

## NHLBI ABE - Automated Bioinformatics Extractor

**NHLBI ABE** is a Java-based standalone program to extract bioinformatics from the National Center for Biotechnology Information (**NCBI**) in real-time fashion.

**NHLBI ABE** uses a list of **protein accession number** or **gene symbol** as an input to extract multiple output types outlined in the below table.

Input	Output
accession number or gene symbol	General information: protein name, gene symbol, amino acid number, and species
	Accession number: RefSeq or Swiss-Prot
	FASTA sequence with or without metadata
	GO term
	Conserved domain

How to start ABE:

1. Make sure that you have the most recent Java Platform. If not, download it from this link <http://www.java.com/en/download/index.jsp>.
2. Prepare a single column input list in Excel (eliminate blank space, if any). Input can be either accession number or gene symbol. Different types of accession number can be used, however, some accession number types can not be used to extract GO term and conserved domain, see the below table.

Accession Number	Output				
	General information	Accession number	FASTA sequence	GO term	Conserved domain
RefSeq (ref)	+	+	+	+	+
Swiss-Prot (sp)	+	+	+	-	-
GenBank (gb)	+	+	+	+	+
EMBL (emb)	+	+	+	+	+
GenInfo Identifier (gi)	+	+	+	-	-

3. Copy and paste the input list into input text field.
4. Select input: accession number or gene symbol. Select species (human, rat, or mouse) if gene symbol is used.
5. Select output. More than one type of output can be selected among general information, accession number, and FASTA sequence. Selection of either GO term or conserved domain will inactivate other output types, to resume other output types, select "None" button in Ontology and Domain panel.
6. Click "Submit" button to start extracting data.
7. When the extraction is done you can either copy data onto clipboard using "Copy" button or save data into a file using "Save" button.