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# Multiple Sequence Alignment and Phylogenetic Tree Construction of Viral Protein 2 of Bluetongue virus

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#### Abstract

Bluetongue is a non contagious disease of animals and spread by the biting midges. Bluetongue disease is mild in goats and severe in sheep as sheep is the primary host of bluetongue virus. There are several clinical symptoms of Bluetongue disease have been found in ruminants like fever, viraemia, sore muzzle, facial oedema, hyperaemia and congestion, erosion of mucous memberane, haemorrhages, vascular permeability. The bluetongue virus is hypervariable in nature therefore there are 24 serotypes of bluetongue virus are well recognised with three newly proposed serotypes BTV 25 from Switzerland and BTV 26 from Quwait and BTV 27 from France. Therefore, there are 27 different serotypes of BTV have been identified according to the specificity of interactions between neutralizing antibodies and the virus outer capsid, the VP2 protein. Bluetongue has a serious economic impact on dairy and wool industry mainly due to high morbidity, mortality and mandatory trade barrier on the movement of BT infected livestock and germplasm. Bioinformatical tools like Clustal X and Clustal Omega are promising and helpful in the construction of phylogenetic tree to check the evolutionary relation among all 24 serotypes of BTV and alignment of the many sequences through Multiple sequence Alignment.

Keywords : BTV, VP2, MSA, FASTA, NCBI, CLUSTAL X, CLUSTAL OMEGA

Bluetongue is a highly infectious vector born viral disease and it is a disease of wild and domestic animals (ruminants). Bluetongue is a non contagious disease of animals and spread by the biting midges (Sperlova, A. and Zendulkova, D. 2011). Bluetongue disease is mild in goats and severe in sheep as sheep is the primary host of bluetongue virus. Cattle act as reservoir of bluetongue virus (Browne, 1971). There are several clinical symptoms of Bluetongue disease have been found in ruminants like fever, viraemia, sore muzzle, facial oedema, hyperaemia and congestion, erosion of mucous memberane, haemorrhages, vascular permeability (OIE, 2014). The bluetongue virus is hypervariable in nature therefore there are 24 serotypes of bluetongue virus are well recognised with three newly proposed serotypes BTV 25 from Switzerland and BTV 26 from Quwait and

BTV 27 from france. Therefore, There are 27 different serotypes of BTV have been identified according to the specificity of interactions between neutralizing antibodies and the virus outer capsid, the VP-2 protein (Roy et al. 1992; Maan et al. 2011; Bumbarov, V. 2012; Zientara et al. 2014; Chand et al. 2015). In India 22 serotypes have been reported of Bluetongue virus (Prasad et al. 2009). Bluetongue virus belongs to family Reoviridae and genus Orbivirus (Tabachnick et al. 2009). Bluetongue has a serious economic impact on dairy and wool industry mainly due to high morbidity, mortality and mandatory trade barrier on the movement of BT infected livestock and germplasm. BT is evolving into newer challenges and poses ever increasing threat to associated environment. Unnatural host like canines have in the past contracted BT infections. Many species of Culicoides have been reported to spread infections. Recently BT has been categorized as multispecies disease by OIE (2014). There is two outer capsid protein VP2and VP5. VP2 is the outermost protein and responsible for cell entry into the vertebrate host cell. VP2 is also responsible for haemagglutination (lysis of RBCs) (Bhattacharya *et al.* 2007; Forzan *et al.* 2007). By a clathrin-dependent endocytosis pathway VP2 is internalised in endosomes after the interaction of BTV with target cell surface (Forzan *et al.* 2007; Pandrangi, A. 2013). After getting entry into the cell VP2 of BTV degraded in acidic medium of endosome exposing VP5 (Forzan *et al.* 2004, 2007).

## **Requirements and Methodology**

For Multiple sequence alignment sequence retrieval in FASTA format is done from NCBI. We get FASTA sequences of VP2 of BTV1 to BTV 24.

Multiple sequence alignment is carried out in CLUSTAL X. Clustal X provides Pairwise Sequence alignment and alignment of 2 or more than 2 Fasta sequences. Here we obtained MSA of 24 sequences of VP2 of Bluetongue virus. For sequence alignment we used FASTA sequence of our VP2 of Bluetongue virus (24 serotypes). Phylogentic tree constructed in Clustal Omega.

## **RESULTS AND DISCUSSION**

MSA (Multiple sequence alignment) is carried out in CLUSTAL X. For sequence alignment we used 24 FASTA sequence of VP2 of BTV. Phylogentic tree constructed in CLUSTAL Omega. Maximum number of amino acid residues is 961.

Study of Phylogenetic tree was conducted to review the sequence alignment and used to asses sequence preservation of Protein, amino acid and nucleotides. A particular conserved sequence support the phylogenetic tree and maintained by evolution.

CLUSTAL 2.1 multiple sequence alignment: Following are the Results of Multiple Sequence Alignment of Viral Protein 2 of BTV 24 Serotypes. CLUSTAL 2.1 multiple sequence alignment

AGJ83602.1	MEEFVIPVFSE-QDMPYALINQYPLAIRTDVKIPDVEGIHDLAKIPESDMIDVPKL
ABB71704.1	MDEFGIPIYLS-SSVPHDLLSDYDFMIDLSDKVVHAGDRHDPKKLKERKAIDVPDG
AGJ83652.1	MEEFVIPVYSE-NEIPYTLLNRYLLAIRTDVKINDVEKKHNVIKIPDSDMIDIPKI
AGJ83612.1	MDELAIPIIDGRFPKEALLEYCCIVELNPASEEDDVDVTTIPOKDMMDIPDA
ABB71694.1	MDELGIPIYGRNYPEHLLKGYEFLINTGVRYPSOGGRHDVSKIPEMFAYDIKDE
AKV60674.1	MDELATPTINGHEPKETLIEYDCITELNPPVEDDAADVVOTPTRDMMDTPNV
AAB30550.1	MEEEVTPVYSE-DETPYALLSRYPLATOTNVKTEDVEGRHNVVETPESDMTDTPRI
AGW27481 1	
ABR71700 1	MEEEVTDVESE_RETDVALTNRVDLATOTOVKTADVEGYHNLVKTDESDMVDVPKL
ADD/1/00.1	
AGC05505.1	
AGJ05472.1	
AGJ83512.1	
AEP22601.1	MEELVIPVIIERFDKRLVGKYDYVIELARPEGDEWSGHDVIHIPDKRMFDIKVQ
CAE51109.1	MEDEPICAIERESVYDEDEIMKYPVIVDLKECVADKKNKIDVSKLEEIKGVCVKSE
AKV60616.1	MEELVIPVISRQFDKKLVGRYEYVIELAEPEQDEWINHDVIQIPGRRMFDVAQQ
AKV60677.1	MEDFP1CV1ERESKFDEDFVVRYPV11DLKECVDDVNGKTDVSKLEETRG1FVRAE
AGJ83462.1	MDELAIPIINGHFPKEALIEYDCIVELNAPSEDDEVDVTQIPTKNMMDIPDV
AGJ83592.1	MDEFAVPIVRG-RTIPYDLIRAYETIIDLDVKVEENEGKHDITKIPESYMCDVPDI
AKV60678.1	MDEFGVPIFRS-SQVPHHILEGYDIKVDLSDRVVQEDGRHDPNKLKERKTIDVPNG
ALI51285.1	MEEFVIPVFSE-RDIPYLLLNHYPLAIQIDVKVDDEGGKHNLIKIPESDMIDVPRL
AMD77980.1	MEELAIPIYTNVFPAELLDGYDYIIDVSSRVEEEGDEPVKRHDVTEIPRNSMFDIKDE
AGJ83582.1	MDELAIPIYTDTFPAGLLDGYDYIIDVSTRVDEPKGRHDVTEIPKRSMFDIKDE
AKV60675.1	MEDFPVSVIERNSTIAPAIIKRYPIIVDLRNMVALSGGKNDVTNIPRVRNIGVRQE
AGW27457.1	MEELVIPVITRQFDKKLVGRYDYVIELTEPEDGEWSGHDVTEIPNRRMFDIKQQ
	*:::: : : : : : : :
AGJ83602.1	DIVSALNYKPVRNDGIVVPRLLDITLKAYDDRKSTKDAQGIKFMTNAGWMKW
ABB71704.1	EARTDLNYNPTDNEGNQLPRALDIALSARLTRKSVRNNDGLDFLTDDKWMEW
AGJ83652.1	
AGJ05012.1 ABB71694 1	GTREALNTEPRANNIGAVETRVVDISESGTDARKTARTSTGGDFESPEEWENW
AKV60674.1	PIRDALKHLPORNDGHVLTRVLDISLSGYDRRKYHKTNSGGEFYSPNEWLNW
AAB30550.1	RIVEAMNYKPARNDGIVVPRLLDITLRAYDDRKSTKSARGIEFMTNARWMKW
AGW27481.1	SIRTALWYNPVRNDGFVLPRVLDITLRGYDGKRAVIDSSKHKIFHTDERWVQW
ABB71700.1	DIVSALNYKPTRNDGIVVPRLLDITLKAYDDRKSVKNARGVDFMTDAKWMKW
AGC83563.1	HIRDAIISKPVSNDGYVLPRILDISLRAFDDRKRIITSGGQSEYHTKADWLQW
AGJ83472.1	AMQDANSAILGRNDGYALPRILDVSIAAYDTRKGYWKYRGIEKMTNQTWLKW
AGJ83512.1	DIVEALAAKPMKNDGIVVPRLLDIILKAYDDKKAIKSAKGVEFMINAKWMKW
CAE51109 1	GVRVALTSRPDPL SHVTTPSALNVLTOAYDRKHKVSLRKREEDGEGVTEYDLDTWVKK
AKV60616.1	GIREAIIYKPLDNDGEVLPRILDMSIACYDMRKTMMKKEGVDEVSNTRWLEW
AKV60677.1	GIRVALNSRPDNLSHVITPSALDVLIRAYDRKHKIALDKRTDDSGRMADHNIDVWVKK
AGJ83462.1	PIREALRVLPQRNDGHVLTRILDISLSGYDRRKYYKTNKGGEFESPKEWLNW
AGJ83592.1	PIQDATTATLSRNDGYALPRILDVSIAAYDTRKGYQKYNGIERMTNQVWLKW
AKV60678.1	EARSDLNYNPTDNEGNQLPRALDIALCARLTRKSFNTNSGVTFHTDHKWMEW
AL151285.1	
AG183582 1	PTREATTYKPVSNDGCVLPRVLDTTLRAEDDRKRVTTNEGHSEEHTRSNWLOW
AKV60675.1	GIRVGLKYRPDTETNVIFPKNLDVLIRAYDHKHRLTRDKRPTDHDADSISDGDVTVWVTN
AGW27457.1	NIREAIEYKPVDNDGEVLPRILDMSIACYDMKKSMMKKDGVDFVSNTKWLEW
	. ::: :: *:
AGJ83602.1	AIDDRMDIQPLKVKLDQH-YSIDYQLFNCVVKAKTANADTMYYDYFPIENK-TKKCNHTN
ABB71704.1	MLSDAMDVQPLKIDLSARNGFVKCDIFNSSIYIRRKYADAIAYRYTSLEDE-SKGCNHTR
AGJ83652.1	AIDDRMDIQPLKVTLDDH-YSVNHQLFNCVVKAKPANADTVYYDYYPLESK-MKKCNHTN
AGJ83612.1	MIRDSMDVQPLKASLEFP-SKIKHSLFSSNVYVSVKKADTISYHIEAKEVE-TRACDHAR
ABB71694.1	MIKDSMDQQPLKISIDEEHSRVVHSLFNCQVKIDAKKADTLSYHLEAIEDA-EKACLHTR
AKV60674.1	MINDSMDVQPLKVSLGLP-PTIRHELFSSSVFISAKKADTTSYHIEPICEK-DKACDHTR
AAB30550.1	A100KMD1QPLKVTLDHY-CSVNHQLFNCVVKANAANADTIYYDYFPLEDH-KKRCNHTN
AGW27481.1	MMKUSMUAQPLKVGLDDRTQKIAHSLHNCVVKIDSKKADTMSYHVEPIEDP-SKGCLHTR
ABB/1/00.1	ALDUKMDIQPLKIILDEH-YAVNHQLFNCIVKAKTANADTIYYDYFPLEDR-AKKCNHTN
AGC83563.1	MIDDAMDVQPLKVDTAHTKIKVSHALFNCTVRLHAKKADTASYHVESVEIE-PNGCNHAW
AGJ834/2.1	
AGJ83512.1	ALUDKMUTUPLKVATUHY-NAVNHULFNCTVKAKSANAUTTYVUYFPLESK-VKKCNHAN
ALF22001.1	
AKV60616 1	
AKV60677 1	ΠΙ ΕΕΩΔΕΙ ΔΑΤΥΗΟΥΕΙ ΓΙΑ ΤΟ ΤΑΤΗΠΑΤΟΙ ΤΑ ΤΑΠΑΤΑΤΑΙ Ε ΓΚΑΕΚΚΟΟΠΥΚ RI ΕΕΩΔΕΙ ΔΑΤΥΗΟΥΕΙ GRGKI KEKMI ΤGI VKI DONVAFT//GVDVAD//DK// CODHON
AG183462 1	
AG183592 1	ATKDEMDVOPI KVSI TDAEGKVRYDI ENCSVRMDAKKAFAVVYGWAAOEVT_DKGCNHAR
AKV60678.1	MLSDAMDVOPLRIDLAAONEYAKCDLFNSSVYVRKKYVDATSYRYTSVFDD-SKGCNHTR
ALI51285.1	AIDDKMDI0PLKVTLDNH-CSVNH0LFNCIVKARSANADTIYYDYYPLENG-AKRCNHTN
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MIDDAMDVQPLKVDIAHTRSRISHALFNCTVRLHSKKADTASYHVEPVEIE-SWGCNHTW

