Protein Interaction Data Sources

Ian Donaldson
Biotechnology Centre of Oslo
University of Oslo

MBV-INF 4410/9410
Monday, November 28th, 2011

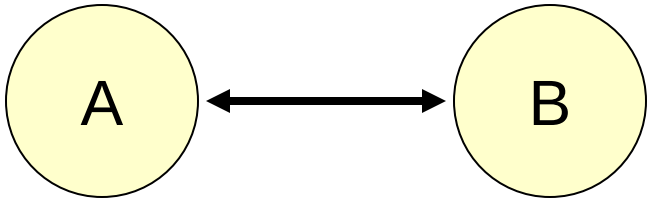
http://donaldson.uio.no/wiki/Protein_Interaction_Resources

http://irefindex.uio.no

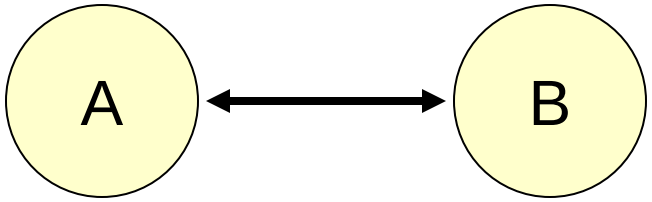
Overview

1. A simple interction record
2. Experimental methods
3. Representation of interactions
4. Interaction databases
5. Identifiers
6. Text mining sources
7. Predicted interaction sources
8. Consolidated databases
9. Visualization tools
10. Applications

A simple interaction record



A simple interaction record

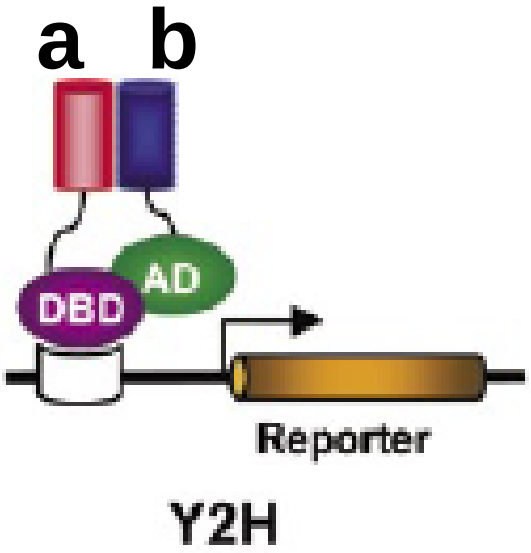


1. Short label
2. Type of molecule
3. Database identifier
4. Origin

5. Short label
6. Type of molecule
7. Database identifier
8. Origin

9. Publication reference

Experimental methods – Yeast Two Hybrid



http://en.wikipedia.org/wiki/Yeast_two-hybrid

Experimental methods
Two Hybrid family

Advantages

- an ”in vivo” binding assay
- easy to automate
- detects binary interactions

Experimental methods
Two Hybrid Family

Limitations

- false positives due to
  - sticky or activating bait or prey
  - overexpression
  - mis-localization (contextual specificity)
  - intermediary proteins

- false negatives due to
  - disruption of interaction by fusion construct
  - absence of intermediary proteins
  - absence of native taxon context

Experimental methods
Affinity purification

- interacting proteins are purified by mea
  of an affinity tag on a ”bait” protein
- proteins are detected via MS
- readout of this experiment type is a list of proteins that somehow interact with the bait protein
- note this is fundamentally different than readout of the Y2H family of experiments (more later)

Suter 2008, Biotechniques

Experimental methods
Affinity purification family

Limitations

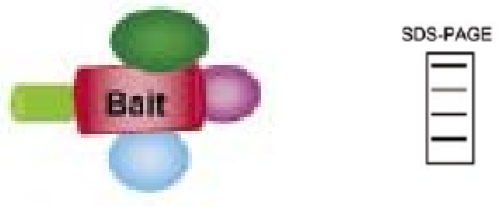
- false positives due to
  - sticky bait or prey
  - mis-identification during MS
  - non-native binding environment

- false negatives due to
  - mis-identification during MS
  - non-native binding environment

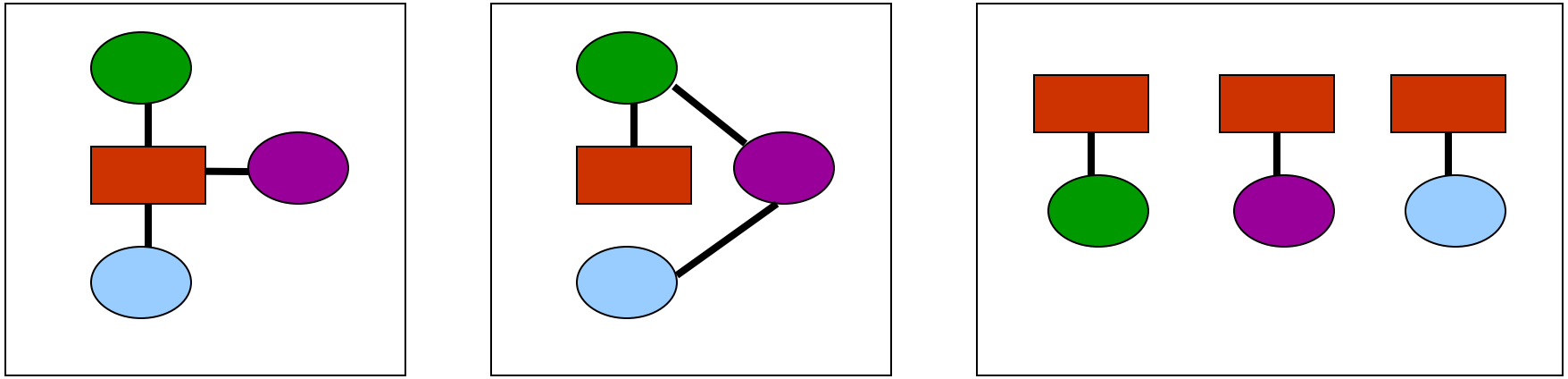
Experimental methods
Affinity purification family

Advantages

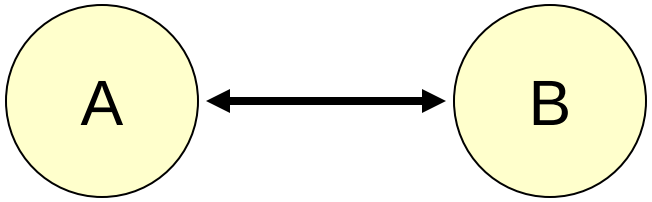
detection of protein complexes but no topology or stoichiometric data



This observation has multiple interpretations:



A simple interaction record



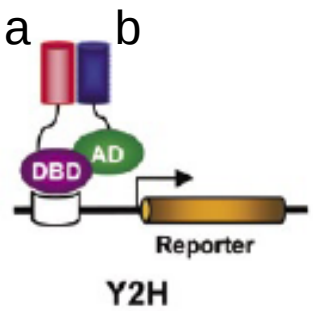
1. Short label
2. Type of molecule
3. Database identifier
4. Origin

