Torgeir R Hvidsten

List of Publications by Year
in descending order

63 papers	**5,788** citations	136950 **32** h-index	133252 **59** g-index
84 all docs	**84** docs citations	**84** times ranked	**8604** citing authors

#	Article	IF	Citations
1	The Norway spruce genome sequence and conifer genome evolution. Nature, 2013, 497, 579-584.	27.8	1,303
2	The Atlantic salmon genome provides insights into rediploidization. Nature, 2016, 533, 200-205.	27.8	1,021
3	Genome interplay in the grain transcriptome of hexaploid bread wheat. Science, 2014, 345, 1250091.	12.6	318
4	Markers of Adenocarcinoma Characteristic of the Site of Origin: Development of a Diagnostic Algorithm. Clinical Cancer Research, 2005, 11, 3766-3772.	7.0	296
5	The Plant Genome Integrative Explorer Resource: PlantGen<scp>IE</scp>.org. New Phytologist, 2015, 208, 1149-1156.	7.3	282
6	Photoperiodic control of seasonal growth is mediated by ABA acting on cell-cell communication. Science, 2018, 360, 212-215.	12.6	272
7	AspWood: High-Spatial-Resolution Transcriptome Profiles Reveal Uncharacterized Modularity of Wood Formation in <i>Populus tremula</i>. Plant Cell, 2017, 29, 1585-1604.	6.6	219
8	Lineage-specific rediploidization is a mechanism to explain time-lags between genome duplication and evolutionary diversification. Genome Biology, 2017, 18, 111.	8.8	136
9	Gene co-expression network connectivity is an important determinant of selective constraint. PLoS Genetics, 2017, 13, e1006402.	3.5	106
10	Predicting Gene Ontology Biological Process From Temporal Gene Expression Patterns. Genome Research, 2003, 13, 965-979.	5.5	88
11	Activity–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
12	Functional and evolutionary genomic inferences in <i>Populus</i> through genome and population sequencing of American and European aspen. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10970-E10978.	7.1	84
13	Learning rule-based models of biological process from gene expression time profiles using Gene Ontology. Bioinformatics, 2003, 19, 1116-1123.	4.1	81
14	NorWood: a gene expression resource for evo–devo studies of conifer wood development. New Phytologist, 2017, 216, 482-494.	7.3	71
15	ComPlEx: conservation and divergence of co-expression networks in A. thaliana, Populus and O. sativa. BMC Genomics, 2014, 15, 106.	2.8	69
16	Subfunctionalization versus neofunctionalization after whole-genome duplication. Nature Genetics, 2018, 50, 908-909.	21.4	67
17	OnPLS integration of transcriptomic, proteomic and metabolomic data shows multi-level oxidative stress responses in the cambium of transgenic hipI- superoxide dismutase Populus plants. BMC Genomics, 2013, 14, 893.	2.8	63
18	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. Nature Communications, 2020, 11, 5773.	12.8	55

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19	Comparative regulomics supports pervasive selection on gene dosage following whole genome duplication. Genome Biology, 2021, 22, 103.	8.8	54
20	Ethylene signaling induces gelatinous layers with typical features of tension wood in hybrid aspen. New Phytologist, 2018, 218, 999-1014.	7.3	52
21	Challenges in microarray class discovery: a comprehensive examination of normalization, gene selection and clustering. BMC Bioinformatics, 2010, 11, 503.	2.6	51
22	Innovation, conservation, and repurposing of gene function in root cell type development. Cell, 2021, 184, 3333-3348.e19.	28.9	48
23	Populus tremula (European aspen) shows no evidence of sexual dimorphism. BMC Plant Biology, 2014, 14, 276.	3.6	45
24	Extracting functional trends from whole genome duplication events using comparative genomics. Biological Procedures Online, 2016, 18, 11.	2.9	45
25	Evolution of Cold Acclimation and Its Role in Niche Transition in the Temperate Grass Subfamily Pooideae. Plant Physiology, 2019, 180, 404-419.	4.8	45
26	The Grayling Genome Reveals Selection on Gene Expression Regulation after Whole-Genome Duplication. Genome Biology and Evolution, 2018, 10, 2785-2800.	2.5	42
27	Discovering regulatory binding-site modules using rule-based learning. Genome Research, 2005, 15, 856-866.	5.5	41
28	PREDICTING GENE FUNCTION FROM GENE EXPRESSIONS AND ONTOLOGIES. , 2000, , 299-310.		40
29	Using multi-data hidden Markov models trained on local neighborhoods of protein structure to predict residue–residue contacts. Bioinformatics, 2009, 25, 1264-1270.	4.1	39
30	Generalized modeling of enzyme-ligand interactions using proteochemometrics and local protein substructures. Proteins: Structure, Function and Bioinformatics, 2006, 65, 568-579.	2.6	38
31	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
32	A Comprehensive Analysis of the Structure-Function Relationship in Proteins Based on Local Structure Similarity. PLoS ONE, 2009, 4, e6266.	2.5	37
33	Quantitative proteomics reveals protein profiles underlying major transitions in aspen wood development. BMC Genomics, 2016, 17, 119.	2.8	35
34	Life–stage–associated remodelling of lipid metabolism regulation in Atlantic salmon. Molecular Ecology, 2018, 27, 1200-1213.	3.9	35
35	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
36	A metabolite roadmap of the wood–forming tissue in <i>Populus tremula</i>. New Phytologist, 2020, 228, 1559-1572.	7.3	32

