

Bioinformatics & Biostatistics

Lecture 2: Bioinformatic Databases

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You Tube



WIKIPEDIA
The Free Encyclopedia



bing™

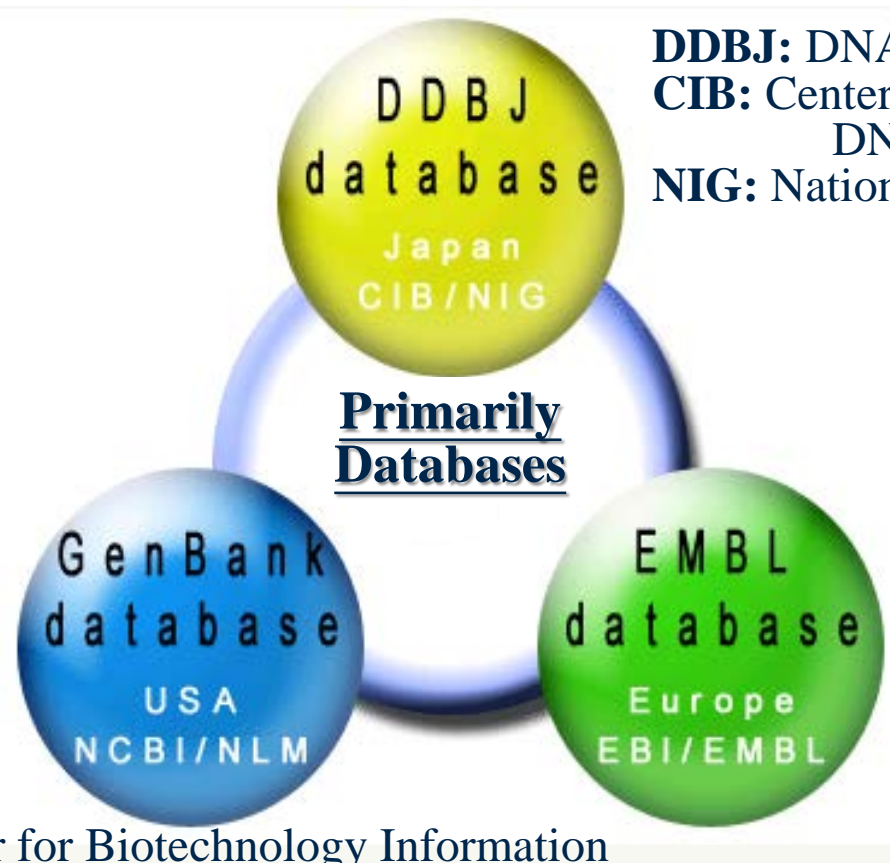
Bai du 百度
www.baidu.com

YAHOO!
INDIA

टांग professor सर्वोत्तम

Search Web

GenBank/EMBL/DDBJ International Nucleotide Sequence Database



DDBJ: DNA Data Bank of Japan
CIB: Center for Information Biology and
DNA Data Bank of Japan
NIG: National Institute of Genetics

Primarily
Databases


EMBL:
European Molecular Biology
Laboratory

EBI:
European Bioinformatics
Institute








NCBI:
National Center for Biotechnology Information

NLM:
National Library of Medicine

GenBank

Nucleotide 

Search

GenBank Submit Genomes WGS HTGs EST/GSS Metagenomes TPA TSA INSDC 

GenBank Overview

What is GenBank?

GenBank[®] is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences (*Nucleic Acids Research*, 2013 Jan;41(D1):D36-42). GenBank is part of the [International Nucleotide Sequence Database Collaboration](#), which comprises the DNA DataBank of Japan (DDBJ), the European Molecular Biology Laboratory (EMBL), and GenBank at NCBI. These three organizations exchange data on a daily basis.

The complete [release notes](#) for the current version of GenBank are available on the NCBI ftp site. A new release is made every two months. GenBank growth [statistics](#) for both the traditional GenBank divisions and the WGS division are available from each release.

An example of a GenBank [record](#) may be viewed for a *Saccharomyces cerevisiae* gene.

Access to GenBank

There are several ways to search and retrieve data from GenBank.

- Search GenBank for sequence identifiers and annotations with [Entrez Nucleotide](#), which is divided into three divisions: [CoreNucleotide](#) (the main collection), [dbEST](#) (Expressed Sequence Tags), and [dbGSS](#) (Genome Survey Sequences).
- Search and align GenBank sequences to a query sequence using [BLAST](#) (Basic Local Alignment Search Tool). BLAST searches CoreNucleotide, dbEST, and dbGSS independently; see [BLAST info](#) for more information about the numerous BLAST databases.
- Search, link, and download sequences programatically using [NCBI e-utilities](#).

GenBank Data Usage

The GenBank database is designed to provide and encourage access within the scientific community to the most up to date and comprehensive DNA sequence information. Therefore, NCBI places no restrictions on the use or distribution of the GenBank data. However, some submitters may claim patent, copyright, or other intellectual property rights in all or a portion of the data they have submitted. NCBI is not in a position to assess the validity of such claims, and therefore cannot provide comment or unrestricted permission concerning the use, copying, or distribution of the information contained in GenBank.

GenBank Resources

[GenBank Home](#)[Submission Types](#)[Submission Tools](#)[Search GenBank](#)[Update GenBank Records](#)

Search All Databases

Search

Clear

Resources

NCBI Home

- All Resources (A-Z)
- 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.

[More about the NCBI](#) | [Mission](#) | [Organization](#) | [Research](#) | [RSS](#)

Genome

1000 prokaryotic genomes are now completed and available in the Genome database.



1 2 3 4

Popular Resources

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

NCBI News

[MyNCBI supports OpenID and InCommons IDs](#)

22 Sep 2010

A list of supported organizations can be found on the MyNCBI

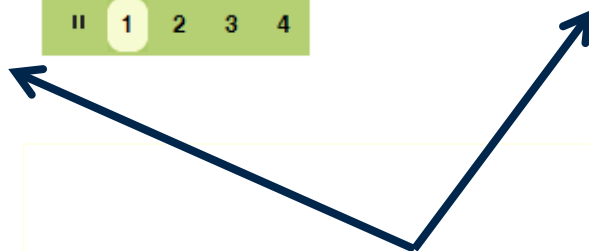
[Personalized settings in MyNCBI](#)

30 Aug 2010

Personalized preferences such as record format and results display

[More...](#)

Secondarily Databases



- [InterPro:Home](#)
- [Advanced Search](#)
- [InterProScan](#)
- [BioMart](#)
- [Help / Documentation](#)
- [About InterPro](#)
- [Release Notes](#)
- [BioMart Manual](#)
- [Tutorial](#)
- [Publications](#)
- [Contributors](#)
- [Web Services](#)
- [Downloads](#)
- [Protein Focus](#)
- [Collagen](#)

EBI > Databases > InterPro

InterPro protein sequence analysis & classification

InterPro is an integrated database of predictive protein "signatures" used for the classification and automatic annotation of proteins and genomes. InterPro classifies sequences at superfamily, family and subfamily levels, predicting the occurrence of functional domains, repeats and important sites. InterPro adds in-depth annotation, including GO terms, to the protein signatures.

Current release: **28.0 11th August 2010** (see [Release Notes](#) for further details)

InterPro:

Do a sequence search of InterPro, via [InterProScan](#)

Extract large datasets by querying our [BioMart](#)

You can access our data programmatically, via [Web Services](#)

Secondarily Databases



FlyBase

A Database of the
Drosophila Genome

 **Saccharomyces Genome Database**

The Genome Database
An international collaboration in support of the Human Genome Project.



 **Mouse Genome Informatics** 



 **Berkeley Drosophila
Genome Project**



[Sanger Centre](#) | [Acedb](#) | [Acebrowser](#) | [Ensembl](#) | [Trace Server](#) | [Library](#)

**The
Sanger Centre**

[Info](#) | [Database Searches](#) | [HGP](#) | [Projects](#) | [Software](#) | [Teams](#) | [Search](#)

[Data Release Policy](#) | [Conditions of Use](#)



[Projects Home](#)

The *C. elegans* Genome Project

The *C. elegans* sequencing project is a collaboration between the [Sanger Centre](#), Hinxton, Cambridge and the [Genome Sequencing Center](#) at the Washington University School of Medicine, St. Louis. The sequence is now essentially complete, as published in *Science* ([additional notes here](#)).

