# 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 | MNX1-HNF1B Axis Is Indispensable for Intraductal Papillary Mucinous Neoplasm Lineages. Gastroenterology, 2022, 162, 1272-1287.e16. | 1.3 | 16 |
| 2 | Complex hereditary peripheral neuropathies caused by novel variants in mitochondrial-related nuclear genes. Journal of Neurology, 2022, 269, 4129-4140. | 3.6 | 2 |
| 3 | Context-dependent DNA polymerization effects can masquerade as DNA modification signals. BMC Genomics, 2022, 23, 249. | 2.8 | 2 |
| 4 | Early prediction of functional prognosis in neurofibromatosis type 2 patients based on genotypeâ€“phenotype correlation with targeted deep sequencing. Scientific Reports, 2022, 12, . | 3.3 | 2 |
| 5 | 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. | 3.2 | 12 |
| 6 | Finding long tandem repeats in long noisy reads. Bioinformatics, 2021, 37, 612-621. | 4.1 | 4 |
| 7 | Splice-site mutations in KIF5A in the Japanese case series of amyotrophic lateral sclerosis. Neurogenetics, 2021, 22, 11-17. | 1.4 | 6 |
| 8 | 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. | 2.3 | 12 |
| 9 | Investigating the mitochondrial genomic landscape of Arabidopsis thaliana by long-read sequencing. PLoS Computational Biology, 2021, 17, e1008597. | 3.2 | 8 |
| 10 | Hamster PIWI proteins bind to piRNAs with stage-specific size variations during oocyte maturation. Nucleic Acids Research, 2021, 49, 2700-2720. | 14.5 | 26 |
| 11 | CTCF looping is established during gastrulation in medaka embryos. Genome Research, 2021, 31, 968-980. | 5.5 | 37 |
| 12 | The time is ripe to investigate human centromeres by long-read sequencing. DNA Research, 2021, 28, . | 3.4 | 5 |
| 13 | CNV analysis using whole exome sequencing identified biallelic CNVs of VPS13B in siblings with intellectual disability. European Journal of Medical Genetics, 2020, 63, 103610. | 1.3 | 14 |
| 14 | A Novel de novo KIF1A Mutation in a Patient with Autism, Hyperactivity, Epilepsy, Sensory Disturbance, and Spastic Paraplegia. Internal Medicine, 2020, 59, 839-842. | 0.7 | 13 |
| 15 | 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 |
| 16 | Comprehensive investigation of RNF213 nonsynonymous variants associated with intracranial artery stenosis. Scientific Reports, 2020, 10, 11942. | 3.3 | 11 |
| 17 | Rapid and ongoing evolution of repetitive sequence structures in human centromeres. Science Advances, 2020, 6, . | 10.3 | 23 |
| 18 | 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 |

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|---|---|---|---|
| 19 | HiC-Hiker: a probabilistic model to determine contig orientation in chromosome-length scaffolds with Hi-C. Bioinformatics, 2020, 36, 3966-3974. | 4.1 | 11 |
| 20 | A framework and an algorithm to detect low-abundance DNA by a handy sequencer and a palm-sized computer. Bioinformatics, 2019, 35, 584-592. | 4.1 | 9 |
| 21 | Noncoding CGG repeat expansions in neuronal intranuclear inclusion disease, oculopharyngodistal myopathy and an overlapping disease. Nature Genetics, 2019, 51, 1222-1232. | 21.4 | 265 |
| 22 | Sporadic progressive myoclonic epilepsy with earlyâ€onset dementia caused by a de novo mutation in PSEN1. Neurology and Clinical Neuroscience, 2019, 7, 294-296. | 0.4 | 0 |
| 23 | Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. Microbiome, 2019, 7, 119. | 11.1 | 65 |
| 24 | Recompleting the Caenorhabditis elegans genome. Genome Research, 2019, 29, 1009-1022. | 5.5 | 108 |
| 25 | Ataxic phenotype with altered CaV3.1 channel property in a mouse model for spinocerebellar ataxia 42. Neurobiology of Disease, 2019, 130, 104516. | 4.4 | 20 |
