

Eric C Rouchka

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

2,361
citations

279798

23
h-index

243625

44
g-index

94
all docs

94
docs citations

94
times ranked

3848
citing authors

#	ARTICLE	IF	CITATIONS
1	Enhancement of the gut barrier integrity by a microbial metabolite through the Nrf2 pathway. <i>Nature Communications</i> , 2019, 10, 89.	12.8	420
2	Gibbs Recursive Sampler: finding transcription factor binding sites. <i>Nucleic Acids Research</i> , 2003, 31, 3580-3585.	14.5	261
3	A Critical Role of the IL-1 β IL-1R Signaling Pathway in Skin Inflammation and Psoriasis Pathogenesis. <i>Journal of Investigative Dermatology</i> , 2019, 139, 146-156.	0.7	152
4	Transcription factor c-Maf is a checkpoint that programs macrophages in lung cancer. <i>Journal of Clinical Investigation</i> , 2020, 130, 2081-2096.	8.2	108
5	A specific low-density neutrophil population correlates with hypercoagulation and disease severity in hospitalized COVID-19 patients. <i>JCI Insight</i> , 2021, 6, .	5.0	79
6	HNRNPA2/B1 is upregulated in endocrine-resistant LCC9 breast cancer cells and alters the miRNA transcriptome when overexpressed in MCF-7 cells. <i>Scientific Reports</i> , 2019, 9, 9430.	3.3	78
7	Involvement of PARP1 in the regulation of alternative splicing. <i>Cell Discovery</i> , 2016, 2, 15046.	6.7	63
8	A comparison of per sample global scaling and per gene normalization methods for differential expression analysis of RNA-seq data. <i>PLoS ONE</i> , 2017, 12, e0176185.	2.5	60
9	Genome-Wide Profiling of PARP1 Reveals an Interplay with Gene Regulatory Regions and DNA Methylation. <i>PLoS ONE</i> , 2015, 10, e0135410.	2.5	55
10	rMAPS: RNA map analysis and plotting server for alternative exon regulation. <i>Nucleic Acids Research</i> , 2016, 44, W333-W338.	14.5	54
11	Transcriptome-wide identification of the RNA-binding landscape of the chromatin-associated protein PARP1 reveals functions in RNA biogenesis. <i>Cell Discovery</i> , 2017, 3, 17043.	6.7	50
12	Inorganic Arsenic-induced cellular transformation is coupled with genome wide changes in chromatin structure, transcriptome and splicing patterns. <i>BMC Genomics</i> , 2015, 16, 212.	2.8	43
13	Decreased ω -6: ω -3 PUFA ratio attenuates ethanol-induced alterations in intestinal homeostasis, microbiota, and liver injury. <i>Journal of Lipid Research</i> , 2019, 60, 2034-2049.	4.2	39
14	Coupling of PARP1-mediated chromatin structural changes to transcriptional RNA polymerase II elongation and cotranscriptional splicing. <i>Epigenetics and Chromatin</i> , 2019, 12, 15.	3.9	39
15	rMAPS2: an update of the RNA map analysis and plotting server for alternative splicing regulation. <i>Nucleic Acids Research</i> , 2020, 48, W300-W306.	14.5	39
16	Polystyrene bead ingestion promotes adiposity and cardiometabolic disease in mice. <i>Ecotoxicology and Environmental Safety</i> , 2022, 232, 113239.	6.0	33
17	Transcriptomic response of breast cancer cells to anacardic acid. <i>Scientific Reports</i> , 2018, 8, 8063.	3.3	32
18	Variant analysis of 1,040 SARS-CoV-2 genomes. <i>PLoS ONE</i> , 2020, 15, e0241535.	2.5	32

