Tabular Column :-

Matrix	BLOSUM 62		
Gap open penalty	1	10	100
Identity	55.6%	54.9%	54.9%
Similarity	57.2%	56.1%	56.1%
Gaps	40.9%	39.6%	39.6%
Score	700.5	676.0	586.0
Length	256	255	255

Matrix	BLOSUM 45		
Gap open penalty	1	10	100
Identity	55.6%	55.3%	54.9%
Similarity	58.0%	57.6%	56.5%
Gaps	40.9%	39.6%	39.6%
Score	844.5	817.5	724.0
Length	257	255	255

Matrix	BLOSUM 50		
Gap open penalty	1	10	100
Identity	55.6%	55.3%	54.9%
Similarity	58.0%	57.6%	56.5%
Gaps	40.9%	39.6%	39.6%
Score	906.5	879.5	787.0
Length	257	255	255

Experiment — 1

Pair wise comparision of sequences
Analysis of parameters affecting alignment.

Aim:- To carry out pair wise sequence alignment of the given sequence using EMBOSS/ JEMBOSS tool at EBT.

Introduction:-
Pair wise alignment is used to find regions of similarity that may indicate structural or evolutionary release relationships between two biological sequences. EMBOSS needle rode two input sequence and wait their optimal global sequences alignment to file. It uses the Needleman wrench alignment algorithm to find the optimum alignment of two sequences along their entire length.
EMBOSS water uses the smith-waterman algorithm to the calculate the local alignment of a sequence to one of more others sequence both of these tools can be used in the following contexts protein sequence & nucleotide sequence.

Query :-
Protein :- Myoglobin.

URL:- www. ebi. ac. uk/emboss/align.

Matrix	PAM 70		
Gap open penalty	1	10	100
Identity	55.4%	55.3%	54.9%
Similarity	57.4%	57.3%	56.5%
Gaps	41.5%	39.6%	39.6%
Score	873.5	844.5	746.0
Length	257	255	255

Matrix	PAM 250		
Gap open penalty	1	10	100
Identity	55.3%	55.3%	54.9%
Similarity	58.4%	58.0%	56.9%
Gaps	40.9%	39.6%	39.6%
Score	662.5	642.5	548.0
Length	25	255	255

Matrix	PAM 350		
Gap open penalty	1	10	100
Identity	55.3%	55.3%	54.9%
Similarity	59.6%	59.6%	58.4%
Gaps	39.6%	39.6%	39.6%
Score	762.5	744.5	647.0
Length	255	255	258

Procedure:-

1) Login to NCBI and retrive protein sequence in FASTA formed.
2) The EMBOSS tool was accessed using URL https://www.ebr.ac.uk/emboss/align.
3) This will lead to EMBOSS tool where the option is provided for local & global alignment
4) The desired alignment option needle was selected for carrying out global alignment
5) The selected sequence in FASTA format were pasted in the windows provided.
6) The alignment was run to get the result
7) The alignment was done using PAM & BLOSUM matrices & the scores were reported.
8) The alignment was run with two Combinations of gap open & extension penalties.

Observation :-

A pair with alignment is carried out with the help of EMBOSS & Needle & 'wunch algorithm.

Protein sequence (general examples):-

```
EMBOSS   00131 LALKGQ TGG OVNIVEMDAAPGG VU--NO
                1.1: 1.: : 1.          ..1 111 .. 1:
EMBOSS  0015  LVLQGI SEG ------ AQAAPGGGAPAVE
                  ↓            ↓        ↓              ↓
               Match       Mismatch  gap        Substitution
```

Result:-

In general for closely related sequences PAM of lower order and BLOSUM of higher order is followed and the reverse for higher divergent sequence.

This is confirmed by the results obtained for alignment using EMBOSS tool and varying the parameters.

P- 10

C - 10

V - 10

P - 18

A8