

Kevin Karplus

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

5,472
citations

236925

25
h-index

395702

33
g-index

46
all docs

46
docs citations

46
times ranked

7694
citing authors

#	ARTICLE	IF	CITATIONS
1	Fallacy of the Unique Genome: Sequence Diversity within Single <i>Helicobacter pylori</i> Strains. <i>MBio</i> , 2017, 8, .	4.1	64
2	Analysis of nanopore data using hidden Markov models. <i>Bioinformatics</i> , 2015, 31, 1897-1903.	4.1	32
3	Error rates for nanopore discrimination among cytosine, methylcytosine, and hydroxymethylcytosine along individual DNA strands. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18910-18915.	7.1	161
4	Automated forward and reverse ratcheting of DNA in a nanopore at 5-Å... precision. <i>Nature Biotechnology</i> , 2012, 30, 344-348.	17.5	528
5	Protein Packing Quality Using Delaunay Complexes. , 2011, , .		0
6	Identification of a Chemoreceptor Zinc-Binding Domain Common to Cytoplasmic Bacterial Chemoreceptors. <i>Journal of Bacteriology</i> , 2011, 193, 4338-4345.	2.2	33
7	Improving protein secondary structure prediction using a simple <i>k</i> -mer model. <i>Bioinformatics</i> , 2010, 26, 596-602.	4.1	54
8	SAM-T08, HMM-based protein structure prediction. <i>Nucleic Acids Research</i> , 2009, 37, W492-W497.	14.5	120
9	Pokefind: a novel topological filter for use with protein structure prediction. <i>Bioinformatics</i> , 2009, 25, i281-i288.	4.1	11
10	Model quality assessment using distance constraints from alignments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 540-549.	2.6	23
11	Applying undertaker cost functions to model quality assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 550-555.	2.6	18
12	Applying Undertaker to quality assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 191-195.	2.6	12
13	Improving physical realism, stereochemistry, and side-chain accuracy in homology modeling: Four approaches that performed well in CASP8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 114-122.	2.6	1,105
14	Predict-2nd: a tool for generalized protein local structure prediction. <i>Bioinformatics</i> , 2008, 24, 2453-2459.	4.1	34
15	Contact prediction using mutual information and neural nets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 159-164.	2.6	95
16	Identification and Characterization of RbmA, a Novel Protein Required for the Development of Rugose Colony Morphology and Biofilm Structure in <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2006, 188, 1049-1059.	2.2	146
17	SAM-T04: What is new in protein-structure prediction for CASP6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 135-142.	2.6	90
18	Calibrating E-values for hidden Markov models using reverse-sequence null models. <i>Bioinformatics</i> , 2005, 21, 4107-4115.	4.1	38

#	ARTICLE	IF	CITATIONS
19	Methods of translating NMR proton distances into their corresponding heavy atom distances for protein structure prediction with limited experimental data. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 597-605.	2.1	1
20	Evaluation of local structure alphabets based on residue burial. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 508-518.	2.6	58
21	Hidden Markov models that use predicted local structure for fold recognition: Alphabets of backbone geometry. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 504-514.	2.6	178
22	Combining local-structure, fold-recognition, and new fold methods for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 491-496.	2.6	269
23	Bioinformatics: A New Field in Engineering Education. <i>Journal of Engineering Education</i> , 2003, 92, 101-104.	3.0	10
24	Predicting reliable regions in protein sequence alignments. <i>Bioinformatics</i> , 2002, 18, 306-314.	4.1	83
25	Information-theoretic dissection of pairwise contact potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 7-14.	2.6	50
26	Assignment of homology to genome sequences using a library of hidden Markov models that represent all proteins of known structure. <i>Journal of Molecular Biology</i> , 2001, 313, 903-919.	4.2	1,092
27	What is the value added by human intervention in protein structure prediction?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 86-91.	2.6	104
28	Predicting protein structure using only sequence information. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 121-125.	2.6	76
29	Predicting protein structure using only sequence information. , 1999, 37, 121.		1
30	Predicting protein structure using only sequence information. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 121-125.	2.6	52
31	Kestrel: A Programmable Array for Sequence Analysis. <i>Journal of Signal Processing Systems</i> , 1998, 19, 115-126.	1.0	20
32	Sequence comparisons using multiple sequences detect three times as many remote homologues as pairwise methods. <i>Journal of Molecular Biology</i> , 1998, 284, 1201-1210.	4.2	498
33	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	2.6	110
34	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	2.6	31
35	A flexible motif search technique based on generalized profiles. <i>Computers & Chemistry</i> , 1996, 20, 3-23.	1.2	275