MIDDAMDYOPLKVDVEHVPSRISHALFNSTVRLHAKRADTASYHIEPVEVE-AYGCNHVW

RTNEFYDIQPIYHTLEDEVCKVKFTSLLGSVSTDSNYAESMSYHYIGVERD---KCDHSK

AMD77980.1

AGJ83582.1

AKV60675.1

AGW27457.1

AGJ83602.1	LDLLRSLTAVEMFHVLQGAAYNLKANHELIANSER-ESLEESYPIGSQKWVHLTRGTKIG	AGJ83602.1	IAATDTQRGRVWRTNPYPCLRGALIAAECELGDVYYSLRHTYRWSLRPEYDQR-ERSLEN
ABB71704.1	VCMVNHLINNGLYNAVQECAYALKDTYVLRVHSQR-ERIDEPFEPGRPKIGSLGRNARID	ABB71704.1	ICATDAYSRRIWRSNPYPCLRGTLIAAECVLGDPYKTLRRKFNWSVRHAADKALEN
AGJ83652.1	LDMLRSLTTMEMYHILQGAAYGLKSTYELKAHAER-ENTGESYPIG-ERLLQIPRGTKIG	AG183652.1	TAATDTOKGRVWRMNPYPCI RGATTAAECEI GDVYETI ROVYSWSI RPEYGOK - EKPLEV
AGJ83612.1	VAMWNNLVRHEMMHSAQEPAYILKPTLDIIVHSER-ASTDVPFELVGQRYISIGKNHRIV	AG183612.1	TAASDTYNSRTWUTNPYPCI RGALTASETSI GDVYWTI RHEYDWSVRPVYSPR-OKERED
ABB71694.1	GQLCNHLARMDLLHAAQEIAYAIKPTYQLIVHSER-ASTSDNFELGRQDVITLRRGHRIQ	ABB71694.1	TAASDTYNSRTWWSNPYPCLRGTLTAAETKLGDVYETLRSWYDWSVRSSYVPR-ERERET
AKV60674.1	VSMWNNLTRHEMMHCAQESAYVLKPTYDITVYSER-ATTDEAFQQVGQKFVTITKNHRVV	AKV60674.1	IAASDTYNSRIWWTNPYPCLRGALIAAETOLGDVYWTLRHFYEWSVRPAYSPR-LRERED
AAB30550.1	LDLLRSLTNMELFHALQGAAYSIKSSYELVANSER-ESLEETYAVGQPKWIHLTRGTRIG	AAB30550.1	TAATDTOKGRVWRTNPYPCI RGALVAAECELGDVYSTLRRVYRWSLRPEYGOH-EROLEN
AGW2/481.1		AGW27481.1	TAASDTENTRVWWSNPYPCI RGTI MASETKI GDVYSMMRSWYDWSVRPTYTPH-EKSREO
ADD/1/00.1		ABB71700 1	TAATDTOKGRVWRTNPYPCI RGALTASECELGDVYYTLRHVYRWSLRPEYGOR-EROLED
AG000000000000000000000000000000000000	SEMEOHVVRCELLNCSQEVAMERI FIELIVIAEK-ASIBBITINGRITELSRGIRVQ	AGC83563.1	TAASDTYEGRTWWSNPYPCI RGSI TAAFAOI GDVYNTMRNGYOWSVRPTYTPY-DRSRES
AG183512.1	I DI I RSI TNTEMEHMI OGAAYSI KSNYEI TINSER-NSTEETYAPGVHNOTRI VRGTRTG	AG183/72 1	TAATDTNRGRTWISNMERCERGALTASETOEGDVYKMERVREEWSVREYSPOADVARON
AEP22601.1	TDIWNHMIRNHLFHAVOESCYIFKPTYKLIVNSER-RTPDEDFOIGNPOFPTLRRNOOIF	AG183512 1	TAATDTORGRTWRTNPYPCI RGAL TAAECEI GDVYHTI ROVYKWSI RODYGRT-EVPLEN
CAE51109.1	EDPLYDFILSGAFQVSKTAGYTLKQTYRLTVRTEVRENNKNELVVNEIYTPGIVRGEQIR	AEP22601 1	TAASDTNINSRVIIJISSNEYPCI RGALTAAECELGDVYYKI RSWYEWSVREGYKPR-DI DROY
AKV60616.1	TEVWNSVVRNHLFNTAQESCYTFKQTYELIVNSER-LSTEEEFRVGAPQFHTIQRNHRMQ	CAE51109 1	TAATDSVRWRTWWSNI IT CERGRETRAECKEGDVTTRERSWTEWSVREGTRER DEDROT
AKV60677.1	VDFLYDFILSGSLQVSKTAGYTLKQTYRLTVHAEANAETRDQLIVNGVYTEGVTRGEEIR	AKV60616_1	TAASDTNNGRVIJJSNI I CERGI TAAECKI GDVYHTI RSKYEJJSNI ETAMSELDICER
AGJ83462.1	VSMWNNLVRHEVMHCAQESAYVLKPTMEIIVHSER-ASTDVPFQLVGQNYVSIGRNHRLV	AKV60677 1	TAATDSVRWRTWWSNPYPCI RGTTTACEMEI GDVYKTI RSTEHWSI RPTYATRKETDRER
AGJ83592.1	SELLQHVIRCELLNCAQESAYMLKPTQKLEPVAEK-TSLSERLLPGSSHLTSMRRGEVFR	AG183/62 1	TAASDTYNCRTWWSNI IT CERGITIACEHEEGDYTRTERSTHWSERI TTATRREIDRER
AKV60678.1	VYSVNHLINCGLYNVAQECAYAFKDINTLIVNSQR-ETTSEPFQPGNPKIGSLGRRARVD	AG183592.1	TAATDTNRGRTWWSNMEPCI RGALTYGETOEGDVYKMLRVREDWSVRNEYSTOADVARON
ALI51285.1		AKV60678 1	
AG183582 1	TERTHHI VNTEMEHSSOEAAYTI KPTYOTTAHAER-AAVGDAENGRTI ELNRNHRTO	ALT51285 1	TAATDTOOGRV/WRTNPYPCI RGALTAAECELGD/YETLROTYKWSLRPEYGOR-ERPLED
AKV60675.1	WHRFFPMLLSDSINLGKEVGYILKETYKIKAIGEAREGOROELRVDVPYTPGIGRNERIS	AMD77980 1	TAASDTNKGRTWWSNPYPCI RGAL TAAEVOLGDVYNLLRNWEOWSVRPTYVPY-DRNRES
AGW27457.1	TAIWNHMVRNHLFNAVQEACYVFKPTYDLIVIGEK-QNREDEFRIGEHNFYTITRNHHMR	AG183582 1	TAASDTNOGRVIIJISSIN II CERGALTAAEVOLGDVYSTLRSWYOWSTRPAYVPY-DRSREN
	*	AKV60675 1	TAATDSERWRTWWNNPYPCI RGCI TACEMEI GDVYKSI KSTYKWTI RSSYSSORETDROI
		AGW27/157 1	
		Adw2/45/.1	*.*:*: *:* * :***** ::: * :** * :: : *::*
AGJ83602.1	-NSGVPYERFISSMVQVVVKGKVPVEIVSEVVRLNEIRTEWINAGFDRSRIRALELCNIL		
ABB71704.1	-MSDPGYSLFKGGMLQITVSGEIPNDIRVEMERLNQIRATWIRDK-SSREVRAIELCTLL		
AGJ83652.1	-SRGEPYNKFVAGLVKVTIKGKVPAEIGEEMNQLNRIKEEWKSASHDRSRIRALELCKIL	AGJ83602.1	NKYVFSRINLFDSNLTVGDKVIHWRYDLTKP-MDTTFDDGYMCVSHEIDGELLCRIDD
AGJ83612.1	<ul> <li>LGDDAYRKTLDGLTRLRVQGRIPELIRNEIQQLHQIRDAWITDSYNPRHIRSLELCRIL</li> </ul>	ABB71704.1	NAYIFTRINLFDTERTPGMRVVHWTQELTMESQTTWDEGYPLKDEAPDDEMHCKIDT
ABB71694.1	-MGDEAYTKLMERLVRLTVQGNVPRKIQSEIEQLEAIRTRWATGRYDPAHINSQDLCRIL	AGJ83652.1	NKYVFNRINLFDSDLTVGDQIVHWRYELYPP-VETTYDDGYLCGSDKEDDELLCEVDE
AKV60674.1	- LGDDAYKKTLGGLTRLRVÖGKIPSLIÖNDIOOLNOIRDTWIRDSYNPRNIRSLELCKLL	AGJ83612.1	DKYLYGRVNLFDLDADPGTQIIHWEYKPITSTVKTTYERGNMCDLFPDVDGITTKFNK
AAB30550.1	-NSGLTYERFISSMVOVIVNGKIPSVIÄNEVÄÖLNRIRAEWITATYDRGRIRALELCNIL	ABB71694.1	EKYIFSKINLFDYEAGPSSKVIHWEYQLYKRERVVTLEKGNPCDLYPDEDDEVIITKFDD
ΔGW27481_1	-MNHNSYEKMVEGI AHI VTRGKTPEL TRDETAKI DETCNRWTRSRHDPGETKAYELCKT	AKV60674.1	DKYIYGRVNLFDLDASPGTKIIHWTYDLITRESKITYHNGNPCDLNPDVDGIITKFNK
ABB71700 1	-NSGLSYNRETSSMV/0V//RGKVPDTTRGETTOLNRTRTEWTSASYDRTRTRALELCNTL	AAB30550.1	NKYVFNRINLFDSNLAVGDQIIHWRYEVKAS-AETTYDSGYMCRHEAEEDELLCKINE
AGC83563 1	-I GDAAYEKI KNGI VOTRTEGKKPOLVEGETNSI NDTRORWTNSGHDRRETKALELOKTI	AGW27481.1	EKYIYGRVNLFDYVAEPGTKIIHWEYKLNQQTKDITYEQGNPCDLFPD-DDEAIITKFDD
AG183/72 1		ABB71700.1	NKYVFGRVNLFDSDLAVGDQVIHWRYEITEP-VKTTYDNGYICNPEEKDDELLCKIDD
AG183512 1		AGC83563.1	DEYIYSRENLFDSALRPGDKIIHWEYKLLNEVREVCIKDGNECDLFPEDEEMTTKFNE
AG5055512.1		AGJ83472.1	ENYVYARVNLFDLVADPATSVIHWEYKLDKP-FKTCYSDGHQCDEYPDEYDLICSFDE
ALF22001.1		AGJ83512.1	NKYVFSRINLFDSNLDVGDQVVHWMYEVDGP-AETTYDNGYMCKTEREDEELVCKISE
CAE51109.1		AEP22601.1	EKYIVGRVNLFDLEAEPGTKVLHWEYELISKLYTISNHGGNQCDLYPDEGEIVTKFDD
AKV60616.1	- LGDNAYDKFLKGLVQLKVSGTTPAKIRDEVAALDVIRDNWIRGSFDRSHIKSLELCKLL	CAE51109.1	KAYPYQRINLFESKLIPGIRIINWLVIRVPLE-KPDISIGRVCMISIESNYILKIDD
AKV60677.1	DMKKMCYSRFRDGWIRATIQPKIVEELRRSKEVLDRISSEWYEKLTTPDVVEICKIV	AKV60616.1	EKYVVGRVNLFDLEGEPATKVTHWEYELTSPTYSVSNHKGNHCDLYPDDVETTKFNE
AGJ83462.1	-LGDEPYKKILQGLIKLRVQGKVPPQIQDEIQQLNRIRDAWIGDAYNPRHIRSLELCRIL	AKV60677.1	
AGJ83592.1	-MGTEQYNRMVQGWYRVKVKGHTPEKIQDEMNELMKIRDRWKVAR-DRREIKSLELCKLL	AGJ05402.1	
AKV60678.1	-MADPGYPLFRAGLLQIIVNGAIPADIRSEMDRLNQIREAWKRDK-NTREVRALDLCVLL	AGJ05552.1	
ALI51285.1	-YRGQPYERFISSLVQVIIKGKIPDEIRTEIAELNRIKDEWKNAAYDRTKIRALELCKIL	ALT51285 1	NKVVEARENEEDTNEAVGDETTHWRVEVVAD_KETTHDDGVTCVSAKGDDELLCEVDE
AMD77980.1	-MGDQGYQKLKEGLVQVRIEGKTPLVIQEEITALNKIREQWIARNFDQREIKVLDLCRLL	AMD77980 1	DKYTYSRTNI EDSTI RPGDKTVHWEYKI I NEVREVSTNKGNECDI EPEDEEETTKEHE
AGJ83582.1	<ul> <li>LGDQGYVKLKKGLVQTRIEGKKPAAIEREIASLNEIRAQWIARGHDRREIKALDLCRIL</li> </ul>	AG183582.1	DKYTYTRTNI EDSALGPGDKTTHWEYOLLNETREVSMSSGNECDLEPE - DEEETTKENE
AKV60675.1	DMKLPVYKRFLEGYIRCQIEPNVPEKLTELKNQLDAICVAWYGGQVPIVADEICKIT	AKV60675.1	NVEPYOKINI EDESGIPGIETIHWRIAHIPVPDETDYEHGYLCPESGDYDIVMAVDD
AGW27457.1	-LGDNAYNQFMKGLVQLRVAGVTPNVIREEMAALDAIRDTWIGGNFERTHIKSLEICKLL	AGW27457.1	EKYIVGRVNLFDLEGEPATKVFHWEYELINKVYHITNHTGNHCDLYPDDVEITAKFDE
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10102602 1		10102602 1	
AGJ65002.1		AGJ65002.1	DRTKEPILERPILQGWDQERFKLIISTLTEP-NLLTTDFEKDATLNSRSELVPPDTFDKWIN
ABB/1/04.1	SKIGKVKWNAEEEPKDEGAMSLRFQNKIDSMFLSENTEKTNIMQNTSGRTDEERFYALLL	ABB/1/04.1	NKYKEMVIQVIDGGWDQENFKIHKLFHDDGNIFLMDFEKDAKLIAQSEVQYPDYYDKWIY
AGJ83652.1	STIGRKMLDAKEEPKDEMDLSTRFQFKLDEKFTKTDSEHINIFRAGGPATDDGRFYALIA	AGJ83652.1	EKYKKMFENMIEGGWDQERFKLHSILTDP-NLLTIDFEKDAYLNSRSELVFPEYFDKWIN
AGJ83612.1	SHIGRKMVHIEEEPKDESDLSVKFQFKLDEKFRINDDERNVIFTSKGQRNDQQRFFVLIM	AGJ83612.1	TAYIDMISELLNGGWNTREFKMYKILESVGNVLTIDFEKDTKLNSRSELSLPYYYDKWIY
ABB71694.1	SRIGRIMLDQEAEPVDEDSLSLRFQRALDEKFRLNDSERNKIFEPKSHRKDEDRFYVLLA	ABB71694.1	AKYSEMVGEIIDGGWNDEEFKMYKLLQEKGNVLTIDFEKDTKLNSTSEVVLPDYYGKWIV
AKV60674.1	SGIGRKMVCIEEEPKNESDLSVKFQFKLDEKFRLDDSERGVIFTNKGQRNDQDRFYVLIM	AKV60674.1	TAYTDMIGELLNGGWNTREFKMYKILESVGNVLTIDFEKDAKLNSRSEFILPDYYDKWIY
AAB30550.1	STIGRKILNTHEEPKDEMDLSTRFQFKLDEKFNRADPEHVNIFGVRGPATDEGRFYALIA	AAB30550.1	DKYKDMLDRMIQGGWDQERFKLHNILTDP-NLLTIDFEKDAYLNLRSELVLPDYFDKWIS
AGW27481.1	STVGRKMLDQEKEPADEASLSIRFQEAIDNKFRQHDPERLKIFEHRNQRRDEDRFYILLM	AGW27481.1	VAYGQMVSDLINGGWDQERFKMHKILKSQGNVLTIDFEKDAKLTSNEGVTMPEYFDKWII
ABB71700.1	SAIGRKMMDAHEEPKDEMDLSTRFQFKLDEKFNTSDSEHVNIFRTSGAATNEGRFYALIA	ABB71700.1	ERYKEMMERLIEGGWDOERFKLHNILTEP-NLLTIDFEKDAYLNSRSELVFPNYFDKWIN
AGC83563.1	STIGRKMLNTEEEPKNEADLSVKFOMELDEIFRPGNNERKNIFGGGNHRKDEDRFYVLIM	AGC83563.1	EKYTEMKGOIIODGWNHRDFKMHKILODGANVLTIDFEKDARIGNGSVLMLPEYYNKWIV
AGJ83472.1	STIGRRMYNMYEEPKDEEAVSLRFOWNLDEIFKTDNREHVNIAVNKNGRTDDERFFALIM	AG183472.1	AKYSEMVORTTEGGWDHKNEKHYKTI KEASNVI TTDEEKDAKI NESSEMNI PYYENKDTA
AG383512_1	SATGRKMI NTHEEPKDEMDL STKEOEKI DDKEKKTDSEHTNTENVRAPATHEGREVALTA	AG183512 1	FKYKTMI DRMTOGGWDOFREKTYSTT TDP-NLLTTDFEKDAHLNTRSFEVLPSVEDOWTV
AFP22601 1	STTGRKMVNI EEEPKDEKDI SI REOHKI DDKEAKNDOERNVTEAOKSORNDODREVVI MV	AED22601 1	ARYSOMTOTTTNECHKOGDEKMEKVI KDECNDI I VDI EKDANCHTVI DRVCRVITEDOVEDDUTV
CAE51109 1	SSTGRRMWNSEETPVDDAMRSRVEOEKI RI I ERVGNSEYDTTOSTSSGOTDI KKEYALLA	CAE51100 1	
AKV60616 1	SSTGRKMVNMEEEPKDEKDI SVKEOEKI DEKESDNDDERNVTETSKTHRTNEDREVVI I V	AV/60616 1	
ΔΚV60677 1		AKV00010.1	
AG183/62 1		AC102462 4	TAVENUTUELI NCCUNTREEVAVILI ERECNULTTREEVASLUERSREVITY NCCUTT ANALAVILITY
AG183502.1		A0J03402.1	TAT SIMILINELLINGGWINT REFRITTALLEDEGINVETTDEEKDARLINENGEN AND SVERVEN
AUV60679 1		AGJ83592.1	INT SEMILUGGWUMKNEKTYKLLKUAGNVLTIDEEKUAKLNEMSEMVMPSYENKKIA
ALTE1305 4		AKV606/8.1	AVIKULVSKVINGGWUVENFKIHKLFVEKGNIFLMDFEKUAKITTVSEVEYPYYYDTWIY
AL151285.1	SALGRKMLUVQEEPKUEMALSIREQEEUEEPKUEKEIKIUQEHVNIFEAGGSATUUGEFYALIA	AL151285.1	UKYKEMFDRMIQGGWDQERFKLHNILTEP-NLLTIDFEKDAYLGARSELVFPPYYDKWIN
AMD//980.1	STIGKKMCNTEEEPKNEADLSVKFQMELDEIFRPGNNERTNIMGGGVHRKNEDRFYVLIM	AMD77980.1	ARYTEMKNQIIQSGWNQRDFKMHKILEDGANVLTIDFEKDAYIGTGSALSLPDYYNKWII
AGJ83582.1	SALGKKMYNIEEEPKNEADMSVKFQMELDEIFKPGNSEHDNIMGGGTHRKDEDRFYVLIV	AGJ83582.1	ERYTEMKGQIIQSGWNHRDFKMHKILEDGANVLTIDFEKDARVGTGSVLTLPDYYDKWIV
AKV60675.1	SKIGKLMWNTEEEPVDETMRSRAFQESIRLMFRTENSEYNNIQAIGSGRTQRQKFYALLI	AKV60675.1	DLYSTFKHRVIDRGWEHQAMKLDELIPQENNIFKMEFEKDAHLDNRNHLVLPPYYNRVVY
AGW27457.1	SSIGRKMVNMEEEPKDERDLSVKFQFKLDDKFSTTDPERNVIFTHKTHRTNQDRFYVLLM	AGW27457.1	ERYGEMIQTIINEGWKHGDFKMFKILKEEGNPLLYDLEKDIRLDSRSQVIFPPYFNKWTH
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AGJ83462.1 AGJ83592.1 AKV60678.1

