David Piquemal

List of Publications by Year in descending order

46 papers	3,321 citations	201674 27 h-index	243625 44 g-index
46 all docs	46 docs citations	46 times ranked	4624 citing authors

#	Article	IF	Citations
1	The Regulation of Hypoxic Genes by Calcium Involves c-Jun/AP-1, Which Cooperates with Hypoxia-Inducible Factor 1 in Response to Hypoxia. Molecular and Cellular Biology, 2002, 22, 1734-1741.	2.3	443
2	Different secretory repertoires control the biomineralization processes of prism and nacre deposition of the pearl oyster shell. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20986-20991.	7.1	287
3	Parallel Evolution of Nacre Building Gene Sets in Molluscs. Molecular Biology and Evolution, 2010, 27, 591-608.	8.9	239
4	Transcriptome and proteome analysis of Pinctada margaritifera calcifying mantle and shell: focus on biomineralization. BMC Genomics, 2010, 11, 613.	2.8	208
5	Role of the putative tumor metastasis suppressor gene Drg-1 in breast cancer progression. Oncogene, 2004, 23, 5675-5681.	5.9	177
6	PenBase, the shrimp antimicrobial peptide penaeidin database: Sequence-based classification and recommended nomenclature. Developmental and Comparative Immunology, 2006, 30, 283-288.	2.3	152
7	Induction of a Peptide with Activity against a Broad Spectrum of Pathogens in the Aedes aegypti Salivary Gland, following Infection with Dengue Virus. PLoS Pathogens, 2011, 7, e1001252.	4.7	149
8	Differential expression of the RTP/Drg1/Ndr1 gene product in proliferating and growth arrested cells. Biochimica Et Biophysica Acta - Molecular Cell Research, 1999, 1450, 364-373.	4.1	128
9	PTEN Up-Regulates the Tumor Metastasis Suppressor Gene Drg-1 in Prostate and Breast Cancer. Cancer Research, 2004, 64, 7655-7660.	0.9	125
10	Whole Transcriptome Profiling of Successful Immune Response to Vibrio Infections in the Oyster Crassostrea gigas by Digital Gene Expression Analysis. PLoS ONE, 2011, 6, e23142.	2.5	115
11	The Tumor Metastasis Suppressor Gene Drg-1 Down-regulates the Expression of Activating Transcription Factor 3 in Prostate Cancer. Cancer Research, 2006, 66, 11983-11990.	0.9	104
12	Transcriptomic Signature of Leishmania Infected Mice Macrophages: A Metabolic Point of View. PLoS Neglected Tropical Diseases, 2012, 6, e1763.	3.0	103
13	The Arabidopsis Root Transcriptome by Serial Analysis of Gene Expression. Gene Identification Using the Genome Sequence. Plant Physiology, 2004, 134, 67-80.	4.8	90
14	High-resolution picture of a venom gland transcriptome: Case study with the marine snail Conus consors. Toxicon, 2012, 59, 34-46.	1.6	76
15	Large-scale discovery of conopeptides and conoproteins in the injectable venom of a fish-hunting cone snail using a combined proteomic and transcriptomic approach. Journal of Proteomics, 2012, 75, 5215-5225.	2.4	74
16	Simultaneous gene expression profiling in human macrophages infected with Leishmania major parasites using SAGE. BMC Genomics, 2008, 9, 238.	2.8	68
17	Lipid Droplet Formation, Their Localization and Dynamics during Leishmania major Macrophage Infection. PLoS ONE, 2016, 11, e0148640.	2.5	62
18	Transcriptome Analysis of Monocytic Leukemia Cell Differentiation. Genomics, 2002, 80, 361-371.	2.9	56

