

Christos A Ouzounis

List of Publications by Year in descending order

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Version: 2024-02-01

170
papers

10,320
citations

36303

51
h-index

38395

95
g-index

180
all docs

180
docs citations

180
times ranked

13646
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein interaction maps for complete genomes based on gene fusion events. <i>Nature</i> , 1999, 402, 86-90.	27.8	1,032
2	Expansion of the BioCyc collection of pathway/genome databases to 160 genomes. <i>Nucleic Acids Research</i> , 2005, 33, 6083-6089.	14.5	570
3	Detection of functional modules from protein interaction networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 49-57.	2.6	362
4	Are splicing mutations the most frequent cause of hereditary disease?. <i>FEBS Letters</i> , 2005, 579, 1900-1903.	2.8	327
5	Stereotyped patterns of somatic hypermutation in subsets of patients with chronic lymphocytic leukemia: implications for the role of antigen selection in leukemogenesis. <i>Blood</i> , 2008, 111, 1524-1533.	1.4	285
6	Genome-wide identification of genes likely to be involved in human genetic disease. <i>Nucleic Acids Research</i> , 2004, 32, 3108-3114.	14.5	226
7	Comparative Genomics of Transcriptional Control in the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2004, 14, 1548-1554.	5.5	221
8	The net of life: Reconstructing the microbial phylogenetic network. <i>Genome Research</i> , 2005, 15, 954-959.	5.5	211
9	A database of protein structure families with common folding motifs. <i>Protein Science</i> , 1992, 1, 1691-1698.	7.6	193
10	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	5.6	190
11	Critical assessment of protein intrinsic disorder prediction. <i>Nature Methods</i> , 2021, 18, 472-481.	19.0	187
12	GeneRAGE: a robust algorithm for sequence clustering and domain detection. <i>Bioinformatics</i> , 2000, 16, 451-457.	4.1	186
13	The Balance of Driving Forces During Genome Evolution in Prokaryotes. <i>Genome Research</i> , 2003, 13, 1589-1594.	5.5	173
14	Transcription regulation and environmental adaptation in bacteria. <i>Trends in Microbiology</i> , 2003, 11, 248-253.	7.7	168
15	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
16	Conserved Clusters of Functionally Related Genes in Two Bacterial Genomes. <i>Journal of Molecular Evolution</i> , 1997, 44, 66-73.	1.8	163
17	Modeling the percolation of annotation errors in a database of protein sequences. <i>Bioinformatics</i> , 2002, 18, 1641-1649.	4.1	153
18	Prediction of Protein Structure by Evaluation of Sequence-structure Fitness. <i>Journal of Molecular Biology</i> , 1993, 232, 805-825.	4.2	146

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19	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	14.5	141
20	Genome evolution reveals biochemical networks and functional modules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15428-15433.	7.1	140
21	Emergence, development and diversification of the TGF- β signalling pathway within the animal kingdom. <i>BMC Evolutionary Biology</i> , 2009, 9, 28.	3.2	137
22	Computational disease gene identification: a concert of methods prioritizes type 2 diabetes and obesity candidate genes. <i>Nucleic Acids Research</i> , 2006, 34, 3067-3081.	14.5	134
23	A minimal estimate for the gene content of the last universal common ancestor—exobiology from a terrestrial perspective. <i>Research in Microbiology</i> , 2006, 157, 57-68.	2.1	130
24	KOW: a novel motif linking a bacterial transcription factor with ribosomal proteins. <i>Trends in Biochemical Sciences</i> , 1996, 21, 425-426.	7.5	120
25	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	14.5	117
26	Protein families and TRIBES in genome sequence space. <i>Nucleic Acids Research</i> , 2003, 31, 4632-4638.	14.5	113
27	Functional associations of proteins in entire genomes by means of exhaustive detection of gene fusions. <i>Genome Biology</i> , 2001, 2, research0034.1.	9.6	108
28	Comprehensive sequence analysis of the 182 predicted open reading frames of yeast chromosome III. <i>Protein Science</i> , 1992, 1, 1677-1690.	7.6	106
29	Early bioinformatics: the birth of a discipline—a personal view. <i>Bioinformatics</i> , 2003, 19, 2176-2190.	4.1	105
30	HipMCL: a high-performance parallel implementation of the Markov clustering algorithm for large-scale networks. <i>Nucleic Acids Research</i> , 2018, 46, e33-e33.	14.5	104
31	Universal Protein Families and the Functional Content of the Last Universal Common Ancestor. <i>Journal of Molecular Evolution</i> , 1999, 49, 413-423.	1.8	103
32	Classification schemes for protein structure and function. <i>Nature Reviews Genetics</i> , 2003, 4, 508-519.	16.3	101
33	Prediction of protein interactions: metabolic enzymes are frequently involved in gene fusion. <i>Nature Genetics</i> , 2000, 26, 141-142.	21.4	91
34	The Phylogenetic Extent of Metabolic Enzymes and Pathways. <i>Genome Research</i> , 2003, 13, 422-427.	5.5	91
35	TFIIB, an evolutionary link between the transcription machineries of archaeobacteria and eukaryotes. <i>Cell</i> , 1992, 71, 189-190.	28.9	90
36	The past, present and future of genome-wide re-annotation. <i>Genome Biology</i> , 2002, 3, comment2001.1.	9.6	86

