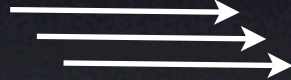


Data Integration using the Distributed Annotation System (DAS)

Andreas Prlić, Ewan Birney, Tony Cox, Thomas A. Down,
Rob Finn, Stefan Gräf, David Jackson, Andreas Kähäri,
Eugene Kulesha, Roger Pettett, James Smith,
Jim Stalker, Tim J. P. Hubbard

- what is DAS
- what do we do with it
- DAS registration server
- latest developments



Ensembl v39 - Jun 2006

Search all Ensembl: Anything

Use Ensembl to...

- Run a BLAST search
- Search Ensembl
- Data mining [BioMart]
- Export data
- Doi load data

Docs and software

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

Other links

- Home
- Sitemap
- Vega
- Pre! Pre Ensembl
- View previous release of page in Archive!
- Stable Archive! link for this page
- Archive! sites
- Trace server

What's New in Ensembl 39

- Honeybee dropped from Ensembl (*Apis mellifera*)
- New Opossum assembly and genebuild (*Monodelphis domestica*)
- New Mouse assembly and genebuild (*Mus musculus*)
- New Ciona savignyi assembly and genebuild (*Ciona savignyi*)
- New Zebrafish assembly and genebuild (*Danio rerio*)

More news...

About Ensembl

Ensembl is a joint project between EMBL, EBI and the Sanger Institute to develop a software system which produces and maintains automatic annotation on selected eukaryotic genomes. Ensembl is primarily funded by the Wellcome Trust.

This site provides free access to all the data and software from the Ensembl project. Click on a species name to browse the data.

Access to all the data produced by

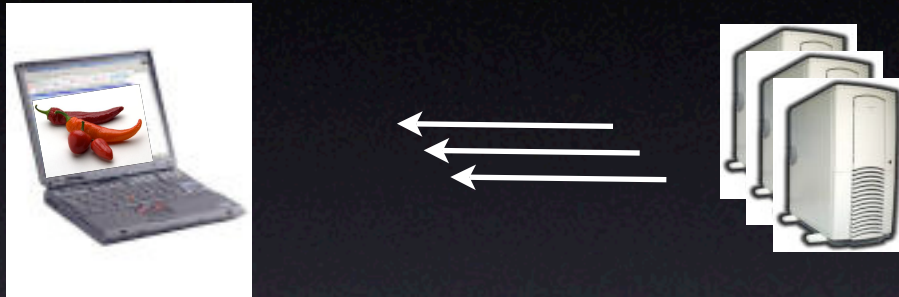
Mammalian genomes

- Homo sapiens* (NCBI 36 | Vega)
- Pan troglodytes* (PanTro 1.0)
- Macaca mulatta* (Mmu1.0.1 | pre!)
- Mus musculus* (UPDATED! NCBI m36 | Vega)
- Rattus norvegicus* (RNO3.4)
- Oryctolagus cuniculus* (RABBIT) (Pre!)
- Canis familiaris* (CanFam 1.0 | Vega | pre!)
- Bos taurus* (Btaur 2.0)
- Dasyurus novemcinctus* (DNO1) (Pre!)
- Loxodonta africana* (LAF1) (Pre!)
- Echinops telfairi* (TEL1) (Pre!)

Other species

- Gallus gallus* (GALLUS 1)
- Xenopus tropicalis* (XOT1.1)
- Danio rerio* (UPDATED! Zv6 | Vega)
- Takifugu rubripes* (Tfugu 4.0)
- Tetraodon nigroviridis* (TETRAODON 7)
- Gasterosteus aculeatus* (GAC1) (Pre!)
- Ciona intestinalis* (CINT) (Pre!)
- Ciona savignyi* (CSAV 2.0) (NEW!)
- Drosophila melanogaster* (DROSC 4)
- Anopheles gambiae* (AGANPS)
- Aedes aegypti* (AEDES 1)

Integration of personal data into bioinf. resources



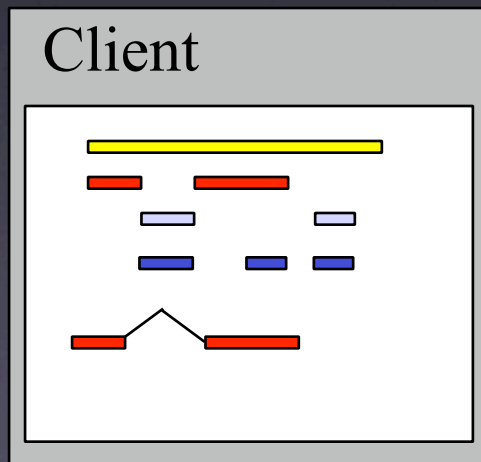
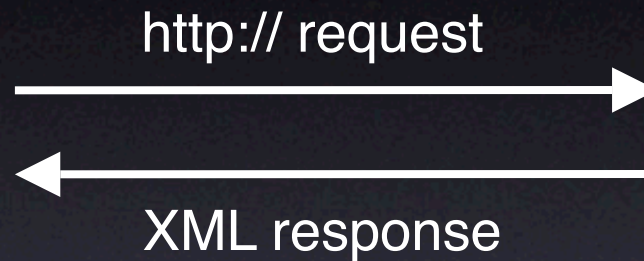
- Integration of annotations from external sources into local applications



- online access to most recent data versions
 - no need for local installations

DAS, how it works

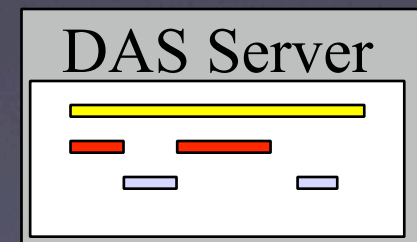
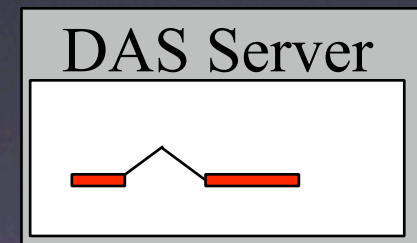
Dowell, Jokerst, Allen, Eddy, Stein
BMC Bioinformatics 2001



get sequence



get features



a few principles...

- Clients are “intelligent” (few)
- Servers are simple and easy to set up (many)
- (most of) data is precalculated
- libraries for server and client
- multiple programming languages

Use Ensembl to...

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- Search Ensembl
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[More news...](#)

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This site provides [free access](#) to all the data and software from the Ensembl project. Click on a species name to browse the data.

Access to all the data produced by the project, and to the software used to analyse and present it, is provided free and without constraints. Some data and software may be subject to [third-party constraints](#).

For all enquiries, please [contact the Ensembl HelpDesk](#) (helpdesk@ensembl.org).

