Las bases de datos del GenBank

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The annual “NAR January Database issue”

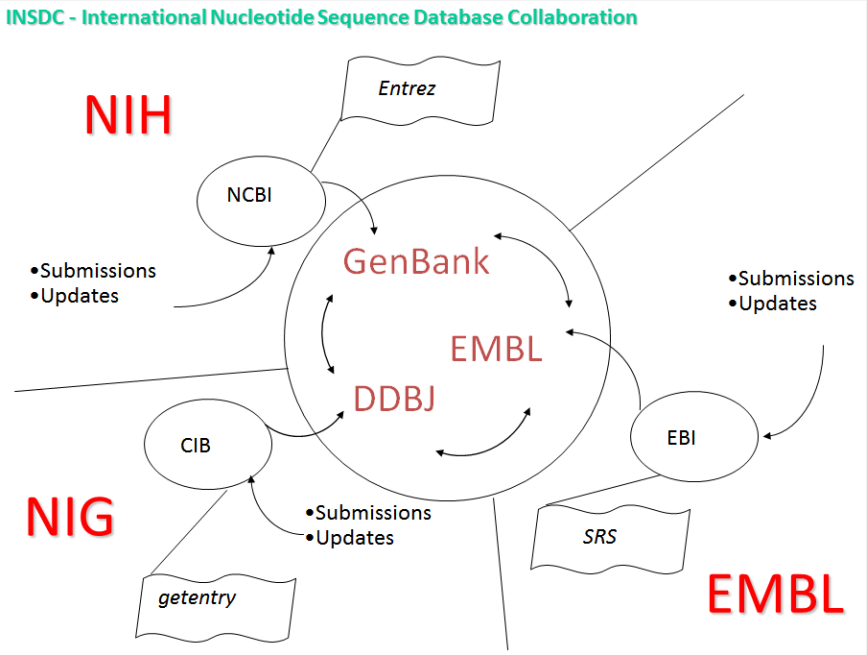
http://www.oxfordjournals.org/nar/database/c/

GenBank

GenBank® is a comprehensive database that contains publicly available nucleotide sequences for more than 300 000 organisms named at the genus level or lower, obtained primarily through submissions from individual laboratories and batch submissions from large-scale sequencing projects. Accession numbers are assigned by GenBank staff upon receipt. Daily data exchange with the European Molecular Biology Laboratory Nucleotide Sequence Database in Europe and the DNA Data Bank of Japan ensures worldwide coverage. GenBank is accessible through the NCBI Entrez retrieval system, which integrates data from the major DNA and protein **sequence** databases along with **taxonomy**, **genome**, **mapping**, **protein structure** and **domain information**, and the biomedical journal **literature via PubMed**. To access GenBank and its related retrieval and analysis services, begin at the NCBI Homepage using the link provided.

