Babajan Banaganapalli

List of Publications by Year
in descending order

83	868	643344 15	721071 23
papers	citations	h-index	g-index

85	85	85	1300
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic association study of NOD2 and IL23R amino acid substitution polymorphisms in Saudi Inflammatory Bowel Disease patients. Journal of King Saud University - Science, 2022, 34, 101726.	1.6	3
2	Integrative system biology and mathematical modeling of genetic networks identifies shared biomarkers for obesity and diabetes. Mathematical Biosciences and Engineering, 2022, 19, 2310-2329.	1.0	9
3	Identifying significant genes and functionally enriched pathways in familial hypercholesterolemia using integrated gene co-expression network analysis. Saudi Journal of Biological Sciences, 2022, 29, 3287-3299.	1.8	4
4	Molecular profiling of melanocortin 4 receptor variants and agouti-related peptide interactions in morbid obese phenotype: a novel paradigm from molecular docking and dynamics simulations. Biologia (Poland), 2022, 77, 1481.	0.8	2
5	Genome-Wide Association Study-Guided Exome Rare Variant Burden Analysis Identifies IL1R1 and CD3E as Potential Autoimmunity Risk Genes for Celiac Disease. Frontiers in Pediatrics, 2022, 10, 837957.	0.9	6
6	Integrative global co-expression analysis identifies key microRNA-target gene networks as key blood biomarkers for obesity. Minerva Medica, 2022, 113, .	0.3	5
7	Identification and functional characterization of 2 Rare LDLR stop gain variants (p.C231* and p.R744*) in Saudi familial hypercholesterolemia patients. Panminerva Medica, 2022, , .	0.2	3
8	Identification of novel mycobacterium tuberculosis leucyl-tRNA synthetase inhibitor using a knowledge-based computational screening approach. Journal of King Saud University - Science, 2022, 34, 102032.	1.6	3
9	Molecular profiling of lamellar ichthyosis pathogenic missense mutations on the structural and stability aspects of TGM1 protein. Journal of Biomolecular Structure and Dynamics, 2021, 39, 4962-4972.	2.0	6
10	Molecular modelling and dynamic simulations of sequestosome 1 (SQSTM1) missense mutations linked to Paget disease of bone. Journal of Biomolecular Structure and Dynamics, 2021, 39, 2873-2884.	2.0	8
11	Structural and Molecular Interaction Studies on Familial Hypercholesterolemia Causative PCSK9 Functional Domain Mutations Reveals Binding Affinity Alterations with LDLR. International Journal of Peptide Research and Therapeutics, 2021, 27, 719-733.	0.9	6
12	Molecular differential analysis of uterine leiomyomas and leiomyosarcomas through weighted gene network and pathway tracing approaches. Systems Biology in Reproductive Medicine, 2021, 67, 209-220.	1.0	7
13	Identification of a Rare Exon 19 Skipping Mutation in ALMS1 Gene in AlstrÃ¶m Syndrome Patients From Two Unrelated Saudi Families. Frontiers in Pediatrics, 2021, 9, 652011.	0.9	8
14	TagSNP approach for HLA risk allele genotyping of Saudi celiac disease patients: effectiveness and pitfalls. Bioscience Reports, 2021, 41, .	1.1	1
15	Saudi Familial Hypercholesterolemia Patients With Rare LDLR Stop Gain Variant Showed Variable Clinical Phenotype and Resistance to Multiple Drug Regimen. Frontiers in Medicine, 2021, 8, 694668.	1.2	8
16	Multilevel systems biology analysis of lung transcriptomics data identifies key miRNAs and potential miRNA target genes for SARS-CoV-2 infection. Computers in Biology and Medicine, 2021, 135, 104570.	3.9	31
17	Novel MYO1D Missense Variant Identified Through Whole Exome Sequencing and Computational Biology Analysis Expands the Spectrum of Causal Genes of Laterality Defects. Frontiers in Medicine, 2021, 8, 724826.	1.2	6
18	Transcriptome-Based Molecular Networks Uncovered Interplay Between Druggable Genes of CD8+ T Cells and Changes in Immune Cell Landscape in Patients With Pulmonary Tuberculosis. Frontiers in Medicine, 2021, 8, 812857.	1.2	3