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37	Exploring the <i>Mycoplasma capricolum</i> genome: a minimal cell reveals its physiology. <i>Molecular Microbiology</i> , 1995, 16, 955-967.	2.5	84
38	The emergence of major cellular processes in evolution. <i>FEBS Letters</i> , 1996, 390, 119-123.	2.8	81
39	Structural and functional properties of genes involved in human cancer. <i>BMC Genomics</i> , 2006, 7, 3.	2.8	75
40	An updated metabolic view of the <i>Bacillus subtilis</i> 168 genome. <i>Microbiology (United Kingdom)</i> , 2013, 159, 757-770.	1.8	72
41	Disentangling the complexity of low complexity proteins. <i>Briefings in Bioinformatics</i> , 2020, 21, 458-472.	6.5	70
42	Measuring genome conservation across taxa: divided strains and united kingdoms. <i>Nucleic Acids Research</i> , 2005, 33, 616-621.	14.5	69
43	Percolation of annotation errors through hierarchically structured protein sequence databases. <i>Mathematical Biosciences</i> , 2005, 193, 223-234.	1.9	67
44	Functional Evolution of the Yeast Protein Interaction Network. <i>Molecular Biology and Evolution</i> , 2004, 21, 1171-1176.	8.9	66
45	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003, 19, 717-726.	4.1	65
46	Tumorigenic Properties of Iron Regulatory Protein 2 (IRP2) Mediated by Its Specific 73-Amino Acids Insert. <i>PLoS ONE</i> , 2010, 5, e10163.	2.5	60
47	Whole-genome sequence annotation: 'Going wrong with confidence'. <i>Molecular Microbiology</i> , 1999, 32, 886-887.	2.5	58
48	What's in a genome?. <i>Nature</i> , 1992, 358, 287-287.	27.8	57
49	Myriads of protein families, and still counting. <i>Genome Biology</i> , 2003, 4, 401.	9.6	55
50	Transcriptome classification reveals molecular subtypes in psoriasis. <i>BMC Genomics</i> , 2012, 13, 472.	2.8	55
51	From genome sequences to protein function. <i>Current Opinion in Structural Biology</i> , 1994, 4, 393-403.	5.7	54
52	Sequence-based feature prediction and annotation of proteins. <i>Genome Biology</i> , 2009, 10, 206.	9.6	53
53	A Systems Model for Immune Cell Interactions Unravels the Mechanism of Inflammation in Human Skin. <i>PLoS Computational Biology</i> , 2010, 6, e1001024.	3.2	51
54	Rise and Demise of Bioinformatics? Promise and Progress. <i>PLoS Computational Biology</i> , 2012, 8, e1002487.	3.2	51

