Arne B Gjuvsland

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Fine Mapping of a Major Backfat QTL Reveals a Causal Regulatory Variant Affecting the CCND2 Gene. Frontiers in Genetics, 2022, 13, .	2.3	9
2	SALARECON connects the Atlantic salmon genome to growth and feed efficiency. PLoS Computational Biology, 2022, 18, e1010194.	3.2	4
3	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
4	Accelerated discovery of functional genomic variation in pigs. Genomics, 2021, 113, 2229-2239.	2.9	16
5	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
6	Loss of function mutations in essential genes cause embryonic lethality in pigs. PLoS Genetics, 2019, 15, e1008055.	3.5	46
7	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
8	Lifeâ€stageâ€associated remodelling of lipid metabolism regulation in Atlantic salmon. Molecular Ecology, 2018, 27, 1200-1213.	3.9	35
9	Disentangling genetic and epigenetic determinants of ultrafast adaptation. Molecular Systems Biology, 2016, 12, 892.	7.2	9
10	The Atlantic salmon genome provides insights into rediploidization. Nature, 2016, 533, 200-205.	27.8	1,021
11	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
12	Concerted Evolution of Life Stage Performances Signals Recent Selection on Yeast Nitrogen Use. Molecular Biology and Evolution, 2015, 32, 153-161.	8.9	86
13	A computational pipeline for quantification of mouse myocardial stiffness parameters. Computers in Biology and Medicine, 2014, 53, 65-75.	7.0	13
14	Bridging the genotype–phenotype gap: what does it take?. Journal of Physiology, 2013, 591, 2055-2066.	2.9	62
15	Propagation of genetic variation in gene regulatory networks. Physica D: Nonlinear Phenomena, 2013, 256-257, 7-20.	2.8	5
16	Effect of Regulatory Architecture on Broad versus Narrow Sense Heritability. PLoS Computational Biology, 2013, 9, e1003053.	3.2	6
17	Ancient Evolutionary Trade-Offs between Yeast Ploidy States. PLoS Genetics, 2013, 9, e1003388.	3.5	85
18	Monotonicity is a key feature of genotype-phenotype maps. Frontiers in Genetics, 2013, 4, 216.	2.3	19

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19	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
20	Parameters in Dynamic Models of Complex Traits are Containers of Missing Heritability. PLoS Computational Biology, 2012, 8, e1002459.	3.2	24
21	Genotype-phenotype map characteristics of an in silico heart cell. Frontiers in Physiology, 2011, 2, 106.	2.8	16
22	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
23	Trait Variation in Yeast Is Defined by Population History. PLoS Genetics, 2011, 7, e1002111.	3.5	311
24	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
25	Allele Interaction – Single Locus Genetics Meets Regulatory Biology. PLoS ONE, 2010, 5, e9379.	2.5	19
26	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
27	Statistical Epistasis Is a Generic Feature of Gene Regulatory Networks. Genetics, 2007, 175, 411-420.	2.9	99
28	Nonlinear regulation enhances the phenotypic expression of trans- acting genetic polymorphisms. BMC Systems Biology, 2007, 1, 32.	3.0	12
29	Threshold-dominated regulation hides genetic variation in gene expression networks. BMC Systems Biology, 2007, 1, 57.	3.0	34
30	Genetically controlled mtDNA deletions prevent ROS damage by arresting oxidative phosphorylation. ELife, 0, 11, .	6.0	9