

INTRODUCTION TO BIOINFORMATICS

Please take the initial BIOINF525 questionnaire:
< <http://tinyurl.com/bioinf525-questions> >

Barry Grant
University of Michigan

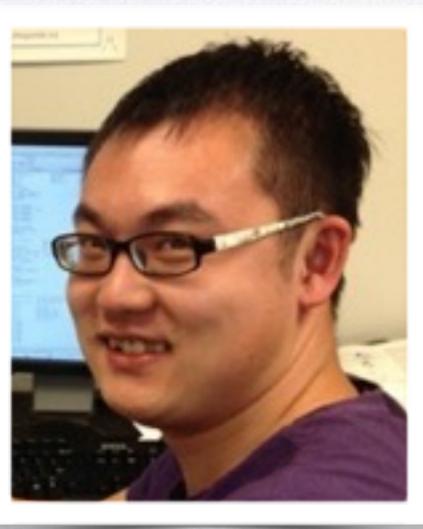
www.thegrantlab.org



Barry Grant, Ph.D.
bjgrant@umich.edu



Ryan Mills, Ph.D.
remills@umich.edu



Hongyang Li (GSI)
hyangl@umich.edu

COURSE LOGISTICS

Lectures: Tuesdays 2:30-4:00 PM
Rm. 2062 Palmer Commons

Labs: Session I: Thursdays 2:30 - 4:00 PM
Session II: Fridays 10:30 - 12:00 PM
Rm. 2036 Palmer Commons

Website: <http://tinyurl.com/bioinf525-w16>
Lecture, lab and background reading material
plus homework and course announcements

MODULE OVERVIEW

Objective: Provide an introduction to the practice of bioinformatics as well as a practical guide to using common bioinformatics databases and algorithms

1.1. ▶ *Introduction to Bioinformatics*

1.2. ▶ *Sequence Alignment and Database Searching*

1.3 ▶ *Structural Bioinformatics*

1.4 ▶ *Genome Informatics: High Throughput Sequencing Applications and Analytical Methods*

TODAYS MENU

Overview of bioinformatics

- The what, why and how of bioinformatics?
- Major bioinformatics research areas.
- Skepticism and common problems with bioinformatics.

Bioinformatics databases and associated tools

- Primary, secondary and composite databases.
 - Nucleotide sequence databases (GenBank & RefSeq).
 - Protein sequence database (UniProt).
 - Composite databases (PFAM & OMIM).

Database usage vignette

- Searching with ENTREZ and BLAST.
- Reference slides and handout on major databases.

HOMEWORK

- Complete the **initial course questionnaire**:
<http://tinyurl.com/bioinf525-questions>
- Check out the “**Background Reading**” material on Ctools:
<http://tinyurl.com/bioinf525-w16>
- Complete the **lecture 1.1 homework questions**:
<http://tinyurl.com/bioinf525-quiz1>

Q. What is Bioinformatics?

Q. What is Bioinformatics?

“Bioinformatics is the application of computers to the collection, archiving, organization, and analysis of biological data.”

[After Orengo, 2003]

- ... Bioinformatics is a hybrid of biology and computer science
- ... **Bioinformatics is computer aided biology!**

Computer based management and analysis of biological and biomedical data with useful applications in many disciplines, particularly genomics, proteomics, metabolomics, etc...

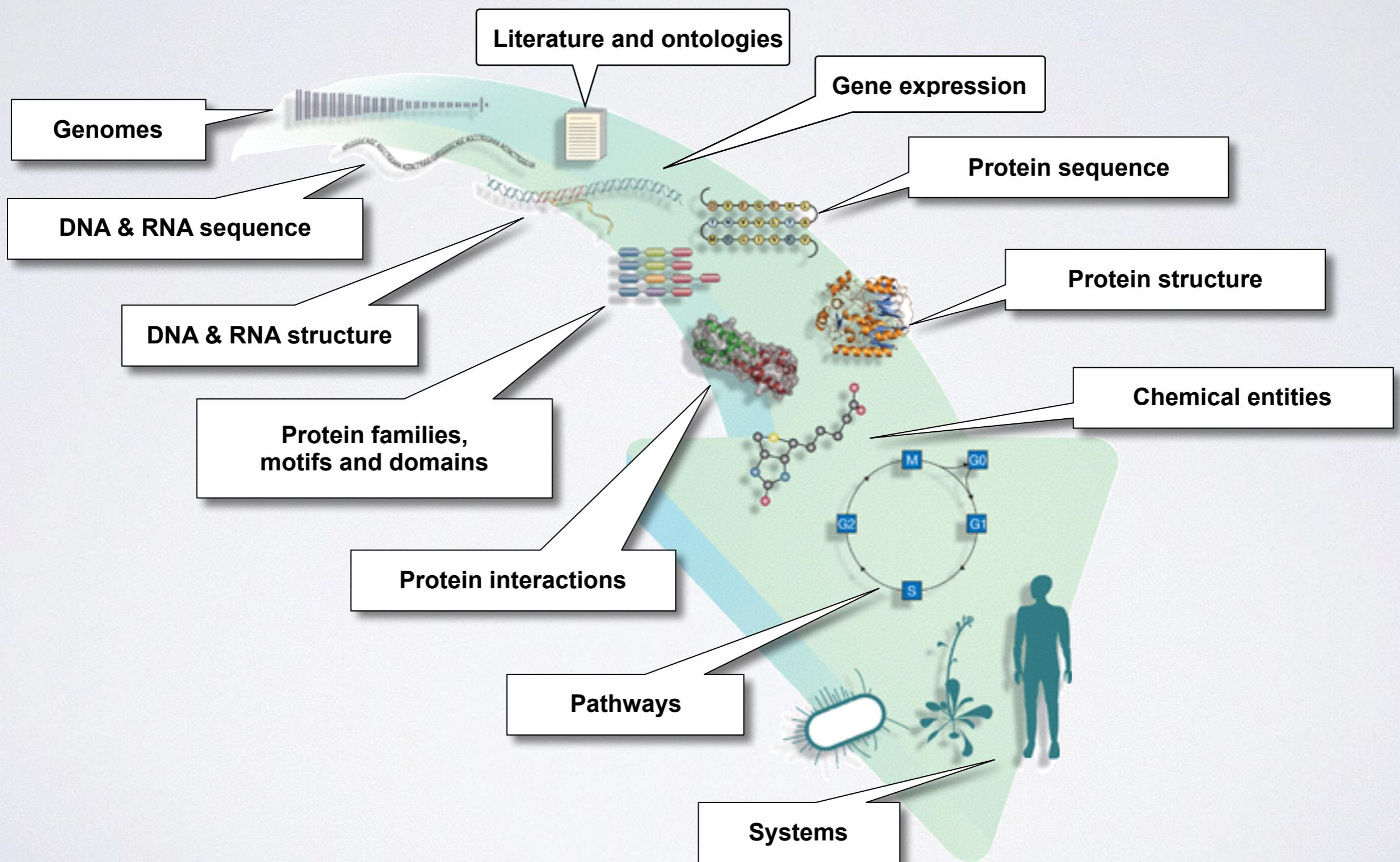
MORE DEFINITIONS

- ▶ “Bioinformatics is conceptualizing biology in terms of **macromolecules** and then applying “**informatics**” techniques (derived from disciplines such as applied maths, computer science, and statistics) to **understand** and **organize** the information associated with these molecules, on a **large-scale**.
Luscombe NM, et al. Methods Inf Med. 2001;40:346.
- ▶ “Bioinformatics is research, development, or application of **computational approaches** for expanding the use of **biological, medical, behavioral or health data**, including those to **acquire, store, organize and analyze** such data.”
National Institutes of Health (NIH) (<http://tinyurl.com/l3gxr6b>)

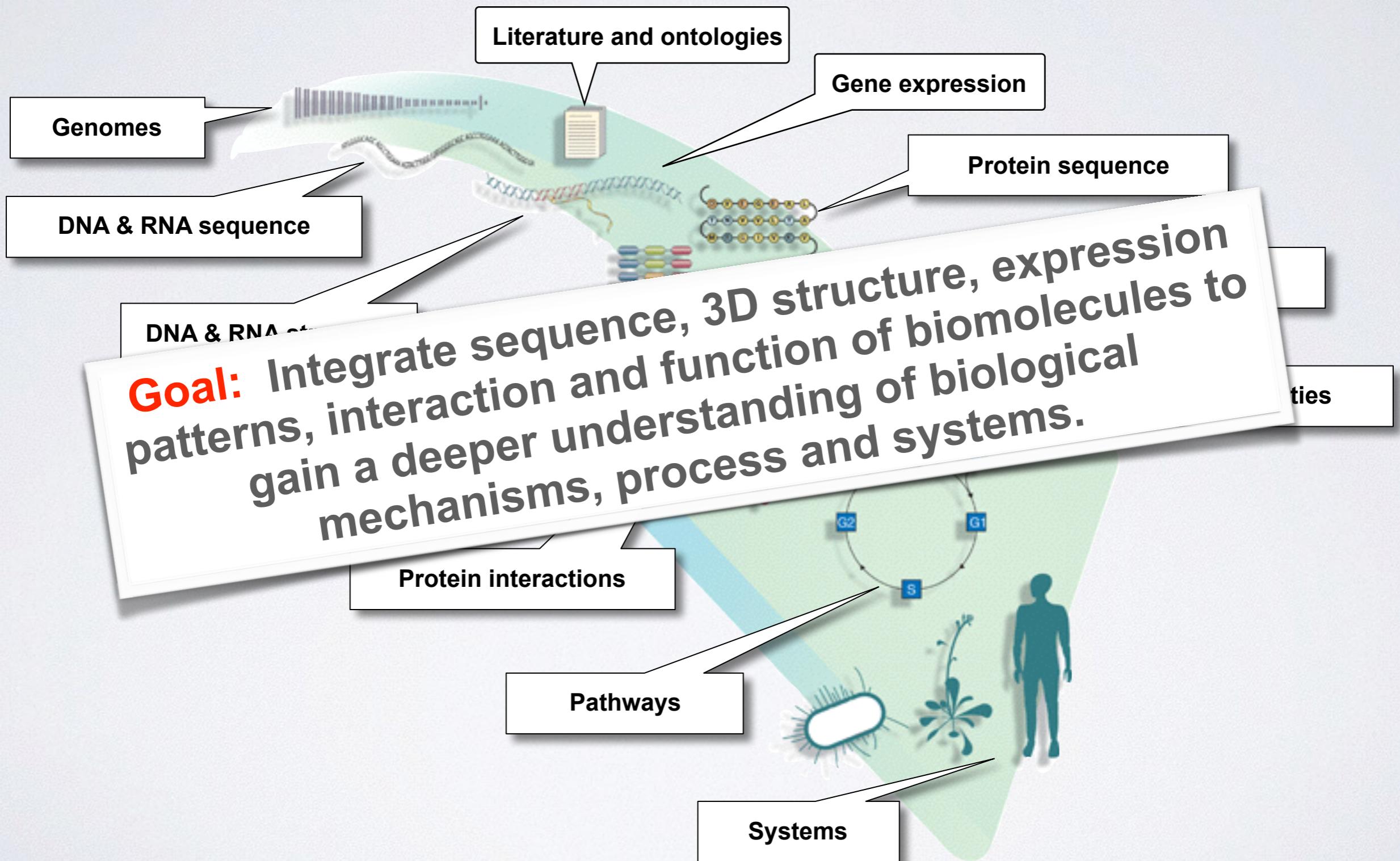
MORE DEFINITIONS

- ▶ “Bioinformatics is conceptualizing biology in terms of **macromolecules** and then applying “**informatics**” (derived from disciplines such as applied mathematics, science, and statistics) to **understand** and **analyze** the information associated with these molecules, on a **large-scale**.
Luscombe NM, et al. Methods 2001;40:346.
 - ▶ “Bioinformatics is the search, development, or application of computer approaches for expanding the use of biological, medical, behavioral or health data, including those to acquire, store, organize and analyze such data.”
National Institutes of Health (NIH) (<http://tinyurl.com/l3gxr6b>)
- Key Point: Bioinformatics is Computer Aided Biology*

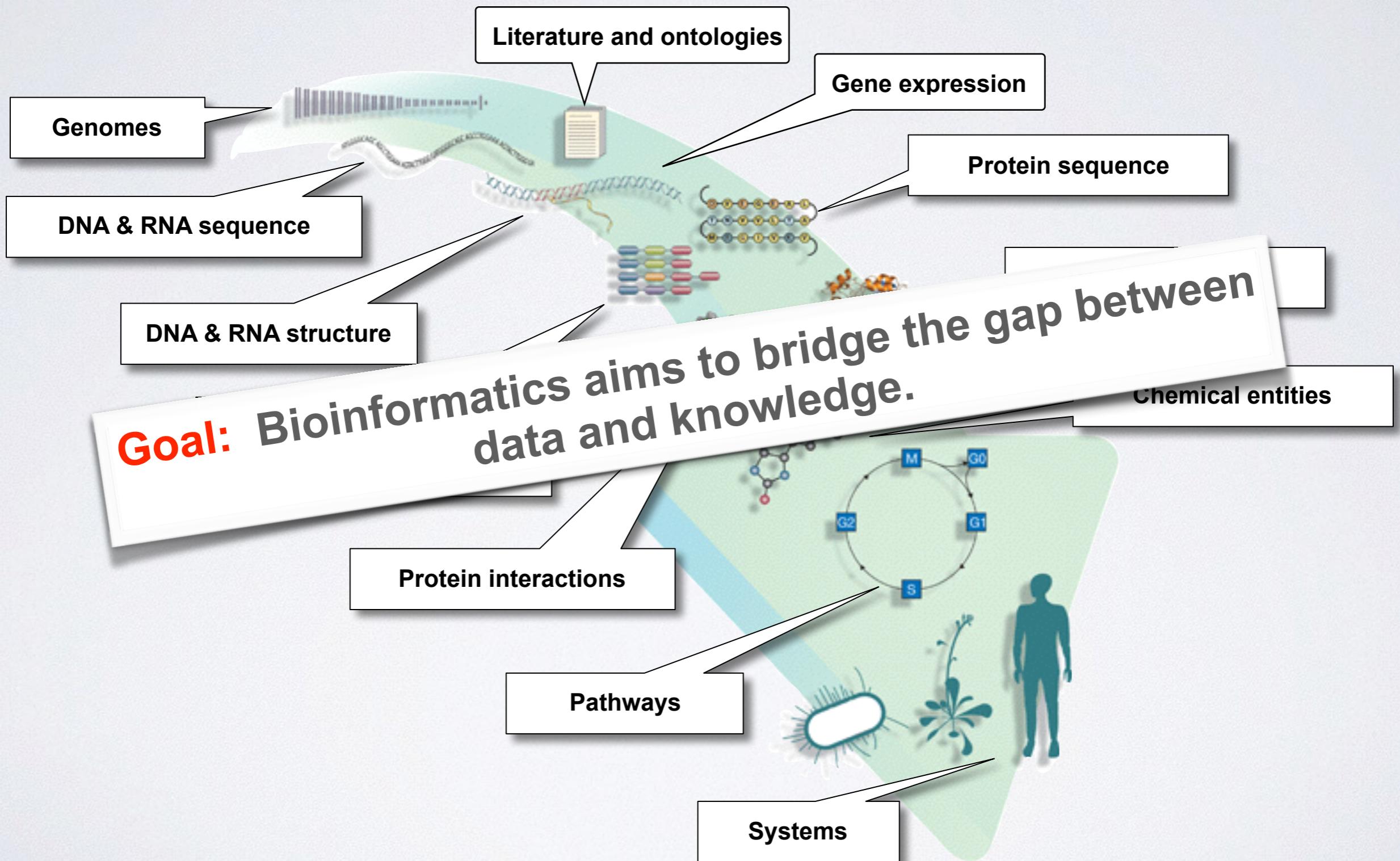
Major types of Bioinformatics Data



Major types of Bioinformatics Data



Major types of Bioinformatics Data



BIOINFORMATICS RESEARCH AREAS

Include but are not limited to:

- Organization, classification, dissemination and analysis of biological and biomedical data (particularly '-omics' data).
- Biological sequence analysis and phylogenetics.
- Genome organization and evolution.
- Regulation of gene expression and epigenetics.
- Biological pathways and networks in healthy & disease states.
- Protein structure prediction from sequence.
- Modeling and prediction of the biophysical properties of biomolecules for binding prediction and drug design.
- Design of biomolecular structure and function.

With applications to Biology, Medicine, Agriculture and Industry

Where did bioinformatics come from?

Bioinformatics arose as molecular biology began to be transformed by the emergence of molecular sequence and structural data

Recap: The key dogmas of molecular biology

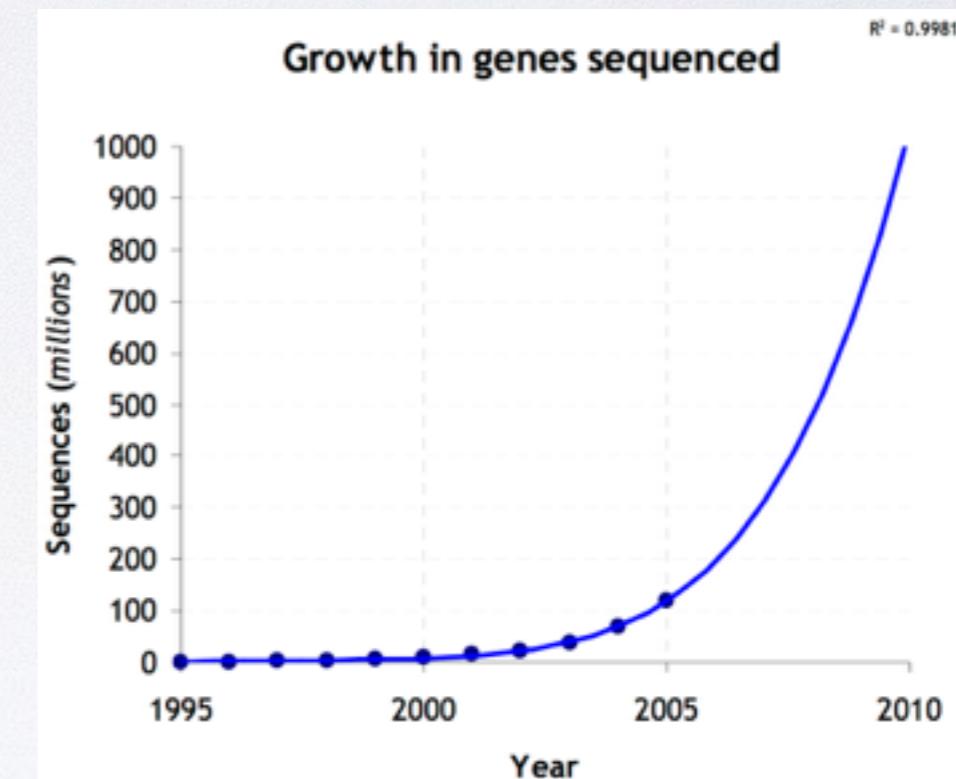
- *DNA sequence determines protein sequence.*
- *Protein sequence determines protein structure.*
- *Protein structure determines protein function.*
- *Regulatory mechanisms (e.g. gene expression) determine the amount of a particular function in space and time.*

Bioinformatics is now essential for the archiving, organization and analysis of data related to these processes.

Why do we need Bioinformatics?

Bioinformatics is necessitated by the rapidly expanding quantities and complexity of biomolecular data

- Bioinformatics provides methods for the efficient:
 - ▶ **storage**
 - ▶ **annotation**
 - ▶ **search and retrieval**
 - ▶ **data integration**
 - ▶ **data mining and analysis**

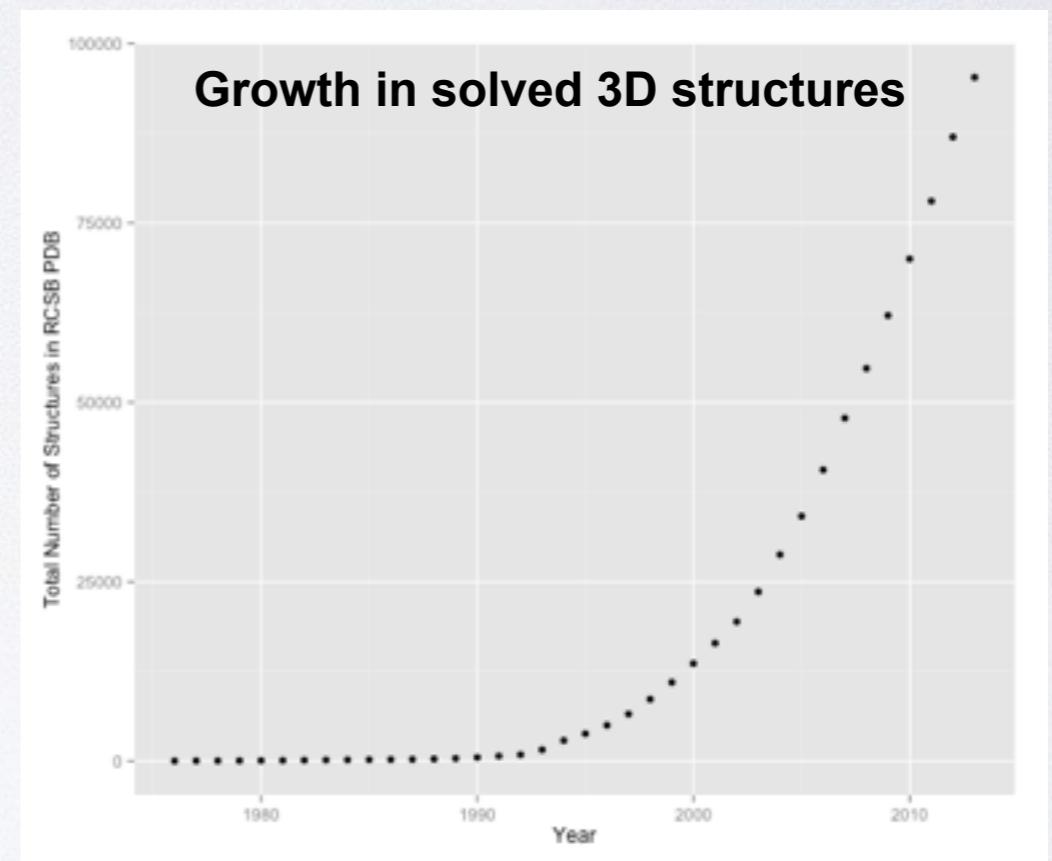


Bioinformatics is essential for the archiving, organization and analysis of data from sequencing, structural genomics, microarrays, proteomics and new high throughput assays.

Why do we need Bioinformatics?

Bioinformatics is necessitated by the rapidly expanding quantities and complexity of biomolecular data

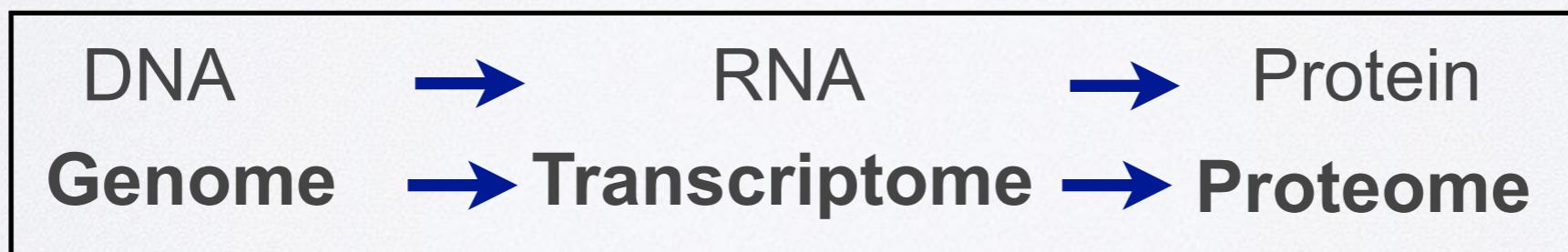
- Bioinformatics provides methods for the efficient:
 - **storage**
 - **annotation**
 - **search and retrieval**
 - **data integration**
 - **data mining and analysis**



Bioinformatics is essential for the archiving, organization and analysis of data from sequencing, structural genomics, microarrays, proteomics and new high throughput assays.

How do we do Bioinformatics?

- A “*bioinformatics approach*” involves the application of **computer algorithms**, **computer models** and **computer databases** with the broad goal of understanding the action of both individual genes, transcripts, proteins and large collections of these entities.



How do we actually do Bioinformatics?

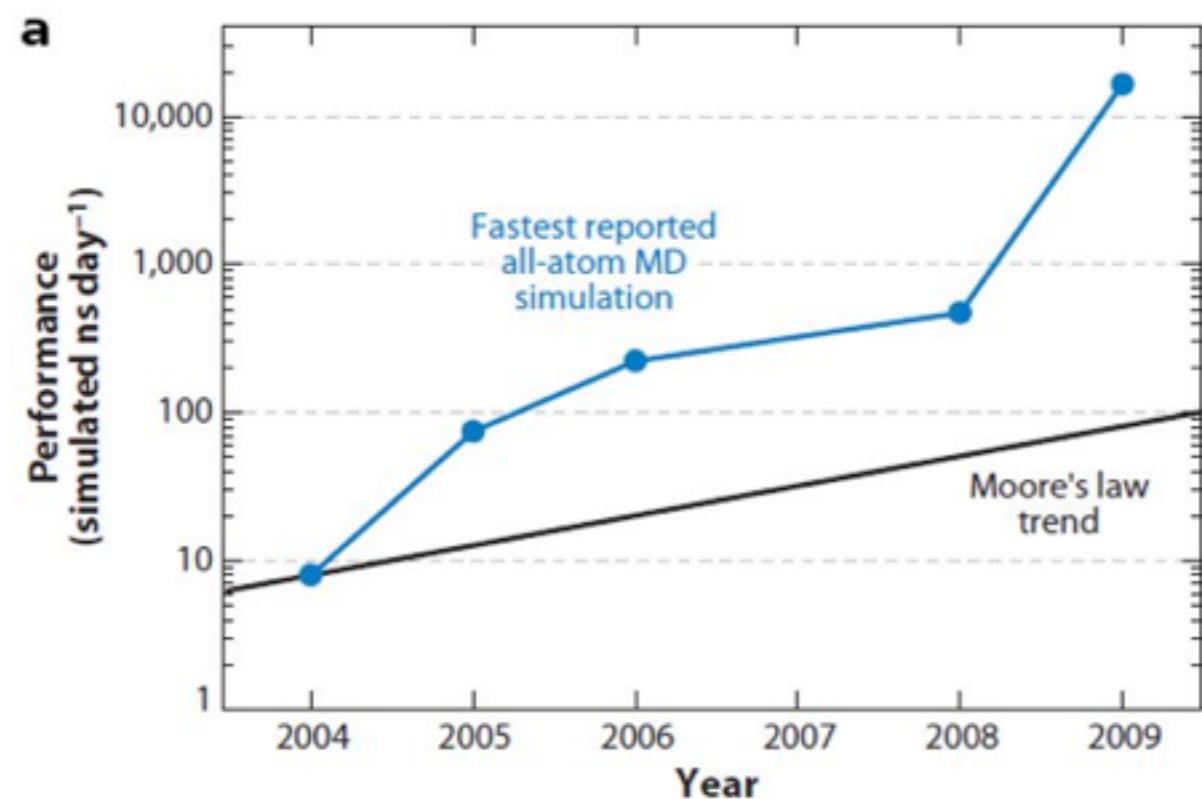
Pre-packaged tools and databases

- ▶ Many online
- ▶ New tools and time consuming methods frequently require downloading
- ▶ Most are free to use

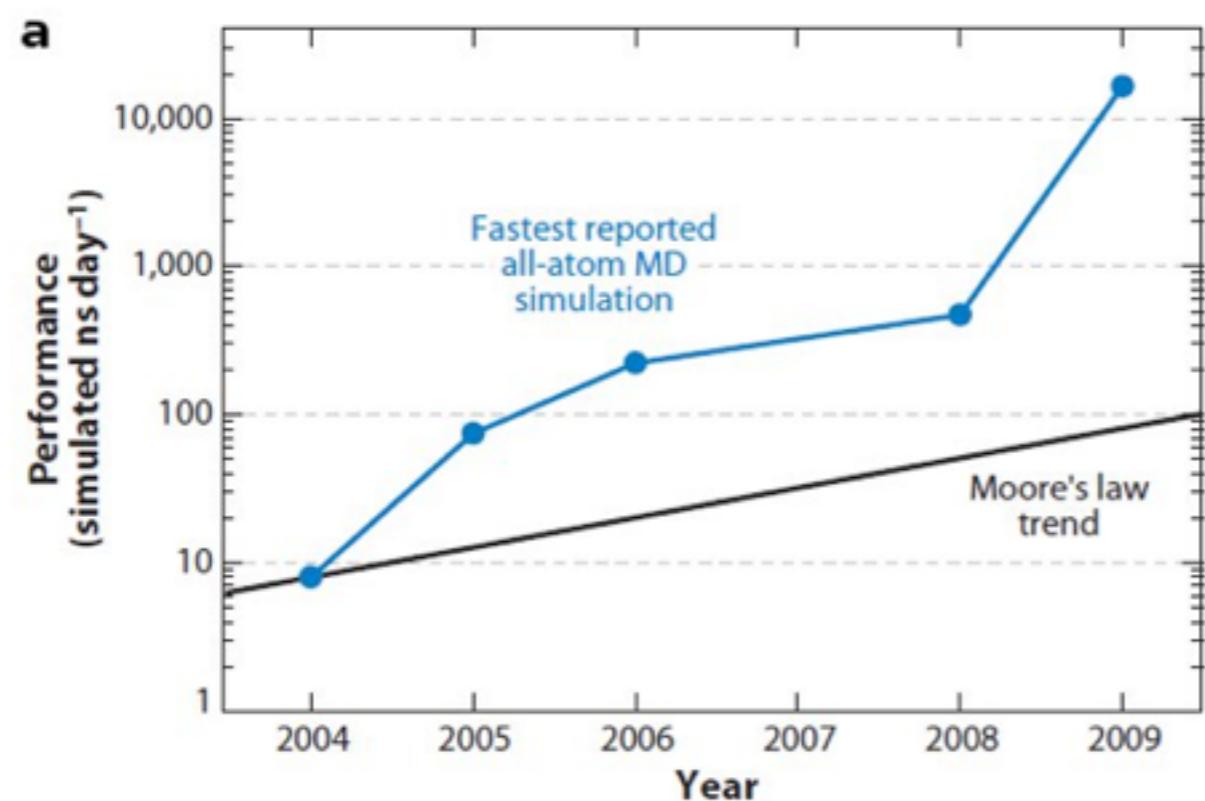
Tool development

- ▶ Mostly on a UNIX environment
- ▶ Knowledge of programming languages frequently required (Python, Perl, R, C Java, Fortran)
- ▶ May require specialized or high performance computing resources...

