

Takashi Ito

List of Publications by Year in descending order

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139
papers

6,881
citations

57758

44
h-index

69250

77
g-index

146
all docs

146
docs citations

146
times ranked

9311
citing authors

#	ARTICLE	IF	CITATIONS
1	Pan-cancer methylome analysis for cancer diagnosis and classification of cancer cell of origin. <i>Cancer Gene Therapy</i> , 2022, 29, 428-436.	4.6	12
2	A GCDGC-specific DNA (cytosine-5) methyltransferase that methylates the GCWGC sequence on both strands and the GCSGC sequence on one strand. <i>PLoS ONE</i> , 2022, 17, e0265225.	2.5	3
3	GET pathway mediates transfer of mislocalized tail-anchored proteins from mitochondria to the ER. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	9
4	Identification of genes associated with endometrial cell ageing. <i>Molecular Human Reproduction</i> , 2021, 27, .	2.8	7
5	Reconstitution of the oocyte transcriptional network with transcription factors. <i>Nature</i> , 2021, 589, 264-269.	27.8	92
6	Catalytically inactive Cas9 impairs DNA replication fork progression to induce focal genomic instability. <i>Nucleic Acids Research</i> , 2021, 49, 954-968.	14.5	24
7	Short single-stranded DNA with putative non-canonical structures comprises a novel class of plasma cell-free DNA. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
8	Maintenance DNA methylation in pre-meiotic germ cells regulates meiotic prophase by facilitating homologous chromosome pairing. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	15
9	Hoxa10 mediates positional memory to govern stem cell function in adult skeletal muscle. <i>Science Advances</i> , 2021, 7, .	10.3	21
10	Simple-to-use CRISPR-SpCas9/SaCas9/AsCas12a vector series for genome editing in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	6
11	The Evolving Genomic Landscape of Esophageal Squamous Cell Carcinoma Under Chemoradiotherapy. <i>Cancer Research</i> , 2021, 81, 4926-4938.	0.9	20
12	Transcriptome dynamics during cholesterol-induced transdifferentiation of human coronary artery smooth muscle cells: A Gene Ontology-centric clustering approach. <i>Biochemistry and Biophysics Reports</i> , 2021, 27, 101061.	1.3	2
13	Nucleosome assembly protein 1 (NAP-1) is a regulator of histone H1 acetylation. <i>Journal of Biochemistry</i> , 2021, , .	1.7	2
14	Limited rejuvenation of aged hematopoietic stem cells in young bone marrow niche. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	42
15	Neuronal activation modulates enhancer activity of genes for excitatory synaptogenesis through <i>de novo</i> DNA methylation. <i>Journal of Reproduction and Development</i> , 2021, , .	1.4	0
16	Short single-stranded DNAs with putative non-canonical structures comprise a new class of plasma cell-free DNA. <i>BMC Biology</i> , 2021, 19, 225.	3.8	19
17	DNA methylation is reconfigured at the onset of reproduction in rice shoot apical meristem. <i>Nature Communications</i> , 2020, 11, 4079.	12.8	42
18	Base-resolution methylomes of gliomas bearing histone H3.3 mutations reveal a G34 mutant-specific signature shared with bone tumors. <i>Scientific Reports</i> , 2020, 10, 16162.	3.3	12

