

Resource Summary Report

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Pig Genomic Informatics System

RRID:SCR_013330

Type: Tool

Proper Citation

Pig Genomic Informatics System (RRID:SCR_013330)

Resource Information

URL: <http://pig.genomics.org.cn/>

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Description: It presents accurate pig gene annotations in all sequenced genomic regions. It integrates various available pig sequence data, including 3.84 million whole-genome-shortgun (WGS) reads and 0.7 million Expressed Sequence Tags (ESTs) generated by Sino-Danish Pig Genome Project, and 1 million miscellaneous GenBank records. The Pig Analysis Database has covered nearly 50% of the whole pig genome and over 70% of the coding sequences (CDS), and aims to provide the most complete pig gene set to date. In addition to gene annotations, the PigGIS also presents expressional information from 98 EST libraries, SNPs detected from both WGS reads and ESTs, oligos that can be used in microarray design and relevant evolutionary data. SIFT analysis of deleterious mutations will come in future.

Abbreviations: PigGIS

Synonyms: Pig Genomic Informatics System

Resource Type: data or information resource, database

Resource Name: Pig Genomic Informatics System

Resource ID: SCR_013330

Alternate IDs: nif-0000-03289

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260905T133206+0000

Ratings and Alerts

No rating or validation information has been found for Pig Genomic Informatics System.

No alerts have been found for Pig Genomic Informatics System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Knowlton MN, et al. (2017) Naming CRISPR alleles: endonuclease-mediated mutation nomenclature across species. Mammalian genome : official journal of the International Mammalian Genome Society, 28(7-8), 367.