

Christoph W Sensen

List of Publications by Year in descending order

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155
papers

10,659
citations

31976

53
h-index

32842

100
g-index

184
all docs

184
docs citations

184
times ranked

12164
citing authors

#	ARTICLE	IF	CITATIONS
1	Non-coding Natural Antisense Transcripts: Analysis and Application. Journal of Biotechnology, 2021, 340, 75-101.	3.8	12
2	Cellular Immune Response Involving Multinucleated Giant Hemocytes with Two-Step Genome Amplification in the Drosophilid <i>Zaprionus indianus</i> . Journal of Innate Immunity, 2020, 12, 257-272.	3.8	7
3	Putative Origins of Cell-Free DNA in Humans: A Review of Active and Passive Nucleic Acid Release Mechanisms. International Journal of Molecular Sciences, 2020, 21, 8062.	4.1	103
4	Circulating cell-free DNA is predominantly composed of retrotransposable elements and non-telomeric satellite DNA. Journal of Biotechnology, 2020, 313, 48-56.	3.8	15
5	Enzymes revolutionize the bioproduction of value-added compounds: From enzyme discovery to special applications. Biotechnology Advances, 2020, 40, 107520.	11.7	97
6	Evaluation of host-based molecular markers for the early detection of human sepsis. Journal of Biotechnology, 2020, 310, 80-88.	3.8	11
7	Enterobacteriaceae dominate the core microbiome and contribute to the resistome of arugula (<i>Eruca</i>) Tj ETQq1 1 0,784314 rgBT /Overl 11.1 84	11.1	84
8	Plasticity of a holobiont: desiccation induces fasting-like metabolism within the lichen microbiota. ISME Journal, 2019, 13, 547-556.	9.8	37
9	Instant Feedback Rapid Prototyping for GPU-Accelerated Computation, Manipulation, and Visualization of Multidimensional Data. International Journal of Biomedical Imaging, 2018, 2018, 1-9.	3.9	0
10	Four distinct types of E.C. 1.2.1.30 enzymes can catalyze the reduction of carboxylic acids to aldehydes. Journal of Biotechnology, 2017, 257, 222-232.	3.8	50
11	Benzene and Naphthalene Degrading Bacterial Communities in an Oil Sands Tailings Pond. Frontiers in Microbiology, 2017, 8, 1845.	3.5	37
12	Oil sands tailings ponds harbour a small core prokaryotic microbiome and diverse accessory communities. Journal of Biotechnology, 2016, 235, 187-196.	3.8	26
13	Special Issue on acib, dedicated to the occasion of Prof. Dr. Helmut Schwab's 65th birthday. Journal of Biotechnology, 2016, 235, 1-2.	3.8	0
14	Carnivorous Nutrition in Pitcher Plants (<i>Nepenthes</i> spp.) via an Unusual Complement of Endogenous Enzymes. Journal of Proteome Research, 2016, 15, 3108-3117.	3.7	51
15	Addressing proteolytic efficiency in enzymatic degradation therapy for celiac disease. Scientific Reports, 2016, 6, 30980.	3.3	54
16	Whole genome sequence-based serogrouping of <i>Listeria monocytogenes</i> isolates. Journal of Biotechnology, 2016, 235, 181-186.	3.8	45
17	Characterization of two novel alcohol short-chain dehydrogenases/reductases from <i>Ralstonia eutropha</i> H16 capable of stereoselective conversion of bulky substrates. Journal of Biotechnology, 2016, 221, 78-90.	3.8	19
18	Structure of a Berberine Bridge Enzyme-Like Enzyme with an Active Site Specific to the Plant Family Brassicaceae. PLoS ONE, 2016, 11, e0156892.	2.5	30