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19	NSD1-deposited H3K36me2 directs de novo methylation in the mouse male germline and counteracts Polycomb-associated silencing. <i>Nature Genetics</i> , 2020, 52, 1088-1098.	21.4	96
20	Tet2 and Tet3 in B cells are required to repress CD86 and prevent autoimmunity. <i>Nature Immunology</i> , 2020, 21, 950-961.	14.5	55
21	ATF7-Dependent Epigenetic Changes Are Required for the Intergenerational Effect of a Paternal Low-Protein Diet. <i>Molecular Cell</i> , 2020, 78, 445-458.e6.	9.7	52
22	TBIO-08. BASE-RESOLUTION METHYLOMES OF GLIOMAS BEARING HISTONE H3.3 MUTATIONS REVEAL A G34 MUTANT-SPECIFIC SIGNATURE SHARED WITH BONE TUMORS. <i>Neuro-Oncology</i> , 2020, 22, iii468-iii468.	1.2	0
23	Base-Resolution Methylome of Retinal Pigment Epithelial Cells Used in the First Trial of Human Induced Pluripotent Stem Cell-Based Autologous Transplantation. <i>Stem Cell Reports</i> , 2019, 13, 761-774.	4.8	20
24	Highly efficient single-stranded DNA ligation technique improves low-input whole-genome bisulfite sequencing by post-bisulfite adaptor tagging. <i>Nucleic Acids Research</i> , 2019, 47, e85-e85.	14.5	51
25	Pioneer Factor NeuroD1 Rearranges Transcriptional and Epigenetic Profiles to Execute Microglia-Neuron Conversion. <i>Neuron</i> , 2019, 101, 472-485.e7.	8.1	161
26	Epigenetic landscape influences the liver cancer genome architecture. <i>Nature Communications</i> , 2018, 9, 1643.	12.8	39
27	Post-Bisulfite Adaptor Tagging for PCR-Free Whole-Genome Bisulfite Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1708, 123-136.	0.9	16
28	Mapping of histone-binding sites in histone replacement-completed spermatozoa. <i>Nature Communications</i> , 2018, 9, 3885.	12.8	53
29	Maternal Protein Restriction Alters the Renal Ptger1 DNA Methylation State in SHRSP Offspring. <i>Nutrients</i> , 2018, 10, 1436.	4.1	7
30	Triazole linking for preparation of a next-generation sequencing library from single-stranded DNA. <i>Nucleic Acids Research</i> , 2018, 46, e95-e95.	14.5	12
31	DMS-Seq for In Vivo Genome-Wide Mapping of Protein-DNA Interactions and Nucleosome Centers. <i>Current Protocols in Molecular Biology</i> , 2018, 123, e60.	2.9	7
32	Epigenome mapping of human normal purified hepatocytes: personal epigenome variation and genome-wide epigenome correlation. <i>Epigenomics</i> , 2018, 10, 955-979.	2.1	3
33	DMS-Seq for In Vivo Genome-wide Mapping of Protein-DNA Interactions and Nucleosome Centers. <i>Cell Reports</i> , 2017, 21, 289-300.	6.4	13
34	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
35	The AP-1 transcription factor JunB is required for Th17 cell differentiation. <i>Scientific Reports</i> , 2017, 7, 17402.	3.3	47
36	Software updates in the Illumina HiSeq platform affect whole-genome bisulfite sequencing. <i>BMC Genomics</i> , 2017, 18, 31.	2.8	29

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37	A strategy for absolute proteome quantification with mass spectrometry by hierarchical use of peptide-concatenated standards. <i>Proteomics</i> , 2016, 16, 1457-1473.	2.2	13
38	DNA Methylation Errors in Cloned Mouse Sperm by Germ Line Barrier Evasion1. <i>Biology of Reproduction</i> , 2016, 94, 128.	2.7	12
39	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
40	Highly sensitive targeted methylome sequencing by post-bisulfite adaptor tagging. <i>DNA Research</i> , 2015, 22, 13-18.	3.4	53
41	DNA methylation and gene expression in <i>Mimulus guttatus</i> . <i>BMC Genomics</i> , 2015, 16, 507.	2.8	34
42	Changepoint detection in base-resolution methylome data reveals a robust signature of methylated domain landscape. <i>BMC Genomics</i> , 2015, 16, 594.	2.8	8
43	Detecting Protein-DNA Interactions Using a Modified Yeast One-Hybrid System. <i>Methods in Molecular Biology</i> , 2014, 1164, 39-50.	0.9	4
44	Synthetic Gene Circuit-Mediated Monitoring of Endogenous Metabolites: Identification of <i>GAL11</i> as a Novel Multicopy Enhancer of <i>S</i> -Adenosylmethionine Level in Yeast. <i>ACS Synthetic Biology</i> , 2013, 2, 425-430.	3.8	43
45	High-resolution DNA methylome analysis of primordial germ cells identifies gender-specific reprogramming in mice. <i>Genome Research</i> , 2013, 23, 616-627.	5.5	239
46	The WD40 protein Morg1 facilitates Par6-aPKC binding to Crb3 for apical identity in epithelial cells. <i>Journal of Cell Biology</i> , 2013, 200, 635-650.	5.2	38
47	Regional DNA methylation differences between humans and chimpanzees are associated with genetic changes, transcriptional divergence and disease genes. <i>Journal of Human Genetics</i> , 2013, 58, 446-454.	2.3	25
48	Mouse Oocyte Methylomes at Base Resolution Reveal Genome-Wide Accumulation of Non-CpG Methylation and Role of DNA Methyltransferases. <i>PLoS Genetics</i> , 2013, 9, e1003439.	3.5	263
49	Amplification-free whole-genome bisulfite sequencing by post-bisulfite adaptor tagging. <i>Nucleic Acids Research</i> , 2012, 40, e136-e136.	14.5	347
50	Highly efficient PCR assay to discriminate allelic DNA methylation status using whole genome amplification. <i>BMC Research Notes</i> , 2011, 4, 179.	1.4	2
51	Translation Initiation: A Regulatory Role for Poly(A) Tracts in Front of the AUG Codon in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2011, 189, 469-478.	2.9	41
52	Remodeling of the SCF complex-mediated ubiquitination system by compositional alteration of incorporated F-box proteins. <i>Proteomics</i> , 2010, 10, 115-123.	2.2	6
53	A yeast one-hybrid system to screen for methylated DNA-binding proteins. <i>Nucleic Acids Research</i> , 2010, 38, e189-e189.	14.5	12
54	MafB protein stability is regulated by the JNK and ubiquitin-proteasome pathways. <i>Archives of Biochemistry and Biophysics</i> , 2010, 494, 94-100.	3.0	11

