

# Protein Interaction Data Sources

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University of Oslo



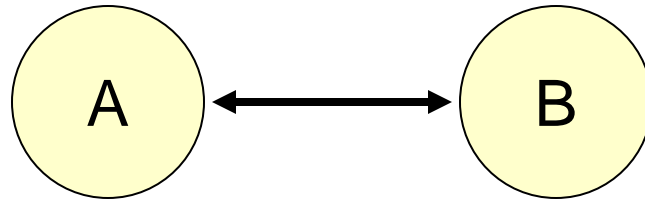
MBV-INF 4410  
Tuesday, September 15th, 2009

[http://donaldson.uio.no/wiki/Protein\\_Interaction\\_Resources](http://donaldson.uio.no/wiki/Protein_Interaction_Resources)  
<http://irefindex.uio.no>

# Overview

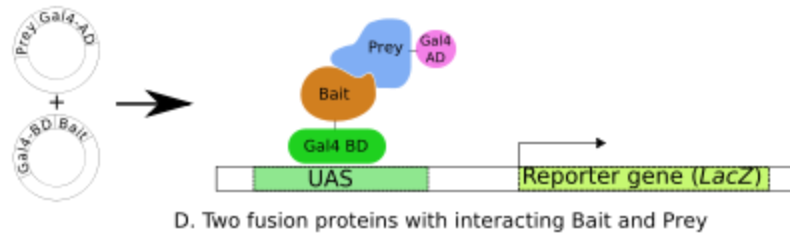
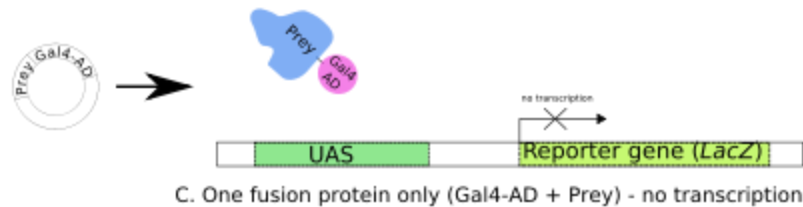
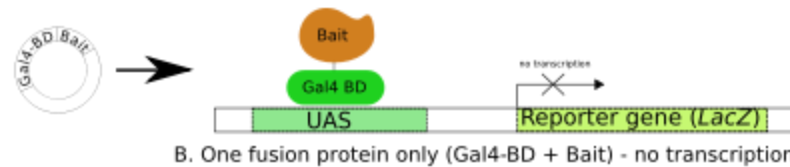
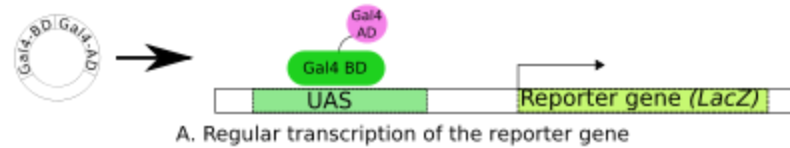
1. A simple interaction record
2. Experimental methods
3. Representation of interactions
4. Interaction databases
5. Identifiers
6. Text mining sources
7. Predicted interaction sources
8. Consolidated databases
9. Visualization tools
10. Applications

# A simple interaction record



- |                          |                        |
|--------------------------|------------------------|
| 1. Short label           | 5. Short label         |
| 2. Type of molecule      | 6. Type of molecule    |
| 3. Database identifier   | 7. Database identifier |
| 4. Origin                | 8. Origin              |
| 9. Publication reference |                        |

# Experimental methods – Yeast Two Hybrid



# Experimental methods – Yeast Two Hybrid

## Advantages

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

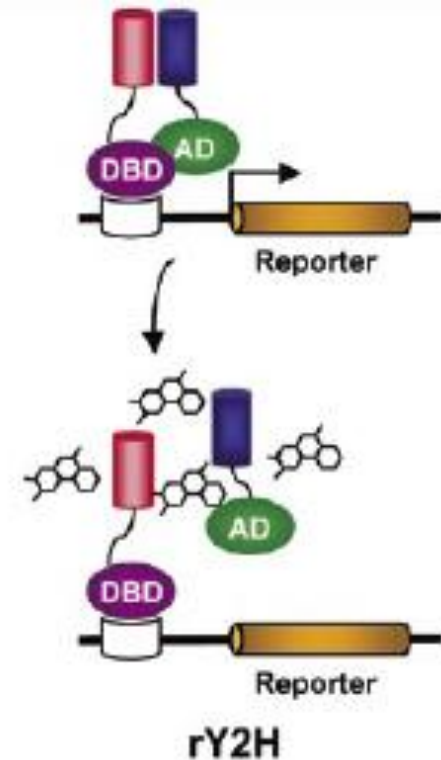
# Experimental methods – Yeast Two Hybrid

## 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

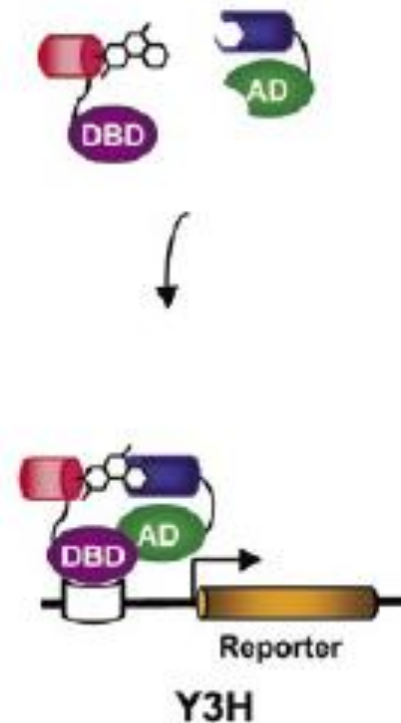
# Experimental methods – reverse Two Hybrid

- screens for small molecules that can disrupt an interaction
- uses a counter-selective strategy



# Experimental methods – Yeast 3 Hybrid

- screens for small molecules or other components that mediate an interaction

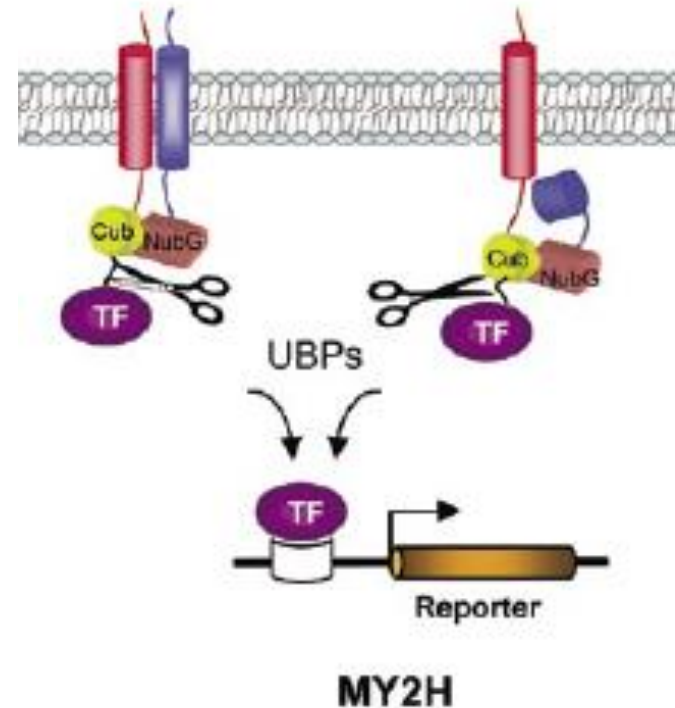




# Experimental methods – membrane Yeast Two-Hybrid (mY2H)

- screens for proteins that interact within or near the membrane
- nearly one third of all proteins are integral membrane proteins not amenable to Y2H

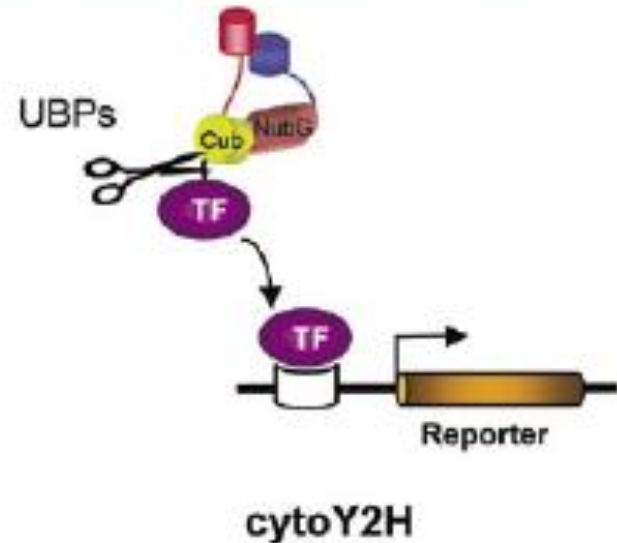
Cub: C-terminus of Ubiquitin  
Nub: N-terminus of Ubiquitin



# Experimental methods – cytosolic Yeast Two-Hybrid (cY2H)

- screens for proteins that interact within cytosol
- alternative for studying proteins in proper context
- alternative for studying proteins that may self activate in Y2H

