

# Kyudong Han

## List of Publications by Year in descending order

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151  
papers

5,166  
citations

136740

32  
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102304

66  
g-index

161  
all docs

161  
docs citations

161  
times ranked

7212  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-exome sequencing reveals rare genetic variations in ovarian granulosa cell tumor. <i>Bosnian Journal of Basic Medical Sciences</i> , 2022, , .	0.6	1
2	A qRT-PCR Method Capable of Quantifying Specific Microorganisms Compared to NGS-Based Metagenome Profiling Data. <i>Microorganisms</i> , 2022, 10, 324.	1.6	6
3	Rapid identification of SARS-CoV-2 in the point-of-care using digital PCR-based Dr. PCR <sup>â</sup> , <sup>¢</sup> Di20K COVID-19 Detection Kit without viral RNA extraction. <i>Genes and Genomics</i> , 2022, 44, 617-628.	0.5	5
4	Microarray analysis of lipopolysaccharide-induced endotoxemia in the cochlea. <i>Gene</i> , 2022, 823, 146347.	1.0	2
5	A Real-Time Detection Device for the Rapid Quantification of Skin Casual Sebum Using the Oil Red O Staining Method. <i>Sensors</i> , 2022, 22, 3016.	2.1	4
6	Identification of Potentially Pathogenic Variants Associated with Recurrence in Medication-Related Osteonecrosis of the Jaw (MRONJ) Patients Using Whole-Exome Sequencing. <i>Journal of Clinical Medicine</i> , 2022, 11, 2145.	1.0	3
7	Evaluation of Lactobacillus Plantarum Additive on Growth Performance, Excreta Microbiota, Nutrient Digestibility, Gas Emission, and Meat Quality in Ross308-Broilers. <i>Brazilian Journal of Poultry Science</i> , 2022, 24, .	0.3	0
8	Comparison of the oral microbial composition between healthy individuals and periodontitis patients in different oral sampling sites using 16S metagenome profiling. <i>Journal of Periodontal and Implant Science</i> , 2022, 52, 394.	0.9	4
9	Alu RNA induces NLRP3 expression through TLR7 activation in Î±-1-antitrypsin <sup>â</sup> deficient macrophages. <i>JCI Insight</i> , 2022, 7, .	2.3	4
10	The Time Sequence of Gene Expression Changes after Spinal Cord Injury. <i>Cells</i> , 2022, 11, 2236.	1.8	2
11	The effect of taxonomic classification by full-length 16S rRNA sequencing with a synthetic long-read technology. <i>Scientific Reports</i> , 2021, 11, 1727.	1.6	71
12	Role of Transposable Elements in Gene Regulation in the Human Genome. <i>Life</i> , 2021, 11, 118.	1.1	31
13	L1 retrotransposons exploit RNA m6A modification as an evolutionary driving force. <i>Nature Communications</i> , 2021, 12, 880.	5.8	32
14	Label-Free Electrochemical Biosensor Based on Au@MoS <sup>â</sup> , <sup>â</sup> PANI for Escherichia coli Detection. <i>Chemosensors</i> , 2021, 9, 49.	1.8	20
15	Human Endogenous Retrovirus (HERV)-K env Gene Knockout Affects Tumorigenic Characteristics of nupr1 Gene in DLD-1 Colorectal Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3941.	1.8	22
16	N,N-Dimethyl-4,4 <sup>â</sup> -azodianiline functionalized magnetic nanoparticles for enhanced sensitivity of nucleic acid amplification tests. <i>Sensors and Actuators B: Chemical</i> , 2021, 332, 129461.	4.0	4
17	A study of transposable element-associated structural variations (TASVs) using a de novo-assembled Korean genome. <i>Experimental and Molecular Medicine</i> , 2021, 53, 615-630.	3.2	9
18	Nuku, a family of primate retrocopies derived from <i>KU70</i>. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	0

