Jean-Baptiste Cazier

List of Publications by Year
in descending order

101 papers	14,083 citations	66343 42 h-index	34986 98 g-index
104 all docs	104 docs citations	104 times ranked	27315 citing authors

#	Article	IF	Citations
1	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
2	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
3	COVID-19 mortality in patients with cancer on chemotherapy or other anticancer treatments: a prospective cohort study. Lancet, The, 2020, 395, 1919-1926.	13.7	908
4	Germline mutations affecting the proofreading domains of POLE and POLD1 predispose to colorectal adenomas and carcinomas. Nature Genetics, 2013, 45, 136-144.	21.4	851
5	A genome-wide association scan of tag SNPs identifies a susceptibility variant for colorectal cancer at 8q24.21. Nature Genetics, 2007, 39, 984-988.	21.4	754
6	A common inversion under selection in Europeans. Nature Genetics, 2005, 37, 129-137.	21.4	747
7	A common variant associated with prostate cancer in European and African populations. Nature Genetics, 2006, 38, 652-658.	21.4	738
8	A genome-wide association study identifies colorectal cancer susceptibility loci on chromosomes 10p14 and 8q23.3. Nature Genetics, 2008, 40, 623-630.	21.4	514
9	Meta-analysis of genome-wide association data identifies four new susceptibility loci for colorectal cancer. Nature Genetics, 2008, 40, 1426-1435.	21.4	498
10	COVID-19 prevalence and mortality in patients with cancer and the effect of primary tumour subtype and patient demographics: a prospective cohort study. Lancet Oncology, The, 2020, 21, 1309-1316.	10.7	473
11	A genome-wide association study shows that common alleles of SMAD7 influence colorectal cancer risk. Nature Genetics, 2007, 39, 1315-1317.	21.4	463
12	Meta-analysis of three genome-wide association studies identifies susceptibility loci for colorectal cancer at 1q41, 3q26.2, 12q13.13 and 20q13.33. Nature Genetics, 2010, 42, 973-977.	21.4	335
13	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	21.4	310
14	Common genetic variants at the CRAC1 (HMPS) locus on chromosome 15q13.3 influence colorectal cancer risk. Nature Genetics, 2008, 40, 26-28.	21.4	277
15	Foxp2 Regulates Gene Networks Implicated in Neurite Outgrowth in the Developing Brain. PLoS Genetics, 2011, 7, e1002145.	3.5	256
16	Distinctive Patterns of MicroRNA Expression Associated with Karyotype in Acute Myeloid Leukaemia. PLoS ONE, 2008, 3, e2141.	2.5	243
17	Linkage of Osteoporosis to Chromosome 20p12 and Association to BMP2. PLoS Biology, 2003, 1, e69.	5.6	222
18	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. Human Molecular Genetics, 2014, 23, 3200-3211.	2.9	222

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19	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	21.4	210
20	Multiple Common Susceptibility Variants near BMP Pathway Loci GREM1, BMP4, and BMP2 Explain Part of the Missing Heritability of Colorectal Cancer. PLoS Genetics, 2011, 7, e1002105.	3.5	188
21	A Whole-Genome Scan and Fine-Mapping Linkage Study of Auditory-Visual Synesthesia Reveals Evidence of Linkage to Chromosomes 2q24, 5q33, 6p12, and 12p12. American Journal of Human Genetics, 2009, 84, 279-285.	6.2	170
22	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. Nature Genetics, 2012, 44, 1131-1136.	21.4	162
23	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	8.2	158
24	Analysis of colorectal cancers in British Bangladeshi identifies early onset, frequent mucinous histotype and a high prevalence of RBFOX1 deletion. Molecular Cancer, 2013, 12, 1.	19.2	154
25	Microdeletions are a general feature of adult and adolescent acute lymphoblastic leukemia: Unexpected similarities with pediatric disease. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6708-6713.	7.1	100
26	Application of whole genome and RNA sequencing to investigate the genomic landscape of common variable immunodeficiency disorders. Clinical Immunology, 2015, 160, 301-314.	3.2	100
27	Segmental uniparental disomy is a commonly acquired genetic event in relapsed acute myeloid leukemia. Blood, 2008, 112, 814-821.	1.4	97
28	Recessive Mutations in SPTBN2 Implicate Î²-III Spectrin in Both Cognitive and Motor Development. PLoS Genetics, 2012, 8, e1003074.	3.5	94
29	Technical and implementation issues in using next-generation sequencing of cancers in clinical practice. British Journal of Cancer, 2013, 109, 827-835.	6.4	91
30	Novel regions of acquired uniparental disomy discovered in acute myeloid leukemia. Genes Chromosomes and Cancer, 2008, 47, 729-739.	2.8	83
31	Differential clonal evolution in oesophageal cancers in response to neo-adjuvant chemotherapy. Nature Communications, 2016, 7, 11111.	12.8	83
32	Whole-genome sequencing of bladder cancers reveals somatic CDKN1A mutations and clinicopathological associations with mutation burden. Nature Communications, 2014, 5, 3756.	12.8	81
33	Development and Validation of a Combined Hypoxia and Immune Prognostic Classifier for Head and Neck Cancer. Clinical Cancer Research, 2019, 25, 5315-5328.	7.0	81
34	Regions of acquired uniparental disomy at diagnosis of follicular lymphoma are associated with both overall survival and risk of transformation. Blood, 2009, 113, 2298-2301.	1.4	75
35	Large Scale Association Analysis Identifies Three Susceptibility Loci for Coronary Artery Disease. PLoS ONE, 2011, 6, e29427.	2.5	75
36	Severity of COVID-19 in children with cancer: Report from the United Kingdom Paediatric Coronavirus Cancer Monitoring Project. British Journal of Cancer, 2021, 124, 754-759.	6.4	72

