Anand Anbarasu

List of Publications by Year
in descending order

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104	1,865	279487	377514
papers	citations	23 h-index	34 g-index

109	109	109	2212
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Discerning molecular interactions: A comprehensive review on biomolecular interaction databases and network analysis tools. Gene, 2018, 642, 84-94.	1.0	117
2	Flavonoid from Carica papaya inhibits NS2B-NS3 protease and prevents Dengue 2 viral assembly. Bioinformation, 2013, 9, 889-895.	0.2	94
3	Computational Analysis Reveals the Association of Threonine 118 Methionine Mutation in PMP22 Resulting in CMT-1A. Advances in Bioinformatics, 2014, 2014, 1-10.	5.7	82
4	Detection of OXA-1 Î²-Lactamase Gene of Klebsiella pneumoniae from Blood Stream Infections (BSI) by Conventional PCR and In-Silico Analysis to Understand the Mechanism of OXA Mediated Resistance. PLoS ONE, 2014, 9, e91800.	1.1	61
5	Molecular docking and molecular dynamics studies on Î²-lactamases and penicillin binding proteins. Molecular BioSystems, 2014, 10, 891-900.	2.9	60
6	Gene network analysis reveals the association of important functional partners involved in antibiotic resistance: A report on an important pathogenic bacterium Staphylococcus aureus. Gene, 2016, 575, 253-263.	1.0	55
7	Gene interaction network studies to decipher the multi-drug resistance mechanism in Salmonella enterica serovar Typhi CT18 reveal potential drug targets. Microbial Pathogenesis, 2020, 142, 104096.	1.3	43
8	Detection and Confirmation of Alkaloids in Leaves of Justicia adhatoda and Bioinformatics Approach to Elicit Its Anti-tuberculosis Activity. Applied Biochemistry and Biotechnology, 2012, 168, 980-990.	1.4	39
9	Vaccine repurposing approach for preventing COVID 19: can MMR vaccines reduce morbidity and mortality?. Human Vaccines and Immunotherapeutics, 2020, 16, 2217-2218.	1.4	37
10	Systems biology studies in Pseudomonas aeruginosa PA01 to understand their role in biofilm formation and multidrug efflux pumps. Microbial Pathogenesis, 2019, 136, 103668.	1.3	36
11	Elucidating the multi-drug resistance mechanism of Enterococcus faecalis V583: A gene interaction network analysis. Gene, 2020, 748, 144704.	1.0	34
12	fabp4 is central to eight obesity associated genes: A functional gene network-based polymorphic study. Journal of Theoretical Biology, 2015, 364, 344-354.	0.8	33
13	Genomic profiling is predictive of response to cisplatin treatment but not to PI3K inhibition in bladder cancer patient-derived xenografts. Oncotarget, 2016, 7, 76374-76389.	0.8	32
14	FtsA as a cidal target for Staphylococcus aureus: Molecular docking and dynamics studies. Journal of Cellular Biochemistry, 2019, 120, 7751-7758.	1.2	31
15	Novel cyclohexanone compound as a potential ligand against SARS-CoV-2 main-protease. Microbial Pathogenesis, 2020, 149, 104546.	1.3	30
16	Aerobactin Seems To Be a Promising Marker Compared With Unstable RmpA2 for the Identification of Hypervirulent Carbapenem-Resistant Klebsiella pneumoniae: In Silico and In Vitro Evidence. Frontiers in Cellular and Infection Microbiology, 2021, 11, 709681.	1.8	30
17	Impact of bedaquiline and capreomycin on the gene expression patterns of multidrugâ€resistant Mycobacterium tuberculosis H37Rv strain and understanding the molecular mechanism of antibiotic resistance. Journal of Cellular Biochemistry, 2019, 120, 14499-14509.	1.2	28
18	Computational gene network study on antibiotic resistance genes of Acinetobacter baumannii. Computers in Biology and Medicine, 2014, 48, 17-27.	3.9	27

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19	In silicoanalysis reveals the anti-malarial potential of quinolinyl chalcone derivatives. Journal of Biomolecular Structure and Dynamics, 2015, 33, 961-977.	2.0	27
