Arne B Gjuvsland

List of Publications by Year
in descending order

30 papers	2,151 citations	516710 16 h-index	477307 29 g-index
33 all docs	33 docs citations	33 times ranked	2932 citing authors

#	Article	IF	Citations
1	The Atlantic salmon genome provides insights into rediploidization. Nature, 2016, 533, 200-205.	27.8	1,021
2	Trait Variation in Yeast Is Defined by Population History. PLoS Genetics, 2011, 7, e1002111.	3.5	311
3	Statistical Epistasis Is a Generic Feature of Gene Regulatory Networks. Genetics, 2007, 175, 411-420.	2.9	99
4	Concerted Evolution of Life Stage Performances Signals Recent Selection on Yeast Nitrogen Use. Molecular Biology and Evolution, 2015, 32, 153-161.	8.9	86
5	Ancient Evolutionary Trade-Offs between Yeast Ploidy States. PLoS Genetics, 2013, 9, e1003388.	3.5	85
6	Life History Shapes Trait Heredity by Accumulation of Loss-of-Function Alleles in Yeast. Molecular Biology and Evolution, 2012, 29, 1781-1789.	8.9	76
7	Bridging the genotype–phenotype gap: what does it take?. Journal of Physiology, 2013, 591, 2055-2066.	2.9	62
8	Hierarchical Cluster-based Partial Least Squares Regression (HC-PLSR) is an efficient tool for metamodelling of nonlinear dynamic models. BMC Systems Biology, 2011, 5, 90.	3.0	48
9	Loss of function mutations in essential genes cause embryonic lethality in pigs. PLoS Genetics, 2019, 15, e1008055.	3.5	46
10	Meta-analysis for milk fat and protein percentage using imputed sequence variant genotypes in 94,321 cattle from eight cattle breeds. Genetics Selection Evolution, 2020, 52, 37.	3.0	41
11	Life–stage–associated remodelling of lipid metabolism regulation in Atlantic salmon. Molecular Ecology, 2018, 27, 1200-1213.	3.9	35
12	Threshold-dominated regulation hides genetic variation in gene expression networks. BMC Systems Biology, 2007, 1, 57.	3.0	34
13	Parameters in Dynamic Models of Complex Traits are Containers of Missing Heritability. PLoS Computational Biology, 2012, 8, e1002459.	3.2	24
14	When Parameters in Dynamic Models Become Phenotypes: A Case Study on Flesh Pigmentation in the Chinook Salmon (Oncorhynchus tshawytscha). Genetics, 2008, 179, 1113-1118.	2.9	19
15	Allele Interaction – Single Locus Genetics Meets Regulatory Biology. PLoS ONE, 2010, 5, e9379.	2.5	19
16	Monotonicity is a key feature of genotype-phenotype maps. Frontiers in Genetics, 2013, 4, 216.	2.3	19
17	Genotype-phenotype map characteristics of an in silico heart cell. Frontiers in Physiology, 2011, 2, 106.	2.8	16
18	Accelerated discovery of functional genomic variation in pigs. Genomics, 2021, 113, 2229-2239.	2.9	16

#	Article	IF	Citations
19	Screening design for computer experiments: metamodelling of a deterministic mathematical model of the mammalian circadian clock. Journal of Chemometrics, 2010, 24, 738-747.	1.3	13
20	A computational pipeline for quantification of mouse myocardial stiffness parameters. Computers in Biology and Medicine, 2014, 53, 65-75.	7.0	13
21	Nonlinear regulation enhances the phenotypic expression of trans- acting genetic polymorphisms. BMC Systems Biology, 2007, 1, 32.	3.0	12
22	Disentangling genetic and epigenetic determinants of ultrafast adaptation. Molecular Systems Biology, 2016, 12, 892.	7.2	9
23	Fine Mapping of a Major Backfat QTL Reveals a Causal Regulatory Variant Affecting the CCND2 Gene. Frontiers in Genetics, 2022, 13, .	2.3	9
24	Genetically controlled mtDNA deletions prevent ROS damage by arresting oxidative phosphorylation. ELife, 0, 11, .	6.0	9
25	Effect of Regulatory Architecture on Broad versus Narrow Sense Heritability. PLoS Computational Biology, 2013, 9, e1003053.	3.2	6
26	Level-biases in estimated breeding values due to the use of different SNP panels over time in ssGBLUP. Genetics Selection Evolution, 2019, 51, 76.	3.0	6
27	Propagation of genetic variation in gene regulatory networks. Physica D: Nonlinear Phenomena, 2013, 256-257, 7-20.	2.8	5
28	SALARECON connects the Atlantic salmon genome to growth and feed efficiency. PLoS Computational Biology, 2022, 18, e1010194.	3.2	4
29	Towards causally cohesive genotype–phenotype modelling for characterization of the soft-tissue mechanics of the heart in normal and pathological geometries. Journal of the Royal Society Interface, 2015, 12, 20141166.	3.4	2
30	Accuracy of genomic prediction of maternal traits in pigs using Bayesian variable selection methods. Journal of Animal Breeding and Genetics, 2022, 139, 654-665.	2.0	2