

Eric Bareke

List of Publications by Year in descending order

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46
papers

1,358
citations

516710

16
h-index

377865

34
g-index

49
all docs

49
docs citations

49
times ranked

2872
citing authors

#	ARTICLE	IF	CITATIONS
1	The histone mark H3K36me2 recruits DNMT3A and shapes the intergenic DNA methylation landscape. <i>Nature</i> , 2019, 573, 281-286.	27.8	338
2	Germline and somatic FGFR1 abnormalities in dysembryoplastic neuroepithelial tumors. <i>Acta Neuropathologica</i> , 2016, 131, 847-863.	7.7	143
3	Debunking Occam's razor: Diagnosing multiple genetic diseases in families by whole-exome sequencing. <i>Clinical Genetics</i> , 2017, 92, 281-289.	2.0	92
4	Next-generation sequencing for diagnosis of rare diseases in the neonatal intensive care unit. <i>Cmaj</i> , 2016, 188, E254-E260.	2.0	86
5	A Unique Morphological Phenotype in Chemoresistant Triple-Negative Breast Cancer Reveals Metabolic Reprogramming and PLIN4 Expression as a Molecular Vulnerability. <i>Molecular Cancer Research</i> , 2019, 17, 2492-2507.	3.4	63
6	Whole-exome sequencing as a diagnostic tool: current challenges and future opportunities. <i>Expert Review of Molecular Diagnostics</i> , 2015, 15, 749-760.	3.1	62
7	TRPV4 and KRAS and FGFR1 gain-of-function mutations drive giant cell lesions of the jaw. <i>Nature Communications</i> , 2018, 9, 4572.	12.8	58
8	H3K27M in Gliomas Causes a One-Step Decrease in H3K27 Methylation and Reduced Spreading within the Constraints of H3K36 Methylation. <i>Cell Reports</i> , 2020, 33, 108390.	6.4	50
9	Whole-exome sequencing is a valuable diagnostic tool for inherited peripheral neuropathies: Outcomes from a cohort of 50 families. <i>Clinical Genetics</i> , 2018, 93, 301-309.	2.0	48
10	Chromatin dysregulation associated with NSD1 mutation in head and neck squamous cell carcinoma. <i>Cell Reports</i> , 2021, 34, 108769.	6.4	42
11	Prognostic and predictive value of circulating tumor DNA during neoadjuvant chemotherapy for triple negative breast cancer. <i>Scientific Reports</i> , 2020, 10, 14704.	3.3	41
12	A benchmark for statistical microarray data analysis that preserves actual biological and technical variance. <i>BMC Bioinformatics</i> , 2010, 11, 17.	2.6	28
13	Recessive mutations in the kinase ZAK cause a congenital myopathy with fibre type disproportion. <i>Brain</i> , 2017, 140, 37-48.	7.6	28
14	Meconium ileus in a Lebanese family secondary to mutations in the GUCY2C gene. <i>European Journal of Human Genetics</i> , 2015, 23, 990-992.	2.8	24
15	SHORT syndrome due to a novel de novo mutation in PRKCE (Protein Kinase C ϵ) impairing TORC2-dependent AKT activation. <i>Human Molecular Genetics</i> , 2017, 26, 3713-3721.	2.9	22
16	Mutation in <i>Eftud2</i> causes craniofacial defects in mice via mis-splicing of <i>Mdm2</i> and increased P53. <i>Human Molecular Genetics</i> , 2021, 30, 739-757.	2.9	20
17	Methylome analysis and whole-exome sequencing reveal that brain tumors associated with encephalocraniocutaneous lipomatosis are midline pilocytic astrocytomas. <i>Acta Neuropathologica</i> , 2018, 136, 657-660.	7.7	18
18	POLR3A variants in hereditary spastic paraplegia and ataxia. <i>Brain</i> , 2018, 141, e1-e1.	7.6	17

