

Peer-reviewed Publications (since 2004)

- [1] Martin Madera, Ryan Calmus, Grant Thiltgen, Kevin Karplus, and Julian Gough. Improving protein secondary structure prediction using a simple k-mer model. *Bioinformatics*, 26(5):596–602, March 2010. doi:10.1093/bioinformatics/btq020
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- [3] John G. Archie, Martin Paluszewski, and Kevin Karplus. Applying undertaker to quality assessment. *Proteins: Structure, Function, and Bioinformatics*, 77(S9):191–195, 12 August 2009. CASP8 special issue. doi:10.1002/prot.22508
- [4] Kevin Karplus. SAM-T08, HMM-based protein structure prediction. *Nucleic Acids Research*, 37(Web Server Issue):W492–W497, 2009. doi:10.1093/nar/gkp403
- [5] Firas Khatib, Carol A. Rohl, and Kevin Karplus. Pokefind: a novel topological filter for use with protein structure prediction. *Bioinformatics*, 25(12):i281–i288, 2009. Presented at ISMB/ECCB 2009. doi:10.1093/bioinformatics/btp198
- [6] John Archie and Kevin Karplus. Applying undertaker cost functions to model quality assessment. *Proteins: Structure, Function, and Bioinformatics*, 75(3):550–555, 2009. published online 30 Sep 2008. doi:10.1002/prot.22288
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- [10] Jiunn C. N. Fong, Kevin Karplus, Gary K. Schoolnik, and Fitnat H. Yildiz. Identification and characterization of RbmA, a novel protein required for the development of rugose colony morphology and biofilm structure in *Vibrio cholera*. *Journal of Bacteriology*, 188(3):1049–1059, February 2006.
- [11] Oscar Hur and Kevin Karplus. 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*, 18(12):597–605, December 2005.
- [12] Kevin Karplus, Sol Katzman, George Shackelford, Martina Koeva, Jenny Draper, Bret Barnes, Marcia Soriano, and Richard Hughey. SAM-T04: what’s new in protein-structure prediction for CASP6. *Proteins: Structure, Function, and Bioinformatics*, 61(S7):135–142, 2005. doi:10.1002/prot.20730
- [13] Kevin Karplus, Rachel Karchin, George Shackelford, and Richard Hughey. Calibrating E-values for hidden Markov models with reverse-sequence null models. *Bioinformatics*, 21(22):4107–4115, 2005. doi:10.1093/bioinformatics/bti629

- [14] Andrea Di Blas, David Dahle, Mark Diekhans, Leslie Grate, Jeffrey Hirschberg, Kevin Karplus, Hansjorg Keller, Francisco J. Kendrick, Mark Mesa-Martinez, David Pease, Eric Rice, Angela Schmid, Don Speck, and Richard Hughey. The UCSC Kestrel parallel processor. *IEEE Transactions on Parallel and Distributed Systems*, 16(1):80–92, January 2005.
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