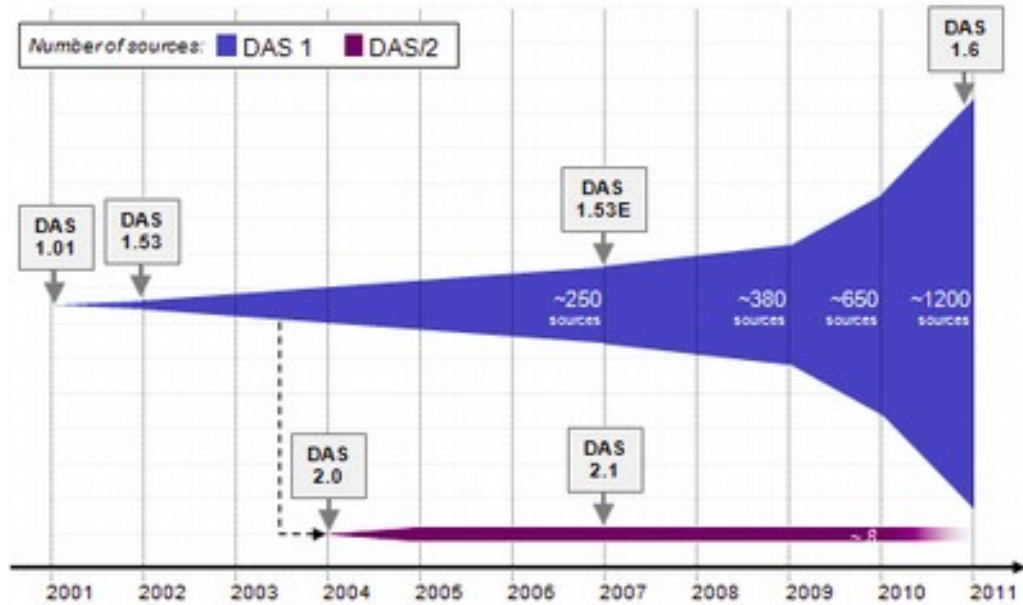


**DAS:**

**Distributed  
Annotation  
Service**

# DAS: Distributed Annotation Service



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

Biodalliance

Browsing ▾

Embedding ▾

Developers ▾

About ▾

Genomes ▾

## Fast, embeddable genome visualization



**Tools**[All tools](#)**BioMart >**

Export custom datasets from Ensembl with this data-mining tool

**BLAST/BLAT >**

Search our genomes for your DNA or protein sequence

**Variant Effect Predictor >**

Analyse your own variants and predict the functional consequences of known and unknown variants

**Search** for**Go**

e.g. [BRCA2](#) or [rat 5:62797383-63627669](#) or [rs699](#) or [coronary heart disease](#)

**All genomes**

- [View full list of all Ensembl species](#)
- [Edit your favourites](#)

