Robert M Maccallum

List of Publications by Year
in descending order

33 papers	5,583 citations	331670 21 h-index	434195 31 g-index
34 all docs	34 docs citations	34 times ranked	7832 citing authors

#	Article	IF	Citations
1	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. Nucleic Acids Research, 2022, 50, D898-D911.	14.5	277
2	Unravelling population structure heterogeneity within the genome of the malaria vector Anopheles gambiae. BMC Genomics, 2021, 22, 422.	2.8	1
3	MIReAD, a minimum information standard for reporting arthropod abundance data. Scientific Data, 2019, 6, 40.	5.3	20
4	The evolution of popular music: USA 1960–2010. Royal Society Open Science, 2015, 2, 150081.	2.4	123
5	VectorBase: an updated bioinformatics resource for invertebrate vectors and other organisms related with human diseases. Nucleic Acids Research, 2015, 43, D707-D713.	14.5	556
6	Highly evolvable malaria vectors: The genomes of 16 *Anopheles* mosquitoes. Science, 2015, 347, 1258522.	12.6	492
7	VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics. Nucleic Acids Research, 2012, 40, D729-D734.	14.5	143
8	Transcriptome of the adult female malaria mosquito vector Anopheles albimanus. BMC Genomics, 2012, 13, 207.	2.8	38
9	Evolution of music by public choice. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12081-12086.	7.1	64
10	An expression map for Anopheles gambiae. BMC Genomics, 2011, 12, 620.	2.8	22
11	A proteogenomic analysis of *Anopheles gambiae* using high-resolution Fourier transform mass spectrometry. Genome Research, 2011, 21, 1872-1881.	5.5	58
12	VectorBase: a data resource for invertebrate vector genomics. Nucleic Acids Research, 2009, 37, D583-D587.	14.5	234
13	The 2007 IEEE CEC simulated car racing competition. Genetic Programming and Evolvable Machines, 2008, 9, 295-329.	2.2	31
14	NucPred Predicting nuclear localization of proteins. Bioinformatics, 2007, 23, 1159-1160.	4.1	313
15	Life cycle transcriptome of the malaria mosquito Anopheles gambiae and comparison with the fruitfly Drosophila melanogaster. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11304-11309.	7.1	70
16	Evolutionary Dynamics of Immune-Related Genes and Pathways in Disease-Vector Mosquitoes. Science, 2007, 316, 1738-1743.	12.6	550
17	Automatic discovery of cross-family sequence features associated with protein function. BMC Bioinformatics, 2006, 7, 16.	2.6	10
18	Improved alignment quality by combining evolutionary information, predicted secondary structure and self-organizing maps. BMC Bioinformatics, 2006, 7, 357.	2.6	12

#	Article	IF	Citations
19	The proteome: structure, function and evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 441-451.	4.0	18
20	CASP6 assessment of contact prediction. Proteins: Structure, Function and Bioinformatics, 2005, 61, 214-224.	2.6	86
21	3D-GENOMICS: a database to compare structural and functional annotations of proteins between sequenced genomes. Nucleic Acids Research, 2004, 32, 245D-250.	14.5	14
22	Striped sheets and protein contact prediction. Bioinformatics, 2004, 20, i224-i231.	4.1	73
23	Evolving Regular Expression-Based Sequence Classifiers for Protein Nuclear Localisation. Lecture Notes in Computer Science, 2004, , 31-40.	1.3	20
24	Evolved Matrix Operations for Post-processing Protein Secondary Structure Predictions. Lecture Notes in Computer Science, 2004, , 220-229.	1.3	0
25	Towards optimal views of proteins. Bioinformatics, 2003, 19, 882-888.	4.1	2
26	Introducing a Perl Genetic Programming System - and Can Meta-evolution Solve the Bloat Problem?. Lecture Notes in Computer Science, 2003, , 364-373.	1.3	10
27	Structural Characterization of the Human Proteome. Genome Research, 2002, 12, 1625-1641.	5.5	66
28	Enhancement of protein modeling by human intervention in applying the automatic programs 3D-JIGSAW and 3D-PSSM. Proteins: Structure, Function and Bioinformatics, 2001, 45, 39-46.	2.6	504
29	SAWTED: Structure Assignment With Text Description--Enhanced detection of remote homologues with automated SWISS-PROT annotation comparisons. Bioinformatics, 2000, 16, 125-129.	4.1	58
30	Enhanced genome annotation using structural profiles in the program 3D-PSSM 1 1Edited by J. Thornton. Journal of Molecular Biology, 2000, 299, 501-522.	4.2	1,361
31	Recognition of remote protein homologies using three-dimensional information to generate a position specific scoring matrix in the program 3D-PSSM. , 1999, , .		27
32	CAFASP-1: Critical assessment of fully automated structure prediction methods. , 1999, 37, 209-217.		110
33	Benchmarking PSI-BLAST in genome annotation 1 1Edited by G. von Heijne. Journal of Molecular Biology, 1999, 293, 1257-1271.	4.2	105