

Richard Reinhardt

List of Publications by Year in descending order

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284
papers

52,752
citations

4960

84
h-index

1424

221
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289
all docs

289
docs citations

289
times ranked

57263
citing authors

#	ARTICLE	IF	CITATIONS
1	Complex and flexible catabolism in <i>Aromatoleum aromaticum</i> . <i>Environmental Microbiology</i> , 2022, 24, 3195-3211.	3.8	4
2	Complete Genomes of the Anaerobic Degradation Specialists <i>Aromatoleum petrolei</i> and <i>Aromatoleum bremense</i> . <i>Microbial Physiology</i> , 2021, 31, 16-35.	2.4	6
3	Genome-wide analysis of European sea bass provides insights into the evolution and functions of single-exon genes. <i>Ecology and Evolution</i> , 2021, 11, 6546-6557.	1.9	0
4	The temperature-regulated DEAD-box RNA helicase CrhR interactome: autoregulation and photosynthesis-related transcripts. <i>Journal of Experimental Botany</i> , 2021, , .	4.8	7
5	Proteogenomic Insights into the Physiology of Marine, Sulfate-Reducing, Filamentous <i>Desulfonema limicola</i> and <i>Desulfonema magnum</i> . <i>Microbial Physiology</i> , 2021, 31, 36-56.	2.4	7
6	SuperSAGE digital expression analysis of differential growth rate in a European sea bass population. <i>Aquaculture and Fisheries</i> , 2019, 4, 17-26.	2.2	5
7	Interplay and Targetome of the Two Conserved Cyanobacterial sRNAs Yfr1 and Yfr2 in <i>Prochlorococcus</i> MED4. <i>Scientific Reports</i> , 2019, 9, 14331.	3.3	10
8	The Systems Architecture of Molecular Memory in Poplar after Abiotic Stress. <i>Plant Cell</i> , 2019, 31, 346-367.	6.6	29
9	Identification of the DNA methyltransferases establishing the methylome of the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>DNA Research</i> , 2018, 25, 343-352.	3.4	38
10	The DNMT3A R882H mutant displays altered flanking sequence preferences. <i>Nucleic Acids Research</i> , 2018, 46, 3130-3139.	14.5	44
11	Benefit from decline: the primary transcriptome of <i>Alteromonas macleodii</i> str. Te101 during <i>Trichodesmium</i> demise. <i>ISME Journal</i> , 2018, 12, 981-996.	9.8	30
12	Single molecule real time sequencing in ADTKD-MUC1 allows complete assembly of the VNTR and exact positioning of causative mutations. <i>Scientific Reports</i> , 2018, 8, 4170.	3.3	40
13	In Vivo Cleavage Map Illuminates the Central Role of RNase E in Coding and Non-coding RNA Pathways. <i>Molecular Cell</i> , 2017, 65, 39-51.	9.7	250
14	Post-polyploidisation morphotype diversification associates with gene copy number variation. <i>Scientific Reports</i> , 2017, 7, 41845.	3.3	73
15	Targeted deep sequencing of flowering regulators in <i>Brassica napus</i> reveals extensive copy number variation. <i>Scientific Data</i> , 2017, 4, 170013.	5.3	32
16	Loss-of-function but not dominant-negative intragenic <i>IKZF1</i> deletions are associated with an adverse prognosis in adult <i>BCR-ABL</i> -negative acute lymphoblastic leukemia. <i>Haematologica</i> , 2017, 102, 1739-1747.	3.5	24
17	H3K14ac is linked to methylation of H3K9 by the triple Tudor domain of SETDB1. <i>Nature Communications</i> , 2017, 8, 2057.	12.8	72
18	Gene-centromere mapping in meiotic gynogenetic European seabass. <i>BMC Genomics</i> , 2017, 18, 449.	2.8	10