20	In silico structure evaluation of BAG3 and elucidating its association with bacterial infections through proteinâ€“protein and hostâ€pathogen interaction analysis. Journal of Cellular Biochemistry, 2022, 123, 115-127.	1.2	27
21	Identification of bioactive natural compounds as efficient inhibitors against Mycobacterium tuberculosis protein-targets: A molecular docking and molecular dynamics simulation study. Journal of Molecular Liquids, 2021, 341, 117340.	2.3	27
22	Natural Inhibitors of HMGâ€CoA Reductaseâ€”An Insilico Approach Through Molecular Docking and Simulation Studies. Journal of Cellular Biochemistry, 2017, 118, 52-57.	1.2	26
23	MurB as a target in an alternative approach to tackle the Vibrio cholerae resistance using molecular docking and simulation study. Journal of Cellular Biochemistry, 2018, 119, 1726-1732.	1.2	25
24	Investigations on Câ€“Hâ‹¯Ï€ interactions in RNA binding proteins. International Journal of Biological Macromolecules, 2007, 41, 251-259.	3.6	24
25	Gene interaction network approach to elucidate the multidrug resistance mechanisms in the pathogenic bacterial strain Proteus mirabilis. Journal of Cellular Physiology, 2021, 236, 468-479.	2.0	24
26	Role of SHV-11, a Class A Î²-Lactamase, Gene in Multidrug Resistance Among Klebsiella pneumoniae Strains and Understanding Its Mechanism by Gene Network Analysis. Microbial Drug Resistance, 2020, 26, 900-908.	0.9	23
27	In-silico strategies to combat COVID-19: A comprehensive review. Biotechnology and Genetic Engineering Reviews, 2021, 37, 64-81.	2.4	23
28	Identification of potential inhibitors for Klebsiella pneumoniae carbapenemase-3: a molecular docking and dynamics study. Journal of Biomolecular Structure and Dynamics, 2019, 37, 4601-4613.	2.0	22
29	Evaluation and Comparison of Radical Scavenging Properties of Solvent Extracts from Justicia adhatoda Leaf Using DPPH Assay. Applied Biochemistry and Biotechnology, 2014, 174, 2413-2425.	1.4	21
30	Gene Network Analysis of Metallo Beta Lactamase Family Proteins Indicates the Role of Gene Partners in Antibiotic Resistance and Reveals Important Drug Targets. Journal of Cellular Biochemistry, 2016, 117, 1330-1339.	1.2	21
31	Insights on inhibition of Plasmodium falciparum plasmepsin I by novel epoxyazadiradione derivatives â€“ molecular docking and comparative molecular field analysis. Journal of Biomolecular Structure and Dynamics, 2019, 37, 3168-3182.	2.0	21
32	Genome sequencing and molecular characterisation of XDR Acinetobacter baumannii reveal complexities in resistance: Novel combination of sulbactamâ€“durlobactam holds promise for therapeutic intervention. Journal of Cellular Biochemistry, 2021, 122, 1946-1957.	1.2	21
33	Ï€â€“Ï€ Interactions in Structural Stability: Role in RNA Binding Proteins. Cell Biochemistry and Biophysics, 2013, 67, 853-863.	0.9	20
34	Study of chemical composition and volatile compounds along with in-vitro assay of antioxidant activity of two medicinal rice varieties: Karungkuravai and Mappilai samba. Journal of Food Science and Technology, 2015, 52, 2572-2584.	1.4	20
35	Molecular docking and dynamics studies on novel benzene sulfonamide substituted pyrazole-pyrazoline analogues as potent inhibitors of Plasmodium falciparum Histo aspartic protease. Journal of Biomolecular Structure and Dynamics, 2020, 38, 3235-3245.	2.0	20
36	Protein aggregation due to nsSNP resulting in P56S VABP protein is associated with amyotrophic lateral sclerosis. Journal of Theoretical Biology, 2014, 354, 72-80.	0.8	19

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37	Molecular dynamics and molecular docking studies on E166A point mutant, R274N/R276N double mutant, and E166A/R274N/R276N triple mutant forms of class A Î²-lactamases. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1953-1968.	2.0	19
38	Molecular Dynamics Studies on D835N Mutation in FLT3â€”Its Impact on FLT3 Protein Structure. Journal of Cellular Biochemistry, 2016, 117, 1439-1445.	1.2	19