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37	NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. Mucosal Immunology, 2018, 11, 562-574.	6.0	71
38	Quantification of subclonal distributions of recurrent genomic aberrations in paired pre-treatment and relapse samples from patients with B-cell chronic lymphocytic leukemia. Leukemia, 2012, 26, 1564-1575.	7.2	65
39	Refinement of the basis and impact of common 11q23.1 variation to the risk of developing colorectal cancer. Human Molecular Genetics, 2008, 17, 3720-3727.	2.9	61
40	Fine-mapping of colorectal cancer susceptibility loci at 8q23.3, 16q22.1 and 19q13.11: refinement of association signals and use of in silico analysis to suggest functional variation and unexpected candidate target genes. Human Molecular Genetics, 2011, 20, 2879-2888.	2.9	56
41	The UK Coronavirus Cancer Monitoring Project: protecting patients with cancer in the era of COVID-19. Lancet Oncology, The, 2020, 21, 622-624.	10.7	53
42	Genome-Wide Association Study in a Lebanese Cohort Confirms PHACTR1 as a Major Determinant of Coronary Artery Stenosis. PLoS ONE, 2012, 7, e38663.	2.5	52
43	Exome Sequencing in an Admixed Isolated Population Indicates NFXL1 Variants Confer a Risk for Specific Language Impairment. PLoS Genetics, 2015, 11, e1004925.	3.5	50
44	Genome-wide analysis of genetic susceptibility to language impairment in an isolated Chilean population. European Journal of Human Genetics, 2011, 19, 687-695.	2.8	47
45	Single Nucleotide Polymorphism Array Analysis Defines a Specific Genetic Fingerprint for Well-Differentiated Cutaneous SCCs. Journal of Investigative Dermatology, 2009, 129, 1562-1568.	0.7	40
46	Nutrigenomics of High Fat Diet Induced Obesity in Mice Suggests Relationships between Susceptibility to Fatty Liver Disease and the Proteasome. PLoS ONE, 2013, 8, e82825.	2.5	39
47	Pharmacogenomics in colorectal cancer: a genome-wide association study to predict toxicity after 5-fluorouracil or FOLFOX administration. Pharmacogenomics Journal, 2013, 13, 209-217.	2.0	37
48	Colorectal Cancer Risk Is Not Associated with Increased Levels of Homozygosity in a Population from the United Kingdom. Cancer Research, 2009, 69, 7422-7429.	0.9	36
49	A colorectal cancer genome-wide association study in a Spanish cohort identifies two variants associated with colorectal cancer risk at 1p33 and 8p12. BMC Genomics, 2013, 14, 55.	2.8	36
50	Erythrocytosis associated with a novel missense mutation in the BPGM gene. Haematologica, 2014, 99, e201-e204.	3.5	35
51	Premalignant SOX2 overexpression in the fallopian tubes of ovarian cancer patients: Discovery and validation studies. EBioMedicine, 2016, 10, 137-149.	6.1	34
52	Mortality Among Adults With Cancer Undergoing Chemotherapy or Immunotherapy and Infected With COVID-19. JAMA Network Open, 2022, 5, e220130.	5.9	34
53	WATER ACTIVITY AND ITS PREDICTION: A REVIEW. International Journal of Food Properties, 2001, 4, 35-43.	3.0	33
54	CNVs leading to fusion transcripts in individuals with autism spectrum disorder. European Journal of Human Genetics, 2012, 20, 1141-1147.	2.8	33

