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	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
2	Integrative analysis of genomic variants reveals new associations of candidate haploinsufficient genes with congenital heart disease. PLoS Genetics, 2021, 17, e1009679.	1.5	17
3	DNA methylation repels binding of hypoxia-inducible transcription factors to maintain tumor immunotolerance. Genome Biology, 2020, 21, 182.	3.8	39
4	Systems genetics analysis identifies calcium-signaling defects as novel cause of congenital heart disease. Genome Medicine, 2020, 12, 76.	3.6	15
5	Overcoming immunotherapy resistance in non-small cell lung cancer (NSCLC) - novel approaches and future outlook. Molecular Cancer, 2020, 19, 141.	7.9	141
6	IGF1R is an entry receptor for respiratory syncytial virus. Nature, 2020, 583, 615-619.	13.7	84
7	Glutamine Metabolism Controls Chondrocyte Identity and Function. Developmental Cell, 2020, 53, 530-544.e8.	3.1	54
8	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling. Cell Research, 2020, 30, 745-762.	5.7	391
9	Lipid availability determines fate of skeletal progenitor cells via SOX9. Nature, 2020, 579, 111-117.	13.7	140
10	DNA methylation-driven EMT is a common mechanism of resistance to various therapeutic agents in cancer. Clinical Epigenetics, 2020, 12, 27.	1.8	64
11	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
12	Single-Cell Transcriptome Atlas of Murine Endothelial Cells. Cell, 2020, 180, 764-779.e20.	13.5	755
13	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
14	Single-Cell RNA Sequencing Maps Endothelial Metabolic Plasticity in Pathological Angiogenesis. Cell Metabolism, 2020, 31, 862-877.e14.	7.2	169
15	A new protocol for single-cell RNA-seq reveals stochastic gene expression during lag phase in budding yeast. ELife, 2020, 9, .	2.8	43
16	Age-related changes in DNA methylation affect renal histology and post-transplant fibrosis. Kidney International, 2019, 96, 1195-1204.	2.6	17
17	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
18	Gene correlation network analysis to identify regulatory factors in idiopathic pulmonary fibrosis. Thorax, 2019, 74, 132-140.	2.7	66

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19	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
20	Osteocytic oxygen sensing controls bone mass through epigenetic regulation of sclerostin. Nature Communications, 2018, 9, 2557.	5.8	92
21	Phenotype molding of stromal cells in the lung tumor microenvironment. Nature Medicine, 2018, 24, 1277-1289.	15.2	1,126
22	Quiescent Endothelial Cells Upregulate Fatty Acid Î²-Oxidation for Vasculoprotection via Redox Homeostasis. Cell Metabolism, 2018, 28, 881-894.e13.	7.2	174
23	A Single-Cell Transcriptome Atlas of the Aging Drosophila Brain. Cell, 2018, 174, 982-998.e20.	13.5	616
24	Itâ€™s T Time for Normal Blood Vessels. Developmental Cell, 2017, 41, 125-126.	3.1	6
25	Lineage-specific functions of TET1 in the postimplantation mouse embryo. Nature Genetics, 2017, 49, 1061-1072.	9.4	96
26	The role of fatty acid Î²-oxidation in lymphangiogenesis. Nature, 2017, 542, 49-54.	13.7	240
27	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
28	Comparative oncogenomics identifies tyrosine kinase FES as a tumor suppressor in melanoma. Journal of Clinical Investigation, 2017, 127, 2310-2325.	3.9	26
29	Genomic and epigenomic analysis of high-risk prostate cancer reveals changes in hydroxymethylation and TET1. Oncotarget, 2016, 7, 24326-24338.	0.8	33
30	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
31	TET enzymes as oxygen-dependent tumor suppressors: exciting new avenues for cancer management. Epigenomics, 2016, 8, 1445-1448.	1.0	9
32	Distinct genetic architectures for syndromic and nonsyndromic congenital heart defects identified by exome sequencing. Nature Genetics, 2016, 48, 1060-1065.	9.4	351
33	Tumour hypoxia causes DNA hypermethylation by reducing TET activity. Nature, 2016, 537, 63-68.	13.7	521
34	Tumors smother their epigenome. Molecular and Cellular Oncology, 2016, 3, e1240549.	0.3	8
35	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
36	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

