# Robert M Maccallum

List of Publications by Year
in descending order

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|---|---|---|---|
| 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 | 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 |
| 2 | 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 |
| 3 | Evolutionary Dynamics of Immune-Related Genes and Pathways in Disease-Vector Mosquitoes. Science, 2007, 316, 1738-1743. | 12.6 | 550 |
| 4 | 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 |
| 5 | Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. Science, 2015, 347, 1258522. | 12.6 | 492 |
| 6 | NucPred Predicting nuclear localization of proteins. Bioinformatics, 2007, 23, 1159-1160. | 4.1 | 313 |
| 7 | VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. Nucleic Acids Research, 2022, 50, D898-D911. | 14.5 | 277 |
| 8 | VectorBase: a data resource for invertebrate vector genomics. Nucleic Acids Research, 2009, 37, D583-D587. | 14.5 | 234 |
| 9 | VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics. Nucleic Acids Research, 2012, 40, D729-D734. | 14.5 | 143 |
| 10 | The evolution of popular music: USA 1960â€"2010. Royal Society Open Science, 2015, 2, 150081. | 2.4 | 123 |
| 11 | CAFASP-1: Critical assessment of fully automated structure prediction methods. , 1999, 37, 209-217. | | 110 |
| 12 | Benchmarking PSI-BLAST in genome annotation 1 1Edited by G. von Heijne. Journal of Molecular Biology, 1999, 293, 1257-1271. | 4.2 | 105 |
| 13 | CASP6 assessment of contact prediction. Proteins: Structure, Function and Bioinformatics, 2005, 61, 214-224. | 2.6 | 86 |
| 14 | Striped sheets and protein contact prediction. Bioinformatics, 2004, 20, i224-i231. | 4.1 | 73 |
| 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 | Structural Characterization of the Human Proteome. Genome Research, 2002, 12, 1625-1641. | 5.5 | 66 |
| 17 | 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 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 19 | A proteogenomic analysis of <i>Anopheles gambiae</i> using high-resolution Fourier transform mass spectrometry. Genome Research, 2011, 21, 1872-1881. | 5.5 | 58 |
| 20 | Transcriptome of the adult female malaria mosquito vector Anopheles albimanus. BMC Genomics, 2012, 13, 207. | 2.8 | 38 |
| 21 | The 2007 IEEE CEC simulated car racing competition. Genetic Programming and Evolvable Machines, 2008, 9, 295-329. | 2.2 | 31 |
| 22 | Recognition of remote protein homologies using three-dimensional information to generate a position specific scoring matrix in the program 3D-PSSM. , 1999, , . |  | 27 |
| 23 | An expression map for Anopheles gambiae. BMC Genomics, 2011, 12, 620. | 2.8 | 22 |
| 24 | MIReAD, a minimum information standard for reporting arthropod abundance data. Scientific Data, 2019, 6, 40. | 5.3 | 20 |
| 25 | Evolving Regular Expression-Based Sequence Classifiers for Protein Nuclear Localisation. Lecture Notes in Computer Science, 2004, , 31-40. | 1.3 | 20 |
| 26 | The proteome: structure, function and evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 441-451. | 4.0 | 18 |
| 27 | 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 |
| 28 | Improved alignment quality by combining evolutionary information, predicted secondary structure and self-organizing maps. BMC Bioinformatics, 2006, 7, 357. | 2.6 | 12 |
| 29 | Automatic discovery of cross-family sequence features associated with protein function. BMC Bioinformatics, 2006, 7, 16. | 2.6 | 10 |
| 30 | 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 |
| 31 | Towards optimal views of proteins. Bioinformatics, 2003, 19, 882-888. | 4.1 | 2 |
| 32 | Unravelling population structure heterogeneity within the genome of the malaria vector Anopheles gambiae. BMC Genomics, 2021, 22, 422. | 2.8 | 1 |
| 33 | Evolved Matrix Operations for Post-processing Protein Secondary Structure Predictions. Lecture Notes in Computer Science, 2004, , 220-229. | 1.3 | 0 |