Other sites using the Ensembl system

- EBL Genome Reviews database

Mammalian genomes

- Homo sapiens*
NCBI 36 | Vega
- Pan troglodytes*
PanTro 1.0
- Macaca mulatta*
MMUL 0.1 | **pre!**
- Mus musculus*
UPDATED! NCBI m36 | Vega
- Rattus norvegicus*
RGSC 3.4 | **pre!**
- Pre!** *Oryctolagus cuniculus*
RABBIT
- Canis familiaris*
CanFam 1.0 | Vega | **pre!**
- Bos taurus*
Btau 2.0
- Pre!** *Dasypus novemcinctus*
ARP1A
- Pre!** *Loxodonta africana*
BROAD E1
- Pre!** *Echinops telfairi*
TENREC
- Monodelphis domestica*
UPDATED! MonDom 4

Other species

- Gallus gallus*
WASHUC 1
- Xenopus tropicalis*
JGI 4.1
- Danio rerio*
UPDATED! Zv 6 | Vega
- Takifugu rubripes*
FUGU 4.0
- Tetraodon nigroviridis*
TETRAODON 7
- Pre!** *Gasterosteus aculeatus*
BROAD S1
- Pre!** *Oryzias latipes*
NEW! MEDAKA 1
- Ciona intestinalis*
JGI2
- Ciona savignyi*
UPDATED! CSAV 2.0
- Drosophila melanogaster*
BDGP 4
- Anopheles gambiae*
AgamP3
- Pre!** *Aedes aegypti*
AEDES 1
- Caenorhabditis elegans*
WS 150
- Saccharomyces cerevisiae*
SGD 1

Rattus norvegicus
3.4 update

- > 20 vertebrates / model organism
- 5 mill. page impressions / week
- 100 mirrors/internal installations worldwide
- open source
- used for other species as well
- MySQL
- 5-10 G / species + 100 G multi species data

Chromosome 12
9,706,323 -
10,559,649

View of Chromosome 12

Graphical view

Graphical overview

Export information about region

Export sequence as FASTA

Export EMBL file

Export Gene info in region

Export SNP info in region

Export Vega info in region

View data stored on another webserver in ContigView

View alignment with ...

View alongside ...

View Syntenic regions ...

View region in NCBI browser

View region in UCSC browser

Ensembl to...

Run a BLAST search

Search Ensembl

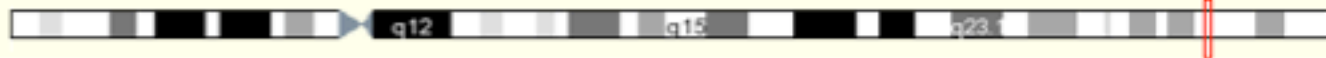
Data mining [BioMart]

Upload and view data chromosome

Export data

Chromosome 12

Chr. 12



Overview

Detailed view

Features ▾ Comparative ▾ DAS Sources ▾ Repeats ▾ Decorations ▾ Export ▾ Image size ▾ Help ▾

Jump to region : CPG island clones Compugen oligos DECIPHER Human SPG predictions Human geneid predictions IMGT Genes Illumina probes NCBI Gnomon OMIM Gene map OMIM Morbid map PDB_Spice RZPD expression clones RZPD gene silencing RZPD verified cDNA RefSeq Sanger Hver Array Toronto Poly Toronto Poly [loc] RZPD verif. cDNA Manage sources... URL based data...

Refresh Band: Refresh

Zoom

<< 5MB < 2MB < 1MB < Window > 1MB > 2MB > 5MB >>

Chr. 12 Length Font

RZPD verified cDNA

RZPD expression clones

RZPD gene silencing

EMBL mRNAs

ENSG00000135100 RZPD:cDNA:ENSG00000135124

RZPD:cDNA:ENSG00000089041 RZPD:cDNA:ENSG00000170833

RZPD:PEC:ENSG00000089041 RZPD:PEC:ENSG00000170833

RZPD:PEC:ENSG00000135124

ENSG00000135100

GENSCAN00000017712 > Ab-initio Genscan trans

Add your own
uses Registry

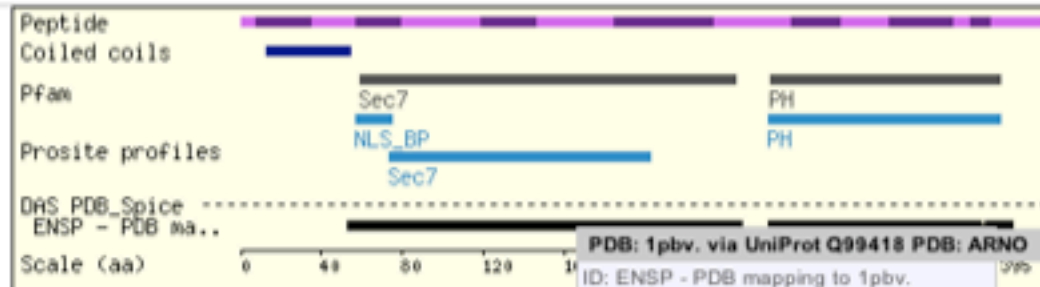
Linking protein structure to e! Peptide view

Prediction Method Genes were annotated by the Ensembl automatic analysis pipeline using either a GeneWise/Exonerate model from a database protein or a set of aligned cDNAs followed by an ORF prediction. GeneWise/Exonerate models are further combined with available aligned cDNAs to annotate UTRs (For more information see V.Curwen et al. , Genome Res. 2004 14:942-50.)

InterPro [IPRO01472](#) Bipartite nuclear localization signal - [\[View other genes with this domain\]](#)
[IPRO00904](#) SEC7-like - [\[View other genes with this domain\]](#)
[IPRO01849](#) Pleckstrin-like - [\[View other genes with this domain\]](#)

Protein Family [ENSF00000001251](#) : CYTOHESIN
This cluster contains 4 Ensembl gene member(s)

Protein Features



Protein Sequence

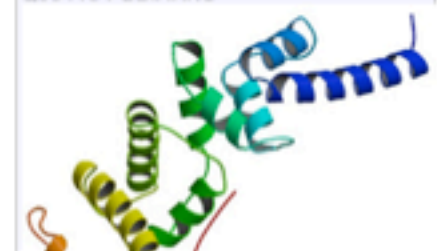
```
MEEDISTYVSDLTREEDQILENINFKKQKILLADIQFLKBYDAEVMNEIINLGSTEEFKKH  
QPKQVWNRKKKTNPKKKGIQFLIENLAKHTCEDIAQIYLYKGGELAKTRIGDYLGEE  
EENIQVLRATVELKREITVQHLVQALQGLINSTRPLGIRAKIDRPHERTARQRCQGNQVY  
QSTVTCYVLSTRAIIPQWTSIADHWKPKPVYERFIAHQDQINDGGLFILLRHLYESIK  
HEPEKIPEDDGHDLTWTIHPDREGWLLKIQQRKTKWQJNEILTNCLLYTEYTWKIF  
RGIIPLNLSIREVEISKKPKCFELYIFDHKDQVIKACKVIADGKVVVEGHRITGSQLDQ  
EKELWIKCQKARISKPTIYEMEARKKKVSSTKPK
```

