

Nickolai N Alexandrov

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

4,135
citations

218677

26
h-index

345221

36
g-index

38
all docs

38
docs citations

38
times ranked

4891
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49. | 27.8 | 1,091 |
| 2 | Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296. | 21.4 | 413 |
| 3 | SNP-Seek database of SNPs derived from 3000 rice genomes. <i>Nucleic Acids Research</i> , 2015, 43, D1023-D1027. | 14.5 | 357 |
| 4 | Rice SNP-seek database update: new SNPs, indels, and queries. <i>Nucleic Acids Research</i> , 2017, 45, D1075-D1081. | 14.5 | 290 |
| 5 | Insights into corn genes derived from large-scale cDNA sequencing. <i>Plant Molecular Biology</i> , 2009, 69, 179-194. | 3.9 | 212 |
| 6 | PDP: protein domain parser. <i>Bioinformatics</i> , 2003, 19, 429-430. | 4.1 | 152 |
| 7 | Full-length messenger RNA sequences greatly improve genome annotation. <i>Genome Biology</i> , 2002, 3, research0029.1. | 9.6 | 147 |
| 8 | Features of Arabidopsis Genes and Genome Discovered using Full-length cDNAs. <i>Plant Molecular Biology</i> , 2006, 60, 69-85. | 3.9 | 145 |
| 9 | GC3 biology in corn, rice, sorghum and other grasses. <i>BMC Genomics</i> , 2010, 11, 308. | 2.8 | 116 |
| 10 | Structural variants in 3000 rice genomes. <i>Genome Research</i> , 2019, 29, 870-880. | 5.5 | 112 |
| 11 | High Resolution Genetic Mapping by Genome Sequencing Reveals Genome Duplication and Tetraploid Genetic Structure of the Diploid <i>Miscanthus sinensis</i> . <i>PLoS ONE</i> , 2012, 7, e33821. | 2.5 | 103 |
| 12 | Common spatial arrangements of backbone fragments in homologous and non-homologous proteins. <i>Journal of Molecular Biology</i> , 1992, 225, 5-9. | 4.2 | 102 |
| 13 | A platinum standard pan-genome resource that represents the population structure of Asian rice. <i>Scientific Data</i> , 2020, 7, 113. | 5.3 | 86 |
| 14 | Towards a deeper haplotype mining of complex traits in rice with <scp>RFGB</scp> v2.0. <i>Plant Biotechnology Journal</i> , 2020, 18, 14-16. | 8.3 | 78 |
| 15 | SARFing the PDB. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 727-732. | 2.1 | 76 |
| 16 | Whole genome sequencing-based association study to unravel genetic architecture of cooked grain width and length traits in rice. <i>Scientific Reports</i> , 2017, 7, 12478. | 3.3 | 69 |
| 17 | Biological meaning, statistical significance, and classification of local spatial similarities in nonhomologous proteins. <i>Protein Science</i> , 1994, 3, 866-875. | 7.6 | 68 |
| 18 | An imputation platform to enhance integration of rice genetic resources. <i>Nature Communications</i> , 2018, 9, 3519. | 12.8 | 65 |

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|----|---|------|-----------|
| 19 | Toward Consistent Assignment of Structural Domains in Proteins. <i>Journal of Molecular Biology</i> , 2004, 339, 647-678. | 4.2 | 63 |
| 20 | Allele mining and enhanced genetic recombination for rice breeding. <i>Rice</i> , 2015, 8, 34. | 4.0 | 57 |
| 21 | Analysis of topological and nontopological structural similarities in the PDB: New examples with old structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 25, 354-365. | 2.6 | 49 |
| 22 | SNP-Seek II: A resource for allele mining and analysis of big genomic data in <i>Oryza sativa</i> . <i>Current Plant Biology</i> , 2016, 7-8, 16-25. | 4.7 | 48 |
| 23 | Nucleotide diversity analysis highlights functionally important genomic regions. <i>Scientific Reports</i> , 2016, 6, 35730. | 3.3 | 48 |
| 24 | Skew in CG content near the transcription start site in <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2003, 19, i313-i314. | 4.1 | 32 |
| 25 | Genome-Wide Discovery of cis-Elements in Promoter Sequences Using Gene Expression. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 139-151. | 2.0 | 32 |
| 26 | Structural argument for N-terminal initiation of protein folding. <i>Protein Science</i> , 1993, 2, 1989-1991. | 7.6 | 27 |
| 27 | A comparative proteomics resource: proteins of <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2003, 4, R51. | 9.6 | 25 |
| 28 | Application of a new method of pattern recognition in DNA sequence analysis: a study of <i>E.coli</i> promoters. <i>Nucleic Acids Research</i> , 1990, 18, 1847-1852. | 14.5 | 22 |
| 29 | Statistical method for rapid homology search. <i>Nucleic Acids Research</i> , 1988, 16, 5169-5173. | 14.5 | 17 |
| 30 | Rice Galaxy: an open resource for plant science. <i>GigaScience</i> , 2019, 8, . | 6.4 | 11 |
| 31 | Shared cis-regulatory architecture identified across defense response genes is associated with broad-spectrum quantitative resistance in rice. <i>Scientific Reports</i> , 2019, 9, 1536. | 3.3 | 6 |
| 32 | Nucleotide binding in β -sheet topologies. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 677-678. | 8.2 | 4 |
| 33 | Progress in single-access information systems for wheat and rice crop improvement. <i>Briefings in Bioinformatics</i> , 2019, 20, 565-571. | 6.5 | 4 |
| 34 | Predicting rice phenotypes with meta and multi-target learning. <i>Machine Learning</i> , 2020, 109, 2195-2212. | 5.4 | 3 |
| 35 | Predicting Rice Phenotypes with Meta-learning. <i>Lecture Notes in Computer Science</i> , 2018, , 144-158. | 1.3 | 2 |
| 36 | Local multiple alignment by consensus matrix. <i>Bioinformatics</i> , 1992, 8, 339-345. | 4.1 | 1 |