

# Laurent Jacob

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6140676/publications.pdf>

Version: 2024-02-01

14  
papers

1,109  
citations

1039880

9  
h-index

1058333

14  
g-index

20  
all docs

20  
docs citations

20  
times ranked

2090  
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein-ligand interaction prediction: an improved chemogenomics approach. <i>Bioinformatics</i> , 2008, 24, 2149-2156.	1.8	310
2	Statistical Methods for Handling Unwanted Variation in Metabolomics Data. <i>Analytical Chemistry</i> , 2015, 87, 3606-3615.	3.2	152
3	A fast and agnostic method for bacterial genome-wide association studies: Bridging the gap between k-mers and genetic events. <i>PLoS Genetics</i> , 2018, 14, e1007758.	1.5	144
4	Efficient peptide-MHC-I binding prediction for alleles with few known binders. <i>Bioinformatics</i> , 2008, 24, 358-366.	1.8	120
5	Virtual screening of GPCRs: An in silico chemogenomics approach. <i>BMC Bioinformatics</i> , 2008, 9, 363.	1.2	90
6	Correcting gene expression data when neither the unwanted variation nor the factor of interest are observed. <i>Biostatistics</i> , 2016, 17, 16-28.	0.9	82
7	More power via graph-structured tests for differential expression of gene networks. <i>Annals of Applied Statistics</i> , 2012, 6, .	0.5	67
8	Efficient RNA isoform identification and quantification from RNA-Seq data with network flows. <i>Bioinformatics</i> , 2014, 30, 2447-2455.	1.8	65
9	Niche specialization and spread of <i>Staphylococcus capitis</i> involved in neonatal sepsis. <i>Nature Microbiology</i> , 2020, 5, 735-745.	5.9	40
10	The healthy ageing gene expression signature for Alzheimer's disease diagnosis: a random sampling perspective. <i>Genome Biology</i> , 2018, 19, 97.	3.8	8
11	A convex formulation for joint RNA isoform detection and quantification from multiple RNA-seq samples. <i>BMC Bioinformatics</i> , 2015, 16, 262.	1.2	7
12	Controlling technical variation amongst 6693 patient microarrays of the randomized MINDACT trial. <i>Communications Biology</i> , 2020, 3, 397.	2.0	7
13	CALDERA: finding all significant de Bruijn subgraphs for bacterial GWAS. <i>Bioinformatics</i> , 2022, 38, i36-i44.	1.8	6
14	PEPA test: fast and powerful differential analysis from relative quantitative proteomics data using shared peptides. <i>Biostatistics</i> , 2019, 20, 632-647.	0.9	1