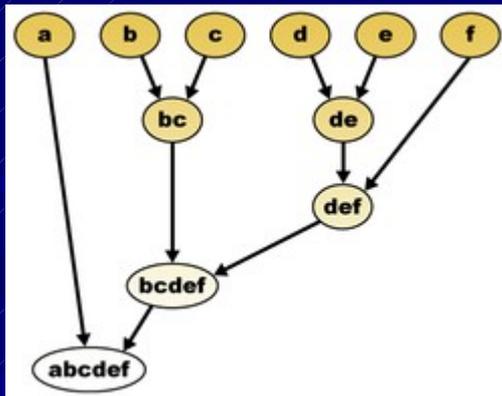


TAXONOMY

Sandra Morales
Gysell Herrera

TAXONOMIA

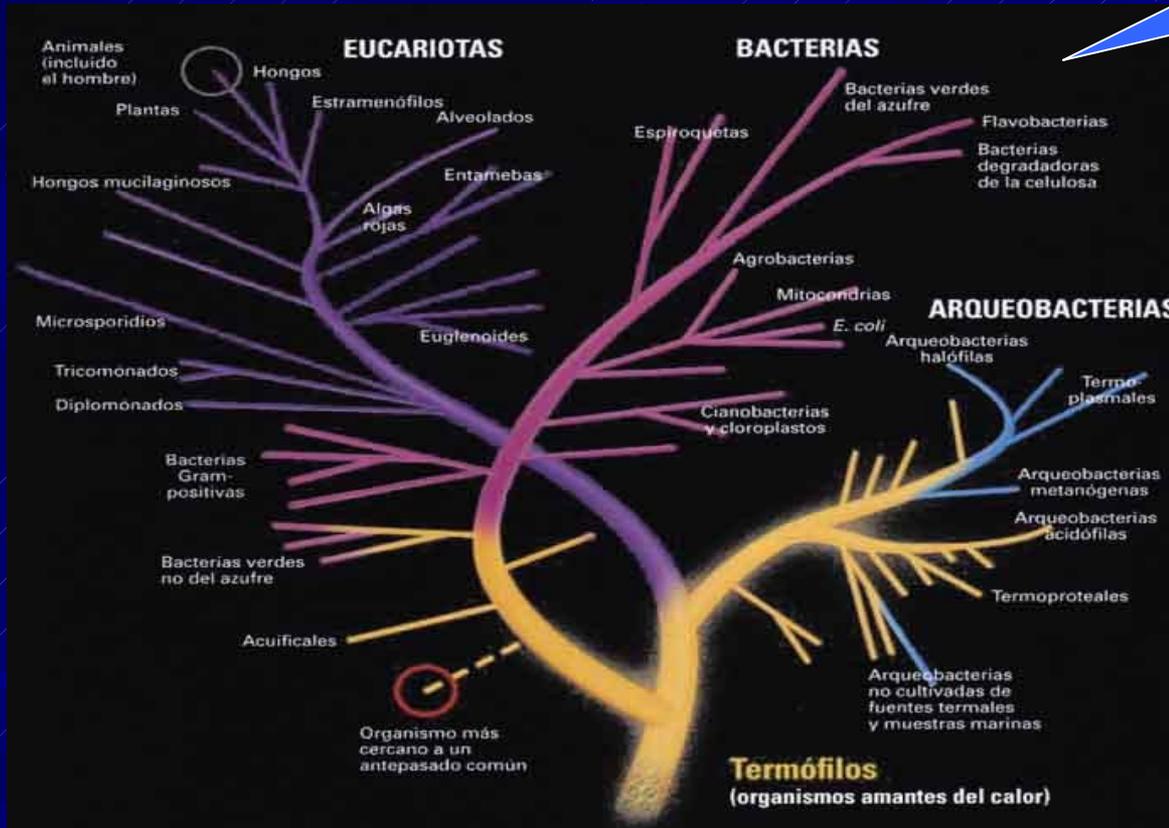
- **Taxonomía Biológica:** la ciencia de ordenar a los organismos en un sistema de clasificación compuesto por taxones agrupados en categorías taxonómicas



Actúa luego de que el árbol filogenético de los organismos ya este resuelto, es decir una vez estén definidas las ramas (clados) y las relaciones de parentesco entre ellos.

