

Yutaka Suzuki

List of Publications by Citations

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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.

338 papers	10,054 citations	49 h-index	89 g-index
358 ext. papers	13,528 ext. citations	8.5 avg, IF	6.05 L-index

#	Paper	IF	Citations
338	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017 , 171, 287-304.e15	56.2	538
337	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016 , 538, 336-343	50.4	510
336	Long noncoding RNA NEAT1-dependent SFPQ relocation from promoter region to paraspeckle mediates IL8 expression upon immune stimuli. <i>Molecular Cell</i> , 2014 , 53, 393-406	17.6	464
335	A single female-specific piRNA is the primary determiner of sex in the silkworm. <i>Nature</i> , 2014 , 509, 633-639	50.4	290
334	Genome-wide determination of RNA stability reveals hundreds of short-lived noncoding transcripts in mammals. <i>Genome Research</i> , 2012 , 22, 947-56	9.7	272
333	Regnase-1 and Roquin Regulate a Common Element in Inflammatory mRNAs by Spatiotemporally Distinct Mechanisms. <i>Cell</i> , 2015 , 161, 1058-1073	56.2	227
332	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018 , 174, 448-464.e24	56.2	213
331	Genomic Landscape of Esophageal Squamous Cell Carcinoma in a Japanese Population. <i>Gastroenterology</i> , 2016 , 150, 1171-1182	13.3	195
330	Genome sequence of the tsetse fly (<i>Glossina morsitans</i>): vector of African trypanosomiasis. <i>Science</i> , 2014 , 344, 380-6	33.3	192
329	DBTSS: DataBase of human Transcriptional Start Sites and full-length cDNAs. <i>Nucleic Acids Research</i> , 2002 , 30, 328-31	20.1	164
328	Extremotolerant tardigrade genome and improved radiotolerance of human cultured cells by tardigrade-unique protein. <i>Nature Communications</i> , 2016 , 7, 12808	17.4	160
327	A genetic mechanism for female-limited Batesian mimicry in <i>Papilio</i> butterfly. <i>Nature Genetics</i> , 2015 , 47, 405-9	36.3	158
326	Expansions of intronic TTTCA and TTTTA repeats in benign adult familial myoclonic epilepsy. <i>Nature Genetics</i> , 2018 , 50, 581-590	36.3	152
325	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites. <i>EMBO Reports</i> , 2001 , 2, 388-93	6.5	141
324	Layer-specific morphological and molecular differences in neocortical astrocytes and their dependence on neuronal layers. <i>Nature Communications</i> , 2018 , 9, 1623	17.4	122
323	Identification of hundreds of novel UPF1 target transcripts by direct determination of whole transcriptome stability. <i>RNA Biology</i> , 2012 , 9, 1370-9	4.8	121
322	Phytochrome controls alternative splicing to mediate light responses in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 18781-6	11.5	115

