



# CLASSIFICATION OF SPECIES OF EBOLA-VIRUS, BASED ON THE PHYSICO-CHEMICAL-PROPERTIES, CONSERVED AMINO-ACIDS, GENE-STRUCTURAL INFORMATION AND INTERPRETING ITS SIGNIFICANCE

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**Abstract— Ebola Infection malady ia an uncommon and Destructive ailment which for the most part two people And non human primates, for example monkeys, gorillas, Chimpanzees. Among the five types of species i.e; Zaire, Sudan, Taiforest, Bundibugyo impacts the people and Reston Ebola virus known to cause disease in non human Primates and pigs. This Ebola infection was first found in 1976 close to ebola water way in majority rule republic Of congo. For Ebola virus sickness casuality rate is 90%. 318 individuals tainted and 280 passings are brought About by this infection with death pace of 88%.**

## I. OBJECTIVES

The extensive target of the subsequent module is that to create a compact, data rich outline of grouping information., illustrate the disparity between a gathering of sequences, Usage of arrangements as models to test hypohthesis, as well as to know whether this model of occasions precisely reflect known organic proof. The primary goal of the third module is to comprehend the essential ideas in quality finding, for example, relationship of protein and nucleotide groupings/exons/introns/coding arrangements/open perusing outlines/agreement properties of exon-intron fringes. Novel highlights of the program incorporate the ability to anticipate different qualities in a succession, to manage fractional just as complete qualities, and to foresee steady arrangements of qualities happening on either or both DNA strands. In the enormous scale investigation of gene, the regular procedure is totally inactivate every quality or over express it. In each case coming about phenotype may not be instructive. The loss of numerous proteins is deadly and this reveals to us that protein is fundamental however donot determine what protein really does. After forecast of quality structure, related with this protein we can research its Structure, Function, diseases, mutations and by utilizing this data we can fix numerous diseases. It utilizes factual example recognizable proof and succession similitude comparision, in which first technique utilizes every single imaginable ways to deal with concentrate the quality structure which incorporates advertiser region, start and end arrangements of intron and exon. As the closeness depends on the

evolution, either our grouping is homologous or not, this procedure depends on the comparability which exploit on the way that if the succession is similar, it will have a similar capacity.

## II. METHODOLOGY

ProtParam registers different physico-substance properties that can be reasoned from a protein succession. No extra data is required about the protein under thought. The protein can either be indicated as a Swiss-Prot/TrEMBL promotion number or ID, or in type of a crude arrangement. Blank area and numbers are disregarded. In the event that you give the promotion number of a Swiss-Prot/TrEMBL passage, you will be incited with a delegate page that enables you to choose the part of the succession on which you might want to play out the investigation. The decision incorporates a choice of develop chains or peptides and spaces from the Swiss-Prot highlight table (which can be picked by tapping on the situations), just as the likelihood to enter start and end position in two boxes.

## III. EXTINCTION COEFFICIENT

The Extinction coefficient shows how much light a protein assimilates at a specific wavelength. It is helpful to have an estimation of this coefficient for following a protein which a spectrophotometer when filtering it. It is conceivable to assess the molar Extinction coefficient of a protein from information of its amino corrosive creation. From the molar extinction coefficient of tyrosine, tryptophan, and cystine (cysteine doesn't ingest considerably at wavelengths >260 nm, while cystine does) at a given wavelength, the termination coefficient of a denatured protein can be figured. Two tables are delivered by ProtParam, the first demonstrating the processed qualities dependent on the supposition that all cysteine deposits show up as half cystines, and the subsequent one accepting that no cysteine shows up as half cystine. Formula for calculating Extinction coefficient is given below.

$$E(\text{Prot}) = \text{Numb}(\text{Tyr}) * \text{Ext}(\text{Tyr}) + \text{Numb}(\text{Trp}) * \text{Ext}(\text{Trp}) + \text{Numb}(\text{Cystine}) * \text{Ext}(\text{Cystine})$$

$$\text{Ext}(\text{Tyr}) = 1490,$$

$$\text{Ext}(\text{Trp}) = 5500,$$

$$\text{Ext}(\text{Cystine}) = 125;$$



#### IV. ALIPHATIC INDEX

The Aliphatic list of a protein is characterized as the relative volume involved by aliphatic side chains (alanine, valine, isoleucine, and leucine). It might be viewed as a positive factor for the expansion of thermostability of globular proteins

$$\text{Aliphatic index} = X(\text{Ala}) + a * X(\text{Val}) + b * (X(\text{Ile}) + X(\text{Leu}))$$

Where,

X(Ala) = Mole percent of Alanine

X(Val) = Mole percent of valine

X(Ile) = Mole percent of Isoleucine

X(Leu) = Mole percent of leucine

#### V. GRAND AVERAGE OF HYDROPHATICITY

The Grand Average of hydrophathy (GRAVY) esteem for a peptide or protein is determined as the entirety of hydrophathy estimations of all the amino acids, isolated by the number of deposits in the succession

#### VI. INVIVO HALF-LIFE

The half-life is an expectation of the time it takes for half of the measure of protein in a cell to vanish after its blend in the cell. The expectation is given for three creatures (human, yeast, and E. coli), yet it is conceivable to extrapolate the outcome to comparative living beings. ProtParam gauges the half-life by taking a gander at the N-terminal amino corrosive of the grouping under investigation.

#### VII. INSTABILITY INDEX

```
# @export instaIndex
# @title Compute the instability index of a protein
sequence
# @description This function calculates the instability
index proposed by Guruprasad (1990). This index predicts
the stability of a protein based on its amino acid
composition, a protein whose instability index is smaller
than 40 is predicted as stable, a value above 40 predicts that
the protein may be unstable.
# @param seq An amino-acids sequence
# @return The computed instability index for a given
amino-acids sequence
# @references Guruprasad K, Reddy BV, Pandit MW
(1990). "Correlation between stability of a protein and its
dipeptide composition: a novel approach for predicting in
vivo stability of a protein from its primary sequence".
Protein Eng. 4 (2): 155 - 61. doi:10.1093/protein/4.2.155
# @examples
# # COMPARED TO ExPASy INSTAINDEX
# # http://web.expasy.org/protparam/
# # SEQUENCE:
QWGRRCCGWGPGRRYCVRWC
# # The instability index (II) is computed to be
83.68
#
# instaIndex(seq
"QWGRRCCGWGPGRRYCVRWC")
# # [1] 83.68
```

```
#
instaIndex <- function(seq) {
# Setting the Guruprasad scale
guruprasad <-
c(
WW = 1,
WC = 1,
WM = 24.68,
WH = 24.68,
WY = 1,
WF = 1,
WQ = 1,
WN = 13.34,
WI = 1,
WR = 1,
WD = 1,
WP = 1,
WT = -14.03,
WK = 1,
WE = 1,
WV = -7.49,
WS = 1,
WG = -9.37,
WA = -14.03,
WL = 13.34,
CW = 24.68,
CC = 1,
CM = 33.6,
CH = 33.6,
CY = 1,
CF = 1,
CQ = -6.54,
CN = 1,
CI = 1,
CR = 1,
CD = 20.26,
CP = 20.26,
CT = 33.6,
CK = 1,
CE = 1,
CV = -6.54,
CS = 1,
CG = 1,
CA = 1,
CL = 20.26,
MW = 1,
MC = 1,
MM = -1.88,
MH = 58.28,
MY = 24.68,
MF = 1,
MQ = -6.54,
MN = 1,
MI = 1,
MR = -6.54,
MD = 1,
MP = 44.94,
MT = -1.88,
MK = 1,
ME = 1,
MV = 1,
```



MS = 44.94,  
MG = 1,  
MA = 13.34,  
ML = 1,  
HW = -1.88,  
HC = 1,  
HM = 1,  
HH = 1,  
HY = 44.94,  
HF = -9.37,  
HQ = 1,  
HN = 24.68,  
HI = 44.94,  
HR = 1,  
HD = 1,  
HP = -1.88,  
HT = -6.54,  
HK = 24.68,  
HE = 1,  
HV = 1,  
HS = 1,  
HG = -9.37,  
HA = 1,  
HL = 1,  
YW = -9.37,  
YC = 1,  
YM = 44.94,  
YH = 13.34,  
YY = 13.34,  
YF = 1,  
YQ = 1,  
YN = 1,  
YI = 1,  
YR = -15.91,  
YD = 24.68,  
YP = 13.34,  
YT = -7.49,  
YK = 1,  
YE = -6.54,  
YV = 1,  
YS = 1,  
YG = -7.49,  
YA = 24.68,  
YL = 1,  
FW = 1,  
FC = 1,  
FM = 1,  
FH = 1,  
FY = 33.6,  
FF = 1,  
FQ = 1,  
FN = 1,  
FI = 1,  
FR = 1,  
FD = 13.34,  
FP = 20.26,  
FT = 1,  
FK = -14.03,  
FE = 1,  
FV = 1,  
FS = 1,

FG = 1,  
FA = 1,  
FL = 1,  
QW = 1,  
QC = -6.54,  
QM = 1,  
QH = 1,  
QY = -6.54,  
QF = -6.54,  
QQ = 20.26,  
QN = 1,  
QI = 1,  
QR = 1,  
QD = 20.26,  
QP = 20.26,  
QT = 1,  
QK = 1,  
QE = 20.26,  
QV = -6.54,  
QS = 44.94,  
QG = 1,  
QA = 1,  
QL = 1,  
NW = -9.37,  
NC = -1.88,  
NM = 1,  
NH = 1,  
NY = 1,  
NF = -14.03,  
NQ = -6.54,  
NN = 1,  
NI = 44.94,  
NR = 1,  
ND = 1,  
NP = -1.88,  
NT = -7.49,  
NK = 24.68,  
NE = 1,  
NV = 1,  
NS = 1,  
NG = -14.03,  
NL = 1,  
IW = 1,  
IC = 1,  
IM = 1,  
IH = 13.34,  
IY = 1,  
IF = 1,  
IQ = 1,  
IN = 1,  
II = 1,  
IR = 1,  
ID = 1,  
IP = -1.88,  
IT = 1,  
IK = -7.49,  
IE = 44.94,  
IV = -7.49,  
IS = 1,  
IG = 1,  
IA = 1,



IL = 20.26,  
RW = 58.28,  
RC = 1,  
RM = 1,  
RH = 20.26,  
RY = -6.54,  
RF = 1,  
RQ = 20.26,  
RN = 13.34,  
RI = 1,  
RR = 58.28,  
RD = 1,  
RP = 20.26,  
RT = 1,  
RK = 1,  
RE = 1,  
RV = 1,  
RS = 44.94,  
RG = -7.49,  
RA = 1,  
RL = 1,  
DW = 1,  
DC = 1,  
DM = 1,  
DH = 1,  
DY = 1,  
DF = -6.54,  
DQ = 1,  
DN = 1,  
DI = 1,  
DR = -6.54,  
DD = 1,  
DP = 1,  
DT = -14.03,  
DK = -7.49,  
DE = 1,  
DV = 1,  
DS = 20.26,  
DG = 1,  
DA = 1,  
DL = 1,  
PW = -1.88,  
PC = -6.54,  
PM = -6.54,  
PH = 1,  
PY = 1,  
PF = 20.26,  
PQ = 20.26,  
PN = 1,  
PI = 1,  
PR = -6.54,  
PD = -6.54,  
PP = 20.26,  
PT = 1,  
PK = 1,  
PE = 18.38,  
PV = 20.26,  
PS = 20.26,  
PG = 1,  
PA = 20.26,  
PL = 1,

TW = -14.03,  
TC = 1,  
TM = 1,  
TH = 1,  
TY = 1,  
TF = 13.34,  
TQ = -6.54,  
TN = -14.03,  
TI = 1,  
TR = 1,  
TD = 1,  
TP = 1,  
TT = 1,  
TK = 1,  
TE = 20.26,  
TV = 1,  
TS = 1,  
TG = -7.49,  
TA = 1,  
TL = 1,  
KW = 1,  
KC = 1,  
KM = 33.6,  
KH = 1,  
KY = 1,  
KF = 1,  
KQ = 24.68,  
KN = 1,  
KI = -7.49,  
KR = 33.6,  
KD = 1,  
KP = -6.54,  
KT = 1,  
KK = 1,  
KE = 1,  
KV = -7.49,  
KS = 1,  
KG = -7.49,  
KA = 1,  
KL = -7.49,  
EW = -14.03,  
EC = 44.94,  
EM = 1,  
EH = -6.54,  
EY = 1,  
EF = 1,  
EQ = 20.26,  
EN = 1,  
EI = 20.26,  
ER = 1,  
ED = 20.26,  
EP = 20.26,  
ET = 1,  
EK = 1,  
EE = 33.6,  
EV = 1,  
ES = 20.26,  
EG = 1,  
EA = 1,  
EL = 1,  
VW = 1,



VC = 1,  
 VM = 1,  
 VH = 1,  
 VY = -6.54,  
 VF = 1,  
 VQ = 1,  
 VN = 1,  
 VI = 1,  
 VR = 1,  
 VD = -14.03,  
 VP = 20.26,  
 VT = -7.49,  
 VK = -1.88,  
 VE = 1,  
 VV = 1,  
 VS = 1,  
 VG = -7.49,  
 VA = 1,  
 VL = 1,  
 SW = 1,  
 SC = 33.6,  
 SM = 1,  
 SH = 1,  
 SY = 1,  
 SF = 1,  
 SQ = 20.26,  
 SN = 1,  
 SI = 1,  
 SR = 20.26,  
 SD = 1,  
 SP = 44.94,  
 ST = 1,  
 SK = 1,  
 SE = 20.26,  
 SV = 1,  
 SS = 20.26,  
 SG = 1,  
 SA = 1,  
 SL = 1,  
 GW = 13.34,  
 GC = 1,  
 GM = 1,  
 GH = 1,  
 GY = -7.49,  
 GF = 1,  
 GQ = 1,  
 GN = -7.49,  
 GI = -7.49,  
 GR = 1,  
 GD = 1,  
 GP = 1,  
 GT = -7.49,  
 GK = -7.49,  
 GE = -6.54,  
 GV = 1,  
 GS = 1,  
 GG = 13.34,  
 GA = -7.49,  
 GL = 1,  
 AW = 1,  
 AC = 44.94,

AM = 1,  
 AH = -7.49,  
 AY = 1,  
 AF = 1,  
 AQ = 1,  
 AN = 1,  
 AI = 1,  
 AR = 1,  
 AD = -7.49,  
 AP = 20.26,  
 AT = 1,  
 AK = 1,  
 AE = 1,  
 AV = 1,  
 AS = 1,  
 AG = 1,  
 AA = 1,  
 AL = 1,  
 LW = 24.68,  
 LC = 1,  
 LM = 1,  
 LH = 1,  
 LY = 1,  
 LF = 1,  
 LQ = 33.6,  
 LN = 1,  
 LI = 1,  
 LR = 20.26,  
 LD = 1,  
 LP = 20.26,  
 LT = 1,  
 LK = -7.49,  
 LE = 1,  
 LV = 1,  
 LS = 1,  
 LG = 1,  
 LA = 1,  
 LL = 1,  
 'NA' = 1

```
) # Divide the amino acid sequence in dipeptides
aa <- aaCheck(seq)
dp <- lapply(aa, function(aa) {
  apply(embed(aa, 2)[, 2:1], 1, paste0, collapse = "")
})
# Apply the formula:
# (10/L)*sum(DIWV(XiYi+1) for each dipeptide)
# Return the index value rounded to 2 decimals
gp <- lapply(dp, function(dp) {
  (10 / (length(dp) + 1)) * sum(guruprasad[dp], na.rm = TRUE)
})
return(unlist(gp))
```

#### VIII. MULTIPLE SEQUENCE ALIGNMENT

##### MODULE-2

We care about the grouping arrangements in the computational science since it gives scientists helpful data about various viewpoints. For instance, it can educate us regarding the advancement of the living beings, we can see which locales of a quality (or its determined protein) are defenseless to change and which can have one buildup supplanted by another without evolving capacity, we can think about Homologous



qualities and can reveal paralogs and Orthologs qualities that are developmental related. In issues, for example, the development of a transformative tree dependent on arrangement information, or in protein designing, where a different arrangement of related groupings may regularly yield the most supportive data on the plan of another protein, an atomic scholar must think about multiple arrangements all the while. A numerous grouping arrangement (MSA) organizes protein successions into a rectangular exhibit with the objective that buildups in a given section are homologous (gotten from a single situation in a hereditary grouping), superposable (in an unbending nearby basic arrangement) or assume a typical practical job. In spite of the fact that these three criteria are basically comparable for firmly related proteins, arrangement, structure and capacity separate over transformative time and various criteria may bring about various arrangements. Physically refined arrangements keep on being better than simply mechanized techniques; there is in this manner a persistent exertion to improve the organic exactness of MSA apparatuses. Also, the high computational expense of most guileless calculations inspires upgrades in speed and memory utilization to suit the quick increment in accessible succession information. The ClustalW calculation has three Important Phases. They are

Stage I: All sets of arrangements are adjusted independently ascertain a Distance Matrix dependent on the level of befuddles each pair of groupings.

Stage II: The guide tree is developed from the separation framework utilizing the Neighbor Joining calculation.

Stage III: The successions are dynamically adjusted after the guide tree.

#### MODULE-3

Genscan is utilized for anticipating the areas and exon-intron structures of qualities in genomic groupings from an assortment of creatures. This server can acknowledge arrangements up to 1 million base sets (1 Mbp) long. On the off chance that you experience difficulty with the web server or on the off chance that you have an enormous number of groupings to process, demand a nearby duplicate of the program. OMICS\_01494 was created by Chris Burge in the examination gathering of Samuel Karlin, Department of Mathematics, Stanford University. OMICS\_10494 is uninhibitedly accessible for scholastic use. Executables are right now accessible for the accompanying Unix stages: Intel/Linux, Sun/Solaris, Intel/Solaris, SGI/Irix, DEC/Tru64, and IBM/AIX. Distinguishes total exon/intron structures of qualities in genomic DNA. OMICS\_01494 utilizes a homogeneous fifth request Markov model of noncoding areas and a three intermittent (inhomogeneous) fifth request Markov model of coding districts. Highlights of the program incorporate the ability to foresee various qualities in a grouping, to manage halfway just as complete qualities, and to anticipate predictable arrangements of qualities happening on either or both DNA strands