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19	Nuclear respiratory factor-1 and bioenergetics in tamoxifen-resistant breast cancer cells. <i>Experimental Cell Research</i> , 2016, 347, 222-231.	2.6	30
20	The induction of peripheral trained immunity in the pancreas incites anti-tumor activity to control pancreatic cancer progression. <i>Nature Communications</i> , 2022, 13, 759.	12.8	30
21	categoryCompare, an analytical tool based on feature annotations. <i>Frontiers in Genetics</i> , 2014, 5, 98.	2.3	29
22	<i>Yersinia pestis</i> Targets the Host Endosome Recycling Pathway during the Biogenesis of the <i>Yersinia</i> -Containing Vacuole To Avoid Killing by Macrophages. <i>MBio</i> , 2018, 9, .	4.1	29
23	Choice of library size normalization and statistical methods for differential gene expression analysis in balanced two-group comparisons for RNA-seq studies. <i>BMC Genomics</i> , 2020, 21, 75.	2.8	29
24	Identification of successful mentoring communities using network-based analysis of mentor-mentee relationships across Nobel laureates. <i>Scientometrics</i> , 2017, 111, 1733-1749.	3.0	28
25	The Adaptor Protein CD2AP Is a Coordinator of Neurotrophin Signaling-Mediated Axon Arbor Plasticity. <i>Journal of Neuroscience</i> , 2016, 36, 4259-4275.	3.6	27
26	Identification of a plasma metabolomic signature of thrombotic myocardial infarction that is distinct from non-thrombotic myocardial infarction and stable coronary artery disease. <i>PLoS ONE</i> , 2017, 12, e0175591.	2.5	27
27	DNA motif detection using particle swarm optimization and expectation-maximization. , 2005, 2005, 181-184.		23
28	Identification of G-quadruplex forming sequences in three manatee papillomaviruses. <i>PLoS ONE</i> , 2018, 13, e0195625.	2.5	22
29	Leukotriene B4-receptor-1 mediated host response shapes gut microbiota and controls colon tumor progression. <i>Oncotarget</i> , 2017, 6, e1361593.	4.6	20
30	Improved locomotor recovery after contusive spinal cord injury in <i>Bmal1</i> ^{-/-} mice is associated with protection of the blood spinal cord barrier. <i>Scientific Reports</i> , 2020, 10, 14212.	3.3	20
31	MPrime: efficient large scale multiple primer and oligonucleotide design for customized gene microarrays. <i>BMC Bioinformatics</i> , 2005, 6, 175.	2.6	19
32	IB4-binding sensory neurons in the adult rat express a novel 3' UTR extended isoform of <i>CaMK4</i> that is associated with its localization to axons. <i>Journal of Comparative Neurology</i> , 2014, 522, 308-336.	1.6	17
33	Transcriptomic analysis of immune response to bacterial lipopolysaccharide in zebra finch (<i>Taeniopygia guttata</i>). <i>BMC Genomics</i> , 2019, 20, 647.	2.8	17
34	Computational Analysis of G-Quadruplex Forming Sequences across Chromosomes Reveals High Density Patterns Near the Terminal Ends. <i>PLoS ONE</i> , 2016, 11, e0165101.	2.5	16
35	Systems characterization of differential plasma metabolome perturbations following thrombotic and non-thrombotic myocardial infarction. <i>Journal of Proteomics</i> , 2017, 160, 38-46.	2.4	15
36	Induction of interferon response by high viral loads at early stage infection may protect against severe outcomes in COVID-19 patients. <i>Scientific Reports</i> , 2021, 11, 15715.	3.3	15

