

Richard Reinhardt

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2096162/publications.pdf>

Version: 2024-02-01

284
papers

52,752
citations

4960

84
h-index

1424

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.	27.8	21,074
2	Revealing structure and assembly cues for <i>Arabidopsis</i> root-inhabiting bacterial microbiota. <i>Nature</i> , 2012, 488, 91-95.	27.8	2,127
3	The Genome of the Kinetoplastid Parasite, <i>Leishmania major</i> . <i>Science</i> , 2005, 309, 436-442.	12.6	1,237
4	The primary transcriptome of the major human pathogen <i>Helicobacter pylori</i> . <i>Nature</i> , 2010, 464, 250-255.	27.8	1,115
5	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005, 434, 325-337.	27.8	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.	21.4	840
7	The genome sequence of Atlantic cod reveals a unique immune system. <i>Nature</i> , 2011, 477, 207-210.	27.8	730
8	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. <i>Science</i> , 2010, 330, 1543-1546.	12.6	725
9	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	27.8	657
10	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014, 505, 546-549.	27.8	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.	21.4	496
12	Dual RNA-seq unveils noncoding RNA functions in host-pathogen interactions. <i>Nature</i> , 2016, 529, 496-501.	27.8	450
13	European sea bass genome and its variation provide insights into adaptation to euryhalinity and speciation. <i>Nature Communications</i> , 2014, 5, 5770.	12.8	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.	21.4	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.	7.8	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.	6.2	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.	21.4	345
18	A conspicuous nickel protein in microbial mats that oxidize methane anaerobically. <i>Nature</i> , 2003, 426, 878-881.	27.8	344

#	ARTICLE	IF	CITATIONS
19	Ktu/PF13 is required for cytoplasmic pre-assembly of axonemal dyneins. <i>Nature</i> , 2008, 456, 611-616.	27.8	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.	3.8	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.	14.5	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.	3.1	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.	7.8	296
24	<i>DNAH5</i> 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.	5.6	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.	21.4	292
26	Hox cluster disintegration with persistent anteroposterior order of expression in <i>Oikopleura dioica</i> . <i>Nature</i> , 2004, 431, 67-71.	27.8	286
27	Genome sequence of the chlorinated compound-respiring bacterium <i>Dehalococcoides</i> species strain CBDB1. <i>Nature Biotechnology</i> , 2005, 23, 1269-1273.	17.5	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.	14.5	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.	7.8	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.	7.1	267
31	The genome sequence of an anaerobic aromatic-degrading denitrifying bacterium, strain EbN1. <i>Archives of Microbiology</i> , 2005, 183, 27-36.	2.2	266
32	Classification and Identification of Bacteria by Mass Spectrometry and Computational Analysis. <i>PLoS ONE</i> , 2008, 3, e2843.	2.5	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.	3.5	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.	6.2	252
35	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. <i>Science</i> , 2010, 330, 1381-1385.	12.6	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.	9.7	250

#	ARTICLE	IF	CITATIONS
37	DNAI2 Mutations Cause Primary Ciliary Dyskinesia with Defects in the Outer Dynein Arm. American Journal of Human Genetics, 2008, 83, 547-558.	6.2	242
38	Parallel Evolution of Nacre Building Gene Sets in Molluscs. Molecular Biology and Evolution, 2010, 27, 591-608.	8.9	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.	2.2	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.	7.1	235
41	CCDC103 mutations cause primary ciliary dyskinesia by disrupting assembly of ciliary dynein arms. Nature Genetics, 2012, 44, 714-719.	21.4	228
42	Efficient targeted DNA methylation with chimeric dCas9-Dnmt3L methyltransferase. Nucleic Acids Research, 2017, 45, 1703-1713.	14.5	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.	3.1	222
44	Dynamic link of DNA demethylation, DNA strand breaks and repair in mouse zygotes. EMBO Journal, 2010, 29, 1877-1888.	7.8	221
45	Metagenome and mRNA expression analyses of anaerobic methanotrophic archaea of the ANME-1 group. Environmental Microbiology, 2010, 12, 422-439.	3.8	221
46	BISMA - Fast and accurate bisulfite sequencing data analysis of individual clones from unique and repetitive sequences. BMC Bioinformatics, 2010, 11, 230.	2.6	215
47	The linear chromosome of the plant-pathogenic mycoplasma 'Candidatus Phytoplasma mali'. BMC Genomics, 2008, 9, 306.	2.8	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.	6.2	207
49	Deep sequencing-based discovery of the Chlamydia trachomatis transcriptome. Nucleic Acids Research, 2010, 38, 868-877.	14.5	206
50	Characterization of a Spontaneous Nonmagnetic Mutant of <i>Magnetospirillum gryphiswaldense</i> Reveals a Large Deletion Comprising a Putative Magnetosome Island. Journal of Bacteriology, 2003, 185, 5779-5790.	2.2	200
51	Accuracy of DNA methylation pattern preservation by the Dnmt1 methyltransferase. Nucleic Acids Research, 2006, 34, 1182-1188.	14.5	186
52	Anaerobic degradation of naphthalene and 2-methylnaphthalene by strains of marine sulfate-reducing bacteria. Environmental Microbiology, 2009, 11, 209-219.	3.8	177
53	Genome of Rice Cluster I Archaea—the Key Methane Producers in the Rice Rhizosphere. Science, 2006, 313, 370-372.	12.6	175
54	SNP and haplotype mapping for genetic analysis in the rat. Nature Genetics, 2008, 40, 560-566.	21.4	172