http://www.ncbi.nlm.nih.gov/
http://www.ncbi.nlm.nih.gov/books/NBK21105/

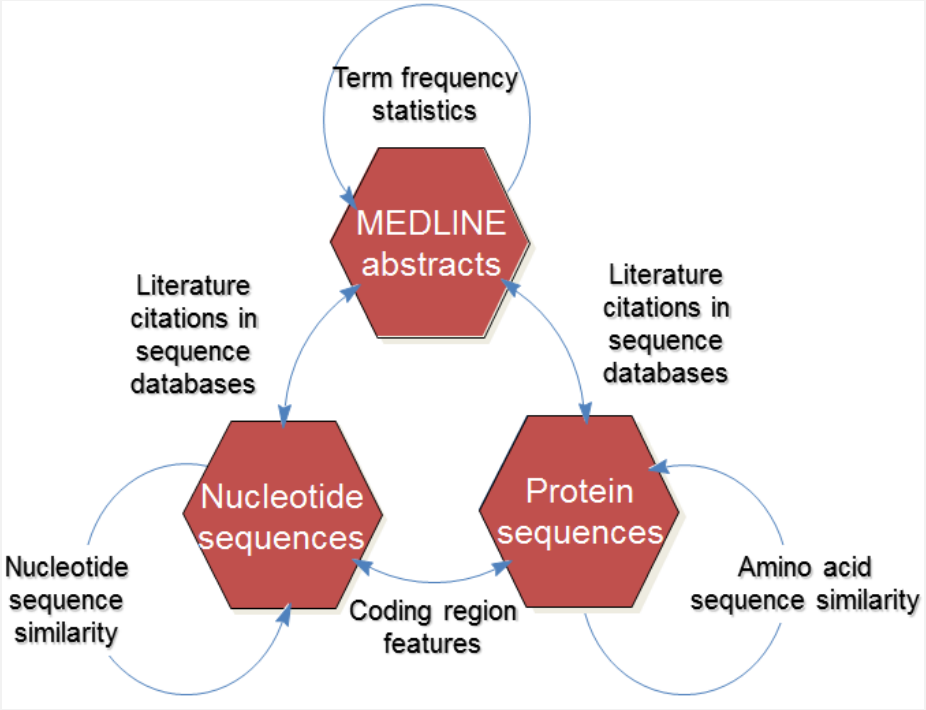
http://www.oxfordjournals.org/nar/database/summary/3



If part of a GenBank nucleotide sequence encodes a protein, a conceptual translation – called a coding region or coding sequence (CDS) – is annotated. A protein accession number (a "protein id") is assigned to the translation product and is noted on the GenBank record.

This protein id is linked to a record for the protein sequence in NCBI's protein databases

NCBI receives and processes about 20,000 direct submission sequences per month, in addition to the approximately 200,000 bulk submissions that are processed automatically



https://www.ncbi.nlm.nih.gov/gquery/gquery.fcgi

NCBI Resources How To

GQuery

NCBI Global Cross-database Search

Search NCBI databases

Search

Literature

PubMed: scientific & medical abstracts/citations
PubMed Central: full-text journal articles
NLM Catalog: books, journals and more in the NLM Collections
MeSH: ontology used for PubMed indexing
Books: books and reports
Site Search: NCBI web and FTP site index

