NCBI FieldGuide Overview

SELECTED DATABASES	*Nucleic Acids Research Database Issue:* *nar.oupjournals.org/cgi/content/full/32/suppl_1/D35*

Literature

	PubMed	Biomedical literature citations and abstracts
	PubMed Central	Free, full text life sciences articles
	OMIM	Online Mendelian Inheritance in Man articles on human genes and phenotypes
	Books	Online biomedical texts

Organism

	Taxonomy	Organisms represented in the NCBI sequence databases

Sequence

	Nucleotide	GenBank, EMBL, DDBJ, PDB, RefSeq, TPA, and patented nucleotide sequences
	Protein	Translations of GenBank, EMBL, and DDBJ records, as well as PDB, PIR, PRF, SWISS-PROT and patented protein sequences
	PopSet	Sets of sequences from population, phylogenetic and mutation studies
	Trace Archives	Raw sequence traces generated by large sequencing projects

Genome

	Genome	Complete Genome records integrated with sequence, genetic and physical maps
	dbSNP	Single nucleotide polymorphism as well as insertion, deletion and microsatellite information
	UniSTS	Sequence Tagged Site marker and mapping data
	Gene	Summary pages of Gene-centered information
	HomoloGene	Computationally-determined homologs among eukaryotic organisms with complete genomes

Expression

	GEO	Gene Expression Omnibus, a repository for gene expression and hybridization array data
	UniGene	Gene-based clusters of EST and mRNA sequences

Structure

	CDD	Conserved Domain Database for identified protein domains
	CDART	Modular domain architecture of proteins
	MMDB/Structure	Experimental 3D structure data from PDB
	PubChem	Information on small molecule chemical compounds and substances assayed for biological activity

SEARCH METHODS

ENTREZ
The Entrez database structure and search protocol integrates the scientific literature, taxonomy, sequence, genome, expression and structure data into a tightly interlinked system. (www.ncbi.nlm.nih.gov/Entrez/)

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 sequences in nucleotide or protein databases and provides statistical information to help decipher the biological significance of the alignment. (www.ncbi.nlm.nih.gov/BLAST/)

VAST
Vector Alignment Search Tool (VAST) is a structure similarity search service. VAST compares the 3D organization of secondary structures of protein structures to those in the MMDB/Structure database and allows for viewing superpositions and alignments using Cn3D. (www.ncbi.nlm.nih.gov/Structure/VAST/vastsearch.html)

SELECTED TOOLS

Sequin	A stand-alone software tool developed by the NCBI for submitting and updating entries to the GenBank, EMBL, or DDBJ sequence databases (www.ncbi.nlm.nih.gov/Sequin/)
VecScreen	Quick identification of nucleic acid sequence that may be due to vector contamination (www.ncbi.nlm.nih.gov/VecScreen/)
MapViewer	Integrated views of sequence, genetic and physical chromosome maps for eukaryotic organisms (www.ncbi.nlm.nih.gov/mapview/)
ePCR	Scanning of DNA sequence for sequence tagged sites in our UniSTS database (www.ncbi.nlm.nih.gov/sutils/e-pcr/)
Model Maker	View evidence for gene annotations on assembled genomic sequence, and create your own model transcripts (www.ncbi.nlm.nih.gov/mapview/static/ModelMakerHelp.html)
Spidey	Alignments of one or more mRNA sequences to a single genomic sequence (www.ncbi.nlm.nih.gov/spidey)
ORFinder	Predictions of all possible ORFs in an RNA sequence (www.ncbi.nlm.nih.gov/gorf/)
Digital Differential Display	Comparisons of mRNA levels in different cell-lines, tissues and organs (www.ncbi.nlm.nih.gov/UniGene/info_ddd.html)
SAGEmap	Gene expression results from SAGE tags mapped to mRNA sequences in GenBank (www.ncbi.nlm.nih.gov/projects/SAGE/)
Cn3D	A helper application for web browsers that allow for simultaneous viewing of 3D structures with sequence alignments. Also has powerful annotation and alignment editing features. (www.ncbi.nlm.nih.gov/Structure/CN3D/cn3d.shtml)
The BLAST Suite	A sequence similarity search program that compares nucleotide or protein queries to sequences in nucleotide or protein databases and provides statistical information to help decipher the biological significance of the alignment. It can be used via a web interface or as a stand-alone tool. (www.ncbi.nlm.nih.gov/BLAST/) The NCBI BLAST ftp site provides standalone blast, client server blast, and wwwblast packages for different platforms. It also provides commonly used blast databases in preformatted as well as FASTA format. (ftp://ftp.ncbi.nih.gov/blast/)

Programming Tools & Information

Batch Entrez	Upload a file of UIDs or accession numbers to retrieve records (www.ncbi.nlm.nih.gov/entrez/batchentrez.cgi?)
E-Utilities	Guidelines for Entrez "URL calls" used to access data at NCBI by scripts (eutils.ncbi.nlm.nih.gov/entrez/query/static/eutils_help.html)
NCBI Toolkit	The NCBI Software Development Toolkit was developed for the production and distribution of GenBank, Entrez, BLAST, and related services by NCBI. Source code is provided as well as information on NCBI's data model, data encoding and programming libraries. (www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=toolkit)
Creating Weblinks	General Entrez Links www.ncbi.nlm.nih.gov/entrez/query/static/linking.html OMIM page Links www.ncbi.nlm.nih.gov/Omim/omimhelp.html#HowToLink UniGene page Links www.ncbi.nlm.nih.gov/UniGene/FAQ.html Structure page Links www.ncbi.nlm.nih.gov/Structure/MISC/linking.html#mmdbsrv Taxonomy page Links www.ncbi.nlm.nih.gov/Taxonomy/taxonomyhome.html/index.cgi?chapter=howlink

NCBI Handbook	**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 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)**

NCBI Training	**Education** **www.ncbi.nlm.nih.gov/Education/** **FieldGuide Home** **www.ncbi.nlm.nih.gov/Class/FieldGuide/**

HELP!	**General Help**	**info@ncbi.nlm.nih.gov**
	BLAST-specific Help	**blast-help@ncbi.nlm.nih.gov**
	GenBank Submissions/Updates Help	**gb-admin@ncbi.nlm.nih.gov**
	Telephone (8^{30}am to 5^{30}pm EST)	**(301) 496-2475**