

Felix Naef

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108
papers

8,140
citations

45
h-index

90
g-index

129
ext. papers

9,648
ext. citations

10.8
avg, IF

5.94
L-index

#	Paper	IF	Citations
108	Circadian gene expression in individual fibroblasts: cell-autonomous and self-sustained oscillators pass time to daughter cells. <i>Cell</i> , 2004 , 119, 693-705	56.2	794
107	Mammalian genes are transcribed with widely different bursting kinetics. <i>Science</i> , 2011 , 332, 472-4	33.3	616
106	Molecular signature of human embryonic stem cells and its comparison with the mouse. <i>Developmental Biology</i> , 2003 , 260, 404-13	3.1	406
105	Transport and conservation laws. <i>Physical Review B</i> , 1997 , 55, 11029-11032	3.3	396
104	Circadian regulation of gene expression systems in the Drosophila head. <i>Neuron</i> , 2001 , 32, 657-71	13.9	383
103	Genome-wide and phase-specific DNA-binding rhythms of BMAL1 control circadian output functions in mouse liver. <i>PLoS Biology</i> , 2011 , 9, e1000595	9.7	333
102	The nodal precursor acting via activin receptors induces mesoderm by maintaining a source of its convertases and BMP4. <i>Developmental Cell</i> , 2006 , 11, 313-23	10.2	231
101	Circadian clock-dependent and -independent rhythmic proteomes implement distinct diurnal functions in mouse liver. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 167-72	11.5	227
100	The circadian clock coordinates ribosome biogenesis. <i>PLoS Biology</i> , 2013 , 11, e1001455	9.7	196
99	Chemotaxis behavior mediated by single larval olfactory neurons in Drosophila. <i>Current Biology</i> , 2005 , 15, 2086-96	6.3	190
98	Cold-inducible RNA-binding protein modulates circadian gene expression posttranscriptionally. <i>Science</i> , 2012 , 338, 379-83	33.3	188
97	A self-regulatory system of interlinked signaling feedback loops controls mouse limb patterning. <i>Science</i> , 2009 , 323, 1050-3	33.3	163
96	Circadian and feeding rhythms differentially affect rhythmic mRNA transcription and translation in mouse liver. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E6579-88	11.5	150
95	Solving the riddle of the bright mismatches: labeling and effective binding in oligonucleotide arrays. <i>Physical Review E</i> , 2003 , 68, 011906	2.4	147
94	Genome-wide RNA polymerase II profiles and RNA accumulation reveal kinetics of transcription and associated epigenetic changes during diurnal cycles. <i>PLoS Biology</i> , 2012 , 10, e1001442	9.7	142
93	Absolute mRNA concentrations from sequence-specific calibration of oligonucleotide arrays. <i>Nucleic Acids Research</i> , 2003 , 31, 1962-8	20.1	135
92	Robust synchronization of coupled circadian and cell cycle oscillators in single mammalian cells. <i>Molecular Systems Biology</i> , 2014 , 10, 739	12.2	132

91	Guidelines for Genome-Scale Analysis of Biological Rhythms. <i>Journal of Biological Rhythms</i> , 2017 , 32, 380-393	3.2	127
90	Cellular oscillators: rhythmic gene expression and metabolism. <i>Current Opinion in Cell Biology</i> , 2005 , 17, 223-9	9	120
89	Circadian gene expression is resilient to large fluctuations in overall transcription rates. <i>EMBO Journal</i> , 2009 , 28, 123-34	13	118
88	Nuclear Proteomics Uncovers Diurnal Regulatory Landscapes in Mouse Liver. <i>Cell Metabolism</i> , 2017 , 25, 102-117	24.6	113
87	The Mouse Microbiome Is Required for Sex-Specific Diurnal Rhythms of Gene Expression and Metabolism. <i>Cell Metabolism</i> , 2019 , 29, 362-382.e8	24.6	109
86	Integration of light and temperature in the regulation of circadian gene expression in Drosophila. <i>PLoS Genetics</i> , 2007 , 3, e54	6	108
85	A process based assessment of the potential to reduce flood runoff by land use change. <i>Journal of Hydrology</i> , 2002 , 267, 74-79	6	105
84	A chemostat array enables the spatio-temporal analysis of the yeast proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 15842-7	11.5	103
83	Control of daily transcript oscillations in Drosophila by light and the circadian clock. <i>PLoS Genetics</i> , 2006 , 2, e39	6	103
82	Freedom and rules: the acquisition and reprogramming of a bird's learned song. <i>Science</i> , 2005 , 308, 1046-9.3	9.3	99
81	Exploring the transcriptional landscape of plant circadian rhythms using genome tiling arrays. <i>Genome Biology</i> , 2009 , 10, R17	18.3	93
80	DNA hybridization to mismatched templates: a chip study. <i>Physical Review E</i> , 2002 , 65, 040902	2.4	93
79	Stimulus-induced modulation of transcriptional bursting in a single mammalian gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 20563-8	11.5	89
78	Two distinct promoter architectures centered on dynamic nucleosomes control ribosomal protein gene transcription. <i>Genes and Development</i> , 2014 , 28, 1695-709	12.6	76
77	Absolute quantification of transcription factors during cellular differentiation using multiplexed targeted proteomics. <i>Nature Methods</i> , 2013 , 10, 570-6	21.6	72
76	Probabilistic base calling of Solexa sequencing data. <i>BMC Bioinformatics</i> , 2008 , 9, 431	3.6	72
75	What shapes eukaryotic transcriptional bursting?. <i>Molecular BioSystems</i> , 2017 , 13, 1280-1290		71
74	Circadian Dbp transcription relies on highly dynamic BMAL1-CLOCK interaction with E boxes and requires the proteasome. <i>Molecular Cell</i> , 2012 , 48, 277-87	17.6	70