#	ARTICLE	IF	CITATIONS
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.	5.5	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.	2.2	159
57	Miniature Genome in the Marine Chordate <i>Oikopleura dioica</i> . <i>Science</i> , 2001, 294, 2506-2506.	12.6	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.	3.5	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.	4.2	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.	2.2	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.	2.4	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.	2.8	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.	2.8	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.	9.8	125
65	Novel JARID1C/SMCX mutations in patients with X-linked mental retardation. <i>Human Mutation</i> , 2006, 27, 389-389.	2.5	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.	2.8	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.	2.2	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.	2.2	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.	7.1	115
70	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
71	Comparative Genomic Analysis of Fruiting Body Formation in Myxococcales. <i>Molecular Biology and Evolution</i> , 2011, 28, 1083-1097.	8.9	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.	14.5	109

#	ARTICLE	IF	CITATIONS
73	The Genomic Sequence and Comparative Analysis of the Rat Major Histocompatibility Complex. <i>Genome Research</i> , 2004, 14, 631-639.	5.5	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.	2.3	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.	9.6	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.	7.1	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.	7.1	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.	3.8	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.	3.8	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.	3.1	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.	3.8	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.	12.8	93
83	EST sequencing of Onychophora and phylogenomic analysis of Metazoa. <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 942-951.	2.7	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.	2.8	92
85	ARE ANTIMITOCHONDRIAL ANTIBODIES IN PRIMARY BILIARY CIRRHOSIS INDUCED BY R(ROUGH)-MUTANTS OF ENTEROBACTERIACEAE?. <i>Lancet</i> , The, 1988, 332, 1166-1170.	13.7	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.	2.2	90
87	Functional proteomic view of metabolic regulation in <i>Aromatoleum aromaticum</i> strain EbN1. <i>Proteomics</i> , 2007, 7, 2222-2239.	2.2	90
88	Phylogenetic diversity and metagenomics of candidate division OP3. <i>Environmental Microbiology</i> , 2010, 12, 1218-1229.	3.8	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.	2.7	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.	1.4	85

#	ARTICLE	IF	CITATIONS
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.	5.9	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.	2.5	84
93	Discovering genes associated with dormancy in the monogonont rotifer <i>Brachionus plicatilis</i> . <i>BMC Genomics</i> , 2009, 10, 108.	2.8	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.	2.8	83
95	Insights into the genomes of archaea mediating the anaerobic oxidation of methane. <i>Environmental Microbiology</i> , 2005, 7, 1937-1951.	3.8	81
96	A global view of the nonprotein-coding transcriptome in <i>Plasmodium falciparum</i> . <i>Nucleic Acids Research</i> , 2010, 38, 608-617.	14.5	80
97	Profiling and Validation of the Circular RNA Repertoire in Adult Murine Hearts. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 216-223.	6.9	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, .	4.1	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.	2.5	77
101	Non-imprinted allele-specific DNA methylation on human autosomes. <i>Genome Biology</i> , 2009, 10, R138.	9.6	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.	2.4	77
103	Targeted epigenome editing of an endogenous locus with chromatin modifiers is not stably maintained. <i>Epigenetics and Chromatin</i> , 2015, 8, 12.	3.9	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.	3.5	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.	3.8	74
106	Transcriptional landscape and essential genes of <i>Neisseria gonorrhoeae</i> . <i>Nucleic Acids Research</i> , 2014, 42, 10579-10595.	14.5	74
107	Post-polyploidisation morphotype diversification associates with gene copy number variation. <i>Scientific Reports</i> , 2017, 7, 41845.	3.3	73
108	Transcriptional activity of paddy soil bacterial communities. <i>Environmental Microbiology</i> , 2009, 11, 960-970.	3.8	72

