

Timir Tripathi

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

97
papers

1,585
citations

22
h-index

35
g-index

105
ext. papers

2,049
ext. citations

4.6
avg, IF

5.96
L-index

| # | Paper | IF | Citations |
|----|--|-----|-----------|
| 97 | Phosphorylation of PPARgamma via active ERK1/2 leads to its physical association with p65 and inhibition of NF-kappabeta. <i>Journal of Cellular Biochemistry</i> , 2003 , 90, 732-44 | 4.7 | 123 |
| 96 | Design of a peptide-based subunit vaccine against novel coronavirus SARS-CoV-2. <i>Microbial Pathogenesis</i> , 2020 , 145, 104236 | 3.8 | 110 |
| 95 | Current and novel therapeutic molecules and targets in Alzheimer's disease. <i>Journal of the Formosan Medical Association</i> , 2016 , 115, 3-10 | 3.2 | 87 |
| 94 | One year update on the COVID-19 pandemic: Where are we now?. <i>Acta Tropica</i> , 2021 , 214, 105778 | 3.2 | 70 |
| 93 | Muscarinic and nicotinic acetylcholine receptor agonists: current scenario in Alzheimer's disease therapy. <i>Journal of Pharmacy and Pharmacology</i> , 2018 , 70, 985-993 | 4.8 | 60 |
| 92 | Distant Phe345 mutation compromises the stability and activity of Mycobacterium tuberculosis isocitrate lyase by modulating its structural flexibility. <i>Scientific Reports</i> , 2017 , 7, 1058 | 4.9 | 53 |
| 91 | Aminoacyl-tRNA synthetases: Structure, function, and drug discovery. <i>International Journal of Biological Macromolecules</i> , 2018 , 111, 400-414 | 7.9 | 51 |
| 90 | Structure-based screening and molecular dynamics simulations offer novel natural compounds as potential inhibitors of Mycobacterium tuberculosis isocitrate lyase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 2045-2057 | 3.6 | 46 |
| 89 | Alterations in conformational topology and interaction dynamics caused by L418A mutation leads to activity loss of Mycobacterium tuberculosis isocitrate lyase. <i>Biochemical and Biophysical Research Communications</i> , 2017 , 490, 276-282 | 3.4 | 43 |
| 88 | Molecular Docking and In Silico ADMET Study Reveals Acylguanidine 7a as a Potential Inhibitor of β Secretase. <i>Advances in Bioinformatics</i> , 2016 , 2016, 9258578 | 5.5 | 40 |
| 87 | Development of multi-epitope driven subunit vaccine against <i>Fasciola gigantica</i> using immunoinformatics approach. <i>International Journal of Biological Macromolecules</i> , 2019 , 138, 224-233 | 7.9 | 39 |
| 86 | High-throughput rational design of the remdesivir binding site in the RdRp of SARS-CoV-2: implications for potential resistance. <i>IScience</i> , 2021 , 24, 101992 | 6.1 | 39 |
| 85 | Identification of potential inhibitors of <i>Fasciola gigantica</i> thioredoxin1: computational screening, molecular dynamics simulation, and binding free energy studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 2147-2162 | 3.6 | 37 |
| 84 | Can SARS-CoV-2 Accumulate Mutations in the S-Protein to Increase Pathogenicity?. <i>ACS Pharmacology and Translational Science</i> , 2020 , 3, 1023-1026 | 5.9 | 36 |
| 83 | Autophagy Modulation as a Treatment of Amyloid Diseases. <i>Molecules</i> , 2019 , 24, | 4.8 | 33 |
| 82 | A combined biochemical and computational studies of the rho-class glutathione s-transferase sll1545 of <i>Synechocystis</i> PCC 6803. <i>International Journal of Biological Macromolecules</i> , 2017 , 94, 378-385 | 7.9 | 31 |
| 81 | Structural insights into natural compounds as inhibitors of <i>Fasciola gigantica</i> thioredoxin glutathione reductase. <i>Journal of Cellular Biochemistry</i> , 2018 , 119, 3067-3080 | 4.7 | 30 |