73	Engineered signaling centers for the spatially controlled patterning of human pluripotent stem cells. <i>Nature Methods</i> , 2019 , 16, 640-648	21.6	69
72	Structure of silent transcription intervals and noise characteristics of mammalian genes. <i>Molecular Systems Biology</i> , 2015 , 11, 823	12.2	69
71	Modulation of transcriptional burst frequency by histone acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 7153-7158	11.5	67
70	In vivo transcriptional profile analysis reveals RNA splicing and chromatin remodeling as prominent processes for adult neurogenesis. <i>Molecular and Cellular Neurosciences</i> , 2006 , 31, 131-48	4.8	61
69	Clock-dependent chromatin topology modulates circadian transcription and behavior. <i>Genes and Development</i> , 2018 , 32, 347-358	12.6	59
68	Transcription factor activity rhythms and tissue-specific chromatin interactions explain circadian gene expression across organs. <i>Genome Research</i> , 2018 , 28, 182-191	9.7	58
67	Transcriptional regulatory logic of the diurnal cycle in the mouse liver. <i>PLoS Biology</i> , 2017 , 15, e2001069	9.7	51
66	Circadian and Feeding Rhythms Orchestrate the Diurnal Liver Acetylome. <i>Cell Reports</i> , 2017 , 20, 1729-1743	13.6	51
65	Empirical characterization of the expression ratio noise structure in high-density oligonucleotide arrays. <i>Genome Biology</i> , 2002 , 3, RESEARCH0018	18.3	51
64	Temperature regulates splicing efficiency of the cold-inducible RNA-binding protein gene Cirbp. <i>Genes and Development</i> , 2016 , 30, 2005-17	12.6	48
63	The telomere-binding protein Tbf1 demarcates snoRNA gene promoters in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2010 , 38, 614-20	17.6	44
62	Molecular and statistical tools for circadian transcript profiling. <i>Methods in Enzymology</i> , 2005 , 393, 341-65	7	43
61	A study of accuracy and precision in oligonucleotide arrays: extracting more signal at large concentrations. <i>Bioinformatics</i> , 2003 , 19, 178-84	7.2	41
60	Similarities and differences of polyadenylation signals in human and fly. <i>BMC Genomics</i> , 2006 , 7, 176	4.5	39
59	Origins and consequences of transcriptional discontinuity. <i>Current Opinion in Cell Biology</i> , 2011 , 23, 657-62	6.2	37
58	Circadian clock-dependent and -independent posttranscriptional regulation underlies temporal mRNA accumulation in mouse liver. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E1916-E1925	11.5	36
57	Dynamical signatures of cellular fluctuations and oscillator stability in peripheral circadian clocks. <i>Molecular Systems Biology</i> , 2007 , 3, 93	12.2	35
56	Genomic and expression analysis of the 12p11-p12 amplicon using EST arrays identifies two novel amplified and overexpressed genes. <i>Cancer Research</i> , 2002 , 62, 6218-23	10.1	34

