Shamsudheen Karuthedath Vellarikkal

List of Publications by Year
in descending order

67 papers	1,711 citations	430874 18 h-index	345221 36 g-index
71 all docs	71 docs citations	71 times ranked	3584 citing authors

#	Article	IF	Citations
1	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	27.8	537
2	Single-Cell Analysis of the Normal Mouse Aorta Reveals Functionally Distinct Endothelial Cell Populations. Circulation, 2019, 140, 147-163.	1.6	231
3	Dynamic Expression of Long Non-Coding RNAs (lncRNAs) in Adult Zebrafish. PLoS ONE, 2013, 8, e83616.	2.5	92
4	Deep learning enables genetic analysis of the human thoracic aorta. Nature Genetics, 2022, 54, 40-51.	21.4	90
5	Comparative Whole-Genome Analysis of Clinical Isolates Reveals Characteristic Architecture of Mycobacterium tuberculosis Pangenome. PLoS ONE, 2015, 10, e0122979.	2.5	49
6	Human 45,X Fibroblast Transcriptome Reveals Distinct Differentially Expressed Genes Including Long Noncoding RNAs Potentially Associated with the Pathophysiology of Turner Syndrome. PLoS ONE, 2014, 9, e100076.	2.5	44
7	RNA sequencing of db/db mice liver identifies lncRNA H19 as a key regulator of gluconeogenesis and hepatic glucose output. Scientific Reports, 2017, 7, 8312.	3.3	42
8	Saliva microbiome in primary SjÃ¶grenâ€™s syndrome reveals distinct set of diseaseâ€associated microbes. Oral Diseases, 2020, 26, 295-301.	3.0	39
9	LncRNA VEAL2 regulates PRKCB2 to modulate endothelial permeability in diabetic retinopathy. EMBO Journal, 2021, 40, e107134.	7.8	32
10	Large scale changes in the transcriptome of Eisenia fetida during regeneration. PLoS ONE, 2018, 13, e0204234.	2.5	31
11	Genomics of rare genetic diseasesâ€”experiences from India. Human Genomics, 2019, 13, 52.	2.9	30
12	mit-o-matic: A Comprehensive Computational Pipeline for Clinical Evaluation of Mitochondrial Variations from Next-Generation Sequencing Datasets. Human Mutation, 2015, 36, 419-424.	2.5	26
13	Screening Currency Notes for Microbial Pathogens and Antibiotic Resistance Genes Using a Shotgun Metagenomic Approach. PLoS ONE, 2015, 10, e0128711.	2.5	25
14	Aptamer-Assisted Detection of the Altered Expression of Estrogen Receptor Alpha in Human Breast Cancer. PLoS ONE, 2016, 11, e0153001.	2.5	25
15	Pharmacogenetic landscape of DPYD variants in south Asian populations by integration of genome-scale data. Pharmacogenomics, 2018, 19, 227-241.	1.3	25
16	Chamber Specific Gene Expression Landscape of the Zebrafish Heart. PLoS ONE, 2016, 11, e0147823.	2.5	24
17	Barcoding of Asian seabass across its geographic range provides evidence for its bifurcation into two distinct species. Frontiers in Marine Science, 2014, 1, .	2.5	21
18	SAGE: a comprehensive resource of genetic variants integrating South Asian whole genomes and exomes. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-10.	3.0	20