### IX. LITERATURE REVIEW

Ebolavirus has a place with the request Mononegavirales and the family Filoviridae. Its RNA genome encodes the accompanying 9 protein items: Spike glycoprotein (GP), Small secreted glycol-protein, Second secreted Glyco-protein, Nucleoprotein (NP), RNA-subordinate RNA polymerase (L), Membrane-related protein (VP24), Minor nucleoprotein (VP30), Polymerase cofactor (VP35), and Matrix protein (VP40). The GP transcript can be altered, and the quality item can be handled by host protease, offering ascend to 4 elective types of

quality items: GP1,2; GP1,2delta; sGP and ssGP. Host furin can sever the longest item interpreted from altered GP mRNA and create GP1,2, which comprises of 2 peptide chains associated by a disulfide bond, GP1 and GP2. GP1,2 is gathered on the layer of Ebolavirus and intercedes cell passage. GP1,2delta is the handled item after evacuation of the C-terminal transmembrane locale of GP1,2 by host ADAM17. Different results of the GP quality, sGP and ssGP are interpreted from the unedited mRNA and then again altered mRNA, respectively. These items share the N-terminal 295 buildups with GP1,2, however vary in their short tails (69 and 3 deposits, separately). GP1,2delta, sGP and ssGP may keep the killing antibodies from restricting GP1,2 on the infection surface, adding to the insusceptible avoidance of the infection. Notwithstanding filling in as basic parts, the Ebolavirus proteins assume numerous jobs in the infection life cycle. GP intercedes cell section and layer combination between the infection and the host cell. NP encapsidates the genome and shields it from nucleases. VP30 is a translation hostile to eliminator and directs the switch among interpretation and replication. VP35 goes about as a cofactor of the polymerase, and VP40 may likewise assume a job in genome replication and interpretation. VP24 and VP35 take an interest in viral nucleocapsid assembly, and VP40 is basic for infection growing and gathering. What's more, GP, VP24, VP30, VP35 and VP40 associate with different host proteins to finish the viral life cycle and to stifle the host insusceptible reaction. In the present examination, we anticipate the 3D structure and utilitarian locales for Ebolavirus protein areas that are not yet portrayed. Also, we think about successions of Ebolavirus proteins' communicating accomplices from RESTV-safe primates with those from RESTV-powerless monkeys. Raised arrangement difference for GP and VP35's collaboration accomplices recommends that these 2 viral proteins might be in charge of host particularity in RESTV. At last, we think about the protein groupings from various Ebolavirus species to distinguish places that are moderated among human pathogenic species yet extraordinary in non-pathogenic (RESTV-explicit transformations). Mapping of these RESTV-explicit transformations and known utilitarian destinations to the 3D structures uncovers bunches of RESTV-explicit changes on the surfaces of GP, VP35 and VP24. These bunches don't cover with the known useful locales and may propose novel connection destinations with host proteins. Based on this review we decided to study physico-chemical properties of Ebolavirus along with Gene structural information and sequence homology to interpret significant aspects on Ebola virus. Ebola Virus Disease (EVD) is a rare and deadly disease in people and nonhuman primates. The viruses that cause EVD are located mainly in sub-Saharan Africa. People can get EVD through direct contact with an infected animal (bat or nonhuman primate) or a sick or dead person infected with Ebola virus. The U.S. Food and Drug Administration (FDA) has approved the Ebola vaccine rVSV-ZEBOV (tradename "Ervebo") for the prevention of EVD. The rVSV-ZEBOV vaccine has been found to be safe and protective against only the Zaire ebolavirus species of ebolavirus. Ebola virus disease (EVD), one of the deadliest viral diseases, was discovered in 1976 when two consecutive outbreaks of fatal hemorrhagic fever occurred in different parts of Central Africa. The first outbreak occurred in the Democratic Republic of Congo (formerly Zaire) in a village near the Ebola River, which gave the virus its name. The second outbreak occurred in what is now South Sudan, approximately 500 miles (850 km) away. Initially, public health officials assumed these outbreaks were a single event associated with an infected person who traveled between the two locations. However, scientists later discovered that the two outbreaks were caused by two genetically distinct viruses: Zaire ebolavirus and Sudan ebolavirus. After this discovery, scientists concluded that the virus came from two



different sources and spread independently to people in each of the affected areas. Viral and epidemiologic data suggest that Ebola virus existed long before these recorded outbreaks occurred. Factors like population growth, encroachment into forested areas, and direct interaction with wildlife (such as bushmeat consumption) may have contributed to the spread of the Ebola virus. Following the discovery of the virus, scientists studied thousands of animals, insects, and plants in search of its source (called reservoir among virologists, people who study viruses). Gorillas, chimpanzees, and other mammals may be implicated when the first cases of an EVD outbreak in people occur. However, they – like people – are “dead-end” hosts, meaning the organism dies following the infection and does not survive and spread the virus to other animals. Like other viruses of its kind, it is possible that the reservoir host animal of Ebola virus does not experience acute illness despite the virus being present in its organs, tissues, and blood. Thus, the virus is likely maintained in the environment by spreading from host to host or through intermediate hosts or vectors. African fruit bats are likely involved in the spread of Ebola virus and may even be the source animal (reservoir host). Scientists continue to search for conclusive evidence of the bat’s role in transmission of Ebola. The most recent Ebola virus to be detected, Bombali virus, was identified in samples from bats collected in Sierra Leone. The use of contaminated needles and syringes during the earliest outbreaks enabled transmission and amplification of Ebola virus. During the first outbreak in Zaire (now Democratic Republic of Congo – DRC), nurses in the Yambuku mission hospital reportedly used five syringes for 300 to 600 patients a day. Close contact with infected blood, reuse of contaminated needles, and improper nursing techniques were the source for much of the human-to-human transmission during early Ebola outbreaks. In 1989, Reston ebolavirus was discovered in research monkeys imported from the Philippines into the U.S. Later, scientists confirmed that the virus spread throughout the monkey population through droplets in the air (aerosolized transmission) in the facility. However, such airborne transmission is not proven to be a significant factor in human outbreaks of Ebola.<sup>4</sup> The discovery of the Reston virus in these monkeys from the Philippines revealed that Ebola was no longer confined to African settings, but was present in Asia as well. By the 1994 Cote d’Ivoire outbreak, scientists and public health officials had a better understanding of how Ebola virus spreads and progress was made to reduce transmission through the use of face masks, gloves and gowns for healthcare personnel. In addition, the use of disposable equipment, such as needles, was introduced. During the 1995 Kikwit, Zaire (now DRC) outbreak, the international public health community played a strong role, as it was now widely agreed that containment and control of Ebola were paramount. Ebola virus disease (EVD) is a life-threatening viral disease with a fatality rate ranging from around 30% to 90%. The first EVD outbreak was reported in the 1970s in Zaire (now the Democratic Republic of the Congo). Until 2013, most outbreaks occurred in the Central Africa region, including Zaire, Sudan and Uganda. However, between March and October 2014, over 10 000 cases of EVD have been recorded in West Africa, such as in Guinea, Liberia, Sierra Leone, and Nigeria, and a few hospital or secondary infections of EVD have occurred in Spain and the United States of America. EVD is presently one of the world’s most feared diseases. In this literature review, we describe the epidemiology, clinical features, diagnosis, and treatment of EVD.

The virus is thought to be initially acquired by exposure to body fluids or tissue from infected animals, such as bats and non-human primates; however, the natural reservoir and mode of transmission to humans has not been confirmed. Laboratory testing of reservoir competence shows that successful infection is possible in bats and rodents, but not in plants or arthropods. Animal to human transmission may occur during hunting and consumption of the reservoir species or infected non-human primates. The practice of butchering or eating bush meat or food contaminated with bat faeces (three species of tree roosting bats have been implicated as a reservoir) is also thought to contribute. Human to human transmission occurs through contact with body fluids from infected patients. In early epidemics, the re-use of non-sterile injections was responsible for many healthcare associated transmissions. However, although this remains a risk, most cases result from close physical contact or contact with body fluids (such as sweat, blood, faeces, vomit, saliva, genital secretions, urine, and breast milk) of infected patients. In a study of viral shedding in various body fluids, Ebola virus was isolated from saliva, breast milk, stool, tears, and semen up to 40 days after the onset of illness, confirming the possibility of delayed sexual transmission. Virus may be found in urine during recovery, and the duration of this phenomenon needs further study. Infection through inhalation is possible in non-human primates, but there is no evidence for airborne transmission in humans. Outside endemic areas, Ebola virus infection is rare and is usually imported. Travellers from affected areas, and laboratory scientists and others working with potentially infected materials and animals, are at high risk.



## RESULTS AND DISCUSSION MODULE-1

|   |                      | Bundibugyo Ebola virus                | Sudan Ebola virus                     | Reston Ebola virus                    | Zaire Ebola virus                     | Tai forest ebola virus                |
|---|----------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|
| Number and composition of amino acids<br><br>NUCLEO-PROTEIN | Alanine (Ala)        | 63(8.5%)                              | 52(7.0%)                              | 60(8.1%)                              | 53(7.2%)                              | 54(7.3%)                              |
|   | Arginine (Arg)       | 31(4.2%)                              | 27(3.7%)                              | 39(5.3%)                              | 33(4.5%)                              | 29(3.9%)                              |
|   | Asparagine (Asn)     | 43(5.8%)                              | 34(4.6%)                              | 40(5.4%)                              | 33(4.5%)                              | 45(6.1%)                              |
|   | Aspartic acid (Asp)  | 57(7.7%)                              | 59(8.0%)                              | 59(8.0%)                              | 59(8.0%)                              | 48(6.5%)                              |
|   | Cysteine (Cys)       | 03(0.4%)                              | 03(0.4%)                              | 03(0.4%)                              | 03(0.4%)                              | 03(0.4%)                              |
|   | Glutamine (Gln)      | 51(6.9%)                              | 47(6.4%)                              | 52(7.0%)                              | 53(7.2%)                              | 49(6.6%)                              |
|   | Glutamic acid (Glu)  | 56(7.6%)                              | 58(7.9%)                              | 59(8.0%)                              | 59(8.0%)                              | 63(8.5%)                              |
|   | Glycine (Gly)        | 37(5.0%)                              | 53(7.2%)                              | 42(5.7%)                              | 41(5.5%)                              | 37(5.0%)                              |
|   | Histidine (His)      | 25(3.4%)                              | 25(3.4%)                              | 28(3.8%)                              | 30(4.1%)                              | 30(4.1%)                              |
|   | Iso-Leucine (Ile)    | 38(5.1%)                              | 29(3.9%)                              | 33(4.5%)                              | 29(3.9%)                              | 34(4.6%)                              |
|   | Leucine (Leu)        | 62(8.4%)                              | 77(10.4%)                             | 74(10.0%)                             | 67(9.1%)                              | 64(8.7%)                              |
|   | Lysine (Lys)         | 37(5.0%)                              | 36(4.9%)                              | 31(4.2%)                              | 38(5.1%)                              | 41(5.5%)                              |
|   | Methionine (Met)     | 20(2.7%)                              | 13(1.8%)                              | 15(2.0%)                              | 20(2.7%)                              | 17(2.3%)                              |
|   | Phenyl Alanine (Phe) | 25(3.4%)                              | 24(3.3%)                              | 25(3.4%)                              | 26(3.5%)                              | 26(3.5%)                              |
|   | Proline (Pro)        | 40(5.4%)                              | 42(5.7%)                              | 40(5.4%)                              | 42(5.7%)                              | 37(5.0%)                              |
|   | Serine (Ser)         | 47(6.4%)                              | 49(6.6%)                              | 44(6.0%)                              | 48(6.5%)                              | 51(6.6%)                              |
|   | Threonine (Thr)      | 41(5.5%)                              | 39(5.3%)                              | 32(4.3%)                              | 38(5.1%)                              | 49(6.9%)                              |
|   | Tryptophan (Trp)     | 04(0.5%)                              | 04(0.5%)                              | 05(0.7%)                              | 04(0.5%)                              | 05(0.7%)                              |
| Tyrosine (Tyr)  | 22(3.0%)             | 22(3.0%)                              | 24(3.2%)                              | 21(2.8%)                              | 21(2.8%)                              |                                       |
| Valine (Val)  | 37(5.0%)             | 45(6.1%)                              | 34(4.6%)                              | 42(5.7%)                              | 36(4.9%)                              |                                       |
| Molecular weight  |                      | 82905.24                              | 81804.90                              | 83452.62                              | 83286.68                              | 83308.50                              |
| Theoretical pI  |                      | 4.90                                  | 4.73                                  | 4.91                                  | 4.98                                  | 5.13                                  |
| Atomic composition  |                      | 11487                                 | 11365                                 | 11557                                 | 11535                                 | 11541                                 |
| Total number of positively charged residues                 |                      | 68                                    | 63                                    | 70                                    | 71                                    | 70                                    |
| Total number of Negatively charged residues                 |                      | 113                                   | 117                                   | 118                                   | 118                                   | 111                                   |
| Extinction coefficient assuming cystine residues            |                      | 54905M <sup>-1</sup> cm <sup>-1</sup> | 54905M <sup>-1</sup> cm <sup>-1</sup> | 63385M <sup>-1</sup> cm <sup>-1</sup> | 53415M <sup>-1</sup> cm <sup>-1</sup> | 58915M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance assuming cystine residues                        |                      | 0.662                                 | 0.671                                 | 0.760                                 | 0.641                                 | 0.707                                 |
| Extinction coefficient with out cystine residues            |                      | 54780M <sup>-1</sup> cm <sup>-1</sup> | 54780M <sup>-1</sup> cm <sup>-1</sup> | 63260M <sup>-1</sup> cm <sup>-1</sup> | 53290M <sup>-1</sup> cm <sup>-1</sup> | 58790M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance with out cystine residues                        |                      | 0.661                                 | 0.670                                 | 0.758                                 | 0.640                                 | 0.706                                 |
| Instability Index   |                      | 45.60                                 | 38.60                                 | 46.18                                 | 50.31                                 | 46.88                                 |
| Aliphatic Index   |                      | 75.82                                 | 80.75                                 | 77.93                                 | 74.32                                 | 73.15                                 |
| Grand Average of Hydrophaticity                             |                      | -0.642                                | -0.565                                | -0.688                                | -0.691                                | -0.714                                |

Table-1: The above table describes different physico-chemical properties associated with the nucleo-protein of Ebola virus species, in which all forms of nucleo-protein in all species of the Ebola virus species have the same number and composition of the amino acids on the whole but vary when compared with the individual amino acids. When we calculated the average isotope mass of the amino acid in the protein and one water molecule, the total molecular weight of the protein is estimated to be in this order: i.e., 83452.62 > 83308.50 > 83286.68 > 82905.24 > 81804.90. i.e., Reston Ebola virus with greater molecular weight and Sudan Ebola virus with the smaller molecular weight. The pI/Mw algorithm is mainly used to enhance a region in a 2-D gel to which a protein which is unmodified should be allowed to run, and point a region in which a modified form of protein should be found if the modifications are documented in the database. When we calculated the sums of different amino acid contributions assuming them as independent with out considering the secondary and tertiary structures, we observed similar values of extinction coefficient for Bundibugyo and Sudan Ebola virus with and without assuming cysteine residues with different absorbance. The nucleo-protein of Sudan Ebola virus is more stable when compared with the other forms of the virus species with a value of 38.60 as the value is less than 40 and Zaire Ebola virus is more unstable as it exceeds a value greater than 40. When we determined the positive factor which explains the increment phenomenon of the globular proteins and volume occupied relatively by the aliphatic side chains, we observed 80.75 (Sudan Ebola virus) > 77.93 (Reston Ebola virus) > 75.82 (Bundibugyo Ebola virus) > 74.32 (Zaire Ebola virus) > 73.15 (Tai forest Ebola virus) and when we studied the phenomenon of the protein that is exhibiting the ability of repelling from the water, the hydrophobicity value of the Sudan Ebola virus (-0.565) is greater and for the Tai forest Ebola virus (-0.714) is less.





| Number and composition of amino acids            |                      | Bundibugyo Ebola virus                | Sudan Ebola virus                     | Reston Ebola virus                    | Zaire Ebola virus                     | Tai forest ebola virus                |
|--|----------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|
| POLYMERASE COMPLEX PROTEIN                       | Alanine (Ala)        | 25(7.3%)                              | 31(9.4%)                              | 23(7.0%)                              | 27(7.9%)                              | 27(7.9%)                              |
|  | Arginine (Arg)       | 16(4.7%)                              | 13(4.0%)                              | 13(4.0%)                              | 18(5.3%)                              | 18(5.3%)                              |
|  | Asparagine (Asn)     | 10(2.9%)                              | 12(3.6%)                              | 14(4.3%)                              | 14(4.1%)                              | 15(4.4%)                              |
|  | Aspartic acid (Asp)  | 18(5.3%)                              | 20(6.1%)                              | 22(6.7%)                              | 17(5.0%)                              | 21(6.2%)                              |
|  | Cysteine (Cys)       | 07(2.1%)                              | 05(1.5%)                              | 07(2.1%)                              | 08(2.4%)                              | 08(2.3%)                              |
|  | Glutamine (Gln)      | 18(5.3%)                              | 18(5.5%)                              | 15(4.6%)                              | 23(6.8%)                              | 20(5.9%)                              |
|  | Glutamic acid (Glu)  | 20(5.9%)                              | 19(5.8%)                              | 17(5.2%)                              | 20(5.9%)                              | 21(6.2%)                              |
|  | Glycine (Gly)        | 19(5.6%)                              | 17(5.2%)                              | 16(4.9%)                              | 20(5.9%)                              | 18(5.3%)                              |
|  | Histidine (His)      | 07(2.1%)                              | 07(2.1%)                              | 05(1.5%)                              | 07(2.1%)                              | 08(2.3%)                              |
|  | Iso-Leucine (Ile)    | 27(7.9%)                              | 27(8.2%)                              | 23(7.0%)                              | 23(6.8%)                              | 28(8.2%)                              |
|  | Leucine (Leu)        | 28(8.2%)                              | 23(7.0%)                              | 29(8.8%)                              | 25(7.4%)                              | 28(8.2%)                              |
|  | Lysine (Lys)         | 21(6.2%)                              | 26(7.9%)                              | 26(7.9%)                              | 16(4.7%)                              | 19(5.6%)                              |
|  | Methionine (Met)     | 07(2.1%)                              | 05(1.5%)                              | 09(2.7%)                              | 08(2.4%)                              | 07(2.1%)                              |
|  | Phenyl Alanine (Phe) | 09(2.6%)                              | 09(2.7%)                              | 07(2.1%)                              | 09(2.6%)                              | 09(2.6%)                              |
|  | Proline (Pro)        | 26(7.6%)                              | 23(7.0%)                              | 24(7.3%)                              | 24(7.1%)                              | 26(7.6%)                              |
|  | Serine (Ser)         | 26(7.6%)                              | 25(7.6%)                              | 26(7.9%)                              | 26(7.6%)                              | 23(6.7%)                              |
|  | Threonine (Thr)      | 30(8.8%)                              | 20(6.1%)                              | 23(7.0%)                              | 28(8.2%)                              | 24(7.0%)                              |
| Tryptophan (Trp)                                 | 03(0.9%)             | 03(0.9%)                              | 03(0.9%)                              | 03(0.9%)                              | 03(0.9%)                              |                                       |
| Tyrosine (Tyr)                                   | 05(1.5%)             | 07(2.1%)                              | 09(2.7%)                              | 06(1.8%)                              | 05(1.5%)                              |                                       |
| Valine (Val)                                     | 19(5.6%)             | 19(5.8%)                              | 18(5.5%)                              | 18(5.3%)                              | 13(3.8%)                              |                                       |
| Molecular weight                                 |                      | 37399.85                              | 36116.21                              | 36409.75                              | 37362.36                              | 37732.92                              |
| Theoretical pI                                   |                      | 6.67                                  | 7.05                                  | 6.95                                  | 6.19                                  | 5.94                                  |
| Atomic composition                               |                      | 5286                                  | 5104                                  | 5135                                  | 5226                                  | 5296                                  |
| Total number of positively charged residues      |                      | 37                                    | 39                                    | 39                                    | 34                                    | 37                                    |
| Total number of Negatively charged residues      |                      | 38                                    | 39                                    | 39                                    | 37                                    | 42                                    |
| Extinction coefficient assuming cystine residues |                      | 24325M <sup>-1</sup> cm <sup>-1</sup> | 27180M <sup>-1</sup> cm <sup>-1</sup> | 30285M <sup>-1</sup> cm <sup>-1</sup> | 25940M <sup>-1</sup> cm <sup>-1</sup> | 24450M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance assuming cystine residues             |                      | 0.650                                 | 0.753                                 | 0.832                                 | 0.694                                 | 0.648                                 |
| Extinction coefficient with out cystine residues |                      | 23950M <sup>-1</sup> cm <sup>-1</sup> | 26930M <sup>-1</sup> cm <sup>-1</sup> | 29910M <sup>-1</sup> cm <sup>-1</sup> | 25440M <sup>-1</sup> cm <sup>-1</sup> | 23950M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance with out cystine residues             |                      | 0.640                                 | 0.746                                 | 0.821                                 | 0.681                                 | 0.635                                 |
| Instability Index                                |                      | 50.17                                 | 45.04                                 | 46.31                                 | 47.32                                 | 46.50                                 |
| Aliphatic Index                                  |                      | 86.39                                 | 85.44                                 | 84.50                                 | 78.35                                 | 83.02                                 |
| Grand Average of Hydrophaticity                  |                      | -0.290                                | -0.369                                | -0.380                                | -0.409                                | -0.438                                |

Table-2: The different physico-chemical properties of polymerase complex protein of the ebola virus is described in the above table in which, the total number shows approximation in its value (Similarity in total number of Amino acids showing similarity in two to three amino acid number) but differs in the individual amino acids. Average isotope mass on protein and one water molecule with respect to each amino acid is calculated, then the total molecular weight of the protein is obtained in this order i.e.; 37732.92 > 37399.85 > 37362.36 > 36409.75 > 36116.21. By this we can say that Tai forest Ebola virus having greater molecular weight and Sudan Ebola virus with smaller molecular weight. Compute pI/Mw algorithm is mainly used to enhance a region in a 2-D gel to which an a protein which is unmodified should allowed to run, and point a region in which modified form of protein should be found if the modifications are documented in the database. Assuming the different independent amino acid contributions with out considering the secondary and tertiary structures, we observed different values of Extinction coefficient with different absorbance values in both cases of assuming and non assuming cysteine residues. All the Polymerase complex proteins in all the Ebola virus species is not stable and this can be justified based upon the values we got i.e.; all the values obtained is greater than 40. When the positive factor which explains the increment phenomenon of the globular protein and volume occupied by the aliphatic side chains is determined the values are 78.35 (Zaire Ebolavirus) > 83.02 (Tai forest Ebolavirus) > 84.50 (Reston Ebolavirus) > 85.44 (Sudan Ebolavirus) > 86.39 (Bundibugyo Ebolavirus). The repelling capacity of the protein in Bundibugyo Ebolavirus (-0.290) is higher and the repelling capacity of protein in the Tai forest Ebola virus (-0.438) is less.