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37	The Rapid Assessment of Aggregated Wastewater Samples for Genomic Surveillance of SARS-CoV-2 on a City-Wide Scale. <i>Pathogens</i> , 2021, 10, 1271.	2.8	15
38	Transcriptional changes in sensory ganglia associated with primary afferent axon collateral sprouting in spared dermatome model. <i>Genomics Data</i> , 2015, 6, 249-252.	1.3	14
39	Dynamic trafficking patterns of IL-17-producing $\gamma\delta$ T cells are linked to the recurrence of skin inflammation in psoriasis-like dermatitis. <i>EBioMedicine</i> , 2022, 82, 104136.	6.1	14
40	rMotifGen: random motif generator for DNA and protein sequences. <i>BMC Bioinformatics</i> , 2007, 8, 292.	2.6	13
41	Shoc2-transduced ERK1/2 motility signals – Novel insights from functional genomics. <i>Cellular Signalling</i> , 2016, 28, 448-459.	3.6	13
42	Whole Transcriptome Analysis Reveals That Filifactor aloisii Modulates TNF α -Stimulated MAPK Activation in Human Neutrophils. <i>Frontiers in Immunology</i> , 2020, 11, 497.	4.8	13
43	Genome-wide miRNA response to anacardic acid in breast cancer cells. <i>PLoS ONE</i> , 2017, 12, e0184471.	2.5	13
44	Effect of single nucleotide polymorphisms on Affymetrix [®] match-mismatch probe pairs. <i>Bioinformatics</i> , 2008, 2, 405-411.	0.5	13
45	RBF-TSS: Identification of Transcription Start Site in Human Using Radial Basis Functions Network and Oligonucleotide Positional Frequencies. <i>PLoS ONE</i> , 2009, 4, e4878.	2.5	12
46	Transcription Factor STAT3 Serves as a Negative Regulator Controlling IgE Class Switching in Mice. <i>ImmunoHorizons</i> , 2018, 2, 349-362.	1.8	12
47	Discovery of a Family of Genomic Sequences Which Interact Specifically with the c-MYC Promoter to Regulate c-MYC Expression. <i>PLoS ONE</i> , 2016, 11, e0161588.	2.5	11
48	Detection of Differentially Expressed Cleavage Site Intervals Within 3 \times Untranslated Regions Using CSI-UTR Reveals Regulated Interaction Motifs. <i>Frontiers in Genetics</i> , 2019, 10, 182.	2.3	11
49	DNA-based random number generation in security circuitry. <i>BioSystems</i> , 2010, 100, 208-214.	2.0	10
50	Framework for reanalysis of publicly available Affymetrix [®] GeneChip [®] data sets based on functional regions of interest. <i>BMC Genomics</i> , 2017, 18, 875.	2.8	10
51	Activity/exercise-induced changes in the liver transcriptome after chronic spinal cord injury. <i>Scientific Data</i> , 2019, 6, 88.	5.3	9
52	Comparative gene expression analysis in melanocytes driven by tumor cell-derived exosomes. <i>Experimental Cell Research</i> , 2020, 386, 111690.	2.6	9
53	Glial granules contain germline proteins in the <i>Drosophila</i> brain, which regulate brain transcriptome. <i>Communications Biology</i> , 2020, 3, 699.	4.4	9
54	DNA media storage. <i>Progress in Natural Science: Materials International</i> , 2008, 18, 603-609.	4.4	8

