

Richard Reinhardt

List of Publications by Year in descending order

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284
papers

52,752
citations

4955

84
h-index

1421

221
g-index

289
all docs

289
docs citations

289
times ranked

57263
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
2	Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. <i>Nature</i> , 2012, 488, 91-95.	13.7	2,127
3	The Genome of the Kinetoplastid Parasite, <i>Leishmania major</i> . <i>Science</i> , 2005, 309, 436-442.	6.0	1,237
4	The primary transcriptome of the major human pathogen <i>Helicobacter pylori</i> . <i>Nature</i> , 2010, 464, 250-255.	13.7	1,115
5	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005, 434, 325-337.	13.7	985
6	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012, 44, 1060-1065.	9.4	840
7	The genome sequence of Atlantic cod reveals a unique immune system. <i>Nature</i> , 2011, 477, 207-210.	13.7	730
8	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. <i>Science</i> , 2010, 330, 1543-1546.	6.0	725
9	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	13.7	657
10	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014, 505, 546-549.	13.7	569
11	Mutations in <i>DNAH5</i> cause primary ciliary dyskinesia and randomization of left-right asymmetry. <i>Nature Genetics</i> , 2002, 30, 143-144.	9.4	496
12	Dual RNA-seq unveils noncoding RNA functions in host-pathogen interactions. <i>Nature</i> , 2016, 529, 496-501.	13.7	450
13	European sea bass genome and its variation provide insights into adaptation to euryhalinity and speciation. <i>Nature Communications</i> , 2014, 5, 5770.	5.8	382
14	Nephrocystin-5, a ciliary IQ domain protein, is mutated in Senior-Loken syndrome and interacts with RPGR and calmodulin. <i>Nature Genetics</i> , 2005, 37, 282-288.	9.4	367
15	An atlas of Hfq-bound transcripts reveals 3' UTRs as a genomic reservoir of regulatory small RNAs. <i>EMBO Journal</i> , 2012, 31, 4005-4019.	3.5	354
16	Mutations in the <i>JARID1C</i> Gene, Which Is Involved in Transcriptional Regulation and Chromatin Remodeling, Cause X-Linked Mental Retardation. <i>American Journal of Human Genetics</i> , 2005, 76, 227-236.	2.6	349
17	Mutations in a novel gene, <i>NPHP3</i> , cause adolescent nephronophthisis, tapeto-retinal degeneration and hepatic fibrosis. <i>Nature Genetics</i> , 2003, 34, 455-459.	9.4	345
18	A conspicuous nickel protein in microbial mats that oxidize methane anaerobically. <i>Nature</i> , 2003, 426, 878-881.	13.7	344

