

# Resource Summary Report

Generated by SPARC SAWG on Sep 12, 2026

## Synergizer

RRID:SCR\_005308

Type: Tool

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### Proper Citation

Synergizer (RRID:SCR\_005308)

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### Resource Information

**URL:** <http://llama.mshri.on.ca/synergizer/translate/>

**Proper Citation:** Synergizer (RRID:SCR\_005308)

**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:** analysis service resource, data access protocol, data analysis service, production service resource, service resource, software resource, web service

**Keywords:** gene, protein, json

**Resource Name:** Synergizer

**Resource ID:** SCR\_005308

**Alternate IDs:** nlx\_144380

**Record Creation Time:** 20220129T080229+0000

**Record Last Update:** 20260912T195624+0000

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### Ratings and Alerts

No rating or validation information has been found for Synergizer.

No alerts have been found for Synergizer.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 9 mentions in open access literature.

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

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

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.

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.

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

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.