Resource Summary Report

Generated by dkNET on Apr 29, 2025

Synergizer

RRID:SCR_005308
Type: Tool

Proper Citation

Synergizer (RRID:SCR_005308)

Resource Information

URL: http://llama.mshri.on.ca/synergizer/translate/

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Description: The Synergizer database is a growing repository of gene and protein identifier synonym relationships. This tool facilitates the conversion of identifiers from one naming scheme (a.k.a namespace) to another. The Synergizer is a service for translating between sets of biological identifiers. It can, for example, translate Ensembl Gene IDs to Entrez Gene IDs, or IPI IDs to HGNC gene symbols, and much more. Unlike some other tools for this purpose, The Synergizer is simple and easy to learn. The Synergizer works via a web interface (for users who are not programmers) or through a web service (for programmatic access).

Abbreviations: Synergizer

Synonyms: The Synergizer

Resource Type: web service, service resource, data access protocol, production service resource, data analysis service, analysis service resource, software resource

Keywords: gene, protein, json

Funding:

Resource Name: Synergizer

Resource ID: SCR_005308

Alternate IDs: nlx_144380

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250429T055000+0000

Ratings and Alerts

No rating or validation information has been found for Synergizer.

No alerts have been found for Synergizer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Balogh P, et al. (2020) RUNX3 levels in human hematopoietic progenitors are regulated by aging and dictate erythroid-myeloid balance. Haematologica, 105(4), 905.

Ahmad S, et al. (2019) Transcriptome Meta-Analysis Deciphers a Dysregulation in Immune Response-Associated Gene Signatures during Sepsis. Genes, 10(12).

Shriwash N, et al. (2019) Identification of differentially expressed genes in small and non-small cell lung cancer based on meta-analysis of mRNA. Heliyon, 5(6), e01707.

Alam A, et al. (2019) Identification and Classification of Differentially Expressed Genes and Network Meta-Analysis Reveals Potential Molecular Signatures Associated With Tuberculosis. Frontiers in genetics, 10, 932.

Sips PY, et al. (2018) Identification of specific metabolic pathways as druggable targets regulating the sensitivity to cyanide poisoning. PloS one, 13(6), e0193889.

Cenik C, et al. (2017) A common class of transcripts with 5'-intron depletion, distinct early coding sequence features, and N1-methyladenosine modification. RNA (New York, N.Y.), 23(3), 270.

Karyala P, et al. (2016) DenHunt - A Comprehensive Database of the Intricate Network of Dengue-Human Interactions. PLoS neglected tropical diseases, 10(9), e0004965.

Bauernfeind AL, et al. (2015) Evolutionary Divergence of Gene and Protein Expression in the Brains of Humans and Chimpanzees. Genome biology and evolution, 7(8), 2276.

Veres DV, et al. (2015) ComPPI: a cellular compartment-specific database for protein-protein

interaction network analysis. Nucleic acids research, 43(Database issue), D485.