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55	Deciphering the genetics of hereditary non-syndromic colorectal cancer. European Journal of Human Genetics, 2008, 16, 1477-1486.	2.8	31
56	Common variation at the adiponectin locus is not associated with colorectal cancer risk in the UK. Human Molecular Genetics, 2009, 18, 1889-1892.	2.9	31
57	mQTL.NMR: An Integrated Suite for Genetic Mapping of Quantitative Variations of ¹H NMR-Based Metabolic Profiles. Analytical Chemistry, 2015, 87, 4377-4384.	6.5	30
58	Germline deletions in the tumour suppressor gene <scp>FOCAD</scp> are associated with polyposis and colorectal cancer development. Journal of Pathology, 2015, 236, 155-164.	4.5	28
59	General lessons from largeâ€scale studies to identify human cancer predisposition genes. Journal of Pathology, 2010, 220, 255-262.	4.5	27
60	Genetic and environmental influences on total plasma homocysteine and its role in coronary artery disease risk. Atherosclerosis, 2012, 222, 180-186.	0.8	27
61	Untargeted Metabolome Quantitative Trait Locus Mapping Associates Variation in Urine Glycerate to Mutant Glycerate Kinase. Journal of Proteome Research, 2012, 11, 631-642.	3.7	25
62	Molecular genetics of the transcription factor GLIS3 identifies its dual function in beta cells and neurons. Genomics, 2018, 110, 98-111.	2.9	22
63	Association between loss of Y chromosome and poor prognosis in male head and neck squamous cell carcinoma. Head and Neck, 2019, 41, 993-1006.	2.0	22
64	Identification of genomic changes associated with cisplatin resistance in testicular germ cell tumor cell lines. Genes Chromosomes and Cancer, 2008, 47, 604-613.	2.8	21
65	Robust hematopoietic specification requires the ubiquitous Sp1 and Sp3 transcription factors. Epigenetics and Chromatin, 2019, 12, 33.	3.9	21
66	A genome-wide association study on copy-number variation identifies a 11q11 loss as a candidate susceptibility variant for colorectal cancer. Human Genetics, 2014, 133, 525-534.	3.8	20
67	Broad-Ranging Natural Metabotype Variation Drives Physiological Plasticity in Healthy Control Inbred Rat Strains. Journal of Proteome Research, 2011, 10, 1675-1689.	3.7	19
68	Refinement of the associations between risk of colorectal cancer and polymorphisms on chromosomes 1q41 and 12q13.13. Human Molecular Genetics, 2012, 21, 934-946.	2.9	19
69	Topological analysis of metabolic networks integrating co-segregating transcriptomes and metabolomes in type 2 diabetic rat congenic series. Genome Medicine, 2016, 8, 101.	8.2	19
70	Transposable element sequence fragments incorporated into coding and noncoding transcripts modulate the transcriptome of human pluripotent stem cells. Nucleic Acids Research, 2021, 49, 9132-9153.	14.5	19
71	SNP rs6457327 in the HLA region on chromosome 6p is predictive of the transformation of follicular lymphoma. Blood, 2011, 117, 3147-3150.	1.4	17
72	Integrative analysis of spontaneous CLL regression highlights genetic and microenvironmental interdependency in CLL. Blood, 2020, 135, 411-428.	1.4	17

