

# Kevin Karplus

## List of Publications by Year in descending order

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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	Fallacy of the Unique Genome: Sequence Diversity within Single <i>Helicobacter pylori</i> Strains. <i>MBio</i> , 2017, 8, .	1.8	64
2	Analysis of nanopore data using hidden Markov models. <i>Bioinformatics</i> , 2015, 31, 1897-1903.	1.8	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.	3.3	161
4	Automated forward and reverse ratcheting of DNA in a nanopore at 5-Å... precision. <i>Nature Biotechnology</i> , 2012, 30, 344-348.	9.4	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.	1.0	33
7	Improving protein secondary structure prediction using a simple <i>k</i> -mer model. <i>Bioinformatics</i> , 2010, 26, 596-602.	1.8	54
8	SAM-T08, HMM-based protein structure prediction. <i>Nucleic Acids Research</i> , 2009, 37, W492-W497.	6.5	120
9	Pokefind: a novel topological filter for use with protein structure prediction. <i>Bioinformatics</i> , 2009, 25, i281-i288.	1.8	11
10	Model quality assessment using distance constraints from alignments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 540-549.	1.5	23
11	Applying undertaker cost functions to model quality assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 550-555.	1.5	18
12	Applying Undertaker to quality assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 191-195.	1.5	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.	1.5	1,105
14	Predict-2nd: a tool for generalized protein local structure prediction. <i>Bioinformatics</i> , 2008, 24, 2453-2459.	1.8	34
15	Contact prediction using mutual information and neural nets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 159-164.	1.5	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.	1.0	146
17	SAM-T04: What is new in protein-structure prediction for CASP6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 135-142.	1.5	90
18	Calibrating E-values for hidden Markov models using reverse-sequence null models. <i>Bioinformatics</i> , 2005, 21, 4107-4115.	1.8	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.	1.0	1
20	Evaluation of local structure alphabets based on residue burial. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 508-518.	1.5	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.	1.5	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.	1.5	269
23	Bioinformatics: A New Field in Engineering Education. <i>Journal of Engineering Education</i> , 2003, 92, 101-104.	1.9	10
24	Predicting reliable regions in protein sequence alignments. <i>Bioinformatics</i> , 2002, 18, 306-314.	1.8	83
25	Information-theoretic dissection of pairwise contact potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 7-14.	1.5	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.	2.0	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.	1.5	104
28	Predicting protein structure using only sequence information. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 121-125.	1.5	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, Suppl 3, 121-5.	1.5	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.	2.0	498
33	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	1.5	110
34	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	1.5	31
35	A flexible motif search technique based on generalized profiles. <i>Computers &amp; Chemistry</i> , 1996, 20, 3-23.	1.2	275