Resource Summary Report

Generated by NIF on Apr 22, 2025

SO

RRID:SCR_004374
Type: Tool

Proper Citation

SO (RRID:SCR_004374)

Resource Information

URL: http://sequenceontology.org/

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Description: A collaborative ontology for the definition of sequence features used in biological sequence annotation. SO was initially developed by the Gene Ontology Consortium. Contributors to SO include the GMOD community, model organism database groups such as WormBase, FlyBase, Mouse Genome Informatics group, and institutes such as the Sanger Institute and the EBI. Input to SO is welcomed from the sequence annotation community. The OBO revision is available here: http://sourceforge.net/p/song/svn/HEAD/tree/ SO includes different kinds of features which can be located on the sequence. Biological features are those which are defined by their disposition to be involved in a biological process. Biomaterial features are those which are intended for use in an experiment such as aptamer and PCR_product. There are also experimental features which are the result of an experiment. SO also provides a rich set of attributes to describe these features such as polycistronic and maternally imprinted. The Sequence Ontologies use the OBO flat file format specification version 1.2, developed by the Gene Ontology Consortium. The ontology is also available in OWL from Open Biomedical Ontologies. This is updated nightly and may be slightly out of sync with the current obo file. An OWL version of the ontology is also available. The resolvable URI for the current version of SO is http://purl.obolibrary.org/obo/so.owl.

Abbreviations: SO

Synonyms: Sequence Ontology Project, Sequence Types and Features Ontology, Sequence Ontology

Resource Type: data or information resource, controlled vocabulary, ontology

Defining Citation: PMID:20796305, PMID:20226267, PMID:18629179, PMID:15892872

Keywords: annotation, sequence, biological sequence, sequence variation, genome, genome annotation, owl, FASEB list

Funding: NHGRI HG02273

Availability: The community can contribute to this resource

Resource Name: SO

Resource ID: SCR_004374

Alternate IDs: nlx_38918

Record Creation Time: 20220129T080224+0000

Record Last Update: 20250421T053433+0000

Ratings and Alerts

No rating or validation information has been found for SO.

No alerts have been found for SO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 43 mentions in open access literature.

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

Tsare EG, et al. (2024) Protein-protein interaction network-based integration of GWAS and functional data for blood pressure regulation analysis. Human genomics, 18(1), 15.

Liu HL, et al. (2023) Mutational spectrum in a Chinese cohort with congenital cataracts. Molecular genetics & genomic medicine, 11(9), e2196.

Josephs KS, et al. (2023) Beyond gene-disease validity: capturing structured data on inheritance, allelic-requirement, disease-relevant variant classes, and disease mechanism for inherited cardiac conditions. medRxiv : the preprint server for health sciences.

Marchesini A, et al. (2023) First genome-wide data from Italian European beech (Fagus

sylvatica L.): Strong and ancient differentiation between Alps and Apennines. PloS one, 18(7), e0288986.

Wei X, et al. (2023) The lingering effects of Neanderthal introgression on human complex traits. eLife, 12.

Duan G, et al. (2023) HGD: an integrated homologous gene database across multiple species. Nucleic acids research, 51(D1), D994.

Takada T, et al. (2022) MoG+: a database of genomic variations across three mouse subspecies for biomedical research. Mammalian genome : official journal of the International Mammalian Genome Society, 33(1), 31.

Ghouse J, et al. (2022) Association of Common and Rare Genetic Variation in the 3-Hydroxy-3-Methylglutaryl Coenzyme A Reductase Gene and Cataract Risk. Journal of the American Heart Association, 11(12), e025361.

Perry MN, et al. (2022) Murine allele and transgene symbols: ensuring unique, concise, and informative nomenclature. Mammalian genome : official journal of the International Mammalian Genome Society, 33(1), 108.

Engel SR, et al. (2022) New data and collaborations at the Saccharomyces Genome Database: updated reference genome, alleles, and the Alliance of Genome Resources. Genetics, 220(4).

Jablonski KP, et al. (2022) Contribution of 3D genome topological domains to genetic risk of cancers: a genome-wide computational study. Human genomics, 16(1), 2.

Kong W, et al. (2021) BTK and PI3K Inhibitors Reveal Synergistic Inhibitory Anti-Tumoral Effects in Canine Diffuse Large B-Cell Lymphoma Cells. International journal of molecular sciences, 22(23).

Giachelle F, et al. (2021) Search, access, and explore life science nanopublications on the Web. PeerJ. Computer science, 7, e335.

Martin FJ, et al. (2021) Accessing Livestock Resources in Ensembl. Frontiers in genetics, 12, 650228.

Arnaud E, et al. (2020) The Ontologies Community of Practice: A CGIAR Initiative for Big Data in Agrifood Systems. Patterns (New York, N.Y.), 1(7), 100105.

Morenikeji OB, et al. (2020) SNP Diversity in CD14 Gene Promoter Suggests Adaptation Footprints in Trypanosome Tolerant N'Dama (Bos taurus) but not in Susceptible White Fulani (Bos indicus) Cattle. Genes, 11(1).

Wei XW, et al. (2020) Mutational landscape and characteristics of ERBB2 in non-small cell lung cancer. Thoracic cancer, 11(6), 1512.

Wang AW, et al. (2019) Genome-wide association study in two populations to determine

genetic variants associated with Toxoplasma gondii infection and relationship to schizophrenia risk. Progress in neuro-psychopharmacology & biological psychiatry, 92, 133.

Ruzicka L, et al. (2019) The Zebrafish Information Network: new support for non-coding genes, richer Gene Ontology annotations and the Alliance of Genome Resources. Nucleic acids research, 47(D1), D867.

Choi J, et al. (2019) Whole genome sequencing identifies high-impact variants in well-known pharmacogenomic genes. The pharmacogenomics journal, 19(2), 127.