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19	Influence of yeast hydrolysate supplement on growth performance, nutrient digestibility, microflora, gas emission, blood profile, and meat quality in broilers. <i>Journal of Animal Science and Technology</i> , 2021, 63, 563-574.	0.8	9
20	Comparative Analysis for Genetic Characterization in Korean Native Jeju Horse. <i>Animals</i> , 2021, 11, 1924.	1.0	0
21	Investigation of high correlation with carcass traits of SNPs of the PLCB1, C/EBP $\beta$ , and TDRKH genes and the combinations of SNPs using the MDR method in the Hanwoo. <i>Genes and Genomics</i> , 2021, 43, 961-973.	0.5	1
22	A comprehensive analysis of gorilla-specific LINE-1 retrotransposons. <i>Genes and Genomics</i> , 2021, 43, 1133-1141.	0.5	3
23	High-accuracy quantitative principle of a new compact digital PCR equipment: Lab On An Array. <i>Genomics and Informatics</i> , 2021, 19, e34.	0.4	6
24	Investigation of single nucleotide polymorphism in TSH- $\beta$ and CaSR associated with body weight in Korean native chickens (Gray Brown). <i>Journal of Animal Reproduction and Biotechnology</i> , 2021, 36, 129-136.	0.3	0
25	Diagnostic evaluation of qRT-PCR-based kit and dPCR-based kit for COVID-19. <i>Genes and Genomics</i> , 2021, 43, 1277-1288.	0.5	8
26	Modulation of Human Mesenchymal Stem Cells by Electrical Stimulation Using an Enzymatic Biofuel Cell. <i>Catalysts</i> , 2021, 11, 62.	1.6	1
27	Comparative analysis of human facial skin microbiome between topical sites compared to entire face. <i>Genes and Genomics</i> , 2021, 43, 1483-1495.	0.5	7
28	Clinical usefulness of anti-muscarinic type 3 receptor autoantibodies in patients with primary Sjögren's syndrome. <i>Clinical and Experimental Rheumatology</i> , 2021, 39, 795-803.	0.4	1
29	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study in multiple populations. <i>Lancet Oncology</i> , 2020, 21, 306-316.	5.1	49
30	AbaR is a LuxR type regulator essential for motility and the formation of biofilm and pellicle in <i>Acinetobacter baumannii</i> . <i>Genes and Genomics</i> , 2020, 42, 1339-1346.	0.5	20
31	Alpha 1 Antitrypsin-Deficient Macrophages Have Impaired Efferocytosis of Apoptotic Neutrophils. <i>Frontiers in Immunology</i> , 2020, 11, 574410.	2.2	11
32	A High Quality Asian Genome Assembly Identifies Features of Common Missing Regions. <i>Genes</i> , 2020, 11, 1350.	1.0	0
33	A single-tube sample preparation method based on a dual-electrostatic interaction strategy for molecular diagnosis of gram-negative bacteria. <i>Mikrochimica Acta</i> , 2020, 187, 558.	2.5	6
34	A comprehensive analysis of chimpanzee ( <i>Pan Troglodytes</i> )-specific AluYb8 element. <i>Genes and Genomics</i> , 2020, 42, 1207-1213.	0.5	0
35	Molecular subtypes of triple-negative breast cancer: understanding of subtype categories and clinical implication. <i>Genes and Genomics</i> , 2020, 42, 1381-1387.	0.5	23
36	Differential expressions of L1-chimeric transcripts in normal and matched-cancer tissues. <i>Analytical Biochemistry</i> , 2020, 600, 113769.	1.1	3

