

Masayoshi Itoh

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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.

137 papers	15,055 citations	39 h-index	122 g-index
154 ext. papers	18,154 ext. citations	9.2 avg, IF	4.87 L-index

#	Paper	IF	Citations
137	The transcriptional landscape of the mammalian genome. <i>Science</i> , 2005 , 309, 1559-63	33.3	2807
136	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014 , 507, 455-461	50.4	1595
135	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
134	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
133	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice. <i>Science</i> , 2003 , 301, 376-9	33.3	772
132	Functional annotation of a full-length Arabidopsis cDNA collection. <i>Science</i> , 2002 , 296, 141-5	33.3	588
131	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017 , 543, 199-204	50.4	581
130	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001 , 409, 685-90	50.4	560
129	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015 , 16, 22	18.3	443
128	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015 , 6, 7866	17.4	393
127	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015 , 347, 1010-4	33.3	384
126	High-efficiency full-length cDNA cloning by biotinylated CAP trapper. <i>Genomics</i> , 1996 , 37, 327-36	4.3	266
125	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <i>Molecular Systems Biology</i> , 2015 , 11, 852	12.2	229
124	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. <i>Genome Research</i> , 2000 , 10, 1617-30	9.7	221
123	Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 520-4	11.5	205
122	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
121	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011 , 21, 1150-9	9.7	143

120	Rapid SNP diagnostics using asymmetric isothermal amplification and a new mismatch-suppression technology. <i>Nature Methods</i> , 2007 , 4, 257-62	21.6	142
119	Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia. <i>Genome Research</i> , 2003 , 13, 1273-89	9.7	141
118	Transcript annotation in FANTOM3: mouse gene catalog based on physical cDNAs. <i>PLoS Genetics</i> , 2006 , 2, e62	6	138
117	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , 2014 , 123, e58-67	2.2	126
116	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014 , 123, e90-9	2.2	101
115	Detecting expressed genes using CAGE. <i>Methods in Molecular Biology</i> , 2014 , 1164, 67-85	1.4	100
114	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017 , 4, 170112	8.2	88
113	Differential roles of epigenetic changes and Foxp3 expression in regulatory T cell-specific transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5289-94	11.5	85
112	High efficiency selection of full-length cDNA by improved biotinylated cap trapper. <i>DNA Research</i> , 1997 , 4, 61-6	4.5	79
111	Balanced-size and long-size cloning of full-length, cap-trapped cDNAs into vectors of the novel lambda-FLC family allows enhanced gene discovery rate and functional analysis. <i>Genomics</i> , 2001 , 77, 79-90	4.3	70
110	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <i>Genome Research</i> , 2014 , 24, 708-17	9.7	66
109	Analysis of the human monocyte-derived macrophage transcriptome and response to lipopolysaccharide provides new insights into genetic aetiology of inflammatory bowel disease. <i>PLoS Genetics</i> , 2017 , 13, e1006641	6	64
108	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , 2014 , 123, e79-89	2.2	59
107	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014 , 123, e68-78	2.2	58
106	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. <i>Cancer Research</i> , 2016 , 76, 216-26	10.1	56
105	Reversible hydrogel formation driven by protein-peptide-specific interaction and chondrocyte entrapment. <i>Biomaterials</i> , 2010 , 31, 58-66	15.6	52
104	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. <i>Genome Research</i> , 2000 , 10, 1757-71	9.7	48
103	Molecular cloning and characterization of the obg gene of <i>Streptomyces griseus</i> in relation to the onset of morphological differentiation. <i>Journal of Bacteriology</i> , 1997 , 179, 170-9	3.5	45

