# Shamsudheen Karuthedath Vellarikkal

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | Deep learning enables genetic analysis of the human thoracic aorta. Nature Genetics, 2022, 54, 40-51. | 21.4 | 90 |
| 2 | Endothelial cell-specific deletion of a microRNA accelerates atherosclerosis. Atherosclerosis, 2022, 350, 9-18. | 0.8 | 4 |
| 3 | COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113. | 27.8 | 537 |
| 4 | LncRNA VEAL2 regulates PRKCB2 to modulate endothelial permeability in diabetic retinopathy. EMBO Journal, 2021, 40, e107134. | 7.8 | 32 |
| 5 | Genome and transcriptome analysis of the mealybug Maconellicoccus hirsutus: Correlation with its unique phenotypes. Genomics, 2021, 113, 2483-2494. | 2.9 | 8 |
| 6 | 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 |
| 7 | 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 |
| 8 | CRISPRâ€Cas9 Genome Editing of Primary Human Vascular Cells In Vitro. Current Protocols, 2021, 1, e291. | 2.9 | 2 |
| 9 | Abstract 11265: Sex-Specific Response to Endothelin-1 Overexpression Mediates Thoracic Aortic Aneurysm Development. Circulation, 2021, 144, . | 1.6 | 0 |
| 10 | Saliva microbiome in primary SjÃ¶grenâ€™s syndrome reveals distinct set of diseaseâ€associated microbes. Oral Diseases, 2020, 26, 295-301. | 3.0 | 39 |
| 11 | 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | 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 |
| 15 | 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 |
| 16 | Abstract 15355: Interleukin-1beta Inhibition Attenuates Accelerated Atherosclerosis in Mice With Tet2 Loss of Function in a Sex-dependent Fashion. Circulation, 2020, 142, . | 1.6 | 1 |
| 17 | Identification of novel circadian transcripts in the zebrafish retina. Journal of Experimental Biology, 2019, 222, . | 1.7 | 3 |
| 18 | Genomics of rare genetic diseasesâ€”experiences from India. Human Genomics, 2019, 13, 52. | 2.9 | 30 |

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|---|---|---|---|
| 19 | Investigating Coronary Artery Disease methylome through targeted bisulfite sequencing. Gene, 2019, 721, 144107. | 2.2 | 10 |
| 20 | Single-Cell Analysis of the Normal Mouse Aorta Reveals Functionally Distinct Endothelial Cell Populations. Circulation, 2019, 140, 147-163. | 1.6 | 231 |
| 21 | 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 |
| 22 | A novel cathepsin D mutation in 2 siblings with late infantile neuronal ceroid lipofuscinosis. Neurology: Genetics, 2019, 5, e302. | 1.9 | 7 |
| 23 | A genome-wide map of circular RNAs in adult zebrafish. Scientific Reports, 2019, 9, 3432. | 3.3 | 19 |
| 24 | 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 |
| 25 | Organellar transcriptome sequencing reveals mitochondrial localization of nuclear encoded transcripts. Mitochondrion, 2019, 46, 59-68. | 3.4 | 8 |
| 26 | 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 |
| 27 | A founder mutation MLC1 c.736delA associated with megalencephalic leukoencephalopathy with subcortical cystsâ€1 in north Indian kindred. Clinical Genetics, 2018, 94, 271-273. | 2.0 | 3 |
| 28 | Pharmacogenetic landscape of DPYD variants in south Asian populations by integration of genome-scale data. Pharmacogenomics, 2018, 19, 227-241. | 1.3 | 25 |
| 29 | RNA secondary structure profiling in zebrafish reveals unique regulatory features. BMC Genomics, 2018, 19, 147. | 2.8 | 9 |
| 30 | Familial Hypertrophic Cardiomyopathy - Identification of cause and risk stratification through exome sequencing. Gene, 2018, 660, 151-156. | 2.2 | 8 |
| 31 | Large scale changes in the transcriptome of Eisenia fetida during regeneration. PLoS ONE, 2018, 13, e0204234. | 2.5 | 31 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | 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 |
| 36 | <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 |

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| 37 | 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 |
| 38 | Autosomal recessive epidermolysis bullosa simplex: report of three cases from India. Clinical and Experimental Dermatology, 2017, 42, 800-803. | 1.3 | 1 |
| 39 | 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 |
| 40 | Unilateral monomorphic hypopigmented macules: A variant of Darier disease. Indian Journal of Dermatology, Venereology and Leprology, 2017, 83, 369. | 0.6 | 0 |
| 41 | Aptamer-Assisted Detection of the Altered Expression of Estrogen Receptor Alpha in Human Breast Cancer. PLoS ONE, 2016, 11, e0153001. | 2.5 | 25 |
| 42 | 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 |
| 43 | 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 |
| 44 | 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 |
| 45 | Case Report: Application of whole exome sequencing for accurate diagnosis of rare syndromes of mineralocorticoid excess. F1000Research, 2016, 5, 1592. | 1.6 | 5 |
| 46 | Case Report: Application of whole exome sequencing for accurate diagnosis of rare syndromes of mineralocorticoid excess. F1000Research, 2016, 5, 1592. | 1.6 | 4 |
| 47 | 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 |
| 48 | Chamber Specific Gene Expression Landscape of the Zebrafish Heart. PLoS ONE, 2016, 11, e0147823. | 2.5 | 24 |
| 49 | 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 |
| 50 | 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 |
| 51 | 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 |
| 52 | Screening Currency Notes for Microbial Pathogens and Antibiotic Resistance Genes Using a Shotgun Metagenomic Approach. PLoS ONE, 2015, 10, e0128711. | 2.5 | 25 |
| 53 | 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 |
| 54 | 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 |

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| 55 | 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 |
| 56 | Comparative Whole-Genome Analysis of Clinical Isolates Reveals Characteristic Architecture of Mycobacterium tuberculosis Pangenome. PLoS ONE, 2015, 10, e0122979. | 2.5 | 49 |
| 57 | 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 |
| 58 | 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 |
| 59 | Draft Genome Sequence of Urease-Producing Sporosarcina pasteurii with Potential Application in Biocement Production. Genome Announcements, 2014, 2, . | 0.8 | 10 |
| 60 | 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 |
| 61 | 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 |
| 62 | Draft Genome Sequence of Multidrug-Resistant Mycobacterium tuberculosis Clinical Isolate OSDD515, Belonging to the Uganda I Genotype. Genome Announcements, 2013, 1, . | 0.8 | 1 |
| 63 | Draft Genome Sequence of an Extensively Drug-Resistant Mycobacterium tuberculosis Clinical Isolate of the Ural Strain OSDD493. Genome Announcements, 2013, 1, . | 0.8 | 2 |
| 64 | Draft Genome Sequence of a Multidrug-Resistant Clinical Isolate of Mycobacterium tuberculosis Belonging to a Novel Spoligotype. Genome Announcements, 2013, 1, . | 0.8 | 0 |
| 65 | Draft Genome Sequence of a Clinical Isolate of Multidrug-Resistant Mycobacterium tuberculosis East African Indian Strain OSDD271. Genome Announcements, 2013, 1, . | 0.8 | 3 |
| 66 | Dynamic Expression of Long Non-Coding RNAs (lncRNAs) in Adult Zebrafish. PLoS ONE, 2013, 8, e83616. | 2.5 | 92 |
| 67 | De novo identification of viral pathogens from cell culture hologenomes. BMC Research Notes, 2012, 5, 11. | 1.4 | 6 |