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55	An Exponential Core in the Heart of the Yeast Protein Interaction Network. <i>Molecular Biology and Evolution</i> , 2005, 22, 421-425.	8.9	50
56	BioLayoutJava. <i>Applied Bioinformatics</i> , 2005, 4, 71-74.	1.6	50
57	Recent developments and future directions in computational genomics. <i>FEBS Letters</i> , 2000, 480, 42-48.	2.8	49
58	Homology of the NifS family of proteins to a new class of pyridoxal phosphate-dependent enzymes. <i>FEBS Letters</i> , 1993, 322, 159-164.	2.8	46
59	GeneTRACE-reconstruction of gene content of ancestral species. <i>Bioinformatics</i> , 2003, 19, 1412-1416.	4.1	46
60	Highly consistent patterns for inherited human diseases at the molecular level. <i>Bioinformatics</i> , 2006, 22, 269-277.	4.1	46
61	Dictionary building via unsupervised hierarchical motif discovery in the sequence space of natural proteins. , 1999, 37, 264-277.		45
62	No wisdom in the crowd: genome annotation in the era of big data – current status and future prospects. <i>Microbial Biotechnology</i> , 2018, 11, 588-605.	4.2	45
63	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	12.6	45
64	A structure-derived sequence pattern for the detection of type I copper binding domains in distantly related proteins. <i>FEBS Letters</i> , 1991, 279, 73-78.	2.8	44
65	Novel protein families in archaean genomes. <i>Nucleic Acids Research</i> , 1995, 23, 565-570.	14.5	40
66	Genome sequences and great expectations. <i>Genome Biology</i> , 2000, 2, interactions0001.1.	9.6	40
67	COmplete GENome Tracking (COGENT): a flexible data environment for computational genomics. <i>Bioinformatics</i> , 2003, 19, 1451-1452.	4.1	40
68	The phylogenetic diversity of eukaryotic transcription. <i>Nucleic Acids Research</i> , 2003, 31, 653-660.	14.5	39
69	From Genes to Genomes: Universal Scale-invariant Properties of Microbial Chromosome Organisation. <i>Journal of Molecular Biology</i> , 2003, 332, 617-633.	4.2	38
70	Annotation inconsistencies beyond sequence similarity-based function prediction – phylogeny and genome structure. <i>Standards in Genomic Sciences</i> , 2015, 10, 108.	1.5	38
71	Ready for a motif submission? A proposed checklist. <i>Trends in Biochemical Sciences</i> , 1995, 20, 104.	7.5	37
72	Novelties from the complete genome of <i>Mycoplasma genitalium</i> . <i>Molecular Microbiology</i> , 1996, 20, 898-900.	2.5	37

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73	Automated metabolic reconstruction for <i>Methanococcus jannaschii</i> . <i>Archaea</i> , 2004, 1, 223-229.	2.3	37
74	PuReD-MCL: a graph-based PubMed document clustering methodology. <i>Bioinformatics</i> , 2008, 24, 1935-1941.	4.1	35
75	Genome coverage, literally speaking. <i>EMBO Reports</i> , 2005, 6, 397-399.	4.5	34
76	Computational complexity of algorithms for sequence comparison, short-read assembly and genome alignment. <i>BioSystems</i> , 2017, 156-157, 72-85.	2.0	34
77	New protein functions in yeast chromosome VIII. <i>Protein Science</i> , 1995, 4, 2424-2428.	7.6	33
78	Stratification of hospitalized COVID-19 patients into clinical severity progression groups by immuno-phenotyping and machine learning. <i>Nature Communications</i> , 2022, 13, 915.	12.8	32
79	Maps, books and other metaphors for systems biology. <i>BioSystems</i> , 2006, 85, 6-10.	2.0	31
80	Complete genome sequence of <i>Arthrobacter phenanthrenivorans</i> type strain (Sphe3). <i>Standards in Genomic Sciences</i> , 2011, 4, 123-130.	1.5	31
81	The modular structure of NifU proteins. <i>Trends in Biochemical Sciences</i> , 1994, 19, 199-200.	7.5	30
82	Taxonomic Identification of Mediterranean Pines and Their Hybrids Based on the High Resolution Melting (HRM) and trnL Approaches: From Cytoplasmic Inheritance to Timber Tracing. <i>PLoS ONE</i> , 2013, 8, e60945.	2.5	30
83	Novel Structural Features of the Human Histocompatibility Molecules HLA-DQ as Revealed by Modeling Based on the Published Structure of the Related Molecule HLA-DR. <i>Journal of Structural Biology</i> , 1996, 117, 145-163.	2.8	29
84	Functional Versatility and Molecular Diversity of the Metabolic Map of <i>Escherichia coli</i> . <i>Genome Research</i> , 2001, 11, 1503-1510.	5.5	29
85	A <i>Drosophila</i> hsp70 gene contains long, antiparallel, coupled open reading frames (LAC ORFs) conserved in homologous loci. <i>Journal of Molecular Evolution</i> , 1995, 41, 414-420.	1.8	28
86	Computational comparisons of model genomes. <i>Trends in Biotechnology</i> , 1996, 14, 280-285.	9.3	28
87	Atypical Divergence of SARS-CoV-2 Orf8 from Orf7a within the Coronavirus Lineage Suggests Potential Stealthy Viral Strategies in Immune Evasion. <i>MBio</i> , 2021, 12, .	4.1	28
88	Bacterial DNA replication initiation factor priA is related to proteins belonging to the "DEAD-box" family. <i>Nucleic Acids Research</i> , 1991, 19, 6953-6953.	14.5	27
89	Primary and secondary structural patterns in eukaryotic cytochrome P-450 families correspond to structures of the helix-rich domain of <i>Pseudomonas putida</i> cytochrome P-450cam. Indications for a similar overall topology. <i>FEBS Journal</i> , 1991, 198, 307-315.	0.2	25
90	Parallel origins of the nucleosome core and eukaryotic transcription from Archaea. <i>Journal of Molecular Evolution</i> , 1996, 42, 234-239.	1.8	25

