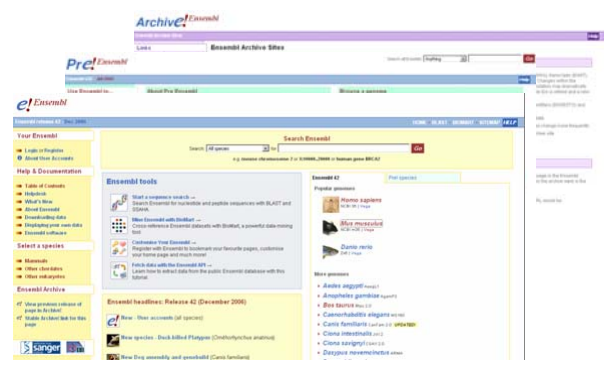


# DAS

## Integration of external annotation data



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## Outline of talk

- DAS
  - What is DAS?
  - DAS client DAS server
- DAS in Ensembl
  - Ensembl as DAS server
  - DAS essentials
  - Examples



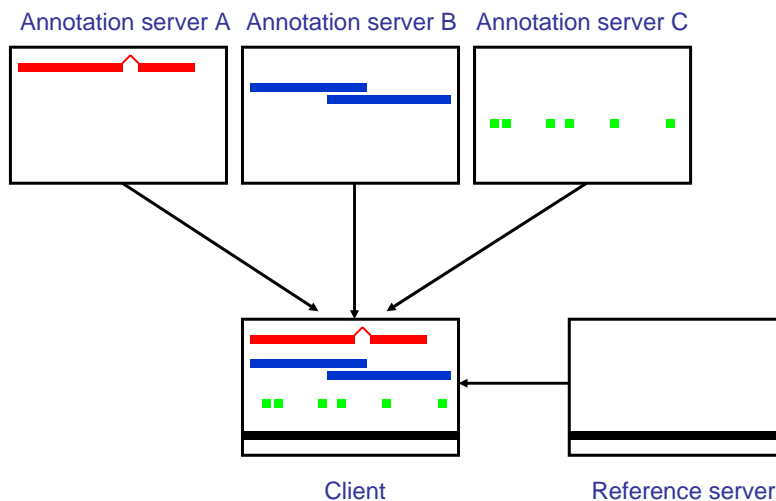
## What is DAS?

### DAS Distributed Annotation System

- Developed by Robin Dowell, Sean Eddy and Lincoln Stein (Dowell *et al.*, 2001)
- Specification of a protocol for requesting and returning sequence and annotation data
- Allows decentralised storage of sequence annotation, and integration on demand basis by client-side software
- Simple protocol that runs over HTTP

... see <http://biodas.org> for details

## DAS concept



## ***DAS concept***

The annotations may be shared more easily.

The amount of data which needs to be stored locally is decreased.

Responsibility for updating and maintaining the data is left with the original data provider.

Conflicting annotations are permitted, encouraging information dissension and dialogue.

Annotation can be stored in a variety of formats.

Other programs, even other types of programs (not annotation viewers), may use the data.

## ***DAS - Annotation***

- Annotation - An entity which:
  - Is anchored to the reference sequence via a stop and start value.
  - Possesses an ID unique to the server and a structured description of its types, methods, and categories.
- Global Annotation:
  - Annotation that applies to the entire reference sequence; start and stop are void

## ***DAS client DAS server***

### Definitions

- A **DAS client** is either an application (*Apollo*) or a web site (*Ensembl*) requesting and displaying annotations for a region of a sequence
- A **DAS server** is designated either as
  - a **reference server**, that provides essential structural information (e.g. entry points or sequence), or
  - an annotation server, that supplies specific annotation and has the knowledge about the sequence and/or annotation data stored in a flat file or database

## ***Ensembl, a DAS client***

### DAS clients in **Ensembl**

- **ContigView**  
Principal data visualisation tool for genome sequence annotation information
- **GeneView**  
Provides detailed information about gene model predictions
- **ProtView**  
Provides detailed information about protein model predictions

## Reference Sequences

- Applicable to **ContigView**
  - Chromosome
  - Contig
  - Clone
- Applicable to **ProtView** or **GeneView**
  - Protein
  - Gene (global annotation only)
  - cDNA (not yet implemented)

## DAS format

URL following a specific, standardised format:

`<prefix>/das/<dsn>/<cmd>?<args>`

- Site-specific prefix (server URL)
  - Keyword “das”
  - Data source name (dsn)
  - Command (cmd)
  - Arguments (args)

Example

`http://www.ebi.ac.uk/das-srv/uniprot/das/aristotle  
/features?segment=P51587`

## ***DAS format***

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- **Arguments (args)**

Example

`http://www.ebi.ac.uk/das-srv/uniprot/das/aristotle  
/features?segment=P51587`

## DAS essentials

<prefix>/das ...

