

# Timothy Ravasi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7157479/publications.pdf>

Version: 2024-02-01

150  
papers

22,068  
citations

31976

53  
h-index

9345

143  
g-index

161  
all docs

161  
docs citations

161  
times ranked

33041  
citing authors

#	ARTICLE	IF	CITATIONS
1	Plasticity to ocean warming is influenced by transgenerational, reproductive, and developmental exposure in a coral reef fish. <i>Evolutionary Applications</i> , 2022, 15, 249-261.	3.1	16
2	A chromosome-scale genome assembly of the false clownfish, <i>Amphiprion ocellaris</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	11
3	Molecular Response of the Brain to Cross-Generational Warming in a Coral Reef Fish. <i>Frontiers in Marine Science</i> , 2022, 9, .	2.5	6
4	The alternative splicing landscape of a coral reef fish during a marine heatwave. <i>Ecology and Evolution</i> , 2022, 12, e8738.	1.9	3
5	Rapid evolution fuels transcriptional plasticity to ocean acidification. <i>Global Change Biology</i> , 2022, 28, 3007-3022.	9.5	23
6	Parents exposed to warming produce offspring lower in weight and condition. <i>Ecology and Evolution</i> , 2022, 12, .	1.9	6
7	Unexpected high abundance of aragonite-forming <i>Nanipora</i> (Octocorallia: Helioporacea) at an acidified volcanic reef in southern Japan. <i>Marine Biodiversity</i> , 2021, 51, 1.	1.0	8
8	Diel $pCO_2$ fluctuations alter the molecular response of coral reef fishes to ocean acidification conditions. <i>Molecular Ecology</i> , 2021, 30, 5105-5118.	3.9	21
9	Sex- and time-specific parental effects of warming on reproduction and offspring quality in a coral reef fish. <i>Evolutionary Applications</i> , 2021, 14, 1145-1158.	3.1	15
10	Molecular basis of parental contributions to the behavioural tolerance of elevated $pCO_2$ in a coral reef fish. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211931.	2.6	9
11	Viral ecogenomics across the Porifera. <i>Microbiome</i> , 2020, 8, 144.	11.1	21
12	Methods matter in repeating ocean acidification studies. <i>Nature</i> , 2020, 586, E20-E24.	27.8	41
13	Functionalization of Magnetic Nanowires for Active Targeting and Enhanced Cell-Killing Efficacy. <i>ACS Applied Bio Materials</i> , 2020, 3, 4789-4797.	4.6	16
14	Probing SWATH-MS as a tool for proteome level quantification in a nonmodel fish. <i>Molecular Ecology Resources</i> , 2020, 20, 1647-1657.	4.8	9
15	Proteomic Responses to Ocean Acidification in the Brain of Juvenile Coral Reef Fish. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	15
16	Symbiodiniaceae diversity of <i>Palythoa tuberculosa</i> in the central and southern Red Sea influenced by environmental factors. <i>Coral Reefs</i> , 2020, 39, 1619-1633.	2.2	2
17	An Epigenetic Signature for Within-Generational Plasticity of a Reef Fish to Ocean Warming. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	31
18	Magnetic core-shell nanowires as MRI contrast agents for cell tracking. <i>Journal of Nanobiotechnology</i> , 2020, 18, 42.	9.1	26

