

Robert M Maccallum

List of Publications by Citations

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33
papers

4,489
citations

22
h-index

34
g-index

34
ext. papers

5,059
ext. citations

9.4
avg, IF

4.97
L-index

#	Paper	IF	Citations
33	Enhanced genome annotation using structural profiles in the program 3D-PSSM. <i>Journal of Molecular Biology</i> , 2000 , 299, 499-520	6.5	1239
32	Evolutionary dynamics of immune-related genes and pathways in disease-vector mosquitoes. <i>Science</i> , 2007 , 316, 1738-43	33.3	461
31	Enhancement of protein modeling by human intervention in applying the automatic programs 3D-JIGSAW and 3D-PSSM. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , Suppl 5, 39-46	4.2	448
30	VectorBase: an updated bioinformatics resource for invertebrate vectors and other organisms related with human diseases. <i>Nucleic Acids Research</i> , 2015 , 43, D707-13	20.1	389
29	Mosquito genomics. Highly evolvable malaria vectors: the genomes of 16 Anopheles mosquitoes. <i>Science</i> , 2015 , 347, 1258522	33.3	372
28	NucPred--predicting nuclear localization of proteins. <i>Bioinformatics</i> , 2007 , 23, 1159-60	7.2	249
27	VectorBase: a data resource for invertebrate vector genomics. <i>Nucleic Acids Research</i> , 2009 , 37, D583-7	20.1	200
26	VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics. <i>Nucleic Acids Research</i> , 2012 , 40, D729-34	20.1	134
25	CAFASP-1: Critical assessment of fully automated structure prediction methods 1999 , 37, 209-217		105
24	Benchmarking PSI-BLAST in genome annotation. <i>Journal of Molecular Biology</i> , 1999 , 293, 1257-71	6.5	99
23	The evolution of popular music: USA 1960-2010. <i>Royal Society Open Science</i> , 2015 , 2, 150081	3.3	89
22	CASP6 assessment of contact prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61 Suppl 7, 214-24	4.2	72
21	Life cycle transcriptome of the malaria mosquito <i>Anopheles gambiae</i> and comparison with the fruitfly <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 11304-9	11.5	59
20	Striped sheets and protein contact prediction. <i>Bioinformatics</i> , 2004 , 20 Suppl 1, i224-31	7.2	59
19	Structural characterization of the human proteome. <i>Genome Research</i> , 2002 , 12, 1625-41	9.7	57
18	SAWTEd: structure assignment with text description--enhanced detection of remote homologues with automated SWISS-PROT annotation comparisons. <i>Bioinformatics</i> , 2000 , 16, 125-9	7.2	54
17	Evolution of music by public choice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 12081-6	11.5	49

16	A proteogenomic analysis of <i>Anopheles gambiae</i> using high-resolution Fourier transform mass spectrometry. <i>Genome Research</i> , 2011 , 21, 1872-81	9.7	47
15	Transcriptome of the adult female malaria mosquito vector <i>Anopheles albimanus</i> . <i>BMC Genomics</i> , 2012 , 13, 207	4.5	31
14	The 2007 IEEE CEC simulated car racing competition. <i>Genetic Programming and Evolvable Machines</i> , 2008 , 9, 295-329	2	26
13	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. <i>Nucleic Acids Research</i> , 2021 ,	20.1	22
12	Recognition of remote protein homologies using three-dimensional information to generate a position specific scoring matrix in the program 3D-PSSM 1999 ,		21
11	An expression map for <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2011 , 12, 620	4.5	19
10	The proteome: structure, function and evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 441-51	5.8	18
9	Evolving Regular Expression-Based Sequence Classifiers for Protein Nuclear Localisation. <i>Lecture Notes in Computer Science</i> , 2004 , 31-40	0.9	15
8	3D-GENOMICS: a database to compare structural and functional annotations of proteins between sequenced genomes. <i>Nucleic Acids Research</i> , 2004 , 32, D245-50	20.1	13
7	MIReAD, a minimum information standard for reporting arthropod abundance data. <i>Scientific Data</i> , 2019 , 6, 40	8.2	12
6	Automatic discovery of cross-family sequence features associated with protein function. <i>BMC Bioinformatics</i> , 2006 , 7, 16	3.6	8
5	Improved alignment quality by combining evolutionary information, predicted secondary structure and self-organizing maps. <i>BMC Bioinformatics</i> , 2006 , 7, 357	3.6	7
4	Introducing a Perl Genetic Programming System - and Can Meta-evolution Solve the Bloat Problem?. <i>Lecture Notes in Computer Science</i> , 2003 , 364-373	0.9	7
3	Towards optimal views of proteins. <i>Bioinformatics</i> , 2003 , 19, 882-8	7.2	2
2	Unravelling population structure heterogeneity within the genome of the malaria vector <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2021 , 22, 422	4.5	1
1	Evolved Matrix Operations for Post-processing Protein Secondary Structure Predictions. <i>Lecture Notes in Computer Science</i> , 2004 , 220-229	0.9	