

Shinichi Morishita

List of Publications by Year in descending order

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167
papers

9,182
citations

61984

43
h-index

48315

88
g-index

180
all docs

180
docs citations

180
times ranked

13795
citing authors

#	ARTICLE	IF	CITATIONS
1	The medaka draft genome and insights into vertebrate genome evolution. <i>Nature</i> , 2007, 447, 714-719.	27.8	1,037
2	The Genome Sequence of Silkworm, <i>Bombyx mori</i> . <i>DNA Research</i> , 2004, 11, 27-35.	3.4	594
3	The genome of a lepidopteran model insect, the silkworm <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 1036-1045.	2.7	592
4	Reconstruction of the vertebrate ancestral genome reveals dynamic genome reorganization in early vertebrates. <i>Genome Research</i> , 2007, 17, 1254-1265.	5.5	444
5	High-dimensional and large-scale phenotyping of yeast mutants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 19015-19020.	7.1	276
6	Human genetic variation database, a reference database of genetic variations in the Japanese population. <i>Journal of Human Genetics</i> , 2016, 61, 547-553.	2.3	270
7	Noncoding CGG repeat expansions in neuronal intranuclear inclusion disease, oculopharyngodistal myopathy and an overlapping disease. <i>Nature Genetics</i> , 2019, 51, 1222-1232.	21.4	265
8	Expansions of intronic TTCA and TTTA repeats in benign adult familial myoclonic epilepsy. <i>Nature Genetics</i> , 2018, 50, 581-590.	21.4	238
9	siDirect: highly effective, target-specific siRNA design software for mammalian RNA interference. <i>Nucleic Acids Research</i> , 2004, 32, W124-W129.	14.5	230
10	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
11	Recurrent DUX4 fusions in B cell acute lymphoblastic leukemia of adolescents and young adults. <i>Nature Genetics</i> , 2016, 48, 569-574.	21.4	198
12	siDirect 2.0: updated software for designing functional siRNA with reduced seed-dependent off-target effect. <i>BMC Bioinformatics</i> , 2009, 10, 392.	2.6	184
13	dsCheck: highly sensitive off-target search software for double-stranded RNA-mediated RNA interference. <i>Nucleic Acids Research</i> , 2005, 33, W589-W591.	14.5	160
14	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites. <i>EMBO Reports</i> , 2001, 2, 388-393.	4.5	154
15	Mining optimized association rules for numeric attributes. , 1996, , .		151
16	Variant between CPT1B and CHKB associated with susceptibility to narcolepsy. <i>Nature Genetics</i> , 2008, 40, 1324-1328.	21.4	141
17	Data mining using two-dimensional optimized association rules. , 1996, , .		136
18	Transversing itemset lattices with statistical metric pruning. , 2000, , .		126

