Ahmad N Abou Tayoun

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6766450/publications.pdf

Version: 2024-02-01

67 papers 2,764 citations

279798 23 h-index 214800 47 g-index

86 all docs 86 docs citations

86 times ranked 5252 citing authors

| # | Article | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Recommendations for interpreting the loss of function PVS1 ACMG/AMP variant criterion. Human Mutation, 2018, 39, 1517-1524. | 2.5 | 511 |
| 2 | Expert specification of the ACMG/AMP variant interpretation guidelines for genetic hearing loss. Human Mutation, 2018, 39, 1593-1613. | 2.5 | 312 |
| 3 | Recommendations for application of the functional evidence PS3/BS3 criterion using the ACMG/AMP sequence variant interpretation framework. Genome Medicine, 2020, 12, 3. | 8.2 | 312 |
| 4 | Understanding Genotypes and Phenotypes in Epileptic Encephalopathies. Molecular Syndromology, 2016, 7, 172-181. | 0.8 | 97 |
| 5 | Regulation of Angiotensin- Converting Enzyme 2 in Obesity: Implications for COVID-19. Frontiers in Physiology, 2020, 11, 555039. | 2.8 | 86 |
| 6 | MicroRNAs as diagnostic markers for pancreatic ductal adenocarcinoma and its precursor, pancreatic intraepithelial neoplasm. Cancer Genetics, 2013, 206, 217-221. | 0.4 | 69 |
| 7 | Host transcriptomic profiling of COVID-19 patients with mild, moderate, and severe clinical outcomes. Computational and Structural Biotechnology Journal, 2021, 19, 153-160. | 4.1 | 69 |
| 8 | Automated Clinical Exome Reanalysis Reveals Novel Diagnoses. Journal of Molecular Diagnostics, 2019, 21, 38-48. | 2.8 | 68 |
| 9 | ClinGen expert clinical validity curation of 164 hearing loss gene–disease pairs. Genetics in Medicine, 2019, 21, 2239-2247. | 2.4 | 67 |
| 10 | Improving hearing loss gene testing: a systematic review of gene evidence toward more efficient next-generation sequencing–based diagnostic testing and interpretation. Genetics in Medicine, 2016, 18, 545-553. | 2.4 | 63 |
| 11 | Consensus interpretation of the p.Met34Thr and p.Val37Ile variants in GJB2 by the ClinGen Hearing Loss Expert Panel. Genetics in Medicine, 2019, 21, 2442-2452. | 2.4 | 56 |
| 12 | Prenatal DNA Sequencing: Clinical, Counseling, and Diagnostic Laboratory Considerations. Prenatal Diagnosis, 2018, 38, 26-32. | 2.3 | 47 |
| 13 | Ceramide kinase regulates phospholipase C and phosphatidylinositol 4, 5, bisphosphate in phototransduction. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20063-20068. | 7.1 | 45 |
| 14 | Use of a Dynamic Genetic Testing Approach for Childhood-Onset Epilepsy. JAMA Network Open, 2019, 2, e192129. | 5.9 | 45 |
| 15 | A Comprehensive Assay for CFTR Mutational Analysis Using Next-Generation Sequencing. Clinical Chemistry, 2013, 59, 1481-1488. | 3.2 | 44 |
| 16 | Democratizing Molecular Diagnostics for the Developing World. American Journal of Clinical Pathology, 2014, 141, 17-24. | 0.7 | 42 |
| 17 | Targeted Droplet-Digital PCR as a Tool for Novel Deletion Discovery at the DFNB1 Locus. Human Mutation, 2016, 37, 119-126. | 2.5 | 37 |
| 18 | De Novo Variants Disturbing the Transactivation Capacity of POU3F3 Cause a Characteristic Neurodevelopmental Disorder. American Journal of Human Genetics, 2019, 105, 403-412. | 6.2 | 35 |

