

Alain Viari

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

4,943
citations

218677

26
h-index

197818

49
g-index

54
all docs

54
docs citations

54
times ranked

10910
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of driver genes for critical forms of COVID-19 in a deeply phenotyped young patient cohort. <i>Science Translational Medicine</i> , 2022, 14, eabj7521.	12.4	71
2	Identification of shared tumor epitopes from endogenous retroviruses inducing high-avidity cytotoxic T cells for cancer immunotherapy. <i>Science Advances</i> , 2022, 8, eabj3671.	10.3	38
3	Characterization of Depressive Symptoms Trajectories After Breast Cancer Diagnosis in Women in France. <i>JAMA Network Open</i> , 2022, 5, e225118.	5.9	9
4	Genetic Analysis of Lung Cancer and the Germline Impact on Somatic Mutation Burden. <i>Journal of the National Cancer Institute</i> , 2022, 114, 1159-1166.	6.3	8
5	<scp>HERVs</scp> characterize normal and leukemia stem cells and represent a source of shared epitopes for cancer immunotherapy. <i>American Journal of Hematology</i> , 2022, 97, 1200-1214.	4.1	8
6	Acquired somatic MMR deficiency is a major cause of MSI tumor in patients suspected for "Lynch-like syndrome" including young patients. <i>European Journal of Human Genetics</i> , 2021, 29, 482-488.	2.8	16
7	CDYL2 Epigenetically Regulates MIR124 to Control NF- κ B/STAT3-Dependent Breast Cancer Cell Plasticity. <i>IScience</i> , 2020, 23, 101141.	4.1	22
8	Ribosomal RNA 2'-O-methylation as a novel layer of inter-tumour heterogeneity in breast cancer. <i>NAR Cancer</i> , 2020, 2, zcaa036.	3.1	40
9	Repurposing rotavirus vaccines for intratumoral immunotherapy can overcome resistance to immune checkpoint blockade. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	49
10	The circular RNome of primary breast cancer. <i>Genome Research</i> , 2019, 29, 356-366.	5.5	85
11	Toll-like receptor 3 downregulation is an escape mechanism from apoptosis during hepatocarcinogenesis. <i>Journal of Hepatology</i> , 2019, 71, 763-772.	3.7	31
12	Mutational Profile of Aggressive, Localised Prostate Cancer from African Caribbean Men Versus European Ancestry Men. <i>European Urology</i> , 2019, 75, 11-15.	1.9	32
13	A gene-expression profiling score for prediction of outcome in patients with follicular lymphoma: a retrospective training and validation analysis in three international cohorts. <i>Lancet Oncology</i> , The, 2018, 19, 549-561.	10.7	165
14	Immunological and classical subtypes of oral premalignant lesions. <i>OncolImmunology</i> , 2018, 7, e1496880.	4.6	35
15	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. <i>Nature Genetics</i> , 2017, 49, 341-348.	21.4	75
16	BCL2 mutations do not confer adverse prognosis in follicular lymphoma patients treated with rituximab. <i>American Journal of Hematology</i> , 2017, 92, 515-519.	4.1	22
17	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. <i>Nature Medicine</i> , 2017, 23, 517-525.	30.7	769
18	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. <i>Nature</i> , 2017, 543, 714-718.	27.8	229

