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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., iIllustrate the disparity between a gathering of sequences, Usage of arrangements as models to test hyphothesis, 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(Prot) = Numb(Tyr)*Ext(Tyr) + Numb(Trp)*Ext(Trp) + Numb(Cystine)*Ext(Cystine)
Ext(Tyr) = 1490,
Ext(Trp) = 5500,
Ext(Cystine) = 125;

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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

Aliphatic index = X(Ala) + a * X(Val) + b * (X(Ile) + X(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 hydropathy (GRAVY) esteem for a peptide or protein is determined as the entirety of hydropathy 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. INSTABILTY 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,

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```
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. Not withstanding 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 protperties 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.4 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.

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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	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%)
NUCLEO-PROTEIN	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
Theoritical 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			$54905M^{-1}cm^{-1}$	$54905M^{-1}cm^{-1}$	$63385M^{-1}cm^{-1}$	$53415M^{-1}cm^{-1}$	$58915M^{-1}cm^{-1}$
Absorbance assuming cystine residues			0.662	0.671	0.760	0.641	0.707
Extinction coefficient with out cystine residues			$54780M^{-1}cm^{-1}$	$54780M^{-1}cm^{-1}$	$63260M^{-1}cm^{-1}$	$53290M^{-1}cm^{-1}$	$58790M^{-1}cm^{-1}$
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 allforms of nucleo-protein in all species of the ebola virus species have same number and composition of the aminoacids on the whole but varieswhen 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;83452.62 >83308.50 >83286.68 >82905.24 >81804.90.i.e; Reston ebola virus with greater molecular weight and Sudan Ebolavirus with the 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 similar values of extinction coefficient for Bundibugyo and Sudan ebola virus with and with out assuming cysteine residues with different absorbance.Thenucleo-protein of sudan ebola virus is more stable when compared with the other forms of the virus species with value 38.60 as the value is less than 40 and Zaire Ebola virus is more unstable as it exceeds 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 Ebolavirus) > 77.93(Reston Ebolavirus) >75.82 (Bundibugyo Ebolavirus)>74.32 (Zaire Ebolavirus) >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 Ebolavirus(-0.565) is greater and for the TaiforestEbolavirus(-0.714)is-less

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			Bundibugyo Ebola virus	Sudan Ebola virus	Reston Ebola virus	Zaire Ebola virus	Tai forest ebola virus
Number and composition of amino acids	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%)
POLYMERASE COMPLEX PROTEIN	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%0
	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
Theoritical 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			$24325M^{-1}cm^{-1}$	$27180M^{-1}cm^{-1}$	$30285M^{-1}cm^{-1}$	$25940M^{-1}cm^{-1}$	$24450M^{-1}cm^{-1}$
Absorbance assuming cystine residues			0.650	0.753	0.832	0.694	0.648
Extinction coefficient with out cystine residues			$23950M^{-1}cm^{-1}$	$26930M^{-1}cm^{-1}$	$29910M^{-1}cm^{-1}$	$25440M^{-1}cm^{-1}$	$23950M^{-1}cm^{-1}$
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 aminoacid 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 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 databaseAssuming 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

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			Tai forest Ebola virus	Sudan Ebola virus	Reston Ebola virus	Zaire Ebola virus
Number and composition of amino acids 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
Theoritical 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			$21555M^{-1}cm^{-1}$	$23045M^{-1}cm^{-1}$	$23045M^{-1}cm^{-1}$	$20065M^{-1}cm^{-1}$
Absorbance assuming cystine residues			0.607	0.650	0.643	0.570
Extinction coefficient with out cystine residues			$21430M^{-1}cm^{-1}$	$22920M^{-1}cm^{-1}$	$22920M^{-1}cm^{-1}$	$19940M^{-1}cm^{-1}$
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 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 databaseWithout considering the secondary and tertiary structures when independent aminoacid 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 phenomeneon 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 order100.73 (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.

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			Bundibugyo Ebola virus	Sudan Ebola virus	Reston Ebola virus	Zaire Ebola virus	Tai forest ebola virus
Number and composition of amino acids	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%)
SECOND SECRETED GLYCO PROTEIN	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
Theoritical 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			$49640M^{-1}cm^{-1}$	$55140M^{-1}cm^{-1}$	$59275M^{-1}cm^{-1}$	$49640M^{-1}cm^{-1}$	$46785M^{-1}cm^{-1}$
Absorbance assuming cystine residues			1.452	1.525	1.587	1.487	1.373
Extinction coefficient with out cystine residues			$49390M^{-1}cm^{-1}$	$54890M^{-1}cm^{-1}$	$58900M^{-1}cm^{-1}$	$49390M^{-1}cm^{-1}$	$46410M^{-1}cm^{-1}$
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 aminoacid and difference when compared individual aminoacids.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 > 3339187.By these studies we concluded that Reston Ebolavirus is having higher molecular weight and Zaire Ebolavirus with small 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 databaseWhen independent aminoacid 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 Taiforest Ebolavirus(-0.220) is greater and in the Reston Ebola virus(-0.440)isless

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			Bundibugyo Ebola virus	Sudan Ebola virus	Reston Ebola virus	Zaire Ebola virus	Tai forest ebola virus
Number and composition of amino acids 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
Theoritical 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			$63870M^{-1}cm^{-1}$	$65360M^{-1}cm^{-1}$	$64900M^{-1}cm^{-1}$	$62380M^{-1}cm^{-1}$	$60890M^{-1}cm^{-1}$
Absorbance assuming cystine residues			1.504	1.535	1.555	1.515	1.462
Extinction coefficient with out cystine residues			$63370M^{-1}cm^{-1}$	$64860M^{-1}cm^{-1}$	$64400M^{-1}cm^{-1}$	$61880M^{-1}cm^{-1}$	$60390M^{-1}cm^{-1}$
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 aminoacids,but varies when compared to individual aminoacids.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 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 the contributions of the independent aminoacids 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 .

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			Bundibugyo Ebola virus	Sudan Ebola virus	Reston Ebola virus	Zaire Ebola virus	Tai forest ebola virus
Number and composition of amino acids							
	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%)
SPIKE GLYCO-PROTEIN	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
Theoritical 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			$100100M^{-1}cm^{-1}$	$101590M^{-1}cm^{-1}$	$103080M^{-1}cm^{-1}$	$100100M^{-1}cm^{-1}$	$95630M^{-1}cm^{-1}$
Absorbance assuming cystine residues			1.323	1.362	1.385	1.344	1.281
Extinction coefficient with out cystine residues			$99350M^{-1}cm^{-1}$	$100840M^{-1}cm^{-1}$	$102330M^{-1}cm^{-1}$	$99350M^{-1}cm^{-1}$	$94880M^{-1}cm^{-1}$
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.

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			Bundibugyo Ebola virus	Sudan Ebola virus	Reston Ebola virus	Zaire Ebola virus	Tai forest ebola virus
Number and composition of amino acids	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%)
MEMBRANE ASSOCIATED PROTEIN	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
Theoritical 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			$30480M^{-1}cm^{-1}$	$34950M^{-1}cm^{-1}$	$31970M^{-1}cm^{-1}$	$31970M^{-1}cm^{-1}$	$30480M^{-1}cm^{-1}$
Absorbance assuming cystine residues			1.082	1.236	1.135	1.133	1.093
Extinction coefficient with out cystine residues			$30480M^{-1}cm^{-1}$	$34950M^{-1}cm^{-1}$	$31970M^{-1}cm^{-1}$	$31970M^{-1}cm^{-1}$	$30480M^{-1}cm^{-1}$
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 allforms of membrane associated 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;28276.97 >28218.85 >28168.88>28163.88 >27887.58 .By this we can say that Sudan Ebolavirus has greater molecular weight and Taiforest Ebolavvirus has 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 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) > 10.50(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

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			Bundibugyo Ebola virus	Sudan Ebola virus	Reston Ebola virus	Zaire Ebola virus	Tai forest ebola virus
Number and composition of amino acids	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%)
MINOR-NUCLEOPROTEIN	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
Theoritical 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			$28335M^{-1}cm^{-1}$	$26845M^{-1}cm^{-1}$	$26845M^{-1}cm^{-1}$	$28460M^{-1}cm^{-1}$	$28460M^{-1}cm^{-1}$
Absorbance assuming cystine residues			0.863	0.836	0.829	0.875	0.873
Extinction coefficient with out cystine residues			$27960M^{-1}cm^{-1}$	$26470M^{-1}cm^{-1}$	$26470M^{-1}cm^{-1}$	$27960M^{-1}cm^{-1}$	$27960M^{-1}cm^{-1}$
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 nucleo- protein of Ebola virus species,in which allforms of minor nucleo 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 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 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 and absorbance in all species of Ebola virus with and with out assuming cysteine residues.The Minor Nucleo-protein 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

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			Bundibugyo Ebola virus	Sudan Ebola virus	Reston Ebola virus	Zaire Ebola virus	Tai forest ebola virus
Number and composition of amino acids	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%)
RNA DEPENDENT RNA POLYMERASE	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
Theoritical 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			$306320M^{-1}cm^{-1}$	$294860M^{-1}cm^{-1}$	$312155M^{-1}cm^{-1}$	$291755M^{-1}cm^{-1}$	$289025M^{-1}cm^{-1}$
Absorbance assuming cystine residues			1.217	1.173	1.236	1.154	1.153
Extinction coefficient with out cystine residues			$303570M^{-1}cm^{-1}$	$292110M^{-1}cm^{-1}$	$309530M^{-1}cm^{-1}$	$289130M^{-1}cm^{-1}$	$286150M^{-1}cm^{-1}$
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 allforms of RNA dependent RNA Polymerase 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 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 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 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 stablewhen 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