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19	Efficient targeted DNA methylation with chimeric dCas9-Dnmt3a-Dnmt3L methyltransferase. <i>Nucleic Acids Research</i> , 2017, 45, 1703-1713.	14.5	224
20	Flowering Time Gene Variation in Brassica Species Shows Evolutionary Principles. <i>Frontiers in Plant Science</i> , 2017, 8, 1742.	3.6	33
21	Three Novel Species with Peptidoglycan Cell Walls form the New Genus <i>Lacunisphaera</i> gen. nov. in the Family Opatutaceae of the Verrucomicrobial Subdivision 4. <i>Frontiers in Microbiology</i> , 2017, 8, 202.	3.5	75
22	Application of dual reading domains as novel reagents in chromatin biology reveals a new H3K9me3 and H3K36me2/3 bivalent chromatin state. <i>Epigenetics and Chromatin</i> , 2017, 10, 45.	3.9	27
23	FUCHS-towards full circular RNA characterization using RNAseq. <i>PeerJ</i> , 2017, 5, e2934.	2.0	45
24	Genome and catabolic subproteomes of the marine, nutritionally versatile, sulfate-reducing bacterium <i>Desulfococcus multivorans</i> DSM 2059. <i>BMC Genomics</i> , 2016, 17, 918.	2.8	43
25	Methylation Markers for the Identification of Body Fluids and Tissues from Forensic Trace Evidence. <i>PLoS ONE</i> , 2016, 11, e0147973.	2.5	62
26	Global RNA recognition patterns of post-transcriptional regulators Hfq and CsrA revealed by UV crosslinking <i>in vivo</i> . <i>EMBO Journal</i> , 2016, 35, 991-1011.	7.8	296
27	The CsrA-FliW network controls polar localization of the dual-function flagellin mRNA in <i>Campylobacter jejuni</i> . <i>Nature Communications</i> , 2016, 7, 11667.	12.8	93
28	miRNA expression profiling of Epstein-Barr virus-associated NKTL cell lines by Illumina deep sequencing. <i>FEBS Open Bio</i> , 2016, 6, 251-263.	2.3	21
29	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.	7.1	103
30	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, .	4.1	78
31	Profiling and Validation of the Circular RNA Repertoire in Adult Murine Hearts. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 216-223.	6.9	79
32	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.	7.1	267
33	Application of recombinant TAF3 PHD domain instead of anti-H3K4me3 antibody. <i>Epigenetics and Chromatin</i> , 2016, 9, 11.	3.9	18
34	Dual RNA-seq unveils noncoding RNA functions in host-pathogen interactions. <i>Nature</i> , 2016, 529, 496-501.	27.8	450
35	Characterization and refinement of growth related quantitative trait loci in European sea bass (<i>Dicentrarchus labrax</i>) using a comparative approach. <i>Aquaculture</i> , 2016, 455, 8-21.	3.5	16
36	Level of tissue differentiation influences the activation of a heat-inducible flower-specific system for genetic containment in poplar (<i>Populus tremula</i> L.). <i>Plant Cell Reports</i> , 2016, 35, 369-384.	5.6	5

