

# Adrian W Briggs

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12103802/publications.pdf>

Version: 2024-02-01

25  
papers

11,837  
citations

279798

23  
h-index

580821

25  
g-index

25  
all docs

25  
docs citations

25  
times ranked

12776  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Hierarchical Clustering Can Identify B Cell Clones with High Confidence in Ig Repertoire Sequencing Data. <i>Journal of Immunology</i> , 2017, 198, 2489-2499.   | 0.8  | 137       |
| 2  | Engineering and optimising deaminase fusions for genome editing. <i>Nature Communications</i> , 2016, 7, 13330.  | 12.8 | 60        |
| 3  | Genetic Evidence of Human Adaptation to a Cooked Diet. <i>Genome Biology and Evolution</i> , 2016, 8, 1091-1103.   | 2.5  | 29        |
| 4  | Massively parallel sequencing of single cells by epicPCR links functional genes with phylogenetic markers. <i>ISME Journal</i> , 2016, 10, 427-436.  | 9.8  | 184       |
| 5  | Neutralizing antibodies against West Nile virus identified directly from human B cells by single-cell analysis and next generation sequencing. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 1587-1597. | 1.3  | 80        |
| 6  | Optimization of scarless human stem cell genome editing. <i>Nucleic Acids Research</i> , 2013, 41, 9049-9061.  | 14.5 | 358       |
| 7  | Iterative capped assembly: rapid and scalable synthesis of repeat-module DNA such as TAL effectors from individual monomers. <i>Nucleic Acids Research</i> , 2012, 40, e117-e117.                                | 14.5 | 185       |
| 8  | A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.   | 12.6 | 1,695     |
| 9  | Preparation of Next-Generation Sequencing Libraries from Damaged DNA. <i>Methods in Molecular Biology</i> , 2012, 840, 143-154.  | 0.9  | 51        |
| 10 | Rapid Retrieval of DNA Target Sequences by Primer Extension Capture. <i>Methods in Molecular Biology</i> , 2012, 772, 145-154.   | 0.9  | 2         |
| 11 | Stable Gene Targeting in Human Cells Using Single-Strand Oligonucleotides with Modified Bases. <i>PLoS ONE</i> , 2012, 7, e36697.  | 2.5  | 28        |
| 12 | Targeted Investigation of the Neandertal Genome by Array-Based Sequence Capture. <i>Science</i> , 2010, 328, 723-725.  | 12.6 | 255       |
| 13 | A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.  | 12.6 | 3,588     |
| 14 | A Complete mtDNA Genome of an Early Modern Human from Kostenki, Russia. <i>Current Biology</i> , 2010, 20, 231-236.  | 3.9  | 252       |
| 15 | Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010, 468, 1053-1060.   | 27.8 | 1,537     |
| 16 | Road blocks on paleogenomesâ€™ polymerase extension profiling reveals the frequency of blocking lesions in ancient DNA. <i>Nucleic Acids Research</i> , 2010, 38, e161-e161.                                     | 14.5 | 47        |
| 17 | Removal of deaminated cytosines and detection of in vivo methylation in ancient DNA. <i>Nucleic Acids Research</i> , 2010, 38, e87-e87.  | 14.5 | 362       |
| 18 | The Neandertal genome and ancient DNA authenticity. <i>EMBO Journal</i> , 2009, 28, 2494-2502.   | 7.8  | 170       |

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 19 | Targeted Retrieval and Analysis of Five Neandertal mtDNA Genomes. <i>Science</i> , 2009, 325, 318-321.  | 12.6 | 456       |
| 20 | Primer Extension Capture: Targeted Sequence Retrieval from Heavily Degraded DNA Sources. <i>Journal of Visualized Experiments</i> , 2009, , 1573.                               | 0.3  | 22        |
| 21 | Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. <i>BMC Evolutionary Biology</i> , 2008, 8, 220.             | 3.2  | 261       |
| 22 | A Complete Neandertal Mitochondrial Genome Sequence Determined by High-Throughput Sequencing. <i>Cell</i> , 2008, 134, 416-426.   | 28.9 | 503       |
| 23 | From micrograms to picograms: quantitative PCR reduces the material demands of high-throughput sequencing. <i>Nucleic Acids Research</i> , 2008, 36, e5-e5.                     | 14.5 | 105       |
| 24 | Patterns of damage in genomic DNA sequences from a Neandertal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14616-14621. | 7.1  | 799       |
| 25 | Analysis of one million base pairs of Neanderthal DNA. <i>Nature</i> , 2006, 444, 330-336.  | 27.8 | 671       |