Fabien Campagne

List of Publications by Year
in descending order

45 papers	5,004 citations	257450 24 h-index	276875 41 g-index
65 all docs	65 docs citations	65 times ranked	8463 citing authors

#	ARTICLE	IF	CITATIONS
1	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
2	DNA Methylation Signatures Identify Biologically Distinct Subtypes in Acute Myeloid Leukemia. Cancer Cell, 2010, 17, 13-27.	16.8	737
3	Minimum information requested in the annotation of biochemical models (MIRIAM). Nature Biotechnology, 2005, 23, 1509-1515.	17.5	553
4	Tas1r3, encoding a new candidate taste receptor, is allelic to the sweet responsiveness locus Sac. Nature Genetics, 2001, 28, 58-63.	21.4	492
5	SNOSID, a proteomic method for identification of cysteine S-nitrosylation sites in complex protein mixtures. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1012-1017.	7.1	334
6	A Polymorphism in CALHM1 Influences Ca2+ Homeostasis, AÎ² Levels, and Alzheimer's Disease Risk. Cell, 2008, 133, 1149-1161.	28.9	310
7	GPCRDB information system for G protein-coupled receptors. Nucleic Acids Research, 2003, 31, 294-297.	14.5	299
8	Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. JAMA Oncology, 2015, 1, 466.	7.1	264
9	Title is missing!. Nature Genetics, 2001, 28, 58-63.	21.4	173
10	Pseudomonas aeruginosa SoxR Does Not Conform to the Archetypal Paradigm for SoxR-Dependent Regulation of the Bacterial Oxidative Stress Adaptive Response. Infection and Immunity, 2005, 73, 2958-2966.	2.2	115
11	Crooked tail (Cd) model of human folate-responsive neural tube defects is mutated in Wnt coreceptor lipoprotein receptor-related protein 6. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12843-12848.	7.1	88
12	Variability in DNA methylation defines novel epigenetic subgroups of DLBCL associated with different clinical outcomes. Blood, 2014, 123, 1699-1708.	1.4	83
13	Gene Expression Profiling Separates Chromophobe Renal Cell Carcinoma from Oncocytoma and Identifies Vesicular Transport and Cell Junction Proteins as Differentially Expressed Genes. Clinical Cancer Research, 2006, 12, 6937-6945.	7.0	79
14	GPCR-OKB: the G Protein Coupled Receptor Oligomer Knowledge Base. Bioinformatics, 2010, 26, 1804-1805.	4.1	74
15	Exome Sequencing and Prediction of Long-Term Kidney Allograft Function. PLoS Computational Biology, 2016, 12, e1005088.	3.2	52
16	Correcting Smad1/5/8, mTOR, and VEGFR2 treats pathology in hereditary hemorrhagic telangiectasia models. Journal of Clinical Investigation, 2020, 130, 942-957.	8.2	48
17	Tacrolimus rescues the signaling and gene expression signature of endothelial ALK1 loss-of-function and improves HHT vascular pathology. Human Molecular Genetics, 2017, 26, 4786-4798.	2.9	45
18	A mouse model of hereditary hemorrhagic telangiectasia generated by transmammary-delivered immunoblocking of BMP9 and BMP10. Scientific Reports, 2016, 6, 37366.	3.3	44

