

Simon Kasif

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

9,488
citations

147801

31
h-index

144013

57
g-index

63
all docs

63
docs citations

63
times ranked

16233
citing authors

#	ARTICLE	IF	CITATIONS
1	Improved microbial gene identification with GLIMMER. <i>Nucleic Acids Research</i> , 1999, 27, 4636-4641.	14.5	2,282
2	Large-Scale Mapping and Validation of <i>Escherichia coli</i> Transcriptional Regulation from a Compendium of Expression Profiles. <i>PLoS Biology</i> , 2007, 5, e8.	5.6	1,308
3	Genomewide Analysis of PRC1 and PRC2 Occupancy Identifies Two Classes of Bivalent Domains. <i>PLoS Genetics</i> , 2008, 4, e1000242.	3.5	878
4	Alignment of whole genomes. <i>Nucleic Acids Research</i> , 1999, 27, 2369-2376.	14.5	766
5	Reconstructing and Reprogramming the Tumor-Propagating Potential of Glioblastoma Stem-like Cells. <i>Cell</i> , 2014, 157, 580-594.	28.9	751
6	Deep Sequencing of the Oral Microbiome Reveals Signatures of Periodontal Disease. <i>PLoS ONE</i> , 2012, 7, e37919.	2.5	329
7	Predicting protein function from protein/protein interaction data: a probabilistic approach. <i>Bioinformatics</i> , 2003, 19, i197-i204.	4.1	317
8	Whole-genome annotation by using evidence integration in functional-linkage networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2888-2893.	7.1	293
9	Network-Based Analysis of Affected Biological Processes in Type 2 Diabetes Models. <i>PLoS Genetics</i> , 2007, 3, e96.	3.5	166
10	Immediate-Early and Delayed Primary Response Genes Are Distinct in Function and Genomic Architecture*. <i>Journal of Biological Chemistry</i> , 2007, 282, 23981-23995.	3.4	159
11	Identification of functional links between genes using phylogenetic profiles. <i>Bioinformatics</i> , 2003, 19, 1524-1530.	4.1	139
12	Optimized Multiplex PCR: Efficiently Closing a Whole-Genome Shotgun Sequencing Project. <i>Genomics</i> , 1999, 62, 500-507.	2.9	131
13	Defects in muscle branched-chain amino acid oxidation contribute to impaired lipid metabolism. <i>Molecular Metabolism</i> , 2016, 5, 926-936.	6.5	124
14	EXTRACTING CONSERVED GENE EXPRESSION MOTIFS FROM GENE EXPRESSION DATA. , 2002, , .		123
15	Computational Identification of Operons in Microbial Genomes. <i>Genome Research</i> , 2002, 12, 1221-1230.	5.5	119
16	GC/AT-content spikes as genomic punctuation marks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16855-16860.	7.1	99
17	RimO, a MiaB-like enzyme, methylthiolates the universally conserved Asp88 residue of ribosomal protein S12 in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1826-1831.	7.1	97
18	Identification of Transcription Factor Binding Sites Upstream of Human Genes Regulated by the Phosphatidylinositol 3-Kinase and MEK/ERK Signaling Pathways. <i>Journal of Biological Chemistry</i> , 2004, 279, 20167-20177.	3.4	86

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19	Probabilistic Protein Function Prediction from Heterogeneous Genome-Wide Data. PLoS ONE, 2007, 2, e337.	2.5	84
20	Accelerated Postnatal Growth Increases Lipogenic Gene Expression and Adipocyte Size in Low Birth Weight Mice. Diabetes, 2009, 58, 1192-1200.	0.6	76
21	Structural Location of Disease-associated Single-nucleotide Polymorphisms. Journal of Molecular Biology, 2003, 327, 1021-1030.	4.2	74
22	The art of gene function prediction. Nature Biotechnology, 2006, 24, 1474-1475.	17.5	69
23	A Systems Biology Approach Identifies Inflammatory Abnormalities Between Mouse Strains Prior to Development of Metabolic Disease. Diabetes, 2010, 59, 2960-2971.	0.6	69
24	Biological context networks: a mosaic view of the interactome. Molecular Systems Biology, 2006, 2, 66.	7.2	68
25	Glycogen Synthase Kinase-3 Represses Cyclic AMP Response Element-binding Protein (CREB)-targeted Immediate Early Genes in Quiescent Cells. Journal of Biological Chemistry, 2007, 282, 9482-9491.	3.4	68
26	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	5.6	54
27	Learning a Hidden Matching. SIAM Journal on Computing, 2004, 33, 487-501.	1.0	52
28	COMBREX: a project to accelerate the functional annotation of prokaryotic genomes. Nucleic Acids Research, 2011, 39, D11-D14.	14.5	47
29	COMBREX-DB: an experiment centered database of protein function: knowledge, predictions and knowledge gaps. Nucleic Acids Research, 2016, 44, D330-D335.	14.5	47
30	Functional characterization of the YmcB and YqeV tRNA methyltransferases of Bacillus subtilis. Nucleic Acids Research, 2010, 38, 6195-6205.	14.5	39
31	Single-cell transcriptional networks in differentiating preadipocytes suggest drivers associated with tissue heterogeneity. Nature Communications, 2020, 11, 2117.	12.8	37
32	Hypermutable DNA chronicles the evolution of human colon cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1889-98.	7.1	35
33	Quantitative Analysis of Single Nucleotide Polymorphisms within Copy Number Variation. PLoS ONE, 2008, 3, e3906.	2.5	34
34	Biological Process Linkage Networks. PLoS ONE, 2009, 4, e5313.	2.5	34
35	Triplet repeat length bias and variation in the human transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17095-17100.	7.1	33
36	Identification of rare germline copy number variations over-represented in five human cancer types. Molecular Cancer, 2015, 14, 25.	19.2	32

