

Finn Drabläs

List of Publications by Year in descending order

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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	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
2	GAPGOM – an R package for gene annotation prediction using GO metrics. <i>BMC Research Notes</i> , 2021, 14, 162.	1.4	1
3	Recommendations for the FAIRification of genomic track metadata. <i>F1000Research</i> , 2021, 10, 268.	1.6	7
4	Robust Distance Measures for <i>k</i> -NN Classification of Cancer Data. <i>Cancer Informatics</i> , 2020, 19, 117693512096554.	1.9	37
5	LSD1 represses a neonatal/repairative gene program in adult intestinal epithelium. <i>Science Advances</i> , 2020, 6, .	10.3	18
6	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
7	Enhanced identification of significant regulators of gene expression. <i>BMC Bioinformatics</i> , 2020, 21, 134.	2.6	3
8	Measures of co-expression for improved function prediction of long non-coding RNAs. <i>BMC Bioinformatics</i> , 2018, 19, 533.	2.6	11
9	Norwegian e-Infrastructure for Life Sciences (NeLS). <i>F1000Research</i> , 2018, 7, 968.	1.6	10
10	Use of multigene panel identifies pathogenic variants in several <i>CRC</i> predisposing genes in patients previously tested for Lynch Syndrome. <i>Clinical Genetics</i> , 2017, 92, 405-414.	2.0	41
11	GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. <i>GigaScience</i> , 2017, 6, 1-12.	6.4	22
12	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
13	A novel non-canonical Wnt signature for prostate cancer aggressiveness. <i>Oncotarget</i> , 2017, 8, 9572-9586.	1.8	59
14	Feature-based classification of human transcription factors into hypothetical sub-classes related to regulatory function. <i>BMC Bioinformatics</i> , 2016, 17, 459.	2.6	15
15	A Balanced Tissue Composition Reveals New Metabolic and Gene Expression Markers in Prostate Cancer. <i>PLoS ONE</i> , 2016, 11, e0153727.	2.5	24
16	TopolCSim: a new semantic similarity measure based on gene ontology. <i>BMC Bioinformatics</i> , 2016, 17, 296.	2.6	24
17	Gene regulation in the immediate-early response process. <i>Advances in Biological Regulation</i> , 2016, 62, 37-49.	2.3	322
18	Pathway Analysis of Skin from Psoriasis Patients after Adalimumab Treatment Reveals New Early Events in the Anti-Inflammatory Mechanism of Anti-TNF- α . <i>PLoS ONE</i> , 2016, 11, e0167437.	2.5	11

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19	EpiFactors: a comprehensive database of human epigenetic factors and complexes. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav067.	3.0	226
20	c-Myb Binding Sites in Haematopoietic Chromatin Landscapes. PLoS ONE, 2015, 10, e0133280.	2.5	20
21	Genome Sequences of 11 Shiga Toxin-Producing Escherichia coli Strains. Genome Announcements, 2015, 3, .	0.8	8
22	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
23	Studies of the photosensitizer disulfonated meso-tetraphenyl chlorin in an orthotopic rat bladder tumor model. Photodiagnosis and Photodynamic Therapy, 2015, 12, 58-66.	2.6	10
24	A novel POLE mutation associated with cancers of colon, pancreas, ovaries and small intestine. Familial Cancer, 2015, 14, 437-448.	1.9	67
25	A property-based analysis of human transcription factors. BMC Research Notes, 2015, 8, 82.	1.4	7
26	Cell cycle regulation of human DNA repair and chromatin remodeling genes. DNA Repair, 2015, 30, 53-67.	2.8	174
27	Safety in numbers: multiple occurrences of highly similar homologs among Azotobacter vinelandii carbohydrate metabolism proteins probably confer adaptive benefits. BMC Genomics, 2014, 15, 192.	2.8	10
28	The microbial communities in two apparently physically separated deep subsurface oil reservoirs show extensive <sc>DNA</sc> sequence similarities. Environmental Microbiology, 2014, 16, 545-558.	3.8	50
29	The eGenVar data management systemâ€”cataloguing and sharing sensitive data and metadata for the life sciences. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau027.	3.0	10
30	Enhanced Efficacy of Bleomycin in Bladder Cancer Cells by Photochemical Internalization. BioMed Research International, 2014, 2014, 1-10.	1.9	14
31	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
32	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
33	Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. BMC Genomics, 2014, 15, 120.	2.8	17
34	Comparative Genomics to Delineate Pathogenic Potential in Non-O157 Shiga Toxin-Producing Escherichia coli (STEC) from Patients with and without Haemolytic Uremic Syndrome (HUS) in Norway. PLoS ONE, 2014, 9, e111788.	2.5	41
35	MotifLab: a tools and data integration workbench for motif discovery and regulatory sequence analysis. BMC Bioinformatics, 2013, 14, 9.	2.6	34
36	Vitamin D receptor ChIP-seq in primary CD4+ cells: relationship to serum 25-hydroxyvitamin D levels and autoimmune disease. BMC Medicine, 2013, 11, 163.	5.5	59

