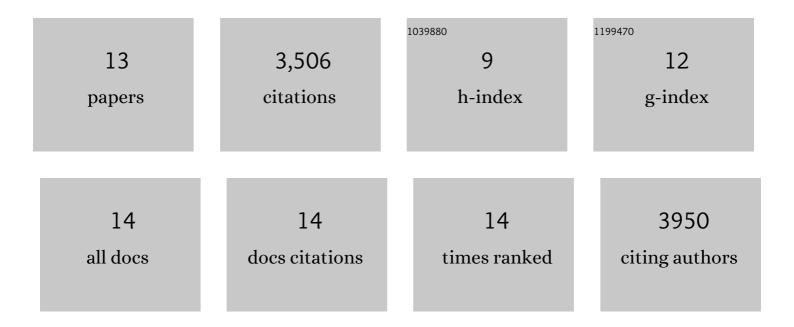
## Gene Myers

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10517689/publications.pdf Version: 2024-02-01



CENE MVEDS

#	Article	IF	CITATIONS
1	Suffix Arrays: A New Method for On-Line String Searches. SIAM Journal on Computing, 1993, 22, 935-948.	0.8	1,468
2	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. Nature Biotechnology, 2019, 37, 1155-1162.	9.4	1,010
3	A fast bit-vector algorithm for approximate string matching based on dynamic programming. Journal of the ACM, 1999, 46, 395-415.	1.8	342
4	Interplay of cell dynamics and epithelial tension during morphogenesis of the Drosophila pupal wing. ELife, 2015, 4, e07090.	2.8	290
5	Efficient Local Alignment Discovery amongst Noisy Long Reads. Lecture Notes in Computer Science, 2014, , 52-67.	1.0	130
6	Monitoring single-cell gene regulation under dynamically controllable conditions with integrated microfluidics and software. Nature Communications, 2018, 9, 212.	5.8	105
7	Why bioimage informatics matters. Nature Methods, 2012, 9, 659-660.	9.0	74
8	Error Tolerant Indexing and Alignment of Short Reads with Covering Template Families. Journal of Computational Biology, 2010, 17, 1397-1411.	0.8	23
9	The genome of the tegu lizard <i>Salvator merianae</i> : combining Illumina, PacBio, and optical mapping data to generate a highly contiguous assembly. GigaScience, 2018, 7, .	3.3	23
10	DENTIST—using long reads for closing assembly gaps at high accuracy. GigaScience, 2022, 11, .	3.3	13
11	A Table-Driven, Full-Sensitivity Similarity Search Algorithm. Journal of Computational Biology, 2003, 10, 103-117.	0.8	9
12	A highly contiguous genome assembly of the bat hawkmoth Hyles vespertilio (Lepidoptera: Sphingidae). GigaScience, 2020, 9, .	3.3	8
13	Crowd sourcing image segmentation with iaSTAPLE. , 2017, , .		6