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19	Molecular modelling and dynamics of CA2 missense mutations causative to carbonic anhydrase 2 deficiency syndrome. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4067-4080.	2.0	20
20	Whole exome sequencing identifies rare biallelic ALMS1 missense and stop gain mutations in familial AlstrÃ¶m syndrome patients. Saudi Journal of Biological Sciences, 2020, 27, 271-278.	1.8	11
21	Exome sequencing and metabolomic analysis of a chronic kidney disease and hearing loss patient family revealed RMND1 mutation induced sphingolipid metabolism defects. Saudi Journal of Biological Sciences, 2020, 27, 324-334.	1.8	13
22	Myocardial infarction biomarker discovery with integrated gene expression, pathways and biological networks analysis. Genomics, 2020, 112, 5072-5085.	1.3	17
23	Exploring celiac disease candidate pathways by global gene expression profiling and gene network cluster analysis. Scientific Reports, 2020, 10, 16290.	1.6	18
24	Low resolution protein mapping and KB-R7943 drug-protein molecular interaction analysis of long-QT syndrome linked KCNH2 mutations. International Journal of Transgender Health, 2020, 13, 183-193.	1.1	3
25	Whole exome sequencing of a Saudi family and systems biology analysis identifies CPED1 as a putative causative gene to Celiac Disease. Saudi Journal of Biological Sciences, 2020, 27, 1494-1502.	1.8	8
26	Unraveling the role of salt-sensitivity genes in obesity with integrated network biology and co-expression analysis. PLoS ONE, 2020, 15, e0228400.	1.1	9
27	Molecular insights into the coding region mutations of lowâ€density lipoprotein receptor adaptor protein 1 (LDLRAP1) linked to familial hypercholesterolemia. Journal of Gene Medicine, 2020, 22, e3176.	1.4	12
28	Association of four missense SNPs with preeclampsia in Saudi women. Saudi Journal of Medicine and Medical Sciences, 2020, 8, 174.	0.3	1
29	Assessing theÂrole ofÂserum prolactin levels and coding region somatic mutations ofÂtheÂprolactin gene in Saudi uterine leiomyoma patients. Archives of Medical Science, 2020, , .	0.4	2
30	Title is missing!. , 2020, 15, e0228400.		0
31	Title is missing!. , 2020, 15, e0228400.		0
32	Title is missing!. , 2020, 15, e0228400.		0
33	Title is missing!. , 2020, 15, e0228400.		0
34	Molecular designing, virtual screening and docking study of novel curcumin analogue as mutation (S769L and K846R) selective inhibitor for EGFR. Saudi Journal of Biological Sciences, 2019, 26, 439-448.	1.8	20
35	The genetic association study of TP53 polymorphisms in Saudi obese patients. Saudi Journal of Biological Sciences, 2019, 26, 1338-1343.	1.8	7
36	Identification of key regulatory genes connected to NF-Î¹B family of proteins in visceral adipose tissues using gene expression and weighted protein interaction network. PLoS ONE, 2019, 14, e0214337.	1.1	23