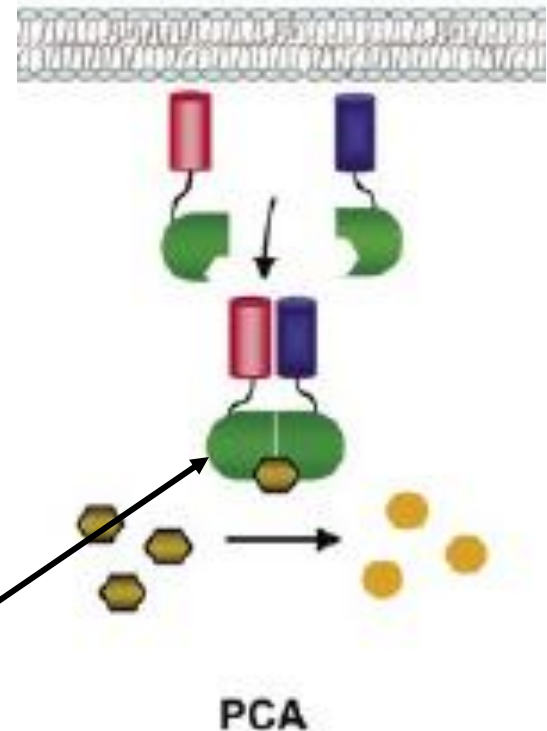
Cub: C-terminus of Ubiquitin  
Nub: N-terminus of Ubiquitin



# Experimental methods – PCA

## Protein Complementation assay

- based on reconstitution of some protein activity
- fusion protein design must prevent spontaneous refolding
- independent of transcription based reporter
- alternatives include assays for luminescence or fluorescence
- useful in a variety of organisms
- other variants of this assay are split TEV protease assay

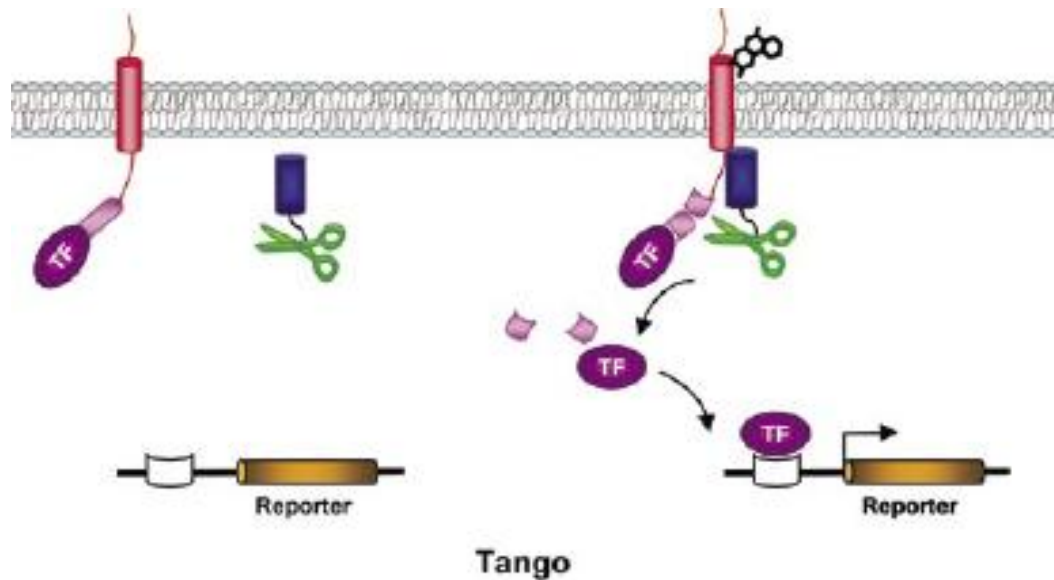


e.g. Reconstituted DHFR activity allows growth on trimethoprim

# Experimental methods – Tango

## State-specific binding assay

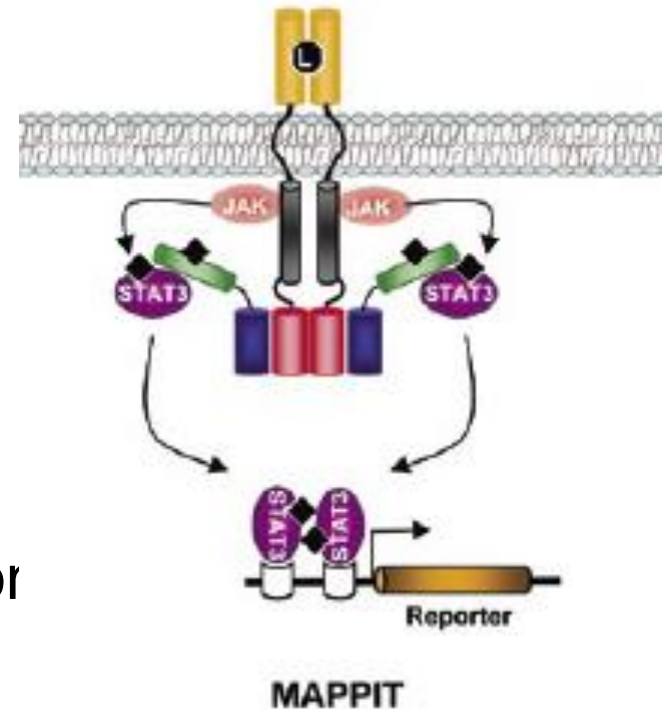
TEV protease is juxtaposed to reporter construct under specific conditions (presence of a ligand).



# Experimental methods – MAPPIT

## Mammalian protein interaction trap

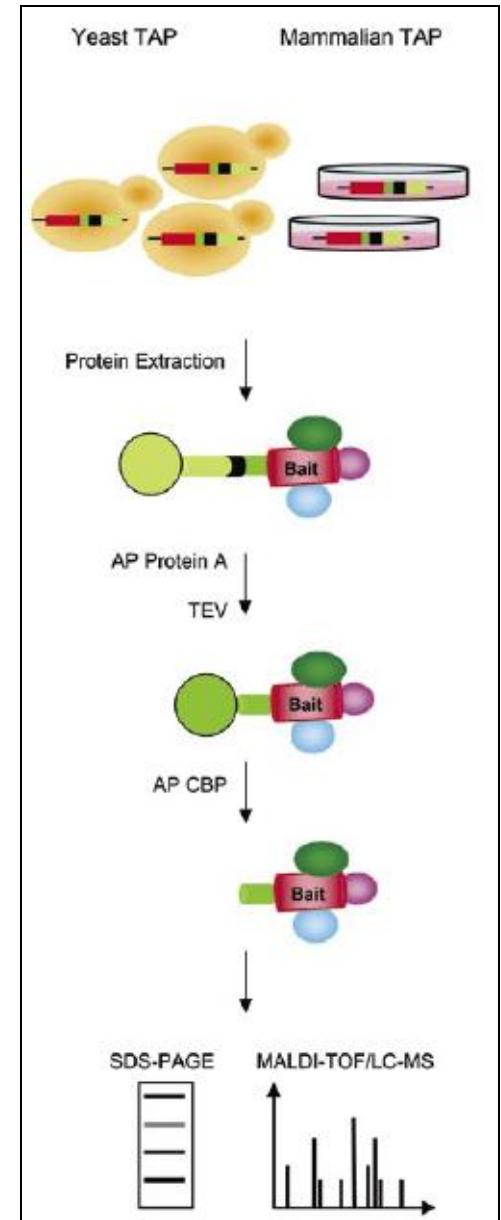
- interaction between bait and prey restores ligand-dependent cytokine receptor signalling
- especially applicable to analysis of cell signalling pathways due to native context of tested bait and prey
- rMAPPIT is used to screen for compounds that disrupt an interaction



# Experimental methods – TAP

## Tandem affinity purification

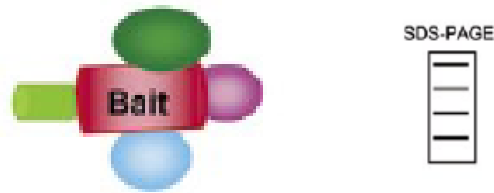
- interacting proteins are purified by means of an affinity tag on a "bait" protein
- proteins are detected via MS
- readout of this experiment type is a list of proteins that somehow interact with the bait protein
- note this is fundamentally different than readout of the Y2H family of experiments (more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