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19	Whole-Genome Sequencing Reveals Breast Cancers with Mismatch Repair Deficiency. <i>Cancer Research</i> , 2017, 77, 4755-4762.	0.9	81
20	A phenotypic and mechanistic perspective on heterogeneity of HER2-positive breast cancers. <i>Molecular and Cellular Oncology</i> , 2016, 3, e1232186.	0.7	5
21	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	1,760
22	Chemical and biological insecticides select distinct gene expression patterns in <i>Aedes aegypti</i> mosquito. <i>Biology Letters</i> , 2014, 10, 20140716.	2.3	24
23	Complex dynamic of dengue virus serotypes 2 and 3 in Cambodia following series of climate disasters. <i>Infection, Genetics and Evolution</i> , 2013, 15, 77-86.	2.3	11
24	Dynamic of H5N1 virus in Cambodia and emergence of a novel endemic sub-clade. <i>Infection, Genetics and Evolution</i> , 2013, 15, 87-94.	2.3	27
25	Biased mutational pattern and quasispecies hypothesis in H5N1 virus. <i>Infection, Genetics and Evolution</i> , 2013, 15, 69-76.	2.3	12
26	Genetic diversity and lineage dynamic of dengue virus serotype 1 (DENV-1) in Cambodia. <i>Infection, Genetics and Evolution</i> , 2013, 15, 59-68.	2.3	26
27	The CanOE Strategy: Integrating Genomic and Metabolic Contexts across Multiple Prokaryote Genomes to Find Candidate Genes for Orphan Enzymes. <i>PLoS Computational Biology</i> , 2012, 8, e1002540.	3.2	32
28	UniPathway: a resource for the exploration and annotation of metabolic pathways. <i>Nucleic Acids Research</i> , 2012, 40, D761-D769.	14.5	83
29	ecoPrimers: inference of new DNA barcode markers from whole genome sequence analysis. <i>Nucleic Acids Research</i> , 2011, 39, e145-e145.	14.5	416
30	Differential strain-specific diagnosis of the heartwater agent: <i>Ehrlichia ruminantium</i> . <i>Infection, Genetics and Evolution</i> , 2008, 8, 459-466.	2.3	5
31	Emergence and Potential of High-Throughput and Integrative Approaches in Pathology. <i>Annals of the New York Academy of Sciences</i> , 2008, 1149, 62-65.	3.8	0
32	PepLine: A Software Pipeline for High-Throughput Direct Mapping of Tandem Mass Spectrometry Data on Genomic Sequences. <i>Journal of Proteome Research</i> , 2008, 7, 1873-1883.	3.7	28
33	<i>Ehrlichia ruminantium</i> : genomic and evolutionary features. <i>Trends in Parasitology</i> , 2007, 23, 414-419.	3.3	28
34	Comparative Genomics of Three Strains of <i>Ehrlichia ruminantium</i> . <i>Annals of the New York Academy of Sciences</i> , 2006, 1081, 417-433.	3.8	19
35	Comparative Genomic Analysis of Three Strains of <i>Ehrlichia ruminantium</i> Reveals an Active Process of Genome Size Plasticity. <i>Journal of Bacteriology</i> , 2006, 188, 2533-2542.	2.2	86
36	Integration of data and methods for genome analysis. <i>Current Opinion in Drug Discovery & Development</i> , 2003, 6, 346-52.	1.9	7

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37	Evolutionary Role of Restriction/Modification Systems as Revealed by Comparative Genome Analysis. <i>Genome Research</i> , 2001, 11, 946-958.	5.5	56
38	Analysis of Intrachromosomal Duplications in Yeast <i>Saccharomyces cerevisiae</i> : A Possible Model for Their Origin. <i>Molecular Biology and Evolution</i> , 2000, 17, 1268-1275.	8.9	69
39	The DB case: pattern matching evidence is not significant. <i>MicroCorrespondence. Molecular Microbiology</i> , 2000, 37, 216-218.	2.5	5
40	Searching genomes for sequences with the potential to form intrastrand triple helices. <i>Journal of Molecular Biology</i> , 2000, 302, 797-809.	4.2	31
41	Implication of gene distribution in the bacterial chromosome for the bacterial cell factory. <i>Journal of Biotechnology</i> , 2000, 78, 209-219.	3.8	36
42	Detecting and Analyzing DNA Sequencing Errors: Toward a Higher Quality of the <i>Bacillus subtilis</i> Genome Sequence. <i>Genome Research</i> , 1999, 9, 1116-1127.	5.5	37
43	Universal replication biases in bacteria. <i>Molecular Microbiology</i> , 1999, 32, 11-16.	2.5	170
44	Functional and evolutionary roles of long repeats in prokaryotes. <i>Research in Microbiology</i> , 1999, 150, 725-733.	2.1	50
45	Pairwise and Multiple Identification of Three-Dimensional Common Substructures in Proteins. <i>Journal of Computational Biology</i> , 1998, 5, 41-56.	1.6	20
46	Automated multiple analysis of protein structures: Application to homology modeling of cytochromes P450. , 1997, 28, 388-404.		20
47	Palingol: a declarative programming language to describe nucleic acids' secondary structures and to scan sequence database. <i>Nucleic Acids Research</i> , 1996, 24, 1395-1403.	14.5	65
48	Searching for flexible repeated patterns using a non-transitive similarity relation. <i>Pattern Recognition Letters</i> , 1995, 16, 233-246.	4.2	25