Andre R O Cavalcanti

List of Publications by Year
in descending order

45 papers	1,091 citations	516561 16 h-index	414303 32 g-index
45 all docs	45 docs citations	45 times ranked	1302 citing authors

#	Article	IF	Citations
1	Soil bacterial assemblage responses to wildfire in low elevation southern California habitats. PLoS ONE, 2022, 17, e0266256.	1.1	3
2	Selection for tandem stop codons in ciliate species with reassigned stop codons. PLoS ONE, 2019, 14, e0225804.	1.1	11
3	Carbon and nitrogen in the topsoils of Inceptisols and Mollisols under native sage scrub and non-native grasslands in southern California. Geoderma Regional, 2018, 14, e00172.	0.9	8
4	Using NCBI BLAST. Current Protocols in Essential Laboratory Techniques, 2017, 14, 11.1.1.	2.6	5
5	Amitotic Chromosome Loss Predicts Distinct Patterns of Senescence and Non-Senescence in Ciliates. Protist, 2015, 166, 224-233.	0.6	5
6	Using NCBI BLAST. Current Protocols in Essential Laboratory Techniques, 2014, 8, 11.1.1.	2.6	3
7	Novel Population Genetics in Ciliates due to Life Cycle and Nuclear Dimorphism. Molecular Biology and Evolution, 2014, 31, 2084-2093.	3.5	5
8	Ambushing the ambush hypothesis: predicting and evaluating off-frame codon frequencies in Prokaryotic Genomes. BMC Genomics, 2013, 14, 418.	1.2	10
9	An Alternative Look at Code Evolution: Using Non-canonical Codes to Evaluate Adaptive and Historic Models for the Origin of the Genetic Code. Journal of Molecular Evolution, 2013, 76, 71-80.	0.8	14
10	A Model for the Evolution of Extremely Fragmented Macronuclei in Ciliates. PLoS ONE, 2013, 8, e64997.	1.1	9
11	Fusion of the subunits Î± and Î² of succinyl-CoA synthetase as a phylogenetic marker for Pezizomycotina fungi. Genetics and Molecular Biology, 2011, 34, 669-675.	0.6	1
12	Multiple Independent Fusions of Glucose-6-Phosphate Dehydrogenase with Enzymes in the Pentose Phosphate Pathway. PLoS ONE, 2011, 6, e22269.	1.1	26
13	Detection of Fused Genes in Eukaryotic Genomes using Gene deFuser: Analysis of the Tetrahymena thermophila genome. BMC Bioinformatics, 2011, 12, 279.	1.2	10
14	Inter-colony comparison of diving behavior of an Arctic top predator: implications for warming in the Greenland Sea. Marine Ecology - Progress Series, 2011, 440, 229-240.	0.9	32
15	1+1â€Š=â€Š3: A Fusion of 2 Enzymes in the Methionine Salvage Pathway of Tetrahymena thermophila Creates a Trifunctional Enzyme That Catalyzes 3 Steps in the Pathway. PLoS Genetics, 2009, 5, e1000701.	1.5	8
16	Tandem Stop Codons in Ciliates That Reassign Stop Codons. Journal of Molecular Evolution, 2009, 68, 424-431.	0.8	28
17	Using NCBI BLAST. Current Protocols in Essential Laboratory Techniques, 2009, 1, 11.1.1.	2.6	1
18	Patterns of Codon Usage in two Ciliates that Reassign the Genetic Code: Tetrahymena thermophila and Paramecium tetraurelia. Protist, 2008, 159, 283-298.	0.6	32

