

Cristina P Vieira

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

1,567
citations

304743
22
h-index

377865
34
g-index

82
all docs

82
docs citations

82
times ranked

1472
citing authors

#	ARTICLE	IF	CITATIONS
1	The pegi3s Bioinformatics Docker Images Project. Lecture Notes in Networks and Systems, 2022, , 31-40.	0.7	4
2	Rewired glycosylation activity promotes scarless regeneration and functional recovery in spiny mice after complete spinal cord transection. Developmental Cell, 2022, 57, 440-450.e7.	7.0	26
3	A new cyanobacterial species with a protective effect on lettuce grown under salinity stress: Envisaging sustainable agriculture practices. Journal of Applied Phycology, 2022, 34, 915-928.	2.8	8
4	The evolution of vitamin C biosynthesis and transport in animals. BMC Ecology and Evolution, 2022, 22, .	1.6	6
5	The identification of the Rosa S-locus and implications on the evolution of the Rosaceae gametophytic self-incompatibility systems. Scientific Reports, 2021, 11, 3710.	3.3	19
6	On the Identification of Clinically Relevant Bacterial Amino Acid Changes at the Whole Genome Level Using Auto-PSS-Genome. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 334-343.	3.6	2
7	Inferences on Mycobacterium Leprae Host Immune Response Escape and Antibiotic Resistance Using Genomic Data and GenomeFastScreen. Advances in Intelligent Systems and Computing, 2021, , 42-50.	0.6	3
8	Comparative Genomics Discloses the Uniqueness and the Biosynthetic Potential of the Marine Cyanobacterium Hyella patelloides. Frontiers in Microbiology, 2020, 11, 1527.	3.5	5
9	Multiple loci linked to inversions are associated with eye size variation in species of the Drosophila virilis phylad. Scientific Reports, 2020, 10, 12832.	3.3	7
10	SEDA: a Desktop Tool Suite for FASTA Files Processing. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	3.0	10
11	Inferring Positive Selection in Large Viral Datasets. Advances in Intelligent Systems and Computing, 2020, , 61-69.	0.6	5
12	EvoPPI: A Web Application to Compare Protein-Protein Interactions (PPIs) from Different Databases and Species. Advances in Intelligent Systems and Computing, 2019, , 149-156.	0.6	1
13	Predicting Specificities Under the Non-self Gametophytic Self-Incompatibility Recognition Model. Frontiers in Plant Science, 2019, 10, 879.	3.6	6
14	Fruit fly identification, population dynamics and fruit damage during fruiting seasons of sweet oranges in Rusitu Valley, Zimbabwe. Scientific Reports, 2019, 9, 13578.	3.3	1
15	EvoPPI 1.0: a Web Platform for Within- and Between-Species Multiple Interactome Comparisons and Application to Nine PolyQ Proteins Determining Neurodegenerative Diseases. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 45-56.	3.6	10
16	BDBM 1.0: A Desktop Application for Efficient Retrieval and Processing of High-Quality Sequence Data and Application to the Identification of the Putative Coffea S-Locus. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 57-67.	3.6	13
17	Didymozoids in Muscle of Atlantic Chub Mackerel (Scomber colias). Acta Parasitologica, 2019, 64, 308-315.	1.1	1
18	ATXN1 N-terminal region explains the binding differences of wild-type and expanded forms. BMC Medical Genomics, 2019, 12, 145.	1.5	6

