

# Robert M Maccallum

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. <i>Nucleic Acids Research</i> , <b>2021</b> ,	20.1	22
32	Unravelling population structure heterogeneity within the genome of the malaria vector <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , <b>2021</b> , 22, 422	4.5	1
31	MIReAD, a minimum information standard for reporting arthropod abundance data. <i>Scientific Data</i> , <b>2019</b> , 6, 40	8.2	12
30	VectorBase: an updated bioinformatics resource for invertebrate vectors and other organisms related with human diseases. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D707-13	20.1	389
29	Mosquito genomics. Highly evolvable malaria vectors: the genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , <b>2015</b> , 347, 1258522	33.3	372
28	The evolution of popular music: USA 1960-2010. <i>Royal Society Open Science</i> , <b>2015</b> , 2, 150081	3.3	89
27	Transcriptome of the adult female malaria mosquito vector <i>Anopheles albimanus</i> . <i>BMC Genomics</i> , <b>2012</b> , 13, 207	4.5	31
26	Evolution of music by public choice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 12081-6	11.5	49
25	VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D729-34	20.1	134
24	An expression map for <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , <b>2011</b> , 12, 620	4.5	19
23	A proteogenomic analysis of <i>Anopheles gambiae</i> using high-resolution Fourier transform mass spectrometry. <i>Genome Research</i> , <b>2011</b> , 21, 1872-81	9.7	47
22	VectorBase: a data resource for invertebrate vector genomics. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D583-7	20.1	200
21	The 2007 IEEE CEC simulated car racing competition. <i>Genetic Programming and Evolvable Machines</i> , <b>2008</b> , 9, 295-329	2	26
20	Evolutionary dynamics of immune-related genes and pathways in disease-vector mosquitoes. <i>Science</i> , <b>2007</b> , 316, 1738-43	33.3	461
19	NucPred--predicting nuclear localization of proteins. <i>Bioinformatics</i> , <b>2007</b> , 23, 1159-60	7.2	249
18	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> , <b>2007</b> , 104, 11304-9	11.5	59
17	Automatic discovery of cross-family sequence features associated with protein function. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 16	3.6	8

16	Improved alignment quality by combining evolutionary information, predicted secondary structure and self-organizing maps. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 357	3.6	7
15	The proteome: structure, function and evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2006</b> , 361, 441-51	5.8	18
14	CASP6 assessment of contact prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 61 Suppl 7, 214-24	4.2	72
13	3D-GENOMICS: a database to compare structural and functional annotations of proteins between sequenced genomes. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D245-50	20.1	13
12	Striped sheets and protein contact prediction. <i>Bioinformatics</i> , <b>2004</b> , 20 Suppl 1, i224-31	7.2	59
11	Evolved Matrix Operations for Post-processing Protein Secondary Structure Predictions. <i>Lecture Notes in Computer Science</i> , <b>2004</b> , 220-229	0.9	
10	Evolving Regular Expression-Based Sequence Classifiers for Protein Nuclear Localisation. <i>Lecture Notes in Computer Science</i> , <b>2004</b> , 31-40	0.9	15
9	Towards optimal views of proteins. <i>Bioinformatics</i> , <b>2003</b> , 19, 882-8	7.2	2
8	Introducing a Perl Genetic Programming System - and Can Meta-evolution Solve the Bloat Problem?. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 364-373	0.9	7
7	Structural characterization of the human proteome. <i>Genome Research</i> , <b>2002</b> , 12, 1625-41	9.7	57
6	Enhancement of protein modeling by human intervention in applying the automatic programs 3D-JIGSAW and 3D-PSSM. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2001</b> , Suppl 5, 39-46	4.2	448
5	SAWTED: structure assignment with text description-enhanced detection of remote homologues with automated SWISS-PROT annotation comparisons. <i>Bioinformatics</i> , <b>2000</b> , 16, 125-9	7.2	54
4	Enhanced genome annotation using structural profiles in the program 3D-PSSM. <i>Journal of Molecular Biology</i> , <b>2000</b> , 299, 499-520	6.5	1239
3	Recognition of remote protein homologies using three-dimensional information to generate a position specific scoring matrix in the program 3D-PSSM <b>1999</b> ,		21
2	CAFASP-1: Critical assessment of fully automated structure prediction methods <b>1999</b> , 37, 209-217		105
1	Benchmarking PSI-BLAST in genome annotation. <i>Journal of Molecular Biology</i> , <b>1999</b> , 293, 1257-71	6.5	99