

**Mz Tools 8 0 119 \_HOT\_**

the ncbi reference sequences database contains the curated, non-redundant nucleotide and amino acid sequences of genes, proteins, and rnas of bacteria, archaea, eukarya and viruses. this resource is designed to provide rapid, convenient access to curated sequence data that are continually being updated as new data become available. the ncbi basic local alignment search tool (blast) service provides both local and non-local sequence comparison. blastn and blastx are tools for large-scale, local sequence alignment of dna or protein sequences. these tools use a translation-independent search of sequence databases. the ncbi map viewer is a publicly accessible map-based sequence viewer. use of this tool involves input of the coordinates of a query region of a chromosome to display the corresponding genomic location and scale. the ncbi genome viewer is a web-accessible sequence viewing tool that allows you to view, manipulate, download and compare a single dna sequence against other sequences in the ncbi databases, or to sequence databases at other web sites. it is a convenient way to view, edit, and analyse dna or protein sequences. the combined analytic tools and databases of chembl are open-source and publicly available. they are freely available through an easy-to-use web interface. the raw data in chembl have been entirely integrated into the ncbi environment, such that users can access and interrogate available protein interactions using biomart and to perform advanced searches using ncbi entrez. the ncbi gene page for a single gene provides the full range of data, including functional annotation, expression, nomenclature, sequence, genomic context, polymorphisms, and clinical reports. the ncbi mutation page provides comprehensive information on a single mutation, including its expression, functional annotation, and nomenclature; it also contains links to other ncbi resources.





medievaldb is a database of dna sequences from the middle ages and renaissance, with the major goal of constructing a reference collection of dna sequences with a high proportion of the temporal and cultural diversity of the sequences currently used for molecular archaeological studies. over 2000 sequences have been reconstructed from fragmented, small, and fragmentary medieval samples by a combination of pcr- and sanger-based sequencing, leading to the assembly of over 3300 sequences. the medievaldb aims to make these data available for use in molecular archaeology and with tools such as blast to aid the researchers. medievaldb, which provides the dna sequences, tools to annotate and query these sequences, and a family tree based on the mtDNA sequences, is freely available via the internet to all academic users. in addition, the ancient dna samples themselves are stored in a repository maintained by ancient dna centre, uppsala university and the värnamo site. the medievaldb website also provides guidance for researchers and students. ncbi biosample is an automated system designed to make available all available nucleic acid sequence data held by the ncbi. it was developed to allow users to explore large collections of sequence data and to link these data to complete reference sequences and/or alignments, created by ncbi and other sequencing centres. current versions of the fda's medical device reporting (mdr) website (mdr.fda.gov). the mdr program helps ensure that manufacturers of medical devices are creating the proper reports for all device-related adverse events. these reports, which are required by law, are filed with fda's center for devices and radiological health.

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