

Kazuho Ikeo

List of Publications by Year in descending order

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111
papers

6,767
citations

94433

37
h-index

64796

79
g-index

114
all docs

114
docs citations

114
times ranked

8100
citing authors

#	ARTICLE	IF	CITATIONS
1	The dynamic genome of Hydra. <i>Nature</i> , 2010, 464, 592-596.	27.8	743
2	Pax 6: mastering eye morphogenesis and eye evolution. <i>Trends in Genetics</i> , 1999, 15, 371-377.	6.7	706
3	Cloning of human, mouse and fission yeast recombination genes homologous to RAD51 and recA. <i>Nature Genetics</i> , 1993, 4, 239-243.	21.4	506
4	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	14.5	295
5	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	5.6	290
6	FGFR-related gene <i>nou-darake</i> restricts brain tissues to the head region of planarians. <i>Nature</i> , 2002, 419, 620-624.	27.8	244
7	The Rice Annotation Project Database (RAP-DB): hub for <i>Oryza sativa</i> ssp. <i>japonica</i> genome information. <i>Nucleic Acids Research</i> , 2006, 34, D741-D744.	14.5	219
8	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	5.5	218
9	Comparative Complete Genome Sequence Analysis of the Amino Acid Replacements Responsible for the Thermostability of <i>Corynebacterium efficiens</i> . <i>Genome Research</i> , 2003, 13, 1572-1579.	5.5	194
10	Origin and evolutionary process of the CNS elucidated by comparative genomics analysis of planarian ESTs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7666-7671.	7.1	172
11	Constrained evolution with respect to gene overlap of hepatitis B virus. <i>Journal of Molecular Evolution</i> , 1997, 44, S83-S90.	1.8	148
12	CIBEX: Center for Information Biology gene EXpression database. <i>Comptes Rendus - Biologies</i> , 2003, 326, 1079-1082.	0.2	138
13	Bone Marrow Adipocytes Facilitate Fatty Acid Oxidation Activating AMPK and a Transcriptional Network Supporting Survival of Acute Monocytic Leukemia Cells. <i>Cancer Research</i> , 2017, 77, 1453-1464.	0.9	123
14	Dissecting planarian central nervous system regeneration by the expression of neural-specific genes. <i>Development Growth and Differentiation</i> , 2002, 44, 135-146.	1.5	120
15	Genome-Wide Association Study Identifies TLL1 Variant Associated With Development of Hepatocellular Carcinoma After Eradication of Hepatitis C Virus Infection. <i>Gastroenterology</i> , 2017, 152, 1383-1394.	1.3	115
16	The expression of neural-specific genes reveals the structural and molecular complexity of the planarian central nervous system. <i>Mechanisms of Development</i> , 2002, 116, 199-204.	1.7	113
17	Histone H4 Lys 20 Monomethylation of the CENP-A Nucleosome Is Essential for Kinetochores Assembly. <i>Developmental Cell</i> , 2014, 29, 740-749.	7.0	101
18	Evolutionary relationship of hepatitis C, pesti-, flavi-, plantviruses, and newly discovered GB hepatitis agents. <i>FEBS Letters</i> , 1996, 378, 232-234.	2.8	93