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|----|--|-----|----|
| 80 | UDP-N-Acetylglucosamine enolpyruvyl transferase (MurA) of <i>Acinetobacter baumannii</i> (AbMurA): Structural and functional properties. <i>International Journal of Biological Macromolecules</i> , 2017 , 97, 106-114 | 7.9 | 26 |
| 79 | Activity loss by H46A mutation in <i>Mycobacterium tuberculosis</i> isocitrate lyase is due to decrease in structural plasticity and collective motions of the active site. <i>Tuberculosis</i> , 2018 , 108, 143-150 | 2.6 | 26 |
| 78 | Identification of novel natural inhibitors of <i>Opisthorchis felineus</i> cytochrome P450 using structure-based screening and molecular dynamic simulation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 3541-3556 | 3.6 | 26 |
| 77 | An efficient protocol to enhance recombinant protein expression using ethanol in <i>Escherichia coli</i> . <i>MethodsX</i> , 2015 , 2, 385-91 | 1.9 | 25 |
| 76 | Unraveling the mechanism of arbidol binding and inhibition of SARS-CoV-2: Insights from atomistic simulations. <i>European Journal of Pharmacology</i> , 2021 , 894, 173836 | 5.3 | 22 |
| 75 | Characterization of a Highly pH Stable Chi-Class Glutathione S-Transferase from <i>Synechocystis</i> PCC 6803. <i>PLoS ONE</i> , 2015 , 10, e0126811 | 3.7 | 20 |
| 74 | Accelerating COVID-19 Research Using Molecular Dynamics Simulation. <i>Journal of Physical Chemistry B</i> , 2021 , 125, 9078-9091 | 3.4 | 20 |
| 73 | An improved method for high-level soluble expression and purification of recombinant amyloid-beta peptide for in vitro studies. <i>Protein Expression and Purification</i> , 2015 , 114, 71-6 | 2 | 18 |
| 72 | <i>Opisthorchis viverrini</i> Proteome and Host-Parasite Interactions. <i>Advances in Parasitology</i> , 2018 , 102, 45-72 | 7.2 | 18 |
| 71 | Structural and energetic understanding of novel natural inhibitors of <i>Mycobacterium tuberculosis</i> malate synthase. <i>Journal of Cellular Biochemistry</i> , 2018 , 120, 2469 | 4.7 | 18 |
| 70 | Direct Interaction between the β -Amyloid Core and Tau Facilitates Cross-Seeding: A Novel Target for Therapeutic Intervention. <i>Biochemistry</i> , 2020 , 59, 341-342 | 3.2 | 15 |
| 69 | Comprehensive analysis of the catalytic and structural properties of a mu-class glutathione s-transferase from <i>Fasciola gigantica</i> . <i>Scientific Reports</i> , 2017 , 7, 17547 | 4.9 | 15 |
| 68 | Glutathione mediated regulation of oligomeric structure and functional activity of <i>Plasmodium falciparum</i> glutathione S-transferase. <i>BMC Structural Biology</i> , 2007 , 7, 67 | 2.7 | 15 |
| 67 | Draft Genome of the Liver Fluke. <i>ACS Omega</i> , 2020 , 5, 11084-11091 | 3.9 | 14 |
| 66 | The mRNA capping enzyme of <i>Saccharomyces cerevisiae</i> has dual specificity to interact with CTD of RNA Polymerase II. <i>Scientific Reports</i> , 2016 , 6, 31294 | 4.9 | 14 |
| 65 | Structural, functional and unfolding characteristics of glutathione S-transferase of <i>Plasmodium vivax</i> . <i>Archives of Biochemistry and Biophysics</i> , 2009 , 487, 115-22 | 4.1 | 14 |
| 64 | Molecular Dynamics Simulation of Protein and Protein-Ligand Complexes 2020 , 133-161 | | 14 |
| 63 | Structural basis of urea-induced unfolding of <i>Fasciola gigantica</i> glutathione S-transferase. <i>Journal of Cellular Physiology</i> , 2019 , 234, 4491-4503 | 7 | 14 |

