Ramu Elango

List of Publications by Year in descending order

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71	1,469	471509	345221
papers	citations	17 h-index	36 g-index

73	73	73	1650
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.	3.5	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.	1.9	9
3	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.	1.9	6
4	Integrative global co-expression analysis identifies key microRNA-target gene networks as key blood biomarkers for obesity. Minerva Medica, 2022, 113, .	0.9	5
5	Exome Sequencing Identifies the Extremely Rare ITGAV and FN1 Variants in Early Onset Inflammatory Bowel Disease Patients. Frontiers in Pediatrics, 2022, 10, .	1.9	3
6	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.	3.5	6
7	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.	3.5	8
8	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.	2.1	7
9	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.	1.9	8
10	TagSNP approach for HLA risk allele genotyping of Saudi celiac disease patients: effectiveness and pitfalls. Bioscience Reports, 2021, 41, .	2.4	1
11	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.	2.6	8
12	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.	7.0	31
13	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.	2.6	6
14	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.	2.6	3
15	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.	3.5	20
16	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.	3.8	11
17	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.	3.8	13
18	Myocardial infarction biomarker discovery with integrated gene expression, pathways and biological networks analysis. Genomics, 2020, 112, 5072-5085.	2.9	17

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19	Exploring celiac disease candidate pathways by global gene expression profiling and gene network cluster analysis. Scientific Reports, 2020, 10, 16290.	3.3	18
20	Identification of Causative Variants Contributing to Nonsyndromic Orofacial Clefts Using Whole-Exome Sequencing in a Saudi Family. Genetic Testing and Molecular Biomarkers, 2020, 24, 723-731.	0.7	8
21	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.	3.8	8
22	Unraveling the role of salt-sensitivity genes in obesity with integrated network biology and co-expression analysis. PLoS ONE, 2020, 15, e0228400.	2.5	9
23	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.	2.8	12
24	Association of four missense SNPs with preeclampsia in Saudi women. Saudi Journal of Medicine and Medical Sciences, 2020, 8, 174.	0.8	1
25	Assessing theÂrole ofÂserum prolactin levels and coding region somatic mutations ofÂtheÂprolactin gene in Saudi uterine leiomyoma patients. Archives of Medical Science, 2020, , .	0.9	2
26	Title is missing!. , 2020, 15, e0228400.		0
27	Title is missing!. , 2020, 15, e0228400.		0
28	Title is missing!. , 2020, 15, e0228400.		0
29	Title is missing!. , 2020, 15, e0228400.		0
30	Rapid detection of type II diabetes mellitus in Saudi patients via simultaneous screening of multiple SNPs. Biotechnology and Biotechnological Equipment, 2019, 33, 1319-1326.	1.3	1
31	Identification of key regulatory genes connected to NF-Î°B family of proteins in visceral adipose tissues using gene expression and weighted protein interaction network. PLoS ONE, 2019, 14, e0214337.	2.5	23
32	Essentials of Bioinformatics, Volume I. , 2019, , .		8
33	Introduction to Biological Databases. , 2019, , 19-27.		0
34	Molecular Docking. , 2019, , 335-353.		3
35	In Silico PCR. , 2019, , 355-371.		2
36	Tools and Methods in Analysis of Complex Sequences. , 2019, , 155-167.		0