ALI51285.1

AMD77980.1 AGJ83582.1

AKV60675.1

AGW27457.1

AGJ83602.1	SPMFNARLRLTHGEIASRKTDDPWNNRVVFGYIKTTTESLDYMLGRYYDVRLQFYGDTLS	AGJ83602.1	LVQNNVGSQRLGVLSSAFPNLANRLLKLREIHFIYDMNVINFLPLLFLVQDNISYWHRQW
ABB71704.1	APIFDTKYKITETEIANAKNLDPAIKRTIDPMMDDPVMLOLSTIGNLYDTRPAVMGSTLS	ABB71704.1	<pre>IIRSSNDANRLKSFELYFPRFGGILRTIKDAKEVSHVTALNFLPYFFLLGDNIIYKHKEW</pre>
AG183652 1	SPMENAKI RI AHGETATRRANDPWINIRAV/HGYTRTSTESI GYALGSYYDI RI OLEGDALS	AG183652 1	I TOKSDGPERI DVI ORNEPNEERREMNI KOVKYTYDI NVVNELPI LEI TODNTSYWHROW
AG303032.1		AG303032.1	VIDDATEKKER FATERFERNESEAVER ACRETITERATION
AGJ83612.1	APMENAKEKITQTEIAQKKADDPSIYKTEAPISSDPIDEQKMCEANYYDVKPAMHGKAES	AGJ83612.1	VIRRVIGKKRLEAISREFPNFGEAVSRLAUPKIVRDVMVINFLPFLFLLGDNMAYEHRQW
ABB71694.1	APMFNSKMRIIETEIATNRSDDPMIKRTLKPMTDDPVELQRYTLARYYDIRPGLMGRSLN	ABB71694.1	RIRSSTGAARMSILEFYFPTFARLISNAREPTYVKDLMALNFLPLLFIVGDNMIYKHRQW
AKV60674.1	APMFNAKLKITEVEIAQAKSDDPDVVRTLAPIGSDPITLQRLCLGNYYDIRPAMHGRALM	AKV60674.1	LIRRVRGKDRLEAIRREFPNFGEAVTILMNPTRVKDVMVINFLPFLILLGDNISYEHRQW
AAB30550.1	SPMENARI RTTKGETGTSKKDDPWNNRAVRGYTKSI AFSI DEVI GPYYDI RI I EEGETI S	AAB30550.1	I TOSI TGTORI DVI KSTEPNEEORI I MI KETKEVRDI NVTNELPI MELVHDNTSYWHROW
ACU17/01 1		ACU17491 1	PTPDAQCONPTNVTTECCOTCOV/LNPTKEATTMOETMVLNEL DLCELVCDNTMVTHKOM
AGW2/401.1	APMENAKLKIKUSEIAQKKUUUPMVKKILSPIAFUPIVLQKLILAKYYUIKPAIMGQALS	AGW2/481.1	KIKDAŐGŐNKINATIEFELIEGIITNKIKEATIMŐETMITNEFELEASDNIMITHKŐM
ABB71700.1	SPMFNARLRITHGEIGSSKTIDPWNRRVVYGYIKTSIESLDYTLGKYYDIRLQLFGDTLS	ABB71700.1	LIQNSTGLQRQEVLKRTFPNFLMRLFKLREVKRICDLNVINFLPLLFLVQDNISYWHRQW
AGC83563.1	APMFNAKLRISETVIAKAHSDDPAVARTAKSFDHDPFNLQRYCLARYYDVRPGLMGRALS	AGC83563.1	KIRSVSGQERLDMIQSFFPRFGRVVRDIAKAKITQDVAHLNFFPLFFIIGDNMAYAHRQW
AG183/172 1	APMERCVI KVCETSTSERHNI OPATSRTMKPMRAKAADI I DYSI GSYVETRSGVMGRTI T	AG183472 1	OTRARKOMORI SYTKOLEDOLYCHIA/SDEDT VCHAOKLALI DI LETTCOMETVEHRON
AC303542.1		A0303472.1	
AGJ65512.1	SPMENARLKIINGEIAIRKSADPWIKRVVFGTIKASIESPETALGQTFDMRIQFTGDALS	AGJ83512.1	LIÓNFDEÞŐKFEWFNAI EÐNEEKHEFKFKDAŐFIZDFUAINEFDFFFAŐDUIZAMHKÓM
AEP22601.1	VPMFNARIKPCEVELAERKSIDPYVRRTLRPLKADCIELMRYHMSQYMDLRVSLQGTSLS	AEP22601.1	LIRSTSGVKRLEVLSRFFPAFSDGLR-IREFKKVRDVMLLNFLPFLFLTGDNIAYEHRQW
CAE51109.1	CPIYHOKIKITEAQMANEWSDDPWVNRVVSGYLGDHVETYGLGYNHIFDTRVPLKGNLLE	CAE51109.1	SIRGSVGAMRWTIFSSSFPTSYRLMKOILVAKRWGDCYIMNFLPLLICGGTSISYLHREW
AKV60616 1	APMENARVKPCDTELAERKNODPEVKRTI KPTKADCVDLLRYHMSHYYDLRPSLKGVSLS	AKV60616_1	I TRTSOGRERI EVTEREEDNVGKAMR_ORDEKKVRDVMEI NEI DEEEL TODNTSVEHROM
AKV60010.1		AKV00010.1	
AKV00077.1	CPMTRKIKITEAEIATSWSDDPWLNKVLNGFLGDRVETFNLGCNRIFDMKVPLKGNLLT	AKV60677.1	AIRSNVGAIRWIMMASAFPISVRLVKGILRAKIWGECYIMNFLPLLICGGSSISYLHREW
AGJ83462.1	APMFNAKLKITETEIAQAKNDDPYVIRTLAPIGSNPFTLQRLCLGNYYDVRPAMHGRALS	AGJ83462.1	TIRRARGRNRLELISREFPNFGRAVARLQSPNTVGDVMVINFLPFLFLMGDNVSYEHRQW
AGJ83592.1	APMFRCILRICETTISVRONADPAVSRTIRPLKAKAADLLDFTLGSYYDTRFGVMGRTLV	AG183592.1	OLRTRKGLNRLDYVKTHEPHLYOWWKASEST YGEAOKLNLLPLLELVGDNETYEHROW
AKV60678 1	APTESTRYKTTETETANAKSI OPATKRTI API SOOPVALOL RAVGHI YOTRPATMGOTI S	AVV/60679 1	OTRESPONDED KMI EREFENAVCOAL REFERATEVOLTTMI NEL DEFELL CONTINUER
ALTE1205 4		AKV00070.1	
AL151285.1	SPMFNAKLKIAKGEIAIWKADDPWSNRAVHGYIKISAESLEYALGPYYDLKLQLFGDILS	ALI51285.1	LIQNTSGAYRLDVLREAFPNFLKHVMNLRDVKRICDLNVINFFPLLFLVQDNISYWHRQW
AMD77980.1	APMFNAKLRITEVVIGTAHTDDPAVGRSAKAFTHDPFDLQRYCLARYYDVRPGMMGRALS	AMD77980.1	KIRSEVGRARIDAIEMTFPRFGRMLRNASQAKINQDIACLNFLPLLFIIGDNISYAHRQW
AGJ83582.1	APMFNAKLRITETVIANAHSDDPAIERSVKPFDHDPSTLORFCLARYYDIRPGLRGRALL	AG183582 1	KTRSSTGRARMEVTETTEPREGI TVKNTTKAKVNODTACI NEEPI EETVGDNMAYAHROW
AKV60675 1		A0000002.1	
ACU07457.4		AKV00075.1	GISTAGKEKKLKLIEKSPETTIKEL®KIKNAKTWKDATAFNFLELLLCAGTNVQTVHKQW
AGW2/45/.1	APMENAKVKPCEVELAQKKNEDPYVKKIVKPIKADCVDLLKYHMSHYMDVKVSMKGLSLA	AGW27457.1	LVRSTQSRDRLSVLKRFFPTFGEGLC-VNNFRKVKDIMLLNFLPFFFLIGDNIAYEHRQW
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40303000 4			
AGJ83602.1	QGQRQSSVFATISQRDDFQILIHIVKDDAICPHAGGSITIFRKTALMLMANTEKIS	AGJ83602.1	AIPMVLFDET-IKLIPVEVGAYANRFGFKSFFNFTRFHPGDSRKKQIADDVHKEFGTICY
ABB71704.1	MRQRQTSLHKTLLDDPQNERFYSSRS-IKKVDDPCPVYYTASLVLQKISELVMSLMIYHV	ABB71704.1	SVPVLTYSDG-I MTWPAOVGANENREGEEGELNYMREHPGTRLRSKVI DDAEKVVAVEMI
AGJ83652.1	LEOROSAVFEHLNKODDFFTLTGYAKDOVVCPHSGGAFYTFRRVALEILSNYEKLT	AG183652 1	SVDVTLYCDT TRITDVEVCAVANRECMESEENETREHDCDSKKKONADDTHKEECLTCE
AG183612 1	KROEOSAVHKNI ANI ADVODTI KRRG-VRKVENPCPI TT-CSYTI EKSALI WIDIMEKHV	AC30303032.1	
ABD71C04 1		A0303012.1	SVFILLTADI-LWFLFVEVOATTWKFGIVSFLETLIFFFSWHMKTVALDEAESKVGKLIL
ADD/1094.1	RIQIQSIFDARVSELSDIERVVSRFGVIKKPIRPCVILI-GRTILERTSLLLIDILRTHI	ABB/1694.1	SIPLLLYIDK-VKVIPLEVGSSNNKQGLVSYLEYMFFFPSLADKISKVDESMIKVSKEVV
AKV60674.1	KKQEQTSYHKTLAKTKDYSDVLNRRG-YRKVEKPCPMVT-CSYVLEKTALFWIDVMEKHV	AKV60674.1	SIPIILHADS-MWFLPVEVGAFYNRFGVISFLEYMMFFPSAQSRESELDEAEIKVSKLIL
AAB30550.1	LKQEQSAVFQYLSQLDDFPALT-QLRGDAVCPHSGGALYTFRKVALFLIGNYEKLS	AAB30550.1	SIPMVLFDDT-IKLIPVEVGAYANRFGFKSFMNFTRFHPGESKKKQIAEDIHKEFGVVAF
AGW27/181 1	ROOGOSTYDEEVSKTEGYAETI ORRGTVOTPKKPCPTVT-AOYTI ERVALELINTI FOHV	ΔGW27481 1	SVPLLLYAHE-LKVTPLEVGSYNDRCGLTSYVEYMVEEPSKAERTSKLDEVOPKTAREM
ADD71700.1		ABR71700 1	
ABB/1/00.1	QKQTQSAVFTYLSGQDDFPALTNYLKGEAVCPHAGGAVYTFRKMALSLIASYEKLS	ADD/1/00.1	SVFMILLFUUA-VILLFVEVUATAMIKFUFNSFTMFINFINFINGUSKKKUUADDMIKETUVACF
AGC83563.1	KEQEASAIANKVAALEDYRDVISRRLGYVEREKRCLTET-AQYILEKTSLYLLNVLSMHV	AGC83563.1	SIPVLLYAHD-IRIIPLEIGAYNNRFGFISYLEYMIFFPSHAIREAVLDESIKECSLALI
AGJ83472.1	TTOKOSDMYKMVODEDDYLSLMVGRGVTDKFANPCPITTACOYALOKTSVMIFSRVEHYF	AGJ83472.1	SYPVILVSHK-LRFVPVELGAYYNRFGLTSLFSYLVFHVGKSKYGLELDEAEKKVLQAAK
AG183512 1	SKONOSAVEOVI SOOFD EPTI TSYAKODVA/CPHSGGAL YTERRVALMI MANYEKI S	AGJ83512.1	AVPMILYDDV-IRLIPVEVGAYANRFGIKSFFNFTRFHPGDAKKRQKADDTHKEFGSISF
A6505512.1		AFP22601.1	AVPVTEYADK - TRTVPAEVGAYYNREGI TCTI EI MMEEPSYDSRNEDI GEDTRACTRPTT
AEP22001.1	VKQVPSSIRQSLAKUASTAGILSKKKENLDTKSQCPIVI-NLFLLEKFFLLIFIIMEKRT	CAE51109 1	SYPMIVITEEDGTKTV/PTMVGRSLPGGSLGEW/SETSEEMGTVHEKTKVEEDELEVLRRCV
CAE51109.1	QEQEISSYHEHLRSDESKEDDTHCALRIFSDKAIRMLFIAIYKKLIHHI		
AKV60616.1	NKQTPSGIHQALVQDDLYSRLLRRRDADLDYSSPCPIIT-NYFLLEKFHILILTIMEKHY	AKV00010.1	SIFILLTADK-LKILFIEVGATTWKFGVICILELLWFFFSTEKREEKLEEDIVLCADAIV
AKV60677 1	OFOATSSYHEHTR	AKV606//.1	SYPMIVVFEDG1KVVPAMIGRSLIQGSLGEWASFVCFFMGSNHEKIKLEEDELEVLRKCV
ACT024C2 4		AGJ83462.1	SVPVILHADV-MWFIPVEVGAFYNRFGVTSFLEYLMFFPSFHMRTVRLDEAEVKVSKLIL
AGJ83462.1	KKQEQSAYHAALVKEKDYEDILIKKG-LKKADKPCPLII-CAYILEKIALLWIDVMEKHI	AG383592.1	AYPAVLISHK-LRFIPVELGAYYNRFGLTSLISHLTFHVGKAKYDONLDOAEOKVFSALK
AGJ83592.1	MSQKQSEMYKMIQEAEDYSELMKSRGVIEKFKNPCPITTACQYTLQKTSVLILSRAQRYF	AKV60678 1	TVPTI TYTDG-VMTWPAOVGANVNREGECGELNVMREHAGSOLRSKVI DDAEKTTAKEMI
AKV60678.1	PRONOTALHKTLLDDPENDRYYEARS-IKKVDNPCSVHYTSSFILOKISELVLSLMIYHI	ALTE100E 1	
ALT51285_1		AL151205.1	SIPHILEDQV-INLIPVEVGATANNEGLASEENFINEHVENGDSKKNQDADDIHKEEGSICE
ALIJI203.1		AMD//980.1	SIPVLLYAHD-IRIIPLEVGAYNNRFGLISYLEYMAFFPSYAIRVAKIDESIKECAIAMA
AMD//980.1	KQQNMSSMTDKLSKQEDYAGIVSKKLEYKERENKCLTET-AQYVFEKTCLYVLELLSKHT	AGJ83582.1	SIPILLYAHD-IRIIPLEVGAYSNRFGLTSYLEYMIFFPSYATRMAMIDEANKECAAALL
AGJ83582.1	KQQDGSTITKKVSALDDYQDVVSRRVNYVQRDVRCPTET-AQYVLEKTSLYLLALFDKHV	AKV60675.1	SYPVLVSMEKGPRIIPAMVGRDLADGNLGDWHAYIKYYMGQHMEDQEVEEDSLEILKISL
AKV60675.1	VAOSMGDYTKYTLGDGWSANSCTGTAYSSRLPTMLFODIFDAITRHL	AGW27457 1	AVPLIEVADK-TRVTPAEVGAVYNREGIVSTLELLTEEPSYEMRKNKVEEDVHACASATI
AGW27457 1	VKOTPSSTHOELARDPLYPGELORRDENLDHKSVCPTVT-NYELLEKEYTLVLTTMEKHY		· * · · * * · · · · ·
Adw2/45/.1	*		
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AC193603 4		40303000 4	EVANITENCO CONTEVA (TTV) DVI VTULACI CACIADETIANTI DVAUDDVCT V TO 100
AGJ65602.1	PELNEGLENQITINPSDGMDTKKTVVDMKDLSQLICFVFDTIFEKKAQLKDPKEAKKILT	AGJ83602.1	EYYMNIRMSQGGVNISVVIIKLDVLKIHLASLCAGLADSIVYILPVAHPRKCIVLIVVGD
ABB/1/04.1	DQDWESTKGAKHb2IT2DE22TA2NTGD12GTAATFEEKK2ATK2AFE2KA11H	ABB71704.1	NYYMRTDIFKGGIQKNVRVTKLSQMEIYHSSLCGGLSDALIYALPISFPIKCLTLIIVGD
AGJ83652.1	PDLHEGLEHQTYTHPKINEYFNRFVLDMKDFSQLICFVFDHFFERHEQLRDVAEARRLVY	AGJ83652.1	EYYTKTKISQGGVDISVVTTKMDTLKVHLASLCSGIADSIVYTLPVAHPKKCVVLIVIGD
AGJ83612.1	GYAP ESEIEFDFPKVNTSTRIGTERIVDISOLVVLMIDWLYEKROTTRSVDEARWTVO	AG183612.1	FEYLNTTTYL GNTOOSVISTKOTLYETYLSSLCGGETEGLWYL PITHPOKCWATEICD
ABB71694.1	EVEE NPOEEETHPRIDSOFKENGNTLSDLNOTVVEIVDYLHEKRNYVRSVYFARYTTS	ABB71694 1	NYYMKTTTSEGGVNI NVVSTKSI I YDTYI SSVCGGVSDGVVWYI PTTHPYKCVV/ATEVCD
AKV60674 1	GDTE - DSTDEEDEPRVDVTI PVETHKVVDVAOLSVI I TDEI VEKRRTVRDTDS APUTTE	AVV/60674 1	
AAD30550 4		AKV000/4.1	
AADJUCCUCDAA		AAB30550.1	EYYINIKISQGSVHIPVMIIKMDVLKIHLSSLCAGLADSIVYTLPVAHPKKCIVLIIVGD
AGW2/481.1	TK21DEDATA2HEKADHKFETAGE2TADT2ŐTATEAEPEKKKIAKÖAAE2KÁMAL	AGW27481.1	KYYTNTKIFEGGINLNVITTKQLLYETYLASLCGGLSDGIVWYLPITHPSKCLVAVEVSD
ABB71700.1	PEMHEGLEHQTYVHPSVNTAYQKQVKDMKDLSQLICFIIDCIFEKRVQIRGVGEARRIVY	ABB71700.1	EYYMNTKISQGGVNVPVVTSKLDTLKIHLASLCSGLADSIVYTLPVAHPKKCIVLIVVGD
AGC83563.1	KPTIDMDIKFKHPSIDTLFDIDTWKIADISQLIVLLFDYLFESRKEIRSVTEARWILF	AGC83563.1	NFYLNTDIHSGEIMRNVVTTKRLLYETHLASLCGGYSDGLLWYVPITHPSKCLVAFEVAD
AGJ83472.1	EEYLK-DDKVEYLSPSLNLEWVEITSRITDISOLIVLTFDVFFEGRROVRTIDESRFILY	AG183472 1	DYYAVATTSEGGINTHSTMTKDPTYOVYI STTCGGI I DSI TYI MPTTHPVKSTMV/TMD
AG383512.1	PDLHEGMEDYTYTHPSIGGAYOKRILEMRDESOLTCETTDYTEERHDOLRDAKEARRTLY	AG182510 1	
AFP22601 1		AGJ0JJJIZ.1	
ALF22001.1		AEP22601.1	NTTLDIIISNGGIQISIISIKALLYEIYLSSICGGESEAILWYLPVIHPSKCLIALEVSD
CAE51109.1	PKEEYAIKEEELLUYISMVEKVKSWDQFIVFIFDFFFENKKGIKIMEEAIQLAK	CAE51109.1	EFYRDVKMVDVIKDTPVRMTKYITCDLAFGSGCGGISESISFILPVTHPNRSLVVFVISD
AKV60616.1	weluusuuvye+PK1DASAFeVUGTLYD1SQTIVHMYDRFFEKRRVLRSIDESRWILH	AKV60616.1	NFYLQTTISNGGVQTSIVSTKALLYEMYLSSICGGYSEGVLWYLPITHPVKCLVALEVSD
AKV60677.1	PKTEYIEREEEVSQYEGLVKRIRTWDQFIIFVFDFFFENRKGLRTTEEATQLAK	AKV60677.1	EFYEGVKMVDIIKDTPVRMTKYIACDLAFGSGCGGTSESLSFILPVTHPNRSLIIFVVAD
AGJ83462.1	SEVT DDSNEFDFPKACVDSPVGTDRIVDVTQLIVLLIDWIYERRKDVRSVDESRWVIE	AG383462.1	DEVLDTTIESGGIOSSVVSTKOILVETVLSSI CGGESEGI VWVI PTTHPTKCVVATEFAD
AG383592.1	REFHG-GDOEEYMSPTLNFEWSDMTSNIYDVAOMVVI VEDVI FERRRVVRGVDESRETI H	AC182502 1	
		AG100002.1	AND A A A A A A A A A A A A A A A A A A

