

Hans J Jansen

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

4,280
citations

331670

21
h-index

345221

36
g-index

41
all docs

41
docs citations

41
times ranked

9671
citing authors

#	ARTICLE	IF	CITATIONS
1	RNAseq Profiling of Leukocyte Populations in Zebrafish Larvae Reveals a cxcl11 Chemokine Gene as a Marker of Macrophage Polarization During Mycobacterial Infection. <i>Frontiers in Immunology</i> , 2019, 10, 832.	4.8	76
2	Deep transcriptome analysis of the heat shock response in an Atlantic sturgeon (<i>Acipenser</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 T	3.6	13
3	Rapid de novo assembly of the European eel genome from nanopore sequencing reads. <i>Scientific Reports</i> , 2017, 7, 7213.	3.3	104
4	De novo whole-genome assembly of a wild type yeast isolate using nanopore sequencing. <i>F1000Research</i> , 2017, 6, 618.	1.6	7
5	De novo whole-genome assembly of a wild type yeast isolate using nanopore sequencing. <i>F1000Research</i> , 2017, 6, 618.	1.6	5
6	MinION Analysis and Reference Consortium: Phase 2 data release and analysis of R9.0 chemistry. <i>F1000Research</i> , 2017, 6, 760.	1.6	107
7	Changes in ovarian gene expression profiles and plasma hormone levels in maturing European eel () Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 14	1.8	19
8	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. <i>F1000Research</i> , 2015, 4, 1075.	1.6	270
9	Testing Tuberculosis Drug Efficacy in a Zebrafish High-Throughput Translational Medicine Screen. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 753-762.	3.2	52
10	A disruptive sequencer meets disruptive publishing. <i>F1000Research</i> , 2015, 4, 1074.	1.6	0
11	Advances in genomics of bony fish. <i>Briefings in Functional Genomics</i> , 2014, 13, 144-156.	2.7	24
12	RNA Sequencing of FACS-Sorted Immune Cell Populations from Zebrafish Infection Models to Identify Cell Specific Responses to Intracellular Pathogens. <i>Methods in Molecular Biology</i> , 2014, 1197, 261-274.	0.9	40
13	The king cobra genome reveals dynamic gene evolution and adaptation in the snake venom system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20651-20656.	7.1	412
14	Robotic injection of zebrafish embryos for high-throughput screening in disease models. <i>Methods</i> , 2013, 62, 246-254.	3.8	84
15	Deep RNA Sequencing of the Skeletal Muscle Transcriptome in Swimming Fish. <i>PLoS ONE</i> , 2013, 8, e53171.	2.5	62
16	Comparison of the Exomes of Common Carp (<i>Cyprinus carpio</i>) and Zebrafish (<i>Danio</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 14	1.1	90
17	First draft genome sequence of the Japanese eel, <i>Anguilla japonica</i> . <i>Gene</i> , 2012, 511, 195-201.	2.2	99
18	Primitive Duplicate Hox Clusters in the European Eel's Genome. <i>PLoS ONE</i> , 2012, 7, e32231.	2.5	128

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19	Scaffolding pre-assembled contigs using SSPACE. <i>Bioinformatics</i> , 2011, 27, 578-579.	4.1	2,214
20	Deep sequencing of the innate immune transcriptomic response of zebrafish embryos to Salmonella infection. <i>Fish and Shellfish Immunology</i> , 2011, 31, 716-724.	3.6	79
21	Identification of Common Carp Innate Immune Genes with Whole-Genome Sequencing and RNA-Seq Data. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 165-175.	1.5	23
22	Analyzing the function of a hox gene: An evolutionary approach. <i>Development Growth and Differentiation</i> , 2011, 53, 982-993.	1.5	8
23	XMeis3 Is Necessary for Mesodermal Hox Gene Expression and Function. <i>PLoS ONE</i> , 2011, 6, e18010.	2.5	4
24	Hox collinearity - a new perspective. <i>International Journal of Developmental Biology</i> , 2011, 55, 899-908.	0.6	31
25	Identification of common carp innate immune genes with whole-genome sequencing and RNA-Seq data. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 169.	1.5	12
26	Retinoid signalling is required for information transfer from mesoderm to neuroectoderm during gastrulation. <i>International Journal of Developmental Biology</i> , 2010, 54, 599-608.	0.6	23
27	The role of the Spemann organizer in anterior-posterior patterning of the trunk. <i>Mechanisms of Development</i> , 2007, 124, 668-681.	1.7	16
28	Extensive Polycistronism and Antisense Transcription in the Mammalian Hox Clusters. <i>PLoS ONE</i> , 2007, 2, e356.	2.5	78
29	Timed interactions between the Hox expressing non-organiser mesoderm and the Spemann organiser generate positional information during vertebrate gastrulation. <i>Developmental Biology</i> , 2004, 268, 207-219.	2.0	93
30	Biochemical differences between Three Subcell-lines Derived from SV40-Transformed Hamster Lens Cells. <i>Experimental Eye Research</i> , 1997, 64, 1037-1041.	2.6	2
31	In vivo footprinting and functional analysis of the human c-sis/PDGF B gene promoter provides evidence for two binding sites for transcriptional activators. <i>Nucleic Acids Research</i> , 1995, 23, 1119-1126.	14.5	17
32	Negative regulation of a special, double AP-1 consensus element in the vimentin promoter: Interference by the retinoic acid receptor. <i>Journal of Cellular Physiology</i> , 1995, 164, 85-92.	4.1	5
33	A novel human c-sis-miRNA species is transcribed from a promoter in c-sis intron 1 and contains the code for an alternative PDGF B-like protein. <i>Nucleic Acids Research</i> , 1995, 23, 2815-2822.	14.5	7
34	Localization and functional analysis of DNase-I-hypersensitive sites in the human c-sis/PDGF-B gene transcription unit and its flanking regions. <i>FEBS Journal</i> , 1993, 211, 509-519.	0.2	16
35	DNase-I-hypersensitive sites located far upstream of the human c-sis/PDGF-B gene comap with transcriptional enhancers and a silencer and are preceded by (part of) a new transcription unit. <i>FEBS Journal</i> , 1993, 216, 487-495.	0.2	18
36	Identification of two silencers flanking an AP-1 enhancer in the vimentin promoter. <i>Gene</i> , 1992, 122, 337-343.	2.2	30