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19	Detection of apoptosis during planarian regeneration by the expression of apoptosis-related genes and TUNEL assay. <i>Gene</i> , 2004, 333, 15-25.	2.2	92
20	Comparative Analysis of Gene Expression for Convergent Evolution of Camera Eye Between Octopus and Human. <i>Genome Research</i> , 2004, 14, 1555-1561.	5.5	78
21	Effect of Wild and Cultivated Rice Genotypes on Rhizosphere Bacterial Community Composition. <i>Rice</i> , 2016, 9, 42.	4.0	75
22	Pirfenidone attenuates lung fibrotic fibroblast responses to transforming growth factor- β 1. <i>Respiratory Research</i> , 2019, 20, 119.	3.6	74
23	Search for the Evolutionary Origin of a Brain: Planarian Brain Characterized by Microarray. <i>Molecular Biology and Evolution</i> , 2003, 20, 784-791.	8.9	73
24	Nematogalectin, a nematocyst protein with GlyXY and galectin domains, demonstrates nematocyte-specific alternative splicing in <i>Hydra</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18539-18544.	7.1	69
25	Neural Network in Planarian Revealed by an Antibody against Planarian Synaptotagmin Homologue. <i>Biochemical and Biophysical Research Communications</i> , 1999, 260, 426-432.	2.1	68
26	The genome stability in <i>Corynebacterium</i> species due to lack of the recombinational repair system. <i>Gene</i> , 2003, 317, 149-155.	2.2	66
27	Acetylation of histone H4 lysine 5 and 12 is required for CENP-A deposition into centromeres. <i>Nature Communications</i> , 2016, 7, 13465.	12.8	66
28	The Scaly-foot Snail genome and implications for the origins of biomineralised armour. <i>Nature Communications</i> , 2020, 11, 1657.	12.8	64
29	Chinese spring wheat (<i>Triticum aestivum</i> L.) chloroplast genome: Complete sequence and contig clones. <i>Plant Molecular Biology Reporter</i> , 2000, 18, 243-253.	1.8	62
30	Induction of a noggin-Like Gene by Ectopic DV Interaction during Planarian Regeneration. <i>Developmental Biology</i> , 2002, 250, 59-70.	2.0	61
31	Lack of interleukin-6 in the tumor microenvironment augments type-1 immunity and increases the efficacy of cancer immunotherapy. <i>Cancer Science</i> , 2017, 108, 1959-1966.	3.9	61
32	<i>HOX</i> genes in the sepiolid squid <i>Euprymna scolopes</i> : Implications for the evolution of complex body plans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2088-2093.	7.1	60
33	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2007, 36, D793-D799.	14.5	57
34	Whole Exome Analysis Identifies Frequent <i>CNGA1</i> Mutations in Japanese Population with Autosomal Recessive Retinitis Pigmentosa. <i>PLoS ONE</i> , 2014, 9, e108721.	2.5	56
35	Transcriptomic changes with increasing algal symbiont reveal the detailed process underlying establishment of coral-algal symbiosis. <i>Scientific Reports</i> , 2018, 8, 16802.	3.3	46
36	Cloning and functional analysis of ascidian <i>Mitf</i> in vivo: insights into the origin of vertebrate pigment cells. <i>Mechanisms of Development</i> , 2003, 120, 1489-1504.	1.7	45

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37	DNA Methylome Analysis Identifies Transcription Factor-Based Epigenomic Signatures of Multilineage Competence in Neural Stem/Progenitor Cells. <i>Cell Reports</i> , 2017, 20, 2992-3003.	6.4	45
38	Maser: one-stop platform for NGS big data from analysis to visualization. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	42
39	HpBase: A genome database of a sea urchin, <i>Hemicentrotus pulcherrimus</i> . <i>Development Growth and Differentiation</i> , 2018, 60, 174-182.	1.5	39
40	Aging of spermatogonial stem cells by Jnk-mediated glycolysis activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16404-16409.	7.1	39
41	HJURP is involved in the expansion of centromeric chromatin. <i>Molecular Biology of the Cell</i> , 2015, 26, 2742-2754.	2.1	38
42	Ascidian tyrosinase gene: Its unique structure and expression in the developing brain. , 1997, 208, 363-374.		37
43	Exogenous mitochondrial transfer and endogenous mitochondrial fission facilitate AML resistance to OxPhos inhibition. <i>Blood Advances</i> , 2021, 5, 4233-4255.	5.2	36
44	The evolutionary relationship between gene duplication and alternative splicing. <i>Gene</i> , 2008, 427, 19-31.	2.2	34
45	Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees. <i>Nucleic Acids Research</i> , 2007, 36, D787-D792.	14.5	33
46	Mutation pattern of human immunodeficiency virus genes. <i>Journal of Molecular Evolution</i> , 1991, 32, 360-363.	1.8	32
47	Function and Evolutionary Origin of Unicellular Camera-Type Eye Structure. <i>PLoS ONE</i> , 2015, 10, e0118415.	2.5	31
48	Structure and developmental expression of the ascidian TRP gene: Insights into the evolution of pigment cell-specific gene expression. <i>Developmental Dynamics</i> , 1999, 215, 225-237.	1.8	29
49	Constitutive centromere-associated network controls centromere drift in vertebrate cells. <i>Journal of Cell Biology</i> , 2017, 216, 101-113.	5.2	29
50	Evolution of pathogenic viruses with special reference to the rates of synonymous and nonsynonymous substitutions.. <i>Japanese Journal of Genetics</i> , 1994, 69, 481-488.	1.0	28
51	CCT2 Mutations Evoke Leber Congenital Amaurosis due to Chaperone Complex Instability. <i>Scientific Reports</i> , 2016, 6, 33742.	3.3	27
52	Evolutionary Process of Amino Acid Biosynthesis in <i>Corynebacterium</i> at the Whole Genome Level. <i>Molecular Biology and Evolution</i> , 2004, 21, 1683-1691.	8.9	26
53	Different Endosymbiotic Interactions in Two Hydra Species Reflect the Evolutionary History of Endosymbiosis. <i>Genome Biology and Evolution</i> , 2016, 8, 2155-2163.	2.5	24
54	<i>RPE65</i> Mutations in Two Japanese Families with Leber Congenital Amaurosis. <i>Ophthalmic Genetics</i> , 2016, 37, 161-169.	1.2	24

