

NCBI FieldGuide Overview

| SELECTED DATABASES | | | Nucleic Acids Research Database Issue: nar.oxfordjournals.org/cgi/content/full/34/suppl_1/D173 |
|--------------------|--|--|---|
| Literature | (M) | PubMed | Biomedical literature citations and abstracts |
| | | PubMed Central | Free, full text life sciences articles |
| | $\overleftarrow{\mathcal{D}}$ | OMIM | "Online Mendelian Inheritance in Man" articles on human genes and phenotypes |
| | B | Books | Online biomedical and scientific texts |
| Organism | | Taxonomy | Organisms represented in the NCBI molecular databases |
| Sequence | Nucle | eotide: Three subset databa nucleotide sequence | ases containing GenBank, EMBL, DDBJ, PDB, RefSeq, TPA and patented es |
| | | CoreNucleotide | A subset of nucleotide sequence records, including the RefSeq collection, that are not included in the EST or GSS databases |
| | | EST | High-throughput Expressed Sequence Tag mRNA records |
| | | ⊕ GSS | High-throughput Genome Survey Sequence DNA records |
| | | Protein | Translations of GenBank, EMBL, and DDBJ records, as well as PDB, PIR, PRF, SWISS-PROT and patented protein sequences |
| | (11) | Genome | Complete genome records integrated with sequence, genetic and physical maps |
| | Og | PopSet | Sets of sequences from population, phylogenetic and mutation studies |
| | | Trace Archives | Raw sequence traces generated by large sequencing projects |
| Genome | Ē | Genome Project | Genome project information |
| | will the same of t | dbSNP | Single nucleotide polymorphism as well as insertion, deletion and microsatellite data |
| | | UniSTS | Sequence Tagged Site marker and mapping data |
| | | Gene | Summary pages of Gene-centered information |
| | #### ##### | HomoloGene | Computationally-determined homologs among selected eukaryotic organisms with complete genomes |
| | | Protein Clusters | A collection of related protein sequences (clusters) encoded by complete prokaryotic and chloroplast plasmids and genomes |
| Expression | | GEO: Profiles & DataSets | "Gene Expression Omnibus", a repository for gene expression and hybridization array data |
| | Ø | UniGene | Gene-based clusters of EST and mRNA sequences |
| | | GenSat | Gene expression atlas of mouse central nervous system |
| | <u></u> | Probe | A public registry of nucleic acid reagents listing effectiveness and distributors |
| Structure | | CDD | "Conserved Domain Database" of identified protein domains |
| | | CDART | Modular domain architecture of proteins |
| | ♣ | MMDB/Structure | Experimental 3D structure data from PDB |
| | 8 | PubChem: Compound, Substance & BioAssay | Information on chemical compounds and substances as well as biological assay data |
| Clinical | | dbGaP | Large-scale patient genotype and phenotype association studies |
| SEARCH ME | THOD |)S | |
| ENTREZ | | | ch protocol allows for keyword searching and integrates databases encompassing my, sequence, genome, expression and structure data into a tightly interlinked n.gov/sites/gquery) |
| BLAST | | Basic Local Alignment Search Tool (BLAST) is a sequence similarity search program that can be used via a web interface or as a stand-alone tool. BLAST compares combinations of nucleotide or protein queries to those in sequence databases and provides statistical information to help decipher the biological significance of the alignment. (www.ncbi.nlm.nih.gov/BLAST) | |
| VAST | | organization of protein seco | ool (VAST) is a structure similarity search service. VAST compares the 3D condary structure elements in the MMDB/Structure database and allows for viewing ents using Cn3D. (www.ncbi.nlm.nih.gov/Structure/VAST/vast.shtml) |
| | | | n queries the PubChem Compound Database with a chemical structure based on ucture binary fingerprints. (pubchem.ncbi.nlm.nih.gov/search/search.cgi) |

SELECTED TOOLS

Stand-alone software and web form tools, respectively, developed by the NCBI for submitting and updating Seguin & Banklt

entries to the GenBank, EMBL, or DDBJ sequence databases (www.ncbi.nlm.nih.gov/Sequin and

www.ncbi.nlm.nih.gov/BankIt)

An interface for uploading a file of UIDs or accession numbers to retrieve records **Batch Entrez**

(www.ncbi.nlm.nih.gov/entrez/batchentrez.cgi)

A stand-alone application integrating the ability to view and analyze sequence data in many ways, **Genome Workbench**

including graphical sequence, varied alignment, phylogenetic tree and tabular views of data

(www.ncbi.nlm.nih.gov/projects/gbench).