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19	Transcriptome analysis of 20 taxonomically related benzylisoquinoline alkaloid-producing plants. <i>BMC Plant Biology</i> , 2015, 15, 227.	3.6	70
20	Comparative analysis of metagenomes from three methanogenic hydrocarbon-degrading enrichment cultures with 41 environmental samples. <i>ISME Journal</i> , 2015, 9, 2028-2045.	9.8	87
21	Roles of Thermophiles and Fungi in Bitumen Degradation in Mostly Cold Oil Sands Outcrops. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6825-6838.	3.1	41
22	Rhizobiales as functional and endosymbiotic members in the lichen symbiosis of <i>Lobaria pulmonaria</i> L. <i>Frontiers in Microbiology</i> , 2015, 6, 53.	3.5	196
23	BRENDA in 2015: exciting developments in its 25th year of existence. <i>Nucleic Acids Research</i> , 2015, 43, D439-D446.	14.5	183
24	Oxidation of Monolignols by Members of the Berberine Bridge Enzyme Family Suggests a Role in Plant Cell Wall Metabolism. <i>Journal of Biological Chemistry</i> , 2015, 290, 18770-18781.	3.4	83
25	LincRNA-p21 acts as a mediator of ING1b-induced apoptosis. <i>Cell Death and Disease</i> , 2015, 6, e1668-e1668.	6.3	30
26	Exploring functional contexts of symbiotic sustain within lichen-associated bacteria by comparative omics. <i>ISME Journal</i> , 2015, 9, 412-424.	9.8	238
27	Transcriptome Profiling of Khat (<i>Catha edulis</i>) and <i>Ephedra sinica</i> Reveals Gene Candidates Potentially Involved in Amphetamine-Type Alkaloid Biosynthesis. <i>PLoS ONE</i> , 2015, 10, e0119701.	2.5	25
28	Diversity of Rumen Bacteria in Canadian Cervids. <i>PLoS ONE</i> , 2014, 9, e89682.	2.5	77
29	Genome research and bioinformatics with relevance to biotechnology. <i>Journal of Biotechnology</i> , 2014, 170, iv.	3.8	0
30	SnowyOwl: accurate prediction of fungal genes by using RNA-Seq and homology information to select among ab initio models. <i>BMC Bioinformatics</i> , 2014, 15, 229.	2.6	30
31	Methanotrophic bacteria in oilsands tailings ponds of northern Alberta. <i>ISME Journal</i> , 2013, 7, 908-921.	9.8	92
32	Phoenix 2: A locally installable large-scale 16S rRNA gene sequence analysis pipeline with Web interface. <i>Journal of Biotechnology</i> , 2013, 167, 393-403.	3.8	53
33	Microbial community and potential functional gene diversity involved in anaerobic hydrocarbon degradation and methanogenesis in an oil sands tailings pond. <i>Genome</i> , 2013, 56, 612-618.	2.0	57
34	Transcriptome analysis based on next-generation sequencing of non-model plants producing specialized metabolites of biotechnological interest. <i>Journal of Biotechnology</i> , 2013, 166, 122-134.	3.8	196
35	Metagenomic analysis of an anaerobic alkane-degrading microbial culture: potential hydrocarbon-activating pathways and inferred roles of community members. <i>Genome</i> , 2013, 56, 599-611.	2.0	82
36	Metagenomics of Hydrocarbon Resource Environments Indicates Aerobic Taxa and Genes to be Unexpectedly Common. <i>Environmental Science & Technology</i> , 2013, 47, 10708-10717.	10.0	179