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19	Ktu/PF13 is required for cytoplasmic pre-assembly of axonemal dyneins. <i>Nature</i> , 2008, 456, 611-616.	13.7	342
20	Whole genome analysis of the marine Bacteroidetes 'Gramella forsetii' reveals adaptations to degradation of polymeric organic matter. <i>Environmental Microbiology</i> , 2006, 8, 2201-2213.	1.8	334
21	Chromatin methylation activity of Dnmt3a and Dnmt3a/3L is guided by interaction of the ADD domain with the histone H3 tail. <i>Nucleic Acids Research</i> , 2010, 38, 4246-4253.	6.5	330
22	Biochemical and Proteomic Analysis of the Magnetosome Membrane in <i>Magnetospirillum gryphiswaldense</i> . <i>Applied and Environmental Microbiology</i> , 2004, 70, 1040-1050.	1.4	318
23	Global <i>scp</i> RNA recognition patterns of post-transcriptional regulators Hfq and CsrA revealed by <i>scp</i> UV crosslinking <i>in vivo</i> . <i>EMBO Journal</i> , 2016, 35, 991-1011.	3.5	296
24	DNAH5 Mutations Are a Common Cause of Primary Ciliary Dyskinesia with Outer Dynein Arm Defects. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2006, 174, 120-126.	2.5	294
25	The coiled-coil domain containing protein CCDC40 is essential for motile cilia function and left-right axis formation. <i>Nature Genetics</i> , 2011, 43, 79-84.	9.4	292
26	Hox cluster disintegration with persistent anteroposterior order of expression in <i>Oikopleura dioica</i> . <i>Nature</i> , 2004, 431, 67-71.	13.7	286
27	Genome sequence of the chlorinated compound-respiring bacterium <i>Dehalococcoides</i> species strain CBDB1. <i>Nature Biotechnology</i> , 2005, 23, 1269-1273.	9.4	277
28	Human box C/D snoRNAs with miRNA like functions: expanding the range of regulatory RNAs. <i>Nucleic Acids Research</i> , 2011, 39, 675-686.	6.5	276
29	Analysis of the host microRNA response to <i>Salmonella</i> uncovers the control of major cytokines by the <i>let-7</i> family. <i>EMBO Journal</i> , 2011, 30, 1977-1989.	3.5	270
30	Grad-seq guides the discovery of ProQ as a major small RNA-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11591-11596.	3.3	267
31	The genome sequence of an anaerobic aromatic-degrading denitrifying bacterium, strain EbN1. <i>Archives of Microbiology</i> , 2005, 183, 27-36.	1.0	266
32	Classification and Identification of Bacteria by Mass Spectrometry and Computational Analysis. <i>PLoS ONE</i> , 2008, 3, e2843.	1.1	261
33	High-Resolution Transcriptome Maps Reveal Strain-Specific Regulatory Features of Multiple <i>Campylobacter jejuni</i> Isolates. <i>PLoS Genetics</i> , 2013, 9, e1003495.	1.5	260
34	Recessive HYDIN Mutations Cause Primary Ciliary Dyskinesia without Randomization of Left-Right Body Asymmetry. <i>American Journal of Human Genetics</i> , 2012, 91, 672-684.	2.6	252
35	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. <i>Science</i> , 2010, 330, 1381-1385.	6.0	251
36	<i>In vivo</i> Cleavage Map Illuminates the Central Role of RNase E in Coding and Non-coding RNA Pathways. <i>Molecular Cell</i> , 2017, 65, 39-51.	4.5	250

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37	DNAI2 Mutations Cause Primary Ciliary Dyskinesia with Defects in the Outer Dynein Arm. American Journal of Human Genetics, 2008, 83, 547-558.	2.6	242
38	Parallel Evolution of Nacre Building Gene Sets in Molluscs. Molecular Biology and Evolution, 2010, 27, 591-608.	3.5	239
39	A Hypervariable 130-Kilobase Genomic Region of Magnetospirillum gryphiswaldense Comprises a Magnetosome Island Which Undergoes Frequent Rearrangements during Stationary Growth. Journal of Bacteriology, 2005, 187, 7176-7184.	1.0	235
40	<i>Helicobacter pylori</i> genome evolution during human infection. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5033-5038.	3.3	235
41	CCDC103 mutations cause primary ciliary dyskinesia by disrupting assembly of ciliary dynein arms. Nature Genetics, 2012, 44, 714-719.	9.4	228
42	Efficient targeted DNA methylation with chimeric dCas9-Dnmt3L methyltransferase. Nucleic Acids Research, 2017, 45, 1703-1713.	6.5	224
43	The Genome of the Alga-Associated Marine Flavobacterium Formosa agariphila KMM 3901 ^T Reveals a Broad Potential for Degradation of Algal Polysaccharides. Applied and Environmental Microbiology, 2013, 79, 6813-6822.	1.4	222
44	Dynamic link of DNA demethylation, DNA strand breaks and repair in mouse zygotes. EMBO Journal, 2010, 29, 1877-1888.	3.5	221
45	Metagenome and mRNA expression analyses of anaerobic methanotrophic archaea of the ANME-1 group. Environmental Microbiology, 2010, 12, 422-439.	1.8	221
46	BISMA - Fast and accurate bisulfite sequencing data analysis of individual clones from unique and repetitive sequences. BMC Bioinformatics, 2010, 11, 230.	1.2	215
47	The linear chromosome of the plant-pathogenic mycoplasma 'Candidatus Phytoplasma mali'. BMC Genomics, 2008, 9, 306.	1.2	207
48	Deletions and Point Mutations of LRRC50 Cause Primary Ciliary Dyskinesia Due to Dynein Arm Defects. American Journal of Human Genetics, 2009, 85, 883-889.	2.6	207
49	Deep sequencing-based discovery of the Chlamydia trachomatis transcriptome. Nucleic Acids Research, 2010, 38, 868-877.	6.5	206
50	Characterization of a Spontaneous Nonmagnetic Mutant of Magnetospirillum gryphiswaldense Reveals a Large Deletion Comprising a Putative Magnetosome Island. Journal of Bacteriology, 2003, 185, 5779-5790.	1.0	200
51	Accuracy of DNA methylation pattern preservation by the Dnmt1 methyltransferase. Nucleic Acids Research, 2006, 34, 1182-1188.	6.5	186
52	Anaerobic degradation of naphthalene and 2-methylnaphthalene by strains of marine sulfate-reducing bacteria. Environmental Microbiology, 2009, 11, 209-219.	1.8	177
53	Genome of Rice Cluster I Archaea—the Key Methane Producers in the Rice Rhizosphere. Science, 2006, 313, 370-372.	6.0	175
54	SNP and haplotype mapping for genetic analysis in the rat. Nature Genetics, 2008, 40, 560-566.	9.4	172