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|----|--|-----|-----------|
| 19 | Diagnosing Cornelia de Lange syndrome and related neurodevelopmental disorders using RNA sequencing. Genetics in Medicine, 2020, 22, 927-936. | 2.4 | 34 |
| 20 | A singleâ€center <i>SCN8Aâ€</i> related epilepsy cohort: clinical, genetic, and physiologic characterization. Annals of Clinical and Translational Neurology, 2019, 6, 1445-1455. | 3.7 | 32 |
| 21 | SARS-CoV-2 Whole Genome Amplification and Sequencing for Effective Population-Based Surveillance and Control of Viral Transmission. Clinical Chemistry, 2020, 66, 1450-1458. | 3.2 | 31 |
| 22 | The Drosophila SK Channel (dSK) Contributes to Photoreceptor Performance by Mediating Sensitivity Control at the First Visual Network. Journal of Neuroscience, 2011, 31, 13897-13910. | 3.6 | 30 |
| 23 | Sequencing-based diagnostics for pediatric genetic diseases: progress and potential. Expert Review of Molecular Diagnostics, 2016, 16, 987-999. | 3.1 | 29 |
| 24 | Multiple early introductions of SARS-CoV-2 into a global travel hub in the Middle East. Scientific Reports, 2020, 10, 17720. | 3.3 | 28 |
| 25 | AUDIOME: a tiered exome sequencing–based comprehensive gene panel for the diagnosis of heterogeneous nonsyndromic sensorineural hearing loss. Genetics in Medicine, 2018, 20, 1600-1608. | 2.4 | 27 |
| 26 | Genetic variation in the Middle East—an opportunity to advance the human genetics field. Genome Medicine, 2020, 12, 116. | 8.2 | 27 |
| 27 | Curating Clinically Relevant Transcripts for the Interpretation of Sequence Variants. Journal of Molecular Diagnostics, 2018, 20, 789-801. | 2.8 | 25 |
| 28 | Allele-Specific Droplet Digital PCR Combined with a Next-Generation Sequencing-Based Algorithm for Diagnostic Copy Number Analysis in Genes with High Homology: Proof of Concept Using Stereocilin. Clinical Chemistry, 2018, 64, 705-714. | 3.2 | 24 |
| 29 | A mutation update for the PCDH19 gene causing early-onset epilepsy in females with an unusual expression pattern. Human Mutation, 2019, 40, 243-257. | 2.5 | 23 |
| 30 | A multiplex PCR assay for the simultaneous detection of Chlamydia trachomatis, Neisseria gonorrhoeae, and Trichomonas vaginalis. Experimental and Molecular Pathology, 2015, 98, 214-218. | 2.1 | 22 |
| 31 | From Your Nose to Your Toes: A Review of Severe Acute Respiratory Syndrome Coronavirus 2 Pandemicâ€'Associated Pernio. Journal of Investigative Dermatology, 2021, 141, 2791-2796. | 0.7 | 21 |
| 32 | PCDH19 -related epilepsy in a male with Klinefelter syndrome: Additional evidence supporting PCDH19 cellular interference disease mechanism. Epilepsy Research, 2018, 145, 89-92. | 1.6 | 20 |
| 33 | Evaluating the impact of in silico predictors on clinical variant classification. Genetics in Medicine, 2022, 24, 924-930. | 2.4 | 20 |
| 34 | Genetic variant pathogenicity prediction trained using disease-specific clinical sequencing data sets. Genome Research, 2019, 29, 1144-1151. | 5.5 | 19 |
| 35 | Recurrent variants in OTOF are significant contributors to prelingual nonsydromic hearing loss in Saudi patients. Genetics in Medicine, 2018, 20, 536-544. | 2.4 | 18 |
| 36 | Considerations for whole exome sequencing unique to prenatal care. Human Genetics, 2020, 139, 1149-1159. | 3.8 | 18 |

