

# Richard H Lathrop

## List of Publications by Year in descending order

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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	CHOPER Filters Enable Rare Mutation Detection in Complex Mutagenesis Populations by Next-Generation Sequencing. PLoS ONE, 2015, 10, e0116877.	2.5	1
2	Tuning cellular response by modular design of bioactive domains in collagen. Biomaterials, 2015, 53, 309-317.	11.4	22
3	Computational identification of a transiently open L1/S3 pocket for reactivation of mutant p53. Nature Communications, 2013, 4, 1407.	12.8	184
4	iCODA: RNAi-Based Inducible Knock-In System in Trypanosoma brucei. Methods in Molecular Biology, 2011, 718, 23-37.	0.9	10
5	Ensemble-Based Computational Approach Discriminates Functional Activity of p53 Cancer and Rescue Mutants. PLoS Computational Biology, 2011, 7, e1002238.	3.2	34
6	All-codon scanning identifies p53 cancer rescue mutations. Nucleic Acids Research, 2010, 38, 7079-7088.	14.5	17
7	Recombinant Human Collagen and Biomimetic Variants Using a De Novo Gene Optimized for Modular Assembly. Biomacromolecules, 2010, 11, 1460-1469.	5.4	20
8	Mechanism of U Insertion RNA Editing in Trypanosome Mitochondria: The Bimodal TUTase Activity of the Core Complex. Journal of Molecular Biology, 2010, 399, 680-695.	4.2	21
9	Predicting Positive p53 Cancer Rescue Regions Using Most Informative Positive (MIP) Active Learning. PLoS Computational Biology, 2009, 5, e1000498.	3.2	49
10	Novel TUTase associates with an editosome-like complex in mitochondria of <i>Trypanosoma brucei</i>. Rna, 2009, 15, 1322-1337.	3.5	28
11	Computationally Optimised DNA Assembly of synthetic genes. International Journal of Bioinformatics Research and Applications, 2008, 4, 324.	0.2	16
12	Choosing where to look next in a mutation sequence space: Active Learning of informative p53 cancer rescue mutants. Bioinformatics, 2007, 23, i104-i114.	4.1	37
13	Heterogeneous biomedical database integration using a hybrid strategy: a p53 cancer research database. Cancer Informatics, 2007, 2, 277-87.	1.9	1
14	Heterogeneous Biomedical Database Integration using a Hybrid Strategy: A P53 Cancer Research Database. Cancer Informatics, 2006, 2, 117693510600200.	1.9	10
15	Functional Census of Mutation Sequence Spaces: The Example of p53 Cancer Rescue Mutants. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 114-125.	3.0	28
16	Predicting oligonucleotide-directed mutagenesis failures in protein engineering. Nucleic Acids Research, 2004, 32, 6407-6413.	14.5	13
17	Information-theoretic dissection of pairwise contact potentials. Proteins: Structure, Function and Bioinformatics, 2002, 49, 7-14.	2.6	50
18	An anytime algorithm for gapped block protein threading with pair interactions. , 1999, , .		0

#	ARTICLE	IF	CITATIONS
19	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
20	Combinatorial Optimization in Rapidly Mutating Drug-Resistant Viruses. Journal of Combinatorial Optimization, 1999, 3, 301-320.	1.3	17
21	Analysis and algorithms for protein sequence-structure alignment. New Comprehensive Biochemistry, 1998, 32, 227-283.	0.1	16
22	Protein Structure Prediction in the Post Genomic Era. , 1998, , .		0
23	Predicting Protein Structure With Probabilistic Models. Advances in Molecular and Cell Biology, 1997, , 447-506.	0.1	28
24	Global Optimum Protein Threading with Gapped Alignment and Empirical Pair Score Functions. Journal of Molecular Biology, 1996, 255, 641-665.	4.2	150
25	The protein threading problem with sequence amino acid interaction preferences is NP-complete. Protein Engineering, Design and Selection, 1994, 7, 1059-1068.	2.1	231
26	Massively parallel symbolic induction of protein structure/function relationships. Lecture Notes in Computer Science, 1993, , 157-173.	1.3	2
27	Acid helix-turn activator motif. Proteins: Structure, Function and Bioinformatics, 1990, 8, 156-163.	2.6	10
28	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
29	ARIADNE: pattern-directed inference and hierarchical abstraction in protein structure recognition. Communications of the ACM, 1987, 30, 909-921.	4.5	68
30	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