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| 62 | Unusual thiol-based redox metabolism of parasitic flukes. <i>Parasitology International</i> , 2017 , 66, 390-395 | 2.1 | 13 |
| 61 | Targeted design of drug binding sites in the main protease of SARS-CoV-2 reveals potential signatures of adaptation. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 555, 147-153 | 3.4 | 13 |
| 60 | Alternate pathway to ascorbate induced inhibition of Mycobacterium tuberculosis. <i>Tuberculosis</i> , 2018 , 111, 161-169 | 2.6 | 12 |
| 59 | Conformational stability and energetics of Plasmodium falciparum glutaredoxin. <i>Biochimie</i> , 2010 , 92, 284-91 | 4.6 | 12 |
| 58 | Quercetin acts as a P-gp modulator via impeding signal transduction from nucleotide-binding domain to transmembrane domain. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 1-9 | 3.6 | 11 |
| 57 | Design of a multi-epitope subunit vaccine for immune-protection against Leishmania parasite. <i>Pathogens and Global Health</i> , 2020 , 114, 471-481 | 3.1 | 11 |
| 56 | Biochemical and thermodynamic comparison of the selenocysteine containing and non-containing thioredoxin glutathione reductase of Fasciola gigantica. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018 , 1862, 1306-1316 | 4 | 11 |
| 55 | Atomic resolution crystal structure of glutaredoxin 1 from Plasmodium falciparum and comparison with other glutaredoxins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 91-100 | | 11 |
| 54 | Structural and stability characteristics of a monothiol glutaredoxin: glutaredoxin-like protein 1 from Plasmodium falciparum. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008 , 1784, 946-524 | | 11 |
| 53 | Fasciola gigantica thioredoxin glutathione reductase: Biochemical properties and structural modeling. <i>International Journal of Biological Macromolecules</i> , 2016 , 89, 152-60 | 7.9 | 10 |
| 52 | Phospho-Tau Impairs Nuclear-Cytoplasmic Transport. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 36-38 | 5.7 | 10 |
| 51 | Preferential regeneration of thioredoxin from parasitic flatworm Fasciola gigantica using glutathione system. <i>International Journal of Biological Macromolecules</i> , 2015 , 81, 983-90 | 7.9 | 9 |
| 50 | Synergistic Effect of Amyloid- β and Tau Disrupts Neural Circuits. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 1129-1130 | 5.7 | 8 |
| 49 | Targeting Nucleotide Binding Domain of Multidrug Resistance-associated Protein-1 (MRP1) for the Reversal of Multi Drug Resistance in Cancer. <i>Scientific Reports</i> , 2018 , 8, 11973 | 4.9 | 8 |
| 48 | Prevalence and functionality of intrinsic disorder in human FG-nucleoporins. <i>International Journal of Biological Macromolecules</i> , 2021 , 175, 156-170 | 7.9 | 8 |
| 47 | Structure-based discovery of phenyl-diketo acids derivatives as malate synthase inhibitors. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 2945-2958 | 3.6 | 8 |
| 46 | Portrait of the Intrinsically Disordered Side of the HTLV-1 Proteome. <i>ACS Omega</i> , 2019 , 4, 10003-10018 | 3.9 | 7 |
| 45 | Eucalyptol, sabinene and cinnamaldehyde: potent inhibitors of salmonella target protein L-asparaginase. <i>3 Biotech</i> , 2017 , 7, 258 | 2.8 | 7 |