- /dsn

Retrieves a list of data sources available from this server

- /<dsn>/types[?segment=<ref>]

Retrieves a list of types available from a data source or particular data source segments

- /<dsn>/features?segment=<ref>

Retrieves the annotations across a segment

Example

<http://www.ensembl.org/das/dsn>

'dsn' - Get the list of available sources

<http://www.ensembl.org/das/dsn>

<http://das.ensembl.org/das/dsn>

```
<?xml version="1.0" standalone="yes"?>
<!DOCTYPE DASDSN SYSTEM "http://www.biodas.org/dtd/dasdsn.dtd">
<DASDSN>
  <DSN>
    <SOURCE id="ena_34_affy10knp">ena_34_affy10knp</SOURCE>
    <MAPMASTER>http://das.ensembl.org/ensembl1834</MAPMASTER>
    <DESCRIPTION>Affymetryrix 10K SNP Array Mapping</DESCRIPTION>
  </DSN>
  <DSN>
    <SOURCE id="ena_35_affy10knp">ena_35_affy10knp</SOURCE>
    <MAPMASTER>http://das.ensembl.org/ensembl2635</MAPMASTER>
    <DESCRIPTION>Affymetryrix 10K SNP Array Mapping</DESCRIPTION>
  </DSN>
  <DSN>
    <SOURCE id="ena_anoph_dros_5_1">ena_anoph_dros_5_1</SOURCE>
    <MAPMASTER>http://servlet.sanger.ac.uk:8080/das/mosquito51</MAPMASTER>
    <DESCRIPTION>Ensembl-mapped Drosophila Genes</DESCRIPTION>
  </DSN>
  <DSN>
    <SOURCE id="ena_cbr25_fgenseh">ena_cbr25_fgenseh</SOURCE>
    <MAPMASTER>http://servlet.sanger.ac.uk:8080/das/cbriggsae1025</MAPMASTER>
    <DESCRIPTION>C. briggsae fgenseh predictions</DESCRIPTION>
  </DSN>
</DASDSN>
```



## ***DAS essentials***

<prefix>/das ...

- /dsn

Retrieves a list of data sources available from this server

- /<dsn>/types[?segment=<ref>]

•Retrieves a list of types available from a data source or particular data source segments

- /<dsn>/features?segment=<ref>

Retrieves the annotations across a segment

Example

[http://genome.dbs.dtu.dk:9000/das/cbs\\_ptm/tyes?segment=P51587](http://genome.dbs.dtu.dk:9000/das/cbs_ptm/tyes?segment=P51587)

## ***DAS essentials***

<prefix>/das ...

- /dsn

Retrieves a list of data sources available from this server

- /<dsn>/types[?segment=<ref>]

Retrieves a list of types available from a data source or particular data source segments

- /<dsn>/features?segment=<ref>

Retrieves the annotations across a segment

Example

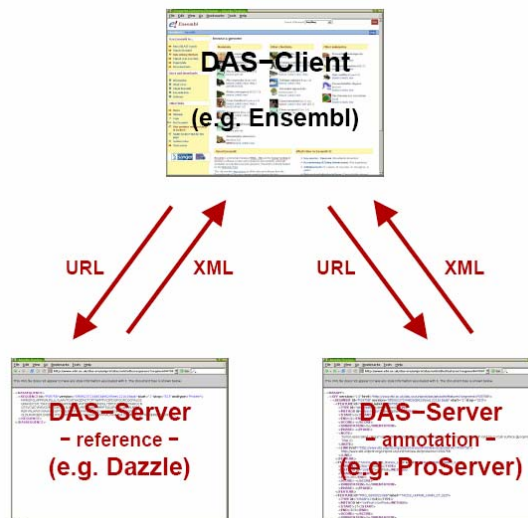
[http://das.ensembl.org/das/ens\\_36\\_refseq/features?segment=1:40000,60000](http://das.ensembl.org/das/ens_36_refseq/features?segment=1:40000,60000)

## 'features' - Get the annotations

[http://www.ebi.ac.uk/das-srv/asd/das/atd\\_human/features?segment=13:3770000,3810000](http://www.ebi.ac.uk/das-srv/asd/das/atd_human/features?segment=13:3770000,3810000)

