William Raymond Pearson

List of Publications by Year in Descending Order

77 papers	**19,578** citations
38 h-index	**86** g-index
86 ext. papers	**20,565** ext. citations
8.9 avg, IF	**6.79** L-index

#	Paper	IF	Citations
77	Bioinformatics core competencies for undergraduate life sciences education. *PLoS ONE*, **2018**, 13, e0196878	3.7	43
76	Query-seeded iterative sequence similarity searching improves selectivity 5-20-fold. *Nucleic Acids Research*, **2017**, 45, e46	20.1	13
75	Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum Task Force of ISCBQ Education Committee). *PLoS Computational Biology*, **2016**, 12, e1004943	5	15
74	GOBLET: the Global Organisation for Bioinformatics Learning, Education and Training. *PLoS Computational Biology*, **2015**, 11, e1004143	5	37
73	Most partial domains in proteins are alignment and annotation artifacts. *Genome Biology*, **2015**, 16, 99	18.3	20
72	The Catalytic Site Atlas 2.0: cataloging catalytic sites and residues identified in enzymes. *Nucleic Acids Research*, **2014**, 42, D485-9	20.1	130
71	An introduction to sequence similarity ("homology") searching. *Current Protocols in Bioinformatics*, **2013**, Chapter 3, Unit3.1	24.2	308
70	Adjusting scoring matrices to correct overextended alignments. *Bioinformatics*, **2013**, 29, 3007-13	7.2	10
69	PSI-Search: iterative HOE-reduced profile SSEARCH searching. *Bioinformatics*, **2012**, 28, 1650-1	7.2	28
68	MACiE: exploring the diversity of biochemical reactions. *Nucleic Acids Research*, **2012**, 40, D783-9	20.1	60
67	Homologous over-extension: a challenge for iterative similarity searches. *Nucleic Acids Research*, **2010**, 38, 2177-89	20.1	41
66	Globally, unrelated protein sequences appear random. *Bioinformatics*, **2010**, 26, 310-8	7.2	27
65	RefProtDom: a protein database with improved domain boundaries and homology relationships. *Bioinformatics*, **2010**, 26, 2361-2	7.2	12
64	Improving pairwise sequence alignment accuracy using near-optimal protein sequence alignments. *BMC Bioinformatics*, **2010**, 11, 146	3.6	9
63	Exploring the relationship between sequence similarity and accurate phylogenetic trees. *Molecular Biology and Evolution*, **2006**, 23, 2090-100	8.3	27
62	Nomenclature for mammalian soluble glutathione transferases. *Methods in Enzymology*, **2005**, 401, 1-8	1.7	236
61	Phylogenies of glutathione transferase families. *Methods in Enzymology*, **2005**, 401, 186-204	1.7	66