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55	An Association Between Core Mutations in Hepatitis B Virus Genotype F1b and Hepatocellular Carcinoma in Alaskan Native People. <i>Hepatology</i> , 2019, 69, 19-33.	7.3	24
56	Establishment of homozygous knock-out sea urchins. <i>Current Biology</i> , 2020, 30, R427-R429.	3.9	24
57	Identification of Novel Mutations in the LRR-Cap Domain of <i>C21orf2</i> in Japanese Patients With Retinitis Pigmentosa and Cone-Rod Dystrophy. <i>Investigative Ophthalmology and Visual Science</i> , 2016, 57, 4255.		23
58	Evolutionary Transitions of MicroRNA-Target Pairs. <i>Genome Biology and Evolution</i> , 2016, 8, 1621-1633.	2.5	23
59	Comprehensive single-cell transcriptome analysis reveals heterogeneity in endometrioid adenocarcinoma tissues. <i>Scientific Reports</i> , 2017, 7, 14225.	3.3	23
60	Comparative genome analyses of nervous system-specific genes. <i>Gene</i> , 2006, 365, 130-136.	2.2	22
61	Comparative miRNAs analysis of Two contrasting broccoli inbred lines with divergent head-forming capacity under temperature stress. <i>BMC Genomics</i> , 2015, 16, 1026.	2.8	22
62	Evolutionary origin of numerous kringles in human and simian apolipoprotein(a). <i>FEBS Letters</i> , 1991, 287, 146-148.	2.8	21
63	Novel <i>C8orf37</i> Mutations in Patients with Early-onset Retinal Dystrophy, Macular Atrophy, Cataracts, and High Myopia. <i>Ophthalmic Genetics</i> , 2016, 37, 1-8.	1.2	17
64	The Human Anatomic Gene Expression Library (H-ANGEL), the H-Inv integrative display of human gene expression across disparate technologies and platforms. <i>Nucleic Acids Research</i> , 2004, 33, D567-D572.	14.5	16
65	RHO Mutations (p.W126L and p.A346P) in Two Japanese Families with Autosomal Dominant Retinitis Pigmentosa. <i>Journal of Ophthalmology</i> , 2014, 2014, 1-10.	1.3	16
66	Construction of complete <i>Tupaia belangeri</i> transcriptome database by whole-genome and comprehensive RNA sequencing. <i>Scientific Reports</i> , 2019, 9, 12372.	3.3	16
67	Accelerated pseudogenization on the neo-X chromosome in <i>Drosophila miranda</i> . <i>Nature Communications</i> , 2016, 7, 13659.	12.8	15
68	Biological Databases at DNA Data Bank of Japan in the Era of Next-Generation Sequencing Technologies. <i>Advances in Experimental Medicine and Biology</i> , 2010, 680, 125-135.	1.6	14
69	Oxphos Inhibition Induces Formation of Tunneling Nanotubes in AML Cells and Facilitates Mitochondrial Transfer from BM Stroma to AML That Contributes to Microenvironment-Mediated Drug-Resistance of AML. <i>Blood</i> , 2019, 134, 911-911.	1.4	11
70	Effects of Cordycepin in <i>Cordyceps militaris</i> during Its Infection to Silkworm Larvae. <i>Microorganisms</i> , 2021, 9, 681.	3.6	10
71	Two-step evolution of endosymbiosis between hydra and algae. <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 19-25.	2.7	9
72	VaProS: a database-integration approach for protein/genome information retrieval. <i>Journal of Structural and Functional Genomics</i> , 2016, 17, 69-81.	1.2	9

