

George Priya Doss C

List of Publications by Citations

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178
papers

3,246
citations

30
h-index

47
g-index

185
ext. papers

3,816
ext. citations

4.4
avg, IF

5.93
L-index

#	Paper	IF	Citations
178	Therapeutic miRNA and siRNA: Moving from Bench to Clinic as Next Generation Medicine. <i>Molecular Therapy - Nucleic Acids</i> , 2017 , 8, 132-143	10.7	464
177	Influence of miRNA in insulin signaling pathway and insulin resistance: micro-molecules with a major role in type-2 diabetes. <i>Wiley Interdisciplinary Reviews RNA</i> , 2014 , 5, 697-712	9.3	142
176	Nanoparticle based insulin delivery system: the next generation efficient therapy for Type 1 diabetes. <i>Journal of Nanobiotechnology</i> , 2015 , 13, 74	9.4	102
175	Molecular Dynamics: New Frontier in Personalized Medicine. <i>Advances in Protein Chemistry and Structural Biology</i> , 2016 , 102, 181-224	5.3	76
174	Identification and in silico analysis of functional SNPs of the BRCA1 gene. <i>Genomics</i> , 2007 , 90, 447-52	4.3	58
173	miRNAs in insulin resistance and diabetes-associated pancreatic cancer: the minute and miracle molecule moving as a monitor in the genomic galaxy. <i>Current Drug Targets</i> , 2013 , 14, 1110-7	3	58
172	Analysis of Differentially Expressed Genes and Molecular Pathways in Familial Hypercholesterolemia Involved in Atherosclerosis: A Systematic and Bioinformatics Approach. <i>Frontiers in Genetics</i> , 2020 , 11, 734	4.5	57
171	Integrative Bioinformatics Approaches to Map Potential Novel Genes and Pathways Involved in Ovarian Cancer. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019 , 7, 391	5.8	50
170	Functionality study of santalin as tyrosinase inhibitor: A potential depigmentation agent. <i>International Journal of Biological Macromolecules</i> , 2016 , 86, 383-9	7.9	43
169	BSA nanoparticle loaded atorvastatin calcium--a new facet for an old drug. <i>PLoS ONE</i> , 2014 , 9, e86317	3.7	43
168	Dysregulation of Signaling Pathways Due to Differentially Expressed Genes From the B-Cell Transcriptomes of Systemic Lupus Erythematosus Patients - A Bioinformatics Approach. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 276	5.8	42
167	TNF/TNFR: drug target for autoimmune diseases and immune-mediated inflammatory diseases. <i>Frontiers in Bioscience - Landmark</i> , 2014 , 19, 1028-40	2.8	42
166	Screening of mutations affecting protein stability and dynamics of FGFR1-A simulation analysis. <i>Applied & Translational Genomics</i> , 2012 , 1, 37-43		42
165	Investigation on the role of nsSNPs in HNPCC genes--a bioinformatics approach. <i>Journal of Biomedical Science</i> , 2009 , 16, 42	13.3	42
164	Influence of V54M mutation in giant muscle protein titin: a computational screening and molecular dynamics approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 917-928	3.6	41
163	Extrapolating the effect of deleterious nsSNPs in the binding adaptability of flavopiridol with CDK7 protein: a molecular dynamics approach. <i>Human Genomics</i> , 2013 , 7, 10	6.8	40
162	Unraveling the inhibition mechanism of cyanidin-3-sophoroside on polyphenol oxidase and its effect on enzymatic browning of apples. <i>Food Chemistry</i> , 2017 , 227, 102-110	8.5	36

