Shinichi Morishita

List of Publications by Year
in descending order

167 papers	9,182 citations	61945 43 h-index	48277 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. Nature, 2007, 447, 714-719.	13.7	1,037
2	The Genome Sequence of Silkworm, Bombyx mori. DNA Research, 2004, 11, 27-35.	1.5	594
3	The genome of a lepidopteran model insect, the silkworm Bombyx mori. Insect Biochemistry and Molecular Biology, 2008, 38, 1036-1045.	1.2	592
4	Reconstruction of the vertebrate ancestral genome reveals dynamic genome reorganization in early vertebrates. Genome Research, 2007, 17, 1254-1265.	2.4	444
5	High-dimensional and large-scale phenotyping of yeast mutants. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 19015-19020.	3.3	276
6	Human genetic variation database, a reference database of genetic variations in the Japanese population. Journal of Human Genetics, 2016, 61, 547-553.	1.1	270
7	Noncoding CGG repeat expansions in neuronal intranuclear inclusion disease, oculopharyngodistal myopathy and an overlapping disease. Nature Genetics, 2019, 51, 1222-1232.	9.4	265
8	ExpansionsÂofÂintronic TTTCA and TTTTA repeats in benign adult familial myoclonic epilepsy. Nature Genetics, 2018, 50, 581-590.	9.4	238
9	siDirect: highly effective, target-specific siRNA design software for mammalian RNA interference. Nucleic Acids Research, 2004, 32, W124-W129.	6.5	230
10	A large-scale full-length cDNA analysis to explore the budding yeast transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17846-17851.	3.3	213
11	Recurrent DUX4 fusions in B cell acute lymphoblastic leukemia of adolescents and young adults. Nature Genetics, 2016, 48, 569-574.	9.4	198
12	siDirect 2.0: updated software for designing functional siRNA with reduced seed-dependent off-target effect. BMC Bioinformatics, 2009, 10, 392.	1.2	184
13	dsCheck: highly sensitive off-target search software for double-stranded RNA-mediated RNA interference. Nucleic Acids Research, 2005, 33, W589-W591.	6.5	160
14	Diverse transcriptional initiation revealed by fine, largeâ€scale mapping of mRNA start sites. EMBO Reports, 2001, 2, 388-393.	2.0	154
15	Mining optimized association rules for numeric attributes. , 1996, , .		151
16	Variant between CPT1B and CHKB associated with susceptibility to narcolepsy. Nature Genetics, 2008, 40, 1324-1328.	9.4	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. American Journal of Human Genetics, 2013, 93, 900-905.	2.6	123
20	Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. Science, 2009, 323, 401-404.	6.0	122
21	5â€²-end SAGE for the analysis of transcriptional start sites. Nature Biotechnology, 2004, 22, 1146-1149.	9.4	115
22	Identification and Characterization of the Potential Promoter Regions of 1031 Kinds of Human Genes. Genome Research, 2001, 11, 677-684.	2.4	115
23	Comparative analysis of chimpanzee and human Y chromosomes unveils complex evolutionary pathway. Nature Genetics, 2006, 38, 158-167.	9.4	110
24	Recompleting the Caenorhabditis elegans genome. Genome Research, 2019, 29, 1009-1022.	2.4	108
25	Data Mining with optimized two-dimensional association rules. ACM Transactions on Database Systems, 2001, 26, 179-213.	1.5	90
26	SCMD: Saccharomyces cerevisiae Morphological Database. Nucleic Acids Research, 2004, 32, 319D-322.	6.5	84
27	Mutations in MME cause an autosomalâ€recessive Charcotâ€“Marieâ€“Tooth disease type 2. Annals of Neurology, 2016, 79, 659-672.	2.8	82
28	A Novel Mutation inELOVL4Leading to Spinocerebellar Ataxia (SCA) With the Hot Cross Bun Sign but Lacking Erythrokeratodermia. JAMA Neurology, 2015, 72, 797.	4.5	79
29	Identification of ATP1A3 Mutations by Exome Sequencing as the Cause of Alternating Hemiplegia of Childhood in Japanese Patients. PLoS ONE, 2013, 8, e56120.	1.1	79