Exon alternating text colour

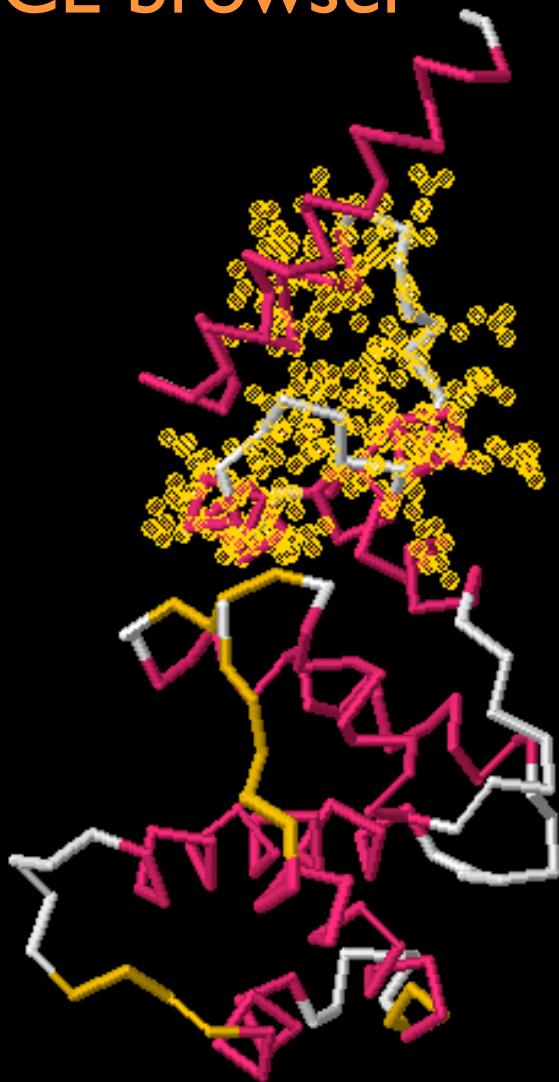
Residue overlap splice site

PDB: 1pbv. via UniProt Q99418 PDB: ARNO

ID: ENSP - PDB mapping to 1pbv.
TYPE: ENSP - PDB mapping
METHOD: Compare, MSD-Mapping of UniProt to PDB
LINK: [http://das.sanger.ac.uk/registry/showspice.jsp?pdb=1pbv.](http://das.sanger.ac.uk/registry/showspice.jsp?pdb=1pbv)
NOTE: PDB: 1pbv. 85%id 49%coverage via UniProt Q99418 PDB:ARNO



SPICE browser



enter RASMOL like command...

SPICE

PDB 1PBV. 195

dssp

SECSTRUC

BEND

BRIDGE

cath

Cath Domain

s3dm

UniProt Q99418

uniprot

description

CHAIN

COILED

SECSTRUC

DOMAIN

ISOFORM

Smart

Scop

PROSITE

ENSP ENSP00000354398

ensp_pdb_mapping

ENSP - PDB

hsa35pep

exon

exon

The image shows the SPICE browser interface for protein 1PBV. It features three main panels: PDB (1PBV. 195), UniProt (Q99418), and ENSP (ENSP00000354398). Each panel displays a horizontal bar representing the protein sequence, with various colored bars indicating different annotations. The PDB panel shows dssp, SECSTRUC, BEND, BRIDGE, cath, Cath Domain, and s3dm. The UniProt panel shows uniprot, description, CHAIN, COILED, SECSTRUC, DOMAIN, ISOFORM, Smart, Scop, and PROSITE. The ENSP panel shows ensp_pdb_mapping, ENSP - PDB, hsa35pep, and exon. A blue heatmap is visible at the bottom of each panel. The interface includes a search bar at the top, a scroll bar on the right, and a command input field at the bottom.

<http://www.efamily.org.uk/software/dasclients/spice>



See exon structure mapped onto 3D

enter RASMOL like command...

PDB 1A17. 159

- dssp
- SECSTRUC
- BEND
- cath
- Cath Domain
- s3dm
- ALPHA-BET

UniProt P53041

- uniprot
- description
- CHAIN
- SECSTRUC
- REPEAT
- REGION
- METAL
- ACT_SITE
- CONFLICT
- Smart

ENSP ENSP00000012443

- MisPred
- hsa35pep
- exon
- exon
- sSNP
- nsSNP

Click

The image shows a vertical stack of three tracks for protein 1A17. The top track is PDB, the middle is UniProt (P53041), and the bottom is ENSP (ENSP00000012443). Each track displays various annotations as colored bars and boxes. An orange arrow points to a feature in the ENSP track, labeled 'Click'.



Show SNPs



A PDB 1S95.A 324

B

dssp

- BEND
- BRIDGE
- SECSTRUC
- 3HELIX

cath

Cath Domain

UniProt P53041

uniprot

- description
- CHAIN
- SECSTRUC
- REPEAT
- REGION
- METAL
- ACT_SITE
- CONFLICT
- Smart

ENSP ENSP00000012443

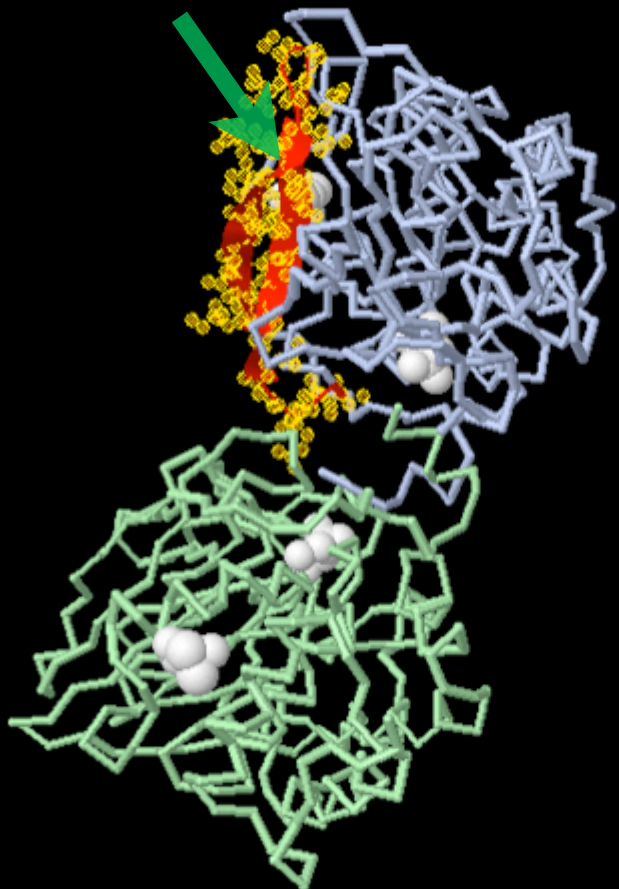
MisPred

hsa35pep

- exon
- exon
- sSNP
- sSNP

enter RASMOL like command...