3 ²¹	DBTSS, DataBase of Transcriptional Start Sites: progress report 2004. <i>Nucleic Acids Research</i> , 2004 , 32, D78-81	20.1	112
3 ²⁰	Long-term expansion of alveolar stem cells derived from human iPS cells in organoids. <i>Nature Methods</i> , 2017 , 14, 1097-1106	21.6	109
3 ¹⁹	Chromatin-associated periodicity in genetic variation downstream of transcriptional start sites. <i>Science</i> , 2009 , 323, 401-4	33.3	108
3 ¹⁸	Genetic basis of the highly efficient yeast <i>Kluyveromyces marxianus</i> : complete genome sequence and transcriptome analyses. <i>Biotechnology for Biofuels</i> , 2015 , 8, 47	7.8	102
3 ¹⁷	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. <i>PLoS Genetics</i> , 2016 , 12, e1005778	6	102
3 ¹⁶	Sensitivity and engineered resistance of myeloid leukemia cells to BRD9 inhibition. <i>Nature Chemical Biology</i> , 2016 , 12, 672-9	11.7	102
3 ¹⁵	NSD3-Short Is an Adaptor Protein that Couples BRD4 to the CHD8 Chromatin Remodeler. <i>Molecular Cell</i> , 2015 , 60, 847-59	17.6	98
3 ¹⁴	RNA-seq Transcriptional Profiling of an Arbuscular Mycorrhiza Provides Insights into Regulated and Coordinated Gene Expression in <i>Lotus japonicus</i> and <i>Rhizophagus irregularis</i> . <i>Plant and Cell Physiology</i> , 2015 , 56, 1490-511	4.9	92
3 ¹³	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016 , 7, 13295	17.4	91
3 ¹²	Massive transcriptional start site analysis of human genes in hypoxia cells. <i>Nucleic Acids Research</i> , 2009 , 37, 2249-63	20.1	87
3 ¹¹	DNA methylation and gene expression dynamics during spermatogonial stem cell differentiation in the early postnatal mouse testis. <i>BMC Genomics</i> , 2015 , 16, 624	4.5	84
3 ¹⁰	DBTSS: DataBase of Human Transcription Start Sites, progress report 2006. <i>Nucleic Acids Research</i> , 2006 , 34, D86-9	20.1	84
3 ⁰⁹	Analysis of small human proteins reveals the translation of upstream open reading frames of mRNAs. <i>Genome Research</i> , 2004 , 14, 2048-52	9.7	83
3 ⁰⁸	The first murine zygotic transcription is promiscuous and uncoupled from splicing and 3R processing. <i>EMBO Journal</i> , 2015 , 34, 1523-37	13	79
3 ⁰⁷	Direct binding of Ataxin-2 to distinct elements in 3RUTRs promotes mRNA stability and protein expression. <i>Molecular Cell</i> , 2014 , 55, 186-98	17.6	79
3 ⁰⁶	Aberrant transcriptional regulations in cancers: genome, transcriptome and epigenome analysis of lung adenocarcinoma cell lines. <i>Nucleic Acids Research</i> , 2014 , 42, 13557-72	20.1	74
3 ⁰⁵	Long terminal repeats power evolution of genes and gene expression programs in mammalian oocytes and zygotes. <i>Genome Research</i> , 2017 , 27, 1384-1394	9.7	72
3 ⁰⁴	Construction of a full-length enriched and a 5Rend enriched cDNA library using the oligo-capping method. <i>Methods in Molecular Biology</i> , 2003 , 221, 73-91	1.4	69

303	Condensin targets and reduces unwound DNA structures associated with transcription in mitotic chromosome condensation. <i>Nature Communications</i> , 2015 , 6, 7815	17.4	64
302	Transcriptome analysis of mouse brain infected with <i>Toxoplasma gondii</i> . <i>Infection and Immunity</i> , 2013 , 81, 3609-19	3.7	63
301	A new lncRNA, APTR, associates with and represses the CDKN1A/p21 promoter by recruiting polycomb proteins. <i>PLoS ONE</i> , 2014 , 9, e95216	3.7	63
300	Methylome diversification through changes in DNA methyltransferase sequence specificity. <i>PLoS Genetics</i> , 2014 , 10, e1004272	6	61
299	Single-cell analysis of lung adenocarcinoma cell lines reveals diverse expression patterns of individual cells invoked by a molecular target drug treatment. <i>Genome Biology</i> , 2015 , 16, 66	18.3	57
298	Dysregulation of spliceosome gene expression in advanced prostate cancer by RNA-binding protein PSF. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 10461-10466	11.5	55
297	Combined Mutation of , and Effectively Drives Metastasis of Intestinal Cancer. <i>Cancer Research</i> , 2018 , 78, 1334-1346	10.1	53
296	Sall1 maintains nephron progenitors and nascent nephrons by acting as both an activator and a repressor. <i>Journal of the American Society of Nephrology: JASN</i> , 2014 , 25, 2584-95	12.7	53
295	BRIC-seq: a genome-wide approach for determining RNA stability in mammalian cells. <i>Methods</i> , 2014 , 67, 55-63	4.6	52
294	ADARB1 catalyzes circadian A-to-I editing and regulates RNA rhythm. <i>Nature Genetics</i> , 2017 , 49, 146-151	36.3	52
293	Minor zygotic gene activation is essential for mouse preimplantation development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E6780-E6788	11.5	52
292	RNA-sequencing-based transcriptome and biochemical analyses of steroidal saponin pathway in a complete set of <i>Allium fistulosum</i> -A. cepa monosomic addition lines. <i>PLoS ONE</i> , 2017 , 12, e0181784	3.7	50
291	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. <i>Nature Communications</i> , 2018 , 9, 2884	17.4	50
290	HTLV-1 bZIP Factor Impairs Anti-viral Immunity by Inducing Co-inhibitory Molecule, T Cell Immunoglobulin and ITIM Domain (TIGIT). <i>PLoS Pathogens</i> , 2016 , 12, e1005372	7.6	50
289	Interactive transcriptome analysis of malaria patients and infecting <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2014 , 24, 1433-44	9.7	47
288	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions. <i>Genome Research</i> , 2004 , 14, 1711-8	9.7	47
287	DBTSS provides a tissue specific dynamic view of Transcription Start Sites. <i>Nucleic Acids Research</i> , 2010 , 38, D98-104	20.1	46
286	Somatic mutations in plasma cell-free DNA are diagnostic markers for esophageal squamous cell carcinoma recurrence. <i>Oncotarget</i> , 2016 , 7, 62280-62291	3.3	46

