Entrez Databases
Entrez is a retrieval system designed for searching several linked databases.

BioSystems - Interacting sets of biomolecules involved in metabolic and signaling pathways, disease states, and other biological processes.
BioSample - Biological source materials used in experimental assays.
BioProject - Searchable collection of complete and incomplete (in-progress) large-scale sequencing, assembly, annotation, and mapping projects for cellular organisms. (redesigned and expanded Genome Project)
Bookshef - Full-text biomedical and scientific books.
Conserved Domains - protein domains represented by sequence alignments and profiles for protein domains conserved in molecular evolution.
dbGaP - Associated genotype and phenotype data.
dbVAR - Large-scale genomic variation.
Epigenomics - results of genome-wide studies on modifications of chromatin in various cell types that assay programmable changes that affect gene expression
EST - Nucleotide database subset containing only Expressed Sequence Tag records.
Gene - Genes and associated information for organisms, including human.
Genome - Genomes of over 1,200 organisms, both completely sequenced organisms and those for which sequencing is in progress.
Genome Project - Organism-specific overviews of complete and in-progress large-scale sequencing, assembly, annotation, and mapping projects for cellular organisms.
GEO Datasets - Curated gene expression and molecular abundance Datasets from NCBI's Gene Expression Omnibus, a gene expression and hybridization array repository.
GEO Profiles - Individual gene expression and molecular abundance profiles assembled from the GEO repository.
GSS - GenBank subset containing only Genome Survey Sequence records.
Homologene - Homologs among the annotated genes of several completely sequenced eukaryotic genomes.
MESH - NLM's controlled vocabulary and classification system for articles.
NCBI Site Search - Database of static NCBI web pages, documentation, and online tools.
NLM Catalog - Records for materials in the NLM collections.
Nucleotide - Nucleotide sequences from GenBank, EMBL, DDBJ (INSDC members), as well as NCBI-curated Reference Sequences, TPA data, and nucleotide sequences from the Protein Databank.
OMIM - Review articles of human genes, genetic disorders, and inherited traits.
PopSet - Population study datasets to analyze evolutionary relatedness of a population.
Probe - Public registry of nucleic acid reagents designed for use in biomedical research applications. Information on reagent distributors, probe effectiveness, and computed sequence similarities.
Protein - Amino acid sequences created from the translations of coding regions provided on nucleotide records.
Protein Clusters - Related protein sequences (clusters) consisting of Reference Sequence proteins that are encoded by complete prokaryotic genomes as well those encoded eukaryotic organelle plastids and genomes.
PubMed Compound - Small molecule chemical structures.
PubMed Substance - Chemical substances screened for bioactivity.
PubMed - 17 million+ citations from MEDLINE and additional life sciences journals.
PubMed Central - Full-text digital archive of life sciences journal literature.
SNP - Repository for both single nucleotide substitutions and short deletion and insertion polymorphisms.
SRA - Sequencing data from the next generation sequencing platforms.
Structure - Molecular Modeling Database of 3D macromolecular structures, including proteins and polynucleotides.
Taxonomy - Names of all organisms represented in the genetic databases with at least one nucleotide or protein sequence.
UniGene - A system for automatically partitioning GenBank sequences into a non-redundant set of gene-oriented clusters containing sequences that represent a unique gene, as well as tissue types and map location.

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Literature Databases
An extended searchable library of the life sciences literature.

Bookshelf - Biomedical and life sciences books and monographs.

Gene Reviews - Expert authored, peer-reviewed disease descriptions.

Journals - Information on journals indexed in NCBI databases.

MeSH - NLM's controlled vocabulary and classification system for articles.

NLM Catalog - Online catalog of NLM.

PubMed - 17 million+ citations from MEDLINE and additional life sciences journals.

PubMed Central - Full-text digital archive of life sciences journal literature.

PubMed Health - Clinical effectiveness reviews for consumers and clinicians.

Nucleotide Databases
Genome data from sequencing projects around the world, the cornerstone of bioinformatics research.

dbGSS - Database of genome survey sequences, or short, single-pass genomic sequences.

dbSNP - population-specific frequency and genotype data, experimental conditions, molecular context, and mapping information for both neutral variations and clinical mutations

GenBank - Annotated collection of all publicly available nucleotide & amino acid sequences.

Nucleotide Database - A collection of nucleotide sequences from several sources, including GenBank, RefSeq, the Third Party Annotation (TPA) database, and PDB

RefSeq - A database of non-redundant reference sequences standards, including genomic DNA contigs, mRNAs, and proteins for known genes. Multiple collaborations, both within NCBI and with external groups, support our data-gathering efforts.

GSS*, Homologene*, SNP*, UniGene*

3D Structure Display Tools
Tools for comparative macromolecular and 3D structural analysis.

CD-Search - Identifies conserved domains present in a protein sequence.

Cn3D - 3D structure & sequence alignment.

CDART - Displays functional domains of a protein & lists proteins with similar domain architectures.

SNP - Repository for both single nucleotide substitutions and short deletion and insertion polymorphisms.

SRA - Sequencing data from the next generation sequencing platforms.

Structure - Molecular Modeling Database of 3D macromolecular structures, including proteins and polynucleotides.

Taxonomy - Names of all organisms represented in the genetic databases with at least one nucleotide or protein sequence.

UniGene - A system for automatically partitioning GenBank sequences into a non-redundant set of gene-oriented clusters containing sequences that represent a unique gene, as well as tissue types and map location.

Data Mining Tools
Data retrieval and submission tools

Text Term Searching
Entrez*

My NCBI - Saves searches & email alerts.

Citation Matcher - Search with PMID.

Taxonomy

Taxonomy Browser - Taxonomy database.

Taxonomy Common Tree - Generates a taxonomic tree for a selected group of organisms.

Taxonomy Statistics - Displays the number of taxonomic nodes in the database for a given rank and date of inclusion.

Sequence Submission

Sequin - Data submission tool includes ORF Finder, alignment view/edit, link PowerBLAST.

Bankit - Web submission tool for one or simple sequence submissions.

Sequence Analysis Tools

BLAST - Finds regions of local similarity between biological sequences.

Blink - Displays the results of BLAST searches that have been done for every protein sequence in the Entrez Protein database.

Conserved Domain (CD Search) - Sequence alignments & profiles representing protein domains conserved in molecular evolution.

Electronic-PCR (e-PCR) - Compare query sequence to mapped sequence-tagged sites to find possible map location for query sequence.

Gene Expression Omnibus (GEO) - Visualization & exploration of curated GEO data.

Genome ProtMap - mapping of each protein from a COG, or in the case of viruses a VOG, back to its genome.

Primer-Blast - uses Primer3 to design PCR primers to a sequence template.

VecScreen - Tool to ID segments of nucleic acid sequence; vector, linker, or adapter origin.

OMIM Morbid Map - Alphabetical listing of diseases and their corresponding cytogenetic map locations, with links to OMIM entries.

Maps
Access to genetic and physical maps.

Map Viewer- Integrated views of chromosome maps for 40 organisms, Human Map, too.

Model Maker - Construct mRNA sequence from genomic data, select exons identified by alignments of mRNAs and ESTs, edit model, test open reading frames, save results.

OMIM Gene Map - Cytogenetic locations of genes reported in literature and determined by mapping methods.

OMIM Morbid Map - Alphabetical listing of diseases and their corresponding cytogenetic map locations, with links to OMIM entries.