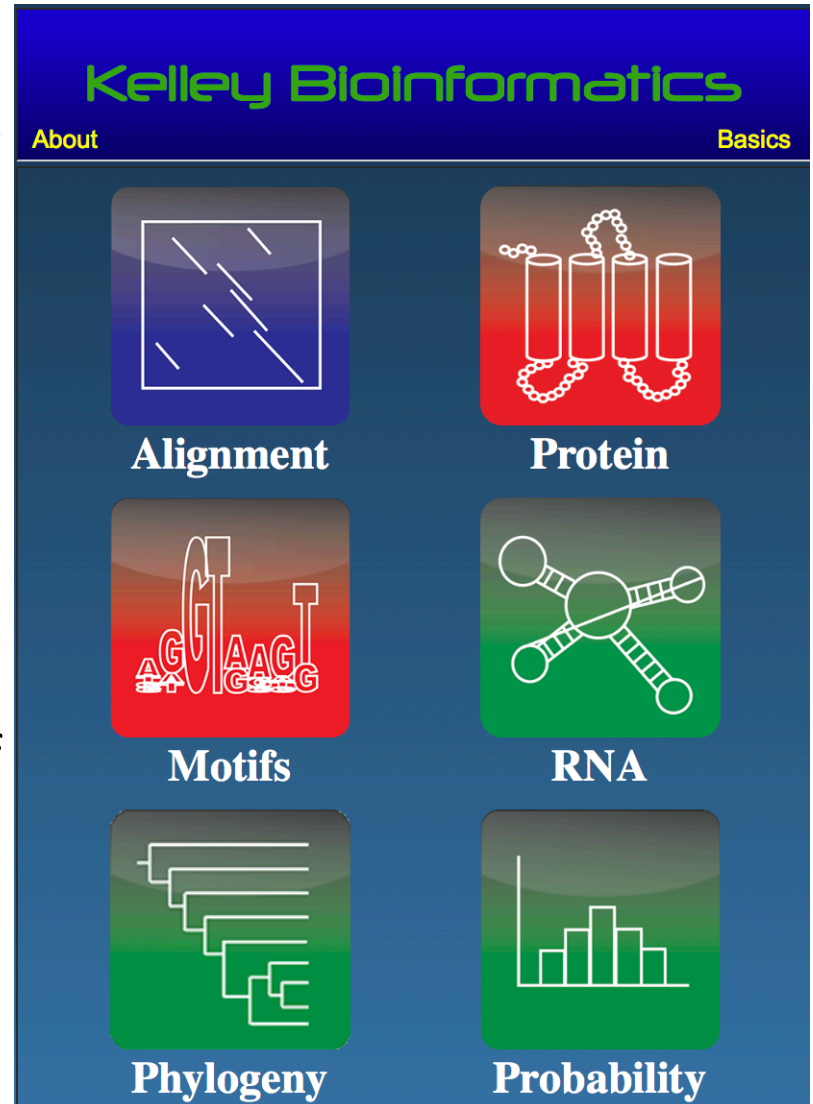


# Homepage Icons

Touching or clicking the icons takes you to a page that teaches specific bioinformatics algorithms and associated software tools on the icon topic.

The **Alignment**, **Motifs** and **Phylogeny** buttons teach algorithms and tools for sequence analyses with DNA, RNA, and proteins. The **Protein** and **RNA** buttons focus on algorithms for predicting structural features of these respective macromolecules, while the **Probability** button teaches how to generate amino acid transition matrices.



# General Site Design: Algorithms

Alignment icon button: The BLAST Exercise example.

Click/Touch to go back to Icon Homepage.

Click/Touch the BLAST link brings up this algorithm. Algorithms begin on Concept Mode.

After studying in Concept mode, use the QUIZ MODE to test yourself. Click "I" Button for more info.

The screenshot shows the Kelley Bioinformatics website interface. At the top is a blue header with the logo and navigation links for 'About' and 'Basics'. Below the header are three main sections: 'Sequence Alignment', 'Methods', and 'Web Resources'. Under 'Sequence Alignment' are buttons for 'MAIN PAGE' and 'PRINT SCREEN'. Under 'Methods' are links for 'BLAST Exercise' and 'Needleman-Wunsch', each with an information icon (I). Under 'Web Resources' are links for 'NCBI BLAST' and 'Clustal Omega', each with 'T' and 'D' icons. Below these sections are input fields for 'Length' (Subject Size: 25, Query Size: 10, Word Size: 5) and 'Scores' (Match: 5, Mismatch: -4). A 'Query' field contains 'ATGGTAATGC'. At the bottom are buttons for 'RANDOM QUERY', 'SUBMIT', and 'QUIZ MODE'. A 'Query' field at the very bottom shows the sequence 'A T G G T A A T G C' with each letter in a different colored box.

# General Site Design: Algorithms

**Kelley Bioinformatics**  
About Basics

Sequence Alignment      Methods      Web Resources

MAIN PAGE      BLAST Exercise      NCBI BLAST  
PRINT SCREEN      Needleman-Wunsch      Clustal Omega

Query Size:  (10 to 15)      Mismatch:   
Word Size:  (5 to 7)  
Query:

RANDOM QUERY      SUBMIT      QUIZ MODE

Query: **A T G G T A A T G C**

The "I" Button stands for "Interactive". This is a tutorial on how to use the Interactive algorithm learning tool.

