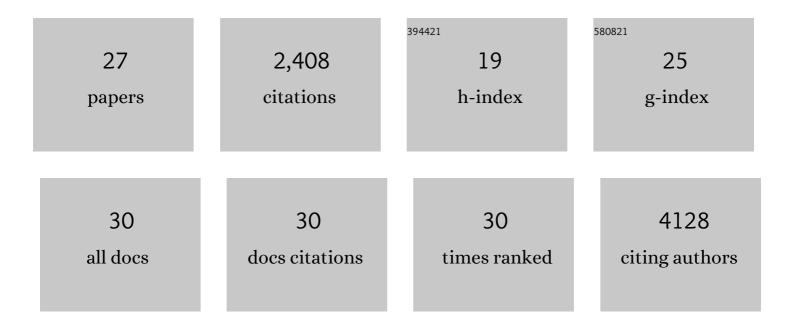
## **Charles Girardot**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9240989/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	The hourglass model of evolutionary conservation during embryogenesis extends to developmental enhancers with signatures of positive selection. Genome Research, 2021, 31, 1573-1581.	5.5	9
2	Lineage-Resolved Enhancer and Promoter Usage during a Time Course of Embryogenesis. Developmental Cell, 2020, 55, 648-664.e9.	7.0	47
3	The Role of Chromatin Accessibility in cis-Regulatory Evolution. Genome Biology and Evolution, 2019, 11, 1813-1828.	2.5	16
4	Expanding the mesodermal transcriptional network by genomeâ€wide identification of Zinc finger homeodomain 1 (Zfh1) targets. FEBS Letters, 2019, 593, 1698-1710.	2.8	2
5	Haploinsufficiency of the intellectual disability gene SETD5 disturbs developmental gene expression and cognition. Nature Neuroscience, 2018, 21, 1717-1727.	14.8	65
6	Dual functionality of <i>cis</i> -regulatory elements as developmental enhancers and Polycomb response elements. Genes and Development, 2017, 31, 590-602.	5.9	71
7	Opbp is a new architectural/insulator protein required for ribosomal gene expression. Nucleic Acids Research, 2017, 45, 12285-12300.	14.5	27
8	Dynamix: dynamic visualization by automatic selection of informative tracks from hundreds of genomic datasets. Bioinformatics, 2017, 33, 2194-2196.	4.1	3
9	Uncoupling evolutionary changes in DNA sequence, transcription factor occupancy and enhancer activity. ELife, 2017, 6, .	6.0	43
10	Identification and <i>in silico</i> modeling of enhancers reveals new features of the cardiac differentiation network. Development (Cambridge), 2016, 143, 4533-4542.	2.5	5
11	Je, a versatile suite to handle multiplexed NGS libraries with unique molecular identifiers. BMC Bioinformatics, 2016, 17, 419.	2.6	121
12	Expanding the Circuitry of Pluripotency by Selective Isolation of Chromatin-Associated Proteins. Molecular Cell, 2016, 64, 624-635.	9.7	84
13	Qualitative Dynamical Modelling Can Formally Explain Mesoderm Specification and Predict Novel Developmental Phenotypes. PLoS Computational Biology, 2016, 12, e1005073.	3.2	10
14	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. Development (Cambridge), 2014, 141, 2633-2643.	2.5	25
15	Subtle Changes in Motif Positioning Cause Tissue-Specific Effects on Robustness of an Enhancer's Activity. PLoS Genetics, 2014, 10, e1004060.	3.5	59
16	A conserved role for Snail as a potentiator of active transcription. Genes and Development, 2014, 28, 167-181.	5.9	73
17	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. Journal of Cell Science, 2014, 127, e1-e1.	2.0	0
18	Analysis of variation at transcription factor binding sites in Drosophila and humans. Genome Biology, 2012, 13, R49.	9.6	83

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#	Article	IF	CITATIONS
19	A Transcription Factor Collective Defines Cardiac Cell Fate and Reflects Lineage History. Cell, 2012, 148, 473-486.	28.9	239
20	Tissue-specific analysis of chromatin state identifies temporal signatures of enhancer activity during embryonic development. Nature Genetics, 2012, 44, 148-156.	21.4	453
21	Model-based method for transcription factor target identification with limited data. Proceedings of the United States of America, 2010, 107, 7793-7798.	7.1	87
22	Combinatorial binding predicts spatio-temporal cis-regulatory activity. Nature, 2009, 462, 65-70.	27.8	361
23	Dynamic Regulation by Polycomb Group Protein Complexes Controls Pattern Formation and the Cell Cycle in Drosophila. Developmental Cell, 2008, 15, 877-889.	7.0	178
24	CoCo: a web application to display, store and curate ChIP-on-chip data integrated with diverse types of gene expression data. Bioinformatics, 2007, 23, 771-773.	4.1	0
25	A core transcriptional network for early mesoderm development in Drosophila melanogaster. Genes and Development, 2007, 21, 436-449.	5.9	268
26	4DXpress: a database for cross-species expression pattern comparisons. Nucleic Acids Research, 2007, 36, D847-D853.	14.5	33
27	Elucidation of an Archaeal Replication Protein Network to Generate Enhanced PCR Enzymes. Journal of Biological Chemistry, 2002, 277, 16179-16188.	3.4	44