Kimmen Sjolander

List of Publications by Year
in descending order

33 papers	4,742 citations	257450 24 h-index	434195 31 g-index
35 all docs	35 docs citations	35 times ranked	5103 citing authors

#	Article	IF	Citations
1	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	4.1	36
2	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	19.0	198
3	The PhyloFacts FAT-CAT web server: ortholog identification and function prediction using fast approximate tree classification. Nucleic Acids Research, 2013, 41, W242-W248.	14.5	25
4	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	7.6	188
5	Ortholog identification in the presence of domain architecture rearrangement. Briefings in Bioinformatics, 2011, 12, 413-422.	6.5	28
6	Getting Started in Structural Phylogenomics. PLoS Computational Biology, 2010, 6, e1000621.	3.2	13
7	Arabidopsis thaliana PGR7 Encodes a Conserved Chloroplast Protein That Is Necessary for Efficient Photosynthetic Electron Transport. PLoS ONE, 2010, 5, e11688.	2.5	18
8	SATCHMO-JS: a webserver for simultaneous protein multiple sequence alignment and phylogenetic tree construction. Nucleic Acids Research, 2010, 38, W29-W34.	14.5	26
9	Berkeley PHOG: PhyloFacts orthology group prediction web server. Nucleic Acids Research, 2009, 37, W84-W89.	14.5	65
10	INTREPID: a web server for prediction of functionally important residues by evolutionary analysis. Nucleic Acids Research, 2009, 37, W390-W395.	14.5	35
11	Automated Protein Subfamily Identification and Classification. PLoS Computational Biology, 2007, 3, e160.	3.2	110
12	Berkeley Phylogenomics Group web servers: resources for structural phylogenomic analysis. Nucleic Acids Research, 2007, 35, W27-W32.	14.5	24
13	PhyloFacts: an online structural phylogenomic encyclopedia for protein functional and structural classification. Genome Biology, 2006, 7, R83.	9.6	50
14	Functional Classification Using Phylogenomic Inference. PLoS Computational Biology, 2006, 2, e77.	3.2	61
15	Predicted hexameric structure of the Agrobacterium VirB4 C terminus suggests VirB4 acts as a docking site during type IV secretion. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1685-1690.	7.1	51
16	Proteome Analysis of the Rice Etioplast. Molecular and Cellular Proteomics, 2005, 4, 1072-1084.	3.8	108
17	Subfamily hmms in functional genomics. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 322-33.	0.7	12
18	Phylogenomic inference of protein molecular function: advances and challenges. Bioinformatics, 2004, 20, 170-179.	4.1	184

#	Article	IF	Citations
19	Arabidopsis Downy Mildew Resistance Gene RPP27 Encodes a Receptor-Like Protein Similar to CLAVATA2 and Tomato Cf-9. Plant Physiology, 2004, 135, 1100-1112.	4.8	52
20	From Endonucleases to Transcription Factors: Evolution of the AP2 DNA Binding Domain in Plants[W]. Plant Cell, 2004, 16, 2265-2277.	6.6	227
21	COACH: profile-profile alignment of protein families using hidden Markov models. Bioinformatics, 2004, 20, 1309-1318.	4.1	86
22	A comparison of scoring functions for protein sequence profile alignment. Bioinformatics, 2004, 20, 1301-1308.	4.1	116
23	The Arabidopsis thaliana Chloroplast Proteome Reveals Pathway Abundance and Novel Protein Functions. Current Biology, 2004, 14, 354-362.	3.9	585
24	SUBFAMILY HMMS IN FUNCTIONAL GENOMICS. , 2004, , .		12
25	SATCHMO: sequence alignment and tree construction using hidden Markov models. Bioinformatics, 2003, 19, 1404-1411.	4.1	91
26	SIMULTANEOUS SEQUENCE ALIGNMENT AND TREE CONSTRUCTION USING HIDDEN MARKOV MODELS. , 2002, , .		6
27	Predicting protein structure using hidden Markov models. Proteins: Structure, Function and Bioinformatics, 1997, 29, 134-139.	2.6	110
28	Predicting protein structure using hidden Markov models. Proteins: Structure, Function and Bioinformatics, 1997, 29, 134-139.	2.6	8
29	Predicting protein structure using hidden Markov models. Proteins: Structure, Function and Bioinformatics, 1997, 29, 134-139.	2.6	31
30	Dirichlet mixtures: a method for improved detection of weak but significant protein sequence homology. Bioinformatics, 1996, 12, 327-345.	4.1	197
31	Hidden Markov Models in Computational Biology. Journal of Molecular Biology, 1994, 235, 1501-1531.	4.2	1,660
32	Stochastic context-free grammers for tRNA modeling. Nucleic Acids Research, 1994, 22, 5112-5120.	14.5	317
33	Recent methods for RNA modeling using stochastic context-free grammars. Lecture Notes in Computer Science, 1994, , 289-306.	1.3	12