

Temple F Smith

List of Publications by Year in descending order

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88
papers

9,394
citations

76196

40
h-index

54797

84
g-index

90
all docs

90
docs citations

90
times ranked

9564
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
2	The ancient regulatory-protein family of WD-repeat proteins. <i>Nature</i> , 1994, 371, 297-300.	13.7	1,409
3	The WD repeat: a common architecture for diverse functions. <i>Trends in Biochemical Sciences</i> , 1999, 24, 181-185.	3.7	1,101
4	Comparison of biosequences. <i>Advances in Applied Mathematics</i> , 1981, 2, 482-489.	0.4	681
5	G Protein Heterodimers: New Structures Propel New Questions. <i>Cell</i> , 1996, 84, 175-178.	13.5	201
6	The statistical distribution of nucleic acid similarities. <i>Nucleic Acids Research</i> , 1985, 13, 645-656.	6.5	198
7	Polytene Chromosomal Maps of 11 <i>Drosophila</i> Species: The Order of Genomic Scaffolds Inferred From Genetic and Physical Maps. <i>Genetics</i> , 2008, 179, 1601-1655.	1.2	191
8	Chromosomal Rearrangement Inferred From Comparisons of 12 <i>Drosophila</i> Genomes. <i>Genetics</i> , 2008, 179, 1657-1680.	1.2	184
9	Folding of Proteins with WD-Repeats: Comparison of Six Members of the WD-Repeat Superfamily to the G Protein β^2 Subunit. <i>Biochemistry</i> , 1996, 35, 13985-13994.	1.2	178
10	Remnants of an Ancient Metabolism without Phosphate. <i>Cell</i> , 2017, 168, 1126-1134.e9.	13.5	175
11	Structural analysis based on state-space modeling. <i>Protein Science</i> , 1993, 2, 305-314.	3.1	169
12	The nature of Lactose operator constitutive mutations. <i>Journal of Molecular Biology</i> , 1971, 59, 273-305.	2.0	158
13	Global Optimum Protein Threading with Gapped Alignment and Empirical Pair Score Functions. <i>Journal of Molecular Biology</i> , 1996, 255, 641-665.	2.0	150
14	Protein classification by stochastic modeling and optimal filtering of amino-acid sequences. <i>Mathematical Biosciences</i> , 1994, 119, 35-75.	0.9	143
15	Diversity of WD-Repeat proteins. <i>Sub-Cellular Biochemistry</i> , 2008, 48, 20-30.	1.0	122
16	Genomic detection of new yeast pre-mRNA 3'-end-processing signals. <i>Nucleic Acids Research</i> , 1999, 27, 888-894.	6.5	118
17	Patterns of Genome Organization in Bacteria. <i>Science</i> , 1998, 279, 1827a-1827.	6.0	105
18	Sites for G $\beta\gamma$ Binding on the G Protein β^2 Subunit Overlap with Sites for Regulation of Phospholipase C β^2 and Adenylyl Cyclase. <i>Journal of Biological Chemistry</i> , 1998, 273, 16265-16272.	1.6	102

