href="mailto:skysanjeev@gmail.com">skysanjeev@gmail.com</a>)</p>	Accepted
44.	<p><b>Flavonoids as Zika virus NS2B-NS3 protease inhibitors: A molecular docking and dynamics simulation study</b></p> <p>Rakhi Yadav, Rajanish Giri*  School of Basic Sciences, Indian Institute of Technology Mandi, Mandi, India, 175005  *E-mail: <a href="mailto:rajanishgiri@iitmandi.ac.in">rajanishgiri@iitmandi.ac.in</a></p>	Accepted
45.	<p><b>An <i>In Silico</i> Approach Towards Inhibition of Precursor Membrane Protein (Prm) to Prevent Dengue Virus Maturation in Trans-Golgi network</b></p> <p>Avinash Ravichandran, Suryanarayanan V, Vijay Prabhu S, Umesh Panwar and Sanjeev Kumar Singh*  Computer Aided Drug Design and Molecular Modelling Lab, Department of Bioinformatics, Alagappa University, Karaikudi-630004, Tamil Nadu, India  (*E-mail: <a href="mailto:skysanjeev@gmail.com">skysanjeev@gmail.com</a>)</p>	Accepted
46.	<p><b>Molecular Mechanism Studies of HIV-1PR Resistance by Active and Inactive Site Mutations for Protease Inhibitors through <i>In Silico</i> Approach</b></p> <p>Chirasmitta Nayak, Ishwar Chandra and Sanjeev Kumar Singh*  Computer Aided Drug Design and Molecular Modeling lab, Department of Bioinformatics, Alagappa University, Karaikudi – 630 004, Tamil Nadu, India.  (Email: <a href="mailto:skysanjeev@gmail.com">skysanjeev@gmail.com</a>)</p>	Accepted
47.	<p><b>Protein-Protein Docking Studies of RANKL-RANK and the Structural Transition Inducement of Hydroxyapatite for Bone Remodelling – <i>In Silico</i> Perspective</b></p>	Accepted

	<p><b>S. Abinaya, J. Josephsahayaran and J. Jeyakanthan</b>  Plant Bioinformatics Lab, Department of Bioinformatics, Science Block, Alagappa University,  Karaikudi - 630 004  (E. mail: <a href="mailto:jjsrbioinformatics2016@gmail.com">jjsrbioinformatics2016@gmail.com</a>)</p>	
48.	<p><b>Understanding the Molecular Evolution, Divergence and their Structural Impact of Selenoprotein P - A computational approach</b>  <b>Aruna lakshmanan, J. Josephsahayaran and J. Jeyakanthan</b>  Plant Bioinformatics Lab, Department of Bioinformatics, Science Block, Alagappa University,  Karaikudi - 630 004  (E. mail: <a href="mailto:jjsrbioinformatics2016@gmail.com">jjsrbioinformatics2016@gmail.com</a>)</p>	Accepted
49.	<p><b>In-silico designing of potential inhibitors for HIV-1 integrase by E-Pharmacophore based Virtual Screening, Docking and Molecular Simulation approaches</b>  <b>Umesh Panwar and Sanjeev Kumar Singh*</b>  Computer Aided Drug Design and Molecular Modelling Lab, Department of Bioinformatics, Alagappa University, Karaikudi-630004, Tamil Nadu, India  (*Email: <a href="mailto:skysanjeev@gmail.com">skysanjeev@gmail.com</a>)</p>	Accepted