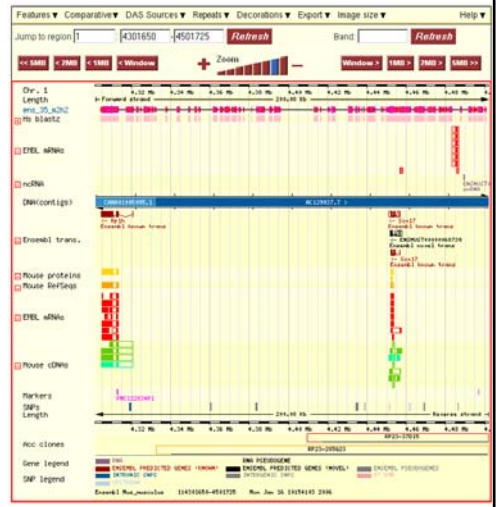
```
<?xml version="1.0" standalone="yes"?>
<!DOCTYPE DASGFF SYSTEM "http://www.biodas.org/dtd/dasgff.dtd">
<DASGFF>
<GFF version="1.01" href="http://web59-nodel.ebi.ac.uk:9100/das/atd_human/features">
<SEGMENT id="13" version="1.0" start="3770000" stop="3810000">
<FEATURE id="6438:1.215740" label="6438:1.215740">
<TYPE id="exon" reference="no" subparts="no" superparts="no">exon</TYPE>
<START>32658014</START>
<END>32658215</END>
<ORIENTATION>-</ORIENTATION>
<LINK href="http://www.ebi.ac.uk/asd-srv/Atd.cgi?method=TRANSCRIPT;origin=AT;product="
<GROUP id="6438" label="ENSG00000133121 AT-1" />
</FEATURE>
<FEATURE id="6438:1.215741" label="6438:1.215741">
<TYPE id="exon" reference="no" subparts="no" superparts="no">exon</TYPE>
<START>32639687</START>
<END>32639758</END>
<ORIENTATION>-</ORIENTATION>
<LINK href="http://www.ebi.ac.uk/asd-srv/Atd.cgi?method=TRANSCRIPT;origin=AT;product="
<GROUP id="6438" label="ENSG00000133121 AT-1" />
</FEATURE>
<FEATURE id="6438:1.215742" label="6438:1.215742">
<TYPE id="exon" reference="no" subparts="no" superparts="no">exon</TYPE>
<START>32637473</START>
<END>32637554</END>
<ORIENTATION>-</ORIENTATION>
<LINK href="http://www.ebi.ac.uk/asd-srv/Atd.cgi?method=TRANSCRIPT;origin=AT;product="
<GROUP id="6438" label="ENSG00000133121 AT-1" />
</FEATURE>
</GFF>
```

## Ensembl - Project

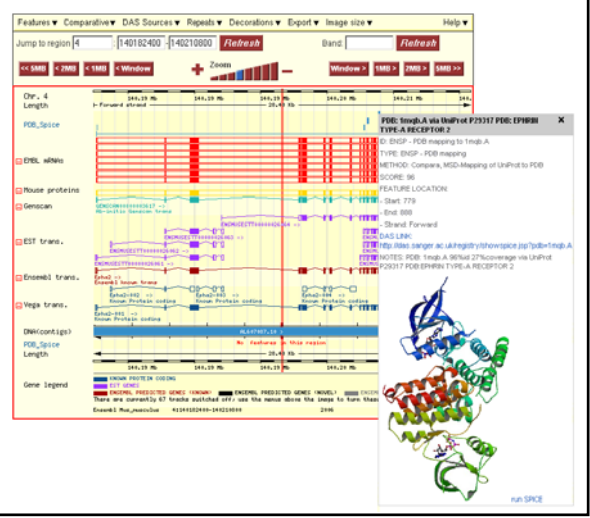




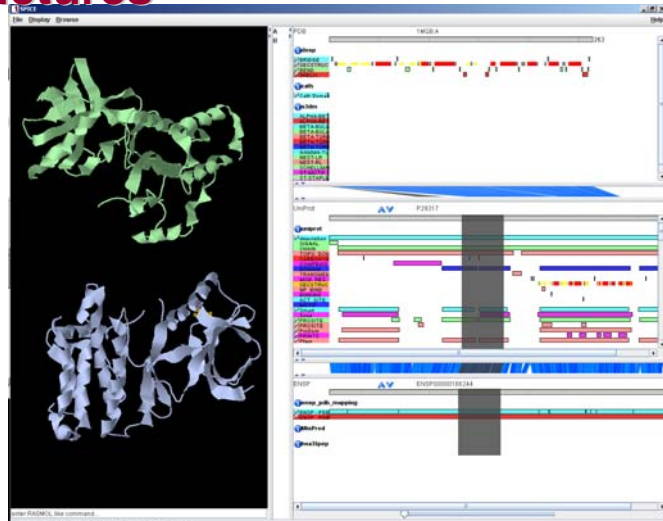
## Display Custom tracks



## Display 3D structures

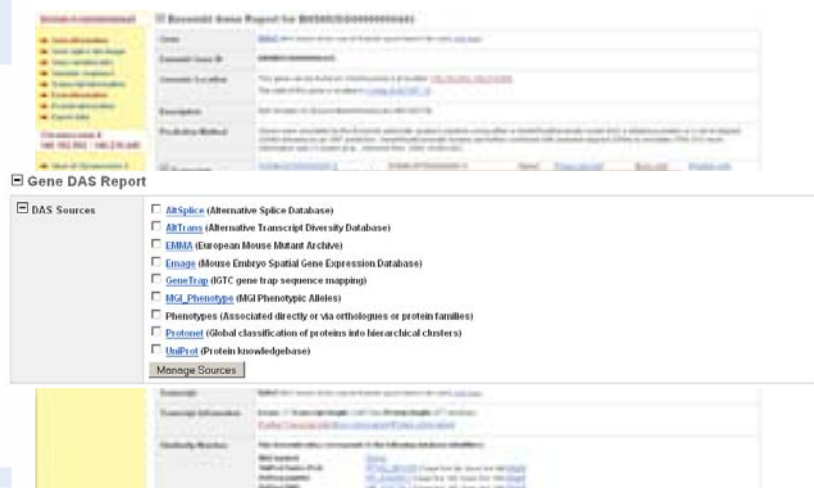


## Display 3D structures



The screenshot displays the Ensembl genome browser interface. On the left, two 3D protein structures are shown: a green ribbon structure and a grey surface structure. The main panel shows genomic tracks for the *TRIOA* gene, including the gene model, transcripts, and protein-coding regions. The interface includes a search bar at the top and various navigation options.

