

Hidemasa U Bono

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

102
papers

11,339
citations

32
h-index

106
g-index

129
ext. papers

13,503
ext. citations

8.5
avg, IF

5.39
L-index

#	Paper	IF	Citations
102	Resistance to chemical carcinogenesis induction via a dampened inflammatory response in naked mole-rats.. <i>Communications Biology</i> , 2022 , 5, 287	6.7	0
101	Activation of transcription factor HIF inhibits IL-1 β -induced NO production in primary cultured rat hepatocytes.. <i>Nitric Oxide - Biology and Chemistry</i> , 2022 ,	5	1
100	RefEX: Reference Expression Dataset 2021 , 117-133		
99	A chromosome-level genome sequence of <i>Chrysanthemum seticuspe</i> , a model species for hexaploid cultivated chrysanthemum. <i>Communications Biology</i> , 2021 , 4, 1167	6.7	1
98	Diversification of mineralocorticoid receptor genes in a subterranean rodent, the naked mole-rat. <i>Journal of Molecular Endocrinology</i> , 2021 , 66, 299-311	4.5	
97	Multi-Omic Meta-Analysis of Transcriptomes and the Bibliome Uncovers Novel Hypoxia-Inducible Genes. <i>Biomedicines</i> , 2021 , 9,	4.8	2
96	De novo transcriptome analysis for examination of the nutrition metabolic system related to the evolutionary process through which stick insects gain the ability of flight (Phasmatodea). <i>BMC Research Notes</i> , 2021 , 14, 182	2.3	0
95	Reference Transcriptome Data in Silkworm. <i>Insects</i> , 2021 , 12,	2.8	5
94	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021 , 12, 3297	17.4	3
93	Polysulfide inhibits hypoxia-elicited hypoxia-inducible factor activation in a mitochondria-dependent manner. <i>Mitochondrion</i> , 2021 , 59, 255-266	4.9	4
92	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. <i>Nucleic Acids Research</i> , 2021 , 49, D892-D898	20.1	19
91	Cigarette Smoke Extract Activates Hypoxia-Inducible Factors in a Reactive Oxygen Species-Dependent Manner in Stroma Cells from Human Endometrium. <i>Antioxidants</i> , 2021 , 10,	7.1	3
90	Inhibiting SARS-CoV-2 infection in vitro by suppressing its receptor, angiotensin-converting enzyme 2, via aryl-hydrocarbon receptor signal. <i>Scientific Reports</i> , 2021 , 11, 16629	4.9	9
89	Full-length 16S rRNA gene amplicon analysis of human gut microbiota using MinION β nanopore sequencing confers species-level resolution. <i>BMC Microbiology</i> , 2021 , 21, 35	4.5	38
88	Meta-Analysis of Hypoxic Transcriptomes from Public Databases. <i>Biomedicines</i> , 2020 , 8,	4.8	12
87	GLIS1, a novel hypoxia-inducible transcription factor, promotes breast cancer cell motility via activation of WNT5A. <i>Carcinogenesis</i> , 2020 , 41, 1184-1194	4.6	7
86	All of gene expression (AOE): An integrated index for public gene expression databases. <i>PLoS ONE</i> , 2020 , 15, e0227076	3.7	11

