

Timir Tripathi

List of Publications by Year in Descending Order

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Version: 2024-04-27

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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	Strategies to improve the expression and solubility of recombinant proteins in E. coli 2022 , 1-12		1
96	Methods to determine the oligomeric structure of proteins 2022 , 49-76		1
95	Experimental methods to study intrinsically disordered proteins 2022 , 505-533		2
94	Phase separation of FG-nucleoporins in nuclear pore complexes.. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2022 , 1869, 119205	4.9	4
93	Methodological advances in the design of peptide-based vaccines.. <i>Drug Discovery Today</i> , 2022 ,	8.8	4
92	Biofunctionalized Chrysin-conjugated gold nanoparticles neutralize Leishmania parasites with high efficacy.. <i>International Journal of Biological Macromolecules</i> , 2022 , 205, 211-219	7.9	2
91	Unraveling the Structural Basis of Urea-induced Unfolding of Fasciola gigantica Cytosolic Malate Dehydrogenase. <i>Journal of Molecular Liquids</i> , 2021 , 118170	6	0
90	Critical Insight into Plausible Acquired Tocopherol Pathway in Neglected Human Trypanosomatids. <i>ACS Omega</i> , 2021 , 6, 31396-31403	3.9	0
89	Prevalence and functionality of intrinsic disorder in human FG-nucleoporins. <i>International Journal of Biological Macromolecules</i> , 2021 , 175, 156-170	7.9	8
88	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
87	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
86	One year update on the COVID-19 pandemic: Where are we now?. <i>Acta Tropica</i> , 2021 , 214, 105778	3.2	70
85	Molecular Dynamics Simulation in Drug Discovery: Opportunities and Challenges 2021 , 295-316		2
84	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
83	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
82	Accelerating COVID-19 Research Using Molecular Dynamics Simulation. <i>Journal of Physical Chemistry B</i> , 2021 , 125, 9078-9091	3.4	20
81	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

80	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
79	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
78	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
77	Design of a peptide-based subunit vaccine against novel coronavirus SARS-CoV-2. <i>Microbial Pathogenesis</i> , 2020 , 145, 104236	3.8	110
76	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
75	Draft Genome of the Liver Fluke. <i>ACS Omega</i> , 2020 , 5, 11084-11091	3.9	14
74	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
73	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
72	A Master Regulator of β Synuclein Aggregation. <i>ACS Chemical Neuroscience</i> , 2020 , 11, 1376-1378	5.7	1
71	Genome-wide identification and characterization of eukaryotic protein kinases. <i>Frontiers in Bioscience - Landmark</i> , 2020 , 25, 1787-1827	2.8	2
70	Molecular Dynamics Simulation of Protein and Protein-Ligand Complexes 2020 , 133-161		14
69	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
68	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
67	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
66	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
65	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
64	Autophagy Modulation as a Treatment of Amyloid Diseases. <i>Molecules</i> , 2019 , 24,	4.8	33
63	Synergistic Effect of Amyloid- β and Tau Disrupts Neural Circuits. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 1129-1130	5.7	8

62	Identification and characterization of glyceraldehyde 3-phosphate dehydrogenase from <i>Fasciola gigantica</i> . <i>Parasitology Research</i> , 2019 , 118, 861-872	2.4	6
61	Autophagy Promotes Memory Formation. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 3337-3339	5.7	6
60	Portrait of the Intrinsically Disordered Side of the HTLV-1 Proteome. <i>ACS Omega</i> , 2019 , 4, 10003-10018	3.9	7
59	Abnormal Microtubule Dynamics Impair the Nuclear-Cytoplasmic Transport in Dementia. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 1133-1134	5.7	3
58	Interaction of β -Synuclein with ATP Synthase: Switching Role from Physiological to Pathological. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 16-17	5.7	5
57	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
56	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
55	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
54	Phospho-Tau Impairs Nuclear-Cytoplasmic Transport. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 36-38	5.7	10
53	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
52	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
51	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
50	Aminoacyl-tRNA synthetases: Structure, function, and drug discovery. <i>International Journal of Biological Macromolecules</i> , 2018 , 111, 400-414	7.9	51
49	Biochemical and thermodynamic comparison of the selenocysteine containing and non-containing thioredoxin glutathione reductase of <i>Fasciola gigantica</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018 , 1862, 1306-1316	4	11
48	Structure-based screening and molecular dynamics simulations offer novel natural compounds as potential inhibitors of <i>Mycobacterium tuberculosis</i> isocitrate lyase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 2045-2057	3.6	46
47	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
46	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
45	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

