Bradley P Coe

List of Publications by Year
in descending order

75 papers	15,154 citations	53794 45 h-index	76900 74 g-index
79 all docs	79 docs citations	79 times ranked	21820 citing authors

#	Article	IF	Citations
1	A family study implicates GBE1 in the etiology of autism spectrum disorder. Human Mutation, 2022, 43, 16-29.	2.5	2
2	Novel biallelic variants affecting the OTU domain of the gene OTUD6B associate with severe intellectual disability syndrome and molecular dynamics simulations. European Journal of Medical Genetics, 2022, 65, 104497.	1.3	1
3	Recent ultra-rare inherited variants implicate new autism candidate risk genes. Nature Genetics, 2021, 53, 1125-1134.	21.4	68
4	Rare copy number variants in over 100,000 European ancestry subjects reveal multiple disease associations. Nature Communications, 2020, 11, 255.	12.8	48
5	Large-scale targeted sequencing identifies risk genes for neurodevelopmental disorders. Nature Communications, 2020, 11, 4932.	12.8	105
6	Integrative Genomic Analyses Identifies GGA2 as a Cooperative Driver of EGFR-Mediated Lung Tumorigenesis. Journal of Thoracic Oncology, 2019, 14, 656-671.	1.1	13
7	Genomic inversions and GOLGA core duplicons underlie disease instability at the 15q25 locus. PLoS Genetics, 2019, 15, e1008075.	3.5	17
8	Molecular Genetic Anatomy and Risk Profile of Hirschsprungâ€™s Disease. New England Journal of Medicine, 2019, 380, 1421-1432.	27.0	131
9	Neurodevelopmental disease genes implicated by de novo mutation and copy number variation morbidity. Nature Genetics, 2019, 51, 106-116.	21.4	231
10	Genome sequencing identifies multiple deleterious variants in autism patients with more severe phenotypes. Genetics in Medicine, 2019, 21, 1611-1620.	2.4	88
11	A genotype-first approach identifies an intellectual disability-overweight syndrome caused by PHIP haploinsufficiency. European Journal of Human Genetics, 2018, 26, 54-63.	2.8	32
12	Inherited and multiple de novo mutations in autism/developmental delay risk genes suggest a multifactorial model. Molecular Autism, 2018, 9, 64.	4.9	114
13	Targeted sequencing identifies 91 neurodevelopmental-disorder risk genes with autism and developmental-disability biases. Nature Genetics, 2017, 49, 515-526.	21.4	443
14	Hotspots of missense mutation identify neurodevelopmental disorder genes and functional domains. Nature Neuroscience, 2017, 20, 1043-1051.	14.8	152
15	Sequencing of sporadic Attentionâ€Deficit Hyperactivity Disorder (ADHD) identifies novel and potentially pathogenic de novo variants and excludes overlap with genes associated with autism spectrum disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 381-389.	1.7	44
16	Genomic Patterns of De Novo Mutation in Simplex Autism. Cell, 2017, 171, 710-722.e12.	28.9	308
17	Recurrent de novo mutations in neurodevelopmental disorders: properties and clinical implications. Genome Medicine, 2017, 9, 101.	8.2	112
18	Analysis of exome sequencing data sets reveals structural variation in the coding region of ABO in individuals of African ancestry. Transfusion, 2016, 56, 2744-2749.	1.6	5

