

Finn Drabås

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/380301/publications.pdf>

Version: 2024-02-01

73
papers

6,405
citations

159585

30
h-index

82547

72
g-index

73
all docs

73
docs citations

73
times ranked

13552
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470. | 27.8 | 1,838 |
| 2 | Alkylation damage in DNA and RNA repair mechanisms and medical significance. <i>DNA Repair</i> , 2004, 3, 1389-1407. | 2.8 | 541 |
| 3 | Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014. | 12.6 | 517 |
| 4 | Uracil in DNA occurrence, consequences and repair. <i>Oncogene</i> , 2002, 21, 8935-8948. | 5.9 | 423 |
| 5 | Gene regulation in the immediate-early response process. <i>Advances in Biological Regulation</i> , 2016, 62, 37-49. | 2.3 | 322 |
| 6 | EpiFactors: a comprehensive database of human epigenetic factors and complexes. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav067. | 3.0 | 226 |
| 7 | Cell cycle regulation of human DNA repair and chromatin remodeling genes. <i>DNA Repair</i> , 2015, 30, 53-67. | 2.8 | 174 |
| 8 | Bioinformatic mapping of AlkB homology domains in viruses. <i>BMC Genomics</i> , 2005, 6, 1. | 2.8 | 166 |
| 9 | Human ABH3 structure and key residues for oxidative demethylation to reverse DNA/RNA damage. <i>EMBO Journal</i> , 2006, 25, 3389-3397. | 7.8 | 157 |
| 10 | Identification of a novel, widespread, and functionally important PCNA-binding motif. <i>Journal of Cell Biology</i> , 2009, 186, 645-654. | 5.2 | 153 |
| 11 | The major histocompatibility class I locus in Atlantic salmon (<i>Salmo salar</i> L.): polymorphism, linkage analysis and protein modelling. <i>Immunogenetics</i> , 2002, 54, 570-581. | 2.4 | 151 |
| 12 | A survey of motif discovery methods in an integrated framework. <i>Biology Direct</i> , 2006, 1, 11. | 4.6 | 135 |
| 13 | Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017, 45, D737-D743. | 14.5 | 116 |
| 14 | Gene duplications in prokaryotes can be associated with environmental adaptation. <i>BMC Genomics</i> , 2010, 11, 588. | 2.8 | 102 |
| 15 | A novel POLE mutation associated with cancers of colon, pancreas, ovaries and small intestine. <i>Familial Cancer</i> , 2015, 14, 437-448. | 1.9 | 67 |
| 16 | A manually curated ChIP-seq benchmark demonstrates room for improvement in current peak-finder programs. <i>Nucleic Acids Research</i> , 2011, 39, e25-e25. | 14.5 | 62 |
| 17 | Detecting periodic patterns in biological sequences. <i>Bioinformatics</i> , 1998, 14, 498-507. | 4.1 | 61 |
| 18 | Improved benchmarks for computational motif discovery. <i>BMC Bioinformatics</i> , 2007, 8, 193. | 2.6 | 61 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Vitamin D receptor ChIP-seq in primary CD4+ cells: relationship to serum 25-hydroxyvitamin D levels and autoimmune disease. <i>BMC Medicine</i> , 2013, 11, 163. | 5.5 | 59 |
| 20 | A novel non-canonical Wnt signature for prostate cancer aggressiveness. <i>Oncotarget</i> , 2017, 8, 9572-9586. | 1.8 | 59 |
| 21 | High coverage sequencing of DNA from microorganisms living in an oil reservoir 2.5 kilometres subsurface. <i>Environmental Microbiology Reports</i> , 2011, 3, 674-681. | 2.4 | 57 |
| 22 | The microbial communities in two apparently physically separated deep subsurface oil reservoirs show extensive DNA sequence similarities. <i>Environmental Microbiology</i> , 2014, 16, 545-558. | 3.8 | 50 |
| 23 | Transcription profiling during the cell cycle shows that a subset of Polycomb-targeted genes is upregulated during DNA replication. <i>Nucleic Acids Research</i> , 2013, 41, 2846-2856. | 14.5 | 48 |
| 24 | EXAFS study of zinc coordination in bacitracin A. <i>BBA - Proteins and Proteomics</i> , 1999, 1431, 433-442. | 2.1 | 47 |
| 25 | Assessment of composite motif discovery methods. <i>BMC Bioinformatics</i> , 2008, 9, 123. | 2.6 | 44 |