Database Retrieving and Manipulation Network

Databases

Literature Database
Sequence Databases -
Primary Databases
Secondarily Databases

Query by
1. Text
2. Sequence

Retrival System

Information

Sequenece, Structure, Image, Document

Softwares

GCG
Vector NTI
CLC
Open Sources
Endnote
MS Office
Adobe

GenBANK
GCG
FASTA
Staden
Image

Formats

Sequence
Converter



Hello 

網頁 圖片 影片 地圖 新聞 更多 ▾ 搜尋工具

約有 108,000,000 項結果 (搜尋時間：0.42 秒)

HELLO! Online: celebrity & royal news, magazine, babies ...

www.hellomagazine.com/ ▾ 翻譯這個網頁

HELLO! Online brings you the latest celebrity & royal news from the UK & around the world, magazine exclusives, celeb babies, weddings, pregnancies and ...

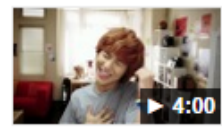
Royalty - William and Kate - Celebrities - This week's issue

Hello - 維基百科，自由的百科全书 - Wikipedia

[zh.wikipedia.org/zh-tw/Hello](http://zh.wikipedia.org/zh-tw>Hello) ▾ 轉為繁體網頁

Hello. Hello是英語中常用的問候語，在英語中意思相同的問候語還有Hi和Hey，早在1883年即有詞典收錄此詞。除了英語，許多歐洲語言中也有類似的詞彙，像是 ...

SHINee(샤이니) _ Hello _ MusicVideo - YouTube



www.youtube.com/watch?v=skZxb5sBoiU ▾

2010年10月4日 - 上傳者：sment

SHINee(샤이니) _ Hello _ MusicVideo ♪ Download on iTunes :

[http://itunes.apple.com/us/album/hello-the ...](http://itunes.apple.com/us/album/hello-the-...)

Gina hello 森 | Facebook

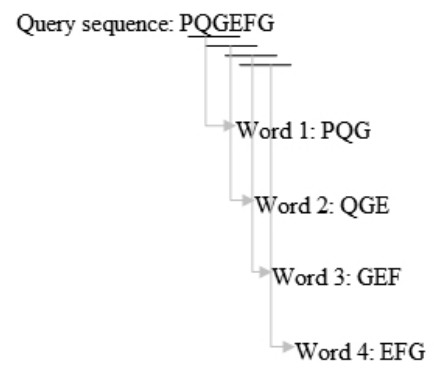
<https://zh-tw.facebook.com/Gina.Hello> ▾


Gina hello 森，臺中市·186163 個讚·26347 人正在談論這個·♥MIMIG 品牌主理 <http://mimig.tw> ♥BLOG: <http://ginahello.com> ♥邀約請 [mail:design.gina@gmail.com](mailto:design.gina@gmail.com)...

Hello Kitty Jet Travels with You! | 首頁

evakitty.evaair.com/ ▾

10月29日起長榮航空Hello Kitty彩繪機直飛巴黎·長榮航空首架777 Hello Kitty Jet — 牽手機，以三麗鷗家族串連全世界... Hello Kitty Jet加持祝Jolin上海演唱會大成功 ...



fuzzy search
(approximate string matching) 

Literature Databases

PubMed

PubMed comprises more than 21 million citations for biomedical literature from MEDLINE, life science journals, and online books. Citations may include links to full-text content from PubMed Central and publisher web sites.

NCBI Resources How To

PubMed.gov
US National Library of Medicine National
Institutes of Health

PubMed

Search

Advanced

Limits

Dates

Published in the Last: Any date

Type of Article

- Clinical Trial
- Editorial
- Letter
- Meta-Analysis
- Review

Species

- Humans
- Animals

Subsets

- AIDS
- Bioethics
- Cancer
- Complementary Medicine
- Complementary Therapies

Text Options

- Links to full text
- Links to free full text
- Abstracts

Languages

- English
- French
- German
- Italian
- Japanese

Sex

- Male
- Female

Ages

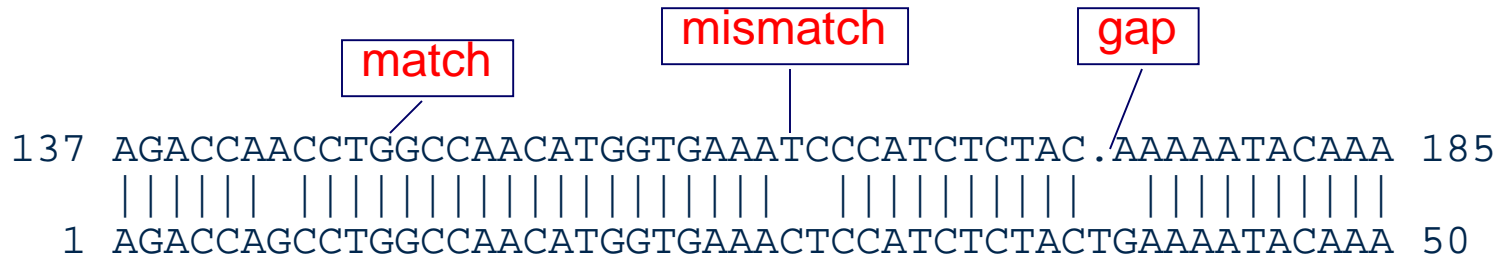
- All Infant: birth-23 months
- All Child: 0-18 years
- All Adult: 19+ years
- Newborn: birth-1 month
- Infant: 1-23 months

Search Field Tags

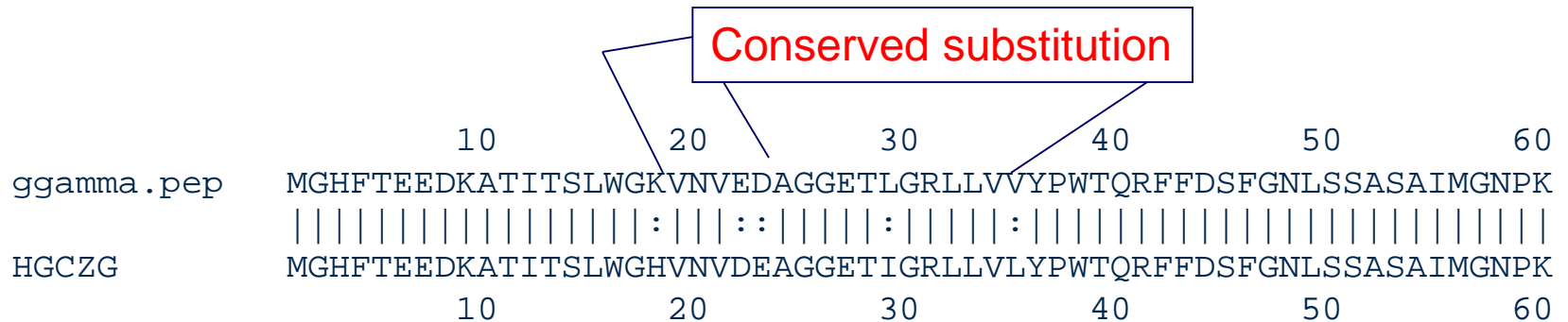
Field: All Fields

Sequence Comparison

Nucleotide sequence alignments



Protein sequence alignments



Residues with shared chemical properties can substitute for each other
Size, charge, hydrophobicity, polarity
scored less than a match, but better than a mismatch
Conservative changes scored as better than non-conservative

Pairwise Comparison

Local Alignment

compares regions within two sequences and
can return several matches

BLAST



VS

Global Alignment

compare entire sequences

FASTA



Query by sequence

Program	QUERY	Database
blastp	amino acid sequence	protein sequence database.
blastn	nucleotide sequence	nucleotide sequence database.
blastx	nucleotide sequence translated in all reading frames	protein sequence database (use this option to find potential translation products of an unknown nucleotide sequence)
tblastn	amino acid sequence	nucleotide sequence database translated in all reading frames
tblastx	six-frame translations of a nucleotide sequence	six-frame translations of a nucleotide sequence database. (tblastx program cannot be used with the nr database on the BLAST Web page because it is computationally intensive)

BLAST principle

1: Query Preprocessing

Break query into words

D**TLV**RAIP -> DTL, **TLV**, LVR, VRA ...

Make a table of similar words

TLV -> TLI, **TIV**, SLV

2: Search query words in indexed table of database words

Find exact match between table word & db.