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55	Genomic Organization of the Human <i>PEX</i> Gene Mutated in X-Linked Dominant Hypophosphatemic Rickets. <i>Genome Research</i> , 1997, 7, 573-585.	2.4	159
56	Comparative Genome Analysis of Four Magnetotactic Bacteria Reveals a Complex Set of Group-Specific Genes Implicated in Magnetosome Biomineralization and Function. <i>Journal of Bacteriology</i> , 2007, 189, 4899-4910.	1.0	159
57	Miniature Genome in the Marine Chordate <i>Oikopleura dioica</i> . <i>Science</i> , 2001, 294, 2506-2506.	6.0	157
58	DNA Methylation Analysis of Chromosome 21 Gene Promoters at Single Base Pair and Single Allele Resolution. <i>PLoS Genetics</i> , 2009, 5, e1000438.	1.5	143
59	Targeted Methylation and Gene Silencing of VEGF-A in Human Cells by Using a Designed Dnmt3a-Dnmt3L Single-Chain Fusion Protein with Increased DNA Methylation Activity. <i>Journal of Molecular Biology</i> , 2013, 425, 479-491.	2.0	138
60	Increasing genomic information in bivalves through new EST collections in four species: Development of new genetic markers for environmental studies and genome evolution. <i>Gene</i> , 2008, 408, 27-36.	1.0	132
61	Alkane degradation under anoxic conditions by a nitrate-reducing bacterium with possible involvement of the electron acceptor in substrate activation. <i>Environmental Microbiology Reports</i> , 2011, 3, 125-135.	1.0	129
62	High-throughput polymorphism detection and genotyping in <i>Brassica napus</i> using next-generation RAD sequencing. <i>BMC Genomics</i> , 2012, 13, 281.	1.2	129
63	Generation and analysis of a 29,745 unique Expressed Sequence Tags from the Pacific oyster (<i>Crassostrea gigas</i>) assembled into a publicly accessible database: the GigasDatabase. <i>BMC Genomics</i> , 2009, 10, 341.	1.2	127
64	<i>Roseobacter</i> clade bacteria are abundant in coastal sediments and encode a novel combination of sulfur oxidation genes. <i>ISME Journal</i> , 2012, 6, 2178-2187.	4.4	125
65	Novel JARID1C/SMCX mutations in patients with X-linked mental retardation. <i>Human Mutation</i> , 2006, 27, 389-389.	1.1	120
66	Transcriptome sequencing and microarray development for the Manila clam, <i>Ruditapes philippinarum</i> : genomic tools for environmental monitoring. <i>BMC Genomics</i> , 2011, 12, 234.	1.2	120
67	Genes involved in the anaerobic degradation of ethylbenzene in a denitrifying bacterium, strain EbN1. <i>Archives of Microbiology</i> , 2002, 178, 506-516.	1.0	118
68	Substrate-Dependent Regulation of Anaerobic Degradation Pathways for Toluene and Ethylbenzene in a Denitrifying Bacterium, Strain EbN1. <i>Journal of Bacteriology</i> , 2005, 187, 1493-1503.	1.0	118
69	Conservation of proteobacterial magnetosome genes and structures in an uncultivated member of the deep-branching <i>Nitrospira</i> phylum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1134-1139.	3.3	115
70	Genome sequence and functional genomic analysis of the oil-degrading bacterium <i>Oleispira antarctica</i> . <i>Nature Communications</i> , 2013, 4, 2156.	5.8	115
71	Comparative Genomic Analysis of Fruiting Body Formation in Myxococcales. <i>Molecular Biology and Evolution</i> , 2011, 28, 1083-1097.	3.5	111
72	Formation of nucleoprotein filaments by mammalian DNA methyltransferase Dnmt3a in complex with regulator Dnmt3L. <i>Nucleic Acids Research</i> , 2008, 36, 6656-6663.	6.5	109