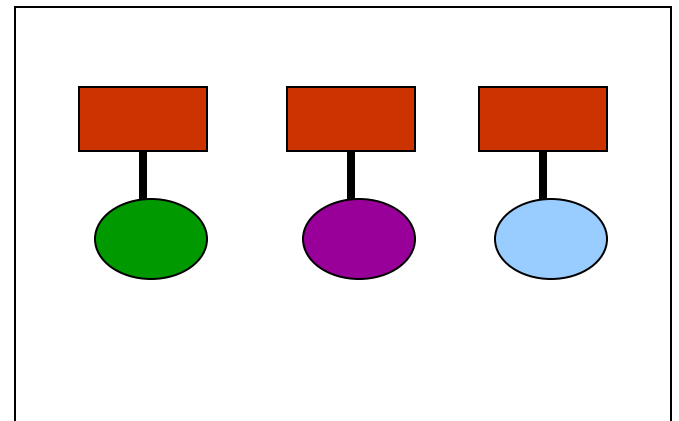
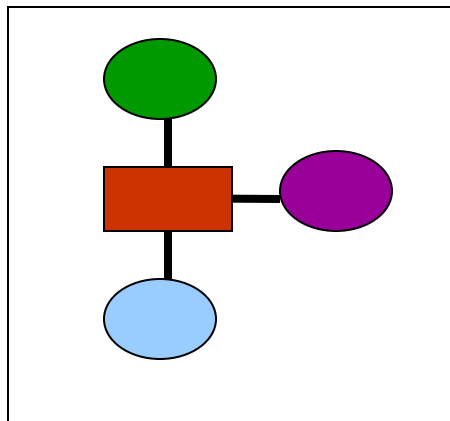
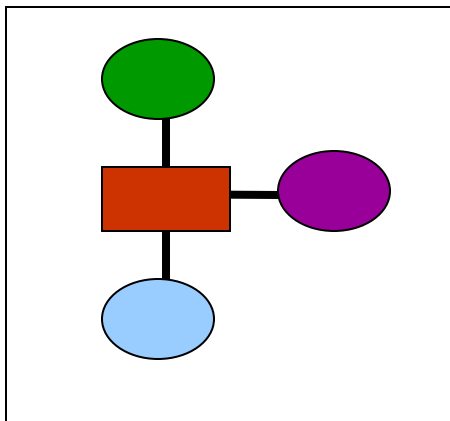
# Experimental methods – AP-MS

## Affinity purification mass spec family

- Advantages
  - detection of protein complexes but no topology or stoichiometric data



three possible interpretations



# Experimental methods – AP-MS

## Affinity purification mass spec family

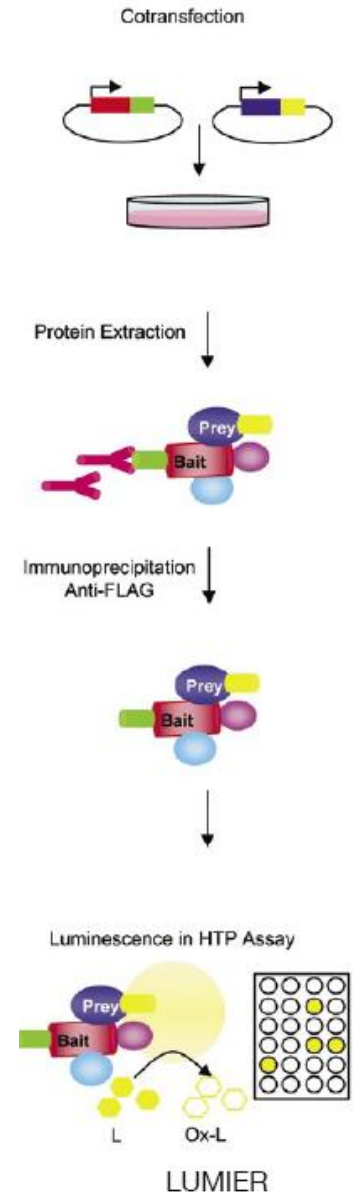
- false positives due to
  - sticky bait or prey
  - mis-identification during MS
  - non-native binding environment
- false negatives due to
  - mis-identification during MS
  - non-native binding environment



# Experimental methods – LUMIER

## Luminescent mammalian interaction assay

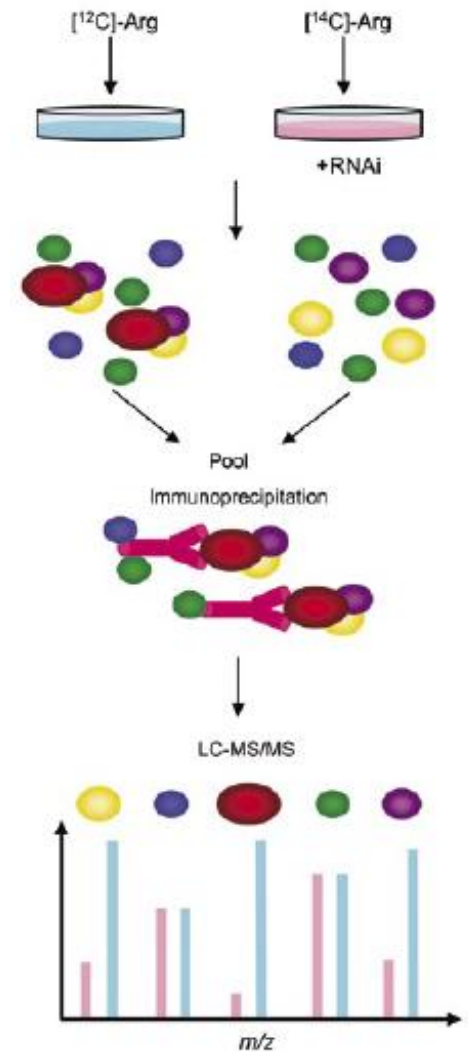
- bait is tagged with FLAG epitope
- prey fused to luciferase
- expression in mammalian cells
- pairwise screening in a high-throughput screen
- pre-tagging of prey aids in non-ambiguous identification



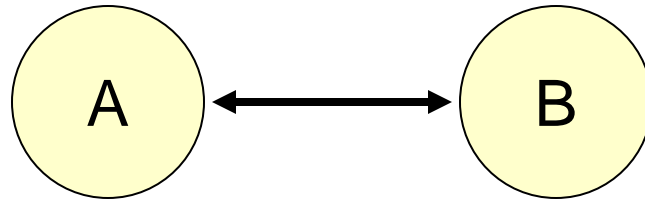
# Experimental methods – QUICK

## Quantitative IP combined with knockdown

- "bait" is knocked down in heavy-labelled sample
- requires antibodies specific to bait (not high throughput)
- reduces noises from non-specifically binding proteins found in IP sample
- no tags, represents native-like cell



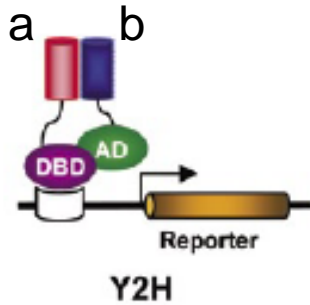
# A simple interaction record



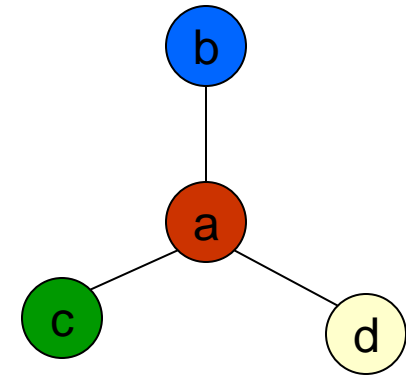
- |                          |                        |
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| 3. Database identifier   | 7. Database identifier |
| 4. Origin                | 8. Origin              |
| 9. Publication reference |                        |

# Representation of interaction data

## binary data versus associative data

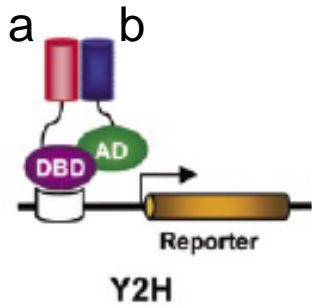


<u>exp</u>	<u>bait</u>	<u>prey</u>
1	a	b
2	a	c
3	a	d

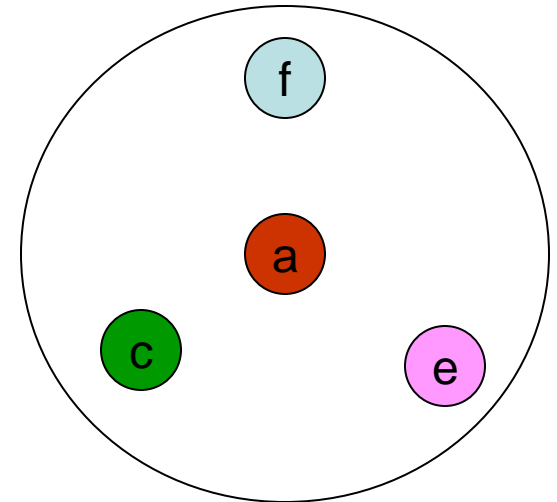
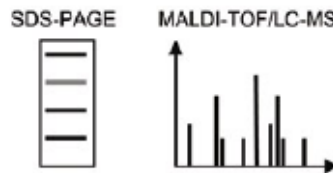
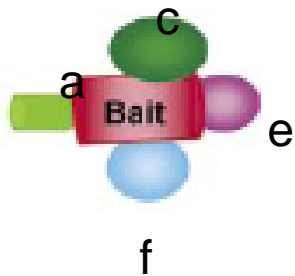
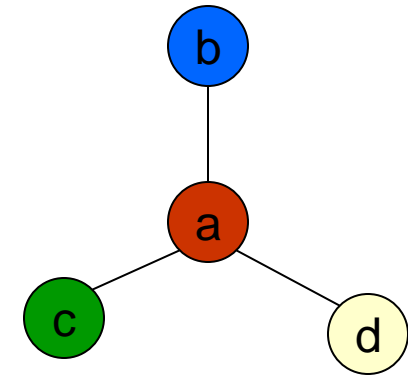