#	Article	IF	Citations
19	Requirements and ontology for a G protein-coupled receptor oligomerization knowledge base. BMC Bioinformatics, 2007, 8, 177.	2.6	42
20	Compression of Structured High-Throughput Sequencing Data. PLoS ONE, 2013, 8, e79871.	2.5	35
21	Characterization of the Mouse Adeno-Associated Virus AAVS1 Ortholog. Journal of Virology, 2004, 78, 8917-8921.	3.4	30
22	Quantitative Information Management for the Biochemical Computation of Cellular Networks. Science Signaling, 2004, 2004, pl11-pl11.	3.6	29
23	CALHM1 P86L Polymorphism Modulates CSF Aβ Levels in Cognitively Healthy Individuals at Risk for Alzheimer's Disease. Molecular Medicine, 2011, 17, 974-979.	4.4	26
24	Building protein diagrams on the web with the residue-based diagram editor RbDe. Nucleic Acids Research, 2003, 31, 3856-3858.	14.5	25
25	Response: CALHM1 Association with Alzheimer's Disease Risk. Cell, 2008, 135, 994-996.	28.9	25
26	GobyWeb: Simplified Management and Analysis of Gene Expression and DNA Methylation Sequencing Data. PLoS ONE, 2013, 8, e69666.	2.5	25
27	Mining expressed sequence tags identifies cancer markers of clinical interest. BMC Bioinformatics, 2006, 7, 481.	2.6	23
28	Growth arrest-specific 1 binds to and controls the maturation and processing of the amyloid-β precursor protein. Human Molecular Genetics, 2011, 20, 2026-2036.	2.9	15
29	Glomerular common gamma chain confers B- and T-cell–independent protection against glomerulonephritis. Kidney International, 2017, 91, 1146-1158.	5.2	15
30	In Silico Analysis of NF2 Gene Missense Mutations in Neurofibromatosis Type 2. Otology and Neurotology, 2015, 36, 908-914.	1.3	13
31	Genome-Wide Profiling of Endothelial Progenitor Cells in Multiple Myeloma: Disease-Relevant Pathways and Overlaps with Common Cancer Biomarkers. Blood, 2008, 112, 626-626.	1.4	13
32	Specific calpain inhibition protects kidney against inflammaging. Scientific Reports, 2017, 7, 8016.	3.3	12
33	Effect of the CALHM1 G330D and R154H Human Variants on the Control of Cytosolic Ca2+ and Aβ Levels. PLoS ONE, 2014, 9, e112484.	2.5	11
34	Batch mode generation of residue-based diagrams of proteins. Bioinformatics, 2003, 19, 1854-1855.	4.1	9
35	BDVal: reproducible large-scale predictive model development and validation in high-throughput datasets. Bioinformatics, 2010, 26, 2472-2473.	4.1	8
36	Beyond tissueInfo: functional prediction using tissue expression profile similarity searches. Nucleic Acids Research, 2008, 36, 3728-3737.	14.5	7

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37	Introduction to the Development and Validation of Predictive Biomarker Models from High-Throughput Data Sets. Methods in Molecular Biology, 2010, 620, 435-470.	0.9	7
38	Critical evaluation of the JDO API for the persistence and portability requirements of complex biological databases. BMC Bioinformatics, 2005, 6, 5.	2.6	6
39	Composable languages for bioinformatics: the NYoSh experiment. PeerJ, 2014, 2, e241.	2.0	5
40	Language workbench user interfaces for data analysis. PeerJ, 2015, 3, e800.	2.0	4
41	Genome-Wide Profiling of Endothelial Progenitor Cells in Multiple Myeloma: Overlaps with Myeloma Tumor Cells and Common Cancer Gene-Pathways.. Blood, 2007, 110, 394-394.	1.4	0
42	DNA Methylation Profiling Predicts Clinical Outcomes and Reveals Unique Insights Into the Molecular Complexity of Acute Myeloid Leukemia.. Blood, 2009, 114, 707-707.	1.4	0
43	Epigenetic Profiling of Primary DLBCLs Reveals Novel DNA Methylation-Based Clusters and New Underlying Mechanisms of Lymphomagenesis. Blood, 2011, 118, 556-556.	1.4	0
44	Epigenetic Profiling of Primary CLL Reveals Novel DNA Methylation-Based Clusters and Novel Mechanisms of Leukemogenesis. Blood, 2012, 120, 3877-3877.	1.4	0
45	Applications, Representation, and Management of Signaling Pathway Information: Introduction to the SigPath Project. , 2007, , 372-392.		0