Resource Summary Report

Generated by NIF on May 24, 2025

KOBAS

RRID:SCR_006350
Type: Tool

Proper Citation

KOBAS (RRID:SCR_006350)

Resource Information

URL: http://kobas.cbi.pku.edu.cn/

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Description: Web server to identify statistically enriched pathways, diseases, and GO terms for a set of genes or proteins, using pathway, disease, and GO knowledge from multiple famous databases. It allows for both ID mapping and cross-species sequence similarity mapping. It then performs statistical tests to identify statistically significantly enriched pathways and diseases. KOBAS 2.0 incorporates knowledge across 1327 species from 5 pathway databases (KEGG PATHWAY, PID, BioCyc, Reactome and Panther) and 5 human disease databases (OMIM, KEGG DISEASE, FunDO, GAD and NHGRI GWAS Catalog). A standalone command line version is also available

Abbreviations: KOBAS

Synonyms: KEGG Orthology Based Annotation System

Resource Type: production service resource, data analysis service, analysis service resource, service resource, software resource

Defining Citation: PMID:21715386

Keywords: ortholog, pathway, disease, gene, protein, annotation, command line, FASEB list

Funding:

Availability: Acknowledgement requested

Resource Name: KOBAS

Resource ID: SCR_006350

Alternate IDs: OMICS_02228

Record Creation Time: 20220129T080235+0000

Record Last Update: 20250524T060120+0000

Ratings and Alerts

No rating or validation information has been found for KOBAS.

No alerts have been found for KOBAS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4397 mentions in open access literature.

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

Li H, et al. (2025) Integrated multi-omics demonstrates enhanced antitumor efficacy of donafenib combined with FADS2 inhibition in hepatocellular carcinoma. Translational oncology, 51, 102142.

You H, et al. (2025) Unravelling distinct patterns of metagenomic surveillance and respiratory microbiota between two P1 genotypes of Mycoplasma pneumoniae. Emerging microbes & infections, 14(1), 2449087.

Bergmann T, et al. (2025) Identification of Quantitative Trait Loci (QTLs) and candidate genes for trichome development in Brassica villosa using genetic, genomic, and transcriptomic approaches. Molecular genetics and genomics : MGG, 300(1), 13.

Liu J, et al. (2025) Subtilisin-like protease 4 regulates cold tolerance through cell wall modification in rice. Scientific reports, 15(1), 426.

Yu R, et al. (2025) Whole-Genome Methylation Sequencing Analysis and Functional Verification of LIM-Homeobox Family Genes in Cervical Cancer. International journal of general medicine, 18, 87.

Li Z, et al. (2025) Integrated Metabolome, Transcriptome, and Physiological Analysis of the Flavonoid and Phenylethanol Glycosides Accumulation in Wild Phlomoides rotata Roots from Different Habitats. International journal of molecular sciences, 26(2).

Shu L, et al. (2025) Comparative Transcriptomic Analysis Reveals New Insights into Spawn Aging in Agaricus bisporus: Mitochondrial Dysfunction. International journal of molecular sciences, 26(2).

Zhang R, et al. (2025) Proteomics and metabolomics analyses of mechanism underlying bovine sperm cryoinjury. BMC genomics, 26(1), 63.

Liu X, et al. (2025) Staphylococcus aureus nt5 gene mutation through CRISPR RNA-guided base editing weakens bacterial virulence and immune evasion. Virulence, 16(1), 2451163.

Chen D, et al. (2025) Sempervirine inhibits proliferation, invasion and metastasis of ovarian cancer cells and induces ultrastructural changes in vivo. Journal of ovarian research, 18(1), 17.

Wang L, et al. (2025) Differential mRNA and lncRNA Expression Profiles Associated with Early Pregnancy Loss in ART Patients. Reproductive sciences (Thousand Oaks, Calif.), 32(1), 229.

Zhang G, et al. (2025) Nanostructure-Mediated Photothermal Effect for Reinforcing Physical Killing Activity of Nanorod Arrays. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(2), e2411997.

Bao Z, et al. (2025) Microbiome dynamics and functional profiles in deep-sea wood-fall micro-ecosystem: insights into drive pattern of community assembly, biogeochemical processes, and lignocellulose degradation. Applied and environmental microbiology, 91(1), e0216524.

Zhang J, et al. (2025) Cpeb1 remodels cell type-specific translational program to promote fear extinction. Science advances, 11(2), eadr8687.

Silva LF, et al. (2025) Insights of cellular and molecular changes in sugarcane response to oxidative signaling. BMC plant biology, 25(1), 54.

Zhou W, et al. (2025) Comparative transcriptome and metabolome analysis reveals the differential response to salinity stress of two genotypes brewing sorghum. Scientific reports, 15(1), 3365.

Wang K, et al. (2025) Transcriptome analysis of muscle atrophy in Leizhou black goats: identification of key genes and insights into limb-girdle muscular dystrophy. BMC genomics, 26(1), 80.

Liao Y, et al. (2025) Functions of thyroid hormone signaling in regulating melanophore, iridophore, erythrophore, and pigment pattern formation in spotted scat (Scatophagus argus). BMC genomics, 26(1), 79.

Liang Z, et al. (2025) Protective effect of ginseng extract and total ginsenosides on hematopoietic stem cell damage by inhibiting cell apoptosis and regulating the intestinal microflora. International journal of molecular medicine, 55(1).

Liu W, et al. (2025) IGF2BP2 orchestrates global expression and alternative splicing profiles associated with glioblastoma development in U251 cells. Translational oncology, 51, 102177.