

Resource Summary Report

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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, THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: KOBAS

Synonyms: KEGG Orthology Based Annotation System

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

Defining Citation: [PMID:21715386](#)

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: KOBAS

Resource ID: SCR_006350

Alternate IDs: OMICS_02228

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260801T042624+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 4787 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Engel K, et al. (2025) Segment specific loss of NFAT5 function in the kidneys is sufficient to induce a global kidney injury like phenotype. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(2), e70352.

Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. GigaScience, 14.

Hu F, et al. (2025) The systemic wrinkled skin phenotype involves aberrant expression and variation of genes related to the oxidative stress and extracellular matrix in Xiang pigs. BMC genomics, 26(1), 1034.

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. GigaScience, 14.

Cao C, et al. (2025) A near telomere-to-telomere genome assembly of the Jinhua pig: enabling more accurate genetic research. GigaScience, 14.

Liu F, et al. (2025) The telomere-to-telomere gapless genome of grass carp provides insights for genetic improvement. GigaScience, 14.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. GigaScience, 14.

Li C, et al. (2025) IGF2BP3 Modulates mRNA Splicing and Stability to Promote Trophoblast Progression via Interaction with PDE3A and Suppression by miR-196a-5p in Preeclampsia. Biomedicines, 13(6).

Dai L, et al. (2025) Multi-omics unveils BCAA metabolism markers L-leucine and HMGS1 as prognostic marker for immunotherapy efficacy in non-small cell lung cancer. Respiratory research, 26(1), 205.

Huang Z, et al. (2025) Transcriptomic insights into the resistance mechanism of *Penaeus vannamei* against highly lethal *Vibrio parahaemolyticus*. *Scientific reports*, 15(1), 13490.

Sun YS, et al. (2025) Convergent musk biosynthesis across host and microbiota in musk deer and muskrat. *Zoological research*, 46(3), 505.

Liu Y, et al. (2025) NRDR Inhibits the Migration of Endometrial Cancer Cells and Affects Their Gene Expression. *Scientifica*, 2025, 2495655.

Wang D, et al. (2025) Gibberellic acid-mediated transcriptional divergence underlies cold stress adaptation in two diploid cotton species. *PeerJ*, 13, e19721.

Hu X, et al. (2025) Clinical and prognostic significance of m6A hypomethylation and IGF2BP3 overexpression in gastric cancer: an integrated epigenomic-transcriptomic analysis. *Human genomics*, 19(1), 95.

Lin X, et al. (2025) Unravelling the Role of PIEZO1 in Adipogenesis of Fibrogenic/Adipogenic Progenitors for Muscle Fat Infiltration After Rotator Cuff Tear. *Journal of cachexia, sarcopenia and muscle*, 16(4), e70004.

Tian X, et al. (2025) Insights into the genetic basis of bilateral head asymmetry in a scale-eating cichlid fish. *Science advances*, 11(31), eadw4406.

Guo M, et al. (2025) Acclimation mechanisms of reef-building coral *Acropora gemmifera* juveniles to long-term CO₂-driven ocean acidification. *Scientific reports*, 15(1), 30655.

Caudal A, et al. (2025) Transcriptomic Profiling of Human Myocardium at Sudden Death to Define Vulnerable Substrate for Lethal Arrhythmias. *JACC. Clinical electrophysiology*, 11(1), 143.

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.

Qu Y, et al. (2025) TSG-6 Protects Against Cerebral Ischemia-Reperfusion Injury via Upregulating Hsp70-1B in Astrocytes. *CNS neuroscience & therapeutics*, 31(3), e70354.