

# Stefano Colella

## List of Publications by Year in descending order

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44  
papers

5,633  
citations

172457

29  
h-index

254184

43  
g-index

48  
all docs

48  
docs citations

48  
times ranked

9778  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and characterization of Vietnamese coffee bacterial endophytes displaying in vitro antifungal and nematicidal activities. <i>Microbiological Research</i> , 2021, 242, 126613.	5.3	28
2	Systemic control of nodule formation by plant nitrogen demand requires autoregulation-dependent and independent mechanisms. <i>Journal of Experimental Botany</i> , 2021, 72, 7942-7956.	4.8	7
3	The transposable element-rich genome of the cereal pest <i>Sitophilus oryzae</i> . <i>BMC Biology</i> , 2021, 19, 241.	3.8	40
4	Host-specific competitiveness to form nodules in <i>Rhizobium leguminosarum</i> symbiovar <i>viciae</i> . <i>New Phytologist</i> , 2020, 226, 555-568.	7.3	33
5	DiCoExpress: a tool to process multifactorial RNAseq experiments from quality controls to co-expression analysis through differential analysis based on contrasts inside GLM models. <i>Plant Methods</i> , 2020, 16, 68.	4.3	29
6	Responses of mature symbiotic nodules to the whole-plant systemic nitrogen signaling. <i>Journal of Experimental Botany</i> , 2020, 71, 5039-5052.	4.8	22
7	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. <i>Genome Biology</i> , 2019, 20, 64.	8.8	114
8	Bacteriocyte Reprogramming to Cope With Nutritional Stress in a Phloem Sap Feeding Hemipteran, the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>Frontiers in Physiology</i> , 2018, 9, 1498.	2.8	15
9	Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. <i>Genome Biology</i> , 2017, 18, 27.	8.8	624
10	Disruption of phenylalanine hydroxylase reduces adult lifespan and fecundity, and impairs embryonic development in parthenogenetic pea aphids. <i>Scientific Reports</i> , 2016, 6, 34321.	3.3	34
11	Direct flow cytometry measurements reveal a fine-tuning of symbiotic cell dynamics according to the host developmental needs in aphid symbiosis. <i>Scientific Reports</i> , 2016, 6, 19967.	3.3	71
12	ArthropodaCyc: a CycADS powered collection of BioCyc databases to analyse and compare metabolism of arthropods. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw081.	3.0	22
13	New insight into the RNA interference response against cathepsin-L gene in the pea aphid, <i>Acyrtosiphon pisum</i> : Molting or gut phenotypes specifically induced by injection or feeding treatments. <i>Insect Biochemistry and Molecular Biology</i> , 2014, 51, 20-32.	2.7	75
14	Tyrosine pathway regulation is host-mediated in the pea aphid symbiosis during late embryonic and early larval development. <i>BMC Genomics</i> , 2013, 14, 235.	2.8	51
15	A Genomic Reappraisal of Symbiotic Function in the Aphid/ <i>Buchnera</i> Symbiosis: Reduced Transporter Sets and Variable Membrane Organisations. <i>PLoS ONE</i> , 2011, 6, e29096.	2.5	44
16	Multimodal dynamic response of the <i>Buchnera aphidicola</i> pLeu plasmid to variations in leucine demand of its host, the pea aphid <i>Acyrtosiphon pisum</i> . <i>Molecular Microbiology</i> , 2011, 81, 1271-1285.	2.5	35
17	CycADS: an annotation database system to ease the development and update of BioCyc databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar008-bar008.	3.0	16
18	Genomic insight into the amino acid relations of the pea aphid, <i>Acyrtosiphon pisum</i> , with its symbiotic bacterium <i>Buchnera aphidicola</i> . <i>Insect Molecular Biology</i> , 2010, 19, 249-258.	2.0	219

