

# Eric Talevich

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6274444/publications.pdf>

Version: 2024-02-01

25  
papers

3,780  
citations

394286

19  
h-index

580701

25  
g-index

29  
all docs

29  
docs citations

29  
times ranked

9813  
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of cryptogenic malignancies from metagenomic whole genome sequencing of body fluids. <i>Genome Medicine</i> , 2021, 13, 98.	3.6	16
2	Correlation Between Surrogate End Points and Overall Survival in a Multi-institutional Clinicogenomic Cohort of Patients With Nonâ€“Small Cell Lung or Colorectal Cancer. <i>JAMA Network Open</i> , 2021, 4, e2117547.	2.8	20
3	Detection of Neoplasms by Metagenomic Next-Generation Sequencing of Cerebrospinal Fluid. <i>JAMA Neurology</i> , 2021, 78, 1355.	4.5	14
4	Genetic Heterogeneity of BRAF Fusion Kinases in Melanoma Affects Drug Responses. <i>Cell Reports</i> , 2019, 29, 573-588.e7.	2.9	62
5	Genomic profiling of combined hepatocellularâ€“cholangiocarcinoma reveals similar genetics to hepatocellular carcinoma. <i>Journal of Pathology</i> , 2019, 248, 164-178.	2.1	82
6	The tumor suppressor <i>BAP1</i> cooperates with <i>BRAFV600E</i> to promote tumor formation in cutaneous melanoma. <i>Pigment Cell and Melanoma Research</i> , 2019, 32, 269-279.	1.5	9
7	A recurrent kinase domain mutation in <i>PRKCA</i> defines chordoid glioma of the third ventricle. <i>Nature Communications</i> , 2018, 9, 810.	5.8	56
8	Adenomatoid tumors of the male and female genital tract are defined by <i>TRAF7</i> mutations that drive aberrant NF- $\kappa$ B pathway activation. <i>Modern Pathology</i> , 2018, 31, 660-673.	2.9	76
9	Targeted next-generation sequencing of pediatric neuro-oncology patients improves diagnosis, identifies pathogenic germline mutations, and directs targeted therapy. <i>Neuro-Oncology</i> , 2017, 19, now254.	0.6	155
10	Genomic profiling of breast secretory carcinomas reveals distinct genetics from other breast cancers and similarity to mammary analog secretory carcinomas. <i>Modern Pathology</i> , 2017, 30, 1086-1099.	2.9	63
11	Gene Copy Number Estimation from Targeted Next-Generation Sequencing of Prostate Cancer Biopsies: Analytic Validation and Clinical Qualification. <i>Clinical Cancer Research</i> , 2017, 23, 6070-6077.	3.2	30
12	Genomic profiling of malignant peritoneal mesothelioma reveals recurrent alterations in epigenetic regulatory genes <i>BAP1</i> , <i>SETD2</i> , and <i>DDX3X</i> . <i>Modern Pathology</i> , 2017, 30, 246-254.	2.9	95
13	CNVkit: Genome-Wide Copy Number Detection and Visualization from Targeted DNA Sequencing. <i>PLoS Computational Biology</i> , 2016, 12, e1004873.	1.5	1,260
14	Genomic profiling of malignant phyllodes tumors reveals aberrations in <i>FGFR1</i> and PI-3 kinase/ <i>RAS</i> signaling pathways and provides insights into intratumoral heterogeneity. <i>Modern Pathology</i> , 2016, 29, 1012-1027.	2.9	54
15	Activating <i>MET</i> kinase rearrangements in melanoma and Spitz tumours. <i>Nature Communications</i> , 2015, 6, 7174.	5.8	139
16	Exome sequencing of desmoplastic melanoma identifies recurrent <i>NFKBIE</i> promoter mutations and diverse activating mutations in the <i>MAPK</i> pathway. <i>Nature Genetics</i> , 2015, 47, 1194-1199.	9.4	221
17	The Genetic Evolution of Melanoma from Precursor Lesions. <i>New England Journal of Medicine</i> , 2015, 373, 1926-1936.	13.9	824
18	ProKinO: A Unified Resource for Mining the Cancer Kinome. <i>Human Mutation</i> , 2015, 36, 175-186.	1.1	47

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19	Prediction and Prioritization of Rare Oncogenic Mutations in the Cancer Kinome Using Novel Features and Multiple Classifiers. <i>PLoS Computational Biology</i> , 2014, 10, e1003545.	1.5	23
20	Structural and evolutionary adaptation of rhopty kinases and pseudokinases, a family of coccidian virulence factors. <i>BMC Evolutionary Biology</i> , 2013, 13, 117.	3.2	74
21	Global Analysis of Protein Expression and Phosphorylation of Three Stages of <i>Plasmodium falciparum</i> Intraerythrocytic Development. <i>Journal of Proteome Research</i> , 2013, 12, 4028-4045.	1.8	161
22	An evolutionary perspective on the kinome of malaria parasites. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 2607-2618.	1.8	53
23	Bio.Phylo: A unified toolkit for processing, analyzing and visualizing phylogenetic trees in Biopython. <i>BMC Bioinformatics</i> , 2012, 13, 209.	1.2	117
24	Structural and evolutionary divergence of eukaryotic protein kinases in Apicomplexa. <i>BMC Evolutionary Biology</i> , 2011, 11, 321.	3.2	83
25	Co-Conserved Features Associated with cis Regulation of ErbB Tyrosine Kinases. <i>PLoS ONE</i> , 2010, 5, e14310.	1.1	14