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37	Contribution of make-up water to the microbial community in an oilfield from which oil is produced by produced water re-injection. <i>International Biodeterioration and Biodegradation</i> , 2013, 81, 44-50.	3.9	20
38	Transcriptome Analysis of <i>Thapsia laciniata</i> Rouy Provides Insights into Terpenoid Biosynthesis and Diversity in Apiaceae. <i>International Journal of Molecular Sciences</i> , 2013, 14, 9080-9098.	4.1	43
39	Genomic compartmentalization of gene families encoding core components of metazoan signaling systems. <i>Genome</i> , 2013, 56, 215-225.	2.0	2
40	Unconventional microarray design reveals the response to obesity is largely tissue specific: analysis of common and divergent responses to diet-induced obesity in insulin-sensitive tissues. <i>Applied Physiology, Nutrition and Metabolism</i> , 2012, 37, 257-268.	1.9	18
41	Complete Genome Sequence of the Fruiting Myxobacterium <i>Coralococcus coralloides</i> DSM 2259. <i>Journal of Bacteriology</i> , 2012, 194, 3012-3013.	2.2	65
42	Molecular and phylogenetic approaches for assessing sources of <i>Cryptosporidium</i> contamination in water. <i>Water Research</i> , 2012, 46, 5135-5150.	11.3	49
43	The Bluejay Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2012, 37, Unit10.9.	25.8	1
44	Methanogenic biodegradation of two-ringed polycyclic aromatic hydrocarbons. <i>FEMS Microbiology Ecology</i> , 2012, 81, 124-133.	2.7	89
45	Synthetic biosystems for the production of high-value plant metabolites. <i>Trends in Biotechnology</i> , 2012, 30, 127-131.	9.3	128
46	Methanogenic toluene metabolism: community structure and intermediates. <i>Environmental Microbiology</i> , 2012, 14, 754-764.	3.8	67
47	A comparative, BAC end sequence enabled map of the genome of the American mink (<i>Neovison vison</i>). <i>Genes and Genomics</i> , 2012, 34, 83-91.	1.4	2
48	Compositions of microbial communities associated with oil and water in a mesothermic oil field. <i>Antonie Van Leeuwenhoek</i> , 2012, 101, 493-506.	1.7	75
49	Metabolomic response to exercise training in lean and diet-induced obese mice. <i>Journal of Applied Physiology</i> , 2011, 110, 1311-1318.	2.5	48
50	Integrative Visualization of Temporally Varying Medical Image Patterns. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 75-84.	1.5	0
51	Carbon and Sulfur Cycling by Microbial Communities in a Gypsum-Treated Oil Sands Tailings Pond. <i>Environmental Science & Technology</i> , 2011, 45, 439-446.	10.0	177
52	Microbial community succession in a bioreactor modeling a souring low-temperature oil reservoir subjected to nitrate injection. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 799-810.	3.6	68
53	Effect of Sodium Bisulfite Injection on the Microbial Community Composition in a Brackish-Water-Transporting Pipeline. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6908-6917.	3.1	74
54	Estimating Cell Count and Distribution in Labeled Histological Samples Using Incremental Cell Search. <i>International Journal of Biomedical Imaging</i> , 2011, 2011, 1-16.	3.9	7