SIDE-NOTE: SUPERCOMPUTERS ANDGPUS



SIDE-NOTE: SUPERCOMPUTERS AND GPUS



HOW COMPUTERS HAVE CHANGED

DATE	COST	SPEED	MEMORY	SIZE
1967	\$40M	0.1 MHz	1 MB	HULL
2013	\$14,000	1 GHz	10 GB	LAPTOP
CHANGE	10,000	10,000	10,000	10,000

If cars were like computers then a new Volvo would cost \$3, would have a top speed of 1,000,000 Km/hr, would carry 50,000 adults and would park in a shed.

Skepticism & Bioinformatics

We have to approach computational results the same way we do wet-lab results:

- Do they make sense?
- Is it what we expected?
- Do we have adequate controls, and how did they come out?
- Modeling is modeling, but biology is different...
What does this model actually contribute?
- Avoid the miss-use of ‘black boxes’

Common problems with Bioinformatics

Confusing multitude of tools available

- ▶ Each with many options and settable parameters

Most tools and databases are written by and for nerds

- ▶ Same is true of documentation - if any exists!

Most are developed independently

Notable exceptions are found at the:

- **EBI** (European Bioinformatics Institute) and
- **NCBI** (National Center for Biotechnology Information)

General Parameters

Max target sequences	500	?	Select the maximum number of aligned sequences to display
Short queries	<input checked="" type="checkbox"/> Automatically adjust parameters for short input sequences		
Expect threshold	10	?	
Word size	3	?	
Max matches in a query range	0	?	

Scoring Parameters

Matrix	BLOSUM62	?
Gap Costs	Existence: 11 Extension: 1	?
Compositional adjustments	Conditional compositional score	

Filters and Masking

Filter	<input type="checkbox"/> Low complexity regions	?
Mask	<input type="checkbox"/> Mask for lookup table only	
	<input type="checkbox"/> Mask lower case letters	?

PSI/PHI/DELTA BLAST

Upload PSSM Optional	Choose File	no file selected
PSI-BLAST Threshold	0.005	?
Pseudocount	0	?

Even Blast has many settable parameters

Related tools with different terminology

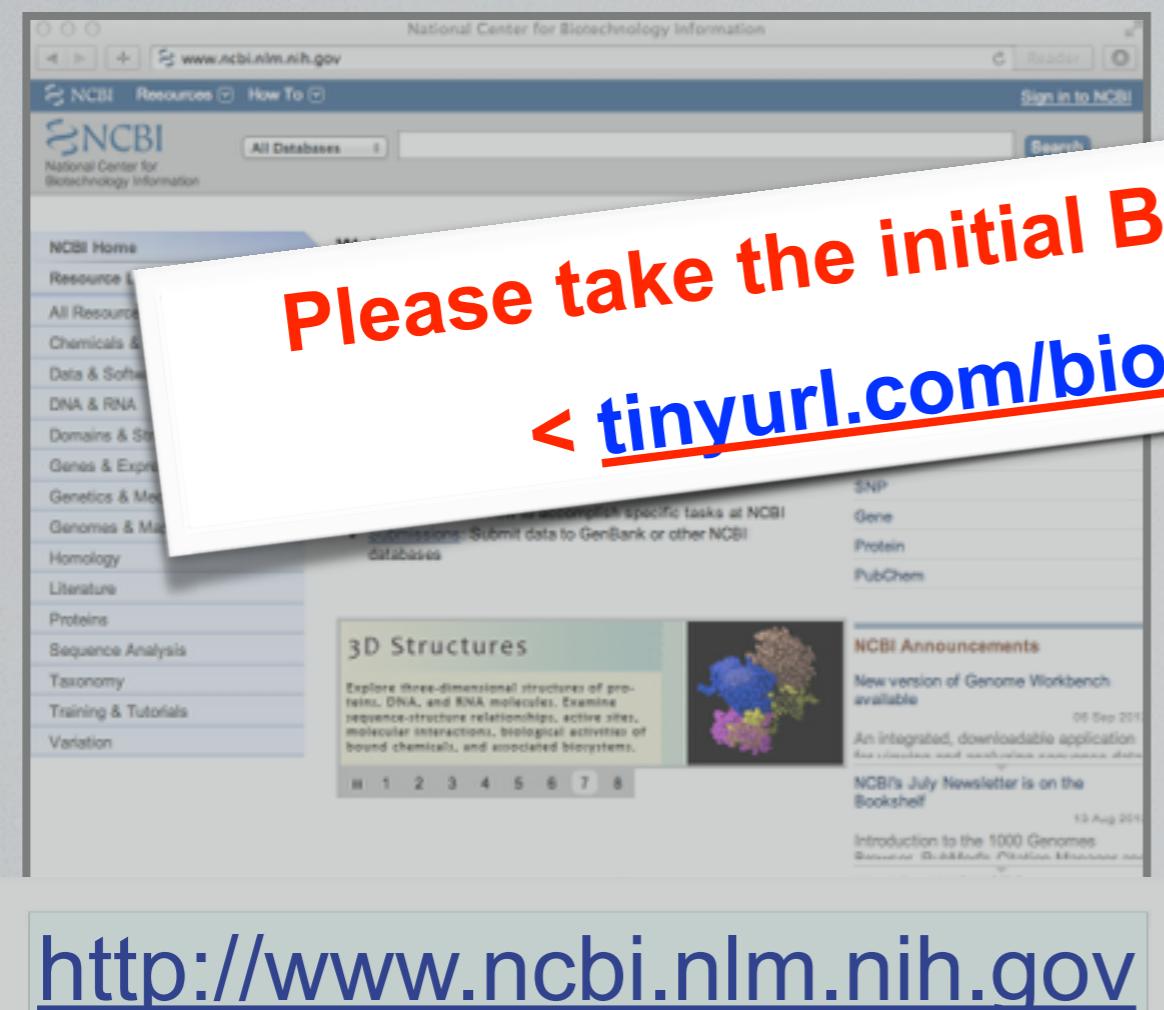
STEP 3 - Set your PROGRAM

FASTA	MATRIX	GAP OPEN	GAP EXTEND	KTUP	EXPECTATION UPPER VALUE	EXPECTATION LOWER VALUE
	BLOSUM50	-10	-2	2	10	0 (default)
	DNA STRAND	HISTOGRAM	FILTER		STATISTICAL ESTIMATES	
	N/A	no	none		Regress	
	SCORES	ALIGNMENTS	SEQUENCE RANGE	DATABASE RANGE		MULTI HSPs
	50	50	START-END	START-END		no
	SCORE FORMAT					
	Default					

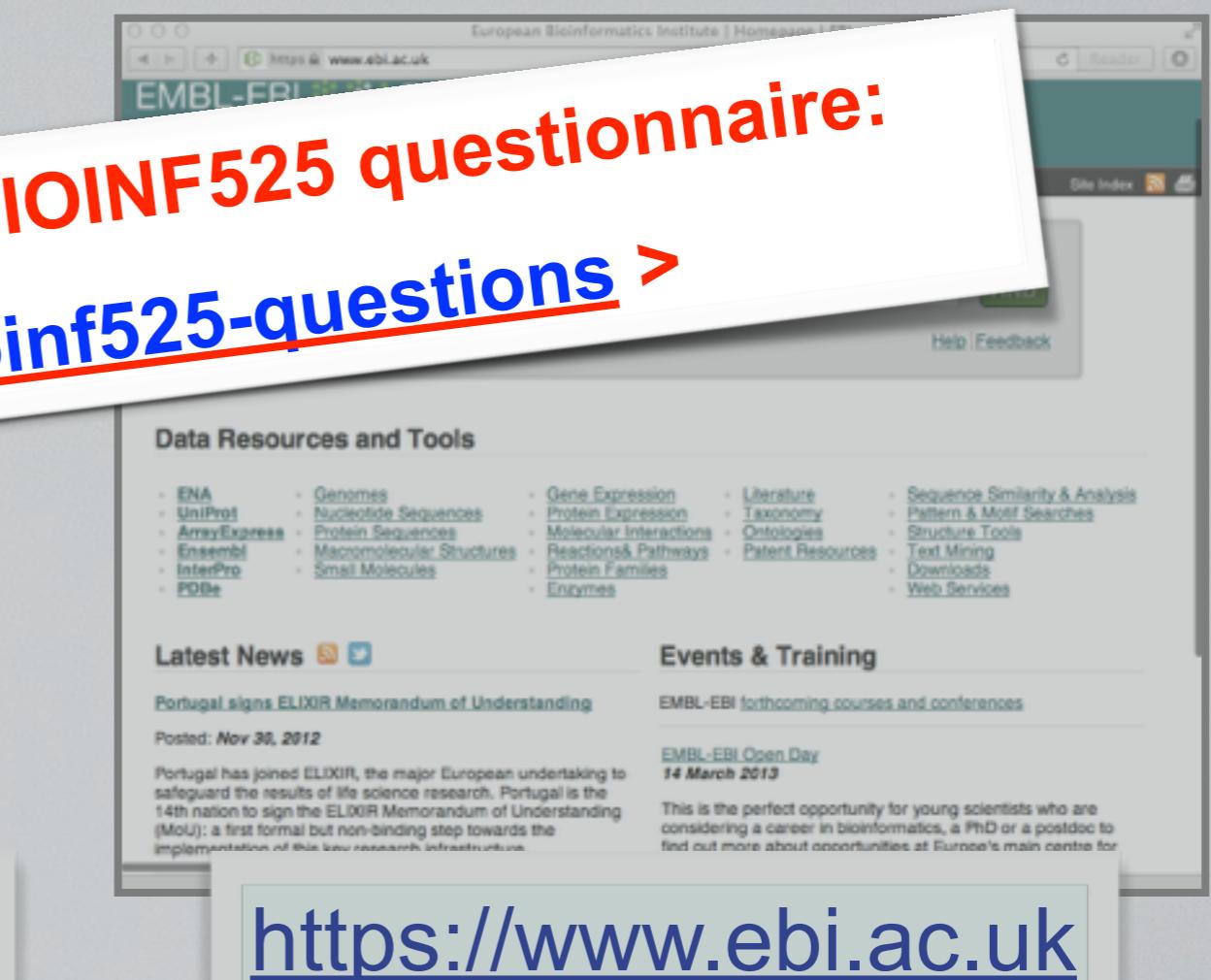
Key Online Bioinformatics Resources: NCBI & EBI

The NCBI and EBI are invaluable, publicly available resources for biomedical research

Please take the initial BIOINF525 questionnaire:
< tinyurl.com/bioinf525-questions >



<http://www.ncbi.nlm.nih.gov>



<https://www.ebi.ac.uk>

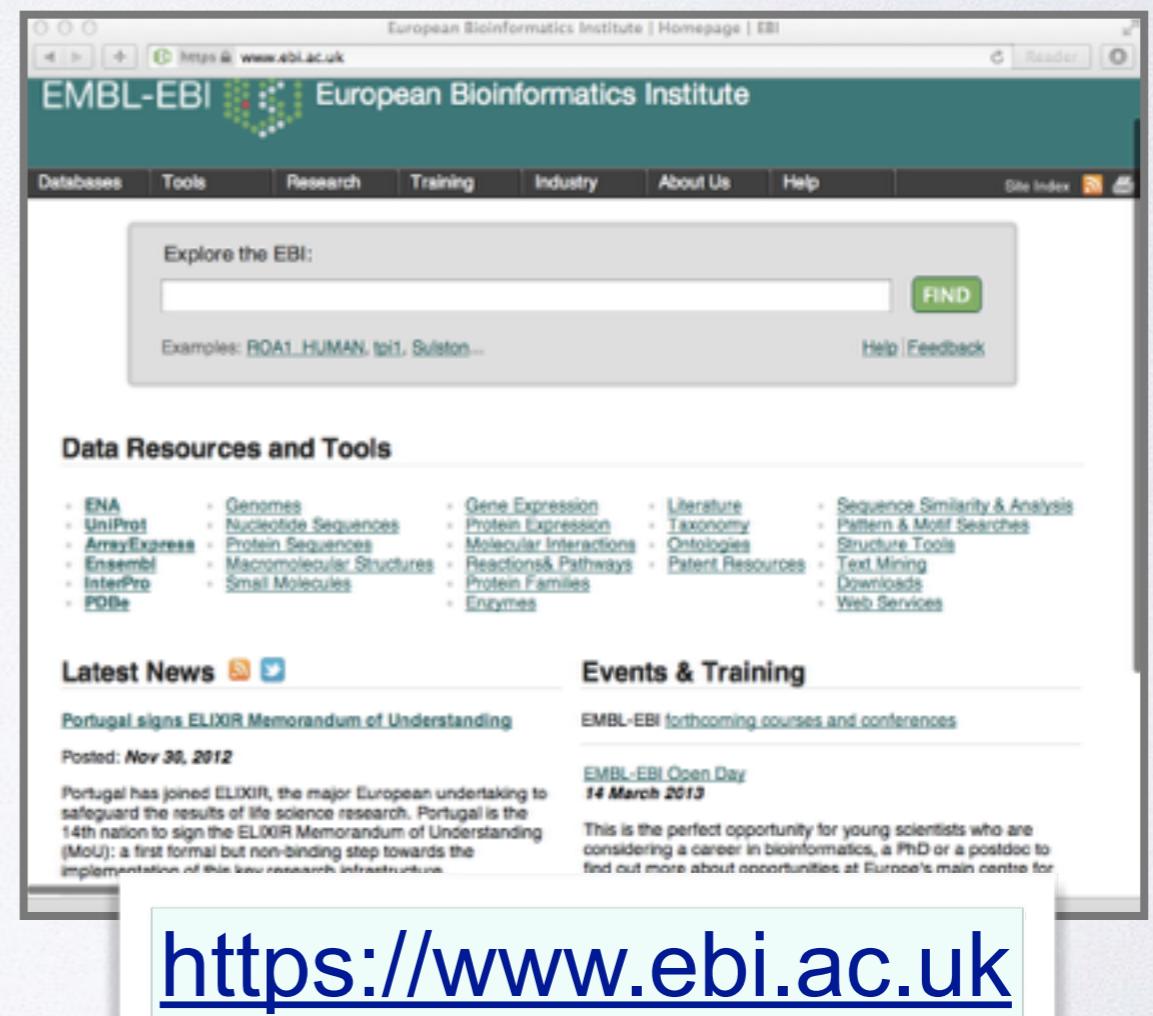
Key Online Bioinformatics Resources: NCBI & EBI

The NCBI and EBI are invaluable, publicly available resources for biomedical research



The screenshot shows the NCBI homepage with a blue header bar containing the NCBI logo, a search bar, and a "Sign in to NCBI" button. Below the header, there's a "Welcome to NCBI" section with a brief introduction and links to "About the NCBI", "Mission", "Organization", "Research", and "RSS Feeds". To the right, there's a "Popular Resources" sidebar listing links to PubMed, Bookshelf, PubMed Central, PubMed Health, BLAST, Nucleotide, Genome, SNP, Gene, Protein, and PubChem. At the bottom left, there's a "3D Structures" section featuring a 3D molecular model and a navigation menu from 1 to 8. A "NCBI Announcements" section is also present.

<http://www.ncbi.nlm.nih.gov>



The screenshot shows the EBI homepage with a green header bar containing the EMBL-EBI logo and the text "European Bioinformatics Institute". Below the header, there's a navigation bar with links to "Databases", "Tools", "Research", "Training", "Industry", "About Us", "Help", and "Site Index". A search bar with a "FIND" button is located in the center. Below the search bar, there's a "Explore the EBI:" input field and a "Examples: ROA1_HUMAN.t01. Sulston..." placeholder. To the right, there's a "Data Resources and Tools" section listing various databases and tools, followed by "Latest News" and "Events & Training" sections.

<https://www.ebi.ac.uk>

National Center for Biotechnology Information (NCBI)

- Created in 1988 as a part of the National Library of Medicine (NLM) at the National Institutes of Health
- NCBI's mission includes:
 - ▶ Establish **public databases**
 - ▶ Develop **software tools**
 - ▶ **Education** on and dissemination of biomedical information
- We will cover a number of core NCBI databases and software tools in the lecture



<http://www.ncbi.nlm.nih.gov>

National Center for Biotechnology Information

NCBI Resources How To Sign in to NCBI

All Databases Search

NCBI Home Resource List (A-Z) All Resources Chemicals & Bioassays Data & Software DNA & RNA Domains & Structures Genes & Expression Genetics & Medicine Genomes & Maps Homology Literature Proteins Sequence Analysis Taxonomy Training & Tutorials Variation

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

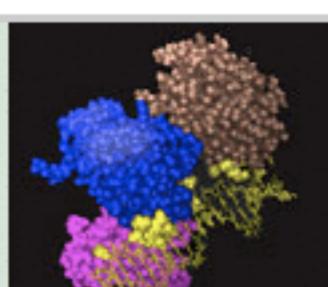
[About the NCBI](#) | [Mission](#) | [Organization](#) | [Research](#) | [RSS Feeds](#)

Get Started

- [Tools](#): Analyze data using NCBI software
- [Downloads](#): Get NCBI data or software
- [How-To's](#): Learn how to accomplish specific tasks at NCBI
- [Submissions](#): Submit data to GenBank or other NCBI databases

3D Structures

Explore three-dimensional structures of proteins, DNA, and RNA molecules. Examine sequence-structure relationships, active sites, molecular interactions, biological activities of bound chemicals, and associated biosystems.



Popular Resources

PubMed
Bookshelf
PubMed Central
PubMed Health
BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem

NCBI Announcements

New version of Genome Workbench available 06 Sep
An integrated, downloadable applicati

<http://www.ncbi.nlm.nih.gov>

National Center for Biotechnology Information

NCBI Resources How To Sign in to NCBI

All Databases Search

NCBI Home Resource List (A-Z) All Resources Chemicals & Bioassays Data & Software DNA & RNA Domains & Structures Genes & Expression Genetics & Medicine Genomes & Maps Homology Literature Proteins Sequence Analysis Taxonomy Training & Tutorials Variation

Welcome to NCBI

The National Center for Biotechnology Information provides access to information and resources that support basic research and health by providing access to databases, tools, and information.

About the NCBI | Mission | Our History

Get Started

- Tools: Analyze data using NCBI tools
- Downloads: Get NCBI data files
- How-To's: Learn how to access and use NCBI resources
- Submissions: Submit data to NCBI databases

3D Structures

Explore three-dimensional structures of proteins, DNA, and RNA molecules. Examine sequence-structure relationships, active sites, molecular interactions, biological activities of bound chemicals, and associated biosystems.

Popular Resources

PubMed Bookshelf PubMed Central PubMed Health BLAST Nucleotide Genome SNP Gene Protein PubChem

Resources

Central Health

Announcements

New version of Genome Workbench available 06 Sep An integrated, downloadable application

A screenshot of the NCBI homepage. The sidebar on the left lists various resources like NCBI Home, Resource List (A-Z), and 3D Structures. The main content area features a 'Welcome to NCBI' section and a 'Get Started' list. On the right, there's a 'Popular Resources' sidebar containing links to PubMed, Bookshelf, PubMed Central, PubMed Health, BLAST, Nucleotide, Genome, SNP, Gene, Protein, and PubChem. A red bracket on the right side of the sidebar groups the 'Gene', 'Protein', and 'PubChem' links, while three separate red arrows point to the 'PubMed', 'BLAST', and 'Gene' links individually.

<http://www.ncbi.nlm.nih.gov>

National Center for Biotechnology Information

NCBI Resources How To Sign in to NCBI

All Databases Search

NCBI Home Resource List (A-Z)

Welcome to NCBI
The National Center for Biotechnology Information advances science

Popular Resources PubMed

Notable NCBI databases include:
GenBank, RefSeq, PubMed, dbSNP

and the search tools ENTREZ and BLAST

Homology Literature Proteins Sequence Analysis Taxonomy Training & Tutorials Variation

databases

3D Structures
Explore three-dimensional structures of proteins, DNA, and RNA molecules. Examine sequence-structure relationships, active sites, molecular interactions, biological activities of bound chemicals and associated biosystems.

Protein PubChem

NCBI Announcements
New version of Genome Workbench available 06 Sep
An integrated, downloadable applicati

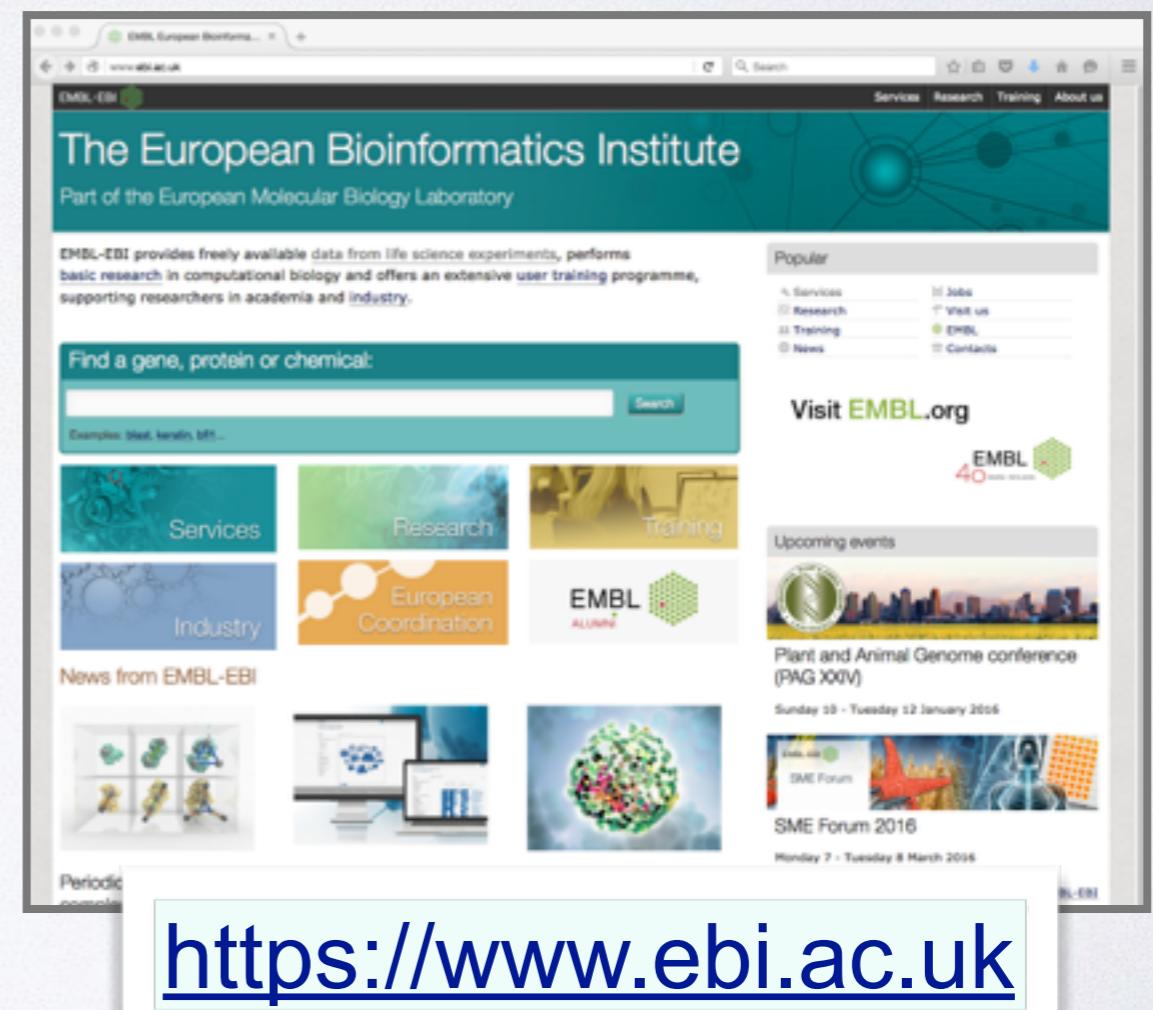
Key Online Bioinformatics Resources: NCBI & EBI

The NCBI and EBI are invaluable, publicly available resources for biomedical research



The screenshot shows the NCBI homepage with a blue header bar containing the NCBI logo, a search bar, and links for "All Databases" and "Search". Below the header, there's a "Welcome to NCBI" section with a brief introduction and links to "About the NCBI", "Mission", "Organization", "Research", and "RSS Feeds". A "Get Started" section lists links for "Tools", "Downloads", "How To", and "Submissions". A "3D Structures" section features a 3D molecular model and a navigation menu from 1 to 8. On the right, there's a "Popular Resources" sidebar with links to PubMed, Bookshelf, PubMed Central, PubMed Health, BLAST, Nucleotide, Genome, SNP, Gene, Protein, and PubChem. A "NCBI Announcements" section highlights the new version of the Genome Workbench and the July Newsletter.

<http://www.ncbi.nlm.nih.gov>



The screenshot shows the EMBL-EBI homepage with a green header bar containing the EMBL-EBI logo, a search bar, and links for "Services", "Research", "Training", and "About us". Below the header, there's a main title "The European Bioinformatics Institute" and a subtitle "Part of the European Molecular Biology Laboratory". A central search bar allows users to "Find a gene, protein or chemical". To the right, there's a "Popular" section with links to "Services", "Research", "Training", and "News". A "Visit EMBL.org" section features the EMBL 40th anniversary logo and links to "Upcoming events", including the "Plant and Animal Genome conference (PAG XXIV)" and the "SME Forum 2016".

<https://www.ebi.ac.uk>

European Bioinformatics Institute (EBI)

- Created in 1997 as a part of the European Molecular Biology Laboratory (EMBL)
- EBI's mission includes:
 - ▶ providing freely available **data and bioinformatics services**
 - ▶ and providing advanced **bioinformatics training**
- We will briefly cover several EBI databases and tools that have advantages over those offered at NCBI



The EBI maintains a number of high quality curated **secondary databases** and associated tools

The screenshot shows the homepage of the European Bioinformatics Institute (EBI) at www.ebi.ac.uk. The page features a dark blue header with the EMBL-EBI logo and navigation links for Services, Research, Training, and About us. Below the header, a large teal banner displays the text: "The European Bioinformatics Institute Part of the European Molecular Biology Laboratory". A central text block states: "EMBL-EBI provides freely available data from life science experiments, performs basic research in computational biology and offers an extensive user training programme, supporting researchers in academia and industry." To the right, a "Popular" sidebar lists links to Services, Research, Training, News, Jobs, Visit us, EMBL, and Contacts. A search bar is located at the top of the main content area. Below the search bar, there's a "Find a gene, protein or chemical:" input field with examples like "blast, keratin, bfl1...". To the right of this input field is a "Search" button. The main content area contains several cards: "Services" (highlighted with a red border), "Research", "Training", "Industry", "European Coordination", and "EMBL ALUMNI". At the bottom left, there's a section for "News from EMBL-EBI" with three small thumbnail images. On the right side, there's a "Visit EMBL.org" section featuring the EMBL 40th anniversary logo and information about the "Plant and Animal Genome conference (PAG XXIV)". The date "Sunday 10 - Tuesday 12 January 2016" is also mentioned.