interact with Menu & RASMOL

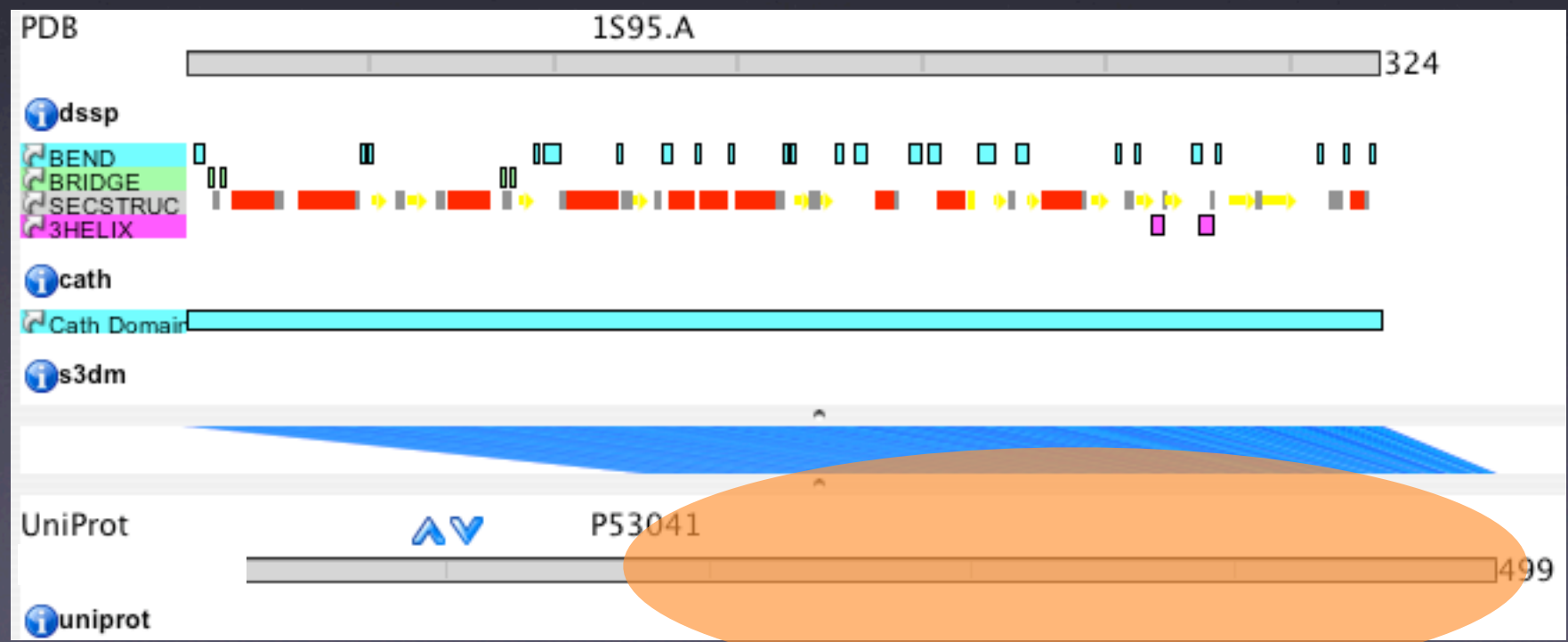
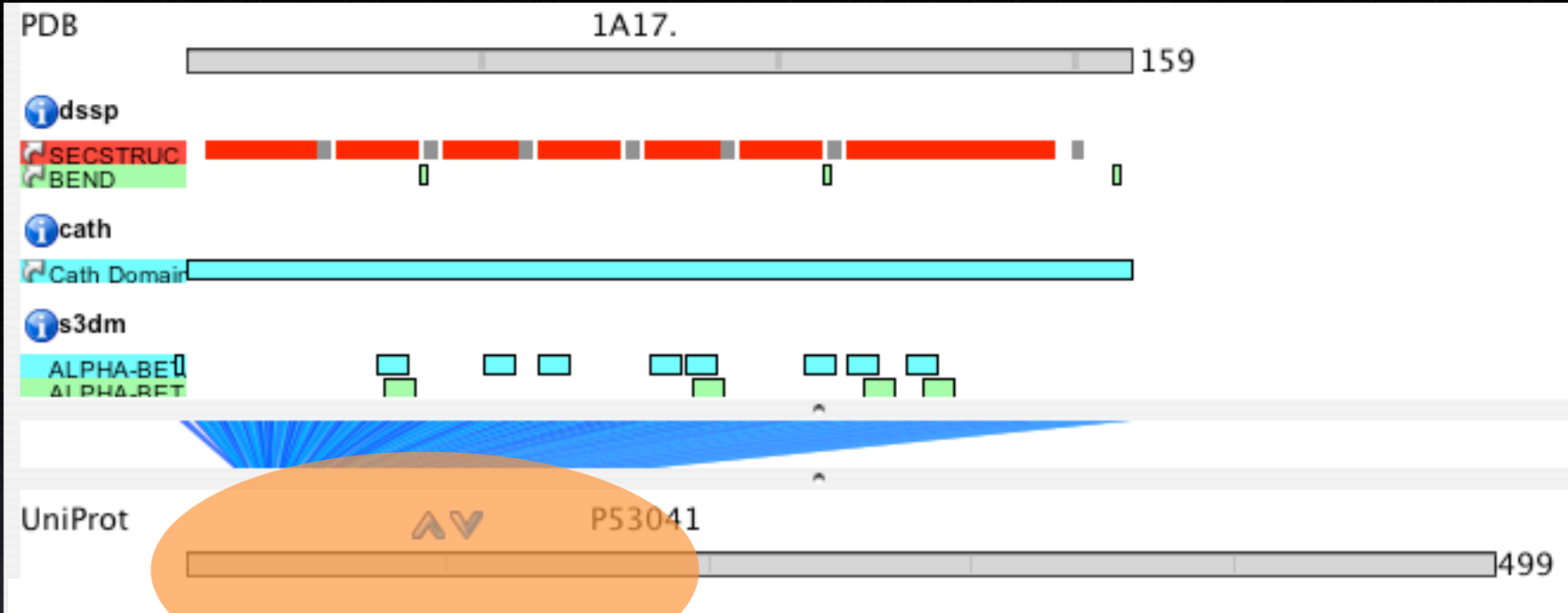


enter RASMOL like command
selected seq: 277 - 304 pdb: 4...479

RASMOL
commands

The screenshot shows the SPICE software interface. At the top, it displays 'SPICE' and 'PDB 1S95.A'. Below this, there is a sequence alignment view with a protein sequence: `K A E G Y E V A H G G R C V T M F S A P N Y C D Q M G N K A S Y I H L Q G S D L R P O F H Q F T A V P H P N V K P M A Y A N T L L`. The alignment is visualized with colored bars (cyan, yellow, purple, red) representing different domains or regions. Below the alignment, there are two more sections: 'UniProt P53041' and 'ENSP ENSP00000012443', each with their respective protein sequences and alignment visualizations. At the bottom right of the interface, there is a zoom slider control with an orange arrow pointing to it.

Zoom



Choose Alignment

alignment for P53041 vs. PDBresnum, Protein Structure

499

1a17. 2.45A XRAY description: SERINE/THREONINE PROTEIN PHOSPHATASE 5

1s95.A 1.6A XRAY description: SERINE-THREONINE PROTEIN PHOSPHATASE 5

1s95.B 1.6A XRAY description: SERINE-THREONINE PROTEIN PHOSPHATASE 5

Close

enter RASMOL like command...