|  |                      | Tai forest Ebola virus                | Sudan Ebola virus                     | Reston Ebola virus                    | Zaire Ebola virus                     |
|--|----------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|
| Number and composition of amino acids<br><br>MATRIX -PROTEIN | Alanine (Ala)        | 19(5.8%)                              | 21(6.4%)                              | 23(6.9%)                              | 22(6.7%)                              |
|  | Arginine (Arg)       | 12(3.7%)                              | 10(3.1%)                              | 11(3.3%)                              | 11(3.4%)                              |
|  | Asparagine (Asn)     | 16(4.9%)                              | 11(3.4%)                              | 13(3.9%)                              | 14(4.3%)                              |
|  | Aspartic acid (Asp)  | 18(5.5%)                              | 19(5.8%)                              | 20(6.0%)                              | 17(5.2%)                              |
|  | Cysteine (Cys)       | 02(0.6%)                              | 02(0.6%)                              | 02(0.6%)                              | 02(0.6%)                              |
|  | Glutamine (Gln)      | 12(3.7%)                              | 15(4.6%)                              | 14(4.2%)                              | 11(3.4%)                              |
|  | Glutamic acid (Glu)  | 08(2.5%)                              | 07(2.1%)                              | 06(1.8%)                              | 09(2.8%)                              |
|  | Glycine (Gly)        | 19(5.8%)                              | 20(6.1%)                              | 19(5.7%)                              | 21(6.4%)                              |
|  | Histidine (His)      | 07(2.1%)                              | 08(2.5%)                              | 09(2.7%)                              | 07(2.1%)                              |
|  | Iso-Leucine (Ile)    | 26(8.0%)                              | 24(7.4%)                              | 25(7.6%)                              | 27(8.3%)                              |
|  | Leucine (Leu)        | 35(10.7%)                             | 35(10.7%)                             | 36(10.9%)                             | 33(10.1%)                             |
|  | Lysine (Lys)         | 16(4.9%)                              | 20(6.1%)                              | 18(5.4%)                              | 18(5.5%)                              |
|  | Methionine (Met)     | 11(3.4%)                              | 11(3.4%)                              | 08(2.4%)                              | 08(2.5%)                              |
|  | Phenyl Alanine (Phe) | 09(2.8%)                              | 09(2.8%)                              | 07(2.1%)                              | 10(3.1%)                              |
|  | Proline (Pro)        | 37(11.3%)                             | 36(11.0%)                             | 40(12.1%)                             | 37(11.3%)                             |
|  | Serine (Ser)         | 22(6.7%)                              | 23(7.1%)                              | 22(6.6%)                              | 22(6.7%)                              |
| Threonine (Thr)  | 31(9.5%)             | 23(7.1%)                              | 23(6.9%)                              | 29(8.9%)                              |                                       |
| Tryptophan (Trp)   | 02(0.6%)             | 02(0.6%)                              | 02(0.6%)                              | 02(0.6%)                              |                                       |
| Tyrosine (Tyr)   | 07(2.1%)             | 08(2.5%)                              | 08(2.4%)                              | 06(1.8%)                              |                                       |
| Valine (Val)   | 17(5.2%)             | 22(6.7%)                              | 25(7.6%)                              | 20(6.1%)                              |                                       |
| Molecular weight   |                      | 35525.19                              | 35475.35                              | 35820.66                              | 35182.83                              |
| Theoretical pI   |                      | 8.44                                  | 8.91                                  | 8.73                                  | 8.76                                  |
| Atomic composition   |                      | 5056                                  | 5064                                  | 5123                                  | 5026                                  |
| Total number of positively charged residues                  |                      | 28                                    | 30                                    | 29                                    | 29                                    |
| Total number of Negatively charged residues                  |                      | 26                                    | 26                                    | 26                                    | 26                                    |
| Extinction coefficient assuming cystine residues             |                      | 21555M <sup>-1</sup> cm <sup>-1</sup> | 23045M <sup>-1</sup> cm <sup>-1</sup> | 23045M <sup>-1</sup> cm <sup>-1</sup> | 20065M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance assuming cystine residues                         |                      | 0.607                                 | 0.650                                 | 0.643                                 | 0.570                                 |
| Extinction coefficient with out cystine residues             |                      | 21430M <sup>-1</sup> cm <sup>-1</sup> | 22920M <sup>-1</sup> cm <sup>-1</sup> | 22920M <sup>-1</sup> cm <sup>-1</sup> | 19940M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance with out cystine residues                         |                      | 0.603                                 | 0.646                                 | 0.640                                 | 0.567                                 |
| Instability Index  |                      | 40.13                                 | 41.76                                 | 41.41                                 | 40.39                                 |
| Aliphatic Index  |                      | 93.93                                 | 96.60                                 | 100.73                                | 96.32                                 |
| Grand Average of Hydrophaticity                              |                      | -0.117                                | -0.063                                | -0.048                                | -0.052                                |

Table-3: The matrix protein of all Ebola virus species shows approximation in the values illustrating total number and composition of the amino acids but completely varies in the individual amino acids. On the protein and Water molecule the average isotope mass with respect to each amino acid is calculated and the values are obtained to be 35820.66 > 35525.19 > 35475.35 > 35458.31 > 35182.83 i.e.; Reston Ebolavirus with the greater molecular weight and Zaire Ebolavirus with smaller molecular weight. Compute pI/Mw algorithm is mainly used to enhance a region in a 2-D gel to which an a protein which is unmodified should allowed to run, and point a region in which modified form of protein should be found if the modifications are documented in the database. Without considering the secondary and tertiary structures when independent amino acid contributions are studied we observed different values of the extinction coefficient with the different values of the absorbance in both the cases i.e.; assuming and non assuming the cysteine residues. The matrix protein of the all the species of the Ebola virus are not stable as the values are greater than 40. The increment phenomenon of the globular protein explaining the positive factor and volume occupied by the aliphatic side chains are studied then the obtained values are in this order 100.73 (Reston Ebolavirus) > 96.63 (Bundibugyo Ebolavirus) > 96.60 (Sudan Ebolavirus) > 96.32 (Zaire Ebolavirus) > 93.93 (Taiforest Ebolavirus). The Protein repelling capacity in the Bundibugyo Ebolavirus (-0.037) is greater and the repelling capacity of the Tai forest Ebola virus (-0.117) is less.



|  |                      | Bundibugyo Ebola virus                | Sudan Ebola virus                     | Reston Ebola virus                    | Zaire Ebola virus                     | Tai forest ebola virus                |
|--|----------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|
| Number and composition of amino acids<br><br>SECOND SECRETED GLYCO PROTEIN | Alanine (Ala)        | 14(4.6%)                              | 20(6.3%)                              | 15(4.5%)                              | 16(5.4%)                              | 17(5.6%)                              |
|  | Arginine (Arg)       | 14(4.6%)                              | 21(6.6%)                              | 20(6.0%)                              | 17(5.7%)                              | 15(5.0%)                              |
|  | Asparagine (Asn)     | 18(6.0%)                              | 15(4.7%)                              | 19(5.7%)                              | 13(4.4%)                              | 17(5.6%)                              |
|  | Aspartic acid (Asp)  | 12(4.0%)                              | 16(5.0%)                              | 13(3.9%)                              | 13(4.4%)                              | 13(4.3%)                              |
|  | Cysteine (Cys)       | 05(1.7%)                              | 05(1.6%)                              | 06(1.8%)                              | 05(1.7%)                              | 06(2.0%)                              |
|  | Glutamine (Gln)      | 08(2.6%)                              | 12(3.8%)                              | 11(3.3%)                              | 09(3.0%)                              | 07(2.3%)                              |
|  | Glutamic acid (Glu)  | 17(5.6%)                              | 17(5.3%)                              | 18(5.4%)                              | 18(6.1%)                              | 16(5.3%)                              |
|  | Glycine (Gly)        | 21(7.0%)                              | 21(6.6%)                              | 24(7.3%)                              | 24(8.1%)                              | 21(7.0%)                              |
|  | Histidine (His)      | 08(2.6%)                              | 07(2.2%)                              | 07(2.1%)                              | 05(1.7%)                              | 08(2.6%)                              |
|  | Iso-Leucine (Ile)    | 11(3.6%)                              | 16(5.0%)                              | 11(3.3%)                              | 14(4.7%)                              | 14(4.6%)                              |
|  | Leucine (Leu)        | 25(8.3%)                              | 29(9.1%)                              | 34(10.3%)                             | 25(8.4%)                              | 25(8.3%)                              |
|  | Lysine (Lys)         | 18(6.0%)                              | 16(5.0%)                              | 19(5.7%)                              | 16(5.4%)                              | 19(6.3%)                              |
|  | Methionine (Met)     | 03(1.0%)                              | 02(0.6%)                              | 04(1.2%)                              | 01(0.3%)                              | 03(1.0%)                              |
|  | Phenyl Alanine (Phe) | 21(7.0%)                              | 21(6.6%)                              | 17(5.1%)                              | 20(6.7%)                              | 22(7.3%)                              |
|  | Proline (Pro)        | 20(6.6%)                              | 18(5.7%)                              | 23(6.9%)                              | 17(5.7%)                              | 18(6.0%)                              |
|  | Serine (Ser)         | 16(5.3%)                              | 22(6.9%)                              | 25(7.6%)                              | 20(6.7%)                              | 17(5.6%)                              |
|  | Threonine (Thr)      | 27(8.9%)                              | 23(7.2%)                              | 27(8.2%)                              | 26(8.8%)                              | 25(8.3%)                              |
| Tryptophan (Trp)   | 06(2.0%)             | 07(2.2%)                              | 08(2.4%)                              | 06(2.0%)                              | 06(2.0%)                              |                                       |
| Tyrosine (Tyr)   | 11(3.6%)             | 11(3.5%)                              | 10(3.0%)                              | 11(3.7%)                              | 09(3.0%)                              |                                       |
| Valine (Val)   | 27(8.9%)             | 19(6.0%)                              | 20(6.0%)                              | 21(7.1%)                              | 24(7.9%)                              |                                       |
| Molecular weight   |                      | 34184.97                              | 36146.05                              | 37352.50                              | 33391.87                              | 34082.99                              |
| Theoretical pI   |                      | 8.49                                  | 8.71                                  | 9.14                                  | 8.19                                  | 8.81                                  |
| Atomic composition   |                      | 4793                                  | 5065                                  | 5235                                  | 4681                                  | 4786                                  |
| Total number of positively charged residues                                |                      | 32                                    | 37                                    | 39                                    | 33                                    | 34                                    |
| Total number of Negatively charged residues                                |                      | 29                                    | 33                                    | 31                                    | 31                                    | 29                                    |
| Extinction coefficient assuming cystine residues                           |                      | 49640M <sup>-1</sup> cm <sup>-1</sup> | 55140M <sup>-1</sup> cm <sup>-1</sup> | 59275M <sup>-1</sup> cm <sup>-1</sup> | 49640M <sup>-1</sup> cm <sup>-1</sup> | 46785M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance assuming cystine residues                                       |                      | 1.452                                 | 1.525                                 | 1.587                                 | 1.487                                 | 1.373                                 |
| Extinction coefficient with out cystine residues                           |                      | 49390M <sup>-1</sup> cm <sup>-1</sup> | 54890M <sup>-1</sup> cm <sup>-1</sup> | 58900M <sup>-1</sup> cm <sup>-1</sup> | 49390M <sup>-1</sup> cm <sup>-1</sup> | 46410M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance with out cystine residues                                       |                      | 1.445                                 | 1.519                                 | 1.577                                 | 1.479                                 | 1.362                                 |
| Instability Index  |                      | 29.22                                 | 37.58                                 | 31.45                                 | 31.11                                 | 27.34                                 |
| Aliphatic Index  |                      | 77.05                                 | 78.81                                 | 75.08                                 | 77.10                                 | 79.04                                 |
| Grand Average of Hydrophaticity  |                      | -0.275                                | -0.339                                | -0.440                                | -0.289                                | -0.220                                |

Table-4: The second Secreted glycol-protein shows approximation in the total number and the composition of the amino acid and difference when compared individual amino acids. The average isotope mass on the protein and water molecule are examined and results are obtained in this order i.e.; 37352.50 > 36146.05 > 34184.97 > 34082.99 > 33391.87. By these studies we concluded that Reston Ebolavirus is having higher molecular weight and Zaire Ebolavirus with small molecular weight. Compute pI/Mw algorithm is mainly used to enhance a region in a 2-D gel to which a protein which is unmodified should be allowed to run, and point a region in which modified form of protein should be found if the modifications are documented in the database. When independent amino acid contributions are studied with out considering the secondary and tertiary structure we observed different values of the extinction coefficient with different absorbance both assuming and not assuming the cysteine residues. When we studied the protein stability the secondary secreted protein of all the Ebola species, every organism shows its stability and this can be justified based on the values obtained and all the values obtained are less than 40. When the positive factor explaining the increment phenomenon of the globular proteins and aliphatic side chains are studied the values are obtained in this order i.e.; 79.04 (Tai forest Ebolavirus) > 78.81 (Sudan Ebolavirus) > 77.10 (Zaire Ebolavirus) > 77.05 (Bundibugyo Ebolavirus) > 75.08 (Reston Ebolavirus). The repelling capacity of the protein in the Tai forest Ebolavirus (-0.220) is greater and in the Reston Ebola virus (-0.440) is less.



|   |                      | Bundibugyo Ebola virus                | Sudan Ebola virus                     | Reston Ebola virus                    | Zaire Ebola virus                     | Tai forest ebola virus                |
|---|----------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|
| Number and composition of amino acids<br><br>SMALL SECRETED GLYCO PROTEIN | Alanine (Ala)        | 17(4.6%)                              | 18(4.8%)                              | 16(4.4%)                              | 17(4.7%)                              | 17(4.7%)                              |
|   | Arginine (Arg)       | 23(6.2%)                              | 24(6.5%)                              | 23(6.3%)                              | 21(5.8%)                              | 24(6.6%)                              |
|   | Asparagine (Asn)     | 17(4.6%)                              | 17(4.6%)                              | 17(4.6%)                              | 13(3.6%)                              | 17(4.7%)                              |
|   | Aspartic acid (Asp)  | 12(3.2%)                              | 15(4.0%)                              | 14(3.8%)                              | 13(3.6%)                              | 13(3.6%)                              |
|   | Cysteine (Cys)       | 08(2.1%)                              | 08(2.2%)                              | 08(2.2%)                              | 08(2.2%)                              | 09(2.5%)                              |
|   | Glutamine (Gln)      | 18(4.8%)                              | 17(4.6%)                              | 16(4.4%)                              | 17(4.7%)                              | 17(4.7%)                              |
|   | Glutamic acid (Glu)  | 19(5.1%)                              | 23(6.2%)                              | 20(5.4%)                              | 22(6.0%)                              | 17(4.7%)                              |
|   | Glycine (Gly)        | 22(5.9%)                              | 25(6.7%)                              | 23(6.3%)                              | 26(7.1%)                              | 21(5.8%)                              |
|   | Histidine (His)      | 08(2.1%)                              | 10(2.7%)                              | 08(2.2%)                              | 04(1.1%)                              | 07(1.9%)                              |
|   | Iso-Leucine (Ile)    | 13(3.5%)                              | 19(5.1%)                              | 13(3.5%)                              | 16(4.4%)                              | 15(4.1%)                              |
|   | Leucine (Leu)        | 29(7.8%)                              | 33(8.9%)                              | 34(9.3%)                              | 34(9.3%)                              | 30(8.2%)                              |
|   | Lysine (Lys)         | 22(5.9%)                              | 22(5.9%)                              | 23(6.3%)                              | 25(6.9%)                              | 23(6.3%)                              |
|   | Methionine (Met)     | 03(0.8%)                              | 04(1.1%)                              | 05(1.4%)                              | 01(0.3%)                              | 03(0.8%)                              |
|   | Phenyl Alanine (Phe) | 23(6.2%)                              | 21(5.6%)                              | 20(5.4%)                              | 22(6.0%)                              | 24(6.6%)                              |
|   | Proline (Pro)        | 30(8.0%)                              | 23(6.2%)                              | 27(7.4%)                              | 20(5.5%)                              | 25(6.8%)                              |
|   | Serine (Ser)         | 23(6.2%)                              | 26(7.0%)                              | 26(7.1%)                              | 25(6.9%)                              | 24(6.6%)                              |
|   | Threonine (Thr)      | 37(9.9%)                              | 25(6.7%)                              | 34(9.3%)                              | 34(9.3%)                              | 35(9.6%)                              |
| Tryptophan (Trp)  | 08(2.1%)             | 08(2.2%)                              | 09(2.5%)                              | 08(2.2%)                              | 08(2.2%)                              |                                       |
| Tyrosine (Tyr)  | 13(3.5%)             | 14(3.8%)                              | 10(2.7%)                              | 12(3.3%)                              | 11(3.0%)                              |                                       |
| Valine (Val)  | 28(7.5%)             | 20(5.4%)                              | 21(5.7%)                              | 26(7.1%)                              | 25(6.8%)                              |                                       |
| Molecular weight  |                      | 42471.48                              | 42584.49                              | 41744.64                              | 41175.11                              | 41655.71                              |
| Theoretical pI  |                      | 9.41                                  | 8.98                                  | 9.31                                  | 9.20                                  | 9.55                                  |
| Atomic composition  |                      | 5959                                  | 5960                                  | 5852                                  | 5809                                  | 5854                                  |
| Total number of positively charged residues                               |                      | 45                                    | 46                                    | 46                                    | 46                                    | 47                                    |
| Total number of Negatively charged residues                               |                      | 31                                    | 38                                    | 34                                    | 35                                    | 30                                    |
| Extinction coefficient assuming cystine residues                          |                      | 63870M <sup>-1</sup> cm <sup>-1</sup> | 65360M <sup>-1</sup> cm <sup>-1</sup> | 64900M <sup>-1</sup> cm <sup>-1</sup> | 62380M <sup>-1</sup> cm <sup>-1</sup> | 60890M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance assuming cystine residues                                      |                      | 1.504                                 | 1.535                                 | 1.555                                 | 1.515                                 | 1.462                                 |
| Extinction coefficient with out cystine residues                          |                      | 63370M <sup>-1</sup> cm <sup>-1</sup> | 64860M <sup>-1</sup> cm <sup>-1</sup> | 64400M <sup>-1</sup> cm <sup>-1</sup> | 61880M <sup>-1</sup> cm <sup>-1</sup> | 60390M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance with out cystine residues                                      |                      | 1.492                                 | 1.523                                 | 1.543                                 | 1.503                                 | 1.450                                 |
| Instability Index   |                      | 39.79                                 | 39.34                                 | 31.30                                 | 34.79                                 | 34.57                                 |
| Aliphatic Index   |                      | 70.24                                 | 74.95                                 | 70.90                                 | 78.96                                 | 72.60                                 |
| Grand Average of Hydrophaticity   |                      | -0.440                                | -0.469                                | -0.494                                | -0.321                                | -0.398                                |

Table-5: The Small Secreted Glyco-Protein although shows approximation in total number and composition of amino acids, but varies when compared to individual amino acids. In the protein and one water molecule when we calculated the average isotope mass, the total molecular weight of the protein the order is obtained in this way i.e; 42584.49 > 42471.48 > 41744.64 > 41655.71 > 41175.11. Hence by this we can say that the molecular weight of the Sudan Ebolavirus is greater and the molecular weight of the Zaire Ebolavirus is smaller. Compute pI/Mw algorithm is mainly used to enhance a region in a 2-D gel to which an a protein which is unmodified should allowed to run, and point a region in which modified form of protein should be found if the modifications are documented in the database. When the contributions of the independent amino acids are studied with out considering the secondary and tertiary structure we observed different values of the extinction coefficient along with their absorbance values both with assuming and with out assuming cysteine residues. The small secreted glycoprotein in all species of the Ebola virus is stable as it has value less than 40. when we determined the positive factor which explains the increment phenomenon of the globular proteins and volume occupied relatively by the aliphatic side chains we observed the values in this order i.e; 78.96 (Zaire Ebolavirus) > 74.95 (Sudan Ebolavirus) > 72.60 (Taiforest Ebolavirus) > 70.90 (Reston Ebolavirus) > 70.24 (Bundibugyo Ebolavirus). and when we studied the phenomenon of the protein that is exhibiting the ability of repelling from the water, the hydrophobicity value of the Zaire Ebolavirus is more (-0.321) and Reston Ebolavirus (-0.494) is less .