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73	Multiple Segmental Uniparental Disomy Associated with Abnormal DNA Methylation of Imprinted Loci in Silver-Russell Syndrome. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E2188-E2193.	3.6	15
74	Harnessing genomics to improve outcomes for women with cancer in India: key priorities for research. Lancet Oncology, The, 2018, 19, e102-e112.	10.7	14
75	COVID-19 in children with haematological malignancies. Archives of Disease in Childhood, 2022, 107, 186-188.	1.9	14
76	Imaging DNA Damage Allows Detection of Preneoplasia in the BALB-neuT Model of Breast Cancer. Journal of Nuclear Medicine, 2014, 55, 2026-2031.	5.0	13
77	Circulating lipid levels and risk of coronary artery disease in a large group of patients undergoing coronary angiography. Journal of Thrombosis and Thrombolysis, 2015, 39, 15-22.	2.1	13
78	Genome-wide Association Study for Tumour Stage, Grade, Size, and Age at Diagnosis of Nonâ€“muscle-invasive Bladder Cancer. European Urology Oncology, 2019, 2, 381-389.	5.4	12
79	Genetic susceptibility to radiation-related differentiated thyroid cancers: a systematic review of literature. Endocrine-Related Cancer, 2019, 26, R583-R596.	3.1	12
80	GREVE: Genomic Recurrent Event ViEwer to assist the identification of patterns across individual cancer samples. Bioinformatics, 2012, 28, 2981-2982.	4.1	11
81	Systems Genetics of Hepatic Metabolome Reveals Octopamine as a Target for Non-Alcoholic Fatty Liver Disease Treatment. Scientific Reports, 2019, 9, 3656.	3.3	11
82	Recurrence of Papillary Thyroid Cancer: A Systematic Appraisal of Risk Factors. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 1392-1406.	3.6	11
83	Transcriptome Profiling in Rat Inbred Strains and Experimental Cross Reveals Discrepant Genetic Architecture of Genome-Wide Gene Expression. G3: Genes, Genomes, Genetics, 2016, 6, 3671-3683.	1.8	9
84	General lessons from largeâ€scale studies to identify human cancer predisposition genes. J Pathol 2010; 220: 255â€“262. Journal of Pathology, 2010, 220, 618-618.	4.5	8
85	Candidate gene variant effects on language disorders in Robinson Crusoe Island. Annals of Human Biology, 2019, 46, 109-119.	1.0	7
86	High-resolution genomic profiling of human papillomavirus-associated vulval neoplasia. British Journal of Cancer, 2010, 102, 1044-1051.	6.4	6
87	Conserved properties of genetic architecture of renal and fat transcriptomes in rat models of insulin resistance. DMM Disease Models and Mechanisms, 2019, 12, .	2.4	6
88	Gene-environment interaction with smoking for increased non- muscle-invasive bladder cancer tumor size. Translational Andrology and Urology, 2020, 9, 1329-1337.	1.4	6
89	Heterogeneity of germline variants in high risk breast and ovarian cancer susceptibility genes in India. Precision Clinical Medicine, 2018, 1, 75-87.	3.3	5
90	Targeting Asparagine and Serine Metabolism in Germinal Centre-Derived B Cells Non-Hodgkin Lymphomas (B-NHL). Cells, 2021, 10, 2589.	4.1	5

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91	Systematic Review: Genetic Associations for Prognostic Factors of Urinary Bladder Cancer. Biomarkers in Cancer, 2019, 11, 1179299X1989725.	3.6	4
92	Novel putative drugs and key initiating genes for neurodegenerative disease determined using networkâ€based genetic integrative analysis. Journal of Cellular Biochemistry, 2019, 120, 5459-5471.	2.6	4
93	External Replication of Urinary Bladder Cancer Prognostic Polymorphisms in the UK Biobank. Frontiers in Oncology, 2019, 9, 1082.	2.8	3
94	A Novel Test for Gene-Ancestry Interactions in Genome-Wide Association Data. PLoS ONE, 2012, 7, e48687.	2.5	3
95	Role of DNA Repair Variants and Diagnostic Radiology Exams in Differentiated Thyroid Cancer Risk: A Pooled Analysis of Two Caseâ€“Control Studies. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1208-1217.	2.5	2
96	Association of coronary artery disease and chronic kidney disease in Lebanese population. International Journal of Clinical and Experimental Medicine, 2015, 8, 15866-77.	1.3	1
97	EPIDERMIS INFLUENCE ON THE GAS EXCHANGES AROUND A PRODUCE. International Journal of Food Properties, 2001, 4, 455-468.	3.0	0
98	The Genetic Population Structure of Robinson Crusoe Island, Chile. Frontiers in Genetics, 2020, 11, 669.	2.3	0
99	Health disparities research is enabled by data diversity but requires much tighter integration of collaborative efforts. Journal of Global Health, 2020, 10, 020351.	2.7	0
100	Development and validation of a combined metabolic and immune prognostic classifier for head and neck cancer.. Journal of Clinical Oncology, 2018, 36, 6049-6049.	1.6	0
101	Integration of Deep Multi-Omics Profiling Veals New Insights into the Biology of Poor-Risk Acute Myeloid Leukemia. Blood, 2020, 136, 39-40.	1.4	0