

# Sarah A Killcoyne

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8945981/publications.pdf>

Version: 2024-02-01

31  
papers

3,246  
citations

516215

16  
h-index

500791

28  
g-index

32  
all docs

32  
docs citations

32  
times ranked

7510  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Integration of biological networks and gene expression data using Cytoscape. <i>Nature Protocols</i> , 2007, 2, 2366-2382.   | 5.5  | 2,275     |
| 2  | Cytoscape: A Community-Based Framework for Network Modeling. <i>Methods in Molecular Biology</i> , 2009, 563, 219-239.   | 0.4  | 191       |
| 3  | The landscape of selection in 551 esophageal adenocarcinomas defines genomic biomarkers for the clinic. <i>Nature Genetics</i> , 2019, 51, 506-516.  | 9.4  | 166       |
| 4  | Genomic copy number predicts esophageal cancer years before transformation. <i>Nature Medicine</i> , 2020, 26, 1726-1732.  | 15.2 | 86        |
| 5  | Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. <i>Nature Genetics</i> , 2020, 52, 1178-1188.  | 9.4  | 79        |
| 6  | Identification of Prognostic Phenotypes of Esophageal Adenocarcinoma in 2 Independent Cohorts. <i>Gastroenterology</i> , 2018, 155, 1720-1728.e4.  | 0.6  | 67        |
| 7  | T1DBase: integration and presentation of complex data for type 1 diabetes research. <i>Nucleic Acids Research</i> , 2007, 35, D742-D746.   | 6.5  | 60        |
| 8  | Identification of Subtypes of Barrett's Esophagus and Esophageal Adenocarcinoma Based on DNA Methylation Profiles and Integration of Transcriptome and Genome Data. <i>Gastroenterology</i> , 2020, 158, 1682-1697.e1.               | 0.6  | 58        |
| 9  | Hydra: a scalable proteomic search engine which utilizes the Hadoop distributed computing framework. <i>BMC Bioinformatics</i> , 2012, 13, 324.  | 1.2  | 48        |
| 10 | Evolution and progression of Barrett's oesophagus to oesophageal cancer. <i>Nature Reviews Cancer</i> , 2021, 21, 731-741.   | 12.8 | 32        |
| 11 | Use of a Cytosponge biomarker panel to prioritise endoscopic Barrett's oesophagus surveillance: a cross-sectional study followed by a real-world prospective pilot. <i>Lancet Oncology</i> , 2022, 23, 270-278.                      | 5.1  | 28        |
| 12 | Systems biology driven software design for the research enterprise. <i>BMC Bioinformatics</i> , 2008, 9, 295.  | 1.2  | 19        |
| 13 | Aneuploidy in targeted endoscopic biopsies outperforms other tissue biomarkers in the prediction of histologic progression of Barrett's oesophagus: A multi-centre prospective cohort study. <i>EBioMedicine</i> , 2020, 56, 102765. | 2.7  | 19        |
| 14 | Adaptable data management for systems biology investigations. <i>BMC Bioinformatics</i> , 2009, 10, 79.  | 1.2  | 18        |
| 15 | Managing Chaos: Lessons Learned Developing Software in the Life Sciences. <i>Computing in Science and Engineering</i> , 2009, 11, 20-29.   | 1.2  | 17        |
| 16 | Limitations of Heartburn and Other Societies' Criteria in Barrett's Screening for Detecting De Novo Esophageal Adenocarcinoma. <i>Clinical Gastroenterology and Hepatology</i> , 2022, 20, 1709-1718.                                | 2.4  | 17        |
| 17 | SAMQA: error classification and validation of high-throughput sequenced read data. <i>BMC Genomics</i> , 2011, 12, 419.  | 1.2  | 13        |
| 18 | Genomic instability signals offer diagnostic possibility in early cancer detection. <i>Trends in Genetics</i> , 2021, 37, 966-972.   | 2.9  | 11        |

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|----|--|-----|-----------|
| 19 | FIGG: Simulating populations of whole genome sequences for heterogeneous data analyses. BMC Bioinformatics, 2014, 15, 149.   | 1.2 | 9         |
| 20 | Methods for visual mining of genomic and proteomic data atlases. BMC Bioinformatics, 2012, 13, 58.   | 1.2 | 8         |
| 21 | Rearrangement processes and structural variations show evidence of selection in oesophageal adenocarcinomas. Communications Biology, 2022, 5, 335.                     | 2.0 | 8         |
| 22 | Comparison of Phenotypes and Risk Factors for Esophageal Adenocarcinoma at Present vs Prior Decades. Clinical Gastroenterology and Hepatology, 2020, 18, 2710-2716.e1. | 2.4 | 5         |
| 23 | Identification of large-scale genomic variation in cancer genomes using <i>in silico</i> reference models. Nucleic Acids Research, 2016, 44, e5-e5.                    | 6.5 | 4         |
| 24 | Mining PeptideAtlas for Biomarkers and Therapeutics in Human Disease. Current Pharmaceutical Design, 2012, 18, 748-754.  | 0.9 | 2         |
| 25 | Managing Chaos: Bridging the cultural divide between engineers and scientists working within the life sciences. Computing in Science and Engineering, 2019, , 1-1.     | 1.2 | 2         |
| 26 | Interfaces to PeptideAtlas: a case study of standard data access systems. Briefings in Bioinformatics, 2012, 13, 615-626.  | 3.2 | 1         |
| 27 | Practical early cancer detection: distinguishing stable from unstable genomes in pre-cancerous tissues. British Journal of Cancer, 2021, 124, 683-685.                 | 2.9 | 1         |
| 28 | An Integration Architecture Designed to Deal with the Issues of Biological Scope, Scale and Complexity. Lecture Notes in Computer Science, 2010, , 179-191.            | 1.0 | 1         |
| 29 | SEQADAPT: an adaptable system for the tracking, storage and analysis of high throughput sequencing experiments. BMC Bioinformatics, 2010, 11, 377.                     | 1.2 | 0         |
| 30 | Howdah - A Flexible Pipeline Framework for Analyzing Genomic Data. , 2010, , .   |     | 0         |
| 31 | Shallow Whole Genome Sequencing can Detect Copy Number Changes in FFPE Material in the Progression of Barrett's Esophagus. Gastroenterology, 2017, 152, S106.          | 0.6 | 0         |