selected seq: 143 - 158 pdb: 143-158

SPICE

PDB

1BOH

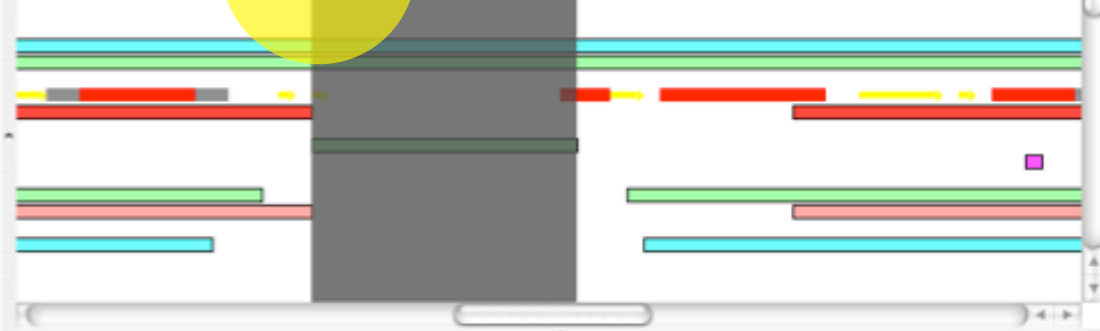
SVL NGG RNLW KEGHP MTS E P SRPE P F KATL NRS L LKTYEQVLE NLESKRFLQV DSRAGGRYL



UniProt

P00586

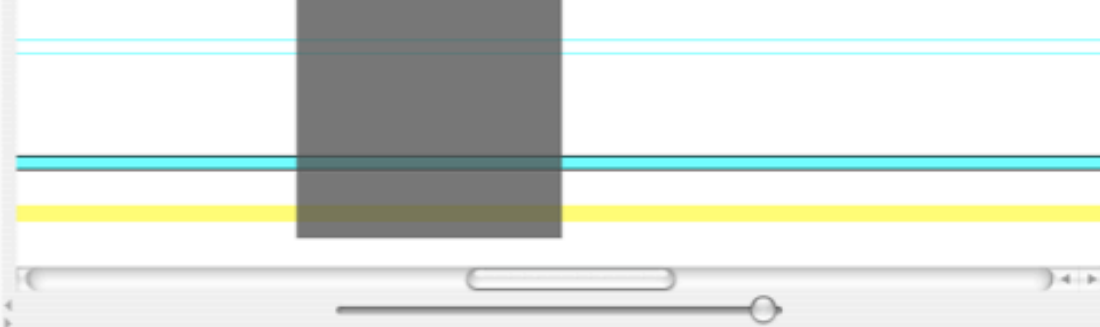
VL NGG RNLW KEGHP MTS E P SRPE P F KATL NRS L LKTYEQVLE NLESKRFLQV DSRAGGRYL



ENSP

ENSP00000249042

L N G R F R N W L K E G H P M T S E P S R P E P A V F K A T L D R S L L K T Y E Q V L E N L E S K R F L Q V D S R S Q G R F L G T E



DAS commands

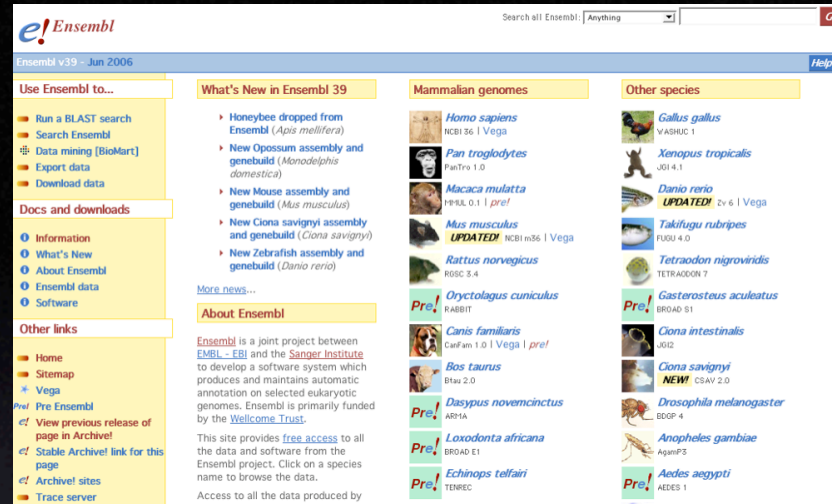
Structure

Features

Alignment

Sequence

The screenshot displays the SPICE web interface. On the left, a 3D protein structure is shown with a pink ribbon backbone and a yellow mesh surface. The structure is set against a black background. On the right, a vertical sidebar contains several panels: 'PDB' with sub-panels for 'dssp', 'SECSTRUC', 'BEND', 'BRIDGE', 'cath', 'Cath Domain', and 's3dm'; 'UniProt' with sub-panels for 'uniprot', 'description', 'CHAIN', 'COILED', 'SECSTRUC DOMAIN', 'ISOFORM', 'Smart', 'Scop', and 'PROSITE'; and 'ENSP' with sub-panels for 'ensp_pdb_mapping', 'ENSP - PDB', and 'hsa35pep'. At the bottom, a command line reads 'enter RASMOL like command...' and a status bar shows 'selected seq: 28 - 67 pdb: 79-118'.



Java Web Start

auto install
latest version
send arguments

DAS registry

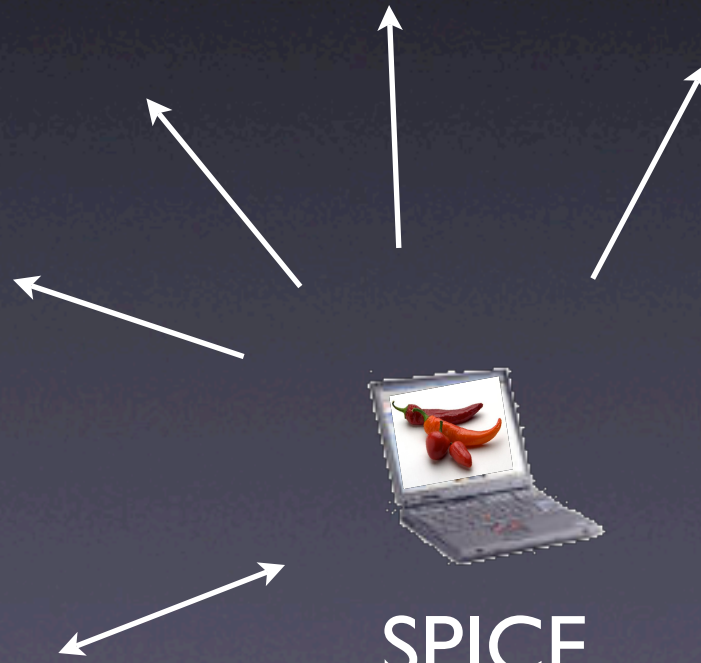


SPICE

Meta information
about DAS servers

DAS registry

SPICE



The DAS registration server

DS_110		dssp	cmbi4.cmbi.ru.nl/das/dssp/	features	PDBresnum,Protein Structure
DS_111		cath	cathwww.biochem ... 0/das/cath_pdb/	features	PDBresnum,Protein Structure
DS_112		structure	das.sanger.ac.uk/das/structure/	structure	PDBresnum,Protein Structure
DS_113		alig_pdb_sp	das.sanger.ac.uk/das/msdpdbsp/	alignment	UniProt,Protein Sequence PDBresnum,Protein Structure
DS_114		signalp	genome.cbs.dtu.dk:9000/das/signalp/	types features	UniProt,Protein Sequence
DS_115		netphos	genome.cbs.dtu.dk:9000/das/netphos/	types features	UniProt,Protein Sequence
DS_116		netoglyc	genome.cbs.dtu.dk:9000/das/netoglyc/	types features	UniProt,Protein Sequence
DS_117		tmhmm	genome.cbs.dtu.dk:9000/das/tmhmm/	types features	UniProt,Protein Sequence

<http://das.sanger.ac.uk/registry/>

DAS registration server

- allows to “publish” DAS servers & share with community
- communicates with clients
- regularly checks servers, sends notification