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37	Identification of genes with fast-evolving regions in microbial genomes. <i>Nucleic Acids Research</i> , 2004, 32, 6347-6357.	14.5	30
38	Thousands of missed genes found in bacterial genomes and their analysis with COMBEX. <i>Biology Direct</i> , 2012, 7, 37.	4.6	28
39	Metabolic modeling of muscle metabolism identifies key reactions linked to insulin resistance phenotypes. <i>Molecular Metabolism</i> , 2015, 4, 151-163.	6.5	28
40	Human-Mouse Gene Identification by Comparative Evidence Integration and Evolutionary Analysis. <i>Genome Research</i> , 2003, 13, 1190-1202.	5.5	27
41	Integrating Extracellular Flux Measurements and Genome-Scale Modeling Reveals Differences between Brown and White Adipocytes. <i>Cell Reports</i> , 2017, 21, 3040-3048.	6.4	24
42	A computational framework for optimal masking in the synthesis of oligonucleotide microarrays. <i>Nucleic Acids Research</i> , 2002, 30, 106e-106.	14.5	23
43	One for all and all for One: Improving replication of genetic studies through network diffusion. <i>PLoS Genetics</i> , 2018, 14, e1007306.	3.5	22
44	On the normalization of RNA equilibrium free energy to the length of the sequence. <i>Nucleic Acids Research</i> , 2003, 31, 49e-49.	14.5	16
45	A Predictive Phosphorylation Signature of Lung Cancer. <i>PLoS ONE</i> , 2009, 4, e7994.	2.5	16
46	Membrane metallo-endopeptidase (Nepriylsin) regulates inflammatory response and insulin signaling in white preadipocytes. <i>Molecular Metabolism</i> , 2019, 22, 21-36.	6.5	15
47	Gene expression module discovery using gibbs sampling. <i>Genome Informatics</i> , 2004, 15, 239-48.	0.4	15
48	To Supplement or Not to Supplement: A Metabolic Network Framework for Human Nutritional Supplements. <i>PLoS ONE</i> , 2013, 8, e68751.	2.5	14
49	Characterization of Two New Aminopeptidases in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2005, 187, 3671-3677.	2.2	13
50	Systems Biology Characterization of Engineered Tissues. <i>Annual Review of Biomedical Engineering</i> , 2013, 15, 55-70.	12.3	13
51	High-throughput mediation analysis of human proteome and metabolome identifies mediators of post-bariatric surgical diabetes control. <i>Nature Communications</i> , 2021, 12, 6951.	12.8	13
52	Objective: biochemical function. <i>Frontiers in Genetics</i> , 2014, 5, 210.	2.3	12
53	Efficient parallel term matching and anti-unification. <i>Journal of Automated Reasoning</i> , 1992, 9, 391-406.	1.4	11
54	Quantifying DNA-protein binding specificities by using oligonucleotide mass tags and mass spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3061-3066.	7.1	11

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55	Some results on the complexity of exploiting data dependency in parallel logic programs. <i>The Journal of Logic Programming</i> , 1989, 6, 229-241.	1.7	10
56	Analysis of brain region-specific co-expression networks reveals clustering of established and novel genes associated with Alzheimer disease. <i>Alzheimer's Research and Therapy</i> , 2020, 12, 103.	6.2	9
57	We need to keep a reproducible trace of facts, predictions, and hypotheses from gene to function in the era of big data. <i>PLoS Biology</i> , 2020, 18, e3000999.	5.6	8
58	Interpretable network propagation with application to expanding the repertoire of human proteins that interact with SARS-CoV-2. <i>GigaScience</i> , 2021, 10, .	6.4	5
59	Systems Biology via Redescription and Ontologies (III): Protein Classification Using Malaria Parasite's Temporal Transcriptomic Profiles. , 2008, , .		3
60	List of contributors* *Authorsâ€™ names are followed by the starting page number(s) of their contribution(s).. <i>New Comprehensive Biochemistry</i> , 1998, 32, xi-xiii.	0.1	0