

Bernard Thienpont

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

9,608
citations

76326

40
h-index

58581

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. <i>Current Opinion in Oncology</i> , 2021, 33, 476-484.	2.4	3
2	Integrative analysis of genomic variants reveals new associations of candidate haploinsufficient genes with congenital heart disease. <i>PLoS Genetics</i> , 2021, 17, e1009679.	3.5	17
3	DNA methylation repels binding of hypoxia-inducible transcription factors to maintain tumor immunotolerance. <i>Genome Biology</i> , 2020, 21, 182.	8.8	39
4	Systems genetics analysis identifies calcium-signaling defects as novel cause of congenital heart disease. <i>Genome Medicine</i> , 2020, 12, 76.	8.2	15
5	Overcoming immunotherapy resistance in non-small cell lung cancer (NSCLC) - novel approaches and future outlook. <i>Molecular Cancer</i> , 2020, 19, 141.	19.2	141
6	IGF1R is an entry receptor for respiratory syncytial virus. <i>Nature</i> , 2020, 583, 615-619.	27.8	84
7	Glutamine Metabolism Controls Chondrocyte Identity and Function. <i>Developmental Cell</i> , 2020, 53, 530-544.e8.	7.0	54
8	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling. <i>Cell Research</i> , 2020, 30, 745-762.	12.0	391
9	Lipid availability determines fate of skeletal progenitor cells via SOX9. <i>Nature</i> , 2020, 579, 111-117.	27.8	140
10	DNA methylation-driven EMT is a common mechanism of resistance to various therapeutic agents in cancer. <i>Clinical Epigenetics</i> , 2020, 12, 27.	4.1	64
11	Regulatory Dynamics of Tet1 and Oct4 Resolve Stages of Global DNA Demethylation and Transcriptomic Changes in Reprogramming. <i>Cell Reports</i> , 2020, 30, 2150-2169.e9.	6.4	9
12	Single-Cell Transcriptome Atlas of Murine Endothelial Cells. <i>Cell</i> , 2020, 180, 764-779.e20.	28.9	755
13	An Integrated Gene Expression Landscape Profiling Approach to Identify Lung Tumor Endothelial Cell Heterogeneity and Angiogenic Candidates. <i>Cancer Cell</i> , 2020, 37, 21-36.e13.	16.8	253
14	Single-Cell RNA Sequencing Maps Endothelial Metabolic Plasticity in Pathological Angiogenesis. <i>Cell Metabolism</i> , 2020, 31, 862-877.e14.	16.2	169
15	A new protocol for single-cell RNA-seq reveals stochastic gene expression during lag phase in budding yeast. <i>ELife</i> , 2020, 9, .	6.0	43
16	Age-related changes in DNA methylation affect renal histology and post-transplant fibrosis. <i>Kidney International</i> , 2019, 96, 1195-1204.	5.2	17
17	Genetic biomarkers in the VEGF pathway predicting response to anti-VEGF therapy in age-related macular degeneration. <i>BMJ Open Ophthalmology</i> , 2019, 4, e000273.	1.6	10
18	Gene correlation network analysis to identify regulatory factors in idiopathic pulmonary fibrosis. <i>Thorax</i> , 2019, 74, 132-140.	5.6	66

