

George Priya Doss C

List of Publications by Year in descending order

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Version: 2024-02-01

183
papers

4,405
citations

126708

33
h-index

155451

55
g-index

185
all docs

185
docs citations

185
times ranked

5795
citing authors

#	ARTICLE	IF	CITATIONS
1	Therapeutic miRNA and siRNA: Moving from Bench to Clinic as Next Generation Medicine. <i>Molecular Therapy - Nucleic Acids</i> , 2017, 8, 132-143.	2.3	600
2	Influence of miRNA in insulin signaling pathway and insulin resistance: microRNAs molecules with a major role in type 2 diabetes. <i>Wiley Interdisciplinary Reviews RNA</i> , 2014, 5, 697-712.	3.2	202
3	Nanoparticle based insulin delivery system: the next generation efficient therapy for Type 1 diabetes. <i>Journal of Nanobiotechnology</i> , 2015, 13, 74.	4.2	145
4	Molecular Dynamics. <i>Advances in Protein Chemistry and Structural Biology</i> , 2016, 102, 181-224.	1.0	132
5	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.	1.1	82
6	Identification and in silico analysis of functional SNPs of the BRCA1 gene. <i>Genomics</i> , 2007, 90, 447-452.	1.3	73
7	Integrative Bioinformatics Approaches to Map Potential Novel Genes and Pathways Involved in Ovarian Cancer. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 391.	2.0	72
8	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, 1110-1117.	1.0	65
9	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.	2.0	57
10	TNF/TNFR: drug target for autoimmune diseases and immune-mediated inflammatory diseases. <i>Frontiers in Bioscience - Landmark</i> , 2014, 19, 1028.	3.0	56
11	Inhibitory effect of brazilein on tyrosinase and melanin synthesis: Kinetics and in silico approach. <i>International Journal of Biological Macromolecules</i> , 2015, 81, 228-234.	3.6	54
12	Screening of mutations affecting protein stability and dynamics of FGFR1" A simulation analysis. <i>Applied & Translational Genomics</i> , 2012, 1, 37-43.	2.1	53
13	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.	4.2	52
14	Functionality study of santalin as tyrosinase inhibitor: A potential depigmentation agent. <i>International Journal of Biological Macromolecules</i> , 2016, 86, 383-389.	3.6	51
15	Studies on flexibility and binding affinity of Asp25 of HIV-1 protease mutants. <i>International Journal of Biological Macromolecules</i> , 2008, 42, 386-391.	3.6	49
16	Investigation on the role of nsSNPs in HNPCC genes " a bioinformatics approach. <i>Journal of Biomedical Science</i> , 2009, 16, 42.	2.6	49
17	BSA Nanoparticle Loaded Atorvastatin Calcium - A New Facet for an Old Drug. <i>PLoS ONE</i> , 2014, 9, e86317.	1.1	49
18	A profound computational study to prioritize the disease-causing mutations in PRPS1 gene. <i>Metabolic Brain Disease</i> , 2018, 33, 589-600.	1.4	49

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19	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.	1.4	47
20	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.	2.0	44
21	Applications of computational algorithm tools to identify functional SNPs. <i>Functional and Integrative Genomics</i> , 2008, 8, 309-316.	1.4	43
22	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.	1.1	43
23	Genotype-phenotype correlation in 18 Egyptian patients with glutaric acidemia type I. <i>Metabolic Brain Disease</i> , 2017, 32, 1417-1426.	1.4	42
24	Investigating the Structural Impacts of I64T and P311S Mutations in APE1-DNA Complex: A Molecular Dynamics Approach. <i>PLoS ONE</i> , 2012, 7, e31677.	1.1	41
25	Integrating <i>In Silico</i> 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, 1-14.	0.9	40
26	DNA barcoding to map the microbial communities: current advances and future directions. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3425-3436.	1.7	40
27	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.	2.0	39
28	Computational Refinement of Functional Single Nucleotide Polymorphisms Associated with ATM Gene. <i>PLoS ONE</i> , 2012, 7, e34573.	1.1	38
29	Structural Analysis of G1691S Variant in the Human <i>Filamin B</i> Gene Responsible for Larsen Syndrome: A Comparative Computational Approach. <i>Journal of Cellular Biochemistry</i> , 2017, 118, 1900-1910.	1.2	38
30	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.	1.4	38
31	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.	1.6	37
32	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.	1.1	36
33	Investigating the Inhibitory Effect of Wortmannin in the Hotspot Mutation at Codon 1047 of PIK3CA Kinase Domain. <i>Advances in Protein Chemistry and Structural Biology</i> , 2016, 102, 267-297.	1.0	36
34	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.	2.3	36
35	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, 1655-1669.	1.7	35
36	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.	1.9	35