**BLAST Method: Initialize Problem**

**PURPOSE:** This Interactive teaches how the BLAST method determines which sequences are the best match to an input sequence. The unknown input sequence is called the QUERY. The BLAST method breaks up the QUERY into little bits, called "Words", and then matches the little bits against other sequences, called the SUBJECTS.

Length		Scores	
Set length of SUBJECT sequences (25 to 50)	Subject Size: <input type="text" value="25"/>	Match: <input type="text" value="5"/>	
Set length of QUERY sequence (10 to 15)	Query Size: <input type="text" value="10"/>	Mismatch: <input type="text" value="-4"/>	
Length to break up the QUERY (5 to 7)	Word Size: <input type="text" value="5"/>		

Query:

RANDOM QUERY      SUBMIT      QUIZ MODE

Query: **A G A T T A A A**

# General Site Design: Tutorials

On the left side are links to usable bioinformatics analysis tools.

The "T" Button stands for "Tutorial" on how to use the analysis software.

The "D" Button stands for "Data". Test data to use with the analysis software.

Web Resources: NCBI BLAST, Clustal Omega

Length: Subject Size: 25 (25 to 50), Query Size: 10  
Scores: Match: 5, Mismatch: -4

Buttons: RANDOM QUERY, SUBMIT, QUIZ MODE

Query: **A T G G T A A T G C**

BLAST home page

Step 1. Click here if you have a DNA sequence.  
(Click here if you have a protein sequence)

```
TEST DATA
DNA sequences
>NucSeq1
ATGAACGACGAAACACAATTTACAATAAGGCCAAGCAAAATATCCGTTTGCCCAAGAAATGGCTCAGG
ATCACAGACATGCTCAGTTACACCAATTCACCTACTTGGCTGATTGTTGAGCCAACGAGGATGGTTC
>NucSeq2
ATGGCTGATTATCCTTTTACTGACAAGCCGCAAGACATTGTCTGATGCGTACTCAATGCACAATCTT
ATGGTCATTCACAATTAACCCCTATTCACATGTCTGCTCTCTTTTGGCCAGTGCAGTAAACGGTAC
>NucSeq3
ATGAACGACGAAACGAAGTTTACGAACAAGCTCTGCATATCATCCATTGCACAGAAACTGCACGAGG
ACCACAGCATTGCAGCTGGTGCCTCTACAGCTGCTTCAGCGTTCGTAGAGACACCTGCTGATGGTATG

Protein Sequences
>LCseedSf1
MKKLTVAISAVVAASVLMAMSAQAAEINXKDSNKLDDYGVKNAHYFSSNDADDGDTTYVRLGFKGETQIN
DQLTGFQWEYEFKGNRAESQSSSKDKTRLAFAGLRFQDYGSLDYGRNYGVAYDIGAWDYLPEFGGDTW
TQIDVFMGRFQVATYRNNDFFGLVDGLFAFAGYQGNDRIDVTEARNGDGFSTTYEYEGFVGATFA
KSDRTNDQVIYGNNSLNASQNAEVAAGLKYDANNILATYVSETQNTVFNHNIAMKQNFVAVQY
QDFGLRPSVAVLQSKGKDLGAWGDQDLEIYIDVGATYFNKMSFTVDYKINLIDKSDPFGKASVATDD
IVAVGLVYQF
>PhoEseedEcol
MKMKKSTLALVVMGIVASASVQAAEINXKDGKLDVYGVKAMHYMSDNDKSGDQSYIRFGFKGETQIN
DQLTGFQWEAEFAGNKAESDTAQKTRLAFAGLKYKDLGSDYGRNLGALYDVEAWTDMFPEFGDSSA
QTDNFMTRKASGLATYRNDFGVYDGLNLTLYQGNRNNRDKQNGDGFSTSLTYDFGGSDFAISGAY
TNSDRTEQNLQSRGTGKRAEAWATGLKYDANNILATYVSETRMTPI TGGFANKQNFVAVQYQDF
GLRPSLQVLSKRGDIEGIDEDLVNIDVGATYFNKMSAFVDYKINQLDSDNKLINNDIVAVGMT
YQF
```

# The Basics Link

The Basics Link

**Kelley Bioinformatics**

About Basics

**Alignment**

**Protein**

**Motifs**

**RNA**

**Phylogeny**

**Probability**

Introductory information on the website, Bioinformatics, and Basic Biology.

Info on how to read different data formats.

Tutorials on more commonly used Bioinformatics websites.

Primers on programming

**Kelley Bioinformatics**

**Basics**

- Using Kelley Bioinfo
- Why Bioinformatics
- DNA → RNA → Protein
- Biology in the Computer

**Data Format**

- Sequence files
- Alignments

**Databases**

- PubMed
- Microbial Genomics
- BLAST
- UniProt
- Ensembl

**Programming**

- Unix
- R
- Python