85	BioHackathon 2015: Semantics of data for life sciences and reproducible research. <i>F1000Research</i> , 2020 , 9, 136	3.6	2
84	Analysis of molecular mechanism for acceleration of polyembryony using gene functional annotation pipeline in <i>Copidosoma floridanum</i> . <i>BMC Genomics</i> , 2020 , 21, 152	4.5	0
83	Characterization of brown adipose tissue thermogenesis in the naked mole-rat (<i>Heterocephalus glaber</i>), a heterothermic mammal. <i>Scientific Reports</i> , 2020 , 10, 19488	4.9	7
82	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020 , 30, 1060-1072	9.7	41
81	Construction of TUATinsecta database that integrated plant and insect database for screening phytophagous insect metabolic products with medicinal potential. <i>Scientific Reports</i> , 2020 , 10, 17509	4.9	0
80	Thyroid Hormone Facilitates in vitro Decidualization of Human Endometrial Stromal Cells via Thyroid Hormone Receptors. <i>Endocrinology</i> , 2020 , 161,	4.8	7
79	All of gene expression (AOE): An integrated index for public gene expression databases 2020 , 15, e0227076		
78	All of gene expression (AOE): An integrated index for public gene expression databases 2020 , 15, e0227076		
77	All of gene expression (AOE): An integrated index for public gene expression databases 2020 , 15, e0227076		
76	All of gene expression (AOE): An integrated index for public gene expression databases 2020 , 15, e0227076		
75	All of gene expression (AOE): An integrated index for public gene expression databases 2020 , 15, e0227076		
74	All of gene expression (AOE): An integrated index for public gene expression databases 2020 , 15, e0227076		
73	Cancerous phenotypes associated with hypoxia-inducible factors are not influenced by the volatile anesthetic isoflurane in renal cell carcinoma. <i>PLoS ONE</i> , 2019 , 14, e0215072	3.7	8
72	Apoptosis-mediated vasa down-regulation controls developmental transformation in Japanese <i>Copidosoma floridanum</i> female soldiers. <i>Developmental Biology</i> , 2019 , 456, 226-233	3.1	0
71	Superoxide dismutase down-regulation and the oxidative stress is required to initiate pupation in <i>Bombyx mori</i> . <i>Scientific Reports</i> , 2019 , 9, 14693	4.9	3
70	Comparative analysis of seven types of superoxide dismutases for their ability to respond to oxidative stress in <i>Bombyx mori</i> . <i>Scientific Reports</i> , 2019 , 9, 2170	4.9	11
69	Suppression of mitochondrial oxygen metabolism mediated by the transcription factor HIF-1 alleviates propofol-induced cell toxicity. <i>Scientific Reports</i> , 2018 , 8, 8987	4.9	15
68	Construction of a simple evaluation system for the intestinal absorption of an orally administered medicine using <i>Bombyx mori</i> larvae. <i>Drug Discoveries and Therapeutics</i> , 2018 , 12, 7-15	5	4

67	Differentiated embryo chondrocyte plays a crucial role in DNA damage response via transcriptional regulation under hypoxic conditions. <i>PLoS ONE</i> , 2018 , 13, e0192136	3.7	5
66	Promotion of malignant phenotype after disruption of the three-dimensional structure of cultured spheroids from colorectal cancer. <i>Oncotarget</i> , 2018 , 9, 15968-15983	3.3	7
65	Identification of functional enolase genes of the silkworm <i>Bombyx mori</i> from public databases with a combination of dry and wet bench processes. <i>BMC Genomics</i> , 2017 , 18, 83	4.5	7
64	Calculating the quality of public high-throughput sequencing data to obtain a suitable subset for reanalysis from the Sequence Read Archive. <i>GigaScience</i> , 2017 , 6, 1-8	7.6	8
63	HIF-1-mediated suppression of mitochondria electron transport chain function confers resistance to lidocaine-induced cell death. <i>Scientific Reports</i> , 2017 , 7, 3816	4.9	34
62	RefEx, a reference gene expression dataset as a web tool for the functional analysis of genes. <i>Scientific Data</i> , 2017 , 4, 170105	8.2	34
61	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017 , 45, D737-D743	20.1	80
60	Next-Generation Sequencing and Bioinformatics 2017 , 97-115		
59	Tumour resistance in induced pluripotent stem cells derived from naked mole-rats. <i>Nature Communications</i> , 2016 , 7, 11471	17.4	54
58	Can the silkworm (<i>Bombyx mori</i>) be used as a human disease model?. <i>Drug Discoveries and Therapeutics</i> , 2016 , 10, 3-8	5	17
57	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015 , 16, 22	18.3	443
56	CRISPRdirect: software for designing CRISPR/Cas guide RNA with reduced off-target sites. <i>Bioinformatics</i> , 2015 , 31, 1120-3	7.2	593
55	Superoxide dismutases, SOD1 and SOD2, play a distinct role in the fat body during pupation in silkworm <i>Bombyx mori</i> . <i>PLoS ONE</i> , 2015 , 10, e0116007	3.7	23
54	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. <i>Journal of Biomedical Semantics</i> , 2014 , 5, 5	2.2	42
53	Identification of key uric acid synthesis pathway in a unique mutant silkworm <i>Bombyx mori</i> model of Parkinson's disease. <i>PLoS ONE</i> , 2013 , 8, e69130	3.7	29
52	Experimental design-based functional mining and characterization of high-throughput sequencing data in the sequence read archive. <i>PLoS ONE</i> , 2013 , 8, e77910	3.7	25
51	Tutorial videos of bioinformatics resources: online distribution trial in Japan named TogoTV. <i>Briefings in Bioinformatics</i> , 2012 , 13, 258-68	13.4	7
50	GGRNA: an ultrafast, transcript-oriented search engine for genes and transcripts. <i>Nucleic Acids Research</i> , 2012 , 40, W592-6	20.1	8