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AKV60678.1

ALI51285.1 AMD77980.1

AGJ83582.1

AKV60675.1 AGW27457.1

KYYMKTDIFSGGVQKNIRVTKSMQMEIYHSSLCGGLSDAVVYALPISFPIKCLTLIIIGD

EYYTTTKISQGEIDVPVVTSKLDTLKLHVASLCAGLADSLVYTLPVAHPKKSIVLIIVGD EFYMNTDIHSGSVMSNVITTKRLLYETYLASLCGGYSDGLLWYLPITHPSKCLVAFEVAD

DYYLSTDVHRGGVMTSVITTKRLLYETYLSSLCGGYSDGLLWYIPITHPLKCLVAFEVAD

EHYMSHSYISNVKDVAVRMTKEIVLDLYFASGCNGVSEMMTFLLPIIHPRKGLVMFCTAD DFYLTTISNGGIQASIVSTKALLYETYLSSVCGGFSEAILWYLPITHPVKCLVALEVSD ..\* :\*\* :: :\*: .\*\*

REHHG-GOQEEVMSPTLNFEWSOMTSNIYDVAQMVLVFDVLFERRRVVRGVDESRFILH EHDW--EPLKQYTHPEISTEFGEISCEICDISQLTVLLIDLFENRRTVRPSEETRYIIH

PSLHEGREHETYMHPAVNDVFRRHVLEMKDFSQLICFVFDYIFEKHVQLRNAKEARRIIY

MPSE--DSEVTFEHPTIDPSVDIETWKIIDVSQLIIEVFOYLEENKKIXROTTEARWILF MPSA--ESEAKFVHPSIDVKHDIETWRIADISQLIVLIFDYLFENKKIVRDTEARWILY PKDK-----LRDQADYFSESRRRVGDIIDWDTFIVYSIYACFERKNQVLREEDATQIVR

