

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	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	12.6	3,588
2	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.	12.6	1,695
3	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010, 468, 1053-1060.	27.8	1,537
4	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
5	Analysis of one million base pairs of Neanderthal DNA. <i>Nature</i> , 2006, 444, 330-336.	27.8	671
6	A Complete Neandertal Mitochondrial Genome Sequence Determined by High-Throughput Sequencing. <i>Cell</i> , 2008, 134, 416-426.	28.9	503
7	Targeted Retrieval and Analysis of Five Neandertal mtDNA Genomes. <i>Science</i> , 2009, 325, 318-321.	12.6	456
8	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
9	Optimization of scarless human stem cell genome editing. <i>Nucleic Acids Research</i> , 2013, 41, 9049-9061.	14.5	358
10	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
11	Targeted Investigation of the Neandertal Genome by Array-Based Sequence Capture. <i>Science</i> , 2010, 328, 723-725.	12.6	255
12	A Complete mtDNA Genome of an Early Modern Human from Kostenki, Russia. <i>Current Biology</i> , 2010, 20, 231-236.	3.9	252
13	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
14	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
15	The Neandertal genome and ancient DNA authenticity. <i>EMBO Journal</i> , 2009, 28, 2494-2502.	7.8	170
16	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
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Engineering and optimising deaminase fusions for genome editing. Nature Communications, 2016, 7, 13330.	12.8	60
20	Preparation of Next-Generation Sequencing Libraries from Damaged DNA. Methods in Molecular Biology, 2012, 840, 143-154.	0.9	51
21	Road blocks on paleogenomesâ€™ polymerase extension profiling reveals the frequency of blocking lesions in ancient DNA. Nucleic Acids Research, 2010, 38, e161-e161.	14.5	47
22	Genetic Evidence of Human Adaptation to a Cooked Diet. Genome Biology and Evolution, 2016, 8, 1091-1103.	2.5	29
23	Stable Gene Targeting in Human Cells Using Single-Strand Oligonucleotides with Modified Bases. PLoS ONE, 2012, 7, e36697.	2.5	28
24	Primer Extension Capture: Targeted Sequence Retrieval from Heavily Degraded DNA Sources. Journal of Visualized Experiments, 2009, , 1573.	0.3	22
25	Rapid Retrieval of DNA Target Sequences by Primer Extension Capture. Methods in Molecular Biology, 2012, 772, 145-154.	0.9	2