39	Î²-Keto esters from ketones and ethyl chloroformate: a rapid, general, efficient synthesis of pyrazolones and their antimicrobial, in silico and in vitro cytotoxicity studies. Organic and Medicinal Chemistry Letters, 2013, 3, 6.	2.0	18
40	Gene and Protein Network Analysis of AmpC Î² Lactamase. Cell Biochemistry and Biophysics, 2015, 71, 1553-1567.	0.9	18
41	Exploring the resistance mechanism of imipenem in carbapenem hydrolysing class D beta-lactamases OXA-143 and its variant OXA-231 (D224A) expressing Acinetobacter baumannii: An in-silico approach. Computational Biology and Chemistry, 2017, 67, 1-8.	1.1	18
42	Influence of cation-Ï€ interactions on RNA-binding proteins. International Journal of Biological Macromolecules, 2007, 40, 479-483.	3.6	17
43	Integrated systems biology approach using gene network analysis to identify the important pathways and new potential drug targets for Neuroblastoma. Gene Reports, 2021, 23, 101101.	0.4	17
44	Emergence of Meropenem Resistance Among Cefotaxime Non-susceptible Streptococcus pneumoniae: Evidence and Challenges. Frontiers in Microbiology, 2021, 12, 810414.	1.5	17
45	Comparative molecular field analysis and molecular docking studies on novel aryl chalcone derivatives against an important drug target cysteine protease in Plasmodium falciparum. Journal of Theoretical Biology, 2016, 403, 110-128.	0.8	16
46	A High-Throughput Cidality Screen for Mycobacterium Tuberculosis. PLoS ONE, 2015, 10, e0117577.	1.1	15
47	Exploring the role of cationâ€“Ï€ interactions in glycoproteins lipid-binding proteins and RNA-binding proteins. Journal of Theoretical Biology, 2007, 247, 346-353.	0.8	14
48	Computational analysis of Nâ€“Hâ‹¯Ï€ interactions and its impact on the structural stability of Î²-lactamases. Computers in Biology and Medicine, 2014, 46, 22-28.	3.9	14
49	Gene interaction network to unravel the role of gut bacterial species in cardiovascular diseases: E. coli O157:H7 host-bacterial interaction study. Computers in Biology and Medicine, 2021, 133, 104417.	3.9	14
50	A Molecular Docking and Dynamics Study to Screen Potent Anti-Staphylococcal Compounds Against Ceftaroline Resistant MRSA. Journal of Cellular Biochemistry, 2016, 117, 542-548.	1.2	13
51	Designing Anti-Microbial Peptides Against Major Î²-Lactamase Enzymes in Clinically Important Gram-Negative Bacterial Pathogens: An In-Silico Study. Probiotics and Antimicrobial Proteins, 2022, 14, 263-276.	1.9	13
52	Influence of C-H...O interactions on the structural stability of Î²-lactamases. Journal of Biological Physics, 2013, 39, 649-663.	0.7	12
53	Investigations on the role of CHâ€¦O interactions and its impact on stability and specificity of penicillin binding proteins. Computers in Biology and Medicine, 2015, 65, 85-92.	3.9	12
54	Computational analysis reveal inhibitory action of nimbin against dengue viral envelope protein. VirusDisease, 2015, 26, 243-254.	1.0	12

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55	A comprehensive review on genomics, systems biology and structural biology approaches for combating antimicrobial resistance in ESKAPE pathogens: computational tools and recent advancements. World Journal of Microbiology and Biotechnology, 2022, 38, .	1.7	12
56	Computation of non-covalent interactions in TNF proteins and interleukins. Cytokine, 2006, 35, 263-269.	1.4	11
57	Investigations on unconventional hydrogen bonds in RNA binding proteins: The role of CHâ‹¯OC interactions. BioSystems, 2007, 90, 792-801.	0.9	11
58	Cationâ€“Ï€ Interactions in Î²-Lactamases: The Role in Structural Stability. Cell Biochemistry and Biophysics, 2013, 66, 147-155.	0.9	11
59	R521C and R521H mutations in FUS result in weak binding with KaryopherinÎ²2 leading to Amyotrophic lateral sclerosis: a molecular docking and dynamics study. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2169-2185.	2.0	11
60	Influence of C-H...pi hydrogen bonds in interleukins. In Silico Biology, 2008, 8, 261-73.	0.4	11