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19	Probabilistic prediction of <i>Saccharomyces cerevisiae</i> mRNA 3'-processing sites. <i>Nucleic Acids Research</i> , 2002, 30, 1851-1858.	6.5	101
20	A Biologically Consistent Model for Comparing Molecular Phylogenies. <i>Journal of Computational Biology</i> , 1995, 2, 493-507.	0.8	89
21	Thirty-plus functional families from a single motif. <i>Protein Science</i> , 2000, 9, 2470-2476.	3.1	88
22	Sites Important for PLC β 2 Activation by the G Protein β 3 Subunit Map to the Sides of the β 2 Propeller Structure. <i>Journal of Biological Chemistry</i> , 1998, 273, 28298-28304.	1.6	86
23	Functional conservation between members of an ancient duplicated transcription factor family, LSF/Grainyhead. <i>Nucleic Acids Research</i> , 2003, 31, 4304-4316.	6.5	84
24	A molecular sequence metric and evolutionary trees. <i>Mathematical Biosciences</i> , 1974, 19, 9-25.	0.9	80
25	The origin and evolution of the ribosome. <i>Biology Direct</i> , 2008, 3, 16.	1.9	71
26	ARIADNE: pattern-directed inference and hierarchical abstraction in protein structure recognition. <i>Communications of the ACM</i> , 1987, 30, 909-921.	3.3	68
27	LFG: a candidate apoptosis regulatory gene family. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2009, 14, 1255-1265.	2.2	64
28	The evolution of the thrombospondin gene family. <i>Journal of Molecular Evolution</i> , 1993, 36, 509-516.	0.8	63
29	Folding a WD Repeat Propeller. <i>Journal of Biological Chemistry</i> , 1998, 273, 9041-9049.	1.6	63
30	Ribosomal protein-sequence block structure suggests complex prokaryotic evolution with implications for the origin of eukaryotes. <i>Molecular Phylogenetics and Evolution</i> , 2004, 33, 615-625.	1.2	63
31	The evolution of Class II Aminoacyl-tRNA synthetases and the first code. <i>FEBS Letters</i> , 2015, 589, 3499-3507.	1.3	59
32	Biology's new Rosetta stone. <i>Nature</i> , 1997, 385, 29-30.	13.7	56
33	Information-theoretic dissection of pairwise contact potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 7-14.	1.5	50
34	Transcription Factor Map Alignment of Promoter Regions. <i>PLoS Computational Biology</i> , 2006, 2, e49.	1.5	50
35	Mapping of the lactose operator. <i>Journal of Molecular Biology</i> , 1971, 62, 139-169.	2.0	49
36	Prediction of a common structural domain in aminoacyl-tRNA synthetases through use of a new pattern-directed inference system. <i>Biochemistry</i> , 1987, 26, 6950-6957.	1.2	49

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37	The challenges of genome sequence annotation or "The devil is in the details". <i>Nature Biotechnology</i> , 1997, 15, 1222-1223.	9.4	49
38	Genome-scale analysis of positionally relocated genes. <i>Genome Research</i> , 2007, 17, 1880-1887.	2.4	49
39	The Evolution of the Ribosome and the Genetic Code. <i>Life</i> , 2014, 4, 227-249.	1.1	48
40	The archaeal origins of the eukaryotic translational system. <i>Archaea</i> , 2006, 2, 1-9.	2.3	41
41	Analysis of the Physical Properties and Molecular Modeling of Sec13: A WD Repeat Protein Involved in Vesicular Trafficking. <i>Biochemistry</i> , 1996, 35, 15215-15221.	1.2	40
42	Current Limitations to Protein Threading Approaches. <i>Journal of Computational Biology</i> , 1997, 4, 217-225.	0.8	40
43	Algorithms for restriction map comparisons. <i>Nucleic Acids Research</i> , 1984, 12, 237-242.	6.5	39
44	Corruption of genomic databases with anomalous sequence. <i>Nucleic Acids Research</i> , 1992, 20, 2741-2747.	6.5	31
45	Yeast "Operons". <i>Microbial & Comparative Genomics</i> , 1998, 3, 133-140.	0.6	28
46	Identifying nature's protein lego set. <i>Advances in Protein Chemistry</i> , 2000, 54, 159-183.	4.4	27
47	Inferring genome-scale rearrangement phylogeny and ancestral gene order: a <i>Drosophila</i> case study. <i>Genome Biology</i> , 2007, 8, R236.	13.9	26
48	Origin of the Genetic Code Is Found at the Transition between a Thioester World of Peptides and the Phosphoester World of Polynucleotides. <i>Life</i> , 2019, 9, 69.	1.1	26
49	The genetic code, information density, and evolution. <i>Mathematical Biosciences</i> , 1969, 4, 179-187.	0.9	25
50	Functional genomics "bioinformatics is ready for the challenge. <i>Trends in Genetics</i> , 1998, 14, 291-293.	2.9	25
51	A homology identification method that combines protein sequence and structure information. <i>Protein Science</i> , 1998, 7, 2499-2510.	3.1	25
52	Techniques for multi-genome synteny analysis to overcome assembly limitations. <i>Genome Informatics</i> , 2006, 17, 152-61.	0.4	24
53	A modified Chou and Fasman protein structure algorithm. <i>Bioinformatics</i> , 1987, 3, 211-216.	1.8	22
54	Recognition of characteristic patterns in sets of functionally equivalent DNA sequences. <i>Bioinformatics</i> , 1987, 3, 223-227.	1.8	20