#	ARTICLE	IF	CITATIONS
19	Species-specific molecular responses of wild coral reef fishes during a marine heatwave. <i>Science Advances</i> , 2020, 6, eaay3423.	10.3	52
20	Testing the Adaptive Potential of Yellowtail Kingfish to Ocean Warming and Acidification. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	2.2	11
21	Nuclear AGO1 Regulates Gene Expression by Affecting Chromatin Architecture in Human Cells. <i>Cell Systems</i> , 2019, 9, 446-458.e6.	6.2	27
22	Iron-Based Core-Shell Nanowires for Combinatorial Drug Delivery and Photothermal and Magnetic Therapy. <i>ACS Applied Materials &amp; Interfaces</i> , 2019, 11, 43976-43988.	8.0	38
23	A genomic view of the reef-building coral <i>Porites lutea</i> and its microbial symbionts. <i>Nature Microbiology</i> , 2019, 4, 2090-2100.	13.3	160
24	Beyond buying time: the role of plasticity in phenotypic adaptation to rapid environmental change. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180174.	4.0	371
25	Neural effects of elevated CO <sub>2</sub> in fish may be amplified by a vicious cycle. , 2019, 7, coz100.		29
26	Finding Nemo's Genes: A chromosome-scale reference assembly of the genome of the orange clownfish <i>Amphiprion percula</i> . <i>Molecular Ecology Resources</i> , 2019, 19, 570-585.	4.8	55
27	Biofunctionalizing Magnetic Nanowires Toward Targeting and Killing Leukemia Cancer Cells. <i>IEEE Transactions on Magnetics</i> , 2019, 55, 1-5.	2.1	15
28	Unusual bilateral color pattern in a regal angelfish from the Red Sea. <i>Bulletin of Marine Science</i> , 2019, 95, 113-114.	0.8	0
29	Transcription Regulatory Networks Analysis Using CAGE. , 2019, , 153-168.		0
30	An interplay between plasticity and parental phenotype determines impacts of ocean acidification on a reef fish. <i>Nature Ecology and Evolution</i> , 2018, 2, 334-342.	7.8	75
31	The epigenetic landscape of transgenerational acclimation to ocean warming. <i>Nature Climate Change</i> , 2018, 8, 504-509.	18.8	124
32	Molecular Response to Extreme Summer Temperatures Differs Between Two Genetically Differentiated Populations of a Coral Reef Fish. <i>Frontiers in Marine Science</i> , 2018, 5, .	2.5	29
33	Phenotypic and molecular consequences of stepwise temperature increase across generations in a coral reef fish. <i>Molecular Ecology</i> , 2018, 27, 4516-4528.	3.9	37
34	Review of In vitro Toxicity of Nanoparticles and Nanorods: Part 1. , 2018, , .		0
35	Inductively actuated micro needles for on-demand intracellular delivery. <i>Scientific Reports</i> , 2018, 8, 9918.	3.3	8
36	Morphological characterization of virus-like particles in coral reef sponges. <i>PeerJ</i> , 2018, 6, e5625.	2.0	27

#	ARTICLE	IF	CITATIONS
37	Mesenchymal stem cells cultured on magnetic nanowire substrates. <i>Nanotechnology</i> , 2017, 28, 055703.	2.6	12
38	The sponge microbiome project. <i>GigaScience</i> , 2017, 6, 1-7.	6.4	193
39	Rapid adaptive responses to climate change in corals. <i>Nature Climate Change</i> , 2017, 7, 627-636.	18.8	327
40	Astrocyte-specific overexpressed gene signatures in response to methamphetamine exposure in vitro. <i>Journal of Neuroinflammation</i> , 2017, 14, 49.	7.2	34
41	Anti-cancer agents in Saudi Arabian herbals revealed by automated high-content imaging. <i>PLoS ONE</i> , 2017, 12, e0177316.	2.5	20
42	Transcriptome and Proteome Studies Reveal Candidate Attachment Genes during the Development of the Barnacle <i>Amphibalanus Amphitrite</i> . <i>Frontiers in Marine Science</i> , 2016, 3, .	2.5	12
43	Genomes of coral dinoflagellate symbionts highlight evolutionary adaptations conducive to a symbiotic lifestyle. <i>Scientific Reports</i> , 2016, 6, 39734.	3.3	303
44	Semi-automated quantification of living cells with internalized nanostructures. <i>Journal of Nanobiotechnology</i> , 2016, 14, 4.	9.1	15
45	Molecular signatures of transgenerational response to ocean acidification in a species of reef fish. <i>Nature Climate Change</i> , 2016, 6, 1014-1018.	18.8	103
46	Shedding light on cell compartmentation in the candidate phylum Poribacteria by high resolution visualisation and transcriptional profiling. <i>Scientific Reports</i> , 2016, 6, 35860.	3.3	31
47	Characterization of piRNAs across postnatal development in mouse brain. <i>Scientific Reports</i> , 2016, 6, 25039.	3.3	34
48	Functionalized magnetic nanowires for chemical and magneto-mechanical induction of cancer cell death. <i>Scientific Reports</i> , 2016, 6, 35786.	3.3	62
49	Sex Change in Clownfish: Molecular Insights from Transcriptome Analysis. <i>Scientific Reports</i> , 2016, 6, 35461.	3.3	88
50	Quantitative analysis of oyster larval proteome provides new insights into the effects of multiple climate change stressors. <i>Global Change Biology</i> , 2016, 22, 2054-2068.	9.5	70
51	Cytotoxic effects of nickel nanowires in human fibroblasts. <i>Toxicology Reports</i> , 2016, 3, 373-380.	3.3	34
52	Hologenome analysis of two marine sponges with different microbiomes. <i>BMC Genomics</i> , 2016, 17, 158.	2.8	60
53	Methamphetamine abuse affects gene expression in brain-derived microglia of SIV-infected macaques to enhance inflammation and promote virus targets. <i>BMC Immunology</i> , 2016, 17, 7.	2.2	53
54	Cytotoxicity and intracellular dissolution of nickel nanowires. <i>Nanotoxicology</i> , 2016, 10, 871-880.	3.0	28

