

Evolutionary Studies/ Phylogenetic Analysis - Analysis of parameters affecting trees.

Aim:-

To carryout Phylogenetic analysis of given sequences.

Introduction:-

CLUSTAL W2 is a general purpose multiple sequences alignment program for DNA or proteins. It attempts to calculate the best match for the selected sequences, and lines them up so that the identities, similarities & differences can be seen. Commonly used phylogenetic tree generation methods provided by the clustal w & program are NJ and UPGMA.

The Phylogenetic tree is build in three steps i) input alignment ii) Setting the parameters iii) Subvision.

Query :- Protein, casein, Myoglobin

url :- 1. www.ebi.ac.uk/clustal.w/

2. [genebee - www.genebee.msu.su/service/phree](http://genebee.msu.su/service/phree).

Procedure:-

1st method [CLUSTAL W] :-

- ① Login to NCBI & retrieve minimum of six queries in FASTA.

- ii) logon to www.ebi.ac.uk/cluster w/.
- iii) Welcome page \rightarrow cluster w \rightarrow launch cluster w/
- iv) Paste the queries & submit
- v) Now click on that & Phylogenetic tree will be displayed.

Method 2:- Simple phylogeny

- \rightarrow logon to cluster w/ & perform multiple sequence alignment for minimum 6 sequences & retrieve the result & copy.
- \rightarrow logon to www.ebi.ac.uk/tools/phylogeny.
- \rightarrow Paste the multiple sequence alignment result already copied the tree previous step.
- \rightarrow Set the tree parameter as NEXUS if option not available set it to default.
- \rightarrow Click on Submit & retrieve result as phylogram
- \rightarrow Interpret the obtained result.

Result

Method 1:-

a phylogenetic analysis for the given 6 sequence is done with the CLUSTAL W tool & result obtained.

we can view of both the cladogram as well as phylogram of obtained tree. Tree can be interpreted and in terms of distances & relationships.

Name of Experiment.....

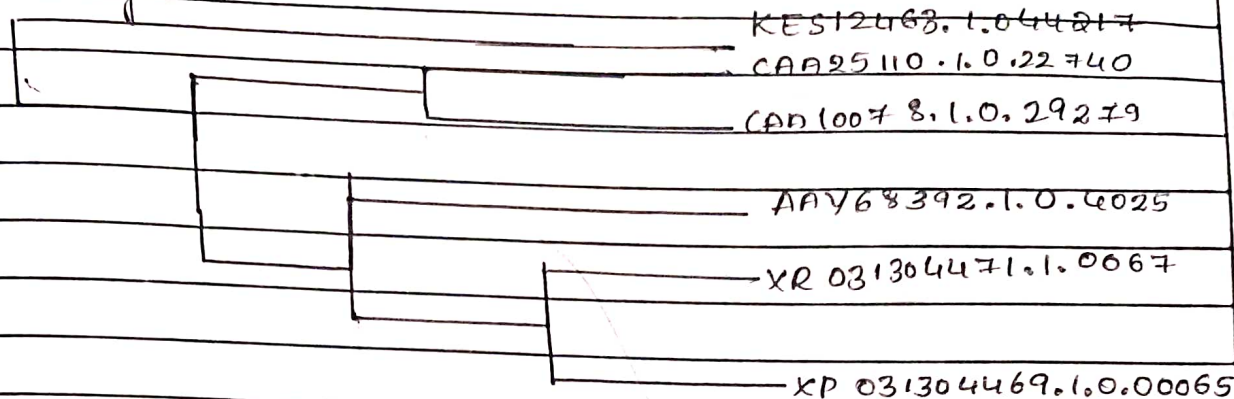
Date..... 20/12/2023

Experiment No.....

Experiment Result.....

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as Phylogenetic tree of sequence is given below
Cladogram



MMKSFELVVITLALT

- MKVFIFT - CLLAVA

- MKVLILA - CLVALA

- MRLILIT - CLVAVA

- MKLIT - CLVAVA

→ gap

→ conserved

sequence

→ Substitution

→ mismatch

Method 2 Simple phylogeny

Simple phylogeny is a tool to perform basic phylogenetic analysis on multiple sequence alignment. It aims to model the substitution that have occurred over evolutionary time & derive & represent the evolutionary relationship b/w sequences.

Results of phylogeny is explained as followed.

as Distance connection can be applied.

as Neighbourhood joining algorithm is employed phylogenetic tree in graphical form is shown below.