| 26 | Use of multigene panel identifies pathogenic variants in several CRC predisposing genes in patients previously tested for Lynch Syndrome. <i>Clinical Genetics</i> , 2017, 92, 405-414. | 2.0 | 41 |
| 27 | Comparative Genomics to Delineate Pathogenic Potential in Non-O157 Shiga Toxin-Producing <i>Escherichia coli</i> (STEC) from Patients with and without Haemolytic Uremic Syndrome (HUS) in Norway. <i>PLoS ONE</i> , 2014, 9, e111788. | 2.5 | 41 |
| 28 | Robust Distance Measures for k-NN Classification of Cancer Data. <i>Cancer Informatics</i> , 2020, 19, 117693512096554. | 1.9 | 37 |
| 29 | Isolation of Mutant Alginate Lyases with Cleavage Specificity for Di-guluronic Acid Linkages. <i>Journal of Biological Chemistry</i> , 2010, 285, 35284-35292. | 3.4 | 34 |
| 30 | MotifLab: a tools and data integration workbench for motif discovery and regulatory sequence analysis. <i>BMC Bioinformatics</i> , 2013, 14, 9. | 2.6 | 34 |
| 31 | The Genomic HyperBrowser: an analysis web server for genome-scale data. <i>Nucleic Acids Research</i> , 2013, 41, W133-W141. | 14.5 | 32 |
| 32 | Clustered ChIP-Seq-defined transcription factor binding sites and histone modifications map distinct classes of regulatory elements. <i>BMC Biology</i> , 2011, 9, 80. | 3.8 | 30 |
| 33 | Directed evolution of the transcription factor XylS for development of improved expression systems. <i>Microbial Biotechnology</i> , 2010, 3, 38-47. | 4.2 | 25 |
| 34 | Structural and functional analysis of the hemagglutinin-esterase of infectious salmon anaemia virus. <i>Virus Research</i> , 2010, 151, 131-141. | 2.2 | 25 |
| 35 | Relationship between operon preference and functional properties of persistent genes in bacterial genomes. <i>BMC Genomics</i> , 2010, 11, 71. | 2.8 | 24 |
| 36 | A Balanced Tissue Composition Reveals New Metabolic and Gene Expression Markers in Prostate Cancer. <i>PLoS ONE</i> , 2016, 11, e0153727. | 2.5 | 24 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 37 | TopolCSim: a new semantic similarity measure based on gene ontology. BMC Bioinformatics, 2016, 17, 296. | 2.6 | 24 |
| 38 | The blind watchmaker and rational protein engineering. Journal of Biotechnology, 1994, 36, 185-220. | 3.8 | 23 |
| 39 | The Pseudomonas syringae Genome Encodes a Combined Mannuronan C-5-epimerase and O-Acetylhydrolase, Which Strongly Enhances the Predicted Gel-forming Properties of Alginates. Journal of Biological Chemistry, 2004, 279, 28920-28929. | 3.4 | 22 |
| 40 | GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. GigaScience, 2017, 6, 1-12. | 6.4 | 22 |
| 41 | Protein Alpha Shape (PAS) Dock: A new gaussian-based score function suitable for docking in homology modelled protein structures. Journal of Computer-Aided Molecular Design, 2006, 20, 131-144. | 2.9 | 21 |
| 42 | c-Myb Binding Sites in Haematopoietic Chromatin Landscapes. PLoS ONE, 2015, 10, e0133280. | 2.5 | 20 |
| 43 | LSD1 represses a neonatal/repairative gene program in adult intestinal epithelium. Science Advances, 2020, 6, . | 10.3 | 18 |
| 44 | Cell-type specificity of ChIP-predicted transcription factor binding sites. BMC Genomics, 2012, 13, 372. | 2.8 | 17 |
| 45 | Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. BMC Genomics, 2014, 15, 120. | 2.8 | 17 |
| 46 | Clustering of non-polar contacts in proteins. Bioinformatics, 1999, 15, 501-509. | 4.1 | 16 |
| 47 | Gene signatures ESC, MYC and ERG-fusion are early markers of a potentially dangerous subtype of prostate cancer. BMC Medical Genomics, 2014, 7, 50. | 1.5 | 16 |
| 48 | Feature-based classification of human transcription factors into hypothetical sub-classes related to regulatory function. BMC Bioinformatics, 2016, 17, 459. | 2.6 | 15 |