5. Short label
6. Type of molecule
7. Database identifier
8. Origin

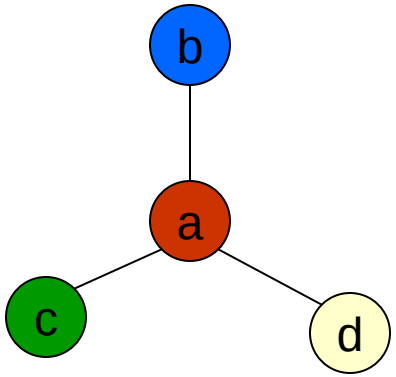
9. Publication reference

Representation of interaction data

binary data versus associative data



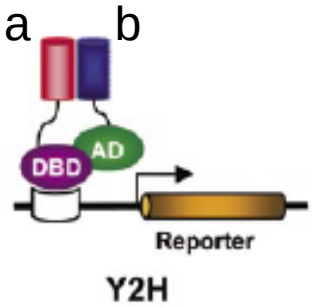
exp	bait	prey
1	a	b
2	a	c
3	a	d



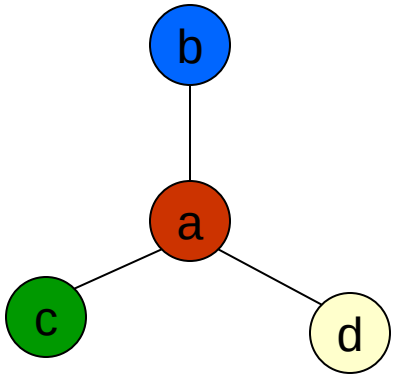
Suter 2008, Biotechniques

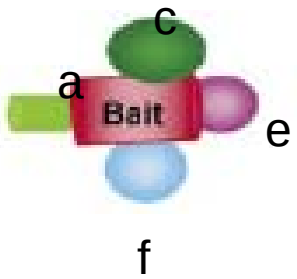
Representation of interaction data

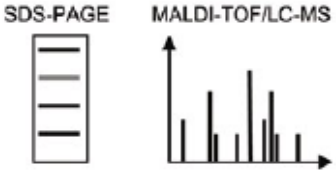
binary data versus associative data

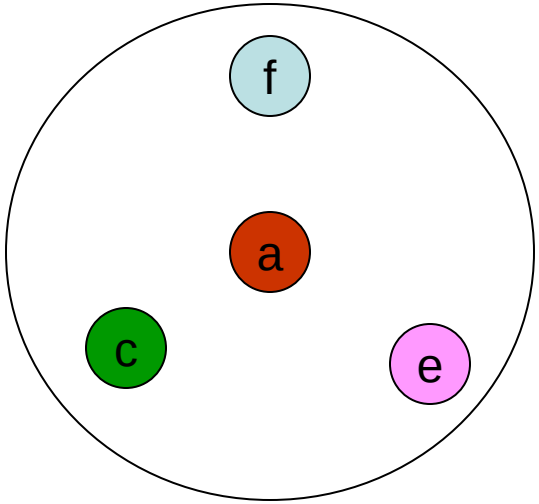


exp	bait	prey
1	a	b
2	a	c
3	a	d





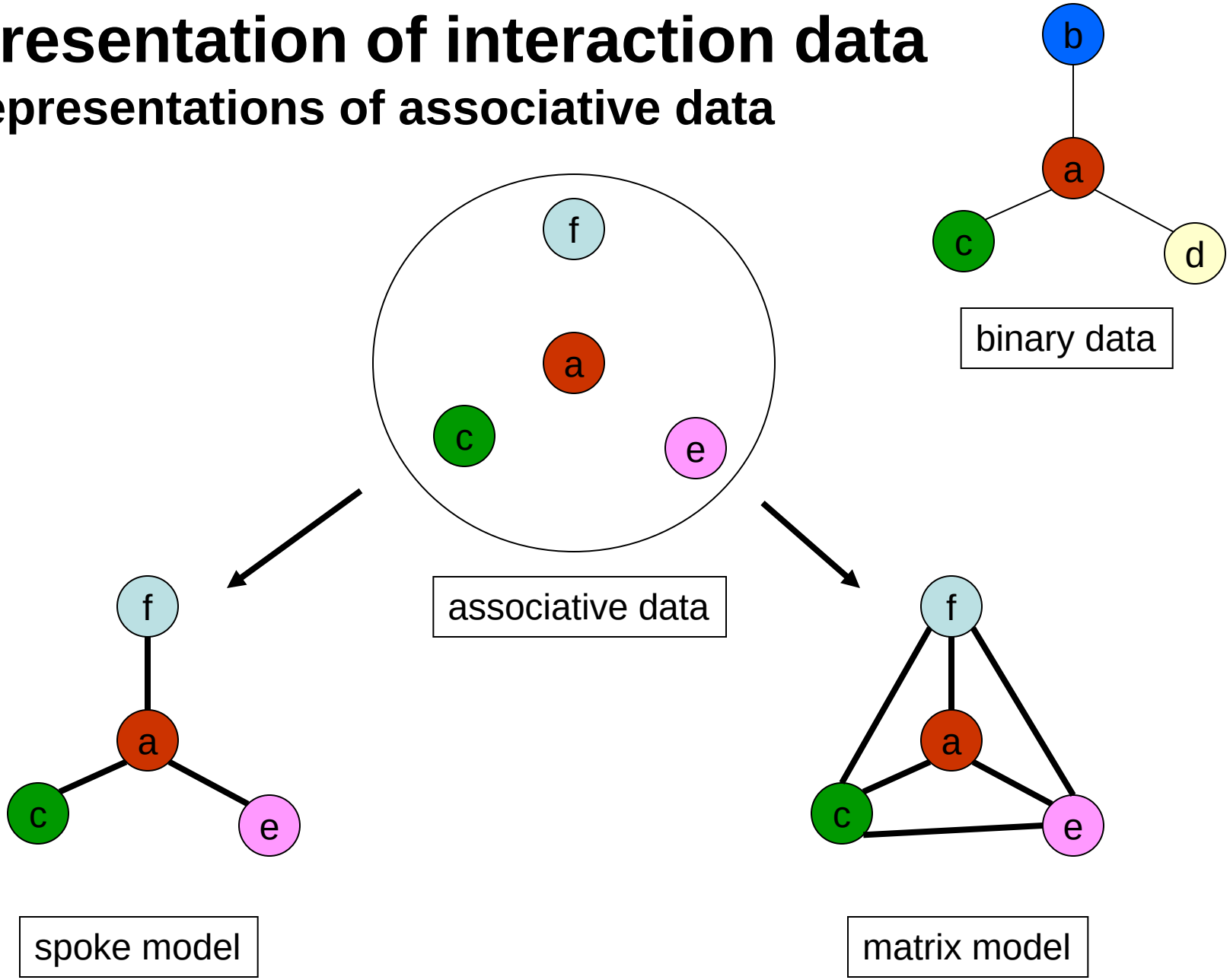




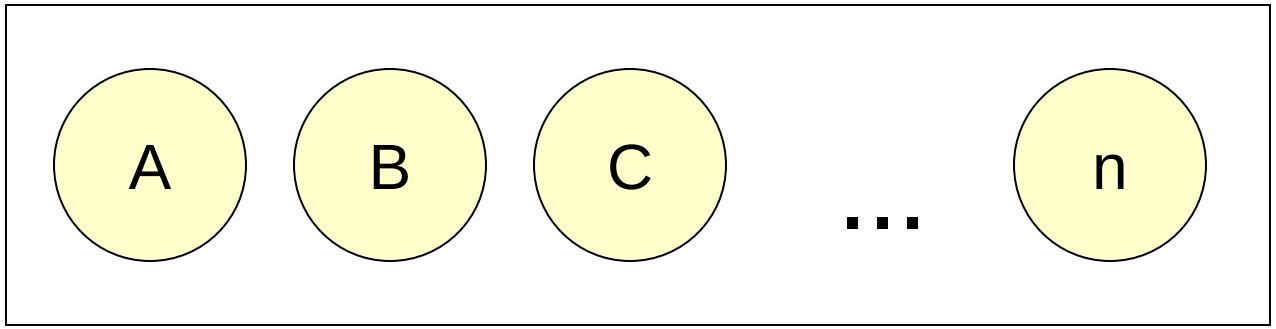
Suter 2008, Biotechniques

Representation of interaction data

misrepresentations of associative data



A simple interaction record



For each interactor

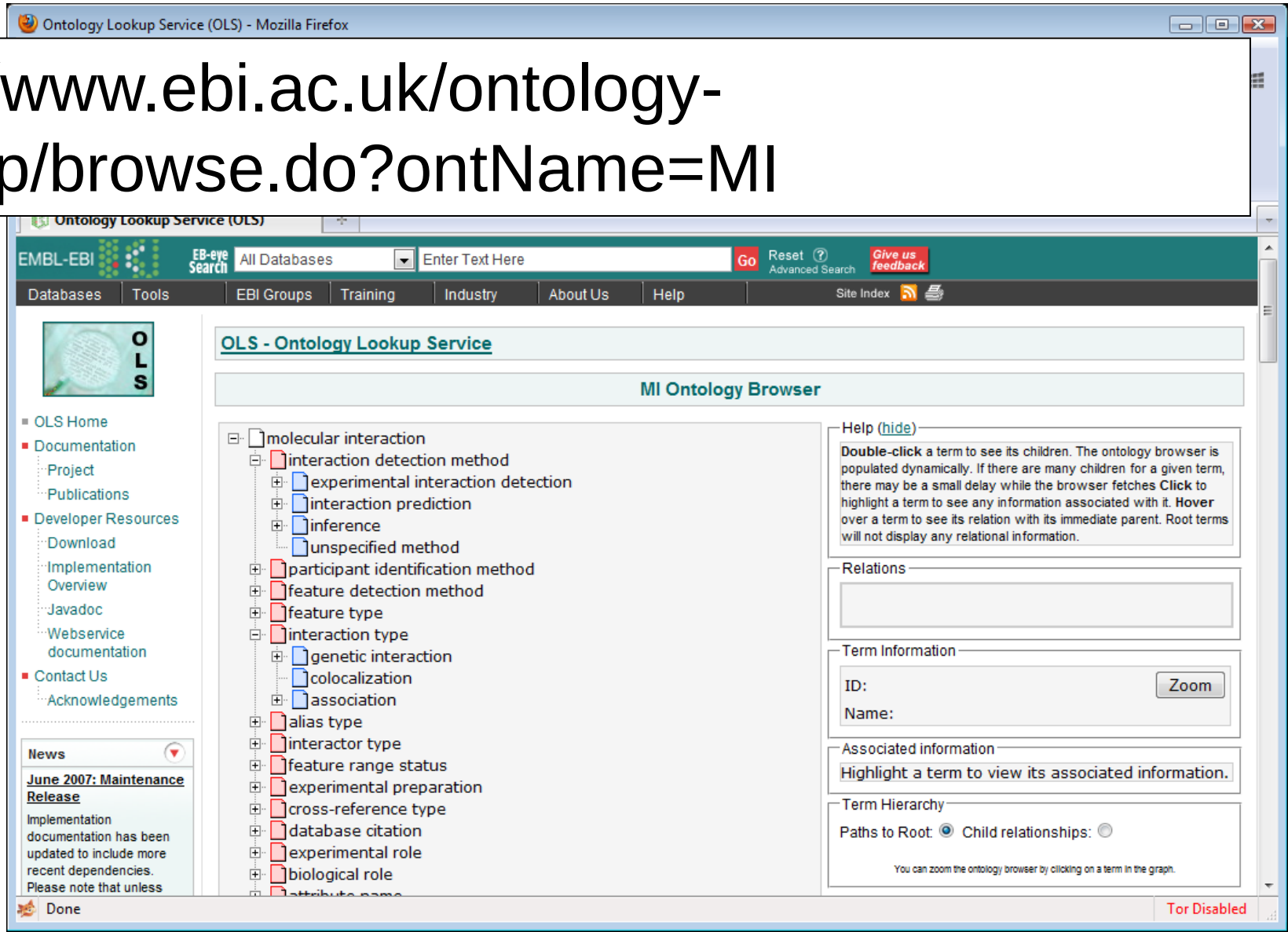
1. Short label
2. Type of molecule
3. Database identifier
4. Origin

For the interaction

5. Publication reference (method)

More about methods and interaction types that they support

http://www.ebi.ac.uk/ontology-lookup/browse.do?ontName=MI



Interaction databases

BIND	inactive
BioGRID	IMEX (Observer)
CORUM	complexes
DIP	IMEX (Archival)
HPRD	human resource
IntAct	IMEX (Archival)
MATRIX	extracellular matrix
MINT	IMEX (Topical)
MPACT	IMEX (Topical) yeast
MPIDB	IMEX (Observer) prokaryotic
MPPI	mammlian
OPHID/I2D	predicted
Many others	

See http://www.pathguide.org/ for URLs

Interaction databases

IMEx
International Molecular Exchange Consortium

IMEx partners exchange data and share curation tasks.

