Eugene W Myers

List of Publications by Citations

56 papers	85,695 citations	27 h-index	65 g-index
65 ext. papers	96,932 ext. citations	19.7 avg, IF	7.18 L-index

#	Paper	IF	Citations
56	Basic local alignment search tool. *Journal of Molecular Biology*, **1990**, 215, 403-10	6.5	65807
55	The sequence of the human genome. *Science*, **2001**, 291, 1304-51	33.3	10609
54	The genome sequence of Drosophila melanogaster. *Science*, **2000**, 287, 2185-95	33.3	4857
53	A Liquid-to-Solid Phase Transition of the ALS Protein FUS Accelerated by Disease Mutation. *Cell*, **2015**, 162, 1066-77	56.2	1388
52	Content-aware image restoration: pushing the limits of fluorescence microscopy. *Nature Methods*, **2018**, 15, 1090-1097	21.6	369
51	The axolotl genome and the evolution of key tissue formation regulators. *Nature*, **2018**, 554, 50-55	50.4	279
50	A platform for brain-wide imaging and reconstruction of individual neurons. *ELife*, **2016**, 5, e10566	8.9	246
49	The fragment assembly string graph. *Bioinformatics*, **2005**, 21 Suppl 2, ii79-85	7.2	237
48	Fast, accurate reconstruction of cell lineages from large-scale fluorescence microscopy data. *Nature Methods*, **2014**, 11, 951-8	21.6	200
47	Towards complete and error-free genome assemblies of all vertebrate species. *Nature*, **2021**, 592, 737-746	50.4	161
46	Efficient Bayesian-based multiview deconvolution. *Nature Methods*, **2014**, 11, 645-8	21.6	154
45	Adaptive light-sheet microscopy for long-term, high-resolution imaging in living organisms. *Nature Biotechnology*, **2016**, 34, 1267-1278	44.5	142
44	The genome of Schmidtea mediterranea and the evolution of core cellular mechanisms. *Nature*, **2018**, 554, 56-61	50.4	113
43	The complete sequence of a human genome.. *Science*, **2022**, 376, 44-53	33.3	107
42	ClearVolume: open-source live 3D visualization for light-sheet microscopy. *Nature Methods*, **2015**, 12, 480-1	21.6	95
41	Bat Biology, Genomes, and the Bat1K Project: To Generate Chromosome-Level Genomes for All Living Bat Species. *Annual Review of Animal Biosciences*, **2018**, 6, 23-46	13.7	88
40	Virtual finger boosts three-dimensional imaging and microsurgery as well as terabyte volume image visualization and analysis. *Nature Communications*, **2014**, 5, 4342	17.4	87

39	Six reference-quality genomes reveal evolution of bat adaptations. *Nature*, **2020**, 583, 578-584	50.4	73
38	A tunable refractive index matching medium for live imaging cells, tissues and model organisms. *ELife*, **2017**, 6,	8.9	66
37	The complete sequence of a human genome		58
36	Differential lateral and basal tension drive folding of Drosophila wing discs through two distinct mechanisms. *Nature Communications*, **2018**, 9, 4620	17.4	58
35	The balance of prickle/spiny-legs isoforms controls the amount of coupling between core and fat PCP systems. *Current Biology*, **2014**, 24, 2111-2123	6.3	52
34	Cell dynamics underlying oriented growth of the wing imaginal disc. *Development (Cambridge)*, **2017**, 144, 4406-4421	6.6	46
33	CLIJ: GPU-accelerated image processing for everyone. *Nature Methods*, **2020**, 17, 5-6	21.6	42
32	Contrasting signatures of genomic divergence during sympatric speciation. *Nature*, **2020**, 588, 106-111	50.4	41
31	BlastNeuron for Automated Comparison, Retrieval and Clustering of 3D Neuron Morphologies. *Neuroinformatics*, **2015**, 13, 487-99	3.2	40
30	Towards complete and error-free genome assemblies of all vertebrate species		38
29	Atlas-builder software and the eNeuro atlas: resources for developmental biology and neuroscience. *Development (Cambridge)*, **2014**, 141, 2524-32	6.6	24
28	Automated detection and quantification of single RNAs at cellular resolution in zebrafish embryos. *Development (Cambridge)*, **2016**, 143, 540-6	6.6	23
27	PreMosa: extracting 2D surfaces from 3D microscopy mosaics. *Bioinformatics*, **2017**, 33, 2563-2569	7.2	19
26	Biobeam-Multiplexed wave-optical simulations of light-sheet microscopy. *PLoS Computational Biology*, **2018**, 14, e1006079	5	19
25	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. *Genome Biology*, **2021**, 22, 120	18.3	19
24	The Earth BioGenome Project 2020: Starting the clock.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	15
23	Non Hybrid Long Read Consensus Using Local De Bruijn Graph Assembly		15
22	Content-Aware Image Restoration: Pushing the Limits of Fluorescence Microscopy		13

21	Rapid and ongoing evolution of repetitive sequence structures in human centromeres. *Science Advances*, **2020**, 6,	14.3	11
20	AUTOMATIC SEGMENTATION OF NUCLEI IN 3D MICROSCOPY IMAGES OF C.ELEGANS **2007**,		11
19	Merfin: improved variant filtering and polishing via k-mer validation		10
18	Rod nuclear architecture determines contrast transmission of the retina and behavioral sensitivity in mice. *ELife*, **2019**, 8,	8.9	9
17	Moral Lineage Tracing **2016**,		7
16	3D Neuron Tip Detection in Volumetric Microscopy Images **2011**,		6
15	Efficient Algorithms for Moral Lineage Tracing **2017**,		5
14	Complete vertebrate mitogenomes reveal widespread gene duplications and repeats		5
13	Large-scale genome sampling reveals unique immunity and metabolic adaptations in bats. *Molecular Ecology*, **2021**, 30, 6449-6467	5.7	5
12	EASI-FISH for thick tissue defines lateral hypothalamus spatio-molecular organization. *Cell*, **2021**,	56.2	5
11	Standards recommendations for the Earth BioGenome Project.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	4
10	Interactive design of GPU-accelerated Image Data Flow Graphs and cross-platform deployment using multi-lingual code generation		4
9	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation.. *Nature Methods*, **2022**,	21.6	3
8	Multi-scale coordination of planar cell polarity in planarians		1
7	CLIJ: GPU-accelerated image processing for everyone		1
6	Long-read Data Revealed Structural Diversity in Human Centromere Sequences		1
5	Expansion-Assisted Iterative-FISH defines lateral hypothalamus spatio-molecular organization		1
4	DENTIST-using long reads for closing assembly gaps at high accuracy.. *GigaScience*, **2022**, 11,	7.6	1

3	Contradictory Phylogenetic Signals in the Laurasiatheria Anomaly Zone. *Genes*, **2022**, 13, 766	4.2	1
2	Constructing 5D developing gene expression patterns without live animal imaging. *Biomedical Engineering Letters*, **2014**, 4, 338-346	3.6	0
1	Finding long tandem repeats in long noisy reads. *Bioinformatics*, **2021**, 37, 612-621	7.2	0