30	Data mining using two-dimensional optimized association rules. SIGMOD Record, 1996, 25, 13-23.	0.7	72
31	KDD Cup 2001 report. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2002, 3, 47-64.	3.2	72
32	Accelerated off-target search algorithm for siRNA. Bioinformatics, 2005, 21, 1316-1324.	1.8	71
33	A recurrent de novo FAM111A mutation causes kennyâ€“caffey syndrome type 2. Journal of Bone and Mineral Research, 2014, 29, 992-998.	3.1	68
34	Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. Microbiome, 2019, 7, 119.	4.9	65
35	Rapid detection of expanded short tandem repeats in personal genomics using hybrid sequencing. Bioinformatics, 2014, 30, 815-822.	1.8	61
36	The transcription start site landscape of C. elegans. Genome Research, 2013, 23, 1348-1361.	2.4	58

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37	DEVELOPMENT OF IMAGE PROCESSING PROGRAM FOR YEAST CELL MORPHOLOGY. Journal of Bioinformatics and Computational Biology, 2004, 01, 695-709.	0.3	57
38	A gain-of-function screen identifies wdb and lkb1 as lifespan-extending genes in Drosophila. Biochemical and Biophysical Research Communications, 2011, 405, 667-672.	1.0	57
39	BodyMap: a human and mouse gene expression database. Nucleic Acids Research, 2000, 28, 136-138.	6.5	56
40	Mining Optimized Association Rules for Numeric Attributes. Journal of Computer and System Sciences, 1999, 58, 1-12.	0.9	55
41	Efficient frequency-based de novo short-read clustering for error trimming in next-generation sequencing. Genome Research, 2009, 19, 1309-1315.	2.4	53
42	ATF6Î±/Î²-mediated adjustment of ER chaperone levels is essential for development of the notochord in medaka fish. Molecular Biology of the Cell, 2013, 24, 1387-1395.	0.9	51
43	Comprehensive and quantitative analysis of yeast deletion mutants defective in apical and isotropic bud growth. Current Genetics, 2009, 55, 365-380.	0.8	50
44	Complete fusion of a transposon and herpesvirus created the Teratorn mobile element in medaka fish. Nature Communications, 2017, 8, 551.	5.8	49
45	Gene expression profile in human leukocytes. Blood, 2003, 101, 3509-3513.	0.6	47
46	G1/S Cyclin-dependent Kinase Regulates Small GTPase Rho1p through Phosphorylation of RhoGEF Tus1p inSaccharomyces cerevisiae. Molecular Biology of the Cell, 2008, 19, 1763-1771.	0.9	47
47	Coordinated Changes in DNA Methylation in Antigen-Specific Memory CD4 T Cells. Journal of Immunology, 2013, 190, 4076-4091.	0.4	46
48	BodyMap: A Collection of 3' ESTs for Analysis of Human Gene Expression Information. Genome Research, 2000, 10, 1817-1827.	2.4	44
49	Dynactin is involved in a checkpoint to monitor cell wall synthesis in Saccharomyces cerevisiae. Nature Cell Biology, 2004, 6, 861-871.	4.6	43
50	Genome-wide profiling of DNA methylation in human cancer cells. Genomics, 2011, 98, 280-287.	1.3	42
51	High-Resolution Analysis of the 5â€²-End Transcriptome Using a Next Generation DNA Sequencer. PLoS ONE, 2009, 4, e4108.	1.1	42
52	Genome-wide genetic variations are highly correlated with proximal DNA methylation patterns. Genome Research, 2012, 22, 1419-1425.	2.4	41
53	Large hypomethylated domains serve as strong repressive machinery for key developmental genes in vertebrates. Development (Cambridge), 2014, 141, 2568-2580.	1.2	41
54	Integrative analysis of genomic alterations in triple-negative breast cancer in association with homologous recombination deficiency. PLoS Genetics, 2017, 13, e1006853.	1.5	39

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55	Mutations in COA7 cause spinocerebellar ataxia with axonal neuropathy. Brain, 2018, 141, 1622-1636.	3.7	38
56	Cooperative scheduling and its application to steelmaking processes. IEEE Transactions on Industrial Electronics, 1991, 38, 150-155.	5.2	37