49	Gene expression profiling in multipotent DFAT cells derived from mature adipocytes. <i>Biochemical and Biophysical Research Communications</i> , 2011 , 407, 562-7	3.4	41
48	Functional Interpretation of Omics Data by Profiling Genes and Diseases Using MeSH Controlled Vocabulary 2011 ,		2
47	Allie: a database and a search service of abbreviations and long forms. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar013	5	22
46	Id4, a new candidate gene for senile osteoporosis, acts as a molecular switch promoting osteoblast differentiation. <i>PLoS Genetics</i> , 2010 , 6, e1001019	6	55
45	Gendoo: functional profiling of gene and disease features using MeSH vocabulary. <i>Nucleic Acids Research</i> , 2009 , 37, W166-9	20.1	29
44	Identification of novel PPARgamma target genes by integrated analysis of ChIP-on-chip and microarray expression data during adipocyte differentiation. <i>Biochemical and Biophysical Research Communications</i> , 2008 , 372, 362-6	3.4	42
43	BioCompass: a novel functional inference tool that utilizes MeSH hierarchy to analyze groups of genes. <i>In Silico Biology</i> , 2008 , 8, 53-61	2	14
42	Identification of novel steroid target genes through the combination of bioinformatics and functional analysis of hormone response elements. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 339, 99-106	3.4	42
41	The transcriptional landscape of the mammalian genome. <i>Science</i> , 2005 , 309, 1559-63	33.3	2807
40	SayaMatcher: genome scale organization and systematic analysis of nuclear receptor response elements. <i>Gene</i> , 2005 , 364, 74-8	3.8	5
39	The study of metabolic pathways in tumors based on the transcriptome. <i>Seminars in Cancer Biology</i> , 2005 , 15, 290-9	12.7	12
38	Gene discovery in genetically labeled single dopaminergic neurons of the retina. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 5069-74	11.5	64
37	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
36	Identification and functional analysis of consensus androgen response elements in human prostate cancer cells. <i>Biochemical and Biophysical Research Communications</i> , 2004 , 325, 1312-7	3.4	24
35	Identification of unique transcripts from a mouse full-length, subtracted inner ear cDNA library. <i>Genomics</i> , 2004 , 83, 1012-23	4.3	21
34	MaXML: mouse annotation XML. <i>In Silico Biology</i> , 2004 , 4, 7-15	2	1
33	The mouse secretome: functional classification of the proteins secreted into the extracellular environment. <i>Genome Research</i> , 2003 , 13, 1350-9	9.7	65
32	Detection of genes with tissue-specific expression patterns using Akaike's information criterion procedure. <i>Physiological Genomics</i> , 2003 , 12, 251-9	3.6	38

