

Torgeir R Hvidsten

List of Publications by Year in descending order

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63
papers

5,788
citations

136950

32
h-index

133252

59
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84
all docs

84
docs citations

84
times ranked

8604
citing authors

#	ARTICLE	IF	CITATIONS
1	A Dual Enrichment Strategy Provides Soil- and Digestate-Competent Nitrous Oxide-Respiring Bacteria for Mitigating Climate Forcing in Agriculture. <i>MBio</i> , 2022, 13, .	4.1	5
2	What can cold-induced transcriptomes of Arctic Brassicaceae tell us about the evolution of cold tolerance?. <i>Molecular Ecology</i> , 2022, 31, 4271-4285.	3.9	5
3	Transkingdom network analysis provides insight into host-microbiome interactions in Atlantic salmon. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1028-1034.	4.1	4
4	Overexpression of vesicle-associated membrane protein PttVAP27-17 as a tool to improve biomass production and the overall saccharification yields in <i>Populus</i> trees. <i>Biotechnology for Biofuels</i> , 2021, 14, 43.	6.2	10
5	Comparative regulomics supports pervasive selection on gene dosage following whole genome duplication. <i>Genome Biology</i> , 2021, 22, 103.	8.8	54
6	Innovation, conservation, and repurposing of gene function in root cell type development. <i>Cell</i> , 2021, 184, 3333-3348.e19.	28.9	48
7	<i>Populus</i> PtERF85 Balances Xylem Cell Expansion and Secondary Cell Wall Formation in Hybrid Aspen. <i>Cells</i> , 2021, 10, 1971.	4.1	11
8	Leaf shape in <i>Populus tremula</i> is a complex, omnigenic trait. <i>Ecology and Evolution</i> , 2020, 10, 11922-11940.	1.9	19
9	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. <i>Nature Communications</i> , 2020, 11, 5773.	12.8	55
10	Integration of absolute multi-omics reveals dynamic protein-to-RNA ratios and metabolic interplay within mixed-domain microbiomes. <i>Nature Communications</i> , 2020, 11, 4708.	12.8	28
11	A metabolite roadmap of the wood-forming tissue in <i>Populus tremula</i> . <i>New Phytologist</i> , 2020, 228, 1559-1572.	7.3	32
12	SalMotifDB: a tool for analyzing putative transcription factor binding sites in salmonid genomes. <i>BMC Genomics</i> , 2019, 20, 694.	2.8	13
13	Evolution of Cold Acclimation and Its Role in Niche Transition in the Temperate Grass Subfamily Pooideae. <i>Plant Physiology</i> , 2019, 180, 404-419.	4.8	45
14	From proteins to polysaccharides: lifestyle and genetic evolution of <i>Coprothermobacter proteolyticus</i> . <i>ISME Journal</i> , 2019, 13, 603-617.	9.8	30
15	Photoperiodic control of seasonal growth is mediated by ABA acting on cell-cell communication. <i>Science</i> , 2018, 360, 212-215.	12.6	272
16	Life-stage-associated remodelling of lipid metabolism regulation in Atlantic salmon. <i>Molecular Ecology</i> , 2018, 27, 1200-1213.	3.9	35
17	A multi-omics approach reveals function of Secretory Carrier-Associated Membrane Proteins in wood formation of <i>Populus</i> trees. <i>BMC Genomics</i> , 2018, 19, 11.	2.8	25
18	Ethylene signaling induces gelatinous layers with typical features of tension wood in hybrid aspen. <i>New Phytologist</i> , 2018, 218, 999-1014.	7.3	52

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19	The Grayling Genome Reveals Selection on Gene Expression Regulation after Whole-Genome Duplication. <i>Genome Biology and Evolution</i> , 2018, 10, 2785-2800.	2.5	42
20	Functional and evolutionary genomic inferences in <i>Populus</i> through genome and population sequencing of American and European aspen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10970-E10978.	7.1	84
21	Subfunctionalization versus neofunctionalization after whole-genome duplication. <i>Nature Genetics</i> , 2018, 50, 908-909.	21.4	67
22	NorWood: a gene expression resource for evo-devo studies of conifer wood development. <i>New Phytologist</i> , 2017, 216, 482-494.	7.3	71
23	Lineage-specific rediploidization is a mechanism to explain time-lags between genome duplication and evolutionary diversification. <i>Genome Biology</i> , 2017, 18, 111.	8.8	136
24	AspWood: High-Spatial-Resolution Transcriptome Profiles Reveal Uncharacterized Modularity of Wood Formation in <i>Populus tremula</i> . <i>Plant Cell</i> , 2017, 29, 1585-1604.	6.6	219
25	Gene co-expression network connectivity is an important determinant of selective constraint. <i>PLoS Genetics</i> , 2017, 13, e1006402.	3.5	106
26	Quantitative proteomics reveals protein profiles underlying major transitions in aspen wood development. <i>BMC Genomics</i> , 2016, 17, 119.	2.8	35
27	The Atlantic salmon genome provides insights into rediploidization. <i>Nature</i> , 2016, 533, 200-205.	27.8	1,021
28	Extracting functional trends from whole genome duplication events using comparative genomics. <i>Biological Procedures Online</i> , 2016, 18, 11.	2.9	45
29	Towards integration of population and comparative genomics in forest trees. <i>New Phytologist</i> , 2016, 212, 338-344.	7.3	31
30	Serendipitous Meta-Transcriptomics: The Fungal Community of Norway Spruce (<i>Picea abies</i>). <i>PLoS ONE</i> , 2015, 10, e0139080.	2.5	27
31	The Plant Genome Integrative Explorer Resource: PlantGenIE.org. <i>New Phytologist</i> , 2015, 208, 1149-1156.	7.3	282
32	<i>Populus tremula</i> (European aspen) shows no evidence of sexual dimorphism. <i>BMC Plant Biology</i> , 2014, 14, 276.	3.6	45
33	ComPlex: conservation and divergence of co-expression networks in <i>A. thaliana</i> , <i>Populus</i> and <i>O. sativa</i> . <i>BMC Genomics</i> , 2014, 15, 106.	2.8	69
34	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014, 345, 1250091.	12.6	318
35	Synergy: A Web Resource for Exploring Gene Regulation in <i>Synechocystis</i> sp. PCC6803. <i>PLoS ONE</i> , 2014, 9, e113496.	2.5	4
36	Co-expression analysis, proteomic and metabolomic study on the impact of a Deg/HtrA protease triple mutant in <i>Synechocystis</i> sp. PCC 6803 exposed to temperature and high light stress. <i>Journal of Proteomics</i> , 2013, 78, 294-311.	2.4	19