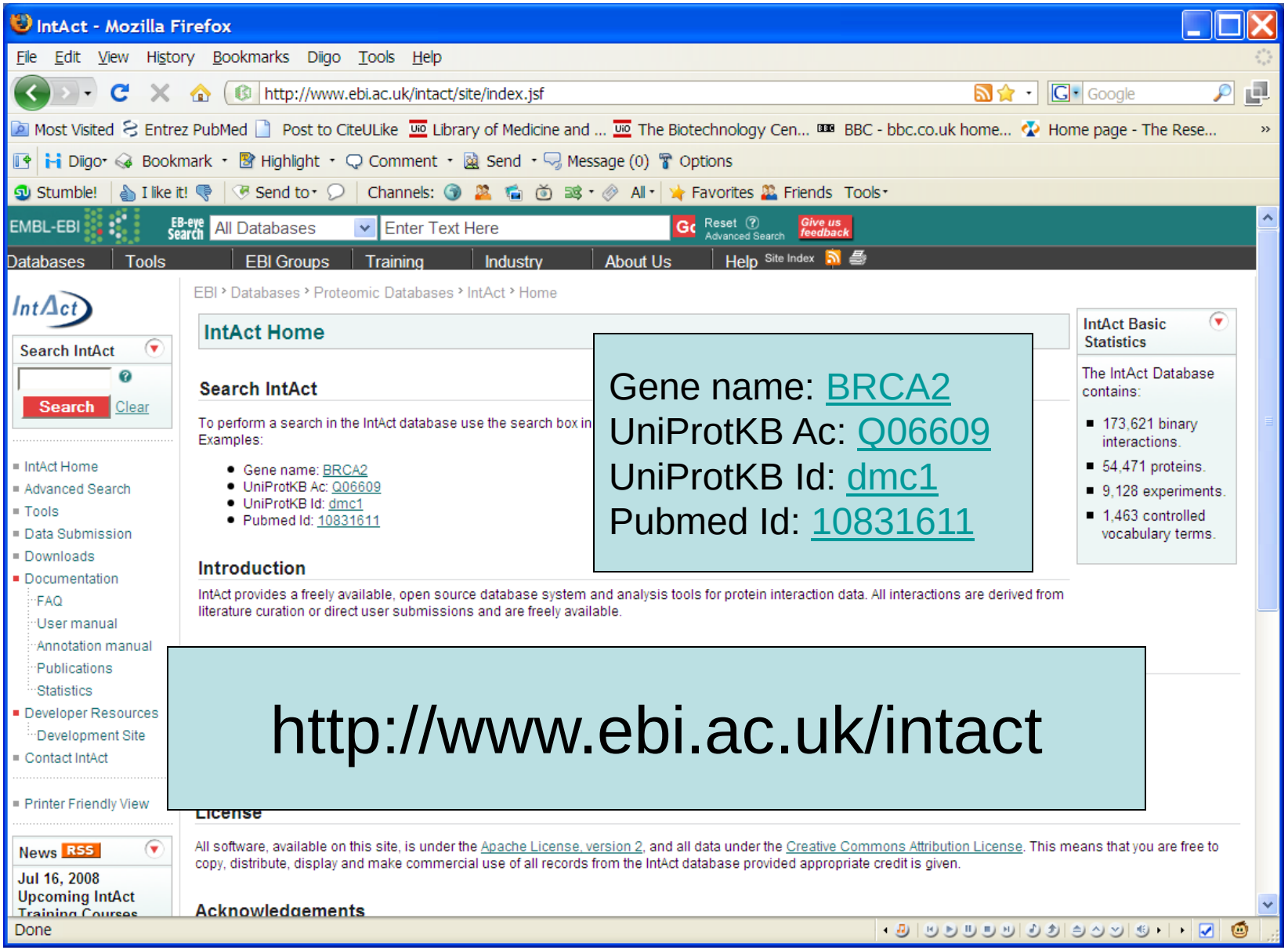
Set standards

They also accept interaction data submissions pre and post publication.

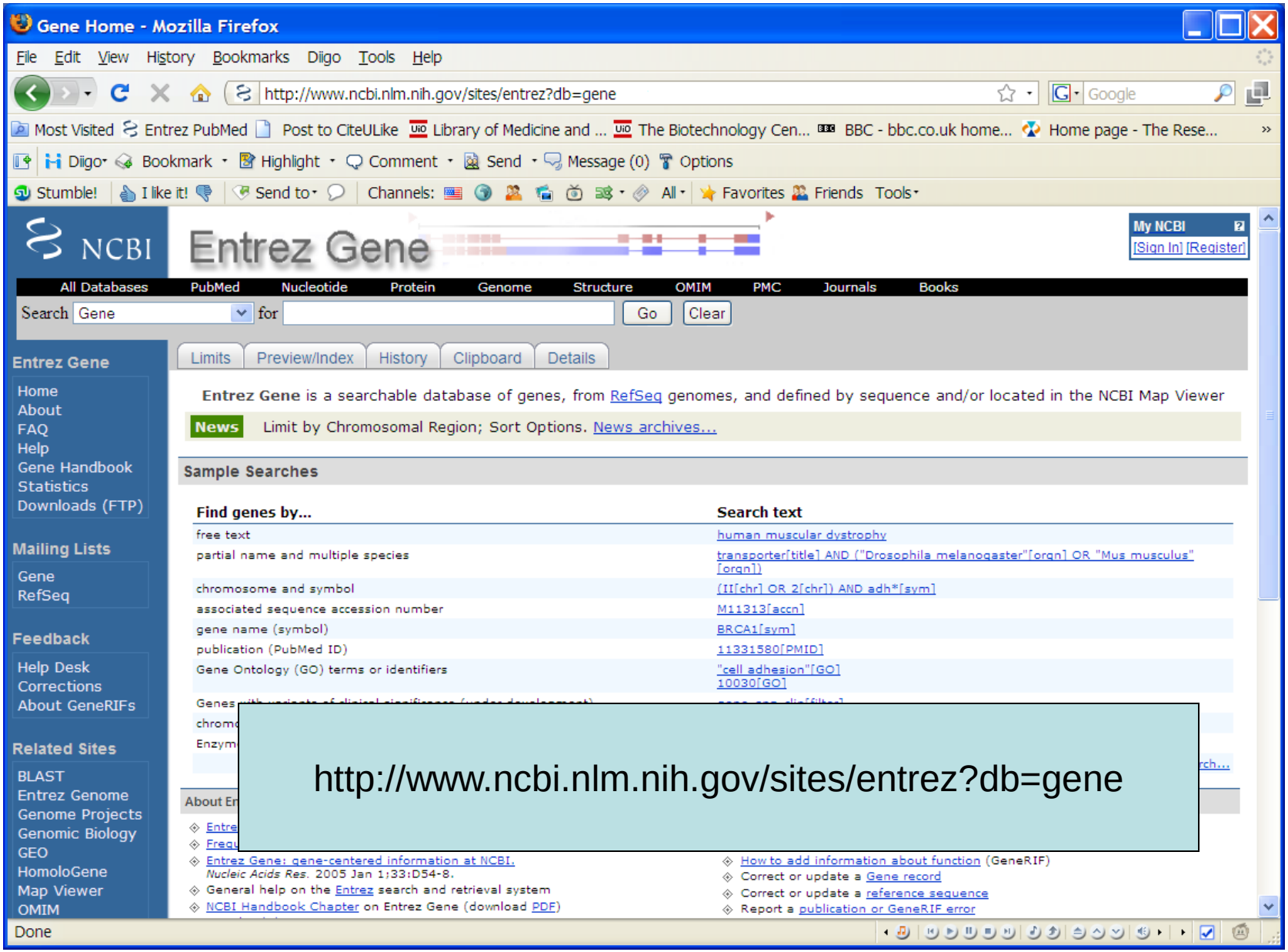
Data consolidation and exchange is an active area of research.

See http://www.imexconsortium.org/

Interaction databases: IntAct



Identifiers: EntrezGene



http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene

Entrez Gene: TNFRSF1A tumor necrosis factor receptor superfamily, member 1A [Homo sapiens] - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene&cmd=Retrieve&dopt=full_report&list_uids=7132

Most Visited | Entrez PubMed | Post to CiteULike | Library of Medicine and ... | The Biotechnology Cen... | BBC - bbc.co.uk home... | Home page - The Rese...