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55	Circular permutation of ligand-binding module improves dynamic range of genetically encoded FRET-based nanosensor. <i>Protein Science</i> , 2009, 18, 2518-2527.	7.6	36
56	NMR Structure of the Heterodimer of Bem1 and Cdc24 PB1 Domains from <i>Saccharomyces Cerevisiae</i> . <i>Journal of Biochemistry</i> , 2009, 146, 317-325.	1.7	12
57	Discrimination between stable and dynamic components of protein complexes by means of quantitative proteomics. <i>Proteomics</i> , 2008, 8, 2366-2370.	2.2	15
58	A parallel affinity purification method for selective isolation of polyubiquitinated proteins. <i>Proteomics</i> , 2008, 8, 3004-3007.	2.2	12
59	Unexpected complexity of the budding yeast transcriptome. <i>IUBMB Life</i> , 2008, 60, 775-781.	3.4	8
60	A proteomic screen reveals the mitochondrial outer membrane protein Mdm34p as an essential target of the Fox protein Mdm30p. <i>Genes To Cells</i> , 2008, 13, 1075-1085.	1.2	23
61	Absolute quantification of the budding yeast transcriptome by means of competitive PCR between genomic and complementary DNAs. <i>BMC Genomics</i> , 2008, 9, 574.	2.8	83
62	Mass Spectrometry-Based Approaches Toward Absolute Quantitative Proteomics. <i>Current Genomics</i> , 2008, 9, 263-274.	1.6	88
63	Unexpected complexity of the budding yeast transcriptome. <i>FASEB Journal</i> , 2008, 22, 100.1.	0.5	0
64	A Novel Cdc42-interacting Domain of the Yeast Polarity Establishment Protein Bem1. <i>Journal of Biological Chemistry</i> , 2007, 282, 29-38.	3.4	43
65	A Synthetic Protein Approach toward Accurate Mass Spectrometric Quantification of Component Stoichiometry of Multiprotein Complexes. <i>Journal of Proteome Research</i> , 2007, 6, 792-800.	3.7	80
66	Regulation of N-cadherin-based cell-cell interaction by JSAP1 scaffold in PC12h cells. <i>Biochemical and Biophysical Research Communications</i> , 2007, 353, 357-362.	2.1	10
67	Structure and Function of the PB1 Domain, a Protein Interaction Module Conserved in Animals, Fungi, Amoebas, and Plants. <i>Science's STKE: Signal Transduction Knowledge Environment</i> , 2007, 2007, re6.	3.9	131
68	Proteomic Analysis of in Vivo 14-3-3 Interactions in the Yeast <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2007, 46, 7781-7792.	2.5	75
69	Methods for Protein-Protein Interaction Analysis. , 2007, , 160-182.		0
70	High-throughput Fluorescence Labelling of Full-length cDNA Products Based on a Reconstituted Translation System. <i>Journal of Biochemistry</i> , 2006, 141, 19-24.	1.7	6
71	Transcriptional activators in yeast. <i>Nucleic Acids Research</i> , 2006, 34, 955-967.	14.5	84
72	Diverse DNA Methylation Statuses at Alternative Promoters of Human Genes in Various Tissues. <i>DNA Research</i> , 2006, 13, 155-167.	3.4	24