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37	The H3K9 dimethyltransferases EHMT1/2 protect against pathological cardiac hypertrophy. Journal of Clinical Investigation, 2016, 127, 335-348.	3.9	99
38	The Cancer Cell Oxygen Sensor PHD2 Promotes Metastasis via Activation of Cancer-Associated Fibroblasts. Cell Reports, 2015, 12, 992-1005.	2.9	66
39	DNA methylation profiling of non-small cell lung cancer reveals a COPD-driven immune-related signature. Thorax, 2015, 70, 1113-1122.	2.7	37
40	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
41	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
42	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
43	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
44	Rare Variants in NR2F2 Cause Congenital Heart Defects in Humans. American Journal of Human Genetics, 2014, 94, 574-585.	2.6	146
45	Mismatch repair deficiency endows tumors with a unique mutation signature and sensitivity to DNA double-strand breaks. ELife, 2014, 3, e02725.	2.8	71
46	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
47	Epigenetics in the heart: the role of histone modifications in cardiac remodelling. Biochemical Society Transactions, 2013, 41, 789-796.	1.6	34
48	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
49	The Dynamics of Genome-wide DNA Methylation Reprogramming in Mouse Primordial Germ Cells. Molecular Cell, 2012, 48, 849-862.	4.5	837
50	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
51	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
52	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
53	Haploinsufficiency of TAB2 Causes Congenital Heart Defects in Humans. American Journal of Human Genetics, 2010, 86, 839-849.	2.6	97
54	Array Comparative Genomic Hybridization as a Diagnostic Tool for Syndromic Heart Defects. Journal of Pediatrics, 2010, 156, 810-817.e4.	0.9	76

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55	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
56	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
57	Collaboratively charting the gene-to-phenotype network of human congenital heart defects. Genome Medicine, 2010, 2, 16.	3.6	25
58	Deletions in theVPS13B(COH1) gene as a cause of Cohen syndrome. Human Mutation, 2009, 30, E845-E854.	1.1	57
59	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
60	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
61	Network Analysis of Differential Expression for the Identification of Disease-Causing Genes. PLoS ONE, 2009, 4, e5526.	1.1	61
62	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
63	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
64	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
65	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
66	Mapping biomedical concepts onto the human genome by mining literature on chromosomal aberrations. Nucleic Acids Research, 2007, 35, 2533-2543.	6.5	27
67	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
68	Left-ventricular non-compaction in a patient with monosomy 1p36. European Journal of Medical Genetics, 2007, 50, 233-236.	0.7	30
69	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
70	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
71	Subtelomeric imbalances in phenotypically normal individuals. Human Mutation, 2007, 28, 958-967.	1.1	72
72	Partial duplications of the ATRX gene cause the ATR-X syndrome. European Journal of Human Genetics, 2007, 15, 1094-1097.	1.4	31

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73	Anterior cervical hypertrichosis and mental retardation. Clinical Dysmorphology, 2006, 15, 189-190.	0.1	11
74	Single-cell chromosomal imbalances detection by array CGH. Nucleic Acids Research, 2006, 34, e68-e68.	6.5	188
75	Sesn1 is a novel gene for leftâ€“right asymmetry and mediating nodal signaling. Human Molecular Genetics, 2006, 15, 3369-3377.	1.4	16
76	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
77	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
78	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
79	25ÂMb deletion of 13q13.3â†'q21.31 in a patient without retinoblastoma. European Journal of Medical Genetics, 2005, 48, 363-366.	0.7	5
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