55	Ribosome profiling and dynamic regulation of translation in mammals. <i>Current Opinion in Genetics and Development</i> , 2017 , 43, 120-127	4.9	33
54	Production of ribosome components in effector CD4+ T cells is accelerated by TCR stimulation and coordinated by ERK-MAPK. <i>Immunity</i> , 2003 , 19, 535-48	32.3	32
53	Whole-embryo modeling of early segmentation in <i>Drosophila</i> identifies robust and fragile expression domains. <i>Biophysical Journal</i> , 2011 , 101, 287-96	2.9	31
52	Single Live Cell Monitoring of Protein Turnover Reveals Intercellular Variability and Cell-Cycle Dependence of Degradation Rates. <i>Molecular Cell</i> , 2018 , 71, 1079-1091.e9	17.6	30
51	Genotypic features of lentivirus transgenic mice. <i>Journal of Virology</i> , 2008 , 82, 7111-9	6.6	29
50	Systematic analysis of differential rhythmic liver gene expression mediated by the circadian clock and feeding rhythms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	29
49	Systems Chronobiology: Global Analysis of Gene Regulation in a 24-Hour Periodic World. <i>Cold Spring Harbor Perspectives in Biology</i> , 2017 , 9,	10.2	28
48	Sleep-wake-driven and circadian contributions to daily rhythms in gene expression and chromatin accessibility in the murine cortex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 25773-25783	11.5	27
47	Modeling an evolutionary conserved circadian cis-element. <i>PLoS Computational Biology</i> , 2008 , 4, e38	5	26
46	Rhythms of the Genome: Circadian Dynamics from Chromatin Topology, Tissue-Specific Gene Expression, to Behavior. <i>Trends in Genetics</i> , 2018 , 34, 915-926	8.5	26
45	Collective synchronization in populations of globally coupled phase oscillators with drifting frequencies. <i>Physical Review E</i> , 2006 , 73, 011104	2.4	25
44	Identifying synergistic regulation involving c-Myc and sp1 in human tissues. <i>Nucleic Acids Research</i> , 2007 , 35, 1098-107	20.1	25
43	Cell-type-specific transcriptomics in chimeric models using transcriptome-based masks. <i>Nucleic Acids Research</i> , 2005 , 33, e1111	20.1	25
42	Autocorrelations from the transfer-matrix density-matrix renormalization-group method. <i>Physical Review B</i> , 1999 , 60, 359-368	3.3	23
41	Characteristic bimodal profiles of RNA polymerase II at thousands of active mammalian promoters. <i>Genome Biology</i> , 2014 , 15, R85	18.3	22
40	Space-time logic of liver gene expression at sub-lobular scale. <i>Nature Metabolism</i> , 2021 , 3, 43-58	14.6	18
39	Non-circadian expression masking clock-driven weak transcription rhythms in U2OS cells. <i>PLoS ONE</i> , 2014 , 9, e102238	3.7	15
38	Reactive hall response. <i>Physical Review Letters</i> , 2000 , 85, 377-80	7.4	14