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MODULE-2

MULTIPLE SEQUENCE ALIGNMENT

MATRIX PROTEIN

```
Sudan           MRRVTVPTAPPAYADIGYPMSMLPIKSSRAVSGIQQKQEVLPGMDTPSNSMRPVADDNID 60
Reston          MRRGVLPTAPPAYNDIAYPMSILPTRPSVIVNETKSDVLAVPGADVPSNSMRPVADDNID 60
TaiForest       MRRIILPTAPPEYMEAVYPMRTMNSGADNTASGPNYTTTGVMTNDTPSNSLRPVADDNID 60
Bundibugyo      MRRAILPTAPPEYIEAVYPMRTVSTSINSTASGPNFPAPDVMMSDTPSNSLRPIADDNID 60
Zaire           ------------------------------------------------------------ 0

Sudan           HTSHTPNGVASAFILEATVNVISGPKVLMKQIPIWLPLGIADQKTYSFDSTTAAIMLASY 120
Reston          HSSHTPSGVASAFILEATVNVISGTKVLMKQIPIWLPLGVADQKIYSFDSTTAAIMLASY 120
TaiForest       HPSHTPNSVASAFILEAMVNVISGPKVLMKQIPIWLPLGVSDQKTYSFDSTTAAIMLASY 120
Bundibugyo      HPSHTPTSVSSAFILEAMVNVISGPKVLMKQIPIWLPLGVADQKTYSFDSTTAAIMLASY 120
Zaire           ----------SAFILEAMVNVISGPKVLMKQIPIWLPLGVADQKTYSFDSTTAAIMLASY 50
                          ******* ****** ***************:**** ***************

Sudan           TITHFGKANNPLVRVNRLGQGIPDHPLRLLRMGNQAFLQEFVLPPVQLPQYFTFDLTALK 180
Reston          TVTHFGKISNPLVRVNRLGPGIPDHPLRLLRLGNQAFLQEFVLPPVQLPQYFTFDLTALK 180
TaiForest       TITHFGKTSNPLVRINRLGPGIPDHPLRLLRIGNQAFLQEFVLPPVQLPQYFTFDLTALK 180
Bundibugyo      TITHFGKTSNPLVRINRLGPGIPDHPLRLLRIGNQAFLQEFVLPPVQLPQYFTFDLTALK 180
Zaire           TITHFGKATNPLVRVNRLGPGIPDHPLRLLRIGNQAFLQEFVLPPVQLPQYFTFDLTALK 110
                *:***** .*****:**** ***********:****************************

Sudan           LVTQPLPAATWTDETPSNLSGALRPGLSFHPKLRPVLLPGKTGKKGHVSDLTAPDKIQTI 240
Reston          LITQPLPAATWTDETPAGAVNALRPGLSLHPKLRPILLPGKTGKKGHASDLTSPDKIQTI 240
TaiForest       LITQPLPAATWTDETPAVSTGTLRPGISFHPKLRPILLPGRAGKKGSNSDLTSPDKIQAI 240
Bundibugyo      LITQPLPAATWTDDTPTGPTGILRPGISFHPKLRPILLPGKTGKRGSSSDLTSPDKIQAI 240
Zaire           LITQPLPAATWTDDTPTGSNGALRPGISFHPKLRPILLPNKSGKKGNSADLTSPEKIQAI 170
                *:************:**:    . ****:*:*******:***.:::**:*   :***:*:***:*

Sudan           VNLMQDFKIVPIDPAKSIIGIEVPELLVHKLTGKKMSQKNGQPIIPVLLPKYIGLDPISP 300
Reston          MNAIPDLKIVPIDPTKNIVGIEVPELLVQRLTGKKPQPKNGQPIIPVLLPKYVGLDPISP 300
TaiForest       MNFLQDLKIVPIDPTKNIMGIEVPELLVHRLTGKKTTTKNGQPIIPILLPKYIGLDPLSQ 300
Bundibugyo      MNFLQDLKLVPIDPAKNIMGIEVPELLVHRLTGKKITTKNGQPIIPILLPKYIGMDPISQ 300
Zaire           MTSLQDFKIVPIDPTKNIMGIEVPETLVHKLTGKKVTSKNGQPIIPVLLPKYIGLDPVAP 230
                :. : *:*:*****:*.*:****** **::*****    ********:*****:*:**::

Sudan           GDLTMVITPDYDDCHSPASCSYLSEK-----     326
Reston          GDLTMVITQDCDSCHSPASHPYHMDKQNSYQ     331
TaiForest       GDLTMVITQDCDSCHSPASLPPVNEK-----     326
Bundibugyo      GDLTMVITQDCDTCHSPASLPPVSEK-----     326
Zaire           GDLTMVITQDCDTCHSPASLPAVIEK-----     256
                ******** * * ******      :*
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MEMBRANE ASSOCIATED PROTEIN

```
Sudan           MAKATGRYNLVTPKRELEQGVVFSDLCNFLVTPTVQGWKVYWAGLEFDVNQKGITLLNRL 60
Reston          MAKATGRYNLVPPKKDMEKGVIFSDLCNFLITQTLQGWKVYWAGIEFDVSQKGMALLTRL 60
Zaire           MAKATGRYNLISPKKDLEKGVVLSDLCNFLVSQTIQGWKVYWAGIEFDVTHKGMALLHRL 60
Taiforest       MAKATGRYNLISPKKDLEKGLVLNDLCTLSVAQTVQGWKVTWAGIEFDVTQKGMALLHRL 60
Bundibugyo      MAKATGRYNLVSPKKDLERGLVLSDLCTFLVDQTIQGWRVTWVGIEFDIAQKGMALLHRL 60

                **********: **:::*:*:::.***.: :  *:***:* *.*:***: :**::** **

Sudan           KVNDFAPAWAMTRNLFPHLFKNQQSEVQTPIWALRVILAAGILDQLMDHSLIEPLSGALN 120
Reston          KTNDFAPAWAMTRNLFPHLFQNPNSVIQSPIWALRVILAAGLQDQLLDHSLVEPLTGALG 120
Zaire           KTNDFAPAWSMTRNLFPHLFQNPNSTIESPLWALRVILAAGIQDQLIDQSLIEPLAGALG 120
Taiforest       KTSDFAPAWSMTRNLFPHLFQNPNSTIESPLWALRVILAAGIQDQLIDQSLIEPLAGALG 120
Bundibugyo      KTADFAPAWSMTRNLFPHLFQNSNSTIESPLWALRVILAAGIQDQLIDQSLVEPLAGALS 120
                *. ******:**********:* :* :::*:**********: ***:*:**:***:***.

Sudan           LIADWLLTTSTNHFNMRTQRVKDQLSMRMLSLIRSNIINFINKLETLHVVNYKGLLSSVE 180
Reston          LISDWLLTTTSTHFNLRTRSVKDQLSLRMLSLIRSNILQFINKLDALHVVNYNGLLSSIE 180
Zaire           LISDWLLTTNTNHFNMRTQRVKEQLSLKMLSLIRSNILKFINKLDALHVVNYNGLLSSIE 180
Taiforest       LIADWLLTTGTNHFQMRTQQAKEQLSLKMLSLVRSNILKFINQLDALHVVNYNGLLSSIE 180
Bundibugyo      LVSDWLLTTNTNHFQMRTQHAKEQLSLKMLSLVRSNILKFISQLDALHVVNYNGLLSSIE 180
                *::****** :.**::**: .*:***::****:****::**.:*::******:******:*

Sudan           IGTPSYAIIITRTNMGYLVEVQEPDKSAMDIRHPGPVKFSLLHESTLKPVATPKPSSITS 240
Reston          IGTSTHTIIITRTNMGFLVEVQEPDKSAMNSKRPGPVKFSLLHESAFKPFTRVPQSGMQS 240
Zaire           IGTQNHTIIITRTNMGFLVELQEPDKSAMNRMKPGPAKFSLLHESTLKAFTQGSSTRMQS 240
Taiforest       IGTKSHTIIITRTNMGFLVELQEPDKSAMNTRKPGPVKFSLLHESTLKTLAKKPATQMQA 240
Bundibugyo      IGTRNHTIIITRTNMGFLVELQEPDKSAMNQKKPGPVKFSLLHESTFKALIKKPATKMQA 240
                *** .::**********:***:*********:  :***.*********::* .     : : :

Sudan           LIMEFNSSLAI       251
Reston          LIMEFNSLLAI       251
Zaire           LILEFNSSLAI       251
Taiforest       LILEFNSSLAI       251
Bundibugyo      LILEFNSSLAI       251
                **:**** ***
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MINOR-NUCLEO PROTEIN

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Reston          MEHSRERGRSSNMRHNSREPYENPSRSRSLSRDPNQVDRRQPRSASQIRVPNLFHRKKTD 60
Sudan           MERGRERGRSRNSRADQQNSTGPQFRTRSISRDKTTTDYRSSRSTSQVRVPTVFHKKGTG 60
Zaire           MEASYERGRPRAARQHSRDGHDHHVRARSSSRENYRGEYRQSRSASQVRVPTVFHKKRVE 60
Taiforest       MEVVHERGRSRISRQNTRDGPSHLVRARSSSRASYRSEYHTPRSASQIRVPTVFHRKKTD 60
Bundibugyo      MDSFHERGRSRTIRQSARDGPSHQVRTRSSSRDSHRSEYHTPRSSSQVRVPTVFHRKRTD 60
                *:   ****    *   ::      *:** **     : :  **:**:***.:**:* .

Reston          ALIVPPAPKDICPTLKKGFLCDSKFCKKDHQLDSLNDHELLLLIARRTCGIIESNSQITS 120
Sudan           TLTVPPAPKDVCPTLRKGFLCDSNFCKKDHQLESLTDRELLLLIARKTCGSTDSSLNIAA 120
Zaire           PLTVPPAPKDICPTLKKGFLCDSSFCKKDHQLESLTDRELLLLIARKTCGSVEQQLNITA 120
Taiforest       LLTVPPAPKDVCPTLKKGFLCDSNFCKKDHQLESLTDRELLLLIARKTCGSTEQQLSIVA 120
Bundibugyo      SLTVPPAPKDICPTLRKGFLCDSNFCKKDHQLESLTDRELLLLIARKTCGSLEQQLNITA 120
                 * *******:****:*******.********:**.*:********:***  :.. .*.:

Reston          PKDMRLANPTAEDFSQGNSPKLTLAVLLQIAEHWATRDLRQIEDSKLRALLTLCAVLTRK 180
Sudan           PKDLRLANPTADDFKQDGSPKLTLKLLVETAEFWANQNINEVDDAKLRALLTLSAVLVRK 180
Zaire           PKDSRLANPTADDFQQEEGPKITLLTLIKTAEHWARQDIRTIEDSKLRALLTLCAVMTRK 180
Taiforest       PKDSRLANPIAEDFQQKDGPKVTLSMLIETAEYWSKQDIKNIDDSRLRALLTLCAVMTRK 180
Bundibugyo      PKDTRLANPIADDFQQKDGPKITLLTLLETAEYWSKQDIKGIDDSRLRALLTLCAVMTRK 180
                *** ***** *:**.*  .**:**  *:: **.*: :::. ::*::*******.**:.**

Reston          FSKSQLGLLCETHLRHEGLGQDQADSVLEVYQRLHSDKGGNFEAALWQQWDRQSLIMFIS 240
Sudan           FSKSQLSQLCESHLRRENLGQDQAESVLEVYQRLHSDKGGAFEAALWQQWDRQSLTMFIS 240
Zaire           FSKSQLSLLCETHLRREGLGQDQAEPVLEVYQRLHSDKGGSFEAALWQQWDRQSLIMFIT 240
Taiforest       FSKSQLSLLCESHLRREGLGQDQSESVLEVYQRLHSDKGGNFEAALWQQWDRQSLIMFIT 240
Bundibugyo      FSKSQLSLLCESHLRREGLGQDQSESVLEVYQRLHSDKGGNFEAALWQQWDRQSLIMFIT 240