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37	Structural analysis of missense mutations in galactokinase 1 (GALK1) leading to galactosemia type 2. Journal of Cellular Biochemistry, 2018, 119, 7585-7598.	1.2	35
38	Comparative computational assessment of the pathogenicity of mutations in the Aspartoacylase enzyme. Metabolic Brain Disease, 2017, 32, 2105-2118.	1.4	34
39	Effect of deleterious nsSNP on the HER2 receptor based on stability and binding affinity with herceptin: A computational approach. Comptes Rendus - Biologies, 2008, 331, 409-417.	0.1	33
40	Role of E542 and E545 missense mutations of PIK3CA in breast cancer: a comparative computational approach. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2745-2757.	2.0	33
41	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 Streptomyces sp. VITJS8 as potential anticancer agent. Applied Microbiology and Biotechnology, 2016, 100, 2869-2882.	1.7	32
42	Genotype-phenotype correlation in patients with isovaleric acidaemia: comparative structural modelling and computational analysis of novel variants. Human Molecular Genetics, 2017, 26, 3105-3115.	1.4	32
43	Two patients with Canavan disease and structural modeling of a novel mutation. Metabolic Brain Disease, 2017, 32, 171-177.	1.4	32
44	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. Journal of Theoretical Biology, 2018, 437, 305-317.	0.8	32
45	Involvement of Essential Signaling Cascades and Analysis of Gene Networks in Diabesity. Genes, 2020, 11, 1256.	1.0	32
46	Next Generation Delivery System for Proteins and Genes of Therapeutic Purpose: Why and How?. BioMed Research International, 2014, 2014, 1-11.	0.9	31
47	Computational modelling approaches as a potential platform to understand the molecular genetics association between Parkinson's and Gaucher diseases. Metabolic Brain Disease, 2018, 33, 1835-1847.	1.4	31
48	Molecular insights of the G2019S substitution in LRRK2 kinase domain associated with Parkinson's disease: A molecular dynamics simulation approach. Journal of Theoretical Biology, 2019, 469, 163-171.	0.8	31
49	A systemic approach to explore the mechanisms of drug resistance and altered signaling cascades in extensively drug-resistant tuberculosis. Advances in Protein Chemistry and Structural Biology, 2021, 127, 343-364.	1.0	30
50	A Molecular Docking and Dynamics Approach to Screen Potent Inhibitors Against Fosfomycin Resistant Enzyme in Clinical Klebsiella pneumoniae. Journal of Cellular Biochemistry, 2017, 118, 4088-4094.	1.2	29
51	Network analysis of transcriptomics data for the prediction and prioritization of membrane-associated biomarkers for idiopathic pulmonary fibrosis (IPF) by bioinformatics approach. Advances in Protein Chemistry and Structural Biology, 2021, 123, 241-273.	1.0	29
52	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. Journal of Biomolecular Structure and Dynamics, 2016, 34, 29-41.	2.0	28
53	Gliptins in managing diabetes - Reviewing computational strategy. Life Sciences, 2016, 166, 108-120.	2.0	27
54	In silico profiling and structural insights of missense mutations in RET protein kinase domain by molecular dynamics and docking approach. Molecular BioSystems, 2014, 10, 421-436.	2.9	25

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55	Draft genome of a hypervirulent <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> with novel sequence type ST2320 isolated from a chronic liver disease patient. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 9, 30-31.	0.9	25
56	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.	1.4	24
57	Implication of salt stress induces changes in pigment production, antioxidant enzyme activity, and qRT-PCR expression of genes involved in the biosynthetic pathway of <i>Bixa orellana</i> L.. <i>Functional and Integrative Genomics</i> , 2019, 19, 565-574.	1.4	24
58	Enzyme therapy: a forerunner in catalyzing a healthy society?. <i>Expert Opinion on Biological Therapy</i> , 2020, 20, 1151-1174.	1.4	24
59	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.	1.0	23
60	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.	0.9	23
61	A New Insight into Structural and Functional Impact of Single-Nucleotide Polymorphisms in PTEN Gene. <i>Cell Biochemistry and Biophysics</i> , 2013, 66, 249-263.	0.9	22
62	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.	1.0	22
63	Effect of UV radiation and its implications on carotenoid pathway in <i>Bixa orellana</i> L.. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2017, 176, 136-144.	1.7	22
64	Bioinformatics classification of mutations in patients with Mucopolysaccharidosis IIIA. <i>Metabolic Brain Disease</i> , 2019, 34, 1577-1594.	1.4	21
65	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.	1.0	21
66	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.	3.9	20
67	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.	1.6	20
68	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.	3.9	19
69	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.	1.0	19
70	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.	2.6	18
71	Identifying a Carotenoid Cleavage Dioxygenase 4a Gene and Its Efficient Agrobacterium-Mediated Genetic Transformation in <i>Bixa orellana</i> L.. <i>Applied Biochemistry and Biotechnology</i> , 2016, 179, 697-714.	1.4	18
72	Integrated approach on azo dyes degradation using laccase enzyme and Cu nanoparticle. <i>SN Applied Sciences</i> , 2021, 3, 1.	1.5	18