161	Inhibitory effect of brazilein on tyrosinase and melanin synthesis: Kinetics and in silico approach. <i>International Journal of Biological Macromolecules</i> , 2015 , 81, 228-34	7.9	36
160	Genotype-phenotype correlation in 18 Egyptian patients with glutaric acidemia type I. <i>Metabolic Brain Disease</i> , 2017 , 32, 1417-1426	3.9	35
159	Computational approach to unravel the impact of missense mutations of proteins (D2HGDH and IDH2) causing D-2-hydroxyglutaric aciduria 2. <i>Metabolic Brain Disease</i> , 2018 , 33, 1699-1710	3.9	34
158	DNA barcoding to map the microbial communities: current advances and future directions. <i>Applied Microbiology and Biotechnology</i> , 2014 , 98, 3425-36	5.7	34
157	Molecular dynamics-based analyses of the structural instability and secondary structure of the fibrinogen gamma chain protein with the D356V mutation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 2714-2724	3.6	34
156	Structural Analysis of G1691S Variant in the Human Filamin B Gene Responsible for Larsen Syndrome: A Comparative Computational Approach. <i>Journal of Cellular Biochemistry</i> , 2017 , 118, 1900-1917	4.7	33
155	A profound computational study to prioritize the disease-causing mutations in PRPS1 gene. <i>Metabolic Brain Disease</i> , 2018 , 33, 589-600	3.9	33
154	Computational refinement of functional single nucleotide polymorphisms associated with ATM gene. <i>PLoS ONE</i> , 2012 , 7, e34573	3.7	33
153	Applications of computational algorithm tools to identify functional SNPs. <i>Functional and Integrative Genomics</i> , 2008 , 8, 309-16	3.8	33
152	Structural signature of the G719S-T790M double mutation in the EGFR kinase domain and its response to inhibitors. <i>Scientific Reports</i> , 2014 , 4, 5868	4.9	32
151	Determining the role of missense mutations in the POU domain of HNF1A that reduce the DNA-binding affinity: A computational approach. <i>PLoS ONE</i> , 2017 , 12, e0174953	3.7	31
150	Investigating the structural impacts of I64T and P311S mutations in APE1-DNA complex: a molecular dynamics approach. <i>PLoS ONE</i> , 2012 , 7, e31677	3.7	31
149	Studies on flexibility and binding affinity of Asp25 of HIV-1 protease mutants. <i>International Journal of Biological Macromolecules</i> , 2008 , 42, 386-91	7.9	31
148	Investigating the Inhibitory Effect of Wortmannin in the Hotspot Mutation at Codon 1047 of PIK3CA Kinase Domain: A Molecular Docking and Molecular Dynamics Approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2016 , 102, 267-97	5.3	30
147	Path to facilitate the prediction of functional amino acid substitutions in red blood cell disorders--a computational approach. <i>PLoS ONE</i> , 2011 , 6, e24607	3.7	30
146	Exploring the interaction between iron oxide nanoparticles (IONPs) and Human serum albumin (HSA): Spectroscopic and docking studies. <i>Journal of Molecular Liquids</i> , 2017 , 241, 793-800	6	29
145	Comparative computational assessment of the pathogenicity of mutations in the Aspartoacylase enzyme. <i>Metabolic Brain Disease</i> , 2017 , 32, 2105-2118	3.9	29
144	Integrating in silico prediction methods, molecular docking, and molecular dynamics simulation to predict the impact of ALK missense mutations in structural perspective. <i>BioMed Research International</i> , 2014 , 2014, 895831	3	29

