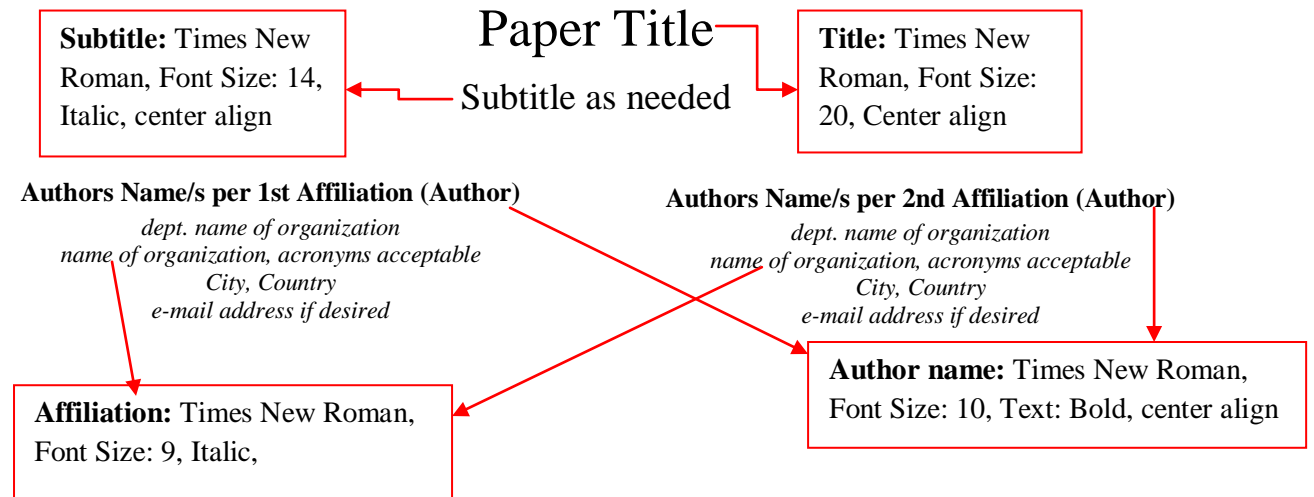


# International Journal of Computational Intelligence and Informatics

## Author Guidelines for Manuscript Preparation

### Front Page Format



### Abstract Format

**Abstract-**This electronic document is a “IJCI” template. The various components of your paper [title, text, heads, etc.] are already defined on the style sheet, as illustrated by the portions given in this document.

Keywords-component, formatting, style, styling

**Keywords:** Times New Roman, Size: 10, Justified

**Abstract:** Times New Roman, Font Size: 10, Bold, Justified

## Text Format

**Heading Level 1**  
(Times New Roman, Font Size 12, center align, Uppercase, Numbering should be 1, 2...)

**Heading Level 2**  
(Times New Roman, Font Size: 11, Left align, Sentence case, Numbering should be 2.1, 2.2 ...)

**Heading Level 3**  
(Times New Roman, Font Size: 10, Left align, Italic text, Sentence case, Numbering should be 2.2.1, 2.2.2 ...)