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19	ERBB4 Mutations that Disrupt the Neuregulin-ErbB4 Pathway Cause Amyotrophic Lateral Sclerosis Type 19. <i>American Journal of Human Genetics</i> , 2013, 93, 900-905.	6.2	123
20	Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. <i>Science</i> , 2009, 323, 401-404.	12.6	122
21	5' end SAGE for the analysis of transcriptional start sites. <i>Nature Biotechnology</i> , 2004, 22, 1146-1149.	17.5	115
22	Identification and Characterization of the Potential Promoter Regions of 1031 Kinds of Human Genes. <i>Genome Research</i> , 2001, 11, 677-684.	5.5	115
23	Comparative analysis of chimpanzee and human Y chromosomes unveils complex evolutionary pathway. <i>Nature Genetics</i> , 2006, 38, 158-167.	21.4	110
24	Recompleting the <i>Caenorhabditis elegans</i> genome. <i>Genome Research</i> , 2019, 29, 1009-1022.	5.5	108
25	Data Mining with optimized two-dimensional association rules. <i>ACM Transactions on Database Systems</i> , 2001, 26, 179-213.	2.8	90
26	SCMD: <i>Saccharomyces cerevisiae</i> Morphological Database. <i>Nucleic Acids Research</i> , 2004, 32, 319D-322.	14.5	84
27	Mutations in <i>MME</i> cause an autosomal recessive Charcot-Marie-Tooth disease type 2. <i>Annals of Neurology</i> , 2016, 79, 659-672.	5.3	82
28	A Novel Mutation in <i>ELOVL4</i> Leading to Spinocerebellar Ataxia (SCA) With the Hot Cross Bun Sign but Lacking Erythrokeratoderma. <i>JAMA Neurology</i> , 2015, 72, 797.	9.0	79
29	Identification of ATP1A3 Mutations by Exome Sequencing as the Cause of Alternating Hemiplegia of Childhood in Japanese Patients. <i>PLoS ONE</i> , 2013, 8, e56120.	2.5	79
30	Data mining using two-dimensional optimized association rules. <i>SIGMOD Record</i> , 1996, 25, 13-23.	1.2	72
31	KDD Cup 2001 report. <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining</i> , 2002, 3, 47-64.	4.0	72
32	Accelerated off-target search algorithm for siRNA. <i>Bioinformatics</i> , 2005, 21, 1316-1324.	4.1	71
33	A recurrent de novo <i>FAM111A</i> mutation causes kennyâ€œcaffey syndrome type 2. <i>Journal of Bone and Mineral Research</i> , 2014, 29, 992-998.	2.8	68
34	Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. <i>Microbiome</i> , 2019, 7, 119.	11.1	65
35	Rapid detection of expanded short tandem repeats in personal genomics using hybrid sequencing. <i>Bioinformatics</i> , 2014, 30, 815-822.	4.1	61
36	The transcription start site landscape of <i>C. elegans</i> . <i>Genome Research</i> , 2013, 23, 1348-1361.	5.5	58

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37	DEVELOPMENT OF IMAGE PROCESSING PROGRAM FOR YEAST CELL MORPHOLOGY. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 01, 695-709.	0.8	57
38	A gain-of-function screen identifies <i>wdb</i> and <i>lkb1</i> as lifespan-extending genes in <i>Drosophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2011, 405, 667-672.	2.1	57
39	BodyMap: a human and mouse gene expression database. <i>Nucleic Acids Research</i> , 2000, 28, 136-138.	14.5	56
40	Mining Optimized Association Rules for Numeric Attributes. <i>Journal of Computer and System Sciences</i> , 1999, 58, 1-12.	1.2	55
41	Efficient frequency-based de novo short-read clustering for error trimming in next-generation sequencing. <i>Genome Research</i> , 2009, 19, 1309-1315.	5.5	53
42	ATF6 \pm / β 2-mediated adjustment of ER chaperone levels is essential for development of the notochord in medaka fish. <i>Molecular Biology of the Cell</i> , 2013, 24, 1387-1395.	2.1	51
43	Comprehensive and quantitative analysis of yeast deletion mutants defective in apical and isotropic bud growth. <i>Current Genetics</i> , 2009, 55, 365-380.	1.7	50
44	Complete fusion of a transposon and herpesvirus created the Teratorn mobile element in medaka fish. <i>Nature Communications</i> , 2017, 8, 551.	12.8	49
45	Gene expression profile in human leukocytes. <i>Blood</i> , 2003, 101, 3509-3513.	1.4	47
46	G1/S Cyclin-dependent Kinase Regulates Small GTPase Rho1p through Phosphorylation of RhoGEF Tus1p in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2008, 19, 1763-1771.	2.1	47
47	Coordinated Changes in DNA Methylation in Antigen-Specific Memory CD4 T Cells. <i>Journal of Immunology</i> , 2013, 190, 4076-4091.	0.8	46
48	BodyMap: A Collection of 3' ESTs for Analysis of Human Gene Expression Information. <i>Genome Research</i> , 2000, 10, 1817-1827.	5.5	44
49	Dynactin is involved in a checkpoint to monitor cell wall synthesis in <i>Saccharomyces cerevisiae</i> . <i>Nature Cell Biology</i> , 2004, 6, 861-871.	10.3	43
50	Genome-wide profiling of DNA methylation in human cancer cells. <i>Genomics</i> , 2011, 98, 280-287.	2.9	42
51	High-Resolution Analysis of the 5' End Transcriptome Using a Next Generation DNA Sequencer. <i>PLoS ONE</i> , 2009, 4, e4108.	2.5	42
52	Genome-wide genetic variations are highly correlated with proximal DNA methylation patterns. <i>Genome Research</i> , 2012, 22, 1419-1425.	5.5	41
53	Large hypomethylated domains serve as strong repressive machinery for key developmental genes in vertebrates. <i>Development (Cambridge)</i> , 2014, 141, 2568-2580.	2.5	41
54	Integrative analysis of genomic alterations in triple-negative breast cancer in association with homologous recombination deficiency. <i>PLoS Genetics</i> , 2017, 13, e1006853.	3.5	39

