# Umashankar Vetrivel

List of Publications by Year
in descending order

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|---|---|---|---|
| 43 papers | 637 citations | 623734<br>14 h-index | 642732<br>23 g-index |
| 43 all docs | 43 docs citations | 43 times ranked | 907 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Ornithine and its role in metabolic diseases: An appraisal. Biomedicine and Pharmacotherapy, 2017, 86, 185-194. | 5.6 | 70 |
| 2 | POAP: A GNU parallel based multithreaded pipeline of open babel and AutoDock suite for boosted high throughput virtual screening. Computational Biology and Chemistry, 2018, 74, 39-48. | 2.3 | 60 |
| 3 | ACUA: A software tool for automated codon usage analysis. Bioinformation, 2007, 2, 62-63. | 0.5 | 55 |
| 4 | A novel in silico approach to identify potential therapeutic targets in human bacterial pathogens. The HUGO Journal, 2011, 5, 25-34. | 4.1 | 40 |
| 5 | Probing the intermolecular interactions of PPARÎ³-LBD with polyunsaturated fatty acids and their anti-inflammatory metabolites to infer most potential binding moieties. Lipids in Health and Disease, 2017, 16, 17. | 3.0 | 37 |
| 6 | Designing and enhancing the antifungal activity of corneal specific cell penetrating peptide using gelatin hydrogel delivery system. International Journal of Nanomedicine, 2019, Volume 14, 605-622. | 6.7 | 30 |
| 7 | Virtual screening, molecular dynamics, and binding free energy calculations on human carbonic anhydrase IX catalytic domain for deciphering potential leads. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2155-2168. | 3.5 | 27 |
| 8 | Agonistic effect of polyunsaturated fatty acids (PUFAs) and its metabolites on brain-derived neurotrophic factor (BDNF) through molecular docking simulation. Lipids in Health and Disease, 2012, 11, 109. | 3.0 | 25 |
| 9 | Structural insights on druggable hotspots in CD147: A bull's eye view. Life Sciences, 2019, 224, 76-87. | 4.3 | 23 |
| 10 | InPACdb - Indian plant anticancer compounds database. Bioinformation, 2009, 4, 71-74. | 0.5 | 21 |
| 11 | In vitro and In silico studies on inhibitory effects of curcumin on multi drug resistance associated protein (MRP1) in retinoblastoma cells. Bioinformation, 2012, 8, 13-19. | 0.5 | 21 |
| 12 | Virtual screening of natural inhibitors targeting ornithine decarboxylase with pharmacophore scaffolding of DFMO and validation by molecular dynamics simulation studies. Journal of Biomolecular Structure and Dynamics, 2019, 37, 766-780. | 3.5 | 19 |
| 13 | Modulation of multidrug resistance 1 expression and function in retinoblastoma cells by curcumin. Journal of Pharmacology and Pharmacotherapeutics, 2013, 4, 103-109. | 0.4 | 17 |
| 14 | PepVis: An integrated peptide virtual screening pipeline for ensemble and flexible docking protocols. Chemical Biology and Drug Design, 2019, 94, 2041-2050. | 3.2 | 14 |
| 15 | Identification of potential drugs targeting L,Lâ€diaminopimelate aminotransferase of Chlamydia trachomatis : An integrative pharmacoinformatics approach. Journal of Cellular Biochemistry, 2019, 120, 2271-2288. | 2.6 | 14 |
| 16 | Virtual screening studies reveal linarin as a potential natural inhibitor targeting CDK4 in retinoblastoma. Journal of Pharmacology and Pharmacotherapeutics, 2013, 4, 256-264. | 0.4 | 13 |
| 17 | Hepatitis C Virus NS3/4A Inhibition and Host Immunomodulation by Tannins from Terminalia chebula: A Structural Perspective. Molecules, 2022, 27, 1076. | 3.8 | 13 |
| 18 | Structure-based drug target prioritisation and rational drug design for targeting <i>Chlamydia trachomatis</i> eye infections. Journal of Biomolecular Structure and Dynamics, 2020, 38, 3131-3143. | 3.5 | 12 |