60	The limits of protein sequence comparison?. *Current Opinion in Structural Biology*, **2005**, 15, 254-60	8.1	64
59	A System for Visualizing and Analyzing Near-Optimal Protein Sequence Alignments. *Information Visualization*, **2005**, 4, 224-237	2.4	5
58	Visualization of near-optimal sequence alignments. *Bioinformatics*, **2004**, 20, 953-8	7.2	8
57	The genome of Cryptosporidium hominis. *Nature*, **2004**, 431, 1107-12	50.4	444
56	Sensitivity and selectivity in protein structure comparison. *Protein Science*, **2004**, 13, 773-85	6.3	105
55	Finding protein and nucleotide similarities with FASTA. *Current Protocols in Bioinformatics*, **2004**, Chapter 3, Unit3.9	24.2	25
54	Identification of residues in glutathione transferase capable of driving functional diversification in evolution. A novel approach to protein redesign. *Journal of Biological Chemistry*, **2003**, 278, 8733-8	5.4	77
53	CRP: Cleavage of Radiolabeled Phosphoproteins. *Nucleic Acids Research*, **2003**, 31, 3859-61	20.1	10
52	Entamoeba histolytica: sequence conservation of the Gal/GalNAc lectin from clinical isolates. *Experimental Parasitology*, **2002**, 101, 157-63	2.1	34
51	Getting more from less: algorithms for rapid protein identification with multiple short peptide sequences. *Molecular and Cellular Proteomics*, **2002**, 1, 139-47	7.6	180
50	Empirical determination of effective gap penalties for sequence comparison. *Bioinformatics*, **2002**, 18, 1500-7	7.2	50
49	Identification and characterization of GSTT3, a third murine Theta class glutathione transferase. *Biochemical Journal*, **2002**, 366, 323-32	3.8	22
48	A strategy for the rapid identification of phosphorylation sites in the phosphoproteome. *Molecular and Cellular Proteomics*, **2002**, 1, 314-22	7.6	41
47	Generalized neighbor-joining: more reliable phylogenetic tree reconstruction. *Molecular Biology and Evolution*, **1999**, 16, 806-16	8.3	41
46	Evolution of protein sequences and structures. *Journal of Molecular Biology*, **1999**, 291, 977-95	6.5	107
45	Distinctive structure of the human GSTM3 gene-inverted orientation relative to the mu class glutathione transferase gene cluster. *Archives of Biochemistry and Biophysics*, **1999**, 361, 85-93	4.1	32
44	Gene structure, expression and chromosomal localization of murine Theta class glutathione transferase mGSTT1-1. *Biochemical Journal*, **1999**, 337, 141	3.8	13
43	Characterization of the human class Mu glutathione S-transferase gene cluster and the GSTM1 deletion. *Journal of Biological Chemistry*, **1998**, 273, 3517-27	5.4	134

42	Empirical statistical estimates for sequence similarity searches. *Journal of Molecular Biology*, **1998**, 276, 71-84	6.5	280
41	Rapid identification of protein phosphatase 1-binding proteins by mixed peptide sequencing and data base searching. Characterization of a novel holoenzymic form of protein phosphatase 1. *Journal of Biological Chemistry*, **1998**, 273, 24396-405	5.4	61
40	Comparison of DNA sequences with protein sequences. *Genomics*, **1997**, 46, 24-36	4.3	505
39	Aligning a DNA sequence with a protein sequence. *Journal of Computational Biology*, **1997**, 4, 339-49	1.7	23
38	Effective protein sequence comparison. *Methods in Enzymology*, **1996**, 266, 227-58	1.7	235
37	On the primer selection problem in polymerase chain reaction experiments. *Discrete Applied Mathematics*, **1996**, 71, 231-246	1	23
36	Comparison of methods for searching protein sequence databases. *Protein Science*, **1995**, 4, 1145-60	6.3	214
35	MIF proteins are not glutathione transferase homologs. *Protein Science*, **1994**, 3, 525-7	6.3	12
34	Primary structure of avian H+/K(+)-ATPase beta-subunit. *Biochimica Et Biophysica Acta - Biomembranes*, **1994**, 1190, 189-92	3.8	9
33	Classification of Adrenergic Receptor Subtypes: Molecular Biologic Approaches. *Methods*, **1994**, 4, 14-19	3	
32	Designing medical informatics research and library--resource projects to increase what is learned. *Journal of the American Medical Informatics Association: JAMIA*, **1994**, 1, 28-33	8.6	76
31	The structure of two murine class-mu glutathione transferase genes coordinately induced by butylated hydroxyanisole. *Archives of Biochemistry and Biophysics*, **1993**, 303, 383-93	4.1	22
30	Differences in induction by xenobiotics in murine tissues and the Hepa1c1c7 cell line of mRNAs encoding glutathione transferase, quinone reductase, and CYP1A P450s. *Pharmacogenetics and Genomics*, **1993**, 3, 167-81		8
29	No pain and gain! Experiences with Mentat on a biological application. *Concurrency and Computation: Practice and Experience*, **1993**, 5, 309-328		9
28	Identification of class-mu glutathione transferase genes GSTM1-GSTM5 on human chromosome 1p13. *American Journal of Human Genetics*, **1993**, 53, 220-33	11	143
27	The origin of nuclear receptor proteins: a single precursor distinct from other transcription factors. *Molecular Endocrinology*, **1992**, 6, 3-7		64
26	Comparing machine-independent versus machine-specific parallelization of a software platform for biological sequence comparison. *Bioinformatics*, **1992**, 8, 167-75	7.2	3
25	Aligning two sequences within a specified diagonal band. *Bioinformatics*, **1992**, 8, 481-7	7.2	63

