Simen RÃ¸d Sandve

List of Publications by Year
in descending order

46 papers	6,222 citations	257101 24 h-index	214527 47 g-index
63 all docs	63 docs citations	63 times ranked	7514 citing authors

#	Article	IF	Citations
1	Genome-Wide Reconstruction of Rediploidization Following Autopolyploidization across One Hundred Million Years of Salmonid Evolution. Molecular Biology and Evolution, 2022, 39, .	3.5	24
2	Transkingdom network analysis provides insight into host-microbiome interactions in Atlantic salmon. Computational and Structural Biotechnology Journal, 2021, 19, 1028-1034.	1.9	4
3	Diet and Life Stage-Associated Lipidome Remodeling in Atlantic Salmon. Journal of Agricultural and Food Chemistry, 2021, 69, 3787-3796.	2.4	5
4	Photoperiod-dependent developmental reprogramming of the transcriptional response to seawater entry in Atlantic salmon (Salmo salar). G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	2
5	Comparative regulomics supports pervasive selection on gene dosage following whole genome duplication. Genome Biology, 2021, 22, 103.	3.8	54
6	Chromosome-Level Genome Assembly of Chinese Sucker (Myxocyprinus asiaticus) Reveals Strongly Conserved Synteny Following a Catostomid-Specific Whole-Genome Duplication. Genome Biology and Evolution, 2021, 13, .	1.1	12
7	Diversified regulation of circadian clock gene expression following whole genome duplication. PLoS Genetics, 2020, 16, e1009097.	1.5	11
8	Genomic regions and signaling pathways associated with indicator traits for feed efficiency in juvenile Atlantic salmon (Salmo salar). Genetics Selection Evolution, 2020, 52, 66.	1.2	9
9	Association of gut microbiota with metabolism in juvenile Atlantic salmon. Microbiome, 2020, 8, 160.	4.9	29
10	The structural variation landscape in 492 Atlantic salmon genomes. Nature Communications, 2020, 11, 5176.	5.8	60
11	Mid and hindgut transcriptome profiling analysis of Atlantic salmon (Salmon salar) under unpredictable chronic stress. Royal Society Open Science, 2020, 7, 191480.	1.1	4
12	Comparative transcriptomics reveals domesticationâ€associated features of Atlantic salmon lipid metabolism. Molecular Ecology, 2020, 29, 1860-1872.	2.0	14
13	SalMotifDB: a tool for analyzing putative transcription factor binding sites in salmonid genomes. BMC Genomics, 2019, 20, 694.	1.2	13
14	The Chromosome-Level Genome Assembly of European Grayling Reveals Aspects of a Unique Genome Evolution Process Within Salmonids. G3: Genes, Genomes, Genetics, 2019, 9, 1283-1294.	0.8	22
15	Evolution of Cold Acclimation and Its Role in Niche Transition in the Temperate Grass Subfamily Pooideae. Plant Physiology, 2019, 180, 404-419.	2.3	45
16	Sex-dependent dominance maintains migration supergene in rainbow trout. Nature Ecology and Evolution, 2019, 3, 1731-1742.	3.4	188
17	Transcriptional regulation of lipid metabolism when salmon fry switches from endogenous to exogenous feeding. Aquaculture, 2019, 503, 422-429.	1.7	4
18	Liver slice culture as a model for lipid metabolism in fish. PeerJ, 2019, 7, e7732.	0.9	8