                ******. ***:***:*.*****:: ************** ************** ***:

Reston          AFLNIALQIPCESSSVVVSGLATLYPAQDNSTPSEATNDTTWSSTVE--   287
Sudan           AFLHVALQLSCESSTVVISGLRLLAPPSVNEGLPPAPGEYTWSEDSTT-   288
Zaire           AFLNIALQLPCESSAVVVSGLRTLVPQSDNEEASTNPGTCSWSDEGTP-   288
Taiforest       AFLNIALQLPCESSSVVISGLRMLIPQSEATEVVTPSETCTWSEGGSSH   289
Bundibugyo      AFLNIALQLPCESSSVVISGLRLLVPQSEDTETSTYTETRAWSEEGGPH   289
                ***::***: ****:**:***  * * .            :**.
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NUCLEO-PROTEIN

```
Sudan           MDKRVRGSWALGGQSEVDLDYHKILTAGLSVQQGIVRQRVIPVYVVSDLEGICQHIIQAF 60
Reston          MDRGTRRIWVSQNQGDTDLDYHKILTAGLTVQQGIVRQKIISVYLVDNLEAMCQLVIQAF 60
Zaire           MDSRPQKIWMAPSLTESDMDYHKILTAGLSVQQGIVRQRVIPVYQVNNLEEICQLIIQAF 60
Taiforest       MESRAHKAWMTHTASGFETDYHKILTAGLSVQQGIVRQRVIQVHQVTNLEEICQLIIQAF 60
Bundibugyo      MDPRPIRTWMMHNTSEVEADYHKILTAGLSVQQGIVRQRIIPVYQISNLEEVCQLIIQAF 60
                *:      *        : **********:*********::* *: : :** :** :****

Sudan           EAGVDFQDNADSFLLLLCLHHAYQGDHRLFLKSDAVQYLEGHGFRFEVREKENVHRLDEL 120
Reston          EAGIDFQENADSFLLMLCLHHAYQGDYKLFLESNAVQYLEGHGFKFELRKKDGVNRLEEL 120
Zaire           EAGVDFQESADSFLLMLCLHHAYQGDYKLFLESGAVKYLEGHGFRFEVKKRDGVKRLEEL 120
Taiforest       EAGVDFQESADSFLLMLCLHHAYQGDYKQFLESNAVKYLEGHGFRFEVRKKEGVKRLEEL 120
Bundibugyo      EAGVDFQDSADSFLLMLCLHHAYQGDYKQFLESNAVKYLEGHGFRFEMKKKEGVKRLEEL 120
                ***:***:.******:**********:: **:*.**:*******:**::::::.*:**:**

Sudan           LPNVTGGKNLRRTLAAMPEEETTEANAGQFLSFASLFLPKLVVGEKACLEKVQRQIQVHA 180
Reston          LPAATSGKNIRRTLAALPEEETTEANAGQFLSFASLFLPKLVVGEKACLEKVQRQIQVHA 180
Zaire           LPAVSSGKNIKRTLAAMPEEETTEANAGQFLSFASLFLPKLVVGEKACLEKVQRQIQVHA 180
Taiforest       LPAASSGKSIRRTLAAMPEEETTEANAGQFLSFASLFLPKLVVGEKACLEKVQRQIQVHS 180
Bundibugyo      LPAASSGKNIKRTLAAMPEEETTEANAGQFLSFASLFLPKLVVGEKACLEKVQRQIQVHA 180
                ** .:.**.::*****:*******************************************:

Sudan           EQGLIQYPTSWQSVGHMMVIFRLMRTNFLIKFLLIHQGMHMVAGHDANDTVISNSVAQAR 240
Reston          EQGLIQYPTAWQSVGHMMVIFRLMRTNFLIKYLLIHQGMHMVAGHDANDAVIANSVAQAR 240
Zaire           EQGLIQYPTAWQSVGHMMVIFRLMRTNFLIKFLLIHQGMHMVAGHDANDAVISNSVAQAR 240
Taiforest       EQGLIQYPTAWQSVGHMMVIFRLMRTNFLIKFLLIHQGMHMVAGHDANDAVIANSVAQAR 240
Bundibugyo      EQGLIQYPTSWQSVGHMMVIFRLMRTNFLIKFLLIHQGMHMVAGHDANDAVIANSVAQAR 240
                *********:**********************:*****************:**:*******

Sudan           FSGLLIVKTVLDHILQKTDLGVRLHPLARTAKVKNEVSSFKAALGSLAKHGEYAPFARLL 300
Reston          FSGLLIVKTVLDHILQKTDQGVRLHPLARTAKVRNEVNAFKAALSSLAKHGEYAPFARLL 300
Zaire           FSGLLIVKTVLDHILQKTERGVRLHPLARTAKVKNEVNSFKAALSSLAKHGEYAPFARLL 300
Taiforest       FSGLLIVKTVLDHILQKTEHGVRLHPLARTAKVKNEVNSFKAALSSLAQHGEYAPFARLL 300
Bundibugyo      FSGLLIVKTVLDHILQKTEHGVRLHPLARTAKVKNEVSSFKAALASLAQHGEYAPFARLL 300
                ******************: *************:***.:*****.***:************

Sudan           NLSGVNNLEHGLYPQLSAIALGVATAHGSTLAGVNVGEQYQQLREAATEAEKQLQQYAET 360
Reston          NLSGVNNLEHGLYPQLSAIALGVATAHGSTLAGVNVGEQYQQLREAATEAEKQLQQYAES 360
Zaire           NLSGVNNLEHGLFPQLSAIALGVATAHGSTLAGVNVGEQYQQLREAATEAEKQLQQYAES 360
Taiforest       NLSGVNNLEHGLFPQLSAIALGVATAHGSTLAGVNVGEQYQQLREAATEAEKQLQKYAES 360
Bundibugyo      NLSGVNNLEHGLFPQLSAIALGVATAHGSTLAGVNVGEQYQQLREAATEAEKQLQKYAES 360
                ************:*****************************************:****:
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Sudan          RELDNLGLDEQEKKILMSFHQKKNEISFQQTNAMVTLRKERLAKLTEAITTASKIKVGDR 420
Reston         RELDSLGLDDQERRILMNFHQKKNEISFQQTNAMVTLRKERLAKLTEAITLASRPNLGSR 420
Zaire          RELDHLGLDDQEKKILMNFHQKKNEISFQQTNAMVTLRKERLAKLTEAITAASLPKTSGH 420
Taiforest      RELDHLGLDDQEKKILKDFHQKKNEISFQQTTAMVTLRKERLAKLTEAITSTSLLKTGKQ 420
Bundibugyo     RELDHLGLDDQEKKILKDFHQKKNEISFQQTTAMVTLRKERLAKLTEAITSTSILKTGRR 420
               **** ****:**::** .************.****************** :*  : . :

Sudan          YPDDNDIPFPGPIYDETHPNPSDDNPDDSRDTTIPGGVVDPYDDESNNYPDYEDSAEGTT 480
Reston         QDDGNEIPFPGPISNNPDQDHLEDDPRDSRDTIIPNGAIDPEDGDFENYNGYHDDEVGTA 480
Zaire          YDDDDDIPFPGPINDDDNPGHQDDDPTDSQDTTIPDVVVDPDDGSYGEYQSYSENGMNAP 480
Taiforest      YDDDNDIPFPGPINDNENSEQQDDDPTDSQDTTIPDIIVDPDDGRYNNYGDYPSETANAP 480
Bundibugyo     YDDDNDIPFPGPINDNENSGQNDDDPTDSQDTTIPDVIIDPNDGGYNNYSDYANDAASAP 480
                 *.::******** :: .    :*:* **:** **.  :** *.   :* .* ..  .:

Sudan          GDLDLFNLDDDDDDSQPGPPDRGQSKERAARTHGLQ-DPTLDGA-------KKVPELTPG 532
Reston         GDLVLFDLDDHEDDNKAFEPQDSSPQS----------QREIER----ERLIHPPPGNNKD 526
Zaire          DDLVLFDLDEDDEDTKPVPNRSTKGGQQKN--S--QKGQHIEGRQTQSRPIQNVPG--P- 533
Taiforest      EDLVLFDLEDGDEDDHRPSSSSENNNKHSL--TGTDSNKTSNWNRNP----TNMPKKDS- 533
Bundibugyo     DDLVLFDLEDEDDADNPAQNTPEKNDRPAT--TKLRNGQDQDGNQGE----TASPRVAP- 533
                ** **:*:: ::  :       .                :              *

Sudan          SHQPG--NLHIT---KP-GSNTNQPQGNMSSTLQSMTPIQEESEPDDQKDDDDESLTSLD 586
Reston         DNRASDNNQQSADSEEQGGQYNWHRGPERTTANRRLSPVHEEDTLMDQGDDDPSSLPPLE 586
Zaire          -------HRTIHHASAPLTDNDRRNEPSGSTSPRMLTPINEEADPLDDADDETSSLPPLE 586
Taiforest      -------TQNNDNPAQRAQEYARDNIQDTPTPHRALTPISEETGSNGHNEDDIDSIPPLE 586
Bundibugyo     -------NQYRDKPMPQVQDRSENHDQTLQTQSRVLTPISEEADPSDHNDGDNESIPPLE 586
                             .          :  : ::*: **    .. :.: .*:  *:

Sudan          SEGDEDVESVSGENNPTVAPPAPVYKDTGVDTNQQNGPSNAVDGQGSESEALPINPEKGS 646
Reston         SDDDDASSSQQDPDYTAVAPPAPVYRSAEAHEPPHKSSNEPAETSQLNEDPDIGQSKSMQ 646
Zaire          SDDEEQDRDGTSNRTPTVAPPAPVYRDHSEKKELPQDEQQDQDHTQEARNQDSDNTQSEH 646
Taiforest      SDEENNTETTITTTKNTTAPPAPVYRSNSEKEPLPQEKSQKQPNQVSGSENTDNKPHSEQ 646
Bundibugyo     SDDEGSTDTTAAETKPATAPPAPVYRSISVDDSVPSENIPAQSNQTNNEDNVRNNAQSEQ 646
               *: :              :.*******:.   .    .              :    : ..

Sudan          ALEETYYHLLKTQGPFEAINYYHLMSDEPIAFSTESGKEYIFPDSLEEAYPPWLSEKEAL 706
Reston         KLEETYHHLLRTQGPFEAINYYHMMKDEPVIFSTDDGKEYTYPDSLEEAYPPWLTEKERL 706
Zaire          SFEEMYRHILRSQGPFDAVLYYHMMKDEPVVFSTSDGKEYTYPDSLEEEYPPWLTEKEAM 706
Taiforest      SVEEMYRHILQTQGPFDAILYYYMMTEEPIVFSTSDGKEYVYPDSLEGEHPPWLSEKEAL 706
Bundibugyo     SIAEMYQHILKTQGPFDAILYYHMMKEEPIIFSTSDGKEYTYPDSLEDEYPPWLSEKEAM 706
                . * * *:*::****:*: **::*.:**: ***..**** :******  :****:*** :

Sudan          EKENRYLVIDGQQFLWPVMSLQDKFLAVLQHD-  738
Reston         DKENRYIYINNQQFFWPVMSPRDKFLAILQHHQ  739
Zaire          NEENRFVTLDGQQFYWPVMNHKNKFMAILQHHQ  739
Taiforest      NEDNRFITMDDQQFYWPVMNHRNKFMAILQHHK  739
Bundibugyo     NEDNRFITMDGQQFYWPVMNHRNKFMAILQHHR  739
               ---***-- -- *** ****  -:**-*-***
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POLYMERASE COMPLEX PROTEIN

