Christos A Ouzounis

List of Publications by Year
in descending order

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	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. Nucleic Acids Research, 2022, 50, D480-D487.	14.5	117
2	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
3	Stratification of hospitalized COVID-19 patients into clinical severity progression groups by immuno-phenotyping and machine learning. Nature Communications, 2022, 13, 915.	12.8	32
4	The Coming of Age for Big Data in Systems Radiobiology, an Engineering Perspective. Big Data, 2021, 9, 63-71.	3.4	2
5	A Strong Seasonality Pattern for Covid-19 Incidence Rates Modulated by UV Radiation Levels. Viruses, 2021, 13, 574.	3.3	13
6	Critical assessment of protein intrinsic disorder prediction. Nature Methods, 2021, 18, 472-481.	19.0	187
7	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	28.9	164
8	Atypical Divergence of SARS-CoV-2 Orf8 from Orf7a within the Coronavirus Lineage Suggests Potential Stealthy Viral Strategies in Immune Evasion. MBio, 2021, 12, .	4.1	28
9	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	14.5	141
10	Disentangling the complexity of low complexity proteins. Briefings in Bioinformatics, 2020, 21, 458-472.	6.5	70
11	A Path toward SARS-CoV-2 Attenuation: Metabolic Pressure on CTP Synthesis Rules the Virus Evolution. Genome Biology and Evolution, 2020, 12, 2467-2485.	2.5	22
12	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
13	The bioinformatics wealth of nations. Bioinformatics, 2020, 36, 2963-2965.	4.1	6
14	Travelling to scientific meetings is a mission, not a vacation. EMBO Reports, 2020, 21, e50388.	4.5	1
15	Ancestral state reconstruction of metabolic pathways across pangenome ensembles. Microbial Genomics, 2020, 6, .	2.0	3
16	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
17	Toward unrestricted use of public genomic data. Science, 2019, 363, 350-352.	12.6	45
18	Consent insufficient for data release—Response. Science, 2019, 364, 446-446.	12.6	5

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19	Establishment of computational biology in Greece and Cyprus: Past, present, and future. PLoS Computational Biology, 2019, 15, e1007532.	3.2	3
20	Understanding Specialized Ribosomal Protein Functions and Associated Ribosomopathies by Navigating Across Sequence, Literature, and Phenotype Information Resources. , 2019, , 35-51.		6
21	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12
22	Hypothesis, analysis and synthesis, it's all Greek to me. ELife, 2019, 8, .	6.0	5
23	HipMCL: a high-performance parallel implementation of the Markov clustering algorithm for large-scale networks. Nucleic Acids Research, 2018, 46, e33-e33.	14.5	104
24	Developing computational biology at meridian 23Â° E, and a little eastwards. Journal of Biological Research, 2018, 25, 18.	2.1	3
25	No wisdom in the crowd: genome annotation in the era of big data â€" current status and future prospects. Microbial Biotechnology, 2018, 11, 588-605.	4.2	45
26	Computational complexity of algorithms for sequence comparison, short-read assembly and genome alignment. BioSystems, 2017, 156-157, 72-85.	2.0	34
27	BioPAXViz: a cytoscape application for the visual exploration of metabolic pathway evolution. Bioinformatics, 2017, 33, 1418-1420.	4.1	5
28	Sequence evidence for common ancestry of eukaryotic endomembrane coatomers. Scientific Reports, 2016, 6, 22311.	3.3	9
29	Brain Radiation Information Data Exchange (BRIDE): integration of experimental data from low-dose ionising radiation research for pathway discovery. BMC Bioinformatics, 2016, 17, 212.	2.6	5
30	Annotation inconsistencies beyond sequence similarity-based function prediction â€" phylogeny and genome structure. Standards in Genomic Sciences, 2015, 10, 108.	1.5	38
31	H3ABioNet computational metagenomics workshop in Mauritius: training to analyse microbial diversity for Africa. Standards in Genomic Sciences, 2015, 10, .	1.5	2
32	Inference of Pathway Decomposition Across Multiple Species Through Gene Clustering. International Journal on Artificial Intelligence Tools, 2015, 24, 1540003.	1.0	0
33	Assessing Proteinase K Resistance of Fish Prion Proteins in a Scrapie-Infected Mouse Neuroblastoma Cell Line. Viruses, 2014, 6, 4398-4421.	3.3	5
34	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	5.6	190
35	Experimental evidence validating the computational inference of functional associations from gene fusion events: a critical survey. Briefings in Bioinformatics, 2014, 15, 443-454.	6.5	19
36	BioTextQuest + : a knowledge integration platform for literature mining and concept discovery. Bioinformatics, 2014, 30, 3249-3256.	4.1	23