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73	The Genomic Sequence and Comparative Analysis of the Rat Major Histocompatibility Complex. <i>Genome Research</i> , 2004, 14, 631-639.	2.4	108
74	Spliced-Leader RNA trans Splicing in a Chordate, <i>Oikopleura dioica</i> , with a Compact Genome. <i>Molecular and Cellular Biology</i> , 2004, 24, 7795-7805.	1.1	104
75	A de novo assembly of the newt transcriptome combined with proteomic validation identifies new protein families expressed during tissue regeneration. <i>Genome Biology</i> , 2013, 14, R16.	13.9	104
76	Natural mutations in a <i>Staphylococcus aureus</i> virulence regulator attenuate cytotoxicity but permit bacteremia and abscess formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3101-10.	3.3	103
77	Genomic insights into the physiology and ecology of the marine filamentous cyanobacterium <i>Lyngbya majuscula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 8815-8820.	3.3	99
78	Comparative genomic analysis of magnetotactic bacteria from the <i>Deltaproteobacteria</i> provides new insights into magnetite and greigite magnetosome genes required for magnetotaxis. <i>Environmental Microbiology</i> , 2013, 15, 2712-2735.	1.8	99
79	Comparative analysis of magnetosome gene clusters in magnetotactic bacteria provides further evidence for horizontal gene transfer. <i>Environmental Microbiology</i> , 2009, 11, 1267-1277.	1.8	96
80	Toward Cloning of the Magnetotactic Metagenome: Identification of Magnetosome Island Gene Clusters in Uncultivated Magnetotactic Bacteria from Different Aquatic Sediments. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3972-3979.	1.4	96
81	Complete genome, catabolic subproteomes and key metabolites of <i>Deltaproteobacteria</i> <i>Desulfobacula toluolica</i> , a marine, aromatic compound-degrading, sulfate-reducing bacterium. <i>Environmental Microbiology</i> , 2013, 15, 1334-1355.	1.8	96
82	The CsrA-FlhW network controls polar localization of the dual-function flagellin mRNA in <i>Campylobacter jejuni</i> . <i>Nature Communications</i> , 2016, 7, 11667.	5.8	93
83	EST sequencing of Onychophora and phylogenomic analysis of Metazoa. <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 942-951.	1.2	92
84	Genome comparison of the epiphytic bacteria <i>Erwinia billingiae</i> and <i>E. tasmaniensis</i> with the pear pathogen <i>E. pyrifoliae</i> . <i>BMC Genomics</i> , 2010, 11, 393.	1.2	92
85	ARE ANTIMITOCHONDRIAL ANTIBODIES IN PRIMARY BILIARY CIRRHOSIS INDUCED BY R(ROUGH)-MUTANTS OF ENTEROBACTERIACEAE?. <i>Lancet</i> , The, 1988, 332, 1166-1170.	6.3	90
86	Genes involved in the anaerobic degradation of toluene in a denitrifying bacterium, strain EbN1. <i>Archives of Microbiology</i> , 2004, 181, 182-194.	1.0	90
87	Functional proteomic view of metabolic regulation in <i>Aromatoleum aromaticum</i> strain EbN1. <i>Proteomics</i> , 2007, 7, 2222-2239.	1.3	90
88	Phylogenetic diversity and metagenomics of candidate division OP3. <i>Environmental Microbiology</i> , 2010, 12, 1218-1229.	1.8	90
89	A 454 sequencing approach for large scale phylogenomic analysis of the common emperor scorpion (<i>Pandinus imperator</i>). <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 826-834.	1.2	87
90	The MLL recombinome of adult CD10-negative B-cell precursor acute lymphoblastic leukemia: results from the GMALL study group. <i>Blood</i> , 2009, 113, 4011-4015.	0.6	85

