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 though 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 probject 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 (STOP), Statistical Tracking of Ontological Phrases

Resource Type: service resource, analysis service resource, data analysis service, production service resource
Keywords: gene ontology, resource:go, gene, protein, annotation

Resource Name: STOP

Resource ID: SCR_005322

Alternate IDs: nlx_144382

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 305 mentions in open access literature.

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


Shtolz N, et al. (2023) The metazoan landscape of mitochondrial DNA gene order and content is shaped by selection and affects mitochondrial transcription. Communications biology, 6(1), 93.


Li HL, et al. (2023) Unifying colors by primes. Light, science & applications, 12(1), 32.

Zapata-Calvente AL, et al. (2023) E-health psychological intervention in pregnant women
exposed to intimate partner violence (eIPV): A protocol for a pilot randomised controlled trial. PloS one, 18(3), e0282997.


de Luxán-Hernández C, et al. (2023) MDF is a conserved splicing factor and modulates cell division and stress response in Arabidopsis. Life science alliance, 6(1).


Guerbaai RA, et al. (2023) Evaluating the implementation fidelity to a successful nurse-led model (INTERCARE) which reduced nursing home unplanned hospitalisations. BMC health services research, 23(1), 138.

Tuckerman J, et al. (2023) Short Message Service Reminder Nudge for Parents and Influenza Vaccination Uptake in Children and Adolescents With Special Risk Medical Conditions: The Flutext-4U Randomized Clinical Trial. JAMA pediatrics, 177(4), 337.


