

Fumiki Katsuoka

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

5,901
citations

101543

36
h-index

76900

74
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95
all docs

95
docs citations

95
times ranked

8604
citing authors

#	ARTICLE	IF	CITATIONS
1	Target Gene Diversity of the Nrf1-MafG Transcription Factor Revealed by a Tethered Heterodimer. <i>Molecular and Cellular Biology</i> , 2022, 42, mcb0052021.	2.3	8
2	CEBPB is required for NRF2-mediated drug resistance in NRF2-activated non-small cell lung cancer cells. <i>Journal of Biochemistry</i> , 2022, 171, 567-578.	1.7	13
3	The I^2 -TrCP-Mediated Pathway Cooperates with the Keap1-Mediated Pathway in Nrf2 Degradation <i>In Vivo</i> . <i>Molecular and Cellular Biology</i> , 2022, 42, .	2.3	13
4	Identification of Dominant Transcripts in Oxidative Stress Response by a Full-Length Transcriptome Analysis. <i>Molecular and Cellular Biology</i> , 2021, 41, .	2.3	7
5	Novel candidates of pathogenic variants of the BRCA1 and BRCA2 genes from a dataset of 3,552 Japanese whole genomes (3.5KJPNv2). <i>PLoS ONE</i> , 2021, 16, e0236907.	2.5	7
6	Loss of Ftsj1 perturbs codon-specific translation efficiency in the brain and is associated with X-linked intellectual disability. <i>Science Advances</i> , 2021, 7, .	10.3	30
7	GWAS Identified IL4R and the Major Histocompatibility Complex Region as the Associated Loci of Total Serum IgE Levels in 9,260 Japanese Individuals. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2749-2752.	0.7	4
8	The association between ERK inhibitor sensitivity and molecular characteristics in colorectal cancer. <i>Biochemical and Biophysical Research Communications</i> , 2021, 560, 59-65.	2.1	4
9	Skeletal muscle-specific Keap1 disruption modulates fatty acid utilization and enhances exercise capacity in female mice. <i>Redox Biology</i> , 2021, 43, 101966.	9.0	15
10	Construction and integration of three de novo Japanese human genome assemblies toward a population-specific reference. <i>Nature Communications</i> , 2021, 12, 226.	12.8	31
11	jMorp updates in 2020: large enhancement of multi-omics data resources on the general Japanese population. <i>Nucleic Acids Research</i> , 2021, 49, D536-D544.	14.5	107
12	Genetic loci for lung function in Japanese adults with adjustment for exhaled nitric oxide levels as airway inflammation indicator. <i>Communications Biology</i> , 2021, 4, 1288.	4.4	13
13	dbTMM: an integrated database of large-scale cohort, genome and clinical data for the Tohoku Medical Megabank Project. <i>Human Genome Variation</i> , 2021, 8, 44.	0.7	7
14	Nrf2 plays a critical role in the metabolic response during and after spaceflight. <i>Communications Biology</i> , 2021, 4, 1381.	4.4	10
15	Landscape of electrophilic and inflammatory stress-mediated gene regulation in human lymphoblastoid cell lines. <i>Free Radical Biology and Medicine</i> , 2020, 161, 71-83.	2.9	4
16	Enhancer remodeling promotes tumor-initiating activity in NRF2-activated non-small cell lung cancers. <i>Nature Communications</i> , 2020, 11, 5911.	12.8	60
17	Nrf2 contributes to the weight gain of mice during space travel. <i>Communications Biology</i> , 2020, 3, 496.	4.4	27
18	Analysis of HLA-G long-read genomic sequences in mother-offspring pairs with preeclampsia. <i>Scientific Reports</i> , 2020, 10, 20027.	3.3	5