Diigo | Bookmark | Highlight | Comment | Send | Message (0) | Options

Stumble! | I like it! | Send to | Channels: | All | Favorites | Friends | Tools

NCBI Entrez Gene

My NCBI [Sign In] [Register]

All Databases | PubMed | Nucleotide | Protein | Genome | Structure | OMIM | PMC | Journals | Books

Search Gene for 7132 Go Clear

Limits | Preview/Index | History | Clipboard | Details

Display Full Report Show 20 Sort by Relevance Send to

All: 1 | Curre... | ...IP GeneView: 1

GeneID: 7132

1: TNFRSF1... superfamily, member 1A [*Homo sapiens*]

updated 12-Oct-2008

Summary

Official Symbol	TNFRSF1A ... ed by HGNC
Official Full Name	tumor necrosis ... provided by HGNC
Primary source	HGNC:11916
See related	Ensembl:ENSG00000067182; HPRD:01861; MIM:191190
Gene type	protein coding
RefSeq status	REVIEWED
Organism	...
Lineage	...orata; Euteleostomi; Mammalia; Eutheria; ...ini; Hominidae; Homo
Also known as	FPF; p55; p60; TBP1; TNF-R; TNFAR; TNFR1; p55-R; CD120a; TNFR55; TNFR60; TNF-R-I; TNF-R55; MGC19588
Summary	The protein encoded by this gene is a member of the TNF-receptor superfamily. This protein is one of the major receptors for the tumor necrosis factor-alpha. This receptor can activate NF-kappaB, mediate apoptosis, and function as a regulator of inflammation. Antiapoptotic protein BCL2-associated athanogene 4 (BAG4/SODD) and adaptor proteins TRADD and TRAF2

GeneID: 7132

Official Symbol: TNFRSF1A
aka Gene Name

Synonyms: TNF-R-I

Entrez Gene Home

Table Of Contents
- Summary
- Genomic regions, transcripts...
- Genomic context
- Bibliography
- HIV-1 protein interactions
- Interactions
- General gene information
- General protein information
- Reference Sequences
- Related Sequences
- Additional Links

Links Explain
- Order cDNA clone
- Conserved Domains
- Genome
- GEO Profiles
- HomoloGene
- Map Viewer
- Nucleotide
- EST
- OMIM
- PubChem Compound
- PubChem Substance
- Full text in PMC
- Probe

Done

Entrez Gene: TNFRSF1A tumor necrosis factor receptor superfamily, member 1A [Homo sapiens] - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene&cmd=Retrieve&dopt=full_report&list_uids=7132

Most Visited | Entrez PubMed | Post to CiteULike | Library of Medicine and ... | The Biotechnology Cen... | BBC - bbc.co.uk home... | Home page - The Rese...

Diigo | Bookmark | Highlight | Comment | Send | Message (0) | Options

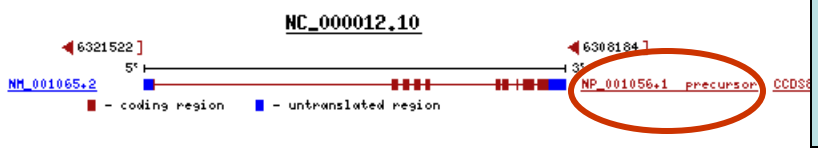
Stumble! | I like it! | Send to | Channels: | All | Favorites | Friends | Tools

have been shown to interact with this receptor, and thus play regulatory roles in the signal transduction mediated by the receptor. Germline mutations of the extracellular domains of this receptor were found to be associated with the autosomal dominant periodic fever syndrome. The impaired receptor clearance is thought to be a mechanism of the disease. [provided by RefSeq]

Genomic regions, transcripts, and products

(minus strand) Go to reference sequence details

Try our new Sequence Viewer

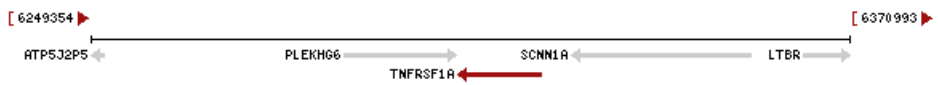


RefSeq Protein Accession: NP_001056

Genomic context

chromosome: 12; Location: 12p13.2

See TNFRSF1A in MapViewer



Bibliography

Related Articles in PubMed

PubMed links

GeneRIFs: Gene References Into Function

What's a GeneRIF?

1. oxidative stress promotes TNFR receptor (TNFR1- and TNFR2) self-interaction and ligand-independent and enhanced ligand-dependent TNF signaling

Probe
Protein
PubMed
PubMed (OMIM)
PubMed (GeneRIF)
SNP
SNP: Genotype
SNP: GeneView
Taxonomy
UniSTS
AceView
CCDS
MGC
ModelMaker
PharmGKB
The registry of TNFRSF1A sequence variants
UniGene

Entrez Gene Info

Feedback

Subscriptions

Done

NCBI Sequence Viewer v2.0 - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_001056.1&dopt=gp

Most Visited | Entrez PubMed | Post to CiteULike | Library of Medicine and ... | The Biotechnology Cen... | BBC - bbc.co.uk home... | Home page - The Rese...

Diigo | Bookmark | Highlight | Comment | Send | Message (0) | Options

Stumble! | I like it! | Send to | Channels: | All | Favorites | Friends | Tools

NCBI Entrez Protein

My NCBI [Sign In] [Register]

PubMed | Nucleotide | Protein | Genome | Structure | PMC | Taxonomy | OMIM | Books

Search Protein for Go Clear

Display GenPept Show 5 Send to

Range: from begin to end Features: SNP CDD HPRD + Refresh

1: NP_001056. Reports tumor necrosis fa...[gi:450757

Conserved Domains, Links

Comment Features Sequence

```
LOCUS       NP_001056                455 aa
DEFINITION  tumor necrosis factor receptor 1 precursor [Homo sapiens]
ACCESSION   NP_001056
VERSION     NP_001056.1  GI:4507575
DBSOURCE    REFSEQ: accession NM_001065.2
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria
            Catarrhini; Homini
REFERENCE   1  (residues 1 to
  AUTHORS   Menon,R., Velez,D.
            Williams,S.M.
  TITLE     Genetic regulation
            receptor concentrations affected by race and preterm birth
  JOURNAL   Hum. Genet. 124 (3), 243-253 (2008)
   PUBMED   18807256
  REMARK    GeneRIF: Observational study of gene-disease association and
            gene-environment interaction. (HuGE Navigator)
REFERENCE   2  (residues 1 to 455)
  AUTHORS   Hosgood,H.D. III, Menashe,I., Shen,M., Yeager,M., Yuenger,J.,
            Rajaraman,P., He,X., Chatterjee,N., Caporaso,N.E., Zhu,Y.,
```