```
Reston         ------------MYNNKLKVCSGPETTGWISEQLMTGKIPVTDIFIDIDNKPDQMEVRLK 48
Sudan          ------------MQQDRTYRHHGPEVSGWFSEQLMTGKIPLTEVFVDVENKPSPAPITII 48
Zaire          -MTTRTKGRGHTAATTQNDRMPGPELSGWISEQLMTGRIPVSDIFCDIENNPGLCYASQM 59
Taiforest      MISTRAAAINDPSLPIRNQCTRGPELSGWISEQLMTGKIPVHEIFNDTEPHISSGSDCLP 60
Bundibugyo     MTSNRARVTYNPPPTTTGTRSCGPELSGWISEQLMTGKIPITDIFNEIETLPSISPSIHS 60
                                  *** :**:********:**: ::* : :    .

Reston         PSSRSSTRTCTSSSQTEVNYVPLLKKVEDTLTMLVNATSRQNAAIEALENRLSTLESSLK 108
Sudan          SKNPKTTRKSDKQVQTDDASSLLTEEVKAAINSVISAVRRQTNAIESLEGRVTTLEASLK 108
Zaire          QQTKPNPKTRNSQTQTDPICNHSFEEVVQTLASLATVVQQQTIASESLEQRITSLENGLK 119
Taiforest      RPKNTAPRTRNTQTQTDPVCNHNFEDVTQALTSLTNVIQKQALNLESLEQRIIDLENGLK 120
Bundibugyo     KIKTPSVQTRSVQTQTDPNCNHDFAEVVKMLTSLTLVVQKQTLATESLEQRITDLEGSLK 120
                  .    :.   . **:          .*   :  :  .  :*    *:** *:  ** .**


Reston         PIQDMGKVISSLNRSCAEMVAKYDLLVMTTGRATSTAAAVDAYWKEHKQPPPGPALYEEN 168
Sudan          PVQDMAKTISSLNRSCAEMVAKYDLLVMTTGRATATAAATEAYWNEHGQAPPGPSLYEDD 168
Zaire          PVYDMAKTISSLNRVCAEMVAKYDLLVMTTGRATATAAATEAYWAEHGQPPPGPSLYEES 179
Taiforest      PMYDMAKVISALNRSCAEMVAKYDLLVMTTGRATATAAATEAYWEEHGQPPPGPSLYEES 180
Bundibugyo     PVSEITKIVSALNRSCAEMVAKYDLLVMTTGRATATAAATEAYWAEHGRPPPGPSLYEED 180
               *: :: * :*:*** ********************:****.:*** ** :  ****:***:.

Reston         ALKGKIDDPNSYVPDAVQEAYKNLDSTSTLTEENFGKPYISAKDLKEIMYDHLPGFGTAF 228
Sudan          AIKAKLKDPNGKVPESVKQAYINLDSTSALNEENFGRPYISAKDLKEIIYDHLPGFGTAF 228
Zaire          AIRGKIESRDETVPQSVREAFNNLNSTTSLTEENFGKPDISAKDLRNIMYDHLPGFGTAF 239
Taiforest      AIRGKINKQEDKVPKEVQEAFRNLDSTSSLTEENFGKPDISAKDLRDIMYDHLPGFGTAF 240
Bundibugyo     AIRTKIGKQGDMVPKEVQEAFRNLDSTALLTEENFGKPDISAKDLRNIMYDHLPGFGTAF 240
               *:: *: .    **. *::*: **:**: *.******:* *******::*:***********

Reston         HQLVQVICKIGKDNNLLDTIHAEFQASLADGDSPQCALIQITKRVPIFQDVPPPIIHIRS 288
Sudan          HQLVQVICKIGKDNNILDIIHAEFQASLAEGDSPQCALIQITKRIPAFQDASPPIVHIKS 288
Zaire          HQLVQVICKLGKDSNSLDIIHAEFQASLAEGDSPQCALIQITKRVPIFQDAAPPVIHIRS 299
Taiforest      HQLVQVICKLGKDNSALDIIHAEFQASLAEGDSPQCALIQITKRIPIFQDATPPTIHIRS 300
Bundibugyo     HQLVQVICKLGKDNSSLDVIHAEFQASLAEGDSPQCALIQITKRIPIFQDAAPPVIHIRS 300
               *********:***.. ** ***********:***************:* ***. ** :**:*

Reston         RGDIPRACQKSLRPAPPSPKIDRGWVCLFKMQDGKTLGLKI   329
Sudan          RGDIPKACQKSLRPVPPSPKIDRGWVCIFQFQDGKALGLKI   329
Zaire          RGDIPRACQKSLRPVPPSPKIDRGWVCVFQLQDGKTLGLKI   340
Taiforest      RGDIPRACQKSLRPVPPSPKIDRGWVCIFQLQDGKTLGLKI   341
Bundibugyo     RGDIPKACQKSLRPVPPSPKIDRGWVCIFQLQDGKTLGLKI   341
               *****:*********.*************:*::*****:*****
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SECOND SECRETED GLYCO PROTEIN

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Taiforest       -MGASGILQLPRERFRKTSFFVWVIILFHKVFSIPLGVVHNNTLQVSDIDKFVCRDKLSS 59
Bundibugyo      -MVTSGILQLPRERFRKTSFFVWVIILFHKVFPIPLGVVHNNTLQVSDIDKLVCRDKLSS 59
Zaire           -MGVTGILQLPRDRFKRTSFFLWVIILFQRTFSIPLGVIHNSTLQVSDVDKLVCRDKLSS 59
Reston          MGSGYQLLQLPRERFRKTSFLVWVIILFQRAISMPLGIVTNSTLKATEIDQLVCRDKLSS 60
Sudan           -MGGLSLLQLPRDKFRKSSFFVWVIILFQKAFSMPLGVVTNSTLEVTEIDQLVCKDHLAS 59
                       :******::*::::**::******::.: :****:: *.**:.:::*::**:*:*:*

Taiforest       TSQLKSVGLNLEGNGVATDVPTATKRWGFRAGVPPKVVNCEAGEWAENCYNLAIKKVDGS 119
Bundibugyo      TSQLKSVGLNLEGNGVATDVPTATKRWGFRAGVPPKVVNYEAGEWAENCYNLDIKKADGS 119
Zaire           TNQLRSVGLNLEGNGVATDVPSATKRWGFRSGVPPKVVNYEAGEWAENCYNLEIKKPDGS 119
Reston          TSQLKSVGLNLEGNGIATDVPSATKRWGFRSGVPPKVVSYEAGEWAENCYNLEIKKSDGS 120
Sudan           TDQLKSVGLNLEGSGVSTDIPSATKRWGFRSGVPPKVVSYEAGEWAENCYNLEIKKPDGS 119
                *.**:*********.*::**:*:********:*******. ************ *** ***

Taiforest       ECLPEAPEGVRDFPRCRYVHKVSGTGPCPGGLAFHKEGAFFLYDRLASTIIYRGTTFAEG 179
Bundibugyo      ECLPEAPEGVRGFPRCRYVHKVSGTGPCPEGYAFHKEGAFFLYDRLASTIIYRSTTFSEG 179
Zaire           ECLPAAPDGIRGFPRCRYVHKVSGTGPCAGDFAFHKEGAFFLYDRLASTVIYRGTTFAEG 179
Reston          ECLPLPPDGVRGFPRCRYVHKVQGTGPCPGDLAFHKNGAFFLYDRLASTVIYRGTTFAEG 180
Sudan           ECLPPPPDGVRGFPRCRYVHKAQGTGPCPGDYAFHKDGAFFLYDRLASTVIYRGVNFAEG 179
                ****  *:*:*.**********..*****  . ****:*************:***...*:**

Taiforest       VIAFLILPKARKDFFQSPPLHEPANMTTDPSSYYHTTTINYVVDNFGTNTTEFLFQVDHL 239
Bundibugyo      VVAFLILPETKKDFFQSPPLHEPANMTTDPSSYYHTVTLNYVADNFGTNMTNFLFQVDHL 239
Zaire           VVAFLILPQAKKDFFSSHPLREPVNATEDPSSGYYSTTIRYQATGFGTNETEYLFEVDNL 239
Reston          VVAFLILSEPKKHFWKATPAHEPVNTTDDSTSYYMTLTLSYEMSNFGGNESNTLFKVDNH 240
Sudan           VIAFLILAKPKETFLQSPPIREAVNYTENTSSYYATSYLEYEIENFGAQHSTTLFKIDNN 239
                *:***** : :: * .: * :* .* * : :* * :  : *   .** : :  **::*:
```

```
Taiforest       TYVQLEARFTPQFLVLLNETIYSDNRRSNTTGKLIWKINPTVDTSMGEWAFWENKKLHKN 299
Bundibugyo      TYVQLEPRFTPQFLVQLNETIYTNGRRSNTTGTLIWKVNPTVDTGVGEWAFWENKKLHKN 299
Zaire           TYVQLESRFTPQFLLQLNETIYTSGKRSNTTGKLIWKVNPEIDTTIGEWAFWETKKPH-- 297
Reston          TYVQLDRPHTPQFLVQLNETLRRNNRLSNSTGRLTWTLDPKIEPDVGEWAFWETKKLFPT 300
Sudan           TFVRLDRPHTPQFLFQLNDTIHLHQQLSNTTGRLIWTLDANINADIGEWAFWENKKSLRT 299
                *:*:*:  .*****. **:*:    : **:** * *.::  ::  :********.**

Taiforest       PFK---------------------------- 302
Bundibugyo      PFK---------------------------- 302
Zaire           ---------------------------- 297
Reston          TSWRKLAFPNSINPHQQLLRSEPGGNCPRKN 331
Sudan           TTWRRAVFRSFIAQRDRRR---------- 318
```

SMALL SECRETED GLYCO PROTEIN

