Kevin Karplus

List of Publications by Year
in descending order

35 papers	5,472 citations	236612 25 h-index	395343 33 g-index
46 all docs	46 docs citations	46 times ranked	7694 citing authors

#	Article	IF	Citations
1	Improving physical realism, stereochemistry, and side‑chain accuracy in homology modeling: Four approaches that performed well in CASP8. Proteins: Structure, Function and Bioinformatics, 2009, 77, 114-122.	1.5	1,105
2	Assignment of homology to genome sequences using a library of hidden Markov models that represent all proteins of known structure. Journal of Molecular Biology, 2001, 313, 903-919.	2.0	1,092
3	Automated forward and reverse ratcheting of DNA in a nanopore at 5-Ã… precision. Nature Biotechnology, 2012, 30, 344-348.	9.4	528
4	Sequence comparisons using multiple sequences detect three times as many remote homologues as pairwise methods. Journal of Molecular Biology, 1998, 284, 1201-1210.	2.0	498
5	A flexible motif search technique based on generalized profiles. Computers & Chemistry, 1996, 20, 3-23.	1.2	275
6	Combining local-structure, fold-recognition, and new fold methods for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2003, 53, 491-496.	1.5	269
7	Hidden Markov models that use predicted local structure for fold recognition: Alphabets of backbone geometry. Proteins: Structure, Function and Bioinformatics, 2003, 51, 504-514.	1.5	178
8	Error rates for nanopore discrimination among cytosine, methylcytosine, and hydroxymethylcytosine along individual DNA strands. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18910-18915.	3.3	161
9	Identification and Characterization of RbmA, a Novel Protein Required for the Development of Rugose Colony Morphology and Biofilm Structure in Vibrio cholerae. Journal of Bacteriology, 2006, 188, 1049-1059.	1.0	146
10	SAM-T08, HMM-based protein structure prediction. Nucleic Acids Research, 2009, 37, W492-W497.	6.5	120
11	Predicting protein structure using hidden Markov models. Proteins: Structure, Function and Bioinformatics, 1997, 29, 134-139.	1.5	110
12	What is the value added by human intervention in protein structure prediction?. Proteins: Structure, Function and Bioinformatics, 2001, 45, 86-91.	1.5	104
13	Contact prediction using mutual information and neural nets. Proteins: Structure, Function and Bioinformatics, 2007, 69, 159-164.	1.5	95
14	SAM-T04: What is new in protein-structure prediction for CASP6. Proteins: Structure, Function and Bioinformatics, 2005, 61, 135-142.	1.5	90
15	Predicting reliable regions in protein sequence alignments. Bioinformatics, 2002, 18, 306-314.	1.8	83
16	Predicting protein structure using only sequence information. Proteins: Structure, Function and Bioinformatics, 1999, 37, 121-125.	1.5	76
17	Fallacy of the Unique Genome: Sequence Diversity within Single *Helicobacter pylori* Strains. MBio, 2017, 8, .	1.8	64
18	Evaluation of local structure alphabets based on residue burial. Proteins: Structure, Function and Bioinformatics, 2004, 55, 508-518.	1.5	58

#	Article	IF	Citations
19	Improving protein secondary structure prediction using a simple *k*-mer model. Bioinformatics, 2010, 26, 596-602.	1.8	54
20	Predicting protein structure using only sequence information. Proteins: Structure, Function and Bioinformatics, 1999, Suppl 3, 121-5.	1.5	52
21	Information-theoretic dissection of pairwise contact potentials. Proteins: Structure, Function and Bioinformatics, 2002, 49, 7-14.	1.5	50
22	Calibrating E-values for hidden Markov models using reverse-sequence null models. Bioinformatics, 2005, 21, 4107-4115.	1.8	38
23	Predict-2nd: a tool for generalized protein local structure prediction. Bioinformatics, 2008, 24, 2453-2459.	1.8	34
24	Identification of a Chemoreceptor Zinc-Binding Domain Common to Cytoplasmic Bacterial Chemoreceptors. Journal of Bacteriology, 2011, 193, 4338-4345.	1.0	33
25	Analysis of nanopore data using hidden Markov models. Bioinformatics, 2015, 31, 1897-1903.	1.8	32
26	Predicting protein structure using hidden Markov models. Proteins: Structure, Function and Bioinformatics, 1997, 29, 134-139.	1.5	31
27	Model quality assessment using distance constraints from alignments. Proteins: Structure, Function and Bioinformatics, 2009, 75, 540-549.	1.5	23
28	Kestrel: A Programmable Array for Sequence Analysis. Journal of Signal Processing Systems, 1998, 19, 115-126.	1.0	20
29	Applying undertaker cost functions to model quality assessment. Proteins: Structure, Function and Bioinformatics, 2009, 75, 550-555.	1.5	18
30	Applying Undertaker to quality assessment. Proteins: Structure, Function and Bioinformatics, 2009, 77, 191-195.	1.5	12
31	Pokefind: a novel topological filter for use with protein structure prediction. Bioinformatics, 2009, 25, i281-i288.	1.8	11
32	Bioinformatics: A New Field in Engineering Education. Journal of Engineering Education, 2003, 92, 101-104.	1.9	10
33	Methods of translating NMR proton distances into their corresponding heavy atom distances for protein structure prediction with limited experimental data. Protein Engineering, Design and Selection, 2005, 18, 597-605.	1.0	1
34	Predicting protein structure using only sequence information. , 1999, 37, 121.		1
35	Protein Packing Quality Using Delaunay Complexes. , 2011, , .		0