Resource Summary Report

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Bioassay Ontology

RRID:SCR_002638
Type: Tool

Proper Citation

Bioassay Ontology (RRID:SCR_002638)

Resource Information

URL: http://bioassayontology.org/

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Description: Ontology to describe and categorize chemical biology and drug screening assays and their results including high-throughput screening (HTS) data for the purpose of categorizing assays and data analysis. BAO is an extensible, knowledge-based, highly expressive (currently SHOIQ(D)) description of biological assays making use of descriptive logic based features of the Web Ontology Language (OWL). BAO currently has over 700 classes and also makes use of several other ontologies. It describes several concepts related to biological screening, including Perturbagen, Format, Meta Target, Design, Detection Technology, and Endpoint. Perturbagens are perturbing agents that are screened in an assay; they are mostly small molecules. Assay Meta Target describes what is known about the biological system and / or its components interrogated in the assay (and influenced by the Perturbagen). Meta target can be directly described as a molecular entity (e.g. a purified protein or a protein complex), or indirectly by a biological process or event (e.g. phosphorylation). Format describes the biological or chemical features common to each test condition in the assay and includes biochemical, cell-based, organism-based, and variations thereof. The assay Design describes the assay methodology and implementation of how the perturbation of the biological system is translated into a detectable signal. Detection Technology relates to the physical method and technical details to detect and record a signal. Endpoints are the final HTS results as they are usually published (such as IC50, percent inhibition, etc). BAO has been designed to accommodate multiplexed assays. All main BAO components include multiple levels of sub-categories and specification classes, which are linked via object property relationships forming an expressive knowledge-based representation.

Abbreviations: BAO

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

Keywords: chemical biology, drug screening, assay, perturbation, high-throughput screening, owl

Funding:

Resource Name: Bioassay Ontology

Resource ID: SCR_002638

Alternate IDs: nlx_156065

Record Creation Time: 20220129T080214+0000

Record Last Update: 20250411T054752+0000

Ratings and Alerts

No rating or validation information has been found for Bioassay Ontology.

No alerts have been found for Bioassay Ontology.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Škuta C, et al. (2025) ECBD: European chemical biology database. Nucleic acids research, 53(D1), D1383.

Bucher E, et al. (2019) Annot: a Django-based sample, reagent, and experiment metadata tracking system. BMC bioinformatics, 20(1), 542.

Kanavy DM, et al. (2019) Comparative analysis of functional assay evidence use by ClinGen Variant Curation Expert Panels. Genome medicine, 11(1), 77.

Hastings J, et al. (2015) eNanoMapper: harnessing ontologies to enable data integration for nanomaterial risk assessment. Journal of biomedical semantics, 6, 10.

Clark AM, et al. (2014) Fast and accurate semantic annotation of bioassays exploiting a

hybrid of machine learning and user confirmation. PeerJ, 2, e524.

Abeyruwan S, et al. (2014) Evolving BioAssay Ontology (BAO): modularization, integration and applications. Journal of biomedical semantics, 5(Suppl 1 Proceedings of the Bio-Ontologies Spec Interest G), S5.

Visser U, et al. (2011) BioAssay Ontology (BAO): a semantic description of bioassays and high-throughput screening results. BMC bioinformatics, 12, 257.