EMBL European Bioinforma...

www.ebi.ac.uk

Search

Services | Research | Training | About us

The European Bioinformatics Institute

Part of the European Molecular Biology Laboratory

EMBL-EBI provides freely available data from life science experiments, performs basic research in computational biology and offers an extensive user training programme, supporting researchers in academia and industry.

Find a gene, protein or chemical:

Examples: blast, keratin, bfl1...

Search

Services

Research

Training

Industry

European Coordination

EMBL ALUMNI

Popular

- Services
- Research
- Training
- News
- Jobs
- Visit us
- EMBL
- Contacts

Visit EMBL.org

EMBL 40 YEARS 1974-2014

Upcoming events

INTERNATIONAL PLANT & ANIMAL GENOME CONFERENCE

Plant and Animal Genome conference (PAG XXIV)

Sunday 10 - Tuesday 12 January 2016

News from EMBL-EBI

The EBI maintains a number of high quality curated **secondary databases** and associated tools

The screenshot shows the EMBL-EBI Services website. At the top, there's a navigation bar with links for Services, Research, Training, and About us. Below the header, a large banner features a blue-toned illustration of molecular structures and a hand holding a test tube. The main content area has a teal header "Services". Below it, a menu bar includes Overview, A to Z, Data submission, and Support. The "Overview" tab is active. The main content is titled "Bioinformatics services" and contains a paragraph about maintaining comprehensive molecular databases. To the right, a "Popular" sidebar lists links to Ensembl, UniProt, PDB, ArrayExpress, ChEMBL, BLAST, Europe PMC, Reactome, Train online, and Support. Another sidebar on the right shows "Service news" with a photo of a butterfly and a "Training" section.

Services < EMBL-EBI

www.ebi.ac.uk/services

Search

Services | Research | Training | About us

Services

Overview | A to Z | Data submission | Support

Bioinformatics services

We maintain the world's most comprehensive range of **freely available** and up-to-date molecular databases. Developed in collaboration with our colleagues worldwide, our services let you share data, perform complex queries and analyse the results in different ways. You can work locally by downloading our data and software, or use our web services to access our resources programmatically. You can read more about our services in the journal *Nucleic Acids Research*.

DNA & RNA
genes, genomes & variation

Gene expression
RNA, protein & metabolite expression

Proteins
sequences, families & motifs

Structures
Molecular & cellular structures

Systems
reactions, interactions & pathways

Chemical biology
chemogenomics & metabolomics

Ontologies
taxonomies & controlled vocabularies

Literature
Scientific publications & patents

Cross domain
cross-domain tools & resources

Popular

- Ensembl
- UniProt
- PDB
- ArrayExpress
- ChEMBL
- BLAST
- Europe PMC
- Reactome
- Train online
- Support

Service news

Training

The EBI maintains a number of high quality curated **secondary databases** and associated tools

The screenshot shows the EBI Services website at www.ebi.ac.uk/services. The page features a navigation bar with links to Services, Research, Training, and About us. Below the navigation is a banner with a molecular structure background. A main heading "Services" is followed by a sub-section "Bioinformatics services". A text block explains the maintenance of comprehensive molecular databases and their availability. Below this are nine service categories arranged in a grid:

- DNA & RNA (genes, genomes & variation)
- Gene expression (RNA, protein & metabolite expression)
- Proteins (sequences, families & motifs) - This box is highlighted with a red border.
- Structures (Molecular & cellular structures)
- Systems (reactions, interactions & pathways)
- Chemical biology (chemogenomics & metabolomics)
- Ontologies (taxonomies & controlled vocabularies)
- Literature (Scientific publications & patents)
- Cross domain (cross-domain tools & resources)

To the right of the services grid is a "Popular" sidebar containing links to Ensembl, UniProt, PDBe, ArrayExpress, and ChEMBL, each with its respective logo. Below the sidebar is a decorative image of a butterfly resting on a molecular structure. At the bottom right, there is a "Training" section with a blurred image of a person working on a computer.

<https://www.ebi.ac.uk>

The EBI makes available a wider variety of **online tools** than NCBI

Proteins

Popular services



UniProt: The Universal Protein Resource

The gold-standard, comprehensive resource for protein sequence and functional annotation data.



InterPro

A database for the classification of proteins into families, domains and conserved sites.



PRIDE: The Proteomics Identifications Database

An archive of protein expression data determined by mass spectrometry.



Pfam

A database of hidden Markov models and alignments to describe conserved protein families and domains.



Clustal Omega

Multiple sequence alignment of DNA or protein sequences. Clustal Omega replaces the older ClustalW alignment tools.



HMMER - protein homology search

Fast sensitive protein homology searches using profile hidden Markov models (HMMs). Variety of different search methods for querying against both sequence and HMM target databases.



InterProScan 5

InterProScan 5 searches sequences against InterPro's predictive protein signatures. Please note that InterProScan 4.8 has been retired.

Quick links

- o Popular services in this category
- o All services in this category
- o Project websites in this category

The EBI also provides a growing selection of **online tutorials** on EBI databases and tools

The screenshot shows the homepage of the European Bioinformatics Institute (EBI). The top navigation bar includes links for Services, Research, Training, and About us. A search bar is located at the top right. The main header features the text "The European Bioinformatics Institute" and "Part of the European Molecular Biology Laboratory". Below the header, a teal-colored box contains a brief description of EMBL-EBI's mission: "EMBL-EBI provides freely available data from life science experiments, performs basic research in computational biology and offers an extensive user training programme, supporting researchers in academia and industry." To the right of this box is a "Popular" sidebar with links to Services, Research, Training, News, Jobs, Visit us, EMBL, and Contacts. A large search input field with a placeholder "Find a gene, protein or chemical:" and a "Search" button is positioned below the mission statement. Below the search field are several colored boxes: a teal "Services" box with a DNA helix icon, a green "Research" box with a brain and microscope icon, an orange "Training" box with a person at a computer icon (this box is highlighted with a red border), a blue "Industry" box with gears and a DNA helix icon, and an orange "European Coordination" box with a network icon. At the bottom left, there is a "News from EMBL-EBI" section with three small thumbnail images. On the right side, there is a "Visit EMBL.org" section featuring the EMBL 40th anniversary logo and a "Upcoming events" section for the "Plant and Animal Genome conference (PAG XXIV)".

EMBL European Bioinforma... www.ebi.ac.uk

EMBL-EBI

The European Bioinformatics Institute

Part of the European Molecular Biology Laboratory

EMBL-EBI provides freely available data from life science experiments, performs basic research in computational biology and offers an extensive user training programme, supporting researchers in academia and industry.

Find a gene, protein or chemical:

Examples: blast, keratin, bfl1...

Search

Popular

- Services
- Research
- Training
- News
- Jobs
- Visit us
- EMBL
- Contacts

Visit EMBL.org

EMBL 40 YEARS 1974-2014

Upcoming events

INTERNATIONAL PLANT & ANIMAL GENOME CONFERENCE

Plant and Animal Genome conference (PAG XXIV)

Sunday 10 - Tuesday 12 January 2016

News from EMBL-EBI

The EBI also provides a growing selection of **online tutorials** on EBI databases and tools

The screenshot shows a web browser displaying the EMBL-EBI Training online course page. The URL in the address bar is www.ebi.ac.uk/training/online/course/using-sequence-similarity-searching-tools-embl-ebi. The page title is "Using sequence similarity searching tools at EMBL-EBI: webinar". The main content area shows a thumbnail of the webinar video, which has a duration of 37:42. The video thumbnail features a blue background with a portrait of Andrew Cowley and text about using sequence similarity search tools at EMBL-EBI. To the left of the video, there is a sidebar with "Course content" sections for "Using sequence similarity searching tools at EMBL-EBI: webinar" and "Contributors". Below these is a "Print Course" link. To the right of the video, there are "Popular" links for "Train online", "Find us", and "Funding", and a "Find us at..." section with links for "Open days and career days", "Conference exhibitions", "EMBL courses and events", "Genome campus events", and "Science for schools". At the bottom of the page, there is a summary of the webinar's focus on using BLAST and PSI-Search to find homologous sequences.

Using sequence similarity searching tools at EMBL-EBI: webinar

Using sequence similarity searching tools at EMBL-EBI: webinar

Using sequence similarity search tools at EMBL-EBI

Finding homologous sequences with BLAST, FASTA, PSI-Search etc.

Andrew Cowley
andrew.cowley@ebi.ac.uk
support@ebi.ac.uk

0:00 / 37:42

This webinar focuses on how to use tools like **BLAST** and PSI-Search to find homologous sequences in EMBL-EBI databases, including tips on which tool and database to use, input formats, how to change parameters and how to interpret the results pages.

The EBI also provides a growing selection of **online tutorials** on EBI databases and tools

A screenshot of a web browser displaying the EBI Train online website. The title bar reads "Train online | EBI Train online". The address bar shows the URL "www.ebi.ac.uk/training/online/". The page header includes the EMBL-EBI logo, a search bar, and links for "Find", "Help", and "Feedback". A red "Beta" badge is visible in the top right corner. The main menu bar has links for "Databases", "Tools", "Research", "Training", "Industry", "About Us", and "Help". A secondary navigation bar on the left is titled "Navigation" and includes a link to "Train online Home". The main content area features a large heading "Notable EBI databases include:" followed by a list of database names.

Notable EBI databases include:
ENA, UniProt, Ensembl

and the tools FASTA, BLAST, InterProScan,
ClustalW, T-Coffee, MUSCLE, DALI, HMMER

Find a course

Browse by subject



[Genes and Genomes](#)



[Gene Expression](#)



[Interactions, Pathways, and Networks](#)

BIOINFORMATICS DATABASES AND ASSOCIATED TOOLS

What is a database?

Computerized store of data that is organized to provide efficient retrieval.

- Uses standardized data (record) formats to enable computer handling

Key database features allow for:

- Adding, changing, removing and merging of records
- User-defined queries and extraction of specified records

Desirable features include:

- Contains the data you are interested in
- Allows fast data access
- Provides annotation and curation of entries
- Provides links to additional information (possibly in other databases)
- Allows you to make discoveries

Bioinformatics Databases

AATDB, AceDb, ACUTS, ADB, AFDB, AGIS, AMSdb, ARR, AsDb, BBDB, BCGD, Beanref, BiolImage, BioMagResBank, BIOMDB, BLOCKS, BovGBASE, BOVMAP, BSORF, BTKbase, CANSITE, CarbBank, CARBHYD, CATH, CAZY, CCDC, CD4OLbase, CGAP, ChickGBASE, Colibri, COPE, CottonDB, CSNDB, CUTG, CyanoBase, dbCFC, dbEST, dbSTS, DDBJ, DGP, DictyDb, Picty_cDB, DIP, DOGS, DOMO, DPD, DPInteract, ECDC, ECGC, EC02DBASE, EcoCyc, EcoGene, EMBL, EMD db, ENZYME, EPD, EpoDB, ESTHER, FlyBase, FlyView, GCRDB, GDB, GENATLAS, Genbank, GeneCards, Genlilesne, GenLink, GENOTK, GenProtEC, GIFTS, GPCRDB, GRAP, GRBase, gRNAsdb, GRR, GSDB, HAEMB, HAMSTERS, HEART-2DPAGE, HEXAdb, HGMD, HIDB, HIDC, HIVdb, HotMolecBase, HOVERGEN, HPDB, HSC-2DPAGE, ICN, ICTVDB, IL2RGbase, IMGT, Kabat, KDNA, KEGG, KloTho, LGIC, MAD, MaizeDb, MDB, Medline, Mendel, MEROPS, MGDB, MGI, MHCPEP5, Micado, MitoDat, MITOMAP, MJDB, MmtDB, Mol-R-U, MPDB, MRR, MutBase, MycDB, NDB, NRSub, O-lycBase, OMIA, OMIM, OPD, ORDB, OWL, PAHdb, PatBase, PDB, PDD, Pfam, PhosphoBase, PigBASE, PIR, PKR, PMD, PPDB, PRESAGE, PRINTS, ProDom, Prolysis, PROSITE, PROTOMAP, RatMAP, RDP, REBASE, RGP, SBASE, SCOP, SeqAnaiRef, SGD, SGP, SheepMap, Soybase, SPAD, SRNA db, SRPDB, STACK, StyGene, Sub2D, SubtiList, SWISS-2DPAGE, SWISS-3DIMAGE, SWISS-MODEL Repository, SWISS-PROT, TeIDB, TGN, tmRDB, TOPS, TRANSFAC, TRR, UniGene, URNADB, V BASE, VDRR, VectorDB, WDCM, WIT, WormPep, etc ..!!!!

Bioinformatics Databases

There are lots of Bioinformatics Databases

For a annotated listing of major bioinformatics databases please see the Ctools handout

< Handout Major Databases.pdf >

Finding Bioinformatics Databases

The screenshot shows a web browser displaying the Oxford Journals | Life Sciences | Nucleic Acids Research | Database Summary Paper Categories page. The URL in the address bar is www.oxfordjournals.org/nar/database/cat/8. The page features a header with the journal's name, navigation links for journal sections like 'ABOUT THIS JOURNAL', 'CONTACT THIS JOURNAL', 'SUBSCRIPTIONS', 'CURRENT ISSUE', 'ARCHIVE', and 'SEARCH'. A sidebar on the right lists categories such as 'Compilation Paper', 'Category List', 'Alphabetical List', 'Category/Paper List', and 'Search Summary Papers'. Below the sidebar, a large blue button contains the URL <http://www.oxfordjournals.org/nar/database/cat/8>.

Oxford Journals | Life Sciences | Nucleic Acids Research | Database Summary Paper Categories
www.oxfordjournals.org/nar/database/cat/8

Oxford Journals | Life Sciences | Nucleic Acids Research | Database Summary Pa... The 2014 Nucleic Acids Research Database Issue and an updated NAR online M...

OXFORD JOURNALS CONTACT US MY BASKET MY ACCOUNT

Nucleic Acids Research

ABOUT THIS JOURNAL CONTACT THIS JOURNAL SUBSCRIPTIONS CURRENT ISSUE ARCHIVE SEARCH

Oxford Journals > Life Sciences > Nucleic Acids Research > Database Summary Paper Categories

2014 NAR Database Summary Paper Category List

- [Nucleotide Sequence Databases](#)
- [RNA sequence databases](#)
- [Protein sequence databases](#)
- [Structure Databases](#)
- [Genomics Databases \(non-vertebrate\)](#)
- [Metabolic and Signaling Pathways](#)
- [Human and other Vertebrate Genomes](#)
- [Human Genes and Diseases](#)
 - [CancerResource](#)
 - [Protein Mutant Database](#)
 - [General human genetics databases](#)
 - [General polymorphism databases](#)
 - [Cancer gene databases](#)
 - [Gene-, system- or disease-specific databases](#)
- [Microarray Data and other Gene Expression Databases](#)
- [Proteomics Resources](#)
- [Other Molecular Biology Databases](#)
- [Organelle databases](#)
- [Plant databases](#)
- [Immunological databases](#)
- [Cell biology](#)

► Compilation Paper
► Category List
► Alphabetical List
► Category/Paper List
► Search Summary Papers

<http://www.oxfordjournals.org/nar/database/cat/8>

► Compilation Paper
► Category List
► Alphabetical List
► Category/Paper List
► Search Summary Papers

Oxford University Press is not responsible for the content of external internet sites.

Major Molecular Databases

The most popular bioinformatics databases focus on:

- Biomolecular sequence (e.g. [GenBank](#), [UniProt](#))
- Biomolecular structure (e.g. [PDB](#))
- Vertebrate genomes (e.g. [Ensemble](#))
- Small molecules (e.g. [PubChem](#))
- Biomedical literature (e.g. [PubMed](#))

The are also many popular “*boutique*” databases for:

- Classifying protein families, domains and motifs (e.g. [PFAM](#), PROSITE)
- Specific organisms (e.g. WormBase, FlyBase)
- Specific proteins of biomedical importance (e.g. KinaseDB, GPCRDB)
- Specific diseases, mutations (e.g. [OMIM](#), HGMD)
- Specific fields or methods of study (e.g. GOA, IEDB)

Major Molecular Databases

The most popular bioinformatics databases focus on:

- Biomolecular sequence (e.g. [GenBank](#), [UniProt](#))
- Biomolecular structure (e.g. [PDB](#))
- Vertebrate genomes (e.g. [Ensemble](#))
- Small molecules (e.g. [PubChem](#))
- Biomedical literature (e.g. [PubMed](#))

There are also many “niche” databases for:

- Classifying families, domains and motifs (e.g. [PFAM](#), [PROSITE](#))
- Specific organisms (e.g. WormBase, FlyBase)
- Specific proteins of biomedical importance (e.g. KinaseDB, GPCRDB)
- Specific diseases, mutations (e.g. [OMIM](#), HGMD)
- Specific fields or methods of study (e.g. GOA, IEDB)

See Online: ‘Handout Major Databases.pdf’

Primary, secondary & composite databases

Bioinformatics databases can be usefully classified into *primary*, *secondary* and *composite* according to their data source.

- **Primary databases** (or archival databases) consist of data derived experimentally.
 - **GenBank**: NCBI's primary nucleotide sequence database.
 - **PDB**: Protein X-ray crystal and NMR structures.
- **Secondary databases** (or derived databases) contain information derived from a primary database.
 - **RefSeq**: non redundant set of curated reference sequences primarily from GenBank
 - **PFAM**: protein sequence families primarily from UniProt and PDB
- **Composite databases** (or *metadatabases*) join a variety of different primary and secondary database sources.
 - **OMIM**: catalog of human genes, genetic disorders and related literature
 - **GENE**: molecular data and literature related to genes with extensive links to other databases.

GENBANK & REFSEQ:

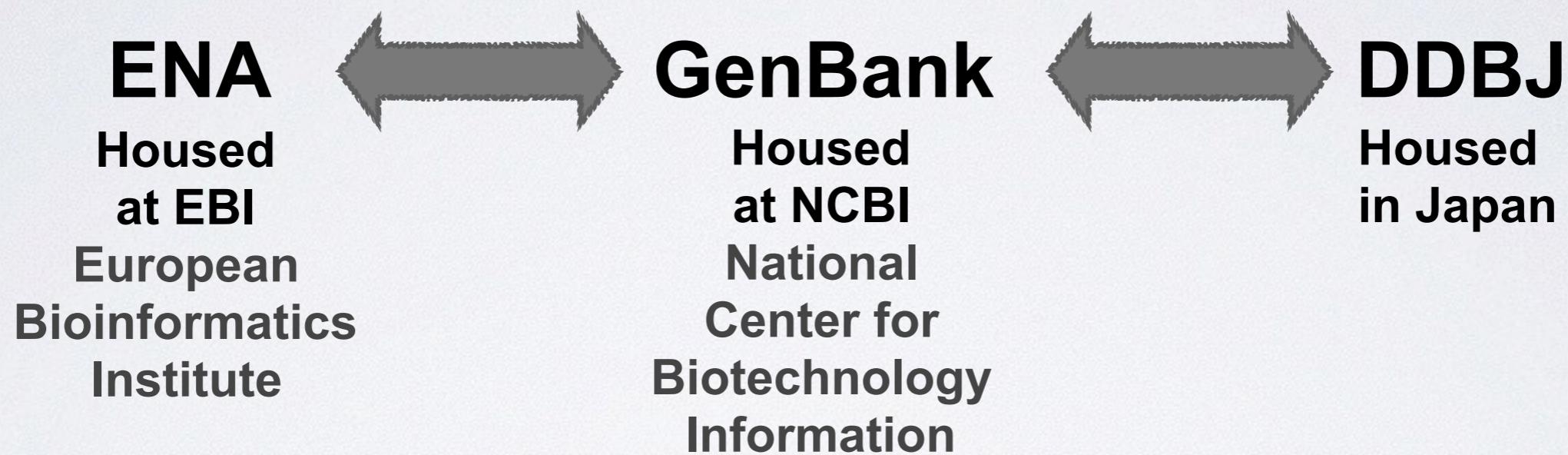
NCBI'S NUCLEOTIDE SEQUENCE DATABASES

What is GenBank?

- GenBank is NCBI's primary nucleotide only sequence database
 - ▶ Archival in nature - reflects the state of knowledge at time of submission
 - ▶ Subjective - reflects the submitter point of view
 - ▶ Redundant - can have many copies of the same nucleotide sequence
- GenBank is actually three collaborating international databases from the US, Japan and Europe
 - ▶ GenBank (US)
 - ▶ DNA Database of Japan (DDBJ)
 - ▶ European Nucleotide Archive (ENA)

GenBank, ENA and DDBJ

Share and synchronize data



- The underlying raw DNA sequences are identical
 - ▶ The different sites provide different views and ways to navigate through the data
- Access to GenBank (and other NCBI databases including RefSeq) is typically through **Entrez**, (the Google of NCBI)
more on this later

GenBank sequence record

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI
www.ncbi.nlm.nih.gov/nuccore/NM_004984.2

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI

NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide (KIF5A) AND "Homo sapiens" Search Help

Display Settings: GenBank Send: Change region shown

Customize view

Homo sapiens kinesin family member 5A (KIF5A), mRNA

NCBI Reference Sequence: NM_004984.2
[FASTA](#) [Graphics](#)

Go to:

LOCUS NM_004984 3897 bp mRNA linear PRI 10-JAN-2014
DEFINITION Homo sapiens kinesin family member 5A (KIF5A), mRNA.
ACCESSION NM_004984
VERSION NM_004984.2 GI:45446748
KEYWORDS RefSeq.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3897)
AUTHORS Kawaguchi,K.
TITLE Role of kinesin-1 in the pathogenesis of SPC10. a rare form of
her
JOURNAL Neu
227
PUBMED Gen
REMARK spa
Rev
REFERENCE 2 Pro
AUTHORS Boh
TITLE alpha-Synuclein oligomers impair neuronal microtubule-kinesin
interplay
JOURNAL J. Biol. Chem. 288 (30), 21742-21754 (2013)
PUBMED 23244021

Analyze this sequence
Run BLAST
Pick Primers
Highlight Sequence Features
Find in this Sequence

Articles about the KIF5A gene
alpha-Synuclein oligomers impair neuronal microtubule-kinesin interplay [J Biol Chem. 2013]

GenBank flat file format has defined fields including unique identifiers such as the **ACCESSION** number.

This same general format is used for other sequence database records too.

Side node: Database accession numbers

Database **accession numbers** are strings of letters and numbers used as **identifying labels** for sequences and other data within databases

- ▶ Examples (all for retinol-binding protein, RBP4):

X02775	GenBank genomic DNA sequence	DNA
NT_030059	Genomic contig	
N91759.1	An expressed sequence tag (1 of 170)	
NM_006744	RefSeq DNA sequence (from a transcript)	RNA
NP_007635	RefSeq protein	
AAC02945	GenBank protein	
Q28369	UniProtKB/SwissProt protein	Protein
1KT7	Protein Data Bank structure record	
PMID: 12205585	PubMed IDs identify articles at NCBI/NIH	Literature

GenBank sequence record

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI

www.ncbi.nlm.nih.gov/nuccore/NM_004984.2

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI

NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide (KIF5A) AND "Homo sapiens" Search Help

Display Settings: GenBank Send:

Homo sapiens kinesin family member 5A (KIF5A), mRNA

NCBI Reference Sequence: NM_004984.2

FASTA Graphics

Go to:

LOCUS NM_004984 3897 bp mRNA linear PRI 10-JAN-2014

DEFINITION Homo sapiens kinesin family member 5A (KIF5A), mRNA.

ACCESSION NM_004984

VERSION NM_004984.2 GI:45446748

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3897)

AUTHORS Kawaguchi, K.

TITLE Role of kinesin-1 in the pathogenesis of SPC10, a rare form of hereditary spastic paraplegia

JOURNAL Neuroscientist 19 (4), 336-344 (2013)

PUBMED 22785106

REMARK GeneRIF: A review of the mechanism of pathogenesis involved in spastic paraplegia type 10 when KIF5A is inactivated by mutations. Review article

REFERENCE 2 (bases 1 to 3897)

AUTHORS Prots, I., Veber, V., Brey, S., Campioni, S., Buder, K., Riek, R., Bohm, K.J. and Winner, B.

TITLE alpha-Synuclein oligomers impair neuronal microtubule-kinesin interplay

JOURNAL J. Biol. Chem. 288 (30), 21742-21754 (2013)

PUBMED 23244021

Send: Change region shown

Customize view

Analyze this sequence

Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

Articles about the KIF5A gene

alpha-Synuclein oligomers impair neuronal microtubule-kinesin interplay [J Biol Chem. 2013]

Molecular motor KIF5A is essential for GABA(A) receptor transport, a [Neuron. 2012]

Systems-wide analysis of ubiquitylation dynamics reveals a key role [Nat Cell Biol. 2012]

See all...

Pathways for the KIF5A gene

Peptide hormone metabolism

MHC class II antigen presentation

GenBank sequence record

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI
www.ncbi.nlm.nih.gov/nuccore/NM_004984.2

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI

NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide (KIF5A) AND "Homo sapiens" Search Help

Display Settings: GenBank Send: Change region shown

FASTA Graphics tomize view

Homo sapiens kinesin family member 5A (KIF5A), mRNA

NCBI Reference Sequence: NM_004984.2

Can set different display formats here

LOCUS NM_004984 3897 bp mRNA linear PRI 10-JAN-2014

DEFINITION Homo sapiens kinesin family member 5A (KIF5A), mRNA.

ACCESSION NM_004984

VERSION NM_004984.2 GI:45446748

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3897)

AUTHORS Kawaguchi,K.

TITLE Role of kinesin-1 in the pathogenesis of SPC10, a rare form of hereditary spastic paraplegia

JOURNAL Neuroscientist 19 (4), 336-344 (2013)

PUBMED 22785106

REMARK GeneRIF: A review of the mechanism of pathogenesis involved in spastic paraplegia type 10 when KIF5A is inactivated by mutations. Review article

REFERENCE 2 (bases 1 to 3897)

AUTHORS Prots,I., Veber,V., Brey,S., Campioni,S., Buder,K., Riek,R., Bohm,K.J. and Winner,B.

TITLE alpha-Synuclein oligomers impair neuronal microtubule-kinesin interplay

JOURNAL J. Biol. Chem. 288 (30), 21742-21754 (2013)

PUBMED 23244021

Analyze this sequence Run BLAST Pick Primers Highlight Sequence Features Find in this Sequence

Articles about the KIF5A gene

alpha-Synuclein oligomers impair neuronal microtubule-kinesin interplay [J Biol Chem. 2013]

Molecular motor KIF5A is essential for GABA(A) receptor transport, a [Neuron. 2012]

Systems-wide analysis of ubiquitylation dynamics reveals a key role [Nat Cell Biol. 2012]

See all...

