

Temple F Smith

List of Publications by Year in descending order

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88
papers

9,394
citations

76326

40
h-index

54911

84
g-index

90
all docs

90
docs citations

90
times ranked

9564
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	2.4	26
2	Remnants of an Ancient Metabolism without Phosphate. <i>Cell</i> , 2017, 168, 1126-1134.e9.	28.9	175
3	The evolution of Class II Aminoacyl-tRNA synthetases and the first code. <i>FEBS Letters</i> , 2015, 589, 3499-3507.	2.8	59
4	Pseudogenization of testis-specific Lfg5 predates human/Neanderthal divergence. <i>Journal of Human Genetics</i> , 2014, 59, 288-291.	2.3	7
5	The Evolution of the Ribosome and the Genetic Code. <i>Life</i> , 2014, 4, 227-249.	2.4	48
6	GTPases and the origin of the ribosome. <i>Biology Direct</i> , 2010, 5, 36.	4.6	16
7	Trichomonas Transmembrane Cyclases Result from Massive Gene Duplication and Concomitant Development of Pseudogenes. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e782.	3.0	16
8	The evolution of the cilium and the eukaryotic cell. <i>Cytoskeleton</i> , 2009, 66, 215-219.	4.4	11
9	LFG: a candidate apoptosis regulatory gene family. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2009, 14, 1255-1265.	4.9	64
10	The origin and evolution of the ribosome. <i>Biology Direct</i> , 2008, 3, 16.	4.6	71
11	Diversity of WD-Repeat proteins. <i>Sub-Cellular Biochemistry</i> , 2008, 48, 20-30.	2.4	122
12	Chromosomal Rearrangement Inferred From Comparisons of 12 Drosophila Genomes. <i>Genetics</i> , 2008, 179, 1657-1680.	2.9	184
13	Polytene Chromosomal Maps of 11 Drosophila Species: The Order of Genomic Scaffolds Inferred From Genetic and Physical Maps. <i>Genetics</i> , 2008, 179, 1601-1655.	2.9	191
14	Genome-scale analysis of positionally relocated genes. <i>Genome Research</i> , 2007, 17, 1880-1887.	5.5	49
15	Inferring genome-scale rearrangement phylogeny and ancestral gene order: a Drosophila case study. <i>Genome Biology</i> , 2007, 8, R236.	9.6	26
16	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
17	Gene expansion in <i>Trichomonas vaginalis</i> : a case study on transmembrane cyclases. <i>Genome Informatics</i> , 2007, 18, 35-43.	0.4	5
18	The archaeal origins of the eukaryotic translational system. <i>Archaea</i> , 2006, 2, 1-9.	2.3	41

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19	Transcription Factor Map Alignment of Promoter Regions. <i>PLoS Computational Biology</i> , 2006, 2, e49.	3.2	50
20	Techniques for multi-genome synteny analysis to overcome assembly limitations. <i>Genome Informatics</i> , 2006, 17, 152-61.	0.4	24
21	Constraining ribosomal RNA conformational space. <i>Nucleic Acids Research</i> , 2005, 33, 5106-5111.	14.5	6
22	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.	2.7	63
23	Functional conservation between members of an ancient duplicated transcription factor family, LSF/Grainyhead. <i>Nucleic Acids Research</i> , 2003, 31, 4304-4316.	14.5	84
24	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.	2.1	18
25	Probabilistic prediction of <i>Saccharomyces cerevisiae</i> mRNA 3'-processing sites. <i>Nucleic Acids Research</i> , 2002, 30, 1851-1858.	14.5	101
26	Triage protein fold prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 654-663.	2.6	11
27	Information-theoretic dissection of pairwise contact potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 7-14.	2.6	50
28	Survey of human mitochondrial diseases using new genomic/proteomic tools. <i>Genome Biology</i> , 2001, 2, research0021.1.	9.6	5
29	A noncanonical WD-repeat protein from the cyanobacterium <i>Synechocystis</i> PCC6803: Structural and functional study. <i>Protein Science</i> , 2001, 10, 293-300.	7.6	16
30	Protein fold recognition by total alignment probability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 40, 451-462.	2.6	16
31	Prediction of interaction partners for orphan nuclear receptors by prior-based protein sequence profiles. <i>Journal of Molecular Recognition</i> , 2000, 13, 117-126.	2.1	0
32	Thirty+ functional families from a single motif. <i>Protein Science</i> , 2000, 9, 2470-2476.	7.6	88
33	Identifying nature's protein lego set. <i>Advances in Protein Chemistry</i> , 2000, 54, 159-183.	4.4	27
34	Comprehensive statistical method for protein fold recognition. , 2000, , .		0
35	A method for optimal design of a threading scoring function. , 1999, , .		1
36	Genomic detection of new yeast pre-mRNA 3'-end-processing signals. <i>Nucleic Acids Research</i> , 1999, 27, 888-894.	14.5	118