143	Next generation delivery system for proteins and genes of therapeutic purpose: why and how?. <i>BioMed Research International</i> , 2014 , 2014, 327950	3	29
142	Effect of deleterious nsSNP on the HER2 receptor based on stability and binding affinity with herceptin: a computational approach. <i>Comptes Rendus - Biologies</i> , 2008 , 331, 409-17	1.4	28
141	Two patients with Canavan disease and structural modeling of a novel mutation. <i>Metabolic Brain Disease</i> , 2017 , 32, 171-177	3.9	27
140	Role of E542 and E545 missense mutations of PIK3CA in breast cancer: a comparative computational approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 2745-2757	3.6	27
139	Computational modelling approaches as a potential platform to understand the molecular genetics association between Parkinson ^R and Gaucher diseases. <i>Metabolic Brain Disease</i> , 2018 , 33, 1835-1847	3.9	26
138	Involvement of Essential Signaling Cascades and Analysis of Gene Networks in Diabesity. <i>Genes</i> , 2020 , 11,	4.2	26
137	Deciphering the impact of somatic mutations in exon 20 and exon 9 of PIK3CA gene in breast tumors among Indian women through molecular dynamics approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016 , 34, 29-41	3.6	25
136	Genotype-phenotype correlation in patients with isovaleric acidaemia: comparative structural modelling and computational analysis of novel variants. <i>Human Molecular Genetics</i> , 2017 , 26, 3105-3115	5.6	25
135	Binding and molecular dynamic studies of sesquiterpenes (2R-acetoxymethyl-1,3,3-trimethyl-4t-(3-methyl-2-buten-1-yl)-1t-cyclohexanol) derived from marine <i>Streptomyces</i> sp. VITJS8 as potential anticancer agent. <i>Applied Microbiology and Biotechnology</i> , 2016 , 100, 2869-82	5.7	24
134	Structural analysis of missense mutations in galactokinase 1 (GALK1) leading to galactosemia type-2. <i>Journal of Cellular Biochemistry</i> , 2018 , 119, 7585-7598	4.7	24
133	Immobilization of β galactosidase from <i>Lactobacillus plantarum</i> HF571129 on ZnO nanoparticles: characterization and lactose hydrolysis. <i>Bioprocess and Biosystems Engineering</i> , 2015 , 38, 1655-69	3.7	24
132	Prospects and progress in the production of valuable carotenoids: Insights from metabolic engineering, synthetic biology, and computational approaches. <i>Journal of Biotechnology</i> , 2018 , 266, 89-101	3.7	23
131	A systemic approach to explore the mechanisms of drug resistance and altered signaling cascades in extensively drug-resistant tuberculosis. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021 , 127, 343-364	5.3	23
130	Gliptins in managing diabetes - Reviewing computational strategy. <i>Life Sciences</i> , 2016 , 166, 108-120	6.8	22
129	Network analysis of transcriptomics data for the prediction and prioritization of membrane-associated biomarkers for idiopathic pulmonary fibrosis (IPF) by bioinformatics approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021 , 123, 241-273	5.3	22
128	In silico profiling and structural insights of missense mutations in RET protein kinase domain by molecular dynamics and docking approach. <i>Molecular BioSystems</i> , 2014 , 10, 421-36		21
127	Substitution impact of highly conserved arginine residue at position 75 in GJB1 gene in association with X-linked Charcot-Marie-tooth disease: A computational study. <i>Journal of Theoretical Biology</i> , 2018 , 437, 305-317	2.3	20
126	A new insight into structural and functional impact of single-nucleotide polymorphisms in PTEN gene. <i>Cell Biochemistry and Biophysics</i> , 2013 , 66, 249-63	3.2	20