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73	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, 607-612.	2.5	17
74	Recent Trends of Polymer Mediated Liposomal Gene Delivery System. <i>BioMed Research International</i> , 2014, 2014, 1-15.	0.9	17
75	Personalized Pharmacoperones for Lysosomal Storage Disorder. <i>Advances in Protein Chemistry and Structural Biology</i> , 2016, 102, 225-265.	1.0	17
76	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.	3.6	17
77	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.	0.8	16
78	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.	2.3	16
79	Mutational landscape of K-Ras substitutions at 12th position-a systematic molecular dynamics approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 1571-1585.	2.0	16
80	An integrative analysis to distinguish between emphysema (EML) and alpha-1 antitrypsin deficiency-related emphysema (ADL)â€™A systems biology approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 127, 315-342.	1.0	16
81	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.	1.1	16
82	Sirtuins Family- Recent Development as a Drug Target for Aging, Metabolism, and Age Related Diseases. <i>Current Drug Targets</i> , 2013, 14, 666-675.	1.0	16
83	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.	2.0	15
84	Probing the Proteinâ€™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.	1.0	15
85	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.	1.1	15
86	Predicting the Impact of Single-Nucleotide Polymorphisms in CDK2â€™Flavopiridol Complex by Molecular Dynamics Analysis. <i>Cell Biochemistry and Biophysics</i> , 2013, 66, 681-695.	0.9	14
87	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.	1.0	14
88	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.	1.4	14
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.	3.9	14
90	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.	2.0	14

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91	First hybrid complete genome of <i>Aeromonas veronii</i> reveals chromosome-mediated novel structural variant mcr-3.30 from a human clinical sample. <i>Access Microbiology</i> , 2020, 2, acmi000103.	0.2	14
92	In Silico Analysis of Prion Protein Mutants: A Comparative Study by Molecular Dynamics Approach. <i>Cell Biochemistry and Biophysics</i> , 2013, 67, 1307-1318.	0.9	13
93	Glutathione-responsive nano-transporter-mediated siRNA delivery: silencing the mRNA expression of Ras. <i>Protoplasma</i> , 2013, 250, 787-792.	1.0	13
94	In silico analysis of structural and functional consequences in p16INK4A by deleterious nsSNPs associated CDKN2A gene in malignant melanoma. <i>Biochimie</i> , 2008, 90, 1523-1529.	1.3	12
95	Impact of single nucleotide polymorphisms in HBB gene causing haemoglobinopathies: in silico analysis. <i>New Biotechnology</i> , 2009, 25, 214-219.	2.4	12
96	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, 1265-1281.	1.4	12
97	Impact of I30T and I30M substitution in MPZ gene associated with Dejerineâ€“Sottas syndrome type B (DSSB): A molecular modeling and dynamics. <i>Journal of Theoretical Biology</i> , 2015, 382, 23-33.	0.8	12
98	Molecular Modeling and Dynamic Simulation of <i>Arabidopsis Thaliana</i> Carotenoid Cleavage Dioxygenase Gene: A Comparison with <i>Bixa orellana</i> and <i>Crocus Sativus</i> . <i>Journal of Cellular Biochemistry</i> , 2017, 118, 2712-2721.	1.2	12
99	Zika: How safe is India?. <i>Infectious Diseases of Poverty</i> , 2017, 6, 37.	1.5	12
100	Computational and modeling approaches to understand the impact of the Fabry's 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.	1.0	12
101	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.	1.0	12
102	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.	1.2	12
103	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.	2.5	12
104	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, 320-346.	2.2	11
105	Computational Resources for Predicting Proteinâ€“Protein Interactions. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018, 110, 251-275.	1.0	11
106	Investigating the Influence of Hotspot Mutations in Proteinâ€“Protein Interaction of IDH1 Homodimer Protein: A Computational Approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018, 111, 243-261.	1.0	11
107	Exploring the codon patterns between CCD and NCED genes among different plant species. <i>Computers in Biology and Medicine</i> , 2019, 114, 103449.	3.9	11
108	Computational Methods to Work as First-Pass Filter in Deleterious SNP Analysis of Alkaptonuria. <i>Scientific World Journal, The</i> , 2012, 2012, 1-9.	0.8	10