```
Taiforest       -MGASGILQLPRERFRKTSFFVWVIILFHKVFSIPLGVVHNNTLQVSDIDKFVCRDKLSS 59
Bundibugyo      -MVTSGILQLPRERFRKTSFFVWVIILFHKVFPIPLGVVHNNTLQVSDIDKLVCRDKLSS 59
Zaire           -MGVTGILQLPRDRFKRTSFFLWVIILFQRTFSIPLGVIHNSTLQVSDVDKLVCRDKLSS 59
Reston          MGSGYQLLQLPRERFRKTSFLVWVIILFQRAISMPLGIVTNSTLKATEIDQLVCRDKLSS 60
Sudan           -MGGLSLLQLPRDKFRKSSFFVWVIILFQKAFSMPLGVVTNSTLEVTEIDQLVCKDHLAS 59
                       :******::*::::**::******::.: :****:: *.**:.:::*::**:*:*:*

Taiforest       TSQLKSVGLNLEGNGVATDVPTATKRWGFRAGVPPKVVNCEAGEWAENCYNLAIKKVDGS 119
Bundibugyo      TSQLKSVGLNLEGNGVATDVPTATKRWGFRAGVPPKVVNYEAGEWAENCYNLDIKKADGS 119
Zaire           TNQLRSVGLNLEGNGVATDVPSATKRWGFRSGVPPKVVNYEAGEWAENCYNLEIKKPDGS 119
Reston          TSQLKSVGLNLEGNGIATDVPSATKRWGFRSGVPPKVVSYEAGEWAENCYNLEIKKSDGS 120
Sudan           TDQLKSVGLNLEGSGVSTDIPSATKRWGFRSGVPPKVVSYEAGEWAENCYNLEIKKPDGS 119
                *.**:*********.*::**:*:********:*******. ************ *** ***

Taiforest       ECLPEAPEGVRDFPRCRYVHKVSGTGPCPGGLAFHKEGAFFLYDRLASTIIYRGTTFAEG 179
Bundibugyo      ECLPEAPEGVRGFPRCRYVHKVSGTGPCPEGYAFHKEGAFFLYDRLASTIIYRSTTFSEG 179
Zaire           ECLPAAPDGIRGFPRCRYVHKVSGTGPCAGDFAFHKEGAFFLYDRLASTVIYRGTTFAEG 179
Reston          ECLPLPPDGVRGFPRCRYVHKVQGTGPCPGDLAFHKNGAFFLYDRLASTVIYRGTTFAEG 180
Sudan           ECLPPPPDGVRGFPRCRYVHKAQGTGPCPGDYAFHKDGAFFLYDRLASTVIYRGVNFAEG 179
                ****  *:*:*.**********..*****  . ****:*************:***...*:**

Taiforest       VIAFLILPKARKDFFQSPPLHEPANMTTDPSSYYHTTTINYVVDNFGTNTTEFLFQVDHL 239
Bundibugyo      VVAFLILPETKKDFFQSPPLHEPANMTTDPSSYYHTVTLNYVADNFGTNMTNFLFQVDHL 239
Zaire           VVAFLILPQAKKDFFSSHPLREPVNATEDPSSGYYSTTIRYQATGFGTNETEYLFEVDNL 239
Reston          VVAFLILSEPKKHFWKATPAHEPVNTTDDSTSYYMTLTLSYEMSNFGGNESNTLFKVDNH 240
Sudan           VIAFLILAKPKETFLQSPPIREAVNYTENTSSYYATSYLEYEIENFGAQHSTTLFKIDNN 239
                *:***** : :: * .: * :* .* * : :* * :  : *   .** : :  **::*:

Taiforest       TYVQLEARFTPQFLVLLNETIYSDNRRSNTTGKLIWKINPTVDTSMGEWAFWENKKTSQK 299
Bundibugyo      TYVQLEPRFTPQFLVQLNETIYTNGRRSNTTGTLIWKVNPTVDTGVGEWAFWENKKTSQK 299
Zaire           TYVQLESRFTPQFLLQLNETIYTSGKRSNTTGKLIWKVNPEIDTTIGEWAFWETKKTSLE 299
Reston          TYVQLDRPHTPQFLVQLNETLRRNNRLSNSTGRLTWTLDPKIEPDVGEWAFWETKKTFPN 300
Sudan           TFVRLDRPHTPQFLFQLNDTIHLHQQLSNTTGRLIWTLDANINADIGEWAFWENKKISPN 299
                *:*:*:  .*****. **:*:    : **:** * *.::  ::  :********.**    :

Taiforest       PFQVKSCLSYLYQKPRTRSLTRQRRSLLPSPPTTTQPKTTKNWFQRIPLQWFRCKTSRER 359
Bundibugyo      PFQVKSCLSYLYQEPRIQAATRRRRSLPPASPTTKPPRTTKTWFQRIPLQWFKCETSRGK 359
Zaire           KFAVKSCLSQLYQTEPKTSVVRVRRELLPTQGPTQQLKTTKSWLQKIPLQWFKCTVKEGK 359
Reston          NFMEKTCISKFHQPTPTTPQIRARRELSKEKLATTHPPTTPSWFQRIPLQWFQCSLQDGQ 360
Sudan           NYVEKSCLSKLYRSTRQKTMMRHRRELQREESPTGPPGSIRTWFQRIPLGWFHCTYQKGK 359
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                  :  *:*:* :::         * **.*      *    :  .*:*:*** **:*  .  :

Taiforest         TQCQPQ--------    365
Bundibugyo        TQCRPHPQTQSPQL    373
Zaire             LQCRI---------    364
Reston            RKCRPKV-------    367
Sudan             QHCRLRIRQKVEE-    372
                   :*:
```

SPIKE GLYCO-PROTEIN

```
Zaire             -MGVTGILQLPRDRFKRTSFFLWVIILFQRTFSIPLGVIHNSTLQVSDVDKLVCRDKLSS 59
Taiforest         -MGASGILQLPRERFRKTSFFVWVIILFHKVFSIPLGVVHNNTLQVSDIDKFVCRDKLSS 59
Bundibugyo        -MVTSGILQLPRERFRKTSFFVWVIILFHKVFPIPLGVVHNNTLQVSDIDKLVCRDKLSS 59
Reston            MGSGYQLLQLPRERFRKTSFLVWVIILFQRAISMPLGIVTNSTLKATEIDQLVCRDKLSS 60
Sudan             -MGGLSLLQLPRDKFRKSSFFVWVIILFQKAFSMPLGVVTNSTLEVTEIDQLVCKDHLAS 59
                        :******::*:::**::*******::.: :****:: *.**:.:::*::**:*:*:*

Zaire             TNQLRSVGLNLEGNGVATDVPSATKRWGFRSGVPPKVVNYEAGEWAENCYNLEIKKPDGS 119
Taiforest         TSQLKSVGLNLEGNGVATDVPTATKRWGFRAGVPPKVVNCEAGEWAENCYNLAIKKVDGS 119
Bundibugyo        TSQLKSVGLNLEGNGVATDVPTATKRWGFRAGVPPKVVNYEAGEWAENCYNLDIKKADGS 119
Reston            TSQLKSVGLNLEGNGIATDVPSATKRWGFRSGVPPKVVSYEAGEWAENCYNLEIKKSDGS 120
Sudan             TDQLKSVGLNLEGSGVSTDIPSATKRWGFRSGVPPKVVSYEAGEWAENCYNLEIKKPDGS 119
                  *.**:*********.*::**:*:********:*******. ************ *** ***

Zaire             ECLPAAPDGIRGFPRCRYVHKVSGTGPCAGDFAFHKEGAFFLYDRLASTVIYRGTTFAEG 179
Taiforest         ECLPEAPEGVRDFPRCRYVHKVSGTGPCPGGLAFHKEGAFFLYDRLASTIIYRGTTFAEG 179
Bundibugyo        ECLPEAPEGVRGFPRCRYVHKVSGTGPCPEGYAFHKEGAFFLYDRLASTIIYRSTTFSEG 179
Reston            ECLPLPPDGVRGFPRCRYVHKVQGTGPCPGDLAFHKNGAFFLYDRLASTVIYRGTTFAEG 180
Sudan             ECLPPPPDGVRGFPRCRYVHKAQGTGPCPGDYAFHKDGAFFLYDRLASTVIYRGVNFAEG 179
                  ****  *:*:*.*********..***** . ****:************:***...*:**

Zaire             VVAFLILPQAKKDFFSSHPLREPVNATEDPSSGYYSTTIRYQATGFGTNETEYLFEVDNL 239
Taiforest         VIAFLILPKARKDFFQSPPLHEPANMTTDPSSYYHTTTINYVVDNFGTNTTEFLFQVDHL 239
Bundibugyo        VVAFLILPETKKDFFQSPPLHEPANMTTDPSSYYHTVTLNYVADNFGTNMTNFLFQVDHL 239
Reston            VVAFLILSEPKKHFWKATPAHEPVNTTDDSTSYYMTLTLSYEMSNFGGNESNTLFKVDNH 240
Sudan             VIAFLILAKPKETFLQSPPIREAVNYTENTSSYYATSYLEYEIENFGAQHSTTLFKIDNN 239
                  *:***** : :: * .: * :* .* * : :* * :  : *   .** : :  **::*:

Zaire             TYVQLESRFTPQFLLQLNETIYTSGKRSNTTGKLIWKVNPEIDTTIGEWAFWETKKNLTR 299
Taiforest         TYVQLEARFTPQFLVLLNETIYSDNRRSNTTGKLIWKINPTVDTSMGEWAFWENKKNFTK 299
Bundibugyo        TYVQLEPRFTPQFLVQLNETIYTNGRRSNTTGTLIWKVNPTVDTGVGEWAFWENKKNFTK 299
Reston            TYVQLDRPHTPQFLVQLNETLRRNNRLSNSTGRLTWTLDPKIEPDVGEWAFWETKKNFSQ 300
Sudan             TFVRLDRPHTPQFLFQLNDTIHLHQQLSNTTGRLIWTLDANINADIGEWAFWENKKNLSE 299
                  *:*:*:  .*****. **:*:    : **:** * *.::  ::  :*******.***::.