125	Computational insights of K1444N substitution in GAP-related domain of NF1 gene associated with neurofibromatosis type 1 disease: a molecular modeling and dynamics approach. <i>Metabolic Brain Disease</i> , 2018 , 33, 1443-1457	3.9	20
124	Computational approaches and resources in single amino acid substitutions analysis toward clinical research. <i>Advances in Protein Chemistry and Structural Biology</i> , 2014 , 94, 365-423	5.3	19
123	A Molecular Docking and Dynamics Approach to Screen Potent Inhibitors Against Fosfomycin Resistant Enzyme in Clinical Klebsiella pneumoniae. <i>Journal of Cellular Biochemistry</i> , 2017 , 118, 4088-4094	4.7	17
122	An extensive computational approach to analyze and characterize the functional mutations in the galactose-1-phosphate uridyl transferase (GALT) protein responsible for classical galactosemia. <i>Computers in Biology and Medicine</i> , 2020 , 117, 103583	7	17
121	Effect of UV radiation and its implications on carotenoid pathway in Bixa orellana L. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2017 , 176, 136-144	6.7	16
120	Personalized Pharmacoperones for Lysosomal Storage Disorder: Approach for Next-Generation Treatment. <i>Advances in Protein Chemistry and Structural Biology</i> , 2016 , 102, 225-65	5.3	16
119	Comprehensive in silico screening and molecular dynamics studies of missense mutations in Sjogren-Larsson syndrome associated with the ALDH3A2 gene. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020 , 120, 349-377	5.3	15
118	Identifying a Carotenoid Cleavage Dioxygenase 4a Gene and Its Efficient Agrobacterium-Mediated Genetic Transformation in Bixa orellana L. <i>Applied Biochemistry and Biotechnology</i> , 2016 , 179, 697-714	3.2	15
117	Recent trends of polymer mediated liposomal gene delivery system. <i>BioMed Research International</i> , 2014 , 2014, 934605	3	15
116	In silico profiling of deleterious amino acid substitutions of potential pathological importance in haemophilia A and haemophilia B. <i>Journal of Biomedical Science</i> , 2012 , 19, 30	13.3	15
115	Sirtuins family--recent development as a drug target for aging, metabolism, and age related diseases. <i>Current Drug Targets</i> , 2013 , 14, 666-75	3	15
114	Draft genome of a hypervirulent Klebsiella quasipneumoniae subsp. similipneumoniae with novel sequence type ST2320 isolated from a chronic liver disease patient. <i>Journal of Global Antimicrobial Resistance</i> , 2017 , 9, 30-31	3.4	14
113	Identification and structural comparison of deleterious mutations in nsSNPs of ABL1 gene in chronic myeloid leukemia: a bio-informatics study. <i>Journal of Biomedical Informatics</i> , 2008 , 41, 607-12	10.2	14
112	DNA Repair Gene (XRCC1) Polymorphism (Arg399Gln) Associated with Schizophrenia in South Indian Population: A Genotypic and Molecular Dynamics Study. <i>PLoS ONE</i> , 2016 , 11, e0147348	3.7	14
111	A comparative computational approach toward pharmacological chaperones (NN-DNJ and ambroxol) on N370S and L444P mutations causing Gaucher's disease. <i>Advances in Protein Chemistry and Structural Biology</i> , 2019 , 114, 315-339	5.3	14
110	An integrative analysis to distinguish between emphysema (EML) and alpha-1 antitrypsin deficiency-related emphysema (ADL)-A systems biology approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021 , 127, 315-342	5.3	14
109	Molecular insights of the G2019S substitution in LRRK2 kinase domain associated with Parkinson's disease: A molecular dynamics simulation approach. <i>Journal of Theoretical Biology</i> , 2019 , 469, 163-171	2.3	13
108	Implication of salt stress induces changes in pigment production, antioxidant enzyme activity, and qRT-PCR expression of genes involved in the biosynthetic pathway of Bixa orellana L. <i>Functional and Integrative Genomics</i> , 2019 , 19, 565-574	3.8	12

107	Understanding the structure-function relationship of HPRT1 missense mutations in association with Lesch-Nyhan disease and HPRT1-related gout by in silico mutational analysis. <i>Computers in Biology and Medicine</i> , 2019 , 107, 161-171	7	12
106	Bioinformatics classification of mutations in patients with Mucopolysaccharidosis IIIA. <i>Metabolic Brain Disease</i> , 2019 , 34, 1577-1594	3.9	12
105	Predicting the impact of single-nucleotide polymorphisms in CDK2-flavopiridol complex by molecular dynamics analysis. <i>Cell Biochemistry and Biophysics</i> , 2013 , 66, 681-95	3.2	12
104	Impact of single nucleotide polymorphisms in HBB gene causing haemoglobinopathies: in silico analysis. <i>New Biotechnology</i> , 2009 , 25, 214-9	6.4	12
103	Glandular hair constituents of <i>Mallotus philippinensis</i> Muell. fruit act as tyrosinase inhibitors: Insights from enzyme kinetics and simulation study. <i>International Journal of Biological Macromolecules</i> , 2018 , 107, 1675-1682	7.9	11
102	Impact of missense mutations in survival motor neuron protein (SMN1) leading to Spinal Muscular Atrophy (SMA): A computational approach. <i>Metabolic Brain Disease</i> , 2018 , 33, 1823-1834	3.9	11
101	In silico analysis of structural and functional consequences in p16INK4A by deleterious nsSNPs associated CDKN2A gene in malignant melanoma. <i>Biochimie</i> , 2008 , 90, 1523-9	4.6	11
100	Mutational landscape of K-Ras substitutions at 12th position-a systematic molecular dynamics approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 1-15	3.6	11
99	A computational method to characterize the missense mutations in the catalytic domain of GAA protein causing Pompe disease. <i>Journal of Cellular Biochemistry</i> , 2019 , 120, 3491-3505	4.7	11
98	Molecular dynamics, residue network analysis, and cross-correlation matrix to characterize the deleterious missense mutations in GALE causing galactosemia III. <i>Cell Biochemistry and Biophysics</i> , 2021 , 79, 201-219	3.2	11
97	Structural insights into the binding mode and conformational changes of BSA induced by bixin and crocin. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 2085-2098	3.6	10
96	Application of evolutionary based in silico methods to predict the impact of single amino acid substitutions in vitelliform macular dystrophy. <i>Advances in Protein Chemistry and Structural Biology</i> , 2014 , 94, 177-267	5.3	10
95	A Computational Approach to Identify the Biophysical and Structural Aspects of Methylenetetrahydrofolate Reductase (MTHFR) Mutations (A222V, E429A, and R594Q) Leading to Schizophrenia. <i>Advances in Protein Chemistry and Structural Biology</i> , 2017 , 108, 105-125	5.3	10
94	Significant fluctuations in ecdysteroid receptor gene (EcR) expression in relation to seasons of molt and reproduction in the grapsid crab, <i>Metopograpsus messor</i> (Brachyura: Decapoda). <i>General and Comparative Endocrinology</i> , 2015 , 211, 39-51	3	10
93	Structure-Based Virtual Screening to Identify Novel Potential Compound as an Alternative to Remdesivir to Overcome the RdRp Protein Mutations in SARS-CoV-2. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 645216	5.6	10
92	Identification of potential inhibitors against pathogenic missense mutations of PMM2 using a structure-based virtual screening approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 171-187	3.6	10
91	A natural anticancer pigment, Pheophytin a, from a seagrass acts as a high affinity human mitochondrial translocator protein (TSPO) ligand, in silico, to reduce mitochondrial membrane Potential ($\Delta\psi$) in adenocarcinomic A549 cells. <i>Phytomedicine</i> , 2019 , 61, 152858	6.5	9
90	Kerala, India is Front Runner in Novel Coronavirus Disease (COVID-19). <i>Frontiers in Medicine</i> , 2020 , 7, 3554.9	4.9	9