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55	Integrative visualization of temporally varying medical image patterns. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 161.	1.5	0
56	Micro-computed tomography-based phenotypic approaches in embryology: procedural artifacts on assessments of embryonic craniofacial growth and development. <i>BMC Developmental Biology</i> , 2010, 10, 18.	2.1	43
57	Building generic anatomical models using virtual model cutting and iterative registration. <i>BMC Medical Imaging</i> , 2010, 10, 5.	2.7	0
58	Phylogenetic Analysis of the MS4A and TMEM176 Gene Families. <i>PLoS ONE</i> , 2010, 5, e9369.	2.5	57
59	Programming-by-Example Meets the Semantic Web: Using Ontologies and Web Services to Close the Semantic Gap. , 2010, , .		1
60	Visualization of biological shape transformation by 3D model morphing. , 2010, , .		0
61	Helping Biologists Effectively Build Workflows, without Programming. <i>Lecture Notes in Computer Science</i> , 2010, , 74-89.	1.3	2
62	Spatiotemporal integration of molecular and anatomical data in virtual reality using semantic mapping. <i>International Journal of Nanomedicine</i> , 2009, 4, 79.	6.7	4
63	Rapid Access to Genes of Biotechnologically Useful Enzymes by Partial Genome Sequencing: The Thermoalkaliphile <i>Anaerobranca gottschalkii</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009, 16, 81-90.	1.0	7
64	Disease-specific motifs can be identified in circulating nucleic acids from live elk and cattle infected with transmissible spongiform encephalopathies. <i>Nucleic Acids Research</i> , 2009, 37, 550-556.	14.5	75
65	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	27.8	243
66	CAVEman, An Object-Oriented Model of the Human Body. , 2009, , 289-300.		2
67	Geometric Morphometrics and the Study of Development. , 2009, , 319-336.		7
68	Virtual Reality Meets Functional Genomics. , 2009, , 601-613.		0
69	Genomic Data Visualization: The Bluejay System. , 2009, , 395-409.		0
70	Fast interactive integration of cross-sectional image datasets and surface data for morphometric analysis. <i>Studies in Health Technology and Informatics</i> , 2009, 142, 183-8.	0.3	1
71	An efficient virtual dissection tool to create generic models for anatomical atlases. <i>Studies in Health Technology and Informatics</i> , 2009, 142, 426-8.	0.3	1
72	CAVEman: Standardized anatomical context for biomedical data mapping. <i>Anatomical Sciences Education</i> , 2008, 1, 10-18.	3.7	14

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73	A novel group of multiâ€GAPâ€domain proteins. <i>Molecular Reproduction and Development</i> , 2008, 75, 1578-1589.	2.0	0
74	Bluejay 1.0: genome browsing and comparison with rich customization provision and dynamic resource linking. <i>BMC Bioinformatics</i> , 2008, 9, 450.	2.6	9
75	Interspecies data mining to predict novel ING-protein interactions in human. <i>BMC Genomics</i> , 2008, 9, 426.	2.8	12
76	Creating Bioinformatics Semantic Web Services from Existing Web Services: A Real-World Application of SAWSDL. , 2008, , .		4
77	Gene Expression by the Sulfate-Reducing Bacterium <i>Desulfovibrio vulgaris</i> Hildenborough Grown on an Iron Electrode under Cathodic Protection Conditions. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2404-2413.	3.1	40
78	Interoperability with Moby 1.0--It's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , 2008, 9, 220-231.	6.5	91
79	Visual Comparison of Multiple Gene Expression Datasets in a Genomic Context. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.5	5
80	Integration of genomic and medical data into a 3D atlas of human anatomy. <i>Studies in Health Technology and Informatics</i> , 2008, 132, 526-31.	0.3	6
81	Visual comparison of multiple gene expression datasets in a genomic context. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.5	1
82	Response of the Hyperthermophilic Archaeon <i>Sulfolobus solfataricus</i> to UV Damage. <i>Journal of Bacteriology</i> , 2007, 189, 8708-8718.	2.2	128
83	Semantic Web Service provision: a realistic framework for Bioinformatics programmers. <i>Bioinformatics</i> , 2007, 23, 1178-1180.	4.1	14
84	Tracking Host Sources of <i>Cryptosporidium</i> spp. in Raw Water for Improved Health Risk Assessment. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3945-3957.	3.1	107
85	Age-dependent change in the 3D structure of cortical porosity at the human femoral midshaft. <i>Bone</i> , 2007, 40, 957-965.	2.9	178
86	Combining a High-Throughput Bioinformatics Grid and Bioinformatics Web Services. , 2007, , 1-10.		0
87	Bluejay: A Highly Scalable and Integrative Visual Environment for Genome Exploration. , 2007, , .		2
88	Using a Novel Data Transformation Technique to Provide the EMBOSS Software Suite as Semantic Web Services. , 2007, , .		6
89	Seahawk: moving beyond HTML in Web-based bioinformatics analysis. <i>BMC Bioinformatics</i> , 2007, 8, 208.	2.6	35
90	Elucidating the transcription cycle of the UV-inducible hyperthermophilic archaeal virus SSV1 by DNA microarrays. <i>Virology</i> , 2007, 365, 48-59.	2.4	56