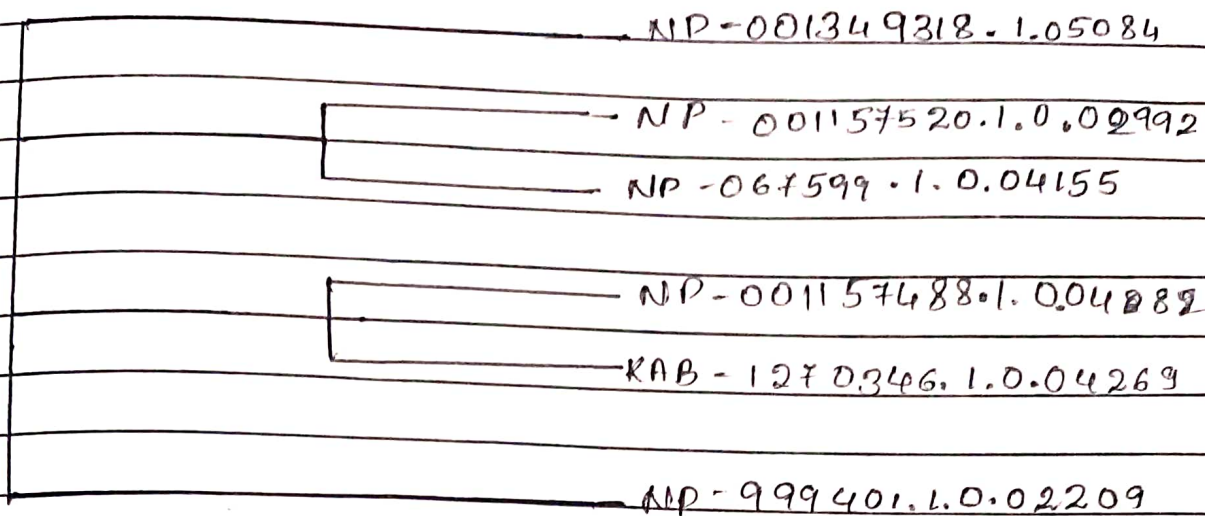
Name of Experiment.....

Date..... 20/12/2023

Experiment No.....

Experiment Result.....

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Discussion:-

Root:- Represents the ancestral lineage.

Tips:- Represents descendent of that ancestor.

Node:- A point of which 2 or more branches diverge indicating point of separation & occurrence of speciation.

Branch:- Linker within tree

Clad:- It is grouping that includes a common ancestor & all the descendent of that ancestor. Clads are nested within one another form nested hierarchy movement forward indicates the movement of time.

9/11/23
P-10
C-10
V-10
R-20
50

Method 01

Clustalw

myoglobin

Myoglobin [Camelus dromedarius]

GenBank: KAB1270346.1

[GenPept Identical Proteins Graphics](#)

>KAB1270346.1 Myoglobin [Camelus dromedarius]

MGLSDGEWQLVLNVWGKVEADVAGHGQEVLRSHVWGECPVLPALLSGVPRALSESHQKRLRKDSRDDDDGD
DGDGDNENDDGGDGGDDGGDDGGDNDDDDGGDGGDDGGDDDRDDSDGGGGGDHADDENGNDGDDDDGHPE
TLEKFDKFKHLKTADMKASEDLKKHGNTVLTALGGILKKKGHHEAELKPLAQSHATKHKIPVKYLEFIS
DAI IHVLQSKHPGDFGADAQAAMNKALELFRNDMAAKYKELGFGQ

myoglobin [Equus caballus]

NCBI Reference Sequence: NP_001157488.1

[GenPept Identical Proteins Graphics](#)

>NP_001157488.1 myoglobin [Equus caballus]

MGLSDGEWQQVLNVWGKVEADIAGHGQEVLRIRLFTGHPETLEKFDKFKHLKTEAMKASEDLKKHGTVV
TALGGILKKKGHHEAELKPLAQSHATKHKIPVKYLEFISDAI IHVLHSHKHPGDFGADAQGAMTKALELFR
NDIAAKYKELGFGQ

myoglobin [Mus musculus]

NCBI Reference Sequence: NP_001157520.1

[GenPept Identical Proteins Graphics](#)

>NP_001157520.1 myoglobin [Mus musculus]

MGLSDGEWQLVLNVWGKVEADLAGHGQEVLRIGLFTKHPETLDKFDKFKNLKSEEDMKGSEDLKKHGCTVL
TALGTILKKKGQHAAEIQPLAQSHATKHKIPVKYLEFISEIIIEVLKKRHSGDFGADAQGAMSKALELFR
NDIAAKYKELGFGQ

Service Announcement

We will be retiring these pages on the **31st of January, 2024**. Please visit our new website at www.ebi.ac.uk/jdispatcher and share your feedback with us!