|  |                      | Bundibugyo Ebola virus                 | Sudan Ebola virus                      | Reston Ebola virus                     | Zaire Ebola virus                      | Tai forest ebola virus                |
|--|----------------------|--|--|--|--|---------------------------------------|
| Number and composition of amino acids<br><br>SPIKE GLYCO-PROTEIN | Alanine (Ala)        | 34(5.0%)                               | 43(6.4%)                               | 41(6.1%)                               | 48(7.1%)                               | 41(6.1%)                              |
|  | Arginine (Arg)       | 35(5.2%)                               | 33(4.9%)                               | 28(4.1%)                               | 33(4.9%)                               | 28(4.1%)                              |
|  | Asparagine (Asn)     | 43(6.4%)                               | 38(5.6%)                               | 43(6.4%)                               | 37(5.5%)                               | 40(5.9%)                              |
|  | Aspartic acid (Asp)  | 34(5.0%)                               | 29(4.3%)                               | 30(4.4%)                               | 35(5.2%)                               | 30(4.4%)                              |
|  | Cysteine (Cys)       | 12(1.8%)                               | 13(1.9%)                               | 13(1.9%)                               | 12(1.8%)                               | 13(1.9%)                              |
|  | Glutamine (Gln)      | 26(3.8%)                               | 28(4.1%)                               | 31(4.6%)                               | 27(4.0%)                               | 25(3.7%)                              |
|  | Glutamic acid (Glu)  | 38(5.6%)                               | 40(5.9%)                               | 35(5.2%)                               | 36(5.3%)                               | 37(5.5%)                              |
|  | Glycine (Gly)        | 40(5.9%)                               | 51(7.5%)                               | 49(7.2%)                               | 53(7.8%)                               | 47(7.0%)                              |
|  | Histidine (His)      | 20(3.0%)                               | 15(2.2%)                               | 15(2.2%)                               | 18(2.7%)                               | 18(2.7%)                              |
|  | Iso-Leucine (Ile)    | 39(5.8%)                               | 48(7.1%)                               | 39(5.8%)                               | 42(6.2%)                               | 40(5.9%)                              |
|  | Leucine (Leu)        | 52(7.7%)                               | 60(8.9%)                               | 57(8.4%)                               | 51(7.5%)                               | 54(8.0%)                              |
|  | Lysine (Lys)         | 26(3.8%)                               | 27(4.0%)                               | 28(4.1%)                               | 30(4.4%)                               | 31(4.6%)                              |
|  | Methionine (Met)     | 06(0.9%)                               | 06(0.9%)                               | 10(1.5%)                               | 04(0.6%)                               | 07(1.0%)                              |
|  | Phenyl Alanine (Phe) | 29(4.3%)                               | 24(3.6%)                               | 22(3.2%)                               | 30(4.4%)                               | 32(4.7%)                              |
|  | Proline (Pro)        | 56(8.3%)                               | 46(6.8%)                               | 51(7.5%)                               | 35(5.2%)                               | 49(7.2%)                              |
|  | Serine (Ser)         | 36(5.3%)                               | 47(7.0%)                               | 55(8.1%)                               | 48(7.1%)                               | 41(6.1%)                              |
|  | Threonine (Thr)      | 81(12.0%)                              | 70(10.4%)                              | 65(9.6%)                               | 73(10.8%)                              | 77(11.4%)                             |
|  | Tryptophan (Trp)     | 14(2.1%)                               | 14(2.1%)                               | 14(2.1%)                               | 14(2.1%)                               | 14(2.1%)                              |
|  | Tyrosine (Tyr)       | 15(2.2%)                               | 16(2.4%)                               | 17(2.5%)                               | 15(2.2%)                               | 12(1.8%)                              |
|  | Valine (Val)         | 40(5.9%)                               | 28(4.1%)                               | 34(5.0%)                               | 35(5.2%)                               | 40(5.9%)                              |
| Molecular weight   |                      | 75689.18                               | 74594.18                               | 74416.73                               | 74464.46                               | 74676.43                              |
| Theoretical pI   |                      | 6.01                                   | 5.97                                   | 5.96                                   | 6.16                                   | 6.16                                  |
| Atomic composition   |                      | 10556                                  | 10434                                  | 10365                                  | 10375                                  | 10441                                 |
| Total number of positively charged residues                      |                      | 61                                     | 60                                     | 56                                     | 63                                     | 59                                    |
| Total number of Negatively charged residues                      |                      | 72                                     | 69                                     | 65                                     | 71                                     | 67                                    |
| Extinction coefficient assuming cystine residues                 |                      | 100100M <sup>-1</sup> cm <sup>-1</sup> | 101590M <sup>-1</sup> cm <sup>-1</sup> | 103080M <sup>-1</sup> cm <sup>-1</sup> | 100100M <sup>-1</sup> cm <sup>-1</sup> | 95630M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance assuming cystine residues                             |                      | 1.323                                  | 1.362                                  | 1.385                                  | 1.344                                  | 1.281                                 |
| Extinction coefficient with out cystine residues                 |                      | 99350M <sup>-1</sup> cm <sup>-1</sup>  | 100840M <sup>-1</sup> cm <sup>-1</sup> | 102330M <sup>-1</sup> cm <sup>-1</sup> | 99350M <sup>-1</sup> cm <sup>-1</sup>  | 94880M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance with out cystine residues                             |                      | 1.313                                  | 1.352                                  | 1.375                                  | 1.334                                  | 1.271                                 |
| Instability Index  |                      | 38.53                                  | 43.39                                  | 42.36                                  | 38.36                                  | 37.21                                 |
| Aliphatic Index  |                      | 74.69                                  | 80.68                                  | 75.92                                  | 75.77                                  | 77.46                                 |
| Grand Average of Hydrophaticity                                  |                      | -0.466                                 | -0.352                                 | -0.404                                 | -0.380                                 | -0.320                                |

Table-6: The above table describes different physico-chemical properties associated with the Spike glycoProtein of Ebola virus species, in which all forms of spike glycol-protein in all species of the ebola virus species have same number and composition of the aminoacids(approximate values) on the whole but varies when compared with the individual aminoacids. When we calculated average isotope mass of the aminoacid in the protein and one watermolecule the total molecular weight of the protein is estimated to be in this order i.e;75689.18 >7467.43 >74594.18 >74464.46 >74416.73,by this we concluded that the Bundibugyo Ebolavirus having greater molecular weight and Reston Ebolavirus with smaller molecular weight.Compute pI/Mw algorithmis mainly used to enhance a region in a 2-D gel to which an a protein which is unmodified should allowed to run,and point a region in which modified form of protein should be found if the modifications are documented in the database.when we calculated the sums of different aminoacid contributions assuming them as independent with out considering the secondary and tertiary structures,we observed different values of extinction coefficient with and with out assuming cysteine residues with different absorbance.The spike glycol-protein of the sudan ebol virus and reston Ebolavirus is more unstable when compared with the other forms of the virus species as values are greater than 40.when we determined the positive factor which explains the increment phenomenon of the globular proteins and volume occupied relatively by the aliphatic side chains we observed 80.68(Sudan Ebolavirus) >77.46(Tai Forest Ebolavirus) >75.92(Reston Ebolavirus) >75.77 (Zaire Ebolavirus)>74.69(Bundibugyo Ebolavirus)and when we studied the phenomenon of the protein that is exhibiting the ability of repelling from the water,the hydrophobicity value of the Taiforest Ebolavirus(-0.320) is more and for Bundibugyo Ebolavirus(-0.466),it is less.



|  |                      | Bundibugyo Ebola virus                | Sudan Ebola virus                     | Reston Ebola virus                    | Zaire Ebola virus                     | Tai forest ebola virus                |
|--|----------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|
| MEMBRANE ASSOCIATED PROTEIN                      | Alanine (Ala)        | 19(7.6%)                              | 15(6.0%)                              | 15(6.0%)                              | 16(6.4%)                              | 20(8.0%)                              |
|  | Arginine (Arg)       | 10(4.0%)                              | 11(4.4%)                              | 11(4.4%)                              | 10(4.0%)                              | 08(3.2%)                              |
|  | Asparagine (Asn)     | 13(5.2%)                              | 16(6.4%)                              | 14(5.6%)                              | 17(6.8%)                              | 13(5.2%)                              |
|  | Aspartic acid (Asp)  | 10(4.0%)                              | 09(3.6%)                              | 10(4.0%)                              | 09(3.6%)                              | 09(3.6%)                              |
|  | Cysteine (Cys)       | 01(0.4%)                              | 01(0.4%)                              | 01(0.4%)                              | 01(0.4%)                              | 01(0.4%)                              |
|  | Glutamine (Gln)      | 14(5.6%)                              | 10(4.0%)                              | 12(4.8%)                              | 12(4.8%)                              | 15(6.0%)                              |
|  | Glutamic acid (Glu)  | 10(4.0%)                              | 11(4.4%)                              | 08(3.2%)                              | 10(4.0%)                              | 10(4.0%)                              |
|  | Glycine (Gly)        | 11(4.4%)                              | 11(4.4%)                              | 13(5.2%)                              | 13(5.2%)                              | 13(5.2%)                              |
|  | Histidine (His)      | 07(2.8%)                              | 06(2.4%)                              | 06(2.4%)                              | 07(2.8%)                              | 06(2.4%)                              |
|  | Iso-Leucine (Ile)    | 17(6.8%)                              | 18(7.2%)                              | 17(6.8%)                              | 19(7.6%)                              | 17(6.8%)                              |
|  | Leucine (Leu)        | 38(15.1%)                             | 33(13.1%)                             | 36(14.3%)                             | 37(14.7%)                             | 39(15.5%)                             |
|  | Lysine (Lys)         | 16(6.4%)                              | 13(5.2%)                              | 13(5.2%)                              | 15(6.0%)                              | 17(6.8%)                              |
|  | Methionine (Met)     | 08(3.2%)                              | 09(3.6%)                              | 09(3.6%)                              | 09(3.6%)                              | 08(3.2%)                              |
|  | Phenyl Alanine (Phe) | 11(4.4%)                              | 10(4.0%)                              | 13(5.2%)                              | 11(4.4%)                              | 09(3.6%)                              |
|  | Proline (Pro)        | 09(3.6%)                              | 13(5.2%)                              | 12(4.8%)                              | 09(3.6%)                              | 10(4.0%)                              |
|  | Serine (Ser)         | 20(8.0%)                              | 19(7.6%)                              | 21(8.4%)                              | 21(8.4%)                              | 18(7.2%)                              |
|  | Threonine (Thr)      | 17(6.8%)                              | 18(7.2%)                              | 18(7.2%)                              | 17(6.8%)                              | 20(8.0%)                              |
|  | Tryptophan (Trp)     | 05(2.0%)                              | 05(2.0%)                              | 05(2.0%)                              | 05(2.0%)                              | 05(2.0%)                              |
| Tyrosine (Tyr)                                   | 02(0.8%)             | 05(2.0%)                              | 03(1.2%)                              | 03(1.2%)                              | 02(0.8%)                              |                                       |
| Valine (Val)                                     | 13(5.2%)             | 18(7.2%)                              | 14(5.6%)                              | 10(4.0%)                              | 11(4.4%)                              |                                       |
| Molecular weight                                 |                      | 28163.88                              | 28276.97                              | 28168.88                              | 28218.85                              | 27887.58                              |
| Theoretical pI                                   |                      | 9.49                                  | 9.18                                  | 9.55                                  | 9.49                                  | 9.46                                  |
| Atomic composition                               |                      | 4031                                  | 4034                                  | 4019                                  | 4023                                  | 3998                                  |
| Total number of positively charged residues      |                      | 26                                    | 24                                    | 24                                    | 25                                    | 25                                    |
| Total number of Negatively charged residues      |                      | 20                                    | 20                                    | 18                                    | 19                                    | 19                                    |
| Extinction coefficient assuming cystine residues |                      | 30480M <sup>-1</sup> cm <sup>-1</sup> | 34950M <sup>-1</sup> cm <sup>-1</sup> | 31970M <sup>-1</sup> cm <sup>-1</sup> | 31970M <sup>-1</sup> cm <sup>-1</sup> | 30480M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance assuming cystine residues             |                      | 1.082                                 | 1.236                                 | 1.135                                 | 1.133                                 | 1.093                                 |
| Extinction coefficient with out cystine residues |                      | 30480M <sup>-1</sup> cm <sup>-1</sup> | 34950M <sup>-1</sup> cm <sup>-1</sup> | 31970M <sup>-1</sup> cm <sup>-1</sup> | 31970M <sup>-1</sup> cm <sup>-1</sup> | 30480M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance with out cystine residues             |                      | 1.082                                 | 1.236                                 | 1.135                                 | 1.133                                 | 1.093                                 |
| Instability Index                                |                      | 35.69                                 | 24.36                                 | 39.95                                 | 36.51                                 | 34.47                                 |
| Aliphatic Index                                  |                      | 108.05                                | 106.02                                | 104.50                                | 104.94                                | 107.69                                |
| Grand Average of Hydrophaticity                  |                      | 0.040                                 | 0.049                                 | 0.078                                 | -0.013                                | 0.028                                 |

Table-1: The above table describes different physico-chemical properties associated with the membrane associated protein of Ebola virus species, in which all forms of membrane associated protein in all species of the Ebola virus species have same number and composition of the amino acids (approximate values) on the whole but varies when compared with the individual amino acids. When we calculated average isotope mass of the amino acid in the protein and one water molecule the total molecular weight of the protein is estimated to be in this order i.e.; 28276.97 > 28218.85 > 28168.88 > 28163.88 > 27887.58. By this we can say that Sudan Ebolavirus has greater molecular weight and Taiforest Ebolavirus has smaller molecular weight. Compute pI/Mw algorithm is mainly used to enhance a region in a 2-D gel to which a protein which is unmodified should be allowed to run, and point a region in which modified form of protein should be found if the modifications are documented in the database. When we calculated the sums of different amino acid contributions assuming them as independent with out considering the secondary and tertiary structures, we observed similar values of extinction coefficient and absorbance in all species of Ebola virus with and with out assuming cysteine residues. The membrane associated protein of all virus species is more stable. When we determined the positive factor which explains the increment phenomenon of the globular proteins and volume occupied relatively by the aliphatic side chains we observed the values in this order i.e.; 108.05 (Bundibugyo Ebolavirus) > 107.69 (Taiforest Ebolavirus) > 106.02 (Sudan Ebolavirus) > 104.94 (Zaire Ebolavirus) > 104.50 (Reston Ebolavirus) and when we studied the phenomenon of the protein that is exhibiting the ability of repelling from the water, the hydrophobicity value of the Zaire Ebolavirus (-0.013) is smaller and Reston Ebolavirus (0.078) is more.



|  |                      | Bundibugyo Ebola virus                | Sudan Ebola virus                     | Reston Ebola virus                    | Zaire Ebola virus                     | Tai forest ebola virus                |
|--|----------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|
| MINOR-NUCLEOPROTEIN                              | Alanine (Ala)        | 14(4.8%)                              | 20(6.9%)                              | 19(6.6%)                              | 21(7.3%)                              | 16(5.5%)                              |
|  | Arginine (Arg)       | 26(9.0%)                              | 23(8.0%)                              | 23(8.0%)                              | 25(8.7%)                              | 23(8.0%)                              |
|  | Asparagine (Asn)     | 05(1.7%)                              | 10(3.5%)                              | 13(4.5%)                              | 06(2.1%)                              | 06(2.1%)                              |
|  | Aspartic acid (Asp)  | 19(6.6%)                              | 18(6.2%)                              | 18(6.3%)                              | 16(5.6%)                              | 15(5.2%)                              |
|  | Cysteine (Cys)       | 07(2.4%)                              | 06(2.1%)                              | 07(2.4%)                              | 08(2.8%)                              | 08(2.8%)                              |
|  | Glutamine (Gln)      | 18(6.2%)                              | 16(5.6%)                              | 17(5.9%)                              | 18(6.2%)                              | 17(5.9%)                              |
|  | Glutamic acid (Glu)  | 18(6.2%)                              | 16(5.6%)                              | 16(5.6%)                              | 21(7.3%)                              | 19(6.6%)                              |
|  | Glycine (Gly)        | 13(4.5%)                              | 14(4.9%)                              | 10(3.5%)                              | 13(4.5%)                              | 12(4.2%)                              |
|  | Histidine (His)      | 09(3.1%)                              | 05(1.7%)                              | 09(3.1%)                              | 09(3.1%)                              | 08(2.8%)                              |
|  | Iso-Leucine (Ile)    | 12(4.2%)                              | 06(2.1%)                              | 13(4.5%)                              | 10(3.5%)                              | 13(4.5%)                              |
|  | Leucine (Leu)        | 35(12.1%)                             | 36(12.5%)                             | 35(12.2%)                             | 32(11.1%)                             | 33(11.4%)                             |
|  | Lysine (Lys)         | 14(4.8%)                              | 16(5.6%)                              | 14(4.9%)                              | 15(5.2%)                              | 16(5.5%)                              |
|  | Methionine (Met)     | 03(1.0%)                              | 02(0.7%)                              | 04(1.4%)                              | 03(1.0%)                              | 05(1.7%)                              |
|  | Phenyl Alanine (Phe) | 09(3.1%)                              | 10(3.5%)                              | 08(2.8%)                              | 08(2.8%)                              | 08(2.8%)                              |
|  | Proline (Pro)        | 13(4.5%)                              | 14(4.9%)                              | 15(5.2%)                              | 15(5.2%)                              | 13(4.5%)                              |
|  | Serine (Ser)         | 33(11.4%)                             | 31(10.8%)                             | 32(11.1%)                             | 27(9.4%)                              | 35(12.1%)                             |
|  | Threonine (Thr)      | 22(7.6%)                              | 23(8.0%)                              | 16(5.6%)                              | 19(6.6%)                              | 18(6.2%)                              |
|  | Tryptophan (Trp)     | 04(1.4%)                              | 04(1.4%)                              | 04(1.4%)                              | 04(1.4%)                              | 04(1.4%)                              |
| Tyrosine (Tyr)                                   | 04(1.4%)             | 03(1.0%)                              | 03(1.0%)                              | 04(1.4%)                              | 04(1.4%)                              |                                       |
| Valine (Val)                                     | 11(3.8%)             | 15(5.2%)                              | 11(3.8%)                              | 14(4.9%)                              | 16(5.5%)                              |                                       |
| Molecular weight                                 |                      | 32839.07                              | 32107.22                              | 32400.65                              | 32520.80                              | 32600.14                              |
| Theoretical pI                                   |                      | 8.46                                  | 8.89                                  | 8.46                                  | 8.40                                  | 8.76                                  |
| Atomic composition                               |                      | 4600                                  | 4509                                  | 4538                                  | 4555                                  | 4582                                  |
| Total number of positively charged residues      |                      | 40                                    | 39                                    | 37                                    | 40                                    | 39                                    |
| Total number of Negatively charged residues      |                      | 37                                    | 34                                    | 34                                    | 37                                    | 34                                    |
| Extinction coefficient assuming cystine residues |                      | 28335M <sup>-1</sup> cm <sup>-1</sup> | 26845M <sup>-1</sup> cm <sup>-1</sup> | 26845M <sup>-1</sup> cm <sup>-1</sup> | 28460M <sup>-1</sup> cm <sup>-1</sup> | 28460M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance assuming cystine residues             |                      | 0.863                                 | 0.836                                 | 0.829                                 | 0.875                                 | 0.873                                 |
| Extinction coefficient with out cystine residues |                      | 27960M <sup>-1</sup> cm <sup>-1</sup> | 26470M <sup>-1</sup> cm <sup>-1</sup> | 26470M <sup>-1</sup> cm <sup>-1</sup> | 27960M <sup>-1</sup> cm <sup>-1</sup> | 27960M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance with out cystine residues             |                      | 0.851                                 | 0.824                                 | 0.817                                 | 0.860                                 | 0.858                                 |
| Instability Index                                |                      | 59.23                                 | 48.85                                 | 53.74                                 | 52.08                                 | 57.49                                 |
| Aliphatic Index                                  |                      | 79.31                                 | 78.92                                 | 82.96                                 | 78.26                                 | 83.67                                 |
| Grand Average of Hydrophaticity                  |                      | -0.624                                | -0.551                                | -0.571                                | -0.607                                | -0.464                                |