**Body Text**  
(Times New Roman, Font Size: 10, justify align)

**Bulletin: Solid circle**

**Numbered list (small case alphabet a), b),....**

1. INTRODUCTION

2. EASE OF USE

2.1. Selecting a Template

2.2. Abbreviations and Acronyms

2.2.1. *Units*

2.2.2. *Authors and Affiliations*

## Table Format

Table numbering as **Table 1, Table 2,...**

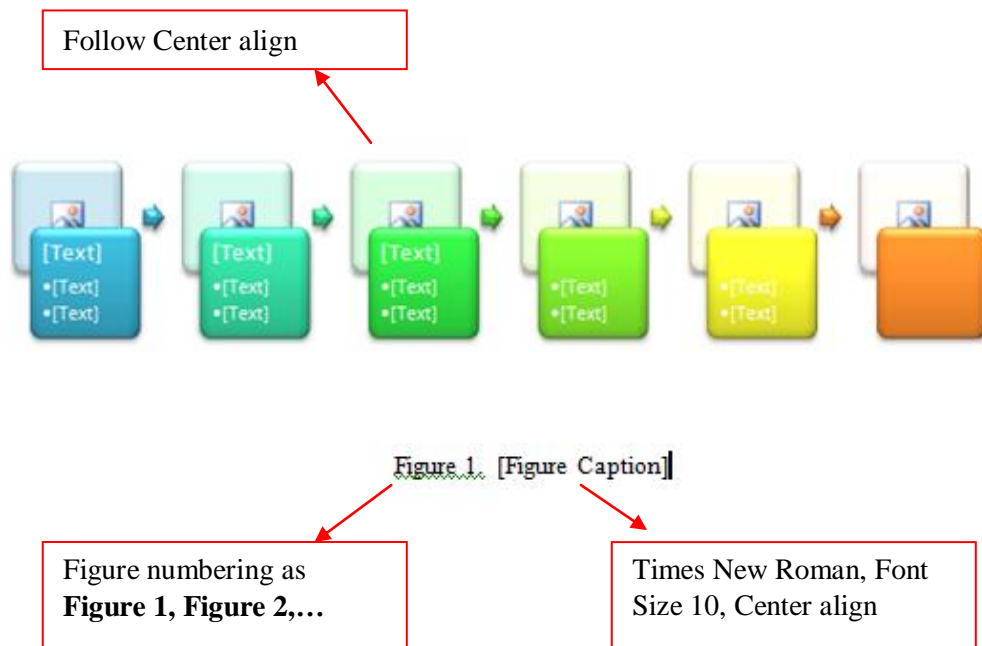
Table Caption: Center align, Font size 10, Times New Roman

Table: 1 [Table Caption]

Column 1	Column2	Column3	Column4	Column5
Value	Value	Value	Value	Value
Value	Value	Value	Value	Value
Value	Value	Value	Value	Value
Value	Value	Value	Value	Value
Value	Value	Value	Value	Value

Center align, Use 'Auto fit to Window'

## Figure Format



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## Figure and Table citation

These significant protein complexes of various organisms are discovered using the computational techniques. Protein complexes are an assembly of proteins that build up a network that commonly spans a dense Sub-network of proteins in a protein interaction network. This would not help much in detecting the functionalities of the gene. Protein sequences and the DNA/mRNA sequence that codes for the protein are shown in the Figure 1. The four basic amino acid combines to form the protein that is shown. The 20 different amino acids that are present in the protein sequence along with their chemical name are listed in the Table 1.

As the protein sequences are in the form of long amino acid sequence, the repeated protein groups are not found manually. The protein structure is of many types denoted as motifs. The protein structure is of many types secondary, tertiary and quaternary in nature. The secondary structures are used in this work. The structural similarity of the detected protein complexes is used to extract the homologous complexes. The functionality of proteins is discovered by various methods like sequence-motif based method, homology based methods, and structure based methods. The motifs can be extracted from the clusters that are generated by various computational techniques.

Refer figure in text as 'Figure 1'

Refer Table in text as 'Table 1'

## Equation Format

**Distance Measure**

The city block distance (Y.Vincent, C.Bernard, a.E, Thangavel.K, Chitralega.M, & Chandrasekhar.T, 2012) is suitable for as 'equation 1' measure deals with n-dimensional data element, it is suitable for this type of sequence profiles. The distance measure is calculated using the equation 4.

$$\text{distance} = \sum_{i=1}^R \sum_{j=1}^A V_k(i,j) - V_c(i,j) \quad (4)$$

where R is the number of residues and A is the number of amino acids (20). The  $V_k(i,j)$  is the value of the profile matrix in row i and column j of segment k. The  $V_c(i,j)$  is the value at row i and column j of the centroid of the cluster c.