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19	Identification of critical genetic variants associated with metabolic phenotypes of the Japanese population. <i>Communications Biology</i> , 2020, 3, 662.	4.4	16
20	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. <i>Nature Communications</i> , 2020, 11, 3175.	12.8	34
21	Impacts of NRF2 activation in non-small cell lung cancer cell lines on extracellular metabolites. <i>Cancer Science</i> , 2020, 111, 667-678.	3.9	29
22	A genotype imputation method for de-identified haplotype reference information by using recurrent neural network. <i>PLoS Computational Biology</i> , 2020, 16, e1008207.	3.2	11
23	Direct and Specific Functional Evaluation of the Nrf2 and MafG Heterodimer by Introducing a Tethered Dimer into Small Maf-Deficient Cells. <i>Molecular and Cellular Biology</i> , 2019, 39, .	2.3	25
24	3.5KJPNv2: an allele frequency panel of 3552 Japanese individuals including the X chromosome. <i>Human Genome Variation</i> , 2019, 6, 28.	0.7	115
25	Construction of JRG (Japanese reference genome) with single-molecule real-time sequencing. <i>Human Genome Variation</i> , 2019, 6, 27.	0.7	9
26	Biobank Establishment and Sample Management in the Tohoku Medical Megabank Project. <i>Tohoku Journal of Experimental Medicine</i> , 2019, 248, 45-55.	1.2	40
27	Estimating carrier frequencies of newborn screening disorders using a whole-genome reference panel of 3552 Japanese individuals. <i>Human Genetics</i> , 2019, 138, 389-409.	3.8	7
28	Maternity Log study: a longitudinal lifelog monitoring and multiomics analysis for the early prediction of complicated pregnancy. <i>BMJ Open</i> , 2019, 9, e025939.	1.9	10
29	Nrf2 activation in myeloid cells and endothelial cells differentially mitigates sickle cell disease pathology in mice. <i>Blood Advances</i> , 2019, 3, 1285-1297.	5.2	17
30	Genome analyses for the Tohoku Medical Megabank Project towards establishment of personalized healthcare. <i>Journal of Biochemistry</i> , 2019, 165, 139-158.	1.7	33
31	Lactate dehydrogenase C is required for the protein expression of a sperm-specific isoform of lactate dehydrogenase A. <i>Journal of Biochemistry</i> , 2019, 165, 323-334.	1.7	15
32	Construction of full-length Japanese reference panel of class I HLA genes with single-molecule, real-time sequencing. <i>Pharmacogenomics Journal</i> , 2019, 19, 136-146.	2.0	12
33	Establishment of Integrated Biobank for Precision Medicine and Personalized Healthcare: The Tohoku Medical Megabank Project. <i>JMA Journal</i> , 2019, 2, 113-122.	0.8	21
34	Identification of somatic mutations in postmortem human brains by whole genome sequencing and their implications for psychiatric disorders. <i>Psychiatry and Clinical Neurosciences</i> , 2018, 72, 280-294.	1.8	9
35	Omics research project on prospective cohort studies from the Tohoku Medical Megabank Project. <i>Genes To Cells</i> , 2018, 23, 406-417.	1.2	38
36	Identification of somatic genetic alterations in ovarian clear cell carcinoma with next generation sequencing. <i>Genes Chromosomes and Cancer</i> , 2018, 57, 51-60.	2.8	83