44	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
43	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	
42	<i>Opisthorchis viverrini</i> Proteome and Host-Parasite Interactions. <i>Advances in Parasitology</i> , 2018 , 102, 45-72	18	
41	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
40	Alternate pathway to ascorbate induced inhibition of <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2018 , 111, 161-169	2.6	12
39	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
38	Studying Parasite Gene Function and Interaction Through Ribozymes and Riboswitches Design Mechanism 2018 , 51-74		
37	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
36	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
35	Yeast and Human Nuclear Pore Complexes: Not So Similar After All. <i>Trends in Cell Biology</i> , 2018 , 28, 589-593	4	
34	Unusual thiol-based redox metabolism of parasitic flukes. <i>Parasitology International</i> , 2017 , 66, 390-395	2.1	13
33	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
32	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
31	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
30	Alterations in conformational topology and interaction dynamics caused by L418A mutation leads to activity loss of <i>Mycobacterium tuberculosis</i> isocitrate lyase. <i>Biochemical and Biophysical Research Communications</i> , 2017 , 490, 276-282	3.4	43
29	Eucalyptol, sabinene and cinnamaldehyde: potent inhibitors of salmonella target protein L-asparaginase. <i>3 Biotech</i> , 2017 , 7, 258	2.8	7
28	Distant Phe345 mutation compromises the stability and activity of <i>Mycobacterium tuberculosis</i> isocitrate lyase by modulating its structural flexibility. <i>Scientific Reports</i> , 2017 , 7, 1058	4.9	53
27	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

26	A combined biochemical and computational studies of the rho-class glutathione s-transferase sll1545 of Synechocystis PCC 6803. <i>International Journal of Biological Macromolecules</i> , 2017 , 94, 378-385	7.9	31
25	Draft Genome Sequence of Strain P5:ABC, Isolated from Hydrocarbon-Contaminated Soil from Noonmati Refinery, Assam, India. <i>Genome Announcements</i> , 2017 , 5,		2
24	Draft Genome Sequence of the Hydrocarbon-Degrading Bacterium Strain ABC Isolated from Noonmati Refinery, Assam, India. <i>Genome Announcements</i> , 2017 , 5,		1
23	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
22	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
21	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
20	<i>Fasciola gigantica</i> thioredoxin glutathione reductase: Biochemical properties and structural modeling. <i>International Journal of Biological Macromolecules</i> , 2016 , 89, 152-60	7.9	10
19	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
18	Preferential regeneration of thioredoxin from parasitic flatworm <i>Fasciola gigantica</i> using glutathione system. <i>International Journal of Biological Macromolecules</i> , 2015 , 81, 983-90	7.9	9
17	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
16	Characterization of a Highly pH Stable Chi-Class Glutathione S-Transferase from <i>Synechocystis PCC 6803</i> . <i>PLoS ONE</i> , 2015 , 10, e0126811	3.7	20
15	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
14	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
13	Functional classification and biochemical characterization of a novel rho class glutathione S-transferase in <i>Synechocystis PCC 6803</i> . <i>FEBS Open Bio</i> , 2015 , 5, 1-7	2.7	7
12	Atomic resolution crystal structure of glutaredoxin 1 from <i>Plasmodium falciparum</i> and comparison with other glutaredoxins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 91-100		11
11	Conformational stability and energetics of <i>Plasmodium falciparum</i> glutaredoxin. <i>Biochimie</i> , 2010 , 92, 284-91	4.6	12
10	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
9	Structural and stability characteristics of a monothiol glutaredoxin: glutaredoxin-like protein 1 from <i>Plasmodium falciparum</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008 , 1784, 946-52	4	11

8	Glutathione mediated regulation of oligomeric structure and functional activity of Plasmodium falciparum glutathione S-transferase. <i>BMC Structural Biology</i> , 2007 , 7, 67	2-7	15
7	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
6	Design of a Peptide-Based Subunit Vaccine against Novel Coronavirus SARS-CoV-2		2
5	How Does Arbidol Inhibit the Novel Coronavirus SARS-CoV-2? Atomistic Insights from Molecular Dynamics Simulations		6
4	How Does Arbidol Inhibit the Novel Coronavirus SARS-CoV-2? Atomistic Insights from Molecular Dynamics Simulations		2
3	High Throughput Designing and Mutational Mapping of RBD-ACE2 Interface Guide Non-Conventional Therapeutic Strategies for COVID-19		6
2	Rational Design of the Remdesivir Binding Site in the RNA-dependent RNA Polymerase of SARS-CoV-2: Implications for Potential Resistance		4
1	Draft genome of the liver fluke Fasciola gigantica		2