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37	Application of NanoString technologies in angioimmunoblastic T cell lymphoma. <i>Genes and Genomics</i> , 2020, 42, 485-494.	0.5	2
38	Performance comparison of fecal preservative and stock solutions for gut microbiome storage at room temperature. <i>Journal of Microbiology</i> , 2020, 58, 703-710.	1.3	12
39	Enhanced Inner-Ear Organoid Formation from Mouse Embryonic Stem Cells by Photobiomodulation. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 17, 556-567.	1.8	19
40	Quantitative evaluation of the molecular marker using droplet digital PCR. <i>Genomics and Informatics</i> , 2020, 18, e4.	0.4	2
41	The nature of triple-negative breast cancer classification and antitumoral strategies. <i>Genomics and Informatics</i> , 2020, 18, e35.	0.4	2
42	Transposable element-mediated structural variation analysis in dog breeds using whole-genome sequencing. <i>Mammalian Genome</i> , 2019, 30, 289-300.	1.0	9
43	Comparison of library construction kits for mRNA sequencing in the Illumina platform. <i>Genes and Genomics</i> , 2019, 41, 1233-1240.	0.5	14
44	A comprehensive analysis of chimpanzee ( <i>Pan troglodytes</i> )-specific LINE-1 retrotransposons. <i>Gene</i> , 2019, 693, 46-51.	1.0	5
45	Complete genome sequence and phylogenetic analysis of nosocomial pathogen <i>Acinetobacter nosocomialis</i> strain NCTC 8102. <i>Genes and Genomics</i> , 2019, 41, 1063-1075.	0.5	6
46	Amelogenic transcriptome profiling in ameloblast-like cells derived from adult gingival epithelial cells. <i>Scientific Reports</i> , 2019, 9, 3736.	1.6	10
47	A comprehensive analysis of the Baboon-specific full-length LINE-1 retrotransposons. <i>Genes and Genomics</i> , 2019, 41, 831-837.	0.5	0
48	Investigation of Hanwoo-specific structural variations using whole-genome sequencing data. <i>Genes and Genomics</i> , 2019, 41, 233-240.	0.5	4
49	Novel Discovery of LINE-1 in a Korean Individual by a Target Enrichment Method. <i>Molecules and Cells</i> , 2019, 42, 87-95.	1.0	1
50	Complete genome sequence of uropathogenic <i>Escherichia coli</i> isolate UPEC 26-1. <i>Genes and Genomics</i> , 2018, 40, 643-655.	0.5	3
51	KoVariome: Korean National Standard Reference Variome database of whole genomes with comprehensive SNV, indel, CNV, and SV analyses. <i>Scientific Reports</i> , 2018, 8, 5677.	1.6	39
52	In vivo evidence on the functional variation within fatty acid synthase gene associated with lipid metabolism in bovine longissimus dorsi muscle tissue. <i>Genes and Genomics</i> , 2018, 40, 289-294.	0.5	6
53	Rapid and sensitive detection of <i>Salmonella</i> based on microfluidic enrichment with a label-free nanobiosensing platform. <i>Sensors and Actuators B: Chemical</i> , 2018, 262, 588-594.	4.0	32
54	Virulence properties of uropathogenic <i>Escherichia coli</i> isolated from children with urinary tract infection in Korea. <i>Genes and Genomics</i> , 2018, 40, 625-634.	0.5	5

