

# Sarath Chandra Janga

## List of Publications by Year in descending order

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Version: 2024-02-01

98  
papers

4,469  
citations

145106

33  
h-index

129628

63  
g-index

108  
all docs

108  
docs citations

108  
times ranked

7770  
citing authors

#	ARTICLE	IF	CITATIONS
1	Penguin: A tool for predicting pseudouridine sites in direct RNA nanopore sequencing data. <i>Methods</i> , 2022, 203, 478-487.	1.9	15
2	CASowary: CRISPR-Cas13 guide RNA predictor for transcript depletion. <i>BMC Genomics</i> , 2022, 23, 172.	1.2	9
3	FOXP3 exon 2 controls T <sub>reg</sub> stability and autoimmunity. <i>Science Immunology</i> , 2022, 7, .	5.6	21
4	A long non-coding <i>lncRNA</i> ( <i>lncRNAP</i> ) modulates brain gene expression and levels of alcohol consumption in rats. <i>Genes, Brain and Behavior</i> , 2021, 20, e12698.	1.1	16
5	Transcriptome-wide high-throughput mapping of protein-RNA occupancy profiles using POP-seq. <i>Scientific Reports</i> , 2021, 11, 1175.	1.6	6
6	Lantern: an integrative repository of functional annotations for lncRNAs in the human genome. <i>BMC Bioinformatics</i> , 2021, 22, 279.	1.2	2
7	Sequoia: an interactive visual analytics platform for interpretation and feature extraction from nanopore sequencing datasets. <i>BMC Genomics</i> , 2021, 22, 513.	1.2	2
8	Mutational Landscape and Interaction of SARS-CoV-2 with Host Cellular Components. <i>Microorganisms</i> , 2021, 9, 1794.	1.6	9
9	Comparative Analysis of Alternative Splicing Profiles in Th Cell Subsets Reveals Extensive Cell Type-Specific Effects Modulated by a Network of Transcription Factors and RNA-Binding Proteins. <i>ImmunoHorizons</i> , 2021, 5, 760-771.	0.8	2
10	Slicelt: A genome-wide resource and visualization tool to design CRISPR/Cas9 screens for editing protein-RNA interaction sites in the human genome. <i>Methods</i> , 2020, 178, 104-113.	1.9	4
11	Role of SARS-CoV-2 in Altering the RNA-Binding Protein and miRNA-Directed Post-Transcriptional Regulatory Networks in Humans. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7090.	1.8	28
12	Granzyme A-producing T helper cells are critical for acute graft-versus-host disease. <i>JCI Insight</i> , 2020, 5, .	2.3	9
13	Long Non-Coding RNA Expression Levels Modulate Cell-Type-Specific Splicing Patterns by Altering Their Interaction Landscape with RNA-Binding Proteins. <i>Genes</i> , 2019, 10, 593.	1.0	16
14	Splicing factor <i>ESRP1</i> controls <i>ER</i> -positive breast cancer by altering metabolic pathways. <i>EMBO Reports</i> , 2019, 20, .	2.0	48
15	Early transcriptome profile of goat peripheral blood mononuclear cells (PBMCs) infected with peste des petits ruminant's vaccine virus (Sungri/96) revealed induction of antiviral response in an interferon independent manner. <i>Research in Veterinary Science</i> , 2019, 124, 166-177.	0.9	10
16	Human protein-RNA interaction network is highly stable across mammals. <i>BMC Genomics</i> , 2019, 20, 1004.	1.2	10
17	A Framework for Identifying Genotypic Information from Clinical Records: Exploiting Integrated Ontology Structures to Transfer Annotations between ICD Codes and Gene Ontologies. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1259-1269.	1.9	4
18	Express: A database of transcriptome profiles encompassing known and novel transcripts across multiple development stages in eye tissues. <i>Experimental Eye Research</i> , 2018, 168, 57-68.	1.2	18