#	ARTICLE	IF	CITATIONS
109	The transcriptional landscape of <i>Chlamydia pneumoniae</i> . <i>Genome Biology</i> , 2011, 12, R98.	9.6	72
110	H3K14ac is linked to methylation of H3K9 by the triple Tudor domain of SETDB1. <i>Nature Communications</i> , 2017, 8, 2057.	12.8	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.	0.8	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.	7.1	67
115	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of <i>Helicobacter pylori</i> . <i>Genetics</i> , 2015, 200, 947-963.	2.9	65
116	A Novel System of Polymorphic and Diverse NK Cell Receptors in Primates. <i>PLoS Genetics</i> , 2009, 5, e1000688.	3.5	64
117	Retroposed SNOfall-A mammalian-wide comparison of platypus snoRNAs. <i>Genome Research</i> , 2008, 18, 1005-1010.	5.5	62
118	Methylation Markers for the Identification of Body Fluids and Tissues from Forensic Trace Evidence. <i>PLoS ONE</i> , 2016, 11, e0147973.	2.5	62
119	Remodelling of the homeobox gene complement in the tunicate <i>Oikopleura dioica</i> . <i>Current Biology</i> , 2005, 15, R12-R13.	3.9	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.	2.8	61
121	DNA Methylation Analysis by Bisulfite Conversion, Cloning, and Sequencing of Individual Clones. <i>Methods in Molecular Biology</i> , 2009, 507, 177-187.	0.9	61
122	Mutational analysis of the NPHP4 gene in 250 patients with nephronophthisis. <i>Human Mutation</i> , 2005, 25, 411-411.	2.5	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.	2.8	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.	3.1	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.	2.5	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.	2.9	59

#	ARTICLE	IF	CITATIONS
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.	3.1	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.	2.8	57
129	High-resolution array comparative genomic hybridization of single micrometastatic tumor cells. <i>Nucleic Acids Research</i> , 2008, 36, e39.	14.5	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.	14.5	56
131	The bovine IGF2 gene is differentially methylated in oocyte and sperm DNA. <i>Genomics</i> , 2006, 88, 222-229.	2.9	55
132	Disruption and pseudoautosomal localization of the major histocompatibility complex in monotremes. <i>Genome Biology</i> , 2007, 8, R175.	9.6	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.	2.4	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	2.8	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.	2.2	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.	2.8	54
137	NUP214-ABL1 in adult T-ALL: the GALL study group experience. <i>Blood</i> , 2006, 108, 3556-3559.	1.4	54
138	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006, 440, 1194-1198.	27.8	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.	2.9	52
140	Profiling of infection specific mRNA transcripts of the European seabass <i>Dicentrarchus labrax</i> . <i>BMC Genomics</i> , 2009, 10, 157.	2.8	52
141	Stress response in tardigrades: differential gene expression of molecular chaperones. <i>Cell Stress and Chaperones</i> , 2010, 15, 423-430.	2.9	52
142	Application of histone modification-specific interaction domains as an alternative to antibodies. <i>Genome Research</i> , 2014, 24, 1842-1853.	5.5	52
143	cDNA Library Enrichment of Full Length Transcripts for SMRT Long Read Sequencing. <i>PLoS ONE</i> , 2016, 11, e0157779.	2.5	51
144	Clone-Based Systematic Haplotyping (CSH): A Procedure for Physical Haplotyping of Whole Genomes. <i>Genome Research</i> , 2003, 13, 2717-2724.	5.5	50