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19	Interchromosomal core duplicons drive both evolutionary instability and disease susceptibility of the Chromosome 8p23.1 region. Genome Research, 2016, 26, 1453-1467.	5.5	37
20	De novo genic mutations among a Chinese autism spectrum disorder cohort. Nature Communications, 2016, 7, 13316.	12.8	293
21	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
22	Recurrent Muscle Weakness with Rhabdomyolysis, Metabolic Crises, and Cardiac Arrhythmia Due to Bi-allelic TANGO2 Mutations. American Journal of Human Genetics, 2016, 98, 347-357.	6.2	98
23	Disruption of POGZ Is Associated with Intellectual Disability and Autism Spectrum Disorders. American Journal of Human Genetics, 2016, 98, 541-552.	6.2	132
24	Maternal Modifiers and Parent-of-Origin Bias of the Autism-Associated 16p11.2 CNV. American Journal of Human Genetics, 2016, 98, 45-57.	6.2	55
25	The Koolen-de Vries syndrome: a phenotypic comparison of patients with a 17q21.31 microdeletion versus a KANSL1 sequence variant. European Journal of Human Genetics, 2016, 24, 652-659.	2.8	108
26	Copy number variant analysis from exome data in 349 patients with epileptic encephalopathy. Annals of Neurology, 2015, 78, 323-328.	5.3	59
27	Global diversity, population stratification, and selection of human copy-number variation. Science, 2015, 349, aab3761.	12.6	293
28	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
29	Excess of rare, inherited truncating mutations in autism. Nature Genetics, 2015, 47, 582-588.	21.4	531
30	The transcriptional regulator ADNP links the BAF (SWI/SNF) complexes with autism. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2014, 166, 315-326.	1.6	68
31	A Higher Mutational Burden in Females Supports a â€œFemale Protective Modelâ€•in Neurodevelopmental Disorders. American Journal of Human Genetics, 2014, 94, 415-425.	6.2	457
32	A SWI/SNF-related autism syndrome caused by de novo mutations in ADNP. Nature Genetics, 2014, 46, 380-384.	21.4	293
33	Refining analyses of copy number variation identifies specific genes associated with developmental delay. Nature Genetics, 2014, 46, 1063-1071.	21.4	583
34	Disruptive CHD8 Mutations Define a Subtype of Autism Early in Development. Cell, 2014, 158, 263-276.	28.9	637
35	Formation of Chimeric Genes by Copy-Number Variation as a Mutational Mechanism in Schizophrenia. American Journal of Human Genetics, 2013, 93, 697-710.	6.2	40
36	Refinement and Discovery of New Hotspots of Copy-Number Variation Associated with Autism Spectrum Disorder. American Journal of Human Genetics, 2013, 92, 221-237.	6.2	279

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37	Response to Benn. Genetics in Medicine, 2013, 15, 317-318.	2.4	0
38	Estimates of penetrance for recurrent pathogenic copy-number variations. Genetics in Medicine, 2013, 15, 478-481.	2.4	277
39	Genomic Deregulation of the E2F/Rb Pathway Leads to Activation of the Oncogene EZH2 in Small Cell Lung Cancer. PLoS ONE, 2013, 8, e71670.	2.5	74
40	Phenotypic Heterogeneity of Genomic Disorders and Rare Copy-Number Variants. New England Journal of Medicine, 2012, 367, 1321-1331.	27.0	519
41	Copy number variation detection and genotyping from exome sequence data. Genome Research, 2012, 22, 1525-1532.	5.5	550
42	Multiplex Targeted Sequencing Identifies Recurrently Mutated Genes in Autism Spectrum Disorders. Science, 2012, 338, 1619-1622.	12.6	1,133
43	Sporadic autism exomes reveal a highly interconnected protein network of de novo mutations. Nature, 2012, 485, 246-250.	27.8	1,960
44	A genetic model for neurodevelopmental disease. Current Opinion in Neurobiology, 2012, 22, 829-836.	4.2	47
45	Divergent Genomic and Epigenomic Landscapes of Lung Cancer Subtypes Underscore the Selection of Different Oncogenic Pathways during Tumor Development. PLoS ONE, 2012, 7, e37775.	2.5	56
46	The genetic variability and commonality of neurodevelopmental disease. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2012, 160C, 118-129.	1.6	101
47	A copy number variation morbidity map of developmental delay. Nature Genetics, 2011, 43, 838-846.	21.4	1,141
48	Genome structural variation discovery and genotyping. Nature Reviews Genetics, 2011, 12, 363-376.	16.3	1,240
49	Relative Burden of Large CNVs on a Range of Neurodevelopmental Phenotypes. PLoS Genetics, 2011, 7, e1002334.	3.5	293
50	Integrating the multiple dimensions of genomic and epigenomic landscapes of cancer. Cancer and Metastasis Reviews, 2010, 29, 73-93.	5.9	51
51	An integrative multi-dimensional genetic and epigenetic strategy to identify aberrant genes and pathways in cancer. BMC Systems Biology, 2010, 4, 67.	3.0	54
52	A sequence-based approach to identify reference genes for gene expression analysis. BMC Medical Genomics, 2010, 3, 32.	1.5	41
53	Transcriptome Profiles of Carcinoma-in-Situ and Invasive Non-Small Cell Lung Cancer as Revealed by SAGE. PLoS ONE, 2010, 5, e9162.	2.5	23
54	FACADE : a fast and sensitive algorithm for the segmentation and calling of high resolution array CGH data. Nucleic Acids Research, 2010, 38, e157-e157.	14.5	14