57	Molecular epidemiological study of familial amyotrophic lateral sclerosis in Japanese population by whole-exome sequencing and identification of novel HNRNPA1 mutation. Neurobiology of Aging, 2018, 61, 255.e9-255.e16.	1.5	37
58	CTCF looping is established during gastrulation in medaka embryos. Genome Research, 2021, 31, 968-980.	2.4	37
59	Constrained clusters of gene expression profiles with pathological features. Bioinformatics, 2004, 20, 3137-3145.	1.8	35
60	CSF1R mutations identified in three families with autosomal dominantly inherited leukoencephalopathy. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 951-957.	1.1	34
61	UTGB/medaka: genomic resource database for medaka biology. Nucleic Acids Research, 2007, 36, D747-D752.	6.5	32
62	Clinical and mutational spectrum of Charcotâ€“Marieâ€“Tooth disease type 2Z caused by MORC2 variants in Japan. European Journal of Neurology, 2017, 24, 1274-1282.	1.7	32
63	Expression profiling of muscles from Fukuyama-type congenital muscular dystrophy and laminin-Î±2 deficient congenital muscular dystrophy; is congenital muscular dystrophy a primary fibrotic disease?. Biochemical and Biophysical Research Communications, 2006, 342, 489-502.	1.0	31
64	Clinical and genetic diversities of Charcotâ€Marieâ€Tooth disease with MFN2 mutations in a large case study. Journal of the Peripheral Nervous System, 2017, 22, 191-199.	1.4	31
65	AgIn: measuring the landscape of CpG methylation of individual repetitive elements. Bioinformatics, 2016, 32, 2911-2919.	1.8	29
66	Burden of rare variants in causative genes for amyotrophic lateral sclerosis (ALS) accelerates age at onset of ALS. Journal of Neurology, Neurosurgery and Psychiatry, 2019, 90, 537-542.	0.9	28
67	Amnionless-mediated glycosylation is crucial for cell surface targeting of cubilin in renal and intestinal cells. Scientific Reports, 2018, 8, 2351.	1.6	27
68	Hamster PIWI proteins bind to piRNAs with stage-specific size variations during oocyte maturation. Nucleic Acids Research, 2021, 49, 2700-2720.	6.5	26
69	Design and implementation of the glue-nail database system. , 1993, , .		25
70	Diversity of Ca2+-Induced Morphology Revealed by Morphological Phenotyping of Ca2+-Sensitive Mutants of Saccharomyces cerevisiae. Eukaryotic Cell, 2007, 6, 817-830.	3.4	24
71	Comparative DNA Sequence Analysis of Mouse and Human CC Chemokine Gene Clusters. Journal of Interferon and Cytokine Research, 2003, 23, 37-45.	0.5	23
72	MachiBase: a Drosophila melanogaster 5'-end mRNA transcription database. Nucleic Acids Research, 2009, 37, D49-D53.	6.5	23

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73	Rapid and ongoing evolution of repetitive sequence structures in human centromeres. Science Advances, 2020, 6, .	4.7	23
74	On Classification and Regression. Lecture Notes in Computer Science, 1998, , 40-57.	1.0	23
75	Modeling neurological diseases with induced pluripotent cells reprogrammed from immortalized lymphoblastoid cell lines. Molecular Brain, 2016, 9, 88.	1.3	21
76	Novel De Novo KCND3 Mutation in a Japanese Patient with Intellectual Disability, Cerebellar Ataxia, Myoclonus, and Dystonia. Cerebellum, 2018, 17, 237-242.	1.4	21
77	Clinicopathological features of the first Asian family having vocal cord and pharyngeal weakness with distal myopathy due to a <scp>MATR3</scp> mutation. Neuropathology and Applied Neurobiology, 2015, 41, 391-398.	1.8	20
78	Ataxic phenotype with altered CaV3.1 channel property in a mouse model for spinocerebellar ataxia 42. Neurobiology of Disease, 2019, 130, 104516.	2.1	20
79	PrimerStation: a highly specific multiplex genomic PCR primer design server for the human genome. Nucleic Acids Research, 2006, 34, W665-W669.	6.5	19