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37	cDNA Library Enrichment of Full Length Transcripts for SMRT Long Read Sequencing. PLoS ONE, 2016, 11, e0157779.	2.5	51
38	Staphylococcus aureus Exploits a Non-ribosomal Cyclic Dipeptide to Modulate Survival within Epithelial Cells and Phagocytes. PLoS Pathogens, 2016, 12, e1005857.	4.7	48
39	Differentiation of <i>Candidatus</i> Phytoplasma cynodontis™ Based on 16S rRNA and <i>groEL</i> Genes and Identification of a New Subgroup, 16SrXIV-C. Plant Disease, 2015, 99, 1578-1583.	1.4	22
40	Generation of an 870Åkb deletion encompassing the Skt/Etl4 locus by combination of inter- and intra-chromosomal recombination. BMC Genetics, 2015, 16, 143.	2.7	1
41	Development and application of primers for the class <i>D</i> (phylum <i>C</i>) enables deep insights into diversity and stratification of subgroups in the marine subsurface. Environmental Microbiology, 2015, 17, 3540-3556.	3.8	22
42	Epstein-Barr Virus EBER Transcripts Affect miRNA-Mediated Regulation of Specific Targets and Are Processed to Small RNA Species. Non-coding RNA, 2015, 1, 170-191.	2.6	7
43	Targeted epigenome editing of an endogenous locus with chromatin modifiers is not stably maintained. Epigenetics and Chromatin, 2015, 8, 12.	3.9	77
44	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of <i>Helicobacter pylori</i> . Genetics, 2015, 200, 947-963.	2.9	65
45	Genome-wide expression profiling and phenotypic evaluation of European maize inbreds at seedling stage in response to heat stress. BMC Genomics, 2015, 16, 123.	2.8	83
46	Rapid and Sensitive Detection of Calreticulin Type 1 and 2 Mutations by Real-Time Quantitative PCR. Molecular Diagnosis and Therapy, 2015, 19, 329-334.	3.8	7
47	Analysis of the Complete Genomes of <i>Acholeplasma brassicae</i> , <i>A. palmae</i> and <i>A. laidlawii</i> and Their Comparison to the Obligate Parasites from <i>Candidatus</i> Phytoplasma'. Journal of Molecular Microbiology and Biotechnology, 2014, 24, 19-36.	1.0	36
48	The Dnmt2 RNA methyltransferase homolog of <i>Geobacter sulfurreducens</i> specifically methylates tRNA-Glu. Nucleic Acids Research, 2014, 42, 6487-6496.	14.5	27
49	On the current status of <i>Phakopsora pachyrhizi</i> genome sequencing. Frontiers in Plant Science, 2014, 5, 377.	3.6	21
50	The oxygen-independent metabolism of cyclic monoterpenes in <i>Castellaniella defragrans</i> 65Phen. BMC Microbiology, 2014, 14, 164.	3.3	19
51	Application of histone modification-specific interaction domains as an alternative to antibodies. Genome Research, 2014, 24, 1842-1853.	5.5	52
52	Transcriptional landscape and essential genes of <i>Neisseria gonorrhoeae</i> . Nucleic Acids Research, 2014, 42, 10579-10595.	14.5	74
53	European sea bass genome and its variation provide insights into adaptation to euryhalinity and speciation. Nature Communications, 2014, 5, 5770.	12.8	382
54	Complete genome determination and analysis of <i>Acholeplasma oculi</i> strain 19L, highlighting the loss of basic genetic features in the <i>Acholeplasmataceae</i> . BMC Genomics, 2014, 15, 931.	2.8	9

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55	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014, 505, 546-549.	27.8	569
56	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.	3.1	60
57	Directed de novo population transcriptome dissects genetic regulation of a balanced polymorphism in phosphorus nutrition/arsenate tolerance in a wild grass, <i>Holcus lanatus</i> . <i>New Phytologist</i> , 2014, 201, 144-154.	7.3	6
58	Cooperative DNA Binding and Protein/DNA Fiber Formation Increases the Activity of the Dnmt3a DNA Methyltransferase. <i>Journal of Biological Chemistry</i> , 2014, 289, 29602-29613.	3.4	44
59	Germline variants in IKZF1, ARID5B, and CEBPE as risk factors for adult-onset acute lymphoblastic leukemia: an analysis from the GMALL study group. <i>Haematologica</i> , 2014, 99, e23-e25.	3.5	21
60	Finished Genome Sequence of the Unicellular Cyanobacterium <i>Synechocystis</i> sp. Strain PCC 6714. <i>Genome Announcements</i> , 2014, 2, .	0.8	13
61	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.	2.5	60
62	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.	9.6	104
63	Erroneous class switching and false VDJ recombination: Molecular dissection of t(8;14)(MYC;IGH) translocations in Burkitt-type lymphoblastic leukemia/B-cell lymphoma. <i>Molecular Oncology</i> , 2013, 7, 850-858.	4.6	22
64	Fine mapping and chromosome walking towards the Ror1 locus in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 2969-2982.	3.6	15
65	The Genome of the Alga-Associated Marine Flavobacterium <i>Formosa agariphila</i> KMM 3901 Reveals a Broad Potential for Degradation of Algal Polysaccharides. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6813-6822.	3.1	222
66	Genome sequence and functional genomic analysis of the oil-degrading bacterium <i>Oleispira antarctica</i> . <i>Nature Communications</i> , 2013, 4, 2156.	12.8	115
67	Ups and downs of a transcriptional landscape shape iron deficiency associated chlorosis of the maize inbreds B73 and Mo17. <i>BMC Plant Biology</i> , 2013, 13, 213.	3.6	11
68	Transcriptome sequencing and microarray design for functional genomics in the extremophile <i>Arabidopsis</i> relative <i>Thellungiella salsuginea</i> (<i>Eutrema salsugineum</i>). <i>BMC Genomics</i> , 2013, 14, 793.	2.8	37
69	Adaptation of <i>Halobacterium salinarum</i> DSM 17395 to growth with complex nutrients. <i>Proteomics</i> , 2013, 13, 2851-2868.	2.2	45
70	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.	4.2	138
71	Dynamics of amino acid utilization in <i>Halobacterium salinarum</i> DSM 17395. <i>Proteomics</i> , 2013, 13, 2869-2885.	2.2	22
72	PTHrP-induced modifications of the sea bream (<i>Sparus auratus</i>) vertebral bone proteome. <i>General and Comparative Endocrinology</i> , 2013, 191, 102-112.	1.8	5