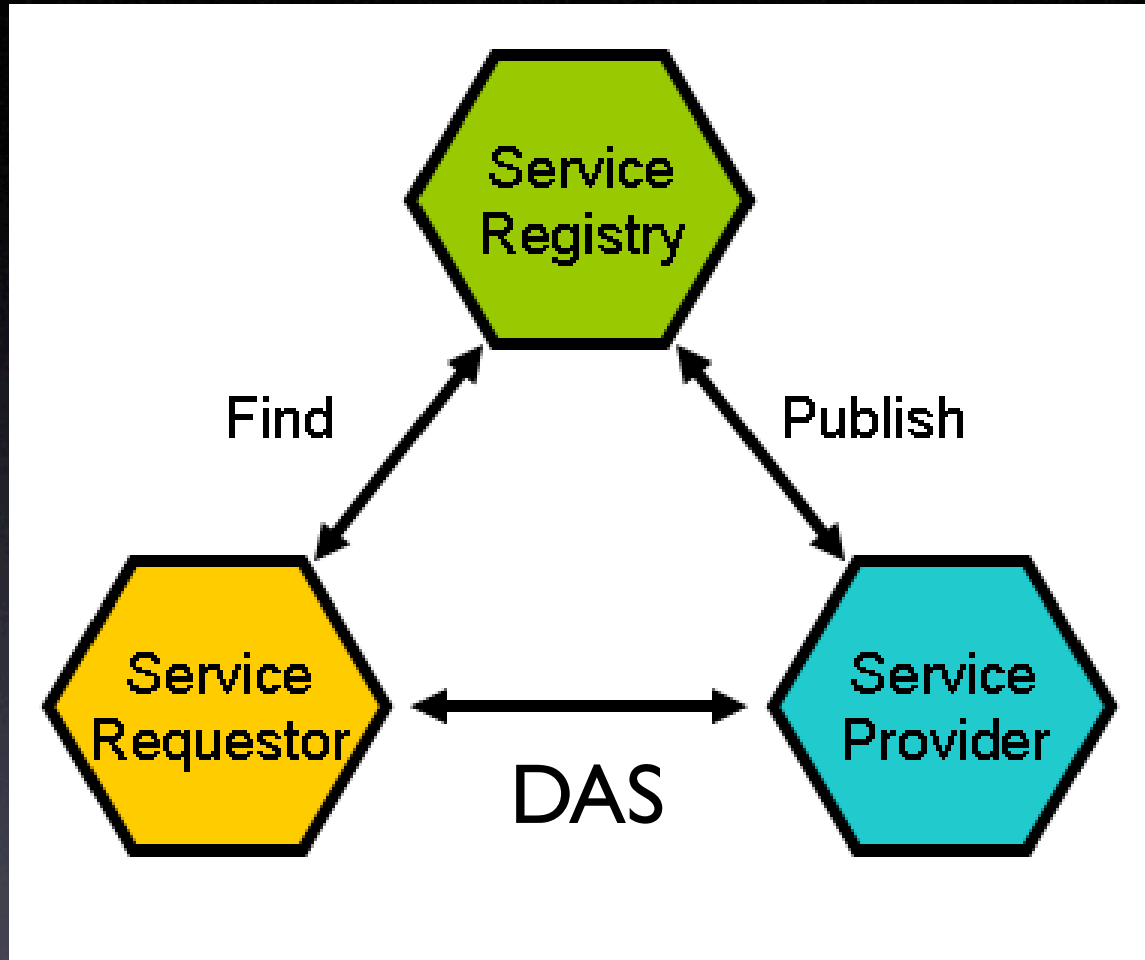
What is the glue?

- “Coordinate Systems”
 - Authority
 - Type of data
 - Version
 - Organism (optional)

Clients and Coordinate Systems

- Ensembl - most of the views can display DAS sources from multiple CS
- SPICE - PDB, UniProt, Ensp
- Dasty - UniProt

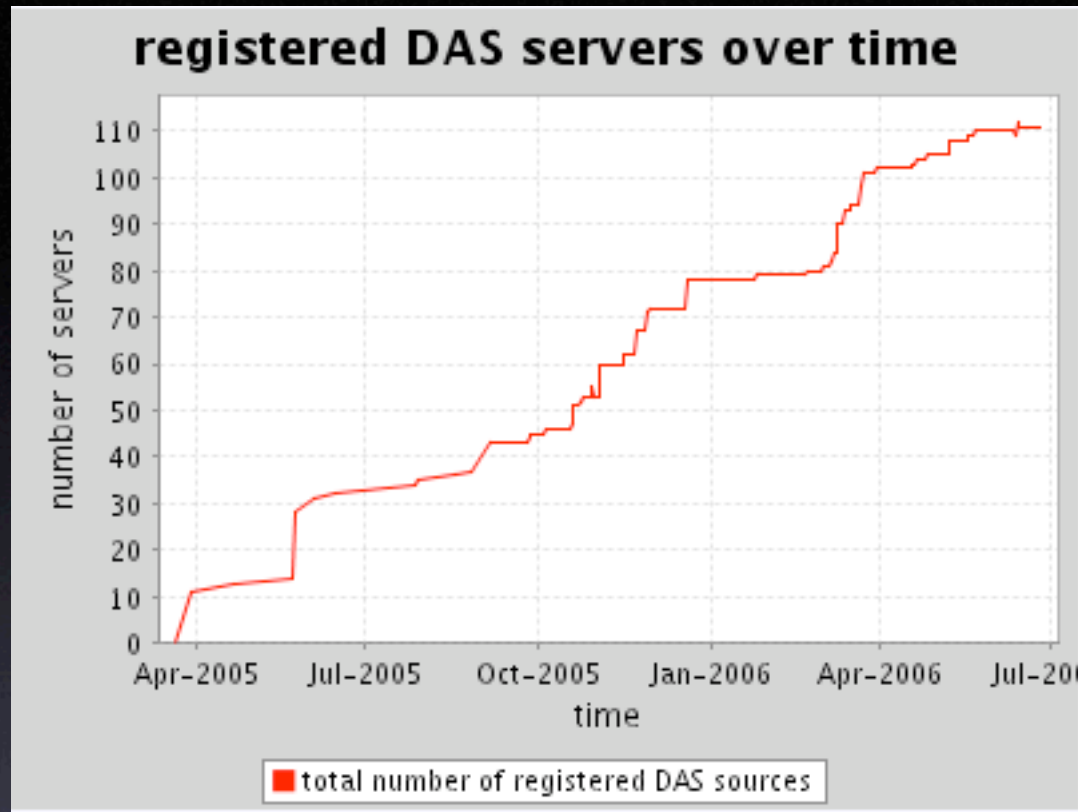
DAS registration server



e.g.
Ensembl,
SPICE

a DAS source

the DAS - SOA



111 DAS sources
 26 institutions
 12 countries



+ others

DAS - issues

- inconsistent implementations
- no consistent use annotation types
- error handling
- searches not possible - in DAS/I
- open sharing of data - low security

SISYPHUS

Submit Query

Structural alignments for proteins with non-trivial relationships



Sisyphus: in greek: crafty

Authors:

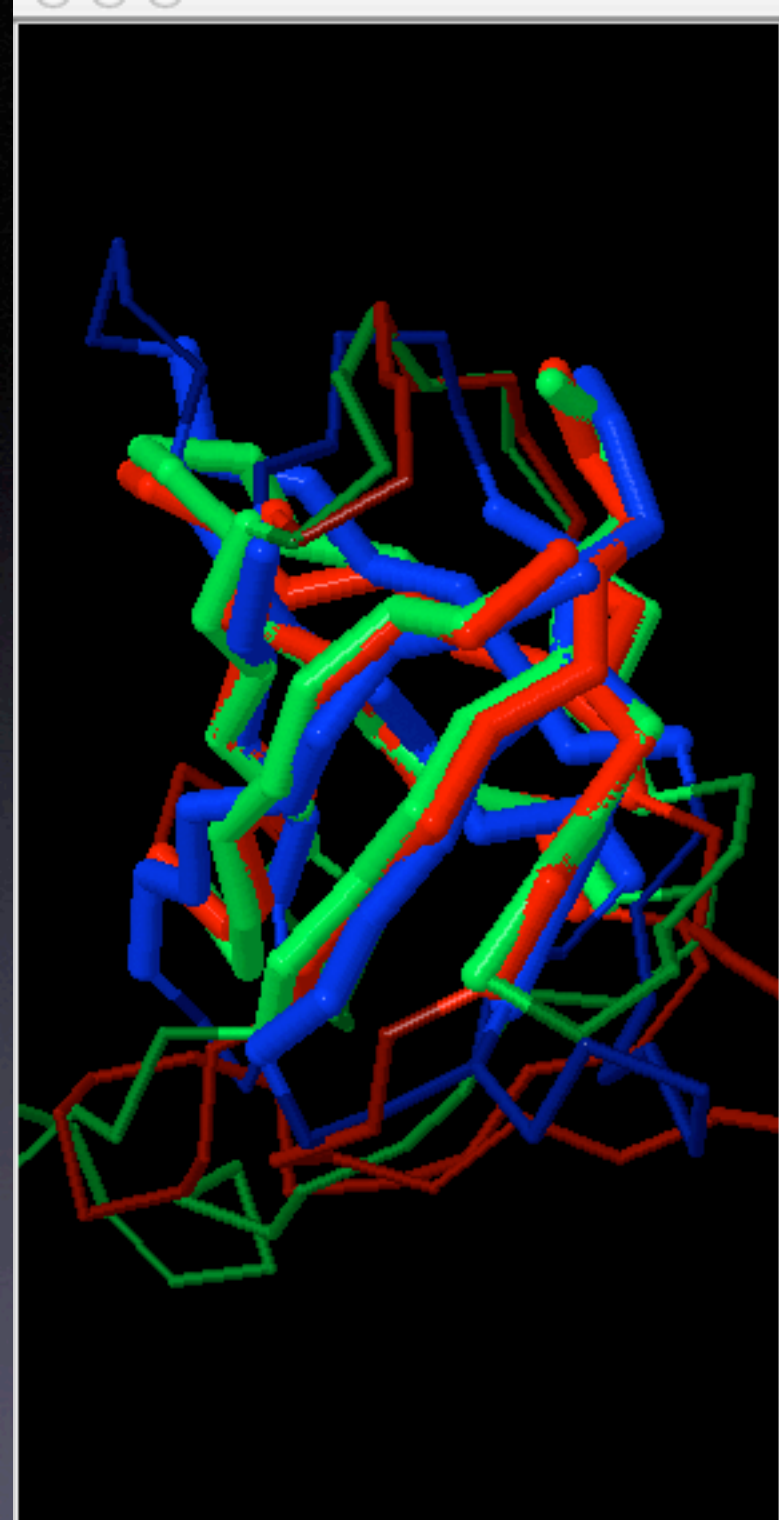
Antonina Andreeva, Andreas Prlic, Tim Hubbard, Alexey Murzin

```

SATVGIFVDagsraenvknNGTAHFLEHLAFkgtqnr-----pgQGIELeienig---shLNAYTsr----eNTVYYAKSLq--edIPKAVDI
TTHIAIALEgvswsap--dYFVALATQAIIVGnwdraigtgtn-----spSPLAVaasqngslansYMSFStsyadsgLWGMYIVTDSnehnVRLIVNE
FSALGLYIDagsrfegrnlKGCTHILDRLAFkstehv-----egRAMAEtlellg---gnYQCTSSr----eNLMYQASVFN--gdVGMKMLQL
LFHIQIGFEGlpidhp--dIYALATLQTLGgggsfsagpgkgmysrlyTHVLNqy---yfvencVAFNhsysdsgIFGISLSCIP--gaAPQAVEV
TCTVGVWIDagsryeseknNGAGYFVEHLAFkgtknr-----pgNALEKevesmg---ahLNAYStr----eHTAYYIKALs--kdLPKAVEL
LAHVAIAVEgpgwahp--dNVALQVANAIIGHydctygggah-----lsSPLASiaatn-klcqsFQTFNicyadtgLLGAHFVCDhms--IDDMMFV
TCTVGVWIDagsryeseknNGAGYFLEHLAFkgtknr-----pgNALEKevesmg---ahLNAYSSr----eHTAYYIKALs--kdVPKAVEL
LAHVAIAVEgpgwahp--dLVALQVANAIIGHydrtyggglh-----ssSPLASiavtn-klcqsFQTFNicysetgLFGEFYFVCDrms--IDDMMFV
TASVGVVFGsgaanenpynNGVSNLWKNIFL-----sKENSavaakeg---laLSSNISr----dFQSYIVSSLp--gsTDKSLDF
KAWISLAVEgepvnsn--nYFVAKLAAQIFGsynafepasrl-----ggIKLLDnigey-qlcdnFNHFSlsykdsGLWGFSTATRnvt-mIDDLIHF
ISTLAVKVHggstryat--kDGVVAHLLNRFNFgntntr-----saLKLVRResellg---gtFKSTLdr----eYITLKATFLk--ddLPYYVNA
DSVAAIGIPvn---ka--sLAQYEVLANYLtsal-----SELSGli-----SSAKLdkftdggLFTLFVRDQ--dsavVSSNIKK
LVHAAIAVESaaigga--eANAFSVLQHVLG-----ANPHVkrngnp---fdVSAFNasysdsgLFGFYTISQaay--AGQVIKA
GSTIGVFIKagsryenssnLGTSHLLRLASSlttkga-----ssFKITRgieavg---gkLSVestr----eNMAYTVECLr--ddVEILMEF
ASRIGLFIKagsryenssnLGTSHLLRLASSlttkga-----ssFKITRgieavg---gkLSVestr----eNMAYTVECLr--ddVDILMEF
LVHAALVAESaaigsa--eANAFSVLQHVLGagphvkragsna-----tSSLYQavakgvhgpfcv---asysds---eYITISQa---GDVIKA

```





- 1efc.A_A301:310_A326
- 1b23.P_P313:322_P338
- 1exm.A_A313:322_A338
- 1d2e.A_A349:358_A371
- 1f60.A_A335:344_A351
- 1skq.A_A323:332_A340
- 1kk0.A_A322:331_A339
- 1s0u.A_A349:358_A371
- 1r5b.A_A557:566_A573
- 1pj5.A_A744:753_A760
- 1nrk.A_A246:255_A262
- 1wos.A_A279:288_A295
- 1vlo.A_A279:288_A295