61	Ethyl 4-(4-methylphenyl)-4-pentenoate from Vetiveria zizanioides Inhibits Dengue NS2Bâ€“NS3 Protease and Prevents Viral Assembly: A Computational Molecular Dynamics and Docking Study. Cell Biochemistry and Biophysics, 2016, 74, 337-351.	0.9	10
62	Essentiality Assessment of Cysteinyl and Lysyl-tRNA Synthetases of Mycobacterium smegmatis. PLoS ONE, 2016, 11, e0147188.	1.1	10
63	Non-classical hydrogen bonds in interleukins: The role of CHâ‹¯O interactions. International Journal of Biological Macromolecules, 2008, 43, 468-473.	3.6	9
64	Aromatic-aromatic interactions: analysis of Ï€-Ï€ interactions in interleukins and TNF proteins. Bioinformation, 2013, 9, 432-439.	0.2	9
65	Exploring the Câ€“Hâ€¦O Interactions in Glycoproteins. Applied Biochemistry and Biotechnology, 2009, 159, 343-354.	1.4	8
66	Non-canonical H-bonds in Î²-lactamases: importance of Câ€“HÂ·Â·Â·Ï€ interactions. Journal of Biological Inorganic Chemistry, 2013, 18, 539-545.	1.1	8
67	In silico study on Penicillin derivatives and Cephalosporins for upper respiratory tract bacterial pathogens. 3 Biotech, 2014, 4, 241-251.	1.1	8
68	An IPTG Inducible Conditional Expression System for Mycobacteria. PLoS ONE, 2015, 10, e0134562.	1.1	8
69	NH - Ï€ Interactions: Investigations on the Evidence and Consequences in RNA Binding Proteins. The Open Structural Biology Journal, 2008, 2, 33-42.	0.1	8
70	Datasets comprising the quality validations of simulated protein-ligand complexes and SYBYL docking scores of bioactive natural compounds as inhibitors of Mycobacterium tuberculosis protein-targets. Data in Brief, 2022, 42, 108146.	0.5	8
71	Leucine to proline substitution by SNP at position 197 in Caspase-9 gene expression leads to neuroblastoma: a bioinformatics analysis. 3 Biotech, 2013, 3, 225-234.	1.1	7
72	Identification of CD4+ T-cell epitope and investigation of HLA distribution for the immunogenic proteins of Burkholderia pseudomallei using in silico approaches â€“ A key vaccine development strategy for melioidosis. Journal of Theoretical Biology, 2016, 400, 11-18.	0.8	7

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73	Structural stability studies in adhesion moleculesâ€"role of cationâ€"Ï€ interactions. Protoplasma, 2011, 248, 673-682.	1.0	6
74	Revealing the Strong Functional Association of adipor2 and cdh13 with adipoq: A Gene Network Study. Cell Biochemistry and Biophysics, 2015, 71, 1445-1456.	0.9	6
75	Tryptophan to Glycine mutation in the position 116 leads to protein aggregation and decreases the stability of the LITAF protein. Journal of Biomolecular Structure and Dynamics, 2015, 33, 1695-1709.	2.0	6
76	Ebolavirus Database: Gene and Protein Information Resource for Ebolaviruses. Advances in Bioinformatics, 2016, 2016, 1-4.	5.7	6
77	Unravelling the Secrets of Mycobacterial Cidality through the Lens of Antisense. PLoS ONE, 2016, 11, e0154513.	1.1	6
78	Full title: Identification of potential drug targets against carbapenem resistant Enterobacteriaceae (CRE) strains using in silico gene network analysis. Gene Reports, 2019, 14, 129-137.	0.4	6
79	Preclinical Evaluation of Sol-gel Synthesized Modulated 45S5-Bioglass Based Biodegradable Bone Graft Intended for Alveolar Bone Regeneration. Journal of Hard Tissue Biology, 2021, 30, 303-308.	0.2	6
80	Epidemiology of Multidrug Resistance among Salmonella enterica serovars typhi and paratyphi A at a Tertiary Pediatric Hospital in India Over a Decade; In-silico Approach to Elucidate the Molecular Mechanism of Quinolone Resistance. International Journal of Infectious Diseases, 2022, 119, 146-149.	1.5	6
81	Analysis of non-synonymous single-nucleotide polymorphisms and population variability of PLD2 gene associated with hypertension. International Journal of Bioinformatics Research and Applications, 2013, 9, 227.	0.1	5
82	Binding site residues in Î²-lactamases: role in non-classical interactions and metal binding. Journal of Coordination Chemistry, 2014, 67, 2898-2910.	0.8	5