#	ARTICLE	IF	CITATIONS
145	First Genome Data from Uncultured Upland Soil Cluster Alpha Methanotrophs Provide Further Evidence for a Close Phylogenetic Relationship to <i>Methylocapsa acidiphila</i> B2 and for High-Affinity Methanotrophy Involving Particulate Methane Monooxygenase. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7472-7482.	3.1	50
146	Analysis of N-acetylglucosamine metabolism in the marine bacterium <i>Pirellula</i> sp. strain 1 by a proteomic approach. <i>Proteomics</i> , 2002, 2, 649-655.	2.2	48
147	<i>Staphylococcus aureus</i> Exploits a Non-ribosomal Cyclic Dipeptide to Modulate Survival within Epithelial Cells and Phagocytes. <i>PLoS Pathogens</i> , 2016, 12, e1005857.	4.7	48
148	Adaptation of <i>Proteobacterium</i> <i>inhibens</i> DSM 17395 to growth with complex nutrients. <i>Proteomics</i> , 2013, 13, 2851-2868.	2.2	45
149	FUCHS towards full circular RNA characterization using RNAseq. <i>PeerJ</i> , 2017, 5, e2934.	2.0	45
150	Hypervariable and Highly Divergent Intron/Exon Organizations in the Chordate <i>Oikopleura dioica</i> . <i>Journal of Molecular Evolution</i> , 2004, 59, 448-457.	1.8	44
151	Retrieval of first genome data for rice cluster I methanogens by a combination of cultivation and molecular techniques. <i>FEMS Microbiology Ecology</i> , 2005, 53, 187-204.	2.7	44
152	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
153	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
154	The DNMT3A R882H mutant displays altered flanking sequence preferences. <i>Nucleic Acids Research</i> , 2018, 46, 3130-3139.	14.5	44
155	Generation, Annotation, Evolutionary Analysis, and Database Integration of 20,000 Unique Sea Urchin EST Clusters. <i>Genome Research</i> , 2003, 13, 2736-2746.	5.5	43
156	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
157	RAI1 is a novel polyglutamine encoding gene that is deleted in Smith-Magenis syndrome patients. <i>Gene</i> , 2001, 270, 69-76.	2.2	42
158	Characteristics of fads2 gene expression and putative promoter in European sea bass (<i>Dicentrarchus labrax</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tff 7-13.	1.1	42
159	Small RNAs of the <i>Bradyrhizobium/Rhodopseudomonas</i> lineage and their analysis. <i>RNA Biology</i> , 2012, 9, 47-58.	3.1	41
160	Late Embryogenesis Abundant (LEA) Proteins in Nondessicated, Encysted, and Diapausing Embryos of Rotifers 1. <i>Biology of Reproduction</i> , 2010, 82, 714-724.	2.7	40
161	Diversity, Molecular Characterization and Expression of T Cell Receptor β^3 in a Teleost Fish, the Sea Bass (<i>Dicentrarchus labrax</i> , L). <i>PLoS ONE</i> , 2012, 7, e47957.	2.5	40
162	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

#	ARTICLE	IF	CITATIONS
163	Gill transcriptome response to changes in environmental calcium in the green spotted puffer fish. BMC Genomics, 2010, 11, 476.	2.8	39
164	Spread of a Distinct Stx2-Encoding Phage Prototype among Escherichia coli O104:H4 Strains from Outbreaks in Germany, Norway, and Georgia. Journal of Virology, 2012, 86, 10444-10455.	3.4	39
165	mRNA-Seq and microarray development for the Grooved carpet shell clam, Ruditapes decussatus: a functional approach to unravel host-parasite interaction. BMC Genomics, 2013, 14, 741.	2.8	39
166	Comparative Analysis of the Conventional and Novel pmo (Particulate Methane Monooxygenase) Operons from Methylocystis Strain SC2. Applied and Environmental Microbiology, 2004, 70, 3055-3063.	3.1	38
167	Growth phase dependent regulation of protein composition in <i>Rhodopirellula baltica</i> . Environmental Microbiology, 2005, 7, 1074-1084.	3.8	38
168	A Small, Variable, and Irregular Killer Cell Ig-Like Receptor Locus Accompanies the Absence of <i>MHC-C</i> and <i>MHC-G</i> in Gibbons. Journal of Immunology, 2010, 184, 1379-1391.	0.8	38
169	Identification of the DNA methyltransferases establishing the methylome of the cyanobacterium Synechocystis sp. PCC 6803. DNA Research, 2018, 25, 343-352.	3.4	38
170	Tissue Gene Expression Analysis Using Arrayed Normalized cDNA Libraries. Genome Research, 2000, 10, 1230-1240.	5.5	37
171	Development of an oligo DNA microarray for the European sea bass and its application to expression profiling of jaw deformity. BMC Genomics, 2010, 11, 354.	2.8	37
172	Transcriptome sequencing and microarray design for functional genomics in the extremophile Arabidopsis relative Thellungiella salsuginea (Eutrema salsugineum). BMC Genomics, 2013, 14, 793.	2.8	37
173	Identification of Genes Essential for Prey-Independent Growth of <i>Bdellovibrio bacteriovorus</i> HD100. Journal of Bacteriology, 2011, 193, 1745-1756.	2.2	36
174	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 'Candidatus Phytoplasma'. Journal of Molecular Microbiology and Biotechnology, 2014, 24, 19-36.	1.0	36
175	X-Ray Structural Analyses of Cyclodecasulfur (S ₁₀) and of a Cyclohexasulfur-Cyclodecasulfur Molecular Addition Compound (S ₆ ·S ₁₀) [1]. Zeitschrift Fur Naturforschung - Section B Journal of Chemical Sciences, 1983, 38, 1548-1556.	0.7	35
176	A Degenerate ParaHox Gene Cluster in a Degenerate Vertebrate. Molecular Biology and Evolution, 2007, 24, 2681-2686.	8.9	34
177	Long-Term Survival of Hydrated Resting Eggs from <i>Brachionus plicatilis</i> . PLoS ONE, 2012, 7, e29365.	2.5	34
178	Flowering Time Gene Variation in Brassica Species Shows Evolutionary Principles. Frontiers in Plant Science, 2017, 8, 1742.	3.6	33
179	MALDI mass spectrometry analysis of single nucleotide polymorphisms by photocleavage and charge-tagging. Nucleic Acids Research, 2003, 31, 63e-63.	14.5	32
180	Physiological and Proteomic Adaptation of <i>Aromatoleum aromaticum</i> N1 to Low Growth Rates in Benzoate-Limited, Anoxic Chemostats. Journal of Bacteriology, 2012, 194, 2165-2180.	2.2	32