285	Single-cell sequencing techniques from individual to multiomics analyses. <i>Experimental and Molecular Medicine</i> , 2020 , 52, 1419-1427	12.8	46
284	Hypermethylation and unique mutational signatures of occupational cholangiocarcinoma in printing workers exposed to haloalkanes. <i>Carcinogenesis</i> , 2016 , 37, 817-826	4.6	46
283	Isolation, tissue expression, and chromosomal assignment of human RGS5, a novel G-protein signaling regulator gene. <i>Journal of Human Genetics</i> , 1998 , 43, 202-5	4.3	45
282	Setdb1 maintains hematopoietic stem and progenitor cells by restricting the ectopic activation of nonhematopoietic genes. <i>Blood</i> , 2016 , 128, 638-49	2.2	44
281	DBTSS as an integrative platform for transcriptome, epigenome and genome sequence variation data. <i>Nucleic Acids Research</i> , 2015 , 43, D87-91	20.1	43
280	Development and validation of a new high-throughput method to investigate the clonality of HTLV-1-infected cells based on provirus integration sites. <i>Genome Medicine</i> , 2014 , 6, 46	14.4	42
279	DBTSS: DataBase of Transcriptional Start Sites progress report in 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D150-4	20.1	42
278	Clinical significance of BRAF non-V600E mutations on the therapeutic effects of anti-EGFR monoclonal antibody treatment in patients with pretreated metastatic colorectal cancer: the Biomarker Research for anti-EGFR monoclonal Antibodies by Comprehensive Cancer genomics (BREAAC) study. <i>British Journal of Cancer</i> , 2017 , 117, 1450-1458	8.7	41
277	Cloning, expression analysis, and chromosomal localization of HIP1R, an isolog of huntingtin interacting protein (HIP1). <i>Journal of Human Genetics</i> , 1998 , 43, 268-71	4.3	41
276	Lanthanide-Dependent Regulation of Methylophony in Strain 22A. <i>MSphere</i> , 2018 , 3,	5	40
275	The CCR4-NOT deadenylase complex controls Atg7-dependent cell death and heart function. <i>Science Signaling</i> , 2018 , 11,	8.8	40
274	The Endosymbiotic Bacterium Wolbachia Selectively Kills Male Hosts by Targeting the Masculinizing Gene. <i>PLoS Pathogens</i> , 2015 , 11, e1005048	7.6	39
273	High-resolution analysis of the 5Rend transcriptome using a next generation DNA sequencer. <i>PLoS ONE</i> , 2009 , 4, e4108	3.7	39
272	Regnase-1 Maintains Iron Homeostasis via the Degradation of Transferrin Receptor 1 and Prolyl-Hydroxylase-Domain-Containing Protein 3 mRNAs. <i>Cell Reports</i> , 2017 , 19, 1614-1630	10.6	38
271	Occupancy of tissue-specific cis-regulatory modules by Otx2 and TLE/Groucho for embryonic head specification. <i>Nature Communications</i> , 2014 , 5, 4322	17.4	38
270	A GC-rich sequence feature in the 3'UTR directs UPF1-dependent mRNA decay in mammalian cells. <i>Genome Research</i> , 2017 , 27, 407-418	9.7	37
269	DBTSS/DBKERO for integrated analysis of transcriptional regulation. <i>Nucleic Acids Research</i> , 2018 , 46, D229-D238	20.1	37
268	Diminished nuclear RNA decay upon infection upregulates antibacterial noncoding RNAs. <i>EMBO Journal</i> , 2018 , 37,	13	36