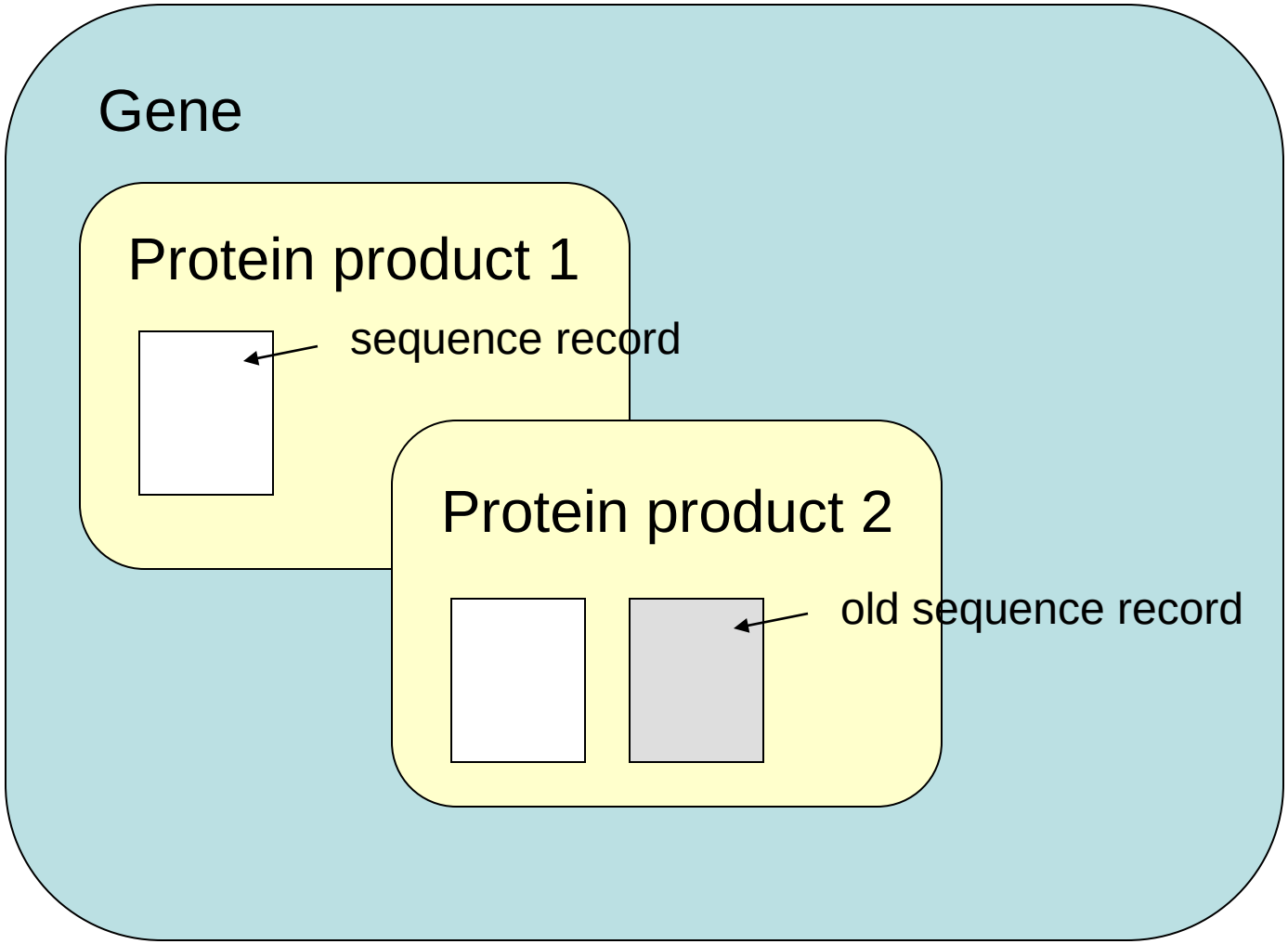
RefSeq Protein Accession: NP_001056

GenInfo Identifier: 4507575

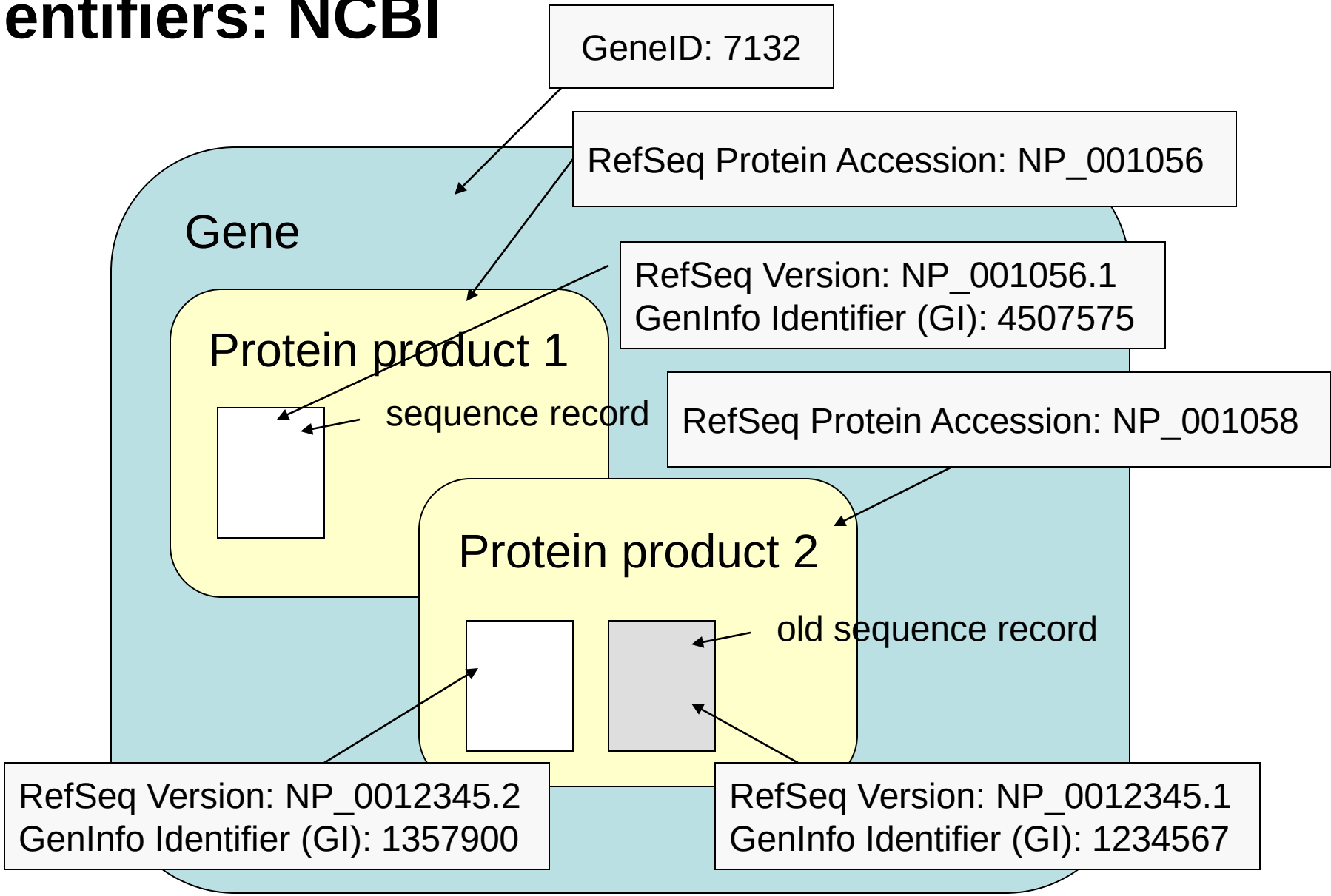
RefSeq Version: NP_001056.1

Done

Identifiers: NCBI



Identifiers: NCBI



Identifiers: UniProtKB

http://www.uniprot.org/

UniProt - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

http://www.uniprot.org/

Most Visited Entrez PubMed Post to CiteULike Library of Medicine and ... The Biotechnology Cen... BBC - bbc.co.uk home... Home page - The Rese...

Diigo Bookmark Highlight Comment Send Message (0) Options

Stumble! I like it! Send to Channels: All Favorites Friends Tools

UniProt

Downloads · Contact · Documentation/Help

Search in: Protein Knowledgebase (UniProtKB)

Query: Search Clear Fields »

Search | Blast | Align | Retrieve | ID Mapping

WELCOME

The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

What we provide

UniProtKB	Protein knowledgebase, consists of two sections: Swiss-Prot, which is manually annotated and reviewed. TrEMBL, which is automatically annotated and is **not** reviewed.
UniRef	Sequence clusters, used to speed up similarity searches.
UniParc	Sequence archive, used to keep track of sequences and their identifiers.
Supporting data	Literature citations, taxonomy, keywords and more.

NEWS

Release 14.3 – Oct 14, 2008

10th anniversary of the Swiss Institute of Bioinformatics

› Statistics for UniProtKB: Swiss-Prot · TrEMBL
› Forthcoming changes
› News archives

SITE TOUR

Learn how to make best use of the tools and data on this site.

Done

DNA repair protein RAD51 homolog 1 - Homo sapiens (Human) - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

http://www.uniprot.org/uniprot/Q06609

Most Visited Entrez PubMed Post to CiteULike Library of Medicine and ... The Biotechnology Cen... BBC - bbc.co.uk home... Home page - The Rese...

Diigo Bookmark Highlight Comment Send Message (0) Options

Stumble! I like it! Send to Channels: All Favorites Friends Tools

DNA repair protein RAD51... | Entrez Gene: RAD51 RAD51 h...

UniProt › UniProtKB Downloads · Contact · Documentation/Help

Search in: Protein Knowledgebase (UniProtKB) | Query

UniProtKB Entry: RAD51_HUMAN

Reviewed, UniProtKB/Swiss-Prot Q06609 (RAD51_HUMAN)

Last modified September 23, 2008. Version 100. History

UniProtKB Accession: Q06609

Contribute: Send feedback

Clusters with 100%, 90%, 50% identity | Documents (... DF/XML GFF FASTA

Names and origin · Protein attributes · General annotation (Comments) · Ontologies · Binary interactions · Alternative products · Sequence annotation (Features) · Sequences · References · Cross-references · Entry information · Relevant documents

Names and origin

Hide | Top

Protein names	*Recommended name:* **DNA repair protein** Short name=hRAD51 Short name=HsRAD51
Gene names	Name: **RAD51** Synonyms: RAD51A, RECA
Organism	**Homo sapiens (Human)**
Taxonomic identifier	9606 [NCBI]
Taxonomic lineage	Eukaryota › Me... ni › Mammalia › Eutheria › Euarchontoglires › Primates › Haplorrhini › Catarrhini › Hominidae › Homo

Gene Name: RAD51

Synonyms: RAD51A

Taxon id: 9606 (human)

Done

DNA repair protein RAD51 homolog 1 - Homo sapiens (Human) - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

http://www.uniprot.org/uniprot/Q06609

Most Visited Entrez PubMed Post to CiteULike Library of Medicine and ... The Biotechnology Cen... BBC - bbc.co.uk home... Home page - The Rese... Wikipedia

Diigo Bookmark Highlight Comment Send Message (0) Options

Stumble! I like it! Send to Channels: All Favorites Friends Tools

Binary interactions

Hide | Top

Binary interactions from IntAct

With	Entry			
itself		1	EBI-297202,EBI-297202	
BRCA2	P51587	7	EBI-297202,EBI-79792	
RAD51AP1	Q96B01-2	2	EBI-297202,EBI-1178743	
RAD51AP1	Q96B01-3	3	EBI-297202,EBI-1178748	
rhp51	P36601	2	EBI-297202,EBI-926960	From a different organism.
TP53	P04637	1	EBI-297202,EBI-366083	

Alternative products

Hide | Top

This entry describes **2** isoforms produced by **alternative splicing**. [Align] [Select]

Isoform 1 (identifier: **Q06609-1**)

This isoform has been chos *try refers to it. This is also the sequence that appears in the downloadable versions of the entry.*

Isoform identifiers

Isoform 2 (identifier: **Q06609-2**)

The sequence of this isoform differs from the canonical sequence as follows:
77-173: Missing.

Notes: No experimental confirmation available.

Find: dmc1 Next Previous Highlight all Match case Reached end of page, continued from top

Done

DNA repair protein RAD51 homolog 1 - Homo sapiens (Human) - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

http://www.uniprot.org/uniprot/Q06609

Most Visited | Entrez PubMed | Post to CiteULike | Library of Medicine and ... | The Biotechnology Cen... | BBC - bbc.co.uk home... | Home page - The Rese... | Wikipedia

Diigo | Bookmark | Highlight | Comment | Send | Message (0) | Options

Stumble! | I like it! | Send to | Channels: | All | Favorites | Friends | Tools

Other Resources

SOURCE	Search...
ProtoNet	Search...