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19	Bioinformatics Protocols for Quickly Obtaining Large-Scale Data Sets for Phylogenetic Inferences. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 1-9.	3.6	18
20	Large Scale Analyses and Visualization of Adaptive Amino Acid Changes Projects. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 24-32.	3.6	14
21	Inferences on specificity recognition at the <i>Malus</i> —domestica gametophytic self-incompatibility system. <i>Scientific Reports</i> , 2018, 8, 1717.	3.3	30
22	Origin and Consequences of Chromosomal Inversions in the <i>virilis</i> Group of <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 3152-3166.	2.5	22
23	Description of new genera and species of marine cyanobacteria from the Portuguese Atlantic coast. <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 18-34.	2.7	92
24	Automated Collection and Sharing of Adaptive Amino Acid Changes Data. <i>Advances in Intelligent Systems and Computing</i> , 2017, , 18-25.	0.6	0
25	The <i>Drosophila melanogaster</i> Muc68E Mucin Gene Influences Adult Size, Starvation Tolerance, and Cold Recovery. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1841-1851.	1.8	2
26	Phylum-wide analysis of genes/proteins related to the last steps of assembly and export of extracellular polymeric substances (EPS) in cyanobacteria. <i>Scientific Reports</i> , 2015, 5, 14835.	3.3	85
27	Convergent Evolution at the Gametophytic Self-Incompatibility System in <i>Malus</i> and <i>Prunus</i> . <i>PLoS ONE</i> , 2015, 10, e0126138.	2.5	63
28	No evidence for Fabaceae Gametophytic self-incompatibility being determined by Rosaceae, Solanaceae, and Plantaginaceae S-RNase lineage genes. <i>BMC Plant Biology</i> , 2015, 15, 129.	3.6	15
29	<i>Drosophila americana</i> Diapausing Females Show Features Typical of Young Flies. <i>PLoS ONE</i> , 2015, 10, e0138758.	2.5	10
30	Genes Belonging to the Insulin and Ecdysone Signaling Pathways Can Contribute to Developmental Time, Lifespan and Abdominal Size Variation in <i>Drosophila americana</i> . <i>PLoS ONE</i> , 2014, 9, e86690.	2.5	2
31	Niche evolution and thermal adaptation in the temperate species <i>Drosophila americana</i> . <i>Journal of Evolutionary Biology</i> , 2014, 27, 1549-1561.	1.7	18
32	<i>Drosophila americana</i> as a Model Species for Comparative Studies on the Molecular Basis of Phenotypic Variation. <i>Genome Biology and Evolution</i> , 2013, 5, 661-679.	2.5	24
33	Patterns of evolution at the gametophytic self-incompatibility <i>Sorbus aucuparia</i> (Pyrinae) S pollen genes support the non-self recognition by multiple factors model. <i>Journal of Experimental Botany</i> , 2013, 64, 2423-2434.	4.8	24
34	Effects of Highly Conserved Major Histocompatibility Complex (MHC) Extended Haplotypes on Iron and Low CD8+ T Lymphocyte Phenotypes in HFE C282Y Homozygous Hemochromatosis Patients from Three Geographically Distant Areas. <i>PLoS ONE</i> , 2013, 8, e79990.	2.5	15
35	The <i>Drosophila melanogaster</i> methuselah Gene: A Novel Gene with Ancient Functions. <i>PLoS ONE</i> , 2013, 8, e63747.	2.5	23
36	The DAIBAM MITE element is involved in the origin of one fixed and two polymorphic <i>Drosophila virilis</i> phylad inversions. <i>Fly</i> , 2012, 6, 71-74.	1.7	13

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37	ADOPS - Automatic Detection Of Positively Selected Sites. Journal of Integrative Bioinformatics, 2012, 9, 18-32.	1.5	17
38	ADOPS--Automatic Detection Of Positively Selected Sites. Journal of Integrative Bioinformatics, 2012, 9, 200.	1.5	25
39	Drosophila Genes That Affect Meiosis Duration Are among the Meiosis Related Genes That Are More Often Found Duplicated. PLoS ONE, 2011, 6, e17512.	2.5	14
40	Resolving the phylogenetic relationships and evolutionary history of the <i>Drosophila virilis</i> group using multilocus data. Molecular Phylogenetics and Evolution, 2011, 60, 249-258.	2.7	33
41	A Comparative Study of the Short Term Cold Resistance Response in Distantly Related <i>Drosophila</i> Species: The Role of regucalcin and Frost. PLoS ONE, 2011, 6, e25520.	2.5	23
42	Evolutionary patterns at the RNase based gametophytic self - incompatibility system in two divergent Rosaceae groups (Maloideae and Prunus). BMC Evolutionary Biology, 2010, 10, 200.	3.2	29
43	<i>Medicago truncatula</i> contains a second gene encoding a plastid located glutamine synthetase exclusively expressed in developing seeds. BMC Plant Biology, 2010, 10, 183.	3.6	34
44	Phylogeny of the <i>teashirt</i> -related zinc finger (<i>tshz</i>) gene family and analysis of the developmental expression of <i>tshz2</i> and <i>tshz3b</i> in the zebrafish. Developmental Dynamics, 2010, 239, 1010-1018.	1.8	16
45	Low numbers of CD8+ T lymphocytes in hereditary haemochromatosis are explained by a decrease of the most mature CD8+ effector memory T cells. Clinical and Experimental Immunology, 2010, 159, 363-371.	2.6	23
46	On the identification of human selected loci in grapevines. Heredity, 2010, 104, 327-328.	2.6	2
47	Gene Classification Based on Amino Acid Motifs and Residues: The DLX (distal-less) Test Case. PLoS ONE, 2009, 4, e5748.	2.5	1
48	RNase-Based Gametophytic Self-Incompatibility Evolution: Questioning the Hypothesis of Multiple Independent Recruitments of the S-Pollen Gene. Journal of Molecular Evolution, 2009, 69, 32-41.	1.8	26
49	Comparative analysis of five immunity-related genes reveals different levels of adaptive evolution in the <i>virilis</i> and <i>melanogaster</i> groups of <i>Drosophila</i> . Heredity, 2009, 102, 573-578.	2.6	14
50	Partitional Clustering of Protein Sequences – An Inductive Logic Programming Approach. Lecture Notes in Computer Science, 2009, , 1001-1004.	1.3	1
51	An S-RNase-Based Gametophytic Self-Incompatibility System Evolved Only Once in Eudicots. Journal of Molecular Evolution, 2008, 67, 179-190.	1.8	70
52	Inferences on the number and frequency of S-pollen gene (SFB) specificities in the polyploid <i>Prunus spinosa</i> . Heredity, 2008, 101, 351-358.	2.6	20
53	Inferring the evolutionary history of <i>Drosophila americana</i> and <i>Drosophila novamexicana</i> using a multilocus approach and the influence of chromosomal rearrangements in single gene analyses. Molecular Ecology, 2008, 17, 2910-2926.	3.9	24
54	Protein evolution of ANTP and PRD homeobox genes. BMC Evolutionary Biology, 2008, 8, 200.	3.2	7

