

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