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19	Mutational landscape of RNA-binding proteins in human cancers. <i>RNA Biology</i> , 2018, 15, 115-129.	1.5	87
20	Great Lakes Bioinformatics Conference (GLBIO) 2015 Special Section Editorial. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1229-1230.	1.9	0
21	A conserved enhancer regulates Il9 expression in multiple lineages. <i>Nature Communications</i> , 2018, 9, 4803.	5.8	26
22	Epitranscriptomic Code and Its Alterations in Human Disease. <i>Trends in Molecular Medicine</i> , 2018, 24, 886-903.	3.5	101
23	Loss of epigenetic regulator TET2 and oncogenic KIT regulate myeloid cell transformation via PI3K pathway. <i>JCI Insight</i> , 2018, 3, .	2.3	18
24	Paracrine IL-2 Is Required for Optimal Type 2 Effector Cytokine Production. <i>Journal of Immunology</i> , 2017, 198, 4352-4359.	0.4	11
25	PSIP1/p75 promotes tumorigenicity in breast cancer cells by promoting the transcription of cell cycle genes. <i>Carcinogenesis</i> , 2017, 38, 966-975.	1.3	25
26	Seten: a tool for systematic identification and comparison of processes, phenotypes, and diseases associated with RNA-binding proteins from condition-specific CLIP-seq profiles. <i>Rna</i> , 2017, 23, 836-846.	1.6	12
27	Community-acquired rhinovirus infection is associated with changes in the airway microbiome. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 312-315.e8.	1.5	26
28	Comparative and temporal transcriptome analysis of peste des petits ruminants virus infected goat peripheral blood mononuclear cells. <i>Virus Research</i> , 2017, 229, 28-40.	1.1	38
29	The RavA-ViaA Chaperone-Like System Interacts with and Modulates the Activity of the Fumarate Reductase Respiratory Complex. <i>Journal of Molecular Biology</i> , 2017, 429, 324-344.	2.0	28
30	Transcriptome analysis of developing lens reveals abundance of novel transcripts and extensive splicing alterations. <i>Scientific Reports</i> , 2017, 7, 11572.	1.6	28
31	RNA Editing in Pathogenesis of Cancer. <i>Cancer Research</i> , 2017, 77, 3733-3739.	0.4	60
32	Differential Expression of miRNAs in Nontumor Liver Tissue of Patients With Hepatocellular Cancer Caused by Nonalcoholic Steatohepatitis Cirrhosis. <i>Clinical Gastroenterology and Hepatology</i> , 2017, 15, 465-467.	2.4	2
33	ExSurv: A Web Resource for Prognostic Analyses of Exons across Human Cancers Using Clinical Transcriptomes. <i>Cancer Informatics</i> , 2016, 15s2, CIN.S39367.	0.9	3
34	Dissecting the expression relationships between RNA-binding proteins and their cognate targets in eukaryotic post-transcriptional regulatory networks. <i>Scientific Reports</i> , 2016, 6, 25711.	1.6	18
35	Cover Image, Volume 7, Issue 4. <i>Wiley Interdisciplinary Reviews RNA</i> , 2016, 7, i-i.	3.2	0
36	Benchmarking of de novo assembly algorithms for Nanopore data reveals optimal performance of OLC approaches. <i>BMC Genomics</i> , 2016, 17, 507.	1.2	21

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37	<sc>RNA</sc>-binding proteins in eye development and disease: implication of conserved <sc>RNA</sc> granule components. Wiley Interdisciplinary Reviews RNA, 2016, 7, 527-557.	3.2	38
38	Prediction and Validation of Transcription Factors Modulating the Expression of Sestrin3 Gene Using an Integrated Computational and Experimental Approach. PLoS ONE, 2016, 11, e0160228.	1.1	5
39	Uncovering RNA binding proteins associated with age and gender during liver maturation. Scientific Reports, 2015, 5, 9512.	1.6	10
40	Database of RNA binding protein expression and disease dynamics (READ DB). Database: the Journal of Biological Databases and Curation, 2015, 2015, bav072.	1.4	9
41	Differential miRNA Expression in Cells and Matrix Vesicles in Vascular Smooth Muscle Cells from Rats with Kidney Disease. PLoS ONE, 2015, 10, e0131589.	1.1	37
42	OperomeDB: A Database of Condition-Specific Transcription Units in Prokaryotic Genomes. BioMed Research International, 2015, 2015, 1-10.	0.9	11
43	Building Integrated Ontological Knowledge Structures with Efficient Approximation Algorithms. BioMed Research International, 2015, 2015, 1-14.	0.9	2
44	Genomic analysis of host " Peste des petits ruminants vaccine viral transcriptome uncovers transcription factors modulating immune regulatory pathways. Veterinary Research, 2015, 46, 15.	1.1	50
45	The human RBPome: From genes and proteins to human disease. Journal of Proteomics, 2015, 127, 61-70.	1.2	106
46	Knowledge Discovery Using Big Data in Biomedical Systems [Guest Editorial]. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 726-728.	1.9	1
47	Expression levels of SF3B3 correlate with prognosis and endocrine resistance in estrogen receptor-positive breast cancer. Modern Pathology, 2015, 28, 677-685.	2.9	28
48	Role of lncRNAs in health and disease--size and shape matter. Briefings in Functional Genomics, 2015, 14, 115-129.	1.3	28
49	Systems and Network-Based Approaches for Personalized Medicine. Current Synthetic and Systems Biology, 2014, 02, .	0.3	1
50	Dissecting the expression landscape of RNA-binding proteins in human cancers. Genome Biology, 2014, 15, R14.	13.9	208
51	Prediction and validation of the unexplored RNA-binding protein atlas of the human proteome. Proteins: Structure, Function and Bioinformatics, 2014, 82, 640-647.	1.5	22
52	Primate vaginal microbiomes exhibit species specificity without universal <i>Lactobacillus</i> dominance. ISME Journal, 2014, 8, 2431-2444.	4.4	149
53	An Intricate Network of Conserved DNA Upstream Motifs and Associated Transcription Factors Regulate the Expression of Uromodulin Gene. Journal of Urology, 2014, 192, 981-989.	0.2	12
54	Diversity and abundance of phosphonate biosynthetic genes in nature. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20759-20764.	3.3	148

