

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	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
2	Amplification-free whole-genome bisulfite sequencing by post-bisulfite adaptor tagging. <i>Nucleic Acids Research</i> , 2012, 40, e136-e136.	14.5	347
3	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
4	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
5	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
6	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
7	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
8	Fluorescent differential display: Arbitrarily primed RT-PCR fingerprinting on an automated DNA sequencer. <i>FEBS Letters</i> , 1994, 351, 231-236.	2.8	179
9	Assembly and Activation of the Phagocyte NADPH Oxidase. <i>Journal of Biological Chemistry</i> , 1996, 271, 22152-22158.	3.4	161
10	Pioneer Factor NeuroD1 Rearranges Transcriptional and Epigenetic Profiles to Execute Microglia-Neuron Conversion. <i>Neuron</i> , 2019, 101, 472-485.e7.	8.1	161
11	Solution structure of the PX domain, a target of the SH3 domain. <i>Nature Structural Biology</i> , 2001, 8, 526-530.	9.7	158
12	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
13	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
14	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
15	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
16	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
17	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
18	The PX Domain as a Novel Phosphoinositide-Binding Module. <i>Biochemical and Biophysical Research Communications</i> , 2001, 287, 733-738.	2.1	98

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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	Reconstitution of the oocyte transcriptional network with transcription factors. <i>Nature</i> , 2021, 589, 264-269.	27.8	92
21	Rapamycin-induced Translational Derepression of GCN4 mRNA Involves a Novel Mechanism for Activation of the eIF2 γ Kinase GCN2. <i>Journal of Biological Chemistry</i> , 2003, 278, 20457-20460.	3.4	88
22	Mass Spectrometry-Based Approaches Toward Absolute Quantitative Proteomics. <i>Current Genomics</i> , 2008, 9, 263-274.	1.6	88
23	Transcriptional activators in yeast. <i>Nucleic Acids Research</i> , 2006, 34, 955-967.	14.5	84
24	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
25	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
26	A Novel G-Protein-Coupled Receptor Gene Expressed in Striatum. <i>Genomics</i> , 2000, 69, 314-321.	2.9	79
27	Molecular Recognition in Dimerization between PB1 Domains. <i>Journal of Biological Chemistry</i> , 2003, 278, 43516-43524.	3.4	78
28	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
29	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
30	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
31	Exploring the protein interactome using comprehensive two-hybrid projects. <i>Trends in Biotechnology</i> , 2001, 19, S23-S27.	9.3	71
32	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
33	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
34	Nuclear factors interacting with an interleukin-6 responsive element of rat β 2-macroglobulin gene. <i>Nucleic Acids Research</i> , 1989, 17, 9425-9435.	14.5	67
35	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
36	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

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37	OPR, PC and AID: all in the PB1 family. Trends in Biochemical Sciences, 2002, 27, 10.	7.5	63
38	Exploring the protein interactome using comprehensive two-hybrid projects. Trends in Biotechnology, 2001, 19, 23-27.	9.3	56
39	Tet2 and Tet3 in B cells are required to repress CD86 and prevent autoimmunity. Nature Immunology, 2020, 21, 950-961.	14.5	55
40	Budding Yeast GCN1 Binds the GI Domain to Activate the eIF2 $\hat{\pm}$ Kinase GCN2. Journal of Biological Chemistry, 2001, 276, 17591-17596.	3.4	54
41	Highly sensitive targeted methylome sequencing by post-bisulfite adaptor tagging. DNA Research, 2015, 22, 13-18.	3.4	53
42	Mapping of histone-binding sites in histone replacement-completed spermatozoa. Nature Communications, 2018, 9, 3885.	12.8	53
43	ATF7-Dependent Epigenetic Changes Are Required for the Intergenerational Effect of a Paternal Low-Protein Diet. Molecular Cell, 2020, 78, 445-458.e6.	9.7	52
44	Photoprotein aequorin: use as a reporter enzyme in studying gene expression in mammalian cells. Gene, 1990, 96, 249-255.	2.2	51
45	Highly efficient single-stranded DNA ligation technique improves low-input whole-genome bisulfite sequencing by post-bisulfite adaptor tagging. Nucleic Acids Research, 2019, 47, e85-e85.	14.5	51
46	The AP-1 transcription factor JunB is required for Th17 cell differentiation. Scientific Reports, 2017, 7, 17402.	3.3	47
47	An SH3 domain-mediated interaction between the phagocyte NADPH oxidase factors p40phox and p47phox. FEBS Letters, 1996, 385, 229-232.	2.8	45
48	DNA Methylome Analysis Identifies Transcription Factor-Based Epigenomic Signatures of Multilineage Competence in Neural Stem/Progenitor Cells. Cell Reports, 2017, 20, 2992-3003.	6.4	45
49	A Novel Cdc42-interacting Domain of the Yeast Polarity Establishment Protein Bem1. Journal of Biological Chemistry, 2007, 282, 29-38.	3.4	43
50	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. ACS Synthetic Biology, 2013, 2, 425-430.	3.8	43
51	Developmentally-regulated expression of mNapor encoding an apoptosis-induced ELAV-type RNA binding protein. Gene, 1999, 237, 135-142.	2.2	42
52	DNA methylation is reconfigured at the onset of reproduction in rice shoot apical meristem. Nature Communications, 2020, 11, 4079.	12.8	42
53	Limited rejuvenation of aged hematopoietic stem cells in young bone marrow niche. Journal of Experimental Medicine, 2021, 218, .	8.5	42
54	Translation Initiation: A Regulatory Role for Poly(A) Tracts in Front of the AUG Codon in <i>Saccharomyces cerevisiae</i> . Genetics, 2011, 189, 469-478.	2.9	41