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37	Functional Genomics Evidence Unearths New Moonlighting Roles of Outer Ring Coat Nucleoporins. Scientific Reports, 2014, 4, 4655.	3.3	20
38	Biological Information Extraction and Co-occurrence Analysis. Methods in Molecular Biology, 2014, 1159, 77-92.	0.9	19
39	An updated metabolic view of the Bacillus subtilis 168 genome. Microbiology (United Kingdom), 2013, 159, 757-770.	1.8	72
40	MEETING REPORT: THE SEVENTH CONFERENCE OF THE HELLENIC SOCIETY FOR COMPUTATIONAL BIOLOGY AND BIOINFORMATICS. Computational and Structural Biotechnology Journal, 2013, 6, e201303006.	4.1	1
41	Gene Network and Proteomic Analyses of Cardiac Responses to Pathological and Physiological Stress. Circulation: Cardiovascular Genetics, 2013, 6, 588-597.	5.1	21
42	Taxonomic Identification of Mediterranean Pines and Their Hybrids Based on the High Resolution Melting (HRM) and trnL Approaches: From Cytoplasmic Inheritance to Timber Tracing. PLoS ONE, 2013, 8, e60945.	2.5	30
43	Detection of Genomic Idiosyncrasies Using Fuzzy Phylogenetic Profiles. PLoS ONE, 2013, 8, e52854.	2.5	16
44	Rise and Demise of Bioinformatics? Promise and Progress. PLoS Computational Biology, 2012, 8, e1002487.	3.2	51
45	Transcriptome classification reveals molecular subtypes in psoriasis. BMC Genomics, 2012, 13, 472.	2.8	55
46	The Chlamydiales Pangenome Revisited: Structural Stability and Functional Coherence. Genes, 2012, 3, 291-319.	2.4	9
47	Multi-genome Core Pathway Identification through Gene Clustering. International Federation for Information Processing, 2012, , 545-555.	0.4	1
48	Complete genome sequence of Mycobacterium sp. strain (Spyr1) and reclassification to Mycobacterium gilvum Spyr1. Standards in Genomic Sciences, 2011, 5, 144-153.	1.5	22
49	Complete genome sequence of Arthrobacter phenanthrenivorans type strain (Sphe3). Standards in Genomic Sciences, 2011, 4, 123-130.	1.5	31
50	Functional Genomics Assistant (FUGA): a toolbox for the analysis of complex biological networks. BMC Research Notes, 2011, 4, 462.	1.4	17
51	Protein coalitions in a core mammalian biochemical network linked by rapidly evolving proteins. BMC Evolutionary Biology, 2011, 11, 142.	3.2	3
52	BioTextQuest: a web-based biomedical text mining suite for concept discovery. Bioinformatics, 2011, 27, 3327-3328.	4.1	13
53	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
54	Genome-wide expression patterns in physiological cardiac hypertrophy. BMC Genomics, 2010, 11, 557.	2.8	17

