

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

CluSTr

RRID:SCR_007600

Type: Tool

Proper Citation

CluSTr (RRID:SCR_007600)

Resource Information

URL: <http://www.ebi.ac.uk/clustr/>

Proper Citation: CluSTr (RRID:SCR_007600)

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 June 24, 2013 as per the Miriam database (<http://www.ebi.ac.uk/miriam/main/collections/MIR:00000021>). The CluSTr database offers an automatic classification of UniProt Knowledgebase and IPI proteins into groups of related proteins. The clustering is based on analysis of all pairwise comparisons between protein sequences. The database provides links to InterPro, which integrates information on protein families, domains and functional sites from PROSITE, PRINTS, Pfam, ProDom, SMART, TIGRFAMs, Gene3D, SUPERFAMILY, PIR Superfamily and PANTHER. To date (2011), CluSTr contains the following information: *

9,450,285 sequences from UniProt Knowledgebase release 15.6 * 308,281 sequences from IPI * 3,636,831,744 similarities, with pairwise alignments generated on-the-fly * 17,616,060 clusters * Clustering for 972 organisms with completely sequenced genomes. For the full list of the genomes see Integr8 * Putative homologues predictions for the above species. For more information see Homologue Selection at Integr8

Synonyms: CluS+Tr

Resource Type: database, data or information resource

Keywords: gene3d, homolog, ipi, pfam, pir superfamily, prints, prodom, prosite, protein classification, protein sequence, protein sequence comparison, superfamily, tigrfams, uniprot, gold standard

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CluSTr

Resource ID: SCR_007600

Alternate IDs: nif-0000-02668

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260725T191148+0000

Ratings and Alerts

No rating or validation information has been found for CluSTr.

No alerts have been found for CluSTr.

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 [nidm-terms](#) .

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.

Grant A, et al. (2004) Progress towards mapping the universe of protein folds. Genome biology, 5(5), 107.

Pruess M, et al. (2003) Bioinformatics Resources for In Silico Proteome Analysis. Journal of biomedicine & biotechnology, 2003(4), 231.

Mulder NJ, et al. (2002) Tools and resources for identifying protein families, domains and motifs. *Genome biology*, 3(1), REVIEWS2001.