

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	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
2	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
3	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
4	Single-cell transcriptional networks in differentiating preadipocytes suggest drivers associated with tissue heterogeneity. <i>Nature Communications</i> , 2020, 11, 2117.	12.8	37
5	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
6	Membrane metallo-endopeptidase (Nepriylsin) regulates inflammatory response and insulin signaling in white preadipocytes. <i>Molecular Metabolism</i> , 2019, 22, 21-36.	6.5	15
7	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
8	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
9	COMBEX-DB: an experiment centered database of protein function: knowledge, predictions and knowledge gaps. <i>Nucleic Acids Research</i> , 2016, 44, D330-D335.	14.5	47
10	Defects in muscle branched-chain amino acid oxidation contribute to impaired lipid metabolism. <i>Molecular Metabolism</i> , 2016, 5, 926-936.	6.5	124
11	Metabolic modeling of muscle metabolism identifies key reactions linked to insulin resistance phenotypes. <i>Molecular Metabolism</i> , 2015, 4, 151-163.	6.5	28
12	Identification of rare germline copy number variations over-represented in five human cancer types. <i>Molecular Cancer</i> , 2015, 14, 25.	19.2	32
13	Objective: biochemical function. <i>Frontiers in Genetics</i> , 2014, 5, 210.	2.3	12
14	Hypermutable DNA chronicles the evolution of human colon cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1889-98.	7.1	35
15	Reconstructing and Reprogramming the Tumor-Propagating Potential of Glioblastoma Stem-like Cells. <i>Cell</i> , 2014, 157, 580-594.	28.9	751
16	Systems Biology Characterization of Engineered Tissues. <i>Annual Review of Biomedical Engineering</i> , 2013, 15, 55-70.	12.3	13
17	The COMBEX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	5.6	54
18	To Supplement or Not to Supplement: A Metabolic Network Framework for Human Nutritional Supplements. <i>PLoS ONE</i> , 2013, 8, e68751.	2.5	14

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19	Thousands of missed genes found in bacterial genomes and their analysis with COMBREX. <i>Biology Direct</i> , 2012, 7, 37.	4.6	28
20	Deep Sequencing of the Oral Microbiome Reveals Signatures of Periodontal Disease. <i>PLoS ONE</i> , 2012, 7, e37919.	2.5	329
21	COMBREX: a project to accelerate the functional annotation of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2011, 39, D11-D14.	14.5	47
22	Functional characterization of the YmcB and YqeV tRNA methyltransferases of <i>Bacillus subtilis</i> . <i>Nucleic Acids Research</i> , 2010, 38, 6195-6205.	14.5	39
23	A Systems Biology Approach Identifies Inflammatory Abnormalities Between Mouse Strains Prior to Development of Metabolic Disease. <i>Diabetes</i> , 2010, 59, 2960-2971.	0.6	69
24	A Predictive Phosphorylation Signature of Lung Cancer. <i>PLoS ONE</i> , 2009, 4, e7994.	2.5	16
25	Accelerated Postnatal Growth Increases Lipogenic Gene Expression and Adipocyte Size in Low Birth Weight Mice. <i>Diabetes</i> , 2009, 58, 1192-1200.	0.6	76
26	Triplet repeat length bias and variation in the human transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17095-17100.	7.1	33
27	Biological Process Linkage Networks. <i>PLoS ONE</i> , 2009, 4, e5313.	2.5	34
28	Systems Biology via Redescription and Ontologies (III): Protein Classification Using Malaria Parasite's Temporal Transcriptomic Profiles. , 2008, , .		3
29	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
30	Genomewide Analysis of PRC1 and PRC2 Occupancy Identifies Two Classes of Bivalent Domains. <i>PLoS Genetics</i> , 2008, 4, e1000242.	3.5	878
31	Quantitative Analysis of Single Nucleotide Polymorphisms within Copy Number Variation. <i>PLoS ONE</i> , 2008, 3, e3906.	2.5	34
32	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
33	Network-Based Analysis of Affected Biological Processes in Type 2 Diabetes Models. <i>PLoS Genetics</i> , 2007, 3, e96.	3.5	166
34	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
35	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
36	Glycogen Synthase Kinase-3 Represses Cyclic AMP Response Element-binding Protein (CREB)-targeted Immediate Early Genes in Quiescent Cells. <i>Journal of Biological Chemistry</i> , 2007, 282, 9482-9491.	3.4	68