| 26 | Neuroimaging, genetic, and enzymatic study in a Japanese family with a GBA gross deletion. Parkinsonism and Related Disorders, 2019, 61, 57-63. | 2.2 | 6 |
| 27 | 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. | 1.9 | 28 |
| 28 | Chromatin Architecture Modulation in B-Cell Acute Lymphoblastic Leukemia Carrying DUX4 Fusions. Blood, 2019, 134, 1240-1240. | 1.4 | 0 |
| 29 | 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 |
| 30 | ExpansionsÂofÂintronic TTTCA and TTTTA repeats in benign adult familial myoclonic epilepsy. Nature Genetics, 2018, 50, 581-590. | 21.4 | 238 |
| 31 | Amnionless-mediated glycosylation is crucial for cell surface targeting of cubilin in renal and intestinal cells. Scientific Reports, 2018, 8, 2351. | 3.3 | 27 |
| 32 | 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. | 3.1 | 15 |
| 33 | Mutations in COA7 cause spinocerebellar ataxia with axonal neuropathy. Brain, 2018, 141, 1622-1636. | 7.6 | 38 |
| 34 | 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. | 3.1 | 37 |
| 35 | Novel De Novo KCND3 Mutation in a Japanese Patient with Intellectual Disability, Cerebellar Ataxia, Myoclonus, and Dystonia. Cerebellum, 2018, 17, 237-242. | 2.5 | 21 |
| 36 | A Statistical Method for Observing Personal Diploid Methylomes and Transcriptomes with Single-Molecule Real-Time Sequencing. Genes, 2018, 9, 460. | 2.4 | 2 |

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| 37 | Novel GBE1 mutation in a Japanese family with adult polyglucosan body disease. Neurology: Genetics, 2017, 3, e138. | 1.9 | 8 |
| 38 | 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. | 1.7 | 17 |
| 39 | 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. | 0.6 | 12 |
| 40 | Slowly progressive d-bifunctional protein deficiency with survival to adulthood diagnosed by whole-exome sequencing. Journal of the Neurological Sciences, 2017, 372, 6-10. | 0.6 | 8 |
| 41 | Altered expression of Crb2 in podocytes expands a variation of CRB2 mutations in steroid-resistant nephrotic syndrome. Pediatric Nephrology, 2017, 32, 801-809. | 1.7 | 12 |
| 42 | TBCD may be a causal gene in progressive neurodegenerative encephalopathy with atypical infantile spinal muscular atrophy. Journal of Human Genetics, 2017, 62, 473-480. | 2.3 | 15 |
| 43 | Complete fusion of a transposon and herpesvirus created the Teratorn mobile element in medaka fish. Nature Communications, 2017, 8, 551. | 12.8 | 49 |
| 44 | 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. | 0.4 | 0 |
| 45 | 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. | 3.3 | 32 |
| 46 | 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. | 3.1 | 31 |
| 47 | Integrative analysis of genomic alterations in triple-negative breast cancer in association with homologous recombination deficiency. PLoS Genetics, 2017, 13, e1006853. | 3.5 | 39 |
| 48 | Hypomethylated domain-enriched DNA motifs prepattern the accessible nucleosome organization in teleosts. Epigenetics and Chromatin, 2017, 10, 44. | 3.9 | 11 |
| 49 | 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 |
| 50 | Atypical parkinsonism caused by Pro105Leu mutation of prion protein. Neurology: Genetics, 2016, 2, e48. | 1.9 | 12 |
| 51 | AgIn: measuring the landscape of CpG methylation of individual repetitive elements. Bioinformatics, 2016, 32, 2911-2919. | 4.1 | 29 |
| 52 | Mutations in MME cause an autosomalâ€recessive Charcotâ€“Marieâ€“Tooth disease type 2. Annals of Neurology, 2016, 79, 659-672. | 5.3 | 82 |
| 53 | Novel COL6A2 mutation in a case of limb girdle muscular dystrophy phenotype with autosomal recessive inheritance. Neurology and Clinical Neuroscience, 2016, 4, 189-191. | 0.4 | 0 |