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55	Mutations in COA7 cause spinocerebellar ataxia with axonal neuropathy. <i>Brain</i> , 2018, 141, 1622-1636.	7.6	38
56	Cooperative scheduling and its application to steelmaking processes. <i>IEEE Transactions on Industrial Electronics</i> , 1991, 38, 150-155.	7.9	37
57	Molecular epidemiological study of familial amyotrophic lateral sclerosis in Japanese population by whole-exome sequencing and identification of novel HNRNPA1 mutation. <i>Neurobiology of Aging</i> , 2018, 61, 255.e9-255.e16.	3.1	37
58	CTCF looping is established during gastrulation in medaka embryos. <i>Genome Research</i> , 2021, 31, 968-980.	5.5	37
59	Constrained clusters of gene expression profiles with pathological features. <i>Bioinformatics</i> , 2004, 20, 3137-3145.	4.1	35
60	<i>CSF1R</i> mutations identified in three families with autosomal dominantly inherited leukoencephalopathy. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012, 159B, 951-957.	1.7	34
61	UTGB/medaka: genomic resource database for medaka biology. <i>Nucleic Acids Research</i> , 2007, 36, D747-D752.	14.5	32
62	Clinical and mutational spectrum of Charcot-Marie-Tooth disease type 2Z caused by <i>MORC2</i> variants in Japan. <i>European Journal of Neurology</i> , 2017, 24, 1274-1282.	3.3	32
63	Expression profiling of muscles from Fukuyama-type congenital muscular dystrophy and laminin- α 2 deficient congenital muscular dystrophy; is congenital muscular dystrophy a primary fibrotic disease?. <i>Biochemical and Biophysical Research Communications</i> , 2006, 342, 489-502.	2.1	31
64	Clinical and genetic diversities of Charcot-Marie-Tooth disease with <i>MFN2</i> mutations in a large case study. <i>Journal of the Peripheral Nervous System</i> , 2017, 22, 191-199.	3.1	31
65	AgIn: measuring the landscape of CpG methylation of individual repetitive elements. <i>Bioinformatics</i> , 2016, 32, 2911-2919.	4.1	29
66	Burden of rare variants in causative genes for amyotrophic lateral sclerosis (ALS) accelerates age at onset of ALS. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2019, 90, 537-542.	1.9	28
67	Amnionless-mediated glycosylation is crucial for cell surface targeting of cubilin in renal and intestinal cells. <i>Scientific Reports</i> , 2018, 8, 2351.	3.3	27
68	Hamster PIWI proteins bind to piRNAs with stage-specific size variations during oocyte maturation. <i>Nucleic Acids Research</i> , 2021, 49, 2700-2720.	14.5	26
69	Design and implementation of the glue-nail database system. , 1993, , .		25
70	Diversity of Ca ²⁺ -Induced Morphology Revealed by Morphological Phenotyping of Ca ²⁺ -Sensitive Mutants of <i>Saccharomyces cerevisiae</i> . <i>Eukaryotic Cell</i> , 2007, 6, 817-830.	3.4	24
71	Comparative DNA Sequence Analysis of Mouse and Human CC Chemokine Gene Clusters. <i>Journal of Interferon and Cytokine Research</i> , 2003, 23, 37-45.	1.2	23
72	MachiBase: a <i>Drosophila melanogaster</i> 5'-end mRNA transcription database. <i>Nucleic Acids Research</i> , 2009, 37, D49-D53.	14.5	23

