# Achuthsankar S Nair

List of Publications by Year
in descending order

| | | 840776 | 642732 |
|:---:|:---:|:---:|:---:|
| **57**<br>papers | **666**<br>citations | **11**<br>h-index | **23**<br>g-index |
| **58**<br>all docs | **58**<br>docs citations | **58**<br>times ranked | **763**<br>citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 1 | Green synthesis and characterization of zinc oxide nanoparticles using Cayratia pedata leaf extract. Biochemistry and Biophysics Reports, 2021, 26, 100995. | 1.3 | 142 |
| 2 | A coding measure scheme employing electron-ion interaction pseudopotential (EIIP). Bioinformation, 2006, 1, 197-202. | 0.5 | 107 |
| 3 | MTar: a computational microRNA target prediction architecture for human transcriptome. BMC Bioinformatics, 2010, 11, S2. | 2.6 | 55 |
| 4 | Composition, Transition and Distribution (CTD) &#x2014; A dynamic feature for predictions based on hierarchical structure of cellular sorting. , 2011, , . | | 41 |
| 5 | Studies on neutralizing effect of Ophiorrhiza mungos root extract against Daboia russelii venom. Journal of Ethnopharmacology, 2014, 151, 543-547. | 4.1 | 29 |
| 6 | Synthesis and Characterization of Zinc Oxide Nanoparticles Using Acacia caesia Bark Extract and Its Photocatalytic and Antimicrobial Activities. Catalysts, 2021, 11, 1507. | 3.5 | 25 |
| 7 | Identification and analysis of novel microRNAs from fragile sites of human cervical cancer: Computational and experimental approach. Genomics, 2011, 97, 333-340. | 2.9 | 20 |
| 8 | Protein location prediction using atomic composition and global features of the amino acid sequence. Biochemical and Biophysical Research Communications, 2010, 391, 1670-1674. | 2.1 | 19 |
| 9 | Making novel proteins from pseudogenes. Bioinformatics, 2015, 31, 33-39. | 4.1 | 18 |
| 10 | The Complete Chloroplast Genome of *Trichopus zeylanicus*, And Phylogenetic Analysis with *Dioscoreales*. Plant Genome, 2019, 12, 1-11. | 2.8 | 17 |
| 11 | Potential protease inhibitors and their combinations to block SARS-CoV-2. Journal of Biomolecular Structure and Dynamics, 2022, 40, 903-917. | 3.5 | 15 |
| 12 | Heat Stress-Induced Cup9-Dependent Transcriptional Regulation of *SIR2*. Molecular and Cellular Biology, 2015, 35, 437-450. | 2.3 | 12 |
| 13 | Identification of Hub Genes and Key Pathways Associated with Anti-VEGF Resistant Glioblastoma Using Gene Expression Data Analysis. Biomolecules, 2021, 11, 403. | 4.0 | 12 |
| 14 | Beijing genotype dominance among circulating Mycobacterium tuberculosis in patients with pulmonary tuberculosis in Belarus. International Journal of Mycobacteriology, 2021, 9, 19. | 0.6 | 11 |
| 15 | Sequence signatures of allosteric proteins towards rational design. Systems and Synthetic Biology, 2010, 4, 271-280. | 1.0 | 9 |
| 16 | High Quality Draft Genome of Arogyapacha (*Trichopus zeylanicus*), an Important Medicinal Plant Endemic to Western Ghats of India. G3: Genes, Genomes, Genetics, 2019, 9, 2395-2404. | 1.8 | 9 |
| 17 | Molecular docking and dynamic studies of crepiside E beta glucopyranoside as an inhibitor of snake venom PLA2. Journal of Molecular Modeling, 2019, 25, 88. | 1.8 | 9 |
| 18 | Temporal VEGFA responsive genes in HUVECs: Gene signatures and potential ligands/receptors fine-tuning angiogenesis. Journal of Cell Communication and Signaling, 2019, 13, 561-571. | 3.4 | 9 |