## GeneDAS



The screenshot shows the GeneDAS report interface. At the top, there is a search bar and a list of sources. Below this, the 'Gene DAS Report' section is expanded, showing a list of DAS sources with checkboxes for selection. The sources include:

- [AltSplice](#) (Alternative Splice Database)
- [ALTtrans](#) (Alternative Transcript Diversity Database)
- [EMMA](#) (European Mouse Mutant Archive)
- [Emage](#) (Mouse Embryo Spatial Gene Expression Database)
- [GeneTrap](#) (IGTC gene trap sequence mapping)
- [MGD\\_Phenotype](#) (MGD Phenotypic Alleles)
- [Phenotypes](#) (Associated directly or via orthologues or protein families)
- [Protomap](#) (Global classification of proteins into hierarchical clusters)
- [UniProt](#) (Protein knowledgebase)

At the bottom of the list, there is a 'Manage Sources' button. The interface also includes a search bar and a list of sources at the top.

# GeneDAS

<b>EMage</b>	description <a href="#">Epha2</a> description expression data in Their Stage <a href="#">[2]</a> in <a href="#">[3]</a> Tissues
<b>MGI Phenotype</b>	Phenotypic Allele <a href="#">MG2248872</a> MGI SYMBOL: Epha2 <sup>206R05A</sup> (hetago)(CNS17m) [NAME: g1 PUMBO: <a href="#">[1]</a> <a href="#">[2]</a> <a href="#">[3]</a> <a href="#">[4]</a> <a href="#">[5]</a> <a href="#">[6]</a> <a href="#">[7]</a> <a href="#">[8]</a> <a href="#">[9]</a> <a href="#">[10]</a> <a href="#">[11]</a> <a href="#">[12]</a> <a href="#">[13]</a> <a href="#">[14]</a> <a href="#">[15]</a> <a href="#">[16]</a> <a href="#">[17]</a> <a href="#">[18]</a> <a href="#">[19]</a> <a href="#">[20]</a> <a href="#">[21]</a> <a href="#">[22]</a> <a href="#">[23]</a> <a href="#">[24]</a> <a href="#">[25]</a> <a href="#">[26]</a> <a href="#">[27]</a> <a href="#">[28]</a> <a href="#">[29]</a> <a href="#">[30]</a> <a href="#">[31]</a> <a href="#">[32]</a> <a href="#">[33]</a> <a href="#">[34]</a> <a href="#">[35]</a> <a href="#">[36]</a> <a href="#">[37]</a> <a href="#">[38]</a> <a href="#">[39]</a> <a href="#">[40]</a> <a href="#">[41]</a> <a 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## Style sheets



## Adding custom data to Ensembl Displays

- Add a new DAS server;
  - Switch on pre-configured server,
  - Configure a new server,
  - Set up your own server (see Ensembl docs),
  - ContigView, ProtView and GeneView.
  
- Use Ensembl DAS server to display your data, made accessible via;
  - file upload,
  - Web page (URL),
  - ContigView only at this time.

## URL-based Upload

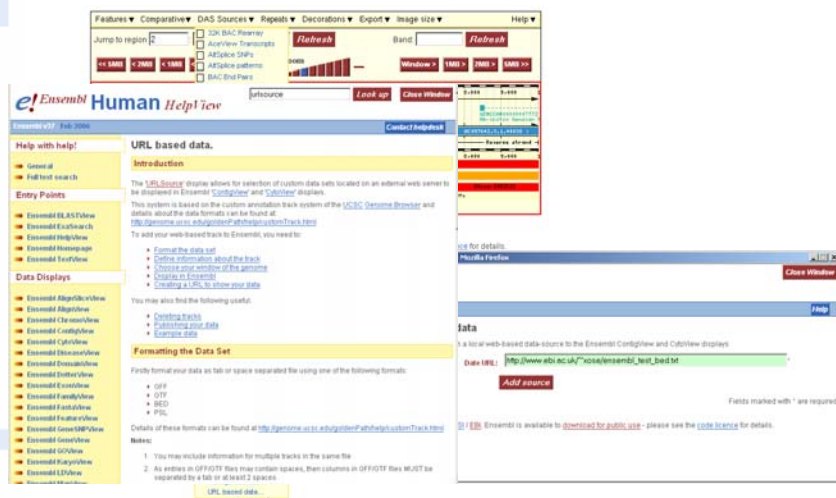
Based on the custom annotation track system of the UCSC browser.