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19	A genome-wide map of circular RNAs in adult zebrafish. Scientific Reports, 2019, 9, 3432.	3.3	19
20	A new strain of white spot syndrome virus affecting Litopenaeus vannamei in Indian shrimp farms. Journal of Fish Diseases, 2018, 41, 1129-1146.	1.9	18
21	Application of whole exome sequencing in elucidating the phenotype and genotype spectrum of junctional epidermolysis bullosa: A preliminary experience of a tertiary care centre in India. Journal of Dermatological Science, 2017, 86, 30-36.	1.9	16
22	Genotypeâ€“Phenotype Correlations of Dystrophic Epidermolysis Bullosa in India: Experience from a Tertiary Care Centre. Acta Dermato-Venereologica, 2018, 98, 873-879.	1.3	16
23	Maternal vitamin B12 deficiency in rats alters DNA methylation in metabolically important genes in their offspring. Molecular and Cellular Biochemistry, 2020, 468, 83-96.	3.1	15
24	Loss of function mutation in the P2X7, a ligand-gated ion channel gene associated with hypertrophic cardiomyopathy. Purinergic Signalling, 2019, 15, 205-210.	2.2	13
25	Role of Tmem163 in zinc-regulated insulin storage of MIN6 cells: Functional exploration of an Indian type 2 diabetes GWAS associated gene. Biochemical and Biophysical Research Communications, 2020, 522, 1022-1029.	2.1	12
26	Spectrum of clinical features and genetic variants in mevalonate kinase (MVK) gene of South Indian families suffering from Hyperimmunoglobulin D Syndrome. PLoS ONE, 2020, 15, e0237999.	2.5	12
27	A Novel Protective Role for Matrix Metalloproteinase-8 in the Pulmonary Vasculature. American Journal of Respiratory and Critical Care Medicine, 2021, 204, 1433-1451.	5.6	11
28	Draft Genome Sequence of Urease-Producing Sporosarcina pasteurii with Potential Application in Biocement Production. Genome Announcements, 2014, 2, .	0.8	10
29	Investigating Coronary Artery Disease methylome through targeted bisulfite sequencing. Gene, 2019, 721, 144107.	2.2	10
30	RNA secondary structure profiling in zebrafish reveals unique regulatory features. BMC Genomics, 2018, 19, 147.	2.8	9
31	The Zebrafish GenomeWiki: a crowdsourcing approach to connect the long tail for zebrafish gene annotation. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau011-bau011.	3.0	8
32	Exome sequencing reveals a novel mutation, p.L325H, in the KRT5 gene associated with autosomal dominant Epidermolysis Bullosa Simplex Koebner type in a large family from western India. Human Genome Variation, 2014, 1, 14007.	0.7	8
33	Wholeâ€exome sequencing solves diagnostic dilemma in a rare case of sporadic acrokeratosis verruciformis. Journal of the European Academy of Dermatology and Venereology, 2016, 30, 695-697.	2.4	8
34	Familial Hypertrophic Cardiomyopathy - Identification of cause and risk stratification through exome sequencing. Gene, 2018, 660, 151-156.	2.2	8
35	Organellar transcriptome sequencing reveals mitochondrial localization of nuclear encoded transcripts. Mitochondrion, 2019, 46, 59-68.	3.4	8
36	Genome and transcriptome analysis of the mealybug Maconellicoccus hirsutus: Correlation with its unique phenotypes. Genomics, 2021, 113, 2483-2494.	2.9	8

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37	<scp>E</scp>gyptian tale from <scp>I</scp>ndia: application of wholeâ€exome sequencing in diagnosis of atypical familial <scp>M</scp>editerranean fever. International Journal of Rheumatic Diseases, 2017, 20, 1770-1775.	1.9	7
38	A novel cathepsin D mutation in 2 siblings with late infantile neuronal ceroid lipofuscinosis. Neurology: Genetics, 2019, 5, e302.	1.9	7
39	De novo identification of viral pathogens from cell culture hologenomes. BMC Research Notes, 2012, 5, 11.	1.4	6
40	Utility of wholeâ€exome sequencing in detecting novel compound heterozygous mutations in <scp>COL</scp>7A1 among families with severe recessive dystrophic epidermolysis bullosa in India â€“ implications on diagnosis, prognosis and prenatal testing. Journal of the European Academy of Dermatology and Venereology, 2018, 32, e433-e435.	2.4	5
41	Case Report: Application of whole exome sequencing for accurate diagnosis of rare syndromes of mineralocorticoid excess. F1000Research, 2016, 5, 1592.	1.6	5
42	Case Report: Whole exome sequencing helps in accurate molecular diagnosis in siblings with a rare co-occurrence of paternally inherited 22q12 duplication and autosomal recessive non-syndromic ichthyosis.. F1000Research, 2015, 4, 446.	1.6	4
43	Case Report: Application of whole exome sequencing for accurate diagnosis of rare syndromes of mineralocorticoid excess. F1000Research, 2016, 5, 1592.	1.6	4
44	Endothelial cell-specific deletion of a microRNA accelerates atherosclerosis. Atherosclerosis, 2022, 350, 9-18.	0.8	4
45	Draft Genome Sequence of a Clinical Isolate of Multidrug-Resistant Mycobacterium tuberculosis East African Indian Strain OSDD271. Genome Announcements, 2013, 1, .	0.8	3
46	AB0188â€…Systematic Analysis of the Oral Microbiome in Primary SjÃ–gren's Syndrome Suggest Enrichment of Distinct Microbes. Annals of the Rheumatic Diseases, 2015, 74, 953.3-954.	0.9	3
47	A founder mutation MLC1 c.736delA associated with megalencephalic leukoencephalopathy with subcortical cystsâ€‘ in north Indian kindred. Clinical Genetics, 2018, 94, 271-273.	2.0	3
48	Identification of novel circadian transcripts in the zebrafish retina. Journal of Experimental Biology, 2019, 222, .	1.7	3
49	Noncanonical role for Ku70/80 in the prevention of allergic airway inflammation via maintenance of airway epithelial cell organelle homeostasis. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2020, 319, L728-L741.	2.9	3
50	Case Report: Whole exome sequencing reveals a novel frameshift deletion mutation p.G2254fs in COL7A1 associated with autosomal recessive dystrophic epidermolysis bullosa. F1000Research, 2016, 5, 900.	1.6	3
51	Draft Genome Sequence of an Extensively Drug-Resistant Mycobacterium tuberculosis Clinical Isolate of the Ural Strain OSDD493. Genome Announcements, 2013, 1, .	0.8	2
52	Draft Genome Sequence of the Extremely Halophilic Bacterium Halomonas salina Strain CIFRI1, Isolated from the East Coast of India. Genome Announcements, 2015, 3, .	0.8	2
53	Interactomics Analyses of Wild-Type and Mutant A1CF Reveal Diverged Functions in Regulating Cellular Lipid Metabolism. Journal of Proteome Research, 2020, 19, 3968-3980.	3.7	2
54	Case Report: Whole exome sequencing reveals a novel frameshift deletion mutation p.G2254fs in COL7A1 associated with autosomal recessive dystrophic epidermolysis bullosa. F1000Research, 2016, 5, 900.	1.6	2

