Bernard Thienpont

List of Publications by Year
in descending order

80 papers	9,608 citations	76294 40 h-index	58549 82 g-index
89 all docs	89 docs citations	89 times ranked	17508 citing authors

#	Article	IF	Citations
1	Phenotype molding of stromal cells in the lung tumor microenvironment. Nature Medicine, 2018, 24, 1277-1289.	15.2	1,126
2	The Dynamics of Genome-wide DNA Methylation Reprogramming in Mouse Primordial Germ Cells. Molecular Cell, 2012, 48, 849-862.	4.5	837
3	Single-Cell Transcriptome Atlas of Murine Endothelial Cells. Cell, 2020, 180, 764-779.e20.	13.5	755
4	A Single-Cell Transcriptome Atlas of the Aging Drosophila Brain. Cell, 2018, 174, 982-998.e20.	13.5	616
5	Tumour hypoxia causes DNA hypermethylation by reducing TET activity. Nature, 2016, 537, 63-68.	13.7	521
6	Inhibition of the Glycolytic Activator PFKFB3 in Endothelium Induces Tumor Vessel Normalization, Impairs Metastasis, and Improves Chemotherapy. Cancer Cell, 2016, 30, 968-985.	7.7	464
7	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling. Cell Research, 2020, 30, 745-762.	5.7	391
8	Distinct genetic architectures for syndromic and nonsyndromic congenital heart defects identified by exome sequencing. Nature Genetics, 2016, 48, 1060-1065.	9.4	351
9	Emerging patterns of cryptic chromosomal imbalance in patients with idiopathic mental retardation and multiple congenital anomalies: a new series of 140 patients and review of published reports. Journal of Medical Genetics, 2006, 43, 625-633.	1.5	342
10	An Integrated Gene Expression Landscape Profiling Approach to Identify Lung Tumor Endothelial Cell Heterogeneity and Angiogenic Candidates. Cancer Cell, 2020, 37, 21-36.e13.	7.7	253
11	The role of fatty acid Î²-oxidation in lymphangiogenesis. Nature, 2017, 542, 49-54.	13.7	240
12	Single-cell chromosomal imbalances detection by array CGH. Nucleic Acids Research, 2006, 34, e68-e68.	6.5	188
13	Submicroscopic chromosomal imbalances detected by array-CGH are a frequent cause of congenital heart defects in selected patients. European Heart Journal, 2007, 28, 2778-2784.	1.0	175
14	Quiescent Endothelial Cells Upregulate Fatty Acid Î²-Oxidation for Vasculoprotection via Redox Homeostasis. Cell Metabolism, 2018, 28, 881-894.e13.	7.2	174
15	Single-Cell RNA Sequencing Maps Endothelial Metabolic Plasticity in Pathological Angiogenesis. Cell Metabolism, 2020, 31, 862-877.e14.	7.2	169
16	Rare Variants in NR2F2 Cause Congenital Heart Defects in Humans. American Journal of Human Genetics, 2014, 94, 574-585.	2.6	146
17	HIF-1Î± Promotes Glutamine-Mediated Redox Homeostasis and Glycogen-Dependent Bioenergetics to Support Postimplantation Bone Cell Survival. Cell Metabolism, 2016, 23, 265-279.	7.2	142
18	Overcoming immunotherapy resistance in non-small cell lung cancer (NSCLC) - novel approaches and future outlook. Molecular Cancer, 2020, 19, 141.	7.9	141

