

Resource Summary Report

Generated by SPARC SAWG on Jul 28, 2026

Distributed Annotation System

RRID:SCR_008427

Type: Tool

Proper Citation

Distributed Annotation System (RRID:SCR_008427)

Resource Information

URL: <http://www.biodas.org>

Proper Citation: Distributed Annotation System (RRID:SCR_008427)

Description: The Distributed Annotation System (DAS) defines a communication protocol used to exchange annotations on genomic or protein sequences. It is motivated by the idea that such annotations should not be provided by single centralized databases, but should instead be spread over multiple sites. Data distribution, performed by DAS servers, is separated from visualization, which is done by DAS clients. The advantages of this system are that control over the data is retained by data providers, data is freed from the constraints of specific organisations and the normal issues of release cycles, API updates and data duplication are avoided. DAS is a client-server system in which a single client integrates information from multiple servers. It allows a single machine to gather up sequence annotation information from multiple distant web sites, collate the information, and display it to the user in a single view. Little coordination is needed among the various information providers. DAS is heavily used in the genome bioinformatics community. Over the last years we have also seen growing acceptance in the protein sequence and structure communities. A DAS-enabled website or application can aggregate complex and high-volume data from external providers in an efficient manner. For the biologist, this means the ability to plug in the latest data, possibly including a user's own data. For the application developer, this means protection from data format changes and the ability to add new data with minimal development cost. Here are some examples of DAS-enabled applications or websites for end users: :- Dalliace Experimental Web/Javascript based Genome Viewer :- IGV Integrative Genome Viewer java based browser for many genomes :- Ensembl uses DAS to pull in genomic, gene and protein annotations. It also provides data via DAS. :- Gbrowse is a generic genome browser, and is both a consumer and provider of DAS. :- IGB is a desktop application for viewing genomic data. :- SPICE is an application for projecting protein annotations onto 3D structures. :- Dasty2 is a web-based viewer for protein annotations :- Jalview is a multiple alignment editor. :- PeppeR is a graphical viewer for 3D electron microscopy data. :- DASMI is an integration portal for protein interaction data. :- DASher is a Java-based viewer for protein annotations. :- EpiC presents structure-function summaries for antibody design. :- STRAP is a STRucture-

based sequence Alignment Program. Hundreds of DAS servers are currently running worldwide, including those provided by the European Bioinformatics Institute, Ensembl, the Sanger Institute, UCSC, WormBase, FlyBase, TIGR, and UniProt. For a listing of all available DAS sources please visit the DasRegistry. Sponsors: The initial ideas for DAS were developed in conversations with LaDeana Hillier of the Washington University Genome Sequencing Center.

Synonyms: BioDAS

Resource Type: narrative resource, software resource, data or information resource, standard specification

Keywords: annotation, database, software, genomic, protein, sequence, visualization, data, client-server, integration, bioinformatics, genome, structure, data integration

Funding: Howard Hughes Medical Institute ;
NHGRI 2-P01-HG00956

Resource Name: Distributed Annotation System

Resource ID: SCR_008427

Alternate IDs: nif-0000-30177

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260728T043304+0000

Ratings and Alerts

No rating or validation information has been found for Distributed Annotation System.

No alerts have been found for Distributed Annotation System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Josset L, et al. (2014) Annotation of long non-coding RNAs expressed in collaborative cross founder mice in response to respiratory virus infection reveals a new class of interferon-stimulated transcripts. RNA biology, 11(7), 875.

Gel Moreno B, et al. (2011) GenExp: an interactive web-based genomic DAS client with client-side data rendering. PloS one, 6(7), e21270.

Sen TZ, et al. (2009) MaizeGDB becomes 'sequence-centric'. Database : the journal of biological databases and curation, 2009, bap020.

Cases I, et al. (2007) CARGO: a web portal to integrate customized biological information. Nucleic acids research, 35(Web Server issue), W16.

Wilson D, et al. (2007) The SUPERFAMILY database in 2007: families and functions. Nucleic acids research, 35(Database issue), D308.

Montaner D, et al. (2006) Next station in microarray data analysis: GEPAS. Nucleic acids research, 34(Web Server issue), W486.

Wilkerson MD, et al. (2006) yrGATE: a web-based gene-structure annotation tool for the identification and dissemination of eukaryotic genes. Genome biology, 7(7), R58.

Sonnhammer EL, et al. (2005) Genome informatics: taming the avalanche of genomic data. Genome biology, 6(1), 301.

Lewis SE, et al. (2002) Apollo: a sequence annotation editor. Genome biology, 3(12), RESEARCH0082.

Taylor MS, et al. (2001) More biology from the sequence. Genome biology, 2(8), REPORTS4018.

Dowell RD, et al. (2001) The distributed annotation system. BMC bioinformatics, 2, 7.