102	Gemin2 plays an important role in stabilizing the survival of motor neuron complex. <i>Journal of Biological Chemistry</i> , 2007 , 282, 11122-34	5.4	44
101	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , 2018 , 8, 6758	4.9	41
100	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020 , 30, 1060-1072	9.7	41
99	Characterization of gene expression in mouse blastocyst using single-pass sequencing of 3995 clones. <i>Genomics</i> , 1998 , 49, 167-79	4.3	39
98	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015 , 43, 6969-82	20.1	38
97	RECLU: a pipeline to discover reproducible transcriptional start sites and their alternative regulation using capped analysis of gene expression (CAGE). <i>BMC Genomics</i> , 2014 , 15, 269	4.5	37
96	Ceruloplasmin is a novel adipokine which is overexpressed in adipose tissue of obese subjects and in obesity-associated cancer cells. <i>PLoS ONE</i> , 2014 , 9, e80274	3.7	36
95	Comparative evaluation of 5Rend-sequence quality of clones in CAP trapper and other full-length-cDNA libraries. <i>Gene</i> , 2001 , 263, 93-102	3.8	36
94	Mechanism of chromium(VI) toxicity in Escherichia coli: is hydrogen peroxide essential in Cr(VI) toxicity?. <i>Journal of Biochemistry</i> , 1995 , 117, 780-6	3.1	35
93	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. <i>Nature Genetics</i> , 2019 , 51, 1369-1379	36.3	33
92	The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , 2015 , 25, 1546-57	9.7	33
91	Rapid screening assay for KRAS mutations by the modified smart amplification process. <i>Journal of Molecular Diagnostics</i> , 2008 , 10, 520-6	5.1	33
90	Novel biomarkers that assist in accurate discrimination of squamous cell carcinoma from adenocarcinoma of the lung. <i>BMC Cancer</i> , 2016 , 16, 760	4.8	30
89	Integration of genetics and miRNA-target gene network identified disease biology implicated in tissue specificity. <i>Nucleic Acids Research</i> , 2018 , 46, 11898-11909	20.1	26
88	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , 2015 , 13, 1493-1504	10.6	25
87	Simple and rapid preparation of plasmid template by a filtration method using microtiter filter plates. <i>Nucleic Acids Research</i> , 1997 , 25, 1315-6	20.1	25
86	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. <i>Genome Research</i> , 2001 , 11, 281-9	9.7	25
85	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. <i>Scientific Reports</i> , 2015 , 5, 11999	4.9	24

84	Exciton Primer-mediated SNP detection in SmartAmp2 reactions. <i>Human Mutation</i> , 2010 , 31, 208-17	4.7	24
83	Use of a competitive probe in assay design for genotyping of the UGT1A1 *28 microsatellite polymorphism by the smart amplification process. <i>BioTechniques</i> , 2007 , 43, 479-84	2.5	24
82	Nanoscale elongating control of the self-assembled protein filament with the cysteine-introduced building blocks. <i>Protein Science</i> , 2009 , 18, 960-9	6.3	23
81	Force measurement for antigen-antibody interaction by atomic force microscopy using a photograft-polymer spacer. <i>Biomacromolecules</i> , 2005 , 6, 2776-84	6.9	23
80	A computer-based method of selecting clones for a full-length cDNA project: simultaneous collection of negligibly redundant and variant cDNAs. <i>Genome Research</i> , 2002 , 12, 1127-34	9.7	23
79	Correlation between sequence conservation of the 5' untranslated region and codon usage bias in <i>Mus musculus</i> genes. <i>Gene</i> , 2001 , 276, 101-5	3.8	23
78	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , 2017 , 15, e2002887	9.7	22
77	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , 2016 , 44, 3233-52	20.1	21
76	Dynamic force spectroscopy of the specific interaction between the PDZ domain and its recognition peptides. <i>Langmuir</i> , 2007 , 23, 2668-73	4	21
75	Constructing ORFeome resources with removable termination codons. <i>BioTechniques</i> , 2006 , 41, 44, 46, 48 passim	2.5	21
74	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. <i>Molecular Cancer Research</i> , 2017 , 15, 1354-1365	6.6	20
73	Role of survival motor neuron complex components in small nuclear ribonucleoprotein assembly. <i>Journal of Biological Chemistry</i> , 2009 , 284, 14609-17	5.4	20
72	Automated Filtration-Based High-Throughput Plasmid Preparation System. <i>Genome Research</i> , 1999 , 9, 463-470	9.7	20
71	High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. <i>Blood</i> , 2014 , 123, e46-57	2.2	19
70	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017 , 66, 218-230	0.9	19
69	Discovery of molecular markers to discriminate corneal endothelial cells in the human body. <i>PLoS ONE</i> , 2015 , 10, e0117581	3.7	19
68	Synthesis of 5-acetyl-2-aminopyrrole C-deoxyribonucleoside. <i>Tetrahedron</i> , 2007 , 63, 12747-12753	2.4	19
67	Automated workflow for preparation of cDNA for cap analysis of gene expression on a single molecule sequencer. <i>PLoS ONE</i> , 2012 , 7, e30809	3.7	18