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55	Integrative Genomic Analyses Identify BRF2 as a Novel Lineage-Specific Oncogene in Lung Squamous Cell Carcinoma. PLoS Medicine, 2010, 7, e1000315.	8.4	87
56	Copy Number Variations in the Human Genome and Strategies for Analysis. Methods in Molecular Biology, 2010, 628, 103-117.	0.9	5
57	Comparative Genomic Hybridization on BAC Arrays. Methods in Molecular Biology, 2009, 556, 7-19.	0.9	3
58	Evolving strategies for global gene expression analysis of cancer. Journal of Cellular Physiology, 2008, 217, 590-597.	4.1	9
59	Inverted duplication with terminal deletion of 5p and no catâ€like cry. American Journal of Medical Genetics, Part A, 2008, 146A, 1173-1179.	1.2	18
60	MD-SeeGH: a platform for integrative analysis of multi-dimensional genomic data. BMC Bioinformatics, 2008, 9, 243.	2.6	27
61	SIGMA2: A system for the integrative genomic multi-dimensional analysis of cancer genomes, epigenomes, and transcriptomes. BMC Bioinformatics, 2008, 9, 422.	2.6	33
62	Integrative genomic and gene expression analysis of chromosome 7 identified novel oncogene loci in non-small cell lung cancer. Genome, 2008, 51, 1032-1039.	2.0	25
63	Genomic markers for malignant progression in pulmonary adenocarcinoma with bronchioloalveolar features. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10155-10160.	7.1	64
64	Comment re: A Comparison of DNA Copy Number Profiling Platforms. Cancer Research, 2008, 68, 4010-4010.	0.9	1
65	Resolving the resolution of array CGH. Genomics, 2007, 89, 647-653.	2.9	163
66	Whole genome tiling path array CGH analysis of segmental copy number alterations in cervical cancer cell lines. International Journal of Cancer, 2007, 120, 436-443.	5.1	34
67	Large fragment Bst DNA polymerase for whole genome amplification of DNA from formalin-fixed paraffin-embedded tissues. BMC Genomics, 2006, 7, 312.	2.8	37
68	SIGMA: A System for Integrative Genomic Microarray Analysis of Cancer Genomes. BMC Genomics, 2006, 7, 324.	2.8	28
69	Gain of a region on 7p22.3, containingMAD1L1, is the most frequent event in small-cell lung cancer cell lines. Genes Chromosomes and Cancer, 2006, 45, 11-19.	2.8	56
70	High-resolution chromosome arm 5p array CGH analysis of small cell lung carcinoma cell lines. Genes Chromosomes and Cancer, 2005, 42, 308-313.	2.8	44
71	High-resolution array CGH increases heterogeneity tolerance in the analysis of clinical samples. Genomics, 2005, 85, 790-793.	2.9	32
72	A tiling resolution DNA microarray with complete coverage of the human genome. Nature Genetics, 2004, 36, 299-303.	21.4	597

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73	Overexpression of LRP12, a gene contained within an 8q22 amplicon identified by high-resolution array CGH analysis of oral squamous cell carcinomas. Oncogene, 2004, 23, 2582-2586.	5.9	61
74	SeeGH--a software tool for visualization of whole genome array comparative genomic hybridization data. BMC Bioinformatics, 2004, 5, 13.	2.6	84
75	Novel regions of amplification on 8q distinct from the MYC locus and frequently altered in oral dysplasia and cancer. Genes Chromosomes and Cancer, 2004, 39, 93-98.	2.8	61