Table-1: The above table describes different physico-chemical properties associated with the minor nucleoprotein of Ebola virus species, in which all forms of minor nucleoprotein in all species of the Ebola virus species have same number and composition of the amino acids (approximate values) on the whole but varies when compared with the individual amino acids. When we calculated average isotope mass of the amino acid in the protein and one water molecule the total molecular weight of the protein is estimated to be in this order i.e.; 32839.07 > 32600.14 > 32520.80 > 21400.65 > 32107.22. By this we can say that Bundibugyo Ebolavirus has greater molecular weight and Sudan Ebolavirus has smaller molecular weight. Compute pI/Mw algorithm is mainly used to enhance a region in a 2-D gel to which a protein which is unmodified should be allowed to run, and point a region in which modified form of protein should be found if the modifications are documented in the database. When we calculated the sums of different amino acid contributions assuming them as independent with out considering the secondary and tertiary structures, we observed different values of extinction coefficient and absorbance in all species of Ebola virus with and with out assuming cysteine residues. The Minor Nucleoprotein of all virus species is more unstable. When we determined the positive factor which explains the increment phenomenon of the globular proteins and volume occupied relatively by the aliphatic side chains we observed the values in this order i.e.; 83.67 (Taiforest Ebolavirus) > 82.96 (Reston Ebolavirus) > 79.31 (Bundibugyo Ebolavirus) > 78.92 (Sudan Ebolavirus) > 78.26 (Zaire Ebolavirus) and when we studied the phenomenon of the protein that is exhibiting the ability of repelling from the water, the hydrophobicity value of the Taiforest Ebolavirus (-0.464) is greater and the value of the Bundibugyo Ebolavirus (-0.624) is less.



|  |                      | Bundibugyo Ebola virus                 | Sudan Ebola virus                      | Reston Ebola virus                     | Zaire Ebola virus                      | Tai forest ebola virus                 |
|--|----------------------|--|--|--|--|--|
| RNA DEPENDENT RNA POLYMERASE                     | Alanine (Ala)        | 121(5.5%)                              | 122(5.5%)                              | 115(5.2%)                              | 119(5.4%)                              | 127(5.7%)                              |
|  | Arginine (Arg)       | 113(5.1%)                              | 131(5.9%)                              | 113(5.1%)                              | 118(5.3%)                              | 119(5.4%)                              |
|  | Asparagine (Asn)     | 109(4.9%)                              | 114(5.2%)                              | 126(5.7%)                              | 106(4.8%)                              | 113(5.1%)                              |
|  | Aspartic acid (Asp)  | 104(4.7%)                              | 98(4.4%)                               | 107(4.8%)                              | 103(4.7%)                              | 98(4.4%)                               |
|  | Cysteine (Cys)       | 44(2.0%)                               | 45(2.0%)                               | 43(1.9%)                               | 43(1.9%)                               | 46(2.1%)                               |
|  | Glutamine (Gln)      | 102(4.6%)                              | 91(4.1%)                               | 103(4.7%)                              | 107(4.8%)                              | 97(4.4%)                               |
|  | Glutamic acid (Glu)  | 107(4.8%)                              | 106(4.8%)                              | 105(4.7%)                              | 109(4.9%)                              | 106(4.8%)                              |
|  | Glycine (Gly)        | 102(4.6%)                              | 107(4.8%)                              | 108(4.9%)                              | 101(4.6%)                              | 103(4.7%)                              |
|  | Histidine (His)      | 70(3.2%)                               | 72(3.3%)                               | 75(3.4%)                               | 76(3.4%)                               | 79(3.6%)                               |
|  | Iso-Leucine (Ile)    | 148(6.7%)                              | 153(6.9%)                              | 144(6.5%)                              | 147(6.6%)                              | 151(6.8%)                              |
|  | Leucine (Leu)        | 255(11.5%)                             | 258(11.7%)                             | 269(12.2%)                             | 250(11.3%)                             | 264(11.9%)                             |
|  | Lysine (Lys)         | 121(5.5%)                              | 101(4.6%)                              | 116(5.2%)                              | 113(5.1%)                              | 107(4.8%)                              |
|  | Methionine (Met)     | 28(1.3%)                               | 38(1.7%)                               | 34(1.5%)                               | 38(1.7%)                               | 25(1.1%)                               |
|  | Phenyl Alanine (Phe) | 106(4.8%)                              | 97(4.4%)                               | 102(4.6%)                              | 116(5.2%)                              | 100(4.5%)                              |
|  | Proline (Pro)        | 105(4.8%)                              | 110(5.0%)                              | 98(4.4%)                               | 102(4.6%)                              | 107(4.8%)                              |
|  | Serine (Ser)         | 191(8.6%)                              | 186(8.4%)                              | 184(8.3%)                              | 184(8.3%)                              | 188(8.5%)                              |
|  | Threonine (Thr)      | 143(6.5%)                              | 153(6.9%)                              | 132(6.0%)                              | 154(7.0%)                              | 151(6.8%)                              |
|  | Tryptophan (Trp)     | 30(1.4%)                               | 29(1.3%)                               | 30(1.4%)                               | 29(1.3%)                               | 29(1.3%)                               |
|  | Tyrosine (Tyr)       | 93(4.2%)                               | 89(4.0%)                               | 97(4.4%)                               | 87(3.9%)                               | 85(3.8%)                               |
|  | Valine (Val)         | 118(5.3%)                              | 110(5.0%)                              | 111(5.0%)                              | 110(5.0%)                              | 115(5.2%)                              |
| Molecular weight                                 |                      | 251649.28                              | 251294.24                              | 252549.04                              | 252724.47                              | 250746.25                              |
| Theoretical pI                                   |                      | 8.64                                   | 8.77                                   | 8.48                                   | 8.55                                   | 8.62                                   |
| Atomic composition                               |                      | 35452                                  | 35386                                  | 35520                                  | 35538                                  | 35339                                  |
| Total number of positively charged residues      |                      | 234                                    | 232                                    | 229                                    | 231                                    | 226                                    |
| Total number of Negatively charged residues      |                      | 211                                    | 204                                    | 212                                    | 212                                    | 204                                    |
| Extinction coefficient assuming cystine residues |                      | 306320M <sup>-1</sup> cm <sup>-1</sup> | 294860M <sup>-1</sup> cm <sup>-1</sup> | 312155M <sup>-1</sup> cm <sup>-1</sup> | 291755M <sup>-1</sup> cm <sup>-1</sup> | 289025M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance assuming cystine residues             |                      | 1.217                                  | 1.173                                  | 1.236                                  | 1.154                                  | 1.153                                  |
| Extinction coefficient with out cystine residues |                      | 303570M <sup>-1</sup> cm <sup>-1</sup> | 292110M <sup>-1</sup> cm <sup>-1</sup> | 309530M <sup>-1</sup> cm <sup>-1</sup> | 289130M <sup>-1</sup> cm <sup>-1</sup> | 286150M <sup>-1</sup> cm <sup>-1</sup> |
| Absorbance with out cystine residues             |                      | 1.206                                  | 1.162                                  | 1.226                                  | 1.144                                  | 1.141                                  |
| Instability Index                                |                      | 39.74                                  | 42.07                                  | 41.60                                  | 41.34                                  | 40.33                                  |
| Aliphatic Index                                  |                      | 92.08                                  | 92.48                                  | 92.57                                  | 89.80                                  | 94.07                                  |
| Grand Average of Hydrophaticity                  |                      | -0.218                                 | -0.206                                 | -0.242                                 | -0.230                                 | -0.191                                 |

Table-1: The above table describes different physico-chemical properties associated with the RNA dependent RNA Polymerase protein of Ebola virus species, in which all forms of RNA dependent RNA Polymerase in all species of the Ebola virus species have same number and composition of the amino acids (approximate values) on the whole but varies when compared with the individual amino acids. When we calculated average isotope mass of the amino acid in the protein and one water molecule the total molecular weight of the protein is estimated to be in this order i.e.; 252724.47 > 252549.04 > 251649.28 > 251294.24 > 250746.25 i.e.; Zaire Ebolavirus with greater molecular weight and Taiforest Ebola virus with small molecular weight. Compute pI/Mw algorithm is mainly used to enhance a region in a 2-D gel to which an a protein which is unmodified should allowed to run, and point a region in which modified form of protein should be found if the modifications are documented in the database. when we calculated the sums of different amino acid contributions assuming them as independent with out considering the secondary and tertiary structures, we observed different values of extinction coefficient and absorbance in all species of Ebola virus with and with out assuming cysteine residues. The RNA dependent RNA polymerase of Bundibugyo Ebolavirus is more stable when compared to other virus species. when we determined the positive factor which explains the increment phenomenon of the globular proteins and volume occupied relatively by the aliphatic side chains we observed the values in this order i.e.; 94.07 (Taiforest Ebolavirus) > 92.57 (Reston Ebolavirus) > 92.48 (Sudan Ebolavirus) > 92.08 (Bundibugyo Ebolavirus) > 89.80 (Zaire Ebolavirus) and when we studied the phenomenon of the protein that is exhibiting the ability of repelling from the water, the hydrophobicity value of the Taiforest Ebolavirus (-0.191) is greater and the value of the Reston Ebolavirus (-0.242) is less







MINOR-NUCLEO PROTEIN

Reston MEHSREGRGRSSNMRHNSREPYENPSRSRSLSRDPNQVDRRQPRASQIRVFNLFHRKKT 60  
 Sudan MERGREGRGRSRNSRADQQNSGTPQFRTRISIRDKTTDYRSRSTSQVVRVTFVHKKGTG 60  
 Zaire MEASYERGRPRAARQHSRDGHDHVRARSSSRENYRGEYRQSRASQVVRVTFVHKKRVE 60  
 Taiforest MEVVHERGRSRI SRQNRTRDGP SHLVRRARSSSRASYRSEYHTPRASQIRVPTVFHRKKT 60  
 Bundibugyo MDSFHERGRSRTIRQSARDGSPHQVTRSSSRDSSHREYHTPRSSSQVVRVTFVHRKRTD 60  
 \*: \*\*\*\* \* : : \* : \* \* : : \* : \* : \* : \* : \* : \*

Reston ALIVPPAPKIDICPTLKKGFCLDSFKCKKDHQLESLDRELLLLIARCTCGIIESNSQITS 120  
 Sudan PLTVPPAPKIDICPTLKKGFCLDSNFCKKDHQLESLDRELLLLIARCTCGSTDSLLNIAA 120  
 Zaire PLTVPPAPKIDICPTLKKGFCLDSNFCKKDHQLESLDRELLLLIARCTCGSVEQQQLNITA 120  
 Taiforest LLTVPPAPKIDICPTLKKGFCLDSNFCKKDHQLESLDRELLLLIARCTCGSTEQQQLSIVA 120  
 Bundibugyo SLTVPPAPKIDICPTLKKGFCLDSNFCKKDHQLESLDRELLLLIARCTCGSLEQQQLNITA 120  
 \* \*\*\*\*\* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Reston PKDMRLANPTAEDFSQGNPKLTLAVLLQIAEHWA TRDLRQIEDSKLRALLTLCVAVLTRK 180  
 Sudan PKDLRLANPTADDFKQDGSFKLTLKLLVETAEFWANQINNEVDDAKLRALLTLCVAVLVRK 180  
 Zaire PKDSRLANPTADDFQEEGPKITLLT LIKTAEHWA RQDIRTIEDSKLRALLTLCVAVMTRK 180  
 Taiforest PKDSRLANPTAEDFQKQDGPKVTLTSM LIETAEYWSKQDIKNIDDSRLRALLTLCVAVMTRK 180  
 Bundibugyo PKDTRLANPTADDFQKDGPKITLLTLETAEYWSKQDIKNIDDSRLRALLTLCVAVMTRK 180  
 \*\*\* \*\*\*\*\* \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Reston FSKSQLGLLCEHLRHEGLGQDQADS VLEVYQRLHSDKGGNFEAALWQQWDRQSLIMFIS 240  
 Sudan FSKSQLSQCESHLLRRENLGQDQAESVLEVYQRLHSDKGGAFEAALWQQWDRQSLTMFIS 240  
 Zaire FSKSQLSLLCEHLRREGLGQDQAEVLEVYQRLHSDKGGSFEAALWQQWDRQSLIMFIT 240  
 Taiforest FSKSQLSLLCEHLRREGLGQDQSES VLEVYQRLHSDKGGNFEAALWQQWDRQSLIMFIT 240  
 Bundibugyo FSKSQLSLLCEHLRREGLGQDQSES VLEVYQRLHSDKGGNFEAALWQQWDRQSLIMFIT 240  
 \*\*\*\*\* . \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Reston AFLNIALQIPCESSVSVVSGLATLYPAQDNSTPSEATNDTTWSSTVE -- 287  
 Sudan AFLHVALQLSCESSVTVVSGLRLLAPPVNEGLPPAPGEYTWSEDST -- 288  
 Zaire AFLNIALQIPCESSAVVSGLR TLVPSQDNEEASTNPGTCSWSDEGTP -- 288  
 Taiforest AFLNIALQIPCESSVVI SGLRMLIPQSEATEVVTPECTWSEGGSSH 289  
 Bundibugyo AFLNIALQIPCESSVVI SGLRLLVPSQEDTETSTYTETRAWSEEGGPH 289  
 \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

NUCLEO-PROTEIN

Sudan MDKRVRGSWALGGQSEVDLDYHKILTAGLSVQQGIVRQRVIPVYVVS DLEGICQHIIQAF 60  
 Reston MDRGTRRIWVSNQGD TDDLYHKILTAGLTVQQGIVRQKIISVYLVDNLEAMCQLVIQAF 60  
 Zaire MDSRFQKIWMAPSLTESDMDYHKILTAGLSVQQGIVRQRVIPVYQVNNLEEICQLIIQAF 60  
 Taiforest MESRAHKAWMHTASGFETDYHKILTAGLSVQQGIVRQRVIQVHQVTNLEEICQLIIQAF 60  
 Bundibugyo MDRPRIRTWMMHNTSEVEADYHKILTAGLSVQQGIVRQRIIPVYQISNLEEVCQLIIQAF 60  
 \*: \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Sudan EAGVDFQDNADSFLLMLCLH HAYQGDHRLFLKSDAVQYLEGHGFRFEVREKENVHRLDEL 120  
 Reston EAGIDFQENADSFLLMLCLH HAYQGDYKLFLESNAVQYLEGHGFKFELRKKDGVNRLDEL 120  
 Zaire EAGVDFQESADSFLLMLCLH HAYQGDYKLFLESNAVQYLEGHGFRFEVVRKRDGVKRLDEL 120  
 Taiforest EAGVDFQESADSFLLMLCLH HAYQGDYKLFLESNAVQYLEGHGFRFEVVRKKEGVKRLDEL 120  
 Bundibugyo EAGVDFQDSADSFLLMLCLH HAYQGDYKLFLESNAVQYLEGHGFRFEMKKKEGVKRLDEL 120  
 \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Sudan LPNVTGGKNLRRTLAAMPEEETTEANAGQFLSFASLFLPKLVVGEKACLEKQVQRQIQVHA 180  
 Reston LPAATSGKNI RRTLAALPEEETTEANAGQFLSFASLFLPKLVVGEKACLEKQVQRQIQVHA 180  
 Zaire LPVAVSSGKNIKRTLAAMPEEETTEANAGQFLSFASLFLPKLVVGEKACLEKQVQRQIQVHA 180  
 Taiforest LPAASSGKNI RRTLAAMPEEETTEANAGQFLSFASLFLPKLVVGEKACLEKQVQRQIQVHS 180  
 Bundibugyo LPAASSGKNIKRTLAAMPEEETTEANAGQFLSFASLFLPKLVVGEKACLEKQVQRQIQVHA 180  
 \* \* . : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Sudan EQGLIQYPTSWQSVGHMMVIFRLMRTNFLIKFLLIHQGMHVMVAGHDANDTVISNSVAQAR 240  
 Reston EQGLIQYPTAWQSVGHMMVIFRLMRTNFLIKYLLIHQGMHVMVAGHDANDAVIANSVAQAR 240  
 Zaire EQGLIQYPTAWQSVGHMMVIFRLMRTNFLIKFLLIHQGMHVMVAGHDANDAVIANSVAQAR 240  
 Taiforest EQGLIQYPTAWQSVGHMMVIFRLMRTNFLIKFLLIHQGMHVMVAGHDANDAVIANSVAQAR 240  
 Bundibugyo EQGLIQYPTSWQSVGHMMVIFRLMRTNFLIKFLLIHQGMHVMVAGHDANDAVIANSVAQAR 240  
 \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Sudan FSGLLIVKTVLDHILQKTDLGVRLHPLARTAKVKNEVNSFKAALGSLAKHGEYAPFARLL 300  
 Reston FSGLLIVKTVLDHILQKTDQVRLHPLARTAKVRNEVNAFKAALS SLAKHGEYAPFARLL 300  
 Zaire FSGLLIVKTVLDHILQKTERGVRLHPLARTAKVKNEVNSFKAALS SLAKHGEYAPFARLL 300  
 Taiforest FSGLLIVKTVLDHILQKTEHGVRLHPLARTAKVKNEVNSFKAALS SLAQHGEYAPFARLL 300  
 Bundibugyo FSGLLIVKTVLDHILQKTEHGVRLHPLARTAKVKNEVNSFKAALA SLAQHGEYAPFARLL 300  
 \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Sudan NLSGVNNLEHGLYPQLSAIALGVATAHGSTLAGVNVGEQYQQLREAA TEAEKQLQYQYAES 360  
 Reston NLSGVNNLEHGLYPQLSAIALGVATAHGSTLAGVNVGEQYQQLREAA TEAEKQLQYQYAES 360  
 Zaire NLSGVNNLEHGLFPQLSAIALGVATAHGSTLAGVNVGEQYQQLREAA TEAEKQLQYQYAES 360  
 Taiforest NLSGVNNLEHGLFPQLSAIALGVATAHGSTLAGVNVGEQYQQLREAA TEAEKQLQYQYAES 360  
 Bundibugyo NLSGVNNLEHGLFPQLSAIALGVATAHGSTLAGVNVGEQYQQLREAA TEAEKQLQYQYAES 360  
 \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*









Zaire ST---ASDTPSATTA-----GPKAEN---TNTSKSTDFL---DPA----- 447  
 Taiforest KT---TSQPTNSTEST-----TLNPTSE-----FSSRGTFSSPTVENTESHAELEGKT 453  
 Bundibugyo TL---ANNPPDNTFES-----TPQDGE-----RTSSHTFSPRPVPTSTIHPTRRETHI 453  
 Reston NTASIEDSPPSASNETIYHSEMDPIQSSNNSAQSPQTKTPEAPTTSPMTQDPQETANSSK 466  
 Sudan TAPSPFA-----QTPPTH-----TSGP-----SVMATEE 440

Zaire TTTSPQNHSETAG-----NNNTHHQDTGEESASSGKLGITNTIAGVAGLITGRRR 500  
 Taiforest PTTLPEQHTAASA-----IPRAVHPDELSGPGFLTNTIRGVNLLTGSRRKR 500  
 Bundibugyo PTTMTTSHDTSN-----RPNPIDISESTEPGLTNTTRGAANLLTGSRRR 500  
 Reston PGTSPGSAAGPS-----QPGLTINTVSKVADSLSPTRKQK 501  
 Sudan PTTFPGSSPGPTTEAPTLTTPENITTAVKTVLPQESTSNGLITSTVGTGILGSLGLRKR 500

Zaire REAIVNAQPKCNPNLHYWTTQDEGAAIGLAWIPYFPGPAEAGIYIEGLMHNQDGLICGLRQ 560  
 Taiforest RDVTPNTQPKCNPNLHYWTALDEGAAIGLAWIPYFPGPAEAGIYIEGLMHNQDGLICGLRQ 560  
 Bundibugyo REITLRTQAKCNPNLHYWTTQDEGAAIGLAWIPYFPGPAEAGIYIEGLMHNQDGLICGLRQ 560  
 Reston RSVRQNTANKCNPDLIYWTAVDEGAAIGLAWIPYFPGPAEAGIYIEGLMHNQDGLICGLRQ 561  
 Sudan RQNTKATGKCNPNLHYWTAQEQHNAAGIAWIPYFPGPAEAGIYIEGLMHNQDGLICGLRQ 560

