Philippe Hupe

List of Publications by Year
in descending order

59 papers	4,775 citations	186265 28 h-index	206112 48 g-index
62 all docs	62 docs citations	62 times ranked	8253 citing authors

#	Article	IF	Citations
1	A critical function for transforming growth factor-Î², interleukin 23 and proinflammatory cytokines in driving and modulating human TH-17 responses. Nature Immunology, 2008, 9, 650-657.	14.5	844
2	Ultrahigh dose-rate FLASH irradiation increases the differential response between normal and tumor tissue in mice. Science Translational Medicine, 2014, 6, 245ra93.	12.4	768
3	Analysis of array CGH data: from signal ratio to gain and loss of DNA regions. Bioinformatics, 2004, 20, 3413-3422.	4.1	465
4	miR-181a and miR-630 Regulate Cisplatin-Induced Cancer Cell Death. Cancer Research, 2010, 70, 1793-1803.	0.9	262
5	Microbe-host interplay in atopic dermatitis and psoriasis. Nature Communications, 2019, 10, 4703.	12.8	217
6	Frequent PTEN genomic alterations and activated phosphatidylinositol 3-kinase pathway in basal-like breast cancer cells. Breast Cancer Research, 2008, 10, R101.	5.0	186
7	Live-Cell Chromosome Dynamics and Outcome of X Chromosome Pairing Events during ES Cell Differentiation. Cell, 2011, 145, 447-458.	28.9	137
8	High PTP4A3 Phosphatase Expression Correlates with Metastatic Risk in Uveal Melanoma Patients. Cancer Research, 2011, 71, 666-674.	0.9	133
9	Genomic Profiling and Identification of High-Risk Uveal Melanoma by Array CGH Analysis of Primary Tumors and Liver Metastases. , 2009, 50, 2572.		122
10	Prognostic Impact of Vitamin B6 Metabolism in Lung Cancer. Cell Reports, 2012, 2, 257-269.	6.4	122
11	Multi-factor data normalization enables the detection of copy number aberrations in amplicon sequencing data. Bioinformatics, 2014, 30, 3443-3450.	4.1	109
12	VAMP: Visualization and analysis of array-CGH, transcriptome and other molecular profiles. Bioinformatics, 2006, 22, 2066-2073.	4.1	106
13	Multiparametric analysis of cytokine-driven human Th17 differentiation reveals a differential regulation of IL-17 and IL-22 production. Blood, 2009, 114, 3610-3614.	1.4	91
14	Frequent genomic structural alterations at HPV insertion sites in cervical carcinoma. Journal of Pathology, 2010, 221, 320-330.	4.5	85
15	Bioinformatics for precision medicine in oncology: principles and application to the SHIVA clinical trial. Frontiers in Genetics, 2014, 5, 152.	2.3	72
16	Spatial normalization of array-CGH data. BMC Bioinformatics, 2006, 7, 264.	2.6	71
17	Search for a Gene Expression Signature of Breast Cancer Local Recurrence in Young Women. Clinical Cancer Research, 2012, 18, 1704-1715.	7.0	67
18	NormaCurve: A SuperCurve-Based Method That Simultaneously Quantifies and Normalizes Reverse Phase Protein Array Data. PLoS ONE, 2012, 7, e38686.	2.5	65

#	Article	IF	Citations
19	High-Resolution Mapping of DNA Breakpoints to Define True Recurrences Among Ipsilateral Breast Cancers. Journal of the National Cancer Institute, 2008, 100, 48-58.	6.3	61
20	Spatiotemporal control of interferon-induced JAK/STAT signalling and gene transcription by the retromer complex. Nature Communications, 2016, 7, 13476.	12.8	50
21	The ERM proteins interact with the HOPS complex to regulate the maturation of endosomes. Molecular Biology of the Cell, 2011, 22, 375-385.	2.1	49
22	Histo€genomic stratification reveals the frequent amplification/overexpression of <scp><i>CCNE</i></scp><i>1</i> and <scp><i>BRD</i></scp><i>4</i> genes in non€BRCAness high grade ovarian carcinoma. International Journal of Cancer, 2015, 137, 1890-1900.	5.1	48
23	Patient€derived xenografts recapitulate molecular features of human uveal melanomas. Molecular Oncology, 2013, 7, 625-636.	4.6	46
24	EMA - A R package for Easy Microarray data analysis. BMC Research Notes, 2010, 3, 277.	1.4	44
25	Extrachromosomal amplification mechanisms in a glioma with amplified sequences from multiple chromosome loci. Human Molecular Genetics, 2010, 19, 1276-1285.	2.9	41
26	Clinical and genetic landscape of treatment naive cervical cancer: Alterations in PIK3CA and in epigenetic modulators associated with sub-optimal outcome. EBioMedicine, 2019, 43, 253-260.	6.1	37
27	Preferential Occurrence of Chromosome Breakpoints within Early Replicating Regions in Neuroblastoma. Cell Cycle, 2005, 4, 1842-1846.	2.6	33
28	CAPweb: a bioinformatics CGH array Analysis Platform. Nucleic Acids Research, 2006, 34, W477-W481.	14.5	32
29	Independent transcriptional reprogramming and apoptosis induction by cisplatin. Cell Cycle, 2012, 11, 3472-3480.	2.6	32
30	Combinatorial code governing cellular responses to complex stimuli. Nature Communications, 2015, 6, 6847.	12.8	32
31	Spi-1/PU.1 Oncogene Accelerates DNA Replication Fork Elongation and Promotes Genetic Instability in the Absence of DNA Breakage. Cancer Research, 2010, 70, 6757-6766.	0.9	29
32	ITALICS: an algorithm for normalization and DNA copy number calling for Affymetrix SNP arrays. Bioinformatics, 2008, 24, 768-774.	4.1	27
33	Multiple-checkpoint inhibition of thymic stromal lymphopoietin€"induced TH2 response by TH17-related cytokines. Journal of Allergy and Clinical Immunology, 2012, 130, 233-240.e5.	2.9	27
34	Proteomic screening identifies a YAP-driven signaling network linked to tumor cell proliferation in human schwannomas. Neuro-Oncology, 2014, 16, 1196-1209.	1.2	27
35	A Quantitative Multivariate Model of Human Dendritic Cell-T Helper Cell Communication. Cell, 2019, 179, 432-447.e21.	28.9	23
36	Spi-1/PU.1 activates transcription through clustered DNA occupancy in erythroleukemia. Nucleic Acids Research, 2012, 40, 8927-8941.	14.5	20