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55	An efficient and tunable parameter to improve variant calling for whole genome and exome sequencing data. <i>Genes and Genomics</i> , 2018, 40, 39-47.	0.5	4
56	Temperature-dependent immune response of olive flounder ( <i>Paralichthys olivaceus</i> ) infected with viral hemorrhagic septicemia virus (VHSV). <i>Genes and Genomics</i> , 2018, 40, 315-320.	0.5	12
57	Accurate, predictable, repeatable micro-assembly technology for polymer, microfluidic modules. <i>Sensors and Actuators B: Chemical</i> , 2018, 254, 1249-1258.	4.0	15
58	Characterization of five complete <i>Cyrtodactylus</i> mitogenome structures reveals low structural diversity and conservation of repeated sequences in the lineage. <i>PeerJ</i> , 2018, 6, e6121.	0.9	5
59	A Simple Guideline to Assess the Characteristics of RNA-Seq Data. <i>BioMed Research International</i> , 2018, 2018, 1-9.	0.9	32
60	Mobile elements contribute to the uniqueness of human genome with 15,000 human-specific insertions and 14ÅMbp sequence increase. <i>DNA Research</i> , 2018, 25, 521-533.	1.5	45
61	Superior single nucleotide polymorphisms that contribute to two main routes of the fatty acid synthesis pathway in Korean cattle. <i>Genes and Genomics</i> , 2018, 40, 945-954.	0.5	1
62	Simple and Low-Cost Sampling of Cell-Free Nucleic Acids from Blood Plasma for Rapid and Sensitive Detection of Circulating Tumor DNA. <i>Advanced Science</i> , 2018, 5, 1800614.	5.6	52
63	A case of interdigitating dendritic cell sarcoma studied by whole-exome sequencing. <i>Genes and Genomics</i> , 2018, 40, 1279-1285.	0.5	4
64	MicroRNAs in Autoimmune Sjögren's Syndrome. <i>Genomics and Informatics</i> , 2018, 16, e19.	0.4	17
65	Chicken ( <i>Gallus gallus</i> ) endogenous retrovirus generates genomic variations in the chicken genome. <i>Mobile DNA</i> , 2017, 8, 2.	1.3	27
66	The Whole-Genome and Transcriptome of the Manila Clam ( <i>Ruditapes philippinarum</i> ). <i>Genome Biology and Evolution</i> , 2017, 9, 1487-1498.	1.1	75
67	Structural variations generated by simian foamy virus-like (SFV) in <i>Crocodylus siamensis</i> . <i>Genes and Genomics</i> , 2017, 39, 1129-1138.	0.5	0
68	Whole-exome sequencing in Tricho-rhino-phalangeal syndrome (TRPS) type I in a Korean family. <i>Genes and Genomics</i> , 2017, 39, 417-422.	0.5	1
69	Targeted next-generation sequencing for identifying genes related to horse temperament. <i>Genes and Genomics</i> , 2017, 39, 1325-1333.	0.5	7
70	Comprehensive Transcriptome Profiling of Balding and Non-Balding Scalps in Trichorhinophalangeal Syndrome Type I Patient. <i>Annals of Dermatology</i> , 2017, 29, 597.	0.3	11
71	Human Primary Epithelial Cells Acquire an Epithelial-Mesenchymal-Transition Phenotype during Long-Term Infection by the Oral Opportunistic Pathogen, <i>Porphyromonas gingivalis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 493.	1.8	81
72	Structural Variation of <i>Alu</i> Element and Human Disease. <i>Genomics and Informatics</i> , 2016, 14, 70.	0.4	76