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73	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.	3.8	99
74	High-Resolution Transcriptome Maps Reveal Strain-Specific Regulatory Features of Multiple <i>Campylobacter jejuni</i> Isolates. <i>PLoS Genetics</i> , 2013, 9, e1003495.	3.5	260
75	Complete genome, catabolic subproteomes and key metabolites of <i>Desulfobacula toluolica</i> , a marine, aromatic compound-degrading, sulfate-reducing bacterium. <i>Environmental Microbiology</i> , 2013, 15, 1334-1355.	3.8	96
76	Alternative Processing as Evolutionary Mechanism for the Origin of Novel Nonprotein Coding RNAs. <i>Genome Biology and Evolution</i> , 2013, 5, 2061-2071.	2.5	11
77	Complete genome sequence of <i>Desulfocapsa sulfexigens</i> , a marine <i>deltaproteobacterium</i> specialized in disproportionating inorganic sulfur compounds. <i>Standards in Genomic Sciences</i> , 2013, 8, 58-68.	1.5	69
78	mRNA-Seq and microarray development for the Grooved carpet shell clam, <i>Ruditapes decussatus</i> : a functional approach to unravel host-parasite interaction. <i>BMC Genomics</i> , 2013, 14, 741.	2.8	39
79	A Rapid Transcriptome Response Is Associated with Desiccation Resistance in Aerially-Exposed Killifish Embryos. <i>PLoS ONE</i> , 2013, 8, e64410.	2.5	17
80	Differential gene expression in <i>Pyropia columbina</i> (Bangiales, Rhodophyta) under natural hydration and desiccation conditions. <i>Latin American Journal of Aquatic Research</i> , 2013, 41, 933-958.	0.6	27
81	Spread of a Distinct Stx2-Encoding Phage Prototype among <i>Escherichia coli</i> O104:H4 Strains from Outbreaks in Germany, Norway, and Georgia. <i>Journal of Virology</i> , 2012, 86, 10444-10455.	3.4	39
82	Experimental tools to identify RNA-protein interactions in <i>Helicobacter pylori</i> . <i>RNA Biology</i> , 2012, 9, 520-531.	3.1	24
83	Small RNAs of the <i>Bradyrhizobium/Rhodopseudomonas</i> lineage and their analysis. <i>RNA Biology</i> , 2012, 9, 47-58.	3.1	41
84	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.	2.2	55
85	Physiological and Proteomic Adaptation of <i>Aromatoleum aromaticum</i> N1 to Low Growth Rates in Benzoate-Limited, Anoxic Chemostats. <i>Journal of Bacteriology</i> , 2012, 194, 2165-2180.	2.2	32
86	<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.	9.8	125
87	Newt-omics: a comprehensive repository for omics data from the newt <i>Notophthalmus viridescens</i> . <i>Nucleic Acids Research</i> , 2012, 40, D895-D900.	14.5	18
88	CCDC103 mutations cause primary ciliary dyskinesia by disrupting assembly of ciliary dynein arms. <i>Nature Genetics</i> , 2012, 44, 714-719.	21.4	228
89	Revealing structure and assembly cues for <i>Arabidopsis</i> root-inhabiting bacterial microbiota. <i>Nature</i> , 2012, 488, 91-95.	27.8	2,127
90	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012, 44, 1060-1065.	21.4	840

