Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

Invitrogen iPath

RRID:SCR_008120
Type: Tool

Proper Citation

Invitrogen iPath (RRID:SCR_008120)

Resource Information

URL: http://escience.invitrogen.com/ipath/

Proper Citation: Invitrogen iPath (RRID:SCR_008120)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on August 26, 2016. LINNEA Pathways is a user-friendly comprehensive online resource for gene- or protein-based scientific research. It is based on a total of 248 signaling and metabolic human biological pathway maps created for Invitrogen by GeneGo. The current version of iPath features 225 maps displaying human regulatory and metabolic pathways established in experimental literature produced by MetaCore from GeneGo, Inc. The map objects (proteins, genes, EC functions, and compounds) are connected via metabolic transformations and physical protein interactions, which were assembled by the GeneGo team of experienced annotators, geneticists, and biochemists. The pathways are organized in a vertical fashion following the general signaling path from signaling molecules and membrane receptors, via signal transduction cascades, to transcription factors and their gene targets. Following the natural organization of cellular machinery with highly interconnected pathways and modules, many maps are linked together via hyperlinked box symbols. Such linkage allows the reconstruction of a big picture view of human cell biology., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: iPath

Resource Type: database, data or information resource

Keywords: gene, genetic, metabolic, molecule, pathway, protein, receptor, research, signaling

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Invitrogen iPath

Resource ID: SCR_008120

Alternate IDs: nif-0000-20864

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260808T190420+0000

Ratings and Alerts

No rating or validation information has been found for Invitrogen iPath.

No alerts have been found for Invitrogen iPath.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 88 mentions in open access literature.

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

Yu MC, et al. (2025) Developing a Label-Free Infrared Spectroscopic Analysis with Chemometrics and Computational Enhancement for Assessing Lupus Nephritis Activity. Biosensors, 15(1).

Elizondo-Reyna E, et al. (2025) Insights from a Genome-Wide Study of Pantoea agglomerans UADEC20: A Promising Strain for Phosphate Solubilization and Exopolysaccharides Production. Current issues in molecular biology, 47(1).

Tang J, et al. (2024) The response mechanism analysis of HMX1 knockout strain to levulinic acid in Saccharomyces cerevisiae. Frontiers in microbiology, 15, 1416903.

Liao H, et al. (2024) Genome-wide identification of resistance genes and response mechanism analysis of key gene knockout strain to catechol in Saccharomyces cerevisiae. Frontiers in microbiology, 15, 1364425.

Cuthbertson L, et al. (2024) Genomic attributes of airway commensal bacteria and mucosa. Communications biology, 7(1), 171.

Wang D, et al. (2024) Serum metabolic alterations in chickens upon infectious bursal disease virus infection. BMC veterinary research, 20(1), 569.

Wang K, et al. (2024) Pharmacological Effects of Antioxidant Mycosporine-Glycine in Alleviating Ultraviolet B-Induced Skin Photodamage: Insights from Metabolomic and Transcriptomic Analyses. Antioxidants (Basel, Switzerland), 14(1).

Hu F, et al. (2024) Maslinic acid induces autophagy and ferroptosis via transcriptomic and metabolomic reprogramming in prostate cancer cells. Frontiers in pharmacology, 15, 1453447.

Park J, et al. (2024) The addition of jogi, Micropogonias undulates, affects amino acid content in kimchi fermentation. PloS one, 19(4), e0300249.

Guo Y, et al. (2024) Crosstalk between human immunodeficiency virus infection and salivary bacterial function in men who have sex with men. Frontiers in cellular and infection microbiology, 14, 1341545.

Zhou K, et al. (2024) Exposure to Molybdate Results in Metabolic Disorder: An Integrated Study of the Urine Elementome and Serum Metabolome in Mice. Toxics, 12(4).

Kim T, et al. (2024) Deficiency in Opu Systems Imparts Salt-Sensitivity to Weizmannia coagulans. Journal of microbiology and biotechnology, 34(7), 1443.

Wang Q, et al. (2024) Characterize the Growth and Metabolism of Acidithiobacillus ferrooxidans under Electroautotrophic and Chemoautotrophic Conditions. Microorganisms, 12(3).

Chen Y, et al. (2024) Metabolome and transcriptome analyses reveal changes of rapeseed in response to ABA signal during early seedling development. BMC plant biology, 24(1), 245.

Han ML, et al. (2024) Arginine catabolism is essential to polymyxin dependence in Acinetobacter baumannii. Cell reports, 43(7), 114410.

Li X, et al. (2024) Integrated phenotypic, transcriptomics and metabolomics: growth status and metabolite accumulation pattern of medicinal materials at different harvest periods of Astragalus Membranaceus Mongholicus. BMC plant biology, 24(1), 358.

Li SH, et al. (2024) Elevated proton motive force is a tetracycline resistance mechanism that leads to the sensitivity to gentamicin in Edwardsiella tarda. Microbial biotechnology, 17(1), e14379.

Li Q, et al. (2024) Unveiling superior phenol detoxification and degradation ability in Candida tropicalis SHC-03: a comparative study with Saccharomyces cerevisiae BY4742. Frontiers in microbiology, 15, 1442235.

Khan SA, et al. (2023) Genome-wide transcriptional response of Escherichia coli O157:H7 to light-emitting diodes with various wavelengths. Scientific reports, 13(1), 1976.

Kim T, et al. (2023) Increased Production of ??-Aminobutyric Acid from Brewer's Spent Grain Through Bacillus Fermentation. Journal of microbiology and biotechnology, 33(4), 527.