66	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , 2015 , 97, 985-995	6.5	17
65	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. <i>PLoS Biology</i> , 2015 , 13, e1002315	9.7	17
64	Correlation of EGFR or KRAS mutation status with 18F-FDG uptake on PET-CT scan in lung adenocarcinoma. <i>PLoS ONE</i> , 2017 , 12, e0175622	3.7	16
63	YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. <i>Scientific Reports</i> , 2016 , 6, 37324	4.9	16
62	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
61	Transcriptional dynamics reveal critical roles for non-coding RNAs in the immediate-early response. <i>PLoS Computational Biology</i> , 2015 , 11, e1004217	5	15
60	Comprehensive sequence analysis of translation termination sites in various eukaryotes. <i>Gene</i> , 2002 , 300, 79-87	3.8	15
59	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , 2019 , 56, 5392-5415	6.2	15
58	Specific mesothelial signature marks the heterogeneity of mesenchymal stem cells from high-grade serous ovarian cancer. <i>Stem Cells</i> , 2014 , 32, 2998-3011	5.8	14
57	Transcriptome analysis of periodontitis-associated fibroblasts by CAGE sequencing identified DLX5 and RUNX2 long variant as novel regulators involved in periodontitis. <i>Scientific Reports</i> , 2016 , 6, 33666	4.9	14
56	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017 , 24, 257-266	8.8	13
55	Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , 2020 , 30, 1073-1081	9.7	13
54	Removal of polyA tails from full-length cDNA libraries for high-efficiency sequencing. <i>BioTechniques</i> , 2001 , 31, 1042, 1044, 1048-9	2.5	13
53	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020 , 30, 951-961	9.7	12
52	Phenotypical Characteristics of POC1B-Associated Retinopathy in Japanese Cohort: Cone Dystrophy With Normal Funduscopy Appearance 2019 , 60, 3432-3446		11
51	Mapping Mammalian Cell-type-specific Transcriptional Regulatory Networks Using KD-CAGE and ChIP-seq Data in the TC-YIK Cell Line. <i>Frontiers in Genetics</i> , 2015 , 6, 331	4.5	11
50	Protein-protein interactions of the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3. <i>Genome Biology</i> , 2005 , 6, R98	18.3	11
49	Computational analysis of full-length mouse cDNAs compared with human genome sequences. <i>Mammalian Genome</i> , 2001 , 12, 673-7	3.2	11

48	DeepCAGE transcriptomics identify HOXD10 as a transcription factor regulating lymphatic endothelial responses to VEGF-C. <i>Journal of Cell Science</i> , 2016 , 129, 2573-85	5.3	11
47	Relatively frequent switching of transcription start sites during cerebellar development. <i>BMC Genomics</i> , 2017 , 18, 461	4.5	10
46	Genetic Spectrum of EYS-associated Retinal Disease in a Large Japanese Cohort: Identification of Disease-associated Variants with Relatively High Allele Frequency. <i>Scientific Reports</i> , 2020 , 10, 5497	4.9	10
45	Sensitive detection of EGFR mutations using a competitive probe to suppress background in the Smart Amplification Process. <i>Biologicals</i> , 2008 , 36, 234-8	1.8	10
44	Proteins that interact with GTP in <i>Streptomyces griseus</i> and its possible implication in morphogenesis. <i>FEMS Microbiology Letters</i> , 1996 , 135, 311-6	2.9	10
43	RNA sequencing analysis revealed the induction of CCL3 expression in human intracranial aneurysms. <i>Scientific Reports</i> , 2019 , 9, 10387	4.9	9
42	Syntheses of pyrido[1,2-a][1,3,5]triazin-4-one C-deoxyribonucleosides. <i>Tetrahedron</i> , 2007 , 63, 11021-11029	4.9	8
41	Synthesis of 8-(2?-deoxy-?-ribofuranosyl)imidazo[1,2-a]-s-triazin-4-one. <i>Tetrahedron Letters</i> , 2007 , 48, 3801-3803	2	8
40	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , 2018 , 14, e1005934	5	8
39	Promoter-level transcriptome in primary lesions of endometrial cancer identified biomarkers associated with lymph node metastasis. <i>Scientific Reports</i> , 2017 , 7, 14160	4.9	7
38	Deep phenotyping of myalgic encephalomyelitis/chronic fatigue syndrome in Japanese population. <i>Scientific Reports</i> , 2020 , 10, 19933	4.9	7
37	Ex vivo conditioning of peripheral blood mononuclear cells of diabetic patients promotes vasculogenic wound healing. <i>Stem Cells Translational Medicine</i> , 2021 , 10, 895-909	6.9	7
36	Cap Analysis of Gene Expression (CAGE): A Quantitative and Genome-Wide Assay of Transcription Start Sites. <i>Methods in Molecular Biology</i> , 2020 , 2120, 277-301	1.4	7
35	High-resolution promoter map of human limbal epithelial cells cultured with keratinocyte growth factor and rho kinase inhibitor. <i>Scientific Reports</i> , 2017 , 7, 2845	4.9	6
34	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping		6
33	Promoter Usage and Dynamics in Vascular Smooth Muscle Cells Exposed to Fibroblast Growth Factor-2 or Interleukin-1. <i>Scientific Reports</i> , 2018 , 8, 13164	4.9	6
32	Restricted Presence of POU6F2 in Human Corneal Endothelial Cells Uncovered by Extension of the Promoter-level Expression Atlas. <i>EBioMedicine</i> , 2017 , 25, 175-186	8.8	5
31	A novel control system for polymerase chain reaction using a RIKEN GS384 thermalcycler. <i>DNA Research</i> , 1997 , 4, 387-91	4.5	5

