Eric Bareke

List of Publications by Year
in descending order

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	HSP90 inhibitors induce GPNMB cell-surface expression by modulating lysosomal positioning and sensitize breast cancer cells to glembatumumab vedotin. Oncogene, 2022, 41, 1701-1717.	5.9	8
2	H3K36 dimethylation shapes the epigenetic interaction landscape by directing repressive chromatin modifications in embryonic stem cells. Genome Research, 2022, , gr.276383.121.	5.5	17
3	Effects of spliceosomal mutations on brain patterning and morphogenesis. FASEB Journal, 2022, 36, .	0.5	0
4	Snrpb is required in murine neural crest cells for proper splicing and craniofacial morphogenesis. DMM Disease Models and Mechanisms, 2022, 15, .	2.4	9
5	A Molecular Diagnosis of LGMDR1 Established by RNA Sequencing. Canadian Journal of Neurological Sciences, 2021, 48, 293-296.	0.5	3
6	Wholeâ€exome sequencing reveals novel vacuolar ATPase genesâ€™ variants and variants in genes involved in lysosomal biology and autophagosomal formation in oral granular cell tumors. Journal of Oral Pathology and Medicine, 2021, 50, 410-417.	2.7	5
7	Mutation in Eftud2 causes craniofacial defects in mice via mis-splicing of Mdm2 and increased P53. Human Molecular Genetics, 2021, 30, 739-757.	2.9	20
8	Chromatin dysregulation associated with NSD1 mutation in head and neck squamous cell carcinoma. Cell Reports, 2021, 34, 108769.	6.4	42
9	H3K27M in Gliomas Causes a One-Step Decrease in H3K27 Methylation and Reduced Spreading within the Constraints of H3K36 Methylation. Cell Reports, 2020, 33, 108390.	6.4	50
10	Prognostic and predictive value of circulating tumor DNA during neoadjuvant chemotherapy for triple negative breast cancer. Scientific Reports, 2020, 10, 14704.	3.3	41
11	Early infantile epileptic encephalopathy due to biallelic pathogenic variants in <scp>PIGQ</scp>: Report of seven new subjects and review of the literature. Journal of Inherited Metabolic Disease, 2020, 43, 1321-1332.	3.6	15
12	Mutation of Eftud2 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
13	The histone mark H3K36me2 recruits DNMT3A and shapes the intergenic DNA methylation landscape. Nature, 2019, 573, 281-286.	27.8	338
14	Neuâ€“Laxova syndrome presenting prenatally with increased nuchal translucency and cystic hygroma: The utility of exome sequencing in deciphering the diagnosis. American Journal of Medical Genetics, Part A, 2019, 179, 813-816.	1.2	15
15	A Unique Morphological Phenotype in Chemoresistant Triple-Negative Breast Cancer Reveals Metabolic Reprogramming and PLIN4 Expression as a Molecular Vulnerability. Molecular Cancer Research, 2019, 17, 2492-2507.	3.4	63
16	Recessive mutation in CD2AP causes focal segmental glomerulosclerosis in humans and mice. Kidney International, 2019, 95, 57-61.	5.2	11
17	Circulating tumor DNA (ctDNA) during and after neoadjuvant chemotherapy and prior to surgery is a powerful prognostic factor in triple-negative breast cancer (TNBC).. Journal of Clinical Oncology, 2019, 37, 594-594.	1.6	6
18	POLR3A variants in hereditary spastic paraplegia and ataxia. Brain, 2018, 141, e1-e1.	7.6	17

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19	Wholeâ€exome sequencing is a valuable diagnostic tool for inherited peripheral neuropathies: Outcomes from a cohort of 50 families. Clinical Genetics, 2018, 93, 301-309.	2.0	48
20	TRPV4 and KRAS and FGFR1 gain-of-function mutations drive giant cell lesions of the jaw. Nature Communications, 2018, 9, 4572.	12.8	58
21	Methylome analysis and whole-exome sequencing reveal that brain tumors associated with encephalocraniocutaneous lipomatosis are midline pilocytic astrocytomas. Acta Neuropathologica, 2018, 136, 657-660.	7.7	18
22	Autosomal dominant cutis laxa with progeroid features due to a novel, de novo mutation in ALDH18A1. Journal of Human Genetics, 2017, 62, 661-663.	2.3	12
23	Debunking Occam's razor: Diagnosing multiple genetic diseases in families by wholeâ€exome sequencing. Clinical Genetics, 2017, 92, 281-289.	2.0	92
24	H3.1 K36M mutation in a congenitalâ€onset soft tissue neoplasm. Pediatric Blood and Cancer, 2017, 64, e26633.	1.5	7
25	Bmp signaling maintains a mesoderm progenitor cell state in the mouse tailbud. Development (Cambridge), 2017, 144, 2982-2993.	2.5	10
26	Recessive mutations in the kinase ZAK cause a congenital myopathy with fibre type disproportion. Brain, 2017, 140, 37-48.	7.6	28
27	SHORT syndrome due to a novel de novo mutation in PRKCE (Protein Kinase CÉ›) impairing TORC2-dependent AKT activation. Human Molecular Genetics, 2017, 26, 3713-3721.	2.9	22
28	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
29	Next-generation sequencing for diagnosis of rare diseases in the neonatal intensive care unit. Cmaj, 2016, 188, E254-E260.	2.0	86
30	Germline and somatic FGFR1 abnormalities in dysembryoplastic neuroepithelial tumors. Acta Neuropathologica, 2016, 131, 847-863.	7.7	143
31	Resolution of refractory hypotension and anuria in a premature newborn with lossâ€ofâ€function of ACE. American Journal of Medical Genetics, Part A, 2015, 167, 1654-1658.	1.2	10
32	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
33	Meconium ileus in a Lebanese family secondary to mutations in the GUCY2C gene. European Journal of Human Genetics, 2015, 23, 990-992.	2.8	24
34	Whole-exome sequencing as a diagnostic tool: current challenges and future opportunities. Expert Review of Molecular Diagnostics, 2015, 15, 749-760.	3.1	62
35	Adaptation of a Bioinformatics Microarray Analysis Workflow for a Toxicogenomic Study in Rainbow Trout. PLoS ONE, 2015, 10, e0128598.	2.5	5
36	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

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37	Joint genotype inference with germline and somatic mutations. BMC Bioinformatics, 2013, 14, S3.	2.6	4
38	A novel mathematical basis for predicting somatic single nucleotide variants from next-generation sequencing. , 2012, , .		0
39	Abstract 4335: The genomic landscape of childhood pre-B acute lymphoblastic leukemia. , 2012, , .		0
40	Abstract 2484: Whole-exome sequencing of a rare case of familial childhood acute lymphoblastic leukemia. , 2012, , .		0
41	gViz, a novel tool for the visualization of co-expression networks. BMC Research Notes, 2011, 4, 452.	1.4	9
42	A benchmark for statistical microarray data analysis that preserves actual biological and technical variance. BMC Bioinformatics, 2010, 11, 17.	2.6	28
43	Functional Analysis: Evaluation of Response Intensities - Tailoring ANOVA for Lists of Expression Subsets. BMC Bioinformatics, 2010, 11, 510.	2.6	7
44	PathEx: a novel multi factors based datasets selector web tool. BMC Bioinformatics, 2010, 11, 528.	2.6	4
45	Meta-analysis of archived DNA microarrays identifies genes regulated by hypoxia and involved in a metastatic phenotype in cancer cells. BMC Cancer, 2010, 10, 176.	2.6	14
46	PHOENIX, a web interface for (re)analysis of microarray data. Open Life Sciences, 2009, 4, 603-618.	1.4	1