#	ARTICLE	IF	CITATIONS
55	Co-transcriptomic Analysis by RNA Sequencing to Simultaneously Measure Regulated Gene Expression in Host and Bacterial Pathogen. <i>Methods in Molecular Biology</i> , 2016, 1390, 145-158.	0.9	6
56	miRNA Repertoires of Demosponges <i>Stylissa carteri</i> and <i>Xestospongia testudinaria</i> . <i>PLoS ONE</i> , 2016, 11, e0149080.	2.5	12
57	Transcriptome and proteome dynamics in larvae of the barnacle <i>Balanus Amphitrite</i> from the Red Sea. <i>BMC Genomics</i> , 2015, 16, 1063.	2.8	18
58	Exploring seascape genetics and kinship in the reef sponge <i>Stylissa carteri</i> in the Red Sea. <i>Ecology and Evolution</i> , 2015, 5, 2487-2502.	1.9	64
59	Proteomic Changes Associated with Successive Reproductive Periods in Male Polychaetous <i>Neanthes arenaceodentata</i> . <i>Scientific Reports</i> , 2015, 5, 13561.	3.3	2
60	Highlighting nonlinear patterns in population genetics datasets. <i>Scientific Reports</i> , 2015, 5, 8140.	3.3	31
61	Selective phosphorylation during early macrophage differentiation. <i>Proteomics</i> , 2015, 15, 3731-3743.	2.2	6
62	The ReFuGe 2020 Consortium using omics approaches to explore the adaptability and resilience of coral holobionts to environmental change. <i>Frontiers in Marine Science</i> , 2015, 2, .	2.5	24
63	Non-chemotoxic induction of cancer cell death using magnetic nanowires. <i>International Journal of Nanomedicine</i> , 2015, 10, 2141.	6.7	90
64	Magnetic nanowires and hyperthermia: How geometry and material affect heat production efficiency. , 2015, , .		1
65	Molecular processes of transgenerational acclimation to a warming ocean. <i>Nature Climate Change</i> , 2015, 5, 1074-1078.	18.8	128
66	The co-transcriptome of uropathogenic <i>Escherichia coli</i> infected mouse macrophages reveals new insights into host-pathogen interactions. <i>Cellular Microbiology</i> , 2015, 17, 730-746.	2.1	90
67	Quantitative Proteomics Study of Larval Settlement in the Barnacle <i>Balanus amphitrite</i> . <i>PLoS ONE</i> , 2014, 9, e88744.	2.5	35
68	Dynamic Epigenetic Control of Highly Conserved Noncoding Elements. <i>PLoS ONE</i> , 2014, 9, e109326.	2.5	5
69	Actinomycetes from Red Sea Sponges: Sources for Chemical and Phylogenetic Diversity. <i>Marine Drugs</i> , 2014, 12, 2771-2789.	4.6	72
70	Draft Genome Sequence of the Antitrypanosomally Active Sponge-Associated Bacterium <i>Actinokineospora</i> sp. Strain EG49. <i>Genome Announcements</i> , 2014, 2, .	0.8	15
71	The Global Invertebrate Genomics Alliance (GIGA): Developing Community Resources to Study Diverse Invertebrate Genomes. <i>Journal of Heredity</i> , 2014, 105, 1-18.	2.4	96
72	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838