WDLD--DSDVAYEFPALDDLAYKTEGALYDVSQVVVHMIDRFFEKRRFLRSVDECRWILH

AGJ33602.1       DKLEPQTRAEQVLSKYYYSRKHVLGVISISVSQDGKLK-VYSSGIVRHRLCEKSILKYI         AGJ3352.1       DWMVQRISKALEFFEHVRDHVRGIASISISRNGUT-THSQGIVKHRLCEKSILKYI         AGJ3352.1       DWVSAQRYCDKLBSRPLSLDHLRGIVIJSVSKRATS-AYSEGIVSHRLCKKNLLKYI         AGJ3352.1       DRVSAQYRCDKLBSRPLSLDHLRGIVIJSIACOMSTK-AYSEGIVSHRLCKKNLLKYI         AKV66674.1       DRVAALRCDRLRLPPLSAHLKGIVVISIACOMTK-AYTEGIVTHRUCKKSLLKH         AKV66674.1       DRVAALRCDRLRLPPLSAHLKGIVVISIACOMTK-AYTEGIVTHRUCKKNLLKYI         AGJ3353.1       DVLPYMSREMITSSYVKHKGIVYQDECKFT-VYSGIVKHKUCKKILKN         AGK353.1       DVVPYSREHIISRPLSSKHLKGIALIAVORINGVS-VTEGIVKHKUCKKILKN         AGG38352.1       DKLPHYRSEQVSKYYSRRHGVGVIDVIV,QWKRPGIVGOTVGUKWUCKKILKKI         AGG38352.1       DKLPHYRSEQVSKYYSRRHGVGVIDVIV,QWKRPGIVGOTVGUKWUCKKILKH         AGG38352.1       DKLPHYRSEQVSKYYSRRHGVGVIDVIV,QWKRPGIVGOTVGUKWUCKKILKH         AGG38362.1       ALTSPELIDVIRTREFLSSHKURGIALIJONNUKYS-VTEGIVKHKUCKKILKH         AKV6061.1       DKLSPSQHAAPAKREFKGTCYTDVIVVVVVVKWPGTVGIVSSWSKHSKIVKKICKHNLKH         AGJ38362.1       DKLSPAQHAPAKREFKGTCYTDVIVVVVVVVVGDQUKWPGTVGIVSSWSKHSKIVKKICKHLKH         AKV60678.1       DKLSPGVFGRDEVSHWYKKKILLKH         AKV60678.1       DKLSPGVFGVFGVVFGNDELMTKLLKH         AGJ38362.1       KVVLVKKGYVFGNDELMTKLLKH         AGJ38362.1       KVVLVKKGYVFGNDELMTKLLKH         AGJ38362.1       RVVLLVKKGYVFGNDELMTKLL				
ABB71704.1       DLAPOPHITSKALLEFFEHVRDHVRGLASISISINGOVT-THSQGTVKVELLKKNILLKN         AG38365.1       DNVSAGYRCDKLRSRFPLSLDHLRGTVILSVSKSRAIS-AYSEGTVSHRLCKKNILGF         AG38365.1       DRVPARLRCDRLRRFPLSADHLKGTVITINVCKSLLKNILKG         AKV60674.1       DRVDARLRCDRLRRFPLSADHLKGTVITISTKDRTVK-AYTEGTTHRUCKKNILGF         AG38350.1       DKLEPHTRSEQTUSAVHYSRHTIGGVSVTVGQISQLR-VHTSGTVKHRVCKKILKNILKN         AG38350.1       DKLEPHTRSEQTUSAVHYSRHTIGGVSVTVGQIQL-VYSGTVHRUCKKNILKNI         AG38370.1       DKLEPHTRSEQTUSAVHYSRHTIGGVSVVTVGQIQL-VYSGTVHRUCKKNILKNI         AG38371.1       DKLEPHTRSEQTVSVYYSRHHIGGVAVSVQEGQLQ-VYSGTVHRUCKKNILKNI         AG38352.1       DKLEPHVRSEQVSKYYSRHHSGTVSTOVGDVNLWKVSURDVITHSCKKNILKNI         AG38352.1       DKLEPHVRSEQVSKYYSRHHSGTVSTOVGDVNLWKPGGVKRNFLKKNILKNI         AG38352.1       DKLEPHVRSEQVSKYYSRHHSGTVSTOVGDVNLWKPGGVSWSEHSKIKTKCKNILKNI         AG38352.1       DKLEPHVRSEQVSKYYSRHHSGTVSTOVGDVNLWKRPGLVSSWSEHSKIKTKCKNINNEHNI         AKV66676.1       TUVGAVVTDKIRRFPLSAHLKGTVQISVHUWKSEHSKIKTKKNIKKNINE         AG38359.1       DKVFQIAARAKRFRERTSVNDVTUJWKRPGLVSSWSEHSKIKTKKNIKKNINNE         AG38362.1       KVYLVRRERILSRFPLSAHLKGTALISTVDRIQKVS-VUGEGIVHRUKKKNILKNIKKNIK         AG38362.1       KVVLVRMSEHSKIKKREKKIKKNIKKNIKKNIKKNIKKNIKKNIKKNIKKNIKKNI	AGJ83602.1	DKLEPQIRAEQVL	SKYYYSRKHVLGVISISVSQDGKLK-VYSSGIVRHRLCEKSILKYKC	
AGJ8362.1       DNVDMQLISEQUALSMYYSRHALAGVSICISQ0GEL-AYSIGUKHRICEKSILKNILGS         AGJ83612.1       DRVPARLRCORLRRFPLSAMHLKGTVLIDIMEGGFD-VTTEGTVTHRVCKKSLLKNILGS         AB871769.1       DRVDAARCORLRRFPLSAMHLKGTVLIDIMEGGFD-VTTEGTVTHRUCKKNILGS         AB80550.1       DRLEPHTRSEQUSSTWINSRHTGGISVTVQ0NSQLA-VHTSGIVKHRVCKSLLKNILGS         AB8172780.1       ERVPASTRASRIKLRFPLSXHLKGTVLIDIDEGGFD-VTTEGTVTHRUCKKNILLSY         AGB3850.1       DRLEPHTRSEQUSSTWINSRHTGGISVTVQ0NSQLA-VHTSGIVKHRVCKSLLKNILGS         AGB72780.1       DRLEPHTRSEQUSSTWINSRHTGGISVTVQ0NQUS-VTSGIVRHRVCKKLLLSY         AGB3851.1       DRLEPHTRSEQUSSTVSTRRHSGISUSVSQ000LV-VTSGIVRHRVCKKTLLKNI         AGB8352.1       DRLEPHTRSEQUSSTVSTRRHSGISTVSQ000LV-VTSGIVTHRUCKKNLLSY         AGB38361.1       DRLEPSPHAARKRFRGTQYDDVILVUWKRPGIVGSWSEHSKISTVRFKETSLIKHL         AGB38362.1       NCVSPAMARKRFRGTQYDDVILVUWKRPGIVGSWSEHSKISTVRFKTRNHEIM         AGS38362.1       NCVSPAMARKRFRGTQYDDVILVUWKRPGIVGSWSEHSKISTVRFKKINLLSY         AGV6661.1       TUVGADVRTINKLRYTQHHTRSSVTSISTSRIGDV-VTEGTVFHKUKKKTLLKN         AGJ83362.1       NKVSAVFCRINERIMYRKSAUSTSINNGOST-VTEGTVFHKUKKKKLLKN         AGV66673.1       DUVPDVKRNKRIKERVSVSISTSRIGDV-VTEGTVFHKUKKKKLLKN         AGJ83362.1       KVVLVKKGYVFGNDELMTKLLN         AGJ8362.1       KVVLVKKGYVFGNDELMTKLLN         AGJ83362.1       DVVPLSKRETISSPHISSHILTTIGNNVV-VTEGTVFHKUKKKKLLKN         AGS3351	ABB71704.1	DLAEPQHRISKAL	EFFEHVRDHVRGIASISISRNGDVT-THSQGIVKVELLKKNILRHQF	
AGJ830211 DIVSAGTAGULTSAGT. DIVSAGTAGUATICUMERSAGT. BR71694.1 DIVSAGTAGUATICSAGT. BR72694.1 DIVVLUKTRETISET. BR72694.1 DIVVLUKTRETISENTICSAGT. BR72694.1 DIVVLUKTRETISENTICSAGT. BR72694.1 DIVVLUKTRETISENTICSAGT. BR72694.1 DIVVLUKTRETISENTICSAGT. BR72694.1 DIVLLKFSGHVFGNDELMTKLLN AGGJ836612.1 RVLLLKFSGHVFGNDELMTKLLN AGGJ836612.1 RVLLLKFSGHVFGNDELMTKLLN AGG383612.1 RVLLLKFSGHVFGNDEMLTKLLN AGG83563.1 DVVLLKFSGHVFGNDELMTKLLN AGG83563.1 DVVLVKVKGYVFGNDELMTKLLN AGG83563.1 DVVLFKFSGYVFGNDEMLTKLLN AGG83563.1 DVVLFKFSGYVFGNDEMLTKLLN AGG83563.1 DVVLFKFSGYVFGNDEMLTKLLN AGG83563.1 DVVLFKFSGYVFGNDELMTKLLN AGG83563.1 DVVLFKFSGYVFGNDELMTKLLN AGG83563.1 DVVLFKFAGUYYGNTGNELTKLLN AGG83563.1 DVVLFKFAGUYYGNTGNELTKLLN AGG83563.1 DVVLFKFAGUYYGNTGNDELTKLLN AGG83563.1 DVVLFKFAGUYYGNTGNDELTKLLN AGG83563.1 DVVLFKFAGUYYGNTGNDELTKLLN AKV60677.1 KVVLVKKGYVFGNDELTKLLN AKV60677.1 KVVLVKKGYVFGNDELTKLLN AKV60677.1 KVVLVKKGYVFGNDELTKLLN AKV60678.1 QVALLKVKGYVFGNDELTKLLN AKV60678.1 QVALLKVKGYVFGNDELTKLLN AKV60678.1 QVALLKVKGYVFGNDELTKLLN	AGJ83652.1	DNVDMQIRSEQAI	SRYYYSRRHIAGVVSICISQDGGLK-AYSTGIVKHRICEKSILKYKC	