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37	Computational Molecular Phenotypic Analysis of PTPN22 (W620R), IL6R (D358A), and TYK2 (P1104A) Gene Mutations of Rheumatoid Arthritis. Frontiers in Genetics, 2019, 10, 168.	1.1	18
38	Exome Analysis Identifies a Novel Compound Heterozygous Alteration in TGM1 Gene Leading to Lamellar Ichthyosis in a Child From Saudi Arabia: Case Presentation. Frontiers in Pediatrics, 2019, 7, 44.	0.9	7
39	Introduction to Biological Databases. , 2019, , 19-27.		0
40	In Silico PCR. , 2019, , 355-371.		2
41	Introduction to Bioinformatics. , 2019, , 1-18.		0
42	Drug Discovery: Concepts and Approaches. , 2019, , 319-334.		0
43	Tools and Methods in Analysis of Complex Sequences. , 2019, , 155-167.		0
44	Salvadora persica L.: A Medicinal Plant with Multifaceted Role in Maintaining Oral Hygiene. , 2019, , 353-371.		2
45	Protective Role of Medicinal Herb Anethum Graveolens (Dill) Against Various Human Diseases and Metabolic Disorders. , 2019, , 181-194.		3
46	ACE insertion/deletion genetic polymorphism, serum ACE levels and high dietary salt intake influence the risk of obesity development among the Saudi adult population. JRAAS - Journal of the Renin-Angiotensin-Aldosterone System, 2019, 20, 147032031987094.	1.0	9
47	Dissecting the Role of NF-Îºb Protein Family and Its Regulators in Rheumatoid Arthritis Using Weighted Gene Co-Expression Network. Frontiers in Genetics, 2019, 10, 1163.	1.1	18
48	Finding a Needle in a Haystack: Variant Effect Predictor (VEP) Prioritizes Disease Causative Variants from Millions of Neutral Ones. , 2019, , 85-104.		1
49	Genetic Association from RFLPs to Millions of Variant Markers: Unravelling the Genetic Complexity of Diseases. , 2019, , 9-23.		0
50	Understanding the Regulatory Features of Co-regulated Genes Using Distant Regulatory Elements (DiRE) Genomic Tool in Health and Disease. , 2019, , 283-299.		0
51	Driving Forces of Bioinformatics. , 2019, , 1-8.		1
52	Diagnostic Revolution Post-Human Genome Sequence Project: High-Throughput Technologies and Bioinformatics. , 2019, , 25-38.		0
53	In Silico Approach to Investigate the Structural and Functional Attributes of Familial Hypercholesterolemia Variants Reported in the Saudi Population. Journal of Computational Biology, 2018, 25, 170-181.	0.8	4
54	Expanded Somatic Mutation Spectrum of MED12 Gene in Uterine Leiomyomas of Saudi Arabian Women. Frontiers in Genetics, 2018, 9, 552.	1.1	18

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55	Protein phenotype diagnosis of autosomal dominant calmodulin mutations causing irregular heart rhythms. Journal of Cellular Biochemistry, 2018, 119, 8233-8248.	1.2	14
56	Computational Protein Phenotype Characterization of IL10RA Mutations Causative to Early Onset Inflammatory Bowel Disease (IBD). Frontiers in Genetics, 2018, 9, 146.	1.1	14
57	Targeted Molecular Sequencing Revealed Allelic Heterogeneity of BRAF and PTPN11 Genes among Arab Noonan Syndrome Patients. Russian Journal of Genetics, 2018, 54, 975-984.	0.2	0
58	Ursolic acid rich Ocimum sanctum L leaf extract loaded nanostructured lipid carriers ameliorate adjuvant induced arthritis in rats by inhibition of COX-1, COX-2, TNF-Î± and IL-1: Pharmacological and docking studies. PLoS ONE, 2018, 13, e0193451.	1.1	39
59	Comprehensive Computational Analysis of GWAS Loci Identifies CCR2 as a Candidate Gene for Celiac Disease Pathogenesis. Journal of Cellular Biochemistry, 2017, 118, 2193-2207.	1.2	17
60	Computational Analysis of Breast Cancer GWAS Loci Identifies the Putative Deleterious Effect of STXBP4 and ZNF404 Gene Variants. Journal of Cellular Biochemistry, 2017, 118, 4296-4307.	1.2	11
61	Induced pluripotent stem cell modelling of HLHS underlines the contribution of dysfunctional NOTCH signalling to impaired cardiogenesis. Human Molecular Genetics, 2017, 26, 3031-3045.	1.4	56
62	Replication of GWAS loci revealed the moderate effect of TNRC6B locus on susceptibility of Saudi women to develop uterine leiomyomas. Journal of Obstetrics and Gynaecology Research, 2017, 43, 330-338.	0.6	18
63	Distribution of <scp>CYP</scp>2C8 and <scp>CYP</scp>2C9 amino acid substitution alleles in South Indian diabetes patients: A genotypic and computational protein phenotype study. Clinical and Experimental Pharmacology and Physiology, 2017, 44, 1171-1179.	0.9	8
64	Whole exome sequencing of a consanguineous family identifies the possible modifying effect of a globally rare AK5 allelic variant in celiac disease development among Saudi patients. PLoS ONE, 2017, 12, e0176664.	1.1	14
65	A Computational Protein Phenotype Prediction Approach to Analyze the Deleterious Mutations of Human MED12 Gene. Journal of Cellular Biochemistry, 2016, 117, 2023-2035.	1.2	27
66	Effect of Silver Nanoparticles Against the Formation of Biofilm by Pseudomonas aeruginosa an In silico Approach. Applied Biochemistry and Biotechnology, 2016, 180, 426-437.	1.4	27
67	Replication of GWAS Coding SNPs Implicates MMEL1 as a Potential Susceptibility Locus among Saudi Arabian Celiac Disease Patients. Disease Markers, 2015, 2015, 1-6.	0.6	11
68	In-Silico Analysis of Inflammatory Bowel Disease (IBD) GWAS Loci to Novel Connections. PLoS ONE, 2015, 10, e0119420.	1.1	23
69	Molecular Modeling and Docking Studies of O-Succinylbenzoate Synthase of M. tuberculosisâ€"a Potential Target for Antituberculosis Drug Design. Applied Biochemistry and Biotechnology, 2014, 172, 1407-1432.	1.4	13
70	Evidence for the presence of somatic mitochondrial DNA mutations in right atrial appendage tissues of coronary artery disease patients. Molecular Genetics and Genomics, 2014, 289, 533-540.	1.0	10
71	Structural and Functional Characterization of Pathogenic Non- Synonymous Genetic Mutations of Human Insulin-Degrading Enzyme by In Silico Methods. CNS and Neurological Disorders - Drug Targets, 2014, 13, 517-532.	0.8	11
72	Synthesis and Biological Activity of New Resveratrol Derivative and Molecular Docking: Dynamics Studies on NFkB. Applied Biochemistry and Biotechnology, 2013, 171, 1639-1657.	1.4	10