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37	Probabilistic Protein Function Prediction from Heterogeneous Genome-Wide Data. PLoS ONE, 2007, 2, e337.	2.5	84
38	Biological context networks: a mosaic view of the interactome. Molecular Systems Biology, 2006, 2, 66.	7.2	68
39	The art of gene function prediction. Nature Biotechnology, 2006, 24, 1474-1475.	17.5	69
40	Characterization of Two New Aminopeptidases in Escherichia coli. Journal of Bacteriology, 2005, 187, 3671-3677.	2.2	13
41	Identification of genes with fast-evolving regions in microbial genomes. Nucleic Acids Research, 2004, 32, 6347-6357.	14.5	30
42	Identification of Transcription Factor Binding Sites Upstream of Human Genes Regulated by the Phosphatidylinositol 3-Kinase and MEK/ERK Signaling Pathways. Journal of Biological Chemistry, 2004, 279, 20167-20177.	3.4	86
43	GC/AT-content spikes as genomic punctuation marks. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16855-16860.	7.1	99
44	Whole-genome annotation by using evidence integration in functional-linkage networks. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2888-2893.	7.1	293
45	Learning a Hidden Matching. SIAM Journal on Computing, 2004, 33, 487-501.	1.0	52
46	Gene expression module discovery using gibbs sampling. Genome Informatics, 2004, 15, 239-48.	0.4	15
47	Structural Location of Disease-associated Single-nucleotide Polymorphisms. Journal of Molecular Biology, 2003, 327, 1021-1030.	4.2	74
48	Human-Mouse Gene Identification by Comparative Evidence Integration and Evolutionary Analysis. Genome Research, 2003, 13, 1190-1202.	5.5	27
49	Identification of functional links between genes using phylogenetic profiles. Bioinformatics, 2003, 19, 1524-1530.	4.1	139
50	On the normalization of RNA equilibrium free energy to the length of the sequence. Nucleic Acids Research, 2003, 31, 49e-49.	14.5	16
51	Predicting protein function from protein/protein interaction data: a probabilistic approach. Bioinformatics, 2003, 19, i197-i204.	4.1	317
52	A computational framework for optimal masking in the synthesis of oligonucleotide microarrays. Nucleic Acids Research, 2002, 30, 106e-106.	14.5	23
53	Computational Identification of Operons in Microbial Genomes. Genome Research, 2002, 12, 1221-1230.	5.5	119
54	EXTRACTING CONSERVED GENE EXPRESSION MOTIFS FROM GENE EXPRESSION DATA. , 2002, , .		123

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55	Alignment of whole genomes. Nucleic Acids Research, 1999, 27, 2369-2376.	14.5	766
56	Improved microbial gene identification with GLIMMER. Nucleic Acids Research, 1999, 27, 4636-4641.	14.5	2,282
57	Optimized Multiplex PCR: Efficiently Closing a Whole-Genome Shotgun Sequencing Project. Genomics, 1999, 62, 500-507.	2.9	131
58	List of contributors* *Authors' names are followed by the starting page number(s) of their contribution(s).. New Comprehensive Biochemistry, 1998, 32, xi-xiii.	0.1	0
59	Efficient parallel term matching and anti-unification. Journal of Automated Reasoning, 1992, 9, 391-406.	1.4	11
60	Some results on the complexity of exploiting data dependency in parallel logic programs. The Journal of Logic Programming, 1989, 6, 229-241.	1.7	10