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|---|---------|-----|-----------|
| 19 | Mutational landscape screening of methylene tetrahydrofolate reductase to predict homocystinuria associated variants: An integrative computational approach. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2020, 819-820, 111687. | 1.0 | 11 |
| 20 | PCOSDB: PolyCystic Ovary Syndrome DataBase for manually curated genes associated with the disease. Bioinformation, 2016, 12, 4-8. | 0.5 | 11 |
| 21 | Genome-wide codon usage profiling of ocular infective Chlamydia trachomatis serovars and drug target identification. Journal of Biomolecular Structure and Dynamics, 2018, 36, 1979-2003. | 3.5 | 9 |
| 22 | Demystifying the pH dependent conformational changes of human heparanase pertaining to structure–function relationships: an in silico approach. Journal of Computer-Aided Molecular Design, 2018, 32, 821-840. | 2.9 | 9 |
| 23 | Microsecond Simulation of the Proteoglycan-like Region of Carbonic Anhydrase IX and Design of Chemical Inhibitors Targeting pH Homeostasis in Cancer Cells. ACS Omega, 2020, 5, 4270-4281. | 3.5 | 9 |
| 24 | In silico analysis and prioritization of drug targets in Fusarium solani. Medical Hypotheses, 2015, 84, 81-84. | 1.5 | 8 |
| 25 | Design of inhibitory peptide targeting Toxoplasma gondii RON4â€"human Î²â€"tubulin interactions by implementing structural bioinformatics methods. Journal of Cellular Biochemistry, 2018, 119, 3236-3246. | 2.6 | 8 |
| 26 | Multilevel Precision-Based Rational Design of Chemical Inhibitors Targeting the Hydrophobic Cleft ofToxoplasma gondiiApical Membrane Antigen 1 (AMA1). Genomics and Informatics, 2016, 14, 53. | 0.8 | 8 |
| 27 | Open discovery: An integrated live Linux platform of Bioinformatics tools. Bioinformation, 2008, 3, 144-146. | 0.5 | 8 |
| 28 | Comparative docking of dual conformations in human fatty acid synthase thioesterase domain reveals potential binding cavity for virtual screening of ligands. Journal of Biomolecular Structure and Dynamics, 2017, 35, 1350-1366. | 3.5 | 7 |
| 29 | Insights on ornithine decarboxylase silencing as a potential strategy for targeting retinoblastoma. Biomedicine and Pharmacotherapy, 2018, 98, 23-28. | 5.6 | 5 |
| 30 | Deciphering ophthalmic adaptive inhibitors targeting RON4 of Toxoplasma gondii: An integrative in silico approach. Life Sciences, 2018, 213, 82-93. | 4.3 | 5 |
| 31 | Understanding the Uptake Mechanism and Interaction Potential of the Designed Peptide and Preparation of Composite Fiber Matrix for Fungal Keratitis. ACS Omega, 2020, 5, 12090-12102. | 3.5 | 3 |
| 32 | Deciphering potential inhibitors targeting THI4 of Fusarium solani sp. to combat fungal keratitis: An integrative computational approach. Computational Biology and Chemistry, 2020, 88, 107350. | 2.3 | 3 |
| 33 | Structure-based design of small molecule and peptide inhibitors for selective targeting of ROCK1: an integrative computational approach. Journal of Biomolecular Structure and Dynamics, 2022, 40, 7450-7468. | 3.5 | 3 |
| 34 | Membrane dynamics simulation and virtual screening reveals potential dual natural inhibitors of endothelin receptors for targeting glaucomatous condition. Life Sciences, 2021, 269, 119082. | 4.3 | 3 |
| 35 | PocketPipe: A computational pipeline for integrated Pocketome prediction and comparison. Bioinformation, 2019, 15, 295-298. | 0.5 | 3 |
| 36 | Elucidating the Therapeutic Potential of Cell-Penetrating Peptides in Human Tenon Fibroblast Cells. ACS Omega, 0, , . | 3.5 | 3 |

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|---|---------|----|-----------| 
| 37 | Microsecond scale sampling of Egr-1 conformational landscape to decipher the impact of its disorder regions on structure–function relationship. Molecular Simulation, 2020, 46, 1255-1264. | 2.0 | 2 |
| 38 | KinomeRun: An interactive utility for kinome target screening and interaction fingerprint analysis towards holistic visualization on kinome tree. Chemical Biology and Drug Design, 2020, 96, 1162-1175. | 3.2 | 2 |
| 39 | Coding-Complete Genome Sequences of NITMA1086 and NITMA1139, Two SARS-CoV-2 Isolates from Belagavi District, Karnataka State, India, Harboring the D614G Mutation. Microbiology Resource Announcements, 2021, 10, . | 0.6 | 2 |
| 40 | Retinoschisis and Norrie disease: a missing link. BMC Research Notes, 2021, 14, 204. | 1.4 | 2 |
| 41 | Importance of ABC transporters in different tissues. Drug Metabolism and Drug Interactions, 2014, 29, 65-66. | 0.3 | 1 |
| 42 | Deciphering novel potential antibacterial targets in tomato pathogen Ralstonia solanacearum GMI1000 through integration of in silico subtractive genomics, codon usage and protein–protein interaction analyses. Australasian Plant Pathology, 0, , 1. | 1.0 | 1 |
| 43 | Deciphering the structural and functional impact of missense mutations in Egr1-DNA interacting interface: an integrative computational approach. Journal of Biomolecular Structure and Dynamics, 2021, , 1-13. | 3.5 | 0 |