

Resource Summary Report

Generated by [kravitz2](#) on Jul 29, 2026

eVOC

RRID:SCR_010704

Type: Tool

Proper Citation

eVOC (RRID:SCR_010704)

Resource Information

URL: <http://www.evocontology.org/site/Main/EvocOntologyDotOrg>

Proper Citation: eVOC (RRID:SCR_010704)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented May 10, 2017. A pilot effort that has developed a centralized, web-based biospecimen locator that presents biospecimens collected and stored at participating Arizona hospitals and biospecimen banks, which are available for acquisition and use by researchers. Researchers may use this site to browse, search and request biospecimens to use in qualified studies. The development of the ABL was guided by the Arizona Biospecimen Consortium (ABC), a consortium of hospitals and medical centers in the Phoenix area, and is now being piloted by this Consortium under the direction of ABRC. You may browse by type (cells, fluid, molecular, tissue) or disease. Common data elements decided by the ABC Standards Committee, based on data elements on the National Cancer Institute's (NCI's) Common Biorepository Model (CBM), are displayed. These describe the minimum set of data elements that the NCI determined were most important for a researcher to see about a biospecimen. The ABL currently does not display information on whether or not clinical data is available to accompany the biospecimens. However, a requester has the ability to solicit clinical data in the request. Once a request is approved, the biospecimen provider will contact the requester to discuss the request (and the requester's questions) before finalizing the invoice and shipment. The ABL is available to the public to browse. In order to request biospecimens from the ABL, the researcher will be required to submit the requested required information. Upon submission of the information, shipment of the requested biospecimen(s) will be dependent on the scientific and institutional review approval. Account required. Registration is open to everyone., documented September 6, 2016. Set of orthogonal controlled vocabularies that unifies gene expression data by facilitating a link between the genome sequence and expression phenotype information. The system associates labelled target cDNAs for microarray experiments, or cDNA libraries and their associated transcripts with controlled terms in a set of hierarchical vocabularies. eVOC consists of four orthogonal controlled vocabularies suitable for describing the domains of human gene expression data including Anatomical System, Cell Type, Pathology and Developmental Stage. The four core eVOC ontologies provide an

appropriate set of detailed human terms that describe the sample source of human experimental material such as cDNA and SAGE libraries. These expression terms are linked to libraries and transcripts allowing the assessment of tissue expression profiles, differential gene expression levels and the physical distribution of expression across the genome. Analysis is currently possible using EST and SAGE data, with microarray data being incorporated. The eVOC data is increasingly being accepted as a standard for describing gene expression and eVOC ontologies are integrated with the Ensembl EnsMart database, the Alternate Transcript Diversity Project and the UniProt Knowledgebase. Several groups are currently working to provide shared development of this resource such that it is of maximum use in unifying transcript expression information.

Abbreviations: eVOC

Synonyms: Expressed Sequence Annotation for Humans, eVOC (Expressed Sequence Annotation for Humans), eVOC Ontologies, eVOContology.org

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

Defining Citation: [PMID:12799354](#)

Keywords: mouse, mapping, cdna, development, microarray, expression, expressed sequence, anatomical system, cell type, developmental stage, experimental technique, microarray platform, pathology, pooling, tissue preparation, treatment, gene expression, genome sequence, expression phenotype, genome, sequence, phenotype, anatomical system, cell type, pathology, anatomy

Funding: South African National Research Foundation ;
European Union ;
Wellcome Trust ;
South African Department of Arts Culture Science and Technology 32146

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: eVOC

Resource ID: SCR_010704

Alternate IDs: nlx_84448

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260729T044255+0000

Ratings and Alerts

No rating or validation information has been found for eVOC.

No alerts have been found for eVOC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Doud MB, et al. (2024) Competition-driven eco-evolutionary feedback reshapes bacteriophage lambda's fitness landscape and enables speciation. Nature communications, 15(1), 863.

Levy D, et al. (2024) Epigenome-wide DNA Methylation Association Study of CHIP Provides Insight into Perturbed Gene Regulation. Research square.

Doud MB, et al. (2023) Competition-driven eco-evolutionary feedback reshapes bacteriophage lambda's fitness landscape and enables speciation. bioRxiv : the preprint server for biology.

Sharp ME, et al. (2017) Toward a comprehensive drug ontology: extraction of drug-indication relations from diverse information sources. Journal of biomedical semantics, 8(1), 2.