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91	The mouse homeobox gene <i>Not</i> is required for caudal notochord development and affected by the truncate mutation. <i>Genes and Development</i> , 2004, 18, 1725-1736.	2.7	84
92	Crystal Structure and Enzyme Kinetics of the (S)-Specific 1-Phenylethanol Dehydrogenase of the Denitrifying Bacterium Strain EbN1. <i>Biochemistry</i> , 2006, 45, 82-93.	1.2	84
93	Discovering genes associated with dormancy in the monogonont rotifer <i>Brachionus plicatilis</i> . <i>BMC Genomics</i> , 2009, 10, 108.	1.2	84
94	Genome-wide expression profiling and phenotypic evaluation of European maize inbreds at seedling stage in response to heat stress. <i>BMC Genomics</i> , 2015, 16, 123.	1.2	83
95	Insights into the genomes of archaea mediating the anaerobic oxidation of methane. <i>Environmental Microbiology</i> , 2005, 7, 1937-1951.	1.8	81
96	A global view of the nonprotein-coding transcriptome in <i>Plasmodium falciparum</i> . <i>Nucleic Acids Research</i> , 2010, 38, 608-617.	6.5	80
97	Profiling and Validation of the Circular RNA Repertoire in Adult Murine Hearts. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 216-223.	3.0	79
98	Single-Cell Genome and Group-Specific <i>dsrAB</i> Sequencing Implicate Marine Members of the Class <i>Dehalococcoidia</i> (Phylum <i>Chloroflexi</i>) in Sulfur Cycling. <i>MBio</i> , 2016, 7, .	1.8	78
99	Ribosomal and DNA binding proteins of the thermoacidophilic archaebacterium <i>Sulfolobus acidocaldarius</i> . <i>BBA - Proteins and Proteomics</i> , 1986, 873, 405-413.	2.1	77
100	Allelic polymorphism and site-specific recombination in the <i>opc</i> locus of <i>Neisseria meningitidis</i> . <i>Molecular Microbiology</i> , 1996, 19, 841-856.	1.2	77
101	Non-imprinted allele-specific DNA methylation on human autosomes. <i>Genome Biology</i> , 2009, 10, R138.	13.9	77
102	An Expressed Sequence Tag Analysis of the Intertidal Brown Seaweeds <i>Fucus serratus</i> (L.) and <i>F. vesiculosus</i> (L.) (Heterokontophyta, Phaeophyceae) in Response to Abiotic Stressors. <i>Marine Biotechnology</i> , 2010, 12, 195-213.	1.1	77
103	Targeted epigenome editing of an endogenous locus with chromatin modifiers is not stably maintained. <i>Epigenetics and Chromatin</i> , 2015, 8, 12.	1.8	77
104	Three Novel Species with Peptidoglycan Cell Walls form the New Genus <i>Lacunisphaera</i> gen. nov. in the Family <i>Opiritaceae</i> of the <i>Verrucomicrobial</i> Subdivision 4. <i>Frontiers in Microbiology</i> , 2017, 8, 202.	1.5	75
105	The genome of <i>Erwinia tasmaniensis</i> strain Et1/99, a non-pathogenic bacterium in the genus <i>Erwinia</i> . <i>Environmental Microbiology</i> , 2008, 10, 2211-2222.	1.8	74
106	Transcriptional landscape and essential genes of <i>Neisseria gonorrhoeae</i> . <i>Nucleic Acids Research</i> , 2014, 42, 10579-10595.	6.5	74
107	Post-polyploidisation morphotype diversification associates with gene copy number variation. <i>Scientific Reports</i> , 2017, 7, 41845.	1.6	73
108	Transcriptional activity of paddy soil bacterial communities. <i>Environmental Microbiology</i> , 2009, 11, 960-970.	1.8	72