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73	A comprehensive analysis of allelic methylation status of CpG islands on human chromosome 11q: Comparison with chromosome 21q. <i>DNA Sequence</i> , 2006, 17, 300-306.	0.7	7
74	A large-scale full-length cDNA analysis to explore the budding yeast transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17846-17851.	7.1	213
75	A novel strategy to design highly specific PCR primers based on the stability and uniqueness of 3' end subsequences. <i>Bioinformatics</i> , 2005, 21, 4363-4370.	4.1	31
76	Comparative genomics approach toward critical determinants for the imprinting of an evolutionarily conserved gene <i>Impact</i> . <i>Biochemical and Biophysical Research Communications</i> , 2005, 329, 824-830.	2.1	20
77	The yeast eIF4E-associated protein Eap1p attenuates GCN4 translation upon TOR-inactivation. <i>FEBS Letters</i> , 2005, 579, 2433-2438.	2.8	21
78	An Evolutionary Scenario for Genomic Imprinting of <i>Impact</i> Lying between Nonimprinted Neighbors. <i>DNA Research</i> , 2004, 11, 381-390.	3.4	9
79	A Comprehensive Analysis of Allelic Methylation Status of CpG Islands on Human Chromosome 21q. <i>Genome Research</i> , 2004, 14, 247-266.	5.5	147
80	Transcriptomic and Proteomic Analysis of a 14-3-3 Gene-Deficient Yeast. <i>Biochemistry</i> , 2004, 43, 6149-6158.	2.5	40
81	Scaffold protein JSAP1 is transported to growth cones of neurites independent of JNK signaling pathways in PC12h cells. <i>Gene</i> , 2004, 329, 51-60.	2.2	27
82	Analysis of gene network regulating yeast multidrug resistance by artificial activation of transcription factors: involvement of Pdr3 in salt tolerance. <i>Gene</i> , 2004, 332, 51-59.	2.2	31
83	A yeast one-hybrid system to detect methylation-dependent DNA-protein interactions. <i>Biochemical and Biophysical Research Communications</i> , 2004, 313, 922-925.	2.1	8
84	SKIP modifies gene expression by affecting both transcription and splicing. <i>Biochemical and Biophysical Research Communications</i> , 2004, 316, 512-517.	2.1	13
85	Mass Spectrometry-Based Proteomics for Quantitative Description of Cellular Events. <i>Current Genomics</i> , 2004, 5, 629-635.	1.6	3
86	The PB1 domain and the PC motif-containing region are structurally similar protein binding modules. <i>EMBO Journal</i> , 2003, 22, 4888-4897.	7.8	38
87	Identification of a five-pass transmembrane protein family localizing in the Golgi apparatus and the ER. <i>Biochemical and Biophysical Research Communications</i> , 2003, 312, 850-857.	2.1	36
88	Phosphorylation of p47phox directs phox homology domain from SH3 domain toward phosphoinositides, leading to phagocyte NADPH oxidase activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4474-4479.	7.1	192
89	Rapamycin-induced Translational Derepression of GCN4 mRNA Involves a Novel Mechanism for Activation of the eIF2 ϵ Kinase GCN2. <i>Journal of Biological Chemistry</i> , 2003, 278, 20457-20460.	3.4	88
90	Molecular Recognition in Dimerization between PB1 Domains. <i>Journal of Biological Chemistry</i> , 2003, 278, 43516-43524.	3.4	78