TIV

SDTDGDKNADGWIE**TIV**RALPTSD

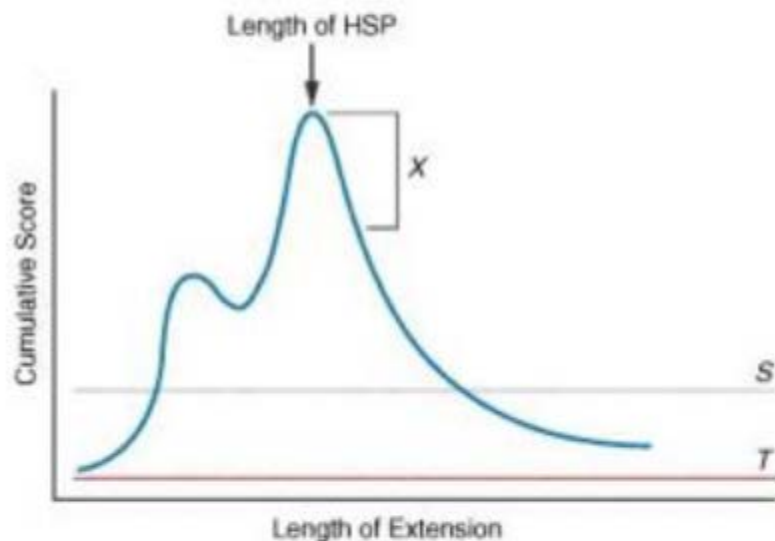
3: Extend query match to HSP

- keep HSPs of significant quality.

DTLVRAIP

SDTDGDKNADGWI**ETIV**RALPTSD

4: Assemble HSPs into gapped alignment



HSP (High Scoring Segment Pair):
An ungapped, high-scoring, local alignment



About NCBI

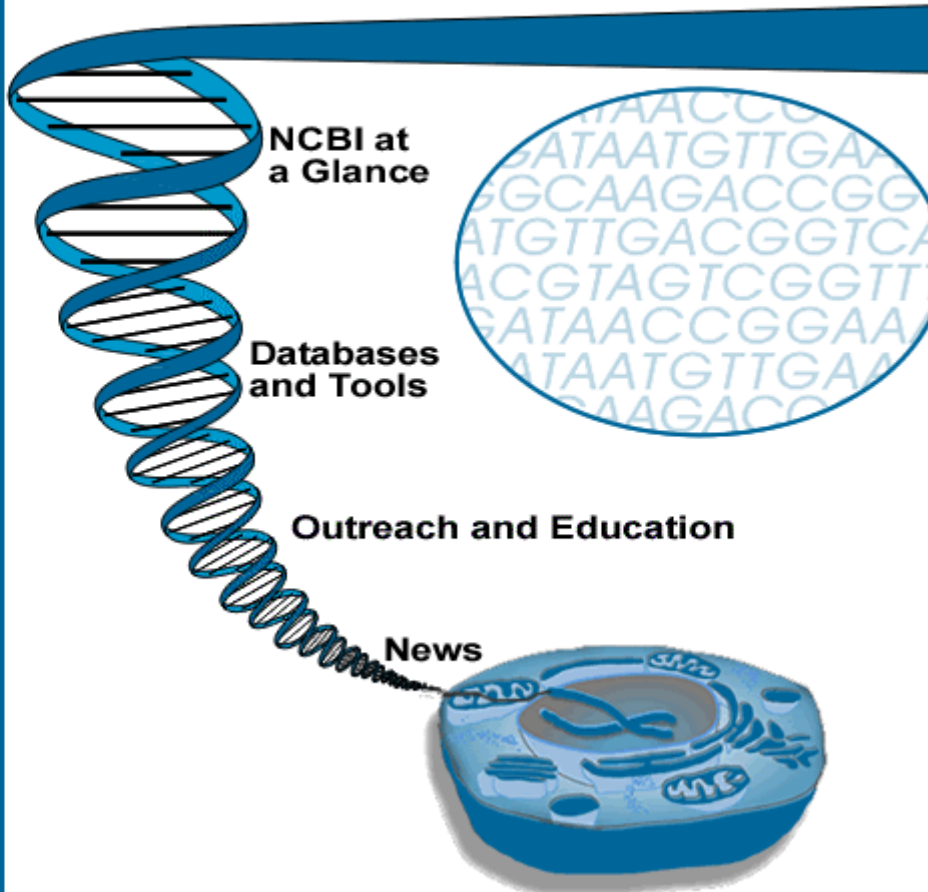
National Center for Biotechnology Information

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[Databases and Tools](#)

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[News](#)



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.

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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

Genotypes and Phenotypes

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



|| 1 2 3 4 5 6 7 8

Popular Resources

PubMed

Bookshelf

PubMed Central

PubMed Health

BLAST

Nucleotide

Genome

SNP

Gene

Protein

PubChem

NCBI Announcements

Try the new My NCBI Feature: SciENcv

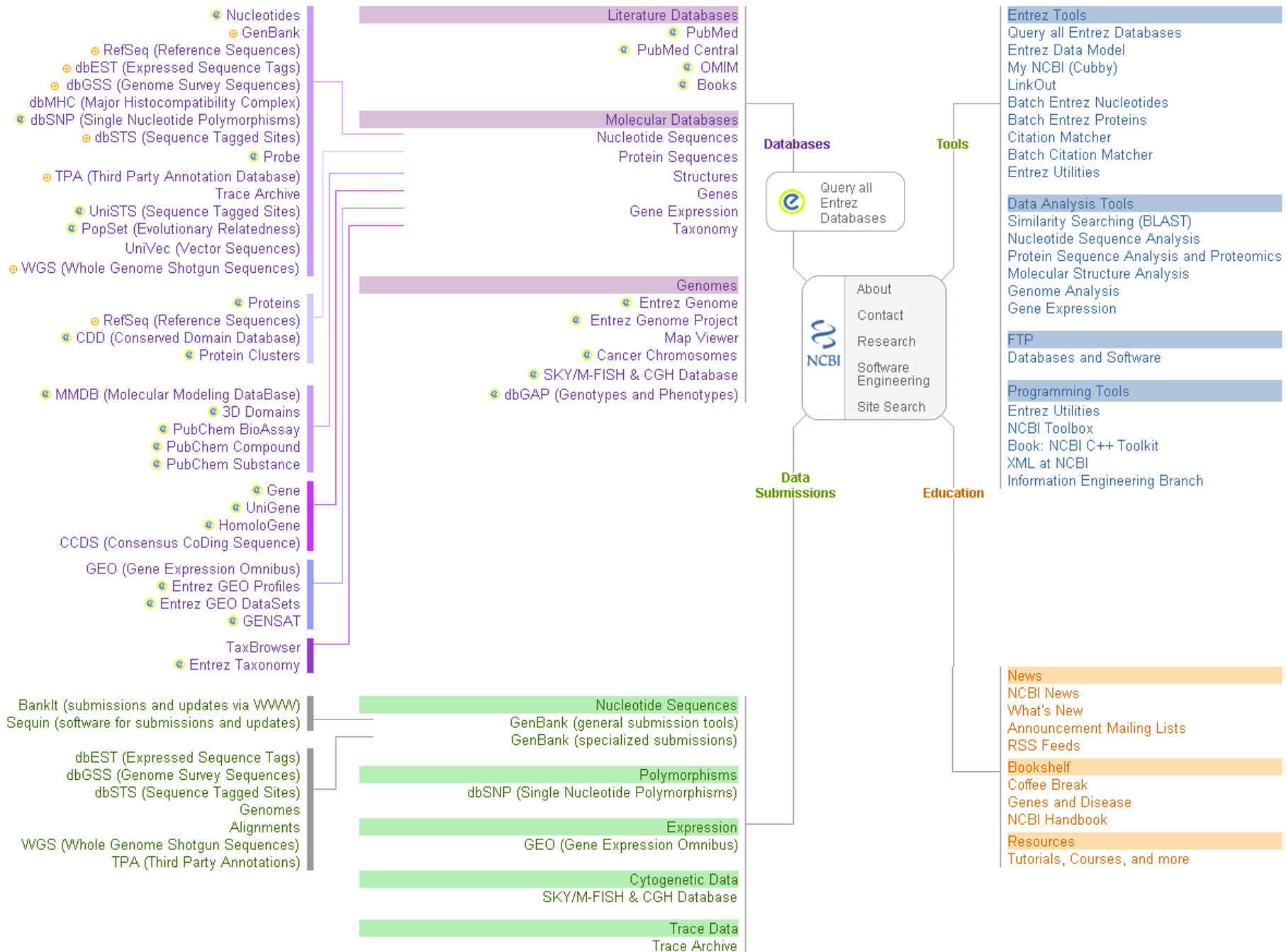
Sep 26, 2013

The National Institutes of Health has issued an invitation to researchers

Comments Requested: NIH genomic data sharing policy

Sep 20, 2013

The National Institutes of Health (NIH) is



Literature

Books	books and reports
MeSH	ontology used for PubMed indexing
NLM Catalog	books, journals and more in the NLM Collections
PubMed	scientific & medical abstracts/citations
PubMed Central	full-text journal articles