#	Article	IF	Citations
19	Factors influencing codon usage bias in genomes. Journal of the Brazilian Chemical Society, 2008, 19, .	0.6	40
20	The Pathway to Detangle a Scrambled Gene. PLoS ONE, 2008, 3, e2330.	1.1	39
21	Consequences of Stop Codon Reassignment on Protein Evolution in Ciliates with Alternative Genetic Codes. Molecular Biology and Evolution, 2007, 25, 179-186.	3.5	15
22	Assessment of a DNA vaccine encoding an anchored-glycosylphosphatidylinositol tegumental antigen complexed to protamine sulphate on immunoprotection against murine schistosomiasis. Memorias Do Instituto Oswaldo Cruz, 2007, 102, 21-27.	0.8	11
23	Interconversion of Germline-Limited and Somatic DNA in a Scrambled Gene. Journal of Molecular Evolution, 2006, 63, 69-73.	0.8	19
24	On the Paucity of Duplicated Genes in Caenorhabditis elegans Operons. Journal of Molecular Evolution, 2006, 62, 765-771.	0.8	5
25	Spliced leader trans-splicing. Current Biology, 2006, 16, R8-R9.	1.8	18
26	Insights into a Biological Computer: Detangling Scrambled Genes in Ciliates. , 2006, , 349-359.		2
27	Decoding the Decoding Region: Analysis of Eukaryotic Release Factor (eRF1) Stop Codon-Binding Residues. Journal of Molecular Evolution, 2005, 60, 337-344.	0.8	26
28	Reciprocal Fusions of Two Genes in the Formaldehyde Detoxification Pathway in Ciliates and Diatoms. Molecular Biology and Evolution, 2005, 22, 1539-1542.	3.5	16
29	Conservation of tandem stop codons in yeasts. Genome Biology, 2005, 6, R31.	13.9	36
30	MDS_IES_DB: a database of macronuclear and micronuclear genes in spirotrichous ciliates. Nucleic Acids Research, 2004, 33, D396-D398.	6.5	29
31	Gene Unscrambler for detangling scrambled genes in ciliates. Bioinformatics, 2004, 20, 800-802.	1.8	10
32	Sequence Features of Oxytricha trifallax (Class Spirotrichea) Macronuclear Telomeric and Subtelomeric Sequences. Protist, 2004, 155, 311-322.	0.6	24
33	Genetic code. Current Biology, 2004, 14, R147.	1.8	3
34	On the Classes of Aminoacyl-tRNA Synthetases, Amino Acids and the Genetic Code. Origins of Life and Evolution of Biospheres, 2004, 34, 407-420.	0.8	18
35	Coding properties of Oxytricha trifallax (Sterkiella histriomuscorum) macronuclear chromosomes: analysis of a pilot genome project. Chromosoma, 2004, 113, 69-76.	1.0	27
36	Genetic code. Current Biology, 2004, 14, R147.	1.8	0

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37	Patterns of Gene Duplication in Saccharomyces cerevisiae and Caenorhabditis elegans. Journal of Molecular Evolution, 2003, 56, 28-37.	0.8	37
38	Sequencing the Oxytricha trifallax macronuclear genome: a pilot project. Trends in Genetics, 2003, 19, 603-607.	2.9	34
39	Genetic Code: What Nature Missed. Current Biology, 2003, 13, R884-R885.	1.8	5
40	Detection of gene duplications and block duplications in eukaryotic genomes. , 2003, , 27-34.		1
41	Detection of gene duplications and block duplications in eukaryotic genomes. Journal of Structural and Functional Genomics, 2003, 3, 27-34.	1.2	12
42	Extent of Gene Duplication in the Genomes of Drosophila, Nematode, and Yeast. Molecular Biology and Evolution, 2002, 19, 256-262.	3.5	422
43	On the relative content of G,C bases in codons of amino acids corresponding to class I and II aminoacyl-tRNA synthetases. , 2001, 31, 257-269.		2
44	On the Classes of Aminoacyl-tRNA Synthetases and the Error Minimization in the Genetic Code. Journal of Theoretical Biology, 2000, 204, 15-20.	0.8	18
45	Vestiges of early molecular processes leading to the genetic code. , 1997, 27, 397-403.		11