AGJ 8350-1 DVN ANEXAMPLEAN PLSAMPLICATURE AVTEGITINE CLKNING AB38550.1 DVLEPHTRSEQUESKIYYSRMTTGCIVSTVTKONSQLE-MTTSGTWKHKUCKKINLLKY AG83572.1 ERVPASTRSRTIKLERPLSAMPLICATUJDEEGKFT-WYSEGIVSRHKUCKKILLKY AG83572.1 OKLEPHTRSEQUESKIYYSRMTIGGWAVSVGGEGQLQ-WYSTGTVRHRUCEKSILKY AG83572.1 OKLEPHVRSEQVUSKYYSRMTIGGWAVSVGGEGQLQ-WYSTGTVRHRUCEKSILKY AG83572.1 OKLEPHVRSEQVUSKYYSRMTIGGWAVSVGDEGUT-WYSSGTVRHRUCEKSILKY AG83512.1 DVLEPHVRSEQVUSKYYSRMTIGGVIDVUQWKRPGLVGSWDEKKSLICKSWLKKT AG83512.1 DVLEPHVRSEQVUSKYYSRMTIGGYIDVUQWKRPGLVGSWDEKKSLICKSWLKKT AG83512.1 DVLEPHVRSEQVUSKYYFSRMVSGTVSICVQDNQLK-WYSSGTWHRVCEKFILKY AG83512.1 DVLEPHVRSEQVUSKYYFSRMVSGTVSICVQGVMQLK-WYSSGTWRHRVCKKTLLKY AG83502.1 DVLSPQ4AAAKRFRGTCYVIDVULWKRPGLVGSWDSEKHSKIICKSMLKY AG83502.1 NVSAVYRCINELRAPPLSSHLKGIVQISVHPNRTFS-WTGGTVKHRVKKKTLLKY AG83502.1 NVSAVYRCINELRAPPLSSHLKGIVJISVMKPGLKAWSEKHSKIICKKNLLKY AG83502.1 DVVPQLKISSMVGTKHVSEHSKVGVGVKSEKHSKLIKKNILKY AG7838.1 DVVPQLKISSMVGAAAKRFGTCYVIDVUVUWKRPGLVGSWDSEKHSKIICKKNLLKY AG7838.1 DVVPQLKISSMVGAALSJUSGNVSISILSDGSIN-TYSEGIAATLCOKSULKY AG7980.1 DVVPQLKRERLISAPPLSSHLKGIAUISVGNVGVVGVGGUK-WHSWGTHRHCKKNLLKY AG78350.1 DVVPJVKRRERLISAPLSSHNKGIAUSSUNGVS-VQTEGIVTHRLCKKNLLKY AKV66075.1 D0V0PJVKRERLISAPLSSHNKGIAUSSUNGVS-VQTEGIVTHRLCKKNLLKY AG83562.1 KVVLVRMPGYVFGNDELLMTKLLN AG83562.1 KVVLVRMPGYVFGNDELLMTKLLN AG983662.1 KVVLVRMPGYVFGNDELLMTKLLN AG983662.1 KVVLVRMPGYVFGNDELLTKLLN AG983662.1 KVVLVRMPGYVFGNDELLTKLLN AG983612.1 RVLLLKFSGHVFGNDEMLTKLLN AG983612.1 RVLLLKFSGHVFGNDEMLTKLLN AG983612.1 KVVLVKMPGYVFGNDELLTKLLN AG983612.1 KVVLVKMPGYVFGNDELMTKLLN AG98350.1 KVILVRMPGYVFGNDELMTKLLN AG983512.1 KVVLVKVKGYVFGNDELLTKLLN AG983512.1 KVVLVKKGYVFGNDELLTKLLN AG983512.1 KVVLVKKGYVFGNDELLTKLLN AG983512.1 KVVLVKKGYVFGNDELLTKLLN AG983512.1 KVVLVKKGYVFGNDELLTKLLN AG983512.1 KVVLVKKGYVFGNDELLTKLLN AG983512.1 KVVLVKKGYVFGNDELLTKLLN AKV60677.1 KVVLVKKGYVFGNDELLTKLLN AKV60678.1 QVALLKVKGYVFGNDELLTKLLN AKV60678.1 QVALLKVKGYVFGNDELLTKLLN	AGJ65012.1 ABB71694 1		I REDI SADHI KGTWITOTNEEGGED_WYTEGTVTHRWCKKSI I KHVC	
AA338550.1       DKLEPHTRSEQTVSRYNYSRKHTCGIVSVTVGQNSQLR-WHTSGIVKHRVCDKFILKH         AGW27481.1       ERVPASTAASRIKLRFPLSVKHLKGIVUQUEEGKFT-VYSEGTVSHRUKKNLLKY         AGW27481.1       DKLEPYMSEQULSVYVSRHUGGVUSVSVEQEQUE/VVSTGVRHRUKKNLLKKNLLKY         AG871700.1       DKLEPYMSEQULSVYVSRHUGGVUSVSVEQEQUE/VVSTGVRHRUKKNLLKKNLLKY         AG838512.1       DKLEPYMSEQULSVYVSRHUGSVUSVEQQUUE/VVSGSGVRHRUKCKKTLLKY         AG383512.1       DKLEPYMSEQULSVYYSRHUSGVUSVQQUUE/VVSGSGVRHRUKCKKTLLKY         AG383512.1       DKLEPSPHARAKRFKGTQYIDDVILQWKRPGIVGVSGQUUE/VVSSGVRHRUKCKKTLLKY         AG383512.1       DKLSPSQHAARAKRFKGTQYIDDVILQWKRPGIVGVSGVQSGUE/VSSGVRKKTLKKYRKKKKKKKKKKKKKKKKKKKKKKKKKKKK         AG25109.1       DKLSPSQHAARAKRFKGTQYIDDVILQWKRPGIVGVSSEKHSKKVKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	AKV60674.1	DRVDAAHRCNRIR	AREPI SAVHI KGTVTI STAKDRTVK-AYTEGTVTHRI CKKNVI GETC	
AGW27481.1       ERVPASIRASŘIKLERPLSVKHLKGIVVIQIDĚGKFT-VYSEGIVSHRICKKNLLKY         ABB71700.1       DKLDPQVRSEQVLSKYYYSRHICKVANSVOGEGUL-VYSTGIVRHRICKKNLLKY         AGR28363.1       DVVPSVRRETRISRNPLSSKHLGLIAUDRNIKVS-VJTGGIVTHRICKKNLLKY         AGR28363.1       DKLEPVVRSEQVSKYFSRHVSGIVSICVGONQLK-VYSSGIVRHVCKKTLLKY         AGR27261.1       ALTSPELRIDKIKRRPLSSCHLKGIVQJSVKPOVTN-VYSEGIVRHVCKKTLLKY         AGR27261.1       DKLEPSQHAARAKRRFKGTCQVIDOVIVLQWKRPCLVGSVNSEKHSKIKVCRNHELMY         AKV60616.1       TLVGADVRIDKIRRFPLSSCHLKGIVQJSVMPNRTFS-VTGGIVSHKVCKKTLLKH         AGR38362.1       DKVSAVYRCNRLRARPFLSSHLRGIALITIGKNNMVD-AYTEGIVSHRUCKKVLCKYLLKH         AGV86675.1       DLVPQLRISRMPYFKHVSEHVRGASISISSMGDS-TYSGGIAKATLCDKSVLVY         AGV9676.1       DLVPQLRISRMPYFKHVSEHVRGASISISMGDS-TYSGGIAKATLCDKSVLVY         AKV60675.1       DVVPATVRKERILMRFPLSSHLKGIALITJOROKVS-VGTGGIVTHRICKKNLLKY         AGJ38362.1       DVVPATVRKERILMRFPLSSHVKGALISVORNKYS-VGTGOVTHRICKKNLLKY         AGJ38362.1       DVVPATVRKERILMRFPLSKHVGGILISVORNKYS-VGTGOVTHRICKKLLKN         AGJ38362.1       DVVPATVRKERILMRFPLSKHVGGALISVORNKYS-VGTGOVTHRICKKLLKN         AGJ38362.1       KVVLVRMPGYVFGNDELMTKLLN         AGJ38362.1       RVVLVKREQUSFFGUNCKHLKKKLLKN         AGJ38362.1       RVVLVKRPGNVFGNDELMTKLLN         AGJ38362.1       RVVLVKRMPGVFGNDELMTKLLN         AGJ38362.1       RVVLLKKFSGHVFGNDEMLTKLLN	AAB30550.1	DKLEPHTRSEOIV	SRYNYSRKHTCGIVSVTVGONSOLR-VHTSGIVKHRVCDKFILKHKC	
ABB71700.1       DKLDPQVRSEQULSKYYYSRHIGKVAVSVGQEGQLQ-VYSTGTVRHRIECKSILKY         AGC83563.1       DVVPSVRRERIISRFPLSSKHLRGIALIAVDRINKVS-VQTEGTVTHRIECKSILKY         AG333472.1       GRGSASOCVRRATRRLRTYQRHIRGSVVSVLRDOUTIN-TYSEGTAKAMLCEKSULKY         AG33312.1       DKLEPHVRSEQVVSKYYFSRHVSGTVSICVGQDQLK-VYSSGTVRHRVCKKTLLKH         AG33312.1       DKLEPHVRSEQVVSKYYFSRHVSGTVSICVGQDQLK-VYSSGTVRHRVCKKTLLKH         AG33312.1       DKLEPHVRSEQVVSKYYFSRHVSGTVSICVGQDQLK-VYSSGTVRHRVCKKTLLKH         AG2510.1       TLVGADVRIDKTRRFPLSAHLKGTQJIDVTVLQMKRPGLVGSVVSKTKVCKRHFLMY         AKV6667.1       DKLSPQHAARAKRFKGTCYVDVTVLQMKRPGLVGMVSKSKKSKTRICKRNFLVKY         AG33352.1       GKGSASOCVRNTFKLRYTQHHTRSSVTSILSOSSIN-TYSEGTAKATLCKNLVGY         AG33352.1       DVVPLQUETSRVDYFKHVSKHRVGKVASISISRNGON-S-VYSEGTAVHELKKNLLKY         AG33352.1       DVVPLSVRRERILSRFPLSARHLGALISTORDKV-VTGGTVFHRLCKKNLLKY         AG33352.1       DVVPLVTRKRETLMRPFLSARHLGALISTORDKVH-VTGGTVFHRLCKKNLLKY         AG33352.1       DVVPLVTRKRETLMRPFLSARHLGALITIDDRSKNKKVCRRNFLKY         AG333562.1       KVVLVRMPGYVFGNDELMTKLLN         AG333662.1       KVVLVRMPGYVFGNDELMTKLLN         AG333662.1       KVVLVRMPGYVFGNDELMTKLLN         AG333662.1       KVVLVRMPGYVFGNDELMTKLLN         AG333662.1       KVVLVKMPGYVFGNDELMTKLLN         AG333662.1       KVVLVKMPGYVFGNDELMTKLLN         AG333662.1 </td <td>AGW27481.1</td> <td>ERVPASIRASŘIK</td> <td>LRFPLSVKHLKGIVVIQIDĚEGŘFT-VYSEGIVSHRICKKNLLKYMC</td> <td></td>	AGW27481.1	ERVPASIRASŘIK	LRFPLSVKHLKGIVVIQIDĚEGŘFT-VYSEGIVSHRICKKNLLKYMC	