Health

ClinVar	human variations of clinical significance
dbGaP	genotype/phenotype interaction studies
GTR	genetic testing registry
MedGen	medical genetics literature and links
OMIM	online mendelian inheritance in man
PubMed Health	clinical effectiveness, disease and drug reports

Genomes

Assembly	genomic assembly information
BioProject	biological projects providing data to NCBI
BioSample	descriptions of biological source materials
Clone	genomic and cDNA clones
dbVar	genome structural variation studies
Epigenomics	epigenomic studies and display tools
Genome	genome sequencing projects by organism
GSS	genome survey sequences
Nucleotide	DNA and RNA sequences
Probe	sequence-based probes and primers
SNP	short genetic variations
SRA	high-throughput DNA and RNA sequence read archive
Taxonomy	taxonomic classification and nomenclature catalog

Genes

EST	expressed sequence tag sequences
Gene	collected information about gene loci
GEO DataSets	functional genomics studies
GEO Profiles	gene expression and molecular abundance profiles
HomoloGene	homologous gene sets for selected organisms
PopSet	sequence sets from phylogenetic and population studies
UniGene	clusters of expressed transcripts

Proteins

Conserved Domains	conserved protein domains
Protein	protein sequences
Protein Clusters	sequence similarity-based protein clusters
Structure	experimentally-determined biomolecular structures

Chemicals

BioSystems	molecular pathways with links to genes, proteins and chemicals
PubChem BioAssay	bioactivity screening studies
PubChem Compound	chemical information with structures, information and links
PubChem Substance	deposited substance and chemical information

Search NCBI databases

Help

p53

x

Search

About 2,054,751 search results for "p53"

Literature

Books	1,434	books and reports
MeSH	162	ontology used for PubMed indexing
NLM Catalog	108	books, journals and more in the NLM Collections
PubMed	73,213	scientific & medical abstracts/citations
PubMed Central	98,959	full-text journal articles

Health

ClinVar	296	human variations of clinical significance
dbGaP	22	genotype/phenotype interaction studies
GTR	133	genetic testing registry
MedGen	72	medical genetics literature and links
OMIM	584	online mendelian inheritance in man
PubMed Health	78	clinical effectiveness, disease and drug reports

Genomes

Assembly	1	genomic assembly information
BioProject	665	biological projects providing data to NCBI
BioSample	319	descriptions of biological source materials
Clone	0	genomic and cDNA clones
dbVar	1,659	genome structural variation studies
Epigenomics	0	epigenomic studies and display tools
Genome	6	genome sequencing projects by organism
GSS	36	genome survey sequences
Nucleotide	47,635	DNA and RNA sequences
Probe	3,518	sequence-based probes and primers
SNP	6,593	short genetic variations
SRA	462	high-throughput DNA and RNA sequence read archive
Taxonomy	0	taxonomic classification and nomenclature catalog

Genes

EST	797	expressed sequence tag sequences
Gene	8,300	collected information about gene loci
GEO DataSets	9,570	functional genomics studies
GEO Profiles	1,749,571	gene expression and molecular abundance profiles
HomoloGene	38	homologous gene sets for selected organisms
PopSet	97	sequence sets from phylogenetic and population studies
UniGene	414	clusters of expressed transcripts

Proteins




Conserved Domains	120	conserved protein domains
Protein	32,168	protein sequences
Protein Clusters	15	sequence similarity-based protein clusters
Structure	1,146	experimentally-determined biomolecular structures

Chemicals

BioSystems	4,040	molecular pathways with links to genes, proteins and chemicals
PubChem BioAssay	11,806	bioactivity screening studies
PubChem Compound	9	chemical information with structures, information and links
PubChem Substance	664	deposited substance and chemical information

Literature Databases

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



Online Mendelian Inheritance in Man

All Databases PubMed Nucleotide Protein Genome Structure PMC OMIM

Search OMIM for

Entrez

OMIM
Search OMIM
Search Gene Map
Help
FAQ
Statistics
Update List

Allied Resources
The Jackson
Laboratory
Human Gene
Nomenclature

Human Genome Resources
Entrez Gene
Genes and Disease
GeneReviews

My NCBI
Welcome petang. [Sign Out](#)

- Enter one or more search terms.
- Use **Limits** to restrict your search by search field, chromosome, and other criteria.
- Use **Index** to browse terms found in OMIM records.
- Use **History** to retrieve records from previous searches, or to combine searches.

NCBI is implementing changes to help you find current content in OMIM based on resources at NCBI, and then directing you to omim.org. Please be aware that you will leave NCBI to view OMIM records. Access to full records from NCBI (e.g. web, ftp, eutils) will no longer be supported.

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 internet starting in 1987. In 1995, OMIM was developed for the World Wide Web by NCBI, the National Center for Biotechnology Information.

OMIM is authored and edited at the McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, under the direction of Dr. Ada Hamosh.

NLM's Profiles in Science -- The McKusick Papers [More...](#)

NOTE: OMIM is intended for use primarily by physicians and other professionals concerned with genetic disorders, by genetics researchers, and by advanced students in science and medicine. While the OMIM database is open to the public, users seeking information about a personal medical or genetic condition are urged to consult with a qualified physician for diagnosis and for answers to personal questions.

[Display Settings:](#) Summary, 20 per page

[Send to:](#)

Filter your results:

Results: 1 to 20 of 584

<< First < Prev Page 1 of 30 Next > Last >>

All (584)

[OMIM UniSTS \(67\)](#)

[OMIM dbSNP \(135\)](#)

[Manage Filters](#)

[*191170 - TUMOR PROTEIN p53; TP53](#)

1. Cytogenetic locations: 17p13.1

OMIM: 191170

[Gene summaries](#) [Genetic tests](#) [Medical literature](#)

[*605426 - TUMOR PROTEIN p53-REGULATED APOPTOSIS-INDUCING PROTEIN 1; TP53AIP1](#)

2. Cytogenetic locations: 11q24.3

OMIM: 605426

[Gene summaries](#) [Genetic tests](#) [Medical literature](#)

[*614502 - CHROMOSOME 9 OPEN READING FRAME 116; C9ORF116](#)

3. Cytogenetic locations: 9q34.3

OMIM: 614502

[Gene summaries](#) [Genetic tests](#) [Medical literature](#)

[*605157 - p53-RESPONSIVE GENE 1](#)

4. Cytogenetic locations: 19q13.31

OMIM: 605157

[Gene summaries](#) [Genetic tests](#) [Medical literature](#)

[*605159 - APOPTOSIS-INDUCING FACTOR, MITOCHONDRION-ASSOCIATED, 2; AIFM2](#)

5. OMIM: 605159

[Gene summaries](#) [Genetic tests](#) [Medical literature](#)

[*606185 - TUMOR PROTEIN p53-INDUCIBLE NUCLEAR PROTEIN 1; TP53INP1](#)

6. Cytogenetic locations: 8q22.1

OMIM: 606185

[Gene summaries](#) [Genetic tests](#) [Medical literature](#)

[*605160 - p53-RESPONSIVE GENE 4](#)

7. OMIM: 605160

[Gene summaries](#) [Genetic tests](#) [Medical literature](#)

Find related data

Database:

Search details

p53[All Fields]

[See more...](#)

Recent activity

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OMIM

[See more...](#)

[Advanced Search](#) | [Display Options](#)***191170****TUMOR PROTEIN p53; TP53***Alternative titles; symbols***P53**

TRANSFORMATION-RELATED PROTEIN 53; TRP53

*HGNC Approved Gene Symbol: TP53**Cytogenetic location: 17p13.1 Genomic coordinates (GRCh37): 17:7,571,719-7,590,867* (from NCBI)**Gene-Phenotype Relationships**