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55	Alignment of protein sequences using secondary structure: a modified dynamic programming method. <i>Protein Engineering, Design and Selection</i> , 1990, 3, 577-581.	1.0	20
56	The binding domain structure of retinoblastoma-binding proteins. <i>Protein Science</i> , 1993, 2, 155-164.	3.1	18
57	A search method for homologs of small proteins. Ubiquitin-like proteins in prokaryotic cells?. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 897-904.	1.0	18
58	Multiple domain protein diagnostic patterns. <i>Protein Science</i> , 1996, 5, 1240-1249.	3.1	17
59	The art of matchmaking: sequence alignment methods and their structural implications. <i>Structure</i> , 1999, 7, R7-R12.	1.6	17
60	Analysis and algorithms for protein sequence-structure alignment. <i>New Comprehensive Biochemistry</i> , 1998, 32, 227-283.	0.1	16
61	Protein fold recognition by total alignment probability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 40, 451-462.	1.5	16
62	A noncanonical WD-repeat protein from the cyanobacterium <i>Synechocystis PCC6803</i> : Structural and functional study. <i>Protein Science</i> , 2001, 10, 293-300.	3.1	16
63	GTPases and the origin of the ribosome. <i>Biology Direct</i> , 2010, 5, 36.	1.9	16
64	<i>Trichomonas</i> Transmembrane Cyclases Result from Massive Gene Duplication and Concomitant Development of Pseudogenes. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e782.	1.3	16
65	Homology Model for the Ligand-Binding Domain of the Human Estrogen Receptor. <i>Journal of Biomolecular Structure and Dynamics</i> , 1998, 15, 841-851.	2.0	15
66	Protein constraints induced by multiframe encoding. <i>Mathematical Biosciences</i> , 1980, 49, 17-26.	0.9	14
67	Triage protein fold prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 654-663.	1.5	11
68	The evolution of the cilium and the eukaryotic cell. <i>Cytoskeleton</i> , 2009, 66, 215-219.	4.4	11
69	Acid helix-turn activator motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 156-163.	1.5	10
70	Visible volume: A robust measure for protein structure characterization. <i>Journal of Molecular Biology</i> , 1997, 273, 338-348.	2.0	9
71	Pattern descriptors and the unidentified reading frame 6 human mtDNA dinucleotide-binding site. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 3, 97-101.	1.5	8
72	Filtered neighbors threading. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 346-359.	1.5	7

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73	Pseudogenization of testis-specific Lfg5 predates human/Neanderthal divergence. <i>Journal of Human Genetics</i> , 2014, 59, 288-291.	1.1	7
74	Constraining ribosomal RNA conformational space. <i>Nucleic Acids Research</i> , 2005, 33, 5106-5111.	6.5	6
75	Sequence banks: Searching for sequence similarities. <i>Nature</i> , 1983, 301, 194-194.	13.7	5
76	Survey of human mitochondrial diseases using new genomic/proteomic tools. <i>Genome Biology</i> , 2001, 2, research0021.1.	13.9	5
77	Gene expansion in <i>Trichomonas vaginalis</i> : a case study on transmembrane cyclases. <i>Genome Informatics</i> , 2007, 18, 35-43.	0.4	5
78	Finite-state and reduced-parameter representations of protein backbone conformations. <i>Journal of Computational Chemistry</i> , 1994, 15, 300-312.	1.5	4
79	Performance of Threading Scoring Functions Designed Using New Optimization Method. <i>Journal of Computational Biology</i> , 1999, 6, 299-311.	0.8	4
80	How Alike are Two Trees?. <i>American Mathematical Monthly</i> , 1980, 87, 552.	0.2	2
81	A taxonomic distance applicable to paleontology. <i>Mathematical Biosciences</i> , 1980, 50, 285-295.	0.9	2
82	Molecular genetics and computer analyses. <i>Bioinformatics</i> , 1987, 3, 167-170.	1.8	2
83	Massively parallel symbolic induction of protein structure/function relationships. <i>Lecture Notes in Computer Science</i> , 1993, , 157-173.	1.0	2
84	Of how great significance?. <i>Nature</i> , 1987, 326, 749-749.	13.7	1
85	A method for optimal design of a threading scoring function. , 1999, , .		1
86	Prediction of interaction partners for orphan nuclear receptors by prior-based protein sequence profiles. <i>Journal of Molecular Recognition</i> , 2000, 13, 117-126.	1.1	0
87	Comprehensive statistical method for protein fold recognition. , 2000, , .		0
88	Sequence Patterns Diagnostic of Structure and Function. , 1997, , 91-104.		0