

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: analysis service resource, data analysis service, production service resource, service resource, software 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: 20260905T132551+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 5008 mentions in open access literature.

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

Li T, et al. (2026) BIN2 phosphorylation of GRF5 suppresses low-nitrate root foraging by inhibiting transcriptional activity and UBP12/13-mediated deubiquitination. Cell reports, 45(5), 117323.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect Cryptophyllum westwoodii provide insights into the evolution of leaf-like masquerade. GigaScience, 15.

Pan X, et al. (2026) Multi-Tissue Genetic Regulation of RNA Editing in Pigs. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(17), e18238.

Song J, et al. (2026) Exploration and analysis of methylglyoxal-driven chronic inflammation in polycystic ovary syndrome. Journal of advanced research, 83, 539.

Zhu M, et al. (2026) GFAT2-mediated HSPD1 O-GlcNAcylation drives chemotherapy resistance in non-small cell lung cancer. Journal of experimental & clinical cancer research : CR, 45(1).

Yan P, et al. (2026) ADH4 deficiency activates the NRF2-CSF1 axis by increased lipid peroxidation in hepatocellular carcinoma. Cancer cell international, 26(1).

Xu J, et al. (2026) Rumen Mycobiome Thiamine Metabolism Contributes to Subacute Rumen Acidosis Tolerance in Goats Through Enhancing Epithelial Cell Proliferation via IGFBP2/IGF1 Axis Activation. Exploration (Beijing, China), 6(2), 70142.

Li Y, et al. (2026) BnaC03.SEIPIN1 improves seed oil content by increasing the number of lipid droplets in Brassica napus. BMC plant biology, 26(1).

Chen T, et al. (2026) Multi-Omics Data Reveal Estrogen-Driven Dysregulation and Stromal-Epithelial Signaling Alterations in Endometrial Polyps. FASEB journal : official

publication of the Federation of American Societies for Experimental Biology, 40(5), e71645.

Alvarez DAN, et al. (2026) Renal proteomics of male offspring exposed to maternal protein restriction: molecular, epigenetic, and nephron-specific signatures of metabolic programming. *Journal of physiology and biochemistry*, 82(1).

Ma B, et al. (2026) Proteome Unravels Mechanism Differences in Embryogenesis Between Honey Bee Drone and Worker (*Apis mellifera* L.). *Molecular & cellular proteomics* : MCP, 25(6), 101579.

Su Z, et al. (2026) Genetic admixture and adaptive signatures of Guanling cattle revealed by whole-genome sequence. *BMC genomics*, 27(1), 122.

Gao F, et al. (2026) Effect of selenium yeast supplementation on drug metabolism genes, oxidative stress, and apoptosis in chicken liver after diquat induction: A proteomic perspective. *Poultry science*, 105(3), 106469.

Wang L, et al. (2026) Transcriptomic response of *Xanthomonas campestris* during xanthan gum production to glutamate concentration. *Scientific reports*, 16(1).

Zhang K, et al. (2026) *Bacillus Calmette-Guérin* ncBCG427 sRNA potentially enhances intracellular bacteria survival by inhibiting apoptosis and inflammatory responses. *BMC microbiology*, 26(1).

Zheng H, et al. (2026) Proteomic analysis of the eating quality of humped cattle beef from Rikaze cattle under various cooking methods. *Food chemistry*: X, 35, 103864.

Liu X, et al. (2026) Identification of multigene predictors of prognosis in patients with ovarian cancer. *iScience*, 29(3), 114932.

Fu X, et al. (2026) Identification and characterization of VC1123, a novel gene required for colonization in *Vibrio cholerae*. *Frontiers in microbiology*, 17, 1758776.

Peng W, et al. (2026) Dual-targeted lipid nanoparticles for TET3 siRNA delivery: nanobiotechnology strategy to remodel tumor immune microenvironment in hepatocellular carcinoma. *Journal of nanobiotechnology*, 24(1).

Liu Z, et al. (2026) Genomic contraction of the LOX gene family limits jasmonic acid biosynthesis and contributes to delayed flower bud opening in honeysuckle (*Lonicera japonica*). *Horticulture research*, 13(6), uhag078.