Zaire LANETTQALQFLRATTELRTFSILNRKAIIDFLLQRWGGTCHILGPDCCIEPHDWTKNIT 620  
 Taiforest LANETTQALQFLRATTELRTFSILNRKAIIDFLLQRWGGTCHILGPDCCIEPHDWTKNIT 620  
 Bundibugyo LANETTQALQFLRATTELRTFSILNRKAIIDFLLQRWGGTCHILGPDCCIEPHDWTKNIT 620  
 Reston LANETTQALQFLRATTELRTYSLLNRKAIIDFLLQRWGGTCHILGPDCCIEPHDWTKNIT 621  
 Sudan LANETTQALQFLRATTELRTYTILNRKAIIDFLLRRWGGTCHILGPDCCIEPHDWTKNIT 620

Zaire DKIDQIIHDFVDKTLFDQGDNDNWWTGWQRWIPAGIGITGVI IAVIALFCICKFVF 676  
 Taiforest DKIDQIIHDFVDNPNLNDNNDNWWTGWQRWIPAGIGITGVI IAI IALLCICKFLL 676  
 Bundibugyo DKIDQIIHDFIDKPLFDQTDNDNWWTGWQRWIPAGIGITGVI IAVIALFCICKFLL 676  
 Reston DEINQIKHDFIDNPLFDHGDVLDNLTGWQRWIPAGIGITGVI IAI IALLCICKILC 677  
 Sudan DKINQIIHDFIDNPLFDQDNDNWWTGWQRWIPAGIGITGVI IAI IALLCICKL 676

RNA DEPENDENT RNA POLYMERASE

Zaire -MATQHTQYDPDARLSSPIVLDQCDLVTRACGLYSSYSLNPQLRCKLPKHIYRLKYDVT 59  
 Tai -MATQHTQYDPDARLSSPIVLDQCDLVTRACGLYSSYSLNPQLKNCRLPKHIYRLKYDT 59  
 Bundibugyo -MATQHTQYDPDARLSSPIVLDQCDLVTRACGLYSSYSLNPQLKNCRLPKHIYRLKFDAT 59  
 Sudan MMATQHTQYDPDARLSSPIVLDQCDLVTRACGLYSEYSLNPKLKTCRLPKHIYRLKYDTIV 60  
 Reston -MATQHTQYDPDARLSSPIVLDQCDLVTRACGLYSSYSLNPQLRQCKLPKHIYRLKFD 59

Zaire TKFLSDVPVATLPIIDFIVPVLKALSGNGFCVPEPRCQFLDEI IKYTMQDALFLKYLLK 119  
 Tai TEFLSDVPVATLPADFLVPTFLRSLGNGSCPIDPKCSQFLDEIVNYTLQDIRFLNYLN 119  
 Bundibugyo TKFLSDVPVATLPIIDYLPDLLRSLGNGFCVPEPRCQFLDEIVSYVLQDAREFLRYFR 119  
 Sudan LRFISDVPVATIPIDYIAPMLINVLADSKNVPLEPPCLSFLDEIVNYTVQDAFLNYLM 120  
 Reston SKFLSDTPVATLPIIDYLPILLRSLTGHGDRPLTPTCNQFLDEIINYTLHDAFLDYLLK 119

Zaire NVGAQEDCVDEHFQEKILSSIQGNEFLHQMFWDYDLAILTRRGRRLNRGNSRSTWFVHDDL 179  
 Tai RAGVHNDHVDRDFGQKIRNLICDNEVLHQMFHWYDLAILARRGRRLNRGNSRSTWFASDNL 179  
 Bundibugyo HVGVHDDNVGKNFEPKIKALIDNEFLQQLFYWDYDLAILTRRGRRLNRGNSRSTWFANDL 179  
 Sudan QIKTQEGVITDQLKQIRRV IHNRYLSALFVHDLAILTRRGRRLNRGNSRSTWFVTNEV 180  
 Reston ATGAQDHLTN IATREKLNELNNDYVHQLFFWHDL IARRGRRLNRGNSRSTWFVHDF 179

Zaire IDILGYGDYVFWKIPISMLPLNTQGI PHAAMDWYQASVFKAEVQGHGTHIVSVSTADVLIM 239  
 Tai VDILGYGDYVFWKIPISMLPLNTQGLPHAAKDWYHESVFKAEVQGHGTHIVSVSTADVLIM 239  
 Bundibugyo IDILGYGDYVFWKIPISMLPLNTQGI PHAAMDWYHESVFKAEVQGHGTHIVSVSTADVLIM 239  
 Sudan VDILGYGDYVFWKIPISMLPLNTQGI PHAAMDWYHESVFKAEVQGHGTHIVSVSTADVLIM 240  
 Reston IDILGYGDYVFWKIPISMLPLNTQGI PHAAMDWYQPTLFPKESILGHSQILSVSTAEILIM 239

Zaire CKDLITCRFNTLLISKIAEIEDPVCSYDYPNFKIVSMYQSGDYLLSILGSDGYKIKFLE 299  
 Tai CKDIIITCRFNTLLIAAVANLEDSVHSYDYPNFKIVSMYQSGDYLLSILGSEGYKVIKLE 299  
 Bundibugyo CKDIIITCRFNTLLIAALANLEDSVHSYDYPNFKIVSMYQSGDYLLSILGSEGYKVIKLE 299  
 Sudan CKDLVTSRFNTLLIAELARLEDPVSADYPLVDNIQSLYNAGDYLLSILGSEGYKIKYLE 300  
 Reston CKDIIITCRFNTSLIASIAKLEDDVSDYDPSDILKIYNAGDYVSIILGSEGYKIKYLE 299

Zaire PLCLAKIQLCSKYTERKGRFLTQMHAVNHTLEETEMRALKPSQAQKIREFHRTLIRLE 359  
 Tai PLCLAKIQLCSNYTERKGRFLTQMHAVNHTLEELTGSRELRPQQIRKVFREFHQLINLK 359  
 Bundibugyo PLCLAKIQLCSNYTERKGRFLTQMHAVNHTLEELIEGRGLKSQDQWKMREFHRLVNLK 359  
 Sudan PLCLAKIQLCSQYTERKGRFLTQMHAVIQTLELRLNRLGLKKSQLSKIREFHQLLLRLR 360  
 Reston PLCLAKIQLCSKFTTERKGRFLTQMHLSVINDLRELSNRRLKDYQEKIRDFHKLILLQLQ 359

Zaire MTPQQLCELFVSIQKHWGHPVLHSETAIQKVKKHATVLKALRPVIFETCYVFKYSIAKHY 419  
 Tai ATPQQLCELFVSIQKHWGHPVLHSEKAIQKVKKHATVIKALRPVIFETCYVFKYSIAKHY 419  
 Bundibugyo STPQQLCELFVSIQKHWGHPVLHSEKAIQKVKKHATVIKALRPVIFETCYVFKYSIAKHY 419  
 Sudan STPQQLCELFVSIQKHWGHPVLHSEKAIQKVKKHATVIKALRPVIFETCYVFKYSIAKHY 420  
 Reston LSPQQLCELFVSIQKHWGHPVILHSEKAIQKVKRHATILKALRPVIFETCYVFKYNIKHY 419

Zaire FDSQGSWYSVTSDRNLTPLGNSYIKRNQFPPLPMIKELLWFEYHLDHPPLFSTKISDLS 479  
 Tai FDSQGSWYSVTSDRCLTPGLSSYIKRNQFPPLPMIKELLWFEYHLDHPPLFSTKISDLS 479  
 Bundibugyo FDSQGSWYSVTSKHLTPGLHSYIKRNQFPPLPMIKDLLWFEYHLDHPPLFSTKISDLS 479  
 Sudan FDSQGSWYSVTSDRCLTPGLNSYIRRNQFPPLPMIKDLLWFEYHLDHPPLFSTKISDLS 480  
 Reston FDSQGSWYSVTSDRNLTPLGNSYIKRNHFPPLPMIKDLLWFEYHLDHPPLFSTKISDLS 479





Zaire PSHYSGNIVHRYNDQYSPHSFMANRMSNSATRLIVSTNTLGEFSGGGQSAARDSNIIFQNV 1319  
 Tai PSHYSGNIVHRYNDQYSPHSFMANRMSNSATRLVSTNTLGEFSGGGQSAARDSNIIFQNV 1319  
 Bundibugyo PSHYSGNIVHRYNDQYSPHSFMANRMSNSATRLVSTNTLGEFSGGGQSAARDSNIIFQNV 1319  
 Sudan PSHYSGNIVHRYNDQYSPHSFMANRMSNSATRLMVSTNTLGEFSGGGQSAARDSNIIFQNV 1318  
 Reston PSHYSGNIVHRYNDQYSPHSFMANRMSNSATRLIVSTNTLGEFSGGGQSAARDSNIIFQNV 1317  
 \*\*\*\*\*

Zaire INYAVALEFDIKFRNTEATDIQYNRAHLHLTKCCTREVPAQYLTYTSTLDDLTRYRENEL 1379  
 Tai INFAVALEFDLFRNVATSSIQHRAHLHLTKCCTREVPAQYLTYTSTLDDLTRYRENEL 1379  
 Bundibugyo INFVALEFDLFRNTEATSSIQHRAHLHLTKCCTREVPAQYLTYTSTLDDLTRYRENEL 1379  
 Sudan INFAVALYDIRFRNTEATSSIQYHRAHLHLTKCCTREVPAQYLTYTSTLDDLTRYRENEL 1378  
 Reston INLAVALYDIRFRNTEATSSIQHRAHLHLTKCCTREVPAQYLTYTSTLDDLTRYRENEL 1377  
 \*\* : \*\* : \*

Zaire IYDSNPLKGGGLNCNLSFDNPFQKQLNIEBDDLIRLPHLSGWELAKTIMQSIISDSNNS 1439  
 Tai IYDNNPLRGGGLNCNLSFDNPLFKGQRLNIEBEDLIRLPHLSGWELAKTIQSIISDSNNS 1439  
 Bundibugyo IYDNNPLKGGGLNCNLSFDNPLFKGQRLNIEBEDLIRLPHLSGWELAKTIQSIISDSNNS 1439  
 Sudan IYDSNPLRGGGLNCNLSFDNPLKGGGLNIEBDDLIRLPHLSGWELAKTIQSIISDSNNS 1438  
 Reston IYDSNPLKGGGLNCNLSFDNPLKGGGLNIEBDDLIRLPHLSGWELAKTIQSIISDSNNS 1437  
 \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \*

Zaire STDPISSGETRSFTTHFLTYPKIGLLYSFGALISYLLGNTIIRTKKLTLDNLFYLYLTQI 1499  
 Tai STDPISSGETRSFTTHFLTYPKIGLLYSFGALISYLLGNTIIRTKKLTLDNLFYLYLTQI 1499  
 Bundibugyo STDPISSGETRSFTTHFLTYPKIGLLYSFGALISYLLGNTIIRTKKLTLDNLFYLYLTQI 1499  
 Sudan STDPISSGETRSFTTHFLTYPKIGLLYSFGALISYLLGNTIIRTKKLTLDNLFYLYLTQI 1498  
 Reston STDPISSGETRSFTTHFLTYPKIGLLYSFGALISYLLGNTIIRTKKLTLDNLFYLYLTQI 1497  
 \*\*\*\*\*

Zaire HNLPHRSLRILKPTFKHASVMSRLMSIDPHFSIYI GGAAGDRGLSDAARFLRTAISFFL 1559  
 Tai HNLPHRSLRILKPTFKHASVMSRLMSIDPHFSIYI GGTAGDRGLSDAARFLRTAISFFL 1559  
 Bundibugyo HNLPHRSLRILKPTFKHVSVISRLMSIDPHFSIYI GGTAGDRGLSDAARFLRTAISFFL 1559  
 Sudan HNLPHRSLRILKPTFKHVSVISRLMSIDPHFSIYI GGTAGDRGLSDAARFLRTAISFFL 1558  
 Reston HNLPHRALRVFKPTFKHASVMSRLMSIDPHFSIYI GGTAGDRGLSDAARFLRTAISFFL 1557  
 \* \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \*

Zaire TFVKEWIIINRGTIVPLWIVYPLEGQNPTEVNNFLYQIVELLVHDSSRQO--AFKTTISDH 1617  
 Tai QFVRKWIIVERKTAIPLWIVYPLEGQNPTEVNNFLYQIVELLVHDSSRQO--AFKTTISDH 1617  
 Bundibugyo QFVKEWIIINRGTIVPLWIVYPLEGQNPTEVNNFLYQIVELLVHDSSRQO--AFKTTISDH 1617  
 Sudan SFVEWVIFRKANIPLWIVYPLEGQNPTEVNNFLYQIVELLVHDSSRQO--AFKTTISDH 1616  
 Reston QFLKSWIIDRQKTIPLWIVYPLEGQNPTEVNNFLYQIVELLVHDSSRQO--AFKTTISDH 1617  
 \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \*

Zaire VHPHDNLVYTCCKSTASNFHASLAYWRSRHRNSNRKYLARDSSTGSSNNSD--G-- 1670  
 Tai VETFDNLVYMCCKSTASNFHASLAYWRSRHRNSNRKYLARDSSTGSSNNSD--G-- 1670  
 Bundibugyo VETFDNLVYMCCKSTASNFHASLAYWRSRHRNSNRKYLARDSSTGSSNNSD--G-- 1670  
 Sudan QKSSNLVYMCCKSTASNFHASLAYWRSRHRNSNRKYLARDSSTGSSNNSD--G-- 1672  
 Reston DLAEENLVYNSKSTASNFHASLAYWRSRHRNSNRKYLARDSSTGSSNNSD--G-- 1673  
 \* \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \*

Zaire ----HIERSQE-----QTRDPHDGTERNLVQLMSHEIKRRTIPQ---ENTHQGPSF 1715  
 Tai PESTAVLGSLQ-----TSLAPPPSA-DEATYDRKNKVLKASRPGKYSQNTTKAPPN 1725  
 Bundibugyo PPSIP--KSKS-----GTQGSFAFF-EKLEYDKERELPTASTPAEQSKTYIKALSS 1725  
 Sudan PPGLDLNRNNDTIPTRIKQIVQGDSTRN--DRTTTT-----RFPF--K-----SRST 1715  
 Reston NH-----QSDEKYYN-----VTCGKSPKQPKERKDFS-----QYRLSNNGQTMNSNRHK 1716  
 . . .

Zaire QSFLSDSACGTANPKLNFDRSRHNKVFQDHNSASKREGHQIISHRLVLPFFTLSSQGTQQL 1775  
 Tai QT-----SCRDVSPNITG-----TDGCPANEGSNSNNNLVSHRIVLPFFTLSSQGTQQL 1775  
 Bundibugyo RIYHGKTPSNAAKDDSTT-----SKGCD-----KEENAVQASHRIVLPFFTLSSQGTQQL 1775  
 Sudan PTKSAPPTKMYEGSTHTQKLTDD---THLDEHNAKEFPSPNPHRLVLPFFTLSSQGTQQL 1772  
 Reston GKFHKNWPKMLMESQRGTIVLTEG---DYFQNNTPPTDDVSSPHRLILPFFTLSSQGTQQL 1773  
 \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \*

Zaire TSSNESQTQDEISKYLRQVRSVIDTIVYCRFTGIVSSMHYKLEDEVLWEIESAVTLAE 1835

Tai PSIRKSEGTTEIVRLTRQLRAIPDITTYCRFTGIVSSMHYKLEDEVLWEIESAVTLAE 1835  
 Bundibugyo PSIRKSEGTTEIVRLTRQLRAIPDITTYCRFTGIVSSMHYKLEDEVLWEIESAVTLAE 1835  
 Sudan IEPSEBESRSNIKGLLQHLRMTDITTYCRFTGIVSSMHYKLEDEVLWEIESAVTLAE 1832  
 Reston DQDAQELMNQNIKQYLLQHLRMTDITTYCRFTGIVSSMHYKLEDEVLWEIESAVTLAE 1833  
 . . .

Zaire GEGAGALLLIQKYQVKTLLFFNTLATESSIESEIVSGMTTPRMLLPVMSKFHNDQIEIILN 1895  
 Tai GEGSALLLLQKYQVKTLLFFNTLATESSIESEIVSGMTTPRMLLPVMSKFHNDQIEIILN 1895  
 Bundibugyo GEGSALLLLQKYQVKTLLFFNTLATESSIESEIVSGMTTPRMLLPVMSKFHNDQIEIILN 1895  
 Sudan GEGSALLLIQKYQVKTLLFFNTLATESSIESEIVSGMTTPRMLLPVMSKFHNDQIEIILN 1892  
 Reston GEGSALLLIQKYQVKTLLFFNTLATESSIESEIVSGMTTPRMLLPVMSKFHNDQIEIILN 1893  
 \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \*

Zaire NSASQITDITNPTWFKDQARARLPKQVEVITMDAETTENINRSKLYEAVYKLILHHIDPSV 1955  
 Tai NSASQITDITNPSWADQKSRIPKQVEIITMDAETTENINRSKLYEAVYKLILHHIDPSV 1955  
 Bundibugyo NSASQITDITNPAWFTDQKSRIPKQVEIITMDAETTENINRSKLYEAVYKLILHHIDPSV 1955  
 Sudan NSASQITDITNPSWADQKSRIPKQVEIITMDAETTENINRSKLYEAVYKLILHHIDPSV 1952  
 Reston NSASQITDITNPSWADQKSRIPKQVEIITMDAETTENINRSKLYEAVYKLILHHIDPSV 1953  
 \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \*

Zaire LKAVVLKVFELSDTEGLMNLNDNLAFFFATGYLIKPIITSSARSSEWYLCLTNFLSTTRKMP 2015  
 Tai LKVVVLKVFELSDTEGLMNLNDNLAFFFATGYLIKPIITSSARSSEWYLCLTNFLSTTRKMP 2015  
 Bundibugyo LKVVVLKVFELSDTEGLMNLNDNLAFFFATGYLIKPIITSSARSSEWYLCLTNFLSTTRKMP 2015  
 Sudan LKVVVLKVFELSDTEGLMNLNDNLAFFFATGYLIKPIITSSARSSEWYLCLTNFLSTTRKMP 2012  
 Reston LKVVVLKVFELSDIEGILWINDYLAFLFAGYLIKPIITSSARSSEWYLCLTNFLSTTRKMP 2013  
 \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \*

Zaire HQNHLSCKQVILTALQIQRSFYWLSHLTQYADCELHLSYIRLGFPSLEKVLVYHRYNLV 2075  
 Tai HQSBHTCMHVITQALQIQRSFYWLSHLTQYADCELHLSYIRLGFPSLEKVLVYHRYNLV 2075  
 Bundibugyo HQSBHTCMHVITQALQIQRSFYWLSHLTQYADCELHLSYIRLGFPSLEKVLVYHRYNLV 2075  
 Sudan HQSBHTCMHVITQALQIQRSFYWLSHLTQYADCELHLSYIRLGFPSLEKVLVYHRYNLV 2072  
 Reston HQTHKACLGVIDALQIQRSFYWLSHLTQYADCELHLSYIRLGFPSLEKVLVYHRYNLV 2073  
 \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \*

Zaire DSKRGPLVSIITQHLALHRAEIRELTDYNDYQQRQSRTOYHYFIRTAKGRITKLVNDYLKFF 2135  
 Tai DSKRGPLVSIITQHLALHRAEIRELTDYNDYQQRQSRTOYHYFIRTAKGRITKLVNDYLKFF 2135  
 Bundibugyo DSKRGPLVSIITQHLALHRAEIRELTDYNDYQQRQSRTOYHYFIRTAKGRITKLVNDYLKFF 2135  
 Sudan DSKRGPLVSIITQHLALHRAEIRELTDYNDYQQRQSRTOYHYFIRTAKGRITKLVNDYLKFF 2132  
 Reston DSKRGPLVSIITQHLALHRAEIRELTDYNDYQQRQSRTOYHYFIRTAKGRITKLVNDYLKFF 2133  
 \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \* \* : \*





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Zaire      LIVQALKHNGTWQAEFKKLPDLISVCNRFYHIRDCNCEERFLVQTLYLHRMQDSEVKLIE 2195
Tai       LIIQALKHNCCTWQEEELRALPDLISVCTRFRYHTRNCSCENRFLVQTLYLHRMQDSEIKLID 2195
Bundibugyo LVVQALKHNCCLWQEEELRTPDLINVCNRFYHIRDCSCEDRFLLIQTLYLHRMQDSEAKLME 2195
Sudan     LVIRALKNNSTWHHELKLLPELIGVCHRFNHRNCTCSEFLVQTLYLHRMQDSEIKLMD 2192
Reston    LIVQALKNNSSWYTELKKLPEVINVCNRFYHHTNCECQEKFFVQTLYLQRLRDAEIKLIE 2193
*:::***:* * * : **::*.** ** * :.* *:::*** ** * : * * * * :
    