Pathways for the KIF5A gene

Peptide hormone metabolism

MHC class II antigen presentation

FASTA sequence record

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI
www.ncbi.nlm.nih.gov/nuccore/45446748?report=fasta

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI

NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide Search Limits Advanced Help

Display Settings: FASTA Send:

Change region shown

Customize view

Homo sapiens kinesin family member 5A (KIF5A), mRNA

NCBI Reference Sequence: NM_004984.2

[GenBank](#) [Graphics](#)

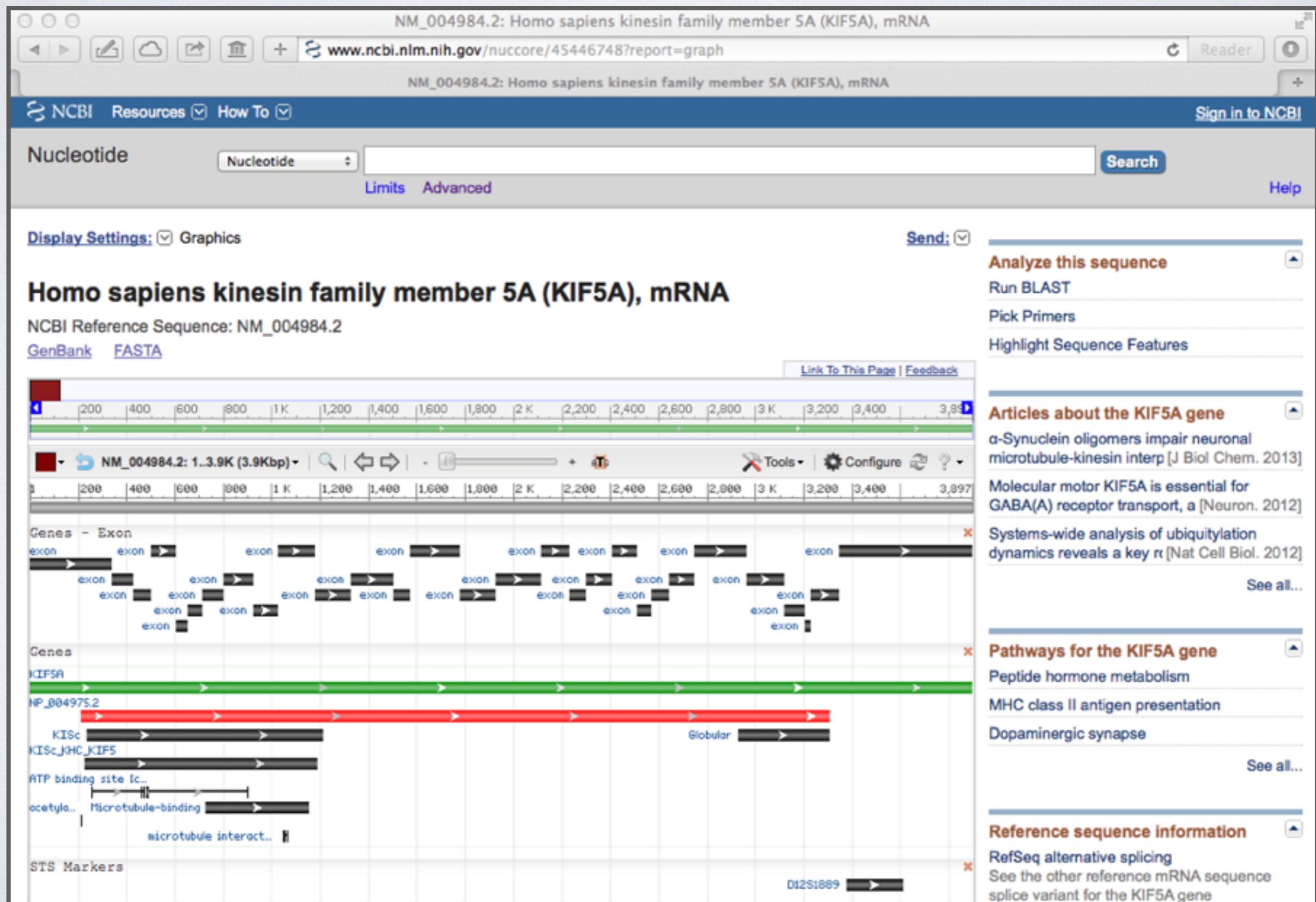
```
>gi|45446748|ref|NM_004984.2| Homo sapiens kinesin family member 5A (KIF5A), mRNA
ACGCCAGTCGCCCCATCCCGCTGCCAGGAGAGACAGCGCCCCGGCCCTGCTCCCCAGGCTT
CGCCCGGGGCCCTCAACTCTGTCCCCAGAGACTGAGCACCTGTCTCCGCCTCGCTGAGAGC
CCTCTCTCTGGAGCACACACCACCCCTGCAGCCAAGAACAGACTCCAGCCCCACGCCGGCTACCACCAT
GCCGGAGACCAACAACGAATGTAGCATCAAGGTGCTCTGCCGATTCCGGCCCTGAACCAGGCTGAGATT
CTCCGGGAGACAAGTCATCCCCATTTCAGGGACGACAGCGCTCGTTATTGGGGGAAGCCATATG
TTTTGACCGTGTATTCCCCAAACACGACTCAAGAGCAAGTTATGCATGTGCCATGCAGATGT
CAAAGATGTCCTTGCTGGCTACAATGGCACCATTTGCTTATGGACAGACATCCTCAGGGAAAACACAT
ACCATGGAGGGAAAGCTGCACGACCCCTCAGCTGATGGAATCATCCTCGAATTGCCGAGACATCTCA
ACCACATCTACTCCATGGATGAGAACCTTGAGTTCCACATCAAGGTTCTTACTTGAAATTACCTGGA
CAAATTCTGTGACCTCTGGATGTGACCAAGACAAATCTGTCGTGACAGGACAAGAACCGGGTGCCA
TTTGTCAAGGGTTGTACTGAACGCTTGTGTCAGCCGGAGGAGATTCTGGATGTGATTGATGAAGGGA
AATCAAATCGTCATGTGCTGTCACCAACATGAAACACAGCTCTCGGAGCCACAGCATCTCTCAT
CAACATCAACCAGGAGAACATGAAACCGAGCAGAACGCTCACTGGAAAGCTGTATCTGGTGGACCTGGCA
GGGACTGAGAACGCTACCAAGACTCGAGCAGAGGGAGCCGTGCTGGACGGAGGAAAGAATATCAACAACT
CACTGTCAGCTCTGGCAATGTGATCTCCGCACTGGCTGAGGGCACTAAAGCTATGTTCCATATCGTGA
CAGCAAAATGACAAGGATTCTCCAGGACTCTCTGGGGAAACTGCCCCACGACTATGTTCATCTGTGC
TCACCATCCAGTTATAATGATGCAGAGACCAAGTCCACCCGTATGTTGGCAGGGCAAAGACCATTA
AGAACACTGCCCTCACTAAATTGGAGTTGACTGCTGAGCAGTGGAAAGAAGAAATATGAGAAGGAGAAGGA
GAAGACAAAGGCCAGAAGGAGACGATTGCAAGCTGGAGGCTGAGCTGAGCCGGTGGCGCAATGGAGAG
AAATGTCCTGAGACAGACGCCCTGGCTGGGAGGAGGAGCCAGGGCTCTGTGAGGAGACCC
CTGTGAATGACAACCTCATCCATCGTGGCCATCGGCCGAGGAGCCAGAAATACGAGGAGGAGAT
CCGCCGTCTCTATAAGCAGCTGACGACAAGGATGATGAAATCAACCAACAAAGCCAACTCATAGAGAAG
CTCAAGCAGCAAATGCTGGACCAGGAAGAGCTGCTGGTGTCCACCCGAGGAGACAACGAGAAGGTCCAGC
GGGAGCTGAGCCACCTGCAATCAGAGAACGATGCCGTAAGGATGAGCTGAAGGAAGTGTGAGGCCCT
CGAGGAGCTGGCTGTGAACTATGACCAGAAGTCCCAGGAGGCTGAGGAGAACAGCCAGCAGAACAGCTT
CTGGTGGATGAGCTCTCAGAAGGTGGCCACCATGCTGTCCCTGGAGTCTGAGTTGAGCCGGCTACAGG
ACGTCAGTGGACACCAGCGAAAACGAATTGCTGAGGTGCTGAACGGCTGATGAAGGATCTGAGCGAGTT
```

FASTA sequence files consist of records where each record begins with a “>” and header information on that same line. Each subsequent line of the record is sequence information.

This format is commonly used by sequence analysis programs.

Pathways for the KIF5A gene
Peptide hormone metabolism
MHC class II antigen presentation

GenBank ‘graphics’ sequence record



GenBank sequence record, cont.

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI

www.ncbi.nlm.nih.gov/nuccore/NM_004984.2

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI

NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide (KIF5A) AND "Homo sapiens" Search Help

Display Settings: GenBank Send:

Homo sapiens kinesin family member 5A (KIF5A), mRNA

NCBI Reference Sequence: NM_004984.2

FASTA Graphics

Go to:

LOCUS NM_004984 3897 bp mRNA linear PRI 10-JAN-2014

DEFINITION Homo sapiens kinesin family member 5A (KIF5A), mRNA.

ACCESSION NM_004984

VERSION NM_004984.2 GI:45446748

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3897)

AUTHORS Kawaguchi, K.

TITLE Role of kinesin-1 in the pathogenesis of SPC10, a rare form of hereditary spastic paraplegia

JOURNAL Neuroscientist 19 (4), 336-344 (2013)

PUBMED 22785106

REMARK GeneRIF: A review of the mechanism of pathogenesis involved in spastic paraplegia type 10 when KIF5A is inactivated by mutations. Review article

REFERENCE 2 (bases 1 to 3897)

AUTHORS Prots, I., Veber, V., Brey, S., Campioni, S., Buder, K., Riek, R., Bohm, K.J. and Winner, B.

TITLE alpha-Synuclein oligomers impair neuronal microtubule-kinesin interplay

JOURNAL J. Biol. Chem. 288 (30), 21742-21754 (2013)

PUBMED 23244071

Send: Change region shown

Customize view

Analyze this sequence

Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

Articles about the KIF5A gene

alpha-Synuclein oligomers impair neuronal microtubule-kinesin interplay [J Biol Chem. 2013]

Molecular motor KIF5A is essential for GABA(A) receptor transport, a [Neuron. 2012]

Systems-wide analysis of ubiquitylation dynamics reveals a key role [Nat Cell Biol. 2012]

See all...

Pathways for the KIF5A gene

Peptide hormone metabolism

MHC class II antigen presentation

GenBank sequence record, cont.

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI

www.ncbi.nlm.nih.gov/nuccore/45446748?report=genbank&to=3897#feature_45446748

Reader

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI

NUC

Disp

Ho

NCB

FAST

Go to

LOCU

DEFI

ACCE

VERS

KEYW

SOUR

OR

REPE

AU

TI

JO

P

RE

REFE

AU

TI

JO

FEATUR

source

gene

exon

misc_feature

CDS

OMIM

Probe

Protein

PubMed

PubMed (RefSeq)

The **FEATURES** section contains annotations including a conceptual translation of the nucleotide sequence.

Recent activity

Turn Off Clear

Homo sapiens kinesin family member 5A (KIF5A), mRNA Nucleotide

(kinesin) AND "Homo sapiens"[orgn] (1351) Nucleotide

kinesin (37064) Nucleotide

See more...

MAETNNNECSIKVLCRFRPLNQAEILRGDKFIPIFQGDDSVVIGG
KPYVFDRVFPNTTQEQQVYHACAMQIVKDVLAGYNGTIFAYGQTSSGKTHMEGKLHD
PQLMGIIPRIARDIFNHIYSMDENLEFHIVSYFEIYLDKIRDLLDVTKTNLSVHEDK
NRVPFVKGCTERFVSSPEEILDVIDEGKSNRHVAVTNMNEHSSRSHSIFLINIKQENM
ETEQKLSGKLYLVDLAGSEKSKTGAEGAVLDEAKNINKSLSALGNVISALAEGTGSY
VPYRDSKMTRILQDSLCCNCRTTMFICCPSSYNDAAETKSTLMPCQRAKTIKNNTASVN

GenBank sequence record, cont.

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI
www.ncbi.nlm.nih.gov/nuccore/45446748?report=genbank&to=389#sequence_45446748 Reader

Homo sapiens kinesin family member 5A (KIF5A), mRNA – Nucleotide – NCBI

/gene="KIF5A"
/gene_synonym="D12S1889; MY050; NKHC; SPC10"
/standard_name="D12S1889"
/db_xref="UniSTS:48006"

ORIGIN

```
1 acgccccaggc cggccgcata ccgtgtccgc aggagagaga cagcgccccc cggccctgt  
61 cccccaggctt cggccggcgc ccctcaactc tttccccaga gactgagcac ctgttcctcg  
121 cctccggcctc tgctgagagc cctcttcctt ggagcacaca ccacccctgc agcccaagaa  
181 gagtcccaggc cccacgcccgg ctaccaccat ggcggagacc aacaacgaat gtacatcaa  
241 ggtgtcttc cgattccggc ccctgaacca ggctgagatt ctgcggggag acaagttcat  
301 ccccatttc caaggggacg acagcgttgt tattgggggg aagccatatg ttttgaccg  
361 tgtattcccc ccaaacacacga ctcaagagca agtttatcat gcatgtgccca tgcagattgt  
421 caaagatgtc ctgtgtggct acaatggcac cattttgtt tatggacaga catcctcagg  
481 gaaaacacat accatggagg gaaagctgca cgacccttagt ctgtatggaa tcatttcctcg  
541 aattgcccga gacatcttca accacatcta ctccatggat gagaaccttg agttccacat  
601 caaggtttct tactttgaaa ttacacttggc caaaatttgtt gaccttctgg atgtgaccgg  
661 gacaaatctg tccgtgcacg aggacaagaa ccgggtgtcca ttgtcaagg gttgtactga  
721 acgttttgtc tccagccccgg aggagattctt ggatgtgtt gatgaaggaa aatcaaatcg  
781 tcatgtggct gtcaccaaca tgaatgaaca cagctctcg agccacacgca tcttcctcat  
841 caacatcaag caggagaaca tggaaacggc gcagaagctc agtgggaagc tgtatctgg  
901 ggacctggca gggagtgaga aggtcagcaa gactggagca gaggggagccg tgctggacga  
961 ggcaaagaat atcaacaagt cactgtcgc tctggcaat gtatctccg cactggctga  
1021 gggcactaaa agctatgttc catatcgta cagcaaaatg acaaggattc tccaggactc  
1081 tctcggggga aactgccggc cgactatgtt catctttgc tcaccatcca gttataatga  
1141 tgcagagacc aagtccaccc tgatgtttgg gcagcgggca aagaccattt agaacactgc  
1201 ctcagtaaat ttggagttga ctgtgtggca gtggaaagaa aaatatgaga aggagaaggaa  
1261 gaagacaaag gcccagaagg agacgattgc gaagctggag gctgagctga gccgtggcg  
1321 caatggagag aatgtgcctg agacagagcg cctggctggg gaggaggcag ccctggggac  
1381 cgagctctgt gaggagaccc ctgtgttgc caactcatcc atctgtgtgc gcacgcgc  
1441 cgaggagcgg cagaaatacg aggaggat ccggcgctc tataaggcgc ttgacgacaa  
1501 ggatgtgaa atcaaccaac aaagccaaact catagagaag ctcaagcgcgaaatgtgtt  
1561 ccaggaagag ctgtgtgggtt ccacccgagg agacaacgag aaggtccagc gggagctgag  
1621 ccacctgcaatc tcaagagaacg atgcccgtaa ggatgtgggtt aagggatgtc tgcaaggccct  
1681 ggaggagctg gtgtgtact atgaccagaa gtcccaaggag gtggaggaga agagccagca  
1741 gaaccagctt ctgggtggatg agctgtctca gaaggtggcc accatgtgtt ccctggagtc  
1801 ttagttgcag cgcttacagg aggtcgttgg acaccacgaa aaaccaattt ctgtgggtct  
1861 gaacgggctg atgaaggatc tgagcgatgtt cagtgttgcatt gtggcaacg gggagattaa  
1921 gctgccatgt gagatcgttggccatcgaa ggaggatgtt actgtggccc gactctacat  
1981 cagaaaaatc aaatcagaag tcaagtctgt ggtcaagcgg tgccggcagc tggagaaccc  
2041 ccagggtggag ttttgcaccgca agatggaaat gaccggcgg gagctctcat cctggccatgt  
2101 cctccatctt cagcatgagg ccaagatccg ctgcgttacg gaatacatgc agacgtgtt  
2161 gctaaagaag cggcacctgg aagagtctt ttttttttttggccatgttggccatgt  
2221 ccaggcccag gaaactgtgc atgaagtggc cctgaaggac aaggaggctt acactcaggaa  
2281 tgcagatgaa gtgaagaagg ctctggatgtt gcaatggag agtcacccggg aggcccatca  
2341 cccggcagctg gcccggatcc gggacgagat caacgagaag cagaagacca ttgtatgtt
```

The actual sequence entry starts after the word **ORIGIN**

RefSeq: NCBI's Derivative Sequence Database

- RefSeq entries are hand curated best representation of a transcript or protein (in their judgement)
- Non-redundant for a given species although alternate transcript forms will be included if there is good evidence

- Experimentally verified transcripts and proteins accession numbers begin with “NM_” or “NP_”
- Model transcripts and proteins based on bioinformatics predictions with little experimental support accession numbers begin with “XM_” or “XP_”
- RefSeq also contains contigs and chromosome records

UNIPROT:

THE PREMIER PROTEIN SEQUENCE DATABASE

UniProt: Protein sequence database

UniProt is a comprehensive, high-quality resource of protein sequence and functional information

- UniProt comprises four databases:

1. **UniProtKB** (Knowledgebase)

Containing Swiss-Prot and TrEMBL components

(these correspond to hand curated and automatically annotated entries respectively)

2. **UniRef** (Reference Clusters)

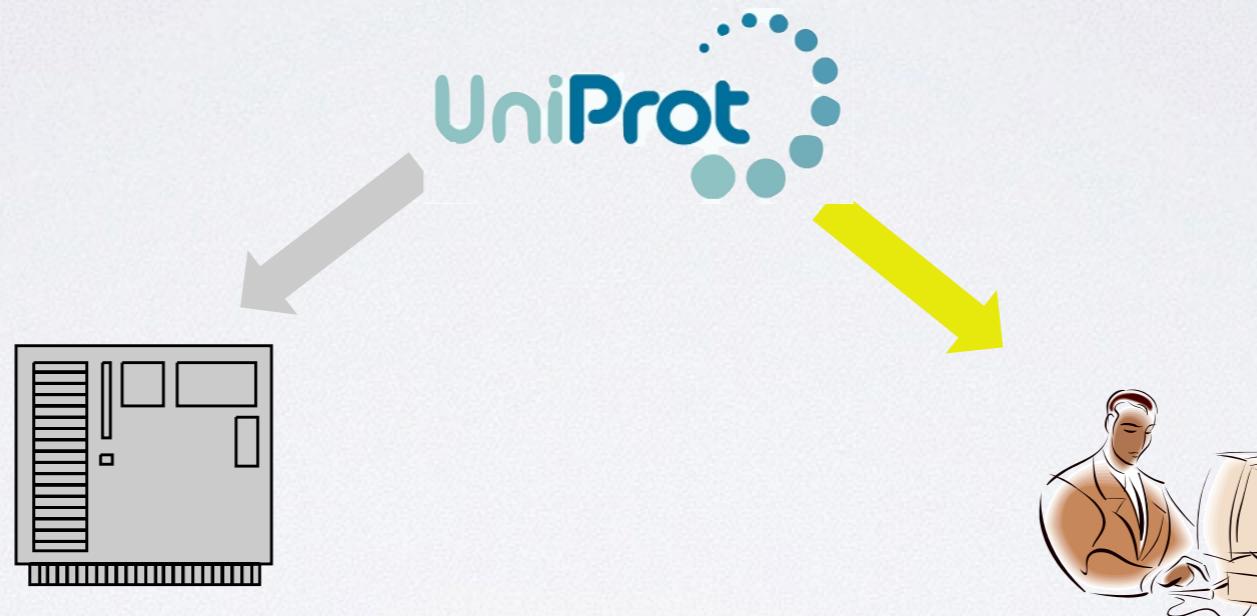
Filtered version of UniProtKB at various levels of sequence identity

e.g. UniRef90 contains sequences with a maximum of 90% sequence identity to each other

3. **UniParc** (Archive) with database cross-references to source.

4. **UniMES** (Metagenomic and Environmental Sequences)

The two sides of UniProtKB



UniProtKB/TrEMBL

Redundant, automatically
annotated - unreviewed

UniProtKB/Swiss-Prot

Non-redundant, high-quality
manual annotation - reviewed

★ Unreviewed, UniProtKB/TrEMBL **Q9N0H9** (Q9N0H9_EQUAS)

★ Reviewed, UniProtKB/Swiss-Prot **P38398** (BRCA1_HUMAN)

Indicators of which part of UniProt an entry belongs
to include the color of the stars and the ID

The main information added to a UniProt/Swiss-Prot entry

[1] "The quaking gene product necessary in embryogenesis and myelination combines features of RNA binding and signal transduction proteins."
Ebersole T.A., Chen Q., Justice M.J., Artzt K.
Nat. Genet. 12:260-265 (1996) [PubMed: 8589716] [Abstract]
Cited for: NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 3), INVOLVEMENT IN QKV, TISSUE SPECIFICITY, MUTAGENESIS

[2] "Genomic organization and alternative splicing of the mouse *Qkv* gene."
Kondo T., Furuta T., Misunaga K., Ebersole T.A., Shichiri M., Wu J., Artzt K., Yamamura K., Abe K.
Mamm. Genome 10:662-669 (1999) [PubMed: 10384037] [Abstract]
Cited for: NUCLEOTIDE SEQUENCE [GENOMIC DNA / mRNA] (ISOFORMS 2; 3; 4 AND 7), ALTERNATIVE SPlicing (ISOFORM 1).
Strain: 129/J.

Literature

Annotations

General annotation (Comments)

Function: RNA-binding protein that plays a central role in myelination. Also required for visceral endoderm function and blood vessel development. Binds to the 5'-ACAUAY-N12-CAUAY-3' RNA core sequence. Acts by regulating pre-mRNA splicing, mRNA export, mRNA stability and protein translation, as well as cellular processes including apoptosis, cell cycle, glial cell fate and development. Required to protect and promote the integrity of the MBP and CD45 mRNAs to maintain oligodendrocyte differentiation. Participates in mRNA transport by regulating the nuclear export of MBP mRNA. Isoform 1 is involved in regulation of mRNA tailoring of MAG pre-mRNA by acting as a negative regulator of MAG exon 12 alternative splicing. Isoform 3 can induce apoptosis, while heterodimerization with other isoforms result in nuclear translocation of isoform 3 and suppression of apoptosis. Isoform 4 acts as a translational repressor for GLT. May also play a role in smooth muscle development.

Subunit structure: Homodimer. Does not require RNA to homodimerize. Able to heterodimerize with BICC1.

Subcellular location: Cytoplasm. Nucleus. Note: Isoform 1 localizes predominantly in the nucleus and at lower level in cytoplasm. It shuttles between the cytoplasm and the nucleus. Isoform 3 localizes predominantly in the cytoplasm and at much lower level in nucleus. Isoform 4 localizes both in the cytosol and nucleus.

Tissue specificity: High expression in brain and peripheral nerve. Expresses in Schwann cells and oligodendrocytes in the central nervous system as well as Schwann cells. Isoform 1 is expressed in the peripheral nerve, but that expression is down-regulated during myelination. Isoform 3 is expressed in the peripheral nerve, but that expression is down-regulated during myelination. Isoform 4 is expressed in the peripheral nerve, but that expression is down-regulated during myelination and migrate away into the emerging nervous system. These have characteristics consistent with the acquisition of a glial rather than neuronal fate (at protein level). First detected in the neuroepithelium of the head folds at E7.5. Expression is strongly present ventrally in the recent brain and neural tube of E8.5 and E9.5 and in the heart. Isoform 1 is expressed in early embryos, while isoform 3 and 4 are expressed later in the embryo. Isoform 4 is expressed in the peripheral nerve, but that expression is down-regulated during myelination.

Developmental stage: Increased expression of isoform 1 is observed in the peripheral nerve during myelination, but that expression is down-regulated during myelination. Isoform 3 is expressed in the peripheral nerve, but that expression is down-regulated during myelination. Isoform 4 is expressed in the peripheral nerve, but that expression is down-regulated during myelination.

Post-translational modification:

Involvement in disease: Defects in *Qkv* are the cause of quaking (qkv). Qkv is a spontaneous mutation resulting in hypomyelination of the central and peripheral nervous systems. Mutant mice develop normally until postnatal day 10 when they display rapid tremors or 'quaking' that is especially pronounced in hindlimbs and experience convulsive tonic-clonic seizures as they mature. Mice with qkv specifically lack isoform 3.

Ontologies

Cell cycle
DNA damage
DNA repair
Fatty acid biosynthesis
Lipid synthesis
Nucleus
Polymorphism
Disease mutation
Repeat
Zinc-finger
DNA-binding
Metal-binding
Zinc
Anti-oncogene
Phosphorylation
3D-structure

Regulation of cell proliferation
Traceable author statement. Source: UniProtKB

Regulation of transcription from RNA polymerase II promoter
Traceable author statement. Source: Protic

Regulation of transcription from RNA polymerase III promoter
Traceable author statement. Source: UniProtKB

Response to estrogen stimulus
Traceable author statement. Source: UniProtKB

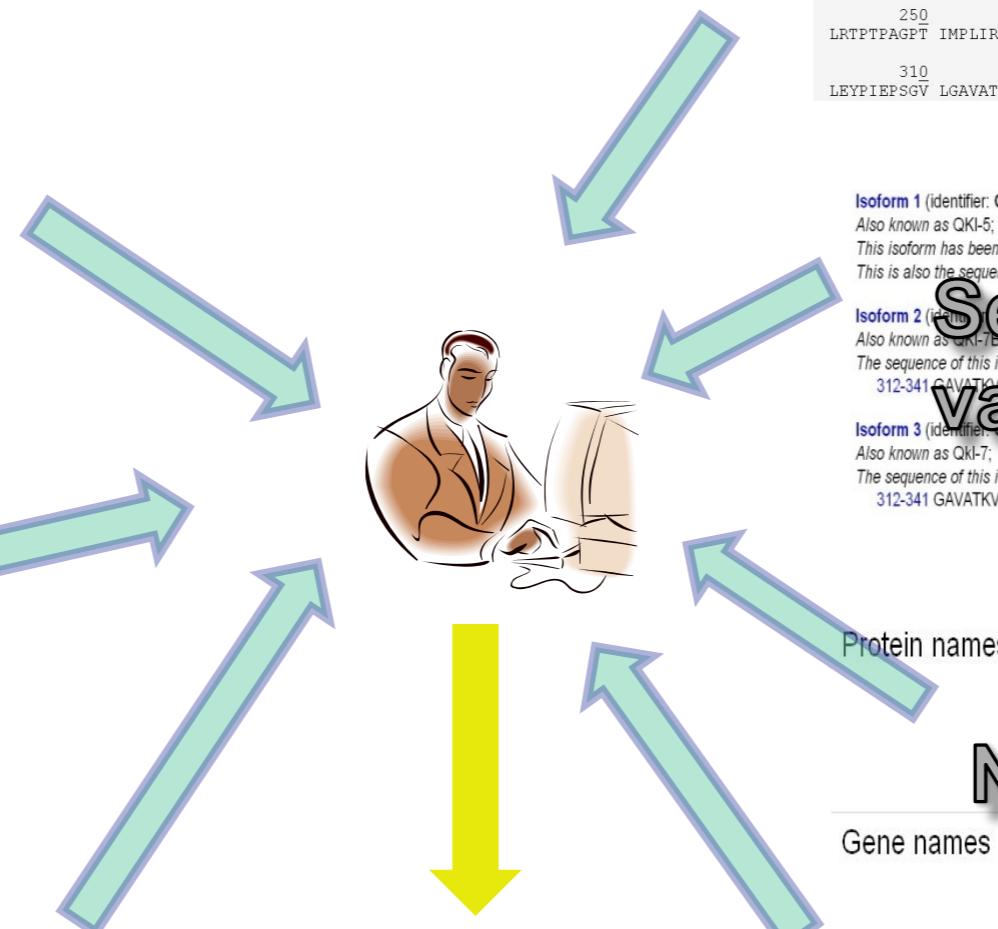
BRCA1-BARD1 complex
Inferred from direct assay. Source: UniProtKB

Gamma-tubulin ring complex
Non-traceable author statement. Source: UniProtKB

DNA binding
Traceable author statement. Source: Protic

Androgen receptor binding
Non-traceable author statement. Source: UniProtKB

Enzyme binding
Inferred from physical interaction. Source: UniProtKB



UniProt /Swiss-Prot

10	20	30	40	50	60
MVGEMETKEK	PKPTPDYLMQ	LMNDKKLMSS	LPNFCGIFNH	LERLLDEEIS	RVRKDMYNDT
70	80	90	100	110	120
LNGSTEKRSA	ELPDAVGIV	QLQEKLKYPV	KEYPDFNFVG	RILGPRGLTA	KQLEAETGCK
130	140	150	160	170	180
IMVRGKGSMR	DYKQKQNG	KENWEEHILNEQ	IHLVLLTVEDA	ONRAEIKLKR	AVEEVKKLLV
190	200	210	220	230	240
PAAEGEDSLK	KMQLMELAIL	NGT	RDANIK	SPALAFSIAA	TAQAAPIIT
250	260	270	280	290	300
LRTPTFAGT	IMPLRQIQT	AVMPNGTPHP	AAIIVPPGPE	AGLIYTPYEY	PTYLAPATSI
310	320	330	340		
LEYPIEPSGV	LGAVATKVRR	HDMRVHPYQR	IVTADRAATG	N	

Sequence

Isoform 1 (identifier: Q9QYS9-1)

Also known as QKI-5;
This isoform has been chosen as the 'canonical' sequence. All positional information in this entry refers to it.
This is also the sequence that appears in the downloadable versions of the entry.