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37	The Genomic HyperBrowser: an analysis web server for genome-scale data. <i>Nucleic Acids Research</i> , 2013, 41, W133-W141.	14.5	32
38	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
39	The Triform algorithm: improved sensitivity and specificity in ChIP-Seq peak finding. <i>BMC Bioinformatics</i> , 2012, 13, 176.	2.6	8
40	Cell-type specificity of ChIP-predicted transcription factor binding sites. <i>BMC Genomics</i> , 2012, 13, 372.	2.8	17
41	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
42	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
43	The differential disease regulome. <i>BMC Genomics</i> , 2011, 12, 353.	2.8	9
44	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
45	A ChIP-Seq Benchmark Shows That Sequence Conservation Mainly Improves Detection of Strong Transcription Factor Binding Sites. <i>PLoS ONE</i> , 2011, 6, e18430.	2.5	12
46	Gene duplications in prokaryotes can be associated with environmental adaptation. <i>BMC Genomics</i> , 2010, 11, 588.	2.8	102
47	Relationship between operon preference and functional properties of persistent genes in bacterial genomes. <i>BMC Genomics</i> , 2010, 11, 71.	2.8	24
48	Directed evolution of the transcription factor XylS for development of improved expression systems. <i>Microbial Biotechnology</i> , 2010, 3, 38-47.	4.2	25
49	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
50	Differential Gene Expression Downstream of Toll-like Receptors (TLRs). <i>Journal of Biological Chemistry</i> , 2010, 285, 17011-17019.	3.4	14
51	PriorsEditor: a tool for the creation and use of positional priors in motif discovery. <i>Bioinformatics</i> , 2010, 26, 2195-2197.	4.1	7
52	Structural and functional analysis of the hemagglutinin-esterase of infectious salmon anaemia virus. <i>Virus Research</i> , 2010, 151, 131-141.	2.2	25
53	Identification of a novel, widespread, and functionally important PCNA-binding motif. <i>Journal of Cell Biology</i> , 2009, 186, 645-654.	5.2	153
54	Assessment of composite motif discovery methods. <i>BMC Bioinformatics</i> , 2008, 9, 123.	2.6	44

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55	Compo: composite motif discovery using discrete models. BMC Bioinformatics, 2008, 9, 527.	2.6	11
56	False Discovery Rates in Identifying Functional DNA Motifs. , 2007, , .		0
57	Improved benchmarks for computational motif discovery. BMC Bioinformatics, 2007, 8, 193.	2.6	61
58	A survey of motif discovery methods in an integrated framework. Biology Direct, 2006, 1, 11.	4.6	135
59	Human ABH3 structure and key residues for oxidative demethylation to reverse DNA/RNA damage. EMBO Journal, 2006, 25, 3389-3397.	7.8	157
60	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
61	Bioinformatic mapping of AlkB homology domains in viruses. BMC Genomics, 2005, 6, 1.	2.8	166
62	Design of Selective Inhibitors of Tyrosine Kinase 2. Letters in Drug Design and Discovery, 2005, 2, 507-515.	0.7	3
63	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
64	Alkylation damage in DNA and RNA repair mechanisms and medical significance. DNA Repair, 2004, 3, 1389-1407.	2.8	541
65	The major histocompatibility class I locus in Atlantic salmon (Salmo salar L.): polymorphism, linkage analysis and protein modelling. Immunogenetics, 2002, 54, 570-581.	2.4	151
66	Uracil in DNA occurrence, consequences and repair. Oncogene, 2002, 21, 8935-8948.	5.9	423
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. Journal of Computer-Aided Molecular Design, 2002, 16, 831-840.	2.9	5
68	Clustering of non-polar contacts in proteins. Bioinformatics, 1999, 15, 501-509.	4.1	16
69	EXAFS study of zinc coordination in bacitracin A. BBA - Proteins and Proteomics, 1999, 1431, 433-442.	2.1	47
70	Detecting periodic patterns in biological sequences. Bioinformatics, 1998, 14, 498-507.	4.1	61
71	The blind watchmaker and rational protein engineering. Journal of Biotechnology, 1994, 36, 185-220.	3.8	23
72	Transformations for mass spectra. Analytica Chimica Acta, 1992, 256, 145-151.	5.4	5

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73	Symmetric distance measures for mass spectra. <i>Analytica Chimica Acta</i> , 1987, 201, 225-239.	5.4	9