Entry information

Hide | Top

Entry name	RAD51_HUMAN
Accession	Primary (citable) accession number: **Q06609** Secondary accession number(s): Q6FHX9, Q9BV60
Entry history	Integrated into UniProtKB/Swiss-Prot: June 1, 1994 Last sequence update: June 1, 19 Last modified: Septembe This is version 100 of the entry and version 1 of the sequence. [Complete history]
Entry status	Reviewed (UniProtKB/Swiss-Prot)
Annotation project	HPI (Human Proteome Initiative)

Secondary (retired) identifiers

Relevant documents

Hide | Top

Human chromosome 15
Human chromosome 15: entries, gene names and cross-references to MIM

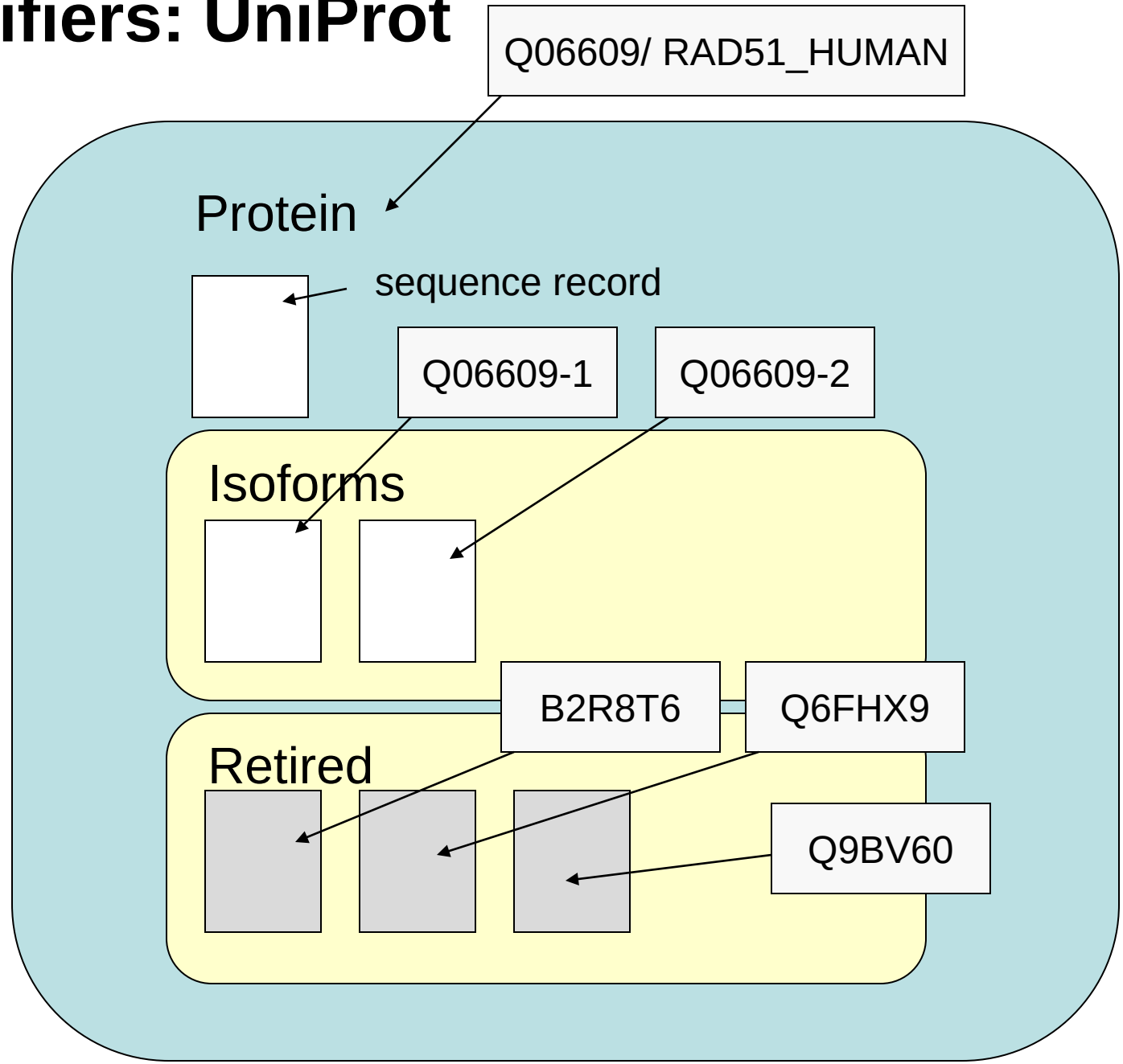
Human entries with polymorphisms or disease mutations
List of human entries with polymorphisms or disease mutations

Human polymorphisms and disease mutations
Index of human polymorphisms and disease mutations

Find: dmc1 | Next | Previous | Highlight all | Match case | Reached end of page, continued from top

Done

Identifiers: UniProt



For your information

Common Identifiers

Gene

Ensembl ENSG00000139618
Entrez Gene 675
Unigene Hs.34012

RNA transcript

GenBank BC026160.1
RefSeq NM_000059
Ensembl ENST00000380152

Protein

Ensembl ENSP00000369497
RefSeq NP_000050.2
UniProt BRCA2_HUMAN or A1YBP1_HUMAN
IPI IPI00412408.1
EMBL AF309413
PDB 1MIU

Species-specific

HUGO HGNC BRCA2
MGI MGI:109337
RGD 2219
ZFIN ZDB-GENE-060510-3
FlyBase CG9097
WormBase WBGene00002299 or ZK1067.1
SGD S000002187 or YDL029W

Annotations

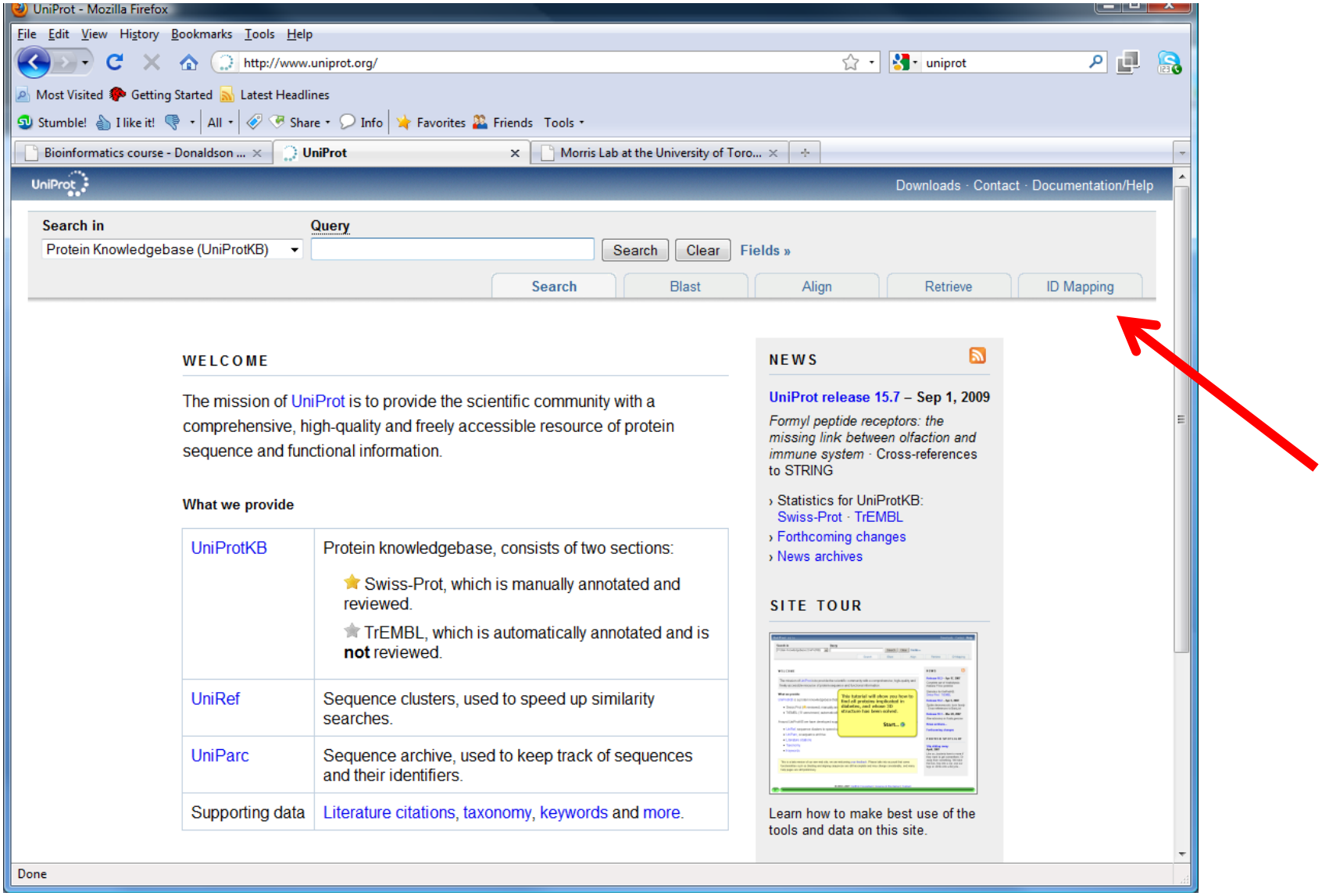
InterPro IPR015252
OMIM 600185
Pfam PF09104
Gene Ontology GO:0000724
SNPs rs28897757