Use Equation Editor, Font Size 12, Left Align

Refer equation in text as 'equation 1'

Define Equation terms as paragraph

Follow equation number as (1), (2), (3),.....

## Reference Format

Follow **APA style** in Microsoft Word. Steps to follow:

1. To add your references in the word document

Choose 'Reference tab' → 'Citation & Bibliography' → 'Manage sources'

The screenshot shows the 'Source Manager' dialog box in Microsoft Word. The 'Sources available in: Master List' section contains one entry: 'Wei Fang, V. S. Shenq, XueZhi Wen, and Wubin Pan; Meteorological Data Analysis Using MapReduce'. The 'Current List' section is empty. A red arrow points to the 'New...' button, with a callout box containing the text 'Choose 'New' to add your references'. The 'Preview (APA):' section shows the citation: 'Citation: (Wei Fang, 2014)' and the full bibliography entry: 'Wei Fang, V. S. (2014). Meteorological Data Analysis Using MapReduce. *The Scientific World Journal*, 10.'

2. Add the details of each reference in this dialog to create a source in word document.

Create Source

Type of Source: Journal Article Language: Default

Bibliography Fields for APA

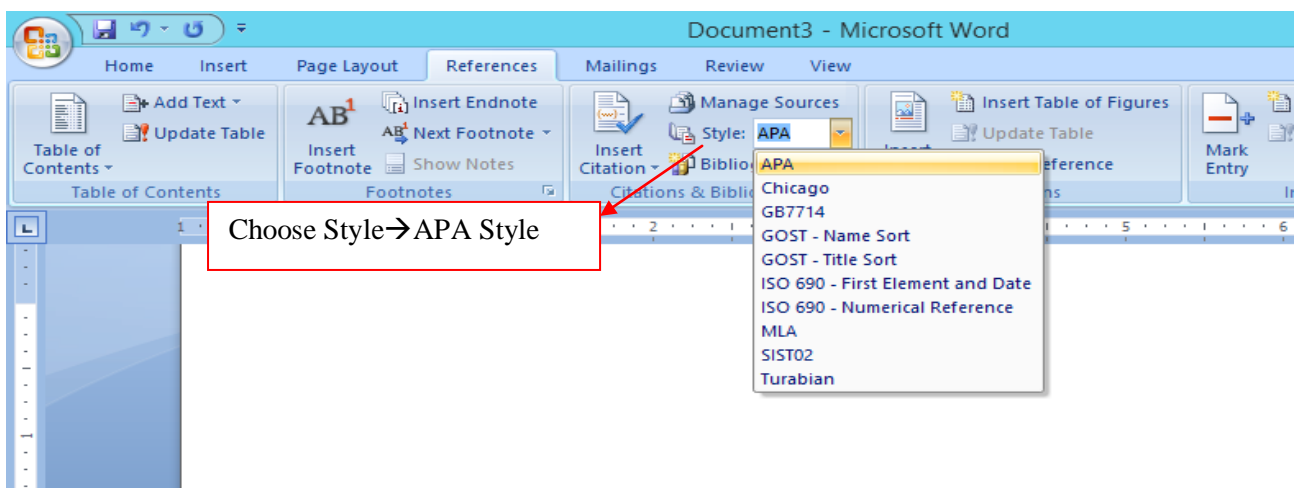
- \* Author [ ] Edit
- Corporate Author [ ]
- \* Title [ ]
- \* Journal Name [ ]
- City [ ]
- \* Year [ ]
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- Day [ ]
- \* Pages [ ]
- Editor [ ] Edit
- Publisher [ ]