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55	Case Report: Whole exome sequencing identifies a novel frameshift insertion c.1325dupT (p.F442fsX2) in the tyrosine kinase domain of BTK gene in a young Indian individual with X-linked agammaglobulinemia. F1000Research, 2016, 5, 2667.	1.6	2
56	Whole exome sequencing in a multi-generation family from India reveals a genetic variation c.10C>T (p.Gln4Ter) in keratin 5 gene associated with Dowlingâ€“Degos disease. Indian Journal of Dermatology, Venereology and Leprology, 2018, 84, 344.	0.6	2
57	Case Report: Whole exome sequencing identifies a novel frameshift insertion c.1325dupT (p.F442fsX2) in the tyrosine kinase domain of BTK gene in a young Indian individual with X-linked agammaglobulinemia. F1000Research, 2016, 5, 2667.	1.6	2
58	CRISPRâ€Cas9 Genome Editing of Primary Human Vascular Cells In Vitro. Current Protocols, 2021, 1, e291.	2.9	2
59	Draft Genome Sequence of Multidrug-Resistant Mycobacterium tuberculosis Clinical Isolate OSDD515, Belonging to the Uganda I Genotype. Genome Announcements, 2013, 1, .	0.8	1
60	Autosomal recessive epidermolysis bullosa simplex: report of three cases from India. Clinical and Experimental Dermatology, 2017, 42, 800-803.	1.3	1
61	Methods to Study Long Noncoding RNA Expression and Dynamics in Zebrafish Using RNA Sequencing. Methods in Molecular Biology, 2019, 1912, 77-110.	0.9	1
62	Case Report: Whole exome sequencing identifies variation c.2308G>A p.E770K in RAG1 associated with B- T- NK+ severe combined immunodeficiency. F1000Research, 2016, 5, 2532.	1.6	1
63	Possible selection bias limits the interpretation of single-cell transcriptomics data of steroid-resistant asthma exacerbation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2102858118.	7.1	1
64	Abstract 15355: Interleukin-1beta Inhibition Attenuates Accelerated Atherosclerosis in Mice With <i>Tet2</i> Loss of Function in a Sex-dependent Fashion. Circulation, 2020, 142, .	1.6	1
65	Draft Genome Sequence of a Multidrug-Resistant Clinical Isolate of Mycobacterium tuberculosis Belonging to a Novel Spoligotype. Genome Announcements, 2013, 1, .	0.8	0
66	Unilateral monomorphic hypopigmented macules: A variant of Darier disease. Indian Journal of Dermatology, Venereology and Leprology, 2017, 83, 369.	0.6	0
67	Abstract 11265: Sex-Specific Response to Endothelin-1 Overexpression Mediates Thoracic Aortic Aneurysm Development. Circulation, 2021, 144, .	1.6	0