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109	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.	1.0	10
110	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.	2.0	10
111	Elucidating the Mutational Landscape in Hepatocyte Nuclear Factor 1 β (HNF1B) by Computational Approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2017, 107, 283-306.	1.0	10
112	An Integrated Computational Framework to Assess the Mutational Landscape of α -L-Galactosidase Gene. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 555-565.	1.2	10
113	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, 5543.	1.7	10
114	Novel biomarker for prostate cancer diagnosis by MRS. <i>Frontiers in Bioscience - Landmark</i> , 2014, 19, 1186.	3.0	9
115	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.	1.2	9
116	In vitro flowering in <i>Oldenlandia umbellata</i> L.. <i>Journal of Ayurveda and Integrative Medicine</i> , 2018, 9, 99-103.	0.9	9
117	Investigating the role of microRNA-27a gene polymorphisms and its interactive effect with risk factors in gastrointestinal cancers. <i>Heliyon</i> , 2020, 6, e03565.	1.4	9
118	Kerala, India's Front Runner in Novel Coronavirus Disease (COVID-19). <i>Frontiers in Medicine</i> , 2020, 7, 355.	1.2	9
119	LSHGD: A database for human leprosy susceptible genes. <i>Genomics</i> , 2012, 100, 162-166.	1.3	8
120	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, 939-956.	0.9	8
121	Computational pipeline to identify and characterize functional mutations in ornithine transcarbamylase deficiency. <i>3 Biotech</i> , 2014, 4, 621-634.	1.1	8
122	Analysis of interactions of clinical mutants of catalase-peroxidase (KatG) responsible for isoniazid resistance in <i>Mycobacterium tuberculosis</i> with derivatives of isoniazid. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 11, 57-67.	0.9	8
123	A computational model to predict the structural and functional consequences of missense mutations in O6-methylguanine DNA methyltransferase. <i>Advances in Protein Chemistry and Structural Biology</i> , 2019, 115, 351-369.	1.0	8
124	Bladder neoplasms and NF- κ B: an unfathomed association. <i>Expert Review of Molecular Diagnostics</i> , 2020, 20, 497-508.	1.5	8
125	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.	2.0	8
126	Comparison of potential inhibitors and targeting fat mass and obesity-associated protein causing diabetes through docking and molecular dynamics strategies. <i>Journal of Cellular Biochemistry</i> , 2021, 122, 1625-1638.	1.2	8

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127	Crucial Protein Based Drug Targets and Potential Inhibitors for Osteoporosis: New Hope and Possibilities. <i>Current Drug Targets</i> , 2013, 14, 1707-1713.	1.0	8
128	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, 3517-3527.	0.8	7
129	Disease-Causing Mutation in Extracellular and Intracellular Domain of FGFR1 Protein: Computational Approach. <i>Applied Biochemistry and Biotechnology</i> , 2013, 169, 1659-1671.	1.4	7
130	Can the chemotherapeutic agents perform anticancer activity through miRNA expression regulation? Proposing a new hypothesis. <i>Protoplasma</i> , 2015, 252, 1603-1610.	1.0	7
131	Interaction of Catechu Dye with DNA: Spectroscopic and In Silico Approach. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2016, 35, 195-210.	0.4	7
132	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.	1.0	7
133	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.	1.0	7
134	Whole-exome sequencing analysis of NSCLC reveals the pathogenic missense variants from cancer-associated genes. <i>Computers in Biology and Medicine</i> , 2022, 148, 105701.	3.9	7
135	Analysis of binding residues between scorpion neurotoxins and D2 dopamine receptor: A computational docking study. <i>Computers in Biology and Medicine</i> , 2008, 38, 1056-1067.	3.9	6
136	In Silico Searching for Disease-Associated Functional DNA Variants. <i>Methods in Molecular Biology</i> , 2011, 760, 239-250.	0.4	6
137	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, 103-115.	2.2	6
138	Disruption of Mitochondrial Complexes in Cancer Stem Cells Through Nano-based Drug Delivery: A Promising Mitochondrial Medicine. <i>Cell Biochemistry and Biophysics</i> , 2013, 67, 1075-1079.	0.9	6
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