24	Dynamic programming algorithms for biological sequence comparison. *Methods in Enzymology*, **1992**, 210, 575-601	1.7	53
23	The origin of nuclear receptor proteins: a single precursor distinct from other transcription factors. *Molecular Endocrinology*, **1992**, 6, 3-7		37
22	A platform for biological sequence comparison on parallel computers. *Bioinformatics*, **1991**, 7, 237-47	7.2	7
21	Cloning, expression, and characterization of a class-mu glutathione transferase from human muscle, the product of the GST4 locus. *Proceedings of the National Academy of Sciences of the United States of America*, **1991**, 88, 4443-7	11.5	61
20	Identifying distantly related protein sequences. *Current Opinion in Structural Biology*, **1991**, 1, 321-326	8.1	11
19	Molecular characterization of alpha 1- and alpha 2-adrenoceptors. *Trends in Pharmacological Sciences*, **1991**, 12, 62-7	13.2	139
18	Searching protein sequence libraries: comparison of the sensitivity and selectivity of the Smith-Waterman and FASTA algorithms. *Genomics*, **1991**, 11, 635-50	4.3	444
17	Hereditary differences in the expression of the human glutathione transferase active on trans-stilbene oxide are due to a gene deletion. *Proceedings of the National Academy of Sciences of the United States of America*, **1988**, 85, 7293-7	11.5	583
16	Improved tools for biological sequence comparison. *Proceedings of the National Academy of Sciences of the United States of America*, **1988**, 85, 2444-8	11.5	9694
15	Tissue-specific induction of murine glutathione transferase mRNAs by butylated hydroxyanisole. *Journal of Biological Chemistry*, **1988**, 263, 13324-32	5.4	49
14	Rapid and sensitive protein similarity searches. *Science*, **1985**, 227, 1435-41	33.3	3665
13	Increased synthesis of glutathione S-transferases in response to anticarcinogenic antioxidants. Cloning and measurement of messenger RNA. *Journal of Biological Chemistry*, **1983**, 258, 2052-62	5.4	98
12	Automatic construction of restriction site maps. *Nucleic Acids Research*, **1982**, 10, 217-27	20.1	43
11	Regulation of synthesis of amyloid A-related protein. *Annals of the New York Academy of Sciences*, **1982**, 389, 106-15	6.5	38
10	Discrete-length repeated sequences in eukaryotic genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **1981**, 78, 4016-20	11.5	6
9	Long and short repeats of sea urchin DNA and their evolution. *Chromosoma*, **1981**, 84, 19-32	2.8	18
8	Repeated DNA sequences near the 5ʹend of the silk fibroin gene. *Journal of Biological Chemistry*, **1981**, 256, 4033-41	5.4	26
7	Computer programs for analysis of nucleic acid hybridization, thermal denaturation, and gel electrophoresis data. *Nucleic Acids Research*, **1979**, 6, 3911-21	20.1	36

6	Kinetic determination of the genome size of the pea. *Plant Physiology*, **1978**, 62, 112-5	6.6	6
5	A program for least squares analysis of reassociation and hybridization data. *Nucleic Acids Research*, **1977**, 4, 1727-37	20.1	196
4	Sequence relationship between long and short repetitive DNA of the rat: a preliminary report. *Proceedings of the National Academy of Sciences of the United States of America*, **1977**, 74, 4382-6	11.5	12
3	Absence of short period interspersion of repetitive and non-repetitive sequences in the DNA of Drosophila melanogaster. *Chromosoma*, **1976**, 56, 309-26	2.8	89
2	Stoichiometry of chromatin proteins. *Biochemical and Biophysical Research Communications*, **1974**, 58, 50-7	3.4	31
1	Barriers to Integration of Bioinformatics into Undergraduate Life Sciences Education		3