267	Sequencing and phasing cancer mutations in lung cancers using a long-read portable sequencer. <i>DNA Research</i> , 2017 , 24, 585-596	4.5	36
266	Zucchini consensus motifs determine the mechanism of pre-piRNA production. <i>Nature</i> , 2020 , 578, 311-316	6.4	35
265	Discovery of an unconventional centromere in budding yeast redefines evolution of point centromeres. <i>Current Biology</i> , 2015 , 25, 2026-33	6.3	35
264	Evaluation and application of RNA-Seq by MinION. <i>DNA Research</i> , 2019 , 26, 55-65	4.5	35
263	PAX6 Isoforms, along with Reprogramming Factors, Differentially Regulate the Induction of Cornea-specific Genes. <i>Scientific Reports</i> , 2016 , 6, 20807	4.9	34
262	Repeated inversions within a pannier intron drive diversification of intraspecific colour patterns of ladybird beetles. <i>Nature Communications</i> , 2018 , 9, 3843	17.4	34
261	Hunt for the tipping point during endocrine resistance process in breast cancer by dynamic network biomarkers. <i>Journal of Molecular Cell Biology</i> , 2019 , 11, 649-664	6.3	33
260	Eosinophil depletion suppresses radiation-induced small intestinal fibrosis. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	32
259	RNA-binding protein NONO promotes breast cancer proliferation by post-transcriptional regulation of SKP2 and E2F8. <i>Cancer Science</i> , 2020 , 111, 148-159	6.9	31
258	Epigenetic control of early dendritic cell lineage specification by the transcription factor IRF8 in mice. <i>Blood</i> , 2019 , 133, 1803-1813	2.2	30
257	Analysis of RNA decay factor mediated RNA stability contributions on RNA abundance. <i>BMC Genomics</i> , 2015 , 16, 154	4.5	30
256	Large hypomethylated domains serve as strong repressive machinery for key developmental genes in vertebrates. <i>Development (Cambridge)</i> , 2014 , 141, 2568-80	6.6	30
255	Genome-wide identification and annotation of HIF-1 α binding sites in two cell lines using massively parallel sequencing. <i>The HUGO Journal</i> , 2010 , 4, 35-48		30
254	The transcriptional cofactor TRIM33 prevents apoptosis in B lymphoblastic leukemia by deactivating a single enhancer. <i>ELife</i> , 2015 , 4, e06377	8.9	29
253	Detection of APC mosaicism by next-generation sequencing in an FAP patient. <i>Journal of Human Genetics</i> , 2015 , 60, 227-31	4.3	28
252	Ezh2 regulates the Lin28/let-7 pathway to restrict activation of fetal gene signature in adult hematopoietic stem cells. <i>Experimental Hematology</i> , 2016 , 44, 282-96.e3	3.1	28
251	Regnase-1 and Roquin Nonredundantly Regulate Th1 Differentiation Causing Cardiac Inflammation and Fibrosis. <i>Journal of Immunology</i> , 2017 , 199, 4066-4077	5.3	28
250	Transcription factor DUO1 generated by neo-functionalization is associated with evolution of sperm differentiation in plants. <i>Nature Communications</i> , 2018 , 9, 5283	17.4	28