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| 37 | Disease-specific ACMG/AMP guidelines improve sequence variant interpretation for hearing loss. Genetics in Medicine, 2021, 23, 2208-2212. | 2.4 | 18 |
| 38 | Clinical evaluation and etiologic diagnosis of hearing loss: A clinical practice resource of the American College of Medical Genetics and Genomics (ACMG). Genetics in Medicine, 2022, 24, 1392-1406. | 2.4 | 18 |
| 39 | Rapid and accurate interpretation of clinical exomes using Phenoxome: a computational phenotype-driven approach. European Journal of Human Genetics, 2019, 27, 612-620. | 2.8 | 17 |
| 40 | The Development and Validation of Clinical Exome-Based Panels Using ExomeSlicer. Journal of Molecular Diagnostics, 2018, 20, 643-652. | 2.8 | 16 |
| 41 | Development of a rapid clinical TPMT genotyping assay. Clinical Biochemistry, 2014, 47, 126-129. | 1.9 | 15 |
| 42 | Using large sequencing data sets to refine intragenic disease regions and prioritize clinical variant interpretation. Genetics in Medicine, 2017, 19, 496-504. | 2.4 | 15 |
| 43 | Utility of clinical exome sequencing in a complex Emirati pediatric cohort. Computational and Structural Biotechnology Journal, 2020, 18, 1020-1027. | 4.1 | 14 |
| 44 | Single-cell transcriptome identifies FCGR3B upregulated subtype of alveolar macrophages in patients with critical COVID-19. IScience, 2021, 24, 103030. | 4.1 | 13 |
| 45 | Genetic and Clinical Characteristics of Patients in the Middle East With Multisystem Inflammatory Syndrome in Children. JAMA Network Open, 2022, 5, e2214985. | 5.9 | 13 |
| 46 | Need for Automated Interactive Genomic Interpretation and Ongoing Reanalysis. JAMA Pediatrics, 2018, 172, 1113. | 6.2 | 12 |
| 47 | The genomic landscape of pediatric rheumatology disorders in the Middle East. Human Mutation, 2021, 42, e1-e14. | 2.5 | 12 |
| 48 | Roles of the Drosophila SK Channel (dSK) in Courtship Memory. PLoS ONE, 2012, 7, e34665. | 2.5 | 12 |
| 49 | Genomic medicine in the Middle East. Genome Medicine, 2021, 13, 184. | 8.2 | 12 |
| 50 | Association of Dromedary Camels and Camel Ticks with Reassortant Crimean-Congo Hemorrhagic Fever Virus, United Arab Emirates. Emerging Infectious Diseases, 2021, 27, 2471-2474. | 4.3 | 11 |
| 51 | VIPâ€HL: Semiâ€automated ACMG/AMP variant interpretation platform for genetic hearing loss. Human Mutation, 2021, 42, 1567-1575. | 2.5 | 10 |
| 52 | Utility of droplet digital PCR and NGS-based CNV clinical assays in hearing loss diagnostics: current status and future prospects. Expert Review of Molecular Diagnostics, 2021, 21, 213-221. | 3.1 | 8 |
| 53 | Genotypeâ€phenotype correlation identified a novel SARSâ€CoVâ€2 variant possibly linked to severe disease. Transboundary and Emerging Diseases, 2021, , . | 3.0 | 8 |
| 54 | A clinical PCR fragment analysis assay for TA repeat sizing in the UGT1A1 promoter region. Clinica Chimica Acta, 2013, 422, 1-4. | 1.1 | 7 |

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| 55 | Ca ²⁺ -Activated K ⁺ Channels Reduce Network Excitability, Improving Adaptability and Energetics for Transmitting and Perceiving Sensory Information. Journal of Neuroscience, 2019, 39, 7132-7154. | 3.6 | 7 |
| 56 | Using Machine Learning to Identify True Somatic Variants from Next-Generation Sequencing. Clinical Chemistry, 2020, 66, 239-246. | 3.2 | 7 |
| 57 | MERSâ€CoV in sheep, goats, and cattle, United Arab Emirates, 2019: Virological and serological investigations reveal an accidental spillover from dromedaries. Transboundary and Emerging Diseases, 2022, 69, 3066-3072. | 3.0 | 7 |
| 58 | Middle Eastern Genetic Variation Improves Clinical Annotation of the Human Genome. Journal of Personalized Medicine, 2022, 12, 423. | 2.5 | 7 |
| 59 | Rapid whole genome sequencing of critically ill pediatric patients from genetically underrepresented populations. Genome Medicine, 2022, 14, . | 8.2 | 7 |
| 60 | A rapid RT-PCR assay for the detection of HIV-1 in human plasma specimens. Experimental and Molecular Pathology, 2014, 97, 111-115. | 2.1 | 5 |
| 61 | Case Report: CMV-Associated Congenital Nephrotic Syndrome. Frontiers in Pediatrics, 2020, 8, 580178. | 1.9 | 5 |
| 62 | Evaluating the thermostability of commercial fast real-time PCR master mixes. Experimental and Molecular Pathology, 2012, 93, 261-263. | 2.1 | 4 |
| 63 | Coexistence of a novel WISP3 pathogenic variant and an MEFV mutation in an Arabic family with progressive pseudorheumatoid dysplasia mimicking polyarticular juvenile idiopathic arthritis. Pediatric Rheumatology, 2020, 18, 69. | 2.1 | 4 |
| 64 | A Rare Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) Mutation Associated With Typical Cystic Fibrosis in an Arab Child. Cureus, 2021, 13, e13526. | 0.5 | 2 |
| 65 | A Simple Practical Guide to Genomic Diagnostics in a Pediatric Setting. Genes, 2021, 12, 818. | 2.4 | 2 |
| 66 | Detection of copy number variants and genes by chromosomal microarray in an Emirati neurodevelopmental disorders cohort. Neurogenetics, 2022, 23, 137-149. | 1.4 | 0 |
| 67 | Comprehensive Genomic Sequencing–Based Screening for Hearing Loss in the Neonatal Intensive Care Setting—Is It Time?. JAMA Network Open, 2022, 5, e2220992. | 5.9 | O |