Show All Bibliography Fields \* Recommended Field

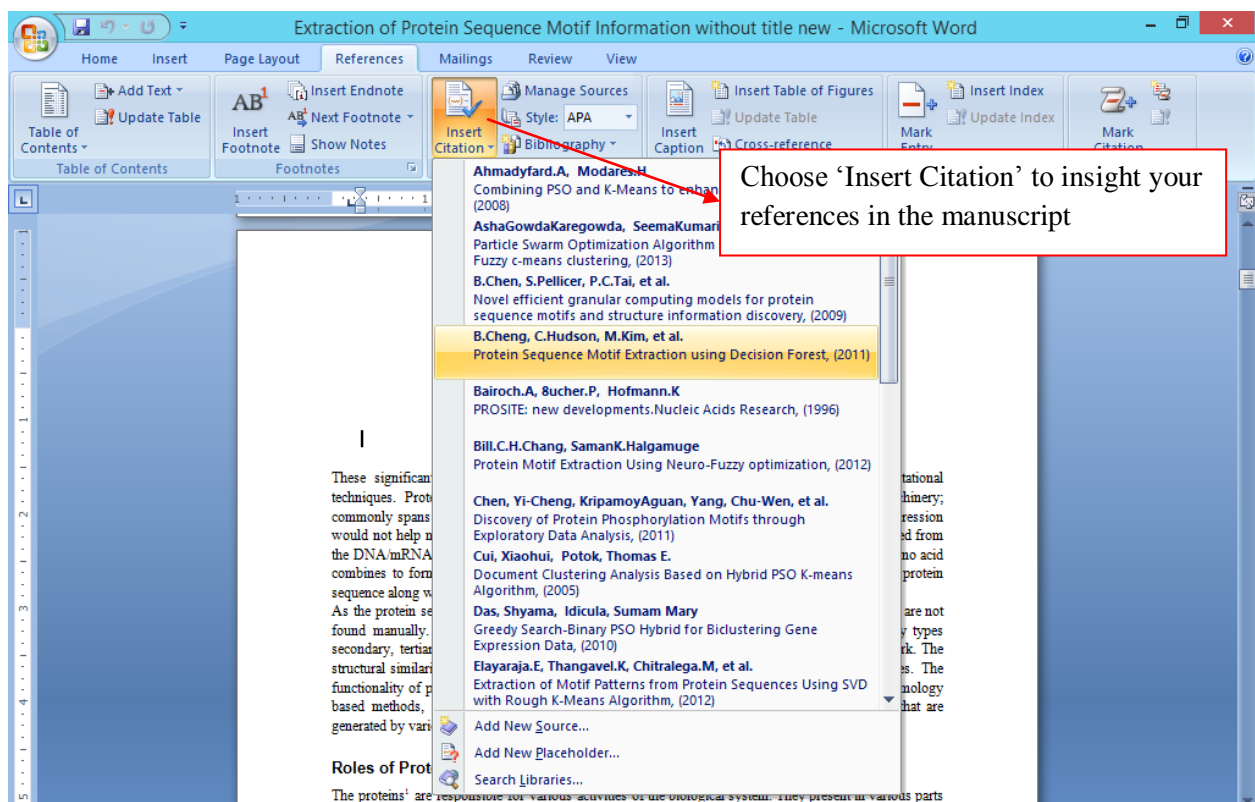
Tag name: Placeholder 1

OK Cancel

3. After adding all the references into 'Manage Source'. Choose Reference Style (Strictly follow APA style)



4. Insert in-text citation of your references in the document. (Place the cursor at the required place where to insert citation)