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37	Performance of Threading Scoring Functions Designed Using New Optimization Method. Journal of Computational Biology, 1999, 6, 299-311.	1.6	4
38	The WD repeat: a common architecture for diverse functions. Trends in Biochemical Sciences, 1999, 24, 181-185.	7.5	1,101
39	The art of matchmaking: sequence alignment methods and their structural implications. Structure, 1999, 7, R7-R12.	3.3	17
40	Filtered neighbors threading. Proteins: Structure, Function and Bioinformatics, 1999, 37, 346-359.	2.6	7
41	Functional genomics—bioinformatics is ready for the challenge. Trends in Genetics, 1998, 14, 291-293.	6.7	25
42	A homology identification method that combines protein sequence and structure information. Protein Science, 1998, 7, 2499-2510.	7.6	25
43	Homology Model for the Ligand-Binding Domain of the Human Estrogen Receptor. Journal of Biomolecular Structure and Dynamics, 1998, 15, 841-851.	3.5	15
44	Sites Important for PLC β 2 Activation by the G Protein β 3 Subunit Map to the Sides of the β 2 Propeller Structure. Journal of Biological Chemistry, 1998, 273, 28298-28304.	3.4	86
45	Patterns of Genome Organization in Bacteria. Science, 1998, 279, 1827-1827.	12.6	105
46	Yeast "Operons". Microbial & Comparative Genomics, 1998, 3, 133-140.	0.4	28
47	Sites for Ca^{2+} Binding on the G Protein β 2 Subunit Overlap with Sites for Regulation of Phospholipase $\text{C}\beta$ 2 and Adenylyl Cyclase. Journal of Biological Chemistry, 1998, 273, 16265-16272.	3.4	102
48	Folding a WD Repeat Propeller. Journal of Biological Chemistry, 1998, 273, 9041-9049.	3.4	63
49	Analysis and algorithms for protein sequence—structure alignment. New Comprehensive Biochemistry, 1998, 32, 227-283.	0.1	16
50	Current Limitations to Protein Threading Approaches. Journal of Computational Biology, 1997, 4, 217-225.	1.6	40
51	Visible volume: A robust measure for protein structure characterization. Journal of Molecular Biology, 1997, 273, 338-348.	4.2	9
52	The challenges of genome sequence annotation or "The devil is in the details". Nature Biotechnology, 1997, 15, 1222-1223.	17.5	49
53	Biology's new Rosetta stone. Nature, 1997, 385, 29-30.	27.8	56
54	Sequence Patterns Diagnostic of Structure and Function. , 1997, , 91-104.		0