80	An alternating fixpoint tailored to magic programs. , 1993, , .		18
81	Segmental duplications in the silkworm genome. BMC Genomics, 2013, 14, 521.	1.2	18
82	Identification of candidate genes involved in the etiology of sporadic Tourette syndrome by exome sequencing. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 712-723.	1.1	17
83	Implementation and Evaluation of Decision Trees with Range and Region Splitting. Constraints, 1997, 2, 401-427.	0.4	16
84	MNX1-HNF1B Axis Is Indispensable for Intraductal Papillary Mucinous Neoplasm Lineages. Gastroenterology, 2022, 162, 1272-1287.e16.	0.6	16
85	The Glue-Nail deductive database system: Design, implementation, and evaluation. VLDB Journal, 1994, 3, 123-160.	2.7	15
86	Data mining tools for the Saccharomyces cerevisiae morphological database. Nucleic Acids Research, 2005, 33, W753-W757.	6.5	15
87	Analysis of a novel gene, Sdgc, reveals sex chromosome-dependent differences of medaka germ cells prior to gonad formation. Development (Cambridge), 2014, 141, 3363-3369.	1.2	15
88	TBCD may be a causal gene in progressive neurodegenerative encephalopathy with atypical infantile spinal muscular atrophy. Journal of Human Genetics, 2017, 62, 473-480.	1.1	15
89	Frequency and characteristics of the TBK1 gene variants in Japanese patients with sporadic amyotrophic lateral sclerosis. Neurobiology of Aging, 2018, 64, 158.e15-158.e19.	1.5	15
90	BodyMap incorporated PCR-based expression profiling data and a gene ranking system. Nucleic Acids Research, 2001, 29, 156-158.	6.5	14

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91	A Simple but Powerful Heuristic Method for Accelerating <formula formulatype="inline"><tex Notation="TeX">k</tex></formula> -Means Clustering of Large-Scale Data in Life Science. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 681-692.	1.9	14
92	CNV analysis using whole exome sequencing identified biallelic CNVs of VPS13B in siblings with intellectual disability. European Journal of Medical Genetics, 2020, 63, 103610.	0.7	14
93	Parallel Branch-and-Bound Graph Search for Correlated Association Rules. Lecture Notes in Computer Science, 2000, , 127-144.	1.0	14
94	Answering the Most Correlated N Association Rules Efficiently. Lecture Notes in Computer Science, 2002, , 410-422.	1.0	13
95	A Novel de novo KIF1A Mutation in a Patient with Autism, Hyperactivity, Epilepsy, Sensory Disturbance, and Spastic Paraplegia. Internal Medicine, 2020, 59, 839-842.	0.3	13
96	Efficient Construction of Regression Trees with Range and Region Splitting. Machine Learning, 2001, 45, 235-259.	3.4	12
97	The Gene Resource Locator: gene locus maps for transcriptome analysis. Nucleic Acids Research, 2002, 30, 221-225.	6.5	12
98	Involvement of Rho-type GTPase in control of cell size inSaccharomyces cerevisiae. FEMS Yeast Research, 2007, 7, 569-578.	1.1	12
99	UTGB toolkit for personalized genome browsers. Bioinformatics, 2009, 25, 1856-1861.	1.8	12
100	Atypical parkinsonism caused by Pro105Leu mutation of prion protein. Neurology: Genetics, 2016, 2, e48.	0.9	12
101	Ataxic form of autosomal recessive PEX10-related peroxisome biogenesis disorders with a novel compound heterozygous gene mutation and characteristic clinical phenotype. Journal of the Neurological Sciences, 2017, 375, 424-429.	0.3	12
102	Altered expression of Crb2 in podocytes expands a variation of CRB2 mutations in steroid-resistant nephrotic syndrome. Pediatric Nephrology, 2017, 32, 801-809.	0.9	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. Journal of Medical Genetics, 2021, 58, 701-711.	1.5	12
104	Loss-of-function variants in NEK1 are associated with an increased risk of sporadic ALS in the Japanese population. Journal of Human Genetics, 2021, 66, 237-241.	1.1	12
