Thierry Voet

List of Publications by Year in descending order

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Version: 2024-02-01

61	10,250	93792	124990
papers	citations	39 h-index	64 g-index

65	65	65	19320
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Single-cell genome-wide concurrent haplotyping and copy-number profiling through genotyping-by-sequencing. Nucleic Acids Research, 2022, 50, e63-e63.	6.5	17
2	Expansion microscopy allows high resolution single cell analysis of epigenetic readers. Nucleic Acids Research, 2022, 50, e100-e100.	6.5	4
3	Development, maturation, and maintenance of human prostate inferred from somatic mutations. Cell Stem Cell, 2021, 28, 1262-1274.e5.	5.2	29
4	Tissue damage induces a conserved stress response that initiates quiescent muscle stem cell activation. Cell Stem Cell, 2021, 28, 1125-1135.e7.	5.2	72
5	A Universal Labeling Strategy for Nucleic Acids in Expansion Microscopy. Journal of the American Chemical Society, 2021, 143, 13782-13789.	6.6	14
6	Evolutionary predictability of genetic versus nongenetic resistance to anticancer drugs in melanoma. Cancer Cell, 2021, 39, 1135-1149.e8.	7.7	83
7	Interstitial Cell Remodeling Promotes Aberrant Adipogenesis in Dystrophic Muscles. Cell Reports, 2020, 31, 107597.	2.9	64
8	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	13.7	108
9	Mechanisms of stretch-mediated skin expansion at single-cell resolution. Nature, 2020, 584, 268-273.	13.7	113
10	Heterotypic cellâ€“cell communication regulates glandular stem cell multipotency. Nature, 2020, 584, 608-613.	13.7	82
11	Identity-by-state-based haplotyping expands the application of comprehensive preimplantation genetic testing. Human Reproduction, 2020, 35, 718-726.	0.4	6
12	Noninvasive prenatal diagnosis by genome-wide haplotyping of cell-free plasma DNA. Genetics in Medicine, 2020, 22, 962-973.	1.1	29
13	Defining the Design Principles of Skin Epidermis Postnatal Growth. Cell, 2020, 181, 604-620.e22.	13.5	65
14	PREIMPLANTATION GENETIC TESTING: Single-cell technologies at the forefront of PGT and embryo research. Reproduction, 2020, 160, A19-A31.	1.1	10
15	Multi-centre evaluation of a comprehensive preimplantation genetic test through haplotyping-by-sequencing. Human Reproduction, 2019, 34, 1608-1619.	0.4	48
16	In vitro fertilization does not increase the incidence of de novo copy number alterations in fetal and placental lineages. Nature Medicine, 2019, 25, 1699-1705.	15.2	43
17	Activation of Skeletal Stem and Progenitor Cells for Bone Regeneration Is Driven by PDGFRÎ² Signaling. Developmental Cell, 2019, 51, 236-254.e12.	3.1	64
18	Zebrafish MITF-Low Melanoma Subtype Models Reveal Transcriptional Subclusters and MITF-Independent Residual Disease. Cancer Research, 2019, 79, 5769-5784.	0.4	36

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19	Identification of the tumour transition states occurring during EMT. Nature, 2018, 556, 463-468.	13.7	1,083
20	A TRP channel trio mediates acute noxious heat sensing. Nature, 2018, 555, 662-666.	13.7	329
21	Early lineage segregation of multipotent embryonic mammary gland progenitors. Nature Cell Biology, 2018, 20, 666-676.	4.6	124
22	Toward Minimal Residual Disease-Directed Therapy in Melanoma. Cell, 2018, 174, 843-855.e19.	13.5	514
23	Single-Cell (Multi)omics Technologies. Annual Review of Genomics and Human Genetics, 2018, 19, 15-41.	2.5	149
24	Single-cell sequencing reveals the origin and the order of mutation acquisition in T-cell acute lymphoblastic leukemia. Leukemia, 2018, 32, 1358-1369.	3.3	66
25	Single-Cell Multiomics: Multiple Measurements from Single Cells. Trends in Genetics, 2017, 33, 155-168.	2.9	392
26	Mutational Processes Shaping the Genome in Early Human Embryos. Cell, 2017, 168, 751-753.	13.5	9
27	Principles guiding embryo selection following genome-wide haplotyping of preimplantation embryos. Human Reproduction, 2017, 32, 687-697.	0.4	40
28	Small chromosomal regions position themselves autonomously according to their chromatin class. Genome Research, 2017, 27, 922-933.	2.4	39
29	Genome stability of bovine in vivo-conceived cleavage-stage embryos is higher compared to in vitro-produced embryos. Human Reproduction, 2017, 32, 2348-2357.	0.4	69
30	Accurate and comprehensive analysis of single nucleotide variants and large deletions of the human mitochondrial genome in DNA and single cells. European Journal of Human Genetics, 2017, 25, 1229-1236.	1.4	16
31	Single-Cell Landscape of Transcriptional Heterogeneity and Cell Fate Decisions during Mouse Early Gastrulation. Cell Reports, 2017, 20, 1215-1228.	2.9	290
32	Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. Genome Biology, 2016, 17, 250.	3.8	68
33	Zygotes segregate entire parental genomes in distinct blastomere lineages causing cleavage-stage chimerism and mixoploidy. Genome Research, 2016, 26, 567-578.	2.4	73
34	Separation and parallel sequencing of the genomes and transcriptomes of single cells using G&T-seq. Nature Protocols, 2016, 11, 2081-2103.	5.5	142
35	Prenatal and pre-implantation genetic diagnosis. Nature Reviews Genetics, 2016, 17, 643-656.	7.7	155
36	Mouse model of chromosome mosaicism reveals lineage-specific depletion of aneuploid cells and normal developmental potential. Nature Communications, 2016, 7, 11165.	5.8	339

