

# Vincent Rj Gardeux

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Deterministic scRNA-seq captures variation in intestinal crypt and organoid composition. <i>Nature Methods</i> , 2022, 19, 323-330.	19.0	33
2	Fly Cell Atlas: A single-nucleus transcriptomic atlas of the adult fruit fly. <i>Science</i> , 2022, 375, eabk2432.	12.6	295
3	A leukemia-protective germline variant mediates chromatin module formation via transcription factor nucleation. <i>Nature Communications</i> , 2022, 13, 2042.	12.8	6
4	Disparate temperature-dependent virus-host dynamics for SARS-CoV-2 and SARS-CoV in the human respiratory epithelium. <i>PLoS Biology</i> , 2021, 19, e3001158.	5.6	79
5	Extensive tissue-specific expression variation and novel regulators underlying circadian behavior. <i>Science Advances</i> , 2021, 7, .	10.3	21
6	ASAP 2020 update: an open, scalable and interactive web-based portal for (single-cell) omics analyses. <i>Nucleic Acids Research</i> , 2020, 48, W403-W414.	14.5	17
7	A parallelized, automated platform enabling individual or sequential ChIP of histone marks and transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13828-13838.	7.1	8
8	cis-regulatory variation modulates susceptibility to enteric infection in the <i>Drosophila</i> genetic reference panel. <i>Genome Biology</i> , 2020, 21, 6.	8.8	14
9	BRB-seq: ultra-affordable high-throughput transcriptomics enabled by bulk RNA barcoding and sequencing. <i>Genome Biology</i> , 2019, 20, 71.	8.8	125
10	Sex-dependent and sex-independent regulatory systems of size variation in natural populations. <i>Molecular Systems Biology</i> , 2019, 15, e9012.	7.2	4
11	Dynamic regulation of chromatin accessibility by pluripotency transcription factors across the cell cycle. <i>ELife</i> , 2019, 8, .	6.0	61
12	kMEN: Analyzing noisy and bidirectional transcriptional pathway responses in single subjects. <i>Journal of Biomedical Informatics</i> , 2017, 66, 32-41.	4.3	15
13	Adaptive pattern search for large-scale optimization. <i>Applied Intelligence</i> , 2017, 47, 319-330.	5.3	10
14	Dissecting the brown adipogenic regulatory network using integrative genomics. <i>Scientific Reports</i> , 2017, 7, 42130.	3.3	20
15	ASAP: a web-based platform for the analysis and interactive visualization of single-cell RNA-seq data. <i>Bioinformatics</i> , 2017, 33, 3123-3125.	4.1	112
16	A genome-by-environment interaction classifier for precision medicine: personal transcriptome response to rhinovirus identifies children prone to asthma exacerbations. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2017, 24, 1116-1126.	4.4	23
17	Profiling of Single-Cell Transcriptomes. <i>Current Protocols in Mouse Biology</i> , 2017, 7, 145-175.	1.2	16
18	N-of-1-pathways MixEnrich: advancing precision medicine via single-subject analysis in discovering dynamic changes of transcriptomes. <i>BMC Medical Genomics</i> , 2017, 10, 27.	1.5	29

#	ARTICLE	IF	CITATIONS
19	The Genetics of Transcription Factor DNA Binding Variation. <i>Cell</i> , 2016, 166, 538-554.	28.9	331
20	Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions. <i>Npj Genomic Medicine</i> , 2016, 1, .	3.8	19
21	eQTL networks unveil enriched mRNA master integrators downstream of complex disease-associated SNPs. <i>Journal of Biomedical Informatics</i> , 2015, 58, 226-234.	4.3	10
22	Computing Molecular Signatures as Optima of a Bi-Objective Function: Method and Application to Prediction in Oncogenomics. <i>Cancer Informatics</i> , 2015, 14, CIN.S21111.	1.9	6
23	Are we able to predict survival in ER-positive HER2-negative breast cancer? A comparison of web-based models. <i>British Journal of Cancer</i> , 2015, 112, 912-917.	6.4	13
24	Towards a PBMC "œvirogram assay" for precision medicine: Concordance between ex vivo and in vivo viral infection transcriptomes. <i>Journal of Biomedical Informatics</i> , 2015, 55, 94-103.	4.3	18
25	Dynamic changes of RNA-sequencing expression for precision medicine: N-of-1-pathways Mahalanobis distance within pathways of single subjects predicts breast cancer survival. <i>Bioinformatics</i> , 2015, 31, i293-i302.	4.1	30
26	"N-of-1- <i>i&gt;pathways&lt;/i&gt;"™ unveils personal deregulated mechanisms from a single pair of RNA-Seq samples: towards precision medicine. <i>Journal of the American Medical Informatics Association: JAMIA</i>, 2014, 21, 1015-1025.</i>	4.4	42
27	Concordance of deregulated mechanisms unveiled in underpowered experiments: PTBP1 knockdown case study. <i>BMC Medical Genomics</i> , 2014, 7, S1.	1.5	16
28	In Silico cancer cell versus stroma cellularity index computed from species-specific human and mouse transcriptome of xenograft models: towards accurate stroma targeting therapy assessment. <i>BMC Medical Genomics</i> , 2014, 7, S2.	1.5	1
29	ARTS: automated randomization of multiple traits for study design. <i>Bioinformatics</i> , 2014, 30, 1637-1639.	4.1	6
30	COPD Hospitalization Risk Increased with Distinct Patterns of Multiple Systems Comorbidities Unveiled by Network Modeling. <i>AMIA ... Annual Symposium proceedings</i> , 2014, 2014, 855-64.	0.2	1
31	The discriminatory cost of ICD-10-CM transition between clinical specialties: metrics, case study, and mitigating tools. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013, 20, 708-717.	4.4	46
32	From Swarm Art Toward Ecosystem Art. <i>International Journal of Swarm Intelligence Research</i> , 2012, 3, 1-18.	0.7	6
33	EM323: a line search based algorithm for solving high-dimensional continuous non-linear optimization problems. <i>Soft Computing</i> , 2011, 15, 2275-2285.	3.6	26
34	Unidimensional Search for Solving Continuous High-Dimensional Optimization Problems. , 2009, , .		13