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19	Lifeâ€stageâ€associated remodelling of lipid metabolism regulation in Atlantic salmon. Molecular Ecology, 2018, 27, 1200-1213.	2.0	35
20	Stable Core Gut Microbiota across the Freshwater-to-Saltwater Transition for Farmed Atlantic Salmon. Applied and Environmental Microbiology, 2018, 84, .	1.4	90
21	The Grayling Genome Reveals Selection on Gene Expression Regulation after Whole-Genome Duplication. Genome Biology and Evolution, 2018, 10, 2785-2800.	1.1	42
22	Subfunctionalization versus neofunctionalization after whole-genome duplication. Nature Genetics, 2018, 50, 908-909.	9.4	67
23	A systemic study of lipid metabolism regulation in salmon fingerlings and early juveniles fed plant oil. British Journal of Nutrition, 2018, 120, 653-664.	1.2	12
24	Transcriptional development of phospholipid and lipoprotein metabolism in different intestinal regions of Atlantic salmon (Salmo salar) fry. BMC Genomics, 2018, 19, 253.	1.2	14
25	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	6.0	2,424
26	Lineage-specific rediploidization is a mechanism to explain time-lags between genome duplication and evolutionary diversification. Genome Biology, 2017, 18, 111.	3.8	136
27	Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. BMC Genomics, 2017, 18, 484.	1.2	99
28	The Atlantic salmon genome provides insights into rediploidization. Nature, 2016, 533, 200-205.	13.7	1,021
29	Extracting functional trends from whole genome duplication events using comparative genomics. Biological Procedures Online, 2016, 18, 11.	1.4	45
30	Two adjacent inversions maintain genomic differentiation between migratory and stationary ecotypes of Atlantic cod. Molecular Ecology, 2016, 25, 2130-2143.	2.0	178
31	Chloroplast phylogeny of Triticum/Aegilops species is not incongruent with an ancient homoploid hybrid origin of the ancestor of the bread wheat Dâ€genome. New Phytologist, 2015, 208, 9-10.	3.5	28
32	Population Structure, Genetic Variation, and Linkage Disequilibrium in Perennial Ryegrass Populations Divergently Selected for Freezing Tolerance. Frontiers in Plant Science, 2015, 6, 929.	1.7	14
33	The evolution and functional divergence of the beta-carotene oxygenase gene family in teleost fishâ€"Exemplified by Atlantic salmon. Gene, 2014, 543, 268-274.	1.0	14
34	Utilization of deletion bins to anchor and order sequences along the wheat 7B chromosome. Theoretical and Applied Genetics, 2014, 127, 2029-2040.	1.8	8
35	Genome interplay in the grain transcriptome of hexaploid bread wheat. Science, 2014, 345, 1250091.	6.0	318
36	Ancient hybridizations among the ancestral genomes of bread wheat. Science, 2014, 345, 1250092.	6.0	629

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37	Integration of mate pair sequences to improve shotgun assemblies of flow-sorted chromosome arms of hexaploid wheat. BMC Genomics, 2013, 14, 222.	1.2	13
38	Evidence for adaptive evolution of lowâ€temperature stress response genes in a Pooideae grass ancestor. New Phytologist, 2013, 199, 1060-1068.	3.5	37
39	Adaptation to seasonality and the winter freeze. Frontiers in Plant Science, 2013, 4, 167.	1.7	120
40	Comparative analyses reveal potential uses of Brachypodium distachyonas a model for cold stress responses in temperate grasses. BMC Plant Biology, 2012, 12, 65.	1.6	46
41	Molecular mechanisms underlying frost tolerance in perennial grasses adapted to cold climates. Plant Science, 2011, 180, 69-77.	1.7	119
42	Identification of candidate genes important for frost tolerance in Festuca pratensis Huds. by transcriptional profiling. Plant Science, 2011, 180, 78-85.	1.7	16
43	Genetic mapping of DArT markers in the Festucaâ€“Lolium complex and their use in freezing tolerance association analysis. Theoretical and Applied Genetics, 2011, 122, 1133-1147.	1.8	27
44	High-throughput genotyping of unknown genomic terrain in complex plant genomes: lessons from a case study. Molecular Breeding, 2010, 26, 711-718.	1.0	2
45	Did gene family expansions during the Eocene-Oligocene boundary climate cooling play a role in Pooideae adaptation to cool climates?. Molecular Ecology, 2010, 19, 2075-2088.	2.0	57
46	Tracking the evolution of a cold stress associated gene family in cold tolerant grasses. BMC Evolutionary Biology, 2008, 8, 245.	3.2	69