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55	Transcriptomic and Proteomic Analysis of a 14-3-3 Gene-Deficient Yeast. <i>Biochemistry</i> , 2004, 43, 6149-6158.	2.5	40
56	Epigenetic landscape influences the liver cancer genome architecture. <i>Nature Communications</i> , 2018, 9, 1643.	12.8	39
57	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
58	The WD40 protein Morg1 facilitates Par6 α PKC binding to Crb3 for apical identity in epithelial cells. <i>Journal of Cell Biology</i> , 2013, 200, 635-650.	5.2	38
59	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
60	Circular permutation of ligand α -binding module improves dynamic range of genetically encoded FRET α -based nanosensor. <i>Protein Science</i> , 2009, 18, 2518-2527.	7.6	36
61	Fluorescent differential display analysis of gene expression in apoptotic neuroblastoma cells1Published in conjunction with A Wisconsin Gathering Honoring Waclaw Szybalski on occasion of his 75th year and 20years of Editorship-in-Chief of <i>Gene</i> , 10 α 11 August 1997, University of Wisconsin, Madison, WI, USA.1. <i>Gene</i> , 1998, 223, 21-31.	2.2	35
62	DNA methylation and gene expression in <i>Mimulus guttatus</i> . <i>BMC Genomics</i> , 2015, 16, 507.	2.8	34
63	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
64	A novel strategy to design highly specific PCR primers based on the stability and uniqueness of 3 α 2-end subsequences. <i>Bioinformatics</i> , 2005, 21, 4363-4370.	4.1	31
65	Software updates in the Illumina HiSeq platform affect whole-genome bisulfite sequencing. <i>BMC Genomics</i> , 2017, 18, 31.	2.8	29
66	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
67	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
68	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
69	Diverse DNA Methylation Statuses at Alternative Promoters of Human Genes in Various Tissues. <i>DNA Research</i> , 2006, 13, 155-167.	3.4	24
70	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
71	A novel procedure for selective cloning ofNotI linking fragments from mammalian genomes. <i>Nucleic Acids Research</i> , 1988, 16, 9177-9184.	14.5	23
72	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

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73	Fluorescent differential display analysis of gene expression in differentiating neuroblastoma cells. <i>Gene</i> , 1997, 184, 73-81.	2.2	23
74	A proteomic screen reveals the mitochondrial outer membrane protein Mdm34p as an essential target of the Foxo protein Mdm30p. <i>Genes To Cells</i> , 2008, 13, 1075-1085.	1.2	23
75	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
76	The yeast eIF4E-associated protein Eap1p attenuates GCN4 translation upon TOR-inactivation. <i>FEBS Letters</i> , 2005, 579, 2433-2438.	2.8	21
77	Hoxa10 mediates positional memory to govern stem cell function in adult skeletal muscle. <i>Science Advances</i> , 2021, 7, .	10.3	21
78	Fluorescent Differential Display. , 1997, 85, 37-44.		20
79	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
80	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
81	The Evolving Genomic Landscape of Esophageal Squamous Cell Carcinoma Under Chemoradiotherapy. <i>Cancer Research</i> , 2021, 81, 4926-4938.	0.9	20
82	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
83	Nuclear matrix association regions of rat β 2-microglobulin gene. <i>Biochemical and Biophysical Research Communications</i> , 1987, 149, 449-454.	2.1	16
84	Affinity capture electrophoresis for sequence-specific DNA purification. <i>Genetic Analysis, Techniques and Applications</i> , 1992, 9, 96-99.	1.5	16
85	Post-Bisulfite Adaptor Tagging for PCR-Free Whole-Genome Bisulfite Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1708, 123-136.	0.9	16
86	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
87	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
88	Discrimination between stable and dynamic components of protein complexes by means of quantitative proteomics. <i>Proteomics</i> , 2008, 8, 2366-2370.	2.2	15
89	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
90	Spatiotemporal, Allelic, and Enforced Expression of <i>Ximpact</i> , the <i>Xenopus</i> Homolog of Mouse Imprinted Gene <i>Impact</i> . <i>Biochemical and Biophysical Research Communications</i> , 1999, 256, 162-169.	2.1	14