Health

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

Organisms

Taxonomy: taxonomic classification and nomenclature catalog

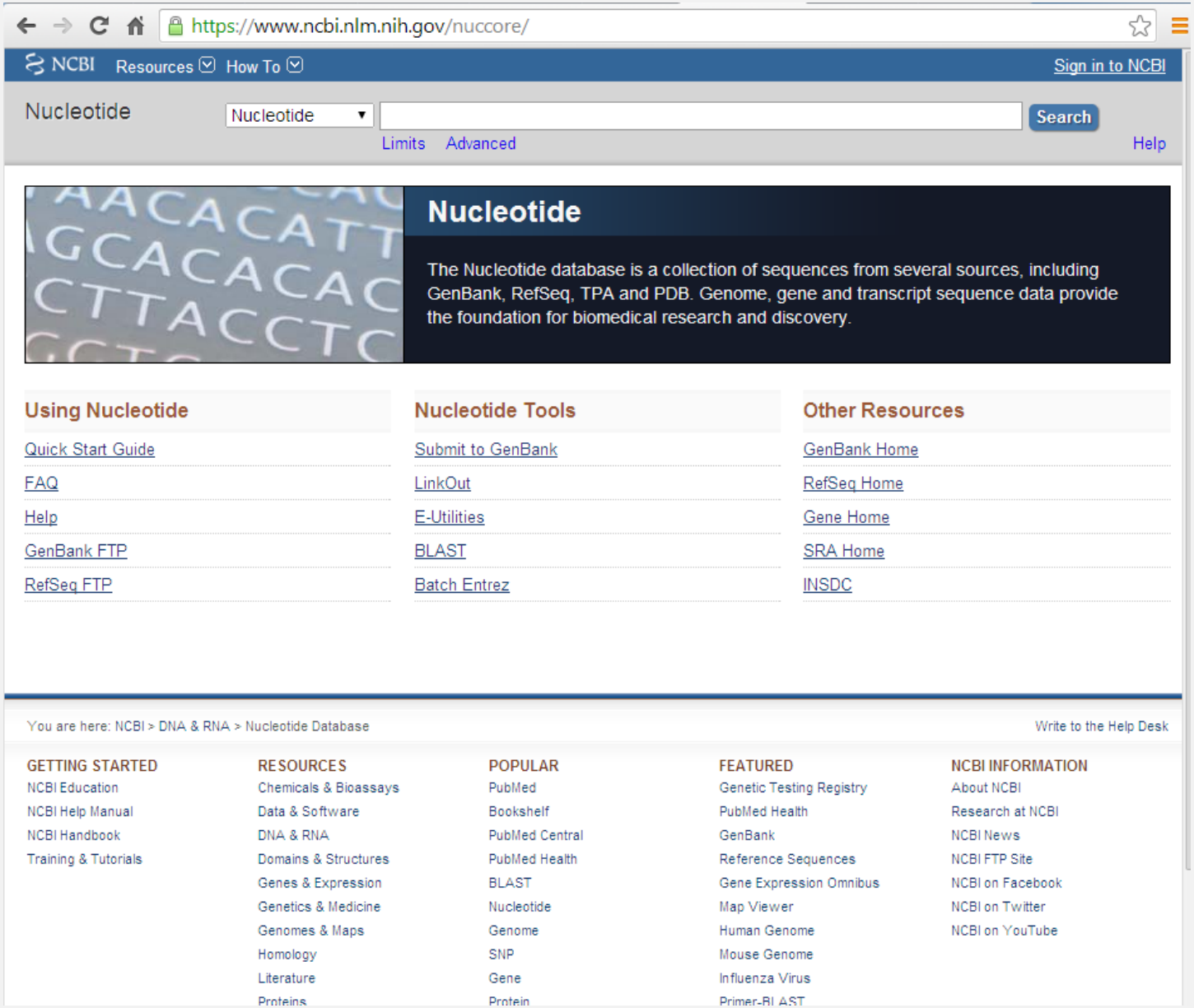
Nucleotide Sequences

Nucleotide: DNA and RNA sequences
GSS: genome survey sequences
EST: expressed sequence tag sequences
SRA: high-throughput DN
PopSet: sequence sets
Probe: sequence-based

Genomes

Genome: genome sequencing projects by organism
Assembly: genomic assembly information
Epigenomics: epigenomic studies and display tools
UniSTS: sequence-tagged sites for genome mapping
dbVar: genome structura
BioProject: biological pr
BioSample: description
Clone: genomic and cDNA clones

https://www.ncbi.nlm.nih.gov/nuccore/



GenBank Flat File

```
LOCUS       BS3588MA1               336 bp    DNA     linear   PLN 27-JUL-2000
DEFINITION  Battarrea stevenii MA-Fungi 35883 18S ribosomal RNA gene, partial
            sequence; internal transcribed spacer 1, complete sequence; and
            5.8S ribosomal RNA gene, partial sequence.
ACCESSION   AF090862
VERSION     AF090862.1  GI:6650341
KEYWORDS    .
SEGMENT     1 of 2
SOURCE      Battarrea stevenii
  ORGANISM  Battarrea stevenii
            Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
            Agaricomycetes; Agaricomycetidae; Agaricales; Agaricaceae;
            Battarrea.
REFERENCE   1  (bases 1 to 336)
  AUTHORS   Martin,M.P. and Johannesson,H.
  TITLE     Battarrea phalloides and B. stevenii, insight into a long-standing
            taxonomic puzzle?
  JOURNAL   Mycotaxon, 67-75 (2000)
REFERENCE   2  (bases 1 to 336)
  AUTHORS   Martin,M.P. and Johannesson,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-1998) Biologia Vegetal (Botanica), Fac. Biologia,
            Univ. Barcelona, Avda. Diagonal 645, Barcelona 08028, Spain
FEATURES             Location/Qualifiers
     source          1..336
                     /organism="Battarrea stevenii"
                     /mol_type="genomic DNA"
                     /strain="MA-Fungi 35883"
                     /db_xref="taxon:107918"
                     /tissue_type="basidiome"
     rRNA            <1..34
                     /product="18S ribosomal RNA"
     misc_RNA        35..319
                     /product="internal transcribed spacer 1"
     rRNA            320..>336
                     /product="5.8S ribosomal RNA"
ORIGIN
        1 ggtttccgta ggtgaacctg cggaaggatc attatcgaat agacttgatg ggttgtcgct
       61 ggctcctagg agcatgtgca cacccgtcat ctttatccat ccacctgtgc acctttttgta
      121 gacttggagg catacaagca catgcatgca atctgggtcc acttacgtgg tccccaggaa
      181 tggagtctgc catgggtggc tgactctgag gctggtgcat gtgcgagtgc ataccctctg
      241 agtctatgtc tttttcatac accacatttg catgtctcgg aatgtattat cacaggctgt
      301 cgtgcctata aaacacaata caactttcag caacgg
//
```