83	Evolutionary Relationship of Penicillin-Binding Protein 2 Coding penA Gene and Understanding the Role in Drug-Resistance Mechanism Using Gene Interaction Network Analysis. Lecture Notes on Multidisciplinary Industrial Engineering, 2020, , 9-25.	0.4	5
84	Nanoscale Biomaterials for 3D printing. IOSR Journal of Pharmacy and Biological Sciences, 2017, 12, 80-86.	0.1	5
85	In silico Evaluation of Non-Synonymous SNPs in IRS-1 gene associated with type II diabetes mellitus.. Research Journal of Pharmacy and Technology, 2018, 11, 1957.	0.2	5
86	Influence of cationâ€"Ï€ interactions to the structural stability of prokaryotic and eukaryotic translation elongation factors. Protoplasma, 2009, 238, 11-20.	1.0	4
87	In silico study of Alzheimerâ€™s disease in relation to FYN gene. Interdisciplinary Sciences, Computational Life Sciences, 2012, 4, 153-160.	2.2	4
88	Network and Polymorphic Analysis of Obesity Candidate Gene-Plin1: A Bioinformatics Approach. International Journal of Human Genetics, 2014, 14, 119-129.	0.1	4
89	Streptococcus pneumoniae Genome Database (SPGDB): A database for strain specific comparative analysis of Streptococcus pneumoniae genes and proteins. Genomics, 2014, 104, 582-586.	1.3	4
90	Rapid and economic synthesis of bone like apatite using simulated body fluid (SBF). Materials Research Innovations, 2019, 23, 149-154.	1.0	4

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91	Comparative Molecular Field Analysis and Molecular Docking Studies on Quinolinone Derivatives Indicate Potential Hepatitis C Virus Inhibitors. Cell Biochemistry and Biophysics, 2019, 77, 139-156.	0.9	3
92	Quorum quenching by 2-Hydroxyanisole extracted from Solanum torvum on Pseudomonas aeruginosa and its inhibitory action upon LasR protein. Gene Reports, 2020, 21, 100802.	0.4	3
93	Arginine and Lysine interactions with p residues in metalloproteins. Bioinformation, 2012, 8, 820-826.	0.2	3
94	A review on Infectious Diseases and their Importance in Developing Biological Databases. Research Journal of Pharmacy and Technology, 2016, 9, 621.	0.2	3
95	Mutation in angiotensin II type 1 receptor disrupts its binding to angiotensin II leading to hypotension: An insight into hydrogen bonding patterns. Frontiers in Biology, 2012, 7, 477-484.	0.7	2
96	Clinical Evaluation of a Polyherbal Nutritional Supplement in Dyslipidemic Volunteers. Journal of Dietary Supplements, 2017, 14, 679-690.	1.4	2
97	An improved unsupervised learning approach for potential human microRNAâ€“disease association inference using cluster knowledge. Network Modeling Analysis in Health Informatics and Bioinformatics, 2021, 10, 1.	1.2	2
98	MOLECULAR DOCKING STUDY OF CATECHINS COMPOUNDS FROM CAMELLIA SINENSIS AGAINST UPPS IN STAPHYLOCOCCUS AUREUS. International Journal for Computational Biology, 2014, 3, 3.	0.1	2
99	Role of Cation-Ï€ Interactions in the Structural Stability of Bacterial Exotoxins. Journal of Microbial & Biochemical Technology, 2009, 01, 022-029.	0.2	2
100	Organ-specific host differential gene expression analysis in systemic candidiasis: A systems biology approach. Microbial Pathogenesis, 2022, 169, 105677.	1.3	2
101	Haemophilus influenzae Genome Database (HIGDB): A single point web resource for Haemophilus influenzae. Computers in Biology and Medicine, 2014, 55, 86-91.	3.9	1
102	Transcriptional expression of secondary resistance genes ccdB and repA2 is enhanced in presence of cephalosporin and carbapenem in Escherichia coli. BMC Microbiology, 2021, 21, 79.	1.3	1
103	Role of Cation-π Interactions in the Structural Stability of Bacterial Adhesins. Protein and Peptide Letters, 2013, 20, 695-704.	0.4	1
104	Regioselective Synthesis of 2-Chloroquinoline Based Ethyl 4-(3-) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td (Hydroxyphenyl)-2,7,7-Trin Evaluation Against P. falciparum Lactate Dehydrogenase. Medicinal Chemistry, 2015, 11, 789-797.	0.7	1