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55	A Systems Model for Immune Cell Interactions Unravels the Mechanism of Inflammation in Human Skin. PLoS Computational Biology, 2010, 6, e1001024.	3.2	51
56	Promoter Complexity and Tissue-Specific Expression of Stress Response Components in Mytilus galloprovincialis, a Sessile Marine Invertebrate Species. PLoS Computational Biology, 2010, 6, e1000847.	3.2	9
57	Tumorigenic Properties of Iron Regulatory Protein 2 (IRP2) Mediated by Its Specific 73-Amino Acids Insert. PLoS ONE, 2010, 5, e10163.	2.5	60
58	Stratification of co-evolving genomic groups using ranked phylogenetic profiles. BMC Bioinformatics, 2009, 10, 355.	2.6	8
59	Emergence, development and diversification of the TGF-β signalling pathway within the animal kingdom. BMC Evolutionary Biology, 2009, 9, 28.	3.2	137
60	Sequence-based feature prediction and annotation of proteins. Genome Biology, 2009, 10, 206.	9.6	53
61	Metabolic innovations towards the human lineage. BMC Evolutionary Biology, 2008, 8, 247.	3.2	14
62	Stereotyped patterns of somatic hypermutation in subsets of patients with chronic lymphocytic leukemia: implications for the role of antigen selection in leukemogenesis. Blood, 2008, 111, 1524-1533.	1.4	285
63	PuReD-MCL: a graph-based PubMed document clustering methodology. Bioinformatics, 2008, 24, 1935-1941.	4.1	35
64	Science communication media for scientists and the public. EMBO Reports, 2007, 8, 886-887.	4.5	3
65	CORRIE: enzyme sequence annotation with confidence estimates. BMC Bioinformatics, 2007, 8, S3.	2.6	14
66	Denoising inferred functional association networks obtained by gene fusion analysis. BMC Genomics, 2007, 8, 460.	2.8	16
67	THE COMPARATIVE GENOMICS OF PROTEIN INTERACTIONS. , 2007, , .		0
68	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
69	The comparative genomics of protein interactions. Genome Informatics, 2007, 19, 131-41.	0.4	1
70	A minimal estimate for the gene content of the last universal common ancestor—exobiology from a terrestrial perspective. Research in Microbiology, 2006, 157, 57-68.	2.1	130
71	Lineage-specific partitions in archaeal transcription. Archaea, 2006, 2, 117-125.	2.3	11
72	Maps, books and other metaphors for systems biology. BioSystems, 2006, 85, 6-10.	2.0	31

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73	Structural and functional properties of genes involved in human cancer. BMC Genomics, 2006, 7, 3.	2.8	75
74	Computational disease gene identification: a concert of methods prioritizes type 2 diabetes and obesity candidate genes. Nucleic Acids Research, 2006, 34, 3067-3081.	14.5	134
75	Highly consistent patterns for inherited human diseases at the molecular level. Bioinformatics, 2006, 22, 269-277.	4.1	46
76	Genome coverage, literally speaking. EMBO Reports, 2005, 6, 397-399.	4.5	34
77	Clustering the annotation space of proteins. BMC Bioinformatics, 2005, 6, 24.	2.6	16
78	Probabilistic annotation of protein sequences based on functional classifications. BMC Bioinformatics, 2005, 6, 302.	2.6	24
79	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
80	Measuring genome conservation across taxa: divided strains and united kingdoms. Nucleic Acids Research, 2005, 33, 616-621.	14.5	69
81	An Exponential Core in the Heart of the Yeast Protein Interaction Network. Molecular Biology and Evolution, 2005, 22, 421-425.	8.9	50
82	Expansion of the BioCyc collection of pathway/genome databases to 160 genomes. Nucleic Acids Research, 2005, 33, 6083-6089.	14.5	570
83	CoGenT++: an extensive and extensible data environment for computational genomics. Bioinformatics, 2005, 21, 3806-3810.	4.1	22
84	The properties of protein family space depend on experimental design. Bioinformatics, 2005, 21, 2618-2622.	4.1	10
85	MagicMatch--cross-referencing sequence identifiers across databases. Bioinformatics, 2005, 21, 3429-3430.	4.1	21
86	Percolation of annotation errors through hierarchically structured protein sequence databases. Mathematical Biosciences, 2005, 193, 223-234.	1.9	67
87	Ancestral state reconstructions for genomes. Current Opinion in Genetics and Development, 2005, 15, 595-600.	3.3	14
88	Are splicing mutations the most frequent cause of hereditary disease?. FEBS Letters, 2005, 579, 1900-1903.	2.8	327
89	BioLayoutJava. Applied Bioinformatics, 2005, 4, 71-74.	1.6	50
90	The net of life: Reconstructing the microbial phylogenetic network. Genome Research, 2005, 15, 954-959.	5.5	211