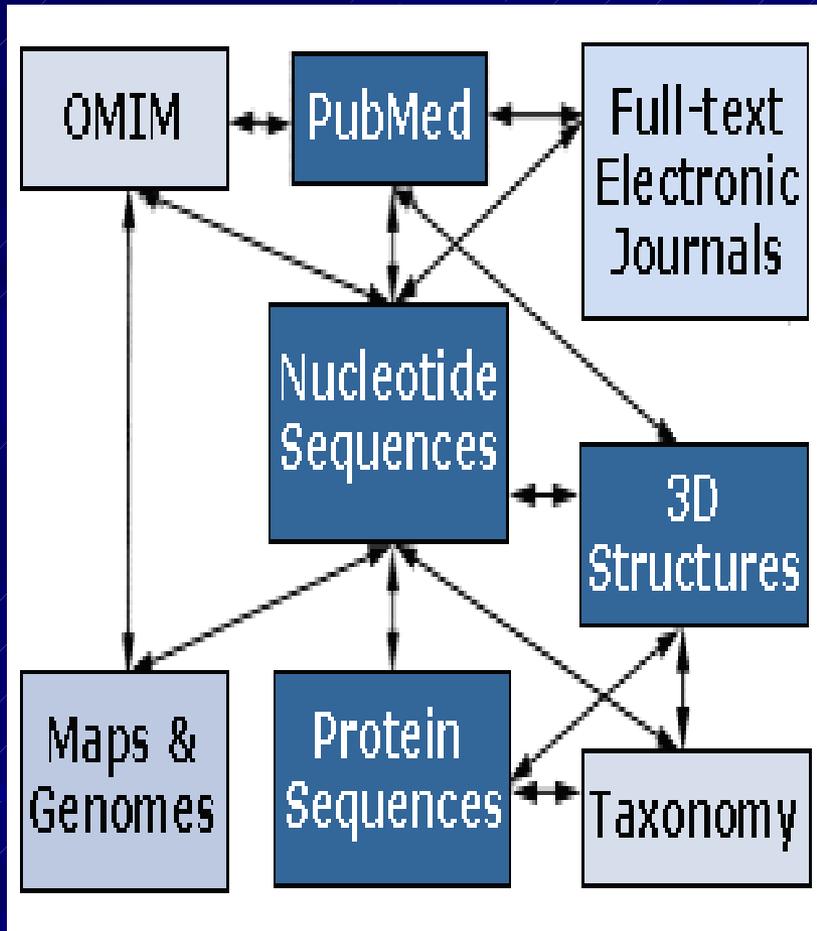
El objetivo fundamental de la Taxonomía es organizar al árbol filogenético en un **sistema de clasificación**.

ARBOL DE LA VIDA



Muestra las relaciones de evolución entre varias especies u otras entidades que se creen tuvieron una descendencia común

NCBI Y ENTREZ



El NCBI desarrolló Entrez como una herramienta para permitir a los usuarios interaccionar estas bases de datos.

ENTREZ es una 'interfaz de usuario' o UI, constituye el nexo entre el usuario y las bases de datos subyacentes.

Permite al usuario realizar consultas simples y obtener resultados, aun desconociendo la arquitectura de las bases de datos.

BASE DE DATOS TAXONOMY

- **TaxBrowser** (*Taxonomy Browser*)
Contiene los nombres de todos los organismos que aparecen en las bases de datos genéticas con al menos una secuencia de nucleótidos o proteínas .
- Taxonomy es una base de datos secundaria de NCBI, utiliza Entrez como sistema de búsqueda y recuperación que permite a los usuarios el acceso a las secuencias, mapas genéticos, taxonomía a nivel molecular. Ultimamente con la herramienta Global Query, permite realizar consultas entre las diferentes bases de datos de Entrez

COMO LLEGAR A TAXONOMY

- Por la Pagina de NCBI → DATABASES
- : <http://www.ncbi.nlm.nih.gov/Taxonomy/>

The screenshot shows the NCBI website interface. On the left, there is a sidebar with navigation options: 'External links to related resources', 'Literature', 'Databases PubMed, OMIM, Books, PubMed Central', 'Related Resources', and 'BLAST'. The main content area is organized into several sections, each with a blue header bar: 'Nucleotide Databases', 'Protein Databases', 'Structure Databases', 'Taxonomy Databases', 'Genome Databases', and 'Expression Databases'. The 'Taxonomy Databases' section is circled with a red dashed oval and contains a single link: 'Taxonomy'. Other sections contain multiple links to various databases.