# Representation of interaction data

## binary data versus associative data

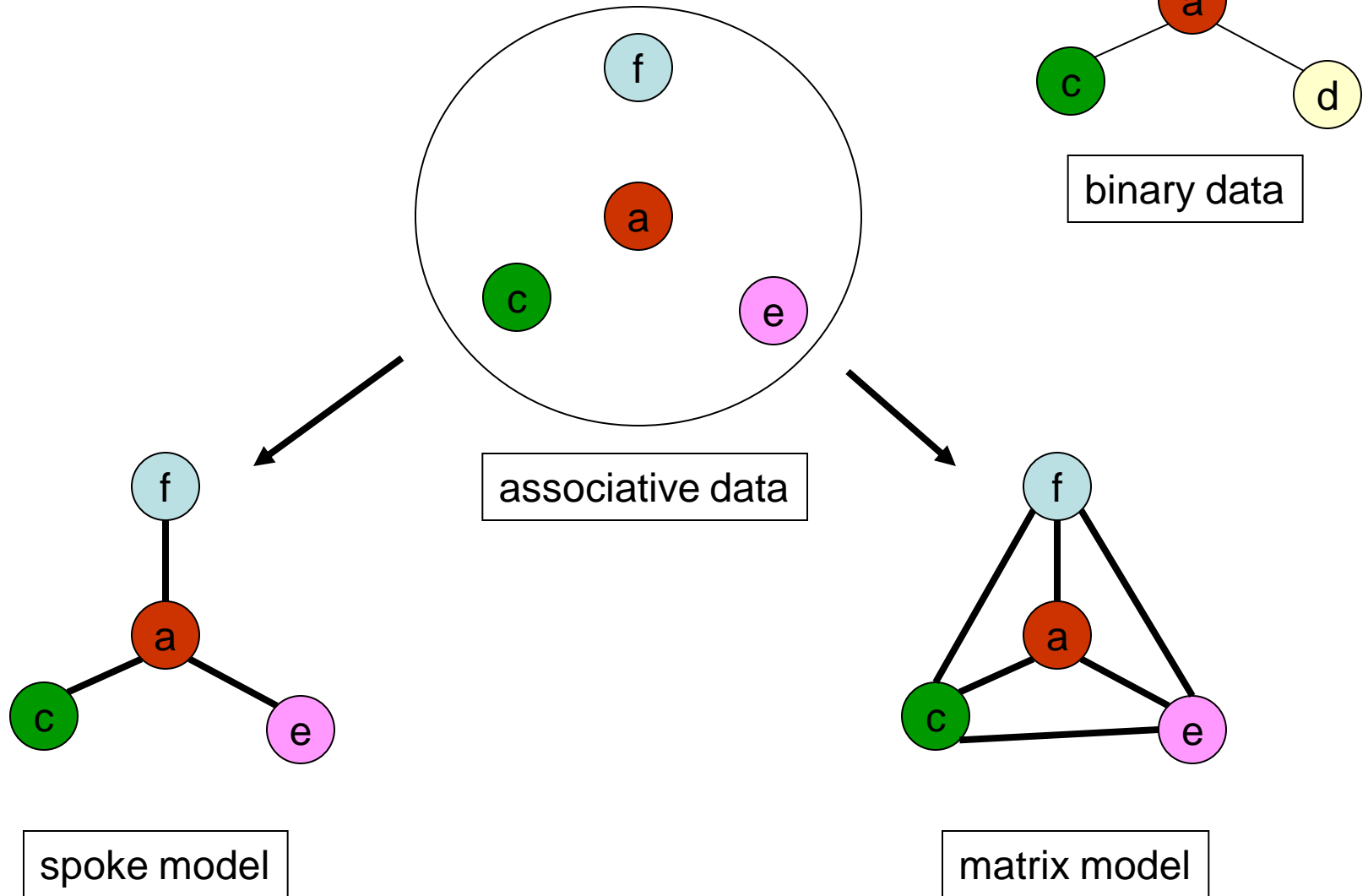


exp	bait	prey
1	a	b
2	a	c
3	a	d

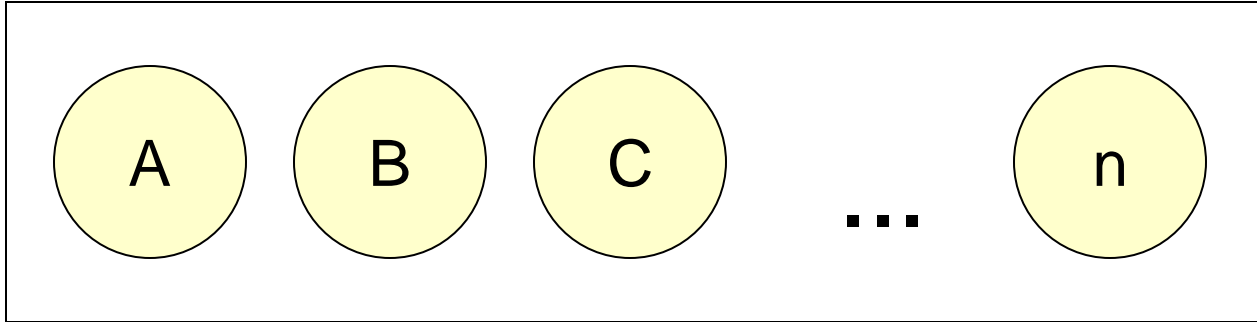


# Representation of interaction data

## 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)

# 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://imex.sourceforge.net/index.html>

# Interaction databases: IntAct

The screenshot shows the IntAct website in a Mozilla Firefox browser. The browser's address bar displays the URL <http://www.ebi.ac.uk/intact/site/index.jsf>. The page content includes a search bar, a navigation menu, and a sidebar with statistics. A large text box highlights the URL <http://www.ebi.ac.uk/intact>.

**IntAct Home**

**Search IntAct**

To perform a search in the IntAct database use the search box in Examples:

- Gene name: [BRCA2](#)
- UniProtKB Ac: [Q06609](#)
- UniProtKB Id: [dmc1](#)
- Pubmed Id: [10831611](#)

**Introduction**

IntAct provides a freely available, open source database system and analysis tools for protein interaction data. All interactions are derived from literature curation or direct user submissions and are freely available.

**IntAct Basic Statistics**

The IntAct Database contains:

- 173,621 binary interactions.
- 54,471 proteins.
- 9,128 experiments.
- 1,463 controlled vocabulary terms.

**License**

All software, available on this site, is under the [Apache License, version 2](#), and all data under the [Creative Commons Attribution License](#). This means that you are free to copy, distribute, display and make commercial use of all records from the IntAct database provided appropriate credit is given.

**Acknowledgements**

# Identifiers: EntrezGene

The screenshot shows the Entrez Gene website interface. At the top, the browser title is "Gene Home - Mozilla Firefox" and the address bar shows the URL "http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene". The page header includes the NCBI logo and "Entrez Gene" text. Below the header is a navigation bar with tabs for "All Databases", "PubMed", "Nucleotide", "Protein", "Genome", "Structure", "OMIM", "PMC", "Journals", and "Books". A search bar is present with the text "Gene" and a "Go" button. The main content area features a description of Entrez Gene as a searchable database of genes. Below this is a "Sample Searches" section with a table of search criteria and their corresponding search text. A large text box is overlaid on the page, containing the URL "http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene".

Gene Home - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

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

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 [ ] Go Clear

Entrez Gene

Home About FAQ Help Gene Handbook Statistics Downloads (FTP)

Mailing Lists

Gene RefSeq

Feedback

Help Desk Corrections About GeneRIFs

Related Sites

BLAST Entrez Genome Genome Projects Genomic Biology GEO HomoloGene Map Viewer OMIM

Entrez Gene is a searchable database of genes, from RefSeq genomes, and defined by sequence and/or located in the NCBI Map Viewer

News Limit by Chromosomal Region; Sort Options. News archives...

Sample Searches

Find genes by...	Search text
free text	<a href="#">human muscular dystrophy</a>
partial name and multiple species	<a href="#">transporter[title] AND ("Drosophila melanogaster"[organ] OR "Mus musculus"[organ])</a>
chromosome and symbol	<a href="#">(II[chr] OR 2[chr]) AND adh*[sym]</a>
associated sequence accession number	<a href="#">M11313[accn]</a>
gene name (symbol)	<a href="#">BRCA1[sym]</a>
publication (PubMed ID)	<a href="#">11331580[PMID]</a>
Gene Ontology (GO) terms or identifiers	<a href="#">"cell adhesion"[GO]</a> <a href="#">10030[GO]</a>
Genes with reports of clinical significance (under development)	<a href="#">...[GO]</a>
chromosome	
Enzyme	

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

About Entrez

- Entrez Gene: gene-centered information at NCBI, Nucleic Acids Res. 2005 Jan 1;33:D54-8.
- General help on the Entrez search and retrieval system
- NCBI Handbook Chapter on Entrez Gene (download PDF)
- How to add information about function (GeneRIF)
- Correct or update a Gene record
- Correct or update a reference sequence
- Report a publication or GeneRIF error

Done



# Entrez Gene

My NCBI  
[Sign In](#) [Register](#)

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search Gene for 7132

Limits Preview/Index History Clipboard Details

Display Full Report Show 20 Sort by Relevance Send to

All: 1 Current P GeneView: 1

GeneID: 7132

1: TNFRSF1A tumor necrosis factor receptor superfamily, member 1A [ Homo sapiens ] updated 12-Oct-2008