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19	Ischemia-Induced DNA Hypermethylation during Kidney Transplant Predicts Chronic Allograft Injury. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 1566-1576.	6.1	27
20	Osteocytic oxygen sensing controls bone mass through epigenetic regulation of sclerostin. <i>Nature Communications</i> , 2018, 9, 2557.	12.8	92
21	Phenotype molding of stromal cells in the lung tumor microenvironment. <i>Nature Medicine</i> , 2018, 24, 1277-1289.	30.7	1,126
22	Quiescent Endothelial Cells Upregulate Fatty Acid β -Oxidation for Vasculoprotection via Redox Homeostasis. <i>Cell Metabolism</i> , 2018, 28, 881-894.e13.	16.2	174
23	A Single-Cell Transcriptome Atlas of the Aging <i>Drosophila</i> Brain. <i>Cell</i> , 2018, 174, 982-998.e20.	28.9	616
24	It's Time for Normal Blood Vessels. <i>Developmental Cell</i> , 2017, 41, 125-126.	7.0	6
25	Lineage-specific functions of TET1 in the postimplantation mouse embryo. <i>Nature Genetics</i> , 2017, 49, 1061-1072.	21.4	96
26	The role of fatty acid β -oxidation in lymphangiogenesis. <i>Nature</i> , 2017, 542, 49-54.	27.8	240
27	Neurogenic Radial Glia-like Cells in Meninges Migrate and Differentiate into Functionally Integrated Neurons in the Neonatal Cortex. <i>Cell Stem Cell</i> , 2017, 20, 360-373.e7.	11.1	64
28	Comparative oncogenomics identifies tyrosine kinase FES as a tumor suppressor in melanoma. <i>Journal of Clinical Investigation</i> , 2017, 127, 2310-2325.	8.2	26
29	Genomic and epigenomic analysis of high-risk prostate cancer reveals changes in hydroxymethylation and TET1. <i>Oncotarget</i> , 2016, 7, 24326-24338.	1.8	33
30	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	5.1	51
31	TET enzymes as oxygen-dependent tumor suppressors: exciting new avenues for cancer management. <i>Epigenomics</i> , 2016, 8, 1445-1448.	2.1	9
32	Distinct genetic architectures for syndromic and nonsyndromic congenital heart defects identified by exome sequencing. <i>Nature Genetics</i> , 2016, 48, 1060-1065.	21.4	351
33	Tumour hypoxia causes DNA hypermethylation by reducing TET activity. <i>Nature</i> , 2016, 537, 63-68.	27.8	521
34	Tumors smother their epigenome. <i>Molecular and Cellular Oncology</i> , 2016, 3, e1240549.	0.7	8
35	Inhibition of the Glycolytic Activator PFKFB3 in Endothelium Induces Tumor Vessel Normalization, Impairs Metastasis, and Improves Chemotherapy. <i>Cancer Cell</i> , 2016, 30, 968-985.	16.8	464
36	HIF-1 β Promotes Glutamine-Mediated Redox Homeostasis and Glycogen-Dependent Bioenergetics to Support Postimplantation Bone Cell Survival. <i>Cell Metabolism</i> , 2016, 23, 265-279.	16.2	142

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37	The H3K9 dimethyltransferases EHMT1/2 protect against pathological cardiac hypertrophy. <i>Journal of Clinical Investigation</i> , 2016, 127, 335-348.	8.2	99
38	The Cancer Cell Oxygen Sensor PHD2 Promotes Metastasis via Activation of Cancer-Associated Fibroblasts. <i>Cell Reports</i> , 2015, 12, 992-1005.	6.4	66
39	DNA methylation profiling of non-small cell lung cancer reveals a COPD-driven immune-related signature. <i>Thorax</i> , 2015, 70, 1113-1122.	5.6	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. <i>British Journal of Cancer</i> , 2015, 113, 1027-1034.	6.4	34
41	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1680-1691.	2.5	24
42	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014, 5, 4051.	12.8	16
43	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105
44	Rare Variants in NR2F2 Cause Congenital Heart Defects in Humans. <i>American Journal of Human Genetics</i> , 2014, 94, 574-585.	6.2	146
45	Mismatch repair deficiency endows tumors with a unique mutation signature and sensitivity to DNA double-strand breaks. <i>ELife</i> , 2014, 3, e02725.	6.0	71
46	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	6.2	98
47	Epigenetics in the heart: the role of histone modifications in cardiac remodelling. <i>Biochemical Society Transactions</i> , 2013, 41, 789-796.	3.4	34
48	BMPR1A is a candidate gene for congenital heart defects associated with the recurrent 10q22q23 deletion syndrome. <i>European Journal of Medical Genetics</i> , 2012, 55, 12-16.	1.3	24
49	The Dynamics of Genome-wide DNA Methylation Reprogramming in Mouse Primordial Germ Cells. <i>Molecular Cell</i> , 2012, 48, 849-862.	9.7	837
50	Congenital heart defects in a novel recurrent 22q11.2 deletion harboring the genes <i>CRKL</i> and <i>MAPK1</i> . <i>American Journal of Medical Genetics, Part A</i> , 2012, 158A, 574-580.	1.2	38
51	High Frequency Of Submicroscopic Chromosomal Deletions in Patients with Idiopathic Congenital Eye Malformations. <i>American Journal of Ophthalmology</i> , 2011, 151, 1087-1094.e45.	3.3	23
52	Challenges of Interpreting Copy Number Variation in Syndromic and Non-Syndromic Congenital Heart Defects. <i>Cytogenetic and Genome Research</i> , 2011, 135, 251-259.	1.1	60
53	Haploinsufficiency of TAB2 Causes Congenital Heart Defects in Humans. <i>American Journal of Human Genetics</i> , 2010, 86, 839-849.	6.2	97
54	Array Comparative Genomic Hybridization as a Diagnostic Tool for Syndromic Heart Defects. <i>Journal of Pediatrics</i> , 2010, 156, 810-817.e4.	1.8	76