Location	Phenotype	Phenotype MIM number	Phenotype mapping key
17p13.1	Adrenal cortical carcinoma	202300	3
	Breast cancer	114480	3
	Choroid plexus papilloma	260500	3
	Colorectal cancer	114500	3
	Hepatocellular carcinoma	114550	3
	Li-Fraumeni syndrome	151623	3
	Nasopharyngeal carcinoma	607107	3
	Osteosarcoma	259500	3
	Pancreatic cancer	260350	3
	{Basal cell carcinoma 7}	614740	3
	{Glioma susceptibility 1}	137800	3

Table of Contents for *191170

- [Title](#)
- [Gene-Phenotype Relationships](#)
- [Text](#)
- [Description](#)
- [Cloning and Expression](#)
- [Gene Structure](#)
- [Mapping](#)
- [Gene Function](#)
- [Biochemical Features](#)
- [Molecular Genetics](#)
- [Animal Model](#)
- [Allelic Variants](#)
- [Table View](#)
- [See Also](#)
- [References](#)
- [Contributors](#)
- [Creation Date](#)
- [Edit History](#)

External Links for Entry:

- [▶ Genome](#)
- [▶ DNA](#)
- [▶ Protein](#)
- [▶ Gene Info](#)
- [▶ Clinical Resources](#)
- [▶ Variation](#)
- [▶ Animal Models](#)
- [▶ Cellular Pathways](#)

- ▶ **Table of Contents for *191170**
- External Links for Entry:
- ▶ **Genome**
- ▶ **DNA**
- ▶ **Ensembl**
- NCBI RefSeq**
- ▶ **UCSC Genome Browser**
- ▶ **Protein**
- ▶ **Gene Info**
- ▶ **Clinical Resources**
- ▶ **Variation**
- ▶ **Animal Models**
- ▶ **Cellular Pathways**

- Results: 18**
- [Homo sapiens tumor protein p53 \(TP53\), transcript variant 4, mRNA](#)
 - 1. 2,651 bp linear mRNA
Accession: NM_001126113.2 GI: 371502116
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)
 - [Homo sapiens tumor protein p53 \(TP53\), transcript variant 3, mRNA](#)
 - 2. 2,724 bp linear mRNA
Accession: NM_001126114.2 GI: 371502117
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)
 - [Homo sapiens tumor protein p53 \(TP53\), transcript variant 6, mRNA](#)
 - 3. 2,404 bp linear mRNA
Accession: NM_001276698.1 GI: 454545206
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)
 - [Homo sapiens tumor protein p53 \(TP53\), transcript variant 8, mRNA](#)
 - 4. 2,708 bp linear mRNA
Accession: NM_001126118.1 GI: 371502118
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)
 - [Homo sapiens tumor protein p53 \(TP53\), transcript variant 2, mRNA](#)
 - 5. 2,588 bp linear mRNA
Accession: NM_001276761.1 GI: 454521556
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)
 - [Homo sapiens tumor protein p53 \(TP53\), transcript variant 1, mRNA](#)
 - 6. 2,591 bp linear mRNA
Accession: NM_000546.5 GI: 371502114
[GenBank](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

Send to: Filter your results:

Choose Destination

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Collections Analysis Tool

Download 18 items.

Format

- Summary
- GenBank
- GenBank (full)
- FASTA
- ASN.1
- XML
- INSDSeq XML
- TinySeq XML
- Feature Table
- Accession List
- GI List

Find related data

Database:

Homo sapiens tumor protein p53 (TP53), transcript variant 4, mRNA

NCBI Reference Sequence: NM_001126113.2
[FASTA](#) [Graphics](#)

[Go to:](#)

```

LOCUS       NM_001126113                2651 bp    mRNA    linear    PRI 04-MAY-2014
DEFINITION  Homo sapiens tumor protein p53 (TP53), transcript variant 4, mRNA.
ACCESSION   NM_001126113 XR_243565
VERSION     NM_001126113.2  GI:371502116
KEYWORDS    RefSeq.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
  
```

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Basic Features

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Gene, RNA, and CDS features only

