## Nicole J Boczek

List of Publications by Year in descending order

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623734 526287 30 940 14 27 citations g-index h-index papers 30 30 30 2041 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Expert specification of the ACMG/AMP variant interpretation guidelines for genetic hearing loss. Human Mutation, 2018, 39, 1593-1613.	2.5	312
2	Bi-allelic Alterations in AEBP1 Lead to Defective Collagen Assembly and Connective Tissue Structure Resulting in a Variant of Ehlers-Danlos Syndrome. American Journal of Human Genetics, 2018, 102, 696-705.	6.2	105
3	Identification and Functional Characterization of a Novel <i>CACNA1C</i> -Mediated Cardiac Disorder Characterized by Prolonged QT Intervals With Hypertrophic Cardiomyopathy, Congenital Heart Defects, and Sudden Cardiac Death. Circulation: Arrhythmia and Electrophysiology, 2015, 8, 1122-1132.	4.8	76
4	Characterization of SEMA3A -Encoded Semaphorin as a Naturally Occurring K $\nu$ 4.3 Protein Inhibitor and its Contribution to Brugada Syndrome. Circulation Research, 2014, 115, 460-469.	4.5	54
5	Best practices for the interpretation and reporting of clinical whole genome sequencing. Npj Genomic Medicine, 2022, 7, 27.	3.8	48
6	Novel long QT syndrome-associated missense mutation, L762F, in CACNA1C-encoded L-type calcium channel imparts a slower inactivation tau and increased sustained and window current. International Journal of Cardiology, 2016, 220, 290-298.	1.7	40
7	Developmental delay and failure to thrive associated with a lossâ€ofâ€function variant in ⟨i⟩WHSC1 (NSD2)⟨ i⟩. American Journal of Medical Genetics, Part A, 2018, 176, 2798-2802.	1.2	33
8	Pharmacogenomic findings from clinical whole exome sequencing of diagnostic odyssey patients. Molecular Genetics & Denomic Medicine, 2017, 5, 269-279.	1.2	30
9	Utility of DNA, RNA, Protein, and Functional Approaches to Solve Cryptic Immunodeficiencies. Journal of Clinical Immunology, 2018, 38, 307-319.	3.8	29
10	De Novo <i>DNM1L</i> Variant in a Teenager With Progressive Paroxysmal Dystonia and Lethal Super-refractory Myoclonic Status Epilepticus. Journal of Child Neurology, 2018, 33, 651-658.	1.4	25
11	Impact of integrated translational research on clinical exome sequencing. Genetics in Medicine, 2021, 23, 498-507.	2.4	24
12	Characterization of three ciliopathy pedigrees expands the phenotype associated with biallelic C2CD3 variants. European Journal of Human Genetics, 2018, 26, 1797-1809.	2.8	19
13	Whole Exome Sequencing and Heterologous Cellular Electrophysiology Studies Elucidate a Novel Loss-of-Function Mutation in the CACNA1A-Encoded Neuronal P/Q-Type Calcium Channel in a Child With Congenital Hypotonia and Developmental Delay. Pediatric Neurology, 2016, 55, 46-51.	2.1	18
14	Disease-specific ACMG/AMP guidelines improve sequence variant interpretation for hearing loss. Genetics in Medicine, 2021, 23, 2208-2212.	2.4	18
15	The prevalence of diseases caused by lysosome-related genes in a cohort of undiagnosed patients. Molecular Genetics and Metabolism Reports, 2017, 13, 46-51.	1.1	17
16	Type 8 long QT syndrome: pathogenic variants in CACNA1C-encoded Cav1.2 cluster in STAC protein binding site. Europace, 2019, 21, 1725-1732.	1.7	15
17	A novel ANO3 variant identified in a 53-year-old woman presenting with hyperkinetic dysarthria, blepharospasm, hyperkinesias, and complex motorÂtics. BMC Medical Genetics, 2016, 17, 93.	2.1	14
18	Multigenerational pedigree with STAR syndrome: A novel FAM58A variant and expansion of the phenotype., 2017, 173, 1328-1333.		11

#	Article	IF	CITATIONS
19	Familial Creutzfeldt-Jakob Disease: Case report and role of genetic counseling in post mortem testing. Prion, 2016, 10, 502-506.	1.8	9
20	Functional validation reveals the novel missense V419L variant in ⟨i⟩TGFBR2⟨li⟩ associated with Loeys–Dietz syndrome (LDS) impairs canonical TGF-β signaling. Journal of Physical Education and Sports Management, 2017, 3, a001727.	1.2	7
21	Earlyâ€onset limbâ€girdle muscular dystrophyâ€2L in a female athlete. Muscle and Nerve, 2017, 55, E19-E21.	2.2	7
22	Co-occurrence of a maternally inherited DNMT3A duplication and a paternally inherited pathogenic variant in EZH2 in a child with growth retardation and severe short stature: atypical Weaver syndrome or evidence of a DNMT3A dosage effect?. Journal of Physical Education and Sports Management, 2018, 4, a002899.	1.2	7
23	Whole exome sequencing of a patient with suspected mitochondrial myopathy reveals novel compound heterozygous variants in <i><scp>RYR</scp>1</i> . Molecular Genetics & amp; Genomic Medicine, 2017, 5, 295-302.	1.2	6
24	Novel Pathogenic Variant in TGFBR2 Confirmed by Molecular Modeling Is a Rare Cause of Loeys-Dietz Syndrome. Case Reports in Genetics, 2017, 2017, 1-4.	0.2	4
25	Expansion of <i>PURA</i> -Related Phenotypes and Discovery of a Novel PURA Variant: A Case Report. Child Neurology Open, 2020, 7, 2329048X2095500.	1.1	4
26	Development and Validation of a Next-Generation Sequencing Panel for Syndromic and Nonsyndromic Hearing Loss. journal of applied laboratory medicine, The, 2020, 5, 467-479.	1.3	4
27	First Report of Bilateral External Auditory Canal Cochlin Aggregates ("Cochlinomasâ€) with Multifocal Amyloid-Like Deposits, Associated with Sensorineural Hearing Loss and a Novel Genetic Variant in COCH Encoding Cochlin. Head and Neck Pathology, 2020, 14, 808-816.	2.6	2
28	Limited diagnostic impact of duplications <1 Mb of uncertain clinical significance: a 10-year retrospective analysis of reporting practices at the Mayo Clinic. Genetics in Medicine, 2020, 22, 2120-2124.	2.4	2
29	Whole Exome Sequencing Leading to the Diagnosis of Dysferlinopathy with a Novel Missense Mutation (c.959G>C). Case Reports in Genetics, 2016, 2016, 1-4.	0.2	0
30	Unconventional Diagnosis Based on Somatic Findings through Germ Line Whole-Exome Sequencing. Clinical Chemistry, 2020, 66, 48-51.	3.2	o