

# Erin L Crowgey

## List of Publications by Citations

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**Version:** 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

31  
papers

377  
citations

9  
h-index

19  
g-index

34  
ext. papers

521  
ext. citations

5.4  
avg, IF

3.38  
L-index

#	Paper	IF	Citations
31	Caught in the middle with multiple displacement amplification: the myth of pooling for avoiding multiple displacement amplification bias in a metagenome. <i>Microbiome</i> , <b>2014</b> , 2, 3	16.6	73
30	An informatics research agenda to support precision medicine: seven key areas. <i>Journal of the American Medical Informatics Association: JAMIA</i> , <b>2016</b> , 23, 791-5	8.6	47
29	Citrullination of myofilament proteins in heart failure. <i>Cardiovascular Research</i> , <b>2015</b> , 108, 232-42	9.9	46
28	Epigenetic machine learning: utilizing DNA methylation patterns to predict spastic cerebral palsy. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 225	3.6	31
27	Impact of immunization technology and assay application on antibody performance--a systematic comparative evaluation. <i>PLoS ONE</i> , <b>2011</b> , 6, e28718	3.7	29
26	Dual Labeling Biotin Switch Assay to Reduce Bias Derived From Different Cysteine Subpopulations: A Method to Maximize S-Nitrosylation Detection. <i>Circulation Research</i> , <b>2015</b> , 117, 846-57	15.7	23
25	Protein S-Nitrosylation Controls Glycogen Synthase Kinase 3 $\beta$ Function Independent of Its Phosphorylation State. <i>Circulation Research</i> , <b>2018</b> , 122, 1517-1531	15.7	23
24	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. <i>Clinical Cancer Research</i> , <b>2009</b> , 15, 6891-900	12.9	17
23	Mapping Citrullinated Sites in Multiple Organs of Mice Using Hypercitrullinated Library. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 2270-2278	5.6	14
22	Protein kinase G signaling in cardiac pathophysiology: Impact of proteomics on clinical trials. <i>Proteomics</i> , <b>2016</b> , 16, 894-905	4.8	9
21	A survey of proteomic biomarkers for heterotopic ossification in blood serum. <i>Journal of Orthopaedic Surgery and Research</i> , <b>2017</b> , 12, 69	2.8	8
20	Accelerating next generation sequencing data analysis: an evaluation of optimized best practices for Genome Analysis Toolkit algorithms. <i>Genomics and Informatics</i> , <b>2020</b> , 18, e10	1.9	8
19	Error-corrected sequencing strategies enable comprehensive detection of leukemic mutations relevant for diagnosis and minimal residual disease monitoring. <i>BMC Medical Genomics</i> , <b>2020</b> , 13, 32	3.7	7
18	Subphenotype meta-analysis of testicular cancer genome-wide association study data suggests a role for RBFOX family genes in cryptorchidism susceptibility. <i>Human Reproduction</i> , <b>2018</b> , 33, 967-977	5.7	7
17	A Systems Biology Approach for Studying Heterotopic Ossification: Proteomic Analysis of Clinical Serum and Tissue Samples. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2018</b> , 16, 212-220	6.5	7
16	An integrated approach for analyzing clinical genomic variant data from next-generation sequencing. <i>Journal of Biomolecular Techniques</i> , <b>2015</b> , 26, 19-28	1.1	7
15	Development of a Novel Next-Generation Sequencing Assay for Carrier Screening in Old Order Amish and Mennonite Populations of Pennsylvania. <i>Journal of Molecular Diagnostics</i> , <b>2019</b> , 21, 687-694	5.1	6

14	Mapping Biological Networks from Quantitative Data-Independent Acquisition Mass Spectrometry: Data to Knowledge Pipelines. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1558, 395-413	1.4	5
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. <i>Human Microbiome Journal</i> , <b>2019</b> , 12, 100057-100057	5.6	3
12	Implementation of a learning healthcare system for sickle cell disease. <i>JAMIA Open</i> , <b>2020</b> , 3, 349-359	2.9	2
11	Development of Bioinformatics Pipeline for Analyzing Clinical Pediatric NGS Data. <i>AMIA Summits on Translational Science Proceedings</i> , <b>2015</b> , 2015, 207-11	1.1	2
10	Transcriptional analysis of muscle tissue and isolated satellite cells in spastic cerebral palsy. <i>Developmental Medicine and Child Neurology</i> , <b>2021</b> , 63, 1213-1220	3.3	2
9	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. <i>Pediatric Gastroenterology, Hepatology and Nutrition</i> , <b>2021</b> , 24, 455-469	2.3	1
8	Germline Sequencing Identifies Rare Variants in Finnish Subjects with Familial Germ Cell Tumors. <i>The Application of Clinical Genetics</i> , <b>2020</b> , 13, 127-137	3.1	0
7	Genomic surveillance of SARS-CoV-2 in the state of Delaware reveals tremendous genomic diversity.. <i>PLoS ONE</i> , <b>2022</b> , 17, e0262573	3.7	0
6	Strong concordance between RNA structural and single nucleotide variants identified via next generation sequencing techniques in primary pediatric leukemia and patient-derived xenograft samples. <i>Genomics and Informatics</i> , <b>2020</b> , 18, e6	1.9	0
5	CBFB-MYH11 fusion transcripts distinguish acute myeloid leukemias with distinct molecular landscapes and outcomes. <i>Blood Advances</i> , <b>2021</b> , 5, 4963-4968	7.8	0
4	Impact of Early Feeding: Metagenomics Analysis of the Infant Gut Microbiome.. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2022</b> , 12, 816601	5.9	0
3	Perspectives on Molecular Diagnostic Testing for the COVID-19 Pandemic in Delaware. <i>Delaware Journal of Public Health</i> , <b>2020</b> , 6, 20-24	0.1	
2	Advancements in Next-Generation Sequencing for Detecting Minimal Residual Disease <b>2019</b> , 159-192		
1	Fundamentals of Drug Metabolism and Pharmacogenomics Within a Learning Healthcare System Workflow Perspective <b>2020</b> , 59-80		