249	Nanopore sequencing of drug-resistance-associated genes in malaria parasites, <i>Plasmodium falciparum</i> . <i>Scientific Reports</i> , 2018 , 8, 8286	4.9	28
248	Serotyping dengue virus with isothermal amplification and a portable sequencer. <i>Scientific Reports</i> , 2017 , 7, 3510	4.9	27
247	ADAR1-mediated RNA editing is required for thymic self-tolerance and inhibition of autoimmunity. <i>EMBO Reports</i> , 2018 , 19,	6.5	27
246	Androgen-induced lncRNA POTEV-AS1 regulates apoptosis-related pathway to facilitate cell survival in prostate cancer cells. <i>Cancer Science</i> , 2017 , 108, 373-379	6.9	26
245	Transcription Factor IRF8 Governs Enhancer Landscape Dynamics in Mononuclear Phagocyte Progenitors. <i>Cell Reports</i> , 2018 , 22, 2628-2641	10.6	26
244	Differential Binding of Three Major Human ADAR Isoforms to Coding and Long Non-Coding Transcripts. <i>Genes</i> , 2017 , 8,	4.2	25
243	p53-inducible DPYSL4 associates with mitochondrial supercomplexes and regulates energy metabolism in adipocytes and cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 8370-8375	11.5	24
242	Targeting in neutrophils enhances the clearance of infected wounds. <i>EMBO Molecular Medicine</i> , 2018 , 10,	12	24
241	Translation-dependent unwinding of stem-loops by UPF1 licenses Regnase-1 to degrade inflammatory mRNAs. <i>Nucleic Acids Research</i> , 2019 , 47, 8838-8859	20.1	23
240	Transition of differential histone H3 methylation in photoreceptors and other retinal cells during retinal differentiation. <i>Scientific Reports</i> , 2016 , 6, 29264	4.9	23
239	LGP2 virus sensor regulates gene expression network mediated by TRBP-bound microRNAs. <i>Nucleic Acids Research</i> , 2018 , 46, 9134-9147	20.1	23
238	A novel diagnostic method for malaria using loop-mediated isothermal amplification (LAMP) and MinION nanopore sequencer. <i>BMC Infectious Diseases</i> , 2017 , 17, 621	4	22
237	Functional D-box sequences reset the circadian clock and drive mRNA rhythms. <i>Communications Biology</i> , 2019 , 2, 300	6.7	22
236	Trans-omic Analysis Reveals Selective Responses to Induced and Basal Insulin across Signaling, Transcriptional, and Metabolic Networks. <i>IScience</i> , 2018 , 7, 212-229	6.1	22
235	Identification of physical interactions between genomic regions by enChIP-Seq. <i>Genes To Cells</i> , 2017 , 22, 506-520	2.3	21
234	Expressed sequence tags from cynomolgus monkey (<i>Macaca fascicularis</i>) liver: a systematic identification of drug-metabolizing enzymes. <i>FEBS Letters</i> , 2008 , 582, 351-8	3.8	21
233	Isolation and chromosomal mapping of a novel human gene showing homology to Na ⁺ /PO ₄ cotransporter. <i>Journal of Human Genetics</i> , 1999 , 44, 190-2	4.3	21
232	Genome-wide identification of pistil-specific genes expressed during fruit set initiation in tomato (<i>Solanum lycopersicum</i>). <i>PLoS ONE</i> , 2017 , 12, e0180003	3.7	21