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37	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.	2.3	18
38	Finding a Needle in a Haystack: Variant Effect Predictor (VEP) Prioritizes Disease Causative Variants from Millions of Neutral Ones. , 2019, , 85-104.		1
39	Genetic Association from RFLPs to Millions of Variant Markers: Unravelling the Genetic Complexity of Diseases. , 2019, , 9-23.		0
40	Understanding the Regulatory Features of Co-regulated Genes Using Distant Regulatory Elements (DiRE) Genomic Tool in Health and Disease. , 2019, , 283-299.		0
41	Driving Forces of Bioinformatics. , 2019, , 1-8.		1
42	Diagnostic Revolution Post-Human Genome Sequence Project: High-Throughput Technologies and Bioinformatics. , 2019, , 25-38.		0
43	iPSC modeling of severe aplastic anemia reveals impaired differentiation and telomere shortening in blood progenitors. Cell Death and Disease, 2018, 9, 128.	6.3	26
44	Expanded Somatic Mutation Spectrum of MED12 Gene in Uterine Leiomyomas of Saudi Arabian Women. Frontiers in Genetics, 2018, 9, 552.	2.3	18
45	Protein phenotype diagnosis of autosomal dominant calmodulin mutations causing irregular heart rhythms. Journal of Cellular Biochemistry, 2018, 119, 8233-8248.	2.6	14
46	Targeted Molecular Sequencing Revealed Allelic Heterogeneity of BRAF and PTPN11 Genes among Arab Noonan Syndrome Patients. Russian Journal of Genetics, 2018, 54, 975-984.	0.6	0
47	Comprehensive Computational Analysis of GWAS Loci Identifies CCR2 as a Candidate Gene for Celiac Disease Pathogenesis. Journal of Cellular Biochemistry, 2017, 118, 2193-2207.	2.6	17
48	Induced pluripotent stem cell modelling of HLHS underlines the contribution of dysfunctional NOTCH signalling to impaired cardiogenesis. Human Molecular Genetics, 2017, 26, 3031-3045.	2.9	56
49	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.	1.3	18
50	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.	1.9	8
51	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.	2.5	14
52	A Computational Protein Phenotype Prediction Approach to Analyze the Deleterious Mutations of Human MED12 Gene. Journal of Cellular Biochemistry, 2016, 117, 2023-2035.	2.6	27
53	Replication of GWAS Coding SNPs Implicates MMEL1 as a Potential Susceptibility Locus among Saudi Arabian Celiac Disease Patients. Disease Markers, 2015, 2015, 1-6.	1.3	11
54	In-Silico Analysis of Inflammatory Bowel Disease (IBD) GWAS Loci to Novel Connections. PLoS ONE, 2015, 10, e0119420.	2.5	23

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55	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.	2.1	10
56	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.	1.4	11
57	LRRK2 Gly2019Ser penetrance in Arabâ€“Berber patients from Tunisia: a case-control genetic study. Lancet Neurology, The, 2008, 7, 591-594.	10.2	172
58	A founding LRRK2 haplotype shared by Tunisian, US, European and Middle Eastern families with Parkinson's disease. Parkinsonism and Related Disorders, 2008, 14, 77-80.	2.2	33
59	PINK1 mutations and parkinsonism. Neurology, 2008, 71, 896-902.	1.1	51
60	Screening for Lrrk2 G2019S and clinical comparison of Tunisian and North American Caucasian Parkinson's disease families. Movement Disorders, 2007, 22, 55-61.	3.9	100
61	Divergent genetic and epigenetic post-zygotic isolation mechanisms in Mus and Peromyscus. Journal of Evolutionary Biology, 2004, 17, 453-460.	1.7	29
62	Fine mapping of Ath6, a quantitative trait locus for atherosclerosis in mice. Mammalian Genome, 2001, 12, 495-500.	2.2	24
63	Generation and mapping of Mus spretus strain-specific markers for rapid genomic scanning. Mammalian Genome, 1996, 7, 340-343.	2.2	11
64	Fragile X syndrome among children with mental retardation. Indian Journal of Pediatrics, 1996, 63, 533-538.	0.8	12
65	Genetic mapping of a pulmonary adenoma resistance locus (Par1) in mouse. Nature Genetics, 1996, 12, 455-457.	21.4	64
66	Toward the construction of integrated physical and genetic maps of the mouse genome using interspersed repetitive sequence PCR (IRS-PCR) genomics.. Genome Research, 1996, 6, 290-299.	5.5	18
67	Efficient high-resolution genetic mapping of mouse interspersed repetitive sequence PCR products, toward integrated genetic and physical mapping of the mouse genome.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 5302-5306.	7.1	36
68	Sequential strategy to identify a susceptibility gene for schizophrenia: Report of potential linkage on chromosome 22q12â€q13.1: Part 1. American Journal of Medical Genetics Part A, 1994, 54, 36-43.	2.4	356
69	Report from the Maryland epidemiology schizophrenia linkage study: No evidence for linkage between schizophrenia and a number of candidate and other genomic regions using a complex dominant model. American Journal of Medical Genetics Part A, 1994, 54, 345-353.	2.4	27
70	Exclusion of linkage between schizophrenia and some candidate genes. Schizophrenia Research, 1993, 9, 123.	2.0	0
71	Complex Inheritance of Rare Missense Variants in PAK2, TAP2, and PLCL1 Genes in a Consanguineous Arab Family With Multiple Autoimmune Diseases Including Celiac Disease. Frontiers in Pediatrics, 0, 10, .	1.9	3