37	Nuclear spin relaxation rates in two-Leg spin ladders. <i>Physical Review Letters</i> , 2000 , 84, 1320-3	7.4	14
36	Robust landscapes of ribosome dwell times and aminoacyl-tRNAs in response to nutrient stress in liver. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 9630-9641	11.5	13
35	Memory and relatedness of transcriptional activity in mammalian cell lineages. <i>Nature Communications</i> , 2019 , 10, 1208	17.4	12
34	Circadian clocks go in vitro: purely post-translational oscillators in cyanobacteria. <i>Molecular Systems Biology</i> , 2005 , 1, 2005.0019	12.2	12
33	Cross-regulatory circuits linking inflammation, high-fat diet, and the circadian clock. <i>Genes and Development</i> , 2018 , 32, 1359-1360	12.6	12
32	Low-dimensional Dynamics of Two Coupled Biological Oscillators. <i>Nature Physics</i> , 2019 , 15, 1086-1094	16.2	11
31	Quantitative analysis and modeling probe polarity establishment in <i>C. elegans</i> embryos. <i>Biophysical Journal</i> , 2015 , 108, 799-809	2.9	9
30	Computational analysis of protein-DNA interactions from ChIP-seq data. <i>Methods in Molecular Biology</i> , 2012 , 786, 263-73	1.4	9
29	Few crucial links assure checkpoint efficiency in the yeast cell-cycle network. <i>Bioinformatics</i> , 2006 , 22, 2539-46	7.2	9
28	Representing perturbed dynamics in biological network models. <i>Physical Review E</i> , 2007 , 76, 011917	2.4	9
27	Analysis of the dynamics of limb transcriptomes during mouse development. <i>BMC Developmental Biology</i> , 2011 , 11, 47	3.1	8
26	The Effects of Time-Restricted Eating versus Standard Dietary Advice on Weight, Metabolic Health and the Consumption of Processed Food: A Pragmatic Randomised Controlled Trial in Community-Based Adults. <i>Nutrients</i> , 2021 , 13,	6.7	8
25	Revealing Assembly of a Pore-Forming Complex Using Single-Cell Kinetic Analysis and Modeling. <i>Biophysical Journal</i> , 2016 , 110, 1574-1581	2.9	7
24	Analysis of precision in chemical oscillators: implications for circadian clocks. <i>Physical Biology</i> , 2013 , 10, 056005	3	7
23	Differential regulation of RNA polymerase III genes during liver regeneration. <i>Nucleic Acids Research</i> , 2019 , 47, 1786-1796	20.1	7
22	Quantitative relationships between SMAD dynamics and target gene activation kinetics in single live cells. <i>Scientific Reports</i> , 2019 , 9, 5372	4.9	6
21	CAST: An automated segmentation and tracking tool for the analysis of transcriptional kinetics from single-cell time-lapse recordings. <i>Methods</i> , 2015 , 85, 3-11	4.6	6
20	Relationship between estrogen receptor alpha location and gene induction reveals the importance of downstream sites and cofactors. <i>BMC Genomics</i> , 2009 , 10, 381	4.5	6

19	ASSET: a robust algorithm for the automated segmentation and standardization of early <i>Caenorhabditis elegans</i> embryos. <i>Developmental Dynamics</i> , 2010 , 239, 3285-96	2.9	6
18	Reply to Comment on Solving the riddle of the bright mismatches: Labeling and effective binding in oligonucleotide arrays <i>Physical Review E</i> , 2006 , 73,	2.4	6
17	What determines eukaryotic translation elongation: recent molecular and quantitative analyses of protein synthesis. <i>Open Biology</i> , 2020 , 10, 200292	7	6
16	Stabilizing patterning in the <i>Drosophila</i> segment polarity network by selecting models in silico. <i>BioSystems</i> , 2010 , 102, 3-10	1.9	5
15	A new promoter element associated with daily time keeping in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2017 , 45, 6459-6470	20.1	4
14	Comment on "Circadian rhythms in the absence of the clock gene ". <i>Science</i> , 2021 , 372,	33.3	3
13	Oscillating and stable genome topologies underlie hepatic physiological rhythms during the circadian cycle. <i>PLoS Genetics</i> , 2021 , 17, e1009350	6	3
12	Characterization of the expression ratio noise structure in high-density oligonucleotide arrays. <i>Genome Biology</i> , 2002 , 3, PREPRINT0001	18.3	3
11	Network inference by combining biologically motivated regulatory constraints with penalized regression. <i>Annals of the New York Academy of Sciences</i> , 2009 , 1158, 114-24	6.5	2
10	Stochastic phase oscillators and circadian bioluminescence recordings. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2007 , 72, 405-11	3.9	2
9	How to tell time: advances in decoding circadian phase from omics snapshots. <i>F1000Research</i> , 2020 , 9,	3.6	2
8	Modeling ribosome dwell times and relationships with tRNA loading and codon usage in mammals		2
7	Stochastic phase oscillator models for circadian clocks. <i>Advances in Experimental Medicine and Biology</i> , 2008 , 641, 141-9	3.6	2
6	Simple and complex interactions between sleep-wake driven and circadian processes shape daily genome regulatory dynamics in the mouse		1
5	Oscillating and stable genome topologies underlie hepatic physiological rhythms during the circadian cycle		1
4	Transcription factor activity rhythms and tissue-specific chromatin interactions explain circadian gene expression across organs		1
3	Systems Biology and Modeling of Circadian Rhythms 2010 , 283-293		1
2	The circadian oscillator analysed at the single-transcript level. <i>Molecular Systems Biology</i> , 2021 , 17, e10135.2	1	1

- 1 A Self-regulatory System of Interlinked Signaling Feedback Loops Controls Mouse Limb Patterning. *Lecture Notes in Computer Science*, **2010**, 575-576 0.9