

# Patrik Koskinen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11356992/publications.pdf>

Version: 2024-02-01

13  
papers

1,850  
citations

840776

11  
h-index

1125743

13  
g-index

13  
all docs

13  
docs citations

13  
times ranked

3113  
citing authors

#	ARTICLE	IF	CITATIONS
1	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
2	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
3	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. <i>Nature Communications</i> , 2014, 5, 4737.	12.8	196
4	Cytokinin and Auxin Display Distinct but Interconnected Distribution and Signaling Profiles to Stimulate Cambial Activity. <i>Current Biology</i> , 2016, 26, 1990-1997.	3.9	170
5	PANNZER: high-throughput functional annotation of uncharacterized proteins in an error-prone environment. <i>Bioinformatics</i> , 2015, 31, 1544-1552.	4.1	123
6	Revised Phylogeny and Novel Horizontally Acquired Virulence Determinants of the Model Soft Rot Phytopathogen <i>Pectobacterium wasabiae</i> SCC3193. <i>PLoS Pathogens</i> , 2012, 8, e1003013.	4.7	93
7	Genome Sequence of <i>Dickeya solani</i> , a New soft Rot Pathogen of Potato, Suggests its Emergence May Be Related to a Novel Combination of Non-Ribosomal Peptide/Polyketide Synthetase Clusters. <i>Diversity</i> , 2013, 5, 824-842.	1.7	54
8	Flight-induced changes in gene expression in the Glanville fritillary butterfly. <i>Molecular Ecology</i> , 2015, 24, 4886-4900.	3.9	28
9	Transcriptome Analysis Reveals Signature of Adaptation to Landscape Fragmentation. <i>PLoS ONE</i> , 2014, 9, e101467.	2.5	24
10	Complete genome sequence of <i>Propionibacterium freudenreichii</i> DSM 20271T. <i>Standards in Genomic Sciences</i> , 2015, 10, 83.	1.5	23
11	Genome sequence of the model plant pathogen <i>Pectobacterium carotovorum</i> SCC1. <i>Standards in Genomic Sciences</i> , 2017, 12, 87.	1.5	16
12	gapFinisher: A reliable gap filling pipeline for SSPACE-LongRead scaffold output. <i>PLoS ONE</i> , 2019, 14, e0216885.	2.5	14
13	Genomic features separating ten strains of <i>Neorhizobium galegae</i> with different symbiotic phenotypes. <i>BMC Genomics</i> , 2015, 16, 348.	2.8	12