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109	The transcriptional landscape of <i>Chlamydia pneumoniae</i> . <i>Genome Biology</i> , 2011, 12, R98.	13.9	72
110	H3K14ac is linked to methylation of H3K9 by the triple Tudor domain of SETDB1. <i>Nature Communications</i> , 2017, 8, 2057.	5.8	72
111	Isolation, characterization and microsequence analysis of a small basic methylated DNA-binding protein from the Archaeobacterium, <i>Sulfolobus solfataricus</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1988, 950, 193-203.	2.4	70
112	Complete genome sequence of <i>Desulfocapsa sulfexigens</i> , a marine deltaproteobacterium specialized in disproportionating inorganic sulfur compounds. <i>Standards in Genomic Sciences</i> , 2013, 8, 58-68.	1.5	69
113	A multiplex PCR for improved detection of typical and atypical BCR-ABL fusion transcripts. <i>Leukemia Research</i> , 2008, 32, 579-585.	0.4	67
114	Novel correlations between the genotype and the phenotype of hypertrophic and dilated cardiomyopathy: results from the German Competence Network Heart Failure. <i>European Journal of Heart Failure</i> , 2011, 13, 1185-1192.	2.9	67
115	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of <i>Helicobacter pylori</i> . <i>Genetics</i> , 2015, 200, 947-963.	1.2	65
116	A Novel System of Polymorphic and Diverse NK Cell Receptors in Primates. <i>PLoS Genetics</i> , 2009, 5, e1000688.	1.5	64
117	Retroposed SNOfall—A mammalian-wide comparison of platypus snoRNAs. <i>Genome Research</i> , 2008, 18, 1005-1010.	2.4	62
118	Methylation Markers for the Identification of Body Fluids and Tissues from Forensic Trace Evidence. <i>PLoS ONE</i> , 2016, 11, e0147973.	1.1	62
119	Remodelling of the homeobox gene complement in the tunicate <i>Oikopleura dioica</i> . <i>Current Biology</i> , 2005, 15, R12-R13.	1.8	61
120	Surviving extreme polar winters by desiccation: clues from Arctic springtail (<i>Onychiurus arcticus</i>) EST libraries. <i>BMC Genomics</i> , 2007, 8, 475.	1.2	61
121	DNA Methylation Analysis by Bisulfite Conversion, Cloning, and Sequencing of Individual Clones. <i>Methods in Molecular Biology</i> , 2009, 507, 177-187.	0.4	61
122	Mutational analysis of the NPHP4 gene in 250 patients with nephronophthisis. <i>Human Mutation</i> , 2005, 25, 411-411.	1.1	60
123	The European sea bass <i>Dicentrarchus labrax</i> genome puzzle: comparative BAC-mapping and low coverage shotgun sequencing. <i>BMC Genomics</i> , 2010, 11, 68.	1.2	60
124	Anaerobic Activation of <i>p</i> -Cymene in Denitrifying Betaproteobacteria: Methyl Group Hydroxylation versus Addition to Fumarate. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7592-7603.	1.4	60
125	Targeted Methylation of the Epithelial Cell Adhesion Molecule (EpCAM) Promoter to Silence Its Expression in Ovarian Cancer Cells. <i>PLoS ONE</i> , 2014, 9, e87703.	1.1	60
126	DNA methylation in the IGF2 intragenic DMR is re-established in a sex-specific manner in bovine blastocysts after somatic cloning. <i>Genomics</i> , 2009, 94, 63-69.	1.3	59