Features added by NCBI

174 SNPs

2 conserved domains

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```

FEATURES             Location/Qualifiers
    source            1..2651
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="17"
                     /map="17p13.1"
    gene              1..2651
                     /gene="TP53"
                     /gene_synonym="BCC7; LFS1; P53; TRP53"
                     /note="tumor protein p53"
                     /db_xref="GeneID:7157"
                     /db_xref="HGNC:HGNC:11998"
                     /db_xref="MIM:191170"
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                     /gene="TP53"
                     /gene_synonym="BCC7; LFS1; P53; TRP53"
                     /inference="alignment:Splign:1.39.8"
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                     /gene="TP53"
                     /gene_synonym="BCC7; LFS1; P53; TRP53"
                     /note="upstream in-frame stop codon"
    exon              175..276
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                     /gene_synonym="BCC7; LFS1; P53; TRP53"
                     /inference="alignment:Splign:1.39.8"
    CDS                203..1243
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                     /gene_synonym="BCC7; LFS1; P53; TRP53"
                     /note="isoform c is encoded by transcript variant 4; tumor
protein 53; mutant tumor protein 53; cellular tumor
antigen p53; phosphoprotein p53; transformation-related
protein 53; p53 tumor suppressor; antigen NY-CO-13"
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                     /product="cellular tumor antigen p53 isoform c"
                     /protein_id="NP_001119585.1"
                     /db_xref="GI:187830823"
                     /db_xref="CCDS:CCDS45605.1"
                     /db_xref="GeneID:7157"
                     /db_xref="HGNC:HGNC:11998"
                     /db_xref="MIM:191170"
                     /translation="MEEPQSDPSEVPEPLSQETFSDLWKLLPENNVLSPLPSQAMDDL
LSPDDIEQWFTEDPGPDEAPRMPEAAPPPVAPAPAAAPTAPAPAPAPSWPLSSSVSPQKT
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PYEPPEVGSDCITIHVNYMCNSSCMGMNRRPILTIITLEDSSGNLLGRNSFEVVRVCA
CPGRDRRTEENLRKKGEPHHELPPGSTKRALPNNTSSSPQPKKPLDGEYFTLQMLL
DLRWCYFLINSS"

```

Display Settings: GenPept [Send to:](#)

cellular tumor antigen p53 isoform c [Homo sapiens]

NCBI Reference Sequence: NP_001119585.1
[FASTA](#) [Graphics](#)

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LOCUS	NP_001119585	346 aa	linear	FRI 04-MAY-2014
DEFINITION	cellular tumor antigen p53 isoform c [Homo sapiens].			
ACCESSION	NP_001119585			
VERSION	NP_001119585.1	GI:187830823		
DBSOURCE	REFSEQ: accession	NM_001126113.2		
KEYWORDS	RefSeq.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.			

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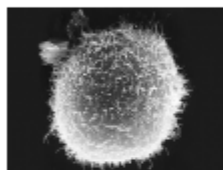
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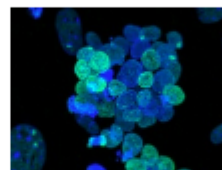
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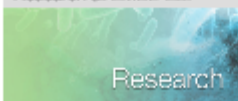
- To provide freely available data and bioinformatics services to all facets of the scientific community
- To contribute to the advancement of biology through basic investigator-driven research
- To provide advanced bioinformatics training to scientists at all levels
- To help disseminate cutting-edge technologies to industry
- To coordinate biological data provision throughout Europe.

Bioinformatics services



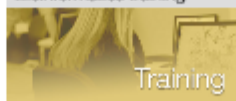
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About the European Nucleotide Archive

The European Nucleotide Archive ([ENA](#)) captures and presents information relating to experimental workflows that are based around nucleotide sequencing. A typical workflow includes the isolation and preparation of material for sequencing, a run of a sequencing machine in which sequencing data are produced and a subsequent bioinformatic analysis pipeline. ENA records this information in a data model that covers input information (sample, experimental setup, machine configuration), output machine data (sequence traces, reads and quality scores) and interpreted information (assembly, mapping, functional annotation).

Data arrive at ENA from a variety of sources. These include submissions of raw data, assembled sequences and annotation from small-scale sequencing efforts, data provision from the major European sequencing centres and routine and comprehensive exchange with our partners in the International Nucleotide Sequence Database Collaboration (INSDC).

Provision of nucleotide sequence data to ENA or its INSDC partners has become a central and mandatory step in the dissemination of research findings to the scientific community. ENA works with publishers of scientific literature and funding bodies to ensure compliance with these principles and to provide optimal submission systems and data access tools that work seamlessly with the published literature.

ENA is made up of a number of distinct databases that includes EMBL-Bank, the newly established Sequence Read Archive (SRA) and the Trace Archive each with their own data formats and standards. ENA data classes and formats are described [here](#).

Although the ENA has almost 30 years of history, the data and services are constantly changing to reflect growing volumes of data, ever improving sequencing technology and the broadening of applications to which sequencing is now put. Latest developments and changes to services are announced [here](#).

As part of the global effort to improve access to and usability of nucleotide sequencing data, we collaborate extensively in the development of our services and technologies and in standards activities.

