Resource Summary Report

Generated by NIF on May 20, 2025

Macaque.org

RRID:SCR_002767
Type: Tool

Proper Citation

Macaque.org (RRID:SCR_002767)

Resource Information

URL: http://www.macaque.org/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented May 10, 2017. A pilot effort that has developed a centralized, web-based biospecimen locator that presents biospecimens collected and stored at participating Arizona hospitals and biospecimen banks, which are available for acquisition and use by researchers. Researchers may use this site to browse, search and request biospecimens to use in qualified studies. The development of the ABL was guided by the Arizona Biospecimen Consortium (ABC), a consortium of hospitals and medical centers in the Phoenix area, and is now being piloted by this Consortium under the direction of ABRC. You may browse by type (cells, fluid, molecular, tissue) or disease. Common data elements decided by the ABC Standards Committee, based on data elements on the National Cancer Institute''s (NCI''s) Common Biorepository Model (CBM), are displayed. These describe the minimum set of data elements that the NCI determined were most important for a researcher to see about a biospecimen. The ABL currently does not display information on whether or not clinical data is available to accompany the biospecimens. However, a requester has the ability to solicit clinical data in the request. Once a request is approved, the biospecimen provider will contact the requester to discuss the request (and the requester''s questions) before finalizing the invoice and shipment. The ABL is available to the public to browse. In order to request biospecimens from the ABL, the researcher will be required to submit the requested required information. Upon submission of the information, shipment of the requested biospecimen(s) will be dependent on the scientific and institutional review approval. Account required. Registration is open to everyone.. Documented on June 8, 2020.Macaque genomic and proteomic resources and how they are providing important new dimensions to research using macaque models of infectious disease. The research encompasses a number of viruses that pose global threats to human health, including influenza, HIV, and SARS-associated coronavirus. By combining macaque infection models with gene expression and protein abundance profiling, they are uncovering exciting new insights into the multitude of molecular and cellular events that occur in response to virus infection. A better understanding of these events may provide the basis for innovative antiviral therapies and improvements to vaccine development strategies.

Abbreviations: Macaque.org

Synonyms: Macaque.org

Resource Type: research forum portal, organization portal, topical portal, disease-related portal, data or information resource, portal, laboratory portal

Keywords: genomic, hiv, infection, proteomic, virus, simian immunodeficiency virus, influenza virus, animal model

Related Condition: Viral infection, Infectious disease

Funding: NCRR ;
NIAID ;
NHLBI ;
NIDA

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Macaque.org

Resource ID: SCR_002767

Alternate IDs: nif-0000-24370

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250519T203219+0000

Ratings and Alerts

No rating or validation information has been found for Macaque.org.

No alerts have been found for Macaque.org.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zhang Z, et al. (2007) Comparative analysis of genome tiling array data reveals many novel primate-specific functional RNAs in human. BMC evolutionary biology, 7 Suppl 1(Suppl 1), S14.

Katze MG, et al. (2007) Lost in the world of functional genomics, systems biology, and translational research: is there life after the Milstein award? Cytokine & growth factor reviews, 18(5-6), 441.

Magness CL, et al. (2005) Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human. Genome biology, 6(7), R60.