

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

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: 20260808T185721+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 [SPARC SAWG](#) .

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.

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.

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

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.

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.

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

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

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

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

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.

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

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.

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.

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

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

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.

Guo M, et al. (2017) Gene signature driving invasive mucinous adenocarcinoma of the lung. *EMBO molecular medicine*, 9(4), 462.

Li XC, et al. (2017) Cis-Regulatory Divergence in Gene Expression between Two Thermally Divergent Yeast Species. *Genome biology and evolution*, 9(5), 1120.

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