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91	Automated metabolic reconstruction for *Methanococcus jannaschii*. Archaea, 2004, 1, 223-229.	2.3	37
92	Comparative Genomics of Transcriptional Control in the Human Malaria Parasite Plasmodium falciparum. Genome Research, 2004, 14, 1548-1554.	5.5	221
93	Genome-wide identification of genes likely to be involved in human genetic disease. Nucleic Acids Research, 2004, 32, 3108-3114.	14.5	226
94	ROBUSTNESS OF METABOLIC MAP RECONSTRUCTION. Journal of Bioinformatics and Computational Biology, 2004, 02, 589-593.	0.8	1
95	Functional Evolution of the Yeast Protein Interaction Network. Molecular Biology and Evolution, 2004, 21, 1171-1176.	8.9	66
96	Mapping Functional Associations in the Entire Genome ofDrosophila melanogasterUsing Fusion Analysis. Comparative and Functional Genomics, 2003, 4, 337-341.	2.0	4
97	Metabolic database systems for the analysis of genome-wide function. Biotechnology and Bioengineering, 2003, 84, 750-755.	3.3	7
98	Detection of functional modules from protein interaction networks. Proteins: Structure, Function and Bioinformatics, 2003, 54, 49-57.	2.6	362
99	Classification schemes for protein structure and function. Nature Reviews Genetics, 2003, 4, 508-519.	16.3	101
100	Early bioinformatics: the birth of a discipline--a personal view. Bioinformatics, 2003, 19, 2176-2190.	4.1	105
101	From Genes to Genomes: Universal Scale-invariant Properties of Microbial Chromosome Organisation. Journal of Molecular Biology, 2003, 332, 617-633.	4.2	38
102	Transcription regulation and environmental adaptation in bacteria. Trends in Microbiology, 2003, 11, 248-253.	7.7	168
103	Beyond 100 genomes. Genome Biology, 2003, 4, 402.	9.6	23
104	Myriads of protein families, and still counting. Genome Biology, 2003, 4, 401.	9.6	55
105	GeneTRACE-reconstruction of gene content of ancestral species. Bioinformatics, 2003, 19, 1412-1416.	4.1	46
106	The phylogenetic diversity of eukaryotic transcription. Nucleic Acids Research, 2003, 31, 653-660.	14.5	39
107	Genome evolution reveals biochemical networks and functional modules. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15428-15433.	7.1	140
108	The Phylogenetic Extent of Metabolic Enzymes and Pathways. Genome Research, 2003, 13, 422-427.	5.5	91