A genome browser displaying integrated views of sequence, genetic and physical chromosome maps for **MapViewer**

eukaryotic organisms (www.ncbi.nlm.nih.gov/mapview)

A tool for viewing evidence for gene annotations on assembled genomic sequence, and create your own **Model Maker**

model transcripts (www.ncbi.nlm.nih.gov/mapview/static/ModelMakerHelp.html)

A stand-alone or web application that aligns cDNA with genomic sequences Splign

(www.ncbi.nlm.nih.gov/sutils/splign)

ORFinder A tool that finds potential ORFs in an RNA sequence (www.ncbi.nlm.nih.gov/gorf/gorf.html)

A stand-alone or web application that identifies MS/MS peptide spectra by searching libraries of known **OMSSA**

protein sequences (pubchem.ncbi.nlm.nih.gov/omssa).

A helper application for web browsers that allow for simultaneous viewing of 3D structures with sequence Cn₃D

alignments. Also has powerful annotation and alignment editing features.

(www.ncbi.nlm.nih.gov/Structure/CN3D/cn3d.shtml)

The NCBI BLAST ftp site provides standalone blast, client server blast, and wwwblast packages for The BLAST Suite

different platforms. It also provides commonly used blast databases in preformatted as well as FASTA

format. (ftp.ncbi.nih.gov/blast)

PROGRAMMING TOOLS & INFORMATION

NCBI Training

The Entrez Programming Utilities are a set of server-side programs that provide a stable interface to **E-Utilities**

access NCBI's databases by scripted "URL calls".

(eutils.ncbi.nlm.nih.gov/entrez/query/static/eutils_help.html)

The NCBI Software Development Toolkit was developed for the production and distribution of GenBank, Entrez, BLAST and other NCBI services. Source code is provided as well as information on NCBI's data **NCBI Toolkit**

model, data encoding and programming libraries. (www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=toolkit.TOC)

General Entrez Links www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=helplinks.chapter.linkshelp

> www.ncbi.nlm.nih.gov/Omim/omimhelp.html#HowToLink OMIM page Links

UniGene page Links www.ncbi.nlm.nih.gov/UniGene/FAQ.shtml Creating Weblinks

> www.ncbi.nlm.nih.gov/Structure/MISC/linking.html#mmdbsrv Structure page Links

www.ncbi.nlm.nih.gov/Taxonomv/taxonomvhome.html/index.cgi?chapter=howlink Taxonomy page Links

MvNCBI is a central place to customize NCBI Web services. You can use Mv NCBI to: **MyNCBI** Save searches, Set up e-mail alerts for new content, Display links to Web resources (LinkOut),

Choose filters that group search results. (http://www.ncbi.nlm.nih.gov/entrez/login.fcgi?)

Individual chapters describing databases, major search algorithms and data processing pipelines; each describes the database design or how the resource works and how the different NCBI Handbook

databases and resources relate to each other, along with a brief overview on using the resource.

(www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=handbook)

Education www.ncbi.nlm.nih.gov/Education

FieldGuide & FieldGuide Plus <u>www.ncbi.nlm.nih.gov/Class/FieldGuide</u> & <u>/FGPlus</u>

MiniCourses www.ncbi.nlm.nih.gov/Class/minicourses

Structure Course www.ncbi.nlm.nih.gov/Class/Structure/course.html PubChem Course www.ncbi.nlm.nih.gov/Class/PubChem/course.html

www.ncbi.nlm.nih.gov/Class/PowerTools PowerTools Workshop

General Help info@ncbi.nlm.nih.gov **BLAST-specific Help** blast-help@ncbi.nlm.nih.gov HELP! GenBank Submissions/Updates Help gb-admin@ncbi.nlm.nih.gov

> Telephone (8³⁰am to 5pm Eastern time) (301) 496-2475