

Fabien Campagne

List of Publications by Year in descending order

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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	Correcting Smad1/5/8, mTOR, and VEGFR2 treats pathology in hereditary hemorrhagic telangiectasia models. <i>Journal of Clinical Investigation</i> , 2020, 130, 942-957.	8.2	48
2	Glomerular common gamma chain confers B- and T-cell-independent protection against glomerulonephritis. <i>Kidney International</i> , 2017, 91, 1146-1158.	5.2	15
3	Tacrolimus rescues the signaling and gene expression signature of endothelial ALK1 loss-of-function and improves HHT vascular pathology. <i>Human Molecular Genetics</i> , 2017, 26, 4786-4798.	2.9	45
4	Specific calpain inhibition protects kidney against inflammaging. <i>Scientific Reports</i> , 2017, 7, 8016.	3.3	12
5	Exome Sequencing and Prediction of Long-Term Kidney Allograft Function. <i>PLoS Computational Biology</i> , 2016, 12, e1005088.	3.2	52
6	A mouse model of hereditary hemorrhagic telangiectasia generated by transmammary-delivered immunoblocking of BMP9 and BMP10. <i>Scientific Reports</i> , 2016, 6, 37366.	3.3	44
7	In Silico Analysis of NF2 Gene Missense Mutations in Neurofibromatosis Type 2. <i>Otology and Neurotology</i> , 2015, 36, 908-914.	1.3	13
8	Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. <i>JAMA Oncology</i> , 2015, 1, 466.	7.1	264
9	Language workbench user interfaces for data analysis. <i>PeerJ</i> , 2015, 3, e800.	2.0	4
10	Effect of the CALHM1 G330D and R154H Human Variants on the Control of Cytosolic Ca ²⁺ and A β Levels. <i>PLoS ONE</i> , 2014, 9, e112484.	2.5	11
11	Variability in DNA methylation defines novel epigenetic subgroups of DLBCL associated with different clinical outcomes. <i>Blood</i> , 2014, 123, 1699-1708.	1.4	83
12	Composable languages for bioinformatics: the NYoSh experiment. <i>PeerJ</i> , 2014, 2, e241.	2.0	5
13	Compression of Structured High-Throughput Sequencing Data. <i>PLoS ONE</i> , 2013, 8, e79871.	2.5	35
14	GobyWeb: Simplified Management and Analysis of Gene Expression and DNA Methylation Sequencing Data. <i>PLoS ONE</i> , 2013, 8, e69666.	2.5	25
15	Epigenetic Profiling of Primary CLL Reveals Novel DNA Methylation-Based Clusters and Novel Mechanisms of Leukemogenesis. <i>Blood</i> , 2012, 120, 3877-3877.	1.4	0
16	CALHM1 P86L Polymorphism Modulates CSF A β Levels in Cognitively Healthy Individuals at Risk for Alzheimer's Disease. <i>Molecular Medicine</i> , 2011, 17, 974-979.	4.4	26
17	Growth arrest-specific 1 binds to and controls the maturation and processing of the amyloid- β precursor protein. <i>Human Molecular Genetics</i> , 2011, 20, 2026-2036.	2.9	15
18	Epigenetic Profiling of Primary DLBCLs Reveals Novel DNA Methylation-Based Clusters and New Underlying Mechanisms of Lymphomagenesis. <i>Blood</i> , 2011, 118, 556-556.	1.4	0