#	ARTICLE	IF	CITATIONS
73	Specificity and transcriptional activity of microbiota associated with low and high microbial abundance sponges from the Red Sea. <i>Molecular Ecology</i> , 2014, 23, 1348-1363.	3.9	139
74	GeoChip-based insights into the microbial functional gene repertoire of marine sponges (high) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707</i> 832-843.	2.7	55
75	Targeted cancer cell death induced by biofunctionalized magnetic nanowires. , 2014, , .		3
76	Exploring the genetics underlying autoimmune diseases with network analysis and link prediction. , 2014, , .		2
77	Revealing microbial functional activities in the <i>Scypha</i> sponge <i>Scyllis carteri</i> by metatranscriptomics. <i>Environmental Microbiology</i> , 2014, 16, 3683-3698.	3.8	64
78	Proteomic profiling during the pre-competent to competent transition of the biofouling polychaete <i>Hydroides elegans</i> . <i>Biofouling</i> , 2014, 30, 921-928.	2.2	2
79	Proteomics insights: proteins related to larval attachment and metamorphosis of marine invertebrates. <i>Frontiers in Marine Science</i> , 2014, 1, .	2.5	10
80	Transcriptome analysis elucidates key developmental components of bryozoan lophophore development. <i>Scientific Reports</i> , 2014, 4, 6534.	3.3	19
81	Proteomic and metabolomic profiles of marine <i>Vibrio</i> sp. 010 in response to an antifoulant challenge. <i>Biofouling</i> , 2013, 29, 789-802.	2.2	8
82	Pivotal role of the muscle-contraction pathway in cryptorchidism and evidence for genomic connections with cardiomyopathy pathways in RASopathies. <i>BMC Medical Genomics</i> , 2013, 6, 5.	1.5	33
83	Novel polymorphic microsatellite markers developed for a common reef sponge, <i>Stylisha carteri</i> . <i>Marine Biodiversity</i> , 2013, 43, 237-241.	1.0	9
84	Exploitation of genetic interaction network topology for the prediction of epistatic behavior. <i>Genomics</i> , 2013, 102, 202-208.	2.9	17
85	Transcriptome and Quantitative Proteome Analysis Reveals Molecular Processes Associated with Larval Metamorphosis in the Polychaete <i>Pseudopolydora vexillosa</i> . <i>Journal of Proteome Research</i> , 2013, 12, 1344-1358.	3.7	13
86	Bacterial community profiles in low microbial abundance sponges. <i>FEMS Microbiology Ecology</i> , 2013, 83, 232-241.	2.7	127
87	From link-prediction in brain connectomes and protein interactomes to the local-community-paradigm in complex networks. <i>Scientific Reports</i> , 2013, 3, 1613.	3.3	311
88	Poster: Observing change in crowded data sets in 3D space - Visualizing gene expression in human tissues. , 2013, , .		0
89	Minimum curvilinearity to enhance topological prediction of protein interactions by network embedding. <i>Bioinformatics</i> , 2013, 29, i199-i209.	4.1	93
90	Questing for Circadian Dependence in ST-Segmentâ€“Elevation Acute Myocardial Infarction. <i>Circulation Research</i> , 2013, 112, e110-4.	4.5	35