#	ARTICLE	IF	CITATIONS
181	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
182	Retroelement Dynamics and a Novel Type of Chordate Retrovirus-like Element in the Miniature Genome of the Tunicate <i>Oikopleura dioica</i> . <i>Molecular Biology and Evolution</i> , 2004, 21, 2022-2033.	8.9	31
183	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
184	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
185	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
186	Onset of Immune Senescence Defined by Unbiased Pyrosequencing of Human Immunoglobulin mRNA Repertoires. <i>PLoS ONE</i> , 2012, 7, e49774.	2.5	30
187	Analysis of the goldfish <i>Carassius auratus</i> olfactory epithelium transcriptome reveals the presence of numerous non-olfactory GPCR and putative receptors for progesterin pheromones. <i>BMC Genomics</i> , 2008, 9, 429.	2.8	29
188	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
189	The Systems Architecture of Molecular Memory in Poplar after Abiotic Stress. <i>Plant Cell</i> , 2019, 31, 346-367.	6.6	29
190	A catabolic gene cluster for anaerobic benzoate degradation in methanotrophic microbial Black Sea mats. <i>Systematic and Applied Microbiology</i> , 2005, 28, 287-294.	2.8	27
191	Anaerobic degradation of 4-methylbenzoate via a specific 4-methylbenzoyl-CoA pathway. <i>Environmental Microbiology</i> , 2012, 14, 1118-1132.	3.8	27
192	The Dnmt2 RNA methyltransferase homolog of <i>Geobacter sulfurreducens</i> specifically methylates tRNA-Glu. <i>Nucleic Acids Research</i> , 2014, 42, 6487-6496.	14.5	27
193	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
194	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
195	Towards the proteome of the marine bacterium <i>Rhodopirellula baltica</i> : Mapping the soluble proteins. <i>Proteomics</i> , 2005, 5, 3654-3671.	2.2	26
196	Gilthead sea bream (<i>Sparus auratus</i>) and European sea bass (<i>Dicentrarchus labrax</i>) expressed sequence tags: Characterization, tissue-specific expression and gene markers. <i>Marine Genomics</i> , 2010, 3, 179-191.	1.1	25
197	Single-nucleotide polymorphisms: analysis by mass spectrometry. <i>Nature Protocols</i> , 2006, 1, 1761-1771.	12.0	24
198	Experimental tools to identify RNA-protein interactions in <i>Helicobacter pylori</i> . <i>RNA Biology</i> , 2012, 9, 520-531.	3.1	24

