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Comparative epigenomic analysis of murine and human adipogenesis

DOI: 10.1016/j.cell.2010.09.006 Cell, 2010, 143, 156-69.

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432	Genome-wide analysis of glucocorticoid receptor binding regions in adipocytes reveal gene network involved in triglyceride homeostasis. <i>PLoS ONE</i> , <b>2010</b> , 5, e15188	3.7	126
431	Tiling histone H3 lysine 4 and 27 methylation in zebrafish using high-density microarrays. <i>PLoS ONE</i> , <b>2010</b> , 5, e15651	3.7	23
430	Epigenetic signatures distinguish multiple classes of enhancers with distinct cellular functions. <i>Genome Research</i> , <b>2011</b> , 21, 1273-83	9.7	402
429	Adipogenesis at a glance. <b>2011</b> , 124, 2681-6		246
428	Identifying novel transcriptional components controlling energy metabolism. 2011, 14, 739-45		20
427	Genome-wide interplay of nuclear receptors with the epigenome. <b>2011</b> , 1812, 818-23		22
426	Molecular basis for gene-specific transactivation by nuclear receptors. <b>2011</b> , 1812, 824-35		55
425	High conservation of transcription factor binding and evidence for combinatorial regulation across six Drosophila species. <b>2011</b> , 43, 414-20		102
424	Forming functional fat: a growing understanding of adipocyte differentiation. <b>2011</b> , 12, 722-34		891
423	Genome-wide CTCF distribution in vertebrates defines equivalent sites that aid the identification of disease-associated genes. <b>2011</b> , 18, 708-14		77
422	Extensive chromatin remodelling and establishment of transcription factor 'hotspots' during early adipogenesis. <b>2011</b> , 30, 1459-72		262
421	Adipogenic hotspots: where the action is. <b>2011</b> , 30, 1418-9		6
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66	Complexity and conservation of regulatory landscapes underlie evolutionary resilience of mammalian gene expression.		2
65	Genome-wide mapping of histone modifications in two species of Leptosphaeria maculans showing contrasting genomic organization and host specialization.		2
64	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development.		1
63	BoostMe accurately predicts DNA methylation values in whole-genome bisulfite sequencing of multiple human tissues.		2
62	Functional Characterization of Enhancer Evolution in the Primate Lineage.		2
61	Heart enhancers with deeply conserved regulatory activity are established early in development.		1
60	Influence of genetic variants on gene expression in human pancreatic islets Implications for type 2 diabetes.		9
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40	Reactive Oxygen Species Regulate the Inflammatory Function of NKT Cells through Promyelocytic Leukemia Zinc Finger.	
39	Temporal epigenomic profiling identifies AHR and GLIS1 as super-enhancer controlled regulators of mesenchymal multipotency.	
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