AG633563.1       DVVPSVRRERIJSRPLSSKHLRGIALIAVDRNQKVS-VDTEGUTHRLCKKNLLKY         AG333472.1       GRGSASDCVRRATRURYTQHIRGSVVSVLRDGVIN-TYSEGLAKAMLCEKSULKY         AG33512.1       DKLEPHVRSEQVSKYYFSRHVSGIVSIVGQVDQLK-VYSGIXHRVCKKTLLKY         AE22601.1       ALTSPELRIDKIKRRFPLSOHLKGIVQISVKPDRTFS-VTTGGIVKHRVCKKTLLKY         AKV60616.1       TLVGADVRIDKIRRFFKGTCQTDDVILQWKRPCTVGWVSSKHSKVRCRRPELKY         AG33362.1       NKVSAVYRCMRLRARPFLSSTHLGIATLITGKNRMVD-AVTEGUSKHSKVRICKRPELKY         AG33362.1       NKVSAVYRCMRLRARPFLSSTHLGIASTICHTGVSVISKHSKVRICKRNELKY         AG33362.1       DVEPQLRISKMVYFKHVSEHVRGVASISISMGVS-VYSGIVHVELLKKNILKY         AG33362.1       DVVPLSVRRERILSFPLSSRHVKGIALISVDRNQKVS-VQTEGIVTHRLCKKNLLKY         AG333662.1       KTTLIRMPGHVFGNDELMTKLLN         AG333662.1       KTVLVKKGYVFGNDELMTKLLKN         AG333662.1       KVVLVVRMPGYVFGNDELMTKLLN         AG333662.1       KVVLVRMPGYVFGNDELMTKLLN         AG333662.1       KVVLVRMPGYVFGNDELMTKLLN         AG333662.1       KVVLVRMPGYVFGNDELMTKLLN         AG333662.1       KVVLVKKGYVFGNDELMTKLLN         AG333662.1       KVVLVRMPGYVFGNDELMTKLLN         AG333662.1       KVVLVRMPGYVFGNDELMTKLLN         AG333662.1       KVVLVRMPGYVFGNDELMTKLLN         AG333662.1       KVVLVKMPGYVFGNDELMTKLLN         AG333662.1       KVVLVKMPGYVFGNDELMTKLLN </td <td>ABB71700.1</td> <td>DKLDPQVRSEQVL</td> <td>SKYYYSRRHICGVVAVSVGQEGQLQ-VYSTGIVRHRICEKSILKYKC</td> <td></td>	ABB71700.1	DKLDPQVRSEQVL	SKYYYSRRHICGVVAVSVGQEGQLQ-VYSTGIVRHRICEKSILKYKC	
AG383472.1       GRGSASDCVRRATERLENTQMELRESVVSVLRDVID-TYSEGLAKAMLCEKSULEYI         AG38352.1       DKLEPHYRSEQVSKSVYSSICKQODQUE.VVSSGVKRHVCKKTLLKYI         CAG38362.1       ALTSPELRIDKIKREPLSSDHLKGIVQISVVPDRTFS-VTTGGIVKHRVCKKTLLKYI         AKV66067.1       DKLSPSQHAARAKREKGTCQYIDDVTULQWKRPGTVGIVVSSKMSKKVCKRTLENYI         AKV6607.1       DKISPAQHAARAKREFKGTCQYIDDVTULQWKRPGTVGIVVSSKMSKKVCKRTLENYI         AG38352.1       DKISPAQHAARAKREFKGTCQYIDVTULQWKRPGTVGIVVSSKMSKKVCKKTLLKYI         AG38352.1       DKVSAVYRCMRLRAFPLSSTHLRGALTITGKNRMVD-AYTEGTVSHRICKKVLKYI         AKV66075.1       DLVEPQLRISRMDVFKHVSEHNRGVSSISISSGSIN-TYSEGIAKATLCOKSVLKYI         AKV66075.1       DKLEPQTRSEQTVIKYYYSRHISGVSICVI0GGQUK-VHSMGTTRHICOKSILKYI         AG38362.1       KVTLVRRETLISRFPLSSHVKGIALISVDRINGKVS-VQTEGTVHRLCKKNLLKYI         AG38362.1       DVVPLSVRRETLSRFPLSARHLGGIALITIDDROKVH-VQTEGTVSHRLCKKNLLKYI         AG383662.1       KTTLLIRMPGHVFGNDELMTKLLN         AG383662.1       KVVLVRMPGYVFGNDELMTKLLN         AG383662.1       KVVLVRMPGYVFGNDELMTKLLN         AG383662.1       KVVLVRMPGYVFGNDELMTKLLN         AG383662.1       KVVLVRMPGYVFGNDELMTKLLN         AG383662.1       KVVLVRMPGYVFGNDELMTKLLN         AG383662.1       KVVLVRMPGYVFGNDELMTKLLN         AG383662.1       RVLLKFSGHVFGNDEMLTKLLN         AG383662.1       KVVLVRMPGYVFGNDELMTKLLN     <	AGC83563.1	DVVPYSVRRERIIS	SRFPLSSKHLRGIALIAVDRNQKVS-VQTEGIVTHRLCKKNLLKYVC	
AG38312.1 DKLEPHVD5QV05KTYF5KHV5GV3LVQDWQL-VT5SG1VKHVCKTLLKY AEP22601.1 DKLSPSQHAARAKRFKGTCQYIDDVIVLQWKRPGLVGSVMSEKHSKTKVCKRNFLIKY AKV6601.1 TLVGADVRIDKIRRRPLSAHLKGTVQISVPPNTFS-VTTGG1VKHVCKKTLLKY AKV6601.1 TLVGADVRIDKIRRRPLSAHLKGTVQISVPNRTFS-VTTGG1VKHVCKKTLKYL AG383462.1 NKVSAVYRCNRLRARFPLSSIHLRGIAILTIGKNRWD-AYTEGIVSHRICKKNLVGY AG383592.1 GKGSASOCVRWTRKLRYTQHIRGSVSISISNGOS-VTSGGIVKATLCOKSUKY AG38359.1 DLVEPQIRSSRVDYFKV9SHNRGVASISISRNGOS-VTSGGIVKHUCKKNLLKY AG38359.1 DLVEPQIRSSRVDYFKV9SHNRGVASISISRNGOS-VTSGGIVKHUCKKNLLKY AG38359.1 DLVEPQIRSEQIVNKYYSRHISGVSICVNQGQLK-VHSMGITRHRICKKNLLKY AG38359.1 DLVEPQIRSEQIVNKYYSRHISGVSICVNQGQLK-VHSMGITRHRICKKNLLKY AG38359.1 DLVEPQIRSEQIVNKYYSRHISGVSICVNQGQLK-VHSMGITRHRICKKLLKY AKV60675.1 DQVQPQVCETALRREPYIREYIHDVIVQVGRPGELKQWKRGSTKVKVCRNFLRYL AG38362.1 KTILIRMPGHVFGNDELLMTKLLN AG38362.1 KVULVRMPGYVFGNDELMTKLLN AG38362.1 KVULVRMPGYVFGNDELMTKLLN AG383612.1 RVLLLKFSGHVFGNDELMTKLLN AG383612.1 RVLLLKFSGHVFGNDELMTKLLN AG383612.1 RVLLLKFSGHVFGNDELMTKLLN AG383612.1 RVLLLKFSGHVFGNDELMTKLLN AG383612.1 KVULVRMPGYVFGNDELMTKLLN AG383612.1 KVLLVRMPGYVFGNDELMTKLLN AG38361.1 DIVLLKFSGHVFGNDELMTKLLN AG827481.1 DIVLLKFSGHVFGNDELMTKLLN AG827481.1 DIVLLKFSGHVFGNDELMTKLLN AG38350.1 KVLVRMPGYVFGNDELMTKLLN AG383512.1 KVVLVRMPGYVFGNDELMTKLLN AG383512.1 KVVLVRMPGYVFGNDELMTKLLN AG383512.1 KVVLVRMPGYVFGNDELMTKLLN AG383512.1 KVVLVKNGYVFGNDELMTKLLN AG383512.1 KVVLVKNGYVFGNDELMTKLLN AG383512.1 KVVLVKNGYVFGNDELMTKLLN AG383512.1 KVVLVKNGYVFGNDELMTKLLN AG38352.1 KVVLVKNGYVFGNDELMTKLLN AG38352.1 KVVLVKNGYVFGNDELMTKLLN AG38352.1 KVVLVKNGYVFGNDELTKLLN AG38352.1 KVVLVKNGYVFGNDELTKLLN AG38352.1 KVVLVKNGYVFGNDELTKLLN AKV60677.1 KVVLTKFAGLVYGNYELITKLAN AKV60677.1 KVVLTKFAGLVYGNYELTKLAN AG38352.1 KVVLTKFAGLVYGNYELTKLN AG38352.1 KVVLTKFAGLVYGNYELTKLN AG38352.1 KVVLTKFAGLVYGNYELTKLN AG38352.1 KVVLTKFAGLVYGNYELTKLN AG38352.1 KVVLTKFAGLVYGNYELTKLN	AGJ83472.1	GRGSASDCVRRAT	RRLRYIQRHIRGSVVVSVLRDGVIN-TYSEGIAKAMLCEKSVLKYNY	
AGJ2301.11 DKLSPSQHAAAAKRRFKGTCQYDDVTULQMKRPGLVGSWJSEKHSKIKVCRRNFLIKH AKV60677.1 DKJSPSQHAAAAKRRFKGTCQYDDVTULQMKRPGLVGSWJSEKHSKIKVCRRNFLIKH AKV60677.1 DKJSPSQHAAAAKRRFKGTCQYDDVTULQMKRPGLVGSWJSEKHSKIKVCRRNFLKY AGJ33452.1 DKLSPSQHAAAAKRFFGTREYVIDVTULQMKRPGLVGSWJSEKHSKIKVCRRNFLKY AGJ33592.1 GKGSASDCVRRVTRKLRYIQHHIRGSVJSILSDGSIN-TYSEGIVSHICKKNULCKY AGJ33592.1 DLVEPQLRJSRVMDVFKHVSEHVRGVASIJSISRNGVS-TYSRGTVHELLKKILKKY AGJ33592.1 DLVEPQLRJSRVMDVFKHVSEHVRGVASIJSISRNGVS-TYSRGTVHELLKKILKIK AGJ3352.1 DLVEPQLRJSRVMDVFKHVSEHVRGVASIJSRNGVS-VQTEGIVTHLCKKNLLKY AGJ3352.1 DVVPATVRKERILSRFPLSSRHVKGIALISVDRNQKVS-VQTEGIVTHLCKKNLLKY AGJ33652.1 DVVPATVRKERILSRFPLSSRHVKGIALISVDRNQKVS-VQTEGIVTHLCKKNLLKY AGJ33652.1 KVVLVRMPGHVFFGNDELLMTKKLLN AGB27457.1 SLVDSNVRIDKIKRFPLSHRHLRGIVQISVRPDRFG-VTTCGIVKHKICKKTLLKQ XV606674.1 DIVLLKFFGHVFFGNDELLMTKKLLN ABB71694.1 DIVLLKFFGHVFFGNDELLMTKLLN AAB30550.1 KVILVRMPGYVFGNDELLTKLLN AGB27481.1 DIVLLKFSGHVFGNDEMLTKLLN AGB27481.1 DIVLLKFSGHVFGNDEMLTKLLN AGJ33472.1 KVVLVRMPGYVFGNDELMTKLLN AGJ33512.1 KVVLVRMPGYVFGNDELMTKLLN AGJ33512.1 KVVLVKMPGYVFGNDELMTKLLN AGJ33512.1 KVVLVKMPGYVFGNDELMTKLLN AGJ33512.1 KVVLVKMPGYVFGNDELMTKLLN AGJ33512.1 KVVLVKMPGYVFGNDELMTKLLN AGJ33512.1 KVVLVKMPGYVFGNDELMTKLLN AGJ33512.1 KVVLVKMPGYVFGNDELMTKLLN AGJ33512.1 KVVLVKKGYVFGNDELMTKLLN AGJ33512.1 KVVLVKKGYVFGNDELMTKLLN AGJ33512.1 KVVLVKKGYVFGNDELMTKLLN AGJ33512.1 KVVLVKKGYVFGNDELMTKLLN AGJ33512.1 KVVLVKKGYVFGNDELMTKLLN AGJ33512.1 KVVLVKKGYVFGNDELMTKLLN AGJ33512.1 KVVLVKKGYVFGNDELMTKLLN AGJ33512.1 KVVLVKKGYVFGNDELMTKLLN AGJ33512.1 KVVLVKKGYVFGNDELMTKLLN AKV60616.1 DVILLQTPGYVFGNDELMTKLLN AKV60616.1 DVILLKFSGHVFGNDELMTKLLN AKV60677.1 KVVLTKFAGLVYGNYELITKLAN AKV60677.1 KVVLTKFAGLVYGNYELTKLAN AGJ33592.1 KVVLIKVKGHVFGNDEMLTKLLN AKV60678.1 QVALLKVKGYVFGNDEMLTKLLN	AGJ83512.1 AED22601 1		SKYYFSKKHVSGIVSICVGQUNQLK-VYSSGIVKHKVCEKFILKYKC	