Header

- Title
- Taxonomy
- Citation

Features (AA seq)

DNA Sequence

http://www.ncbi.nlm.nih.gov/Sitemap/samplerecord.html

from: Fiona Brinkman, MBB

EMBL Flat File

```
ID   AF115338   standard; DNA; PRO; 591 BP.
AC   AF115338;
SV   AF115338.1
DT   03-JUN-1999 (Rel. 59, Created)
DT   23-AUG-1999 (Rel. 60, Last updated, Version 2)
DE   Pseudomonas fluorescens ECF sigma factor SigX (sigX) gene, complete cds.
KW   .
OS   Pseudomonas fluorescens
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.
RN   [1]
RP   1-591
RX   MEDLINE; 99369842.
RA   Brinkman F.S., Schoofs G., Hancock R.E., De Mot R.;
RT   "Influence of a putative ECF sigma factor on expression of the major outer
RT   membrane protein, OprF, in Pseudomonas aeruginosa and Pseudomonas
RT   fluorescens";
RL   J. Bacteriol. 181(16):4746-4754(1999).
RN   [2]
RP   1-591
RA   De Mot R.;
RT   ;
RL   Submitted (04-DEC-1998) to the EMBL/GenBank/DDBJ databases.
RL   F.A. Janssens Laboratory of Genetics, Applied Plant Sciences, K.
RL   Mercierlaan 92, Heverlee B-3001, Belgium
DR   SPTREMBL; Q9X4L7; Q9X4L7.
FH   Key             Location/Qualifiers
FH
FT   source 1..591
FT                   /db_xref="taxon:294"
FT                   /organism="Pseudomonas fluorescens"
FT                   /strain="M114"
FT   CDS 1..591
FT                   /codon_start=1
FT                   /db_xref="SPTREMBL:Q9X4L7"
FT                   /transl_table=11
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FT                   /protein_id="AAD34329.1"
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FT                   RRKRRLMDALSLDPLEEASEEKALQPEEKGGLDRWLVYVNPIDRGILVLRFVAELEFQE
FT                   IADIMHMGLSATKMRYKRALDKLREKFAGETET"
SQ   Sequence 591 BP; 157 A; 133 C; 170 G; 131 T; 0 other;
     atgaataaag cccaaacgct atccacgcgc tacgaccccc gcgagctctc tgatgaggag        60
     ttggtcgcgc gctcgcatac cgagcttttt cacgtaacgc gcgcctatga agaactgatg       120
     cggcgttacc agcgaacatt atttaacgtt tgtgcgagat atcttgggaa cgatcgcgac       180
     gcagacgatg tctgtcagga agtcatgttg aaggtgctgt atggcctgaa gaacctcgag       240
     gggaaatcga agttcaaaac gtggctctac agcatcacgt acaacgaatg tattacgcag       300
     tatcggaagg aacggcgaaa gcgtcgcttg atggacgcat tgagtcttga ccccctcgag       360
```

Header

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Features (AA seq)

DNA Sequence

from: Fiona Brinkman, MBB

LOCUS vs Accession vs PID vs protein_id: What's the difference?

