Stig W Omholt

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10393416/publications.pdf

Version: 2024-02-01

52	5,512	136950	182427
papers	citations	32 h-index	51 g-index

54	54	54	5926
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Aging as a consequence of selection to reduce the environmental risk of dying. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	9
2	Cardiovascular models for personalised medicine: Where now and where next?. Medical Engineering and Physics, 2019, 72, 38-48.	1.7	42
3	Interstitial solute transport in 3D reconstructed neuropil occurs by diffusion rather than bulk flow. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9894-9899.	7.1	216
4	Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. BMC Genomics, 2017, 18, 484.	2.8	99
5	Disentangling genetic and epigenetic determinants of ultrafast adaptation. Molecular Systems Biology, 2016, 12, 892.	7.2	9
6	A novel role for pigment genes in the stress response in rainbow trout (Oncorhynchus mykiss). Scientific Reports, 2016, 6, 28969.	3.3	19
7	The Atlantic salmon genome provides insights into rediploidization. Nature, 2016, 533, 200-205.	27.8	1,021
8	Roadmap for cardiovascular circulation model. Journal of Physiology, 2016, 594, 6909-6928.	2.9	33
9	Towards causally cohesive genotypeâ€“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
10	High-Throughput Biochemical Fingerprinting of Saccharomyces cerevisiae by Fourier Transform Infrared Spectroscopy. PLoS ONE, 2015, 10, e0118052.	2.5	38
11	Concerted Evolution of Life Stage Performances Signals Recent Selection on Yeast Nitrogen Use. Molecular Biology and Evolution, 2015, 32, 153-161.	8.9	86
12	Arterial Stiffening Provides Sufficient Explanation for Primary Hypertension. PLoS Computational Biology, 2014, 10, e1003634.	3.2	42
13	A computational pipeline for quantification of mouse myocardial stiffness parameters. Computers in Biology and Medicine, 2014, 53, 65-75.	7.0	13
14	Evolution evolves: physiology returns to centre stage. Journal of Physiology, 2014, 592, 2237-2244.	2.9	102
15	Life-History Evolution and the Polyphenic Regulation of Somatic Maintenance and Survival. Quarterly Review of Biology, 2013, 88, 185-218.	0.1	97
16	Bridging the genotypeâ€“phenotype gap: what does it take?. Journal of Physiology, 2013, 591, 2055-2066.	2.9	62
17	Propagation of genetic variation in gene regulatory networks. Physica D: Nonlinear Phenomena, 2013, 256-257, 7-20.	2.8	5
18	From sequence to consequence and back. Progress in Biophysics and Molecular Biology, 2013, 111, 75-82.	2.9	13

#	Article	IF	Citations
19	Effect of Regulatory Architecture on Broad versus Narrow Sense Heritability. PLoS Computational Biology, 2013, 9, e1003053.	3.2	6
20	Ancient Evolutionary Trade-Offs between Yeast Ploidy States. PLoS Genetics, 2013, 9, e1003388.	3.5	85
21	Electrodiffusive Model for Astrocytic and Neuronal Ion Concentration Dynamics. PLoS Computational Biology, 2013, 9, e1003386.	3.2	51
22	Monotonicity is a key feature of genotype-phenotype maps. Frontiers in Genetics, 2013, 4, 216.	2.3	19
23	A computational analysis of the long-term regulation of arterial pressure. F1000Research, 2013, 2, 208.	1.6	34
24	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
25	Parameters in Dynamic Models of Complex Traits are Containers of Missing Heritability. PLoS Computational Biology, 2012, 8, e1002459.	3.2	24
26	Genotype-phenotype map characteristics of an in silico heart cell. Frontiers in Physiology, 2011, 2, 106.	2.8	16
27	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
28	A dense SNP-based linkage map for Atlantic salmon (Salmo salar) reveals extended chromosome homeologies and striking differences in sex-specific recombination patterns. BMC Genomics, 2011, 12, 615.	2.8	226
29	Trait Variation in Yeast Is Defined by Population History. PLoS Genetics, 2011, 7, e1002111.	3.5	311
30	Allele Interaction â€“ Single Locus Genetics Meets Regulatory Biology. PLoS ONE, 2010, 5, e9379.	2.5	19
31	Sequencing the genome of the Atlantic salmon (Salmo salar). Genome Biology, 2010, 11, 403.	8.8	250
32	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
33	Statistical Epistasis Is a Generic Feature of Gene Regulatory Networks. Genetics, 2007, 175, 411-420.	2.9	99
34	Nonlinear regulation enhances the phenotypic expression of trans- acting genetic polymorphisms. BMC Systems Biology, 2007, 1, 32.	3.0	12
35	Threshold-dominated regulation hides genetic variation in gene expression networks. BMC Systems Biology, 2007, 1, 57.	3.0	34
36	A new method for rearing genetically manipulated honey bee workers. Apidologie, 2005, 36, 293-299.	2.0	22

#	Article	IF	Citations
37	Hormonal control of the yolk precursor vitellogenin regulates immune function and longevity in honeybees. Experimental Gerontology, 2004, 39, 767-773.	2.8	304
38	Altered Physiology in Worker Honey Bees (Hymenoptera: Apidae) Infested with the Mite <I>Varroa destructor</I> (Acari: Varroidae): A Factor in Colony Loss During Overwintering?. Journal of Economic Entomology, 2004, 97, 741-747.	1.8	141
39	Epigenetic Regulation of Aging in Honeybee Workers. Science of Aging Knowledge Environment: SAGE KE, 2004, 2004, pe28-pe28.	0.8	61
40	The hive bee to forager transition in honeybee colonies: the double repressor hypothesis. Journal of Theoretical Biology, 2003, 223, 451-464.	1.7	237
41	Disruption of vitellogenin gene function in adult honeybees by intra-abdominal injection of double-stranded RNA. BMC Biotechnology, 2003, 3, 1.	3.3	243
42	Social exploitation of vitellogenin. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1799-1802.	7.1	338
43	The Regulatory Basis of Melanogenic Switching. Journal of Theoretical Biology, 2002, 215, 449-468.	1.7	38
44	The Regulatory Anatomy of Honeybee Lifespan. Journal of Theoretical Biology, 2002, 216, 209-228.	1.7	222
45	Gene Regulatory Networks Generating the Phenomena of Additivity, Dominance and Epistasis. Genetics, 2000, 155, 969-980.	2.9	143
46	Description and Analysis of Switchlike Regulatory Networks Exemplified by a Model of Cellular Iron Homeostasis. Journal of Theoretical Biology, 1998, 195, 339-350.	1.7	15
47	A methodological basis for description and analysis of systems with complex switch-like interactions. Journal of Mathematical Biology, 1998, 36, 321-348.	1.9	85
48	A mathematical framework for describing and analysing gene regulatory networks. Journal of Theoretical Biology, 1995, 176, 291-300.	1.7	241
49	FEEDBACK LOOPS, STABILITY AND MULTISTATIONARITY IN DYNAMICAL SYSTEMS. Journal of Biological Systems, 1995, 03, 409-413.	1.4	111
50	Relationships between worker longevity and the intracolonial population dynamics of the honeybee. Journal of Theoretical Biology, 1988, 130, 275-284.	1.7	16
51	Thermoregulation in the winter cluster of the honeybee, Apis Mellifera. Journal of Theoretical Biology, 1987, 128, 219-231.	1.7	41
52	Genetically controlled mtDNA deletions prevent ROS damage by arresting oxidative phosphorylation. ELife, 0, 11, .	6.0	9