

# Kimmen Sjolander

## List of Publications by Year in descending order

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33  
papers

4,742  
citations

257357

24  
h-index

434063

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. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
2	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430.	9.0	198
3	The PhyloFacts FAT-CAT web server: ortholog identification and function prediction using fast approximate tree classification. <i>Nucleic Acids Research</i> , 2013, 41, W242-W248.	6.5	25
4	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	3.1	188
5	Ortholog identification in the presence of domain architecture rearrangement. <i>Briefings in Bioinformatics</i> , 2011, 12, 413-422.	3.2	28
6	Getting Started in Structural Phylogenomics. <i>PLoS Computational Biology</i> , 2010, 6, e1000621.	1.5	13
7	<i>Arabidopsis thaliana</i> PGR7 Encodes a Conserved Chloroplast Protein That Is Necessary for Efficient Photosynthetic Electron Transport. <i>PLoS ONE</i> , 2010, 5, e11688.	1.1	18
8	SATCHMO-JS: a webserver for simultaneous protein multiple sequence alignment and phylogenetic tree construction. <i>Nucleic Acids Research</i> , 2010, 38, W29-W34.	6.5	26
9	Berkeley PHOG: PhyloFacts orthology group prediction web server. <i>Nucleic Acids Research</i> , 2009, 37, W84-W89.	6.5	65
10	INTREPID: a web server for prediction of functionally important residues by evolutionary analysis. <i>Nucleic Acids Research</i> , 2009, 37, W390-W395.	6.5	35
11	Automated Protein Subfamily Identification and Classification. <i>PLoS Computational Biology</i> , 2007, 3, e160.	1.5	110
12	Berkeley Phylogenomics Group web servers: resources for structural phylogenomic analysis. <i>Nucleic Acids Research</i> , 2007, 35, W27-W32.	6.5	24
13	PhyloFacts: an online structural phylogenomic encyclopedia for protein functional and structural classification. <i>Genome Biology</i> , 2006, 7, R83.	13.9	50
14	Functional Classification Using Phylogenomic Inference. <i>PLoS Computational Biology</i> , 2006, 2, e77.	1.5	61
15	Predicted hexameric structure of the <i>Agrobacterium</i> VirB4 C terminus suggests VirB4 acts as a docking site during type IV secretion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1685-1690.	3.3	51
16	Proteome Analysis of the Rice Etioplast. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1072-1084.	2.5	108
17	Subfamily hmms in functional genomics. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005, , 322-33.	0.7	12
18	Phylogenomic inference of protein molecular function: advances and challenges. <i>Bioinformatics</i> , 2004, 20, 170-179.	1.8	184

#	ARTICLE	IF	CITATIONS
19	Arabidopsis Downy Mildew Resistance Gene RPP27 Encodes a Receptor-Like Protein Similar to CLAVATA2 and Tomato Cf-9. <i>Plant Physiology</i> , 2004, 135, 1100-1112.	2.3	52
20	From Endonucleases to Transcription Factors: Evolution of the AP2 DNA Binding Domain in Plants[W]. <i>Plant Cell</i> , 2004, 16, 2265-2277.	3.1	227
21	COACH: profile-profile alignment of protein families using hidden Markov models. <i>Bioinformatics</i> , 2004, 20, 1309-1318.	1.8	86
22	A comparison of scoring functions for protein sequence profile alignment. <i>Bioinformatics</i> , 2004, 20, 1301-1308.	1.8	116
23	The Arabidopsis thaliana Chloroplast Proteome Reveals Pathway Abundance and Novel Protein Functions. <i>Current Biology</i> , 2004, 14, 354-362.	1.8	585
24	SUBFAMILY HMMS IN FUNCTIONAL GENOMICS. , 2004, , .		12
25	SATCHMO: sequence alignment and tree construction using hidden Markov models. <i>Bioinformatics</i> , 2003, 19, 1404-1411.	1.8	91
26	SIMULTANEOUS SEQUENCE ALIGNMENT AND TREE CONSTRUCTION USING HIDDEN MARKOV MODELS. , 2002, , .		6
27	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	1.5	110
28	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	1.5	8
29	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	1.5	31
30	Dirichlet mixtures: a method for improved detection of weak but significant protein sequence homology. <i>Bioinformatics</i> , 1996, 12, 327-345.	1.8	197
31	Hidden Markov Models in Computational Biology. <i>Journal of Molecular Biology</i> , 1994, 235, 1501-1531.	2.0	1,660
32	Stochastic context-free grammars for tRNA modeling. <i>Nucleic Acids Research</i> , 1994, 22, 5112-5120.	6.5	317
33	Recent methods for RNA modeling using stochastic context-free grammars. <i>Lecture Notes in Computer Science</i> , 1994, , 289-306.	1.0	12