| 54 | 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 |

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| 55 | Human genetic variation database, a reference database of genetic variations in the Japanese population. Journal of Human Genetics, 2016, 61, 547-553. | 2.3 | 270 |
| 56 | Modeling neurological diseases with induced pluripotent cells reprogrammed from immortalized lymphoblastoid cell lines. Molecular Brain, 2016, 9, 88. | 2.6 | 21 |
| 57 | Assessing Cell-to-Cell DNA Methylation Variability on Individual Long Reads. Scientific Reports, 2016, 6, 21317. | 3.3 | 11 |
| 58 | Recurrent DUX4 fusions in B cell acute lymphoblastic leukemia of adolescents and young adults. Nature Genetics, 2016, 48, 569-574. | 21.4 | 198 |
| 59 | A linear time algorithm for detecting long genomic regions enriched with a specific combination of epigenetic states. BMC Genomics, 2015, 16, S8. | 2.8 | 1 |
| 60 | 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 |
| 61 | A Novel Mutation inELOVL4Leading to Spinocerebellar Ataxia (SCA) With the Hot Cross Bun Sign but Lacking Erythrokeratodermia. JAMA Neurology, 2015, 72, 797. | 9.0 | 79 |
| 62 | 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. | 3.2 | 20 |
| 63 | 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. | 3.0 | 14 |
| 64 | Rapid detection of expanded short tandem repeats in personal genomics using hybrid sequencing. Bioinformatics, 2014, 30, 815-822. | 4.1 | 61 |
| 65 | A recurrent de novo FAM111A mutation causes kennyâ€“caffey syndrome type 2. Journal of Bone and Mineral Research, 2014, 29, 992-998. | 2.8 | 68 |
| 66 | Exome sequencing shows a novel de novo mutation in <scp>ATL</scp>1. Neurology and Clinical Neuroscience, 2014, 2, 1-4. | 0.4 | 2 |
| 67 | 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. | 2.5 | 15 |
| 68 | Large hypomethylated domains serve as strong repressive machinery for key developmental genes in vertebrates. Development (Cambridge), 2014, 141, 2568-2580. | 2.5 | 41 |
| 69 | Segmental duplications in the silkworm genome. BMC Genomics, 2013, 14, 521. | 2.8 | 18 |
| 70 | Exome analysis reveals a Japanese family with spinocerebellar ataxia, autosomal recessive 1. Journal of the Neurological Sciences, 2013, 331, 158-160. | 0.6 | 5 |
| 71 | ERBB4 Mutations that Disrupt the Neuregulin-ErbB4 Pathway Cause Amyotrophic Lateral Sclerosis Type 19. American Journal of Human Genetics, 2013, 93, 900-905. | 6.2 | 123 |
| 72 | The transcription start site landscape of C. elegans. Genome Research, 2013, 23, 1348-1361. | 5.5 | 58 |

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| 73 | 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. | 2.1 | 51 |
| 74 | Coordinated Changes in DNA Methylation in Antigen-Specific Memory CD4 T Cells. Journal of Immunology, 2013, 190, 4076-4091. | 0.8 | 46 |
| 75 | Identification of ATP1A3 Mutations by Exome Sequencing as the Cause of Alternating Hemiplegia of Childhood in Japanese Patients. PLoS ONE, 2013, 8, e56120. | 2.5 | 79 |
| 76 | Modeling Chronic Myelomonocytic Leukemia Through Patient-Derived Induced Pluripotent Stem Cells. Blood, 2013, 122, 864-864. | 1.4 | 0 |
| 77 | CSF1R mutations identified in three families with autosomal dominantly inherited leukoencephalopathy. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 951-957. | 1.7 | 34 |
| 78 | Extremely slow rate of evolution in the HOX cluster revealed by comparison between Tanzanian and Indonesian coelacanths. Gene, 2012, 505, 324-332. | 2.2 | 9 |
| 79 | Genome-wide genetic variations are highly correlated with proximal DNA methylation patterns. Genome Research, 2012, 22, 1419-1425. | 5.5 | 41 |