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|---|---------|----|-----------| 
| 19 | Molecular docking and molecular dynamics simulation identify a novel Radicicol derivative that predicts exclusive binding to Plasmodium falciparum Topoisomerase VIB. Journal of Biomolecular Structure and Dynamics, 2021, , 1-13. | 3.5 | 9 |
| 20 | Looking for a sequence based allostery definition: A statistical journey at different resolution scales. Journal of Theoretical Biology, 2012, 304, 211-218. | 1.7 | 8 |
| 21 | In silico study of peptide inhibitors against BACE 1. Systems and Synthetic Biology, 2015, 9, 67-72. | 1.0 | 7 |
| 22 | SPARK-MSNA: Efficient algorithm on Apache Spark for aligning multiple similar DNA/RNA sequences with supervised learning. Scientific Reports, 2019, 9, 6631. | 3.3 | 7 |
| 23 | Identifying pseudogenes from hypothetical proteins for making synthetic proteins. Systems and Synthetic Biology, 2014, 8, 169-171. | 1.0 | 6 |
| 24 | Computational identification of novel microRNAs and their targets in the malarial vector, Anopheles stephensi. Systems and Synthetic Biology, 2015, 9, 11-17. | 1.0 | 5 |
| 25 | Fractality of numeric and symbolic sequences. IEEE Potentials, 2010, 29, 36-39. | 0.3 | 4 |
| 26 | Application of Recurrence Quantification Analysis (RQA) in Biosequence Pattern Recognition. Communications in Computer and Information Science, 2011, , 284-293. | 0.5 | 4 |
| 27 | Function annotation of peptides generated from the non-coding regions of D. melanogaster genome. Bioinformation, 2016, 12, 202-208. | 0.5 | 4 |
| 28 | Glu-108 in Saccharomyces cerevisiae Rad51 Is Critical for DNA Damage-Induced Nuclear Function. MSphere, 2019, 4, . | 2.9 | 4 |
| 29 | Rutaretin1â€²-(6â€³-sinapoylglucoside): promising inhibitor of COVID 19 m$^{pro}$ catalytic dyad from the leaves of *Pittosporum dasycaulon* miq (Pittosporaceae). Journal of Biomolecular Structure and Dynamics, 2022, 40, 12557-12573. | 3.5 | 4 |
| 30 | Computational study of â€˜HUBâ€™ microRNA in human cardiac diseases. Bioinformation, 2017, 13, 17-20. | 0.5 | 4 |
| 31 | *In silico* screening and epitope mapping of leptospiral outer membrane proteinâ€"Lsa46. Journal of Biomolecular Structure and Dynamics, 2023, 41, 26-44. | 3.5 | 4 |
| 32 | Identification of potential lead compounds against BACE1 through in-silico screening of phytochemicals of Medhya rasayana plants for Alzheimer's disease management. Computers in Biology and Medicine, 2022, 145, 105422. | 7.0 | 4 |
| 33 | Bagging with CTD â€" A Novel Signature for the Hierarchical Prediction of Secreted Protein Trafficking in Eukaryotes. Genomics, Proteomics and Bioinformatics, 2013, 11, 385-390. | 6.9 | 3 |
| 34 | Complete chloroplast genome of the medicinal plant Evolvulus alsinoides: comparative analysis, identification of mutational hotspots and evolutionary dynamics with species of Solanales. Physiology and Molecular Biology of Plants, 2021, 27, 1867-1884. | 3.1 | 3 |
| 35 | Bioinformatics screening of ETV4 transcription factor oncogenes and identifying smallâ€molecular anticancer drugs. Chemical Biology and Drug Design, 2022, 99, 277-285. | 3.2 | 3 |
| 36 | Decahydroquinolines from the venom of a formicinae ant, Oecophylla smaragdina. Toxicon, 2014, 92, 50-53. | 1.6 | 2 |

