

# Leonid Brodsky

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7192393/publications.pdf>

Version: 2024-02-01

16  
papers

1,212  
citations

687363

13  
h-index

996975

15  
g-index

16  
all docs

16  
docs citations

16  
times ranked

2488  
citing authors

#	ARTICLE	IF	CITATIONS
1	Defective viral genomes as therapeutic interfering particles against flavivirus infection in mammalian and mosquito hosts. <i>Nature Communications</i> , 2021, 12, 2290.	12.8	32
2	Intra and inter-cellular modeling of dynamic interaction between Zika virus and its naturally occurring defective viral genomes. <i>Journal of Virology</i> , 2021, 95, e0097721.	3.4	0
3	A defective viral genome strategy elicits broad protective immunity against respiratory viruses. <i>Cell</i> , 2021, 184, 6037-6051.e14.	28.9	33
4	Poliovirus intrahost evolution is required to overcome tissue-specific innate immune responses. <i>Nature Communications</i> , 2017, 8, 375.	12.8	58
5	Adaptation of the pine fungal pathogen <i>Grosmannia clavigera</i> to monoterpenes: Biochemical mechanisms revealed by RNA-seq analysis. <i>Forest Pathology</i> , 2017, 47, e12372.	1.1	4
6	FACT is a sensor of DNA torsional stress in eukaryotic cells. <i>Nucleic Acids Research</i> , 2017, 45, gkw1366.	14.5	75
7	RNA Recombination Enhances Adaptability and Is Required for Virus Spread and Virulence. <i>Cell Host and Microbe</i> , 2016, 19, 493-503.	11.0	133
8	Brain region-specific methylation in the promoter of the murine oxytocin receptor gene is involved in its expression regulation. <i>Psychoneuroendocrinology</i> , 2014, 39, 121-131.	2.7	52
9	Mutational and fitness landscapes of an RNA virus revealed through population sequencing. <i>Nature</i> , 2014, 505, 686-690.	27.8	343
10	Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , 2014, 5, 3966.	12.8	124
11	High-resolution metabolic mapping of cell types in plant roots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1232-41.	7.1	131
12	Diversity of Long Terminal Repeat Retrotransposon Genome Distribution in Natural Populations of the Wild Diploid Wheat <i>Aegilops speltoides</i> . <i>Genetics</i> , 2012, 190, 263-274.	2.9	38
13	Tandem repeats on an eco-geographical scale: outcomes from the genome of <i>Aegilops speltoides</i> . <i>Chromosome Research</i> , 2011, 19, 607-623.	2.2	36
14	Transposable elements in a marginal plant population: temporal fluctuations provide new insights into genome evolution of wild diploid wheat. <i>Mobile DNA</i> , 2010, 1, 6.	3.6	85
15	A binary search approach to whole-genome data analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16893-16898.	7.1	7
16	Evaluation of Peak Picking Quality in LC-MS Metabolomics Data. <i>Analytical Chemistry</i> , 2010, 82, 9177-9187.	6.5	61