#	ARTICLE	IF	CITATIONS
91	Proteomic Changes between Male and Female Worms of the Polychaetous Annelid <i>Neanthes arenaceodentata</i> before and after Spawning. <i>PLoS ONE</i> , 2013, 8, e72990.	2.5	4
92	Identification and Predictive Value of Interleukin-6 and Interleukin-10 and Interleukin-6 and Interleukin-10 Cytokine Patterns in ST-Elevation Acute Myocardial Infarction. <i>Circulation Research</i> , 2012, 111, 1336-1348.	4.5	72
93	First Proteome of the Egg Perivitelline Fluid of a Freshwater Gastropod with Aerial Oviposition. <i>Journal of Proteome Research</i> , 2012, 11, 4240-4248.	3.7	54
94	Defining the protein interaction network of human malaria parasite <i>Plasmodium falciparum</i> . <i>Genomics</i> , 2012, 99, 69-75.	2.9	28
95	The evolution of ultraconserved elements with different phylogenetic origins. <i>BMC Evolutionary Biology</i> , 2012, 12, 236.	3.2	22
96	Involvement of Wnt Signaling Pathways in the Metamorphosis of the Bryozoan <i>Bugula neritina</i> . <i>PLoS ONE</i> , 2012, 7, e33323.	2.5	21
97	SECOM: A Novel Hash Seed and Community Detection Based-Approach for Genome-Scale Protein Domain Identification. <i>PLoS ONE</i> , 2012, 7, e39475.	2.5	15
98	Computational Tools for Genome-Wide miRNA Prediction and Study. <i>The Open Biology Journal</i> , 2012, 5, 23-30.	0.5	3
99	Intramacrophage survival of uropathogenic <i>Escherichia coli</i> : Differences between diverse clinical isolates and between mouse and human macrophages. <i>Immunobiology</i> , 2011, 216, 1164-1171.	1.9	61
100	Quantitative Proteomics Identify Molecular Targets That Are Crucial in Larval Settlement and Metamorphosis of <i>Bugula neritina</i> . <i>Journal of Proteome Research</i> , 2011, 10, 349-360.	3.7	22
101	Unexpected complexity of the Reef-Building Coral <i>Acropora millepora</i> transcription factor network. <i>BMC Systems Biology</i> , 2011, 5, 58.	3.0	9
102	Novel systems biology insights using antifibrotic approaches for diabetic kidney disease. <i>Expert Review of Endocrinology and Metabolism</i> , 2010, 5, 127-135.	2.4	1
103	Dependency on de novo protein synthesis and proteomic changes during metamorphosis of the marine bryozoan <i>Bugula neritina</i> . <i>Proteome Science</i> , 2010, 8, 25.	1.7	15
104	Rapid transcriptome and proteome profiling of a non-model marine invertebrate, <i>Bugula neritina</i> . <i>Proteomics</i> , 2010, 10, 2972-2981.	2.2	46
105	Study of monocyte membrane proteome perturbation during lipopolysaccharide-induced tolerance using iTRAQ-based quantitative proteomic approach. <i>Proteomics</i> , 2010, 10, 2780-2789.	2.2	45
106	Nonlinear dimension reduction and clustering by Minimum Curvilinearity unfold neuropathic pain and tissue embryological classes. <i>Bioinformatics</i> , 2010, 26, i531-i539.	4.1	61
107	Coevolution within a transcriptional network by compensatory trans and cis mutations. <i>Genome Research</i> , 2010, 20, 1672-1678.	5.5	62
108	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	28.9	667

#	ARTICLE	IF	CITATIONS
109	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 141, 369.	28.9	4
110	Evolutionary divergence in the fungal response to fluconazole revealed by soft clustering. <i>Genome Biology</i> , 2010, 11, R77.	9.6	38
111	An Integrated Systems Analysis Implicates EGR1 Downregulation in Simian Immunodeficiency Virus Encephalitis-Induced Neural Dysfunction. <i>Journal of Neuroscience</i> , 2009, 29, 12467-12476.	3.6	37
112	Pirfenidone Is Renoprotective in Diabetic Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2009, 20, 1765-1775.	6.1	147
113	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
114	Transcription Regulatory Networks Analysis Using CAGE. , 2009, , 153-168.		0
115	Integrative Systems Approaches to Study Innate Immunity. , 2009, , 1-13.		0
116	Integrated approaches to uncovering transcription regulatory networks in mammalian cells. <i>Genomics</i> , 2008, 91, 219-231.	2.9	38
117	A systems approach to delineate functions of paralogous transcription factors: Role of the Yap family in the DNA damage response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2934-2939.	7.1	55
118	<i>Gpnmb</i> Is Induced in Macrophages by IFN- $\gamma$ and Lipopolysaccharide and Acts as a Feedback Regulator of Proinflammatory Responses. <i>Journal of Immunology</i> , 2007, 178, 6557-6566.	0.8	191
119	Differential Effects of CpG DNA on IFN- $\gamma$ Induction and STAT1 Activation in Murine Macrophages versus Dendritic Cells: Alternatively Activated STAT1 Negatively Regulates TLR Signaling in Macrophages. <i>Journal of Immunology</i> , 2007, 179, 3495-3503.	0.8	44
120	Mouse neutrophilic granulocytes express mRNA encoding the macrophage colony-stimulating factor receptor (CSF-1R) as well as many other macrophage-specific transcripts and can transdifferentiate into macrophages in vitro in response to CSF-1. <i>Journal of Leukocyte Biology</i> , 2007, 82, 111-123.	3.3	155
121	PU.1 and ICSBP control constitutive and IFN- $\gamma$ -regulated Tlr9 gene expression in mouse macrophages. <i>Journal of Leukocyte Biology</i> , 2007, 81, 1577-1590.	3.3	41
122	Concordant Epigenetic Silencing of Transforming Growth Factor- $\beta$ Signaling Pathway Genes Occurs Early in Breast Carcinogenesis. <i>Cancer Research</i> , 2007, 67, 11517-11527.	0.9	76
123	Transcriptional Regulatory Networks in Macrophages. <i>Novartis Foundation Symposium</i> , 2007, 281, 2-24.	1.1	23
124	Systems biology of transcription control in macrophages. <i>BioEssays</i> , 2007, 29, 1215-1226.	2.5	44
125	Histone deacetylase inhibitors decrease Toll-like receptor-mediated activation of proinflammatory gene expression by impairing transcription factor recruitment. <i>Immunology</i> , 2007, 122, 596-606.	4.4	155
126	Transcriptional network dynamics in macrophage activation. <i>Genomics</i> , 2006, 88, 133-142.	2.9	125