Allowed formats: GFF, GTF, BED, PSL (see *also* <http://genome.ucsc.edu/goldenPath/help/customTrack.html>).

Display data by either entering the URL of the data file on the Urlsource page (ContigView: Data sources > URL based data ...) or by creating the following URL:

[http://www.ensembl.org/species/contigview?data\\_URL=URL](http://www.ensembl.org/species/contigview?data_URL=URL)

## Display of uploaded data



The screenshot shows the Ensembl Human Help page. The main content area is titled 'URL based data' and includes an 'Introduction' section. The introduction states: 'The URLSource display allows for selection of custom data sets located on an external web server to be displayed in Ensembl. ContigView and CustomTrack displays. This system is based on the custom annotation track system of the UCSC Genome Browser and details about the data formats can be found at: <http://genome.ucsc.edu/goldenPath/help/customTrack.html>'. Below this, it says 'To add your web-based track to Ensembl, you need to:'. A list of steps follows: 'Format the data set', 'Define information about the track', 'Specify your website of the genome', 'Create an Ensembl track', and 'Create a URL to show your data'. A note says 'You may also find the following useful:'. A 'Formatting the Data Set' section follows, stating 'Firstly format your data as tab or space separated by using one of the following formats:'. A list of formats is provided: 'GFF', 'GTF', 'BED', and 'PSL'. Below this, it says 'Details of these formats can be found at <http://genome.ucsc.edu/goldenPath/help/customTrack.html>'. A 'Notes' section follows with two points: '1. You may include information for multiple tracks in the same file.' and '2. As entries in GFF/GTF files may contain spaces, then columns in GFF/GTF files MUST be separated by a tab or at least 2 spaces.' At the bottom, there is a 'data' section with a 'Data URL' field containing 'http://www.ncbi.nlm.nih.gov/ensembl\_test\_data' and an 'Add source' button. A note at the bottom right says 'Fields marked with \* are required'.

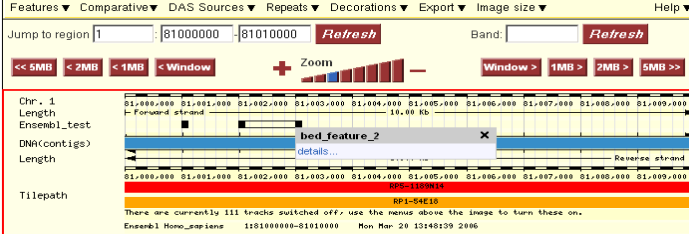


## URL-based

```

browser position chr2:1-10000
track name=Ensembl_test description="Ensembl
workshop (BED)" color=000000
url=http://www.ebi.ac.uk/~xose/ensembl_test.html
2      1000   1100   bed_feature_1 1000   +
2      2000   2100   bed_feature_2 500    +
2      3000   3100   bed_feature_2 100    +
    
```

## Display of data via URL



The screenshot shows the Ensembl genome browser interface. At the top, there are navigation menus: Features, Comparative, DAS Sources, Repeats, Decorations, Export, Image size, and Help. Below these is a search bar with 'Jump to region' and a 'Refresh' button. The search bar contains '1' and '81000000-81010000'. To the right is a 'Band:' field with another 'Refresh' button. Below the search bar are navigation buttons: '<< 5MB', '< 2MB', '< 1MB', '< Window', a zoom control with a '+' sign and a bar chart, 'Window >', '1MB >', '2MB >', and '5MB >>'. The main content area shows a genomic track for 'Chr. 1' with a length of 19,400 kb. A track named 'Ensembl\_test' is visible, containing a feature 'bed\_feature\_2' with a length of 1000 bp. Below the track is a 'Tilepath' section with a yellow background and the text 'There are currently 111 tracks switched off; use the menus above the image to turn these on.' At the bottom, it says 'Ensembl Home\_page 1081000000-810100000 Mon Mar 20 15:49:19 2006'.

## Display of uploaded data

### DAS Wizard Step 2 of 3: Data appearance

Coordinate System: Provided by Registry

Enable on:  geneview  proteinview  transview  
 coreview  cybrowser

[Back](#) [Next](#)

### DAS Wizard Step 3 of 3: Display configuration

#### DAS sources

Name	DAS Server
das_32K	http://das1:
das_ACEVIEW	http://das.er
das_ALTSPUCE	http://www.e
das_ALTSPUCENP	http://www.e
das_ABas	http://db.sys
das_ABasPlasma	http://db.sys
das_BAC	http://das1:
das_CHORIS07	http://das1:
das_CHORI_243	http://das.er
das_CISRED	http://stand
das_COMPUOEN	http://das.er
das_CPG	http://das.er
das_Decipher	http://das1:
das_DOTB	http://das1:
das_FIRSTEF	http://das1:
das_FOSMD	http://das1:
das_GCS_EnoFish	http://www.e
das_GCS_mRNA	http://www.e

