Hidemasa U Bono

List of Publications by Citations

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	KEGG: Kyoto Encyclopedia of Genes and Genomes. *Nucleic Acids Research*, **1999**, 27, 29-34	20.1	3093
101	The transcriptional landscape of the mammalian genome. *Science*, **2005**, 309, 1559-63	33.3	2807
100	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. *Nature*, **2002**, 420, 563-73	50.4	1350
99	CRISPRdirect: software for designing CRISPR/Cas guide RNA with reduced off-target sites. *Bioinformatics*, **2015**, 31, 1120-3	7.2	593
98	Functional annotation of a full-length mouse cDNA collection. *Nature*, **2001**, 409, 685-90	50.4	560
97	Gateways to the FANTOM5 promoter level mammalian expression atlas. *Genome Biology*, **2015**, 16, 22	18.3	443
96	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. *PLoS Biology*, **2004**, 2, e162	9.7	255
95	Delineating developmental and metabolic pathways in vivo by expression profiling using the RIKEN set of 18,816 full-length enriched mouse cDNA arrays. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 2199-204	11.5	182
94	Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia. *Genome Research*, **2003**, 13, 1273-89	9.7	141
93	Reconstruction of amino acid biosynthesis pathways from the complete genome sequence. *Genome Research*, **1998**, 8, 203-10	9.7	136
92	Protein-protein interaction panel using mouse full-length cDNAs. *Genome Research*, **2001**, 11, 1758-65	9.7	89
91	Discovery of imprinted transcripts in the mouse transcriptome using large-scale expression profiling. *Genome Research*, **2003**, 13, 1402-9	9.7	87
90	Two-component response regulators from Arabidopsis thaliana contain a putative DNA-binding motif. *Plant and Cell Physiology*, **1998**, 39, 1232-9	4.9	86
89	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. *Nucleic Acids Research*, **2017**, 45, D737-D743	20.1	80
88	The mouse secretome: functional classification of the proteins secreted into the extracellular environment. *Genome Research*, **2003**, 13, 1350-9	9.7	65
87	Gene discovery in genetically labeled single dopaminergic neurons of the retina. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 5069-74	11.5	64
86	Systematic expression profiling of the mouse transcriptome using RIKEN cDNA microarrays. *Genome Research*, **2003**, 13, 1318-23	9.7	62

85	Id4, a new candidate gene for senile osteoporosis, acts as a molecular switch promoting osteoblast differentiation. *PLoS Genetics*, **2010**, 6, e1001019	6	55
84	Tumour resistance in induced pluripotent stem cells derived from naked mole-rats. *Nature Communications*, **2016**, 7, 11471	17.4	54
83	Preprocessing implementation for microarray (PRIM): an efficient method for processing cDNA microarray data. *Physiological Genomics*, **2001**, 4, 183-8	3.6	54
82	FANTOM DB: database of Functional Annotation of RIKEN Mouse cDNA Clones. *Nucleic Acids Research*, **2002**, 30, 116-8	20.1	48
81	Molecular basis of constitutive production of basement membrane components. Gene expression profiles of Engelbreth-Holm-Swarm tumor and F9 embryonal carcinoma cells. *Journal of Biological Chemistry*, **2003**, 278, 50691-701	5.4	43
80	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. *Journal of Biomedical Semantics*, **2014**, 5, 5	2.2	42
79	Identification of novel PPARgamma target genes by integrated analysis of ChIP-on-chip and microarray expression data during adipocyte differentiation. *Biochemical and Biophysical Research Communications*, **2008**, 372, 362-6	3.4	42
78	Identification of novel steroid target genes through the combination of bioinformatics and functional analysis of hormone response elements. *Biochemical and Biophysical Research Communications*, **2006**, 339, 99-106	3.4	42
77	Gene expression profiling in multipotent DFAT cells derived from mature adipocytes. *Biochemical and Biophysical Research Communications*, **2011**, 407, 562-7	3.4	41
76	Functional annotation of human long noncoding RNAs via molecular phenotyping. *Genome Research*, **2020**, 30, 1060-1072	9.7	41
75	Detection of genes with tissue-specific expression patterns using Akaike's information criterion procedure. *Physiological Genomics*, **2003**, 12, 251-9	3.6	38
74	Continued discovery of transcriptional units expressed in cells of the mouse mononuclear phagocyte lineage. *Genome Research*, **2003**, 13, 1360-5	9.7	38
73	Full-length 16S rRNA gene amplicon analysis of human gut microbiota using MinION™ nanopore sequencing confers species-level resolution. *BMC Microbiology*, **2021**, 21, 35	4.5	38
72	HIF-1-mediated suppression of mitochondria electron transport chain function confers resistance to lidocaine-induced cell death. *Scientific Reports*, **2017**, 7, 3816	4.9	34
71	RefEx, a reference gene expression dataset as a web tool for the functional analysis of genes. *Scientific Data*, **2017**, 4, 170105	8.2	34
70	READ: RIKEN Expression Array Database. *Nucleic Acids Research*, **2002**, 30, 211-3	20.1	31
69	Gendoo: functional profiling of gene and disease features using MeSH vocabulary. *Nucleic Acids Research*, **2009**, 37, W166-9	20.1	29
68	Identification of key uric acid synthesis pathway in a unique mutant silkworm Bombyx mori model of Parkinson's disease. *PLoS ONE*, **2013**, 8, e69130	3.7	29