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91	An atlas of Hfq-bound transcripts reveals 3â€™ UTRs as a genomic reservoir of regulatory small RNAs. <i>EMBO Journal</i> , 2012, 31, 4005-4019.	7.8	354
92	Complete Sequence Analysis of Two Methanotroph-Specific <i>repABC</i> -Containing Plasmids from <i>Methylocystis</i> sp. Strain SC2. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4373-4379.	3.1	16
93	Transcriptome analysis of enriched <i>Golovinomyces orontii</i> haustoria by deep 454 pyrosequencing. <i>Fungal Genetics and Biology</i> , 2012, 49, 470-482.	2.1	44
94	Genomic characterization of the European sea bass <i>Dicentrarchus labrax</i> reveals the presence of a novel uncoupling protein (UCP) gene family member in the teleost fish lineage. <i>BMC Evolutionary Biology</i> , 2012, 12, 62.	3.2	11
95	High-throughput polymorphism detection and genotyping in <i>Brassica napus</i> using next-generation RAD sequencing. <i>BMC Genomics</i> , 2012, 13, 281.	2.8	129
96	Maternal 3â€™UTRs: from egg to onset of zygotic transcription in Atlantic cod. <i>BMC Genomics</i> , 2012, 13, 443.	2.8	17
97	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.	6.2	252
98	Characteristics of <i>fads2</i> gene expression and putative promoter in European sea bass (<i>Dicentrarchus labrax</i>). <i>Overlock 10</i> 7-13.	1.1	42
99	Structure and activity of the cold-active and anion-activated carboxyl esterase OLEI01171 from the oil-degrading marine bacterium <i>Oleispira antarctica</i> . <i>Biochemical Journal</i> , 2012, 445, 193-203.	3.7	31
100	Long-Term Survival of Hydrated Resting Eggs from <i>Brachionus plicatilis</i> . <i>PLoS ONE</i> , 2012, 7, e29365.	2.5	34
101	Diversity, Molecular Characterization and Expression of T Cell Receptor Î³ in a Teleost Fish, the Sea Bass (<i>Dicentrarchus labrax</i> , L). <i>PLoS ONE</i> , 2012, 7, e47957.	2.5	40
102	Anaerobic degradation of 4-methylbenzoate via a specific 4-methylbenzoyl-CoA pathway. <i>Environmental Microbiology</i> , 2012, 14, 1118-1132.	3.8	27
103	Molecular analysis of the t(2;8)(q24;q24) MYC-IGK translocation in high-grade lymphoma/leukemia by long-distance inverse PCR. <i>Genes Chromosomes and Cancer</i> , 2012, 51, 290-299.	2.8	10
104	Onset of Immune Senescence Defined by Unbiased Pyrosequencing of Human Immunoglobulin mRNA Repertoires. <i>PLoS ONE</i> , 2012, 7, e49774.	2.5	30
105	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.	7.1	115
106	In silico mining and characterization of simple sequence repeats from gilthead sea bream (<i>Sparus aurata</i>) multiplexing and cross-species assays. <i>Marine Genomics</i> , 2011, 4, 83-91.	1.1	21
107	Comparative analysis of intronless genes in teleost fish genomes: Insights into their evolution and molecular function. <i>Marine Genomics</i> , 2011, 4, 109-119.	1.1	21
108	Expressed sequence tags from heat-shocked seagrass <i>Zostera noltii</i> (Hornemann) from its southern distribution range. <i>Marine Genomics</i> , 2011, 4, 181-188.	1.1	29

