

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

STOP

RRID:SCR_005322

Type: Tool

Proper Citation

STOP (RRID:SCR_005322)

Resource Information

URL: <http://www.mooneygroup.org/stop/input>

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Description: STOP is a multi-ontology enrichment analysis tool. It is intended to be used to help from hypothesis about large sets of genes or proteins. The annotations used for enrichment analysis are obtained automatically applying text descriptions of genes and proteins to the NCBO annotator. Text for genes is found using NCBI entrez gene, and text for proteins is found using UniProt. The text is then run through NCBO annotator with all the available ontologies. For more information about the NCBO annotator please visit: <http://bioportal.bioontology.org/> The goal of National Center for Biomedical Ontology (NCBO) is to support biomedical researchers in their knowledge-intensive work, by providing online tools and a Web portal enabling them to access, review, and integrate disparate ontological resources in all aspects of biomedical investigation and clinical practice. A major focus of our work involves the use of biomedical ontologies to aid in the management and analysis of data derived from complex experiments. This work is an expansion of the work of Rob Tirrell and others on RANSUM This project would not be possible without the contributions of Emily Howe, Uday Evani, Corey Powell, Mathew Fleisch, Tobias Wittkop, Ari Berman, Nigam Shah and Sean Mooney An account is required.

Abbreviations: STOP

Synonyms: Statistical Tracking of Ontological Phrases, Statistical Tracking of Ontological Phrases (STOP)

Resource Type: data analysis service, service resource, production service resource, analysis service resource

Keywords: gene ontology, resource:go, gene, protein, annotation

Resource Name: STOP

Resource ID: SCR_005322

Alternate IDs: nlx_144382

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260801T190932+0000

Ratings and Alerts

No rating or validation information has been found for STOP.

No alerts have been found for STOP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 451 mentions in open access literature.

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

De Jaeger-Braet J, et al. (2025) The recruitment of the A-type cyclin TAM to stress granules is crucial for meiotic fidelity under heat. Science advances, 11(32), eadr5694.

Saito S, et al. (2025) Effects of Stop-Work orders on HIV testing, treatment and programmes for prevention of vertical transmission in four sub-Saharan African countries. Journal of the International AIDS Society, 28(9), e70034.

Zang Y, et al. (2025) The GoSPGF-GoPGF-GhWRKYs transcriptional cascade positively regulates pigment gland formation in the stem of upland cotton. Plant biotechnology journal, 23(10), 4506.

Ngan J, et al. (2025) Rationale and design of a randomised phase II multicentre crossover trial investigating a sodium-glucose co-transporter 2 inhibitor, dapagliflozin, combined with a novel continuous ketone monitor in adults with type 1 diabetes to reduce the risk of diabetic ketoacidosis: the PARTNER study. BMJ open, 15(5), e098457.

Pasqua M, et al. (2025) Engineering a Human-Sized Common Bile Duct Prototype with Regenerative Potential: In Vitro Evaluation of Mechanics, Function, Degradation, and Immune Modulation. Advanced healthcare materials, 14(21), e2501660.

Köhler CA, et al. (2025) Improving data sharing and knowledge transfer via the Neuroelectrophysiology Analysis Ontology (NEAO). Scientific data, 12(1), 907.

Fung CH, et al. (2025) A multisite feasibility study of integrated cognitive-behavioral treatment for co-existing nocturia and chronic insomnia. Journal of the American Geriatrics Society, 73(2), 558.

Pitkänen M, et al. (2025) Temporal and sleep stage-dependent agreement in manual scoring of respiratory events. *Journal of sleep research*, 34(3), e14391.

Wei H, et al. (2025) Structural insights into brassinosteroid export mediated by the Arabidopsis ABC transporter ABCB1. *Plant communications*, 6(1), 101181.

Carlton M, et al. (2025) Salivary Proteome Is Altered in Children With Small Area Thermal Burns. *Proteomics. Clinical applications*, 19(2), e202300107.

Houdroge F, et al. (2025) The costs and benefits of a prison needle and syringe program in Australia, 2025-30: a modelling study. *The Medical journal of Australia*, 222(8), 396.

Eid L, et al. (2025) A Digital Mental Health Intervention for Paranoia (the STOP App): Qualitative Study on User Acceptability. *JMIR human factors*, 12, e70181.

Örd M, et al. (2025) High-throughput investigation of cyclin docking interactions reveals the complexity of motif binding determinants. *Nature communications*, 16(1), 7622.

Mazzola R, et al. (2025) Association between lung function and sleep disorder symptoms in a community-based multi-site case-finding study. *Journal of sleep research*, 34(3), e14356.

Gagliardini M, et al. (2025) Deciphering Auditory Hyperexcitability in Otogl Mutant Mice Unravels an Auditory Neuropathy Mechanism. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(19), e2410776.

Breusegem SY, et al. (2025) A multiparametric anti-aging CRISPR screen uncovers a role for BAF in protein synthesis regulation. *Nature communications*, 16(1), 1681.

Stricker PEF, et al. (2025) Proteomic Characterization of Extracellular Vesicles from Human Neural Precursor Cells: A Promising Advanced Therapy for Neurodegenerative Diseases. *International journal of nanomedicine*, 20, 6675.

Bicka M, et al. (2025) Heterogeneity of radial spoke components in Tetrahymena cilia. *Cellular and molecular life sciences : CMLS*, 82(1), 329.

Suryanarayana SM, et al. (2025) Distinct neurogenic pathways shape the diversification and mosaic organization of cortical output channels. *bioRxiv : the preprint server for biology*.

Huxford C, et al. (2025) Exploring two-way text messages for post-discharge follow-up and quality improvement in rural Uganda. *PloS one*, 20(8), e0322969.