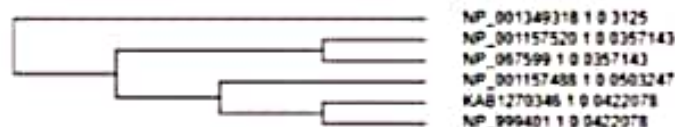
Results for job clustalo-l20231220-085834-0250-18948874-p1m

[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)

[Download Guide Tree Data](#)

Phylogram

Branch length: ☒ Clustogram ☐ Real



Guide Tree

```
|
| NP_001349318 & 0.3125
|
|
| NP_001157520 & 0.3357143
|
| NP_067599 & 0.3357143
| & 0.3357143
|
| NP_001157488 & 0.3503247
|
|
| KAB1270346 & 0.3422078
|
| NP_999401 & 0.3422078
| & 0.3422078
| & 0.3422078
| & 0.3422078
|
```

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Results for job clustalo-l20231220-085834-0250-18948874-p1m

[Alignments](#) [Result Summary](#) [Guide Tree](#) [Phylogenetic Tree](#) [Results Viewers](#) [Submission Details](#)

[Download Phylogenetic Tree Data](#)

Phylogenetic Tree

This is a Neighbour-joining tree without distance corrections

Branch length: ☒ Clustogram ☐ Real



Tree Data

```
|
| NP_001349318 & 0.30804
|
| NP_001157520 & 0.32962
| NP_067599 & 0.34151
| & 0.34151
|
| NP_001157488 & 0.34822
| KAB1270346 & 0.34208
| & 0.34208
|
| NP_999401 & 0.32208
```

Phylogeny

 Feedback

Tools > Phylogeny

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Simple Phylogeny

Phylogenetic tree generation using the ClustalW2 program

 [Launch Simple Phylogeny](#)

The tools described on this page are provided using [Search and sequence analysis tools services from EMBL-EBI in 2022](#)

Please read the provided Help & Documentation and FAQs before seeking help from our support staff. If you have any feedback or encountered any issues please let us know via [EMBL-EBI Support](#). If you plan to use these services during a course please [contact us](#). Read our [Privacy Notice](#) if you are concerned with your privacy and how we handle personal information.

Simple Phylogeny

This tool provides access to phylogenetic tree generation methods from the ClustalW2 package. Please note this is NOT a multiple sequence alignment tool. To perform a multiple sequence alignment please use one of our MSA tools.

STEP 1 - Enter your multiple sequence alignment

Enter or paste a multiple sequence alignment in any supported format.

CLUSTAL O(1.2.4) multiple sequence alignment

```
NP_001349318.1  ---MADHDLVLKQWGAVEADYAANGGEVLNRLF  30
NP_001157520.1  MQLSDGEWQVLVNVWGKVEADLAGHGQEVLIQLF  34
NP_067599.1     MQLSDGEWQVLVNVWGKVEADLAGHGQEVLIQLF  34
NP_001157488.1  MQLSDGEWQVLVNVWGKVEADLAGHGQEVLIQLF  34
KAB1270346.1    MQLSDGEWQVLVNVWGKVEADLAGHGQEVLIQLF  34
NP_999401.1     MQLSDGEWQVLVNVWGKVEADLAGHGQEVLIQLF  34
```

Or, upload a file to be chosen

[Use a example sequence](#) | [Clear sequence](#) | [See more example inputs](#)

STEP 2 - Set your Phylogeny options

TREE FORMAT	DISTANCE CORRECTION	EXCLUDE GAPS	CLUSTERING METHOD	P1 M
Default	off	off	Neighbour-joining	off

STEP 3 - Submit your job

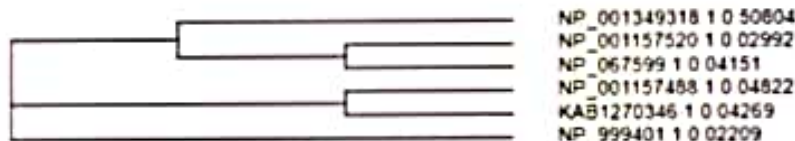
☐ Be notified by email (Tick this box if you want to be notified by email when the results are available)

Results for job simple_phylogeny-l20231220-095325-0486-86358151-p1m

[Phylogenetic Tree](#) [Result Summary](#) [Submission Details](#)

Phylogram

Branch length ☒ Cladogram ☐ Real



Phylogenetic Tree

[View Phylogenetic Tree File](#)

```
{
  NP_001349318.1 0.50604,
  {
    NP_001157520.1 0.02992,
    NP_067599.1 0.04151,
    {
      NP_001157488.1 0.04822,
      {
        KAB1270346.1 0.04269,
        NP_999401.1 0.02209
      }
    }
  }
}
```