231	Local potentiation of stress-responsive genes by upstream noncoding transcription. <i>Nucleic Acids Research</i> , 2016 , 44, 5174-89	20.1	20
230	Exome Analyses of Long QT Syndrome Reveal Candidate Pathogenic Mutations in Calmodulin-Interacting Genes. <i>PLoS ONE</i> , 2015 , 10, e0130329	3.7	20
229	NanoPipe-a web server for nanopore MinION sequencing data analysis. <i>GigaScience</i> , 2019 , 8,	7.6	19
228	Assignment of 118 novel cDNAs of cynomolgus monkey brain to human chromosomes. <i>Gene</i> , 2001 , 275, 31-7	3.8	19
227	Identification of long non-coding RNAs in advanced prostate cancer associated with androgen receptor splicing factors. <i>Communications Biology</i> , 2020 , 3, 393	6.7	19
226	Dramatic improvement in genome assembly achieved using doubled-haploid genomes. <i>Scientific Reports</i> , 2014 , 4, 6780	4.9	18
225	Long non-coding RNA exchange during the oocyte-to-embryo transition in mice. <i>DNA Research</i> , 2017 , 24, 129-141	4.5	18
224	Regulation of ectopic heterochromatin-mediated epigenetic diversification by the JmjC family protein Epe1. <i>PLoS Genetics</i> , 2019 , 15, e1008129	6	17
223	Molecular evidence for recent divergence of X- and Y-linked gene pairs in <i>Spinacia oleracea</i> L. <i>PLoS ONE</i> , 2019 , 14, e0214949	3.7	17
222	Deep sequencing of the prothoracic gland transcriptome reveals new players in insect ecdysteroidogenesis. <i>PLoS ONE</i> , 2017 , 12, e0172951	3.7	17
221	Three-step transcriptional priming that drives the commitment of multipotent progenitors toward B cells. <i>Genes and Development</i> , 2018 , 32, 112-126	12.6	17
220	Selective control of up-regulated and down-regulated genes by temporal patterns and doses of insulin. <i>Science Signaling</i> , 2016 , 9, ra112	8.8	17
219	Genomic structure and evolution of the mating type locus in the green seaweed <i>Ulva partita</i> . <i>Scientific Reports</i> , 2017 , 7, 11679	4.9	17
218	The Exon Junction Complex Controls the Efficient and Faithful Splicing of a Subset of Transcripts Involved in Mitotic Cell-Cycle Progression. <i>International Journal of Molecular Sciences</i> , 2016 , 17,	6.3	17
217	A computational tool to detect DNA alterations tailored to formalin-fixed paraffin-embedded samples in cancer clinical sequencing. <i>Genome Medicine</i> , 2018 , 10, 44	14.4	17
216	Directed induction of alveolar type I cells derived from pluripotent stem cells via Wnt signaling inhibition. <i>Stem Cells</i> , 2021 , 39, 156-169	5.8	17
215	Comprehensive single-cell transcriptome analysis reveals heterogeneity in endometrioid adenocarcinoma tissues. <i>Scientific Reports</i> , 2017 , 7, 14225	4.9	16
214	An integrated genome-wide multi-omics analysis of gene expression dynamics in the preimplantation mouse embryo. <i>Scientific Reports</i> , 2019 , 9, 13356	4.9	16

213	Transcriptome profiling reveals infection strategy of an insect maculavirus. <i>DNA Research</i> , 2018 ,	4.5	16
212	Bone-protective Functions of Netrin 1 Protein. <i>Journal of Biological Chemistry</i> , 2016 , 291, 23854-23868	5.4	16
211	Flexible selection of diversified Na(+)/K(+)-ATPase β subunit isoforms for osmoregulation in teleosts. <i>Zoological Letters</i> , 2016 , 2, 15	3	16
210	Evolutionarily conserved autoregulation of alternative pre-mRNA splicing by ribosomal protein L10a. <i>Nucleic Acids Research</i> , 2016 , 44, 5585-5596	20.1	16
209	Characterization of STAT6 target genes in human B cells and lung epithelial cells. <i>DNA Research</i> , 2011 , 18, 379-92	4.5	16
208	Isolation, tissue expression, and chromosomal assignment of a novel human gene which encodes a protein with RING finger motif. <i>Journal of Human Genetics</i> , 1998 , 43, 272-4	4.3	16
207	A novel human gene whose product shares significant homology with the bovine brain-specific protein p25 on chromosome 5p15.3. <i>Journal of Human Genetics</i> , 1999 , 44, 121-2	4.3	16
206	H-NS Facilitates Sequence Diversification of Horizontally Transferred DNAs during Their Integration in Host Chromosomes. <i>PLoS Genetics</i> , 2016 , 12, e1005796	6	16
205	Aberrant splicing isoforms detected by full-length transcriptome sequencing as transcripts of potential neoantigens in non-small cell lung cancer. <i>Genome Biology</i> , 2021 , 22, 9	18.3	16
204	Expression of miR-26a exhibits a negative correlation with HMGA1 and regulates cancer progression by targeting HMGA1 in lung adenocarcinoma cells. <i>Molecular Medicine Reports</i> , 2017 , 15, 534-542	2.9	15
203	Analysis of Müller glia specific genes and their histone modification using Hes1-promoter driven EGFP expressing mouse. <i>Scientific Reports</i> , 2017 , 7, 3578	4.9	15
202	Spatial Interplay between Polycomb and Trithorax Complexes Controls Transcriptional Activity in T Lymphocytes. <i>Molecular and Cellular Biology</i> , 2015 , 35, 3841-53	4.8	15
201	Indoleamine 2,3-dioxygenase 1 is highly expressed in glioma stem cells. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 524, 723-729	3.4	15
200	Non-invasive diagnosis of cutaneous leishmaniasis by the direct boil loop-mediated isothermal amplification method and MinION nanopore sequencing. <i>Parasitology International</i> , 2018 , 67, 34-37	2.1	15
199	Identification of Minimal Promoter Region Regulated by MALAT1 in Human Lung Adenocarcinoma Cells. <i>Frontiers in Genetics</i> , 2017 , 8, 208	4.5	15
198	Genome-wide characterization of DNA methylation, small RNA expression, and histone H3 lysine nine di-methylation in Brassica rapa L. <i>DNA Research</i> , 2018 , 25, 511-520	4.5	15
197	Identification of Arabidopsis genic and non-genic promoters by paired-end sequencing of TSS tags. <i>Plant Journal</i> , 2017 , 90, 587-605	6.9	14
196	Molecular mechanisms underlying active desalination and low water permeability in the esophagus of eels acclimated to seawater. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2017 , 312, R231-R244	3.2	14

