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1	DeepBlue: Diving into Epigenomic Data	Felipe ALBRECHT
2	IHEC Data Portal 2016 update: datasets quality control, permanent sessions, public API	David BUJOLD
3	Dynamic metabolic epigenome landscape in human tissues from Korea Epigenome Project	Jae-Bum BAE
4	The BLUEPRINT of human hematopoietic differentiation inscribed in DNA methylation	Matthias FARLIK
5	Cell type specific chromatin architecture defines erythropoiesis and megakaryopoiesis.	Romina PETERSEN
6	Combining transcription factor binding affinities with an open chromatin prior for accurate gene expression prediction	Florian SCHMIDT
7	Epigenetic and functional dynamics of human bone marrow myeloid differentiation to mature blood neutrophils	Farzin POURFARZAD
8	A short lamin B1 isoform required for neutrophil nuclear lobulation and extracellular trap formation	Farzin POURFARZAD
9	The effect of common genetic variation on transcription factor binding, chromatin structure and their influence on cellular phenotype	Stephen WATT
10	Distinct epigenetic architectures in bidirectional promoters revealed by single cell analysis	Fatemeh BEHJATI ARDAKANI
11	eFORGE: a tool for identifying cell type-specific signal in epigenomic data	Charles BREEZE
12	Epigenetics and moral responsibility: the challenging task of identifying epigenetic normality and the internal contradiction of plasticity+inheritance	Charles DUPRAS
13	Genetic variations in the transcriptome and epigenome of human immune cells	Louella Vasquez
14	The epigenomic landscape of adult de novo AMLs	Guoqiang YI
15	An efficient method for NGS library preparation from single-stranded DNA	Fumihito MIURA
16	A community-wide comparison of DNA methylation assays for biomarker development and clinical applications	Florian HALBRITTER
17	Computational Methods for the DEEP Characterization of DNA Methylation BLUEPRINTs	Fabian MÜLLER
18	MeDeCom discovers and quantifies latent components of heterogeneous methylomes	Pavlo LUTSIK
19	iMethyl: an integrative human DNA methylation variation database	Atsushi SHIMIZU
20	HOXA transcription factors play a key role in the epigenetic regulation of TCRalpha enhancer activity	Agata CIESLAK
21	Dynamic DNA methylation in healthy and neoplastic blood cells	Angelika MERKEL



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22	IHEC on Twitter: First Year	Cath ENNIS
23	Canadian Epigenetics, Environment and Health Research Consortium (CEEHRC) Network: enabling and advancing Canadian epigenetics research	Martin HIRST
24	Revisiting digital footprinting of DNase-seq for detection of cell-specific binding sites	Ivan COSTA
25	Using the IHEC data through the Genomic Efficient Correlator (GeEC) tool	Pierre-Étienne JACQUES
26	Regulation of intron retention in human blood cells	Sebastian ULLRICH
27	Fast and efficient Post-Bisulfite-Seq Library construction with QIAseq Ultralow Input DNA Library Protocol	Ioanna ANDREOU
28	Age-related DNA methylation changes in mouse spermatozoa	Norio KOBAYASHI
29	Benchmarking of splinted adaptor tagging (SPLAT), a novel bisulphite sequencing library preparation method	Jessica NORDLUND
30	Reference Epigenomes at the ENCODE portal	Jason HILTON
31	The Relevance of epigenetic signature in blood with target tissues in chronic diseases	Suman LEE
32	Discovery of new molecular subgroups in pediatric ALL using DNA methylation classification and RNA-sequencing	Yanara MARINCEVIC-ZUNIGA
33	Epigenomic reset induced by HAT/EZH2 modulation leads to cancer-selective death both in solid and hematological cancers, overcoming acquired resistance.	Francesca PETRAGLIA
34	Searching for the chromatin determinants of human hematopoiesis	Enrique CARRILLO
35	EPICO platform: a reference cyber-infrastructure for comparative epigenomics. The BLUEPRINT Data Analysis Portal as a practical case	Jose Maria FERNANDEZ
36	Integrative analysis of the epigenetic regulation of neutrophil differentiation	Felipe WERE
37	Unravelling Epigenomic Communication through Social Network Science: the influential role of 5hmC in the context of 3D chromatin interaction network	David JUAN
38	Protocols and programs for standardized chromatin research	Laura ARRIGONI
39	Association analysis of the multiple sclerosis susceptibility gene TNFSF14 in the Italian population: high density fine mapping and functional analysis of the identified primary associated variant	Miriam ZUCCALA
40	Mapping functional non-coding transcripts in primate immune cells using comparative epigenomics	David VENUTO



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41	Epigenetic reprogramming of diffuse large B-cell lymphoma cell lines: a drug screening to investigate drug resistance	Chiara FACCIOTTO
42	Analysis and visualization of DNA methylation whole genome bisulfite sequencing data in diffuse large B-cell lymphoma	Chiara FACCIOTTO
43	The hematopoietic transcription factors RUNX1 and ERG prevent AML1-ETO oncogene overexpression and onset of the apoptosis program in t(8;21) AMLs	Amit MANDOLI
44	Epigenomic profiling in innate immune memory reveals avenues for blocking and reversing immunological tolerance in humans	Boris NOVAKOVIC
45	Epigenetic regulation of Osteoclast differentiation	Robab DAVAR
46	Shape-based peak calling	Philipp BENNER
47	FindER: A Sensitive Analytical Tool to Study Epigenetic Modifications and Protein-DNA Binding from ChIP-Seq data	Misha BILENKY
48	Next Generation Epigenetics – Innovative Research Tools for the Accurate Analysis of DNA Modifications	Dominique FAUVIN
49	Childhood Abuse in Post-Mortem Human Amygdala: Combining Gene Expression, DNA Methylation and Histone Modification Data.	Marc-Aurèle CHAY
50	Integrative analysis of reference epigenomes for uterine endometrium	Kenichiro HATA
51	Modelling epigenetic control of lineage fate decisions	Jens PRZYBILLA
52	Integrating epigenetic datasets in cancer using a network based approach highlights tumor specific pathways	Carl HERRMANN
53	Profiling DNA modifications at base pair resolution reveals expanded low gene body methylation and associated cell specific epigenomic states	Nicolas WALKER
54	Single Cell Transcriptome Conservation in Cryopreserved Cells and Tissues	Holger HEYN
55	Development of microfluidic chip for automated Chromatin Immunoprecipitation and library construction	Rene DIRKS
56	Characterization of the HIV-1 cis-regulatory intragenic region	Roxane VERDIKT
57	Z-DNA Formation and Transcriptional Activation in the Human Genome.	Tae-Young ROH