Experimental Platform

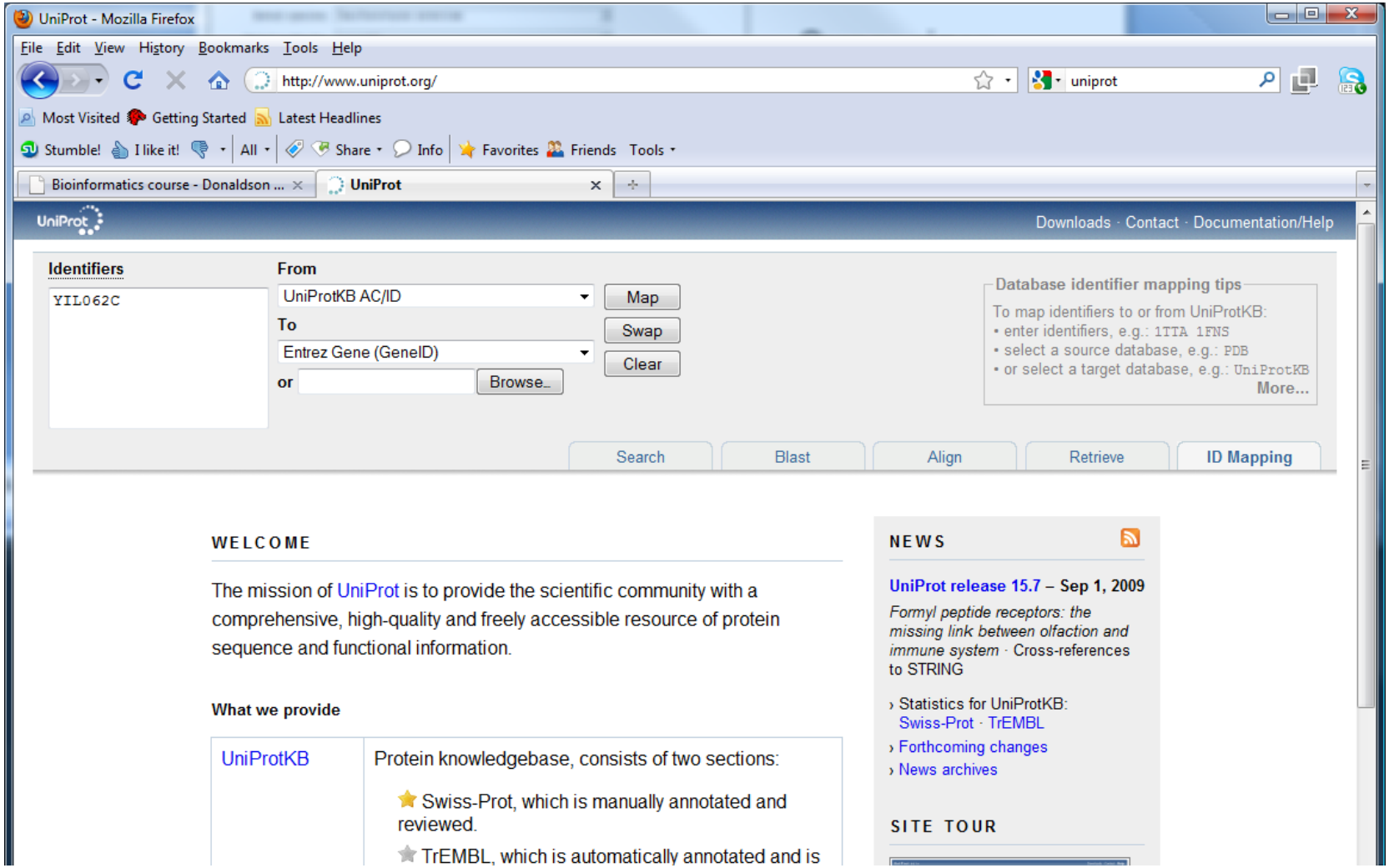
Affymetrix 208368_3p_s_at
Agilent A_23_P99452
CodeLink GE60169
Illumina GI_4502450-S

Red = Recommended

UniProt ID Mapping Service

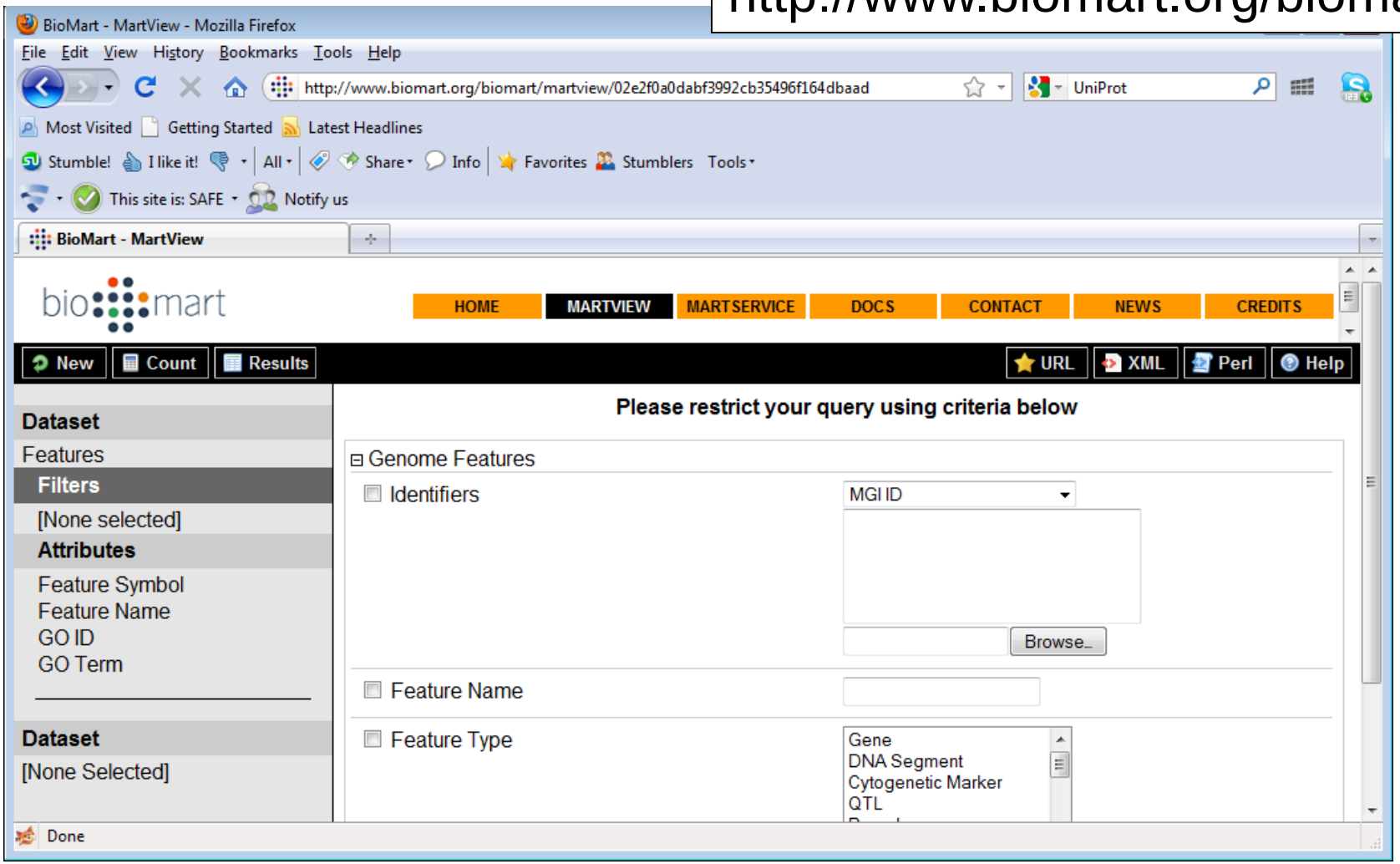


UniProt ID Mapping Service



Ensembl BioMart

http://www.biomart.org/biomart



ID Mapping Challenges

- Avoid errors: map IDs correctly
- Gene name ambiguity – not a good ID
  - e.g. FLJ92943, LFS1, TRP53, p53
  - Better to use the standard gene symbol: TP53
- Excel error-introduction
  - OCT4 is changed to October-4
- Problems reaching 100% coverage
  - E.g. due to version issues
  - Use multiple sources to increase coverage

Zeeberg BR et al. Mistaken identifiers: gene name errors can be introduced inadvertently when using Excel in bioinformatics BMC Bioinformatics. 2004 Jun 23;5:80

ID Mapping Challenges

- Spot-test any ID mapping service you use.
- Check samples from first, last and middle of your list of identifiers to be converted.
- Ask for help if you are uncertain.

Identifiers: Why can’t I find my protein

Are you using a sequence record identifier?

Is the identifier retired?

Are you using the identifier for the correct organism?

Have you tried searching for identifiers for all products of the gene?

Try different identifier systems (Entrez Gene, UniProt)

Remember that only 10% to 50% of all proteins have interaction information.

You always have recourse to text-mining and predicted interactions.

Overview

1. A simple interction record
2. Experimental methods
3. Representation of interactions
4. Interaction databases
5. Identifiers
6. Text mining sources
7. Predicted interaction sources
8. Consolidated databases
9. Visualization tools
10. Applications

Text mining resources

Most are based on co-ocurrence of gene name mentions.

Start at http://zope.bioinfo.cnio.es/bionlp_tools

iHOP	http://www.ihop-net.org/UniPub/iHOP/
EBIMed	http://www.ebi.ac.uk/Rebholz-srv/ebimed/index.jsp
FACTA	http://text0.mib.man.ac.uk/software/facta/
PubGene	http://www.pubgene.org/
InfoPubMed	https://www-tsujii.is.s.u-tokyo.ac.jp/info-pubmed/
Chillibot	http://www.chilibot.net/
MedEvi	http://www.ebi.ac.uk/tc-test/textmining/medevi/
FABLE	http://fable.chop.edu/overview.jsp
BCMS	http://bcms.bioinfo.cnio.es/
BioText	http://biosearch.berkeley.edu/

Text mining resources: iHOP

iHOP - Information Hyperlinked over Proteins - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

http://www.ihop-net.org/UniPub/iHOP/index.html?field=all&search=RAD51&organism_id=0

Most Visited | Entrez PubMed | Post to CiteULike | Library of Medicine and ... | The Biotechnology Cen... | BBC - bbc.co.uk home... | Home page - The Rese... | Wikipedia

Diigo | Bookmark | Highlight | Comment | Send | Message (0) | Options

Stumble! | I like it! | Send to | Channels: | All | Favorites | Friends | Tools

iHOP - Inf... | EBIMed | FACTA | PubGene - Find... | Chilibot: finding... | MedEvi - a per... | FABLE - Overvi... | BioCreative Met... | BioText Search ...

iHOP

information hyperlinked over proteins

Search Gene

RAD51

Gene Model Developer's Zone

new

How to cite iHOP

Contact

Links

Help

Concept & Implementation by Robert Hoffmann

Symbol	Name	Synonym/ DB-reference	Organism	Results
	Life cycles of successful genes			
RAD51	**RAD51** homolog (RecA homolog, E. coli) (S. cerevisiae)		Homo sapiens	
Rad51	**RAD51** homolog (S. cerevisiae)		Mus musculus	
RAD51	Strand exchange protein, forms a helical filament with DNA that searches for ...		Saccharomyces cerevisiae	
rad51	**RAD51** homolog (RecA homolog, E. coli) (S. cerevisiae)		Danio rerio	
RAD51	Le**RAD51**		Lycopersicon esculentum	
rad51	**rad51** protein		Xenopus laevis	
RAD51	**RAD51** homolog (RecA homolog, E. coli) (S. cerevisiae)		Gallus gallus	
RAD51	**RAD51** homolog (RecA homolog, E. coli) (S. cerevisiae)		Canis familiaris	
rad51	DNA repair protein **Rad51** homolog		Guillardia theta	
rad51	DNA repair protein		Giardia lamblia ATCC 50803	
RAD51L1	**RAD51**-like 1 (S. cerevisiae)		Homo sapiens	
RAD51C	**RAD51** homolog C (S. cerevisiae)		Homo sapiens	
RAD51L3	**RAD51**-like 3 (S. cerevisiae)		Homo sapiens	
RAD51AP1	**RAD51** associated protein 1		Homo sapiens	
Rad51l3	**RAD51**-like 3 (S. cerevisiae)		Mus musculus	

Interaction information for this gene.