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19	DNA Methylation Signatures Identify Biologically Distinct Subtypes in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2010, 17, 13-27.	16.8	737
20	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	17.5	795
21	GPCR-OKB: the G Protein Coupled Receptor Oligomer Knowledge Base. <i>Bioinformatics</i> , 2010, 26, 1804-1805.	4.1	74
22	BDVal: reproducible large-scale predictive model development and validation in high-throughput datasets. <i>Bioinformatics</i> , 2010, 26, 2472-2473.	4.1	8
23	Introduction to the Development and Validation of Predictive Biomarker Models from High-Throughput Data Sets. <i>Methods in Molecular Biology</i> , 2010, 620, 435-470.	0.9	7
24	DNA Methylation Profiling Predicts Clinical Outcomes and Reveals Unique Insights Into the Molecular Complexity of Acute Myeloid Leukemia.. <i>Blood</i> , 2009, 114, 707-707.	1.4	0
25	A Polymorphism in CALHM1 Influences Ca ²⁺ Homeostasis, A β ² Levels, and Alzheimer's Disease Risk. <i>Cell</i> , 2008, 133, 1149-1161.	28.9	310
26	Response: CALHM1 Association with Alzheimer's Disease Risk. <i>Cell</i> , 2008, 135, 994-996.	28.9	25
27	Beyond tissueInfo: functional prediction using tissue expression profile similarity searches. <i>Nucleic Acids Research</i> , 2008, 36, 3728-3737.	14.5	7
28	Genome-Wide Profiling of Endothelial Progenitor Cells in Multiple Myeloma: Disease-Relevant Pathways and Overlaps with Common Cancer Biomarkers. <i>Blood</i> , 2008, 112, 626-626.	1.4	13
29	Requirements and ontology for a G protein-coupled receptor oligomerization knowledge base. <i>BMC Bioinformatics</i> , 2007, 8, 177.	2.6	42
30	Genome-Wide Profiling of Endothelial Progenitor Cells in Multiple Myeloma: Overlaps with Myeloma Tumor Cells and Common Cancer Gene-Pathways.. <i>Blood</i> , 2007, 110, 394-394.	1.4	0
31	Applications, Representation, and Management of Signaling Pathway Information: Introduction to the SigPath Project. , 2007, , 372-392.		0
32	Mining expressed sequence tags identifies cancer markers of clinical interest. <i>BMC Bioinformatics</i> , 2006, 7, 481.	2.6	23
33	Gene Expression Profiling Separates Chromophobe Renal Cell Carcinoma from Oncocytoma and Identifies Vesicular Transport and Cell Junction Proteins as Differentially Expressed Genes. <i>Clinical Cancer Research</i> , 2006, 12, 6937-6945.	7.0	79
34	SNOSID, a proteomic method for identification of cysteine S-nitrosylation sites in complex protein mixtures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1012-1017.	7.1	334
35	Minimum information requested in the annotation of biochemical models (MIRIAM). <i>Nature Biotechnology</i> , 2005, 23, 1509-1515.	17.5	553
36	Critical evaluation of the JDO API for the persistence and portability requirements of complex biological databases. <i>BMC Bioinformatics</i> , 2005, 6, 5.	2.6	6

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37	<i>Pseudomonas aeruginosa</i> SoxR Does Not Conform to the Archetypal Paradigm for SoxR-Dependent Regulation of the Bacterial Oxidative Stress Adaptive Response. <i>Infection and Immunity</i> , 2005, 73, 2958-2966.	2.2	115
38	Crooked tail (Cd) model of human folate-responsive neural tube defects is mutated in Wnt coreceptor lipoprotein receptor-related protein 6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12843-12848.	7.1	88
39	Characterization of the Mouse Adeno-Associated Virus AAVS1 Ortholog. <i>Journal of Virology</i> , 2004, 78, 8917-8921.	3.4	30
40	Quantitative Information Management for the Biochemical Computation of Cellular Networks. <i>Science Signaling</i> , 2004, 2004, p111-p111.	3.6	29
41	GPCRDB information system for G protein-coupled receptors. <i>Nucleic Acids Research</i> , 2003, 31, 294-297.	14.5	299
42	Building protein diagrams on the web with the residue-based diagram editor RbDe. <i>Nucleic Acids Research</i> , 2003, 31, 3856-3858.	14.5	25
43	Batch mode generation of residue-based diagrams of proteins. <i>Bioinformatics</i> , 2003, 19, 1854-1855.	4.1	9
44	Tas1r3, encoding a new candidate taste receptor, is allelic to the sweet responsiveness locus Sac. <i>Nature Genetics</i> , 2001, 28, 58-63.	21.4	492
45	Title is missing!. <i>Nature Genetics</i> , 2001, 28, 58-63.	21.4	173