Zaire             KIRSEELSFTVVSNGAKNISGQSPARTSSDPGTNTTTEDHKIMASENSSAMVQVHSQGRE 359
Taiforest         TLSSEELSFVPVPETQNQVLDTTATVSPPISAHNHAAEDHKELVSEDSTPVVQMQNIKGK 359
Bundibugyo        TLSSEELSVIFVPRAQDPGSNQKTKVTPTSFANNQTSKNHEDLVPEDPASVVQVRDLQRE 359
Reston            QLHGENLHFQIPSTHTNNSSDQSPAGTVQGKISYHPPANNSELVPTDSPPVVSVLTAGRT 360
Sudan             QLRGEELSFEALSLNETEDDDAASSRITKGRISDRATRKYSDLVPKNSPGMVPLHIPEGE 359
                   : .*:* .           .                  . . :.  :   :* :

Zaire             AAVSHLTTLATISTS--P-QSLTTKPGPDNST-HNTPVYKLD-ISEATQVEQHHRRTDND 414
Taiforest         DTMPTTVT-----------GVPTTTPSPFPINARNTDHTKSFIGLEGPQ-ED-HSTTQPA 406
Bundibugyo        NTVPTPPP-----------DTVPTTLIPDTMEEQTTSHYEPPNISRNHQ-ER-NNTAHPE 406
Reston            EEMSTQGLTNGETITGFTANPMTTTIAPS-------PTMT------SEV-DNNVPSEQPN 406
Sudan             TTLPSQNSTEGRRVGVNTQETITETAATI--IGTNGNHMQISTIGIRPS-SSQIPSSSPT 416
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Zaire          ST---ASDTPSATTAA------GPPKAEN---TNTSKSTDFL---DPA----------447
Taiforest      KT---TSQPTNSTEST------TLNPTSE----PSSRGTGPSSPTVPNTTESHAELGKTT453
Bundibugyo     TL---ANNPPDNTTPS------TPPQDGE----RTSSHTTPSPRPVPTSTIHPTTRETHI453
Reston         NTASIEDSPPSASNETIYHSEMDPIQGSNNSAQSPQTKTTPAPTTSPMTQDPQETANSSK466
Sudan          TAPSPEA-------------------------QTPTTH-----TSGP------SVMATEE440

Zaire          TTTSPQNHSETAG-------NNNTHHQDTGEESASSGKLGLITNTIAGVAGLITGGRRTR500
Taiforest      PTTLPEQHTAASA-------------IPRAVHPDELSGPGFLTNTIRGVTNLLTGSRRKR500
Bundibugyo     PTTMTTSHDTDSN--------------RPNPIDISESTEPGPLTNTTRGAANLLTGSRRTR500
Reston         PGTSPGSAAGPS---------------------QPGLTINTVSKVADSLSPTRKQK501
Sudan          PTTPPGSSPGPTTEAPTLTTPENITTAVKTVLPQESTSNGLITSTVTGILGSLGLRKRSR500

Zaire          REAIVNAQPKCNPNLHYWTTQDEGAAIGLAWIPYFGPAAEGIYIEGLMHNQDGLICGLRQ560
Taiforest      RDVTPNTQPKCNPNLHYWTALDEGAAIGLAWIPYFGPAAEGIYTEGIMENQNGLICGLRQ560
Bundibugyo     REITLRTQAKCNPNLHYWTTQDEGAAIGLAWIPYFGPAAEGIYTEGIMHNQNGLICGLRQ560
Reston         RSVRQNTANKCNPDLYYWTAVDEGAAVGLAWIPYFGPAAEGIYIEGVMHNQNGLICGLRQ561
Sudan          RQTNTKATGKCNPNLHYWTAQEQHNAAGIAWIPYFGPGAEGIYTEGLMHNQNALVCGLRQ560

Zaire          LANETTQALQLFLRATTELRTFSILNRKAIDFLLQRWGGTCHILGPDCCIEPHDWTKNIT620
Taiforest      LANETTQALQLFLRATTELRTFSILNRKAIDFLLQRWGGTCHILGPDCCIEPQDWTKNIT620
Bundibugyo     LANETTQALQLFLRATTELRTFSILNRKAIDFLLQRWGGTCHILGPDCCIEPHDWTKNIT620
Reston         LANETTQALQLFLRATTELRTYSLLNRKAIDFLLQRWGGTCRILGPSCCIEPHDWTKNIT621
Sudan          LANETTQALQLFLRATTELRTYTILNRKAIDFLLRRWGGTCRILGPDCCIEPHDWTKNIT620