Sequence variants

Isoform 2 (identifier: Q9QYS9-2)

Also known as QKI-7B;
The sequence of this isoform differs from the canonical sequence as follows:
312-341 GAVATKVRRHDMRVPHQVIRTADRAATGN → VWLSQRKAKNSRTVLTEPSSDLNLNTA

Isoform 3 (identifier: Q9QYS9-3)

Also known as QKI-7;
The sequence of this isoform differs from the canonical sequence as follows:
312-341 GAVATKVRRHDMRVPHQVIRTADRAATGN → EWIEMPVMPDISAH

Protein names

Protein quaking

Also known as:

Mqkl

Qkv

Gene names

Name: **Qki**

Synonyms: Qk, Qk1, Qka1

Molecule processing

Chain

1 – 341 341 Protein quaking



Regions

Domain

87 – 153 67 KH



Motif

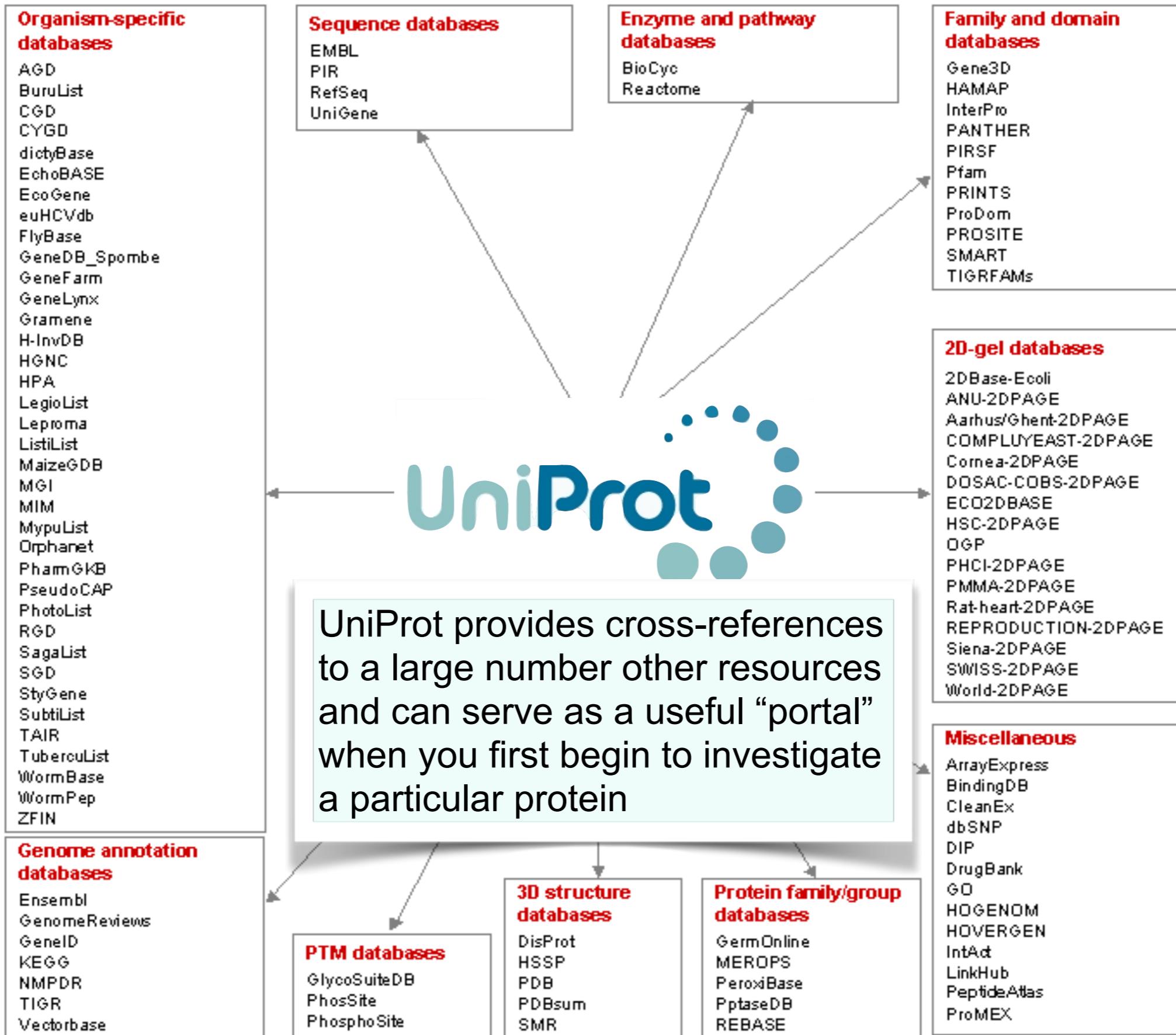
276 – 286 10 C-terminal g



Motif

324 – 330 7 Nuclear localization signal

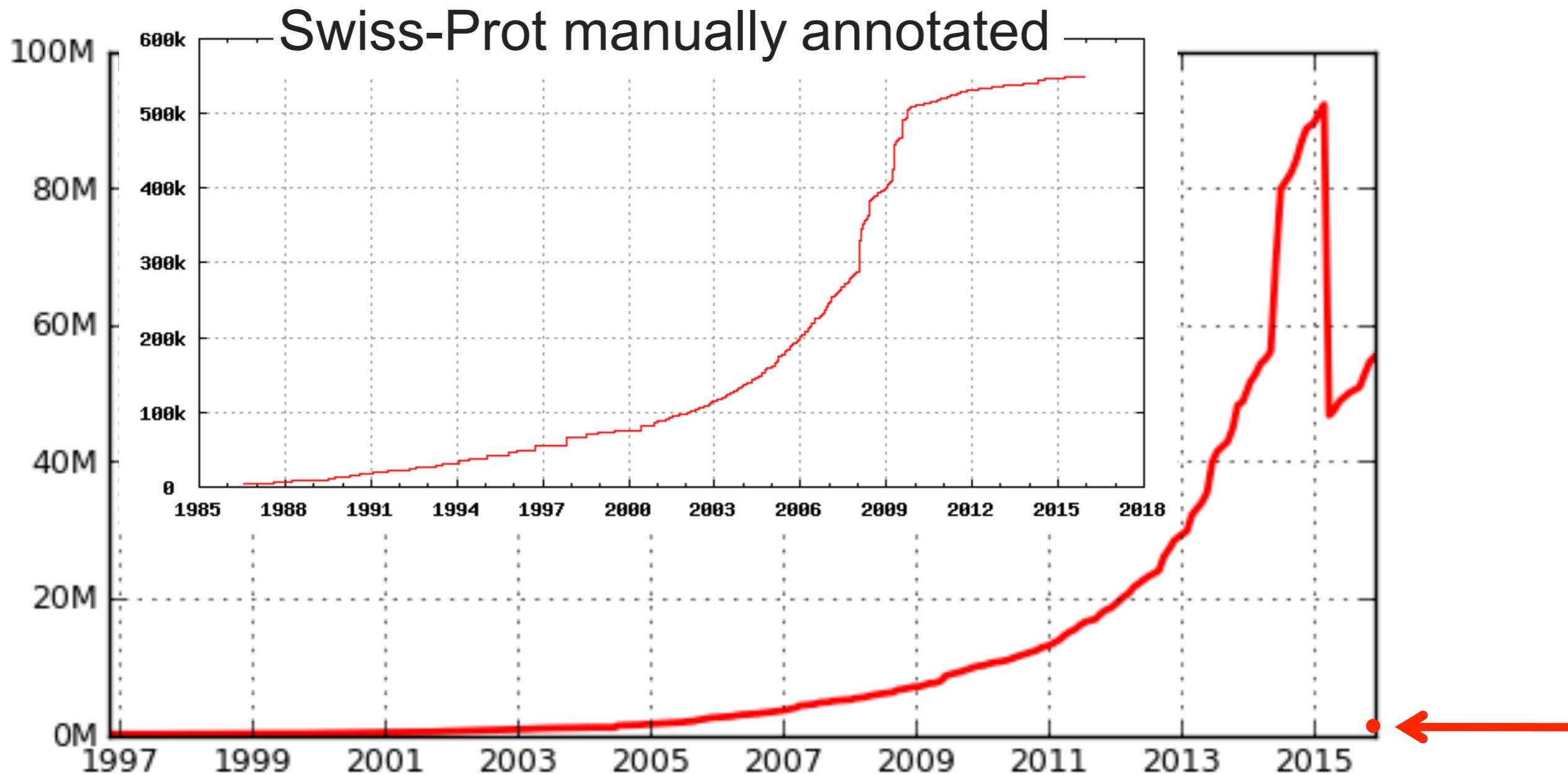
Sequence features



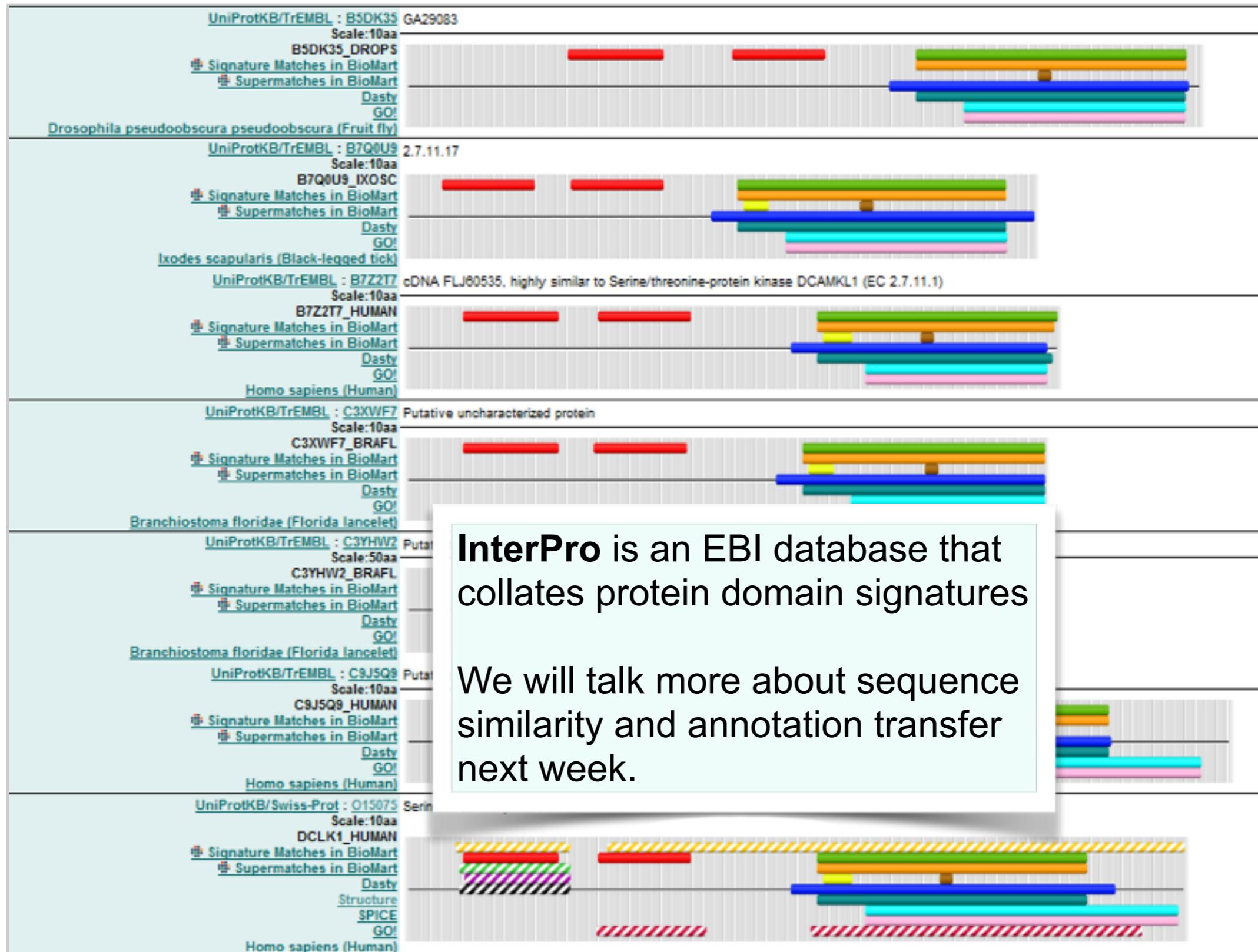
UniProt/Swiss-Prot vs UniProt/TrEMBL

- UniProtKB/Swiss-Prot is a **non-redundant** database with one entry per protein
- UniProtKB/TrEMBL is a **redundant** database with one entry per translated ENA entry (ENA is the EBI's equivalent of GenBank)
 - ▶ Therefore TrEMBL can contain multiple entries for the same protein
 - ▶ Multiple UniProtKB/TrEMBL entries for the same protein can arise due to:
 - Erroneous gene model predictions
 - Sequence errors (Frame shifts)
 - Polymorphisms
 - Alternative start sites
 - Isoforms
 - OR because the same sequence was submitted by different people

Side note: Automatic Annotation (sharing the wealth)



Same domain composition = same function = annotation transfer



DATABASE VIGNETTE

You have just come out a seminar about gastric cancer and one of your co-workers asks:

“What do you know about that ‘Kras’ gene the speaker kept taking about?”

You have some recollection about hearing of ‘Ras’ before. How would you find out more?

- Google?
- Library?
- **Bioinformatics databases at NCBI and EBI!**

<http://www.ncbi.nlm.nih.gov/>

<http://www.ncbi.nlm.nih.gov/>

Hands on demo (or see following slides)

National Center for Biotech X www.ncbi.nlm.nih.gov NCBI Resources How To Sign in to NCBI

All Databases ras Search

NCBI National Center for Biotechnology Information

NCBI Home Resource List (A-Z) All Resources Chemicals & Bioassays Data & Software DNA & RNA Domains & Structures Genes & Expression Genetics & Medicine Genomes & Maps Homology Literature Proteins Sequence Analysis Taxonomy Training & Tutorials Variation

Welcome to NCBI

The National Center for Biotechnology Information advances health by providing access to biomedical information.

About the NCBI | Mission | Organization | NCBI News

Get Started

- [Data](#): Search and analyze data using NCBI software
- [Tools](#): Get NCBI data or software
- [How Tos](#): Learn how to accomplish specific tasks at NCBI
- [Submissions](#): Submit data to GenBank or other NCBI databases

Genotypes and Phenotypes

Data from Genome Wide Association studies that link genes and diseases. See study variables, protocols, and analysis.

NCBI Announcements

RefSeq release 69 available on

The full RefSeq release 69 is now available on the FTP site with 74 records describing 50,070,460 ...

The screenshot shows the NCBI homepage with a search bar containing 'ras'. A red box highlights the search term 'ras'. The page features a sidebar with various resource links and a main content area with sections like 'Welcome to NCBI', 'Get Started', and 'Genotypes and Phenotypes'.

ras - GQuery: Global Cross X

www.ncbi.nlm.nih.gov/gquery/?term=ras

NCBI Resources How To Sign in to NCBI

Search NCBI databases

Help

ras

About 2,978,774 search results for "ras"

Literature		Genes		
Books	1,677	books and reports	EST	3,985 expressed sequence tag sequences
MeSH	402	ontology used for PubMed indexing	Gene	87,165 collected information about gene loci
NLM Catalog	223	books, journals and more in the NLM Collections	GEO DataSets	3,732 functional genomics studies
PubMed	54,672	scientific & medical abstracts/citations	GEO Profiles	1,622,789 gene expression and molecular abundance profiles
PubMed Central	96,114	full-text journal articles	HomoloGene	696 homologous gene sets for selected organisms
Health			PopSet	2,254 sequence sets from phylogenetic and population studies
ClinVar	759	human variations of clinical significance	UniGene	4,770 clusters of expressed transcripts
dbGaP	120	genotype/phenotype interaction studies	Proteins	
GTR	1,879	genetic testing registry		

A red box highlights the "Gene" entry in the "Genes" section.

77

ras - Gene - NCBI x
 www.ncbi.nlm.nih.gov/gene/?term=ras

NCBI Resources How To Sign in to NCBI

Gene Gene ras x Search Save search Advanced Help

[Show additional filters](#) [Display Settings:](#) Tabular, 20 per page, Sorted by Relevance [Send to:](#) [Hide sidebar >>](#)

[Filters: Manage Filters](#)

Did you mean ras as a gene symbol?
 Search Gene for [ras](#) as a symbol.

<< First < Prev Page 1 of 4282 Next > Last >>

Results: 1 to 20 of 85633

i Filters activated: Current only. [Clear all](#) to show 87165 items.

Name/Gene ID	Description	Location	Aliases
ras ID: 19412	resistance to audiogenic seizures [<i>Mus</i> <i>musculus</i> (house mouse)]		asr
ras ID: 43873	rasberry [<i>Drosophila</i> <i>melanogaster</i> (fruit fly)]	Chromosome X, NC_004354.4 (10744502..10749097)	Dmel_CG1799, CG11485, CG1799, Dmel\CG1799, EP(X)1093,

Top Organisms [Tree]

- Homo sapiens (1126)** (highlighted with a red box)
- Mus musculus (823)
- Rattus norvegicus (625)
- Oreochromis niloticus (533)
- Neolamprologus brichardi (507)
- All other taxa (82019)

[More...](#)

Find related data
 Database: Select Find items

Search details
 ras[All Fields] AND alive[property]

(ras) AND "Homo sapiens" [porgn:txid9606]

Gene

Gene (ras) AND "Homo sapiens"[porgn:txid9606] Search Help

Show additional filters Hide sidebar >

Display Settings: Tabular, 20 per page, Sorted by Relevance Send to:

Results: 1 to 20 of 1126 << First < Prev Page 1 of 57 Next > Last >>

i Filters activated: Current only. [Clear all](#) to show 1499 items.

Filters: Manage Filters

Find related data

Database: Select

Find items

Search details

```
ras[All Fields] AND "Homo sapiens"[porgn] AND alive[property]
```

Search See more...

Recent activity

Turn Off Clear

Name/Gene ID	Description	Location	Aliases
<input type="checkbox"/> NRAS ID: 4893	neuroblastoma RAS viral (v-ras) oncogene homolog [<i>Homo sapiens</i> (human)]	Chromosome 1, NC_000001.11 (114704464..114716894, complement)	RP5-1000E10.2, ALPS4, CMNS, N-ras, NCMS1, NS6, NRAS
<input type="checkbox"/> KRAS ID: 3845	Kirsten rat sarcoma viral oncogene homolog [<i>Homo sapiens</i> (human)]	Chromosome 12, NC_000012.12 (25205246..25250923, complement)	C-K-RAS, CFC2, K-RAS2A, K-RAS2B, K-RAS4A, K-RAS4B, K-RAS1, KRAS2, NS, NS2, RASK2

Gene sources

Genomic Categories

- Alternatively spliced
- Annotated genes
- Non-coding
- Protein-coding
- Pseudogene

Sequence content

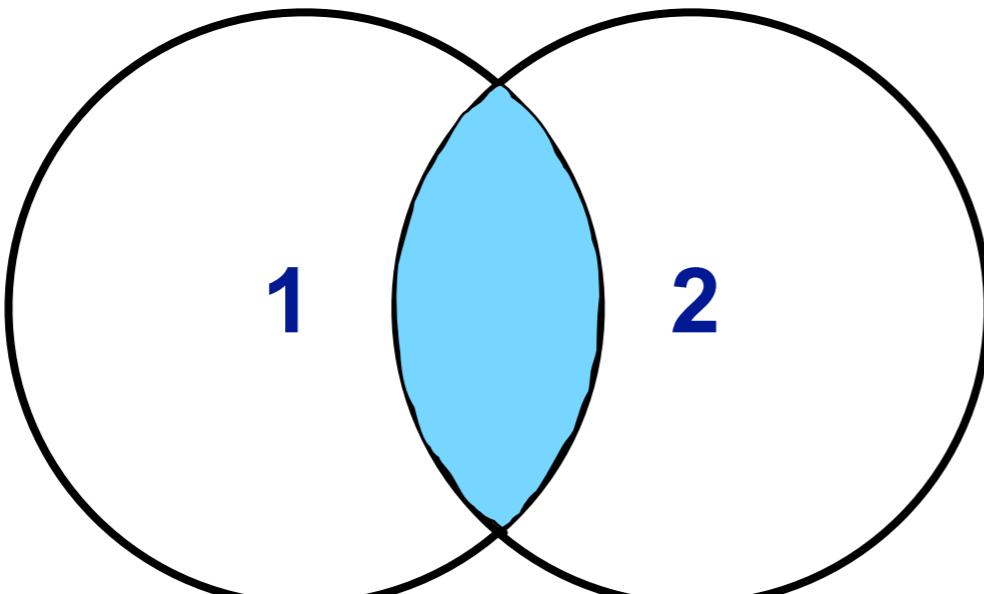
CCDS Ensembl RefSeq

Status clear

Current only

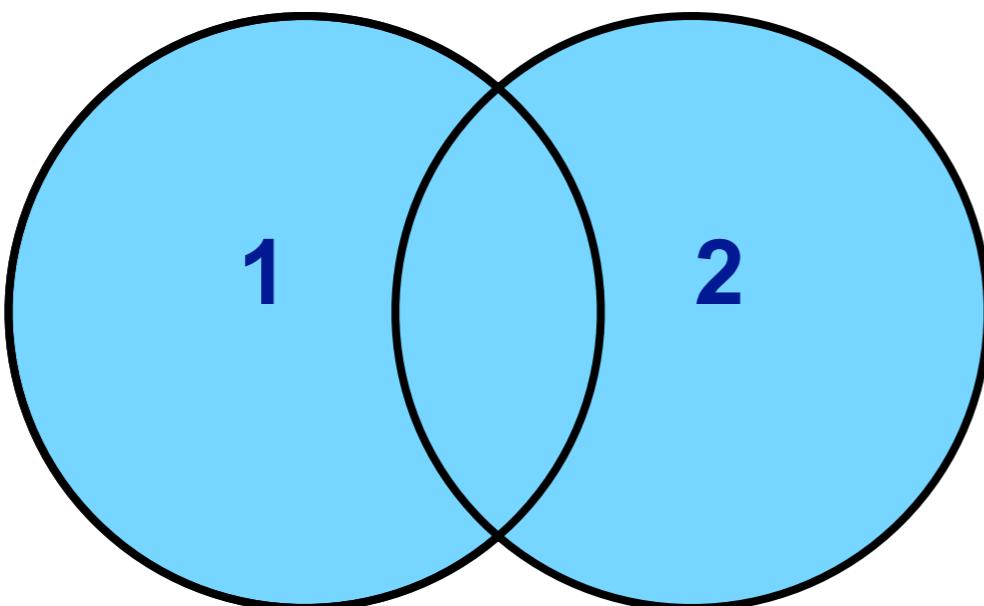
Chromosome locations Select

1 AND 2



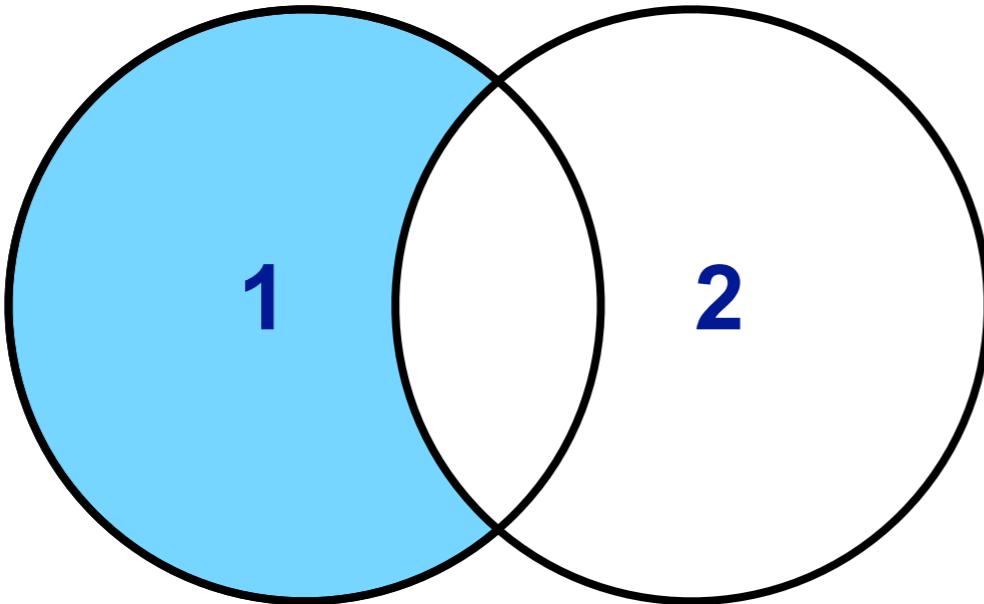
**ras AND disease
(1185 results)**

1 OR 2



**ras OR disease
(134,872 results)**

1 NOT 2



**ras NOT disease
(84,448 results)**

(ras) AND "Homo sapiens" X

www.ncbi.nlm.nih.gov/gene

NCBI Resources How To Sign in to NCBI

Gene Gene (ras) AND "Homo sapiens"[porgn:txid9606] Search Save search Advanced Help

Show additional filters Hide sidebar >>

Results: 1 to 20 of 1126 << First < Prev Page 1 of 57 Next > Last >>

i Filters activated: Current only. [Clear all](#) to show 1499 items.

Name/Gene ID	Description	Location	Aliases
<input type="checkbox"/> NRAS ID: 4893	neuroblastoma RAS viral (v-ras) oncogene homolog [Homo sapiens (human)]	Chromosome 1, NC_000001.11 (114704464..114716894, complement)	RP5-1000E10.2, ALPS4, CMNS, N-ras, NCMS1, NS6, NRAS
<input type="checkbox"/> KRAS ID: 3845	Kirsten rat sarcoma viral oncogene homolog [Homo sapiens (human)]	Chromosome 12, NC_000012.12 (25205246..25250923, complement)	C-K-RAS, CFC2, K-RAS2A, K-RAS2B, K-RAS4A, K-RAS4B, K-RAS1, KRAS2, NS, NS2, RASK2

Filters: [Manage Filters](#)

Find related data

Database: Select

Find items

Search details

```
ras[All Fields] AND "Homo sapiens"[porgn] AND alive[property]
```

Search See more...

Recent activity Turn Off Clear

Chromosome locations Select

KRAS Kirsten rat sarcoma viral oncogene homolog [*Homo sapiens* (human)]

Gene ID: 3845, updated on 4-Jan-2015

Summary

Official Symbol KRAS provided by HGNC

Official Full Name Kirsten rat sarcoma viral oncogene homolog provided by HGNC

Primary source HGNC:HGNC:6407

See related Ensembl:ENSG00000133703; HPRD:01817; MIM:190070;
Vega:OTTHUMG00000171193

Gene type protein coding

RefSeq status REVIEWED

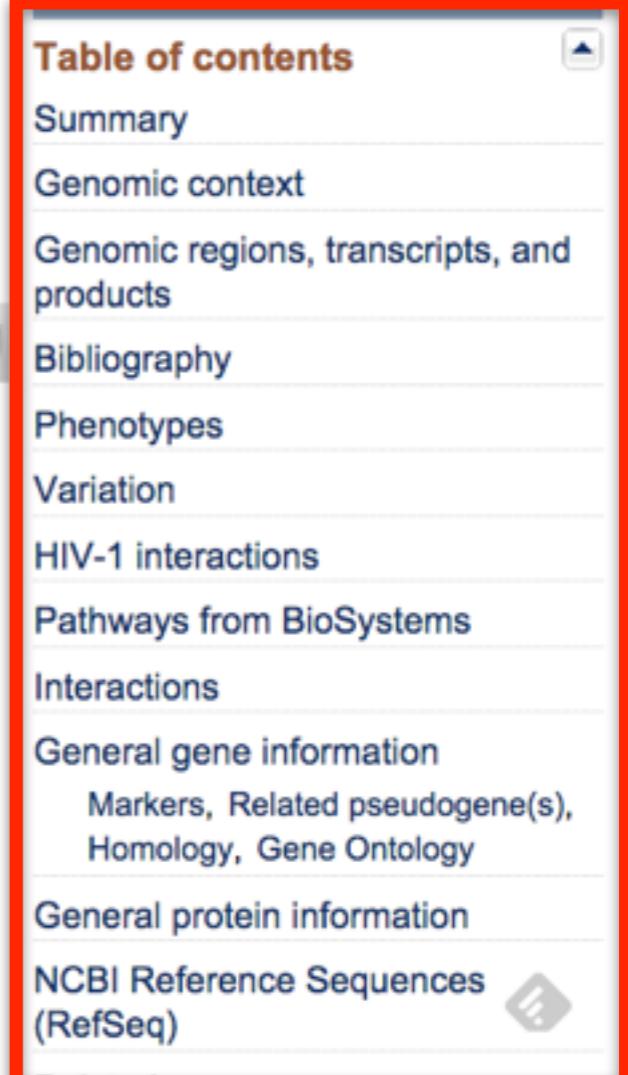
Organism *Homo sapiens*

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini;
Hominidae; Homo

Also known as NS; NS3; CFC2; KRAS1; KRAS2; RASK2; KI-RAS; C-K-RAS; K-RAS2A; K-

Table of contents

- Summary
- Genomic context
- Genomic regions, transcripts, and products
- Bibliography
- Phenotypes
- Variation
- HIV-1 interactions
- Pathways from BioSystems
- Interactions
- General gene information
- Markers, Related pseudogene(s), Homology, Gene Ontology
- General protein information
- NCBI Reference Sequences (RefSeq)



KRAS Kirsten rat sarcoma

www.ncbi.nlm.nih.gov/gene/3845

NCBI Resources How To Sign in to NCBI

Gene Search Help

Display S Hide sidebar >

KRAS (human)

Example Questions:
What chromosome location and what genes are in the vicinity?