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109	PseuRECA: genome annotation and gene context analysis for Pseudomonas aeruginosa PAO1. Bioinformatics, 2003, 19, 1457-1460.	4.1	8
110	Comparison of sequence masking algorithms and the detection of biased protein sequence regions. Bioinformatics, 2003, 19, 1672-1681.	4.1	20
111	Evaluation of annotation strategies using an entire genome sequence. Bioinformatics, 2003, 19, 717-726.	4.1	65
112	COmplete GENome Tracking (COGENT): a flexible data environment for computational genomics. Bioinformatics, 2003, 19, 1451-1452.	4.1	40
113	Protein families and TRIBES in genome sequence space. Nucleic Acids Research, 2003, 31, 4632-4638.	14.5	113
114	The Balance of Driving Forces During Genome Evolution in Prokaryotes. Genome Research, 2003, 13, 1589-1594.	5.5	173
115	Automated Genome Functional Annotation for Structural Genomics. , 2003, , 349-368.		0
116	Modeling the percolation of annotation errors in a database of protein sequences. Bioinformatics, 2002, 18, 1641-1649.	4.1	153
117	Bioinformatics and the theoretical foundations of molecular biology. Bioinformatics, 2002, 18, 377-378.	4.1	23
118	The past, present and future of genome-wide re-annotation. Genome Biology, 2002, 3, comment2001.1.	9.6	86
119	Genome-wide detection and family clustering of ion channels. FEBS Letters, 2002, 514, 129-134.	2.8	12
120	Genetic variation between Helicobacter pylori strains: gene acquisition or loss?. Trends in Microbiology, 2002, 10, 445-447.	7.7	18
121	Functional associations of proteins in entire genomes by means of exhaustive detection of gene fusions. Genome Biology, 2001, 2, research0034.1.	9.6	108
122	Functional Versatility and Molecular Diversity of the Metabolic Map of Escherichia coli. Genome Research, 2001, 11, 1503-1510.	5.5	29
123	Prediction of protein interactions: metabolic enzymes are frequently involved in gene fusion. Nature Genetics, 2000, 26, 141-142.	21.4	91
124	GeneRAGE: a robust algorithm for sequence clustering and domain detection. Bioinformatics, 2000, 16, 451-457.	4.1	186
125	Recent developments and future directions in computational genomics. FEBS Letters, 2000, 480, 42-48.	2.8	49
126	Genome sequences and great expectations. Genome Biology, 2000, 2, interactions0001.1.	9.6	40

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127	Whole-genome sequence annotation: 'Going wrong with confidence'. Molecular Microbiology, 1999, 32, 886-887.	2.5	58
128	Protein interaction maps for complete genomes based on gene fusion events. Nature, 1999, 402, 86-90.	27.8	1,032
129	Universal Protein Families and the Functional Content of the Last Universal Common Ancestor. Journal of Molecular Evolution, 1999, 49, 413-423.	1.8	103
130	The PWI motif: a new protein domain in splicing factors. Trends in Biochemical Sciences, 1999, 24, 179-180.	7.5	25
131	Dictionary building via unsupervised hierarchical motif discovery in the sequence space of natural proteins. , 1999, 37, 264-277.		45
132	Reproducibility in genome sequence annotation: the Plasmodium falciparum chromosome 2 case. FEBS Letters, 1999, 451, 354-355.	2.8	14
133	A ferredoxin-like domain in RNA polymerase 30/40-kDa subunits. Trends in Biochemical Sciences, 1998, 23, 169-170.	7.5	8
134	RGD sequences in several receptor proteins: novel cell adhesion function of receptors?. International Journal of Biological Macromolecules, 1998, 22, 51-57.	7.5	17
135	Errors in Genome Reviews. , 1998, 281, 1453c-1453.		18
136	Sequence analysis of the Methanococcus jannaschii genome and the prediction of protein function. Bioinformatics, 1997, 13, 481-483.	4.1	16
137	Evolution of immunoglobulin-like modules in chitinases: their structural flexibility and functional implications. Folding & Design, 1997, 2, 291-294.	4.5	25
138	ThiD-TenA: A Gene Pair Fusion in Eukaryotes. Journal of Molecular Evolution, 1997, 45, 708-711.	1.8	8
139	Conserved Clusters of Functionally Related Genes in Two Bacterial Genomes. Journal of Molecular Evolution, 1997, 44, 66-73.	1.8	163
140	Genomes with distinct function composition. FEBS Letters, 1996, 389, 96-101.	2.8	22
141	The emergence of major cellular processes in evolution. FEBS Letters, 1996, 390, 119-123.	2.8	81
142	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. Journal of Structural Biology, 1996, 117, 145-163.	2.8	29
143	Computational comparisons of model genomes. Trends in Biotechnology, 1996, 14, 280-285.	9.3	28
144	Parallel origins of the nucleosome core and eukaryotic transcription from Archaea. Journal of Molecular Evolution, 1996, 42, 234-239.	1.8	25