PDB 1EFC.A

dssp

SECSTRUC

BEND

3HELIX

BRIDGE

cath

s3dm

UniProt P02990

uniprot

description

INIT MET

CHAIN

MOD RES

SECSTRUC

NP_BIND

MUTAGEN

VARIANT

TIGRFAMs

TIGRFAMs

ENSP 0

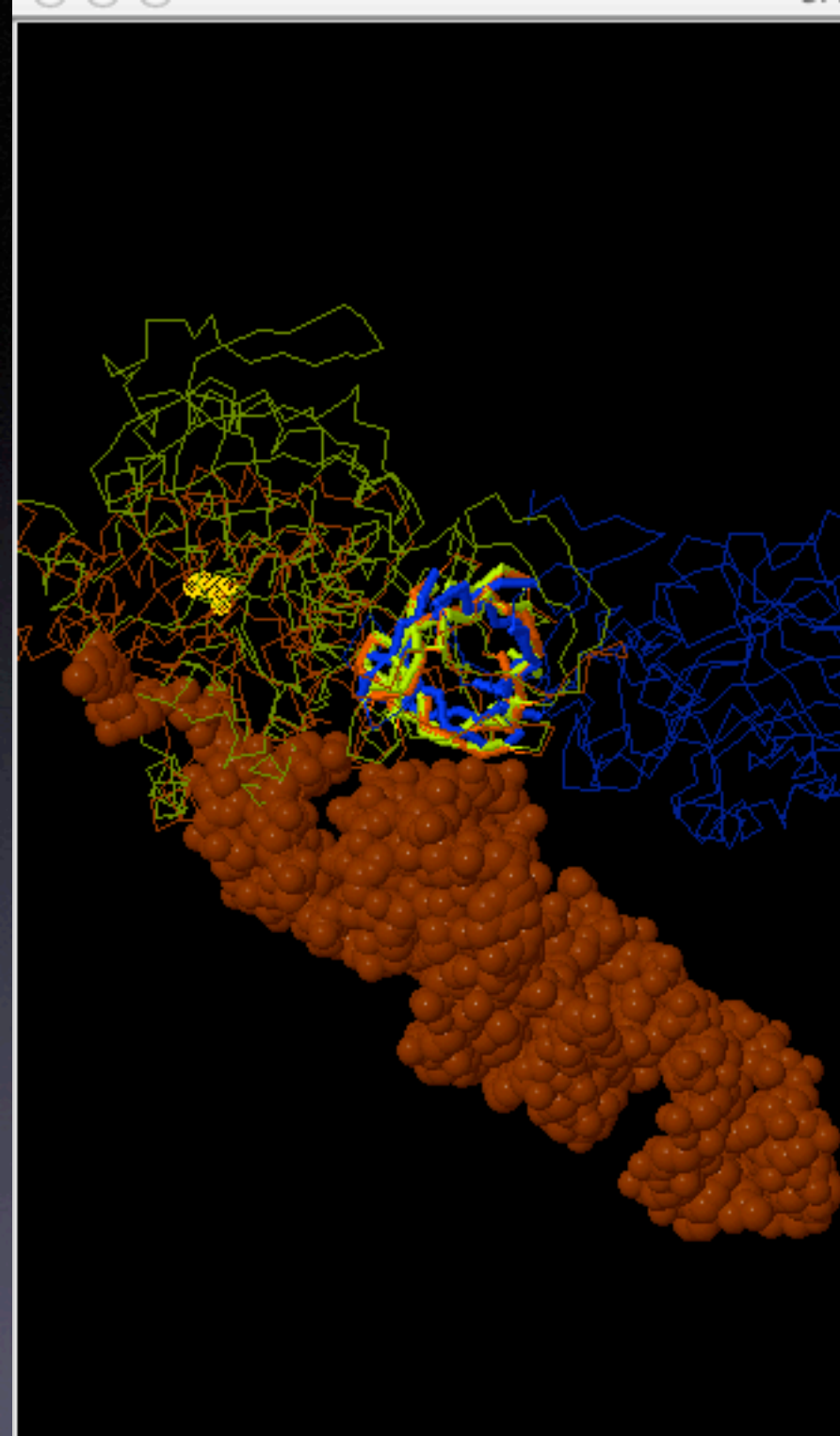
superfam

cbs_sort

cbs_ptm

cbs_func

enter RASMOL like command...



- 1efc.A_A301:310_A326
- 1b23.P_P313:322_P338
- 1exm.A_A313:322_A338
- 1d2e.A_A349:358_A374
- 1f60.A_A335:344_A351
- 1skq.A_A323:332_A340
- 1kk0.A_A322:331_A338
- 1s0u.A_A349:358_A374
- 1r5b.A_A557:566_A573
- 1pj5.A_A744:753_A760
- 1nrk.A_A246:255_A262
- 1wos.A_A279:288_A294
- 1vlo.A_A279:288_A294

PDB 1B23.P

[dssp](#)

BRIDGE
BEND
SECSTRUC
3HELIX

[cath](#)

[s3dm](#)

UniProt Q01698

[uniprot](#)

description
INIT MET
CHAIN
SECSTRUC
NP_BIND
TIGRFAMs
TIGRFAMs
Scop
PROSITE
PRINTS

ENSP 0

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[cbs_sort](#)

[cbs_ptm](#)

[cbs_func](#)

- Alignment DAS:
- rotation matrices, shift vectors
- range information (optional)

MuscleWS alignment of Uniref50 Sequences - FASTA

Search View Colour Calculate Web Service

110 120 130

A/1-97 SCAGK IAGGAVDQT DGNFLDD DQLEEGWVLT CVAY
 N/1-144 SCAGK IAGGAVDQT DGNFLDD DQLEEGWVLT CVAY
 ES/1-144 SCAGKVTAGSVDQSDG NFLDE DQEAAGFVLT CVAY
 DLTU/1-144 SCAGKVTAGTVDQSDG KFLDD DQEAAGFVLT CVAY
 /1-149 SCAGKVVGG EVDQSDG SFLDD EQIEAGFVLT CVAY
 RIPR/1-152 SCAGKVVNGN VNOEDG SFLDD EQIEGGWVLT
 CR/1-148 SCAGKVTSGS VNOEDG SFLDD DQIEGGWVLT
 DL/1-147 SCAGKLTGSLN QDDQS FLLDD DQIEGGWVLT
 SA/1-96 SCAGKVVSGS VQSDQS FLLDD DQIEAGFVLT
 H/1-148 SCAGKVVSGS VQSDQS FLLDD EQIEGEGFVLT
 A/1-96 SCAGKVVSGF VQSDDES FLLDD DQIEAGFVLT
 TH/1-148 SCAGKVVSGS IDQSDQS FLLDD EQMSEGYVLT
 RATH/1-118 SCAGKVVSGS IDQSDQS FLLDD -----
 TE/1-150 SCAGKVVSGS VQSDQS YLDD GQIADGWVLT
 AIZ

Fe 4 5 6 7

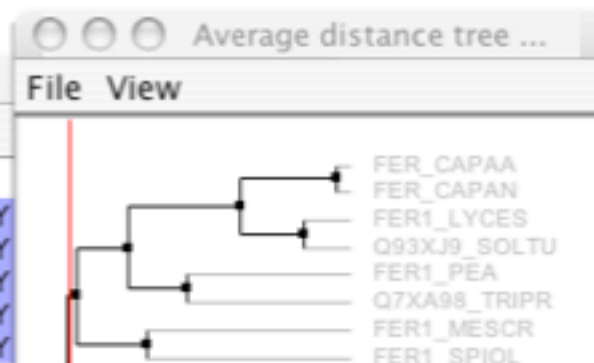
Fe

9 3 6 3 9 9 6 4 5 9 9 9 0 1 0 0 0 3 2 3 2 2

Boundary Structure

Sulphur Contacts

Conservation SCAGKVVSGSVDQSD+SFLDDDQIEAGWVLT



Preferences

Visual Connections Output Editing **DAS Settings**

Nickname	Use Source
uniprot	<input checked="" type="checkbox"/>
dssp	<input type="checkbox"/>
cath	<input type="checkbox"/>
structure	<input type="checkbox"/>
alig_pdb_sp	<input type="checkbox"/>
signalp	<input checked="" type="checkbox"/>
netphos	<input checked="" type="checkbox"/>
netoglyc	<input type="checkbox"/>
tmhmm	<input checked="" type="checkbox"/>

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All Protein Sequence Protein Structure Gene_ID Chromosome

All UniProt PDBresnum Ensembl ZV4 MGI

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