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55	Folding of Proteins with WD-Repeats:â€‰ Comparison of Six Members of the WD-Repeat Superfamily to the G Protein Î² Subunit. <i>Biochemistry</i> , 1996, 35, 13985-13994.	2.5	178
56	Analysis of the Physical Properties and Molecular Modeling of Sec13:Â A WD Repeat Protein Involved in Vesicular Trafficâ€. <i>Biochemistry</i> , 1996, 35, 15215-15221.	2.5	40
57	Global Optimum Protein Threading with Gapped Alignment and Empirical Pair Score Functions. <i>Journal of Molecular Biology</i> , 1996, 255, 641-665.	4.2	150
58	G Protein Heterodimers: New Structures Propel New Questions. <i>Cell</i> , 1996, 84, 175-178.	28.9	201
59	Multiple domain protein diagnostic patterns. <i>Protein Science</i> , 1996, 5, 1240-1249.	7.6	17
60	A Biologically Consistent Model for Comparing Molecular Phylogenies. <i>Journal of Computational Biology</i> , 1995, 2, 493-507.	1.6	89
61	Finite-state and reduced-parameter representations of protein backbone conformations. <i>Journal of Computational Chemistry</i> , 1994, 15, 300-312.	3.3	4
62	The ancient regulatory-protein family of WD-repeat proteins. <i>Nature</i> , 1994, 371, 297-300.	27.8	1,409
63	Protein classification by stochastic modeling and optimal filtering of amino-acid sequences. <i>Mathematical Biosciences</i> , 1994, 119, 35-75.	1.9	143
64	The evolution of the thrombospondin gene family. <i>Journal of Molecular Evolution</i> , 1993, 36, 509-516.	1.8	63
65	The binding domain structure of retinoblastomaâ€binding proteins. <i>Protein Science</i> , 1993, 2, 155-164.	7.6	18
66	Structural analysis based on stateâ€space modeling. <i>Protein Science</i> , 1993, 2, 305-314.	7.6	169
67	Massively parallel symbolic induction of protein structure/function relationships. <i>Lecture Notes in Computer Science</i> , 1993, , 157-173.	1.3	2
68	Corruption of genomic databases with anomalous sequence. <i>Nucleic Acids Research</i> , 1992, 20, 2741-2747.	14.5	31
69	Acid helix-turn activator motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 156-163.	2.6	10
70	Alignment of protein sequences using secondary structure: a modified dynamic programming method. <i>Protein Engineering, Design and Selection</i> , 1990, 3, 577-581.	2.1	20
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.	2.6	8
72	Molecular genetics and computer analyses. <i>Bioinformatics</i> , 1987, 3, 167-170.	4.1	2

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73	ARIADNE: pattern-directed inference and hierarchical abstraction in protein structure recognition. Communications of the ACM, 1987, 30, 909-921.	4.5	68
74	A modified Chou and Fasman protein structure algorithm. Bioinformatics, 1987, 3, 211-216.	4.1	22
75	Recognition of characteristic patterns in sets of functionally equivalent DNA sequences. Bioinformatics, 1987, 3, 223-227.	4.1	20
76	Prediction of a common structural domain in aminoacyl-tRNA synthetases through use of a new pattern-directed inference system. Biochemistry, 1987, 26, 6950-6957.	2.5	49
77	Of how great significance?. Nature, 1987, 326, 749-749.	27.8	1
78	The statistical distribution of nucleic acid similarities. Nucleic Acids Research, 1985, 13, 645-656.	14.5	198
79	Algorithms for restriction map comparisons. Nucleic Acids Research, 1984, 12, 237-242.	14.5	39
80	Sequence banks: Searching for sequence similarities. Nature, 1983, 301, 194-194.	27.8	5
81	Comparison of biosequences. Advances in Applied Mathematics, 1981, 2, 482-489.	0.7	681
82	How Alike are Two Trees?. American Mathematical Monthly, 1980, 87, 552.	0.3	2
83	A taxonomic distance applicable to paleontology. Mathematical Biosciences, 1980, 50, 285-295.	1.9	2
84	Protein constraints induced by multiframe encoding. Mathematical Biosciences, 1980, 49, 17-26.	1.9	14
85	A molecular sequence metric and evolutionary trees. Mathematical Biosciences, 1974, 19, 9-25.	1.9	80
86	Mapping of the lactose operator. Journal of Molecular Biology, 1971, 62, 139-169.	4.2	49
87	The nature of Lactose operator constitutive mutations. Journal of Molecular Biology, 1971, 59, 273-305.	4.2	158
88	The genetic code, information density, and evolution. Mathematical Biosciences, 1969, 4, 179-187.	1.9	25