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55	An old bilbo-like non-LTR retroelement insertion provides insight into the relationship of species of the virilis group. <i>Gene</i> , 2008, 425, 48-55.	2.2	12
56	Genetic and molecular characterization of three novel S-haplotypes in sour cherry (<i>Prunus cerasus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	4.8	34
57	Recombination at <i>Prunus</i> S-Locus Region SLFL1 Gene. <i>Genetics</i> , 2008, 180, 483-491.	2.9	11
58	The <i>Prunus</i> Self-Incompatibility Locus (S locus) Is Seldom Rearranged. <i>Journal of Heredity</i> , 2008, 99, 657-660.	2.4	7
59	The number, age, sharing and relatedness of <i>S</i> -locus specificities in <i>Prunus</i> . <i>Genetical Research</i> , 2008, 90, 17-26.	0.9	17
60	Different Positively Selected Sites at the Gametophytic Self-Incompatibility Pistil S-RNase Gene in the Solanaceae and Rosaceae (<i>Prunus</i> , <i>Pyrus</i> , and <i>Malus</i>). <i>Journal of Molecular Evolution</i> , 2007, 65, 175-185.	1.8	51
61	Comparative polytene chromosome maps of <i>D. montana</i> and <i>D. virilis</i> . <i>Chromosoma</i> , 2007, 116, 21-27.	2.2	11
62	Variability patterns and positively selected sites at the gametophytic self-incompatibility pollen SFB gene in a wild self-incompatible <i>Prunus spinosa</i> (Rosaceae) population. <i>New Phytologist</i> , 2006, 172, 577-587.	7.3	75
63	The Evolutionary History of the Transposable Element Penelope in the <i>Drosophila virilis</i> Group of Species. <i>Journal of Molecular Evolution</i> , 2006, 63, 262-273.	1.8	14
64	On the location of the gene(s) harbouring the advantageous variant that maintains the X/4 fusion of <i>Drosophila americana</i> . <i>Genetical Research</i> , 2006, 87, 163-174.	0.9	17
65	Evidence for introgression in differentiated North-American and Finnish <i>Drosophila montana</i> populations. <i>Genetica</i> , 2005, 123, 285-293.	1.1	5
66	Dynamics and function of intron sequences of the wingless gene during the evolution of the <i>Drosophila</i> genus. <i>Evolution & Development</i> , 2004, 6, 325-335.	2.0	7
67	Genomic characterization of a repetitive motif strongly associated with developmental genes in <i>Drosophila</i> . <i>BMC Genomics</i> , 2003, 4, 52.	2.8	4
68	Evidence for rare recombination at the gametophytic self-incompatibility locus. <i>Heredity</i> , 2003, 91, 262-267.	2.6	33
69	Inferences on the Evolutionary History of the <i>Drosophila americana</i> Polymorphic <i>X4</i> Fusion From Patterns of Polymorphism at the <i>X</i> -Linked <i>paralytic</i> and <i>elav</i> Genes. <i>Genetics</i> , 2003, 164, 1459-1469.	2.9	25
70	Polymorphic Microsatellites in <i>Antirrhinum</i> (Scrophulariaceae), a Genus With Low Levels of Nuclear Sequence Variability. , 2002, 93, 217-221.		15
71	Molecular variation at the self-incompatibility locus in natural populations of the genera <i>Antirrhinum</i> and <i>Misopates</i> . <i>Heredity</i> , 2002, 88, 172-181.	2.6	25
72	Low Diversity and Divergence in the <i>fil1</i> Gene Family of <i>Antirrhinum</i> (Scrophulariaceae). <i>Journal of Molecular Evolution</i> , 2001, 52, 171-181.	1.8	11

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73	Low Rates of Silent Substitution in Nuclear Genes of Two Distantly Related Scrophulariaceae (<i>Antirrhinum</i> and <i>Verbascum</i>). <i>Molecular Biology and Evolution</i> , 2001, 18, 1940-1951.	8.9	3
74	Evolution of the cycloidea gene family in <i>Antirrhinum</i> and <i>Misopates</i> . <i>Molecular Biology and Evolution</i> , 1999, 16, 1474-1483.	8.9	29
75	Factors contributing to the hybrid dysgenesis syndrome in <i>Drosophila virilis</i> . <i>Genetical Research</i> , 1998, 71, 109-117.	0.9	50
76	The evolution of small gene clusters: evidence for an independent origin of the maltase gene cluster in <i>Drosophila virilis</i> and <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 1997, 14, 985-993.	8.9	23
77	A framework physical map of <i>Drosophila virilis</i> based on P1 clones: applications in genome evolution. <i>Chromosoma</i> , 1997, 106, 99-107.	2.2	42
78	Discordant Rates of Chromosome Evolution in the <i>Drosophila virilis</i> Species Group. <i>Genetics</i> , 1997, 147, 223-230.	2.9	39