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37	OnPLS integration of transcriptomic, proteomic and metabolomic data shows multi-level oxidative stress responses in the cambium of transgenic hipl- superoxide dismutase Populus plants. BMC Genomics, 2013, 14, 893.	2.8	63
38	Characterization of cytokinin signaling and homeostasis gene families in two hardwood tree species: Populus trichocarpa and Prunus persica. BMC Genomics, 2013, 14, 885.	2.8	38
39	The Norway spruce genome sequence and conifer genome evolution. Nature, 2013, 497, 579-584.	27.8	1,303
40	Activityâ€‘dormancy transition in the cambial meristem involves stage-specific modulation of auxin response in hybrid aspen. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3418-3423.	7.1	86
41	A systems biology model of the regulatory network in Populusleaves reveals interacting regulators and conserved regulation. BMC Plant Biology, 2011, 11, 13.	3.6	26
42	Classification of microarrays; synergistic effects between normalization, gene selection and machine learning. BMC Bioinformatics, 2011, 12, 390.	2.6	27
43	Challenges in microarray class discovery: a comprehensive examination of normalization, gene selection and clustering. BMC Bioinformatics, 2010, 11, 503.	2.6	51
44	A Computer Scientist's Guide to the Regulatory Genome. Fundamenta Informaticae, 2010, 103, 323-332.	0.4	2
45	A Comprehensive Analysis of the Structure-Function Relationship in Proteins Based on Local Structure Similarity. PLoS ONE, 2009, 4, e6266.	2.5	37
46	Using multi-data hidden Markov models trained on local neighborhoods of protein structure to predict residueâ€‘residue contacts. Bioinformatics, 2009, 25, 1264-1270.	4.1	39
47	Gene expression trends and protein features effectively complement each other in gene function prediction. Bioinformatics, 2009, 25, 322-330.	4.1	5
48	Local descriptors of protein structure: A systematic analysis of the sequenceâ€‘structure relationship in proteins using shortâ€‘and longâ€‘range interactions. Proteins: Structure, Function and Bioinformatics, 2009, 75, 870-884.	2.6	15
49	A segmental maximum a posteriori approach to genome-wide copy number profiling. Bioinformatics, 2008, 24, 751-758.	4.1	29
50	Interaction Model Based on Local Protein Substructures Generalizes to the Entire Structural Enzyme-Ligand Space. Journal of Chemical Information and Modeling, 2008, 48, 2278-2288.	5.4	33
51	Differential gene expression in the olfactory bulb following exposure to the olfactory toxicant 2,6-dichlorophenyl methylsulphone and its 2,5-dichlorinated isomer in mice. NeuroToxicology, 2007, 28, 1120-1128.	3.0	1
52	Revealing cell cycle control by combining model-based detection of periodic expression with novel cis-regulatory descriptors. BMC Systems Biology, 2007, 1, 45.	3.0	8
53	Rough Sets in Bioinformatics. , 2007, , 225-243.		10
54	Generalized modeling of enzyme-ligand interactions using proteochemometrics and local protein substructures. Proteins: Structure, Function and Bioinformatics, 2006, 65, 568-579.	2.6	38

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55	Using local gene expression similarities to discover regulatory binding site modules. BMC Bioinformatics, 2006, 7, 505.	2.6	12
56	Discovering regulatory binding-site modules using rule-based learning. Genome Research, 2005, 15, 856-866.	5.5	41
57	Markers of Adenocarcinoma Characteristic of the Site of Origin: Development of a Diagnostic Algorithm. Clinical Cancer Research, 2005, 11, 3766-3772.	7.0	296
58	Predicting Gene Ontology Biological Process From Temporal Gene Expression Patterns. Genome Research, 2003, 13, 965-979.	5.5	88
59	Learning rule-based models of biological process from gene expression time profiles using Gene Ontology. Bioinformatics, 2003, 19, 1116-1123.	4.1	81
60	A novel approach to fold recognition using sequence-derived properties from sets of structurally similar local fragments of proteins. Bioinformatics, 2003, 19, ii81-ii91.	4.1	25
61	Towards Knowledge Discovery from cDNA Microarray Gene Expression Data. Lecture Notes in Computer Science, 2000, , 470-475.	1.3	0
62	PREDICTING GENE FUNCTION FROM GENE EXPRESSIONS AND ONTOLOGIES. , 2000, , 299-310.		40
63	Bioinformatic Strategies for cDNA-Microarray Data Processing. , 0, , 61-74.		1