Section	Links
Nucleotide Databases	dbEST , dbGSS , dbSNP , dbSTS , Nucleotide , GenBank , HomoloGene , MGC , PopSet , Probe , RefSeq , TPA , Trace Archive , UniGene , UniSTS
Protein Databases	3D Domains , Proteins , PROW , RefSeq
Structure Databases	Conserved Domains , 3D Domains , Structure (MMDB)
Taxonomy Databases	Taxonomy
Genome Databases	Cancer Chromosomes , COGs , Gene , Genome Project , Genomes
Expression Databases	

TAXONOMY BROWSER

Version traduca de <http://130.14.29.110/Taxonomy/> - Microsoft Internet Explorer

Archivo Edición Ver Favoritos Herramientas Ayuda

Dirección <D:\SANDRA\UNAL\BIOINFORMATICA\bases de datos NCBI\taxonomy\recorrido\inicio.htm> Ir Vínculos >>

Google™ Esta página se la tradujo de forma automática de Inglés. [Volver a los resultados de la búsqueda](#)
[Ver la Página Web Original](#) [Eliminar frame](#)

NCBI Taxonomy Browser

PubMed Entrez BLAST OMIM Taxonomy Structure

Search for As lock

The NCBI Taxonomy Homepage

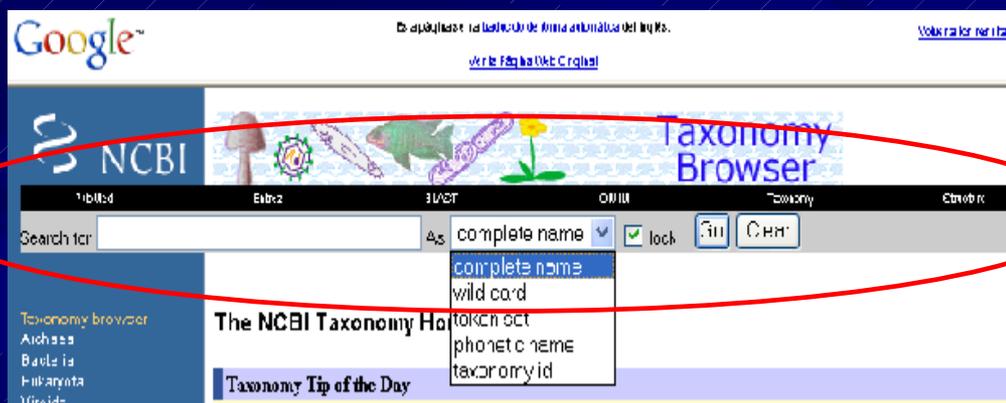
Taxonomy Tip of the Day

Did you know

that a small number of sequences extracted from extinct organisms have been deposited at GenBank? These include DNA from the Neanderthal man, the woolly mammoth, the saber-toothed cat, and several giant New Zealand birds (moas) among others. A more complete list of extinct organisms that are represented in the public sequence database can be found [here](#).

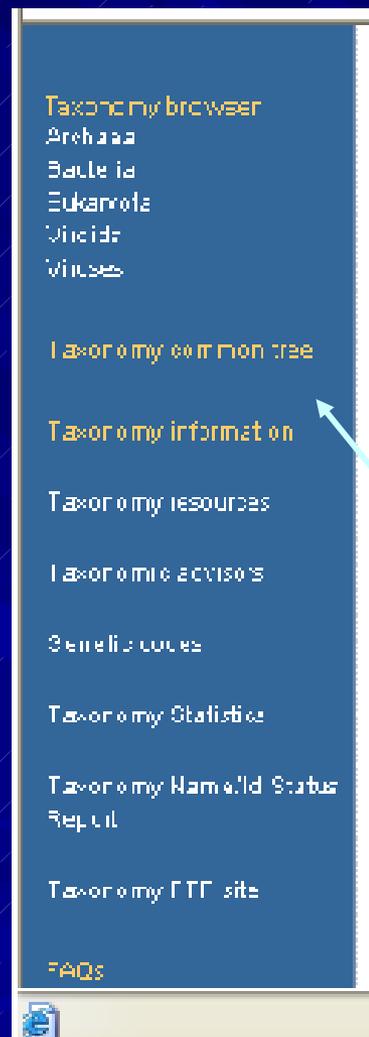
Inicio EXPOSICION ... recorrido PATRON EXP... Versión tradu... ES 04:04 a.m.

