

# Michal Levy-Sakin

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11025622/publications.pdf>

Version: 2024-02-01

16  
papers

1,109  
citations

687363

13  
h-index

940533

16  
g-index

20  
all docs

20  
docs citations

20  
times ranked

2627  
citing authors

#	ARTICLE	IF	CITATIONS
1	A hybrid approach for de novo human genome sequence assembly and phasing. <i>Nature Methods</i> , 2016, 13, 587-590.	19.0	225
2	Light-emitting self-assembled peptide nucleic acids exhibit both stacking interactions and Watson-Crick base pairing. <i>Nature Nanotechnology</i> , 2015, 10, 353-360.	31.5	136
3	Complete Phenotypic Recovery of an Alzheimer's Disease Model by a Quinone-Tryptophan Hybrid Aggregation Inhibitor. <i>PLoS ONE</i> , 2010, 5, e11101.	2.5	129
4	Genome maps across 26 human populations reveal population-specific patterns of structural variation. <i>Nature Communications</i> , 2019, 10, 1025.	12.8	123
5	Beyond sequencing: optical mapping of DNA in the age of nanotechnology and nanoscopy. <i>Current Opinion in Biotechnology</i> , 2013, 24, 690-698.	6.6	103
6	A Blood-Brain Barrier (BBB) Disrupter Is Also a Potent $\alpha$ -Synuclein ( $\alpha$ -syn) Aggregation Inhibitor. <i>Journal of Biological Chemistry</i> , 2013, 288, 17579-17588.	3.4	84
7	De novo human genome assemblies reveal spectrum of alternative haplotypes in diverse populations. <i>Nature Communications</i> , 2018, 9, 3040.	12.8	81
8	Targeting insulin amyloid assembly by small aromatic molecules: Toward rational design of aggregation inhibitors. <i>Islets</i> , 2009, 1, 210-215.	1.8	53
9	Toward Single-Molecule Optical Mapping of the Epigenome. <i>ACS Nano</i> , 2014, 8, 14-26.	14.6	42
10	One-Pot Chemoenzymatic Cascade for Labeling of the Epigenetic Marker 5-Hydroxymethylcytosine. <i>ChemBioChem</i> , 2015, 16, 1857-1860.	2.6	32
11	The Influence of Chemical Chaperones on Enzymatic Activity under Thermal and Chemical Stresses: Common Features and Variation among Diverse Chemical Families. <i>PLoS ONE</i> , 2014, 9, e88541.	2.5	27
12	Application of full-genome analysis to diagnose rare monogenic disorders. <i>Npj Genomic Medicine</i> , 2021, 6, 77.	3.8	22
13	Accurate assembly of the olive baboon ( <i>Papio anubis</i> ) genome using long-read and Hi-C data. <i>GigaScience</i> , 2020, 9, .	6.4	18
14	The Driver of Extreme Human-Specific Olduvai Repeat Expansion Remains Highly Active in the Human Genome. <i>Genetics</i> , 2020, 214, 179-191.	2.9	14
15	Three patients with homozygous familial hypercholesterolemia: Genomic sequencing and kindred analysis. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e1007.	1.2	5
16	Whole-exome sequencing reveals damaging gene variants associated with hypoalphalipoproteinemia. <i>Journal of Lipid Research</i> , 2022, 63, 100209.	4.2	2