| 80 | Poster: Robust estimation of DNA methylation with local regression. , 2011, , . | | 0 |
| 81 | A gain-of-function screen identifies wdb and lkb1 as lifespan-extending genes in Drosophila. Biochemical and Biophysical Research Communications, 2011, 405, 667-672. | 2.1 | 57 |
| 82 | Genome-wide profiling of DNA methylation in human cancer cells. Genomics, 2011, 98, 280-287. | 2.9 | 42 |
| 83 | Invited: Searching massive epigenome data for evolutionarily conserved sequence motifs. , 2011, , . | | 0 |
| 84 | Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. , 2011, , 39-47. | | 1 |
| 85 | Reconstruction of the Vertebrate Ancestral Genome Reveals Dynamic Genome Reorganization in Early Vertebrates. , 2011, , 307-322. | | 1 |
| 86 | Accelerating Path-free XML Queries in RDBMS. IPSJ Online Transactions, 2010, 3, 206-217. | 0.1 | 0 |
| 87 | Cost-Effective Sequencing of Full-Length cDNA Clones Powered by a De Novo-Reference Hybrid Assembly. PLoS ONE, 2010, 5, e10517. | 2.5 | 11 |
| 88 | Robust and accurate recognition of veins in fruit fly wings. , 2009, , . | | 1 |
| 89 | UTGB toolkit for personalized genome browsers. Bioinformatics, 2009, 25, 1856-1861. | 4.1 | 12 |
| 90 | Efficient frequency-based de novo short-read clustering for error trimming in next-generation sequencing. Genome Research, 2009, 19, 1309-1315. | 5.5 | 53 |

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| 91 | Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. Science, 2009, 323, 401-404. | 12.6 | 122 |
| 92 | MachiBase: a Drosophila melanogaster 5'-end mRNA transcription database. Nucleic Acids Research, 2009, 37, D49-D53. | 14.5 | 23 |
| 93 | siDirect 2.0: updated software for designing functional siRNA with reduced seed-dependent off-target effect. BMC Bioinformatics, 2009, 10, 392. | 2.6 | 184 |
| 94 | Comprehensive and quantitative analysis of yeast deletion mutants defective in apical and isotropic bud growth. Current Genetics, 2009, 55, 365-380. | 1.7 | 50 |
| 95 | High-Resolution Analysis of the 5â€²-End Transcriptome Using a Next Generation DNA Sequencer. PLoS ONE, 2009, 4, e4108. | 2.5 | 42 |
| 96 | Variant between CPT1B and CHKB associated with susceptibility to narcolepsy. Nature Genetics, 2008, 40, 1324-1328. | 21.4 | 141 |
| 97 | The genome of a lepidopteran model insect, the silkworm Bombyx mori. Insect Biochemistry and Molecular Biology, 2008, 38, 1036-1045. | 2.7 | 592 |
| 98 | Relational-style XML query. , 2008, , . | | 7 |
| 99 | 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. | 2.1 | 47 |
| 100 | A Unique Center for Bioinformatics Research. Asia Pacific Biotech News, 2007, 11, 1068-1068. | 0.0 | 0 |
| 101 | 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 |
| 102 | Reconstruction of the vertebrate ancestral genome reveals dynamic genome reorganization in early vertebrates. Genome Research, 2007, 17, 1254-1265. | 5.5 | 444 |
| 103 | UTGB/medaka: genomic resource database for medaka biology. Nucleic Acids Research, 2007, 36, D747-D752. | 14.5 | 32 |
| 104 | The medaka draft genome and insights into vertebrate genome evolution. Nature, 2007, 447, 714-719. | 27.8 | 1,037 |
| 105 | Involvement of Rho-type GTPase in control of cell size inSaccharomyces cerevisiae. FEMS Yeast Research, 2007, 7, 569-578. | 2.3 | 12 |
| 106 | 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. | 2.1 | 31 |
| 107 | Comparative analysis of chimpanzee and human Y chromosomes unveils complex evolutionary pathway. Nature Genetics, 2006, 38, 158-167. | 21.4 | 110 |
| 108 | Evaluation of image processing programs for accurate measurement of budding and fission yeast morphology. Current Genetics, 2006, 49, 237-247. | 1.7 | 11 |