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73	Genome-Wide Association Study Identifies ZNF354C Variants Associated with Depression from Interferon-Based Therapy for Chronic Hepatitis C. <i>PLoS ONE</i> , 2016, 11, e0164418.	2.5	9
74	Inhibition of BCL2A1 by STAT5 inactivation overcomes resistance to targeted therapies of FLT3-ITD/D835 mutant AML. <i>Translational Oncology</i> , 2022, 18, 101354.	3.7	9
75	Gene-by-gene or localized dosage compensation on the neo-X chromosome in <i>Drosophila miranda</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 1875-1881.	2.5	8
76	Collagen adhesion gene is associated with bloodstream infections caused by methicillin-resistant <i>Staphylococcus aureus</i> . <i>International Journal of Infectious Diseases</i> , 2020, 91, 22-31.	3.3	8
77	DOCK11 and DENND2A play pivotal roles in the maintenance of hepatitis B virus in host cells. <i>PLoS ONE</i> , 2021, 16, e0246313.	2.5	8
78	Coevolution of Axon Guidance Molecule Slit and Its Receptor Robo. <i>PLoS ONE</i> , 2014, 9, e94970.	2.5	7
79	Molecular phylogeny of ten intertidal hermit crabs of the genus <i>Pagurus</i> inferred from multiple mitochondrial genes, with special emphasis on the evolutionary relationship of <i>Pagurus lanuginosus</i> and <i>Pagurus maculosus</i> . <i>Genetica</i> , 2018, 146, 369-381.	1.1	7
80	Multiple analysis of root exudates and microbiome in rice (<i>Oryza sativa</i>) under low P conditions. <i>Archives of Microbiology</i> , 2021, 203, 5599-5611.	2.2	7
81	Specific Features of Fibrotic Lung Fibroblasts Highly Sensitive to Fibrotic Processes Mediated via TGF- β -ERK5 Interaction. <i>Cellular Physiology and Biochemistry</i> , 2019, 52, 822-837.	1.6	7
82	Hydrophilic Shell Matrix Proteins of <i>Nautilus pompilius</i> and the Identification of a Core Set of Conchiferan Domains. <i>Genes</i> , 2021, 12, 1925.	2.4	7
83	<sc>IFN</sc> β -mediated <sc>NK2R</sc> expression is related to the malignancy of colon cancer cells. <i>Cancer Science</i> , 2022, , .	3.9	7
84	Gene dosage imbalance of human chromosome 21 in mouse embryonic stem cells differentiating to neurons. <i>Gene</i> , 2011, 481, 93-101.	2.2	6
85	Clonal analysis revealed functional heterogeneity in cancer stem-like cell phenotypes in uterine endometrioid adenocarcinoma. <i>Experimental and Molecular Pathology</i> , 2019, 106, 78-88.	2.1	6
86	Development of a time-series shotgun metagenomics database for monitoring microbial communities at the Pacific coast of Japan. <i>Scientific Reports</i> , 2021, 11, 12222.	3.3	6
87	The reduction of miR146b-5p in monocytes and T cells could contribute to the immunopathogenesis of hepatitis C virus infection. <i>Scientific Reports</i> , 2019, 9, 13393.	3.3	5
88	The increased frequency of methicillin-resistant <i>Staphylococcus aureus</i> with low MIC of beta-lactam antibiotics isolated from hospitalized patients. <i>Journal of Infection and Chemotherapy</i> , 2020, 26, 604-610.	1.7	5
89	Diversity and functions of bacterial communities in water and sediment from the watershed of the Tama River flowing a highly urbanized area. <i>Fisheries Science</i> , 2021, 87, 697-715.	1.6	5
90	Metagenomic analysis provides functional insights into seasonal change of a non-cyanobacterial prokaryotic community in temperate coastal waters. <i>PLoS ONE</i> , 2021, 16, e0257862.	2.5	5

