Resource Summary Report

Generated by nidm-terms on Jul 30, 2026

BIOBASE Corporation

RRID:SCR_010271
Type: Tool

Proper Citation

BIOBASE Corporation (RRID:SCR_010271)

Resource Information

URL: http://www.biobase-international.com

Proper Citation: BIOBASE Corporation (RRID:SCR_010271)

Description: THIS RESOURCE IS OUT OF SERVICE, documented on February 1st,2022. BIOBASE offers academic and non-profit organizations free access to TRANSFAC?? non-professional version with much reduced functionality and content compared to our professional database.

Resource Type: commercial organization

Keywords: FASEB list

Availability: THIS RESOURCE IS OUT OF SERVICE

Resource Name: BIOBASE Corporation

Resource ID: SCR_010271

Alternate IDs: nlx_156933

Record Creation Time: 20220129T080257+0000

Record Last Update: 20260725T190656+0000

Ratings and Alerts

No rating or validation information has been found for BIOBASE Corporation.

No alerts have been found for BIOBASE Corporation.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 183 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Pornsukjantra T, et al. (2024) An increase in ER stress and unfolded protein response in iPSCs-derived neuronal cells from neuronopathic Gaucher disease patients. Scientific reports, 14(1), 9177.

Lakkhana P, et al. (2024) Exploring molecular spectrum in thai patients with maple syrup urine disease: unveiling a common variant. Orphanet journal of rare diseases, 19(1), 396.

Rojananuangnit K, et al. (2023) Microspherophakic Angle Closure Glaucoma in a Patient with Coffin-Siris Syndrome: Case Report. The application of clinical genetics, 16, 165.

Tidy AC, et al. (2022) Sporophytic control of pollen meiotic progression is mediated by tapetum expression of ABORTED MICROSPORES. Journal of experimental botany, 73(16), 5543.

Rojnueangnit K, et al. (2022) Genetic diagnosis for adult patients at a genetic clinic. Cold Spring Harbor molecular case studies, 8(7).

Phetthong T, et al. (2021) Gaucher disease: clinical phenotypes and refining GBA mutational spectrum in Thai patients. Orphanet journal of rare diseases, 16(1), 519.

Singh P, et al. (2021) Squamous cell carcinoma subverts adjacent histologically normal epithelium to promote lateral invasion. The Journal of experimental medicine, 218(6).

Micheu MM, et al. (2020) Yield of Rare Variants Detected by Targeted Next-Generation Sequencing in a Cohort of Romanian Index Patients with Hypertrophic Cardiomyopathy. Diagnostics (Basel, Switzerland), 10(12).

Thongpradit S, et al. (2020) Novel SOX10 Mutations in Waardenburg Syndrome: Functional Characterization and Genotype-Phenotype Analysis. Frontiers in genetics, 11, 589784.

Lin S, et al. (2019) Intrinsic adriamycin resistance in p53-mutated breast cancer is related to the miR-30c/FANCF/REV1-mediated DNA damage response. Cell death & disease, 10(9), 666.

Uyhelji HA, et al. (2018) Exploring gene expression biomarker candidates for neurobehavioral impairment from total sleep deprivation. BMC genomics, 19(1), 341.

van B??mmel A, et al. (2018) coTRaCTE predicts co-occurring transcription factors within cell-type specific enhancers. PLoS computational biology, 14(8), e1006372.

Cao Q, et al. (2018) Leptin suppresses microRNA-122 promoter activity by phosphorylation of foxO1 in hepatic stellate cell contributing to leptin promotion of mouse

liver fibrosis. Toxicology and applied pharmacology, 339, 143.

Carruthers NJ, et al. (2018) Low level Hg2+ exposure modulates the B-cell cytoskeletal phosphoproteome. Journal of proteomics, 173, 107.

Kusano C, et al. (2017) A novel mutation in the C-propeptide of COL2A1 causes atypical spondyloepiphyseal dysplasia congenita. Human genome variation, 4, 17003.

Sancisi V, et al. (2017) RUNX2 expression in thyroid and breast cancer requires the cooperation of three non-redundant enhancers under the control of BRD4 and c-JUN. Nucleic acids research, 45(19), 11249.

Stafford JL, et al. (2017) Reanalysis of BRCA1/2 negative high risk ovarian cancer patients reveals novel germline risk loci and insights into missing heritability. PloS one, 12(6), e0178450.

Qian Y, et al. (2017) Multiple gene variations contributed to congenital heart disease via GATA family transcriptional regulation. Journal of translational medicine, 15(1), 69.

Forleo C, et al. (2017) Targeted next-generation sequencing detects novel gene-phenotype associations and expands the mutational spectrum in cardiomyopathies. PloS one, 12(7), e0181842.

Kaplun A, et al. (2016) Establishing and validating regulatory regions for variant annotation and expression analysis. BMC genomics, 17 Suppl 2(Suppl 2), 393.