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| 37 | Fingerprint-based similarity search identified <i>p</i>-anisidine as an anticancer agent in HeLa and a prospective phytochemical ETV1 transcription factor inhibitor. Journal of Biomolecular Structure and Dynamics, 2021, 39, 4973-4980. | 3.5 | 2 |
| 38 | Compression of Large genomic datasets using COMRAD on Parallel Computing Platform. Bioinformation, 2015, 11, 267-271. | 0.5 | 2 |
| 39 | Exploring the potent inhibitor Î²-stigmasterol from <i>Pittosporum dasycaulon</i> Miq. leaves against snake venom phospholipase A2 protein through <i>inÂvitro</i> and molecular dynamics behavior approach. Toxin Reviews, 2023, 42, 85-98. | 3.4 | 2 |
| 40 | Are categorical periodograms and indicator sequences of genomes spectrally equivalent?. In Silico Biology, 2006, 6, 215-22. | 0.9 | 2 |
| 41 | A bio-sequence k-mer frequency counter (kFC). , 2014, , . | | 1 |
| 42 | NGS read data compression using parallel computing algorithm. , 2015, , . | | 1 |
| 43 | Predicting stable functional peptides from the intergenic space of E. coli. Systems and Synthetic Biology, 2015, 9, 135-140. | 1.0 | 1 |
| 44 | Effect of retroactivity in the dynamics of mixed feedback loop. , 2016, , . | | 1 |
| 45 | Mathematical modelling of nonlinear dynamics generated from modular interconnections in cellular SOS response system. Nonlinear Dynamics, 2018, 93, 643-652. | 5.2 | 1 |
| 46 | RBLOSUM performs better than CorBLOSUM with lesser error per query. BMC Research Notes, 2018, 11, 328. | 1.4 | 1 |
| 47 | A computational-cum-experimental study provides some clues on the druggable binding site and design of anticancer therapeutics on ETV1 transcription factor oncoprotein. Molecular Systems Design and Engineering, 0, , . | 3.4 | 1 |
| 48 | HYPO: A Database of Human Hypothetical Proteins. Protein and Peptide Letters, 2018, 25, 799-803. | 0.9 | 1 |
| 49 | Classification of proteins in intracellular and secretory pathway using global descriptors of amino acid sequence. , 2011, , . | | 0 |
| 50 | A Novel Algorithm for Prediction of Hub Proteins from Primary Structure in Eukaryotic Proteome Using Dipeptide Compositional Skew Information and Amino Acid Sequence Likeness. , 2012, , 33-40. | | 0 |
| 51 | Virtual screening for NS5B inhibitors of Hepatitis C virus. Nature Precedings, 2012, , . | 0.1 | 0 |
| 52 | Cell Phenomena Are Reminiscent of Electric Circuits. IEEE Potentials, 2013, 32, 32-35. | 0.3 | 0 |
| 53 | Effect of Transducer Positioning in Active Noise Control. , 2018, , . | | 0 |
| 54 | An Approach to Reveal the Possible Underlying Mechanisms Inherent to Oecophylla smaragdina as a Biocontrol Agent. Proceedings of the National Academy of Sciences India Section B - Biological Sciences, 2019, 89, 313-319. | 1.0 | 0 |

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|---|---|---|---|
| 55 | Lacunarity Analysis of Protein Sequences Reveal Fractal Like Behavior of Amino Acid Distributions. Communications in Computer and Information Science, 2011, , 320-327. | 0.5 | 0 |
| 56 | A Novel Algorithm for Hub Protein Identification in Prokaryotic Proteome Using Di-Peptide Composition and Hydrophobicity Ratio. Communications in Computer and Information Science, 2012, , 204-211. | 0.5 | 0 |
| 57 | A Novel Algorithm for Hub Protein Identification in H.Sapiens Using Global Amino Acid Features. Advances in Intelligent Systems and Computing, 2013, , 13-22. | 0.6 | 0 |