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91	Effect of Voxel Size on 3D Micro-CT Analysis of Cortical Bone Porosity. <i>Calcified Tissue International</i> , 2007, 80, 211-219.	3.1	86
92	Gene transcript and metabolite profiling of elicitor-induced opium poppy cell cultures reveals the coordinate regulation of primary and secondary metabolism. <i>Planta</i> , 2007, 225, 1085-1106.	3.2	98
93	Enhancing Bluejay with Scalability, Genome Comparison and Microarray Visualization. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2007, , 557-568.	0.2	0
94	Expressed sequence tags from Madagascar periwinkle (<i>Catharanthus roseus</i>). <i>FEBS Letters</i> , 2006, 580, 4501-4507.	2.8	49
95	Creating hierarchical models of protein families based on Expressed Sequence Tags: The "Sprockets" analysis pipeline. <i>Analytica Chimica Acta</i> , 2006, 564, 123-132.	5.4	0
96	Reconstructing the Mosaic Glycolytic Pathway of the Anaerobic Eukaryote <i>Monocercomonoides</i> . <i>Eukaryotic Cell</i> , 2006, 5, 2138-2146.	3.4	38
97	On the way to building an integrated computational environment for the study of developmental patterns and genetic diseases. <i>International Journal of Nanomedicine</i> , 2006, 1, 89-96.	6.7	7
98	Maintenance of ancestral complexity and non-metazoan genes in two basal cnidarians. <i>Trends in Genetics</i> , 2005, 21, 633-639.	6.7	315
99	Phylogenetic Analysis of the ING Family of PHD Finger Proteins. <i>Molecular Biology and Evolution</i> , 2005, 22, 104-116.	8.9	164
100	Jabiru: Harnessing Java 3D Behaviors for Device and Display Portability. <i>IEEE Computer Graphics and Applications</i> , 2005, 25, 70-80.	1.2	5
101	MODULAR NEURAL NETWORKS AND THEIR APPLICATION IN EXON PREDICTION. , 2005, , .		2
102	Bioinformatics visualization and integration with open standards: the Bluejay genomic browser. <i>In Silico Biology</i> , 2005, 5, 187-98.	0.9	13
103	Reconstruction of the Central Carbohydrate Metabolism of <i>Thermoproteus tenax</i> by Use of Genomic and Biochemical Data. <i>Journal of Bacteriology</i> , 2004, 186, 2179-2194.	2.2	66
104	Osprey: a comprehensive tool employing novel methods for the design of oligonucleotides for DNA sequencing and microarrays. <i>Nucleic Acids Research</i> , 2004, 32, e133-e133.	14.5	47
105	4D Bioinformatics: A New Look at the Ribosome as an Example. <i>IUBMB Life</i> , 2003, 55, 279-283.	3.4	7
106	From model organisms to organismal models: visualizing complex genomic datasets. <i>Biosilico</i> , 2003, 1, 23-26.	0.5	1
107	The analysis of 100 genes supports the grouping of three highly divergent amoebae: <i>Dictyostelium</i> , <i>Entamoeba</i> , and <i>Mastigamoeba</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1414-1419.	7.1	352
108	Transcription Profiling of <i>Candida albicans</i> Cells Undergoing the Yeast-to-Hyphal Transition. <i>Molecular Biology of the Cell</i> , 2002, 13, 3452-3465.	2.1	346