GeneID: 7132  
Summary

Official Symbol: TNFRSF1A  
aka Gene Name

Official Symbol TNFRSF1A

Official Full Name tumor necrosis factor receptor superfamily, member 1A

Primary source [HGNC:11916](#)

See related [Ensembl:ENSG00000067182](#); [HPRD:01861](#); [MIM:191190](#)

Gene type protein coding

RefSeq status REVIEWED

Organism Homo sapiens  
Lineage Eukaryota; Metazoa; Chordata; Euteleostomi; Mammalia; Eutheria; Primates; Hominidae; Homo

Synonyms: TNF-R-I

Also known as TNFRSF1A; 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

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

protein... 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]

- Probe
- Protein
- PubMed
- PubMed (OMIM)
- PubMed (GeneRIF)
- SNP
- SNP: Genotype
- SNP: GeneView
- Taxonomy
- UniSTS
- AceView
- CCDS

### Genomic regions, transcripts, and products

(minus strand) Go to [reference sequence details](#)

[Try our new Sequence Viewer](#)



RefSeq Protein Accession:  
NP\_001056

- MGC
- ModelMaker
- PharmGKB
- The registry of TNFRSF1A sequence variants
- UniGene

### Genomic context

chromosome: 12; Location: 12p13.2

[See TNFRSF1A in MapViewer](#)



Entrez Gene Info

Feedback

Subscriptions

### 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

NCBI Sequence Viewer v2.0 - Mozilla Firefox

File Edit View History Bookmarks Digo 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...

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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:4507575] 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; Cephalopoda; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homini

REFERENCE 1 (residues 1 to 455)

AUTHORS Menon,R., Velez,D., Williams,S.M.

TITLE Genetic regulation of tumor necrosis factor 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.,

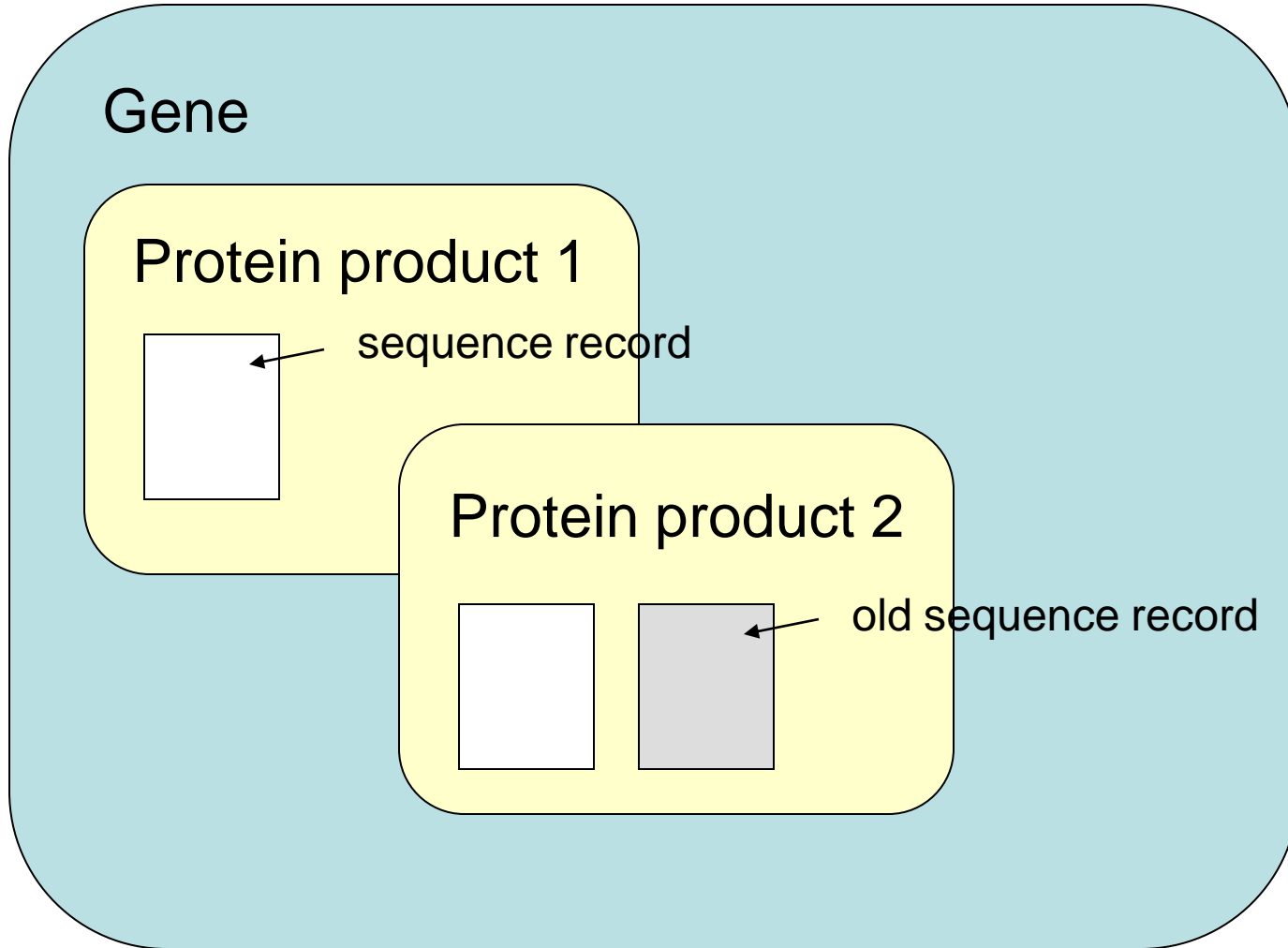
Done

RefSeq Protein Accession: NP\_001056

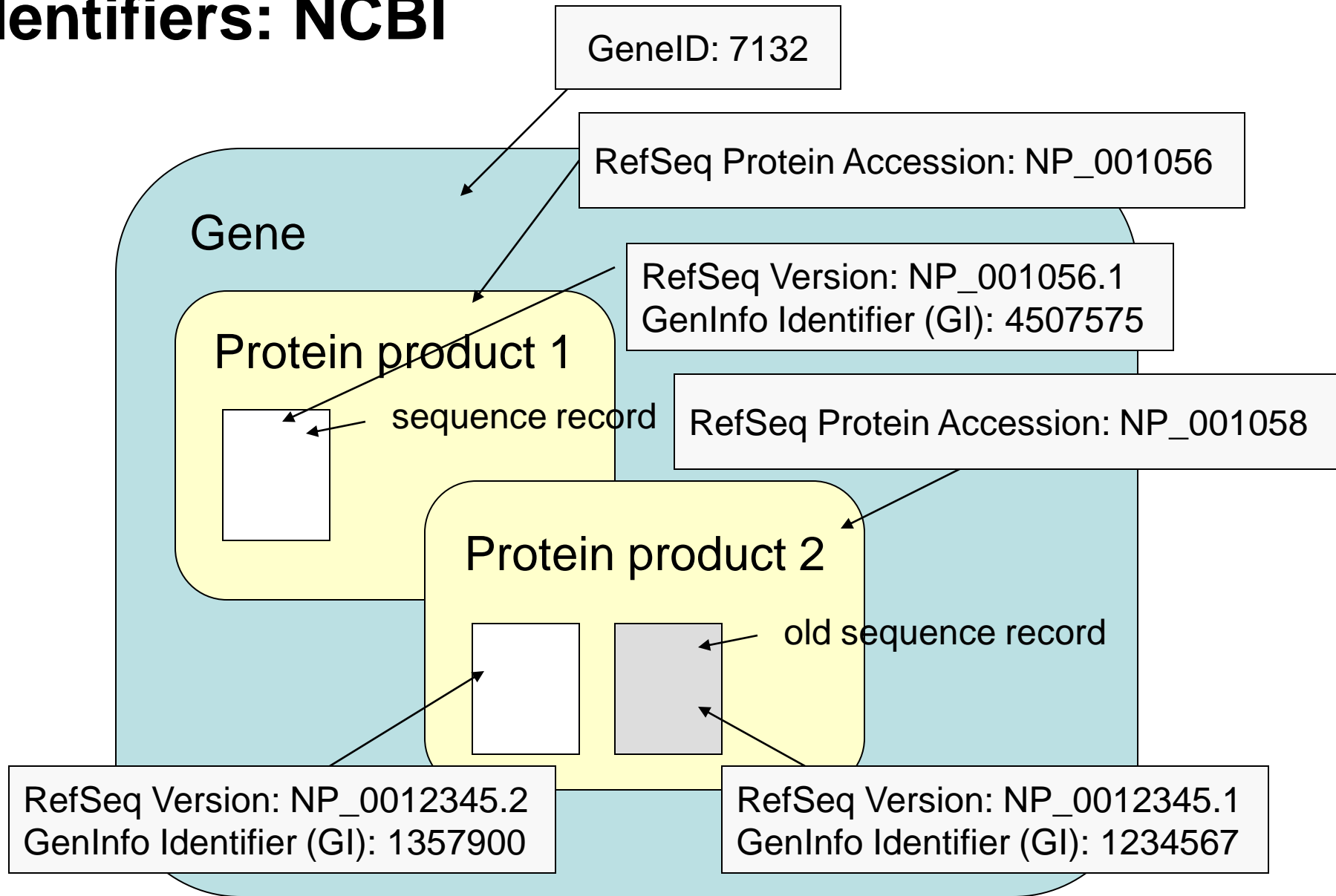
GenInfo Identifier: 4507575

RefSeq Version: NP\_001056.1

# Identifiers: NCBI



# Identifiers: NCBI





# Identifiers: UniProtKB

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

The screenshot shows the UniProt website in a Mozilla Firefox browser. The browser's address bar displays <http://www.uniprot.org/>. The page features a search bar at the top with a dropdown menu set to "Protein Knowledgebase (UniProtKB)". Below the search bar are buttons for "Search", "Blast", "Align", "Retrieve", and "ID Mapping".