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73	A Genome-Wide Methylation Approach Identifies a New Hypermethylated Gene Panel in Ulcerative Colitis. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1291.	1.8	29
74	An adaptive detection method for fetal chromosomal aneuploidy using cell-free DNA from 447 Korean women. <i>BMC Medical Genomics</i> , 2016, 9, 61.	0.7	10
75	Modulation of LINE-1 retrotransposition by a human SAMHD1 polymorphism. <i>Virology Reports</i> , 2016, 6, 53-60.	0.4	10
76	Comparison of two high-throughput semiconductor chip sequencing platforms in noninvasive prenatal testing for Down syndrome in early pregnancy. <i>BMC Medical Genomics</i> , 2016, 9, 22.	0.7	9
77	Analysis of L1-chimeric transcripts derived from bidirectional promoter of human-specific L1. <i>Genes and Genomics</i> , 2016, 38, 69-79.	0.5	3
78	Whole Genome Re-Sequencing of Three Domesticated Chicken Breeds. <i>Zoological Science</i> , 2016, 33, 73.	0.3	12
79	Identification of transposable element-mediated deletions in 27 Korean individuals based on whole genome sequencing data. <i>Genes and Genomics</i> , 2016, 38, 179-192.	0.5	1
80	Relationship between Single Nucleotide Polymorphisms in the Peroxisome Proliferator-Activated Receptor Gamma Gene and Fatty Acid Composition in Korean Native Cattle. <i>Asian-Australasian Journal of Animal Sciences</i> , 2016, 29, 184-194.	2.4	3
81	Mutational Analysis of Extranodal NK/T-Cell Lymphoma Using Targeted Sequencing with a Comprehensive Cancer Panel. <i>Genomics and Informatics</i> , 2016, 14, 78.	0.4	17
82	The first whole genome and transcriptome of the cinereous vulture reveals adaptation in the gastric and immune defense systems and possible convergent evolution between the Old and New World vultures. <i>Genome Biology</i> , 2015, 16, 215.	3.8	41
83	Dynamic changes in host gene expression associated with H5N8 avian influenza virus infection in mice. <i>Scientific Reports</i> , 2015, 5, 16512.	1.6	40
84	Meeting report: The biology of genomes and proteomes. <i>Genes and Genomics</i> , 2015, 37, 567-570.	0.5	0
85	Evolutionary fate of SVA2 elements in primate genomes. <i>Genes and Genomics</i> , 2015, 37, 153-159.	0.5	1
86	Transposable element-driven transcript diversification and its relevance to genetic disorders. <i>Gene</i> , 2015, 558, 187-194.	1.0	21
87	An automated analysis pipeline for a large set of ChIP-seq data: AutoChIP. <i>Genes and Genomics</i> , 2015, 37, 305-311.	0.5	2
88	Gene structure variation in segmental duplication block C of human chromosome 7q 11.23 during primate evolution. <i>Gene</i> , 2015, 573, 285-295.	1.0	2
89	Genome-Wide Analysis of DNA Methylation before and after Exercise in the Thoroughbred Horse with MeDIP-Seq. <i>Molecules and Cells</i> , 2015, 38, 210-220.	1.0	36
90	Simple Method for Markerless Gene Deletion in Multidrug-Resistant <i>Acinetobacter baumannii</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 3357-3368.	1.4	73

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91	Genome-wide target site triplication of Alu elements in the human genome. <i>Gene</i> , 2015, 561, 283-291.	1.0	5
92	Identification and expression analysis of human endogenous retrovirus Y (HERV-Y) in various human tissues. <i>Archives of Virology</i> , 2015, 160, 2161-2168.	0.9	2
93	Identification of human-specific AluS elements through comparative genomics. <i>Gene</i> , 2015, 555, 208-216.	1.0	5
94	TE composition of human long noncoding RNAs and their expression patterns in human tissues. <i>Genes and Genomics</i> , 2015, 37, 87-95.	0.5	6
95	BLAT-Based Comparative Analysis for Transposable Elements: BLATCAT. <i>BioMed Research International</i> , 2014, 2014, 1-7.	0.9	0
96	Genome-Wide Copy Number Variation Analysis Identifies Deletion Variants Associated With Ankylosing Spondylitis. <i>Arthritis and Rheumatology</i> , 2014, 66, 2103-2112.	2.9	29
97	Endogenous retrovirus-mediated genomic variations in chimpanzees. <i>Mobile Genetic Elements</i> , 2014, 4, 1-4.	1.8	7
98	<i>Mucilaginibacter koreensis</i> sp. nov., isolated from leaf mould. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2274-2279.	0.8	16
99	Genome-wide analysis of DNA methylation patterns in horse. <i>BMC Genomics</i> , 2014, 15, 598.	1.2	33
100	Comparative study of different molecular methods for typing of <i>Acinetobacter baumannii</i> clinical isolates from University Hospitals. <i>Genes and Genomics</i> , 2014, 36, 551-558.	0.5	1
101	Whole genome sequence and analysis of the Marwari horse breed and its genetic origin. <i>BMC Genomics</i> , 2014, 15, S4.	1.2	30
102	Chimpanzee-Specific Endogenous Retrovirus Generates Genomic Variations in the Chimpanzee Genome. <i>PLoS ONE</i> , 2014, 9, e101195.	1.1	10
103	Identification and characterization of transposable elements inserted into the coding sequences of horse genes. <i>Genes and Genomics</i> , 2013, 35, 483-489.	0.5	17
104	DNA methylation of mobile genetic elements in human cancers. <i>Genes and Genomics</i> , 2013, 35, 265-271.	0.5	4
105	Meeting report: Frontiers in genetics: genomics and epigenomics. <i>Genes and Genomics</i> , 2013, 35, 559-562.	0.5	0
106	Co-existence of bla OXA-23 and armA in multidrug-resistant <i>Acinetobacter baumannii</i> isolated from a hospital in South Korea. <i>Journal of Medical Microbiology</i> , 2013, 62, 836-844.	0.7	14
107	Human-Specific HERV-K Insertion Causes Genomic Variations in the Human Genome. <i>PLoS ONE</i> , 2013, 8, e60605.	1.1	62
108	The novel MER transposon-derived miRNAs in human genome. <i>Gene</i> , 2013, 512, 422-428.	1.0	25