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19	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	5.6	913
20	The anatomy of an aphid genome: From sequence to biology. <i>Comptes Rendus - Biologies</i> , 2010, 333, 464-473.	0.2	20
21	A statistical approach for detecting genomic aberrations in heterogeneous tumor samples from single nucleotide polymorphism genotyping data. <i>Genome Biology</i> , 2010, 11, R92.	8.8	125
22	Altered Intra-Nuclear Organisation of Heterochromatin and Genes in ICF Syndrome. <i>PLoS ONE</i> , 2010, 5, e11364.	2.5	25
23	Genome-Wide Hypomethylation in Head and Neck Cancer Is More Pronounced in HPV-Negative Tumors and Is Associated with Genomic Instability. <i>PLoS ONE</i> , 2009, 4, e4941.	2.5	114
24	Systemic analysis of the symbiotic function of <i>Buchnera aphidicola</i> , the primary endosymbiont of the pea aphid <i>Acyrtosiphon pisum</i> . <i>Comptes Rendus - Biologies</i> , 2009, 332, 1034-1049.	0.2	49
25	Molecular signatures of metastasis in head and neck cancer. <i>Head and Neck</i> , 2008, 30, 1273-1283.	2.0	27
26	MicroRNA-10b and breast cancer metastasis. <i>Nature</i> , 2008, 455, E8-E9.	27.8	134
27	GenoSNP: a variational Bayes within-sample SNP genotyping algorithm that does not require a reference population. <i>Bioinformatics</i> , 2008, 24, 2209-2214.	4.1	65
28	hsa-miR-210 Is Induced by Hypoxia and Is an Independent Prognostic Factor in Breast Cancer. <i>Clinical Cancer Research</i> , 2008, 14, 1340-1348.	7.0	617
29	Analysis of DNA Methylation at the Human Alpha Globin Cluster during Hematopoiesis. <i>Blood</i> , 2008, 112, 1861-1861.	1.4	0
30	QuantiSNP: an Objective Bayes Hidden-Markov Model to detect and accurately map copy number variation using SNP genotyping data. <i>Nucleic Acids Research</i> , 2007, 35, 2013-2025.	14.5	525
31	LRRTM1 on chromosome 2p12 is a maternally suppressed gene that is associated paternally with handedness and schizophrenia. <i>Molecular Psychiatry</i> , 2007, 12, 1129-1139.	7.9	300
32	Haemoglobin stabilising protein is a quantitative trait gene that modifies the phenotype of $\alpha$ -thalassaemia. <i>British Journal of Haematology</i> , 2006, 133, 675-682.	2.5	79
33	Matrix-Assisted Laser Desorption/Ionisation, Time-of-Flight Mass Spectrometry in Genomics Research. <i>PLoS Genetics</i> , 2006, 2, e100.	3.5	103
34	N-(4-Hydroxyphenyl)retinamide and nitric oxide pro-drugs exhibit apoptotic and anti-invasive effects against bone metastatic breast cancer cells. <i>Carcinogenesis</i> , 2006, 27, 568-577.	2.8	37
35	Genome-wide loss of heterozygosity analysis of WT1-wild-type and WT1-mutant Wilms tumors. <i>Genes Chromosomes and Cancer</i> , 2005, 43, 172-180.	2.8	29
36	Sensitive and quantitative universal Pyrosequencing methylation analysis of CpG sites. <i>BioTechniques</i> , 2003, 35, 146-150.	1.8	457

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37	Reduced expression of the A? subunit of protein phosphatase 2A in human gliomas in the absence of mutations in the A? and A? subunit genes. <i>International Journal of Cancer</i> , 2001, 93, 798-804.	5.1	60
38	Mutation analysis of hBUB1, hBUBR1 and hBUB3 genes in glioblastomas. <i>Acta Neuropathologica</i> , 2001, 101, 297-304.	7.7	29
39	Loss of Heterozygosity on Chromosome 10 Is More Extensive in Primary (De Novo) Than in Secondary Glioblastomas. <i>Laboratory Investigation</i> , 2000, 80, 65-72.	3.7	145
40	Identical mutations in the CSB gene associated with either Cockayne syndrome or the DeSanctis-Cacchione variant of xeroderma pigmentosum. <i>Human Molecular Genetics</i> , 2000, 9, 1171-1175.	2.9	53
41	Alterations in the CSB Gene in Three Italian Patients with the Severe Form of Cockayne Syndrome (CS) But Without Clinical Photosensitivity. <i>Human Molecular Genetics</i> , 1999, 8, 935-941.	2.9	49
42	Molecular Analysis of Mutations in the CSB(ERCC6) Gene in Patients with Cockayne Syndrome. <i>American Journal of Human Genetics</i> , 1998, 62, 77-85.	6.2	145
43	Cloning a new human gene from chromosome 21q22.3 encoding a glutamic acid-rich protein expressed in heart and skeletal muscle. <i>Human Genetics</i> , 1997, 99, 387-392.	3.8	34
44	Prenatal diagnosis of 30 fetuses at risk for fragile X syndrome. , 1996, 64, 187-190.		2