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| 44 | Functional classification and biochemical characterization of a novel rho class glutathione S-transferase in <i>Synechocystis</i> PCC 6803. <i>FEBS Open Bio</i> , 2015 , 5, 1-7 | 2.7 | 7 |
| 43 | Interface-based design of the favipiravir-binding site in SARS-CoV-2 RNA-dependent RNA polymerase reveals mutations conferring resistance to chain termination. <i>FEBS Letters</i> , 2021 , 595, 2366-2382 | 3.8 | 7 |
| 42 | Purification and characterization of two-domain glutaredoxin in the parasitic helminth <i>Fasciola gigantica</i> . <i>Parasitology International</i> , 2017 , 66, 432-435 | 2.1 | 6 |
| 41 | Identification and characterization of glyceraldehyde 3-phosphate dehydrogenase from <i>Fasciola gigantica</i> . <i>Parasitology Research</i> , 2019 , 118, 861-872 | 2.4 | 6 |
| 40 | Autophagy Promotes Memory Formation. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 3337-3339 | 5.7 | 6 |
| 39 | Designing a vaccine for fascioliasis using immunogenic 24kDa mu-class glutathione s-transferase. <i>Infection, Genetics and Evolution</i> , 2020 , 83, 104352 | 4.5 | 6 |
| 38 | How Does Arbidol Inhibit the Novel Coronavirus SARS-CoV-2? Atomistic Insights from Molecular Dynamics Simulations | | 6 |
| 37 | High Throughput Designing and Mutational Mapping of RBD-ACE2 Interface Guide Non-Conventional Therapeutic Strategies for COVID-19 | | 6 |
| 36 | Salt-regulated reversible fibrillation of <i>Mycobacterium tuberculosis</i> isocitrate lyase: Concurrent restoration of structure and activity. <i>International Journal of Biological Macromolecules</i> , 2017 , 104, 89-96 | 7.9 | 5 |
| 35 | Recombinant expression, purification and preliminary characterization of the mRNA export factor MEX67 of <i>Saccharomyces cerevisiae</i> . <i>Protein Expression and Purification</i> , 2015 , 107, 56-61 | 2 | 5 |
| 34 | Interaction of α -Synuclein with ATP Synthase: Switching Role from Physiological to Pathological. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 16-17 | 5.7 | 5 |
| 33 | Cloning, soluble expression, and purification of the RNA polymerase II subunit RPB5 from <i>Saccharomyces cerevisiae</i> . <i>Bioengineered</i> , 2015 , 6, 62-6 | 5.7 | 5 |
| 32 | Unfolding of <i>Acinetobacter baumannii</i> MurA proceeds through a metastable intermediate: A combined spectroscopic and computational investigation. <i>International Journal of Biological Macromolecules</i> , 2019 , 126, 941-951 | 7.9 | 5 |
| 31 | Structure-function studies of the asparaginyl-tRNA synthetase from understanding the role of catalytic and non-catalytic domains. <i>Biochemical Journal</i> , 2018 , 475, 3377-3391 | 3.8 | 5 |
| 30 | Soluble expression and purification of a full-length asparaginyl tRNA synthetase from <i>Fasciola gigantica</i> . <i>Protein Expression and Purification</i> , 2018 , 143, 9-13 | 2 | 4 |
| 29 | Phase separation of FG-nucleoporins in nuclear pore complexes.. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2022 , 1869, 119205 | 4.9 | 4 |
| 28 | Rational Design of the Remdesivir Binding Site in the RNA-dependent RNA Polymerase of SARS-CoV-2: Implications for Potential Resistance | | 4 |
| 27 | Yeast and Human Nuclear Pore Complexes: Not So Similar After All. <i>Trends in Cell Biology</i> , 2018 , 28, 589-593 | 5.1 | 4 |