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109	Phylogeny of Flavobacteria Group Isolated from Freshwater Using Multilocus Sequencing Analysis. <i>Genomics and Informatics</i> , 2013, 11, 272.	0.4	6
110	Persistence of Hölder continuity for non-local integro-differential equations. <i>Discrete and Continuous Dynamical Systems</i> , 2013, 33, 1741-1771.	0.5	0
111	UniPrimer: A Web-Based Primer Design Tool for Comparative Analyses of Primate Genomes. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-8.	2.0	4
112	High Levels of Sequence Diversity in the 5' UTRs of Human-Specific L1 Elements. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-8.	2.0	11
113	Human Genomic Deletions Generated by SVA-Associated Events. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-7.	2.0	14
114	mRNA sequence analysis and quantitative expression of the ADAMTS4 gene in the thoroughbred horse. <i>Genes and Genomics</i> , 2012, 34, 441-445.	0.5	3
115	<i>Flavobacterium dankookense</i> sp. nov., isolated from a freshwater reservoir, and emended descriptions of <i>Flavobacterium cheonanense</i> , <i>F. chungnamense</i> , <i>F. koreense</i> and <i>F. aquatile</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 2378-2382.	0.8	38
116	Identification of ORF sequences and exercise-induced expression change in thoroughbred horse OXCT1 gene. <i>Gene</i> , 2012, 496, 45-48.	1.0	7
117	First case of <i>Nocardia nova</i> spinal abscess in an immunocompetent patient. <i>Brazilian Journal of Infectious Diseases</i> , 2012, 16, 196-199.	0.3	9
118	Transposable Elements: No More 'Junk DNA'. <i>Genomics and Informatics</i> , 2012, 10, 226.	0.4	51
119	First case of <i>Nocardia nova</i> spinal abscess in an immunocompetent patient. <i>Brazilian Journal of Infectious Diseases</i> , 2012, 16, 196-199.	0.3	3
120	In vitro CpG methylation and garcinol reduce PERV LTR promoter activity. <i>Genes and Genomics</i> , 2012, 34, 217-222.	0.5	2
121	<i>Arenimonas aquaticum</i> sp. nov., a member of the gammaproteobacterium, isolated from a freshwater reservoir. <i>Journal of Microbiology</i> , 2012, 50, 354-358.	1.3	11
122	Quantitative analysis of transcript variants of CHM gene containing LTR12C element in humans. <i>Gene</i> , 2011, 489, 1-5.	1.0	11
123	Characterization of <i>Acinetobacter baumannii</i> Co-producing Carbapenemases OXA-23 and OXA-66, and armA16S Ribosomal RNA Methylase at a University Hospital in South Korea. <i>Taehan Hmsang Misaengmul Hakhoe Chi = Korean Journal of Clinical Microbiology</i> , 2011, 14, 67.	0.5	3
124	Evolutionary diversification of DYX1C1 transcripts via an HERV-H LTR integration event. <i>Genes and Genetic Systems</i> , 2011, 86, 277-284.	0.2	1
125	A vertically stacked, polymer, microfluidic point mutation analyzer: Rapid high accuracy detection of low-abundance K-ras mutations. <i>Analytical Biochemistry</i> , 2011, 417, 211-219.	1.1	18
126	Transcriptional variations mediated by an alternative promoter of the FPR3 gene. <i>Mammalian Genome</i> , 2011, 22, 621-633.	1.0	5