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73	Rapid and ongoing evolution of repetitive sequence structures in human centromeres. <i>Science Advances</i> , 2020, 6, .	10.3	23
74	On Classification and Regression. <i>Lecture Notes in Computer Science</i> , 1998, , 40-57.	1.3	23
75	Modeling neurological diseases with induced pluripotent cells reprogrammed from immortalized lymphoblastoid cell lines. <i>Molecular Brain</i> , 2016, 9, 88.	2.6	21
76	Novel De Novo KCND3 Mutation in a Japanese Patient with Intellectual Disability, Cerebellar Ataxia, Myoclonus, and Dystonia. <i>Cerebellum</i> , 2018, 17, 237-242.	2.5	21
77	Clinicopathological features of the first Asian family having vocal cord and pharyngeal weakness with distal myopathy due to a <i>MATR3</i> mutation. <i>Neuropathology and Applied Neurobiology</i> , 2015, 41, 391-398.	3.2	20
78	Ataxic phenotype with altered CaV3.1 channel property in a mouse model for spinocerebellar ataxia 42. <i>Neurobiology of Disease</i> , 2019, 130, 104516.	4.4	20
79	PrimerStation: a highly specific multiplex genomic PCR primer design server for the human genome. <i>Nucleic Acids Research</i> , 2006, 34, W665-W669.	14.5	19
80	An alternating fixpoint tailored to magic programs. , 1993, , .		18
81	Segmental duplications in the silkworm genome. <i>BMC Genomics</i> , 2013, 14, 521.	2.8	18
82	Identification of candidate genes involved in the etiology of sporadic Tourette syndrome by exome sequencing. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 712-723.	1.7	17
83	Implementation and Evaluation of Decision Trees with Range and Region Splitting. <i>Constraints</i> , 1997, 2, 401-427.	0.7	16
84	MXN1-HNF1B Axis Is Indispensable for Intraductal Papillary Mucinous Neoplasm Lineages. <i>Gastroenterology</i> , 2022, 162, 1272-1287.e16.	1.3	16
85	The Glue-Nail deductive database system: Design, implementation, and evaluation. <i>VLDB Journal</i> , 1994, 3, 123-160.	4.1	15
86	Data mining tools for the <i>Saccharomyces cerevisiae</i> morphological database. <i>Nucleic Acids Research</i> , 2005, 33, W753-W757.	14.5	15
87	Analysis of a novel gene, <i>Sdgc</i> , reveals sex chromosome-dependent differences of medaka germ cells prior to gonad formation. <i>Development (Cambridge)</i> , 2014, 141, 3363-3369.	2.5	15
88	TBCD may be a causal gene in progressive neurodegenerative encephalopathy with atypical infantile spinal muscular atrophy. <i>Journal of Human Genetics</i> , 2017, 62, 473-480.	2.3	15
89	Frequency and characteristics of the TBK1 gene variants in Japanese patients with sporadic amyotrophic lateral sclerosis. <i>Neurobiology of Aging</i> , 2018, 64, 158.e15-158.e19.	3.1	15
90	BodyMap incorporated PCR-based expression profiling data and a gene ranking system. <i>Nucleic Acids Research</i> , 2001, 29, 156-158.	14.5	14