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37	Evaluation of reported pathogenic variants and their frequencies in a Japanese population based on a whole-genome reference panel of 2049 individuals. <i>Journal of Human Genetics</i> , 2018, 63, 213-230.	2.3	35
38	<i>O</i> -GlcNAcylation Signal Mediates Proteasome Inhibitor Resistance in Cancer Cells by Stabilizing NRF1. <i>Molecular and Cellular Biology</i> , 2018, 38, .	2.3	43
39	Regional genetic differences among Japanese populations and performance of genotype imputation using whole-genome reference panel of the Tohoku Medical Megabank Project. <i>BMC Genomics</i> , 2018, 19, 551.	2.8	14
40	Derepression of the DNA Methylation Machinery of the Gata1 Gene Triggers the Differentiation Cue for Erythropoiesis. <i>Molecular and Cellular Biology</i> , 2017, 37, .	2.3	13
41	GATA2 haploinsufficiency accelerates EVI1-driven leukemogenesis. <i>Blood</i> , 2017, 130, 908-919.	1.4	30
42	Halofuginone enhances the chemo-sensitivity of cancer cells by suppressing NRF2 accumulation. <i>Free Radical Biology and Medicine</i> , 2017, 103, 236-247.	2.9	117
43	Genome-wide identification of inter-individually variable DNA methylation sites improves the efficacy of epigenetic association studies. <i>Npj Genomic Medicine</i> , 2017, 2, 11.	3.8	59
44	Monitoring of minimal residual disease in early T-cell precursor acute lymphoblastic leukaemia by next-generation sequencing. <i>British Journal of Haematology</i> , 2017, 176, 318-321.	2.5	7
45	A Histologic Categorization of Aqueous Outflow Routes in Familial Open-Angle Glaucoma and Associations With Mutations in the <i>MYOC</i> Gene in Japanese Patients. , 2017, 58, 2818.		13
46	Nrf2-Mediated Regulation of Skeletal Muscle Glycogen Metabolism. <i>Molecular and Cellular Biology</i> , 2016, 36, 1655-1672.	2.3	101
47	Small Maf proteins (MafF, MafG, MafK): History, structure and function. <i>Gene</i> , 2016, 586, 197-205.	2.2	174
48	The structural origin of metabolic quantitative diversity. <i>Scientific Reports</i> , 2016, 6, 31463.	3.3	18
49	Small Maf deficiency recapitulates the liver phenotypes of Nrf1 and Nrf2 deficient mice. <i>Genes To Cells</i> , 2016, 21, 1309-1319.	1.2	21
50	Unique cistrome defined as CsMBE is strictly required for Nrf2-sMaf heterodimer function in cytoprotection. <i>Free Radical Biology and Medicine</i> , 2016, 91, 45-57.	2.9	55
51	Discovery of an NRF-specific inducer from a large-scale chemical library using a direct NRF-protein monitoring system. <i>Genes To Cells</i> , 2015, 20, 563-577.	1.2	7
52	iJGVD: an integrative Japanese genome variation database based on whole-genome sequencing. <i>Human Genome Variation</i> , 2015, 2, 15050.	0.7	100
53	DNA methyltransferase 3a regulates osteoclast differentiation by coupling to an S-adenosylmethionine-producing metabolic pathway. <i>Nature Medicine</i> , 2015, 21, 281-287.	30.7	190
54	Rare variant discovery by deep whole-genome sequencing of 1,070 Japanese individuals. <i>Nature Communications</i> , 2015, 6, 8018.	12.8	352

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55	Transcription factor <i>NF-κB</i> -related factor 1 impairs glucose metabolism in mice. <i>Genes To Cells</i> , 2014, 19, 650-665.	1.2	43
56	An efficient quantitation method of next-generation sequencing libraries by using MiSeq sequencer. <i>Analytical Biochemistry</i> , 2014, 466, 27-29.	2.4	47
57	Validation of multiple single nucleotide variation calls by additional exome analysis with a semiconductor sequencer to supplement data of whole-genome sequencing of a human population. <i>BMC Genomics</i> , 2014, 15, 673.	2.8	10
58	Nrf2 deficiency leads to behavioral, neurochemical and transcriptional changes in mice. <i>Genes To Cells</i> , 2013, 18, 899-908.	1.2	33
59	NF-E2-Related Factor 1 (Nrf1) Serves as a Novel Regulator of Hepatic Lipid Metabolism through Regulation of the <i>Lipin1</i> and <i>PGC-1β</i> Genes. <i>Molecular and Cellular Biology</i> , 2012, 32, 2760-2770.	2.3	89
60	Embryonic Lethality and Fetal Liver Apoptosis in Mice Lacking All Three Small Maf Proteins. <i>Molecular and Cellular Biology</i> , 2012, 32, 808-816.	2.3	55
61	Nrf2-Maf heterodimers contribute globally to antioxidant and metabolic networks. <i>Nucleic Acids Research</i> , 2012, 40, 10228-10239.	14.5	317
62	Constitutive Expression of Aryl Hydrocarbon Receptor in Keratinocytes Causes Inflammatory Skin Lesions. <i>Molecular and Cellular Biology</i> , 2012, 32, 1759-1759.	2.3	0
63	Nrf2 degron-fused reporter system: a new tool for specific evaluation of Nrf2 inducers. <i>Genes To Cells</i> , 2011, 16, 406-415.	1.2	19
64	Central nervous system-specific deletion of transcription factor Nrf1 causes progressive motor neuronal dysfunction. <i>Genes To Cells</i> , 2011, 16, 692-703.	1.2	90
65	Molecular Determinants for Small Maf Protein Control of Platelet Production. <i>Molecular and Cellular Biology</i> , 2011, 31, 151-162.	2.3	15
66	NF-E2 domination over Nrf2 promotes ROS accumulation and megakaryocytic maturation. <i>Blood</i> , 2010, 115, 677-686.	1.4	84
67	Nrf1 and Nrf2 Play Distinct Roles in Activation of Antioxidant Response Element-dependent Genes. <i>Journal of Biological Chemistry</i> , 2008, 283, 33554-33562.	3.4	275
68	Hepatocyte-Specific Deletion of Heme Oxygenase-1 Disrupts Redox Homeostasis in Basal and Oxidative Environments. <i>Tohoku Journal of Experimental Medicine</i> , 2008, 216, 331-339.	1.2	30
69	Pharmacodynamic characterization of chemopreventive triterpenoids as exceptionally potent inducers of Nrf2-regulated genes. <i>Molecular Cancer Therapeutics</i> , 2007, 6, 154-162.	4.1	268
70	Molecular Basis Distinguishing the DNA Binding Profile of Nrf2-Maf Heterodimer from That of Maf Homodimer. <i>Journal of Biological Chemistry</i> , 2007, 282, 33681-33690.	3.4	92
71	Two-site substrate recognition model for the Keap1-Nrf2 system: a hinge and latch mechanism. <i>Biological Chemistry</i> , 2006, 387, 1311-20.	2.5	397
72	MafG Sumoylation Is Required for Active Transcriptional Repression. <i>Molecular and Cellular Biology</i> , 2006, 26, 4652-4663.	2.3	49