195	Integrative Genomic Analysis of OCT1 Reveals Coordinated Regulation of Androgen Receptor in Advanced Prostate Cancer. <i>Endocrinology</i> , 2019 , 160, 463-472	4.8	14
194	Combinatory use of distinct single-cell RNA-seq analytical platforms reveals the heterogeneous transcriptome response. <i>Scientific Reports</i> , 2018 , 8, 3482	4.9	14
193	Pulmonary Regnase-1 orchestrates the interplay of epithelium and adaptive immune systems to protect against pneumonia. <i>Mucosal Immunology</i> , 2018 , 11, 1203-1218	9.2	14
192	A missense mutation in solute carrier family 12, member 1 (SLC12A1) causes hydrallantois in Japanese Black cattle. <i>BMC Genomics</i> , 2016 , 17, 724	4.5	14
191	Different gene expression profiles between normal and thermally selected strains of rainbow trout, <i>Oncorhynchus mykiss</i> , as revealed by comprehensive transcriptome analysis. <i>Gene</i> , 2016 , 576, 637-643	3.8	14
190	In silico identification of lysocin biosynthetic gene cluster from <i>Lysobacter</i> sp. RH2180-5. <i>Journal of Antibiotics</i> , 2017 , 70, 204-207	3.7	14
189	Genome-wide analysis of the chromatin composition of histone H2A and H3 variants in mouse embryonic stem cells. <i>PLoS ONE</i> , 2014 , 9, e92689	3.7	14
188	Long-read sequencing for non-small-cell lung cancer genomes. <i>Genome Research</i> , 2020 , 30, 1243-1257	9.7	14
187	PSF Promotes ER-Positive Breast Cancer Progression via Posttranscriptional Regulation of and. <i>Cancer Research</i> , 2020 , 80, 2230-2242	10.1	14
186	Kmt2b conveys monovalent and bivalent H3K4me3 in mouse spermatogonial stem cells at germline and embryonic promoters. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	14
185	A Single Pheromone Receptor Gene Conserved across 400 My of Vertebrate Evolution. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2928-2939	8.3	14
184	PHLDA1, another PHLDA family protein that inhibits Akt. <i>Cancer Science</i> , 2018 , 109, 3532-3542	6.9	14
183	Regnase-1-mediated post-transcriptional regulation is essential for hematopoietic stem and progenitor cell homeostasis. <i>Nature Communications</i> , 2019 , 10, 1072	17.4	13
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181	The Number of Transcription Factors at an Enhancer Determines Switch-like Gene Expression. <i>Cell Reports</i> , 2020 , 31, 107724	10.6	13
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