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55	Relationship between Differential Hepatic microRNA Expression and Decreased Hepatic Cytochrome P450 3A Activity in Cirrhosis. PLoS ONE, 2013, 8, e74471.	1.1	37
56	From specific to global analysis of posttranscriptional regulation in eukaryotes: posttranscriptional regulatory networks. Briefings in Functional Genomics, 2012, 11, 505-521.	1.3	16
57	Extensive cross-talk and global regulators identified from an analysis of the integrated transcriptional and signaling network in Escherichia coli. Molecular BioSystems, 2012, 8, 3028.	2.9	10
58	Synthesis of Methylphosphonic Acid by Marine Microbes: A Source for Methane in the Aerobic Ocean. Science, 2012, 337, 1104-1107.	6.0	263
59	DNA Sequence Preferences of Transcriptional Activators Correlate More Strongly than Repressors with Nucleosomes. Molecular Cell, 2012, 47, 183-192.	4.5	26
60	The RNA-Binding Protein Musashi1 Affects Medulloblastoma Growth via a Network of Cancer-Related Genes and Is an Indicator of Poor Prognosis. American Journal of Pathology, 2012, 181, 1762-1772.	1.9	73
61	Comparative analysis of gene expression and regulation of replicative aging associated genes in S. cerevisiae. Molecular BioSystems, 2011, 7, 403-410.	2.9	2
62	MicroRNAs as Post-Transcriptional Machines and their Interplay with Cellular Networks. Advances in Experimental Medicine and Biology, 2011, 722, 59-74.	0.8	78
63	Construction, Structure and Dynamics of Post-Transcriptional Regulatory Network Directed by RNA-Binding Proteins. Advances in Experimental Medicine and Biology, 2011, 722, 103-117.	0.8	22
64	Interplay between Posttranscriptional and Posttranslational Interactions of RNA-Binding Proteins. Journal of Molecular Biology, 2011, 409, 466-479.	2.0	43
65	Transcriptional profiling of fetal hypothalamic TRH neurons. BMC Genomics, 2011, 12, 222.	1.2	8
66	Network-based function prediction and interactomics: The case for metabolic enzymes. Metabolic Engineering, 2011, 13, 1-10.	3.6	43
67	Structural Coupling between RNA Polymerase Composition and DNA Supercoiling in Coordinating Transcription: a Global Role for the Omega Subunit?. MBio, 2011, 2, .	1.8	34
68	A Screen for RNA-Binding Proteins in Yeast Indicates Dual Functions for Many Enzymes. PLoS ONE, 2010, 5, e15499.	1.1	122
69	Dissecting the expression patterns of transcription factors across conditions using an integrated network-based approach. Nucleic Acids Research, 2010, 38, 6841-6856.	6.5	8
70	Identification and Genomic Analysis of Transcription Factors in Archaeal Genomes Exemplifies Their Functional Architecture and Evolutionary Origin. Molecular Biology and Evolution, 2010, 27, 1449-1459.	3.5	72
71	Genome-wide analysis of mRNA decay patterns during early Drosophila development. Genome Biology, 2010, 11, R93.	13.9	124
72	Dissecting the expression dynamics of RNA-binding proteins in posttranscriptional regulatory networks. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20300-20305.	3.3	85

