

# Elisabeth R M Tillier

## List of Publications by Year in descending order

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25  
papers

2,078  
citations

471509

17  
h-index

642732

23  
g-index

25  
all docs

25  
docs citations

25  
times ranked

3701  
citing authors

#	ARTICLE	IF	CITATIONS
1	Coevolution Reveals a Network of Human Proteins Originating with Multicellularity. <i>Molecular Biology and Evolution</i> , 2013, 30, 332-346.	8.9	21
2	MSH3 Polymorphisms and Protein Levels Affect CAG Repeat Instability in Huntington's Disease Mice. <i>PLoS Genetics</i> , 2013, 9, e1003280.	3.5	128
3	A Census of Human Soluble Protein Complexes. <i>Cell</i> , 2012, 150, 1068-1081.	28.9	781
4	Using Coevolution to Predict Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2011, 781, 237-256.	0.9	21
5	A new, fast algorithm for detecting protein coevolution using maximum compatible cliques. <i>Algorithms for Molecular Biology</i> , 2011, 6, 17.	1.2	17
6	Mining bacterial genomes for novel arylesterase activity. <i>Microbial Biotechnology</i> , 2010, 3, 677-690.	4.2	12
7	Faster coevolution detection of proteins using maximum similar cliques. , 2010, , .		0
8	Loss and gain of GroEL in the Mollicutes This paper is one of a selection of papers published in this special issue entitled "Canadian Society of Biochemistry, Molecular & Cellular Biology 52nd Annual Meeting - Protein Folding: Principles and Diseases" and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2010, 88, 185-194.	2.0	34
9	The human protein coevolution network. <i>Genome Research</i> , 2009, 19, 1861-1871.	5.5	48
10	A fast and flexible approach to oligonucleotide probe design for genomes and gene families. <i>Bioinformatics</i> , 2007, 23, 1195-1202.	4.1	31
11	Aligning two RNA secondary structures with I-block. <i>New Biotechnology</i> , 2007, 24, 321-326.	2.7	1
12	Positional homology in bacterial genomes. <i>Evolutionary Bioinformatics</i> , 2007, 2, 77-90.	1.2	7
13	A Bayesian approach to pairwise RNA Secondary Structure Alignment. , 2006, , .		0
14	Positional Homology in Bacterial Genomes. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	1.2	1
15	Codep: Maximizing co-evolutionary interdependencies to discover interacting proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 822-831.	2.6	31
16	The accuracy of several multiple sequence alignment programs for proteins. <i>BMC Bioinformatics</i> , 2006, 7, 471.	2.6	122
17	SIMPROT: using an empirically determined indel distribution in simulations of protein evolution. <i>BMC Bioinformatics</i> , 2005, 6, 236.	2.6	38
18	A Transition Probability Model for Amino Acid Substitutions from Blocks. <i>Journal of Computational Biology</i> , 2003, 10, 997-1010.	1.6	132

#	ARTICLE	IF	CITATIONS
19	Using multiple interdependency to separate functional from phylogenetic correlations in protein alignments. <i>Bioinformatics</i> , 2003, 19, 750-755.	4.1	118
20	Empirical Models for Substitution in Ribosomal RNA. <i>Molecular Biology and Evolution</i> , 2003, 21, 419-427.	8.9	36
21	Exploring the Set of All Minimal Sequences of Reversals " An Application to Test the Replication-Directed Reversal Hypothesis. <i>Lecture Notes in Computer Science</i> , 2002, , 300-315.	1.3	28
22	Genome rearrangement by replication-directed translocation. <i>Nature Genetics</i> , 2000, 26, 195-197.	21.4	182
23	Replication Orientation Affects the Rate and Direction of Bacterial Gene Evolution. <i>Journal of Molecular Evolution</i> , 2000, 51, 459-463.	1.8	42
24	The Contributions of Replication Orientation, Gene Direction, and Signal Sequences to Base-Composition Asymmetries in Bacterial Genomes. <i>Journal of Molecular Evolution</i> , 2000, 50, 249-257.	1.8	161
25	High Apparent Rate of Simultaneous Compensatory Base-Pair Substitutions in Ribosomal RNA. <i>Genetics</i> , 1998, 148, 1993-2002.	2.9	86