BUSQUEDAS



Modulo de Busqueda:

- Nombre completo
- Ficha
- Simbolo fijo
- Nombre fonetico
- Id taxonomico



Menu

Search for As

Taxonomy browser

- Archaea
- Bacteria
- Eukaryota**
- Viroids
- Viruses

Taxonomy common tree

Taxonomy information

Taxonomy

The NCBI Taxonomy Browser

Taxonomy Tip of the Day

that a small number of sequenced genomes, including the woolly mammoth, the sequenced genomes are represented in the public

DOMINIOS



Archaea, Bacteria y Eukarya

Search for Eukaryota as complete name link

Display 3 levels using filter: none

Nucleotide Protein Structure Complete Sequences Genome Projects Popset SRF
 3D Objects Domains GLU Datasets GLU Expressions UniGene UniSTS Pubmed Central
 Gene Unichrome MapView LinkOut PLAGT TRAC

[Lineage](#) [Full root](#) [Other organisms](#)

o [Eukaryota \(eucaryotes\)](#) Click on organism names to get more information.

- o [Acanthamoebidae](#)
 - o [Acanthamoeba](#)
 - [Acanthamoeba astronyxis](#)
 - [Acanthamoeba castellanii](#)
 - [Acanthamoeba comanioni](#)
 - [Acanthamoeba culbertsoni](#)
 - [Acanthamoeba divionensis](#)
 - [Acanthamoeba echinulata](#)
 - [Acanthamoeba griffini](#)
 - [Acanthamoeba hatchetti](#)
 - [Acanthamoeba healyi](#)
 - [Acanthamoeba jacobsi](#)
 - [Acanthamoeba leucolata](#)
 - [Acanthamoeba lugdunensis](#)
 - [Acanthamoeba mauritanensis](#)
 - [Acanthamoeba palestinensis](#)
 - [Acanthamoeba pearcei](#)
 - [Acanthamoeba polyphaga](#)
 - [Acanthamoeba pusulosa](#)
 - [Acanthamoeba quina](#)
 - [Acanthamoeba rhyssodes](#)
 - [Acanthamoeba rostrata](#)
 - [Acanthamoeba stevensoni](#)
 - [Acanthamoeba terricola](#)
 - [Acanthamoeba triangularis](#)
 - [Acanthamoeba tubiashi](#)
 - [Acanthamoeba sp.](#)
 - unclassified Acanthamoeba
 - environmental samples
 - o [Comandouia](#)
 - [Comandouia operculata](#)
 - o [Protacanthamoeba](#)

ORGANISMOS Y ESPECIES

Taxonomy browser (Arabidopsis thaliana) - Microsoft Internet Explorer provided by Universidad Nacional

http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Undefined&name=Arabidopsis+thaliana&lvl=0&srchmode=1

Search for Arabidopsis thaliana as complete name lock Go Clear

Display 0 levels using filter: none

Arabidopsis thaliana

Taxonomy ID: 3702
 Genbank common name: **thale cress**
 Rank: species
 Genetic code: [Translation table 1 \(Standard\)](#)
 Mitochondrial genetic code: [Translation table 1 \(Standard\)](#)
 Other names:
 synonym: **Arabidopsis thaliana (L.) Heynh.**
 common name: **thale-cress**
 common name: **mouse-ear cress**

[Lineage \(full\)](#)
[cellular organisms](#); [Eukaryota](#); [Viridiplantae](#); [Streptophyta](#); [Streptophytina](#); [Embryophyta](#); [Tracheophyta](#); [Euphyllophyta](#); [Spermatophyta](#); [Magnoliophyta](#); [eudicotyledons](#); [core eudicotyledons](#); [rosids](#); [eurosids II](#); [Brassicales](#); [Brassicaceae](#); [Arabidopsis](#)

Entrez records	
Database name	Direct links
Nucleotide	1,970,975
Protein	126,903
Structure	233
Genome Sequences	7
Genome Projects	1
Popset	233
3D Domains	735
Domains	39
GEO Datasets	579
GEO Expressions	1,325,088
UniGene	29,224
UniSTS	641
PubMed Central	8,390
Gene	31,392
HomoloGene	10,929
Taxonomy	1

Comments and References:

O'Kane and Al-Shehbaz 1997
 O'Kane, S.L., Jr. and I.H. Al-Shehbaz, 1997. A synopsis of Arabidopsis (Brassicaceae). Novon 7: 323-327.

