

Richard H Lathrop

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12081824/publications.pdf>

Version: 2024-02-01

30
papers

1,130
citations

516710

16
h-index

501196

28
g-index

30
all docs

30
docs citations

30
times ranked

1071
citing authors

#	ARTICLE	IF	CITATIONS
1	The protein threading problem with sequence amino acid interaction preferences is NP-complete. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 1059-1068.	2.1	231
2	Computational identification of a transiently open L1/S3 pocket for reactivation of mutant p53. <i>Nature Communications</i> , 2013, 4, 1407.	12.8	184
3	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
4	ARIADNE: pattern-directed inference and hierarchical abstraction in protein structure recognition. <i>Communications of the ACM</i> , 1987, 30, 909-921.	4.5	68
5	Information-theoretic dissection of pairwise contact potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 7-14.	2.6	50
6	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.	2.5	49
7	Predicting Positive p53 Cancer Rescue Regions Using Most Informative Positive (MIP) Active Learning. <i>PLoS Computational Biology</i> , 2009, 5, e1000498.	3.2	49
8	Choosing where to look next in a mutation sequence space: Active Learning of informative p53 cancer rescue mutants. <i>Bioinformatics</i> , 2007, 23, i104-i114.	4.1	37
9	Ensemble-Based Computational Approach Discriminates Functional Activity of p53 Cancer and Rescue Mutants. <i>PLoS Computational Biology</i> , 2011, 7, e1002238.	3.2	34
10	Predicting Protein Structure With Probabilistic Models. <i>Advances in Molecular and Cell Biology</i> , 1997, , 447-506.	0.1	28
11	Functional Census of Mutation Sequence Spaces: The Example of p53 Cancer Rescue Mutants. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 114-125.	3.0	28
12	Novel TUTase associates with an editosome-like complex in mitochondria of <i>Trypanosoma brucei</i> . <i>Rna</i> , 2009, 15, 1322-1337.	3.5	28
13	Tuning cellular response by modular design of bioactive domains in collagen. <i>Biomaterials</i> , 2015, 53, 309-317.	11.4	22
14	Mechanism of U Insertion RNA Editing in Trypanosome Mitochondria: The Bimodal TUTase Activity of the Core Complex. <i>Journal of Molecular Biology</i> , 2010, 399, 680-695.	4.2	21
15	Recombinant Human Collagen and Biomimetic Variants Using a De Novo Gene Optimized for Modular Assembly. <i>Biomacromolecules</i> , 2010, 11, 1460-1469.	5.4	20
16	Combinatorial Optimization in Rapidly Mutating Drug-Resistant Viruses. <i>Journal of Combinatorial Optimization</i> , 1999, 3, 301-320.	1.3	17
17	All-codon scanning identifies p53 cancer rescue mutations. <i>Nucleic Acids Research</i> , 2010, 38, 7079-7088.	14.5	17
18	Analysis and algorithms for protein sequence-structure alignment. <i>New Comprehensive Biochemistry</i> , 1998, 32, 227-283.	0.1	16

#	ARTICLE	IF	CITATIONS
19	Computationally Optimised DNA Assembly of synthetic genes. International Journal of Bioinformatics Research and Applications, 2008, 4, 324.	0.2	16
20	Predicting oligonucleotide-directed mutagenesis failures in protein engineering. Nucleic Acids Research, 2004, 32, 6407-6413.	14.5	13
21	Acid helix-turn activator motif. Proteins: Structure, Function and Bioinformatics, 1990, 8, 156-163.	2.6	10
22	An Anytime Local-to-Global Optimization Algorithm for Protein Threading in $O(m^2n^2)$ Space. Journal of Computational Biology, 1999, 6, 405-418.	1.6	10
23	Heterogeneous Biomedical Database Integration using a Hybrid Strategy: A P53 Cancer Research Database. Cancer Informatics, 2006, 2, 117693510600200.	1.9	10
24	iCODA: RNAi-Based Inducible Knock-In System in Trypanosoma brucei. Methods in Molecular Biology, 2011, 718, 23-37.	0.9	10
25	Pattern descriptors and the unidentified reading frame 6 human mtDNA dinucleotide-binding site. Proteins: Structure, Function and Bioinformatics, 1988, 3, 97-101.	2.6	8
26	Massively parallel symbolic induction of protein structure/function relationships. Lecture Notes in Computer Science, 1993, , 157-173.	1.3	2
27	CHOPER Filters Enable Rare Mutation Detection in Complex Mutagenesis Populations by Next-Generation Sequencing. PLoS ONE, 2015, 10, e0116877.	2.5	1
28	Heterogeneous biomedical database integration using a hybrid strategy: a p53 cancer research database. Cancer Informatics, 2007, 2, 277-87.	1.9	1
29	An anytime algorithm for gapped block protein threading with pair interactions. , 1999, , .		0
30	Protein Structure Prediction in the Post Genomic Era. , 1998, , .		0