**Favourite genomes****Human**

GRCh38.p12

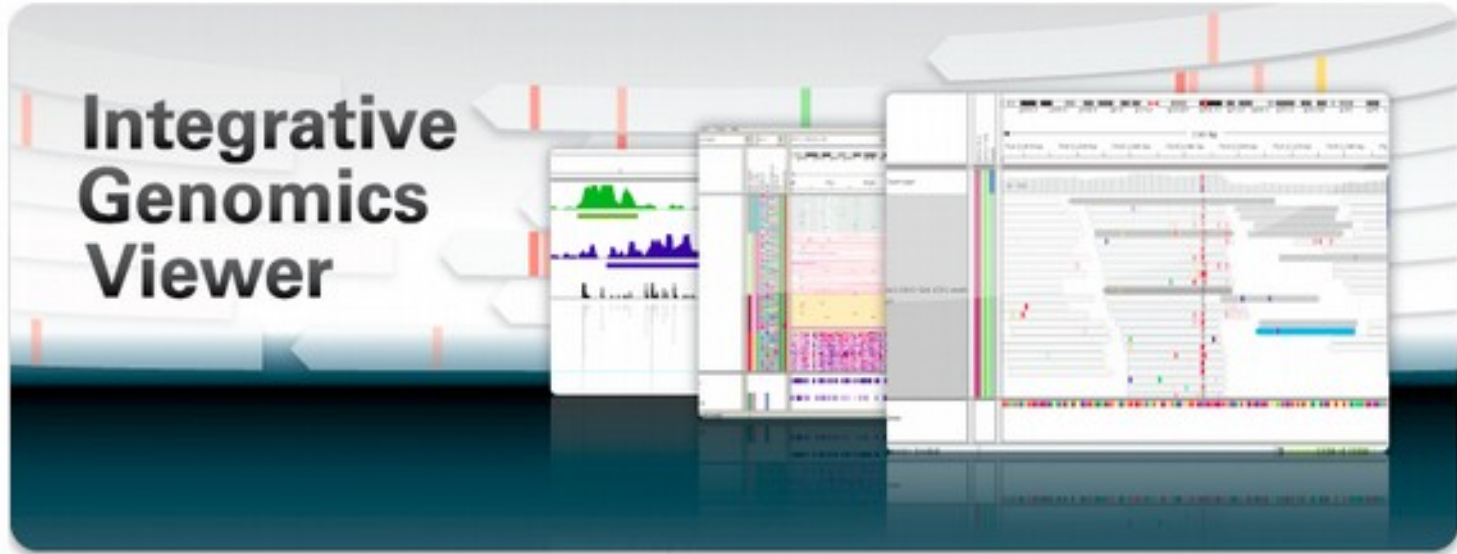
[Still using GRCh37?](#)**Mouse**

GRCm38.p6

**Zebrafish**

GRCz11

<http://software.broadinstitute.org/software/igv/>



# The ProteomeBinders Eptope Choice Resource (beta release)



EpiC collates and presents a structure-function summary and antigenicity prediction of your prote help you design antibodies that are appropriate to your planned experiments.

Antibodies are invaluable research tools but any given antibody will be suitable for some experiments but will not work in others. EpiC utilises information on both the protein target and the various experiments that you plan to carry out and helps in the prediction of antigenicity and therefore epitopes. At least for the better annotated proteins, EpiC should give you an idea of how many antibodies you need to make and where to target the epitopes. Click on the tabs below to start designing your "virtual" experiment. Please remember EpiC is in an early stage of the software development, please get in touch if you want to see a service included or notice any reliability issues. If you notice anything amiss please contact by e-mail niall.haslam at ucd dot ie. Bear in mind that the EpiC resource collates data by connecting to multiple remote servers and cannot guarantee their uptime. For the moment, if a particular remote service fails you will have to reload the page later. It has been tested and will work in Firefox, however the other browsers, such as Safari, Opera and IE with Compatibility Mode on, should work.



**About the Protein** About the Experiment Explore Epitopes Help About

**Please enter the protein information here:** Hide

Please enter the UniProt ID and click Fetch:

e.g. P04637

Alternatively enter the raw sequence by click on the button below:

**Questions about subcellular localisation:** Hide

- Are you interested in signal peptide information?
- Are you interested in localisation information?
- Are you interested in nuclear localisation information?

**Questions about the state of the protein:** Hide

Please select the state of the protein in the experiment:

# STRAP

Intuitive Editor for annotated multiple Sequence and Structure Alignments


## Try it

Demo 1 

Demo 2 

Demo 3 

Demo 4 

 Not Starting?

## Get it

Either Java Web Start   
or [Download & Install](#)


In case of problems introduced with the new version, use the [Previous Strap version ...](#) as a fall back.

[Archive](#)

## Create it

Interactive JavaScript and HTML5 based multiple sequence alignment for web sites

- Interactively in the browser: [Server in the US](#) or [Server in Germany](#)
- [From the program Strap](#)
- [Programmatically](#)

 Java-based. For most cases now obsolete

<http://www.bioinformatics.org/strap/>