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127	Identification of a <i>Leishmania infantum</i> gene mediating resistance to ϵ and SbIII. <i>International Journal for Parasitology</i> , 2008, 38, 1411-1423.	1.3	57
128	A second generation genetic map of the bumblebee <i>Bombus terrestris</i> (Linnaeus, 1758) reveals slow genome and chromosome evolution in the Apidae. <i>BMC Genomics</i> , 2011, 12, 48.	1.2	57
129	High-resolution array comparative genomic hybridization of single micrometastatic tumor cells. <i>Nucleic Acids Research</i> , 2008, 36, e39.	6.5	56
130	Bisulfite sequencing Data Presentation and Compilation (BDPC) web server--a useful tool for DNA methylation analysis. <i>Nucleic Acids Research</i> , 2008, 36, e34-e34.	6.5	56
131	The bovine IGF2 gene is differentially methylated in oocyte and sperm DNA. <i>Genomics</i> , 2006, 88, 222-229.	1.3	55
132	Disruption and pseudoautosomal localization of the major histocompatibility complex in monotremes. <i>Genome Biology</i> , 2007, 8, R175.	13.9	55
133	Comparative Analysis of Expressed Sequence Tag (EST) Libraries in the Seagrass <i>Zostera marina</i> Subjected to Temperature Stress. <i>Marine Biotechnology</i> , 2008, 10, 297-309.	1.1	55
134	Development and validation of a gene expression oligo microarray for the gilthead sea bream (<i>Sparus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.2	55
135	Complete Genome Sequence of <i>Methylocystis</i> sp. Strain SC2, an Aerobic Methanotroph with High-Affinity Methane Oxidation Potential. <i>Journal of Bacteriology</i> , 2012, 194, 6008-6009.	1.0	55
136	The amino acid sequence of a small DNA binding protein from the archaeobacterium <i>Sulfolobus solfataricus</i> . <i>FEBS Letters</i> , 1984, 176, 176-178.	1.3	54
137	NUP214-ABL1 in adult T-ALL: the GIMALL study group experience. <i>Blood</i> , 2006, 108, 3556-3559.	0.6	54
138	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006, 440, 1194-1198.	13.7	53
139	Identification and Analysis of Axonemal Dynein Light Chain 1 in Primary Ciliary Dyskinesia Patients. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2005, 33, 41-47.	1.4	52
140	Profiling of infection specific mRNA transcripts of the European seabass <i>Dicentrarchus labrax</i> . <i>BMC Genomics</i> , 2009, 10, 157.	1.2	52
141	Stress response in tardigrades: differential gene expression of molecular chaperones. <i>Cell Stress and Chaperones</i> , 2010, 15, 423-430.	1.2	52
142	Application of histone modification-specific interaction domains as an alternative to antibodies. <i>Genome Research</i> , 2014, 24, 1842-1853.	2.4	52
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281	Isolation and characterization of Rac1 pseudogenes (~ 1 Rac1 ~ 4 Rac1) in the human genome. <i>Gene</i> , 2004, 341, 189-197.	1.0	2
282	Analyses of the <i>vrl</i> Gene Cluster in <i>Desulfococcus multivorans</i> ; Homologous to the Virulence-Associated Locus of the Ovine Footrot Pathogen <i>Dichelobacter nodosus</i> ; Strain A198. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2007, 13, 156-164.	1.0	1
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