67	G protein-coupled receptor genes in the FANTOM2 database. *Genome Research*, **2003**, 13, 1466-77	9.7	28
66	Analysis of the mouse transcriptome for genes involved in the function of the nervous system. *Genome Research*, **2003**, 13, 1395-401	9.7	26
65	Experimental design-based functional mining and characterization of high-throughput sequencing data in the sequence read archive. *PLoS ONE*, **2013**, 8, e77910	3.7	25
64	Development and evaluation of an automated annotation pipeline and cDNA annotation system. *Genome Research*, **2003**, 13, 1542-51	9.7	24
63	Identification and functional analysis of consensus androgen response elements in human prostate cancer cells. *Biochemical and Biophysical Research Communications*, **2004**, 325, 1312-7	3.4	24
62	Superoxide dismutases, SOD1 and SOD2, play a distinct role in the fat body during pupation in silkworm Bombyx mori. *PLoS ONE*, **2015**, 10, e0116007	3.7	23
61	Comprehensive analysis of the mouse metabolome based on the transcriptome. *Genome Research*, **2003**, 13, 1345-9	9.7	23
60	Allie: a database and a search service of abbreviations and long forms. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, bar013	5	22
59	Identification of unique transcripts from a mouse full-length, subtracted inner ear cDNA library. *Genomics*, **2004**, 83, 1012-23	4.3	21
58	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. *Nucleic Acids Research*, **2021**, 49, D892-D898	20.1	19
57	Can the silkworm (Bombyx mori) be used as a human disease model?. *Drug Discoveries and Therapeutics*, **2016**, 10, 3-8	5	17
56	Inferring alternative splicing patterns in mouse from a full-length cDNA library and microarray data. *Genome Research*, **2002**, 12, 1286-93	9.7	16
55	Suppression of mitochondrial oxygen metabolism mediated by the transcription factor HIF-1 alleviates propofol-induced cell toxicity. *Scientific Reports*, **2018**, 8, 8987	4.9	15
54	Functional transcriptomes: comparative analysis of biological pathways and processes in eukaryotes to infer genetic networks among transcripts. *Current Opinion in Structural Biology*, **2002**, 12, 355-61	8.1	15
53	BioCompass: a novel functional inference tool that utilizes MeSH hierarchy to analyze groups of genes. *In Silico Biology*, **2008**, 8, 53-61	2	14
52	Meta-Analysis of Hypoxic Transcriptomes from Public Databases. *Biomedicines*, **2020**, 8,	4.8	12
51	The study of metabolic pathways in tumors based on the transcriptome. *Seminars in Cancer Biology*, **2005**, 15, 290-9	12.7	12
50	All of gene expression (AOE): An integrated index for public gene expression databases. *PLoS ONE*, **2020**, 15, e0227076	3.7	11

49	Comparative analysis of seven types of superoxide dismutases for their ability to respond to oxidative stress in Bombyx mori. *Scientific Reports*, **2019**, 9, 2170	4.9	11
48	Gene expression profile of normal lungs predicts genetic predisposition to lung cancer in mice. *Carcinogenesis*, **2003**, 24, 1819-26	4.6	9
47	Inhibiting SARS-CoV-2 infection in vitro by suppressing its receptor, angiotensin-converting enzyme 2, via aryl-hydrocarbon receptor signal. *Scientific Reports*, **2021**, 11, 16629	4.9	9
46	Calculating the quality of public high-throughput sequencing data to obtain a suitable subset for reanalysis from the Sequence Read Archive. *GigaScience*, **2017**, 6, 1-8	7.6	8
45	Cancerous phenotypes associated with hypoxia-inducible factors are not influenced by the volatile anesthetic isoflurane in renal cell carcinoma. *PLoS ONE*, **2019**, 14, e0215072	3.7	8
44	GGRNA: an ultrafast, transcript-oriented search engine for genes and transcripts. *Nucleic Acids Research*, **2012**, 40, W592-6	20.1	8
43	Identification of functional enolase genes of the silkworm Bombyx mori from public databases with a combination of dry and wet bench processes. *BMC Genomics*, **2017**, 18, 83	4.5	7
42	GLIS1, a novel hypoxia-inducible transcription factor, promotes breast cancer cell motility via activation of WNT5A. *Carcinogenesis*, **2020**, 41, 1184-1194	4.6	7
41	Tutorial videos of bioinformatics resources: online distribution trial in Japan named TogoTV. *Briefings in Bioinformatics*, **2012**, 13, 258-68	13.4	7
40	Promotion of malignant phenotype after disruption of the three-dimensional structure of cultured spheroids from colorectal cancer. *Oncotarget*, **2018**, 9, 15968-15983	3.3	7
39	Characterization of brown adipose tissue thermogenesis in the naked mole-rat (Heterocephalus glaber), a heterothermic mammal. *Scientific Reports*, **2020**, 10, 19488	4.9	7
38	Thyroid Hormone Facilitates in vitro Decidualization of Human Endometrial Stromal Cells via Thyroid Hormone Receptors. *Endocrinology*, **2020**, 161,	4.8	7
37	Human disease genes and their cloned mouse orthologs: exploration of the FANTOM2 cDNA sequence data set. *Genome Research*, **2003**, 13, 1496-500	9.7	6
36	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping		6
35	Differentiated embryo chondrocyte plays a crucial role in DNA damage response via transcriptional regulation under hypoxic conditions. *PLoS ONE*, **2018**, 13, e0192136	3.7	5
34	SayaMatcher: genome scale organization and systematic analysis of nuclear receptor response elements. *Gene*, **2005**, 364, 74-8	3.8	5
33	Reference Transcriptome Data in Silkworm. *Insects*, **2021**, 12,	2.8	5
32	Construction of a simple evaluation system for the intestinal absorption of an orally administered medicine using Bombyx mori larvae. *Drug Discoveries and Therapeutics*, **2018**, 12, 7-15	5	4