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91	Evolution of immunoglobulin-like modules in chitinases: their structural flexibility and functional implications. <i>Folding & Design</i> , 1997, 2, 291-294.	4.5	25
92	The PWI motif: a new protein domain in splicing factors. <i>Trends in Biochemical Sciences</i> , 1999, 24, 179-180.	7.5	25
93	Probabilistic annotation of protein sequences based on functional classifications. <i>BMC Bioinformatics</i> , 2005, 6, 302.	2.6	24
94	Bioinformatics and the theoretical foundations of molecular biology. <i>Bioinformatics</i> , 2002, 18, 377-378.	4.1	23
95	Beyond 100 genomes. <i>Genome Biology</i> , 2003, 4, 402.	9.6	23
96	BioTextQuest + : a knowledge integration platform for literature mining and concept discovery. <i>Bioinformatics</i> , 2014, 30, 3249-3256.	4.1	23
97	Barley β -glucosidase: Expression during seed germination and maturation and partial amino acids sequences. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 1994, 1199, 52-58.	2.4	22
98	Genomes with distinct function composition. <i>FEBS Letters</i> , 1996, 389, 96-101.	2.8	22
99	CoGenT++: an extensive and extensible data environment for computational genomics. <i>Bioinformatics</i> , 2005, 21, 3806-3810.	4.1	22
100	Complete genome sequence of <i>Mycobacterium</i> sp. strain (Spir1) and reclassification to <i>Mycobacterium gilvum</i> Spir1. <i>Standards in Genomic Sciences</i> , 2011, 5, 144-153.	1.5	22
101	A Path toward SARS-CoV-2 Attenuation: Metabolic Pressure on CTP Synthesis Rules the Virus Evolution. <i>Genome Biology and Evolution</i> , 2020, 12, 2467-2485.	2.5	22
102	MagicMatch—cross-referencing sequence identifiers across databases. <i>Bioinformatics</i> , 2005, 21, 3429-3430.	4.1	21
103	Gene Network and Proteomic Analyses of Cardiac Responses to Pathological and Physiological Stress. <i>Circulation: Cardiovascular Genetics</i> , 2013, 6, 588-597.	5.1	21
104	Comparison of sequence masking algorithms and the detection of biased protein sequence regions. <i>Bioinformatics</i> , 2003, 19, 1672-1681.	4.1	20
105	Functional Genomics Evidence Unearths New Moonlighting Roles of Outer Ring Coat Nucleoporins. <i>Scientific Reports</i> , 2014, 4, 4655.	3.3	20
106	Experimental evidence validating the computational inference of functional associations from gene fusion events: a critical survey. <i>Briefings in Bioinformatics</i> , 2014, 15, 443-454.	6.5	19
107	Biological Information Extraction and Co-occurrence Analysis. <i>Methods in Molecular Biology</i> , 2014, 1159, 77-92.	0.9	19
108	Genetic variation between <i>Helicobacter pylori</i> strains: gene acquisition or loss?. <i>Trends in Microbiology</i> , 2002, 10, 445-447.	7.7	18