LOCUS: Unique string of 10 letters and numbers in the database. Not maintained amongst databases.
ACCESSION: A unique identifier to that record (particular sequence) in GenBank/EMBL/DDBJ that does not change when record is updated.
Nucleotide gi: Geninfo identifier (gi), a unique integer specific for GenBank which will change every time the sequence changes.
VERSION: System started in 1999 for GenBank/EMBL/DDBJ where the accession and version play the same function as the accession and gi number. Format: accession.version

from: Fiona Brinkman, MBB

Which of these would you use to cite a sequence? When would you use one over another?

- **LOCUS:** Unique string of 10 letters and numbers in the database. Not maintained amongst databases.
- **ACCESSION:** A unique identifier to that record (particular sequence) in GenBank/EMBL/DDBJ that does not change when record is updated.
- **Nucleotide gi:** Geninfo identifier (gi), a unique integer specific for GenBank which will change every time the sequence changes. (*and can disappear*!)
- **VERSION:** System started in 1999 for GenBank/EMBL/DDBJ where the accession and version play the same function as the accession and gi number. Format: accession.version

Tomato graphics from www.rottentomatoes.com

from: Fiona Brinkman, MBB

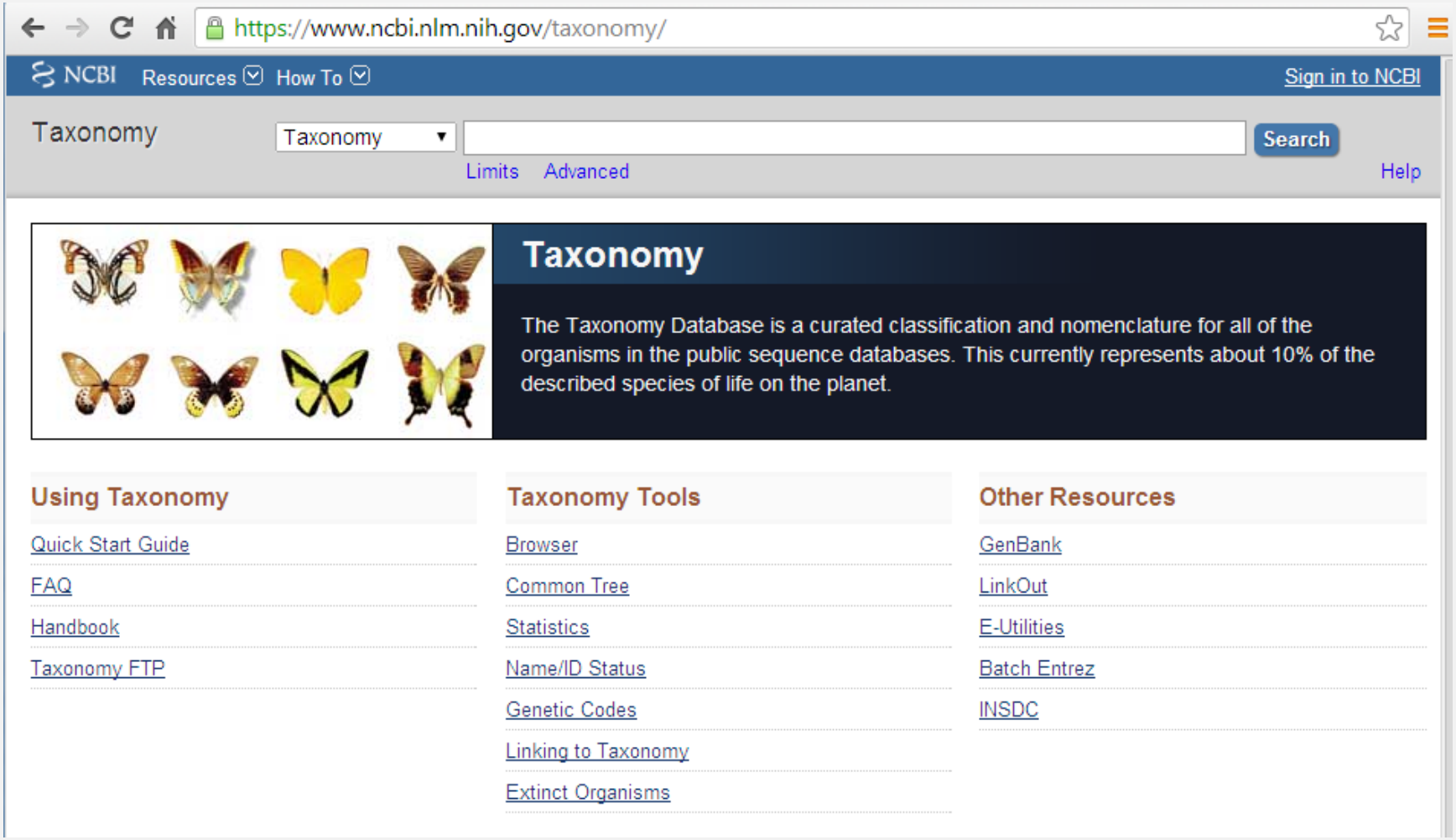
Briefly…Examples of Functional Divisions