31	Full-length 16S rRNA gene amplicon analysis of human gut microbiota using MinION nanopore sequencing confers species-level resolution		4
30	Polysulfide inhibits hypoxia-elicited hypoxia-inducible factor activation in a mitochondria-dependent manner. *Mitochondrion*, **2021**, 59, 255-266	4.9	4
29	Superoxide dismutase down-regulation and the oxidative stress is required to initiate pupation in Bombyx mori. *Scientific Reports*, **2019**, 9, 14693	4.9	3
28	All of gene expression (AOE): an integrated index for public gene expression databases		3
27	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. *Nature Communications*, **2021**, 12, 3297	17.4	3
26	Cigarette Smoke Extract Activates Hypoxia-Inducible Factors in a Reactive Oxygen Species-Dependent Manner in Stroma Cells from Human Endometrium. *Antioxidants*, **2021**, 10,	7.1	3
25	Functional Interpretation of Omics Data by Profiling Genes and Diseases Using MeSH-Controlled Vocabulary **2011**,		2
24	BioHackathon 2015: Semantics of data for life sciences and reproducible research. *F1000Research*, **2020**, 9, 136	3.6	2
23	Reference transcriptome data in silkworm Bombyx mori		2
22	Senescent cell death as an aging resistance mechanism in naked mole-rat		2
21	Meta-analysis of hypoxic transcriptomes from public databases		2
20	Multi-Omic Meta-Analysis of Transcriptomes and the Bibliome Uncovers Novel Hypoxia-Inducible Genes. *Biomedicines*, **2021**, 9,	4.8	2
19	A chromosome-level genome sequence of Chrysanthemum seticuspe, a model species for hexaploid cultivated chrysanthemum. *Communications Biology*, **2021**, 4, 1167	6.7	1
18	MaXML: mouse annotation XML. *In Silico Biology*, **2004**, 4, 7-15	2	1
17	Activation of transcription factor HIF inhibits IL-1-induced NO production in primary cultured rat hepatocytes.. *Nitric Oxide - Biology and Chemistry*, **2022**,	5	1
16	Apoptosis-mediated vasa down-regulation controls developmental transformation in Japanese Copidosoma floridanum female soldiers. *Developmental Biology*, **2019**, 456, 226-233	3.1	0
15	Analysis of molecular mechanism for acceleration of polyembryony using gene functional annotation pipeline in Copidosoma floridanum. *BMC Genomics*, **2020**, 21, 152	4.5	0
14	Construction of TUATinsecta database that integrated plant and insect database for screening phytophagous insect metabolic products with medicinal potential. *Scientific Reports*, **2020**, 10, 17509	4.9	0

LIST OF PUBLICATIONS

13	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). *BMC Research Notes*, **2021**, 14, 182	2.3	0
12	Resistance to chemical carcinogenesis induction via a dampened inflammatory response in naked mole-rats.. *Communications Biology*, **2022**, 5, 287	6.7	0
11	RefEX: Reference Expression Dataset **2021**, 117-133		
10	Expression Profiling of Parietal Endoderm Cells and Development of Systems for Large Scale Production of Laminins **2003**, 7-11		
9	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. *F1000Research*,8, 1677	3.6	
8	Next-Generation Sequencing and Bioinformatics **2017**, 97-115		
7	Diversification of mineralocorticoid receptor genes in a subterranean rodent, the naked mole-rat. *Journal of Molecular Endocrinology*, **2021**, 66, 299-311	4.5	
6	All of gene expression (AOE): An integrated index for public gene expression databases **2020**, 15, e0227076		
5	All of gene expression (AOE): An integrated index for public gene expression databases **2020**, 15, e0227076		
4	All of gene expression (AOE): An integrated index for public gene expression databases **2020**, 15, e0227076		
3	All of gene expression (AOE): An integrated index for public gene expression databases **2020**, 15, e0227076		
2	All of gene expression (AOE): An integrated index for public gene expression databases **2020**, 15, e0227076		
1	All of gene expression (AOE): An integrated index for public gene expression databases **2020**, 15, e0227076		