[FOC Checklist](#)
 Name verified on date of entry into database in: Flora of China Checklist - TROPICOS nomenclature database, Missouri Botanical Garden, St. Louis, Missouri, USA

Genome Information

[Go to NCBI genomic BLAST page for Arabidopsis thaliana](#)

[Genome view: 5 chromosomes](#)

Información
General

Registro que
aparecen en
otras bases

Taxonomy browser (Arabidopsis thaliana) - Microsoft Internet Explorer provided by Universidad Nacional

Go to NCBI genomic BLAST page for Arabidopsis thaliana

Genome view: 5 chromosomes

See the [mitochondrion Genome](#)

Trace records (raw single-pass reads of DNA sequence)

Center name	Record counts per type		
	PRIMERWALK	SHOTGUN	ALL
TIGR_JCVIJC - The Institute for Genomic Research, Traces generated at JCVIJC	538	79,286	79,824
Total	538	79,286	79,824

External Information Resources (NCBI LinkOut)

LinkOut	Subject	LinkOut Provider
Arabidopsis thaliana (L.) Heynh.	taxonomy/phylogenetic	Global Biodiversity Information Facility
Related Immune Epitope Information	gene/protein/disease-specific	Immune Epitope Database and Analysis Resource
Arabidopsis thaliana (L.) Heynh.	taxonomy/phylogenetic	Integrated Taxonomic Information System
EST Index	companies/research institutes	Kazusa DNA Research Institute
KAOS	companies/research institutes	NCBI Plastid Genomes
NCBI Plastids	DNA/protein sequence	NCBI taxonomy bookmarks
ABRC	taxonomy/phylogenetic	
AGR	taxonomy/phylogenetic	
DATA	taxonomy/phylogenetic	
MATDB	taxonomy/phylogenetic	
TAIR	taxonomy/phylogenetic	
Arabidopsis thaliana	taxonomy/phylogenetic	PLANTS Database (USDA/NRCS)
TIGR	companies/research institutes	The Institute for Genomic Research
Arabidopsis thaliana	taxonomy/phylogenetic	The International Plant Names Index
INTF: Arabidopsis thaliana	herbarium/museum collections	The New York Botanical Garden
Arabidopsis	organism-specific	Trans-NIH Model Organism Initiative
Arabidopsis thaliana	taxonomy/phylogenetic	TreeBase
Arabidopsis thaliana (L.) Heynh.	taxonomy/phylogenetic	USDA-ARS GRIN Taxonomy
search W3TROPICOS	taxonomy/phylogenetic	Vascular Tropicos
Arabidopsis thaliana	taxonomy/phylogenetic	electronic Plant Information Centre

Informacion del genoma

Informacion Externa



Enter Genome View - Microsoft Internet Explorer provided by Universidad Nacional

NCBI Map Viewer

Search for: Find

Arabidopsis thaliana (mouse-ear cress) genome view

Build 6.0 statistics

Lineage: Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eucomidiales; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis; Arabidopsis thaliana

The Arabidopsis Information Resource (TAIR) has announced the release of the latest version of the Arabidopsis genome (TAIR6) at TAIR and NCBI. TAIR has assumed primary responsibility for maintaining the Arabidopsis genome annotation in North America following TIGR's final release (TIGR5). The latest release builds on the gene structures of the previous TIGR5 release using new cDNA and EST data released in the intervening period as well as community input regarding missing and incorrectly annotated genes. This version is available for [download](#) and is displayed in Map Viewer. Additional map features seen along the sequence in the Map Viewer are based on the contigs, clones, genes, STSs and ESTs.

The TAIR6 release contains a total of 26,751 protein coding genes, 3,818 pseudogenes and 838 non-coding RNA genes (31,407 genes in all), providing the most comprehensive Arabidopsis genome annotation to date. A total of 437 new genes were added and nine genes were deleted. Updates were made to 973 genes including 831 updates to coding sequences, 14 gene splits and 7 gene merges and the addition of 1200 new splice variants. A total of 3159 Arabidopsis genes (10%) now have annotated splice variants. No changes were made to the chromosome sequences for this release.