89	A computational approach for investigating the mutational landscape of RAC-alpha serine/threonine-protein kinase (AKT1) and screening inhibitors against the oncogenic E17K mutation causing breast cancer. <i>Computers in Biology and Medicine</i> , 2019 , 115, 103513	7	9
88	In silico analysis of prion protein mutants: a comparative study by molecular dynamics approach. <i>Cell Biochemistry and Biophysics</i> , 2013 , 67, 1307-18	3.2	9
87	Glutathione-responsive nano-transporter-mediated siRNA delivery: silencing the mRNA expression of Ras. <i>Protoplasma</i> , 2013 , 250, 787-92	3.4	9
86	Novel biomarker for prostate cancer diagnosis by MRS. <i>Frontiers in Bioscience - Landmark</i> , 2014 , 19, 1186-201	2.01	9
85	Computational and modeling approaches to understand the impact of the Fabry disease causing mutation (D92Y) on the interaction with pharmacological chaperone 1-deoxygalactonojirimycin (DGJ). <i>Advances in Protein Chemistry and Structural Biology</i> , 2019 , 114, 341-407	5.3	9
84	Molecular Modeling and Dynamic Simulation of Arabidopsis Thaliana Carotenoid Cleavage Dioxygenase Gene: A Comparison with Bixa orellana and Crocus Sativus. <i>Journal of Cellular Biochemistry</i> , 2017 , 118, 2712-2721	4.7	8
83	Impact of I30T and I30M substitution in MPZ gene associated with Dejerine-Sottas syndrome type B (DSSB): A molecular modeling and dynamics. <i>Journal of Theoretical Biology</i> , 2015 , 382, 23-33	2.3	8
82	Enzyme therapy: a forerunner in catalyzing a healthy society?. <i>Expert Opinion on Biological Therapy</i> , 2020 , 20, 1151-1174	5.4	8
81	Analysis of interactions of clinical mutants of catalase-peroxidase (KatG) responsible for isoniazid resistance in Mycobacterium tuberculosis with derivatives of isoniazid. <i>Journal of Global Antimicrobial Resistance</i> , 2017 , 11, 57-67	3.4	8
80	Crucial protein based drug targets and potential inhibitors for osteoporosis: new hope and possibilities. <i>Current Drug Targets</i> , 2013 , 14, 1707-13	3	8
79	A review of novel coronavirus disease (COVID-19): based on genomic structure, phylogeny, current shreds of evidence, candidate vaccines, and drug repurposing. <i>3 Biotech</i> , 2021 , 11, 198	2.8	8
78	A Computational Approach to Identify a Potential Alternative Drug With Its Positive Impact Toward PMP22. <i>Journal of Cellular Biochemistry</i> , 2017 , 118, 3730-3743	4.7	7
77	Deciphering the Role of Filamin B Calponin-Homology Domain in Causing the Larsen Syndrome, Boomerang Dysplasia, and Atelosteogenesis Type I Spectrum Disorders via a Computational Approach. <i>Molecules</i> , 2020 , 25,	4.8	7
76	An Integrated Computational Framework to Assess the Mutational Landscape of β -Iduronidase IDUA Gene. <i>Journal of Cellular Biochemistry</i> , 2018 , 119, 555-565	4.7	7
75	An integrated in silico approach to analyze the involvement of single amino acid polymorphisms in FANCD1/BRCA2-PALB2 and FANCD1/BRCA2-RAD51 complex. <i>Cell Biochemistry and Biophysics</i> , 2014 , 70, 939-56	3.2	7
74	Assessing reproductive toxicity and antioxidant enzymes on beta asarone induced male Wistar albino rats: In vivo and computational analysis. <i>Life Sciences</i> , 2017 , 173, 150-160	6.8	7
73	LSHGD: a database for human leprosy susceptible genes. <i>Genomics</i> , 2012 , 100, 162-6	4.3	7
72	Computational methods to work as first-pass filter in deleterious SNP analysis of alkaptonuria. <i>Scientific World Journal, The</i> , 2012 , 2012, 738423	2.2	7