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37	Towards integration of population and comparative genomics in forest trees. New Phytologist, 2016, 212, 338-344.	7.3	31
38	From proteins to polysaccharides: lifestyle and genetic evolution of *Coprothermobacter proteolyticus*. ISME Journal, 2019, 13, 603-617.	9.8	30
39	A segmental maximum a posteriori approach to genome-wide copy number profiling. Bioinformatics, 2008, 24, 751-758.	4.1	29
40	Integration of absolute multi-omics reveals dynamic protein-to-RNA ratios and metabolic interplay within mixed-domain microbiomes. Nature Communications, 2020, 11, 4708.	12.8	28
41	Classification of microarrays; synergistic effects between normalization, gene selection and machine learning. BMC Bioinformatics, 2011, 12, 390.	2.6	27
42	Serendipitous Meta-Transcriptomics: The Fungal Community of Norway Spruce (Picea abies). PLoS ONE, 2015, 10, e0139080.	2.5	27
43	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
44	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
45	A multi-omics approach reveals function of Secretory Carrier-Associated Membrane Proteins in wood formation of‌ ‌‌Populus‌‌ ‌trees. BMC Genomics, 2018, 19, 11.	2.8	25
46	Co-expression analysis, proteomic and metabolomic study on the impact of a Deg/HtrA protease triple mutant in Synechocystis sp. PCC 6803 exposed to temperature and high light stress. Journal of Proteomics, 2013, 78, 294-311.	2.4	19
47	Leaf shape in Populus tremula is a complex, omnigenic trait. Ecology and Evolution, 2020, 10, 11922-11940.	1.9	19
48	Local descriptors of protein structure: A systematic analysis of the sequence–structure relationship in proteins using short–and long–range interactions. Proteins: Structure, Function and Bioinformatics, 2009, 75, 870-884.	2.6	15
49	SalMotifDB: a tool for analyzing putative transcription factor binding sites in salmonid genomes. BMC Genomics, 2019, 20, 694.	2.8	13
50	Using local gene expression similarities to discover regulatory binding site modules. BMC Bioinformatics, 2006, 7, 505.	2.6	12
51	PopulusPtERF85 Balances Xylem Cell Expansion and Secondary Cell Wall Formation in Hybrid Aspen. Cells, 2021, 10, 1971.	4.1	11
52	Overexpression of vesicle-associated membrane protein PttVAP27-17 as a tool to improve biomass production and the overall saccharification yields in Populus trees. Biotechnology for Biofuels, 2021, 14, 43.	6.2	10
53	Rough Sets in Bioinformatics. , 2007, , 225-243.		10
54	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

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55	Gene expression trends and protein features effectively complement each other in gene function prediction. Bioinformatics, 2009, 25, 322-330.	4.1	5
56	A Dual Enrichment Strategy Provides Soil- and Digestate-Competent Nitrous Oxide-Respiring Bacteria for Mitigating Climate Forcing in Agriculture. MBio, 2022, 13, .	4.1	5
57	What can cold‑induced transcriptomes of Arctic Brassicaceae tell us about the evolution of cold tolerance?. Molecular Ecology, 2022, 31, 4271-4285.	3.9	5
58	Transkingdom network analysis provides insight into host-microbiome interactions in Atlantic salmon. Computational and Structural Biotechnology Journal, 2021, 19, 1028-1034.	4.1	4
59	Synergy: A Web Resource for Exploring Gene Regulation in Synechocystis sp. PCC6803. PLoS ONE, 2014, 9, e113496.	2.5	4
60	A Computer Scientist's Guide to the Regulatory Genome. Fundamenta Informaticae, 2010, 103, 323-332.	0.4	2
61	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
62	Bioinformatic Strategies for cDNA-Microarray Data Processing. , 0, , 61-74.		1
63	Towards Knowledge Discovery from cDNA Microarray Gene Expression Data. Lecture Notes in Computer Science, 2000, , 470-475.	1.3	0