

Emily S Wong

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

2,359
citations

331259

21
h-index

476904

29
g-index

35
all docs

35
docs citations

35
times ranked

3536
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183. | 13.7 | 657 |
| 2 | Single-Cell Transcriptomic Analysis of Cardiac Differentiation from Human PSCs Reveals HOPX-Dependent Cardiomyocyte Maturation. <i>Cell Stem Cell</i> , 2018, 23, 586-598.e8. | 5.2 | 215 |
| 3 | Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , 2011, 12, R81. | 13.9 | 167 |
| 4 | Defensins and the convergent evolution of platypus and reptile venom genes. <i>Genome Research</i> , 2008, 18, 986-994. | 2.4 | 137 |
| 5 | Venom evolution through gene duplications. <i>Gene</i> , 2012, 496, 1-7. | 1.0 | 120 |
| 6 | Proteomics and Phylogenetic Analysis of the Cathepsin L Protease Family of the Helminth Pathogen <i>Fasciola hepatica</i> . <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1111-1123. | 2.5 | 118 |
| 7 | Characterization of the opossum immune genome provides insights into the evolution of the mammalian immune system. <i>Genome Research</i> , 2007, 17, 982-991. | 2.4 | 100 |
| 8 | Deep conservation of the enhancer regulatory code in animals. <i>Science</i> , 2020, 370, . | 6.0 | 89 |
| 9 | Novel venom gene discovery in the platypus. <i>Genome Biology</i> , 2010, 11, R95. | 13.9 | 72 |
| 10 | Ancient Antimicrobial Peptides Kill Antibiotic-Resistant Pathogens: Australian Mammals Provide New Options. <i>PLoS ONE</i> , 2011, 6, e24030. | 1.1 | 72 |
| 11 | Non-genetic determinants of malignant clonal fitness at single-cell resolution. <i>Nature</i> , 2022, 601, 125-131. | 13.7 | 71 |
| 12 | Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution. <i>Nature Communications</i> , 2017, 8, 1092. | 5.8 | 60 |
| 13 | Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. <i>Nature Genetics</i> , 2017, 49, 1714-1721. | 9.4 | 57 |
| 14 | Decoupling of evolutionary changes in transcription factor binding and gene expression in mammals. <i>Genome Research</i> , 2015, 25, 167-178. | 2.4 | 54 |
| 15 | MHC-linked and un-linked class I genes in the wallaby. <i>BMC Genomics</i> , 2009, 10, 310. | 1.2 | 48 |
| 16 | Comparative genomics indicates the mammalian CD33rSiglec locus evolved by an ancient large-scale inverse duplication and suggests all Siglecs share a common ancestral region. <i>Immunogenetics</i> , 2009, 61, 401-417. | 1.2 | 42 |
| 17 | Proteomics and Deep Sequencing Comparison of Seasonally Active Venom Glands in the Platypus Reveals Novel Venom Peptides and Distinct Expression Profiles. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1354-1364. | 2.5 | 39 |
| 18 | A Limited Role for Gene Duplications in the Evolution of Platypus Venom. <i>Molecular Biology and Evolution</i> , 2012, 29, 167-177. | 3.5 | 33 |

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|----|--|-----|-----------|
| 19 | SVM-Based Prediction of Propeptide Cleavage Sites in Spider Toxins Identifies Toxin Innovation in an Australian Tarantula. PLoS ONE, 2013, 8, e66279. | 1.1 | 30 |
| 20 | Immunome database for marsupials and monotremes. BMC Immunology, 2011, 12, 48. | 0.9 | 27 |
| 21 | Identification of natural killer cell receptor clusters in the platypus genome reveals an expansion of C-type lectin genes. Immunogenetics, 2009, 61, 565-579. | 1.2 | 24 |
| 22 | Transcriptomic analysis supports similar functional roles for the two thymuses of the tammar wallaby. BMC Genomics, 2011, 12, 420. | 1.2 | 21 |
| 23 | Identification of natural killer cell receptor genes in the genome of the marsupial Tasmanian devil (<i>Sarcophilus harrisi</i>). Immunogenetics, 2013, 65, 25-35. | 1.2 | 21 |
| 24 | <i>Cis</i> -acting variation is common across regulatory layers but is often buffered during embryonic development. Genome Research, 2021, 31, 211-224. | 2.4 | 19 |
| 25 | Echidna Venom Gland Transcriptome Provides Insights into the Evolution of Monotreme Venom. PLoS ONE, 2013, 8, e79092. | 1.1 | 18 |
| 26 | Hatching time for monotreme immunology. Australian Journal of Zoology, 2009, 57, 185. | 0.6 | 11 |
| 27 | Genomic Identification of Chemokines and Cytokines in Opossum. Journal of Interferon and Cytokine Research, 2011, 31, 317-330. | 0.5 | 10 |
| 28 | Distal regulation, silencers, and a shared combinatorial syntax are hallmarks of animal embryogenesis. Genome Research, 2022, 32, 474-487. | 2.4 | 7 |
| 29 | Use of Genomic Information to Gain Insights into Immune Function in Marsupials: A Review of Divergent Immune Genes. , 2010, , 381-400. | | 5 |
| 30 | Quantitative analysis of chromatin interaction changes upon a 4.3 Mb deletion at mouse 4E2. BMC Genomics, 2015, 16, 982. | 1.2 | 2 |