2. *Protein Function Analysis*

These groups of programs allow you to compare protein sequences to the protein database that contain information on motifs, and protein domains. These allow you to approximate the biochemical function of query protein.

3. *Structural Analysis*

These sets of tools allow you to compare structures with the known structural databases. The determination of a protein's 2D or 3D structure is crucial in the study of its function.

4. *Sequence Analysis*

This set of tools allows you to carry out further, more detailed analysis on your query sequence including evolutionary analysis, identification of mutations, etc.

Examples of Bioinformatics Tools:

i. **BLAST** - **B**asic **L**ocal **A**lignment **S**earch **T**ool

BLAST comes under Homology and Similarity Tool. BLAST is used to perform fast similarity searches to find a match against the queried nucleotide or protein sequence. It is developed at NCBI.

Depending on the type of sequences to compare, there are different programs:

Blast p: Compares an aminoacid query sequence against a protein sequence database.
Blast n: Compares a nucleotide query sequence against a nucleotide sequence database.
Blast x: Compares a nucleotide query sequence against a protein sequence database.
t Blast n: Compares a protein query sequence against a nucleotide sequence database.

Program	***Query sequence***	***Database***
Blast p	Protein	Protein
Blast n	Nucleic acid	Nucleic acid
Blast x	Translated nucleic acid	Protein
t Blast n	Protein	Translated nucleic acid

ii. **FASTA** - **FAST** homology search **A**ll sequences

FASTA is an alignment program for protein sequences and it can locate the highly matching segments between two sequences. FASTA search similarities between one sequence (the query) and any group of sequences of the same type (nucleic acid or protein) as the query sequence. It is generally best to make protein-protein comparisons, but it can also compare DNA sequence to DNA databanks.

A sequence in FASTA format is represented as a series of lines each of which do not exceed 80 characters. The first line in a FASTA file starts either with a greater than (>) symbol or a semicolon (;). Following the initial line is the actual sequence in standard one letter code. The sequence ends with an asterisk.
>MCHU- Calmodulin-Human, rabbit, rat, and chicken
ACCTGAGGCTCCGAACGTCCGATTCAC*