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91	A Simple but Powerful Heuristic Method for Accelerating k -Means Clustering of Large-Scale Data in Life Science. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 681-692.	3.0	14
92	CNV analysis using whole exome sequencing identified biallelic CNVs of VPS13B in siblings with intellectual disability. <i>European Journal of Medical Genetics</i> , 2020, 63, 103610.	1.3	14
93	Parallel Branch-and-Bound Graph Search for Correlated Association Rules. <i>Lecture Notes in Computer Science</i> , 2000, , 127-144.	1.3	14
94	Answering the Most Correlated N Association Rules Efficiently. <i>Lecture Notes in Computer Science</i> , 2002, , 410-422.	1.3	13
95	A Novel <i>de novo</i> KIF1A Mutation in a Patient with Autism, Hyperactivity, Epilepsy, Sensory Disturbance, and Spastic Paraplegia. <i>Internal Medicine</i> , 2020, 59, 839-842.	0.7	13
96	Efficient Construction of Regression Trees with Range and Region Splitting. <i>Machine Learning</i> , 2001, 45, 235-259.	5.4	12
97	The Gene Resource Locator: gene locus maps for transcriptome analysis. <i>Nucleic Acids Research</i> , 2002, 30, 221-225.	14.5	12
98	Involvement of Rho-type GTPase in control of cell size in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2007, 7, 569-578.	2.3	12
99	UTGB toolkit for personalized genome browsers. <i>Bioinformatics</i> , 2009, 25, 1856-1861.	4.1	12
100	Atypical parkinsonism caused by Pro105Leu mutation of prion protein. <i>Neurology: Genetics</i> , 2016, 2, e48.	1.9	12
101	Ataxic form of autosomal recessive PEX10-related peroxisome biogenesis disorders with a novel compound heterozygous gene mutation and characteristic clinical phenotype. <i>Journal of the Neurological Sciences</i> , 2017, 375, 424-429.	0.6	12
102	Altered expression of Crb2 in podocytes expands a variation of CRB2 mutations in steroid-resistant nephrotic syndrome. <i>Pediatric Nephrology</i> , 2017, 32, 801-809.	1.7	12
103	Targeted deep sequencing of DNA from multiple tissue types improves the diagnostic rate and reveals a highly diverse phenotype of mosaic neurofibromatosis type 2. <i>Journal of Medical Genetics</i> , 2021, 58, 701-711.	3.2	12
104	Loss-of-function variants in NEK1 are associated with an increased risk of sporadic ALS in the Japanese population. <i>Journal of Human Genetics</i> , 2021, 66, 237-241.	2.3	12
105	Evaluation of image processing programs for accurate measurement of budding and fission yeast morphology. <i>Current Genetics</i> , 2006, 49, 237-247.	1.7	11
106	Cost-Effective Sequencing of Full-Length cDNA Clones Powered by a De Novo-Reference Hybrid Assembly. <i>PLoS ONE</i> , 2010, 5, e10517.	2.5	11
107	Assessing Cell-to-Cell DNA Methylation Variability on Individual Long Reads. <i>Scientific Reports</i> , 2016, 6, 21317.	3.3	11
108	Hypomethylated domain-enriched DNA motifs prepattern the accessible nucleosome organization in teleosts. <i>Epigenetics and Chromatin</i> , 2017, 10, 44.	3.9	11