#	Article	IF	Citations
19	A relationship between antimicrobial peptide gene expression and capacity of a selected shrimp line to survive a Vibrio infection. Molecular Immunology, 2008, 45, 3438-3445.	2.2	56
20	Atlas of gene expression in the mouse kidney: new features of glomerular parietal cells. Physiological Genomics, 2011, 43, 161-173.	2.3	54
21	Of Mice and Men: Divergence of Gene Expression Patterns in Kidney. PLoS ONE, 2012, 7, e46876.	2.5	51
22	Transforming growth factor-?1 is an autocrine mediator of U937 cell growth arrest and differentiation induced by vitamin D3 and retinoids. , 1999, 178, 109-119.		47
23	Gene profiling during development and after a peripheral nerve traumatism reveals genes specifically induced by injury in dorsal root ganglia. Molecular and Cellular Neurosciences, 2006, 32, 217-229.	2.2	44
24	A hemocyte gene expression signature correlated with predictive capacity of oysters to survive Vibrio infections. BMC Genomics, 2012, 13, 252.	2.8	38
25	Mining SAGE data allows large-scale, sensitive screening of antisense transcript expression. Nucleic Acids Research, 2004, 32, e163-e163.	14.5	34
26	Pharmacogenomic analysis of acute promyelocytic leukemia cells highlights CYP26 cytochrome metabolism in differential all-trans retinoic acid sensitivity. Blood, 2007, 109, 4450-4460.	1.4	33
27	Correlation of N-myc downstream-regulated gene 1 expression with clinical outcomes of colorectal cancer patients of different race/ethnicity. World Journal of Gastroenterology, 2007, 13, 2803.	3.3	31
28	Gene expression profiling from leukocytes of horses affected by osteochondrosis. Journal of Orthopaedic Research, 2010, 28, 965-970.	2.3	29
29	Recruitment of Glycosyl Hydrolase Proteins in a Cone Snail Venomous Arsenal: Further Insights into Biomolecular Features of Conus Venoms. Marine Drugs, 2012, 10, 258-280.	4.6	26
30	The intellectual disability of trisomy 21: differences in gene expression in a case series of patients with lower and higher IQ. European Journal of Human Genetics, 2013, 21, 1253-1259.	2.8	25
31	Modification of gene expression: Help to detect doping with erythropoiesisâ€stimulating agents. American Journal of Hematology, 2009, 84, 755-759.	4.1	24
32	Parental diuron-exposure alters offspring transcriptome and fitness in Pacific oyster Crassostrea gigas. Ecotoxicology and Environmental Safety, 2017, 142, 51-58.	6.0	23
33	Analysis of remnant reticulocyte mRNA reveals new genes and antisense transcripts expressed in the human erythroid lineage. Haematologica, 2004, 89, 1434-8.	3.5	20
34	Blood cells RNA biomarkers as a first longâ€term detection strategy for EPO abuse in horseracing. Drug Testing and Analysis, 2010, 2, 339-345.	2.6	19
35	Serial analysis of gene expression (SAGE) in bovine trypanotolerance: preliminary results. Genetics Selection Evolution, 2003, 35, S35-47.	3.0	15
36	Analysis of human reticulocyte genes reveals altered erythropoiesis: potential use to detect recombinant human erythropoietin doping. Haematologica, 2004, 89, 991-7.	3.5	14

#	Article	IF	Citations
37	Efficiency and limits of the Serial Analysis of Gene Expression (SAGE) method: Discussions based on first results in bovine trypanotolerance. Veterinary Immunology and Immunopathology, 2005, 108, 59-69.	1.2	13
38	Study of Bovine Trypanotolerance by Whole Transcriptome Analysis. Annals of the New York Academy of Sciences, 2008, 1149, 71-76.	3.8	12
39	Evidence of zoonotic Poxviridae coinfections in clinically diagnosed papillomas using a newly developed mini-array test. Journal of Veterinary Diagnostic Investigation, 2016, 28, 59-64.	1.1	11
40	Bovine Transcriptome Analysis by SAGE Technology during an ExperimentalTrypanosoma congolenseInfection. Annals of the New York Academy of Sciences, 2006, 1081, 286-299.	3.8	10
41	Identification of Differentially Expressed Genes between Fetal and Adult Mouse Kidney: Candidate Gene in Kidney Development. Nephron Physiology, 2006, 102, p81-p91.	1.2	10
42	Leishmania Parasites Differently Regulate Antioxidant Genes in Macrophages Derived From Resistant and Susceptible Mice. Frontiers in Cellular and Infection Microbiology, 2021, 11, 748738.	3.9	10
43	New prognostic markers, determined using gene expression analyses, reveal two distinct subtypes of chronic myelomonocytic leukaemia patients. British Journal of Haematology, 2012, 157, 347-356.	2.5	8
44	Use of the Serial Analysis of Gene Expression (SAGE) Method in Veterinary Research: A Concrete Application in the Study of the Bovine Trypanotolerance Genetic Control. Annals of the New York Academy of Sciences, 2004, 1026, 171-182.	3.8	6
45	All Trans Retinoic Acid (atRA) Differentiation Markers in Normal and Retinoid-Resistant Acute Promyelocytic Leukemia Cells Revealed Induction of atRA Metabolism as Relevant Prognostic of APL Sensitivity to Therapy.. Blood, 2005, 106, 3256-3256.	1.4	2
46	Les nouvelles opportunitÃ©s et outils de gÃ©nomique dans la lutte contre le dopage. Revue Francophone Des Laboratoires, 2008, 2008, 61-68.	0.0	0