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91	A functional single-nucleotide polymorphism in the human cytidine deaminase gene contributing to ara-C sensitivity. <i>Pharmacogenetics and Genomics</i> , 2003, 13, 29-38.	5.7	102
92	Roles for the Two-hybrid System in Exploration of the Yeast Protein Interactome. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 561-566.	3.8	105
93	OPR, PC and AID: all in the PB1 family. <i>Trends in Biochemical Sciences</i> , 2002, 27, 10.	7.5	63
94	Appearance of Osteonectin-expressing Fibroblastic Cells in Early Rat Stomach Carcinogenesis and Stomach Tumors Induced with N-Methyl-N- ϵ -nitro-N-nitrosoguanidine. <i>Japanese Journal of Cancer Research</i> , 2002, 93, 960-967.	1.7	9
95	The adaptor protein p40phox as a positive regulator of the superoxide-producing phagocyte oxidase. <i>EMBO Journal</i> , 2002, 21, 6312-6320.	7.8	128
96	The PX Domain as a Novel Phosphoinositide- Binding Module. <i>Biochemical and Biophysical Research Communications</i> , 2001, 287, 733-738.	2.1	98
97	Differential display analysis of mutants for the transcription factor Pdr1p regulating multidrug resistance in the budding yeast. <i>FEBS Letters</i> , 2001, 505, 103-108.	2.8	11
98	Human homologues of the <i>Caenorhabditis elegans</i> cell polarity protein PAR6 as an adaptor that links the small GTPases Rac and Cdc42 to atypical protein kinase C. <i>Genes To Cells</i> , 2001, 6, 107-119.	1.2	123
99	Solution structure of the PX domain, a target of the SH3 domain. <i>Nature Structural Biology</i> , 2001, 8, 526-530.	9.7	158
100	Exploring the protein interactome using comprehensive two-hybrid projects. <i>Trends in Biotechnology</i> , 2001, 19, 23-27.	9.3	56
101	Exploring the protein interactome using comprehensive two-hybrid projects. <i>Trends in Biotechnology</i> , 2001, 19, S23-S27.	9.3	71
102	Discovery of a novel compound: insight into mechanisms for acrylamide-induced axonopathy and colchicine-induced apoptotic neuronal cell death. <i>Brain Research</i> , 2001, 909, 8-19.	2.2	25
103	Budding Yeast GCN1 Binds the GI Domain to Activate the eIF2 γ Kinase GCN2. <i>Journal of Biological Chemistry</i> , 2001, 276, 17591-17596.	3.4	54
104	Comparative Genome Analysis of the Mouse Imprinted Gene <i>Impact</i> and Its Nonimprinted Human Homolog <i>IMPACT</i> : Toward the Structural Basis for Species-Specific Imprinting. <i>Genome Research</i> , 2000, 10, 1878-1889.	5.5	66
105	GI Domain-mediated Association of the Eukaryotic Initiation Factor 2 γ Kinase GCN2 with Its Activator GCN1 Is Required for General Amino Acid Control in Budding Yeast. <i>Journal of Biological Chemistry</i> , 2000, 275, 20243-20246.	3.4	68
106	A Novel G-Protein-Coupled Receptor Gene Expressed in Striatum. <i>Genomics</i> , 2000, 69, 314-321.	2.9	79
107	Mechanism for Phosphorylation-induced Activation of the Phagocyte NADPH Oxidase Protein p47. <i>Journal of Biological Chemistry</i> , 1999, 274, 33644-33653.	3.4	212
108	Developmentally-regulated expression of mNapor encoding an apoptosis-induced ELAV-type RNA binding protein. <i>Gene</i> , 1999, 237, 135-142.	2.2	42