Zaire          DKIDQIIHDFVDKTLPDQGDNDNWWTGWRQWIPAGIGVTGVIIAVIALFCICKFVF     676
Taiforest      DKIDQIIHDFVDNNLPNQNDGSNWWTGWKQWVPAGIGITGVIIAIIALLCICKFML     676
Bundibugyo     DKIDQIIHDFIDKPLPDQTDNDNWWTGWRQWVPAGIGITGVIIAVIALLCICKFLL     676
Reston         DEINQIKHDFIDNPLPDHGDDLNLWTGWRQWIPAGIGIIGVIIAIIALLCICKILC     677
Sudan          DKINQIIHDFIDNPLPNQDNDDNWWTGWRQWIPAGIGITGIIIAIIALLCVCKLLC     676
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RNA DEPENDENT RNA POLYMERASE

```
Zaire          -MATQHTQYPDARLSSPIVLDQCDLVTRACGLYSSYSLNPQLRNCKLPKHIYRLKYDVTV59
Tai            -MATQHTQYPDARLSSPIVLDQCDLVTRACGLYSAYSLNPQLKNCRLPKHIYRLKYDTTV59
Bundibugyo     -MATQHTQYPDARLSSPIVLDQCDLVTRACGLYSSYSLNPQLKNCRLPKHIYRLKFDATV59
Sudan          MMATQHTQYPDARLSSPIVLDQCDLVTRACGLYSEYSLNPKLKTCRLPKHIYRLKYDTIV60
Reston         -MATQHTQYPDARLSSPIVLDQCDLVTRACGLYSSYSLNPQLRQCKLPKHIYRLKFDTIV59

Zaire          TKFLSDVPVATLPIDFIVPVLLKALSGNGFCPVEPRCQQFLDEIIKYTMQDALFLKYYLK119
Tai            TEFLSDVPVATLPADFLVPTFLRTLSGNGSCPIDPKCSQFLEEIVNYTLQDIRFLNYYLN119
Bundibugyo     TKFLSDVPIVTLPIDYLTPLLLRTLSGEGLCPVEPKCSQFLDEIVSYVLQDARFLRYYFR119
Sudan          LRFISDVPVATIPIDYIAPMLINVLADSKNVPLEPPCLSFLDEIVNYTVQDAAFLNYYMN120
Reston         SKFLSDTPVATLPIDYLVPILLRSLTGHGDRPLTPTCNQFLDEIINYTLHDAAFLDYYLK119

Zaire          NVGAQEDCVDEHFQEKILSSIQGNEFLHQMFFWYDLAILTRRGRLNRGNSRSTWFVHDDL179
Tai            RAGVHNDHVDRDFGQKIRNLICDNEVLHQMFHWYDLAILARRGRLNRGNNRSTWFASDNL179
Bundibugyo     HVGVHDDNVGKNFEPKIKALIYDNEFLQQLFYWYDLAILTRRGRLNRGNNRSTWFANDDL179
Sudan          QIKTQEGVITDQLKQNIRRVIHKNRYLSALFFWHDLAILTRRGRMNRGNVRSTWFVTNEV180
Reston         ATGAQDHLTNIATREKLKNEILNNDYVHQLFFWHDLSILARRGRLNRGNNRSTWFVHDEF179

Zaire          IDILGYGDYVFWKIPISMLPLNTQGIPHAAMDWYQASVFKEAVQGHTHIVSVSTADVLIM239
Tai            VDILGYGDYIFWKIPLSLLPVDTQGLPHAAKDWYHESVFKEAIQGHTHIVSISTADVLIM239
Bundibugyo     IDILGYGDYIFWKIPLSLLSLNTEGIPHAAKDWYHASIFKEAVQGHTHIVSVSTADVLIM239
Sudan          VDILGYGDYIFWKIPIALLPMNTANVPHASTDWYQPNIFKEAIQGHTHIISVSTAEVLIM240
Reston         IDILGYGDYIFWKIPLSLLPVTIDGVPHAATDWYQPTLFKESILGHSQILSVSTAEILIM239

Zaire          CKDLITCRFNTTLISKIAEIEDPVCSDYPNFKIVSMLYQSGDYLLSILGSDGYKIIKFLE299
Tai            CKDIITCRFNTTLIAAVANLEDSVHSDYPLPETVSDLYKAGDYLISLLGSEGYKVIKFLE299
Bundibugyo     CKDIITCRFNTTLIAALANLEDSICSDYPQPETISNLYKAGDYLISILGSEGYKVIKFLE299
Sudan          CKDLVTSRFNTLLIAELARLEDPVSADYPLVDNIQSLYNAGDYLLSILGSEGYKIIKYLE300
Reston         CKDIITCRFNTSLIASIAKLEDVDVSDYPDPSDILKIYNAGDYVISILGSEGYKIIKYLE299

Zaire          PLCLAKIQLCSKYTERKGRFLTQMHLAVNHTLEEITEMRALKPSQAQKIREFHRTLIRLE359
Tai            PLCLAKIQLCSNYTERKGRFLTQMHLAVNHTLEELTGSRELRPQQIRKVREFHQMLINLK359
Bundibugyo     PLCLAKIQLCSNYTERKGRFLTQMHLAVNHTLEELIEGRGLKSQQDWKMREFHRILVNLK359
Sudan          PLCLAKIQLCSQYTERKGRFLTQMHLAVIQTLRELLLNRGLKKSQLSKIREFHQLLLRLR360
Reston         PLCLAKIQLCSKFTERKGRFLTQMHLSVINDLRELISNRRLKDYQQEKIRDFHKILLQLQ359

Zaire          MTPQQLCELFSIQKHWGHPVLHSETAIQKVKKHATVLKALRPIVIFETYCVFKYSIAKHY419
Tai            ATPQQLCELFSVQKHWGHPVLHSEKAIQKVKKHATVIKALRPIIIFETYCVFKYSIAKHY419
Bundibugyo     STPQQLCELFSVQKHWGHPVLHSEKAIQKVKKHATVIKALRPVIIFETYCVFKYSIAKHY419
Sudan          STPQQLCELFSIQKHWGHPVLHSEKAIQKVKNHATVLKALRPIIIFETYCVFKYSVAKHF420
Reston         LSPQQFCELFSVQKHWGHPILHSEKAIQKVKRHATILKALRPNVIFETYCVFKYNIAKHY419

Zaire          FDSQGSWYSVTSDRNLTPGLNSYIKRNQFPPLPMIKELLWEFYHLDHPPLFSTKIISDLS479
Tai            FDSQGTWYSVTSDRCLTPGLSSYIKRNQFPPLPMIKELLWEFYHLDHPPLFSTKVISDLS479
Bundibugyo     FDSQGSWYSVISDKHLTPGLHSYIKRNQFPPLPMIKDLLWEFYHLDHPPLFSTKIISDLS479
Sudan          FDSQGTWYSVISDRCLTPGLNSYIRRNQFPPLPMIKDLLWEFYHLDHPPLFSTKIISDLS480
Reston         FDSQGTWYSVISDRNLTPGLNSFIKRNHFPSLPMIKDLLWEFYHLNHPPLFSTKVISDLS479
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Zaire          IFIKDRATAVERTCWDAVFEPNVLGYNPPHKFSTKRVPEQFLEQENFSIENVLSYAQKLE 539
Tai            IFIKDRATAVEKTCWDAVFEPNVLGYNPPNKFATKRVPEQFLEQENFSIESVLHYAQRLE 539
Bundibugyo     IFIKDRATAVEKTCWDAVFEPNVLGYSPPNKFSTKRVPEQFLEQENFSIDSVLTYAQRLD 539
Sudan          IFIKDRATAVEQTCWDAVFEPNVLGYSPPYRFNTKRVPEQFLEQEDFSIESVLQYAQELR 540
Reston         IFIKDRATAVEQTCWDAVFEPNVLGYNPPNKFSTKRVPEQFLEQEDFSIESVLNYAQELH 539
               ***********:**************.** :* ************:***:.** ***.*

Zaire          YLLPQYRNFSFSLKEKELNVGRTFGKLPYPTRNVQTLCEALLADGLAKAFPSNMMVVTER 599
Tai            YLLPEYRNFSFSLKEKELNIGRAFGKLPYPTRNVQTLCEALLADGLAKAFPSNMMVVTER 599
Bundibugyo     YLLPQYRNFSFSLKEKELNVGRAFGKLPYPTRNVQTLCEALLADGLAKAFPSNMMVVTER 599
Sudan          YLLPQNRNFSFSLKEKELNVGRTFGKLPYLTRNVQTLCEALLADGLAKAFPSNMMVVTER 600
Reston         YLLPQNRNFSFSLKEKELNIGRTFGKLPYLTRNVQTLCEALLADGLAKAFPSNMMVVTER 599
               ****: **************:**:****** ********************************

Zaire          EQKESLLHQASWHHTSDDFGEHATVRGSSFVTDLEKYNLAFRYEFTAPFIEYCNRCYGVK 659
Tai            EQKESLLHQASWHHTSDDFGENATVRGSSFVTDLEKYNLAFRYEFTAPFIEYCNRCYGVR 659
Bundibugyo     EQKESLLHQASWHHTSDDFGENATVRGSSFVTDLEKYNLAFRYEFTAPFIEYCNRCYGVK 659
Sudan          EQKESLLHQASWHHTSDDFGEHATVRGSSFVTDLEKYNLAFRYEFTAPFIKYCNQCYGVR 660
Reston         EQKESLLHQASWHHTSDDFGENATVRGSSFVTDLEKYNLAFRYEFTAPFIEYCNHCYGVR 659
               **********************:********************************:***:****:

Zaire          NVFNWMHYTIPQCYMHVSDYYNPPHNLTLENRDNPPEGPSSYRGHMGGIEGLQQKLWTSI 719
Tai            NLFNWMHYTIPQCYIHVSDYYNPPHGVSLENRENPPEGPSSYRGHLGGIEGLQQKLWTSI 719
Bundibugyo     NLFNWMHYTIPQCYIHVSDYYNPPHGVSLENREDPPEGPSSYRGHLGGIEGLQQKLWTSI 719
Sudan          NVFDWMHFLIPQCYMHVSDYYNPPHNVTLENREYPPEGPSAYRGHLGGIEGLQQKLWTSI 720

Reston         NVFNWMHYLIPQCYMHVSDYYNPPHNVNLSNREYPPEGPSSYRGHLGGIEGLQQKLWTSI 719
               *:*:***: *****:**********.:.*.**: ******:****:***************

Zaire          SCAQISLVEIKTGFKLRSAVMGDNQCITVLSVFPLETDADEQEQSAEDNAARVAASLAKV 779
Tai            SCAQISLVEIKTGFKLRSAVMGDNQCITVLSVFPLETESSEQELSSEDNAARVAASLAKV 779
Bundibugyo     SCAQISLVEIKTGFKLRSAVMGDNQCITVLSVFPLETDSNEQEHSSEDNAARVAASLAKV 779
Sudan          SCAQISLVEIKTGFKLRSAVMGDNQCITVLSVFPLESSPNEQERCAEDNAARVAASLAKV 780
Reston         SCAQISLVEIKTGFKLRSAVMGDNQCITVLSVFPLKTDPEEQEQSAEDNAARVAASLAKV 779
               ****************************************::. .*** .:***************

Zaire          TSACGIFLKPDETFVHSGFIYFGKKQYLNGVQLPQSLKTATRMAPLSDAIFDDLQGTLAS 839
Tai            TSACGIFLKPDETFVHSGFIYFGKKQYLNGVQLPQSLKTATRIAPLSDAIFDDLQGTLAS 839
Bundibugyo     TSACGIFLKPDETFVHSGFIYFGKKQYLNGVQLPQSLKTATRIAPLSDAIFDDLQGTLAS 839
Sudan          TSACGIFLKPDETFVHSGFIYFGKKQYLNGIQLPQSLKTAARMAPLSDAIFDDLQGTLAS 840
Reston         TSACGIFLKPDETFVHSGFIYFGKKQYLNGVQLPQSLKTAARMAPLSDAIFDDLQGTLAS 839
               **********************************:*********:*:****************

Zaire          IGTAFERSISETRHIFPCRITAAFHTFFSVRILQYHHLGFNKGFDLGQLTLGKPLDFGTI 899
Tai            IGTAFERSISETRHVVPCRVAAAFHTFFSVRILQYHHLGFNKGTDLGQLSLSKPLDFGTI 899
Bundibugyo     IGTAFERSISETRHVYPCRVVAAFHTFFSVRILQYHHLGFNKGTDLGQLSLSKPLDFGTI 899
Sudan          IGTAFERSISETRHILPCRVAAAFHTYFSVRILQHHHLGFHKGSDLGQLAINKPLDFGTI 900
Reston         IGTAFERAISETRHILPCRIVAAFHTYFAVRILQYHHLGFNKGIDLGQLSLSKPLDYGTI 899
               ********:*******: ***:.*****:*:******:*****:** ******::.****:***

Zaire          SLALAVPQVLGGLSFLNPEKCFYRNLGDPVTSGLFQLKTYLRMIEMDDLFLPLIAKNPGN 959
Tai            TLALAVPQVLGGLSFLNPEKCFYRNLGDPVTSGLFQLKTYLQMIHMDDLFLPLIAKNPGN 959
Bundibugyo     TLALAVPQVLGGLSFLNPEKCFYRNLGDPVTSGLFQLRTYLQMINMDDLFLPLIAKNPGN 959
Sudan          ALSLAVPQVLGGLSFLNPEKCLYRNLGDPVTSGLFQLKHYLSMVGMSDIFHALIAKSPGN 960
Reston         TLTLAVPQVLGGLSFLNPEKCFYRNFGDPVTSGLFQLRVYLEMVNMKDLFCPLISKNPGN 959
               :*:**********************:***:************: ** *: *.*:*  **:*.***

Zaire          CTAIDFVLNPSGLNVPGSQDLTSFLRQIVRRTITLSAKNKLINTLFHASADFEDEMVCKW 1019
Tai            CSAIDFVLNPSGLNVPGSQDLTSFLRQIVRRTITLSAKNKLINTLFHSSADLEDEMVCKW 1019
Bundibugyo     CSAIDFVLNPSGLNVPGSQDLTSFLRQIVRRTITLSAKNKLINTLFHSSADLEDEMVCKW 1019
Sudan          CSAIDFVLNPGGLNVPGSQDLTSFLRQIVRRSITLSARNKLINTLFHASADLEDELVCKW 1020
Reston         CSAIDFVLNPSGLNVPGSQDLTSFLRQIVRRSITLTARNKLINTLFHASADLEDEMVCKW 1019
               *:*********.**********************:***:*:**********:***:***:****

Zaire          LLSSTPVMSRFAADIFSRTPSGKRLQILGYLEGTRTLLASKIINNNTETPVLDRLRKITL 1079
Tai            LLSSTPVMSRFAADIFSRTPSGKRLQILGYLEGTRTLLASKIINHNTETPILDRLRKITL 1079
Bundibugyo     LLSSTPVMSRFAADIFSRTPSGKRLQILGYLEGTRTLLASKVINNNAETPILDRLRKITL 1079
Sudan          LLSSTPVMSRFAADIFSRTPSGKRLQILGYLEGTRTLLASKMISNNAETPILERLRKITL 1080
Reston         LLSSNPVMSRFAADIFSRTPSGKRLQILGYLEGTRTLLASKIINNSETPVLDKLRKITL 1079
               *****.*****************************************:*.:*:***:*::******

Zaire          QRWSLWFSYLDHCDNILAEALTQITCTVDLAQILREYSWAHILEGRPLIGATLPCMIEQF 1139
Tai            QRWSLWFSYLDHCDQVLADALTQITCTVDLAQILREYTWAHILEGRQLIGATLPCILEQL 1139
Bundibugyo     QRWSLWFSYLDHCDQVLADALIKVSCTVDLAQILREYTWAHILEGRQLIGATLPCMLEQF 1139
Sudan          QRWNLWFSYLDHCDPALMEAIQPIKCTVDIAQILREYSWAHILDGRQLIGATLPCIPEQF 1140
Reston         QRWNLWFSYLDHCDQLLADALQKISCTVDLAQILREYTWSHILEGRSLIGATLPCMVEQF 1139
               ***.***********  * :*:  :.*****:********:*:****:** *********: **:

Zaire          KVFWLKPYEQCPQCSNAKQPGGKPFVSVAVKKHIVSAWPNASRISWTIGDGIPYIGSRTE 1199
Tai            NVIWLKPYEHCPKCAKSANPKGEPFVSIAIKKHVVSAWPDQSRLSWTIGDGIPYIGSRTE 1199
Bundibugyo     NVFWLKSYEQCPKCAKSRNPKGEPFVSIAIKKQVVSAWPNQSRLNWTIGDGVPYIGSRTE 1199
Sudan          QTTWLKPYEQCVECSSTN--NSSPYVSVALKRNVVSAWPDASRLGWTIGDGIPYIGSRTE 1198
Reston         KVKWLGQYEPCPECLNKK--GSNAYVSVAVKDQVVSAWPNTSRISWTIGSGVPYIGSRTE 1197
               :. **  ** * :* .    .. :**:*:* ::******: **:.****.*:*********

Zaire          DKIGQPAIKPKCPSAALREAIELASRLTWVTQGSSNSDLLIKPFLEARVNLSVQEILQMT 1259
Tai            DKIGQPAIKPKCPSAALREAIELTSRLTWVTQGGANSDLLVKPFIEARVNLSVQEILQMT 1259
Bundibugyo     DKIGQPAIKPKCPSAALREAIELTSRLTWVTQGGANSDLLVKPFVEARVNLSVQEILQMT 1259
Sudan          DKIGQPAIKPRCPSAALREAIELTSRLTWVTQGSANSDQLIRPFLEARVNLSVQEILQMT 1258
Reston         DKIGQPAIKPRCPSSALKEAIELASRLTWVTQGGSNSEQLIRPFLEARVNLSVSEVLQMT 1257
               **********:***:**:******:**********.:***: *::**:********.*:****
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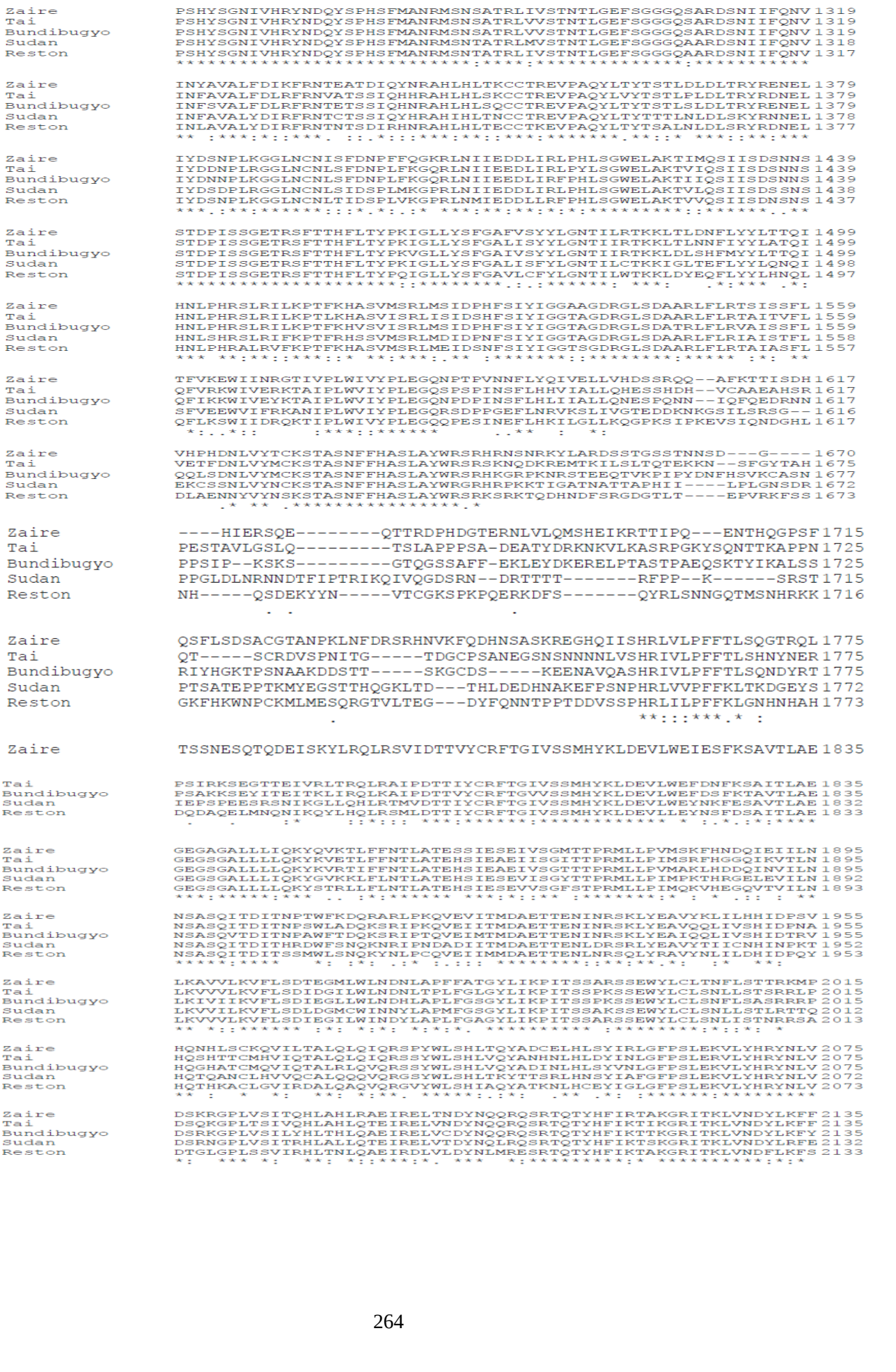

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```
Zaire           LIVQALKHNGTWQAEFKKLPELISVCNRFYHIRDCNCEERFLVQTLYLHRMQDSEVKLIE 2195
Tai             LIIQALKHNCTWQEELRALPDLISVCTRFYHTRNCSCENRFLVQTLYLSRMQDSEIKLID 2195
Bundibugyo      LVVQALKHNCLWQEELRTLPDLINVCNRFYHIRDCSCEDRFLIQTLYLTRMQDSEAKLME 2195
Sudan           LVIRALKNNSTWHHELYLLPELIGVCHRFNHTRNCTCSERFLVQTLYLHRMSDAEIKLMD 2192
Reston          LIVQALKNNSSWYTELKKLPEVINVCNRFYHTHNCECQEKFFVQTLYLQRLRDAEIKLIE 2193
                *:::***:*  *  *:  **::*.** ** * ::* *.::*::***** *: *:* **::

Zaire           RLTGLLSLFPDGLYRFD--        2212
Tai             RLTGLLSLCPNGFFR----        2210
Bundibugyo      RLTGFLGLYPNGINA----        2210
Sudan           RLTSLVNMFPEGFRSSSV-        2210
Reston          RLTGLMRFYPEGLIYSNHT        2212
                ***.:: : *:*:
```