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| 109 | PrimerStation: a highly specific multiplex genomic PCR primer design server for the human genome. Nucleic Acids Research, 2006, 34, W665-W669. | 14.5 | 19 |
| 110 | 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. | 7.1 | 213 |
| 111 | Large-Scale Genome Sequence Processing. , 2006, , . | | 7 |
| 112 | Accelerated off-target search algorithm for siRNA. Bioinformatics, 2005, 21, 1316-1324. | 4.1 | 71 |
| 113 | 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. | 7.1 | 276 |
| 114 | dsCheck: highly sensitive off-target search software for double-stranded RNA-mediated RNA interference. Nucleic Acids Research, 2005, 33, W589-W591. | 14.5 | 160 |
| 115 | Data mining tools for the Saccharomyces cerevisiae morphological database. Nucleic Acids Research, 2005, 33, W753-W757. | 14.5 | 15 |
| 116 | SCMD: Saccharomyces cerevisiae Morphological Database. Nucleic Acids Research, 2004, 32, 319D-322. | 14.5 | 84 |
| 117 | 5'SAGE: 5'-end Serial Analysis of Gene Expression database. Nucleic Acids Research, 2004, 33, D550-D552. | 14.5 | 9 |
| 118 | COMPUTING HIGHLY SPECIFIC AND NOISE-TOLERANT OLIGOMERS EFFICIENTLY. Journal of Bioinformatics and Computational Biology, 2004, 02, 21-46. | 0.8 | 9 |
| 119 | Report on BIOKDD04. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2004, 6, 153-154. | 4.0 | 0 |
| 120 | 5â€²-end SAGE for the analysis of transcriptional start sites. Nature Biotechnology, 2004, 22, 1146-1149. | 17.5 | 115 |
| 121 | Dynactin is involved in a checkpoint to monitor cell wall synthesis in Saccharomyces cerevisiae. Nature Cell Biology, 2004, 6, 861-871. | 10.3 | 43 |
| 122 | DEVELOPMENT OF IMAGE PROCESSING PROGRAM FOR YEAST CELL MORPHOLOGY. Journal of Bioinformatics and Computational Biology, 2004, 01, 695-709. | 0.8 | 57 |
| 123 | Constrained clusters of gene expression profiles with pathological features. Bioinformatics, 2004, 20, 3137-3145. | 4.1 | 35 |
| 124 | The Genome Sequence of Silkworm, Bombyx mori. DNA Research, 2004, 11, 27-35. | 3.4 | 594 |
| 125 | siDirect: highly effective, target-specific siRNA design software for mammalian RNA interference. Nucleic Acids Research, 2004, 32, W124-W129. | 14.5 | 230 |
| 126 | Itemset Classified Clustering. Lecture Notes in Computer Science, 2004, , 398-409. | 1.3 | 5 |

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|---|---|---|---|
| 127 | Comparative DNA Sequence Analysis of Mouse and Human CC Chemokine Gene Clusters. Journal of Interferon and Cytokine Research, 2003, 23, 37-45. | 1.2 | 23 |
| 128 | A Fast and Sensitive Algorithm for Aligning ESTs to the Human Genome. Journal of Bioinformatics and Computational Biology, 2003, 01, 363-386. | 0.8 | 7 |
| 129 | Gene expression profile in human leukocytes. Blood, 2003, 101, 3509-3513. | 1.4 | 47 |
| 130 | The Gene Resource Locator: gene locus maps for transcriptome analysis. Nucleic Acids Research, 2002, 30, 221-225. | 14.5 | 12 |
| 131 | KDD Cup 2001 report. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2002, 3, 47-64. | 4.0 | 72 |
| 132 | Answering the Most Correlated N Association Rules Efficiently. Lecture Notes in Computer Science, 2002, , 410-422. | 1.3 | 13 |
| 133 | Computing Optimal Hypotheses Efficiently for Boosting. Lecture Notes in Computer Science, 2002, , 471-481. | 1.3 | 9 |
| 134 | Practical Software for Aligning ESTs to Human Genome. Lecture Notes in Computer Science, 2002, , 1-16. | 1.3 | 0 |
| 135 | Diverse transcriptional initiation revealed by fine, largeâ€scale mapping of mRNA start sites. EMBO Reports, 2001, 2, 388-393. | 4.5 | 154 |