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73	Transgenic expression of BACH1 transcription factor results in megakaryocytic impairment. <i>Blood</i> , 2005, 105, 3100-3108.	1.4	40
74	Nrf2 Transcriptionally Activates the mafG Gene through an Antioxidant Response Element. <i>Journal of Biological Chemistry</i> , 2005, 280, 4483-4490.	3.4	94
75	Genetic Evidence that Small Maf Proteins Are Essential for the Activation of Antioxidant Response Element-Dependent Genes. <i>Molecular and Cellular Biology</i> , 2005, 25, 8044-8051.	2.3	250
76	Constitutive Expression of Aryl Hydrocarbon Receptor in Keratinocytes Causes Inflammatory Skin Lesions. <i>Molecular and Cellular Biology</i> , 2005, 25, 9360-9368.	2.3	144
77	Small Maf proteins serve as transcriptional cofactors for keratinocyte differentiation in the Keap1-Nrf2 regulatory pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6379-6384.	7.1	293
78	Transgenic Expression of Bach1 Transcription Factor Results in Down-Regulation of the p45 Target Genes in Megakaryocytic Lineage Cells. <i>Blood</i> , 2004, 104, 1605-1605.	1.4	1
79	Small Maf Compound Mutants Display Central Nervous System Neuronal Degeneration, Aberrant Transcription, and Bach Protein Mislocalization Coincident with Myoclonus and Abnormal Startle Response. <i>Molecular and Cellular Biology</i> , 2003, 23, 1163-1174.	2.3	46
80	Integration and diversity of the regulatory network composed of Maf and CNC families of transcription factors. <i>Gene</i> , 2002, 294, 1-12.	2.2	412
81	Solution structure of the DNA-binding domain of MafG. <i>Nature Structural Biology</i> , 2002, 9, 252-256.	9.7	42
82	An embryonic/fetal beta-type globin gene repressor contains a nuclear receptor TR2/TR4 heterodimer. <i>EMBO Journal</i> , 2002, 21, 3434-3442.	7.8	100
83	Functional characterization of the two alternative promoters of human p45 NF-E2 gene. <i>Experimental Hematology</i> , 2000, 28, 1113-1119.	0.4	19
84	One enhancer mediates mafK transcriptional activation in both hematopoietic and cardiac muscle cells. <i>EMBO Journal</i> , 2000, 19, 2980-2991.	7.8	23
85	Positive or Negative MARE-Dependent Transcriptional Regulation Is Determined by the Abundance of Small Maf Proteins. <i>Cell</i> , 2000, 103, 865-876.	28.9	136
86	Characterization of the Murine mafF Gene. <i>Journal of Biological Chemistry</i> , 1999, 274, 21162-21169.	3.4	51
87	Type II Alveolar Epithelial Cells in Lung Express Receptor for Advanced Glycation End Products (RAGE) Gene. <i>Biochemical and Biophysical Research Communications</i> , 1997, 238, 512-516.	2.1	87