Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 14, 2025

Wellcome Trust Sanger Institute; Hinxton; United Kingdom

RRID:SCR_011784
Type: Tool

Proper Citation

Wellcome Trust Sanger Institute; Hinxton; United Kingdom (RRID:SCR_011784)

Resource Information

URL: http://www.sanger.ac.uk/

Proper Citation: Wellcome Trust Sanger Institute; Hinxton; United Kingdom (RRID:SCR_011784)

Description: Non profit research organization for genome sequences to advance understanding of biology of humans and pathogens in order to improve human health globally. Provides data which can be translated for diagnostics, treatments or therapies including over 100 finished genomes, which can be downloaded. Data are publicly available on limited basis, and provided more extensively upon request.

Abbreviations: WTSI, Sanger

Synonyms: Wellcome Trust Sanger Institute, Genome Research Limited, The Wellcome Sanger Institute, Sanger Institute, Wellcome Trust Sanger Institute Genome Research Limited

Resource Type: institution

Keywords: research, genome, sequence, human, health, project, global, data, treatment, therapy

Funding: Wellcome Trust

Resource Name: Wellcome Trust Sanger Institute; Hinxton; United Kingdom

Resource ID: SCR_011784

Alternate IDs: ISNI: 0000 0004 0606 5382, nlx_91258, grid.10306.34, Wikidata: Q1142544

Alternate URLs: https://ror.org/05cy4wa09

Record Creation Time: 20220129T080306+0000

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Ratings and Alerts

No rating or validation information has been found for Wellcome Trust Sanger Institute; Hinxton; United Kingdom.

No alerts have been found for Wellcome Trust Sanger Institute; Hinxton; United Kingdom.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 519 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Chen H, et al. (2025) Atlas of Fshr expression from novel reporter mice. eLife, 13.

Goldberg LR, et al. (2025) Atp1a2 and Kcnj9 Are Candidate Genes Underlying Sensitivity to Oxycodone-Induced Locomotor Activation and Withdrawal-Induced Anxiety-Like Behaviors in C57BL/6 Substrains. Genes, brain, and behavior, 24(1), e70009.

Anselmino N, et al. (2024) Integrative Molecular Analyses of the MD Anderson Prostate Cancer Patient-derived Xenograft (MDA PCa PDX) Series. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(10), 2272.

Deng G, et al. (2024) SPI1+CD68+ macrophages as a biomarker for gastric cancer metastasis: a rationale for combined antiangiogenic and immunotherapy strategies. Journal for immunotherapy of cancer, 12(10).

Mehta H, et al. (2024) Probing the Effects of Retinoblastoma Binding Protein 6 (RBBP6) Knockdown on the Sensitivity of Cisplatin in Cervical Cancer Cells. Cells, 13(8).

Sunaga N, et al. (2024) The oncogenic role of LGR6 overexpression induced by aberrant Wnt/?-catenin signaling in lung cancer. Thoracic cancer, 15(2), 131.

Wei H, et al. (2024) MMPs-related risk model identification and SAA1 promotes clear cell

renal cell carcinoma migration via ERK-AP1-MMPs axis. Scientific reports, 14(1), 9411.

Spiers AJ, et al. (2023) Bioinformatics characterization of BcsA-like orphan proteins suggest they form a novel family of pseudomonad cyclic-?-glucan synthases. PloS one, 18(6), e0286540.

Kim M, et al. (2023) Integrative analysis of hepatic transcriptional profiles reveals genetic regulation of atherosclerosis in hyperlipidemic Diversity Outbred-F1 mice. Scientific reports, 13(1), 9475.

Kotler O, et al. (2023) SUMOylation of NaV1.2 channels regulates the velocity of backpropagating action potentials in cortical pyramidal neurons. eLife, 12.

Maruapula D, et al. (2023) Archived rilpivirine-associated resistance mutations among ART-naive and virologically suppressed people living with HIV-1 subtype C in Botswana: implications for cabotegravir/rilpivirine use. The Journal of antimicrobial chemotherapy, 78(10), 2489.

Zuze BJL, et al. (2023) Fostemsavir resistance-associated polymorphisms in HIV-1 subtype C in a large cohort of treatment-naïve and treatment-experienced individuals in Botswana. Microbiology spectrum, 11(6), e0125123.

Liu Z, et al. (2023) Epigenetic reprogramming of Runx3 reinforces CD8?+?T-cell function and improves the clinical response to immunotherapy. Molecular cancer, 22(1), 84.

Geyer SH, et al. (2022) The venous system of E14.5 mouse embryos-reference data and examples for diagnosing malformations in embryos with gene deletions. Journal of anatomy, 240(1), 11.

Sutton M, et al. (2022) Detection of SARS-CoV-2 B.1.351 (Beta) Variant through Wastewater Surveillance before Case Detection in a Community, Oregon, USA. Emerging infectious diseases, 28(6), 1101.

Zou X, et al. (2022) Mammalian splicing divergence is shaped by drift, buffering in trans, and a scaling law. Life science alliance, 5(4).

Kayser N, et al. (2022) Clock genes rescue nphp mutations in zebrafish. Human molecular genetics, 31(24), 4143.

Bareng OT, et al. (2022) Doravirine-associated resistance mutations in antiretroviral therapy naïve and experienced adults with HIV-1 subtype C infection in Botswana. Journal of global antimicrobial resistance, 31, 128.

Marcianò G, et al. (2021) Kinetoplastid kinetochore proteins KKT2 and KKT3 have unique centromere localization domains. The Journal of cell biology, 220(8).

Kariuki S, et al. (2021) Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya. eLife, 10.