71	Prioritization of candidate SNPs in colon cancer using bioinformatics tools: an alternative approach for a cancer biologist. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2010 , 2, 320-46	3.5	7
70	Elucidating the role of interacting residues of the MSH2-MSH6 complex in DNA repair mechanism: A computational approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2019 , 115, 325-350	5.3	7
69	Functional and structural characterization of missense mutations in PAX6 gene. <i>Frontiers in Biology</i> , 2015 , 10, 377-385		6
68	Computational Resources for Predicting Protein-Protein Interactions. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018 , 110, 251-275	5.3	6
67	Investigating the Influence of Hotspot Mutations in Protein-Protein Interaction of IDH1 Homodimer Protein: A Computational Approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018 , 111, 243-261	5.3	6
66	Molecular docking and molecular dynamics study on the effect of ERCC1 deleterious polymorphisms in ERCC1-XPF heterodimer. <i>Applied Biochemistry and Biotechnology</i> , 2014 , 172, 1265-81	3.2	6
65	In silico discrimination of nsSNPs in hTERT gene by means of local DNA sequence context and regularity. <i>Journal of Molecular Modeling</i> , 2013 , 19, 3517-27	2	6
64	Elucidating the Mutational Landscape in Hepatocyte Nuclear Factor 1 (HNF1B) by Computational Approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2017 , 107, 283-306	5.3	6
63	Computational biophysical, biochemical, and evolutionary signature of human R-spondin family proteins, the member of canonical Wnt/βcatenin signaling pathway. <i>BioMed Research International</i> , 2014 , 2014, 974316	3	6
62	Analysis of binding residues between scorpion neurotoxins and D2 dopamine receptor: a computational docking study. <i>Computers in Biology and Medicine</i> , 2008 , 38, 1056-67	7	6
61	Computational model to analyze and characterize the functional mutations of NOD2 protein causing inflammatory disorder - Blau syndrome. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020 , 120, 379-408	5.3	6
60	Mixed azo dyes degradation by an intracellular azoreductase enzyme from alkaliphilic <i>Bacillus subtilis</i> : a molecular docking study. <i>Archives of Microbiology</i> , 2021 , 203, 3033-3044	3	6
59	Investigating mutations at the hotspot position of the ERBB2 and screening for the novel lead compound to treat breast cancer - a computational approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021 , 123, 49-71	5.3	6
58	In vitro flowering in <i>Oldenlandia umbellata</i> L. <i>Journal of Ayurveda and Integrative Medicine</i> , 2018 , 9, 99-103		6
57	Can the chemotherapeutic agents perform anticancer activity through miRNA expression regulation? Proposing a new hypothesis [corrected]. <i>Protoplasma</i> , 2015 , 252, 1603-10	3.4	5
56	Influence of the SNPs on the structural stability of CBS protein: Insight from molecular dynamics simulations. <i>Frontiers in Biology</i> , 2014 , 9, 504-518		5
55	Computational pipeline to identify and characterize functional mutations in ornithine transcarbamylase deficiency. <i>3 Biotech</i> , 2014 , 4, 621-634	2.8	5
54	Predicting the impact of deleterious single point mutations in SMAD gene family using structural bioinformatics approach. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2012 , 4, 103-15	3.5	5