#	ARTICLE	IF	CITATIONS
37	Telomere crisis in kidney epithelial cells promotes the acquisition of a microRNA signature retrieved in aggressive renal cell carcinomas. Carcinogenesis, 2013, 34, 1173-1180.	2.8	19
38	ART-DeCo: easy tool for detection and characterization of cross-contamination of DNA samples in diagnostic next-generation sequencing analysis. European Journal of Human Genetics, 2019, 27, 792-800.	2.8	18
39	From prospective biobanking to precision medicine: BIO-RAIDs â€" an EU study protocol in cervical cancer. BMC Cancer, 2015, 15, 842.	2.6	16
40	Precision medicine in cancer: challenges and recommendations from an EU-funded cervical cancer biobanking study. British Journal of Cancer, 2016, 115, 1575-1583.	6.4	13
41	ACTuDB, a new database for the integrated analysis of array-CGH and clinical data for tumors. Oncogene, 2007, 26, 6641-6652.	5.9	12
42	SMETHILLIUM: spatial normalization METHod for ILLumina InfinIUM HumanMethylation BeadChip. Bioinformatics, 2011, 27, 1693-1695.	4.1	10
43	Whole-genome profiling helps to classify phyllodes tumours of the breast. Journal of Clinical Pathology, 2016, 69, 1081-1087.	2.0	10
44	Assessment of the novel online delineation workshop dummy run approach using FALCON within a European multicentre trial in cervical cancer (RAIDs). Radiotherapy and Oncology, 2017, 124, 130-138.	0.6	7
45	A comparison of Sars-Cov-2 vaccine platforms: the CoviCompare project. Nature Medicine, 2022, 28, 882-884.	30.7	7
46	Using Transcriptional Signatures to Assess Immune Cell Function: From Basic Mechanisms to Immune-Related Disease. Journal of Molecular Biology, 2015, 427, 3356-3367.	4.2	6
47	QUARTIC: QUick pArallel algoRithms for high-Throughput sequencIng data proCessing. F1000Research, 2020, 9, 240.	1.6	6
48	biogitflow: development workflow protocols for bioinformatics pipelines with git and GitLab. F1000Research, 2020, 9, 632.	1.6	2
49	QUARTIC: QUick pArallel algoRithms for high-Throughput sequencIng data proCessing. F1000Research, 2020, 9, 240.	1.6	2
50	Stability-Based Comparison of Class Discovery Methods for DNA Copy Number Profiles. PLoS ONE, 2013, 8, e81458.	2.5	1
51	QUARTIC: QUick pArallel algoRithms for high-Throughput sequencIng data proCessing. F1000Research, 0, 9, 240.	1.6	1
52	P23: CAP: aÂWeb-based platform forÂCGH-array management andÂanalysis. European Journal of Medical Genetics, 2005, 48, 471-472.	1.3	0
53	Bioinformatics for Precision Medicine in Oncology. , 2015, , 69-99.		0
54	Geniac: Automatic Configuration GENerator and Installer for nextflow pipelines. Open Research Europe, 0, 1, 76.	2.0	0

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55	Analytical Platforms 1: Use of Cultured Cells and Fluorescent Read-Out Coupled to NormaCurve Normalization in RPPA. Advances in Experimental Medicine and Biology, 2019, 1188, 77-93.	1.6	0
56	biogitflow: development workflow protocols for bioinformatics pipelines with git and GitLab. F1000Research, 2020, 9, 632.	1.6	0
57	biogitflow: development workflow protocols for bioinformatics pipelines with git and GitLab. F1000Research, 0, 9, 632.	1.6	0
58	Geniac: Automatic Configuration GENerator and Installer for nextflow pipelines. Open Research Europe, 0, 1, 76.	2.0	0
59	INFLUENCE OF FLG LOSS-OF-FUNCTION MUTATIONS IN HOSTâ€"MICROBE INTERACTIONS DURING ATOPIC SKIN INFLAMMATION. Journal of Dermatological Science, 2022, , .	1.9	0