Name: As nickname in registry  
 Label: As nickname in registry

Help URL:   
 Link Text:   
 Link URL:

Track colour:

Group features:

Display on:

Label features:

Apply stylesheet:   
 Use score:

[Back](#) [Finish](#)

#### DAS sources

Name	DAS Server	Data Source	Coordinate System
das_32K	http://das1	sanger.ac.uk:7070/peridas	ens_ncbi_35_22array
das_ACEVIEW	http://das.ensembl.org/das	ens_35_aceview	Ensembl Location
das_ALTSPUCE	http://www.ebi.ac.uk/das-srvs/das	ssd_human	Ensembl Location
das_ALTSPUCENP	http://www.ebi.ac.uk/das-srvs/das	ssd_stg_human	Ensembl Location
das_ABas	http://db.systemsbiology.net:8080/das	Human_Ena30_NCBI05_APD0405_P09	Ensembl Location
das_ABasPlasma	http://db.systemsbiology.net:8080/das	HumanPlasma_ALL_Ena32_P09	Ensembl Location

## File upload-based

```
#<col1>      <col2>      <col3>      <col4>
#<group>     <name>       <type>     <subtype>

Similarity   Fake_match_1  homology    wublastn
Transcription Fake_tscr_1   transcript  exon
Transcription Fake_tscr_1   transcript  exon

#<col5> <col6> <col7> <col8> <col9> <col10>
#<chr>  <start> <end> <strand> <phase> <score>

2      4000    4050   +        .        100
2      4200    4300   +        .        100
2      4400    4500   +        .        100
```

e!  
Ensembl

# Example: Epigenomic ChIP-chip data

e! Ensembl Mouse ContigView

Ensembl v85 - Apr 2006

Chromosome 17  
19,558,400 - 19,658,400

- View of Chromosome 17
- Graphical overview
- Export information about region
- Export sequence as FASTA
- Export ENML file
- Export Gene info in region
- Export SNP info in region
- Export Vega info in region
- View alignment with ...
- View alongside ...
- View Systemic regions ...
- View regions in Ensembl NCBI/Ensembl
- View region in UCSC browser

Use Ensembl to...

- Run a BLAST search
- Search Ensembl
- Data mining (BioMart)
- Upload your own data
- Export data
- Download data

Docs and downloads

- Information
- What's New
- About Ensembl
- Ensembl data
- Software

Chromosome 17

Dr. 17

Overview

Dr. 17 band

WtContigs

Ensembl Genes

Gene legend

Detailed view

Features Comparative DAS Sources Repeats Decorations Export Image size Help

Jump to region 17

Band: Refresh

5MB 2MB 1MB Window 1MB 2MB 5MB

Chr. 17

Length

Ensembl trans.

DNA(contigs)

GEN-HU\_H3K4me3\_NCBI

Length

ZIG

Gene legend

MMUchr17P20085384

Method: ChIP-chip (NimbleGen)

Score: 2.51717210759535

Category: epigenomic modification

Feature location:

- Start: 19602397

- End: 19602447

- Strand: Forward

NOTES:

MEFB1\_H3K4me3\_v9\_HFB1\_NCBIin35

e!  
Ensembl

# Example: Epigenomic ChIP-chip data

Detailed view

Features Comparative DAS Sources Repeats Decorations Export Image size Help

Jump to region 17 : 19558400 -19658400 Refresh Band: Refresh

5MB 2MB 1MB Window Zoom Window 1MB 2MB 5MB

Chr. 17

Length

Ensembl trans.

DNA(contigs)

GEN-HU\_H3K4me3\_NCBI

Length

ZIG

Gene legend

MMUchr17P20085384

Method: ChIP-chip (NimbleGen)

Score: 2.51717210759535

Category: epigenomic modification

Feature location:

- Start: 19602397


- End: 19602447


- Strand: Forward

NOTES:

MEFB1\_H3K4me3\_v9\_HFB1\_NCBIin35

Basepair view





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## DAS Registry

available DAS services

Keyword search:

EMBL-EBI  European Bioinformatics Institute

UniProt DAS 

• UniProt DAS Home  
• Access DAS Server  
• Download DAS Server  
• Contact Us

**UniProt DAS Services at the EBI**

The distributed annotation system (DAS) is a client-server system in which a single client integrates information from multiple servers. The UniProt DAS server allows researchers to show their research results, for example identified peptides or signal sequences, on the UniProt reference sequence server, in the context of UniProt/Swiss-Prot annotation.

**The UniProt of Protein DAS Reference Server**

- Access the UniProt of DAS Server

The UniProt DAS Reference Server serves both sequence and feature data from UniProt/Swiss-Prot and UniProt/TrEMBL. In addition to this, feature links to InterPro for all the proteins in UniProt are provided, including basic information (position, id and a brief description) and internet addresses to the relevant data source.