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91	<scp>TrBase</scp>: A genome and transcriptome database of <i>Temnopleurus reevesii</i>. Development Growth and Differentiation, 2022, 64, 210-218.	1.5	5
92	Ascidian tyrosinase gene: Its unique structure and expression in the developing brain. Developmental Dynamics, 1997, 208, 363-374.	1.8	4
93	Upregulation of Bcl-2 Confers Resistance to FLT3 Inhibition in FLT3-ITD AML with Secondary Acquired Mutations. Blood, 2018, 132, 3944-3944.	1.4	4
94	Genomic and Transcriptomic Analyses of Bioluminescence Genes in the Enope Squid Watasenia scintillans. Marine Biotechnology, 2020, 22, 760-771.	2.4	3
95	Metatranscriptomic Analysis of Corals Inoculated With Tolerant and Non-Tolerant Symbiont Exposed to High Temperature and Light Stress. Frontiers in Physiology, 2022, 13, 806171.	2.8	3
96	Diverse Mechanisms of Resistance to Decitabine and Venetoclax Therapy in Newly Diagnosed and Relapsed/Refractory AML Inferred By Transcriptome Analysis. Blood, 2021, 138, 2244-2244.	1.4	2
97	Evolutionary origin of sex-related genes in the mouse brain. Gene, 2007, 406, 108-112.	2.2	1
98	Eukaryotic nuclear structure explains the evolutionary rate difference of ribosome export factors. Gene, 2008, 421, 7-13.	2.2	1
99	Colour variation of the intertidal hermit crab <i>Clibanarius virescens</i> considering growth stage, geographic area in the Indo-West Pacific Ocean, and molecular phylogeny. Journal of the Marine Biological Association of the United Kingdom, 2020, 100, 1107-1121.	0.8	1
100	Combined Targeting of Bcl-2 and XPO1 Overcomes Acquired Resistance to Tyrosine Kinase Inhibitors in the FLT3-ITD/TKD Double Mutant AML. Blood, 2018, 132, 2640-2640.	1.4	1
101	Cap Analysis of Gene Expression (CAGE) Sequencing Reveals Alterations of the Transcript Signatures in Acute Monocytic Leukemia Cells By Fatty Acid Oxidation Inhibition. Blood, 2015, 126, 3631-3631.	1.4	1
102	Mutation patterns for two flaviviruses: hepatitis C virus and GB virus C/hepatitis G virus. FEBS Letters, 1999, 450, 294-298.	2.8	0
103	Genome Network Project: An Integrated Genomic Platform. Nature Precedings, 2009, , .	0.1	0
104	DDBJ Activities: Contribution to the Research in Information Biology. Nature Precedings, 2009, , .	0.1	0
105	Molecular Cloning of Secreted Luciferases from Marine Planktonic Copepods. Methods in Molecular Biology, 2016, 1461, 33-41.	0.9	0
106	Cap Analysis of Gene Expression (CAGE) Sequencing Reveals Alterations of the Transcriptional Signatures of FLT3-ITD with Secondary D835 TKD Mutations in Acute Myeloid Leukemia. Blood, 2016, 128, 1530-1530.	1.4	0
107	Mitochondrial Transfer Confers Microenvironment-Mediated Resistance to Oxphos Inhibition in AML. Blood, 2018, 132, 430-430.	1.4	0
108	Cage Transcriptome Analysis Reveals BCL2A1 Upregulation in FLT3-ITD/D835 Dual Mutated AML Cells Harboring Complex Co-Mutations. Blood, 2019, 134, 1264-1264.	1.4	0

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109	Usage of the Sea Urchin <i>Hemicentrotus pulcherrimus</i> Database, HpBase. <i>Methods in Molecular Biology</i> , 2021, 2219, 267-275.	0.9	0
110	BCL2A1: A Novel Target in Refractory Acute Myeloid Leukemia with FLT3-ITD/D835 Dual Mutations. <i>Blood</i> , 2020, 136, 32-33.	1.4	0
111	The Direct Interactions with Bone Marrow Microenvironment Confer Resistance to the Inhibition of Oxidative Phosphorylation in AML. <i>Blood</i> , 2020, 136, 11-11.	1.4	0