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91	[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
92	SKIP modifies gene expression by affecting both transcription and splicing. <i>Biochemical and Biophysical Research Communications</i> , 2004, 316, 512-517.	2.1	13
93	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
94	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
95	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
96	A parallel affinity purification method for selective isolation of polyubiquitinated proteins. <i>Proteomics</i> , 2008, 8, 3004-3007.	2.2	12
97	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
98	A yeast one-hybrid system to screen for methylated DNA-binding proteins. <i>Nucleic Acids Research</i> , 2010, 38, e189-e189.	14.5	12
99	DNA Methylation Errors in Cloned Mouse Sperm by Germ Line Barrier Evasion1. <i>Biology of Reproduction</i> , 2016, 94, 128.	2.7	12
100	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
101	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
102	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
103	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
104	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
105	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
106	Sequence-Tagged NotI Sites of Human Chromosome 21: Sequence Analysis and Mapping. <i>Genomics</i> , 1993, 17, 39-44.	2.9	9
107	[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
108	Appearance of Osteonectin-expressing Fibroblastic Cells in Early Rat Stomach Carcinogenesis and Stomach Tumors Induced with N-Methyl-N ² -nitro-N-nitrosoguanidine. <i>Japanese Journal of Cancer Research</i> , 2002, 93, 960-967.	1.7	9

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109	An Evolutionary Scenario for Genomic Imprinting of Impact Lying between Nonimprinted Neighbors. <i>DNA Research</i> , 2004, 11, 381-390.	3.4	9
110	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
111	Pulsed-field polyacrylamide gel electrophoresis: Basic phenomena and applications. <i>Electrophoresis</i> , 1993, 14, 278-282.	2.4	8
112	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
113	Unexpected complexity of the budding yeast transcriptome. <i>IUBMB Life</i> , 2008, 60, 775-781.	3.4	8
114	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
115	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
116	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
117	Maternal Protein Restriction Alters the Renal Ptger1 DNA Methylation State in SHRSP Offspring. <i>Nutrients</i> , 2018, 10, 1436.	4.1	7
118	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
119	Identification of genes associated with endometrial cell ageing. <i>Molecular Human Reproduction</i> , 2021, 27, .	2.8	7
120	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
121	Sixty New STSs (Sequence-Tagged Sites) of Human Chromosome 21. <i>DNA Research</i> , 1994, 1, 85-89.	3.4	6
122	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
123	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
124	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
125	Isolation and Expression Study of a Maternally Expressed Novel <i>Xenopus</i> Gene <i>Xem1</i> Encoding a Putative Evolutionarily Conserved Membrane Protein. <i>Biochemical and Biophysical Research Communications</i> , 1997, 238, 899-904.	2.1	5
126	Detecting Protein-DNA Interactions Using a Modified Yeast One-Hybrid System. <i>Methods in Molecular Biology</i> , 2014, 1164, 39-50.	0.9	4

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127	A nuclear factor which interacts with an at-cluster in the first intron of rat $\hat{\pm}2$ -macroglobulin gene. <i>Biochemical and Biophysical Research Communications</i> , 1987, 147, 824-830.	2.1	3
128	Epigenome mapping of human normal purified hepatocytes: personal epigenome variation and genomeâ€“epigenome correlation. <i>Epigenomics</i> , 2018, 10, 955-979.	2.1	3
129	Mass Spectrometry-Based Proteomics for Quantitative Description of Cellular Events. <i>Current Genomics</i> , 2004, 5, 629-635.	1.6	3
130	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
131	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
132	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
133	Nucleosome assembly protein 1 (NAP-1) is a regulator of histone H1 acetylation. <i>Journal of Biochemistry</i> , 2021, , .	1.7	2
134	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
135	Short singleâ€“stranded DNA with putative nonâ€“canonical structures comprises a novel class of plasma cellâ€“free DNA. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
136	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
137	Unexpected complexity of the budding yeast transcriptome. <i>FASEB Journal</i> , 2008, 22, 100.1.	0.5	0
138	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
139	Methods for Protein-Protein Interaction Analysis. , 2007, , 160-182.		0