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109	The transcriptional landscape of <i>Chlamydia pneumoniae</i> . <i>Genome Biology</i> , 2011, 12, R98.	9.6	72
110	Analysis of single nucleotide polymorphisms in three chromosomes of European sea bass <i>Dicentrarchus labrax</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 70-75.	1.0	14
111	Directed sequencing and annotation of three <i>Dicentrarchus labrax</i> L. chromosomes by applying Sanger- and pyrosequencing technologies on pooled DNA of comparatively mapped BAC clones. <i>Genomics</i> , 2011, 98, 202-212.	2.9	15
112	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.	2.4	129
113	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.	21.4	292
114	Hybridisation-based resequencing of 17 X-linked intellectual disability genes in 135 patients reveals novel mutations in ATRX, SLC6A8 and PQBP1. <i>European Journal of Human Genetics</i> , 2011, 19, 717-720.	2.8	21
115	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.	7.8	270
116	Fine structure of translocation breakpoints within the major breakpoint region in BCR-ABL1-positive leukemias. <i>DNA Repair</i> , 2011, 10, 1131-1137.	2.8	9
117	Cloning, Tissue Expression Analysis, and Functional Characterization of Two Δ^6 -Desaturase Variants of Sea Bass (<i>Dicentrarchus labrax</i> L.). <i>Marine Biotechnology</i> , 2011, 13, 22-31.	2.4	31
118	Sequence analysis of the grey mouse lemur (<i>Microcebus murinus</i>) MHC class II DQ and DR region. <i>Immunogenetics</i> , 2011, 63, 85-93.	2.4	17
119	Natural history of SLC11 genes in vertebrates: tales from the fish world. <i>BMC Evolutionary Biology</i> , 2011, 11, 106.	3.2	20
120	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.	2.8	120
121	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.	2.8	57
122	A <i>BACH2</i> - <i>BCL2L1</i> fusion gene resulting from a t(6;20)(q15;q11.2) chromosomal translocation in the lymphoma cell line BLUE1. <i>Genes Chromosomes and Cancer</i> , 2011, 50, 389-396.	2.8	22
123	Deep sequencing of naupliar-, cyprid- and adult-specific normalised Expressed Sequence Tag (EST) libraries of the acorn barnacle <i>Balanus amphitrite</i> . <i>Biofouling</i> , 2011, 27, 367-374.	2.2	19
124	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.	7.1	67
125	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.	7.1	99
126	A Comparative BAC Map for the Gilthead Sea Bream (<i>Sparus aurata</i> L.). <i>Journal of Biomedicine and Biotechnology</i> , 2011, 2011, 1-7.	3.0	13

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127	Human box C/D snoRNAs with miRNA like functions: expanding the range of regulatory RNAs. <i>Nucleic Acids Research</i> , 2011, 39, 675-686.	14.5	276
128	<i>Helicobacter pylori</i> genome evolution during human infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5033-5038.	7.1	235
129	Identification of Genes Essential for Prey-Independent Growth of <i>Bdellovibrio bacteriovorus</i> HD100. <i>Journal of Bacteriology</i> , 2011, 193, 1745-1756.	2.2	36
130	The genome sequence of Atlantic cod reveals a unique immune system. <i>Nature</i> , 2011, 477, 207-210.	27.8	730
131	Comparative Genomic Analysis of Fruiting Body Formation in Myxococcales. <i>Molecular Biology and Evolution</i> , 2011, 28, 1083-1097.	8.9	111
132	Parallel Evolution of Nacre Building Gene Sets in Molluscs. <i>Molecular Biology and Evolution</i> , 2010, 27, 591-608.	8.9	239
133	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.	2.4	77
134	Stress response in tardigrades: differential gene expression of molecular chaperones. <i>Cell Stress and Chaperones</i> , 2010, 15, 423-430.	2.9	52
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