Gene ID: 3845, updated on 4-Jan-2015

Summary

Official Symbol KRAS provided by HGNC

Official Full Name Kirsten rat sarcoma viral oncogene homolog provided by HGNC

Primary source HGNC:HGNC:6407

See related Ensembl:ENSG00000133703; HPRD:01817; MIM:190070;
Vega:OTTHUMG00000171193

Gene type protein coding

RefSeq status REVIEWED

Organism Homo sapiens

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini;
Hominidae; Homo

Also known as NS; NS3; CFC2; KRAS1; KRAS2; RASK2; KI-RAS; C-K-RAS; K-RAS2A; K-

Table of contents

Summary

Genomic context

Genomic regions, transcripts, and products

Bibliography

Phenotypes

Variation

HIV-1 interactions

Pathways from BioSystems

Interactions

General gene information

Markers, Related pseudogene(s), Homology, Gene Ontology

General protein information

NCBI Reference Sequences (RefSeq)

Related documents

83

KRAS Kirsten rat sarcoma

www.ncbi.nlm.nih.gov/gene/3845#genomic-context

Genomic context

Location: 12p12.1 **Exon count:** 6

See KRAS in [Epigenomics](#), [MapViewer](#)

Annotation release	Status	Assembly	Chr	Location
106	current	GRCh38 (GCF_000001405.26)	12	NC_000012.12 (25205246..25250923, complement)
105	previous assembly	GRCh37.p13 (GCF_000001405.25)	12	NC_000012.11 (25358180..25403870, complement)

Chromosome 12 - NC_000012.12

[25052101 ►] [25436297 ►]

LRMP → LYRMS ← CASC1 ← KRAS ← LOC100421617 ← RPL39P27

Genomic regions, transcripts, and products

Go to [reference sequence details](#)

Genomic Sequence: NC_000012.12 chromosome 12 reference GRCh38 Primary Assembly

Go to nucleotide: [Graphics](#) [FASTA](#) [GenBank](#)

BioAssay by Target (List)
BioAssay by Target (Summary)
BioAssay, by Gene target
BioAssays, RNAi Target, Active
BioAssays, RNAi Target, Tested
BioProjects
BioSystems
Books
CCDS
ClinVar
Conserved Domains
dbVar
EST
Full text in PMC
Full text in PMC_nucleotide
Gene neighbors
Genome
GEO Profiles
GTR
HomoloGene
Map Viewer
MedGen
Nucleotide

KRAS Kirsten rat sarcoma

www.ncbi.nlm.nih.gov/gene/3845

NCBI Resources How To Sign in to NCBI

Gene

Display Settings

KRAS Ki
(human)]

Gene ID: 3845

Summary

Example Questions:

What ‘molecular functions’, ‘biological processes’, and ‘cellular component’ information is available?

Official Symbol KRAS provided by HGNC

Official Full Name Kirsten rat sarcoma viral oncogene homolog provided by HGNC

Primary source HGNC:HGNC:6407

See related Ensembl:ENSG00000133703; HPRD:01817; MIM:190070;
Vega:OTTHUMG00000171193

Gene type protein coding

RefSeq status REVIEWED

Organism Homo sapiens

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini;
Hominidae; Homo

Also known as NS; NS3; CFC2; KRAS1; KRAS2; RASK2; KI-RAS; C-K-RAS; K-RAS2A; K-

Search Help Hide sidebar >>

Table of contents

Summary

Genomic context

Genomic regions, transcripts, and products

Bibliography

Phenotypes

Variation

HIV-1 interactions

Pathways from BioSystems

Interactions

General gene information

Markers, Related pseudogene(s), Homology, Gene Ontology

General protein information

NCBI Reference Sequences (RefSeq)

Related documents

85

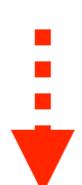
KRAS Kirsten rat sarcoma

Gene Ontology Provided by GOA

Function	Evidence Code	Pubs
GDP binding	IEA	
GMP binding	IEA	
GTP binding	IEA	
LRR domain binding	IEA	
protein binding	IPI	PubMed
protein complex binding	IDA	PubMed

Items 1 - 25 of 33 < Prev Page 1 of 2 Next >

Process	Evidence Code	Pubs
Fc-epsilon receptor signaling pathway	TAS	
GTP catabolic process	IEA	
MAPK cascade	TAS	
Ras protein signal transduction	TAS	
actin cytoskeleton organization	IEA	
activation of MAPKK activity	TAS	
axon guidance	TAS	
blood coagulation	TAS	



GO: Gene Ontology

GO provides a controlled vocabulary of terms for describing gene product characteristics and gene product annotation data

The screenshot shows the UniProt-GOA database homepage. At the top, there's a navigation bar with tabs for 'Services', 'Research', 'Training', and 'About us'. Below the navigation bar, the main title 'UniProt-GOA' is displayed. To the right of the title is a search bar with examples like 'GO:0006915, tropomyosin, P06727' and a 'Search' button. A menu on the right side lists various resources and initiatives, such as 'Downloads', 'Searching UniProt-GOA', 'Annotation Methods', 'Annotation Tutorial', 'Manual Annotation Efforts', 'Reference Genome Annotation Initiative', 'Cardiovascular Gene Ontology Annotation Initiative', 'Renal Gene Ontology Annotation Initiative', and 'Exosome Gene'. At the bottom left, there's a paragraph about the UniProt GO annotation program and a note that UniProt is a member of the GO Consortium.

KRAS Kirsten rat sarcoma × UniProt-GOA < EMBL-EBI ×

www.ebi.ac.uk/GOA

EMBL-EBI

Services Research Training About us

UniProt-GOA

Search

Examples: GO:0006915, tropomyosin, P06727

Overview New to UniProt-GOA FAQ Contact Us

Gene Ontology Annotation (UniProt-GOA) Database

The UniProt GO annotation program aims to provide high-quality Gene Ontology (GO) annotations to proteins in the UniProt Knowledgebase (UniProtKB). The assignment of GO terms to UniProt records is an integral part of [UniProt biocuration](#). UniProt manual and electronic GO annotations are supplemented with manual annotations supplied by external collaborating GO Consortium groups, to ensure a comprehensive GO annotation dataset is supplied to users .

UniProt is a member of the [GO Consortium](#).

Menu

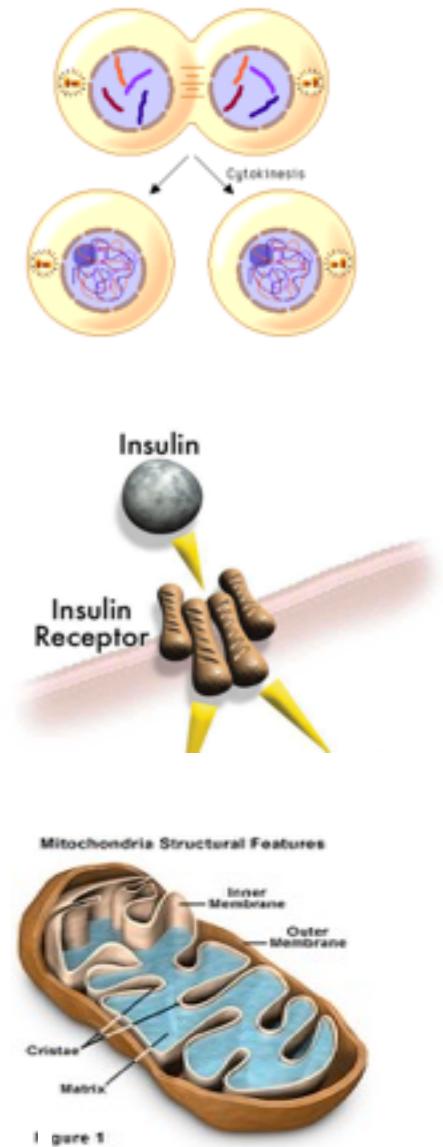
- [Downloads](#)
- [Searching UniProt-GOA](#)
- [Annotation Methods](#)
- [Annotation Tutorial](#)
- [Manual Annotation Efforts](#)
 - [Reference Genome Annotation Initiative](#)
 - [Cardiovascular Gene Ontology Annotation Initiative](#)
 - [Renal Gene Ontology Annotation Initiative](#)
 - [Exosome Gene](#)

Why do we need Ontologies?

- Annotation is essential for capturing the understanding and knowledge associated with a sequence or other molecular entity
- Annotation is traditionally recorded as “free text”, which is easy to read by humans, but has a number of disadvantages, including:
 - ▶ Difficult for computers to parse
 - ▶ Quality varies from database to database
 - ▶ Terminology used varies from annotator to annotator
- Ontologies are annotations using standard vocabularies that try to address these issues
- GO is integrated with UniProt and many other databases including a number at NCBI

GO Ontologies

- There are three ontologies in GO:
 - ▶ **Biological Process**
A commonly recognized series of events
e.g. cell division, mitosis,
 - ▶ **Molecular Function**
An elemental activity, task or job
e.g. kinase activity, insulin binding
 - ▶ **Cellular Component**
Where a gene product is located
e.g. mitochondrion, mitochondrial membrane



KRAS Kirsten rat sarcoma

Gene Ontology Provided by GOA

Function	Evidence Code	Pubs
GDP binding		
GMP binding		
GTP binding		
LRR domain binding		
protein binding		
protein complex binding		

Process	Code	Pubs
Fc-epsilon receptor signaling pathway	TAS	
GTP catabolic process	IEA	
MAPK cascade	TAS	
Ras protein signal transduction	TAS	
actin cytoskeleton organization	IEA	
activation of MAPKK activity	TAS	
axon guidance	TAS	
blood coagulation	TAS	

The 'Gene Ontology' or GO is actually maintained by the EBI so lets switch or link over to UniProt also from the EBI.

↓ Scroll down to
UniProt link

UniProt will detail much more information for protein coding genes such as this one

KRAS Kirsten rat sarcoma X www.ncbi.nlm.nih.gov/gene/3845#gene-ontology

genomic X01669.1 CAA25828.1

Items 1 - 25 of 43 < Prev Page 1 of 2 Next >

Protein Accession	Links
P01116.1	GenPept Link UniProtKB Link GenPept UniProtKB/Swiss-Prot:P01116

Additional links

You are here: NCBI > Genes & Expression > Gene Write to the Help Desk

GETTING STARTED

- NCBI Education
- NCBI Help Manual
- NCBI Handbook
- Training & Tutorials

RESOURCES

- Chemicals & Bioassays
- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature
- Proteins
- Sequence Analysis
- Taxonomy

POPULAR

- PubMed
- Bookshelf
- PubMed Central
- PubMed Health
- BLAST
- Nucleotide
- Genome
- SNP
- Gene
- Protein
- PubChem

FEATURED

- Genetic Testing Registry
- PubMed Health
- GenBank
- Reference Sequences
- Gene Expression Omnibus
- Map Viewer
- Human Genome
- Mouse Genome
- Influenza Virus
- Primer-BLAST
- Sequence Read Archive

NCBI INFORMATION

- About NCBI
- Research at NCBI
- NCBI News
- NCBI FTP Site
- NCBI on Facebook
- NCBI on Twitter
- NCBI on YouTube

Scroll down to UniProt link

UniProt will detail much more information for protein coding genes

The screenshot shows the UniProtKB interface for the protein P01116, which corresponds to KRAS in Homo sapiens (Human). The top navigation bar includes links for UniProtKB, Advanced search, Help, Contact, and a Basket. The main content area displays the protein's name, ID, and organism. A red box highlights the 'Status' section, which indicates the protein is 'Reviewed' with experimental evidence at the protein level. Another red box surrounds the 'Display' sidebar on the left, which lists various data categories like Function, Names & Taxonomy, and Sequences. A red arrow points down from the bottom of the sidebar towards the main content area.

P01116 - RASK_HUMAN

Protein: GTPase KRas
Gene: KRAS
Organism: Homo sapiens (Human)
Status: Reviewed - Experimental evidence at protein levelⁱ

Display: None

FUNCTION
 NAMES & TAXONOMY
 SUBCELL LOCATION
 PATHOL/BIOTECH
 PTM / PROCESSING
 EXPRESSION
 INTERACTION
 STRUCTURE
 FAMILY & DOMAINS
 SEQUENCES (2)
 CROSS-REFERENCES

Functionⁱ

Ras proteins bind GDP/GTP and possess intrinsic GTPase activity. Plays an important role in the regulation of cell proliferation (PubMed:23698361, PubMed:22711838). 2 Publications Curated

Enzyme regulationⁱ

Alternates between an inactive form bound to GDP and an active form bound to GTP. Activated by a guanine nucleotide-exchange factor (GEF) and inactivated by a GTPase-activating protein (GAP). Interaction with SOS1 promotes exchange of bound GDP by GTP. 3 Publications

Regions

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Nucleotide binding ⁱ	10 – 18	9	GTP 2 Publications			
Nucleotide binding ⁱ	29 – 35	7	GTP 2 Publications			
Nucleotide binding ⁱ	59 – 60	2	GTP 2 Publications			

KRAS - GTPase KRas precursor

www.uniprot.org/uniprot/P01116

UniProtKB Advanced

BLAST Align Retrieve/ID Mapping Help Contact Basket

P01116 - RASK_HUMAN

Protein: GTPase KRas
Gene: KRAS
Organism: Homo sapiens (Human)
Status: Reviewed - 5 stars

Display: None

FUNCTION NAMES & TAXONOMY SUBCELL LOCATION PATHOL/BIOTECH PTM / PROCESSING EXPRESSION INTERACTION STRUCTURE FAMILY & DOMAINS SEQUENCES (2) CROSS-REFERENCES

Function

Ras proteins bind GDP/GTP and possess intrinsic GTPase activity. Plays an important role in the regulation of cell proliferation (PubMed:23698361, PubMed:22711838). 2 Publications Curated

Enzyme regulation

Alternates between an inactive form bound to GDP and an active form bound to GTP. Activated by a guanine nucleotide-exchange factor (GEF) and inactivated by a GTPase-activating protein (GAP). Interaction with SOS1 promotes exchange of bound GDP by GTP. 3 Publications

Regions

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Nucleotide binding	10 – 18	9	GTP 2 Publications			
Nucleotide binding	29 – 35	7	GTP 2 Publications			
Nucleotide binding	59 – 60	2	GTP 2 Publications			

Example Questions:
What positions in the protein are responsible for GTP binding?

Example Questions:

What variants of this enzyme are involved in gastric cancer and other human diseases?

KRAS - GTPase KRas prec X

www.uniprot.org/uniprot/P01116

Display None

FUNCTION

NAMES & TAXONOMY

SUBCELL LOCATION

PATHOL/BIOTECH

PTM / PROCESSING

EXPRESSION

INTERACTION

STRUCTURE

FAMILY & DOMAINS

SEQUENCES (2)

CROSS-REFERENCES

PUBLICATIONS

ENTRY INFORMATION

MISCELLANEOUS

SIMILAR PROTEINS

▲ Top

Pathology & Biotech

Involvement in diseaseⁱ

LEUKEMIA, ACUTE MYELOGENOUS (AML)

[MIM:601626]: A subtype of acute leukemia, a cancer of the white blood cells. AML is a malignant disease of bone marrow characterized by maturational arrest of hematopoietic precursors at an early stage of development. Clonal expansion of myeloid blasts occurs in bone marrow, blood, and other tissue. Myelogenous leukemias develop from changes in cells that normally produce neutrophils, basophils, eosinophils and monocytes. 1 Publication ▾

Note: The disease is caused by mutations affecting the gene represented in this entry.

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Natural variant ⁱ	10 – 10		1 G → GG in one individual with AML; expression in 3T3 cell causes cellular transformation; expression in COS cells activates the Ras-MAPK signaling pathway; lower GTPase activity; faster GDP dissociation rate. 1 Publication ▾		VAR_034601	

LEUKEMIA, JUVENILE MYELOMONOCYTIC (JMML)

[MIM:607785]: An aggressive pediatric myelodysplastic syndrome/myeloproliferative disorder characterized by malignant transformation in the hematopoietic stem cell compartment with proliferation of differentiated progeny. Patients have splenomegaly, enlarged lymph nodes, rashes, and hemorrhages.

Note: The disease is caused by mutations affecting the gene represented in this entry.

NOONAN SYNDROME 3 (NS3)

[MIM:609942]: A form of Noonan syndrome, a disease characterized by short stature, facial dysmorphic features such as hypertelorism, a downward eyeslant and low-set posteriorly rotated ears, and a high incidence of congenital heart

Example Questions:

Are high resolution protein structures available to examine the details of these mutations?

KRAS - GTPase KRas prec X

www.uniprot.org/uniprot/P01116

Display None

FUNCTION

NAMES & TAXONOMY

SUBCELL LOCATION

PATHOL/BIOTECH

PTM / PROCESSING

EXPRESSION

INTERACTION

STRUCTURE

FAMILY & DOMAINS

SEQUENCES (2)

CROSS-REFERENCES

PUBLICATIONS

ENTRY INFORMATION

MISCELLANEOUS

SIMILAR PROTEINS

▲ Top

Structure

Secondary structure

1

Legend: Helix Turn Beta strand

Show more details

3D structure databases

Select the link destinations:

PDBeⁱ

RCSB PDBⁱ

PDBjⁱ

Entry	Method	Resolution (Å)	Chain	Positions	PDBsum
1D8D	X-ray	2.00	P	178-188	[»]
1D8E	X-ray	3.00	P	178-188	[»]
1KZO	X-ray	2.20	C	169-173	[»]
1KZP	X-ray	2.10	C	169-173	[»]
3GFT	X-ray	2.27	A/B/C/D/E/F	1-164	[»]
4DSN	X-ray	2.03	A	2-164	[»]
4DSO	X-ray	1.85	A	2-164	[»]
4EPR	X-ray	2.00	A	1-164	[»]
4EPT	X-ray	2.00	A	1-164	[»]
4EPV	X-ray	1.35	A	1-164	[»]
4EPW	X-ray	1.70	A	1-164	[»]
4EPX	X-ray	1.76	A	1-164	[»]
4EPY	X-ray	1.80	A	1-164	[»]
4L8G	X-ray	1.52	A	1-169	[»]
4LDJ	X-ray	1.15	A	1-164	[»]
4LPK	X-ray	1.50	A/B	1-169	[»]

Example Questions:

What is known about the protein family, its species distribution, number in humans and residue-wise conservation, etc... ?

KRAS - GTPase KRas prec X
www.uniprot.org/uniprot/P01116

Display None

FUNCTION

NAMES & TAXONOMY

SUBCELL LOCATION

PATHOL/BIOTECH

PTM / PROCESSING

EXPRESSION

INTERACTION

STRUCTURE

FAMILY & DOMAINS

SEQUENCES (2)

CROSS-REFERENCES

PUBLICATIONS

ENTRY INFORMATION

MISCELLANEOUS

SIMILAR PROTEINS

OrthoDB EVO
PhylomeDBⁱ P01116
TreeFamⁱ TF3

Family and domain databases

Gene3D ⁱ	3.40.50.300. 1 hit.
InterPro ⁱ	IPR027417. P-loop_NTPase. IPR005225. Small_GTP-bd_dom. IPR001806. Small_GTPase. IPR020849. Small_GTPase_Ras. [Graphical view]
PANTHER ⁱ	PTHR24070. PTHR24070. 1 hit
Pfam ⁱ	PF00071. Ras. 1 hit. [Graphical view]
PRINTS ⁱ	PR00449. RASTRNSFRMNG.
SMART ⁱ	SM00173. RAS. 1 hit. [Graphical view]
SUPFAM ⁱ	SSF52540. SSF52540. 1 hit.
TIGRFAMs ⁱ	TIGR00231. small_GTP. 1 hit.
PROSITE ⁱ	PS51421. RAS. 1 hit. [Graphical view]

▲ Top

Sequences (2)ⁱ

Sequence statusⁱ: Complete.

Sequence processingⁱ: The displayed sequence is further processed into a mature form.

This entry describes 2 isoformsⁱ produced by alternative splicing. Align

PFAM is one of the best protein family databases

Example Questions:

What is known about the protein family, its **species distribution**, number in humans and residue-wise conservation, etc... ?

KRAS - GTPase KRas prec > Me Pfam: Family: Ras (PF00071) >

EMBL-EBI  HOME | SEARCH

Family: Ras (PF00071)

Summary

Domain organisation

Clan

Alignments

HMM logo

Trees

Curation & model

Species (selected)

Interactions

Structures

Jump to... ↻

enter ID/acc

Summary: Ras family

Pfam includes annotations and additional family information from a range of different sources. These sources can be accessed via the tabs below.

[Wikipedia: Ras subfamily](#) [Wikipedia: Ras superfamily](#) [Pfam](#) [InterPro](#)

This is the Wikipedia entry entitled "[Ras subfamily](#)". [More...](#)

Ras subfamily [Edit Wikipedia article](#)

This article is about p21/Ras protein. For the p21/waf1 protein, see [p21](#).

Ras is the name given to a [family of related proteins](#) which is ubiquitously expressed in all cell lineages and organs. All Ras protein family members belong to a class of protein called [small GTPase](#), and are involved in transmitting signals within cells ([cellular signal transduction](#)). Ras is the prototypical member of the [Ras superfamily](#) of proteins, which are all related in 3D structure and regulate diverse cell behaviours.

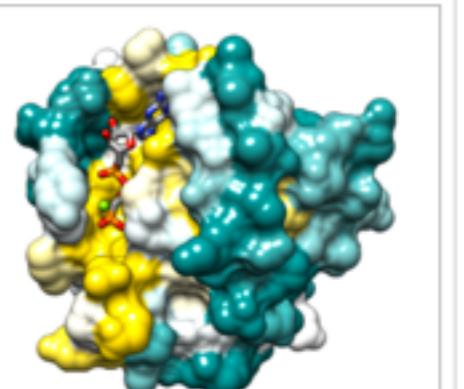
The name 'Ras' is an abbreviation of 'Rat sarcoma', reflecting the way the first members of the protein family were discovered. The name ras is also used to refer to the family of [genes](#) encoding those proteins.

When Ras is 'switched on' by incoming signals, it subsequently switches on other proteins, which ultimately turn on genes involved in [cell growth](#), [differentiation](#) and [survival](#). As a result, mutations in ras genes can lead to the production of permanently activated Ras proteins. This can cause unintended and overactive signalling inside the cell, even in the absence of incoming signals.

Because these signals result in cell growth and division, overactive Ras signaling can ultimately lead to [cancer](#).^[1] The 3 Ras genes in humans ([HRAS](#), [KRAS](#), and [NRAS](#)) are the most common [oncogenes](#) in human [cancer](#); mutations that permanently activate Ras are found in 20% to 25% of all human tumors and up to 90% in certain types of cancer (e.g., [pancreatic cancer](#)).^[2] For this reason, Ras inhibitors are being studied as a treatment for cancer, and other diseases with Ras overexpression.

[Contents \[hide\]](#)

1 History
2 Structure
3 Function
 3.1 Activation and deactivation
 3.2 Membrane attachment
4 Members
5 Ras in cancer
 5.1 Inappropriate activation
 5.2 Constitutively active Ras



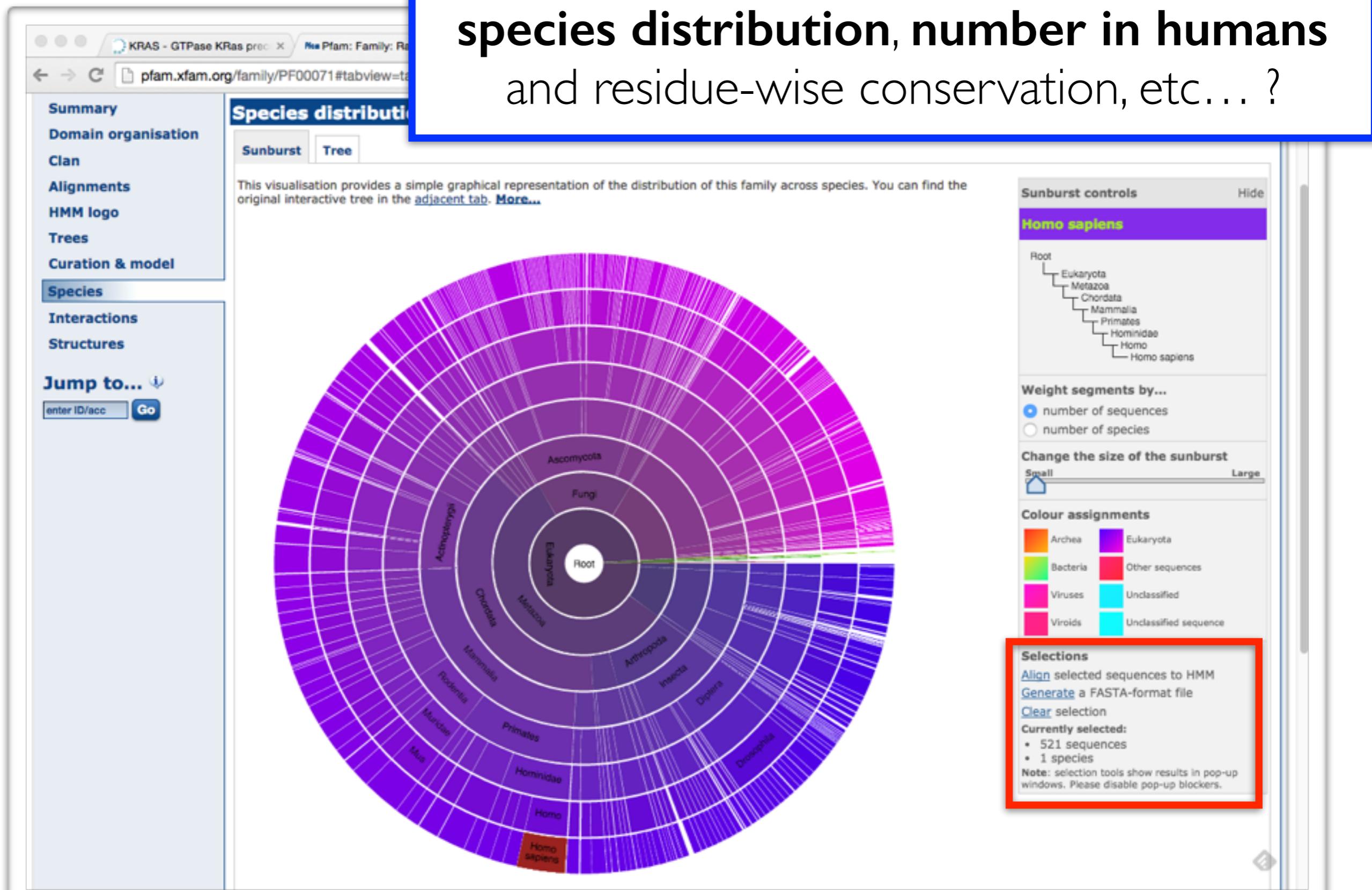
H-Ras structure PDB 121p, surface colored by conservation in Pfam seed alignment: gold, most conserved; dark cyan, least conserved.