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19	H3K36 dimethylation shapes the epigenetic interaction landscape by directing repressive chromatin modifications in embryonic stem cells. <i>Genome Research</i> , 2022, , gr.276383.121.	5.5	17
20	Neurolaxova syndrome presenting prenatally with increased nuchal translucency and cystic hygroma: The utility of exome sequencing in deciphering the diagnosis. <i>American Journal of Medical Genetics, Part A</i> , 2019, 179, 813-816.	1.2	15
21	Early infantile epileptic encephalopathy due to biallelic pathogenic variants in <i>PIGQ</i> : Report of seven new subjects and review of the literature. <i>Journal of Inherited Metabolic Disease</i> , 2020, 43, 1321-1332.	3.6	15
22	Meta-analysis of archived DNA microarrays identifies genes regulated by hypoxia and involved in a metastatic phenotype in cancer cells. <i>BMC Cancer</i> , 2010, 10, 176.	2.6	14
23	Autosomal dominant cutis laxa with progeroid features due to a novel, de novo mutation in <i>ALDH18A1</i> . <i>Journal of Human Genetics</i> , 2017, 62, 661-663.	2.3	12
24	Recessive mutation in <i>CD2AP</i> causes focal segmental glomerulosclerosis in humans and mice. <i>Kidney International</i> , 2019, 95, 57-61.	5.2	11
25	Resolution of refractory hypotension and anuria in a premature newborn with loss of function of <i>ACE</i> . <i>American Journal of Medical Genetics, Part A</i> , 2015, 167, 1654-1658.	1.2	10
26	<i>Bmp</i> signaling maintains a mesoderm progenitor cell state in the mouse tailbud. <i>Development (Cambridge)</i> , 2017, 144, 2982-2993.	2.5	10
27	<i>gViz</i> , a novel tool for the visualization of co-expression networks. <i>BMC Research Notes</i> , 2011, 4, 452.	1.4	9
28	<i>Snrpb</i> is required in murine neural crest cells for proper splicing and craniofacial morphogenesis. <i>DMM Disease Models and Mechanisms</i> , 2022, 15, .	2.4	9
29	HSP90 inhibitors induce GPNMB cell-surface expression by modulating lysosomal positioning and sensitize breast cancer cells to glembatumumab vedotin. <i>Oncogene</i> , 2022, 41, 1701-1717.	5.9	8
30	Functional Analysis: Evaluation of Response Intensities - Tailoring ANOVA for Lists of Expression Subsets. <i>BMC Bioinformatics</i> , 2010, 11, 510.	2.6	7
31	H3.1 K36M mutation in a congenital-onset soft tissue neoplasm. <i>Pediatric Blood and Cancer</i> , 2017, 64, e26633.	1.5	7
32	Circulating tumor DNA (ctDNA) during and after neoadjuvant chemotherapy and prior to surgery is a powerful prognostic factor in triple-negative breast cancer (TNBC).. <i>Journal of Clinical Oncology</i> , 2019, 37, 594-594.	1.6	6
33	Whole-exome sequencing reveals novel vacuolar ATPase genes'™ variants and variants in genes involved in lysosomal biology and autophagosomal formation in oral granular cell tumors. <i>Journal of Oral Pathology and Medicine</i> , 2021, 50, 410-417.	2.7	5
34	Adaptation of a Bioinformatics Microarray Analysis Workflow for a Toxicogenomic Study in Rainbow Trout. <i>PLoS ONE</i> , 2015, 10, e0128598.	2.5	5
35	PathEx: a novel multi factors based datasets selector web tool. <i>BMC Bioinformatics</i> , 2010, 11, 528.	2.6	4
36	Joint genotype inference with germline and somatic mutations. <i>BMC Bioinformatics</i> , 2013, 14, S3.	2.6	4

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37	A Molecular Diagnosis of LGMDR1 Established by RNA Sequencing. Canadian Journal of Neurological Sciences, 2021, 48, 293-296.	0.5	3
38	Meta-Analysis and Gene Set Analysis of Archived Microarrays Suggest Implication of the Spliceosome in Metastatic and Hypoxic Phenotypes. PLoS ONE, 2014, 9, e86699.	2.5	2
39	PHOENIX, a web interface for (re)analysis of microarray data. Open Life Sciences, 2009, 4, 603-618.	1.4	1
40	A novel mathematical basis for predicting somatic single nucleotide variants from next-generation sequencing. , 2012, , .		0
41	MG-109â€¦Revisiting a clinical diagnosis 15 years later with the aid of whole exome sequencing: Osteopetrosis versus harderophorphyria. Journal of Medical Genetics, 2015, 52, A4.1-A4.	3.2	0
42	Abstract 4335: The genomic landscape of childhood pre-B acute lymphoblastic leukemia. , 2012, , .		0
43	Abstract 2484: Whole-exome sequencing of a rare case of familial childhood acute lymphoblastic leukemia. , 2012, , .		0
44	Bmp signaling maintains a mesoderm progenitor cell state in the mouse tailbud. Journal of Cell Science, 2017, 130, e1.2-e1.2.	2.0	0
45	Mutation of <i>Eftud2</i> in Mouse Neural Crest Cells Models MFDM and Reveals Contribution of P53 in Abnormal Craniofacial Development. FASEB Journal, 2020, 34, 1-1.	0.5	0
46	Effects of spliceosomal mutations on brain patterning and morphogenesis. FASEB Journal, 2022, 36, .	0.5	0