The ENA is developed and maintained at the EMBL-EBI under the guidance of the INSDC International Advisory Committee and a newly formed Scientific Advisory Board.

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Macromolecular structures (422 results found)

[DNA-free p53 Tetramer Reconstruction](#)*Authors:* Pham N, Lucumi A, Cheung N, Viadiu H*Method:* single-particle reconstruction*Specimen state:* particle

Related data

Views


Source: EMDB
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[tumor protein p53](#)*Approved Symbol:* TP53 *Approved Name:* tumor protein **p53** *Status:* (Approved)*Aliases:* **p53** LFS1*Locus Type:* gene with protein product*Chromosome:* 17p13.1

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Views

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ID: HGNC:11998 **Summary information is available for this gene**[View all 704 results for Genomes](#)

Nucleotide sequences (20,113 results found)

[AB020317](#)Mus musculus mRNA for **p53**, complete cds.

Related data

Views

Source: Sequence (Release)
ID: AB020317[AB021961](#)Mus musculus mutant **p53** mRNA, complete cds.

Related data

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ID: AB021961[View all 20113 results for Nucleotide sequences](#)

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IntAct Interactions (226 results found)

[p53-p53-1](#)Homodimerization of **p53** shown by ubiquitin reconstruction[p53-p21_promoter](#)DNA binding properties of **p53**[p53-p21_p53bind](#)DNA binding properties of **p53**[gnl3-p53](#)Coimmunoprecipitation reveals interaction between the nucleostemin protein and **P53** protein[p53-p21_p53bind-1](#)DNA binding properties of **p53**

Reactome (137 results found)

[Stabilization of p53](#)

... al, 1998; Banin et al, 1998 and Khanna et al, 1998). ATM also regulates the phosphorylation of **p53** ... (Chehab et al, 2000; Shieh et al, 2000; Hirao et al 2000). Phosphorylation of **p53** at Ser-20 interferes with **p53**-MDM2 interaction. MDM2 is transcriptionally activated by **p53** and is a negative regulator of ...



Kyoto Encyclopedia of Genes & Genomes <http://www.genome.ad.jp/kegg/>



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KEGG: Kyoto Encyclopedia of Genes and Genomes

KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies (See [Release notes](#) for new and updated features).
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Database: KEGG - Search term: p53

KEGG PATHWAY

map04115
p53 signaling pathway

KEGG BRITE

ko00001
KO; KEGG Orthology (KO)
ko00002
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ko01000
Enzyme; Enzymes
ko01001
Kinase; Protein kinases
ko01009
Protein phosphatases and associated proteins; Protein phosphatases and associated proteins
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KEGG ORTHOLOGY

K04451
TP53, P53; tumor protein p53
K05627
BAIAP2, IRSP53; BAI1-associated protein 2
K08851
TP53RK, PRPK, BUD32; TP53 regulating kinase [EC:2.7.11.1]
K10128
RPRM; reprimin, TP53-dependent G2 arrest mediator candidate
K10133
TP53I3; tumor protein p53-inducible protein 3 [EC:1.-.-.-]
... » display all

KEGG GENES

hsa:27296
TP53TG5, C20orf10, CLG01; TP53 target 5
hsa:8925
HERC1, p532, p619; HECT and RLD domain containing E3 ubiquitin protein ligase family member 1; K10594 E3 ubiquitin-protein ligase HERC1 [EC:6.3.2.19]
hsa:112858
TP53RK, BUD32, C20orf64, Nori-2, Nori-2p, PRPK, dJ101A2; TP53 regulating kinase [EC:2.7.11.1]; K08851 TP53 regulating kinase [EC:2.7.11.1]
hsa:90313
TP53I13, DSCP1; tumor protein p53 inducible protein 13
hsa:10458
BAIAP2, BAP2, FLAF3, IRSP53; BAI1-associated protein 2; K05627 BAI1-associated protein 2
... » display all

KEGG DGENES

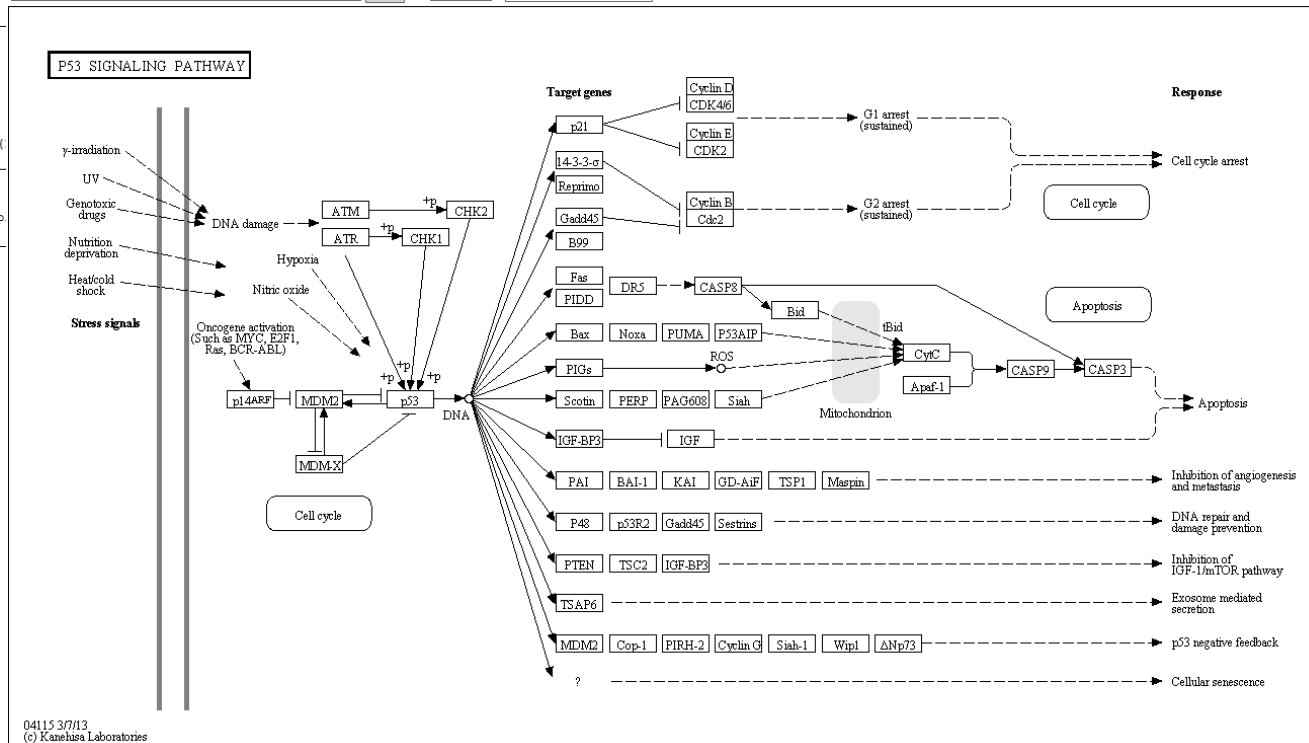
T10002:9129
K08851 TP53 regulating kinase [EC:2.7.11.1]
T10003:9362
K08851 TP53 regulating kinase [EC:2.7.11.1]
T10004:9514
K08851 TP53 regulating kinase [EC:2.7.11.1]
T10005:1048
K10133 tumor protein p53-inducible protein 3 [EC:1.-.-.-]
T10005:2716
K10136 TP53 apoptosis effector
... » display all

KEGG MGENES

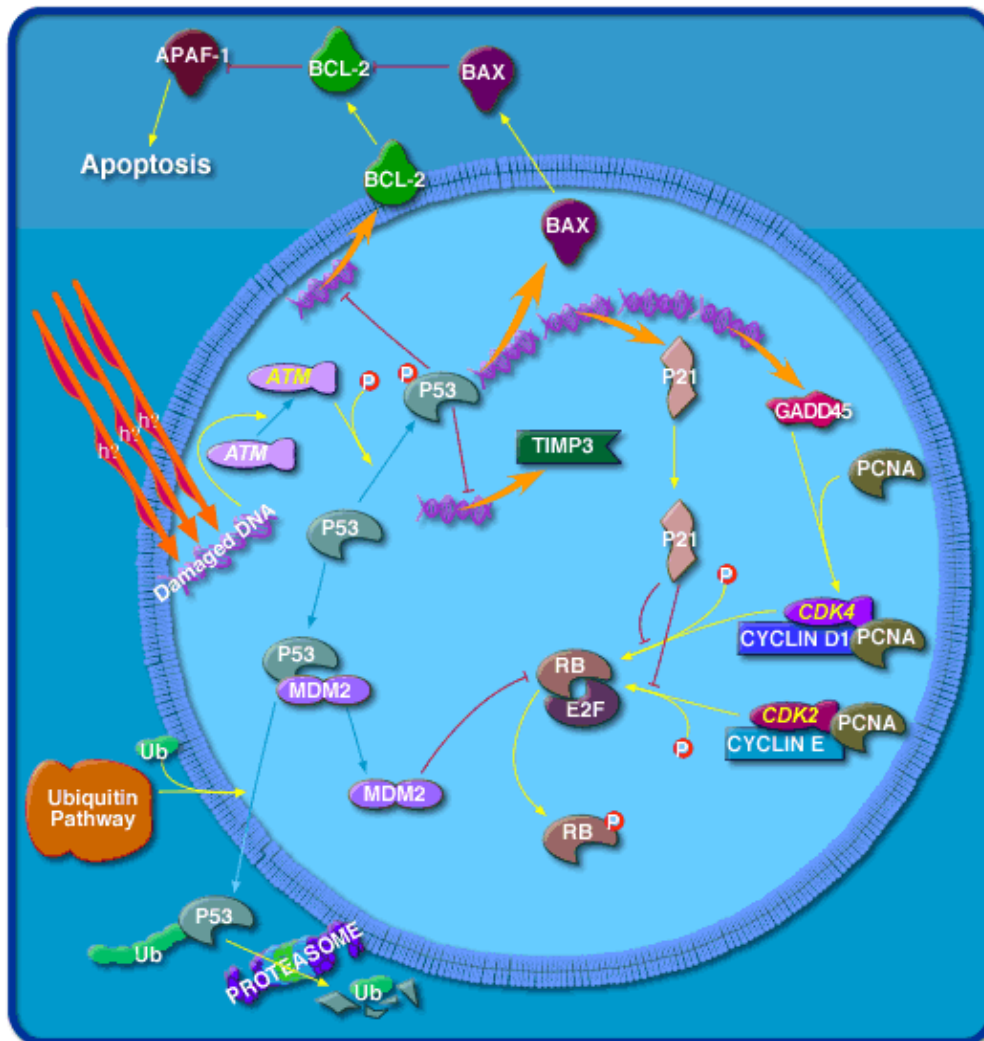
T30027:GL0163842
[Lack_3'-end][KO:K01409][COG:COG3642]; K08851 TP53 regulating kinase [EC:2.7.11.1]
T30027:GL0239786
[Lack_5'-end][KO:K08851][COG:COG3642][KOG:KOG3087][eggNOG:fuNOG06542 meNOG17527 veNOG18025]; K08851 TP53 regulating kinase [EC:2.7.11.1]
T30079:GL0055487
[Complete][KO:K08851][COG:COG3642][KOG:KOG3087]; K08851 TP53 regulating kinase [EC:2.7.11.1]
T30126:GL0061334
[Lack_3'-end][KO:K00344]; K10133 tumor protein p53-inducible protein 3 [EC:1.-.-.-]
T30146:73081
similar to uniprot|P53189 saccharomyces cerevisiae YGL028c SCW11
... » display all

Entry	map04115	Pathway
Name	p53 signaling pathway	
Description	p53 activation is induced by a number of stress signals, including DNA damage, oxidative stress and activated oncogenes. The p53 protein is employed as a transcriptional activator of p53-regulated genes. This results in three major outputs; cell cycle arrest, cellular senescence or apoptosis. Other p53-regulated gene functions communicate with adjacent cells, repair the damaged DNA or set up positive and negative feedback loops that enhance or attenuate the functions of the p53 protein and integrate these stress responses with other signal transduction pathways.	
Class	Cellular Processes; Cell growth and death	
	BRITE hierarchy	
Pathway map	map04115 p53 signaling pathway	
	All organisms Ortholog table	
Disease	H00409 Type II diabetes mellitus H00848 Ataxia with ocular apraxia (AOA) H00881 Li-Fraumeni syndrome H00896 Lymphangioliomyomatosis (LAM) H00915 Tuberous sclerosis complex (TSC) H00992 Seckel syndrome H01007 Choroid plexus papilloma H01106 Plasminogen activator inhibitor type 1 (PAI-1) H01195 VACTERL/VATER association	
Reference	PMID:16557269	