#	ARTICLE	IF	CITATIONS
199	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
200	Crystal and Molecular Structure of cyclo-Heptasulfur (?-S ₇). <i>Angewandte Chemie International Edition in English</i> , 1977, 16, 715-715.	4.4	23
201	Gene identification and analysis of transcripts differentially regulated in fracture healing by EST sequencing in the domestic sheep. <i>BMC Genomics</i> , 2006, 7, 172.	2.8	23
202	High-throughput sequencing of microdissected chromosomal regions. <i>European Journal of Human Genetics</i> , 2010, 18, 457-462.	2.8	23
203	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
204	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
205	Dynamics of amino acid utilization in <i>Proteomics</i> , 2013, 13, 2869-2885.	2.2	22
206	Differentiation of <i>Candidatus</i> <i>Phytoplasma cynodontis</i> ™ Based on 16S rRNA and <i>groEL</i> Genes and Identification of a New Subgroup, 16SrXIV-C. <i>Plant Disease</i> , 2015, 99, 1578-1583.	1.4	22
207	Development and application of primers for the class <i>D</i> (<i>ehalococcoidia</i>) (phylum <i>C</i> (<i>chloroflexi</i>)) enables deep insights into diversity and stratification of subgroups in the marine subsurface. <i>Environmental Microbiology</i> , 2015, 17, 3540-3556.	3.8	22
208	Bond Interaction in Sulfur Rings: Crystal and Molecular Structure of cyclo-Heptasulfur Oxide, S ₇ O. <i>Angewandte Chemie International Edition in English</i> , 1977, 16, 716-716.	4.4	21
209	Genomic sequences and genetic differentiation at associated tandem repeat markers in growth hormone, somatotactin and insulin-like growth factor-1 genes of the sea bass, <i>Dicentrarchus labrax</i> . <i>Aquatic Living Resources</i> , 2010, 23, 285-296.	1.2	21
210	In silico mining and characterization of simple sequence repeats from gilthead sea bream (<i>Sparus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 multiplexing and cross-species assays. <i>Marine Genomics</i> , 2011, 4, 83-91.	1.1	21
211	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
212	Hybridisation-based resequencing of 17 X-linked intellectual disability genes in 135 patients reveals novel mutations in <i>ATRX</i> , <i>SLC6A8</i> and <i>PQBP1</i> . <i>European Journal of Human Genetics</i> , 2011, 19, 717-720.	2.8	21
213	On the current status of <i>Phakopsora pachyrhizi</i> genome sequencing. <i>Frontiers in Plant Science</i> , 2014, 5, 377.	3.6	21
214	Germline variants in <i>IKZF1</i> , <i>ARID5B</i> , and <i>CEBPE</i> 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
215	miRNA expression profiling of Epstein-Barr virus-associated <i>NKTL</i> cell lines by Illumina deep sequencing. <i>FEBS Open Bio</i> , 2016, 6, 251-263.	2.3	21
216	Darstellung, Schwingungsspektren und Röntgenstrukturanalyse von Trifluor- und Trichloracetyltrischwefeltrinitrid, CX ₃ CO-NS ₃ N ₂ 1 / Synthesis, Vibrational Spectra, and X-ray Structure Analysis of Trifluoro and Trichloroacetyl Trisulfurtrinitride, CX ₃ CO-NS ₃ N ₂ 1. <i>Zeitschrift Fur Naturforschung - Section B Journal of Chemical Sciences</i> , 1977, 32, 488-494.	0.7	20

