Erin L Crowgey

List of Publications by Year
in descending order

33 papers	**607** citations	759233 **12** h-index	610901 **24** g-index
34 all docs	**34** docs citations	**34** times ranked	**1212** citing authors

#	Article	IF	Citations
1	Genomic surveillance of SARS-CoV-2 in the state of Delaware reveals tremendous genomic diversity. PLoS ONE, 2022, 17, e0262573.	2.5	6
2	Impact of Early Feeding: Metagenomics Analysis of the Infant Gut Microbiome. Frontiers in Cellular and Infection Microbiology, 2022, 12, 816601.	3.9	7
3	The PNPLA3 rs738409 Variant but not MBOAT7 rs641738 is a Risk Factor for Nonalcoholic Fatty Liver Disease in Obese U.S. Children of Hispanic Ethnicity. Pediatric Gastroenterology, Hepatology and Nutrition, 2021, 24, 455.	1.2	9
4	Transcriptional analysis of muscle tissue and isolated satellite cells in spastic cerebral palsy. Developmental Medicine and Child Neurology, 2021, 63, 1213-1220.	2.1	7
5	CBFB-MYH11 fusion transcripts distinguish acute myeloid leukemias with distinct molecular landscapes and outcomes. Blood Advances, 2021, 5, 4963-4968.	5.2	4
6	Error-corrected sequencing strategies enable comprehensive detection of leukemic mutations relevant for diagnosis and minimal residual disease monitoring. BMC Medical Genomics, 2020, 13, 32.	1.5	14
7	Germline Sequencing Identifies Rare Variants in Finnish Subjects with Familial Germ Cell Tumors . The Application of Clinical Genetics, 2020, Volume 13, 127-137.	3.0	1
8	Accelerating next generation sequencing data analysis: an evaluation of optimized best practices for Genome Analysis Toolkit algorithms. Genomics and Informatics, 2020, 18, e10.	0.8	39
9	Fundamentals of Drug Metabolism and Pharmacogenomics Within a Learning Healthcare System Workflow Perspective. Computers in Health Care, 2020, , 59-80.	0.3	0
10	Strong concordance between RNA structural and single nucleotide variants identified via next generation sequencing techniques in primary pediatric leukemia and patient-derived xenograft samples. Genomics and Informatics, 2020, 18, e6.	0.8	2
11	Perspectives on molecular diagnostic testing for the COVID-19 pandemic in Delaware. Delaware Journal of Public Health, 2020, 6, 20-24.	0.3	0
12	Implementation of a learning healthcare system for sickle cell disease. JAMIA Open, 2020, 3, 349-359.	2.0	7
13	Whole genome metagenomic analysis of the gut microbiome of differently fed infants identifies differences in microbial composition and functional genes, including an absent CRISPR/Cas9 gene in the formula-fed cohort. Human Microbiome Journal, 2019, 12, 100057.	3.8	8
14	Mapping Citrullinated Sites in Multiple Organs of Mice Using Hypercitrullinated Library. Journal of Proteome Research, 2019, 18, 2270-2278.	3.7	30
15	Development of a Novel Next-Generation Sequencing Assay for Carrier Screening in Old Order Amish and Mennonite Populations of Pennsylvania. Journal of Molecular Diagnostics, 2019, 21, 687-694.	2.8	13
16	Advancements in Next-Generation Sequencing for Detecting Minimal Residual Disease. , 2019, , 159-192.		0
17	Subphenotype meta-analysis of testicular cancer genome-wide association study data suggests a role for RBFOX family genes in cryptorchidism susceptibility. Human Reproduction, 2018, 33, 967-977.	0.9	10
18	Protein <i>S</i>-Nitrosylation Controls Glycogen Synthase Kinase 3β Function Independent of Its Phosphorylation State. Circulation Research, 2018, 122, 1517-1531.	4.5	40

#	Article	IF	Citations
19	Epigenetic machine learning: utilizing DNA methylation patterns to predict spastic cerebral palsy. BMC Bioinformatics, 2018, 19, 225.	2.6	45
20	A Systems Biology Approach for Studying Heterotopic Ossification: Proteomic Analysis of Clinical Serum and Tissue Samples. Genomics, Proteomics and Bioinformatics, 2018, 16, 212-220.	6.9	9
21	Abstract 2076: Identification of novel fusion genes and expression variants in primary and patient-derived xenograft samples of pediatric leukemia using error-corrected RNA sequencing. , 2018, , .		0
22	A survey of proteomic biomarkers for heterotopic ossification in blood serum. Journal of Orthopaedic Surgery and Research, 2017, 12, 69.	2.3	13
23	Mapping Biological Networks from Quantitative Data-Independent Acquisition Mass Spectrometry: Data to Knowledge Pipelines. Methods in Molecular Biology, 2017, 1558, 395-413.	0.9	7
24	Protein kinase G signaling in cardiac pathophysiology: Impact of proteomics on clinical trials. Proteomics, 2016, 16, 894-905.	2.2	10
25	An informatics research agenda to support precision medicine: seven key areas. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 791-795.	4.4	61
26	An Integrated Approach for Analyzing Clinical Genomic Variant Data from Next-Generation Sequencing. Journal of Biomolecular Techniques, 2015, 26, 19-28.	1.5	9
27	Citrullination of myofilament proteins in heart failure. Cardiovascular Research, 2015, 108, 232-242.	3.8	64
28	Dual Labeling Biotin Switch Assay to Reduce Bias Derived From Different Cysteine Subpopulations. Circulation Research, 2015, 117, 846-857.	4.5	31
29	Development of Bioinformatics Pipeline for Analyzing Clinical Pediatric NGS Data. AMIA Summits on Translational Science Proceedings, 2015, 2015, 207-11.	0.4	2
30	Caught in the middle with multiple displacement amplification: the myth of pooling for avoiding multiple displacement amplification bias in a metagenome. Microbiome, 2014, 2, 3.	11.1	105
31	Impact of Immunization Technology and Assay Application on Antibody Performance â€" A Systematic Comparative Evaluation. PLoS ONE, 2011, 6, e28718.	2.5	35
32	Combined Inhibition of Janus Kinase 1/2 for the Treatment of JAK2V617F-Driven Neoplasms: Selective Effects on Mutant Cells and Improvements in Measures of Disease Severity. Clinical Cancer Research, 2009, 15, 6891-6900.	7.0	19
33	The Use of Machine Learning and Phonetic Endophenotypes to Discover Genetic Variants Associated with Speech Sound Disorder. , 0, , .		0