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73	Global Functional Atlas of Escherichia coli Encompassing Previously Uncharacterized Proteins. PLoS Biology, 2009, 7, e1000096.	2.6	331
74	Transcriptional regulation shapes the organization of genes on bacterial chromosomes. Nucleic Acids Research, 2009, 37, 3680-3688.	6.5	57
75	Plasticity of transcriptional machinery in bacteria is increased by the repertoire of regulatory families. Computational Biology and Chemistry, 2009, 33, 261-268.	1.1	12
76	Structure and organization of drug-target networks: insights from genomic approaches for drug discovery. Molecular BioSystems, 2009, 5, 1536.	2.9	95
77	Scaling relationship in the gene content of transcriptional machinery in bacteria. Molecular BioSystems, 2009, 5, 1494.	2.9	36
78	Transcript stability in the protein interaction network of Escherichia coli. Molecular BioSystems, 2009, 5, 154-162.	2.9	14
79	Operons and the effect of genome redundancy in deciphering functional relationships using phylogenetic profiles. Proteins: Structure, Function and Bioinformatics, 2008, 70, 344-352.	1.5	27
80	Network-based approaches for linking metabolism with environment. Genome Biology, 2008, 9, 239.	13.9	34
81	Functional organisation of Escherichia coli transcriptional regulatory network. Journal of Molecular Biology, 2008, 381, 238-247.	2.0	143
82	Eukaryotic gene regulation in three dimensions and its impact on genome evolution. Current Opinion in Genetics and Development, 2008, 18, 571-582.	1.5	43
83	Transcriptional regulation constrains the organization of genes on eukaryotic chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15761-15766.	3.3	72
84	Ten Simple Rules for Organizing a Scientific Meeting. PLoS Computational Biology, 2008, 4, e1000080.	1.5	23
85	Coordination logic of the sensing machinery in the transcriptional regulatory network of Escherichia coli. Nucleic Acids Research, 2007, 35, 6963-6972.	6.5	21
86	Structure and evolution of gene regulatory networks in microbial genomes. Research in Microbiology, 2007, 158, 787-794.	1.0	47
87	Internal Versus External Effector and Transcription Factor Gene Pairs Differ in Their Relative Chromosomal Position in Escherichia coli. Journal of Molecular Biology, 2007, 368, 263-272.	2.0	15
88	Conservation of transcriptional sensing systems in prokaryotes: A perspective from Escherichia coli. FEBS Letters, 2007, 581, 3499-3506.	1.3	6
89	Prediction and evolution of transcription factors and their evolutionary families in prokaryotes. BMC Systems Biology, 2007, 1, .	3.0	0
90	Internal-sensing machinery directs the activity of the regulatory network in Escherichia coli. Trends in Microbiology, 2006, 14, 22-27.	3.5	78

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91	Identification and analysis of DNA-binding transcription factors in Bacillus subtilis and other Firmicutes- a genomic approach. BMC Genomics, 2006, 7, 147.	1.2	63
92	The distinctive signatures of promoter regions and operon junctions across prokaryotes. Nucleic Acids Research, 2006, 34, 3980-3987.	6.5	14
93	Bacterial regulatory networks are extremely flexible in evolution. Nucleic Acids Research, 2006, 34, 3434-3445.	6.5	207
94	The partitioned Rhizobium etli genome: Genetic and metabolic redundancy in seven interacting replicons. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3834-3839.	3.3	365
95	Nebulon: a system for the inference of functional relationships of gene products from the rearrangement of predicted operons. Nucleic Acids Research, 2005, 33, 2521-2530.	6.5	44
96	The Network of Transcriptional Interactions Imposes Linear Constrains in the Genome. OMICS A Journal of Integrative Biology, 2005, 9, 139-145.	1.0	4
97	Conservation of adjacency as evidence of paralogous operons. Nucleic Acids Research, 2004, 32, 5392-5397.	6.5	36
98	Transcriptional regulatory networks. , 0, , 14-35.		0