#	ARTICLE	IF	CITATIONS
127	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635.	21.4	1,201
128	Systems biology of innate immunity. <i>Cellular Immunology</i> , 2006, 244, 105-109.	3.0	35
129	Transcript Annotation in FANTOM3: Mouse Gene Catalog Based on Physical cDNAs. <i>PLoS Genetics</i> , 2006, 2, e62.	3.5	165
130	The JNK Are Important for Development and Survival of Macrophages. <i>Journal of Immunology</i> , 2006, 176, 2219-2228.	0.8	100
131	LPS regulates proinflammatory gene expression in macrophages by altering histone deacetylase expression. <i>FASEB Journal</i> , 2006, 20, 1315-1327.	0.5	210
132	Antisense Transcription in the Mammalian Transcriptome. <i>Science</i> , 2005, 309, 1564-1566.	12.6	1,553
133	An Inflammatory Role for the Mammalian Carboxypeptidase Inhibitor Latexin: Relationship to Cystatins and the Tumor Suppressor TIG1. <i>Structure</i> , 2005, 13, 309-317.	3.3	71
134	Pilot studies on the parallel production of soluble mouse proteins in a bacterial expression system. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 13-20.	1.2	7
135	Inflammation suppressor genes: please switch out all the lights. <i>Journal of Leukocyte Biology</i> , 2005, 78, 9-13.	3.3	88
136	Transcription Factor Tfec Contributes to the IL-4-Inducible Expression of a Small Group of Genes in Mouse Macrophages Including the Granulocyte Colony-Stimulating Factor Receptor. <i>Journal of Immunology</i> , 2005, 174, 7111-7122.	0.8	81
137	Experimental validation of the regulated expression of large numbers of non-coding RNAs from the mouse genome. <i>Genome Research</i> , 2005, 16, 11-19.	5.5	461
138	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
139	LPS regulates a set of genes in primary murine macrophages by antagonising CSF-1 action. <i>Immunobiology</i> , 2005, 210, 97-107.	1.9	58
140	Interferon- $\beta$ : an overview of signals, mechanisms and functions. <i>Journal of Leukocyte Biology</i> , 2004, 75, 163-189.	3.3	3,315
141	Probing the S100 protein family through genomic and functional analysis. <i>Genomics</i> , 2004, 84, 10-22.	2.9	153
142	Genetic control of the innate immune response. <i>BMC Immunology</i> , 2003, 4, 5.	2.2	119
143	Identification and Analysis of Chromodomain-Containing Proteins Encoded in the Mouse Transcriptome. <i>Genome Research</i> , 2003, 13, 1416-1429.	5.5	50
144	Systematic Characterization of the Zinc-Finger-Containing Proteins in the Mouse Transcriptome. <i>Genome Research</i> , 2003, 13, 1430-1442.	5.5	89

#	ARTICLE	IF	CITATIONS
145	Continued Discovery of Transcriptional Units Expressed in Cells of the Mouse Mononuclear Phagocyte Lineage. <i>Genome Research</i> , 2003, 13, 1360-1365.	5.5	41
146	Phosphoregulators: Protein Kinases and Protein Phosphatases of Mouse. <i>Genome Research</i> , 2003, 13, 1443-1454.	5.5	43
147	Generation of Diversity in the Innate Immune System: Macrophage Heterogeneity Arises from Gene-Autonomous Transcriptional Probability of Individual Inducible Genes. <i>Journal of Immunology</i> , 2002, 168, 44-50.	0.8	94
148	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	27.8	1,548
149	The mononuclear phagocyte system revisited. <i>Journal of Leukocyte Biology</i> , 2002, 72, 621-7.	3.3	264
150	Review of In Vitro Toxicity of Nanoparticles and Nanorods Part 2. , 0, , .		0