| 49 | Differential Gene Expression Downstream of Toll-like Receptors (TLRs). Journal of Biological Chemistry, 2010, 285, 17011-17019. | 3.4 | 14 |
| 50 | Enhanced Efficacy of Bleomycin in Bladder Cancer Cells by Photochemical Internalization. BioMed Research International, 2014, 2014, 1-10. | 1.9 | 14 |
| 51 | A ChIP-Seq Benchmark Shows That Sequence Conservation Mainly Improves Detection of Strong Transcription Factor Binding Sites. PLoS ONE, 2011, 6, e18430. | 2.5 | 12 |
| 52 | Compo: composite motif discovery using discrete models. BMC Bioinformatics, 2008, 9, 527. | 2.6 | 11 |
| 53 | Measures of co-expression for improved function prediction of long non-coding RNAs. BMC Bioinformatics, 2018, 19, 533. | 2.6 | 11 |
| 54 | Pathway Analysis of Skin from Psoriasis Patients after Adalimumab Treatment Reveals New Early Events in the Anti-Inflammatory Mechanism of Anti-TNF- α . PLoS ONE, 2016, 11, e0167437. | 2.5 | 11 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 55 | Safety in numbers: multiple occurrences of highly similar homologs among <i>Azotobacter vinelandii</i> carbohydrate metabolism proteins probably confer adaptive benefits. <i>BMC Genomics</i> , 2014, 15, 192. | 2.8 | 10 |
| 56 | The eGenVar data management system—cataloguing and sharing sensitive data and metadata for the life sciences. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau027. | 3.0 | 10 |
| 57 | Studies of the photosensitizer disulfonated meso-tetraphenyl chlorin in an orthotopic rat bladder tumor model. <i>Photodiagnosis and Photodynamic Therapy</i> , 2015, 12, 58-66. | 2.6 | 10 |
| 58 | Norwegian e-Infrastructure for Life Sciences (NeLS). <i>F1000Research</i> , 2018, 7, 968. | 1.6 | 10 |
| 59 | Symmetric distance measures for mass spectra. <i>Analytica Chimica Acta</i> , 1987, 201, 225-239. | 5.4 | 9 |
| 60 | The differential disease regulome. <i>BMC Genomics</i> , 2011, 12, 353. | 2.8 | 9 |
| 61 | The Triform algorithm: improved sensitivity and specificity in ChIP-Seq peak finding. <i>BMC Bioinformatics</i> , 2012, 13, 176. | 2.6 | 8 |
| 62 | Genome Sequences of 11 Shiga Toxin-Producing <i>Escherichia coli</i> Strains. <i>Genome Announcements</i> , 2015, 3, . | 0.8 | 8 |
| 63 | PriorsEditor: a tool for the creation and use of positional priors in motif discovery. <i>Bioinformatics</i> , 2010, 26, 2195-2197. | 4.1 | 7 |
| 64 | A property-based analysis of human transcription factors. <i>BMC Research Notes</i> , 2015, 8, 82. | 1.4 | 7 |
| 65 | Recommendations for the FAIRification of genomic track metadata. <i>F1000Research</i> , 2021, 10, 268. | 1.6 | 7 |
| 66 | Transformations for mass spectra. <i>Analytica Chimica Acta</i> , 1992, 256, 145-151. | 5.4 | 5 |
| 67 | Protein Alpha Shape Similarity Analysis (PASSA): a new method for mapping protein binding sites. Application in the design of a selective inhibitor of tyrosine kinase 2. <i>Journal of Computer-Aided Molecular Design</i> , 2002, 16, 831-840. | 2.9 | 5 |
| 68 | Targeted sequencing of genes associated with the mismatch repair pathway in patients with endometrial cancer. <i>PLoS ONE</i> , 2020, 15, e0235613. | 2.5 | 4 |
| 69 | Design of Selective Inhibitors of Tyrosine Kinase 2. <i>Letters in Drug Design and Discovery</i> , 2005, 2, 507-515. | 0.7 | 3 |
| 70 | Enhanced identification of significant regulators of gene expression. <i>BMC Bioinformatics</i> , 2020, 21, 134. | 2.6 | 3 |
| 71 | FunHoP: Enhanced Visualization and Analysis of Functionally Homologous Proteins in Complex Metabolic Networks. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 848-859. | 6.9 | 2 |
| 72 | GAPGOM—an R package for gene annotation prediction using GO metrics. <i>BMC Research Notes</i> , 2021, 14, 162. | 1.4 | 1 |

| # | ARTICLE | IF | CITATIONS |
|----|---|----|-----------|
| 73 | False Discovery Rates in Identifying Functional DNA Motifs. , 2007, , . | | 0 |