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127	Quantitative analysis of the HERV pol gene in human tissues. <i>Genes and Genomics</i> , 2011, 33, 439-443.	0.5	3
128	Development of GEBRET: a web-based analysis tool for retroelements in primate genomes. <i>Genes and Genomics</i> , 2011, 33, 679-684.	0.5	2
129	Alu pair exclusions in the human genome. <i>Mobile DNA</i> , 2011, 2, 10.	1.3	15
130	Identification of a Genomic Reservoir for New TRIM Genes in Primate Genomes. <i>PLoS Genetics</i> , 2011, 7, e1002388.	1.5	98
131	Genomic Structure and Expression Analyses of the PYGM Gene in the Thoroughbred Horse. <i>Zoological Science</i> , 2011, 28, 276.	0.3	4
132	Laboratory Methods for the Analysis of Primate Mobile Elements. <i>Methods in Molecular Biology</i> , 2010, 628, 153-179.	0.4	2
133	Distribution of Four HIV Type 1-Resistance Polymorphisms (CCR5-Δ32, CCR5-m303, CCR2-64I, and SDF1-3'ΔA) in the Bahraini Population. <i>AIDS Research and Human Retroviruses</i> , 2009, 25, 973-977.	0.5	22
134	Allele frequencies of the human platelet antigen-1 in the Egyptian population. <i>BMC Research Notes</i> , 2009, 2, 90.	0.6	7
135	Phylogeny of the macaques (Cercopithecidae: Macaca) based on Alu elements. <i>Gene</i> , 2009, 448, 242-249.	1.0	113
136	A multi-function, microfluidic module for mutation detection. , 2009, , .		2
137	Mobile elements create structural variation: Analysis of a complete human genome. <i>Genome Research</i> , 2009, 19, 1516-1526.	2.4	267
138	L1 recombination-associated deletions generate human genomic variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 19366-19371.	3.3	127
139	Chromosomal Inversions between Human and Chimpanzee Lineages Caused by Retrotransposons. <i>PLoS ONE</i> , 2008, 3, e4047.	1.1	84
140	Alu Recombination-Mediated Structural Deletions in the Chimpanzee Genome. <i>PLoS Genetics</i> , 2007, 3, e184.	1.5	94
141	Mobile DNA in Old World Monkeys: A Glimpse Through the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 238-240.	6.0	116
142	Endonuclease-independent insertion provides an alternative pathway for L1 retrotransposition in the human genome. <i>Nucleic Acids Research</i> , 2007, 35, 3741-3751.	6.5	68
143	Different evolutionary fates of recently integrated human and chimpanzee LINE-1 retrotransposons. <i>Gene</i> , 2007, 390, 18-27.	1.0	65
144	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283

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145	Human Genomic Deletions Mediated by Recombination between Alu Elements. <i>American Journal of Human Genetics</i> , 2006, 79, 41-53.	2.6	289
146	Genomic rearrangements by LINE-1 insertion-mediated deletion in the human and chimpanzee lineages. <i>Nucleic Acids Research</i> , 2005, 33, 4040-4052.	6.5	127
147	A mobile element based phylogeny of Old World monkeys. <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 872-880.	1.2	90
148	Under the genomic radar: The Stealth model of Alu amplification. <i>Genome Research</i> , 2005, 15, 655-664.	2.4	65
149	SVA Elements: A Hominid-specific Retroposon Family. <i>Journal of Molecular Biology</i> , 2005, 354, 994-1007.	2.0	319
150	Imipenem-resistant <i>Achromobacter xylosoxidans</i> carrying blaVIM-2-containing class 1 integron. <i>Diagnostic Microbiology and Infectious Disease</i> , 2005, 53, 215-220.	0.8	26
151	Alu Element Mutation Spectra: Molecular Clocks and the Effect of DNA Methylation. <i>Journal of Molecular Biology</i> , 2004, 344, 675-682.	2.0	78