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37	Heterogeneity in Oct4 and Sox2 Targets Biases Cell Fate in 4-Cell Mouse Embryos. Cell, 2016, 165, 61-74.	13.5	385
38	Single-Cell RNA-Sequencing Reveals a Continuous Spectrum of Differentiation in Hematopoietic Cells. Cell Reports, 2016, 14, 966-977.	2.9	164
39	Urine of Preterm Neonates as a Novel Source of Kidney Progenitor Cells. Journal of the American Society of Nephrology: JASN, 2016, 27, 2762-2770.	3.0	32
40	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. Nature Methods, 2016, 13, 229-232.	9.0	602
41	SNES makes sense? Single-cell exome sequencing evolves. Genome Biology, 2015, 16, 86.	3.8	3
42	Concurrent Whole-Genome Haplotyping and Copy-Number Profiling of Single Cells. American Journal of Human Genetics, 2015, 96, 894-912.	2.6	110
43	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. Cell Stem Cell, 2015, 16, 712-724.	5.2	376
44	G&T-seq: parallel sequencing of single-cell genomes and transcriptomes. Nature Methods, 2015, 12, 519-522.	9.0	633
45	On the identification of low allele frequency mosaic mutations in the brains of Alzheimer's disease patients. Alzheimer's and Dementia, 2015, 11, 1265-1276.	0.4	57
46	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. Nature Genetics, 2015, 47, 367-372.	9.4	380
47	Homozygous missense mutation in STYXL1 associated with moderate intellectual disability, epilepsy and behavioural complexities. European Journal of Medical Genetics, 2015, 58, 205-210.	0.7	11
48	Pseudoautosomal Region 1 Length Polymorphism in the Human Population. PLoS Genetics, 2014, 10, e1004578.	1.5	24
49	Single Cell Genomics: Advances and Future Perspectives. PLoS Genetics, 2014, 10, e1004126.	1.5	337
50	Single cell segmental aneuploidy detection is compromised by S phase. Molecular Cytogenetics, 2014, 7, 46.	0.4	23
51	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. Science, 2014, 346, 251-256.	6.0	962
52	Single cell analysis of cancer genomes. Current Opinion in Genetics and Development, 2014, 24, 82-91.	1.5	120
53	Single-cell paired-end genome sequencing reveals structural variation per cell cycle. Nucleic Acids Research, 2013, 41, 6119-6138.	6.5	142
54	Preimplantation genetic diagnosis guided by single-cell genomics. Genome Medicine, 2013, 5, 71.	3.6	45

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55	Nonallelic homologous recombination between retrotransposable elements is a driver of de novo unbalanced translocations. Genome Research, 2013, 23, 411-418.	2.4	90
56	Next-Generation Sequencing of Disseminated Tumor Cells. Frontiers in Oncology, 2013, 3, 320.	1.3	32
57	Breakage-fusion-bridge cycles leading to inv dup del occur in human cleavage stage embryos. Human Mutation, 2011, 32, 783-793.	1.1	60
58	What next for preimplantation genetic screening? High mitotic chromosome instability rate provides the biological basis for the low success rate. Human Reproduction, 2009, 24, 2679-2682.	0.4	87
59	Chromosome instability is common in human cleavage-stage embryos. Nature Medicine, 2009, 15, 577-583.	15.2	710
60	Controlled transgene dosage and PAC-mediated transgenesis in mice using a chromosomal vector. Genomics, 2003, 82, 596-605.	1.3	24
61	Telomere-independent homologue pairing and checkpoint escape of accessory ring chromosomes in male mouse meiosis. Journal of Cell Biology, 2003, 162, 795-808.	2.3	32