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| 26 | Methodological advances in the design of peptide-based vaccines.. <i>Drug Discovery Today</i> , 2022 , | 8.8 | 4 |
| 25 | Abnormal Microtubule Dynamics Impair the Nuclear-Cytoplasmic Transport in Dementia. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 1133-1134 | 5.7 | 3 |
| 24 | Engineering glutathione S-transferase with a point mutation at conserved F136 residue increases the xenobiotic-metabolizing activity. <i>International Journal of Biological Macromolecules</i> , 2020 , 163, 1117-1126 | 7.9 | 3 |
| 23 | Identification and characterization of cytosolic malate dehydrogenase from the liver fluke <i>Fasciola gigantica</i> . <i>Scientific Reports</i> , 2020 , 10, 13372 | 4.9 | 3 |
| 22 | Conserved Arg451 residue is critical for maintaining the stability and activity of thioredoxin glutathione reductase. <i>Archives of Biochemistry and Biophysics</i> , 2019 , 674, 108098 | 4.1 | 2 |
| 21 | Draft Genome Sequence of Strain P5:ABC, Isolated from Hydrocarbon-Contaminated Soil from Noonmati Refinery, Assam, India. <i>Genome Announcements</i> , 2017 , 5, | | 2 |
| 20 | Experimental methods to study intrinsically disordered proteins 2022 , 505-533 | | 2 |
| 19 | Design of a Peptide-Based Subunit Vaccine against Novel Coronavirus SARS-CoV-2 | | 2 |
| 18 | Genome-wide identification and characterization of eukaryotic protein kinases. <i>Frontiers in Bioscience - Landmark</i> , 2020 , 25, 1787-1827 | 2.8 | 2 |
| 17 | How Does Arbidol Inhibit the Novel Coronavirus SARS-CoV-2? Atomistic Insights from Molecular Dynamics Simulations | | 2 |
| 16 | Draft genome of the liver fluke <i>Fasciola gigantica</i> | | 2 |
| 15 | Intrinsically Disordered Human T Lymphotropic Virus Type 1 p30 Protein: Experimental and Computational Evidence. <i>AIDS Research and Human Retroviruses</i> , 2019 , 35, 477-487 | 1.6 | 2 |
| 14 | Molecular Dynamics Simulation in Drug Discovery: Opportunities and Challenges 2021 , 295-316 | | 2 |
| 13 | Role of the glutaredoxin domain and FAD in the stabilization of thioredoxin glutathione reductase. <i>Archives of Biochemistry and Biophysics</i> , 2018 , 656, 38-45 | 4.1 | 2 |
| 12 | Biofunctionalized Chrysin-conjugated gold nanoparticles neutralize <i>Leishmania</i> parasites with high efficacy.. <i>International Journal of Biological Macromolecules</i> , 2022 , 205, 211-219 | 7.9 | 2 |
| 11 | A Master Regulator of β Synuclein Aggregation. <i>ACS Chemical Neuroscience</i> , 2020 , 11, 1376-1378 | 5.7 | 1 |
| 10 | Draft Genome Sequence of the Hydrocarbon-Degrading Bacterium Strain ABC Isolated from Noonmati Refinery, Assam, India. <i>Genome Announcements</i> , 2017 , 5, | | 1 |
| 9 | Strategies to improve the expression and solubility of recombinant proteins in <i>E. coli</i> 2022 , 1-12 | | 1 |

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| 8 | Methods to determine the oligomeric structure of proteins 2022 , 49-76 | | 1 |
| 7 | nucleoside diphosphate kinase shows interaction with putative ATP binding cassette (ABC) transporter, Rv1273c. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 38, 1083-1093 | 3.6 | 1 |
| 6 | Potent Inhibitors of Thioredoxin Glutathione Reductase: Grail of Anti-Schistosome Drug within Reach?. <i>ACS Infectious Diseases</i> , 2020 , 6, 893-895 | 5.5 | 0 |
| 5 | Unraveling the Structural Basis of Urea-induced Unfolding of <i>Fasciola gigantica</i> Cytosolic Malate Dehydrogenase. <i>Journal of Molecular Liquids</i> , 2021 , 118170 | 6 | 0 |
| 4 | Critical Insight into Plausible Acquired Tocopherol Pathway in Neglected Human Trypanosomatids. <i>ACS Omega</i> , 2021 , 6, 31396-31403 | 3.9 | 0 |
| 3 | Therapeutic p28 peptide targets essential H1N1 influenza virus proteins: insights from docking and molecular dynamics simulations. <i>Molecular Diversity</i> , 2021 , 25, 1929-1943 | 3.1 | 0 |
| 2 | Point mutation A394E in the central intrinsic disordered region of Rna14 leads to chromosomal instability in fission yeast. <i>International Journal of Biological Macromolecules</i> , 2018 , 119, 785-791 | 7.9 | |
| 1 | Studying Parasite Gene Function and Interaction Through Ribozymes and Riboswitches Design Mechanism 2018 , 51-74 | | |