105	Evaluation of image processing programs for accurate measurement of budding and fission yeast morphology. Current Genetics, 2006, 49, 237-247.	0.8	11
106	Cost-Effective Sequencing of Full-Length cDNA Clones Powered by a De Novo-Reference Hybrid Assembly. PLoS ONE, 2010, 5, e10517.	1.1	11
107	Assessing Cell-to-Cell DNA Methylation Variability on Individual Long Reads. Scientific Reports, 2016, 6, 21317.	1.6	11
108	Hypomethylated domain-enriched DNA motifs prepattern the accessible nucleosome organization in teleosts. Epigenetics and Chromatin, 2017, 10, 44.	1.8	11

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109	Comprehensive investigation of RNF213 nonsynonymous variants associated with intracranial artery stenosis. Scientific Reports, 2020, 10, 11942.	1.6	11
110	HiC-Hiker: a probabilistic model to determine contig orientation in chromosome-length scaffolds with Hi-C. Bioinformatics, 2020, 36, 3966-3974.	1.8	11
111	5'SAGE: 5'-end Serial Analysis of Gene Expression database. Nucleic Acids Research, 2004, 33, D550-D552.	6.5	9
112	COMPUTING HIGHLY SPECIFIC AND NOISE-TOLERANT OLIGOMERS EFFICIENTLY. Journal of Bioinformatics and Computational Biology, 2004, 02, 21-46.	0.3	9
113	Extremely slow rate of evolution in the HOX cluster revealed by comparison between Tanzanian and Indonesian coelacanths. Gene, 2012, 505, 324-332.	1.0	9
114	A framework and an algorithm to detect low-abundance DNA by a handy sequencer and a palm-sized computer. Bioinformatics, 2019, 35, 584-592.	1.8	9
115	Computing Optimal Hypotheses Efficiently for Boosting. Lecture Notes in Computer Science, 2002, , 471-481.	1.0	9
116	An Extension of Van Gelder's Alternating Fixpoint to Magic Programs. Journal of Computer and System Sciences, 1996, 52, 506-521.	0.9	8
117	Novel GBE1 mutation in a Japanese family with adult polyglucosan body disease. Neurology: Genetics, 2017, 3, e138.	0.9	8
118	Slowly progressive d-bifunctional protein deficiency with survival to adulthood diagnosed by whole-exome sequencing. Journal of the Neurological Sciences, 2017, 372, 6-10.	0.3	8
119	Investigating the mitochondrial genomic landscape of Arabidopsis thaliana by long-read sequencing. PLoS Computational Biology, 2021, 17, e1008597.	1.5	8
120	Studies on drug metabolism by use of isotopes. XVI. Species differences in metabolism of 1-butyryl-4-cinnamylpiperazine hydrochloride.. Chemical and Pharmaceutical Bulletin, 1975, 23, 1949-1954.	0.6	7
121	Studies on drug metabolism by use of isotopes. 23. Metabolic study of 1-butyryl-4-cinnamylpiperazine in the rat during development of tolerance by using two kinds of deuterium-labeled forms. Journal of Medicinal Chemistry, 1978, 21, 525-529.	2.9	7
122	A Fast and Sensitive Algorithm for Aligning ESTs to the Human Genome. Journal of Bioinformatics and Computational Biology, 2003, 01, 363-386.	0.3	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. Parkinsonism and Related Disorders, 2019, 61, 57-63.	1.1	6
126	Splice-site mutations in KIF5A in the Japanese case series of amyotrophic lateral sclerosis. Neurogenetics, 2021, 22, 11-17.	0.7	6

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127	SONAR. , 1996, , .		5
128	Avoiding Cartesian products for multiple joins. Journal of the ACM, 1997, 44, 57-85.	1.8	5
129	Itemset Classified Clustering. Lecture Notes in Computer Science, 2004, , 398-409.	1.0	5
130	Exome analysis reveals a Japanese family with spinocerebellar ataxia, autosomal recessive 1. Journal of the Neurological Sciences, 2013, 331, 158-160.	0.3	5
131	The time is ripe to investigate human centromeres by long-read sequencing. DNA Research, 2021, 28, .	1.5	5
132	Prolog computation model BPM and its debugger PROEDIT2. Lecture Notes in Computer Science, 1987, , 147-158.	1.0	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.	1.1	4