MODULE-3

Nucleoprotein:

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

Polymerase complex protein

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

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Initiation signal/3'-Splice site score	E-1 =42	E-1 = 75 E-2 = ( )	E-1 =71 E-2 = ( )	E-1 = 66 E-2 = ( )	E-1 = 69 E-2 = ( )
Termination signal/5'-Splice site score	E-1=3	E-1 = 45 E-2 =( )	E-1 = 43 E-2 = ( )	E-1 = 52 E-2 = ( )	E-1 = 48 E-2 = ( )
Coding Region score	E-1 =568	E-1 = 296 E-2 =( )	E-1 = 819 E-2 = ( )	E-1 = 843 E-2 = ( )	E-1 = 813 E-2 = ( )
Probability of Exon	E-1 = 0.455	E-1 = 0.283 E-2 = ( )	E-1 = 0.534 E-2 = ( )	E-1 = 0.847 E-2 = ( )	E-1 = 0.846 E-1 = ( )
Exon score	E-1=37.93	E-1 = 21.09 E-2 = 1.05	E-1 = 72.31 E-2 = -1.75	E-1 = 75.31 E-2 = -1.75	E-1 = 72.01 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 Exon number = 01 Type of Exon = Init	Gene number = 01 Exon number = 01 Type of Exon = Init	Gene number = 01 Exon number = 01 Type of Exon = Sngl	Gene number = 01 Exon number = 01 Type of Exon = Sngl	Gene number = 01 Exon number = 01 Type of Exon = Sngl
	Gene number = 01 Exon number = 02 Type of Exon = Term	Gene number = 01 Exon number =02 Type of Exon =Intr	Gene number = 01 Exon number = 02 Type of Exon = PlyA	Gene number = 01 Exon number = 02 Type of Exon =PlyA	Gene number = 01 Exon number = 02 Type of Exon = PlyA
Type of DNA Strand **+ = Input Strand** **- = Output Strand**	E-1(+ = Input strand) E-2(+ = Input strand)	E-1(+ = Input strand) E-2(+ = Input strand)	E-1(+ = Input strand) E-2(+ = Input strand)	E-1(+ = Input strand) E-2(+ = Input strand)	E-1(+ = Input Strand) E-2(+ = Input Strand)
Beginning of Exon/Signal	E-1 = 90 E-2 = 1098	E-1 = 90 E-2 = 1046	E-1 = 90 E-2 = 1293	E-1 = 90 E-2 =1435	E-1 = 90 E-2 = 1274
Ending of Exon/signal	E-1 = 990 E-2 = 1498	E-1 = 1004 E-1 = 1225	E-1 = 1070 E-2 = 1298	E-1 = 1070 E-2 = 1440	E-1 = 1085 E-2 = 1279
Length of Exon/signal	E-1 = 901 E-2 = 401	E-1 = 915 E-2 = 180	E-1 = 981 E-2 = 06	E-1 = 981 E-2 = 06	E-1 = 996 E-2 = 06
Reading Frame	E-1 = 02 E-2 = 01	E-1 = 02 E-2 = 01	E-1 = 02 E-2 = ( )	E-1 = 02 E-2 = ( )	E-1 = 02 E-2 = ( )
Net-Phase of Exon/Signal	E-1 = 01 E-2 = 02	E-1 = 00 E-2 = 00	E-1 = 00 E-2 = ( )	E-1 = 00 E-2 = ( )	E-1 = 00 E-2 = ( )
Initiation signal/3'-Splice site score	E-1 = 81 E-2 = 20	E-1 = 101 E-2 = 72	E-1 =64 E-2 = ( )	E-1 = 48 E-2 = ( )	E-1 = 60 E-2 = ( )
Termination signal/5'-Splice site score	E-1 = 53 E-2 = 48	E-1 = -6 E-2 = 69	E-1 = 37 E-2 = ( )	E-1 = 32 E-2 = ( )	E-1 = 28 E-2 = ( )
Coding Region score	E-1 = 349 E-2 = 287	E-1 = 427 E-2 = 239	E-1 = 279 E-2 = ( )	E-1 = 837 E-2 = ( )	E-1 = 692 E-2 = ( )
Probability of Exon	E-1 = 0.752 E-2 = 0.989	E-1 = 0.769 E-2 = 0.823	E-1 = 0.632 E-2 = ( )	E-1 = 0.840 E-2 =( )	E-1 = 0.728 E-2 = ( )
Exon score	E-1 = 25.13 E-2 = 13.18	E-1 = 28.67 E-2 = 20.46	E-1 = 17.22 E-2 = -1.75	E-1 = 70.65 E-2 = -0.45	E-1 = 57.05 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 Exon number = 01 Type of Exon= Init	Gene number = 01 Exon number = 01 Type of Exon = Init	Gene number = 01 Exon number = 01 Type of Exon = Init	Gene number = 01 Exon number = 01 Type of Exon = Intr	Gene number = 01 Exon Number = 01 Type of Exon = Init
	Gene number = 01	Gene number = 01	Gene number = 01	Gene number = 01	Gene number = 01

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

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

Spike Glycoprotein:

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

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

RNA Dependent RNA Polymerase:

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

Membrane Associated Protein:

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

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

Minor Nucleoprotein:

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

Intrepretation 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 occurance of ailment.

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