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GimmeMotifs: an analysis framework for transcription factor motif analysis

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32	Open collaborative writing with Manubot. <i>PLoS Computational Biology</i> , 2019 , 15, e1007128	5	24
31	Dynamic transcriptional and chromatin accessibility landscape of medaka embryogenesis. <i>Genome Research</i> , 2020 , 30, 924-937	9.7	9
30	Transcriptomic and open chromatin atlas of high-resolution anatomical regions in the rhesus macaque brain. <i>Nature Communications</i> , 2020 , 11, 474	17.4	14
29	TAD cliques predict key features of chromatin organization. <i>BMC Genomics</i> , 2021 , 22, 499	4.5	2
28	ANANSE: an enhancer network-based computational approach for predicting key transcription factors in cell fate determination. <i>Nucleic Acids Research</i> , 2021 , 49, 7966-7985	20.1	3
27	Heterochromatin diversity modulates genome compartmentalization and loop extrusion barriers.		2
26	ANANSE: An enhancer network-based computational approach for predicting key transcription factors in cell fate determination.		0
25	Bayesian Linear Mixed Models for Motif Activity Analysis.		
24	Epigenome dysregulation resulting from NSD1 mutation in head and neck squamous cell carcinoma.		0
23	Combinatorial action of transcription factors in open chromatin contributes to early cellular heterogeneity and organizer mesendoderm specification.		0
22	Loss of PRC2 subunits primes lineage choice during exit of pluripotency.		
21	TAD cliques predict key features of chromatin organization.		
20	Loss of PRC2 subunits primes lineage choice during exit of pluripotency. <i>Nature Communications</i> , 2021 , 12, 6985	17.4	2
19	Integration of single-cell transcriptomes and chromatin landscapes reveals regulatory programs driving pharyngeal organ development.. <i>Nature Communications</i> , 2022 , 13, 457	17.4	1
18	Assessing Chromatin Accessibility During WBR in Acoels.. <i>Methods in Molecular Biology</i> , 2022 , 2450, 549-561		1
17	FindIT2: an R/Bioconductor package to identify influential transcription factor and targets based on multi-omics data.. <i>BMC Genomics</i> , 2022 , 23, 272	4.5	
16	Chromatin regulates genome-wide transcription factor binding affinities.		0

15	Nucleome programming is required for the foundation of totipotency in mammalian germline development. <i>EMBO Journal</i> ,	13	1
14	Insights into deuterostome evolution from the biphasic transcriptional programmes of hemichordates.		
13	FOXA2 controls the antioxidant response in FH-deficient cells independent of NRF2.		
12	ONECUT2 restricts Microfold cell numbers in the small intestine; a multi-omics study.		0
11	Loss of MLL3/4 decouples enhancer H3K4 monomethylation, H3K27 acetylation, and gene activation during ESC differentiation.		0
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7	ONECUT2 regulates RANKL-dependent enterocyte and microfold cell differentiation in the small intestine; a multi-omics study.		0
6	Computational approaches to understand transcription regulation in development.		1
5	Loss of MLL3/4 decouples enhancer H3K4 monomethylation, H3K27 acetylation, and gene activation during embryonic stem cell differentiation. 2023 , 24,		0
4	scANANSE gene regulatory network and motif analysis of single-cell clusters. 12, 243		0
3	Quantification of absolute transcription factor binding affinities in the native chromatin context using BANC-seq.		0
2	Cross-species regulatory landscapes and elements revealed by novel joint systematic integration of human and mouse blood cell epigenomes.		0
1	Multi-omics analysis reveals a crucial role for Retinoic Acid in promoting epigenetic and transcriptional competence of an in vitro model of human Pharyngeal Endoderm.		0