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145	The core histone fold: Limits to functional versatility. Journal of Molecular Evolution, 1996, 43, 541-542.	1.8	3
146	KOW: a novel motif linking a bacterial transcription factor with ribosomal proteins. Trends in Biochemical Sciences, 1996, 21, 425-426.	7.5	120
147	Novelties from the complete genome of Mycoplasma genitalium. Molecular Microbiology, 1996, 20, 898-900.	2.5	37
148	Ready for a motif submission? A proposed checklist. Trends in Biochemical Sciences, 1995, 20, 104.	7.5	37
149	A Drosophila hsp70 gene contains long, antiparallel, coupled open reading frames (LAC ORFs) conserved in homologous loci. Journal of Molecular Evolution, 1995, 41, 414-420.	1.8	28
150	Nucleic acid-binding metabolic enzymes: Living fossils of stereochemical interactions?. Journal of Molecular Evolution, 1995, 40, 564-569.	1.8	16
151	New protein functions in yeast chromosome VIII. Protein Science, 1995, 4, 2424-2428.	7.6	33
152	Exploring the <i>Mycoplasma capricolum</i> genome: a minimal cell reveals its physiology. Molecular Microbiology, 1995, 16, 955-967.	2.5	84
153	Novel protein families in archaean genomes. Nucleic Acids Research, 1995, 23, 565-570.	14.5	40
154	The functional composition of living machines as a design principle for artificial organisms. Lecture Notes in Computer Science, 1995, , 841-851.	1.3	1
155	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
156	The modular structure of NifU proteins. Trends in Biochemical Sciences, 1994, 19, 199-200.	7.5	30
157	From genome sequences to protein function. Current Opinion in Structural Biology, 1994, 4, 393-403.	5.7	54
158	Barley Î²-glucosidase: Expression during seed germination and maturation and partial amino acids sequences. Biochimica Et Biophysica Acta - General Subjects, 1994, 1199, 52-58.	2.4	22
159	Mechanisms of Specificity in mRNA Degradation: Autoregulation and Cognate Interactions. Journal of Theoretical Biology, 1993, 163, 373-392.	1.7	14
160	Commentary response. FEBS Letters, 1993, 330, 242-242.	2.8	0
161	Homology of the NifS family of proteins to a new class of pyridoxal phosphate-dependent enzymes. FEBS Letters, 1993, 322, 159-164.	2.8	46
162	Prediction of Protein Structure by Evaluation of Sequence-structure Fitness. Journal of Molecular Biology, 1993, 232, 805-825.	4.2	146

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163	TFIIB, an evolutionary link between the transcription machineries of archaebacteria and eukaryotes. Cell, 1992, 71, 189-190.	28.9	90
164	Comprehensive sequence analysis of the 182 predicted open reading frames of yeast chromosome III. Protein Science, 1992, 1, 1677-1690.	7.6	106
165	A database of protein structure families with common folding motifs. Protein Science, 1992, 1, 1691-1698.	7.6	193
166	What's in a genome?. Nature, 1992, 358, 287-287.	27.8	57
167	A structure-derived sequence pattern for the detection of type I copper binding domains in distantly related proteins. FEBS Letters, 1991, 279, 73-78.	2.8	44
168	Primary and secondary structural patterns in eukaryotic cytochrome P-450 families correspond to structures of the helix-rich domain of Pseudomonas putida cytochrome P-450cam. Indications for a similar overall topology. FEBS Journal, 1991, 198, 307-315.	0.2	25
169	Bacterial DNA replication initiation factor priA is related to proteins belonging to the â€˜DEAD-boxâ€™ family. Nucleic Acids Research, 1991, 19, 6953-6953.	14.5	27
170	Preliminary evidence for seasonality of Covid-19 due to ultraviolet radiation. F1000Research, 0, 9, 658.	1.6	6