Identifiers

Symbol	Ras
Pfam	PF00071
InterPro	IPR013753
PROSITE	PDOC00017
SCOP	Sp21
SUPERFAMILY	Sp21

Example Questions:

What is known about the protein family, its **species distribution, number in humans** and residue-wise conservation, etc... ?



Example Questions:

What is known about the protein family, its species distribution, number in humans and **residue-wise conservation**, etc... ?

KRAS - GTPase KRas prec X Me Pfam: Family: Ra

← → C pfam.xfam.org/family/PF00071#tabview=tab1

Summary **Species distribution**

Domain organisation

Clan

Alignment

HMM log

Trees

Curation

Species

Interact

Structure

Jump to

enter ID/acc

Pfam: Pfam alignment viewer

pfam.xfam.org/family/PF00071/alignment/view?jobId=EDCA403E-9836-11E4-B360-10B3298E2F76

EMBL-EBI

Alignment for selected sequences

Currently showing rows 1 to 30 of 536 rows in this alignment. Show 30 rows of alignment

P11234/16-178	.KIVIMVSGGVGKSAITL.....Q.....FM.....Y..D..EF..V....E.DYEFTK.-AD...SYRKVVLD.....
P01112/5-165	.KLVVVGAGGVGKSAITL.....Q.....LI.....Q..N..HF..V....D.EYDFTI.-ED...SYRKQVVID.....
Q14088/38-204	.KIIIVGDSNVGKTCIYT.....R.....FC.....G..S..TY..P....D.KTEATI.GVD...FREKTVEIE.....
Q9BM83/7-173	.KCILAGDPAVGKTAQ.....I.....FR.....S..DgaHF.Q....K.SYTATI.GMD...LVVKTVPVpd.....
P15153/5-178	.KCVVVGCGAVGKTCIIT.....S.....YT.....T..N..AF..P....E.EYIFTW.-FD...NYSANVMVD.....
Q00194/11-183	.KLLALGDSOVGKTCIPLY.....R.....YT.....D..N..KF..N....P.KFITTW.GID...FREKRVVYNaqgn.....
Q15907/13-174	.KVVLLGDSGVGKSNLIS.....R.....FT.....R..N..EF..N....L.ESKSTI.GVE...PATRSIQVD.....
P10114/5-166	.KVVVLGSGGVGKSAITV.....O.....FV.....T..S..TF..I....E.KYDFTI.-ED...FYRKEIEVD.....
P51153/10-171	.KLLLIGDSGVGKTCIIT.....R.....FA.....E..D..NF..N....N.TYISTI.GID...FKIRTVDIE.....
P55040/77-241	.RVVLLIGEQGVGKSTLAN.....I.....FA.....Gvhd..SM.D....S.D-CEVL.GED...TYERTLMVD.....
P55042/93-253	.KVLLLGAPGVGKESALAR.....I.....FG.....G..V..ED..G....P.EAEAAG.--H...TYDRSIVVD.....
P01116/5-165	.KLVVVGAGGVGKSAITL.....Q.....LI.....Q..N..HF..V....D.EYDFTI.-ED...SYRKQVVID.....
Q9H07/21-182	.KLVLLGCGSVGKSSLAL.....R.....YW.....K..N..DF..K....S..ILPTW.GCA...FPTKVVWD.....
Q9ULC3/11-171	.KVVVVGNGAVGKSSMIQ.....R.....YC.....K..S..IF..T....K.DYKNTI.GVD...FLEROQIWN.....
Q14807/15-177	.KLVVVGDGGVGKSAITI.....Q.....FF.....Q..K..IF..V....P.DYDFTI.-ED...SYLKHTEID.....
Q9NX57/7-202	.KIVLLCDMMNVGKTSILQ.....R.....YM.....E..R..RF..P....D..T-VSW.GEA...FYLEQW--.....
Q9H082/35-201	.KIIIVGDSNVGKTCIYT.....R.....FC.....A..S..RF..P....D.RTEATI.GVD...FRERAVEID.....
Q969Q5/9-174	.KVVMLGKEYVGKTSLVE.....R.....YW.....H..D..RFIV....E.PYQNTI.GAA...FVAKVMSC.....
P51149/10-175	.KVIILGDSGVGKTSNN.....Q.....YW.....N..K..KF..S....N.QYKATI.GAD...FLTKEVMD.....
Q9ULN5/65-227	.KVMVLGDSGVGKTCIIV.....R.....FK.....D..S..AF..L....AqTFISTW.GID...FRNKVLQVD.....
P57735/14-175	.KVVLLIGESCVGKTNLLS.....R.....FT.....R..N..EF..S....H.DSRTTI.GVE...FSTRTVML.....
P51159/11-183	.KFLALGDSGVGKTSVLY.....Q.....YT.....D..S..KF..N....S.KFITTW.GID...FREKRVVYRasgp.....
P01111/5-165	.KLVVVGAGGVGKSAITI.....Q.....LI.....Q..N..HF..V....D.EYDFTI.-ED...SYRKQVVID.....
P11233/16-177	.KIVIMVSGGVGKSAITL.....Q.....FM.....Y..D..EF..V....E.DYEFTK.-AD...SYRKVVLD.....
Q9UL25/21-182	.KVVLLGEGCVGKTSLVL.....R.....YC.....E..N..KF..N....D.KHITTL.QAS...FLTKKLNI.....
Q9NP72/10-171	.KILIIGESCVGKSSILL.....R.....FT.....D..D..TF..D....P.ELAATI.GVD...FKVKTISVD.....
Q9H04/10-171	.KLLLIGDSGVGKSCILL.....R.....FA.....D..D..TY..T....E.SYISTI.GVD...FKIRTIELD.....
Q9UL26/7-168	.KVCILGDTGVGKSSIVW.....R.....FV.....E..D..SF..D....P.NINFTI.GAS...FMTKTVYO.....
Q9UBK7/23-179	.KIIICLGDSAVGKSKIME.....R.....FL.....M..D..GT..Q....P.QQLSTI.ALT...LYKHTATWD.....
P51157/14-179	.KIVVILGDSAGSKTSLTT.....C.....FA.....Q..E..TF..G....K.QYKOTI.GLD...FFLRRITLP.....

1 2 3 4 5 6 7 8 9 10 11 ...

There are 18 pages in this alignment. Show page 1

Download this alignment.

Close window

can find the

Sunburst controls Hide

Homo sapiens

Root
Eukaryota
Metazoa
Chordata
Mammalia
Primates
Hominoidea
Homo
Homo sapiens

Weight segments by...
 number of sequences
 number of species

Change the size of the sunburst
 Small Large

Colour assignments

Archea	Eukaryota
Bacteria	Other sequences
Viruses	Unclassified
Viroids	Unclassified sequence

Selections

Align selected sequences to HMM
Generate a FASTA-format file
Clear selection
Currently selected:
* 521 sequences
* 1 species
Note: selection tools show results in pop-up windows. Please disable pop-up blockers.

Example Questions:

What is known about the protein family, its species distribution, number in humans and **residue-wise conservation**, etc... ?

KRAS - GTPase KRas prec X Me Pfam: Family: Ra

← → C pfam.xfam.org/family/PF00071#tabview=tab4

EMBL-EBI

HOME | SEARCH | BROWSE | FTP | HELP | ABOUT

Pfam keyword search Go

Family: Ras (PF00071)

Summary Domain organisation Clan Alignments **HMM logo** HMM logo Trees Curation & model Species Interactions Structures

Jump to... enter ID/acc Go

Comments or questions on the site? Send a mail to pfam-help@ebi.ac.uk. European Molecular Biology Laboratory

Family: Kinesin (PF00225)

 Loading page components (1 remaining)... 126 architectures  4150 sequences  6 Interactions  248 species  114 structures[Summary](#)[Domain organisation](#)[Clans](#)[Alignments](#)[HMM logo](#)[Trees](#)[Curation & models](#)[Species](#)[Interactions](#)[Structures](#)[Jump to... !\[\]\(626e6083350fea1607a4aa287aee6985_img.jpg\)](#)[enter ID/acc](#)[Go](#)

Interactions

There are **6** interactions for this family. [More...](#)

[Tubulin](#)
[Tubulin_C](#)[Tubulin_C](#)[Kinesin](#)[Tubulin](#)[Kinesin](#)

Family: Kinesin (PF00225)

126 architectures
4150 sequences
6 Interactions
248 species
114 structures
Summary**Domain organisation****Clans****Alignments****HMM logo****Trees****Curation & models****Species****Interactions****Structures****Jump to...**

enter ID/acc

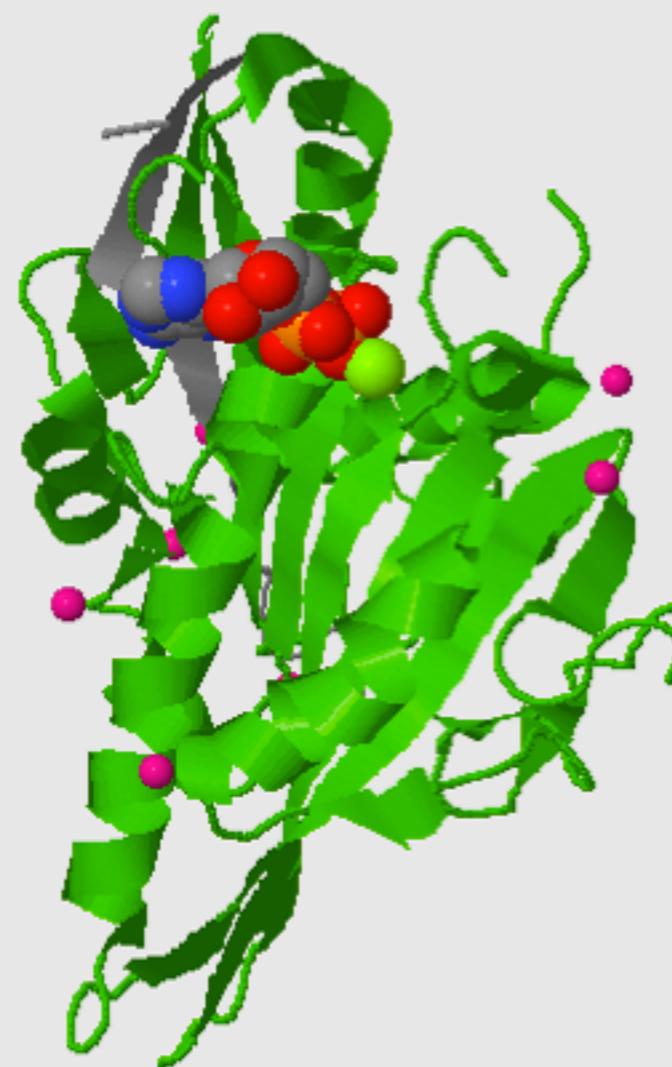
Structures

For those sequences which have a structure in the [Protein DataBank](#), we use the mapping between [UniProt](#), PDB and Pfam coordinate systems from the [PDBe](#) group, to allow us to map Pfam domains onto UniProt sequences and three-dimensional protein structures. The table below shows the structures on which the **Kinesin** domain has been found.

UniProt entry	UniProt residues	PDB ID	PDB chain ID	PDB residues	View
A8BKD1_GIALA	11 - 335	2vvg	A	11 - 335	Jmol AstexViewer SPICE
			B	11 - 335	Jmol AstexViewer SPICE
CENPE_HUMAN	12 - 329	1t5c	A	12 - 329	Jmol AstexViewer SPICE
			B	12 - 329	Jmol AstexViewer SPICE
KAR3_YEAST	392 - 723	1f9t	A	392 - 723	Jmol AstexViewer SPICE
		1f9u	A	392 - 723	Jmol AstexViewer SPICE
		1f9v	A	392 - 723	Jmol AstexViewer SPICE
		1f9w	A	392 - 723	Jmol AstexViewer SPICE
		3kar	A	392 - 723	Jmol AstexViewer SPICE
KI13B_HUMAN	11 - 352	3qbj	A	11 - 352	Jmol AstexViewer SPICE
			B	11 - 352	Jmol AstexViewer SPICE
			C	11 - 352	Jmol AstexViewer SPICE
		1ii6	A	24 - 359	Jmol AstexViewer SPICE
			B	24 - 359	Jmol AstexViewer SPICE
		1q0b	A	24 - 359	Jmol AstexViewer SPICE
			B	24 - 359	Jmol AstexViewer SPICE
		1x88	A	24 - 359	Jmol AstexViewer SPICE
			B	24 - 359	Jmol AstexViewer SPICE
		1	A	24 - 359	Jmol AstexViewer SPICE



PDB entry 3bfm



Jmol

PDB			UniProt			Pfam family		Colour
Chain	Start	End	ID	Start	End			
A	49	368	KIF22_HUMAN	49	368	Kinesin (PF00225)		

 [Close window](#)

ENTREZ & BLAST:

TOOLS FOR SEARCHING AND ACCESSING MOLECULAR DATA AT NCBI

Entrez: Integrated search of NCBI databases

The screenshot shows the NCBI homepage with the Entrez sidebar open. The sidebar is titled "All Databases" and lists various NCBI databases: PubMed, Protein, Nucleotide, GSS, EST, Structure, Genome, BioProject, BioSample, BioSystems, Books, Conserved Domains, Clone, dbGaP, dbVar, Epigenomics, Gene, GEO DataSets, GEO Profiles, HomoloGene, MeSH, NCBI Web Site, NLM Catalog, OMIA, OMIM, PMC, PopSet, Probe, Protein Clusters, PubChem BioAssay, PubChem Compound, PubChem Substance, PubMed Health, SNP, SRA, Taxonomy, ToolKit, ToolKitAll, UniGene, and UniSTS.

Welcome to NCBI

NCBI Center for Biotechnology Information advances science by providing access to biomedical and genomic information.

[NCBI](#) | [Mission](#) | [Organization](#) | [Research](#) | [RSS Feeds](#)

Entrez

Analyze data using NCBI software
Downloads: Get NCBI data or software
Tutorials: Learn how to accomplish specific tasks at NCBI
Submissions: Submit data to GenBank or other NCBI databases

Entrez is available from the main NCBI homepage or from the homepage of individual databases

3 4 5 6 7 8

Popular Resources

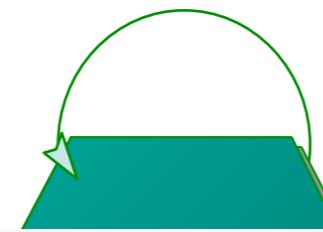
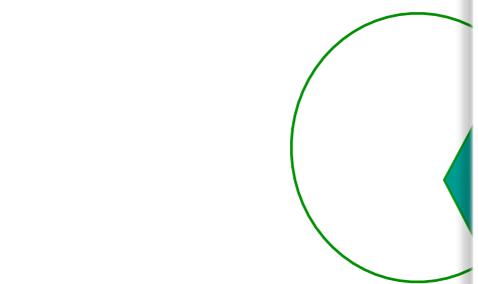
- PubMed
- Bookshelf
- PubMed Central
- PubMed Health
- BLAST
- Nucleotide
- Genome
- SNP
- Gene
- Protein

NCBI Announcements

- NCBI's April Newsletter is on the Bookshelf 04 May 2012
- Information about May's Discovery Workshop, the new GTR and Assembly 04 May 2012
- New Filter Sidebar will be added to PubMed 03 May 2012
- A Filter Sidebar will be added soon to the PubMed result pages. The useful 03 May 2012
- DELTA BLAST - more sensitive protein searching 30 Apr 2012
- Domain Enhanced Lookup Time Accelerated BLAST (DELTA-BLAST) 30 Apr 2012

[More...](#)

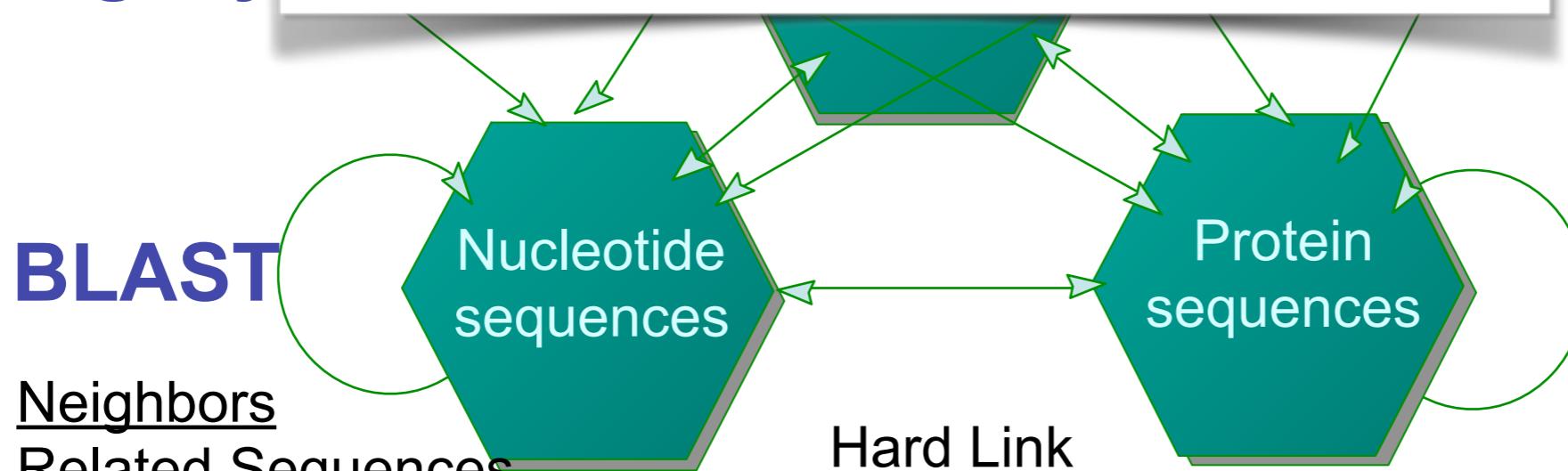
Entrez: navigating across databases



Entrez was setup to allow you to navigate to related data in different databases without having to run additional searches.

Relies on pre-computed and pre-compiled data links:

- Neighbor knowledge based on calculations
- Hard links based on things we know about



Global Entrez Query: All NCBI Databases

ras - GQuery: Global Cross X

www.ncbi.nlm.nih.gov/gquery/?term=ras

NCBI Resources How To Sign in to NCBI

Search NCBI databases Help

ras Search

About 2,978,774 search results for "ras"

Literature

Books 1,333 Books and reports

MeSH 402 ontology used for PubMed indexing

NLM Catalog 223 Catalog of books and other materials about gene

PubMed 54,672 genetics studies

PubMed Central 96,114 and molecular

Health

ClinVar 759 human variations of clinical abundance profiles

dbGaP 120 genotype/phenotype interaction homologous gene sets for selected organisms

GTR 1,879 genetic testing registry sequence sets from phylogenetic and population studies

The Entrez system: 38 (and counting) clusters of expressed transcripts

integrated databases

GEO Profiles 1,622,789

HomoloGene 696

PopSet 2,254

UniGene 4,770

Proteins

<http://www.ncbi.nlm.nih.gov/gquery/>

Search Results

Nucleotide Nucleotide zebrafish creatine kinase

Save search Limits Advanced

Display Settings: Summary, 20 per page, Sorted by Default order

Send to: Filter your results:

All (35)

Bacteria (0)

INSDC (GenBank) (27)

mRNA (32)

RefSeq (8)

[Manage Filters](#)

Results: 1 to 20 of 35 << First < Prev Page of 2 Next > Last >>

[Danio rerio creatine kinase, muscle b \(ckmb\), mRNA](#)

1. 1,463 bp linear mRNA
Accession: NM_001105683.1 GI: 157787180
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio zgc:63663 \(zgc:63663\), mRNA](#)

2. 2,476 bp linear mRNA
Accession: NM_200614.1 GI: 41055386
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio creatine kinase, muscle](#)

3. 1,552 bp linear mRNA
Accession: NM_130932.1 GI: 18858426
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio creatine kinase, mitochondrial 2 \(sarcomeric\), mRNA \(cDNA clone MGC:198091](#)

4. IMAGE:9039080, complete cds
1,296 bp linear mRNA
Accession: BC171364.1 GI: 213624628
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio creatine kinase, mitochondrial 2 \(sarcomeric\), mRNA \(cDNA clone MGC:172259](#)

5. IMAGE:8798676, complete cds
1,400 bp linear mRNA
Accession: BC154617.1 GI: 159155933
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

Discovery Column
(sort, filter, link)

▼ Top Organisms [Tree]
Danio rerio (29)
Ictalurus furcatus (6)

Find related data
Database:

Search details
("Danio rerio"[Organism]
OR zebrafish[All Fields])
AND creatine kinase[All Fields]

See more...

Recent activity

Limits

Limits

Published in the last

Any Date

Search Field Tags

Field: All Fields

Source database

Any

Gene Location

Any

Modified in the last

Any Date

Segmented Sequences

Any

Molecule

Any

Exclude

- STSs
- working draft
- TPA
- patents

Search Results

Nucleotide Nucleotide zebrafish creatine kinase

Save search Limits Advanced

Display Settings: Summary, 20 per page, Sorted by Default order

Send to: Filter your results:

All (35)

Bacteria (0)

INSDC (GenBank) (27)

mRNA (32)

RefSeq (8)

[Manage Filters](#)

Results: 1 to 20 of 35 << First < Prev Page of 2 Next > Last >>

[Danio rerio creatine kinase, muscle b \(ckmb\), mRNA](#)

1. 1,463 bp linear mRNA
Accession: NM_001105683.1 GI: 157787180
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio zgc:63663 \(zgc:63663\), mRNA](#)

2. 2,476 bp linear mRNA
Accession: NM_200614.1 GI: 41055386
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio creatine kinase, muscle](#)

3. 1,552 bp linear mRNA
Accession: NM_130932.1 GI: 18858426
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio creatine kinase, mitochondrial 2 \(sarcomeric\), mRNA \(cDNA clone MGC:198091](#)

4. IMAGE:9039080, complete cds
1,296 bp linear mRNA
Accession: BC171364.1 GI: 213624628
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio creatine kinase, mitochondrial 2 \(sarcomeric\), mRNA \(cDNA clone MGC:172259](#)

5. IMAGE:8798676, complete cds
1,400 bp linear mRNA
Accession: BC154617.1 GI: 159155933
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

Discovery Column
(sort, filter, link)

▼ Top Organisms [Tree]
Danio rerio (29)
Ictalurus furcatus (6)

Find related data
Database:

Search details
("Danio rerio"[Organism]
OR zebrafish[All Fields])
AND creatine kinase[All Fields]

See more...

Recent activity

Advanced: Search Builder

Nucleotide Advanced Search Builder

zebrafish[Organism] AND "creatin kinase"[Title]

[Clear](#)

Helps build complex fielded queries

Organism

zebrafish

AND

Title

"creatin kinase"[Title]

[Show index list](#)

[Hide index list](#)

creatin kinase (749)

creatin kinase 1 (6)
creatin kinase 2 (2)
creatin kinase b (30)
creatin kinase b gene (3)
creatin kinase b mrna (3)
creatin kinase b pseudogene 1 (1)
creatin kinase b subunit (1)
creatin kinase brain (43)
creatin kinase chain b (1)

[Previous 200](#)

[Next 200](#)

[Refresh index](#)

AND

All Fields

[Show index list](#)

[Search](#)

or [Add to history](#)

Items from search history can be included / combined / modified

History

[Clear history](#)

Search	Add to builder	Query	Items found	Time
#7	Add	Search zebrafish[organism] AND actin[title]	71	12:41:16
#4	Add	Search zebrafish actin	1288	12:40:07
#1	Add	Search zebrafish creatine kinase	34	12:39:02

Complex Query Results

Display Settings: Summary, 20 per page, Sorted by Default order

Send to: Filter your results:

Results: 6

[Danio rerio creatine kinase, brain a \(ckba\), mRNA](#)
1. 1,481 bp linear mRNA
Accession: NM_001077163.1 GI: 116004536
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio creatine kinase, mitochondrial 1 \(ckmt1\), nuclear gene encoding mitochondrial protein, mRNA](#)
2. mRNA

("Danio rerio"[Organism] AND "creatin kinase"[Title]) AND "refseq"[Filter] AND mrna[Filter]

[Danio rerio creatine kinase, muscle a \(ckma\), mRNA](#)
3. 1,552 bp linear mRNA
Accession: NM_130932.1 GI: 18858426
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio creatine kinase, mitochondrial 2 \(sarcomeric\) \(ckmt2\), nuclear gene encoding mitochondrial protein, mRNA](#)
4. 1,401 bp linear mRNA
Accession: NM_200697.1 GI: 41152341
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio creatine kinase, muscle b \(ckmb\), mRNA](#)
5. 1,463 bp linear mRNA
Accession: NM_001105683.1 GI: 157787180
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Danio rerio creatine kinase, brain b \(ckbb\), mRNA](#)
6. 1,459 bp linear mRNA
Accession: NM_173222.1 GI: 27545192
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

All (6)

Bacteria (0)

INSDC (GenBank) (0)

[mRNA \(6\)](#)

[RefSeq \(6\)](#)

[Manage Filters](#)

Analyze these sequences

[Run BLAST](#)

Find related data

Database:

[Find items](#)

Search details

```
("Danio rerio"[Organism]
AND "creatin kinase"
[Title]) AND "refseq"
[Filter]
```

[Search](#) [See more...](#)

Recent activity

Controlled Vocabularies

- Taxonomy primary controlled vocabulary / classification system for molecular databases at NCBI

The screenshot shows the Nucleotide database search interface. The search term 'sponges' is entered in the search bar. The search details panel on the right shows the query: "'Porifera' [Organism] OR sponges [All Fields]".

- ▶ Medical Subject Headings (MeSH) primary controlled vocabulary / classification system (ontology) for molecular databases at NCBI

The screenshot shows the PubMed search interface. The search term 'sponges' is entered in the search bar. The search details panel on the right shows the query: "'porifera' [MeSH Terms] OR 'porifera' [All Fields] OR 'sponges' [All Fields]".

BLAST is a very important tool available from the NCBI Homepage

<http://www.ncbi.nlm.nih.gov/guide/>

The screenshot shows the NCBI homepage with a red border around the main content area. In the top right corner of this red box is a red arrow pointing to the left towards the 'Popular Resources' sidebar.

NCBI Home

- Site Map (A-Z)
- All Resources
- Chemicals & Bioassays
- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature
- Proteins
- Sequence Analysis
- Taxonomy
- Training & Tutorials
- Variation

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

[About the NCBI](#) | [Mission](#) | [Organization](#) | [Research](#) | [RSS Feeds](#)

Get Started

- [Tools](#): Analyze data using NCBI software
- [Downloads](#): Get NCBI data or software
- [How-To's](#): Learn how to accomplish specific tasks at NCBI
- [Submissions](#): Submit data to GenBank or other NCBI databases

PubMed Central

Free Full Text. Over 1,500,000 articles from over 450 journals. Linked to PubMed and fully searchable.

1 2 3 4

Popular Resources

- [BLAST](#)
- [Bookshelf](#)
- [Gene](#)
- [Genome](#)
- [Nucleotide](#)
- [OMIM](#)
- [Protein](#)
- [PubChem](#)
- [PubMed](#)
- [PubMed Central](#)
- [SNP](#)

NCBI News

NAR's 2011 Database Issue is out with 9 NCBI-Authored Papers 05 Jan 2011

New articles are available describing the new Epigenomics

New NCBI News Issue 29 Nov 2010

BLAST – Basic Local Alignment Search Tool

<http://blast.ncbi.nlm.nih.gov/Blast.cgi>

The screenshot shows the NCBI BLAST homepage. At the top, there's a navigation bar with links for Home, Recent Results, Saved Strategies, and Help. On the right, there's a "My NCBI" section with links for Sign In and Register. Below the navigation, a banner says "BLAST finds regions of similarity between biological sequences." A red box highlights a new feature: "Aligning Multiple Protein Sequences? Try the COBALT Multiple Alignment Tool." The main content area has a section titled "BLAST Assembled RefSeq Genomes" where users can choose a species genome to search. It lists several organisms with checkboxes: Human, Mouse, Rat, Arabidopsis thaliana, Oryza sativa, Bos taurus, Danio rerio, Drosophila melanogaster, Gallus gallus, Pan troglodytes, Microbes, and Apis mellifera. Below this is a "Basic BLAST" section for choosing a BLAST program to run. It includes links for nucleotide blast, protein blast, blastx, tblastn, and tblastx, each with a brief description and algorithm information. To the right, there's a "News" sidebar with a link to a new WGS BLAST page, a tip of the day about batch jobs, and a "More tips..." link. A large callout box in the bottom right corner states: "BLAST performs sequence similarity searches of query sequences vs sequence databases. We will cover this in detail in the next lecture."