## Biclustering

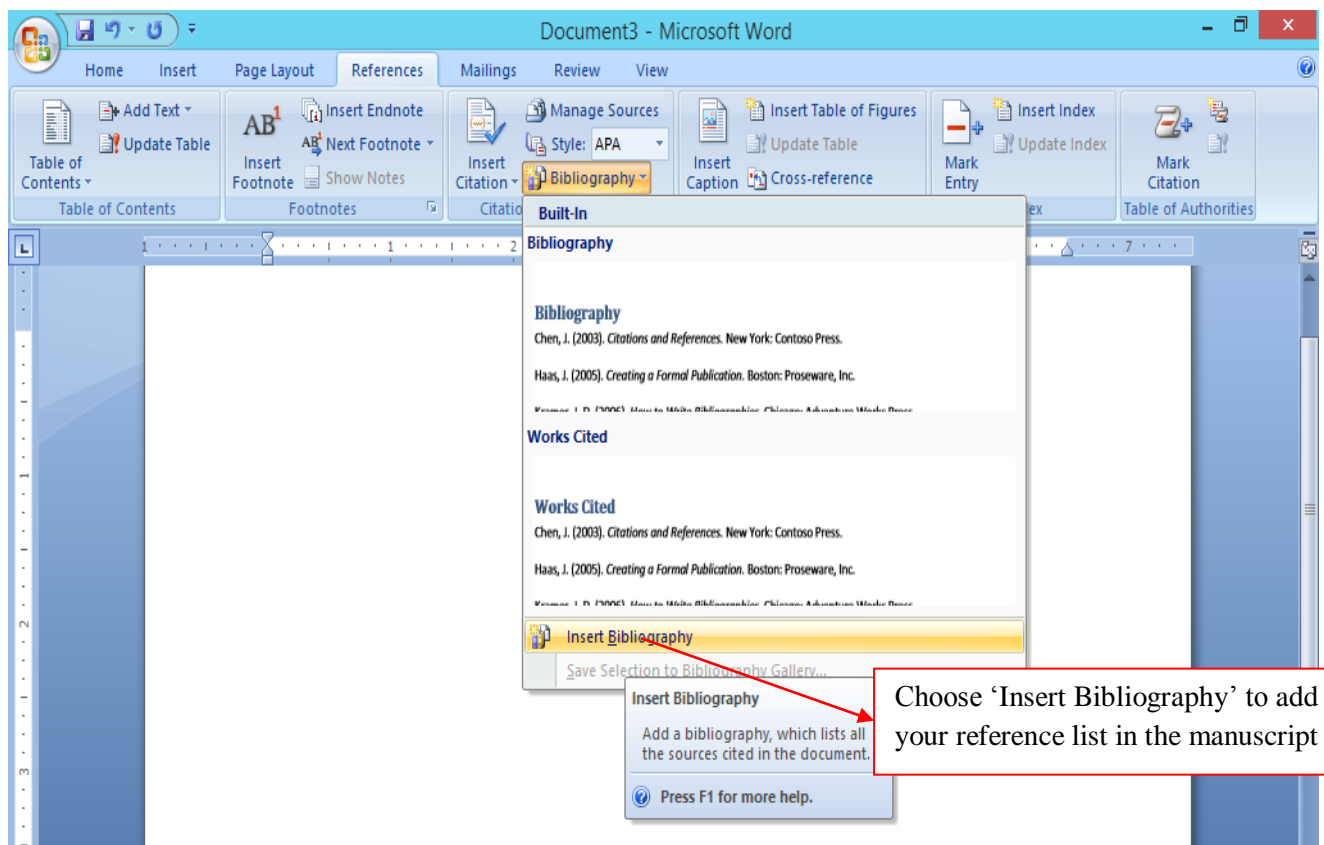
Biclustering (Madeira.S.C & Oliveira.A.L., 2004) is another data mining technique. It is also named as Co-Clustering, Two Way Clustering. It generates biclusters of different sizes and characteristics. The process of grouping data based on both the rows (segments) and columns (amino acids). Biclustering is useful for Bioinformatics and many other research areas. It is NP-Complete.

The major difference (PavelBerkhin, 2002)(Madeira.S.C & Oliveira.A.L., 2004) between the clustering and biclustering are as follows.

1. Clustering applied to any one of the dimensions of the dataset, biclustering applied to both dimensions.
2. Clustering derives the global model, biclustering derives the local model.
3. Biclustering groups more similar patterns than the clustering process.

Citations will be inserted like this in your document

5. At the Reference part of your manuscript insert entire reference list as follows.



List of references will be added as follows

**REFERENCES|**

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References will be added like this