Authors	Levine AJ, Hu W, Feng Z.	
Title	The P53 pathway: what questions remain to be explored?	
Journal	Cell Death Differ 13:1027-36 (2006)	

http://www.genome.jp/kegg-bin/show_pathway?map04115



Metabolic & Signalling Pathways



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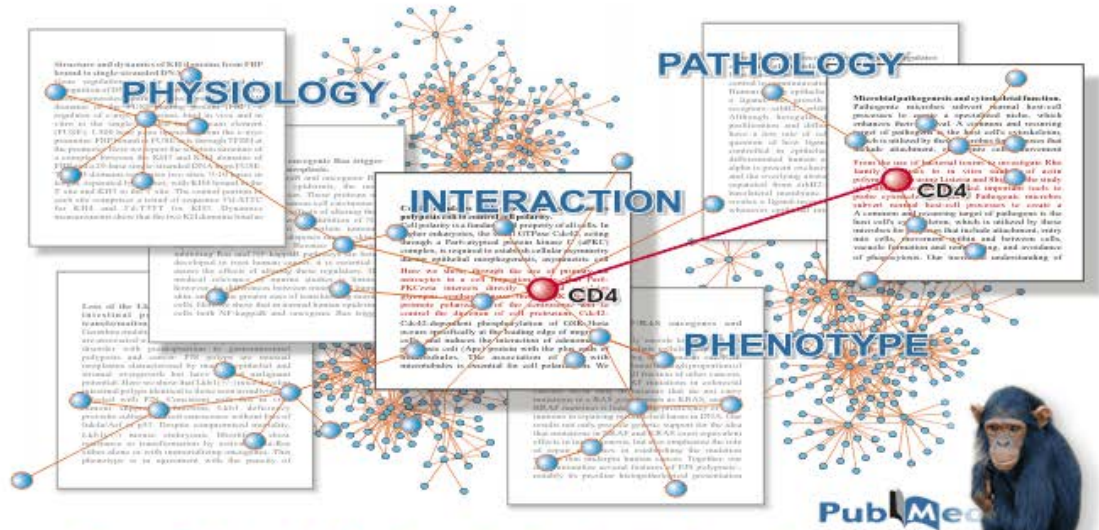
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Symbol	Name	Synonym/ DB-reference	Organism	Results
				<p>Life cycles of successful genes</p>
p53	p53		Drosophila melanogaster	
P53	tumor suppressor p53		Sus scrofa	
P53	P53 protein		Ovis aries	
p53	tumor suppressor protein p53		Oryzias latipes	
TP53	tumor protein p53		Homo sapiens	
Trp53	transformation related protein 53		Mus musculus	
tp53	tumor protein p53		Danio rerio	
tp53	tumor protein p53		Xenopus tropicalis	
Trp53	transformation related protein 53		Rattus norvegicus	
p53-ps	Wistar clone pR53P1 p53 pseudogene		Rattus norvegicus	
TP53	tumor protein p53		Monodelphis domestica	
APSE-1_53	P53		Acyrtosiphon pisum bacteriophage APSE-1	
PaP2_gp53	hypothetical protein		Pseudomonas aeruginosa bacteriophage PaP2	
betaTub60D	beta-Tubulin at 60D	p53	Drosophila melanogaster	
hth	homothorax	P53	Drosophila melanogaster	
AT5G06720	peroxidase, putative	P53	Arabidopsis thaliana	
LOC396767	p53 protein		Sus scrofa	
LChV-2p07	ORF6	p53	Little cherry virus 2	

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Symbol	Name	Synonym/ DB-reference	Organism	Results
Life cycles of successful genes				
p53	p53		Drosophila melanogaster	
P53	tumor suppressor p53		Sus scrofa	
P53	P53 protein		Oris aries	
p53	tumor suppressor protein p53		Oryzias latipes	
TP53	tumor protein p53		Homo sapiens	
Trp53	transformation related protein 53		Mus musculus	
tp53	tumor protein p53		Danio rerio	
tp53	tumor protein p53		Xenopus tropicalis	
Trp53	transformation related protein 53		Rattus norvegicus	
p53-ps	Wistar clone pR53P1 p53 pseudogene		Rattus norvegicus	
TP53	tumor protein p53		Monodelphis domestica	
APSE-1_53	p53		Acyrthosiphon pisum bacteriophage APSE-1	
PaP2_gp53	hypothetical protein		Pseudomonas aeruginosa bacteriophage PaP2	
betaTub60D	beta-Tubulin at 60D	p53	Drosophila melanogaster	
hth	homothorax	P53	Drosophila melanogaster	
AT5G06720	peroxidase, putative	P53	Arabidopsis thaliana	
LOC396767	p53 protein		Sus scrofa	
LCHV-2p07	ORF6	p53	Little cherry virus 2	

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Minimal information for this gene



Most recent information for this gene



Interaction information for this gene



Defining information for this gene

Symbol	Name	Synonyms	Organism
p53	CG33336 gene product from transcript CG33336-RB	CG10873, CG31325, CG33336, Dmel\CG33336, dmp53, Dmp53, DmP53, Dm-P53, dp53, Dp53, D-p53, prac	Drosophila melanogaster
WikiGenes	edit this page new		
NCBI Gene	2768677		
NCBI RefSeq	NP_996268 , NP_996267		
NCBI RefSeq	NM_001170223 , NM_206544		
NCBI UniGene	2768677		
NCBI Accession	AF250918 , DQ191318		

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Experimental evidence for the association between **p53** and **CG4753** from Y2H.





Most recent information for this gene.

Symbol	Name	Synonyms	Organism
p53	CG33336 gene product from transcript CG33336-RB	CG10873, CG31325, CG33336, Dmel\CG33336, dmp53, Dmp53, DmP53, Dm-P53, dp53, Dp53, D-p53, prac	Drosophila melanogaster

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 NCBI RefSeq [NM_001170223](#), [NM_206544](#)
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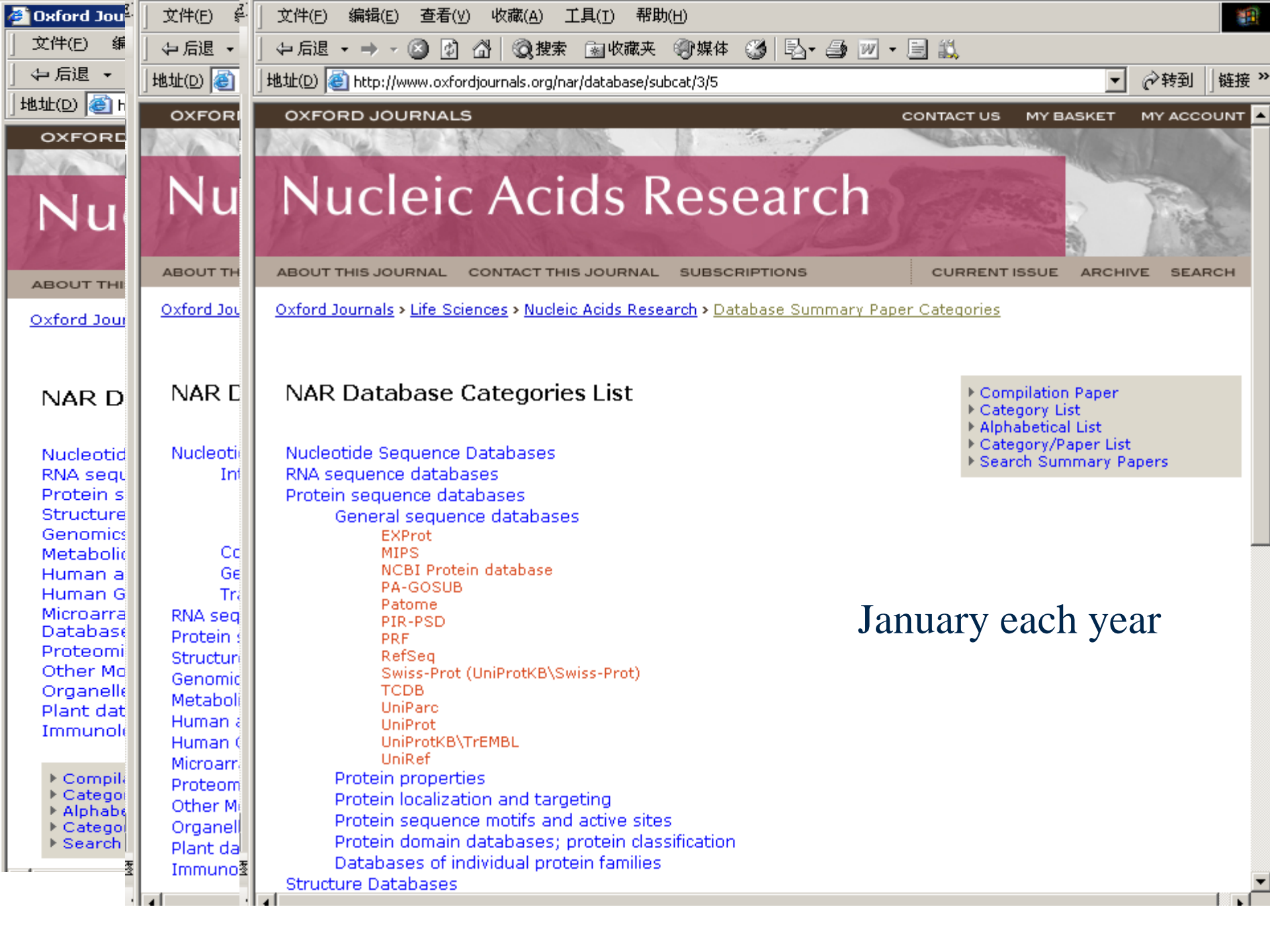
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- We report here that [dE2F1](#) promotes IR-induced [p53](#) -independent [apoptosis](#) in larval imaginal discs. [2010]
- [DmChk2](#) induced [cell death](#) was not suppressed by [Dmp53](#) mutant, revealing for the first time that in Drosophila, over-expression of [DmChk2](#) can induce [cell death](#) which is independent of [Dmp53](#) . [2010]
- [E2F1](#) and [E2F2](#) have opposite effects on radiation-induced [p53](#) -independent [apoptosis](#) in Drosophila. [2010]
- Moreover, our results demonstrate that although [DmChk2](#) and [Dmp53](#) affect different stages of ovarian development, loss of ovarian [stem cells](#) by [p53](#) expression and mid-oogenesis [cell death](#) induced by [DmChk2](#) do not require caspase activity. [2010]
- Furthermore, a rough eye [phenotype](#) because of overexpression of [DREF](#) in Drosophila eye imaginal disks could be **suppressed** by half dose reduction of the [dmp53](#) gene. [2010]
- [DREF](#) binds specifically to DRE sequences in the Drosophila [p53](#) ([dmp53](#)) gene promoter as shown using anti-[DREF](#) antibodies in [chromatin immunoprecipitation](#) assays. [2010]
- The data demonstrate that wild-type [p53](#) over-expression can **regulate** life span independent of [foxo](#) , and suggest that [foxo](#) acts in males to **produce** sexually antagonistic life span effects of [p53](#) . [2010]
- We propose that in response to UV irradiation, [Dmp53](#) enhances the expression of the [dKDM4B](#) histone demethylase, which demethylates H3K9me3 preferentially in heterochromatin regions. [2010]
- In addition, the level of mRNA of [dmp53](#) was decreased in [DREF](#) -knockdown cells and transient expression of the luciferase gene under control of the wild-type [dmp53](#) gene promoter showed strong promoter activity in [S2](#) cells, but this was almost completely abrogated with a DRE-mutated promoter. [2010]
- The ability of [ionizing radiation](#) (IR) to induce [apoptosis](#) independent of [p53](#) is crucial for successful therapy of cancers bearing [p53](#) mutations. [p53](#) -independent [apoptosis](#), however, remains poorly understood relative to [p53](#) -dependent [apoptosis](#). [2010]



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