Resource Summary Report

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Genome Center BLAST Server

RRID:SCR_007190
Type: Tool

Proper Citation

Genome Center BLAST Server (RRID:SCR_007190)

Resource Information

URL: http://genome.wustl.edu/tools/blast

Proper Citation: Genome Center BLAST Server (RRID:SCR_007190)

Description: This is the portal to the BLAST Server provided by the WUSTL Genome Ceneter BLAST Server. The Genome Center is a world leader in the fast-paced, constantly changing field of genomics. A truly unique institution, The Genome Center is pushing the limits of academic research by creating, testing, and implementing new approaches to the study of biology with the goal of understanding human health and disease, as well as evolution and the biology of other organisms. The Genome Center is helping to lead the way in high-speed, comprehensive genomics. Since its inception in 1993, The Genome Center has played a vital role in the field of genome sequencing, receiving over 800 million in funding. The Genome Center began as a key player in the Human Genome Project an international effort to decode all 3 billion letters of our genetic blueprint ultimately contributing 25 percent of the finished sequence. Sponsors: This resource is supported by the NIH. Keywords: Genome, BLAST, SErver, Genomics, Academic, Research,

Synonyms: Genome BLAST Server

Resource Type: data or information resource, portal, topical portal

Resource Name: Genome Center BLAST Server

Resource ID: SCR_007190

Alternate IDs: nif-0000-30151

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260808T185847+0000

Ratings and Alerts

No rating or validation information has been found for Genome Center BLAST Server.

No alerts have been found for Genome Center BLAST Server.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Reitmeier S, et al. (2020) Comparing Circadian Rhythmicity in the Human Gut Microbiome. STAR protocols, 1(3), 100148.

James-Zorn C, et al. (2018) Navigating Xenbase: An Integrated Xenopus Genomics and Gene Expression Database. Methods in molecular biology (Clifton, N.J.), 1757, 251.

Guo CJ, et al. (2017) Discovery of Reactive Microbiota-Derived Metabolites that Inhibit Host Proteases. Cell, 168(3), 517.

Zheng RS, et al. (2017) An investigation of fungal contamination on the surface of medicinal herbs in China. Chinese medicine, 12, 2.

Fiz-Palacios O, et al. (2013) Did terrestrial diversification of amoebas (amoebozoa) occur in synchrony with land plants? PloS one, 8(9), e74374.

Davies MR, et al. (2013) Horizontally acquired glycosyltransferase operons drive salmonellae lipopolysaccharide diversity. PLoS genetics, 9(6), e1003568.

Gibson MS, et al. (2012) Identification, cloning and characterisation of interleukin-1F5 (IL-36RN) in the chicken. Developmental and comparative immunology, 38(1), 136.

McFerrin LG, et al. (2011) Evolution of the Max and Mlx networks in animals. Genome biology and evolution, 3, 915.

Chen J, et al. (2010) [Investigation of fungal populations in seven ochratoxin A contaminated root herbs]. Zhongguo Zhong yao za zhi = Zhongguo zhongyao zazhi = China journal of Chinese materia medica, 35(20), 2647.

Hellgren O, et al. (2010) Evolution of a cluster of innate immune genes (beta-defensins) along the ancestral lines of chicken and zebra finch. Immunome research, 6, 3.

Tao Y, et al. (2007) A sex-ratio meiotic drive system in Drosophila simulans. II: an X-linked distorter. PLoS biology, 5(11), e293.

Rapkins RW, et al. (2006) Recent assembly of an imprinted domain from non-imprinted components. PLoS genetics, 2(10), e182.