The server can be queried using any of the following:



- UniProt Accession numbers e.g. Q35202 *sequence, features*
- Swiss-Prot ID's e.g. A4\_Human *sequence, features*
- TrEMBL ID's e.g. Q12368 *sequence, features*
- SP ID's e.g. IPH0201571 *sequence*
- UniParc ID's e.g. UP000012665 *sequence*

All of these kinds of identifier will return sequence information. Identifier types marked with an \* will also return UniProt and InterPro feature hits.

For further details of the UniProt DAS server click on the link above that will take you to the UniProt DAS home page. This includes example requests using the DAS protocol for real proteins that can be found in UniProt.

<http://www.dasregistry.org>



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## DAS Server Registration

Central DAS data source registration service at:

<http://www.dasregistry.org/>

A registered data source

- Becomes publicly available
- can automatically be activated
  - in various DAS clients (Ensembl, SPICE, Dasty, etc.)
- gets “health”-checked

## DAS Server Implementations

Most commonly used DAS-Server implementations:

- **LDAS**  
The Lightweight DAS server using Perl, Apache and MySQL  
... see <http://www.biodas.org/servers/>
- **DAZZLE**  
DAS server written in Java  
... see <http://www.derkholm.net/thomas/dazzle>
- **ProServer**  
DAS server written in Perl  
... see <http://www.sanger.ac.uk/proserver>

## Ensembl as DAS server

- list of reference servers

<http://www.ensembl.org/das/dsn>

```
- <DSN>
  <SOURCE id="Homo_sapiens" version="37_35">Homo_sapiens</SOURCE>
  <MAPMASTER>http://www.ensembl.org/das/Homo_sapiens</MAPMASTER>
- <DESCRIPTION>
  Homo_sapiens Reference server based on NCBI35. Contains 111 entry points of the highest assembly tier.
</DESCRIPTION>
</DSN>
- <DSN>
  <SOURCE id="Macaca_mulatta" version="37_1a">Macaca_mulatta</SOURCE>
  <MAPMASTER>http://www.ensembl.org/das/Macaca_mulatta</MAPMASTER>
- <DESCRIPTION>
  Macaca_mulatta Reference server based on MMUL_0_1. Contains 192158 entry points of the highest assembly tier.
</DESCRIPTION>
</DSN>
- <DSN>
  <SOURCE id="Monodelphis_domestica" version="37_2a">Monodelphis_domestica</SOURCE>
  <MAPMASTER>http://www.ensembl.org/das/Monodelphis_domestica</MAPMASTER>
- <DESCRIPTION>
  Monodelphis_domestica Reference server based on BROADO2. Contains 5078 entry points of the highest assembly tier.
</DESCRIPTION>
</DSN>
```

# Ensembl as DAS server

- list of entry points

[http://www.ensembl.org/das/Homo\\_sapiens.NCBI36.reference/entry\\_points](http://www.ensembl.org/das/Homo_sapiens.NCBI36.reference/entry_points)

```

-<DASEP>
  -<ENTRY_POINTS href="Homo_sapiens.NCBI36.reference" version="1.0">
    <SEGMENT id="NT_113917" start="1" stop="19840" orientation="+">NT_113917</SEGMENT>
    <SEGMENT id="NT_113886" start="1" stop="96249" orientation="+">NT_113886</SEGMENT>
    <SEGMENT id="NT_113912" start="1" stop="185143" orientation="+">NT_113912</SEGMENT>
    <SEGMENT id="NT_113878" start="1" stop="106433" orientation="+">NT_113878</SEGMENT>
    <SEGMENT id="NT_113957" start="1" stop="166452" orientation="+">NT_113957</SEGMENT>
    <SEGMENT id="NT_113889" start="1" stop="161147" orientation="+">NT_113889</SEGMENT>
    <SEGMENT id="NT_113905" start="1" stop="183161" orientation="+">NT_113905</SEGMENT>
    <SEGMENT id="NT_113952" start="1" stop="184355" orientation="+">NT_113952</SEGMENT>
    <SEGMENT id="NT_113927" start="1" stop="111864" orientation="+">NT_113927</SEGMENT>
    <SEGMENT id="NT_113908" start="1" stop="13036" orientation="+">NT_113908</SEGMENT>
    <SEGMENT id="NT_113962" start="1" stop="217385" orientation="+">NT_113962</SEGMENT>
    <SEGMENT id="NT_113938" start="1" stop="44580" orientation="+">NT_113938</SEGMENT>
    <SEGMENT id="NT_113941" start="1" stop="37498" orientation="+">NT_113941</SEGMENT>
    <SEGMENT id="NT_113870" start="1" stop="145186" orientation="+">NT_113870</SEGMENT>
    <SEGMENT id="NT_113939" start="1" stop="147354" orientation="+">NT_113939</SEGMENT>
    <SEGMENT id="NT_113901" start="1" stop="182896" orientation="+">NT_113901</SEGMENT>
    <SEGMENT id="NT_113916" start="1" stop="173443" orientation="+">NT_113916</SEGMENT>
    <SEGMENT id="NT_113949" start="1" stop="159169" orientation="+">NT_113949</SEGMENT>
    <SEGMENT id="NT_113880" start="1" stop="185571" orientation="+">NT_113880</SEGMENT>
    <SEGMENT id="NT_113953" start="1" stop="131056" orientation="+">NT_113953</SEGMENT>
    <SEGMENT id="NT_113926" start="1" stop="119514" orientation="+">NT_113926</SEGMENT>
    <SEGMENT id="NT_113951" start="1" stop="152296" orientation="+">NT_113951</SEGMENT>
    <SEGMENT id="NT_113944" start="1" stop="182567" orientation="+">NT_113944</SEGMENT>
    <SEGMENT id="NT_113921" start="1" stop="39615" orientation="+">NT_113921</SEGMENT>
    <SEGMENT id="NT_113873" start="1" stop="51825" orientation="+">NT_113873</SEGMENT>
    <SEGMENT id="NT_113882" start="1" stop="172475" orientation="+">NT_113882</SEGMENT>
    <SEGMENT id="NT_113948" start="1" stop="92689" orientation="+">NT_113948</SEGMENT>
    <SEGMENT id="NT_113924" start="1" stop="139260" orientation="+">NT_113924</SEGMENT>
    <SEGMENT id="NT_113900" start="1" stop="112804" orientation="+">NT_113900</SEGMENT>
    <SEGMENT id="NT_113943" start="1" stop="81310" orientation="+">NT_113943</SEGMENT>
  