30	CREB3L1 overexpression as a potential diagnostic marker of Philadelphia chromosome-negative myeloproliferative neoplasms. <i>Cancer Science</i> , 2021 , 112, 884-892	6.9	5
29	Monitoring transcription initiation activities in rat and dog. <i>Scientific Data</i> , 2017 , 4, 170173	8.2	4
28	Computer-Based Methods for the Mouse Full-Length cDNA Encyclopedia: Real-Time Sequence Clustering for Construction of a Nonredundant cDNA Library. <i>Genome Research</i> , 2001 , 11, 281-289	9.7	4
27	Cancer-associated fibroblast migration in non-small cell lung cancers is modulated by increased integrin $\alpha 1$ expression. <i>Molecular Oncology</i> , 2021 , 15, 1507-1527	7.9	4
26	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , 2019 , 20, 718	4.5	3
25	CXCL4/PF4 is a predictive biomarker of cardiac differentiation potential of human induced pluripotent stem cells. <i>Scientific Reports</i> , 2019 , 9, 4638	4.9	3
24	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. <i>Stem Cells and Development</i> , 2017 , 26, 314-327	4.4	3
23	Expression of a plasmid-encoded gene for cadmium resistance of <i>Pseudomonas putida</i> GAM-1 in <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 1992 , 73, 314-316		3
22	Development of a Tet-On Inducible Expression System for the Anhydrobiotic Cell Line, Pv11. <i>Insects</i> , 2020 , 11,	2.8	3
21	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021 , 12, 3297	17.4	3
20	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. <i>Open Biology</i> , 2018 , 8,	7	3
19	Transcription start site profiling of 15 anatomical regions of the <i>Macaca mulatta</i> central nervous system. <i>Scientific Data</i> , 2017 , 4, 170163	8.2	2
18	Mapping of 19032 mouse cDNAs on mouse chromosomes. <i>Journal of Structural and Functional Genomics</i> , 2002 , 2, 23-8		2
17	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease		2
16	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. <i>Cerebellum</i> , 2018 , 17, 308-325	4.3	1
15	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. <i>PLoS ONE</i> , 2015 , 10, e0144176	3.7	1
14	In vitro protein phosphorylation associated with cellular differentiation of <i>Streptomyces griseus</i> . <i>Archives of Microbiology</i> , 1998 , 169, 174-7	3	1
13	Cadmium resistance acquirement by IS1 transposition into <i>Escherichia coli</i> C600. <i>Journal of Bioscience and Bioengineering</i> , 1994 , 78, 466-468		1

12	Scanning single-molecule counting system for Eprobe with highly simple and effective approach. <i>PLoS ONE</i> , 2020 , 15, e0243319	3.7	1
11	Development of a Tet-On inducible expression system for the anhydrobiotic cell line, Pv11		1
10	Low Quantity single strand CAGE (LQ-ssCAGE) maps regulatory enhancers and promoters		1
9	Evidence of transcription at polyT short tandem repeats		1
8	Functional annotation of human long noncoding RNAs using chromatin conformation data		1
7	Low Quantity Single Strand CAGE (LQ-ssCAGE) Maps Regulatory Enhancers and Promoters. <i>Methods in Molecular Biology</i> , 2021 , 2351, 67-90	1.4	1
6	Nanopore sequencing reveals TACC2 locus complexity and diversity of isoforms transcribed from an intronic promoter. <i>Scientific Reports</i> , 2021 , 11, 9355	4.9	0
5	High quality genome assembly of the "anhydrobiotic midge" provides insights on a single chromosome-based emergence of extreme desiccation tolerance.. <i>NAR Genomics and Bioinformatics</i> , 2022 , 4, lqac029	3.7	0
4	New pyrosequencing method to analyze the function of the Klenow fragment (EXO-) for unnatural nucleic acids: pyrophosphorolysis and incorporation efficiency. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2012 , 31, 608-15	1.4	
3	CREB3L1 Overexpression Can Reliably Discriminate Ph-MPNs from Reactive Cases. <i>Blood</i> , 2020 , 136, 41-41	2.2	
2	Association between the EGFR or KRAS mutation status and the FDG-PET findings in surgically resected lung adenocarcinoma.. <i>Journal of Clinical Oncology</i> , 2015 , 33, 7535-7535	2.2	
1	The choice of negative control antisense oligonucleotides dramatically impacts downstream analysis depending on the cellular background. <i>BMC Genomic Data</i> , 2021 , 22, 33	0	