The main content area is divided into several sections:

- WELCOME**: A paragraph stating the mission of UniProt: "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**: A table listing various UniProt services and their descriptions.
- NEWS**: A section titled "Release 14.3 – Oct 14, 2008" with a sub-heading "10th anniversary of the Swiss Institute of Bioinformatics". It includes links for "Statistics for UniProtKB: Swiss-Prot · TrEMBL", "Forthcoming changes", and "News archives".
- SITE TOUR**: A section with a sub-heading "Learn how to make best use of the tools and data on this site." and a small thumbnail image of a tutorial page.

Service	Description
<a href="#">UniProtKB</a>	Protein knowledgebase, consists of two sections: <ul style="list-style-type: none"><li>★ Swiss-Prot, which is manually annotated and reviewed.</li><li>★ TrEMBL, which is automatically annotated and is <b>not</b> reviewed.</li></ul>
<a href="#">UniRef</a>	Sequence clusters, used to speed up similarity searches.
<a href="#">UniParc</a>	Sequence archive, used to keep track of sequences and their identifiers.
Supporting data	<a href="#">Literature citations</a> , <a href="#">taxonomy</a> , <a href="#">keywords</a> and <a href="#">more</a> .

Search in

Query

Protein Knowledgebase (UniProtKB)

UniProtKB Entry: RAD51\_HUMAN

★ Reviewed, UniProtKB/Swiss-Prot **Q06609** (RAD51\_HUMAN)

Last modified September 23, 2008. Version 100. History

Contribute Send feedback

UniProtKB Accession: Q06609

Clusters with 100%, 90%, 50% identity Documents (FASTA) 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

Gene Name: RAD51

Short name=hRAD51

Short name=HsRAD51

Gene names

Name:

**RAD51**

Synonyms: RAD51A

Synonyms: RAD51A, RECA

Organism

**Homo sapiens (Human)**

Taxonomic identifier

**9606 [NCBI]**

Taxon id: 9606 (human)

Taxonomic lineage

Eukaryota › Metazoa › Chordata › Mammalia › Eutheria › Euarchontoglires › Primates › Haplorhini › Catarrhini › Hominoidea › Homo

Binary interactions

Binary interactions from IntAct

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

Alternative products

This entry describes **2** isoforms produced by **alternative splicing**. [\[Align\]](#) [\[Select\]](#)

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

This isoform has been chosen as the canonical sequence. This entry 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.



Other Resources

SOURCE	<a href="#">Search...</a>
ProtoNet	<a href="#">Search...</a>

Entry information

Hide | Top

Entry name	RAD51_HUMAN	
Accession	Primary (citable) accession number: <b>Q06609</b> Secondary accession number(s): <u>Q6FHX9, Q9BV60</u>	
Entry history	Integrated into UniProtKB/Swiss-Prot:	June 1, 1994
	Last sequence update:	June 1, 1994
	Last modified:	September 1, 2009
	This is version 100 of the entry and version 1 of the sequence. <a href="#">[Complete history]</a>	
Entry status	Reviewed (UniProtKB/Swiss-Prot)	
Annotation project	<a href="#">HPI (Human Proteome Initiative)</a>	

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

# **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?**

**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 interaction 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-occurrence of gene name mentions.

Start at [http://zope.bioinfo.cnio.es/bionlp\\_tools](http://zope.bioinfo.cnio.es/bionlp_tools)

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

# Text mining resources: iHOP

iHOP - Information Hyperlinked over Proteins - Mozilla Firefox

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

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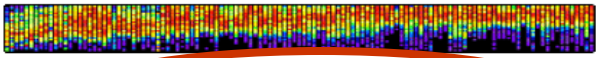




























































iHOP - Inf... EBIMed FACTA PubGene - Find... Chilibot: finding... MedEvi - a per... FABLE - Overvi... BioCreative Met... BioText Search ...

**iHOP**  
Information hyperlinked over proteins

Search Gene  
RAD51

Gene Model Developer's Zone  
How to cite iHOP

Contact Links Help

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	LeRAD51		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	   
Rad51I3	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); }





Search Gene

Show overview

Find in this Page

Filter and options

Gene Model

Developer's Zone

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.

Found in this page: interacts (21)

Find in this Page

(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.

Show all Order by relevance

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

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. [2003]



Find: dmc1

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

Done



# Text mining resources: EBIMed

EBIMed - Mozilla Firefox

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http://www.ebi.ac.uk/Rebholz-srv/ebimed/excerptResults.jsp?queryId=QueryDMYHMSms19102008213500843&key=P3: biotext

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**EBIMed**  
Excerpts table

RAD51 Search  
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Abstracts per page  
5 Update

first << 1/14 >> last

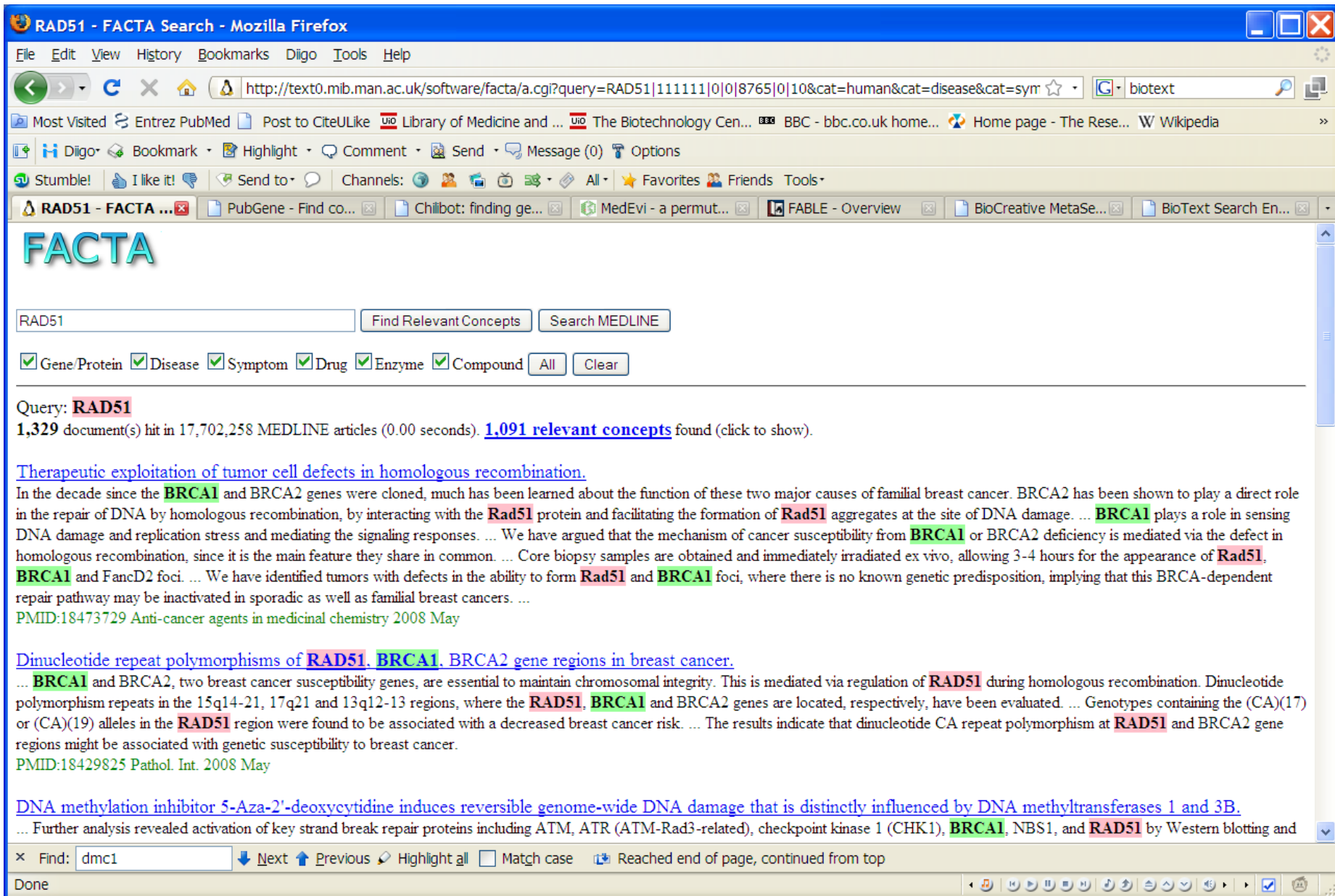
Rows 1 to 5 (out of 67)