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109	Errors in Genome Reviews. , 1998, 281, 1453c-1453.		18
110	RGD sequences in several receptor proteins: novel cell adhesion function of receptors?. International Journal of Biological Macromolecules, 1998, 22, 51-57.	7.5	17
111	Genome-wide expression patterns in physiological cardiac hypertrophy. BMC Genomics, 2010, 11, 557.	2.8	17
112	Functional Genomics Assistant (FUGA): a toolbox for the analysis of complex biological networks. BMC Research Notes, 2011, 4, 462.	1.4	17
113	Nucleic acid-binding metabolic enzymes: Living fossils of stereochemical interactions?. Journal of Molecular Evolution, 1995, 40, 564-569.	1.8	16
114	Sequence analysis of the Methanococcus jannaschii genome and the prediction of protein function. Bioinformatics, 1997, 13, 481-483.	4.1	16
115	Clustering the annotation space of proteins. BMC Bioinformatics, 2005, 6, 24.	2.6	16
116	Denosing inferred functional association networks obtained by gene fusion analysis. BMC Genomics, 2007, 8, 460.	2.8	16
117	A recent origin of Orf3a from M protein across the coronavirus lineage arising by sharp divergence. Computational and Structural Biotechnology Journal, 2020, 18, 4093-4102.	4.1	16
118	Detection of Genomic Idiosyncrasies Using Fuzzy Phylogenetic Profiles. PLoS ONE, 2013, 8, e52854.	2.5	16
119	Mechanisms of Specificity in mRNA Degradation: Autoregulation and Cognate Interactions. Journal of Theoretical Biology, 1993, 163, 373-392.	1.7	14
120	Reproducibility in genome sequence annotation: the Plasmodium falciparum chromosome 2 case. FEBS Letters, 1999, 451, 354-355.	2.8	14
121	Ancestral state reconstructions for genomes. Current Opinion in Genetics and Development, 2005, 15, 595-600.	3.3	14
122	CORRIE: enzyme sequence annotation with confidence estimates. BMC Bioinformatics, 2007, 8, S3.	2.6	14
123	Metabolic innovations towards the human lineage. BMC Evolutionary Biology, 2008, 8, 247.	3.2	14
124	BioTextQuest: a web-based biomedical text mining suite for concept discovery. Bioinformatics, 2011, 27, 3327-3328.	4.1	13
125	A Strong Seasonality Pattern for Covid-19 Incidence Rates Modulated by UV Radiation Levels. Viruses, 2021, 13, 574.	3.3	13
126	Copy Number and Loss of Heterozygosity Detected by SNP Array of Formalin-Fixed Tissues Using Whole-Genome Amplification. PLoS ONE, 2011, 6, e24503.	2.5	13

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127	Genome-wide detection and family clustering of ion channels. FEBS Letters, 2002, 514, 129-134.	2.8	12
128	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12
129	Lineage-specific partitions in archaeal transcription. Archaea, 2006, 2, 117-125.	2.3	11
130	The properties of protein family space depend on experimental design. Bioinformatics, 2005, 21, 2618-2622.	4.1	10
131	Promoter Complexity and Tissue-Specific Expression of Stress Response Components in <i>Mytilus galloprovincialis</i> , a Sessile Marine Invertebrate Species. PLoS Computational Biology, 2010, 6, e1000847.	3.2	9
132	The Chlamydiales Pangenome Revisited: Structural Stability and Functional Coherence. Genes, 2012, 3, 291-319.	2.4	9
133	Sequence evidence for common ancestry of eukaryotic endomembrane coatomers. Scientific Reports, 2016, 6, 22311.	3.3	9
134	ThiD-TenA: A Gene Pair Fusion in Eukaryotes. Journal of Molecular Evolution, 1997, 45, 708-711.	1.8	8
135	A ferredoxin-like domain in RNA polymerase 30/40-kDa subunits. Trends in Biochemical Sciences, 1998, 23, 169-170.	7.5	8
136	PseuRECA: genome annotation and gene context analysis for <i>Pseudomonas aeruginosa</i> PAO1. Bioinformatics, 2003, 19, 1457-1460.	4.1	8
137	Stratification of co-evolving genomic groups using ranked phylogenetic profiles. BMC Bioinformatics, 2009, 10, 355.	2.6	8
138	Metabolic database systems for the analysis of genome-wide function. Biotechnology and Bioengineering, 2003, 84, 750-755.	3.3	7
139	Sensitive detection of sequence similarity using combinatorial pattern discovery: A challenging study of two distantly related protein families. Proteins: Structure, Function and Bioinformatics, 2005, 61, 926-937.	2.6	7
140	Annotating unknown species of urban microorganisms on a global scale unveils novel functional diversity and local environment association. Environmental Research, 2022, 207, 112183.	7.5	7
141	Reverse Interpretation: A Hypothetical Selection Mechanism for Adaptive Mutagenesis Based on Autoregulated mRNA Stability. Journal of Theoretical Biology, 1994, 167, 373-380.	1.7	6
142	Understanding Specialized Ribosomal Protein Functions and Associated Ribosomopathies by Navigating Across Sequence, Literature, and Phenotype Information Resources. , 2019, , 35-51.		6
143	The bioinformatics wealth of nations. Bioinformatics, 2020, 36, 2963-2965.	4.1	6
144	Preliminary evidence for seasonality of Covid-19 due to ultraviolet radiation. F1000Research, 0, 9, 658.	1.6	6