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Zaire      RLTGLLSLFPDGLYRFD--          2212
Tai       RLTGLLSLCPNGFFR----          2210
Bundibugyo RLTGFLGLYPNGINA----          2210
Sudan     RLTSLVNMFPPEGFRSSSV-        2210
Reston    RLTGLMRFYPEGLIYSNHT          2212
***.::: : *:*:
    
```

### MODULE-3

#### Nucleoprotein:

|  | Tai Forest Ebolavirus                                       | Bundibugyo Ebolavirus                                       | Sudan Ebolavirus  | Zaire Ebolavirus  | Reston Ebolavirus   |
|--|---|---|---|---|---|
| <b>Gene number; Exon number and Exon type</b>                      | Gene Number = 01<br>Exon Number = 01<br>Type of Exon = Sngl | Gene Number = 01<br>Exon Number = 01<br>Type of Exon = Sngl | Gene Number = 01<br>Exon Number = 01<br>Type of Exon = Sngl | Gene Number = 01<br>Exon Number = 01<br>Type of Exon = Sngl | Gene Number = 01<br>Exon Number = 01<br>Type of Exon = Sngl |
|  | Gene Number = 01<br>Exon Number = 02<br>Type of Exon = PlyA |   | Gene Number = 01<br>Exon Number = 02<br>Type of Exon = PlyA | Gene Number = 01<br>Exon Number = 02<br>Type of Exon = PlyA | Gene Number = 01<br>Exon Number = 02<br>Type of Exon = PlyA |
| <b>Type of DNA Strand</b><br>+ = Input Strand<br>- = Output Strand | E-1(+=Input strand)<br>E-2(+=Input Strand)                  | E-1(+= Input Strand)  | E-1(+=Input Strand)<br>E-2(+=Input Strand)                  | E-1(+=Input Strand)<br>E-2(+=Input strand)                  | E-1(+=Input Strand)<br>E-2(+=Input Strand)                  |
| <b>Beginning of Exon/Signal</b>                                    | E-1=409<br>E-2=2677   | E-1=403   | E-1 = 403<br>E-2 = 2734                                     | E-1= 415<br>E-2= 2743                                       | E-1= 409<br>E-2= 2947                                       |
| <b>Ending of Exon/signal</b>                                       | E-1=2628<br>E-2=2682  | E-1=2622  | E-1= 2619<br>E-2 = 2739                                     | E-1= 2634<br>E-2= 2748                                      | E-1= 2628<br>E-2= 2952                                      |
| <b>Length of Exon/signal</b>                                       | E-1=2220<br>E-2=06  | E-1=2220  | E-1 = 2217<br>E-2 = 06                                      | E-1= 2220<br>E-2= 06  | E-1= 2220<br>E-2= 06  |
| <b>Reading Frame</b>   | E-1=0<br>E-2=( )  | E-1=0   | E-1 = 0<br>E-2 = ( )  | E-1= 0<br>E-2 = ( )   | E-1 = 0<br>E-2 = ( )  |
| <b>Net-Phase of Exon/Signal</b>                                    | E-1=0<br>E-2=( )  | E-1=0   | E-1 = 0<br>E-2 = ( )  | E-1 = 0<br>E-2 = ( )  | E-1 = 0<br>E-2 = ( )  |
| <b>Initiation signal/3'-Splice site score</b>                      | E-1=99<br>E-2=( )   | E-1=75  | E-1 = 81<br>E-2 = ( )                                       | E-1= 55<br>E-2= ( )   | E-1 = 71<br>E-2 = ( )                                       |
| <b>Termination signal/5'-Splice site score</b>                     | E-1=28<br>E-2=( )   | E-1=42  | E-1 = 55<br>E-2 = ( )                                       | E-1 = 42<br>E-2 = ( )                                       | E-1 = 41<br>E-2 = ( )                                       |
| <b>Coding Region score</b>   | E-1=1622<br>E-2=( )   | E-1=1481  | E-1 = 1662<br>E-2 = ( )                                     | E-1 = 1366<br>E-2 = ( )                                     | E-1 = 1420<br>E-2 = ( )                                     |
| <b>Probability of Exon</b>   | E-1=0.776<br>E-2=( )  | E-1=0.478   | E-1 = 0.998<br>E-2 = ( )                                    | E-1 = 0.578<br>E-2 = ( )                                    | E-1 = 0.921<br>E-2 = ( )                                    |
| <b>Exon score</b>  | E-1=151.05<br>E-2=-3.64                                     | E-1=135.75  | E-1 = 155.98<br>E-2 = 1.05                                  | E-1 = 122.45<br>E-2 = 1.05                                  | E-1 = 129.35<br>E-2 = -1.75                                 |

#### Polymerase complex protein

|  | Tai Forest Ebolavirus                                       | Bundibugyo Ebolavirus                                       | Sudan Ebolavirus  | Zaire Ebolavirus  | Reston Ebolavirus   |
|--|---|---|---|---|---|
| <b>Gene number; Exon number and Exon type</b>                      | Gene number = 01<br>Exon Number = 01<br>Type of Exon = Init | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl |
|  |   | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA |
| <b>Type of DNA Strand</b><br>+ = Input Strand<br>- = Output Strand | E-1(+=Input Strand)   | E-1(+= Input strand)<br>E-2(+=Input Strand)                 | E-1(+=Input strand)<br>E-2(+=Input Strand)                  | E-1(+=Input strand)<br>E-2(+=Input strand)                  | E-1(+=Input strand)<br>E-2(+=Input strand)                  |
| <b>Beginning of Exon/Signal</b>                                    | E-1 = 89  | E-1 = 89<br>E-2 = 1303                                      | E-1= 126<br>E-2 = 1343                                      | E-1= 98<br>E-2= 1238  | E-1 = 137<br>E-2 = 1218                                     |
| <b>Ending of Exon/signal</b>                                       | E-1 = 1004  | E-1 = 1114<br>E-2 = 1308                                    | E-1 = 1115<br>E-2 = 1348                                    | E-1 = 1120<br>E-2 = 1243                                    | E-1 = 1126<br>E-2 = 1223                                    |
| <b>Length of Exon/signal</b>                                       | E-1 = 916   | E-1 = 1026<br>E-2 = 06                                      | E-1 = 990<br>E-2 = 06                                       | E-1 = 1023<br>E-2 = 06                                      | E-1 = 990<br>E-2 = 06                                       |
| <b>Reading Frame</b>   | E-1 = 01  | E-1 = 01<br>E-2 = ( )                                       | E-1 = 02<br>E-2 = ( )                                       | E-1 = 01<br>E-2 = ( )                                       | E-1 = 01<br>E-2 = ( )                                       |
| <b>Net-Phase of Exon/Signal</b>                                    | E-1 = 01  | E-1 = 00<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = ( )                                       |



|   |             |                           |                            |                            |                            |
|---|-------------|---------------------------|----------------------------|----------------------------|----------------------------|
| Initiation signal/3'-Splice site score  | E-1 =42     | E-1 = 75<br>E-2 = ( )     | E-1 =71<br>E-2 = ( )       | E-1 = 66<br>E-2 = ( )      | E-1 = 69<br>E-2 = ( )      |
| Termination signal/5'-Splice site score | E-1=3       | E-1 = 45<br>E-2=( )       | E-1 = 43<br>E-2 = ( )      | E-1 = 52<br>E-2 = ( )      | E-1 = 48<br>E-2 = ( )      |
| Coding Region score                     | E-1 =568    | E-1 = 296<br>E-2=( )      | E-1 = 819<br>E-2 = ( )     | E-1 = 843<br>E-2 = ( )     | E-1 = 813<br>E-2 = ( )     |
| Probability of Exon                     | E-1 = 0.455 | E-1 = 0.283<br>E-2 = ( )  | E-1 = 0.534<br>E-2 = ( )   | E-1 = 0.847<br>E-2 = ( )   | E-1 = 0.846<br>E-1 = ( )   |
| Exon score                              | E-1=37.93   | E-1 = 21.09<br>E-2 = 1.05 | E-1 = 72.31<br>E-2 = -1.75 | E-1 = 75.31<br>E-2 = -1.75 | E-1 = 72.01<br>E-2 = -1.75 |

### **Matrix Protein:**

|   | Tai Forest Ebolavirus                                       | Bundibugyo Ebolavirus  | Sudan Ebolavirus   | Zaire Ebolavirus   | Reston Ebolavirus  |
|---|---|--|--|--|--|
| Gene number;Exon number and Exon type                       | Gene number = 01<br>Exon number = 01<br>Type of Exon = Init | Gene number = 01<br>Exon number = 01<br>Type of Exon = Init  | Gene number = 01<br>Exon number = 01<br>Type of Exon = Snagl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Snagl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Snagl |
|   | Gene number = 01<br>Exon number = 02<br>Type of Exon = Term | Gene number = 01<br>Exon number = 02<br>Type of Exon = Intra | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA  | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA  | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA  |
| Type of DNA Strand<br>+ = Input Strand<br>- = Output Strand | E-1(+ = Input strand)<br>E-2(+ = Input strand)              | E-1(+ = Input strand)<br>E-2(+ = Input strand)               | E-1(+ = Input strand)<br>E-2(+ = Input strand)               | E-1(+ = Input strand)<br>E-2(+ = Input strand)               | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)               |
| Beginning of Exon/Signal                                    | E-1 = 90<br>E-2 = 1098                                      | E-1 = 90<br>E-2 = 1046                                       | E-1 = 90<br>E-2 = 1293                                       | E-1 = 90<br>E-2 = 1435                                       | E-1 = 90<br>E-2 = 1274                                       |
| Ending of Exon/signal                                       | E-1 = 990<br>E-2 = 1498                                     | E-1 = 1004<br>E-1 = 1225                                     | E-1 = 1070<br>E-2 = 1298                                     | E-1 = 1070<br>E-2 = 1440                                     | E-1 = 1085<br>E-2 = 1279                                     |
| Length of Exon/signal                                       | E-1 = 901<br>E-2 = 401                                      | E-1 = 915<br>E-2 = 180                                       | E-1 = 981<br>E-2 = 06  | E-1 = 981<br>E-2 = 06  | E-1 = 996<br>E-2 = 06  |
| Reading Frame   | E-1 = 02<br>E-2 = 01  | E-1 = 02<br>E-2 = 01   | E-1 = 02<br>E-2 = ( )  | E-1 = 02<br>E-2 = ( )  | E-1 = 02<br>E-2 = ( )  |
| Net-Phase of Exon/Signal                                    | E-1 = 01<br>E-2 = 02  | E-1 = 00<br>E-2 = 00   | E-1 = 00<br>E-2 = ( )  | E-1 = 00<br>E-2 = ( )  | E-1 = 00<br>E-2 = ( )  |
| Initiation signal/3'-Splice site score                      | E-1 = 81<br>E-2 = 20  | E-1 = 101<br>E-2 = 72  | E-1 = 64<br>E-2 = ( )  | E-1 = 48<br>E-2 = ( )  | E-1 = 60<br>E-2 = ( )  |
| Termination signal/5'-Splice site score                     | E-1 = 53<br>E-2 = 48  | E-1 = -6<br>E-2 = 69   | E-1 = 37<br>E-2 = ( )  | E-1 = 32<br>E-2 = ( )  | E-1 = 28<br>E-2 = ( )  |
| Coding Region score   | E-1 = 349<br>E-2 = 287                                      | E-1 = 427<br>E-2 = 239                                       | E-1 = 279<br>E-2 = ( )                                       | E-1 = 837<br>E-2 = ( )                                       | E-1 = 692<br>E-2 = ( )                                       |
| Probability of Exon   | E-1 = 0.752<br>E-2 = 0.989                                  | E-1 = 0.769<br>E-2 = 0.823                                   | E-1 = 0.632<br>E-2 = ( )                                     | E-1 = 0.840<br>E-2 = ( )                                     | E-1 = 0.728<br>E-2 = ( )                                     |
| Exon score  | E-1 = 25.13<br>E-2 = 13.18                                  | E-1 = 28.67<br>E-2 = 20.46                                   | E-1 = 17.22<br>E-2 = -1.75                                   | E-1 = 70.65<br>E-2 = -0.45                                   | E-1 = 57.05<br>E-2 = -1.75                                   |

### **Small Secreted Glycoprotein:**

|                                       | Tai Forest Ebolavirus                                      | Bundibugyo Ebolavirus                                       | Sudan Ebolavirus  | Zaire Ebolavirus   | Reston Ebolavirus   |
|---------------------------------------|--|---|---|--|---|
| Gene number;Exon number and Exon type | Gene number = 01<br>Exon number = 01<br>Type of Exon= Init | Gene number = 01<br>Exon number = 01<br>Type of Exon = Init | Gene number = 01<br>Exon number = 01<br>Type of Exon = Init | Gene number = 01<br>Exon number = 01<br>Type of Exon = Intra | Gene number = 01<br>Exon Number = 01<br>Type of Exon = Init |
|                                       | Gene number = 01   | Gene number = 01  | Gene number = 01  | Gene number = 01   | Gene number = 01  |



|   |  |  |  |  |  |
|---|--|--|--|--|--|
|   | Exon number = 02<br>Type of Exon = Term<br>Gene number = 01<br>Exon number = 03<br>Type of Exon = PlyA | Exon number = 02<br>Type of Exon = Term<br>Gene number = 01<br>Exon number = 03<br>Type of Exon = PlyA | Exon number = 02<br>Type of Exon = Term        | Exon number = 02<br>Type of Exon = Intr        | Exon number = 02<br>Type of Exon = Intr        |
| Type of DNA Strand<br>+ = Input Strand<br>- = Output Strand | E-1(+ = Input strand)<br>E-2(+ = Input strand)<br>E-3(+ = Input strand)                                | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)<br>E-3(+ = Input Strand)                                | E-1(+ = Input Strand)<br>E-2(+ = Input Strand) | E-1(+ = Input Strand)<br>E-2(+ = Input Strand) | E-1(+ = Input strand)<br>E-2(+ = Input Strand) |
| Beginning of Exon/Signal                                    | E-1 = 140<br>E-2 = 1076<br>E-3 = 2356  | E-1 = 140<br>E-2 = 1052<br>E-3 = 2373  | E-1 = 116<br>E-2 = 1043                        | E-1 = 425<br>E-2 = 1035                        | E-1 = 142<br>E-2 = 1102                        |
| Ending of Exon/signal                                       | E-1 = 995<br>E-2 = 2169<br>E-3 = 2361  | E-1 = 995<br>E-2 = 2169<br>E-3 = 2378  | E-1 = 971<br>E-2 = 2145                        | E-1 = 999<br>E-2 = 2101                        | E-1 = 1000<br>E-2 = 1938                       |
| Length of Exon/signal                                       | E-1 = 856<br>E-2 = 1094<br>E-3 = 06  | E-1 = 856<br>E-2 = 1118<br>E-3 = 06  | E-1 = 856<br>E-2 = 1103                        | E-1 = 575<br>E-2 = 1067                        | E-1 = 859<br>E-2 = 837                         |
| Reading Frame   | E-1 = 01<br>E-2 = 00<br>E-3 = ( )  | E-1 = 01<br>E-2 = 00<br>E-3 = ( )  | E-1 = 01<br>E-2 = 00                           | E-1 = 01<br>E-2 = 00                           | E-1 = 00<br>E-2 = 02                           |
| Net-Phase of Exon/Signal                                    | E-1 = 01<br>E-2 = 02<br>E-3 = ( )  | E-1 = 01<br>E-2 = 02<br>E-3 = ( )  | E-1 = 01<br>E-2 = 02                           | E-1 = 02<br>E-2 = 02                           | E-1 = 01<br>E-2 = 00                           |
| Initiation signal/3'-Splice site score                      | E-1 = 84<br>E-2 = 35<br>E-3 = ( )  | E-1 = 87<br>E-2 = -37<br>E-3 = ( )   | E-1 = 82<br>E-2 = -50                          | E-1 = 39<br>E-2 = -12                          | E-1 = 87<br>E-2 = 34                           |
| Termination signal/5'-Splice site score                     | E-1 = 92<br>E-2 = 43<br>E-3 = ( )  | E-1 = 36<br>E-2 = 33<br>E-3 = ( )  | E-1 = -4<br>E-2 = 42                           | E-1 = -12<br>E-2 = 72                          | E-1 = 97<br>E-2 = 67                           |
| Coding Region score   | E-1 = 285<br>E-2 = 497<br>E-3 = ( )  | E-1 = 496<br>E-2 = 430<br>E-3 = ( )  | E-1 = 305<br>E-2 = 578                         | E-1 = 423<br>E-2 = 611                         | E-1 = 415<br>E-2 = 425                         |
| Probability of Exon   | E-1 = 0.896<br>E-2 = 0.979<br>E-3 = ( )  | E-1 = 0.908<br>E-2 = 0.134<br>E-3 = ( )  | E-1 = 0.237<br>E-2 = 0.309                     | E-1 = 0.365<br>E-2 = 0.734                     | E-1 = 0.835<br>E-2 = 0.362                     |
| Exon score  | E-1 = 23.30<br>E-2 = 32.16<br>E-3 = 1.05   | E-1 = 39.10<br>E-2 = 17.20<br>E-3 = 1.05   | E-1 = 15.51<br>E-2 = 31.64                     | E-1 = 18.94<br>E-2 = 39.43                     | E-1 = 37.09<br>E-2 = 26.36                     |

**Second Secreted Glycoprotein:**

|   |   |   |   |   |   |
|---|---|---|---|---|---|
|   | Tai Forest Ebolavirus   | Bundibugyo Ebolavirus   | Sudan Ebolavirus  | Zaire Ebolavirus  | Reston Ebolavirus   |
| Gene number; Exon number and Exon type                      | Gene number = 01<br>Exon number = 01<br>Type of Exon = init             | Gene number = 01<br>Exon number = 01<br>Type of Exon = Init             | Gene number = 01<br>Exon number = 01<br>Type of Exon = Init | Gene number = 01<br>Exon number = 01<br>Type of Exon = Intr | Gene number = 01<br>Exon number = 01<br>Type of Exon = Init |
|   | Gene number = 01<br>Exon number = 02<br>Type of Exon = Term             | Gene number = 01<br>Exon number = 02<br>Type of Exon = Term             | Gene number = 01<br>Exon number = 02<br>Type of exon = Term | Gene number = 01<br>Exon number = 02<br>Type of exon = Intr | Gene number = 01<br>Exon number = 02<br>Type of exon = Intr |
|   | Gene number = 01<br>Exon number = 03<br>Type of Exon = PlyA             | Gene number = 01<br>Exon number = 03<br>Type of Exon = PlyA             |   |   |   |
| Type of DNA Strand<br>+ = Input Strand<br>- = Output Strand | E-1(+ = Input Strand)<br>E-2(+ = Input strand)<br>E-3(+ = Input strand) | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)<br>E-3(+ = Input Strand) | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input strand)<br>E-2(+ = Input strand)              |
| Beginning of Exon/Signal                                    | E-1 = 140<br>E-2 = 1076<br>E-3 = 2356                                   | E-1 = 140<br>E-2 = 1052<br>E-3 = 2373                                   | E-1 = 116<br>E-2 = 1043                                     | E-1 = 425<br>E-2 = 1035                                     | E-1 = 142<br>E-2 = 1102                                     |
| Ending of Exon/signal                                       | E-1 = 995<br>E-2 = 2169<br>E-3 = 2361                                   | E-1 = 995<br>E-2 = 2169<br>E-3 = 2378                                   | E-1 = 971<br>E-2 = 2145                                     | E-1 = 999<br>E-2 = 2101                                     | E-1 = 1000<br>E-2 = 1938                                    |
| Length of Exon/signal                                       | E-1 = 856<br>E-2 = 1094<br>E-3 = 06                                     | E-1 = 856<br>E-2 = 1118<br>E-3 = 06                                     | E-1 = 856<br>E-2 = 1103                                     | E-1 = 575<br>E-2 = 1067                                     | E-1 = 859<br>E-2 = 837                                      |
| Reading Frame   | E-1 = 01<br>E-2 = 00<br>E-3 = ( )                                       | E-1 = 01<br>E-2 = 00<br>E-3 = ( )                                       | E-1 = 01<br>E-2 = 00  | E-1 = 01<br>E-2 = 00  | E-1 = 00<br>E-2 = 02  |



|  |  |  |                            |                            |                            |
|--|--|--|----------------------------|----------------------------|----------------------------|
| <b>Net-Phase of Exon/Signal</b>                | E-1 = 01<br>E-2 = 02<br>E-3 = ( )        | E-1 = 01<br>E-2 = 02<br>E-3 = ( )        | E-1 = 01<br>E-2 = 02       | E-1 = 02<br>E-2 = 02       | E-1 = 01<br>E-2 = 00       |
| <b>Initiation signal/3'-Splice site score</b>  | E-1 = 84<br>E-2 = 35<br>E-3 = ( )        | E-1 = 87<br>E-2 = -37<br>E-3 = ( )       | E-1 = 82<br>E-2 = -50      | E-1 = 39<br>E-2 = -12      | E-1 = 87<br>E-2 = 34       |
| <b>Termination signal/5'-Splice site score</b> | E-1 = 92<br>E-2 = 43<br>E-3 = ( )        | E-1 = 36<br>E-2 = 33<br>E-3 = ( )        | E-1 = -4<br>E-2 = 42       | E-1 = -12<br>E-2 = 72      | E-1 = 97<br>E-2 = 67       |