53	In silico analyses of COMT, an important signaling cascade of dopaminergic neurotransmission pathway, for drug development of Parkinson's disease. <i>Applied Biochemistry and Biotechnology</i> , 2012 , 167, 845-60	3.2	5
52	In silico searching for disease-associated functional DNA variants. <i>Methods in Molecular Biology</i> , 2011 , 760, 239-50	1.4	5
51	Interaction of Catechu Dye with DNA: Spectroscopic and In Silico Approach. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2016 , 35, 195-210	1.4	5
50	A computational model to predict the structural and functional consequences of missense mutations in O-methylguanine DNA methyltransferase. <i>Advances in Protein Chemistry and Structural Biology</i> , 2019 , 115, 351-369	5.3	5
49	Molecular dynamics simulations to decipher the structural and functional consequences of pathogenic missense mutations in the galactosylceramidase (GALC) protein causing Krabbe's disease. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 1795-1810	3.6	5
48	Probing the Protein-Protein Interaction Network of Proteins Causing Maturity Onset Diabetes of the Young. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018 , 110, 167-202	5.3	5
47	In vitro efficacy and in silico analysis of cefixime-ofloxacin combination for Salmonella Typhi from bloodstream infection. <i>Journal of Applied Microbiology</i> , 2017 , 123, 615-624	4.7	4
46	Analyzing the Effect of V66M Mutation in BDNF in Causing Mood Disorders: A Computational Approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2017 , 108, 85-103	5.3	4
45	Disease-causing mutation in extracellular and intracellular domain of FGFR1 protein: computational approach. <i>Applied Biochemistry and Biotechnology</i> , 2013 , 169, 1659-71	3.2	4
44	In Silico Identification and Analysis of Drug Resistant Mutants of ABL Tyrosine Kinase Based on Detrimental Missense Mutations. <i>Current Signal Transduction Therapy</i> , 2011 , 6, 396-404	0.8	4
43	Computational and structural analysis of deleterious functional SNPs in ARNT oncogene. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2009 , 1, 220-8	3.5	4
42	First hybrid complete genome of reveals chromosome-mediated novel structural variant from a human clinical sample. <i>Access Microbiology</i> , 2020 , 2, acmi000103	1	4
41	Enhanced production of anthraquinones by gamma-irradiated cell cultures of <i>Rubia cordifolia</i> in a bioreactor. <i>Industrial Crops and Products</i> , 2020 , 145, 111987	5.9	4
40	Integrated approach on azo dyes degradation using laccase enzyme and Cu nanoparticle. <i>SN Applied Sciences</i> , 2021 , 3, 1	1.8	4
39	Exploring the codon patterns between CCD and NCED genes among different plant species. <i>Computers in Biology and Medicine</i> , 2019 , 114, 103449	7	3
38	Investigating the role of microRNA-27a gene polymorphisms and its interactive effect with risk factors in gastrointestinal cancers. <i>Heliyon</i> , 2020 , 6, e03565	3.6	3
37	Computational identification of pathogenic associated nsSNPs and its structural impact in UROD gene: a molecular dynamics approach. <i>Cell Biochemistry and Biophysics</i> , 2014 , 70, 735-46	3.2	3
36	CoagVDb: a comprehensive database for coagulation factors and their associated SAPs. <i>Biological Research</i> , 2015 , 48, 35	7.6	3

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