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145	Assessing Proteinase K Resistance of Fish Prion Proteins in a Scrapie-Infected Mouse Neuroblastoma Cell Line. <i>Viruses</i> , 2014, 6, 4398-4421.	3.3	5
146	Brain Radiation Information Data Exchange (BRIDE): integration of experimental data from low-dose ionising radiation research for pathway discovery. <i>BMC Bioinformatics</i> , 2016, 17, 212.	2.6	5
147	BioPAXViz: a cytoscape application for the visual exploration of metabolic pathway evolution. <i>Bioinformatics</i> , 2017, 33, 1418-1420.	4.1	5
148	Consent insufficient for data release—Response. <i>Science</i> , 2019, 364, 446-446.	12.6	5
149	Hypothesis, analysis and synthesis, it's all Greek to me. <i>ELife</i> , 2019, 8, .	6.0	5
150	Mapping Functional Associations in the Entire Genome of <i>Drosophila melanogaster</i> Using Fusion Analysis. <i>Comparative and Functional Genomics</i> , 2003, 4, 337-341.	2.0	4
151	The core histone fold: Limits to functional versatility. <i>Journal of Molecular Evolution</i> , 1996, 43, 541-542.	1.8	3
152	Science communication media for scientists and the public. <i>EMBO Reports</i> , 2007, 8, 886-887.	4.5	3
153	Protein coalitions in a core mammalian biochemical network linked by rapidly evolving proteins. <i>BMC Evolutionary Biology</i> , 2011, 11, 142.	3.2	3
154	Developing computational biology at meridian 23° E, and a little eastwards. <i>Journal of Biological Research</i> , 2018, 25, 18.	2.1	3
155	Establishment of computational biology in Greece and Cyprus: Past, present, and future. <i>PLoS Computational Biology</i> , 2019, 15, e1007532.	3.2	3
156	Ancestral state reconstruction of metabolic pathways across pangenome ensembles. <i>Microbial Genomics</i> , 2020, 6, .	2.0	3
157	H3ABioNet computational metagenomics workshop in Mauritius: training to analyse microbial diversity for Africa. <i>Standards in Genomic Sciences</i> , 2015, 10, .	1.5	2
158	The Coming of Age for Big Data in Systems Radiobiology, an Engineering Perspective. <i>Big Data</i> , 2021, 9, 63-71.	3.4	2
159	ROBUSTNESS OF METABOLIC MAP RECONSTRUCTION. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 589-593.	0.8	1
160	MEETING REPORT: THE SEVENTH CONFERENCE OF THE HELLENIC SOCIETY FOR COMPUTATIONAL BIOLOGY AND BIOINFORMATICS. <i>Computational and Structural Biotechnology Journal</i> , 2013, 6, e201303006.	4.1	1
161	Multi-genome Core Pathway Identification through Gene Clustering. <i>International Federation for Information Processing</i> , 2012, , 545-555.	0.4	1
162	The functional composition of living machines as a design principle for artificial organisms. <i>Lecture Notes in Computer Science</i> , 1995, , 841-851.	1.3	1

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163	Travelling to scientific meetings is a mission, not a vacation. EMBO Reports, 2020, 21, e50388.	4.5	1
164	Sequence variation, common tissue expression patterns and learning models: a genome-wide survey of vertebrate ribosomal proteins. NAR Genomics and Bioinformatics, 2020, 2, lqaa088.	3.2	1
165	The comparative genomics of protein interactions. Genome Informatics, 2007, 19, 131-41.	0.4	1
166	Commentary response. FEBS Letters, 1993, 330, 242-242.	2.8	0
167	Automated Genome Functional Annotation for Structural Genomics. , 2003, , 349-368.		0
168	Inference of Pathway Decomposition Across Multiple Species Through Gene Clustering. International Journal on Artificial Intelligence Tools, 2015, 24, 1540003.	1.0	0
169	THE COMPARATIVE GENOMICS OF PROTEIN INTERACTIONS. , 2007, , .		0
170	Stereotyped Patterns of Somatic Hypermutation (SHM) in Subsets of Patients with Chronic Lymphocytic Leukemia (CLL): Implications for the Role of Antigen Selection in Leukemogenesis.. Blood, 2007, 110, 744-744.	1.4	0