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19	Lipid availability determines fate of skeletal progenitor cells via SOX9. Nature, 2020, 579, 111-117.	13.7	140
20	Genotype-phenotype correlation in 21 patients with Wolf-Hirschhorn syndrome using high resolution array comparative genome hybridisation (CGH). Journal of Medical Genetics, 2007, 45, 71-80.	1.5	111
21	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
22	The H3K9 dimethyltransferases EHMT1/2 protect against pathological cardiac hypertrophy. Journal of Clinical Investigation, 2016, 127, 335-348.	3.9	99
23	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	2.6	98
24	Haploinsufficiency of TAB2 Causes Congenital Heart Defects in Humans. American Journal of Human Genetics, 2010, 86, 839-849.	2.6	97
25	Lineage-specific functions of TET1 in the postimplantation mouse embryo. Nature Genetics, 2017, 49, 1061-1072.	9.4	96
26	Osteocytic oxygen sensing controls bone mass through epigenetic regulation of sclerostin. Nature Communications, 2018, 9, 2557.	5.8	92
27	IGF1R is an entry receptor for respiratory syncytial virus. Nature, 2020, 583, 615-619.	13.7	84
28	Array Comparative Genomic Hybridization as a Diagnostic Tool for Syndromic Heart Defects. Journal of Pediatrics, 2010, 156, 810-817.e4.	0.9	76
29	Subtelomeric imbalances in phenotypically normal individuals. Human Mutation, 2007, 28, 958-967.	1.1	72
30	Mismatch repair deficiency endows tumors with a unique mutation signature and sensitivity to DNA double-strand breaks. ELife, 2014, 3, e02725.	2.8	71
31	The Cancer Cell Oxygen Sensor PHD2 Promotes Metastasis via Activation of Cancer-Associated Fibroblasts. Cell Reports, 2015, 12, 992-1005.	2.9	66
32	Gene correlation network analysis to identify regulatory factors in idiopathic pulmonary fibrosis. Thorax, 2019, 74, 132-140.	2.7	66
33	Neurogenic Radial Glia-like Cells in Meninges Migrate and Differentiate into Functionally Integrated Neurons in the Neonatal Cortex. Cell Stem Cell, 2017, 20, 360-373.e7.	5.2	64
34	DNA methylation-driven EMT is a common mechanism of resistance to various therapeutic agents in cancer. Clinical Epigenetics, 2020, 12, 27.	1.8	64
35	Network Analysis of Differential Expression for the Identification of Disease-Causing Genes. PLoS ONE, 2009, 4, e5526.	1.1	61
36	Challenges of Interpreting Copy Number Variation in Syndromic and Non-Syndromic Congenital Heart Defects. Cytogenetic and Genome Research, 2011, 135, 251-259.	0.6	60

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37	Deletions in theVPS13B(COH1) gene as a cause of Cohen syndrome. Human Mutation, 2009, 30, E845-E854.	1.1	57
38	Glutamine Metabolism Controls Chondrocyte Identity and Function. Developmental Cell, 2020, 53, 530-544.e8.	3.1	54
39	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	2.3	51
40	A novel genomic disorder: a deletion of the SACS gene leading to Spastic Ataxia of Charlevoixâ€“Saguenay. European Journal of Human Genetics, 2008, 16, 1050-1054.	1.4	48
41	Duplications of the critical Rubinstein-Taybi deletion region on chromosome 16p13.3 cause a novel recognisable syndrome. Journal of Medical Genetics, 2010, 47, 155-161.	1.5	47
42	A new protocol for single-cell RNA-seq reveals stochastic gene expression during lag phase in budding yeast. ELife, 2020, 9, .	2.8	43
43	DNA methylation repels binding of hypoxia-inducible transcription factors to maintain tumor immunotolerance. Genome Biology, 2020, 21, 182.	3.8	39
44	Congenital heart defects in a novel recurrent 22q11.2 deletion harboring the genes CRKL and MAPK1. American Journal of Medical Genetics, Part A, 2012, 158A, 574-580.	0.7	38
45	DNA methylation profiling of non-small cell lung cancer reveals a COPD-driven immune-related signature. Thorax, 2015, 70, 1113-1122.	2.7	37
46	Epigenetics in the heart: the role of histone modifications in cardiac remodelling. Biochemical Society Transactions, 2013, 41, 789-796.	1.6	34
47	Evaluation of efficacy and safety markers in a phase II study of metastatic colorectal cancer treated with aflibercept in the first-line setting. British Journal of Cancer, 2015, 113, 1027-1034.	2.9	34
48	Genomic and epigenomic analysis of high-risk prostate cancer reveals changes in hydroxymethylation and TET1. Oncotarget, 2016, 7, 24326-24338.	0.8	33
49	Partial duplications of the ATRX gene cause the ATR-X syndrome. European Journal of Human Genetics, 2007, 15, 1094-1097.	1.4	31
50	ModuleMiner - improved computational detection of cis-regulatory modules: are there different modes of gene regulation in embryonic development and adult tissues?. Genome Biology, 2008, 9, R66.	13.9	31
51	Left-ventricular non-compaction in a patient with monosomy 1p36. European Journal of Medical Genetics, 2007, 50, 233-236.	0.7	30
52	Molecular karyotyping of patients with MCA/MR: the blurred boundary between normal and pathogenic variation. Cytogenetic and Genome Research, 2006, 115, 225-230.	0.6	29
53	Mapping biomedical concepts onto the human genome by mining literature on chromosomal aberrations. Nucleic Acids Research, 2007, 35, 2533-2543.	6.5	27
54	Ischemia-Induced DNA Hypermethylation during Kidney Transplant Predicts Chronic Allograft Injury. Journal of the American Society of Nephrology: JASN, 2018, 29, 1566-1576.	3.0	27