#	ARTICLE	IF	CITATIONS
217	X-Ray Structure Analysis of cyclo-Decasulfur, S ₁₀ . <i>Angewandte Chemie International Edition in English</i> , 1978, 17, 57-58.	4.4	20
218	Natural history of SLC11 genes in vertebrates: tales from the fish world. <i>BMC Evolutionary Biology</i> , 2011, 11, 106.	3.2	20
219	Criteria for gene identification and features of genome organization: analysis of 6.5 Mb of DNA sequence from human chromosome 21. <i>Gene</i> , 2000, 247, 215-232.	2.2	19
220	Genomics and Diversity of the Common Marmoset Monkey NK Complex. <i>Journal of Immunology</i> , 2007, 178, 7151-7161.	0.8	19
221	Novel method for high-throughput colony PCR screening in nanoliter-reactors. <i>Nucleic Acids Research</i> , 2009, 37, e57-e57.	14.5	19
222	Haplotype divergence in <i>Beta vulgaris</i> and microsynteny with sequenced plant genomes. <i>Plant Journal</i> , 2009, 57, 14-26.	5.7	19
223	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
224	The oxygen-independent metabolism of cyclic monoterpenes in <i>Castellaniella defragrans</i> 65Phen. <i>BMC Microbiology</i> , 2014, 14, 164.	3.3	19
225	Identification and characterisation of a novel immune-type receptor (NITR) gene cluster in the European sea bass, <i>Dicentrarchus labrax</i> , reveals recurrent gene expansion and diversification by positive selection. <i>Immunogenetics</i> , 2009, 61, 773-788.	2.4	18
226	Different Phylogenomic Approaches to Resolve the Evolutionary Relationships among Model Fish Species. <i>Molecular Biology and Evolution</i> , 2010, 27, 2757-2774.	8.9	18
227	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
228	Application of recombinant TAF3 PHD domain instead of anti-H3K4me3 antibody. <i>Epigenetics and Chromatin</i> , 2016, 9, 11.	3.9	18
229	A novel aminopeptidase associated with the 60 kDa chaperonin in the thermophilic archaeon <i>Sulfolobus solfataricus</i> . <i>Molecular Microbiology</i> , 1998, 29, 775-785.	2.5	17
230	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
231	Maternal 3' UTRs: from egg to onset of zygotic transcription in Atlantic cod. <i>BMC Genomics</i> , 2012, 13, 443.	2.8	17
232	A Rapid Transcriptome Response Is Associated with Desiccation Resistance in Aerially-Exposed Killifish Embryos. <i>PLoS ONE</i> , 2013, 8, e64410.	2.5	17
233	Kristall- und Molekülstruktur von cyclo-Heptaschwefel (C ₇). <i>Angewandte Chemie</i> , 1977, 89, 756-757.	2.0	16
234	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

#	ARTICLE	IF	CITATIONS
235	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
236	Physical and Transcriptional Mapping of the 17p13.3 Region That Is Frequently Deleted in Human Cancer. <i>Genomics</i> , 2000, 70, 26-33.	2.9	15
237	Analysis of a normalised expressed sequence tag (EST) library from a key pollinator, the bumblebee <i>Bombus terrestris</i> . <i>BMC Genomics</i> , 2010, 11, 110.	2.8	15
238	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
239	Fine mapping and chromosome walking towards the <i>Ror1</i> locus in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 2969-2982.	3.6	15
240	Analysis of the Spermine Synthase Gene Region in <i>Fugu rubripes</i> , <i>Tetraodon fluviatilis</i> , and <i>Danio rerio</i> . <i>Genomics</i> , 1999, 57, 164-168.	2.9	14
241	Mapping of Protein-Protein Interaction Sites by the "Absence of Interference"™ Approach. <i>Journal of Molecular Biology</i> , 2008, 376, 1091-1099.	4.2	14
242	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
243	Characterization of a Highly Complex Region in Xq13 and Mapping of Three Isodicentric Breakpoints Associated with Preleukemia. <i>Genomics</i> , 2000, 64, 221-229.	2.9	13
244	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
245	Finished Genome Sequence of the Unicellular Cyanobacterium <i>Synechocystis</i> sp. Strain PCC 6714. <i>Genome Announcements</i> , 2014, 2, .	0.8	13
246	Genetic and diet effects on Ppar- α and Ppar- β signaling pathways in the Berlin Fat Mouse Inbred line with genetic predisposition for obesity. <i>Lipids in Health and Disease</i> , 2010, 9, 99.	3.0	12
247	Sequencing and genotypic analysis of the triosephosphate isomerase (TPI1) locus in a large sample of long-lived Germans. <i>BMC Genetics</i> , 2008, 9, 38.	2.7	11
248	Multi-transcript expression patterns in the gastrolith disk and the hypodermis of the crayfish <i>Cherax quadricarinatus</i> at premolt. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 171-177.	1.0	11
249	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
250	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
251	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
252	Molecular analysis of the t(2;8)(p11;p11) 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