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109	Comprehensive investigation of RNF213 nonsynonymous variants associated with intracranial artery stenosis. <i>Scientific Reports</i> , 2020, 10, 11942.	3.3	11
110	HiC-Hiker: a probabilistic model to determine contig orientation in chromosome-length scaffolds with Hi-C. <i>Bioinformatics</i> , 2020, 36, 3966-3974.	4.1	11
111	5'SAGE: 5'-end Serial Analysis of Gene Expression database. <i>Nucleic Acids Research</i> , 2004, 33, D550-D552.	14.5	9
112	COMPUTING HIGHLY SPECIFIC AND NOISE-TOLERANT OLIGOMERS EFFICIENTLY. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 21-46.	0.8	9
113	Extremely slow rate of evolution in the HOX cluster revealed by comparison between Tanzanian and Indonesian coelacanths. <i>Gene</i> , 2012, 505, 324-332.	2.2	9
114	A framework and an algorithm to detect low-abundance DNA by a handy sequencer and a palm-sized computer. <i>Bioinformatics</i> , 2019, 35, 584-592.	4.1	9
115	Computing Optimal Hypotheses Efficiently for Boosting. <i>Lecture Notes in Computer Science</i> , 2002, , 471-481.	1.3	9
116	An Extension of Van Gelder's Alternating Fixpoint to Magic Programs. <i>Journal of Computer and System Sciences</i> , 1996, 52, 506-521.	1.2	8
117	Novel GBE1 mutation in a Japanese family with adult polyglucosan body disease. <i>Neurology: Genetics</i> , 2017, 3, e138.	1.9	8
118	Slowly progressive d-bifunctional protein deficiency with survival to adulthood diagnosed by whole-exome sequencing. <i>Journal of the Neurological Sciences</i> , 2017, 372, 6-10.	0.6	8
119	Investigating the mitochondrial genomic landscape of <i>Arabidopsis thaliana</i> by long-read sequencing. <i>PLoS Computational Biology</i> , 2021, 17, e1008597.	3.2	8
120	Studies on drug metabolism by use of isotopes. XVI. Species differences in metabolism of 1-butyl-4-cinnamylpiperazine hydrochloride.. <i>Chemical and Pharmaceutical Bulletin</i> , 1975, 23, 1949-1954.	1.3	7
121	Studies on drug metabolism by use of isotopes. 23. Metabolic study of 1-butyl-4-cinnamylpiperazine in the rat during development of tolerance by using two kinds of deuterium-labeled forms. <i>Journal of Medicinal Chemistry</i> , 1978, 21, 525-529.	6.4	7
122	A Fast and Sensitive Algorithm for Aligning ESTs to the Human Genome. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 363-386.	0.8	7
123	Relational-style XML query. , 2008, , .		7
124	Large-Scale Genome Sequence Processing. , 2006, , .		7
125	Neuroimaging, genetic, and enzymatic study in a Japanese family with a GBA gross deletion. <i>Parkinsonism and Related Disorders</i> , 2019, 61, 57-63.	2.2	6
126	Splice-site mutations in KIF5A in the Japanese case series of amyotrophic lateral sclerosis. <i>Neurogenetics</i> , 2021, 22, 11-17.	1.4	6

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127	SONAR. , 1996, , .		5
128	Avoiding Cartesian products for multiple joins. Journal of the ACM, 1997, 44, 57-85.	2.2	5
129	Itemset Classified Clustering. Lecture Notes in Computer Science, 2004, , 398-409.	1.3	5
130	Exome analysis reveals a Japanese family with spinocerebellar ataxia, autosomal recessive 1. Journal of the Neurological Sciences, 2013, 331, 158-160.	0.6	5
131	The time is ripe to investigate human centromeres by long-read sequencing. DNA Research, 2021, 28, .	3.4	5
132	Prolog computation model BPM and its debugger PROEDIT2. Lecture Notes in Computer Science, 1987, , 147-158.	1.3	4
133	Clinical and molecular genetic characterization of two female patients harboring the Xq27.3q28 deletion with different ratios of X chromosome inactivation. Human Mutation, 2020, 41, 1447-1460.	2.5	4
134	Finding long tandem repeats in long noisy reads. Bioinformatics, 2021, 37, 612-621.	4.1	4
135	Implementation and Evaluation of Decision Trees with Range and Region Splitting. , 1997, , 163-189.		4
136	Unlinking the methylome pattern from nucleotide sequence, revealed by large-scale in vivo genome engineering and methylome editing in medaka fish. PLoS Genetics, 2017, 13, e1007123.	3.5	4
137	How should Prolog computation Be represented for practical use?. New Generation Computing, 1990, 8, 95-112.	3.3	3
138	SONAR. SIGMOD Record, 1996, 25, 553.	1.2	3
139	Associations between nucleosome phasing, sequence asymmetry, and tissue-specific expression in a set of inbred Medaka species. BMC Genomics, 2015, 16, 978.	2.8	3
140	Clinical usefulness of multigene screening with phenotype-driven bioinformatics analysis for the diagnosis of patients with monogenic diabetes or severe insulin resistance. Diabetes Research and Clinical Practice, 2020, 169, 108461.	2.8	3
141	Design and implementation of the glue-nail database system. SIGMOD Record, 1993, 22, 147-156.	1.2	2
142	Exome sequencing shows a novel <i>de novo</i> mutation in <i>ATL1</i> . Neurology and Clinical Neuroscience, 2014, 2, 1-4.	0.4	2
143	Comparative Analysis of Genome and Epigenome in Closely Related Medaka Species Identifies Conserved Sequence Preferences for DNA Hypomethylated Domains. Zoological Science, 2016, 33, 358.	0.7	2
144	Overexpression of Larp4B downregulates dMyc and reduces cell and organ sizes in Drosophila. Biochemical and Biophysical Research Communications, 2018, 497, 762-768.	2.1	2