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109	Using CAVEÂ® Technology for Functional Genomics Studies. <i>Diabetes Technology and Therapeutics</i> , 2002, 4, 867-871.	4.4	11
110	First insight into the genome of an uncultivated crenarchaeote from soil. <i>Environmental Microbiology</i> , 2002, 4, 603-611.	3.8	161
111	The Phylogenetic Position of the Pelobiont <i>Mastigamoeba balamuthi</i> Based on Sequences of rDNA and Translation Elongation Factors EF-1alpha and EF-2. <i>Journal of Eukaryotic Microbiology</i> , 2002, 49, 1-10.	1.7	35
112	Bluejay: A Browser for Linear Units in Java. , 2002, , 183-194.		1
113	Properties of the recombinant Î±-glucosidase from <i>Sulfolobus solfataricus</i> in relation to starch processing. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2001, 11, 787-794.	1.8	13
114	Presence of Prokaryotic and Eukaryotic Species in All Subgroups of the PP i-Dependent Group II Phosphofruktokinase Protein Family. <i>Journal of Bacteriology</i> , 2001, 183, 6714-6716.	2.2	30
115	The complete genome of the crenarchaeon <i>Sulfolobus solfataricus</i> P2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 7835-7840.	7.1	718
116	Two different and highly organized mechanisms of translation initiation in the archaeon <i>Sulfolobus solfataricus</i> . <i>Extremophiles</i> , 2000, 4, 175-179.	2.3	115
117	Enolase from <i>Trypanosoma brucei</i> , from the Amitochondriate Protist <i>Mastigamoeba balamuthi</i> , and from the Chloroplast and Cytosol of <i>Euglena gracilis</i> : Pieces in the Evolutionary Puzzle of the Eukaryotic Glycolytic Pathway. <i>Molecular Biology and Evolution</i> , 2000, 17, 989-1000.	8.9	65
118	High Spontaneous Mutation Rate in the Hyperthermophilic Archaeon <i>Sulfolobus solfataricus</i> Is Mediated by Transposable Elements. <i>Journal of Bacteriology</i> , 2000, 182, 2574-2581.	2.2	116
119	Identification and Molecular Characterization of the First Î±-Xylosidase from an Archaeon. <i>Journal of Biological Chemistry</i> , 2000, 275, 22082-22089.	3.4	68
120	MAGPIE/EGRET Annotation of the 2.9-Mb <i>Drosophila melanogaster</i> Adh Region. <i>Genome Research</i> , 2000, 10, 502-510.	5.5	19
121	Gene content and organization of a 281-kbp contig from the genome of the extremely thermophilic archaeon, <i>Sulfolobus solfataricus</i> P2. <i>Genome</i> , 2000, 43, 116-136.	2.0	2
122	Mutations in ABC1 in Tangier disease and familial high-density lipoprotein deficiency. <i>Nature Genetics</i> , 1999, 22, 336-345.	21.4	1,609
123	Mutations in the ABC 1 gene in familial HDL deficiency with defective cholesterol efflux. <i>Lancet</i> , The, 1999, 354, 1341-1346.	13.7	345
124	Two DNA polymerase sliding clamps from the thermophilic archaeon <i>Sulfolobus solfataricus</i> . <i>Journal of Molecular Biology</i> , 1999, 291, 47-57.	4.2	52
125	Molecular Analysis of pDL10 from <i>Acidianus ambivalens</i> Reveals a Family of Related Plasmids from Extremely Thermophilic and Acidophilic Archaea. <i>Genetics</i> , 1999, 152, 1307-1314.	2.9	40
126	Completing the sequence of the <i>Sulfolobus solfataricus</i> P2 genome. <i>Extremophiles</i> , 1998, 2, 305-312.	2.3	58