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73	Mycobacterial Hsp65 potentially cross-reacts with autoantibodies of diabetes sera and also induces (in vitro) cytokine responses relevant to diabetes mellitus. Molecular BioSystems, 2013, 9, 2932.	2.9	5
74	Experimental and Computational Studies on Newly Synthesized Resveratrol Derivative: A New Method for Cancer Chemoprevention and Therapeutics?. OMICS A Journal of Integrative Biology, 2013, 17, 568-583.	1.0	11
75	Design and evaluation of new chemotherapeutics of aloe-emodin (AE) against the deadly cancer disease: an in silico study. Journal of Chemical Biology, 2013, 6, 141-153.	2.2	5
76	Synthesis and evaluation of resveratrol derivatives as new chemical entities for cancer. Journal of Molecular Graphics and Modelling, 2013, 41, 43-54.	1.3	19
77	Molecular characterization of Mtb-OMP decarboxylase by modeling, docking and dynamic studies. Interdisciplinary Sciences, Computational Life Sciences, 2012, 4, 142-152.	2.2	4
78	Comprehensive structural and functional characterization of Mycobacterium tuberculosis UDP-NAG enolpyruvyl transferase (Mtb-MurA) and prediction of its accurate binding affinities with inhibitors. Interdisciplinary Sciences, Computational Life Sciences, 2011, 3, 204-216.	2.2	21
79	Probing ligand binding modes of Mycobacterium tuberculosis MurC ligase by molecular modeling, dynamics simulation and docking. Journal of Molecular Modeling, 2010, 16, 77-85.	0.8	20
80	Exploring the molecular basis for selective binding of Mycobacterium tuberculosis Asp kinase toward its natural substrates and feedback inhibitors: A docking and molecular dynamics study. Journal of Molecular Modeling, 2010, 16, 1357-1367.	0.8	30
81	Novel Derivative of Benzofuran Induces Cell Death Mostly by G2/M Cell Cycle Arrest through p53-dependent Pathway but Partially by Inhibition of NF-ÎºB. Journal of Biological Chemistry, 2010, 285, 22318-22327.	1.6	36
82	Inhibiting TRAF2-mediated Activation of NF-ÎºB Facilitates Induction of AP-1. Journal of Biological Chemistry, 2010, 285, 11617-11627.	1.6	27
83	Insights from Streptococcus pneumoniae glucose kinase structural model. Bioinformation, 2009, 3, 308-310.	0.2	1