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109	Spatiotemporal, Allelic, and Enforced Expression of Ximpact, the Xenopus Homolog of Mouse Imprinted Gene Impact. <i>Biochemical and Biophysical Research Communications</i> , 1999, 256, 162-169.	2.1	14
110	[17] Fluorescent differential display: A fast and reliable method for message display polymerase chain reaction. <i>Methods in Enzymology</i> , 1999, 303, 298-309.	1.0	13
111	Functional modules and expression of mouse p40 phox and p67phox, SH3-domain-containing proteins involved in the phagocyte NADPH oxidase complex. <i>FEBS Journal</i> , 1998, 251, 573-582.	0.2	67
112	The PC motif : a novel and evolutionarily conserved sequence involved in interaction between p40 phox and p67phox, SH3 domain-containing cytosolic factors of the phagocyte NADPH oxidase. <i>FEBS Journal</i> , 1998, 251, 583-589.	0.2	73
113	Fluorescent differential display analysis of gene expression in apoptotic neuroblastoma cells Published in conjunction with A Wisconsin Gathering Honoring Waclaw Szybalski on occasion of his 75th year and 20 years of Editorship-in-Chief of <i>Gene</i> , 10 th August 1997, University of Wisconsin, Madison, WI, USA. <i>Gene</i> , 1998, 223, 21-31.	2.2	35
114	Anionic Amphiphile-independent Activation of the Phagocyte NADPH Oxidase in a Cell-free System by p47 and p67 , Both in C Terminally Truncated Forms. <i>Journal of Biological Chemistry</i> , 1998, 273, 4232-4236.	3.4	68
115	Fluorescent Differential Display. , 1997, 85, 37-44.		20
116	Isolation and Expression Study of a Maternally Expressed Novel Xenopus Gene Xem1 Encoding a Putative Evolutionarily Conserved Membrane Protein. <i>Biochemical and Biophysical Research Communications</i> , 1997, 238, 899-904.	2.1	5
117	Fluorescent differential display analysis of gene expression in differentiating neuroblastoma cells. <i>Gene</i> , 1997, 184, 73-81.	2.2	23
118	Rare Occurrence of ras and p53 Gene Mutations in Mouse Stomach Tumors Induced by N-Methyl-N-nitrosourea. <i>Japanese Journal of Cancer Research</i> , 1997, 88, 363-368.	1.7	21
119	An SH3 domain-mediated interaction between the phagocyte NADPH oxidase factors p40phox and p47phox. <i>FEBS Letters</i> , 1996, 385, 229-232.	2.8	45
120	[12] Fluorescent differential display method for high-speed scanning of tissue- or cell-specific transcripts. <i>Methods in Molecular Genetics</i> , 1996, , 229-245.	0.6	9
121	Assembly and Activation of the Phagocyte NADPH Oxidase. <i>Journal of Biological Chemistry</i> , 1996, 271, 22152-22158.	3.4	161
122	Differential display analysis of gene expression in developing embryos of <i>Xenopus laevis</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1995, 1262, 43-51.	2.4	23
123	Mapping of Regions of Physical Deletion on Chromosome 16q in Prostate Cancer Cells by Fluorescence in Situ Hybridization (FISH). <i>Journal of Urology</i> , 1995, 153, 249-254.	0.4	71
124	Sixty New STSs (Sequence-Tagged Sites) of Human Chromosome 21. <i>DNA Research</i> , 1994, 1, 85-89.	3.4	6
125	Fluorescent differential display: Arbitrarily primed RT-PCR fingerprinting on an automated DNA sequencer. <i>FEBS Letters</i> , 1994, 351, 231-236.	2.8	179
126	Pulsed-field polyacrylamide gel electrophoresis: Basic phenomena and applications. <i>Electrophoresis</i> , 1993, 14, 278-282.	2.4	8

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127	Sequence-Tagged NotI Sites of Human Chromosome 21: Sequence Analysis and Mapping. <i>Genomics</i> , 1993, 17, 39-44.	2.9	9
128	Triplex affinity capture of a single copy clone from a yeast genomic library. <i>Nucleic Acids Research</i> , 1992, 20, 3524-3524.	14.5	15
129	Affinity capture electrophoresis for sequence-specific DNA purification. <i>Genetic Analysis, Techniques and Applications</i> , 1992, 9, 96-99.	1.5	16
130	An improved pulsed-field polyacrylamide gel electrophoresis system for physical selection of linking clones: Isolation of SfiI linking clones from a chromosome 21-specific library. <i>Genomics</i> , 1991, 9, 707-712.	2.9	6
131	Photoprotein aequorin: use as a reporter enzyme in studying gene expression in mammalian cells. <i>Gene</i> , 1990, 96, 249-255.	2.2	51
132	Risk factors for the complication of cerebral infarction in Japanese patients with acute myocardial infarction.. <i>International Heart Journal</i> , 1989, 30, 635-643.	0.6	7
133	Nuclear factors interacting with an interleukin-6 responsive element of rat $\hat{I}\pm 2$ -macroglobulin gene. <i>Nucleic Acids Research</i> , 1989, 17, 9425-9435.	14.5	67
134	A novel procedure for selective cloning of NotI linking fragments from mammalian genomes. <i>Nucleic Acids Research</i> , 1988, 16, 9177-9184.	14.5	23
135	Nuclear matrix association regions of rat $\hat{I}\pm 2$ -macroglobulin gene. <i>Biochemical and Biophysical Research Communications</i> , 1987, 149, 449-454.	2.1	16
136	A nuclear factor which interacts with an at-cluster in the first intron of rat $\hat{I}\pm 2$ -macroglobulin gene. <i>Biochemical and Biophysical Research Communications</i> , 1987, 147, 824-830.	2.1	3
137	Mechanisms for improvement of cardiac performance by nifedipine in an acute mitral regurgitation in dogs.. <i>International Heart Journal</i> , 1985, 26, 1019-1028.	0.6	2
138	Ambulatory electrocardiograms obtained by holter monitoring system in patients with permanent demand pacemakers.. <i>International Heart Journal</i> , 1985, 26, 23-32.	0.6	13
139	Primary thrombocythemia and myocardial infarction in a 26-year-old woman with normal coronary arteriogram.. <i>International Heart Journal</i> , 1981, 22, 439-445.	0.6	16