NCBI/BLAST Home

BLAST finds regions of similarity between biological sequences. [more...](#)

New Aligning Multiple Protein Sequences? Try the [COBALT Multiple Alignment Tool](#). [Go](#)

BLAST Assembled RefSeq Genomes

Choose a species genome to search, or [list all genomic BLAST databases](#).

[Human](#) [Oryza sativa](#) [Gallus gallus](#)
 [Mouse](#) [Bos taurus](#) [Pan troglodytes](#)
 [Rat](#) [Danio rerio](#) [Microbes](#)
 [Arabidopsis thaliana](#) [Drosophila melanogaster](#) [Apis mellifera](#)

Basic BLAST

Choose a BLAST program to run.

[nucleotide blast](#) Search a nucleotide database using a nucleotide query
Algorithms: [blastn](#), [megablast](#), [discontiguous megablast](#)

[protein blast](#) Search protein database using a protein query
Algorithms: [blastp](#), [psi-blast](#), [phi-blast](#)

[blastx](#) Search protein database using a translated nucleotide query

[tblastn](#) Search translated nucleotide database using a protein query

[tblastx](#) Search translated nucleotide database using a translated nucleotide query

Specialized BLAST

News

[New WGS BLAST page](#)

A new WGS BLAST page allows selection of search sets by organism.
Mon, 22 Nov 2010 09:00:00 EST

[More BLAST news...](#)

Tip of the Day

[How to do Batch BLAST jobs](#)

BLAST makes it easy to examine a large group of potential gene candidates.

[More tips...](#)

BLAST performs sequence similarity searches of query sequences vs sequence databases. We will cover this in detail in the next lecture.

SUMMARY

- Bioinformatics is computer aided biology.
- Bioinformatics deals with the collection, archiving, organization, and interpretation of a wide range of biological data.
- There are a large number of primary, secondary and tertiary bioinformatics databases.
- The NCBI and EBI are major online bioinformatics service providers.
- Introduced GenBank, RefSeq, UniProt, PDB databases as well as a number of ‘boutique’ databases including PFAM and OMIM.
- Introduced the notion of *controlled vocabularies* and *ontologies*.
- Described the use of ENTREZ and BLAST for searching databases.

HOMEWORK

- Complete the **initial course questionnaire**:
<http://tinyurl.com/bioinf525-questions>
- Check out the “**Background Reading**” material on Ctools:
<http://tinyurl.com/bioinf525-w16>
- Complete the **lecture 1.1 homework questions**:
<http://tinyurl.com/bioinf525-quiz1>

THANK YOU

ADDITIONAL DATABASES OF NOTE (SLIDES FOR YOUR REFERENCE)

NCBI Metadatabases

- **Gene**
 - ▶ molecular data and literature related to genes
- **HomoloGene**
 - ▶ automated collection of homologous genes from selected eukaryotes
- **Taxonomy**
 - ▶ access to NCBI data through source organism taxonomic classification
- **PubChem**
 - ▶ small organic molecules and their biological activities
- **BioSystems**
 - ▶ biochemical pathways and processes linked to NCBI genes, gene products, small molecules, and structures

PubMed

- Curated database of biomedical journal articles
- Data records are annotated with MeSH terms (Medical Subject Headings)
- Contract workers actually read all of the articles and classify them with the MeSH terms
- PubMed entries contain article abstracts
- PubMed Central contains full journal articles, but the majority are not freely re-distributable

PubMed results

Limits and Advanced search can be used to refine searches

The screenshot shows the PubMed search results page. A red arrow points from the text above to the 'Limits' link in the top navigation bar. The search term entered is 'corticotrop* AND receptor AND human[orgn]'. The results section displays 20 of 2363 articles, with the first few listed below:

- [Distribution of retinoic acid receptor- \$\alpha\$ immunoreactivity in the human hypothalamus.](#)
1. Meng QY, Chen XN, Zhao J, Swaab DF, Zhou JN.
Neuroscience. 2010 Dec 3. [Epub ahead of print]
PMID: 21130848 [PubMed - as supplied by publisher]
[Related citations](#)
- [Caloric restriction experience reprograms stress and orexigenic pathways and promotes binge eating.](#)
2. Pankevich DE, Teegarden SL, Hedin AD, Jensen CL, Bale TL.
J Neurosci. 2010 Dec 1;30(48):16399-407.
PMID: 21123586 [PubMed - Indexed for MEDLINE]
[Related citations](#)
- [Glucocorticoids Differentially Regulate the Expression of CRFR1 and CRFR2 \$\alpha\$ in MIN6 Insulinoma Cells and Rodent Islets.](#)
3. Huisng MO, Pilbrow AP, Matsumoto M, van der Meulen T, Park H, Vaughan JM, Lee S, Vale WW.
Endocrinology. 2011 Jan;152(1):138-50. Epub 2010 Nov 24.
PMID: 21106875 [PubMed - in process]
[Related citations](#)
- [The benzodiazepine diazepam demonstrates the usefulness of Syrian hamsters as a model for anxiety testing: Evaluation of other classes of anxiolytics in comparison to diazepam.](#)
4. Gannon RL, Lungwitz E, Batista N, Hester I, Huntley C, Peacock A, Delagrange P, Millan MJ.
Behav Brain Res. 2010 Nov 20. [Epub ahead of print]
PMID: 21094664 [PubMed - as supplied by publisher]
[Related citations](#)

On the right side, there are sections for 'Titles with your search terms' and '215 free full-text articles in PubMed Central', each with a 'See more...' link. At the bottom, there is a 'Find related data' section with a 'Database: Select' dropdown.

Small molecule databases have been added at NCBI

<http://pubchem.ncbi.nlm.nih.gov/>

The screenshot shows the homepage of the PubChem database. At the top, there is a navigation bar with links for "Databases", "Deposition", "Services", "Help", and "more". Below the navigation bar is the PubChem logo. Underneath the logo are three main search tabs: "BioAssay", "Compound", and "Substance". To the right of these tabs is a search bar with a "GO" button and a link to "Advanced search". Below the search bar are two blue links: "Chemical structure search" and "BioActivity analysis". A green box contains a "New" announcement about the addition of over 2.5 million structures from IBM BAO. At the bottom of the page, there are links for "Write to Helpdesk", "Disclaimer", "Privacy Statement", "Accessibility", "Data Citation Guidelines", "National Center for Biotechnology Information", "NLM", "NIH", and "HHS". On the right side of the page, there is a vertical sidebar with various links and icons, including "Bioactivity summary", "Bioactivity datatable", "Bioactivity structure-activity", "Chemical structure search", "3D conformer viewer", "Chemical structure clustering", "Deposition gateway", "Structure download", "Bioassay download", and "PubChem FTP".

Databases Deposition Services Help more

PubChem

BioAssay Compound Substance

GO Advanced search

Chemical structure search | BioActivity analysis

New More than 2.5 million structures from the IBM BAO (Business Analytics and Optimization) strategic IP insight platform (SIIP) are now available in PubChem. See [more..](#) and [related news](#).

more ...

Write to Helpdesk | Disclaimer | Privacy Statement | Accessibility | Data Citation Guidelines
National Center for Biotechnology Information
NLM | NIH | HHS

Bioactivity summary

Bioactivity datatable

Bioactivity structure-activity

Chemical structure search

3D conformer viewer

Chemical structure clustering

Deposition gateway

Structure download

Bioassay download

PubChem FTP

HomoloGene - Homologous genes from different organisms <http://www.ncbi.nlm.nih.gov/homologene>

NCBI

HomoloGene Discover Homologs

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search HomoloGene for Go Clear

Limits Preview/Index History Clipboard Details

HomoloGene Homepage Query Tips Build Procedure FTP site

Genome Resources Homo sapiens Mus musculus Rattus norvegicus Danio rerio

HomoloGene is a system for automated detection of homologs among the annotated genes of several completely sequenced eukaryotic genomes.

HomoloGene Release 65 Statistics

Initial numbers of genes from complete genomes, numbers of genes placed in a homology group, and the numbers of groups for each species.

Species	Number of Genes		HomoloGene groups
	Input	Grouped	
Homo sapiens	19,943*	18,981	18,431
Pan troglodytes	25,096	16,850	15,980
Canis familiaris	19,766	16,708	15,951
Bos taurus	22,049	18,180	16,224
Mus musculus	25,388	21,766	19,005
Rattus norvegicus	21,991	19,229	17,473
Gallus gallus	17,959	13,142	11,905
Danio rerio	26,690*	21,084	14,067
Drosophila melanogaster	13,827*	9,282	7,749
Anopheles gambiae	12,460	8,867	7,541
Caenorhabditis elegans	20,132*	8,678	4,810
Schizosaccharomyces pombe	5,043	3,225	2,935
Saccharomyces cerevisiae	5,880	4,851	4,370
Kluyveromyces lactis	5,335	4,459	4,382
Eremothecium gossypii	4,722	3,928	3,884
Magnaporthe grisea	12,832	7,330	6,399
Neurospora crassa	9,821*	6,287	6,144
Arabidopsis thaliana	27,000*	19,961	11,243

What's New

HomoloGene release 65 includes updated annotations for the following species: Homo sapiens (NCBI release 37.2), Danio rerio (NCBI release 4.1), Drosophila melanogaster (NCBI release 9.3) Caenorhabditis elegans (NCBI release 9.1), Arabidopsis thaliana (NCBI release 9.1).

Related Resources

Entrez Genomes

A collection of complete genome sequences that includes more than 1000 viruses and over hundred microbes

- Archaea
- Bacteria
- Eukaryota

Online Mendelian Inheritance in Man – OMIM

<http://www.ncbi.nlm.nih.gov/omim>

The screenshot shows the OMIM homepage within the NCBI interface. The top navigation bar includes links for All Databases, PubMed, Nucleotide, Protein, Genome, Structure, PMC, and OMIM. A search bar is present, and the right side features a "My NCBI" section with "Sign In" and "Register" buttons. The main content area has tabs for Entrez, OMIM, Help, FAQ, and OMIM Facts. The OMIM tab is active, showing search instructions and a welcome message. The welcome message highlights OMIM's role as a comprehensive compendium of human genes and genetic phenotypes, containing over 12,000 entries and focusing on the relationship between phenotype and genotype.

Entrez

OMIM

Search OMIM
Search Gene Map
Search Morbid Map

Help

OMIM Help
How to Link

FAQ

Numbering System
Symbols
How to Print
Citing OMIM
Download

OMIM Facts
Statistics
Update Log

OMIM® - Online Mendelian Inheritance in Man

Welcome to OMIM®, Online Mendelian Inheritance in Man®. OMIM is a comprehensive, authoritative, and timely compendium of human genes and genetic phenotypes. The full-text, referenced overviews in OMIM contain information on all known mendelian disorders and over 12,000 genes. OMIM focuses on the relationship between phenotype and genotype. It is updated daily, and the entries contain copious links to other genetics resources.

This database was initiated in the early 1960s by Dr. Victor A. McKusick as a catalog of mendelian traits and disorders, entitled Mendelian Inheritance in Man (MIM). Twelve book editions of MIM were published between 1966 and 1998. The online version, OMIM, was created in 1985 by a collaboration between the National Library of Medicine and the William H. Welch Medical Library at Johns Hopkins. It was made generally available on the

OMIM is essentially a set of reviews of human genes, gene function and phenotypes. Includes causative mutations where known.

The NCBI Bookshelf includes many well known molecular biology texts.

<http://www.ncbi.nlm.nih.gov/books/>

The Bookshelf is a growing collection of biomedical books that can be searched directly by typing a concept into the textbox above and selecting "Go". Try one of these searches:

► [cell cycle control](#) ► [immunodeficiency](#) ► [protein evolution](#)

► **New on the Bookshelf:**

 [Health, United States, 2009](#)
Hyattsville (MD): [National Center for Health Statistics \(US\)](#); 2010

 [Human Herpesviruses: Biology, Therapy, and Immunoprophylaxis](#)
Arvin, Ann; Campadelli-Fiume, Gabriella; Mocarski, Edward; Moore, Patrick S.; Roizman, Bernard; Whitley, Richard; Yamanishi, Koichi, editors
Cambridge: [Cambridge University Press](#); 2007

 [NIH Molecular Libraries Probe Reports from the Molecular Libraries Program](#)
NIH Molecular Libraries
Bethesda (MD): [National Center for Biotechnology Information \(US\)](#); 2010

 [StemBook](#)
Cambridge (MA): [Harvard Stem Cell Institute](#); 2008-

 [VA Evidence-based Synthesis Program Reports](#)
Washington (DC): [Department of Veterans Affairs \(US\)](#); 2007-

GEO: Gene Expression Omnibus

- Gene expression data (mostly from microarrays but also RNA-seq data, 2 methods for measuring RNA levels)

Query browse and download data sets

Gene Expression Omnibus: a public functional genomics data repository supporting MIAME-compliant data submissions. Array- and sequence-based data are accepted. Tools are provided to help users query and download experiments and curated gene expression profiles. [More information »](#)

GEO navigation

QUERY

- DataSets [GO](#)
- Gene profiles [GO](#)
- GEO accession [GO](#)
- GEO BLAST

BROWSE

- DataSets
- GEO accessions
 - Platforms
 - Samples
 - Series

Site contents

Public data

Platforms	8,246
Samples	514,893
Series	20,827

Documentation

- [Overview](#)
- [FAQ](#)
- [Find](#)
- [Submission guide](#)
- [Linking & citing](#)
- [Journal citations](#)
- [Construct a Query](#)
- [Programmatic access](#)
- [DataSet clusters](#)
- [GEO announce list](#)
- [Data disclaimer](#)
- [GEO staff](#)

Query & Browse

- [Repository browser](#)
- [Submitters](#)

Submitter login

- **Series** - (GSEXXX) is an original submitter-supplied record that summarizes a study. May contain multiple individual **Samples** (GSMXXX).

GEO Accession viewer
www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3541

NCBI **GEO**

Platforms (1) [GPL4091 Agilent-014693 Human Genome CGH Microarray 244A \(Feature number version\)](#)

Samples (4) [GSM495808 Aspc1 Cell Line](#)
[GSM495809 JH39 Xenograft](#)
[GSM495810 JH21 Xenograft](#)

Download family

Format
SOFT formatted family file(s)
MINiML formatted family file(s)
Series Matrix File(s)

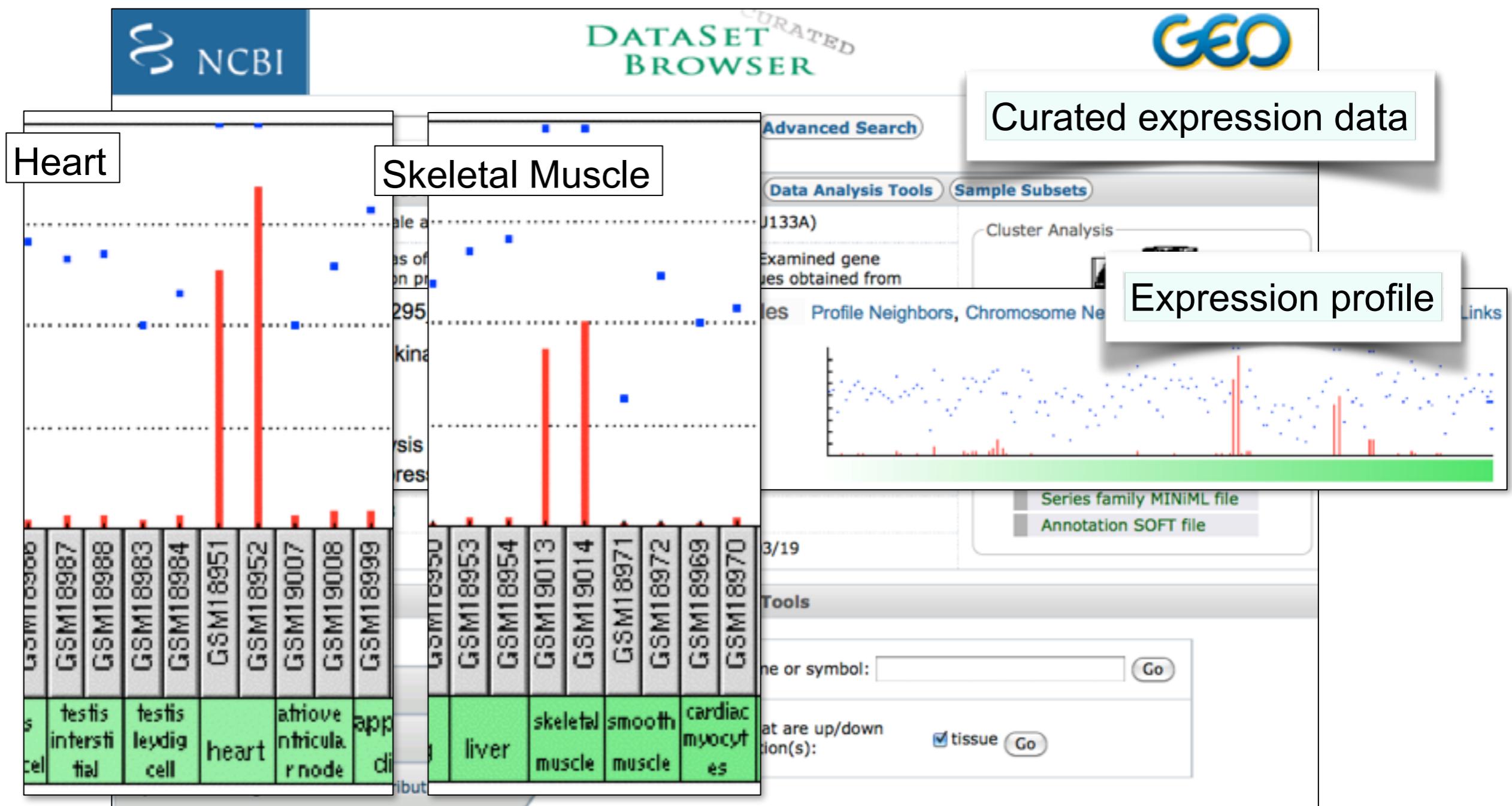
Supplementary file **Size** **Download** **File type/resource**

GSE19852_RAW.tar	170.7 Mb	(ftp)(http)	TAR (of TXT)
----------------------------------	----------	-----------------------------	--------------

NLM | NIH | GEO Help | Disclaimer | Section 508 |

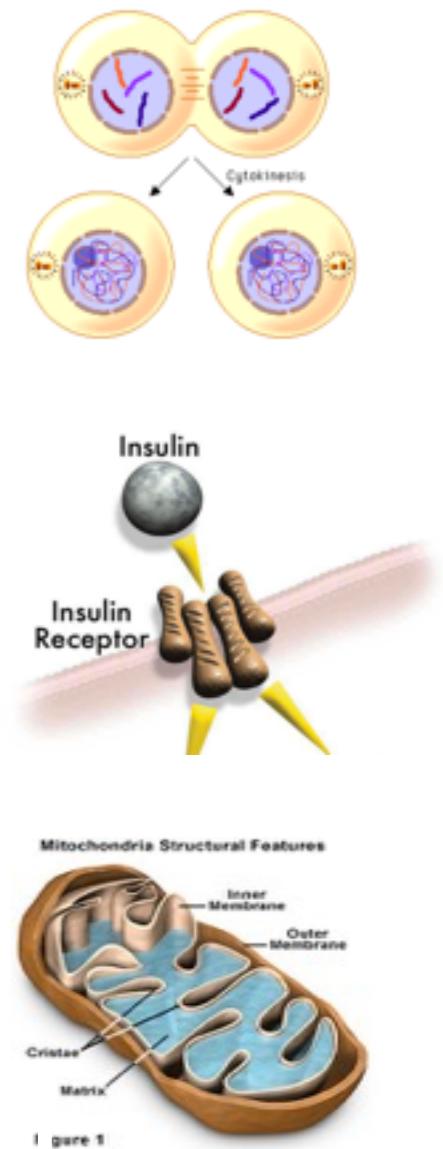
uter. Significance Analysis of Microarrays (SAM) identified 92 genes differentially expressed by strain. Interestingly, several members of the solute carrier family of amino acid transporters, genes involved in amino acid synthesis and development, and amiloride-sensitive epithelial sodium channel gene were induced by strain. These results were confirmed by quantitative real-time polymerase chain reaction (qRT-PCR). Thus, this study identifies genes induced by strain that may be important for amino acid signaling pathways, protein

- DataSets - (GDSxxx) are curated collections of selected Samples that are biologically and statistically comparable



GO Ontologies

- There are three ontologies in GO:
 - ▶ **Biological Process**
A commonly recognized series of events
e.g. cell division, mitosis,
 - ▶ **Molecular Function**
An elemental activity, task or job
e.g. kinase activity, insulin binding
 - ▶ **Cellular Component**
Where a gene product is located
e.g. mitochondrion, mitochondrial membrane



QuickGO is a fast web-based browser of the Gene Ontology and Gene Ontology annotation data

The screenshot shows the QuickGO homepage on a web browser. The URL in the address bar is www.ebi.ac.uk/QuickGO/. The page has a dark green header with the EMBL-EBI logo and navigation links for Databases, Tools, Research, Training, Industry, About Us, Help, Terms of Use, Privacy, Cookies, Site Index, and a download icon.

The main content area features a sidebar on the left with links to QuickGO Help, Reference, FAQs, Video tutorials, Downloads, geneontology.org, UniProt-GOA project, and Web Services. The main content area includes a search bar with placeholder "Enter Text Here", a "Find" button, and links to "Web Services", "Dataset", and "Term Basket: 0". Below this is a section titled "Search and Filter GO annotation sets" with a description of how filters can generate specific subsets of annotations. Another section, "Investigate GO slims", explains what GO slims are and how they can be used to categorize proteins/genes. A third section, "View the history of changes to GO", allows users to view historical changes. To the right, there is a "QuickGO News" sidebar with links to news items from August 2011, June 2011, and April 2011, along with links to the "QuickGO News Archive", "QuickGO Tips", and "Tutorial".

GO annotation in UniProt

An example UniProt entry for hemoglobin beta (HBB_human, P68871) with GO annotation displayed.

Hemoglobin subunit beta – Homo sapiens (Human)

www.uniprot.org/uniprot/P68871

Hemoglobin subunit beta – Homo sapiens (Human)

Names · Attributes · General annotation · Ontologies · Interactions · Sequence annotation · Sequences · References · Web links · Cross-refs · Entry Info · Documents · Customize order

Gene Ontology (GO)

Biological_process	bicarbonate transport Traceable author statement. Source: Reactome
	blood coagulation Traceable author statement. Source: Reactome
	hydrogen peroxide catabolic process Inferred from direct assay PubMed 19740759 . Source: BHF-UCL
	nitric oxide transport Non-traceable author statement PubMed 8292032 . Source: UniProtKB
	positive regulation of cell death Inferred from direct assay PubMed 19740759 . Source: BHF-UCL
	positive regulation of nitric oxide biosynthetic process Non-traceable author statement PubMed 7965120 . Source: UniProtKB
	protein heterooligomerization Inferred from direct assay PubMed 19740759 . Source: BHF-UCL
	regulation of blood pressure Inferred from electronic annotation. Source: UniProtKB-KW
	regulation of blood vessel size Inferred from electronic annotation. Source: UniProtKB-KW
	renal absorption Inferred from mutant phenotype PubMed 18465053 PubMed 18974585 . Source: UniProtKB
	small molecule metabolic process Traceable author statement. Source: Reactome
Cellular_component	endocytic vesicle lumen Traceable author statement. Source: Reactome
	extracellular region Traceable author statement. Source: Reactome
	haptoglobin-hemoglobin complex Inferred from direct assay PubMed 19740759 . Source: BHF-UCL
	hemoglobin complex Non-traceable author statement Ref.33 Ref.72 . Source: UniProtKB
Molecular_function	heme binding Inferred from electronic annotation. Source: InterPro

GO annotation in UniProt

An example UniProt entry for hemoglobin beta (HBB_human, P68871) with GO annotation displayed.

The screenshot shows a web browser window with two tabs. The top tab is titled "Hemoglobin subunit beta - Homo sapiens (Human)" and displays the UniProt entry for HBB_human (P68871). The bottom tab is titled "GO:0020037 heme binding" and displays the QuickGO annotation details for this term. The QuickGO page includes navigation links like "EBI > Databases > QuickGO" and "GO:0020037 heme binding". It features a search bar, a "Quick GO" logo, and various links for "Web Services", "Dataset", and "Term Basket: 0". The main content area shows the term's ID (GO:0020037), name (heme binding), ontology (Molecular Function), definition (Interacting selectively and non-covalently with heme, any compound of iron complexed in a porphyrin (tetrapyrrole) ring.), and a GONUTS link. Below this, there are tabs for "Synonyms", "Annotation Guidance", "Cross-Ontology Relations", and "Cross-references". A note about synonyms is present, and a table shows one synonym: Type: exact, Synonym: haem binding. The UniProt tab also shows standard protein information like document count, gene count, and protein length.

DAVID: a online tool for assessing GO term enrichment in gene lists

The screenshot shows the DAVID Bioinformatics Resources 6.7 homepage. The top navigation bar includes links for Home, Start Analysis, Shortcut to DAVID Tools, Technical Center, Downloads & APIs, Term of Service, Why DAVID?, and About Us. The main content area features the DAVID logo and the text "DAVID Bioinformatics Resources 6.7" and "National Institute of Allergy and Infectious Diseases (NIAID), NIH". A sidebar on the left provides links to Functional Annotation, Gene Functional Classification, Gene ID Conversion, Gene Name Batch Viewer, and NIAID Pathogen Annotation Browser. The central content area discusses the latest release (v6.7) and highlights its features, including functional annotation clustering, charting, and tables. A sidebar on the right lists "What's Important in DAVID?" such as current release notes and citation requirements. A large callout box in the bottom right corner states: "DAVID allows you to upload lists of genes and search for enriched GO and search for functionally related genes not in your list". Below this is a URL link: <http://david.abcc.ncifcrf.gov>.

DAVID Functional Annotation Bioinformatics Microarray Analysis

david.abcc.ncifcrf.gov/home.jsp

DAVID Functional Annotation Bioinformatics Microarray Analysis DAVID: Database for Annotation, Visualization, and Integrated...

DAVID Bioinformatics Resources 6.7
National Institute of Allergy and Infectious Diseases (NIAID), NIH

Home Start Analysis Shortcut to DAVID Tools Technical Center Downloads & APIs Term of Service Why DAVID? About Us

Functional Annotation

- Functional Annotation Clustering
- Functional Annotation Chart
- Functional Annotation Table

Gene Functional Classification

Gene ID Conversion

Gene Name Batch Viewer

NIAID Pathogen Annotation Browser

er published in *Nature Protocols* describes step-by-step procedure to use DAVID!

Shortcut to DAVID 6.7

003 - 2013

What's Important in DAVID?

- Current (v 6.7) release note
- New requirement to cite DAVID
- IDs of Affy Exon and Gene arrays supported

DAVID allows you to upload lists of genes and search for enriched GO and search for functionally related genes not in your list

<http://david.abcc.ncifcrf.gov>

Example output: enriched functions from GO

DAVID: Database for Annotation, Visualization, and Integrat...ID); Science Applications International Corporation (SAIC) david.abcc.ncifcrf.gov/chartReport.jsp?annot=25 Reader +

DAVID: Functional Annotation Result Summary Database for Annotation, Visualization, and Integrated Discov...

DAVID Bioinformatics Resources 6.7
National Institute of Allergy and Infectious Diseases (NIAID), NIH

Functional Annotation Chart

Help and Manual

Current Gene List: List_1
Current Background: Homo sapiens
14 DAVID IDs
Options

Rerun Using Options Create Sublist

10 chart records

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of osteoclast differentiation	RT		2	14.3	2.1E-2	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to organic substance	RT		4	28.6	2.9E-2	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of myeloid leukocyte differentiation	RT		2	14.3	3.9E-2	9.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of transcription from RNA polymerase II promoter	RT		3	21.4	4.8E-2	9.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of myeloid cell differentiation	RT		2	14.3	6.5E-2	9.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cartilage development	RT		2	14.3	6.9E-2	9.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of transcription, DNA-dependent	RT		3	21.4	7.5E-2	9.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of RNA metabolic process	RT		3	21.4	7.6E-2	8.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to protein stimulus	RT		2	14.3	9.8E-2	9.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of transcription	RT		3	21.4	1.0E-1	9.1E-1

Download File

8 gene(s) from your list are not in the output.