Abstract	Sentences
<a href="#">17991895</a> <i>Palii Stela S et al. (2007)</i>	Further analysis revealed activation of key strand break repair proteins including <a href="#">ATM</a> , <a href="#">ATR</a> (ATM-Rad3-related), checkpoint kinase 1 ( <a href="#">CHK1</a> ), <a href="#">BRCA1</a> , <a href="#">NBS1</a> , and <a href="#">RAD51</a> by Western blotting and immunofluorescence .
<a href="#">17999359</a> <i>Antoniou Antonis C et al. (2007)</i>	<div style="border: 2px solid red; padding: 5px;">RAD51 is an important component of double-stranded DNA-repair mechanisms that interacts with both <a href="#">BRCA1</a> and <a href="#">BRCA2</a> .</div> <p>A single-nucleotide polymorphism (SNP) in the 5' untranslated region (UTR) of <a href="#">RAD51</a>, 135G-&gt;C, has been suggested as a possible modifier of breast cancer risk in <a href="#">BRCA1</a> and <a href="#">BRCA2</a> mutation carriers .</p> <p><a href="#">RAD51</a> is the first gene to be reliably identified as a modifier of risk among <a href="#">BRCA1/2</a> mutation carriers .</p>
<a href="#">17001309</a>	Several studies have revealed that the recombinational repair genes, <a href="#">RAD51</a> and <a href="#">BRCA1</a> , and the DNA mismatch repair genes, <a href="#">MLH1</a> and <a href="#">MSH2</a> , are decreased in

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

Done

# Text mining resources: FACTA



**RAD51 - FACTA Search - Mozilla Firefox**

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http://text0.mib.man.ac.uk/software/facta/a.cgi?query=RAD51|111111|0|0|8765|0|10&cat=human&cat=disease&cat=sym ☆ biotext

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## FACTA

RAD51 Find Relevant Concepts Search MEDLINE

Gene/Protein  Disease  Symptom  Drug  Enzyme  Compound All Clear

Query: **RAD51**  
1,329 document(s) hit in 17,702,258 MEDLINE articles (0.00 seconds). [1,091 relevant concepts](#) found (click to show).

[Therapeutic exploitation of tumor cell defects in homologous recombination.](#)  
In the decade since the **BRCA1** and **BRCA2** genes were cloned, much has been learned about the function of these two major causes of familial breast cancer. **BRCA2** has been shown to play a direct role in the repair of DNA by homologous recombination, by interacting with the **Rad51** protein and facilitating the formation of **Rad51** aggregates at the site of DNA damage. ... **BRCA1** plays a role in sensing DNA damage and replication stress and mediating the signaling responses. ... We have argued that the mechanism of cancer susceptibility from **BRCA1** or **BRCA2** deficiency is mediated via the defect in homologous recombination, since it is the main feature they share in common. ... Core biopsy samples are obtained and immediately irradiated ex vivo, allowing 3-4 hours for the appearance of **Rad51**, **BRCA1** and FancD2 foci. ... We have identified tumors with defects in the ability to form **Rad51** and **BRCA1** foci, where there is no known genetic predisposition, implying that this **BRCA**-dependent repair pathway may be inactivated in sporadic as well as familial breast cancers. ...  
PMID:18473729 *Anti-cancer agents in medicinal chemistry* 2008 May

[Dinucleotide repeat polymorphisms of \*\*RAD51\*\*, \*\*BRCA1\*\*, \*\*BRCA2\*\* gene regions in breast cancer.](#)  
... **BRCA1** and **BRCA2**, two breast cancer susceptibility genes, are essential to maintain chromosomal integrity. This is mediated via regulation of **RAD51** during homologous recombination. Dinucleotide polymorphism repeats in the 15q14-21, 17q21 and 13q12-13 regions, where the **RAD51**, **BRCA1** and **BRCA2** genes are located, respectively, have been evaluated. ... Genotypes containing the (CA)(17) or (CA)(19) alleles in the **RAD51** region were found to be associated with a decreased breast cancer risk. ... The results indicate that dinucleotide CA repeat polymorphism at **RAD51** and **BRCA2** gene regions might be associated with genetic susceptibility to breast cancer.  
PMID:18429825 *Pathol. Int.* 2008 May

[DNA methylation inhibitor 5-Aza-2'-deoxycytidine induces reversible genome-wide DNA damage that is distinctly influenced by DNA methyltransferases 1 and 3B.](#)  
... Further analysis revealed activation of key strand break repair proteins including ATM, ATR (ATM-Rad3-related), checkpoint kinase 1 (CHK1), **BRCA1**, NBS1, and **RAD51** by Western blotting and

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

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Browse literature or sequence neighbours.

**Organism** Homo sapiens Select one or "all organisms"

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

**Biological term** and/or 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...
Organism	Homo sapiens
Article ...	4905
Term T...	PubGene Gene/Prot...
External...	EG
Chrom...	
Alt. Sym...	BRCC5
Alt. Sym...	HRAD51
Alt. Sym...	HsRad51
Alt. Sym...	HsT16930
Alt. Sym...	RAD51A
Alt. Sym...	RECA

Network view Table view

The network graph displays RAD51 (red node) at the center, connected to several other genes/proteins (red nodes): POLG2, ATRX, POLA1, BRCAX, BRCA2, DIAPH8, TP53, and STK32C. ATP5E is also shown as a grey node at the bottom, connected to STK32C. The nodes are arranged in a roughly circular pattern around the central RAD51 node.

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

Applet pubgenegraph.GraphController started

# Text mining resources: Chillibot

Chilibot: finding gene and protein relationships from MEDLINE - a text mining approach - Mozilla Firefox

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Last update: 08/04/07

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### RAD51 & BRCA2

Retrieving synonyms..

Retrieving abstracts .. [RAD51/BRCA2 .....

Performing linguistic analysis ..

---

Analyzed 100 *most recent* abstracts out of 207 available.  
Found 103 interactive sentences and 70 parallel sentences.

[View all relevant sentences.](#)

---

#### Interactive relationship (e.g. stimulation, inhibition, etc)

- These findings indicate that **BRCA2** inhibits **Rad51** cleavage and subsequent apoptosis. [Ref. Radiat Res. 2008](#)
- Similarly, reducing **BRCA2** by 50% reduces **RAD51** and BCCIP foci. [Ref. Mol Cell Biol. 2005](#)
- **BRCA2** expression also modulates **Rad51** protein levels such that **Rad51** protein is relatively decreased in **BRCA2** defective cancer cells. [Ref. Mol Carcinog. 2008](#)
- **BRCA2** is essential for homologous recombination in vivo, but isolated BRC repeat peptides can prevent the assembly of **RAD51** into active nucleoprotein filaments in vitro, suggesting a model in which **BRCA2** sequesters **RAD51** in undamaged cells, and promotes recombinase function after DNA damage. [Ref. Nucleic Acids Res. 2006](#)
- The interactions of **BRCA2** with **RAD51** and DMC1 lead us to suggest that the **BRCA2** tumour suppressor is a universal regulator of recombinase actions. [Ref. Oncogene. 2007](#)
- The **BRCA2** tumour suppressor regulates the RAD 51 [RAD51] recombinase during double strand break (DSB) repair by homologous recombination (HR) but how **BRCA2** executes its functions is not well understood. [Ref. J Mol Biol. 2006](#)
- The crystallographic analysis shows that the BRC motif of the **BRCA2** tumor suppressor is in contact with the subunit subunit interface of **Rad51** and could thus prevent filament formation of **Rad51**. [Ref. Genes Cells. 2008](#)
- From these results, we conclude that (i) **BRCA2** regulates **RAD51** recombination in response to the type of DNA damage and (ii) **BRCA2** suppresses SCRS, suggesting a role for **BRCA2** in sister chromatids cohesion and or alignment. [Ref. Cancer Res. 2005](#)
- Inhibition of filament formation of human **Rad51** protein by a small peptide derived from the BRC motif of the **BRCA2** protein. [Ref. Genes Cells. 2008](#)
- Brh2, the ortholog of the **BRCA2** tumor suppressor in *Ustilago maydis*, works hand in hand with **Rad51** to promote repair of DNA by homologous recombination. [Ref. Proc Natl Acad Sci U S A. 2008](#)
- The **BRCA2** tumor suppressor functions in repair of DNA by homologous recombination through regulating the action of **Rad51**. [Ref. DNA Repair \(Amst\). 2007](#)

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Done



# Text mining resources: Chillibot

Chilibot: finding gene and protein relationships from MEDLINE - a text mining approach - Mozilla Firefox

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## Chilibot

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Last update: 08/04/07

We recommend Firefox browser.

### Two lists search, context restriction

Context: substance abuse OR addiction

```
graph TD; P[POLYMORPHISM] --- 8[8] --- TH; P --- 5[5] --- SCT; P --- 6[6] --- GABRG1; P --- 5[5] --- GABRB1; P --- 5[5] --- GABRA4; P --- 29[29] --- GABRA2; P --- 5[5] --- DRD4; P --- 21[21] --- CCKBR; P --- BDNF; P --- ADH5;
```

Searching for polymorphism of genes associated with substance abuse or addiction. A list of 27 genes was first identified in a data mining study. This Chilibot search found that the polymorphism of 10 of them were known to be associated with substance abuse/addiction.