#	ARTICLE	IF	CITATIONS
253	Gene-centromere mapping in meiotic gynogenetic European seabass. <i>BMC Genomics</i> , 2017, 18, 449.	2.8	10
254	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
255	Induction of putative tumor-suppressing genes in Rat-1 fibroblasts by oncogenic Raf-1 as evidenced by robot-assisted complex hybridization. <i>Journal of Molecular Medicine</i> , 2000, 78, 380-388.	3.9	9
256	New clustering module in BDPC bisulfite sequencing data presentation and compilation web application for DNA methylation analyses. <i>BioTechniques</i> , 2009, 47, 781-783.	1.8	9
257	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
258	Complete genome determination and analysis of <i>Acholeplasma oculi</i> strain 19L, highlighting the loss of basic genetic features in the <i>Acholeplasmataceae</i> . <i>BMC Genomics</i> , 2014, 15, 931.	2.8	9
259	Konformationsanalyse, X. Konformation des Oxacycloheptanringes im 1,6-Anhydro-L-idit. <i>Chemische Berichte</i> , 1975, 108, 3201-3209.	0.2	8
260	German Human Methyloome Project Started. <i>Cancer Research</i> , 2006, 66, 7378-7378.	0.9	8
261	Matrix-Assisted Laser Desorption/Ionization Mass Spectrometric Analysis of DNA on Microarrays. <i>Clinical Chemistry</i> , 2006, 52, 1303-1310.	3.2	7
262	Epstein-Barr Virus EBER Transcripts Affect miRNA-Mediated Regulation of Specific Targets and Are Processed to Small RNA Species. <i>Non-coding RNA</i> , 2015, 1, 170-191.	2.6	7
263	Rapid and Sensitive Detection of Calreticulin Type 1 and 2 Mutations by Real-Time Quantitative PCR. <i>Molecular Diagnosis and Therapy</i> , 2015, 19, 329-334.	3.8	7
264	The temperature-regulated DEAD-box RNA helicase CrhR interactome: autoregulation and photosynthesis-related transcripts. <i>Journal of Experimental Botany</i> , 2021, , .	4.8	7
265	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
266	A Role for Molecular Studies in Unveiling the Pathways for Formation of Rotifer Resting Eggs and Their Survival During Dormancy. <i>Topics in Current Genetics</i> , 2010, , 109-132.	0.7	7
267	Purification of ribosomal 30S proteins from the archae-bacterium <i>sulfolobus acidocaldarius</i> by ion-exchange and discontinuous reversed-phase high-performance liquid chromatography. <i>Journal of Chromatography A</i> , 1987, 397, 327-338.	3.7	6
268	Trait-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
269	Complete Genomes of the Anaerobic Degradation Specialists <i>Aromatoleum petrolei</i> and <i>Aromatoleum bremense</i> and <i>PbN1</i> and <i>T</i> . <i>Microbial Physiology</i> , 2021, 31, 16-35.	2.4	6
270	Automated solid-phase extraction for purification of single nucleotide polymorphism genotyping products prior to matrix-assisted laser desorption/ionisation time-of-flight mass spectrometric analysis. <i>Journal of Chromatography A</i> , 2004, 1049, 9-16.	3.7	6

#	ARTICLE	IF	CITATIONS
271	Fluorescent labelling of sequencing primers for automated oligonucleotide synthesis. <i>DNA Sequence</i> , 1992, 2, 273-279.	0.7	5
272	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
273	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
274	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
275	Synthesis and Application of a New Fluorescein Derivative for Fluorescent Labelling of Oligonucleotides and as a Novel Tool for Non-radioactive DNA Sequencing. <i>Liebigs Annalen Der Chemie</i> , 1993, 1993, 1051-1056.	0.8	4
276	Analysis of 41%kb of the DNA sequence from the right arm of chromosome II of <i>Schizosaccharomyces pombe</i> . <i>Yeast</i> , 2001, 18, 1111-1116.	1.7	4
277	Complex and flexible catabolism in <i>Aromatoleum aromaticum</i> . <i>Environmental Microbiology</i> , 2022, 24, 3195-3211.	3.8	4
278	A novel sporadic Burkitt lymphoma cell line (BLUE-1) with a unique t(6;20)(q15;q11.2) rearrangement. <i>Leukemia Research</i> , 2006, 30, 1417-1423.	0.8	3
279	A MLL-KIAA0284 fusion gene in a patient with secondary acute myeloid leukemia and t(11;14)(q23;q32). <i>Blood Cells, Molecules, and Diseases</i> , 2008, 41, 210-214.	1.4	3
280	Ribosomal Proteins and DNA-Binding Protein II from the Extreme Thermophile <i>Bacillus caldolyticus</i> . <i>Biological Chemistry Hoppe-Seyler</i> , 1987, 368, 121-130.	1.4	2
281	Isolation and characterization of Rac1 pseudogenes (~ 1 Rac1 ~ 4 Rac1) in the human genome. <i>Gene</i> , 2004, 341, 189-197.	2.2	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
283	Generation of an 870kb deletion encompassing the <i>Skt/Etl4</i> locus by combination of inter- and intra-chromosomal recombination. <i>BMC Genetics</i> , 2015, 16, 143.	2.7	1
284	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