134	Finding long tandem repeats in long noisy reads. Bioinformatics, 2021, 37, 612-621.	1.8	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.	1.5	4
137	How should Prolog computation Be represented for practical use?. New Generation Computing, 1990, 8, 95-112.	2.5	3
138	SONAR. SIGMOD Record, 1996, 25, 553.	0.7	3
139	Associations between nucleosome phasing, sequence asymmetry, and tissue-specific expression in a set of inbred Medaka species. BMC Genomics, 2015, 16, 978.	1.2	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.	1.1	3
141	Design and implementation of the glue-nail database system. SIGMOD Record, 1993, 22, 147-156.	0.7	2
142	Exome sequencing shows a novel de novo mutation in <scp>ATL</scp>1. Neurology and Clinical Neuroscience, 2014, 2, 1-4.	0.2	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.	0.3	2
144	Overexpression of Larp4B downregulates dMyc and reduces cell and organ sizes in Drosophila. Biochemical and Biophysical Research Communications, 2018, 497, 762-768.	1.0	2

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145	A Statistical Method for Observing Personal Diploid Methylomes and Transcriptomes with Single-Molecule Real-Time Sequencing. Genes, 2018, 9, 460.	1.0	2
146	Complex hereditary peripheral neuropathies caused by novel variants in mitochondrial-related nuclear genes. Journal of Neurology, 2022, 269, 4129-4140.	1.8	2
147	Context-dependent DNA polymerization effects can masquerade as DNA modification signals. BMC Genomics, 2022, 23, 249.	1.2	2
148	Early prediction of functional prognosis in neurofibromatosis type 2 patients based on genotypeâ€“phenotype correlation with targeted deep sequencing. Scientific Reports, 2022, 12, .	1.6	2
149	Use of stable isotopes in the pharmacokinetics of drugs by mass fragmentography. I. Urinary excretion of 1-butyryl-4-cinnamylpiperazine in man.. Journal of Pharmacobio-dynamics, 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. BMC Genomics, 2015, 16, S8.	1.2	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. Lecture Notes in Computer Science, 1999, , 345-346.	1.0	1
155	Report on BIOKDD04. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2004, 6, 153-154.	3.2	0
156	A Unique Center for Bioinformatics Research. Asia Pacific Biotech News, 2007, 11, 1068-1068.	0.5	0
157	Accelerating Path-free XML Queries in RDBMS. IPSJ Online Transactions, 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 COL6A2 mutation in a case of limb girdle muscular dystrophy phenotype with autosomal recessive inheritance. Neurology and Clinical Neuroscience, 2016, 4, 189-191.	0.2	0
161	Novel mutation in the membrane metalloendopeptidase gene in a patient with the autosomal recessive form of Charcot-Marie-Tooth disease. Neurology and Clinical Neuroscience, 2017, 5, 124-126.	0.2	0
162	Sporadic progressive myoclonic epilepsy with earlyâ€onset dementia caused by a de novo mutation in PSEN1. Neurology and Clinical Neuroscience, 2019, 7, 294-296.	0.2	0

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163	Practical Software for Aligning ESTs to Human Genome. Lecture Notes in Computer Science, 2002, , 1-16.	1.0	0
164	Modeling Chronic Myelomonocytic Leukemia Through Patient-Derived Induced Pluripotent Stem Cells. Blood, 2013, 122, 864-864.	0.6	0
165	Lattice programming methodology. Lecture Notes in Computer Science, 1989, , 96-107.	1.0	0
166	Chromatin Architecture Modulation in B-Cell Acute Lymphoblastic Leukemia Carrying DUX4 Fusions. Blood, 2019, 134, 1240-1240.	0.6	0
167	Expression profile analysis in cells overexpressing <scp>DRPLA cDNA</scp> to explore the roles of <scp>DRPLAp</scp> as a transcriptional coregulator. Neurology and Clinical Neuroscience, 0, , .	0.2	0