

David B Searls

List of Publications by Year in descending order

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41
papers

1,546
citations

394421
19
h-index

315739
38
g-index

43
all docs

43
docs citations

43
times ranked

1546
citing authors

#	ARTICLE	IF	CITATIONS
1	Lessons from the CAGIâ€¢4 Hopkins clinical panel challenge. <i>Human Mutation</i> , 2017, 38, 1155-1168.	2.5	6
2	A New Online Computational Biology Curriculum. <i>PLoS Computational Biology</i> , 2014, 10, e1003662.	3.2	10
3	A primer in macromolecular linguistics. <i>Biopolymers</i> , 2013, 99, 203-217.	2.4	13
4	An Online Bioinformatics Curriculum. <i>PLoS Computational Biology</i> , 2012, 8, e1002632.	3.2	16
5	Ten Simple Rules for Online Learning. <i>PLoS Computational Biology</i> , 2012, 8, e1002631.	3.2	21
6	The Roots of Bioinformatics. <i>PLoS Computational Biology</i> , 2010, 6, e1000809.	3.2	29
7	Ten Simple Rules for Choosing between Industry and Academia. <i>PLoS Computational Biology</i> , 2009, 5, e1000388.	3.2	12
8	Omic Empiricism. <i>Science Signaling</i> , 2009, 2, eg6.	3.6	0
9	Can literature analysis identify innovation drivers in drug discovery?. <i>Nature Reviews Drug Discovery</i> , 2009, 8, 865-878.	46.4	93
10	Literature mining in support of drug discovery. <i>Briefings in Bioinformatics</i> , 2008, 9, 479-492.	6.5	70
11	A View from the Dark Side. <i>PLoS Computational Biology</i> , 2007, 3, e105.	3.2	3
12	Risk in drug trials. <i>Lancet</i> , The, 2006, 368, 2205.	13.7	6
13	Grammatical Representations of Macromolecular Structure. <i>Journal of Computational Biology</i> , 2006, 13, 1077-1100.	1.6	40
14	Data integration: challenges for drug discovery. <i>Nature Reviews Drug Discovery</i> , 2005, 4, 45-58.	46.4	161
15	Clusters of Adjacent and Similarly Expressed Genes across Normal Human Tissues Complicate Comparative Transcriptomic Discovery. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 351-363.	2.0	6
16	Managing genomic and proteomic knowledge. <i>Drug Discovery Today: Technologies</i> , 2005, 2, 197-204.	4.0	4
17	Trees of life and of language. <i>Nature</i> , 2003, 426, 391-392.	27.8	32
18	Pharmacophylogenomics: genes, evolution and drug targets. <i>Nature Reviews Drug Discovery</i> , 2003, 2, 613-623.	46.4	78

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19	Data integrationâ€”connecting the dots. <i>Nature Biotechnology</i> , 2003, 21, 844-845.	17.5	11
20	The language of genes. <i>Nature</i> , 2002, 420, 211-217.	27.8	339
21	From Jabberwocky to Genome: Lewis Carroll and Computational Biology. <i>Journal of Computational Biology</i> , 2001, 8, 339-348.	1.6	6
22	Using bioinformatics in gene and drug discovery. <i>Drug Discovery Today</i> , 2000, 5, 135-143.	6.4	54
23	BIOINFORMATICSTOOLS FORWHOLEGENOMES. <i>Annual Review of Genomics and Human Genetics</i> , 2000, 1, 251-279.	6.2	30
24	Formal language theory and biological macromolecules. <i>DIMACS Series in Discrete Mathematics and Theoretical Computer Science</i> , 1999, , 117-140.	0.0	21
25	Grand challenges in computational biology. <i>New Comprehensive Biochemistry</i> , 1998, , 3-10.	0.1	8
26	Analysis of EST-Driven Gene Annotation in Human Genomicâ‰%Sequence. <i>Genome Research</i> , 1998, 8, 362-376.	5.5	72
27	Linguistic approaches to biological sequences. <i>Bioinformatics</i> , 1997, 13, 333-344.	4.1	38
28	Computational gene discovery and human disease. <i>Current Opinion in Genetics and Development</i> , 1997, 7, 416-423.	3.3	35
29	Visualizing the Genome. , 1997, , 185-204.		2
30	Sequence alignment through pictures. <i>Trends in Genetics</i> , 1996, 12, 35-37.	6.7	9
31	String variable grammar: A logic grammar formalism for the biological language of DNA. <i>The Journal of Logic Programming</i> , 1995, 24, 73-102.	1.7	48
32	bioTk: Componentry for genome informatics graphical user interfaces. <i>Gene</i> , 1995, 163, GC1-GC16.	2.2	17
33	SORTEZ: a relational translator for NCBI's ASN.1 database. <i>Bioinformatics</i> , 1994, 10, 369-378.	4.1	10
34	Gene Structure Prediction by Linguistic Methods. <i>Genomics</i> , 1994, 23, 540-551.	2.9	142
35	Document Image Analysis Using Logic-Grammar-Based Syntactic Pattern Recognition. , 1992, , 520-545.		6
36	Fast Fourier transform-based correlation of DNA sequences using complex plane encoding. <i>Bioinformatics</i> , 1991, 7, 143-154.	4.1	15

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37	Logic-based configuration with a semantic network. <i>The Journal of Logic Programming</i> , 1990, 8, 53-73.	1.7	15
38	Analysis of early antigenic changes on heterokaryons between L-cells and a teratocarcinoma-derived cell line, TerC. <i>Somatic Cell Genetics</i> , 1982, 8, 587-604.	2.7	0
39	Lipid composition and lateral diffusion in plasma membranes of teratocarcinoma-derived cell lines. <i>Cell</i> , 1981, 24, 511-517.	28.9	26
40	An improved colorimetric assay for plasminogen activator. <i>Analytical Biochemistry</i> , 1980, 107, 64-70.	2.4	16
41	Plasma membrane isolation on DEAE-Sephadex beads. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1980, 602, 207-212.	2.6	20