| <b>Coding Region score</b>                     | E-1 = 285<br>E-2 = 497<br>E-3 = ( )      | E-1 = 496<br>E-2 = 430<br>E-3 = ( )      | E-1 = 305<br>E-2 = 578     | E-1 = 423<br>E-2 = 611     | E-1 = 415<br>E-2 = 425     |
| <b>Probability of Exon</b>                     | E-1 = 0.896<br>E-2 = 0.979<br>E-3 = ( )  | E-1 = 0.908<br>E-2 = 0.134<br>E-3 = ( )  | E-1 = 0.237<br>E-2 = 0.309 | E-1 = 0.365<br>E-2 = 0.734 | E-1 = 0.835<br>E-2 = 0.362 |
| <b>Exon score</b>                              | E-1 = 23.30<br>E-2 = 32.16<br>E-3 = 1.05 | E-1 = 39.10<br>E-2 = 17.20<br>E-3 = 1.05 | E-1 = 15.51<br>E-2 = 31.64 | E-1 = 18.94<br>E-2 = 39.43 | E-1 = 37.09<br>E-2 = 26.36 |

**Spike Glycoprotein:**

|  | <b>Tai Forest Ebolavirus</b>  | <b>Bundibugyo Ebolavirus</b>  | <b>Sudan Ebolavirus</b>                                     | <b>Zaire Ebolavirus</b>                                     | <b>Reston Ebolavirus</b>                                    |
|--|---|---|---|---|---|
| <b>Gene number; Exon number and Exon type</b>                      | Gene number = 01<br>Exon number = 01<br>Type of Exon = Init             | Gene number = 01<br>Exon number = 01<br>Type of Exon = Init             | Gene number = 01<br>Exon number = 01<br>Type of Exon = Init | Gene number = 01<br>Exon number = 01<br>Type of Exon = Intr | Gene number = 01<br>Exon number = 01<br>Type of Exon = Init |
|  | Gene number = 01<br>Exon number = 02<br>Type of Exon = Term             | Gene number = 01<br>Exon number = 02<br>Type of Exon = Term             | Gene number = 01<br>Exon number = 02<br>Type of Exon = Term | Gene number = 01<br>Exon number = 02<br>Type of Exon = Intr | Gene number = 01<br>Exon number = 02<br>Type of Exon = Intr |
|  | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA             | Gene number = 01<br>Exon number = 03<br>Type of Exon = PlyA             |   |   |   |
| <b>Type of DNA Strand</b><br>+ = Input Strand<br>- = Output Strand | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)<br>E-3(+ = Input Strand) | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)<br>E-3(+ = Input Strand) | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              |
| <b>Beginning of Exon/Signal</b>                                    | E-1 = 140<br>E-2 = 1076<br>E-3 = 2356                                   | E-1 = 140<br>E-2 = 1052<br>E-3 = 2373                                   | E-1 = 116<br>E-2 = 1043                                     | E-1 = 425<br>E-2 = 1035                                     | E-1 = 142<br>E-2 = 1102                                     |
| <b>Ending of Exon/signal</b>                                       | E-1 = 995<br>E-2 = 2169<br>E-3 = 2361                                   | E-1 = 995<br>E-2 = 2169<br>E-3 = 2378                                   | E-1 = 971<br>E-2 = 2145                                     | E-1 = 999<br>E-2 = 2101                                     | E-1 = 1000<br>E-2 = 1938                                    |
| <b>Length of Exon/signal</b>                                       | E-1 = 856<br>E-2 = 1094<br>E-3 = 06                                     | E-1 = 856<br>E-2 = 1118<br>E-3 = 06                                     | E-1 = 856<br>E-2 = 1103                                     | E-1 = 575<br>E-2 = 1067                                     | E-1 = 859<br>E-2 = 837                                      |
| <b>Reading Frame</b>   | E-1 = 01<br>E-2 = 00<br>E-3 = ( )                                       | E-1 = 01<br>E-2 = 00<br>E-3 = ( )                                       | E-1 = 01<br>E-2 = 00  | E-1 = 01<br>E-2 = 00  | E-1 = 00<br>E-2 = 02  |
| <b>Net-Phase of Exon/Signal</b>                                    | E-1 = 01<br>E-2 = 02<br>E-3 = ( )                                       | E-1 = 01<br>E-2 = 02<br>E-3 = ( )                                       | E-1 = 01<br>E-2 = 02  | E-1 = 02<br>E-2 = 02  | E-1 = 01<br>E-2 = 00  |
| <b>Initiation signal/3'-Splice site score</b>                      | E-1 = 84<br>E-2 = 35<br>E-3 = ( )                                       | E-1 = 87<br>E-2 = -37<br>E-3 = ( )                                      | E-1 = 82<br>E-2 = -50                                       | E-1 = 39<br>E-2 = -12                                       | E-1 = 87<br>E-2 = 34  |
| <b>Termination signal/5'-Splice site score</b>                     | E-1 = 92<br>E-2 = 43<br>E-3 = ( )                                       | E-1 = 36<br>E-2 = 33<br>E-3 = ( )                                       | E-1 = -4<br>E-2 = 42  | E-1 = -12<br>E-2 = 72                                       | E-1 = 97<br>E-2 = 67  |



|                            |  |  |                            |                            |                            |
|----------------------------|--|--|----------------------------|----------------------------|----------------------------|
| <b>Coding Region score</b> | E-1 = 285<br>E-2 = 497<br>E-3 = ( )      | E-1 = 496<br>E-2 = 430<br>E-3 = ( )      | E-1 = 305<br>E-2 = 578     | E-1 = 423<br>E-2 = 611     | E-1 = 415<br>E-2 = 425     |
| <b>Probability of Exon</b> | E-1 = 0.896<br>E-2 = 0.979<br>E-3 = ( )  | E-1 = 0.908<br>E-2 = 0.134<br>E-3 = ( )  | E-1 = 0.237<br>E-2 = 0.309 | E-1 = 0.365<br>E-2 = 0.734 | E-1 = 0.835<br>E-2 = 0.362 |
| <b>Exon score</b>          | E-1 = 23.30<br>E-2 = 32.16<br>E-3 = 1.05 | E-1 = 39.10<br>E-2 = 17.20<br>E-3 = 1.05 | E-1 = 15.51<br>E-2 = 31.64 | E-1 = 18.94<br>E-2 = 39.43 | E-1 = 37.09<br>E-2 = 26.36 |

**RNA Dependent RNA Polymerase:**

|  | <b>Tai Forest Ebolavirus</b>                                | <b>Bundibugyo Ebolavirus</b>                                | <b>Sudan Ebolavirus</b>                                     | <b>Zaire Ebolavirus</b>                                     | <b>Reston Ebolavirus</b>                                    |
|--|---|---|---|---|---|
| <b>Gene number; Exon number and Exon type</b>                        | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl |
|  | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA |
| <b>Type of DNA Strand<br/>+ = Input Strand<br/>- = Output Strand</b> | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              |
| <b>Beginning of Exon/Signal</b>                                      | E-1 = 81<br>E-2 = 6959                                      | E-1 = 81<br>E-2 = 6803                                      | E-1 = 82<br>E-2 = 6986                                      | E-1 = 81<br>E-2 = 6775                                      | E-1 = 87<br>E-2 = 7202                                      |
| <b>Ending of Exon/signal</b>   | E-1 = 6713<br>E-2 = 6964                                    | E-1 = 6713<br>E-2 = 6808                                    | E-1 = 6711<br>E-2 = 6991                                    | E-1 = 6719<br>E-2 = 6780                                    | E-1 = 6725<br>E-2 = 7207                                    |
| <b>Length of Exon/signal</b>   | E-1 = 6633<br>E-2 = 06                                      | E-1 = 6633<br>E-2 = 06                                      | E-1 = 6630<br>E-2 = 06                                      | E-1 = 6639<br>E-2 = 06                                      | E-1 = 6639<br>E-2 = 06                                      |
| <b>Reading Frame</b>   | E-1 = 02<br>E-2 = ( )                                       | E-1 = 02<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = ( )                                       | E-1 = 02<br>E-2 = 00  | E-1 = 02<br>E-2 = ( )                                       |
| <b>Net-Phase of Exon/Signal</b>                                      | E-1 = 00<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = 00  | E-1 = 00<br>E-2 = ( )                                       |
| <b>Initiation signal/3'-Splice site score</b>                        | E-1 = 87<br>E-2 = ( )                                       | E-1 = 36<br>E-2 = ( )                                       | E-1 = 52<br>E-2 = ( )                                       | E-1 = 15<br>E-2 = ( )                                       | E-1 = 40<br>E-2 = ( )                                       |
| <b>Termination signal/5'-Splice site score</b>                       | E-1 = 49<br>E-2 = ( )                                       | E-1 = 44<br>E-2 = ( )                                       | E-1 = 31<br>E-2 = ( )                                       | E-1 = 38<br>E-2 = ( )                                       | E-1 = 43<br>E-2 = ( )                                       |
| <b>Coding Region score</b>   | E-1 = 2393<br>E-2 = ( )                                     | E-1 = 2459<br>E-2 = ( )                                     | E-1 = 2403<br>E-2 = ( )                                     | E-1 = 2927<br>E-2 = ( )                                     | E-1 = 2884<br>E-2 = ( )                                     |
| <b>Probability of Exon</b>   | E-1 = 0.884<br>E-2 = ( )                                    | E-1 = 0.996<br>E-2 = ( )                                    | E-1 = 0.967<br>E-2 = ( )                                    | E-1 = 0.972<br>E-2 = ( )                                    | E-1 = 0.975<br>E-2 = ( )                                    |
| <b>Exon score</b>  | E-1 = 227.53<br>E-2 = -3.44                                 | E-1 = 228.53<br>E-2 = -0.45                                 | E-1 = 223.23<br>E-2 = -1.75                                 | E-1 = 272.63<br>E-2 = -3.44                                 | E-1 = 271.33<br>E-2 = 1.05                                  |

**Membrane Associated Protein:**

|   | <b>Tai Forest Ebolavirus</b>                                | <b>Bundibugyo Ebolavirus</b>                                | <b>Sudan Ebolavirus</b>                                     | <b>Zaire Ebolavirus</b>                                     | <b>Reston Ebolavirus</b>                                    |
|---|---|---|---|---|---|
| <b>Gene number; Exon number and Exon type</b> | Gene number = 01<br>Exon number = 01<br>Type of Exon = Term | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl |
|   | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA |
| <b>Type of DNA Strand</b>                     | E-1(+ = Input Strand)                                       | E-1(+ = Input Strand)                                       | E-1(+ = Input Strand)                                       | E-1(+ = Input Strand)                                       | E-1(+ = Input Strand)                                       |



|  |                            |                           |                           |                           |                            |
|--|----------------------------|---------------------------|---------------------------|---------------------------|----------------------------|
| + = Input Strand<br>- = Output Strand          | E-2(+ = Input Strand)      | E-2(+ = Input Strand)     | E-2(+ = Input Strand)     | E-2(+ = Input Strand)     | E-2(+ = Input Strand)      |
| <b>Beginning of Exon/Signal</b>                | E-1 = 327<br>E-2 = 1439    | E-1 = 467<br>E-2 = 1348   | E-1 = 474<br>E-2 = 1237   | E-1 = 461<br>E-2 = 1310   | E-1 = 472<br>E-2 = 1241    |
| <b>Ending of Exon/signal</b>                   | E-1 = 1222<br>E-2 = 1444   | E-1 = 1222<br>E-2 = 1353  | E-1 = 1229<br>E-2 = 1242  | E-1 = 1216<br>E-2 = 1315  | E-1 = 1227<br>E-2 = 1246   |
| <b>Length of Exon/signal</b>                   | E-1 = 896<br>E-2 = 06      | E-1 = 756<br>E-2 = 06     | E-1 = 756<br>E-2 = 06     | E-1 = 756<br>E-2 = 06     | E-1 = 756<br>E-2 = 06      |
| <b>Reading Frame</b>                           | E-1 = 01<br>E-2 = ( )      | E-1 = 01<br>E-2 = ( )     | E-1 = 02<br>E-2 = ( )     | E-1 = 01<br>E-2 = ( )     | E-1 = 00<br>E-2 = ( )      |
| <b>Net-Phase of Exon/Signal</b>                | E-1 = 02<br>E-2 = ( )      | E-1 = 00<br>E-2 = ( )     | E-1 = 00<br>E-2 = ( )     | E-1 = 00<br>E-2 = ( )     | E-1 = 00<br>E-2 = ( )      |
| <b>Initiation signal/3'-Splice site score</b>  | E-1 = 45<br>E-2 = ( )      | E-1 = 80<br>E-2 = ( )     | E-1 = 80<br>E-2 = ( )     | E-1 = 88<br>E-2 = ( )     | E-1 = 83<br>E-2 = ( )      |
| <b>Termination signal/5'-Splice site score</b> | E-1 = 35<br>E-2 = ( )      | E-1 = 37<br>E-2 = ( )     | E-1 = 32<br>E-2 = ( )     | E-1 = 36<br>E-2 = ( )     | E-1 = 42<br>E-2 = ( )      |
| <b>Coding Region score</b>                     | E-1 = 535<br>E-2 = ( )     | E-1 = 450<br>E-2 = ( )    | E-1 = 504<br>E-2 = ( )    | E-1 = 622<br>E-2 = ( )    | E-1 = 299<br>E-2 = ( )     |
| <b>Probability of Exon</b>                     | E-1 = 0.795<br>E-2 = ( )   | E-1 = 0.776<br>E-2 = ( )  | E-1 = 0.992<br>E-2 = ( )  | E-1 = 0.999<br>E-2 = ( )  | E-1 = 0.922<br>E-2 = ( )   |
| <b>Exon score</b>                              | E-1 = 35.47<br>E-2 = -1.75 | E-1 = 34.99<br>E-2 = 1.05 | E-1 = 39.89<br>E-2 = 1.05 | E-1 = 52.89<br>E-2 = 1.05 | E-1 = 20.69<br>E-2 = -3.24 |

**Minor Nucleoprotein:**

|  | <b>Tai Forest Ebolavirus</b>                                | <b>Bundibugyo Ebolavirus</b>                                | <b>Sudan Ebolavirus</b>                                     | <b>Zaire Ebolavirus</b>                                     | <b>Reston Ebolavirus</b>                                    |
|--|---|---|---|---|---|
| <b>Gene number; Exon number and Exon type</b>                        | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl | Gene number = 01<br>Exon number = 01<br>Type of Exon = Sngl |
|  | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA | Gene number = 01<br>Exon number = 02<br>Type of Exon = PlyA |
| <b>Type of DNA Strand<br/>+ = Input Strand<br/>- = Output Strand</b> | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              | E-1(+ = Input Strand)<br>E-2(+ = Input Strand)              |
| <b>Beginning of Exon/Signal</b>                                      | E-1 = 228<br>E-2 = 1174                                     | E-1 = 228<br>E-2 = 1174                                     | E-1 = 218<br>E-2 = 1161                                     | E-1 = 222<br>E-2 = 1401                                     | E-1 = 229<br>E-2 = 1132                                     |
| <b>Ending of Exon/signal</b>   | E-1 = 1097<br>E-2 = 1179                                    | E-1 = 1097<br>E-2 = 1179                                    | E-1 = 1084<br>E-2 = 1166                                    | E-1 = 1088<br>E-2 = 1406                                    | E-1 = 1092<br>E-2 = 1137                                    |
| <b>Length of Exon/signal</b>   | E-1 = 870<br>E-1 = 06                                       | E-1 = 870<br>E-2 = 06                                       | E-1 = 867<br>E-2 = 06                                       | E-1 = 867<br>E-2 = 06                                       | E-1 = 864<br>E-2 = 06                                       |
| <b>Reading Frame</b>   | E-1 = 02<br>E-2 = ( )                                       | E-1 = 02<br>E-2 = ( )                                       | E-1 = 01<br>E-2 = ( )                                       | E-1 = 02<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = ( )                                       |
| <b>Net-Phase of Exon/Signal</b>                                      | E-1 = 00<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = ( )                                       | E-1 = 00<br>E-2 = ( )                                       |
| <b>Initiation signal/3'-Splice site score</b>                        | E-1 = 78<br>E-2 = ( )                                       | E-1 = 52<br>E-2 = ( )                                       | E-1 = 73<br>E-2 = ( )                                       | E-1 = 06<br>E-2 = ( )                                       | E-1 = 77<br>E-2 = ( )                                       |
| <b>Termination signal/5'-Splice site score</b>                       | E-1 = 48<br>E-2 = ( )                                       | E-1 = 38<br>E-2 = ( )                                       | E-1 = 38<br>E-2 = ( )                                       | E-1 = 38<br>E-2 = ( )                                       | E-1 = 43<br>E-2 = ( )                                       |
| <b>Coding Region score</b>   | E-1 = 595<br>E-2 = ( )                                      | E-1 = 540<br>E-2 = ( )                                      | E-1 = 513<br>E-2 = ( )                                      | E-1 = 414<br>E-2 = ( )                                      | E-1 = 566<br>E-2 = ( )                                      |
| <b>Probability of Exon</b>   | E-1 = 0.990<br>E-2 = ( )                                    | E-1 = 0.865<br>E-2 = ( )                                    | E-1 = 0.971<br>E-2 = ( )                                    | E-1 = 0.891<br>E-2 = ( )                                    | E-1 = 0.693<br>E-2 = ( )                                    |
| <b>Exon score</b>  | E-1 = 50.17<br>E-2 = 1.05                                   | E-1 = 41.07<br>E-2 = -1.75                                  | E-1 = 40.44<br>E-2 = 1.05                                   | E-1 = 23.84<br>E-2 = -0.45                                  | E-1 = 46.62<br>E-2 = 1.05                                   |



**Interpretation Of Data-** The above data provides Gene structural information of the genes encoded by Ebola virus proteins. The data represented in the above table shows different terminologies involving gene structure i.e. Exon Number, Type of Exon [Init = Initial exon (ATG to 5' splice site); Intr = Internal exon (3' splice site to 5' splice site); Term = Terminal exon (3' splice site to stop codon); Sngl = Single exon gene (ATG to stop); Prom = Promoter (TATA box/ initiation site); Ply A = poly A signal (consensus: AATAAA)]. We also study DNA strand i.e. (+) = input strand and (-) = negative strand. We also studied beginning of the exon / signal, end of the exon/signal, Length of exon, Reading frame, Net phase of exon, Initial signal/3' splice site score, Termination signal/5' splice site score, Coding region score, probability of exon along with exon score.

## X. CONCLUSION

This three module study help us to know different angles i.e; the Extinction coefficient estimations of proteins help us to distinguish the adjustment in light collecting proficiency and surface inclusion esteem with submersion solvent, Immersion time and drenching focus in the protein. It is likewise used to ponder the effect of dissolvable to control the adsorption kinetics. This is utilized to characterize the scope of wavelength where the light has its greatest profundity of infiltration in tissue. This is the inherent property of various species so it is utilized to separate between the molecules. Instability record clarifies the steady property of protein. Aliphatic file estimates the dissolvability of focused proteins. We even assessed whether the protein is hydrophobic/hydrophilic dependent on the amazing normal of hydrophaticity values. we can anticipate the protein structure, Function and developmental history of groupings and its utilization structure superposition programs and phylogenetic examination programmes. By the quality basic data we can discover infection seriousness and foresee quality structure to explore function, expression level, disease, mutation. By this quality basic investigation we can avoid the sickness by postponement of occurrence of ailment.

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