Arabidopsis thaliana is a small flowering plant of mustard family, brassicaceae (Cruciferae). It was selected as a model organism for genome sequencing in plants based on the fact that it has (1) a small genome of ~120 Mb with a simple structure having few repeated sequences and high gene density, (2) short generation time of six weeks from seed germination to seed set (3) produces large numbers of seeds, and (4) is easy to transform. The sequencing was done by an international collaboration, collectively termed the [Arabidopsis Genome Initiative \(AGI\)](#). The project was initiated in 1996 and completed in 2000 ([Nature](#), 408:796-815).

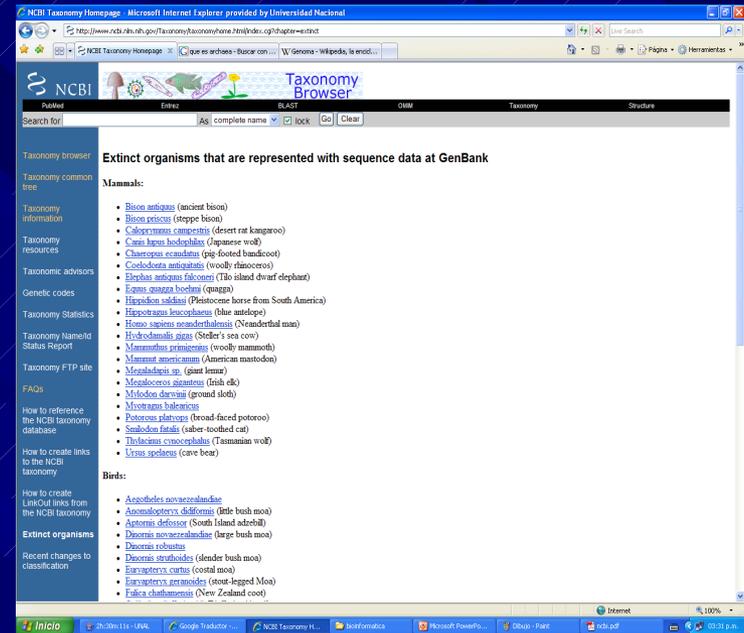
Available Documentation:

- NCBI Handbook: Map Viewer chapter - resource description
- NCBI Handbook: Map Viewer Examples - tutorials and examples
- Map Viewer Help - details about navigation and customizing your display
- Genome Assembly - description of genome assembly and annotation process
- Genomes - description of NCBI's Hidden Markov Model (HMM) *ab initio* prediction program

MENU

- **Taxonomy resources** Compilacion de las referencias y recursos en linea usados por GenBank clasificados por Algas, plantas , vertebrados...
- **Taxonomic advisors:**
Contribuciones de GenBank a la BD Taxonomy
- **Genetic codes**
- **Taxonomy Statistics: 243.037**
Taxones representados hasta 26-02-07

- Organismos Extintos
- Sitio para FTP: Protocolo de transferencia de ficheros entre sistemas. Se conecta a un servidor en donde se pueden alojar o descargar archivos sin importar el SO en uso.



Current directory is /pub/taxonomy

[Up to higher level directory](#)

qi_taxid.readme	817 bytes	Fri Apr 6 00:00:00 2001
qi_taxid_nucl.dmp.gz	215359 Kb	Mon Feb 26 07:21:00 2007
qi_taxid_nucl.diff...	314 Kb	Mon Feb 26 07:21:00 2007
qi_taxid_prot.dmp.gz	28262 Kb	Mon Feb 26 07:21:00 2007
qi_taxid_prot.diff...	91 Kb	Mon Feb 26 07:21:00 2007
taxcat.tar.Z	1746 Kb	Sun Feb 26 20:37:00 2006
taxcat.tar.gz	1088 Kb	Sun Feb 26 20:37:00 2006
taxcat.zip	1088 Kb	Sun Feb 26 20:37:00 2006
taxdmp.zip	9086 Kb	Sun Feb 26 20:20:00 2006
taxdump.tar.Z	12492 Kb	Sun Feb 26 20:20:00 2006
taxdump.tar.gz	9088 Kb	Sun Feb 26 20:20:00 2006
taxdump_readme.txt	4 Kb	Tue Jun 13 00:00:00 2006