| 136 | Data Mining with optimized two-dimensional association rules. ACM Transactions on Database Systems, 2001, 26, 179-213. | 2.8 | 90 |
| 137 | Efficient Construction of Regression Trees with Range and Region Splitting. Machine Learning, 2001, 45, 235-259. | 5.4 | 12 |
| 138 | BodyMap incorporated PCR-based expression profiling data and a gene ranking system. Nucleic Acids Research, 2001, 29, 156-158. | 14.5 | 14 |
| 139 | Identification and Characterization of the Potential Promoter Regions of 1031 Kinds of Human Genes. Genome Research, 2001, 11, 677-684. | 5.5 | 115 |
| 140 | BodyMap: A Collection of 3' ESTs for Analysis of Human Gene Expression Information. Genome Research, 2000, 10, 1817-1827. | 5.5 | 44 |
| 141 | Transversing itemset lattices with statistical metric pruning. , 2000, , . | | 126 |
| 142 | BodyMap: a human and mouse gene expression database. Nucleic Acids Research, 2000, 28, 136-138. | 14.5 | 56 |
| 143 | Parallel Branch-and-Bound Graph Search for Correlated Association Rules. Lecture Notes in Computer Science, 2000, , 127-144. | 1.3 | 14 |
| 144 | Mining Optimized Association Rules for Numeric Attributes. Journal of Computer and System Sciences, 1999, 58, 1-12. | 1.2 | 55 |

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| 145 | Weighted Majority Decision among Region Rules for a Categorical Dataset. Lecture Notes in Computer Science, 1999, , 345-346. | 1.3 | 1 |
| 146 | On Classification and Regression. Lecture Notes in Computer Science, 1998, , 40-57. | 1.3 | 23 |
| 147 | Avoiding Cartesian products for multiple joins. Journal of the ACM, 1997, 44, 57-85. | 2.2 | 5 |
| 148 | Implementation and Evaluation of Decision Trees with Range and Region Splitting. Constraints, 1997, 2, 401-427. | 0.7 | 16 |
| 149 | Implementation and Evaluation of Decision Trees with Range and Region Splitting. , 1997, , 163-189. | | 4 |
| 150 | Mining optimized association rules for numeric attributes. , 1996, , . | | 151 |
| 151 | An Extension of Van Gelder's Alternating Fixpoint to Magic Programs. Journal of Computer and System Sciences, 1996, 52, 506-521. | 1.2 | 8 |
| 152 | Data mining using two-dimensional optimized association rules. SIGMOD Record, 1996, 25, 13-23. | 1.2 | 72 |
| 153 | SONAR. SIGMOD Record, 1996, 25, 553. | 1.2 | 3 |
| 154 | Data mining using two-dimensional optimized association rules. , 1996, , . | | 136 |
| 155 | SONAR. , 1996, , . | | 5 |
| 156 | The Glue-Nail deductive database system: Design, implementation, and evaluation. VLDB Journal, 1994, 3, 123-160. | 4.1 | 15 |
| 157 | Design and implementation of the glue-nail database system. SIGMOD Record, 1993, 22, 147-156. | 1.2 | 2 |
| 158 | An alternating fixpoint tailored to magic programs. , 1993, , . | | 18 |
| 159 | Design and implementation of the glue-nail database system. , 1993, , . | | 25 |
| 160 | Cooperative scheduling and its application to steelmaking processes. IEEE Transactions on Industrial Electronics, 1991, 38, 150-155. | 7.9 | 37 |
| 161 | How should Prolog computation Be represented for practical use?. New Generation Computing, 1990, 8, 95-112. | 3.3 | 3 |
| 162 | Lattice programming methodology. Lecture Notes in Computer Science, 1989, , 96-107. | 1.3 | 0 |

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| 163 | Prolog computation model BPM and its debugger PROEDIT2. Lecture Notes in Computer Science, 1987, , 147-158. | 1.3 | 4 |
| 164 | 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. | 6.4 | 7 |
| 165 | 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 |
| 166 | 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. | 1.3 | 7 |
| 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, , . | 0.4 | 0 |