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127	Sulfolobus islandicus plasmids pRN1 and pRN2 share distant but common evolutionary ancestry. <i>Extremophiles</i> , 1998, 2, 391-393.	2.3	44
128	NUCLEOTIDE SEQUENCES OF SMALL-SUBUNIT AND INTERNAL TRANSCRIBED SPACER REGIONS OF NUCLEAR rRNA GENES SUPPORT THE AUTONOMY OF SOME GENERA OF THE GELIDIALES (RHODOPHYTA). <i>Journal of Phycology</i> , 1998, 34, 299-305.	2.3	18
129	Sulfolobus genome: from genomics to biology. <i>Current Opinion in Microbiology</i> , 1998, 1, 584-588.	5.1	23
130	Sequencing the Genome of Sulfolobus solfataricus P2. , 1998, , 552-558.		0
131	MAGPIE: A Multipurpose Automated Genome Project Investigation Environment for Ongoing Sequencing Projects. , 1998, , 559-566.		0
132	Evolutionary analysis of the hisCGABdFDEHI gene cluster from the archaeon Sulfolobus solfataricus P2. <i>Journal of Bacteriology</i> , 1997, 179, 4429-4432.	2.2	17
133	Fully automated genome analysis that reflects user needs and preferences. A detailed introduction to the MAGPIE system architecture. <i>Biochimie</i> , 1996, 78, 302-310.	2.6	116
134	TheSulfolobus solfataricusP2 genome project. <i>FEBS Letters</i> , 1996, 389, 88-91.	2.8	21
135	MAGPIE: automated genome interpretation. <i>Trends in Genetics</i> , 1996, 12, 76-78.	6.7	106
136	Complete Nucleotide Sequence of theSulfolobus islandicusMulticopy Plasmid pRN1. <i>Plasmid</i> , 1996, 35, 141-144.	1.4	63
137	Organizational characteristics and information content of an archaeal genome: 156kb of sequence from Sulfolobus solfataricus P2. <i>Molecular Microbiology</i> , 1996, 22, 175-191.	2.5	93
138	An archaeobacterial homolog of pelota, a meiotic cell division protein in eukaryotes. <i>FEMS Microbiology Letters</i> , 1996, 144, 151-155.	1.8	0
139	The origin of land plants: Phylogenetic relationships among charophytes, bryophytes, and vascular plants inferred from complete small-subunit ribosomal RNA gene sequences. <i>Journal of Molecular Evolution</i> , 1995, 41, 74-84.	1.8	107
140	Nucleotide sequence and analysis of the centromeric region of yeast chromosome IX. <i>Yeast</i> , 1995, 11, 61-78.	1.7	21
141	Complete DNA sequence of yeast chromosome XI. <i>Nature</i> , 1994, 369, 371-378.	27.8	382
142	Sequencing and analysis of 51Â·6 kilobases on the left arm of chromosome XI fromSaccharomyces cerevisiae reveals 23 open reading frames including theFAS1 gene. <i>Yeast</i> , 1993, 9, 1343-1348.	1.7	9
143	The production of clonal and axenic cultures of microalgae using fluorescence-activated cell sorting. <i>European Journal of Phycology</i> , 1993, 28, 93-97.	2.0	68
144	Separation of up to 1000 bases on a modified A.L.F. DNA sequencer. <i>Nucleic Acids Research</i> , 1993, 21, 6042-6044.	14.5	18

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145	Molecular Phylogeny of Algal Plastids: A Brief Review of Host/Endosymbiont Genome Development Based on Sequence Comparisons. , 1992, , 171-192.		0
146	Bioinformatics: Genomic Data Representation through Imagesâ€™ MAGPIE as an Example. , 0, , 345-363.		2
147	Ethical, Legal and Social Issues: Genomicsâ€™ Five Years from Now. , 0, , 397-405.		0
148	Genome Data Representation Through Images: The MAGPIE/Bluejay System. , 0, , 383-414.		3
149	Systems Biology. , 0, , 491-505.		0
150	The (Im)perfect Humanâ€™ His Own Creator? Bioethics and Genetics at the Beginning of Life. , 0, , 561-570.		0
151	The Future of Large-Scale Life Science Research. , 0, , 572-584.		0
152	Yeast Two-hybrid Technologies. , 0, , 261-272.		0
153	Structural Genomics. , 0, , 273-295.		0
154	Sequencing Microbial Genomes. , 0, , 1-9.		3
155	Genomics-Five Years from Now. , 0, , 431-439.		0