31	Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia. <i>Genome Research</i> , 2003 , 13, 1273-89	9.7	141
30	Gene expression profile of normal lungs predicts genetic predisposition to lung cancer in mice. <i>Carcinogenesis</i> , 2003 , 24, 1819-26	4.6	9
29	Molecular basis of constitutive production of basement membrane components. Gene expression profiles of Engelbreth-Holm-Swarm tumor and F9 embryonal carcinoma cells. <i>Journal of Biological Chemistry</i> , 2003 , 278, 50691-701	5.4	43
28	Development and evaluation of an automated annotation pipeline and cDNA annotation system. <i>Genome Research</i> , 2003 , 13, 1542-51	9.7	24
27	Systematic expression profiling of the mouse transcriptome using RIKEN cDNA microarrays. <i>Genome Research</i> , 2003 , 13, 1318-23	9.7	62
26	Discovery of imprinted transcripts in the mouse transcriptome using large-scale expression profiling. <i>Genome Research</i> , 2003 , 13, 1402-9	9.7	87
25	Comprehensive analysis of the mouse metabolome based on the transcriptome. <i>Genome Research</i> , 2003 , 13, 1345-9	9.7	23
24	Human disease genes and their cloned mouse orthologs: exploration of the FANTOM2 cDNA sequence data set. <i>Genome Research</i> , 2003 , 13, 1496-500	9.7	6
23	Analysis of the mouse transcriptome for genes involved in the function of the nervous system. <i>Genome Research</i> , 2003 , 13, 1395-401	9.7	26
22	G protein-coupled receptor genes in the FANTOM2 database. <i>Genome Research</i> , 2003 , 13, 1466-77	9.7	28
21	Continued discovery of transcriptional units expressed in cells of the mouse mononuclear phagocyte lineage. <i>Genome Research</i> , 2003 , 13, 1360-5	9.7	38
20	Expression Profiling of Parietal Endoderm Cells and Development of Systems for Large Scale Production of Laminins 2003 , 7-11		
19	Functional transcriptomes: comparative analysis of biological pathways and processes in eukaryotes to infer genetic networks among transcripts. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 355-61	8.1	15
18	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002 , 420, 563-73	50.4	1350
17	FANTOM DB: database of Functional Annotation of RIKEN Mouse cDNA Clones. <i>Nucleic Acids Research</i> , 2002 , 30, 116-8	20.1	48
16	Inferring alternative splicing patterns in mouse from a full-length cDNA library and microarray data. <i>Genome Research</i> , 2002 , 12, 1286-93	9.7	16
15	READ: RIKEN Expression Array Database. <i>Nucleic Acids Research</i> , 2002 , 30, 211-3	20.1	31
14	Delineating developmental and metabolic pathways in vivo by expression profiling using the RIKEN set of 18,816 full-length enriched mouse cDNA arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 2199-204	11.5	182

13	Protein-protein interaction panel using mouse full-length cDNAs. <i>Genome Research</i> , 2001 , 11, 1758-65	9.7	89
12	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001 , 409, 685-90	50.4	560
11	Preprocessing implementation for microarray (PRIM): an efficient method for processing cDNA microarray data. <i>Physiological Genomics</i> , 2001 , 4, 183-8	3.6	54
10	KEGG: Kyoto Encyclopedia of Genes and Genomes. <i>Nucleic Acids Research</i> , 1999 , 27, 29-34	20.1	3093
9	Reconstruction of amino acid biosynthesis pathways from the complete genome sequence. <i>Genome Research</i> , 1998 , 8, 203-10	9.7	136
8	Two-component response regulators from <i>Arabidopsis thaliana</i> contain a putative DNA-binding motif. <i>Plant and Cell Physiology</i> , 1998 , 39, 1232-9	4.9	86
7	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , 8, 1677	3.6	
6	Reference transcriptome data in silkworm <i>Bombyx mori</i>		2
5	Full-length 16S rRNA gene amplicon analysis of human gut microbiota using MinION nanopore sequencing confers species-level resolution		4
4	Senescent cell death as an aging resistance mechanism in naked mole-rat		2
3	Meta-analysis of hypoxic transcriptomes from public databases		2
2	All of gene expression (AOE): an integrated index for public gene expression databases		3
1	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping		6