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55	Transcriptional profile of immediate response to ionizing radiation exposure. <i>Genomics Data</i> , 2016, 7, 82-85.	1.3	8
56	Regulation of miR-29b-1/a transcription and identification of target mRNAs in CHO-K1 cells. <i>Molecular and Cellular Endocrinology</i> , 2017, 444, 38-47.	3.2	8
57	Transcriptome of dorsal root ganglia caudal to a spinal cord injury with modulated behavioral activity. <i>Scientific Data</i> , 2019, 6, 83.	5.3	7
58	Multimiomics analysis of the impact of polychlorinated biphenyls on environmental liver disease in a mouse model. <i>Environmental Toxicology and Pharmacology</i> , 2022, 94, 103928.	4.0	7
59	Detecting and accounting for multiple sources of positional variance in peak list registration analysis and spin system grouping. <i>Journal of Biomolecular NMR</i> , 2017, 68, 281-296.	2.8	6
60	<i>Pas de deux</i>: An Intricate Dance of Anther Smut and Its Host. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 505-518.	1.8	6
61	A combined approach with gene-wise normalization improves the analysis of RNA-seq data in human breast cancer subtypes. <i>PLoS ONE</i> , 2018, 13, e0201813.	2.5	6
62	Dataset for dose and time-dependent transcriptional response to ionizing radiation exposure. <i>Data in Brief</i> , 2019, 27, 104624.	1.0	5
63	Ileum Gene Expression in Response to Acute Systemic Inflammation in Mice Chronically Fed Ethanol: Beneficial Effects of Elevated Tissue n-3 PUFAs. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1582.	4.1	5
64	Exposure to Fine Particulate Matter Air Pollution Alters mRNA and miRNA Expression in Bone Marrow-Derived Endothelial Progenitor Cells from Mice. <i>Genes</i> , 2021, 12, 1058.	2.4	5
65	Database of exact tandem repeats in the Zebrafish genome. <i>BMC Genomics</i> , 2010, 11, 347.	2.8	4
66	DNA-based dynamic logic circuitry. , 2010, , .		4
67	Data set for transcriptional response to depletion of the Shoc2 scaffolding protein. <i>Data in Brief</i> , 2016, 7, 770-778.	1.0	4
68	Feature Selection in Cancer Classification from mRNA Data Based on Localized Dimension Reduction. , 2009, , .		3
69	Transcriptional signatures of the small intestinal mucosa in response to ethanol in transgenic mice rich in endogenous n3 fatty acids. <i>Scientific Reports</i> , 2020, 10, 19930.	3.3	3
70	Affymetrix® Mismatch (MM) Probes: Useful after All. , 2012, , .		2
71	Adjusted Sample Size Calculation for RNA-seq Data in the Presence of Confounding Covariates. <i>BioMedInformatics</i> , 2021, 1, 47-63.	2.0	2
72	Computational Prediction of Genes Translationally Regulated by Cytoplasmic Polyadenylation Elements. <i>Lecture Notes in Computer Science</i> , 2009, , 353-361.	1.3	2

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73	Inference and Sample Size Calculations Based on Statistical Tests in a Negative Binomial Distribution for Differential Gene Expression in RNAseq Data. <i>Journal of Biometrics & Biostatistics</i> , 2017, 08, .	4.0	2
74	Interval Trees for Detection of Overlapping Genetic Entities. , 2011, , .		1
75	An Island-Based Approach for Differential Expression Analysis. , 2013, 2013, 419-429.		1
76	RNA-seq data of soleus muscle tissue after spinal cord injury under conditions of inactivity and applied exercise. <i>Data in Brief</i> , 2020, 28, 105056.	1.0	1
77	Sex-Based Differences in Cardiac Gene Expression and Function in BDNF Val66Met Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7002.	4.1	1
78	Combined exposure to polychlorinated biphenyls and high-fat diet modifies the global epitranscriptomic landscape in mouse liver. <i>Environmental Epigenetics</i> , 2021, 7, dvab008.	1.8	1
79	A Heuristic Algorithm for Detecting Intercellular Interactions. , 2011, , .		0
80	A comparison of combined p-value methods for gene differential expression using RNA-seq data. , 2014, , .		0
81	Region-based custom chip description formats for reanalysis of publicly available affymetrix® genechip® data sets. , 2016, , .		0
82	Cover Image, Volume 85, Issue 5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, C1-C1.	2.6	0
83	Dietary copper&fructose interactions alter gut microbiome in a sex&differential manner likely contributes to the sex differences in the metabolic phenotype. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.5	0
84	Differential Expression of Long Noncoding RNAs in Murine Myoblasts After Short Hairpin RNA-Mediated Dysferlin Silencing In Vitro: Microarray Profiling. <i>JMIR Bioinformatics and Biotechnology</i> , 2022, 3, e33186.	0.9	0