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145	A Statistical Method for Observing Personal Diploid Methylomes and Transcriptomes with Single-Molecule Real-Time Sequencing. <i>Genes</i> , 2018, 9, 460.	2.4	2
146	Complex hereditary peripheral neuropathies caused by novel variants in mitochondrial-related nuclear genes. <i>Journal of Neurology</i> , 2022, 269, 4129-4140.	3.6	2
147	Context-dependent DNA polymerization effects can masquerade as DNA modification signals. <i>BMC Genomics</i> , 2022, 23, 249.	2.8	2
148	Early prediction of functional prognosis in neurofibromatosis type 2 patients based on genotype-phenotype correlation with targeted deep sequencing. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
149	Use of stable isotopes in the pharmacokinetics of drugs by mass fragmentography. I. Urinary excretion of 1-butyryl-4-cinnamylpiperazine in man.. <i>Journal of Pharmacobio-dynamics</i> , 1978, 1, 222-229.	0.5	1
150	Robust and accurate recognition of veins in fruit fly wings. , 2009, , .		1
151	A linear time algorithm for detecting long genomic regions enriched with a specific combination of epigenetic states. <i>BMC Genomics</i> , 2015, 16, S8.	2.8	1
152	Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. , 2011, , 39-47.		1
153	Reconstruction of the Vertebrate Ancestral Genome Reveals Dynamic Genome Reorganization in Early Vertebrates. , 2011, , 307-322.		1
154	Weighted Majority Decision among Region Rules for a Categorical Dataset. <i>Lecture Notes in Computer Science</i> , 1999, , 345-346.	1.3	1
155	Report on BLOKDD04. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2004, 6, 153-154.	4.0	0
156	A Unique Center for Bioinformatics Research. <i>Asia Pacific Biotech News</i> , 2007, 11, 1068-1068.	0.0	0
157	Accelerating Path-free XML Queries in RDBMS. <i>IPSJ Online Transactions</i> , 2010, 3, 206-217.	0.1	0
158	Poster: Robust estimation of DNA methylation with local regression. , 2011, , .		0
159	Invited: Searching massive epigenome data for evolutionarily conserved sequence motifs. , 2011, , .		0
160	Novel <i>COL6A2</i> mutation in a case of limb girdle muscular dystrophy phenotype with autosomal recessive inheritance. <i>Neurology and Clinical Neuroscience</i> , 2016, 4, 189-191.	0.4	0
161	Novel mutation in the membrane metalloendopeptidase gene in a patient with the autosomal recessive form of Charcot-Marie-Tooth disease. <i>Neurology and Clinical Neuroscience</i> , 2017, 5, 124-126.	0.4	0
162	Sporadic progressive myoclonic epilepsy with early-onset dementia caused by a de novo mutation in PSEN1. <i>Neurology and Clinical Neuroscience</i> , 2019, 7, 294-296.	0.4	0

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163	Practical Software for Aligning ESTs to Human Genome. Lecture Notes in Computer Science, 2002, , 1-16.	1.3	0
164	Modeling Chronic Myelomonocytic Leukemia Through Patient-Derived Induced Pluripotent Stem Cells. Blood, 2013, 122, 864-864.	1.4	0
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