Vincent Rj Gardeux

List of Publications by Year
in descending order

34 papers	1,561 citations	516710 16 h-index	395702 33 g-index
46 all docs	46 docs citations	46 times ranked	2555 citing authors

#	Article	IF	Citations
1	The Genetics of Transcription Factor DNA Binding Variation. Cell, 2016, 166, 538-554.	28.9	331
2	Fly Cell Atlas: A single-nucleus transcriptomic atlas of the adult fruit fly. Science, 2022, 375, eabk2432.	12.6	295
3	BRB-seq: ultra-affordable high-throughput transcriptomics enabled by bulk RNA barcoding and sequencing. Genome Biology, 2019, 20, 71.	8.8	125
4	ASAP: a web-based platform for the analysis and interactive visualization of single-cell RNA-seq data. Bioinformatics, 2017, 33, 3123-3125.	4.1	112
5	Disparate temperature-dependent virus–host dynamics for SARS-CoV-2 and SARS-CoV in the human respiratory epithelium. PLoS Biology, 2021, 19, e3001158.	5.6	79
6	Dynamic regulation of chromatin accessibility by pluripotency transcription factors across the cell cycle. ELife, 2019, 8, .	6.0	61
7	The discriminatory cost of ICD-10-CM transition between clinical specialties: metrics, case study, and mitigating tools. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 708-717.	4.4	46
8	â€˜N-of-1-<i>pathways</i>â€™ unveils personal deregulated mechanisms from a single pair of RNA-Seq samples: towards precision medicine. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 1015-1025.	4.4	42
9	Deterministic scRNA-seq captures variation in intestinal crypt and organoid composition. Nature Methods, 2022, 19, 323-330.	19.0	33
10	Dynamic changes of RNA-sequencing expression for precision medicine: N-of-1-pathways Mahalanobis distance within pathways of single subjects predicts breast cancer survival. Bioinformatics, 2015, 31, i293-i302.	4.1	30
11	N-of-1-pathways MixEnrich: advancing precision medicine via single-subject analysis in discovering dynamic changes of transcriptomes. BMC Medical Genomics, 2017, 10, 27.	1.5	29
12	EM323: a line search based algorithm for solving high-dimensional continuous non-linear optimization problems. Soft Computing, 2011, 15, 2275-2285.	3.6	26
13	A genome-by-environment interaction classifier for precision medicine: personal transcriptome response to rhinovirus identifies children prone to asthma exacerbations. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 1116-1126.	4.4	23
14	Extensive tissue-specific expression variation and novel regulators underlying circadian behavior. Science Advances, 2021, 7, .	10.3	21
15	Dissecting the brown adipogenic regulatory network using integrative genomics. Scientific Reports, 2017, 7, 42130.	3.3	20
16	Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions. Npj Genomic Medicine, 2016, 1, .	3.8	19
17	Towards a PBMC â€œvirogram assayâ€•for precision medicine: Concordance between ex vivo and in vivo viral infection transcriptomes. Journal of Biomedical Informatics, 2015, 55, 94-103.	4.3	18
18	ASAP 2020 update: an open, scalable and interactive web-based portal for (single-cell) omics analyses. Nucleic Acids Research, 2020, 48, W403-W414.	14.5	17

#	Article	IF	Citations
19	Concordance of deregulated mechanisms unveiled in underpowered experiments: PTBP1 knockdown case study. BMC Medical Genomics, 2014, 7, S1.	1.5	16
20	Profiling of Single‐Cell Transcriptomes. Current Protocols in Mouse Biology, 2017, 7, 145-175.	1.2	16
21	kMEn: Analyzing noisy and bidirectional transcriptional pathway responses in single subjects. Journal of Biomedical Informatics, 2017, 66, 32-41.	4.3	15
22	cis-regulatory variation modulates susceptibility to enteric infection in the Drosophila genetic reference panel. Genome Biology, 2020, 21, 6.	8.8	14
23	Unidimensional Search for Solving Continuous High-Dimensional Optimization Problems. , 2009, , .		13
24	Are we able to predict survival in ER-positive HER2-negative breast cancer? A comparison of web-based models. British Journal of Cancer, 2015, 112, 912-917.	6.4	13
25	eQTL networks unveil enriched mRNA master integrators downstream of complex disease-associated SNPs. Journal of Biomedical Informatics, 2015, 58, 226-234.	4.3	10
26	Adaptive pattern search for large-scale optimization. Applied Intelligence, 2017, 47, 319-330.	5.3	10
27	A parallelized, automated platform enabling individual or sequential ChIP of histone marks and transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13828-13838.	7.1	8
28	ARTS: automated randomization of multiple traits for study design. Bioinformatics, 2014, 30, 1637-1639.	4.1	6
29	Computing Molecular Signatures as Optima of a Bi-Objective Function: Method and Application to Prediction in Oncogenomics. Cancer Informatics, 2015, 14, CIN.S21111.	1.9	6
30	From Swarm Art Toward Ecosystem Art. International Journal of Swarm Intelligence Research, 2012, 3, 1-18.	0.7	6
31	A leukemia-protective germline variant mediates chromatin module formation via transcription factor nucleation. Nature Communications, 2022, 13, 2042.	12.8	6
32	Sex‐dependent and sex‐independent regulatory systems of size variation in natural populations. Molecular Systems Biology, 2019, 15, e9012.	7.2	4
33	In Silicocancer cell versus stroma cellularity index computed from species-specific human and mouse transcriptome of xenograft models: towards accurate stroma targeting therapy assessment. BMC Medical Genomics, 2014, 7, S2.	1.5	1
34	COPD Hospitalization Risk Increased with Distinct Patterns of Multiple Systems Comorbidities Unveiled by Network Modeling. AMIA ... Annual Symposium proceedings, 2014, 2014, 855-64.	0.2	1