

Charles Girardot

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9240989/publications.pdf>

Version: 2024-02-01

27
papers

2,408
citations

394421

19
h-index

580821

25
g-index

30
all docs

30
docs citations

30
times ranked

4128
citing authors

#	ARTICLE	IF	CITATIONS
1	Tissue-specific analysis of chromatin state identifies temporal signatures of enhancer activity during embryonic development. <i>Nature Genetics</i> , 2012, 44, 148-156.	21.4	453
2	Combinatorial binding predicts spatio-temporal cis-regulatory activity. <i>Nature</i> , 2009, 462, 65-70.	27.8	361
3	A core transcriptional network for early mesoderm development in <i>Drosophila melanogaster</i> . <i>Genes and Development</i> , 2007, 21, 436-449.	5.9	268
4	A Transcription Factor Collective Defines Cardiac Cell Fate and Reflects Lineage History. <i>Cell</i> , 2012, 148, 473-486.	28.9	239
5	Dynamic Regulation by Polycomb Group Protein Complexes Controls Pattern Formation and the Cell Cycle in <i>Drosophila</i> . <i>Developmental Cell</i> , 2008, 15, 877-889.	7.0	178
6	Je, a versatile suite to handle multiplexed NGS libraries with unique molecular identifiers. <i>BMC Bioinformatics</i> , 2016, 17, 419.	2.6	121
7	Model-based method for transcription factor target identification with limited data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7793-7798.	7.1	87
8	Expanding the Circuitry of Pluripotency by Selective Isolation of Chromatin-Associated Proteins. <i>Molecular Cell</i> , 2016, 64, 624-635.	9.7	84
9	Analysis of variation at transcription factor binding sites in <i>Drosophila</i> and humans. <i>Genome Biology</i> , 2012, 13, R49.	9.6	83
10	A conserved role for Snail as a potentiator of active transcription. <i>Genes and Development</i> , 2014, 28, 167-181.	5.9	73
11	Dual functionality of cis-regulatory elements as developmental enhancers and Polycomb response elements. <i>Genes and Development</i> , 2017, 31, 590-602.	5.9	71
12	Haploinsufficiency of the intellectual disability gene SETD5 disturbs developmental gene expression and cognition. <i>Nature Neuroscience</i> , 2018, 21, 1717-1727.	14.8	65
13	Subtle Changes in Motif Positioning Cause Tissue-Specific Effects on Robustness of an Enhancer's Activity. <i>PLoS Genetics</i> , 2014, 10, e1004060.	3.5	59
14	Lineage-Resolved Enhancer and Promoter Usage during a Time Course of Embryogenesis. <i>Developmental Cell</i> , 2020, 55, 648-664.e9.	7.0	47
15	Elucidation of an Archaeal Replication Protein Network to Generate Enhanced PCR Enzymes. <i>Journal of Biological Chemistry</i> , 2002, 277, 16179-16188.	3.4	44
16	Uncoupling evolutionary changes in DNA sequence, transcription factor occupancy and enhancer activity. <i>ELife</i> , 2017, 6, .	6.0	43
17	4DXpress: a database for cross-species expression pattern comparisons. <i>Nucleic Acids Research</i> , 2007, 36, D847-D853.	14.5	33
18	Opbp is a new architectural/insulator protein required for ribosomal gene expression. <i>Nucleic Acids Research</i> , 2017, 45, 12285-12300.	14.5	27

#	ARTICLE	IF	CITATIONS
19	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. <i>Development (Cambridge)</i> , 2014, 141, 2633-2643.	2.5	25
20	The Role of Chromatin Accessibility in cis-Regulatory Evolution. <i>Genome Biology and Evolution</i> , 2019, 11, 1813-1828.	2.5	16
21	Qualitative Dynamical Modelling Can Formally Explain Mesoderm Specification and Predict Novel Developmental Phenotypes. <i>PLoS Computational Biology</i> , 2016, 12, e1005073.	3.2	10
22	The hourglass model of evolutionary conservation during embryogenesis extends to developmental enhancers with signatures of positive selection. <i>Genome Research</i> , 2021, 31, 1573-1581.	5.5	9
23	Identification and <i>in silico</i> modeling of enhancers reveals new features of the cardiac differentiation network. <i>Development (Cambridge)</i> , 2016, 143, 4533-4542.	2.5	5
24	Dynamix: dynamic visualization by automatic selection of informative tracks from hundreds of genomic datasets. <i>Bioinformatics</i> , 2017, 33, 2194-2196.	4.1	3
25	Expanding the mesodermal transcriptional network by genome-wide identification of Zinc finger homeodomain 1 (Zfh1) targets. <i>FEBS Letters</i> , 2019, 593, 1698-1710.	2.8	2
26	CoCo: a web application to display, store and curate ChIP-on-chip data integrated with diverse types of gene expression data. <i>Bioinformatics</i> , 2007, 23, 771-773.	4.1	0
27	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. <i>Journal of Cell Science</i> , 2014, 127, e1-e1.	2.0	0