

Resource Summary Report

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Catholic University of the Sacred Heart; Milan; Italy

RRID:SCR_000958

Type: Tool

Proper Citation

Catholic University of the Sacred Heart; Milan; Italy (RRID:SCR_000958)

Resource Information

URL: <http://www.ucsc.it/>

Proper Citation: Catholic University of the Sacred Heart; Milan; Italy
(RRID:SCR_000958)

Description: An Italian private research university that offers undergraduate, graduate and postdoctoral level degrees in both Italian and English.

Abbreviations: UCSC

Synonyms: Catholic University of the Sacred Heart, Università Cattolica del Sacro Cuore, Università Cattolica del Sacro Cuore, Università Cattolica, Università Cattolica

Resource Type: university

Keywords: italy, private, research, undergraduate, graduate, english, italian

Resource Name: Catholic University of the Sacred Heart; Milan; Italy

Resource ID: SCR_000958

Alternate IDs: ISNI:0000 0001 0941 3192, Wikidata:Q229022, nlx_158321, grid.8142.f, Crossref funder ID:501100005743

Alternate URLs: <https://ror.org/03h7r5v07>

Record Creation Time: 20220129T080204+0000

Record Last Update: 20260801T190134+0000

Ratings and Alerts

No rating or validation information has been found for Catholic University of the Sacred Heart; Milan; Italy.

No alerts have been found for Catholic University of the Sacred Heart; Milan; Italy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 154 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#) .

Nguyen QH, et al. (2018) Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. *GigaScience*, 7(3), 1.

Yu F, et al. (2018) LnChrom: a resource of experimentally validated lncRNA-chromatin interactions in human and mouse. *Database : the journal of biological databases and curation*, 2018.

Zheng LL, et al. (2018) dreamBase: DNA modification, RNA regulation and protein binding of expressed pseudogenes in human health and disease. *Nucleic acids research*, 46(D1), D85.

Forrest ME, et al. (2018) Colon Cancer-Upregulated Long Non-Coding RNA lincDUSP Regulates Cell Cycle Genes and Potentiates Resistance to Apoptosis. *Scientific reports*, 8(1), 7324.

Feulner PGD, et al. (2018) A Dense Linkage Map of Lake Victoria Cichlids Improved the Pundamilia Genome Assembly and Revealed a Major QTL for Sex-Determination. *G3 (Bethesda, Md.)*, 8(7), 2411.

Hung LY, et al. (2018) An Evolutionary Landscape of A-to-I RNA Editome across Metazoan Species. *Genome biology and evolution*, 10(2), 521.

Pham HTT, et al. (2018) STAT5BN642H is a driver mutation for T cell neoplasia. *The Journal of clinical investigation*, 128(1), 387.

Khor SS, et al. (2018) Genome-wide association study of self-reported food reactions in Japanese identifies shrimp and peach specific loci in the HLA-DR/DQ gene region. *Scientific reports*, 8(1), 1069.

Bao S, et al. (2018) Derivation of hypermethylated pluripotent embryonic stem cells with high potency. *Cell research*, 28(1), 22.

Jöud M, et al. (2018) Identification of human glycosyltransferase genes expressed in erythroid cells predicts potential carbohydrate blood group loci. *Scientific reports*, 8(1), 6040.

Han X, et al. (2018) Distinct epigenomic patterns are associated with haploinsufficiency and predict risk genes of developmental disorders. *Nature communications*, 9(1), 2138.

Koufariotis LT, et al. (2018) Variance explained by whole genome sequence variants in coding and regulatory genome annotations for six dairy traits. *BMC genomics*, 19(1), 237.

Lee KS, et al. (2018) Selection on the regulation of sympathetic nervous activity in humans and chimpanzees. *PLoS genetics*, 14(4), e1007311.

Haas J, et al. (2018) Genomic structural variations lead to dysregulation of important coding and non-coding RNA species in dilated cardiomyopathy. *EMBO molecular medicine*, 10(1), 107.

Batut PJ, et al. (2017) Conserved noncoding transcription and core promoter regulatory code in early *Drosophila* development. *eLife*, 6.

Kanduri C, et al. (2017) Genome build information is an essential part of genomic track files. *Genome biology*, 18(1), 175.

Ehrlund A, et al. (2017) Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. *Diabetes*, 66(1), 218.

Song YX, et al. (2017) Non-coding RNAs participate in the regulatory network of CLDN4 via ceRNA mediated miRNA evasion. *Nature communications*, 8(1), 289.

Yuen KC, et al. (2017) Condensin II is anchored by TFIIIC and H3K4me3 in the mammalian genome and supports the expression of active dense gene clusters. *Science advances*, 3(6), e1700191.

Zhang LQ, et al. (2017) Estimating the effects of transcription factors binding and histone modifications on gene expression levels in human cells. *Oncotarget*, 8(25), 40090.