### Hypothesis generation

```
graph TD; CREB --- 10[10] --- ACTIN; CREB --- 23[23] --- CAMKII; CREB --- 14[14] --- ZIF268; CREB --- 14[14] --- TAU; CREB --- 30[30] --- AMPA; CREB --- 30[30] --- NMDA; CREB --- 13[13] --- PKA; CREB --- 5[5] --- PKC; CREB --- 13[13] --- TRKB; CREB --- 5[5] --- TRKA; CREB --- 13[13] --- PLC; CREB --- 5[5] --- SYNAPSIN_I[SYNAPSIN I]; CREB --- 2[2] --- LTP; SYNAPTOTAGMIN --- 13[13] --- ACTIN; SYNAPTOTAGMIN --- 5[5] --- CAMKII; SYNAPTOTAGMIN --- 14[14] --- ZIF268; SYNAPTOTAGMIN --- 14[14] --- TAU; SYNAPTOTAGMIN --- 6[6] --- AMPA; SYNAPTOTAGMIN --- 14[14] --- NMDA; SYNAPTOTAGMIN --- 14[14] --- PKA; SYNAPTOTAGMIN --- 2[2] --- PKC; SYNAPTOTAGMIN --- 14[14] --- TRKB; SYNAPTOTAGMIN --- 2[2] --- TRKA; SYNAPTOTAGMIN --- 2[2] --- PLC; SYNAPTOTAGMIN --- 2[2] --- SYNAPSIN_I; SYNAPTOTAGMIN --- 2[2] --- LTP;
```

From a complex of relationship network, Chilibot suggested that CREB may have a relationship (e.g. regulation) with synaptotagmin, based on 1) there is no known relationship between CREB and synaptotagmin; and 2) they are both connected to many gene/protein and are both involved in similar biological process (e.g. LTP). The original search included one keyword ("LTP") and 22 other genes. CREB was first selected by clicking on the graph. Hypothesis was generated by clicking on the "CREB might be related to.." button. See [here](#) for details.

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

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# Text mining resources: MedEvi

MedEvi - a permuted concordancer for Medline - Mozilla Firefox

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http://www.ebi.ac.uk/tc-test/textmining/medevi/results.jsp?query=BRCA1+AND+bind\*+AND+RAD51&options=side+AND+ef

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Query: BRCA1 AND bind\* AND RAD51

3 permuted occurrences of 25 filtered documents of 25 hit documents (4.59s). [List keywords](#) [List multiword terms](#)

Jump to result set: [ABC](#) [BCA](#)

**Set 1: BRCA1 AND bind\* AND RAD51** [Top](#)

[1](#) radiation ( IR ) and exhibit [defective DNA repair](#) . Both BRCA1 and [BRCA2](#) have been reported to bind Rad51 , [a protein](#) essential for homologous recombination

[2](#) sensitivity to DNA-damaging agents . In human cells , BRCA1 binds to both [Rad50](#) and Rad51 and colocalizes with these proteins at repair foci .

**Set 2: bind\* AND RAD51 AND BRCA1** [Top](#)

[1](#) the zinc finger domain ( exons 2 , 3 and 5 ) and the binding domain with Rad51 ( exon 11 ) of the BRCA1 protein . An identical nonsense mutation at codon 63

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Find: dmc1     Match case

Done

# Text mining resources: FABLE

**FABLE** - Gene Lister query [brca1 AND rad51] - Mozilla Firefox

Fast Automated Biomedical Literature Extraction

Why use FABLE?  
FABLE Help

Gene Lister  Article Finder

brca1 rad51  Synonyms:  Sort by:  Results/page:

Next > Last > | 1-25 of 186 unique genes found in articles containing *brca1* AND *rad51* | Download:

Gene	Articles	Synonyms	LitTrack	Links
<a href="#">RAD51</a>	<a href="#">163</a>	▷ RAD51	<a href="#">15q15.1</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">BRCA1</a>	<a href="#">150</a>	▷ BRCA1	<a href="#">17q21.31</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">BRCA2</a>	<a href="#">95</a>	▷ BRCA2	<a href="#">13q13.1</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">TP53</a>	<a href="#">34</a>	▷ TP53	<a href="#">17p13.1</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">NBN</a>	<a href="#">24</a>	▷ NBN	<a href="#">8q21.3</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">ATM</a>	<a href="#">21</a>	▷ ATM	<a href="#">11q22.3</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">NLRP2</a>	<a href="#">20</a>	▷ NLRP2	<a href="#">19q13.42</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">FANCD2</a>	<a href="#">19</a>	▷ FANCD2	<a href="#">3p25.3</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">FANCA</a>	<a href="#">17</a>	▷ FANCA	<a href="#">16q24.3</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">RAD50</a>	<a href="#">17</a>	▷ RAD50	<a href="#">5q31.1</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">FXN</a>	<a href="#">16</a>	▷ FXN	<a href="#">9q21.11</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">MRE11A</a>	<a href="#">16</a>	▷ MRE11A	<a href="#">11q21</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">RAD52</a>	<a href="#">16</a>	▷ RAD52	<a href="#">12p13.33</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">BARD1</a>	<a href="#">15</a>	▷ BARD1	<a href="#">2q35</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">ATRX</a>	<a href="#">12</a>	▷ ATRX	<a href="#">Xq21.1</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">UBE2S</a>	<a href="#">10</a>	▷ UBE2S	<a href="#">19q13.42</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">CHEK2</a>	<a href="#">9</a>	▷ CHEK2	<a href="#">22q12.1</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">ATR</a>	<a href="#">8</a>	▷ ATR	<a href="#">3q23</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>
<a href="#">XRCC3</a>	<a href="#">8</a>	▷ XRCC3	<a href="#">14q32.33</a>	<a href="#">NCBI Gene</a>   <a href="#">UCSC</a>   <a href="#">SvmAtlas</a>   <a href="#">Google</a>   <a href="#">GeneCards</a>   <a href="#">GeneLynx</a>



# Text mining resources: BioText

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RAD51 AND BRCA2

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**$\gamma$ -H2AX in recognition and signaling of DNA double-strand breaks in the context of chromatin**

Kinner, A., Wu, W., Staudt, C., Iliakis, G. (2008) *Nucleic Acids Research*.

**FIGURE CAPTION**

Figure 2.. DSB repair pathways. (A) Homologous recombination repair (HRR). After the initial sensing of the DSB by MRN and the activation of ATM, H2AX is phosphorylated, which in turn elicits a sequence of signaling events thought to ultimately cause the activation of nucleases such as Mre11 and CtIP to process the DNA ends and generate ssDNA with 3' overhangs. ssDNA is bound by RPA, which is subsequently exchanged by **Rad51** and **Rad51** paralogs. This exchange is facilitated by Rad52, Rad54 and **BRCA2**. The Rad51-decorated DNA fiber initiates strand invasion into an intact homologous DNA molecule that leads to the formation of a Holiday junction. The DNA sequence around the DSB is copied by DNA synthesis associated with branch migration, and the process is completed by resolution of the Holiday junction. HRR is a templated repair process and is therefore error free (15–17). (B) DNA-PK-dependent nonhomologous end joining (D-NHEJ). DNA ends are recognized by Ku, which recruits, after processing by Tdp1 or PNKP, DNA-PKcs. Upon end-binding, DNA-PKcs is activated and phosphorylates itself and possibly also other proteins (like H2AX on an adjacent nucleosome). Phosphorylated DNA-PKcs is thought to be released from the DNA end, which allows the DNA ligase IV/XRCC4/XLF complex to mediate end-ligation possibly with the help of a DNA polymerase that catalyzes gap filling (19,149,150). (C) Backup pathway of nonhomologous end joining (B-NHEJ). There is evidence that cells of higher eukaryotes with defects in D-NHEJ rejoin the majority of DSBs using an alternative repair pathway that is not utilizing any of the HRR-associated activities (19). This pathway is therefore termed backup NHEJ (B-NHEJ). Although details of this pathway remain to be elucidated, there is evidence that it utilizes the PARP-1/DNA Ligase III/XRCC1 repair module known to be involved in the repair of SSB and base damages (151–155), and that its function is facilitated by the linker histone H1 (156). (D) Single strand annealing (SSA). This repair pathway shares features of HRR and NHEJ, and is best described in yeast (17). After the initial sensing of the DSBs

# Overview

1. A simple interaction 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

<b>STRING</b>	<a href="http://string.embl.de/"><u>http://string.embl.de/</u></a>
<b>OPHID/I2D</b>	<a href="http://ophid.utoronto.ca/ophidv2.201/"><u>http://ophid.utoronto.ca/ophidv2.201/</u></a>
<b>InteroPorc</b>	<a href="http://biodev.extra.cea.fr/interoporc"><u>http://biodev.extra.cea.fr/interoporc</u></a>
<b>FunCoup</b>	<a href="http://FunCoup.sbc.su.se"><u>http://FunCoup.sbc.su.se</u></a>

# **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 multiple data sources.**

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

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# Consolidated databases

**cPATH**

<http://cbio.mskcc.org/cpath/>

**Pathway Commons**

<http://www.pathwaycommons.org/pc/>

**MiMI**

<http://mimi.ncibi.org/MimiWeb/main-page.jsp>

**iRefIndex**

<http://irefindex.uio.no/wiki/iRefIndex>

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# 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 coimmunoprecipitation 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.**