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55	Comparative oncogenomics identifies tyrosine kinase FES as a tumor suppressor in melanoma. Journal of Clinical Investigation, 2017, 127, 2310-2325.	3.9	26
56	Collaboratively charting the gene-to-phenotype network of human congenital heart defects. Genome Medicine, 2010, 2, 16.	3.6	25
57	Position effect leading to haploinsufficiency in a mosaic ring chromosome 14 in a boy with autism. European Journal of Human Genetics, 2008, 16, 1187-1192.	1.4	24
58	BMPR1A is a candidate gene for congenital heart defects associated with the recurrent 10q22q23 deletion syndrome. European Journal of Medical Genetics, 2012, 55, 12-16.	0.7	24
59	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	1.1	24
60	High Frequency Of Submicroscopic Chromosomal Deletions in Patients with Idiopathic Congenital Eye Malformations. American Journal of Ophthalmology, 2011, 151, 1087-1094.e45.	1.7	23
61	A microduplication of CBP in a patient with mental retardation and a congenital heart defect. American Journal of Medical Genetics, Part A, 2007, 143A, 2160-2164.	0.7	20
62	Age-related changes in DNA methylation affect renal histology and post-transplant fibrosis. Kidney International, 2019, 96, 1195-1204.	2.6	17
63	Integrative analysis of genomic variants reveals new associations of candidate haploinsufficient genes with congenital heart disease. PLoS Genetics, 2021, 17, e1009679.	1.5	17
64	Sesn1 is a novel gene for leftâ€“right asymmetry and mediating nodal signaling. Human Molecular Genetics, 2006, 15, 3369-3377.	1.4	16
65	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
66	Systems genetics analysis identifies calcium-signaling defects as novel cause of congenital heart disease. Genome Medicine, 2020, 12, 76.	3.6	15
67	Anterior cervical hypertrichosis and mental retardation. Clinical Dysmorphology, 2006, 15, 189-190.	0.1	11
68	Genetic biomarkers in the VEGF pathway predicting response to anti-VEGF therapy in age-related macular degeneration. BMJ Open Ophthalmology, 2019, 4, e000273.	0.8	10
69	Molecular cytogenetic characterization of a constitutional complex intrachromosomal 4q rearrangement in a patient with multiple congenital anomalies. Cytogenetic and Genome Research, 2006, 114, 338-341.	0.6	9
70	TET enzymes as oxygen-dependent tumor suppressors: exciting new avenues for cancer management. Epigenomics, 2016, 8, 1445-1448.	1.0	9
71	Regulatory Dynamics of Tet1 and Oct4 Resolve Stages of Global DNA Demethylation and Transcriptomic Changes in Reprogramming. Cell Reports, 2020, 30, 2150-2169.e9.	2.9	9
72	Tumors smother their epigenome. Molecular and Cellular Oncology, 2016, 3, e1240549.	0.3	8

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73	A complex submicroscopic chromosomal imbalance in 19p13.11 with one microduplication and two microtriplications. European Journal of Medical Genetics, 2008, 51, 219-225.	0.7	7
74	Refining the locus of branchio-otic syndrome 2 (BOS2) to a 5.25ÂMb locus on chromosome 1q31.3q32.1. European Journal of Medical Genetics, 2009, 52, 393-397.	0.7	7
75	Congenital anterolateral bowing of the tibia with ipsilateral polydactyly of the great toe associated with cerebral cyst: a new entity?. Clinical Dysmorphology, 2009, 18, 195-200.	0.1	7
76	Itâ€™s T Time for Normal Blood Vessels. Developmental Cell, 2017, 41, 125-126.	3.1	6
77	25ÂMb deletion of 13q13.3â†'q21.31 in a patient without retinoblastoma. European Journal of Medical Genetics, 2005, 48, 363-366.	0.7	5
78	A second patient with Tsukahara syndrome: Type A1 brachydactyly, short stature, hearing loss, microcephaly, mental retardation and ptosis. American Journal of Medical Genetics, Part A, 2010, 152A, 947-949.	0.7	4
79	Novel next-generation sequencing-based methodologies to characterize the mutational consequences of (prenatal) chemotherapy exposure in noncancerous tissue. Current Opinion in Oncology, 2021, 33, 476-484.	1.1	3
80	Temporal Dynamics of Tet1 and Oct4 Gene Activation Resolve Distinct Stages of Global DNA Demethylation and Transcriptomic Changes in the Final Phases of Induced Pluripotency. SSRN Electronic Journal, 0, , .	0.4	0