Find: dmc1 | Next | Previous | Highlight all | Match case | Reached end of page, continued from top

javascript:if(window.name=='') { window.location.href='./nil'; } else { doaction('IHOP', 91604, 1); }

iHOP - Information Hyperlinked over Proteins [RAD51] - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

http://www.ihop-net.org/UniPub/iHOP/gs/91604.html?IN=1

Most Visited | Entrez PubMed | Post to CiteULike | Library of Medicine and ... | The Biotechnology Cen... | BBC - bbc.co.uk home... | Home page - The Rese... | Wikipedia

Diigo | Bookmark | Highlight | Comment | Send | Message (0) | Options

Stumble! | I like it! | Send to | Channels: | All | Favorites | Friends | Tools

iHOP - Inf... | EBIMed | FACTA | PubGene - Find... | Chilibot: finding... | MedEvi - a per... | FABLE - Overvi... | BioCreative Met... | BioText Search ...

iHOP

information hyperlinked over proteins

Search Gene

Show overview new

Find in this Page

Filter and options

Gene Model

Developer's Zone new

Help

Concept & Implementation by Robert Hoffmann

WARNING: Please keep in mind that gene detection is done automatically and can exhibit a certain error. Read more about synonym ambiguity and the iHOP confidence value.

Find in this Page

Found in this page: interacts (**21**)

(Click here to show sentences in the default order)

Sentences in this view contain interactions of RAD51 - Interaction Information is available whenever you see this symbol - Read more.

For a summary overview of the information in this page click here. new

Show all

Order by relevance

The results provide insight into why mutation in just one of the eight BRC repeats would affect the way that BRCA2 protein **interacts** with the RAD51 filament. [2005]

The RAD51 recombinase **interacts** directly with the breast cancer-**associated** tumour suppressor BRCA2, an interaction that is required for normal recombination proficiency, radiation resistance and genome stability. [2003]

It is known that BRCA2 **interacts** directly with RAD51 through a series of degenerative motifs known as the BRC repeats. [2004]

The breast cancer susceptibility gene BRCA2 **encodes** a critical accessory protein that **interacts** with the RAD51 recombinase and this interaction fluctuates during the cell cycle. [2007]

BRCA2 protein **interacts** directly with the RAD51 recombinase and regulates recombination-mediated DSB repair, accounting for the high levels of spontaneous chromosomal aberrations seen in BRCA2-defective cells. [2007]

Whereas BRCA2 **interacts** directly with and **regulates** RAD51, the role of BRCA1 in this process is unclear. [2005]

RAD51 is an important component of double-stranded DNA-repair mechanisms that **interacts** with both BRCA1 and BRCA2 . [2007]

Previous data report that wild-type p53 **suppresses** homologous recombination and physically **interacts** with Rad51. [2006]

p53 **interacts** with hRAD51 and hRAD54, and directly modulates homologous recombination. [2003]

Previously we reported that HsRad51 **interacts** with XRCC3, and Rad51C interacts with XRCC3, Rad51B, and HsRad51

Find: dmc1 | Next | Previous | Highlight all | Match case | Reached end of page, continued from top

Done

Text mining resources: PubGene

Network based on co-occurrence in article for the "RAD51" Gene and Proteins in Homo sapiens - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

http://www.pubgene.org/

Most Visited Entrez PubMed Post to CiteULike Library of Medicine and ... The Biotechnology Cen... BBC - bbc.co.uk home... Home page - The Rese... Wikipedia Google Translate

Diigo Bookmark Highlight Comment Send Message (0) Options

Stumble! I like it! Send to Channels: All Favorites Friends Tools

PubGene - Find ... | Chilibot: finding ... | MedEvi - a perm... | FABLE - Overview | BioCreative Met... | BioText Search ... | RAD51 - Google... | RAD51 - Google... | Network base...

PubGene Beta

FAQ
Users Guide
Demo Tutorials
Feedback

Bio Networks | Bio Associations | Sequence Homology | My Workspace Login

Browse literature or sequence neighbours.

Organism: Homo sapiens — Select one or "all organisms"

Gene / Protein *: RAD51 — Terms separated by comma, eg. *BRCA1*, *LEP*

and/or

Biological term: One term, eg. *Alzheimer Disease*. Supported categories

Network displays genes/proteins important for the biological term

Submit | Advanced Options | Network Parameters

Network based on co-occurrence in article for the "RAD51" Gene and Proteins in Homo sapiens

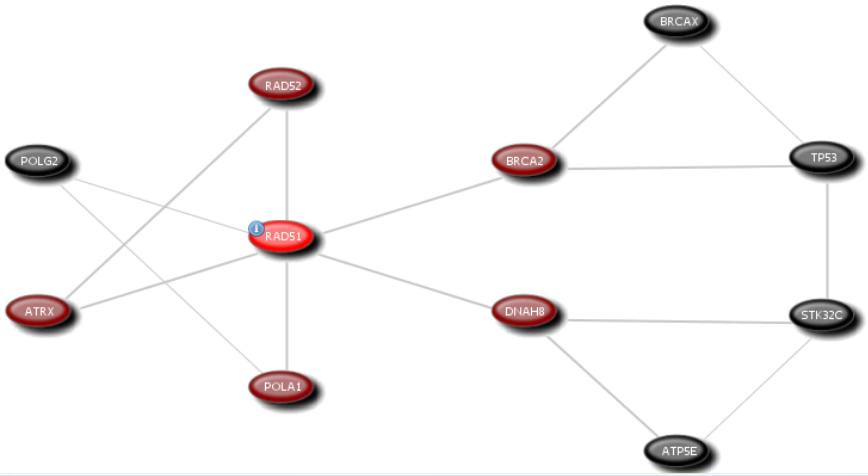
Send selected terms to Choose PubGene Tool — Legend

Information about 'RAD51'

Key information | Related terms

Property	Value
Term	RAD51
Name	RAD51 homolog (Re...
Organi...	Homo sapiens
Article ...	4905
Term T...	PubGene Gene/Prot...
Externa...	EG
Chrom...	
Alt. Sym...	BRCC5
Alt. Sym...	HRAD51
Alt. Sym...	HsRad51
Alt. Sym...	HsT16930
Alt. Sym...	RAD51A
Alt. Sym...	RECA

Network view | Table view



Find: dmc1 Next Previous Highlight all Match case Reached end of page, continued from top

Applet pubgenegraph.GraphController started

Overview

1. A simple interction record
2. Experimental methods
3. Representation of interactions
4. Interaction databases
5. Identifiers
6. Text mining sources
7. Predicted interaction sources
8. Consolidated databases
9. Visualization tools
10. Applications

Predicted interaction resources

STRING	http://string.embl.de/
OPHID/I2D	http://ophid.utoronto.ca/ophidv2.201/
FunCoup	http://FunCoup.sbc.su.se

Finding interaction information

The take home message:

There is no single place to collect interaction information.

Users are placed in a ”go-fish” position and are responsible for distinguishing and sorting through multilple data sources.

There are a few reources that are focusing on providing an integrated data resource...

Overview

1. A simple interction record
2. Experimental methods
3. Representation of interactions
4. Interaction databases
5. Identifiers
6. Text mining sources
7. Predicted interaction sources
8. Consolidated databases
9. Visualization tools
10. Applications

Consolidated databases

APID2NET	http://bioinfow.dep.usal.es/apid/apid2net.html
Pathway Commons	http://www.pathwaycommons.org/pc/
MiMI	http://mimi.ncibi.org/MimiWeb/main-page.jsp
iRefIndex	http://irefindex.uio.no

Finding interaction information

The take home message:

There is no single place to collect interaction information.

Users are placed in a ”go-fish” position and are responsible for distinguishing and sorting through multilple data sources.

There are a few reources that are focusing on providing an integrated data resource...

Overview

1. A simple interction record
2. Experimental methods
3. Representation of interactions
4. Interaction databases
5. Identifiers
6. Text mining sources
7. Predicted interaction sources
8. Consolidated databases
9. Visualization tools
10. Applications

Visualization Tools

Cytoscape http://www.cytoscape.org/
VisAnt http://visant.bu.edu/

There are over 30 visualization tools listed in a recent review

Suderman M, Hallett M: Tools for visually exploring biological networks. *Bioinformatics* 2007, 23(20):2651-2659.

Cytoscape will be covered in a following talk.

Conclusions

Interaction data is an important bioinformatics data source.

Interaction detection techniques have evolved past the simple Y2H and coimmpunoprecipitation methods.

Finding data is still a non-trivial task.

There is no de facto source of data and users are faced with doing their own collection and curation.

Data integration and accessibility is an ongoing area of research.