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55	A second patient with Tsukahara syndrome: Type A1 brachydactyly, short stature, hearing loss, microcephaly, mental retardation and ptosis. <i>American Journal of Medical Genetics, Part A</i> , 2010, 152A, 947-949.	1.2	4
56	Duplications of the critical Rubinstein-Taybi deletion region on chromosome 16p13.3 cause a novel recognisable syndrome. <i>Journal of Medical Genetics</i> , 2010, 47, 155-161.	3.2	47
57	Collaboratively charting the gene-to-phenotype network of human congenital heart defects. <i>Genome Medicine</i> , 2010, 2, 16.	8.2	25
58	Deletions in the <i>VPS13B</i> (<i>COH1</i>) gene as a cause of Cohen syndrome. <i>Human Mutation</i> , 2009, 30, E845-E854.	2.5	57
59	Refining the locus of branchio-otic syndrome 2 (BOS2) to a 5.25 Mb locus on chromosome 1q31.3q32.1. <i>European Journal of Medical Genetics</i> , 2009, 52, 393-397.	1.3	7
60	Congenital anterolateral bowing of the tibia with ipsilateral polydactyly of the great toe associated with cerebral cyst: a new entity?. <i>Clinical Dysmorphology</i> , 2009, 18, 195-200.	0.3	7
61	Network Analysis of Differential Expression for the Identification of Disease-Causing Genes. <i>PLoS ONE</i> , 2009, 4, e5526.	2.5	61
62	A novel genomic disorder: a deletion of the SACS gene leading to Spastic Ataxia of Charlevoix-Saguenay. <i>European Journal of Human Genetics</i> , 2008, 16, 1050-1054.	2.8	48
63	Position effect leading to haploinsufficiency in a mosaic ring chromosome 14 in a boy with autism. <i>European Journal of Human Genetics</i> , 2008, 16, 1187-1192.	2.8	24
64	ModuleMiner - improved computational detection of cis-regulatory modules: are there different modes of gene regulation in embryonic development and adult tissues?. <i>Genome Biology</i> , 2008, 9, R66.	9.6	31
65	A complex submicroscopic chromosomal imbalance in 19p13.11 with one microduplication and two microtriplications. <i>European Journal of Medical Genetics</i> , 2008, 51, 219-225.	1.3	7
66	Mapping biomedical concepts onto the human genome by mining literature on chromosomal aberrations. <i>Nucleic Acids Research</i> , 2007, 35, 2533-2543.	14.5	27
67	Genotype-phenotype correlation in 21 patients with Wolf-Hirschhorn syndrome using high resolution array comparative genome hybridisation (CGH). <i>Journal of Medical Genetics</i> , 2007, 45, 71-80.	3.2	111
68	Left-ventricular non-compaction in a patient with monosomy 1p36. <i>European Journal of Medical Genetics</i> , 2007, 50, 233-236.	1.3	30
69	Submicroscopic chromosomal imbalances detected by array-CGH are a frequent cause of congenital heart defects in selected patients. <i>European Heart Journal</i> , 2007, 28, 2778-2784.	2.2	175
70	A microduplication of <i>CBP</i> in a patient with mental retardation and a congenital heart defect. <i>American Journal of Medical Genetics, Part A</i> , 2007, 143A, 2160-2164.	1.2	20
71	Subtelomeric imbalances in phenotypically normal individuals. <i>Human Mutation</i> , 2007, 28, 958-967.	2.5	72
72	Partial duplications of the ATRX gene cause the ATR-X syndrome. <i>European Journal of Human Genetics</i> , 2007, 15, 1094-1097.	2.8	31

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73	Anterior cervical hypertrichosis and mental retardation. <i>Clinical Dysmorphology</i> , 2006, 15, 189-190.	0.3	11
74	Single-cell chromosomal imbalances detection by array CGH. <i>Nucleic Acids Research</i> , 2006, 34, e68-e68.	14.5	188
75	Sesn1 is a novel gene for left-right asymmetry and mediating nodal signaling. <i>Human Molecular Genetics</i> , 2006, 15, 3369-3377.	2.9	16
76	Molecular cytogenetic characterization of a constitutional complex intrachromosomal 4q rearrangement in a patient with multiple congenital anomalies. <i>Cytogenetic and Genome Research</i> , 2006, 114, 338-341.	1.1	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. <i>Journal of Medical Genetics</i> , 2006, 43, 625-633.	3.2	342
78	Molecular karyotyping of patients with MCA/MR: the blurred boundary between normal and pathogenic variation. <i>Cytogenetic and Genome Research</i> , 2006, 115, 225-230.	1.1	29
79	25ÂMb deletion of 13q13.3â†’q21.31 in a patient without retinoblastoma. <i>European Journal of Medical Genetics</i> , 2005, 48, 363-366.	1.3	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. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0