```

# Ensembl as DAS server

- Exploring assembly:

<http://www.ensembl.org/das/.../features?segment=1:1,1000000>

```

-<DASGFF>
-<GFF>
  -<SEGMENT id="1" start="1" stop="1000000">
    -<FEATURE id="1">
      <START>1</START>
      <STOP>1000000</STOP>
      <TYPE id="chromosome" category="component" reference="yes" superparts="no" subparts="yes">chromosome</TYPE>
      <TARGET id="1" start="1" stop="1000000">1</TARGET>
    </FEATURE>
    -<FEATURE id="supercontig:NT_077912">
      <START>357583</START>
      <STOP>511231</STOP>
      <TYPE id="supercontig" category="component" reference="yes" superparts="yes" subparts="yes">supercontig</TYPE>
      <TARGET id="NT_077912" start="1" stop="153649">supercontig NT_077912</TARGET>
    </FEATURE>
    -<FEATURE id="supercontig:NT_077913">
      <START>561232</START>
      <STOP>1000000</STOP>
      <TYPE id="supercontig" category="component" reference="yes" superparts="yes" subparts="yes">supercontig</TYPE>
      <TARGET id="NT_077913" start="1" stop="438769">supercontig NT_077913</TARGET>
    </FEATURE>
    -<FEATURE id="supercontig:NT_077402">
      <START>1</START>
      <STOP>167280</STOP>
  
```

## Ensembl as DAS server

### • Exploring assembly:

[http://www.ensembl.org/das/.../features?segment=NT\\_077912](http://www.ensembl.org/das/.../features?segment=NT_077912)

```
-<DASGFF>
-<GFF>
  -<SEGMENT id="NT_077912" start="" stop="">
    -<FEATURE id="NT_077912">
      <START/>
      <STOP/>
      <TYPE id="supercontig" category="component" reference="yes" superparts="yes" subparts="yes">supercontig</TYPE>
      <TARGET id="NT_077912" start="" stop="">NT_077912</TARGET>
    </FEATURE>
    -<FEATURE id="clone:AL732372.15">
      <START>1</START>
      <STOP>153649</STOP>
      <TYPE id="clone" category="component" reference="yes" superparts="yes" subparts="yes">clone</TYPE>
      <TARGET id="AL732372.15" start="1" stop="153649">clone AL732372.15</TARGET>
    </FEATURE>
    -<FEATURE id="chromosome:1">
      <START>1</START>
      <STOP>153649</STOP>
      <TYPE id="chromosome" category="supercomponent" reference="yes" superparts="no" subparts="yes"/>
      <TARGET id="1" start="357583" stop="511231"/>
    </FEATURE>
  </SEGMENT>
</GFF>
</DASGFF>
```

## Ensembl as DAS server

### • Exploring assembly:

<http://www.ensembl.org/das/.../features?segment=AL732372.15.1.153649>

```
-<DASGFF>
-<GFF>
  -<SEGMENT id="AL732372.15.1.153649" start="" stop="">
    -<FEATURE id="AL732372.15.1.153649">
      <START/>
      <STOP/>
      <TYPE id="contig" category="component" reference="yes" superparts="yes" subparts="no">contig</TYPE>
      <TARGET id="AL732372.15.1.153649" start="" stop="">AL732372.15.1.153649</TARGET>
    </FEATURE>
    -<FEATURE id="clone:AL732372.15">
      <START>1</START>
      <STOP>153649</STOP>
      <TYPE id="clone" category="supercomponent" reference="yes" superparts="yes" subparts="yes"/>
      <TARGET id="AL732372.15" start="1" stop="153649"/>
    </FEATURE>
  </SEGMENT>
</GFF>
</DASGFF>
```