PAT Patent
EST Expressed Sequence Tags
STS Sequence Tagged Site
GSS Genome Survey Sequence
HTG High Throughput Genome (unfinished)
HTC High throughput cDNA (unfinished)

Genbank overview:
http://www.ncbi.nlm.nih.gov/bookshelf/br.fcgi?book=handbook&part=ch1

from: Fiona Brinkman, MBB

https://www.ncbi.nlm.nih.gov/taxonomy/



- Species that have not yet appeared in public entries in another Entrez database will not appear in Entrez Taxonomy (**only species in Entrez**).
- The Entrez Taxonomy database **is curated** by a small group of taxonomists at the NCBI, based on the current consensus classification in the systematic literature.
- **~10% of the total** number of described species on the planet (c. 210.000 sp.)
- It is becoming increasingly common to include some **sequence data in the description of a new species**.

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=107918

NCBI Taxonomy Browser

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

Search for [ ] as [complete name] [x] lock [Go] [Clear]

Display [3] levels using filter: [none]

Battarrea stevenii

Taxonomy ID: 107918
Inherited blast name: **basidiomycetes**
Rank: species
Genetic code: Translation table 1 (Standard)
Mitochondrial genetic code: Translation table 4 (Mold Mitochondrial; Protozoan Mitochondrial; Coelenterate Mitochondrial; Mycoplasma; Spiroplasma)

Lineage (full)

cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Agaricaceae; Battarrea

Entrez records

Database name	Direct links
Nucleotide	24
Popset	1
Taxonomy	1

External Information Resources (NCBI LinkOut)

LinkOut	Subject	LinkOut Provider
search GBIF	taxonomy/phylogenetic	Global Biodiversity Information Facility
MA-Fungi 32476	culture/stock collections	Herbarium, Real Jardin Botanico-CSIC, Madrid
MA-Fungi 28224	culture/stock collections	
MA-Fungi 32477	culture/stock collections	
MA-Fungi 33554	culture/stock collections	
MA-Fungi 35883	culture/stock collections	
MA-Fungi 31719	culture/stock collections	
MA-Fungi 31720	culture/stock collections	
MA-Fungi 31008	culture/stock collections	
MA-Fungi 29283	culture/stock collections	
Battarrea stevenii (Libosch.) Fr. 1829	taxonomy/phylogenetic	Index Fungorum
Battarrea stevenii (Liboschitz) Fries	taxonomy/phylogenetic	MycoBank
Battarrea stevenii (taxon passport)	culture/stock collections	StrainInfo
Battarrea stevenii	taxonomy/phylogenetic	Systematic Mycology and Microbiology Laboratory, Fungal Databases

How do I update or correct errors in the Databases?

- Example: For Gene names, citations, new protein name, sequencing errors in Genbank…

  update@ncbi.nlm.nih.gov

- But most people don't bother to correct things that they notice are wrong…

→ increased need for more focused community-based projects

from: Fiona Brinkman, MBB

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