AKV60616.1 TLVGADVRIDKIRRRFPLSAKHLKGIVQISVHPNRTFS-VTTCGIVKHKVCKKTLLKH AKV60677.1 DKISPAQHAARAKRRFRGTREYVNUDIVLQWKRPGTVGINWSEKHSKVTCCRFNFLKY AGJ83592.1 GKGSASDCVRRVTRKLRYIQHIRGSVJSILSOGSIN-TYSEGIVARILCKKNULKY ALSI285.1 DLVEPQLRISEVNVYSKHVSEHVRGVASISISRNGDVS-TYSRGTVHELLKKILLKY ALSI285.1 DLVEPQLRISEVNVYYSRHISGVVSICVNQGQULK-VHSMGITRHLICKKILLKY AMD7980.1 DLVPJVRREEILSRPPJSRHNKGIALISVDNKVS-VQTEGIVTHLCKKILLKY AGJ83582.1 DVVPJVRREEILSRPPJSRHVKGIALISVDNKVS-VQTEGIVTHLCKKILLKY AGJ83662.1 KTILIRMPGHVFGNDELLMTKLLN AGJ83652.1 KVULVRMPGYVFGNDELLMTKLLN AGJ83652.1 KVULVRMPGYVFGNDELLMTKLLN AGJ83612.1 RVLLLKFSGHVFGNDEMLTKLLN AGJ83652.1 KVULVRMPGYVFGNDEMLTKLLN AGJ83652.1 KVULVRMPGYVFGNDEMLTKLLN AGJ83612.1 RVLLLKFSGHVFGNDEMLTKLLN AGJ83612.1 RVLLLKFSGHVFGNDEMLTKLLN AGB71694.1 DIVLLKFSGHVFGNDEMLTKLLN AGB27481.1 DIVLLKFSGHVFGNDEMLTKLLN AGB27481.1 DIVLLKFSGHVFGNDEMLTKLLN AGJ83512.1 KVVLVRMPGYVFGNDELMTKLLN AGJ83512.1 KVVLVRMPGYVFGNDELMTKLLN AGJ83512.1 KVVLVKMPGYVFGNDELMTKLLN AGJ83512.1 KVVLVKMPGYVFGNDELMTKLLN AGJ83512.1 KVVLVKKGYVFGNDELLTKLLN AGJ83512.1 KVVLVKKGYVFGNDELLTKLLN AGJ83512.1 KVVLVKVKGYVFGNDELLTKLLN AGJ83512.1 KVVLVKVKGYVFGNDELLTKLLN AGJ83512.1 KVVLVKVKGYVFGNDELLTKLLN AGJ8352.1 KVVLVKVKGYVFGNDELLTKLLN AGJ8352.1 KVVLVKKGYVFGNDELLTKLLN AGJ8352.1 KVVLVKKGYVFGNDELLTKLLN AGJ8352.1 KVVLVKKGYVFGNDELLTKLLN AGJ8352.1 KVVLVKKGYVFGNDELLTKLLN AGJ8352.1 KVVLVKKGYVFGNDELLTKLLN AGJ8352.1 KVVLVKKGYVFGNDELLTKLLN AGJ8352.1 KVVLVKKGYVFGNDELLTKLLN AGJ8352.1 KVVLVKKGYVFGNDELLTKLLN AGJ8352.1 KVVLKKGYVFGNDELLTKLLN AGJ8352.1 KVVLTKFAGLVYGNYELTKLAN AKV60677.1 KVVLTKFAGLVYGNYELTKLAN AGJ8352.1 KVVLTKKGHVFGNDEMLTKLLN AGJ8352.1 KVVLTKKGHVFGNDEMLTKLLN AKV60678.1 QVALLKVKGYVFGNDELLTKLLN AKV60678.1 QVALLKVKGYVFGNDELLTKLLN	CAF51109.1	DKI SPSOHAARAKI	RREKGTCOYTDDVTVI OMKRPGI VGSVWSEKHSKTKVCRRNEI NYDH	
AKV60677.1DKISPAQHAARAKRFRGTRETVINDVI VLQMKRPGTVGNVMSEKHSKVRICRRNFLKYDAG333462.1NKVSAVYRCINRLRARPLSSISHLRGIALITGKNRMD-AYTEGTVSHRICKKILLGYAG333462.1NKVSAVYRCINRLRARPLSSISHLRGIALITGKNRMD-AYTEGTVSHRICKKILLGYAKV60678.1DLVEPQLRISRVMDYFKHVSEHVRGVASISISRNGDVS-TYSRGTVHVELLKKNILKYDALS1285.1DKLEPQIRSEQTVIKYYSRRHISGVSICVNQGQUL-VHSMGTRHRICDKSLLKYJAMD77980.1DVVPLSVRRERILSRFPLSSRHVKGIALISVDRNQKYS-VQTEGTVHRLCKKNILLKYDAGJ33362.1DVVPLSVRRERILSRFPLSSRHVKGIALISVDRNQKYS-VQTEGTVHRLCKKNILLKYDAGJ33362.1KTTLIRMPGHVFGNDELMTKLLNAGJ33362.1RVALLKVKGYVFGNDELMTKLLKNAGJ333612.1RVALLKVKGYVFGNDELMTKLLNAGJ333612.1RVLLLKFSGHVFGNDEMLTKLLNAGJ333612.1RVLLLKFSGHVFGNDEMLTKLLNAGJ333612.1RVLLLKFSGHVFGNDEMLTKLLNAGJ333612.1RVLLKFSGHVFGNDEMLTKLLNAGJ333612.1RVLLKFSGHVFGNDEMLTKLLNAGJ333612.1RVLLKFSGHVFGNDEMLTKLLNAGJ33361.1DIVLLKFSGHVFGNDEMLTKLLNAGB3362.1KVILVRMPGYVFGNDELMTKLLNAGJ33361.1DIVLLKFSGHVFGNDEMLTKLLNAGJ33361.1DVLLKFSGHVFGNDEMLTKLLNAGJ33361.1DVLLKFSGHVFGNDELMTKLLNAGJ33351.1DVVLFKFSGYVFGNDELMTKLLNAGB3351.1DVLLKFSGHVFGNDELMTKLLNAGJ33351.1CVLVKVKKGYVFGNDELLTKLLNAGJ33351.1DVVLFKFSGYVFGNDELLTKLLNAGG333472.1KVVLVKNGYVFGNDELLTKLLNAGJ33512.1KVVLVKKKGYVFGNDELLTKLLNAKV60616.1DVILLQTPGYVFGNDELLTKLLNAGJ33592.1KVVLVKKGHVFGNDEMLTKLLNAGJ33592.1KVVLTKKGHVFGNDEMLTKLLN<	AKV60616.1	TLVGADVRIDKIR	RRFPLSAKHLKGIVQISVHPNRTFS-VTTCGIVKHKVCKKTLLKHRC	
AG383462.1NKVSAVYRONRLRARFPLSSTHLRGTALLTIGKNRVUO-AYTEGIVSHICKKIVLGYAG383592.1GKGSASDCVRVTRKLRYIQHHIRGSVISILSDGSIN-TYSEGIAKATLCKKIVLGYALI51285.1DLVEPQLRISRVHOYFKHVSEHVRGVASISISRBOVS-TYSEGIAKATLCKKILLKYAG383582.1DVVPLSVRERILSRPLSSRHVKGTALISVDRNQKVS-VQTEGITHRLCKKILLKYAG383602.1KTILIRMPGIVGRPGELKQWKRGSTKVKVCRNFLKYIAG383602.1KTILIRMPGHVFGNDELMTKLLNAG38362.1KVVLVRNPGYVFGNDELMTKLLNAG38362.1KVVLVRMPGYVFGNDELMTKLLNAG38362.1KVVLVRMPGYVFGNDELMTKLLNAG38362.1KVVLVRMPGYVFGNDELMTKLLNAG383612.1RVLLLKFSGHVFGNDEMLTKLLNAG383612.1RVLLLKFSGHVFGNDEMLTKLLNAG383612.1RVLLLKFSGHVFGNDEMLTKLLNAG383612.1RVLLLKFSGHVFGNDEMLTKLLNAG827481.1DIVLLKFSGHVFGNDEMLTKLLNAGW27481.1DIVLLKFSGHVFGNDEMLTKLLNAG83563.1DVVLFKFSGYVFGNDELMTKLLNAG383472.1KVVLVKNGYVFGNDELMTKLLNAG383512.1KVVLVKNGYVFGNDELMTKLLNAG383512.1KVVLVKKGYVFGNDELMTKLLNAG83553.1DVVLFKFSGYVFGNDELLTKLLNAG83553.1DVVLFKFSGYVFGNDELLTKLLNAG383512.1KVVLVKNGYVFGNDELLTKLLNAG383512.1KVVLVKNGYVFGNDELLTKLLNAG383512.1KVVLVKNPGYVFGNDELLTKLLNAG383512.1KVVLVKNPGYVFGNDELLTKLLNAKV60677.1KVVLTKFAGLVYGNYELITKLANAG383512.1KVVLVKNPGYVFGNDELLTKLLNAG383592.1KVVLTKFAGLVYGNYELITKLANAG06677.1KVVLTKFAGLVYGNDEMLTKLLNAKV60678.1QVALLKVKGYVFGNDEMLTKLLNAKV60678.1QVALLKVKGYVFGNDEM	AKV60677.1	DKISPAQHAARAK	RRFRGTREYVNDVIVLQMKRPGTVGNVWSEKHSKVRICRRNFLKYDH	
AG383592.1       GK6SASDCVRRVTRKLRY1QHHIRGSVISILSDGSIN-TYSEGIAATICDKSVLKYY         AKV60678.1       DLVEPQLRISRVMDYFKHVSEHVRGVASISISIRNGVS-TYSRGIVHVELLKKNILKYI         ALIS1285.1       DKLEPQIRSEGIVIKYYVSRHISGVSICVIQGEQLK-VHSMGITRHRICDKSILKYI         AG383582.1       DVVPLSVREREISRPHSSRHVKGIALISVDRIQKVS-VQTEGIVTHRICKKNILLKYI         AG383582.1       DVVPATVRKERILRRPVTREYTUDVIJQUGVRGVFGELKQWKRCSTKVKVCRRIFLKYI         AG4027457.1       SLVDSNVRIDKIKRRFPLSHRHLRGIVDISVRPORTFG-VTTCGIVKHCKKILLKYI         AG383602.1       KVTLVRMPGHVFGNDELMTKLLN         AG383602.1       KVVLVRMPGYVFGNDELMTKLLN         AG383602.1       KVVLVRMPGYVFGNDELMTKLLN         AG383612.1       RVLLLKFSGHVFGNDEMLTKLLN         AG383612.1       RVLLLKFSGHVFGNDEMLTKLLN         AG383612.1       RVLLLKFSGHVFGNDEMLTKLLN         AG50674.1       QILLLKFSGHVFGNDEMLTKLLN         AG8027481.1       DIVLLKFHGHVFGNDELMTKLLN         AG8027481.1       DIVLLKFSGHVFGNDELLTKLLN         AG8027481.1       DIVLLKFSGHVFGNDELMTKLLN         AG83563.1       DVVLFKFSGYVFGNDELMTKLLN         AG83563.1       DVVLFKFSGYVFGNDELLTKLLN         AG383472.1       KVVLVKNGYVFGNDELLTKLLN         AG383512.1       KVVLVKNGYVFGNDELLTKLLN         AG66673.1       DVILLQTPGYVFGNDELLTKLLN         AG86677.1       KVVLVKNGVFGNDEMLTKL	AGJ83462.1	NKVSAVYRCNRLR	ARFPLSSIHLRGIAILTIGKNRMVD-AYTEGIVSHRICKKNVLGYTC	
AKV60678.1 DUVEPQLEISKVINUYFKNYSEHVKGVASISISKNGUVS-IYSRCIHVELKKNILKKY AMD77980.1 DUVPLSVRRERILSRFPLSSRHVKGIALISVDRNQKVS-VQTEGIVTHRLCKKNLLKY AGJ83582.1 DVVPATVRKERILMRFPLSARHLRGIALITIDRDRKVH-VQTEGIVSHRLCKKNLLKY AKV60675.1 DQVQPQVQCETALRRFPYTREYIHDVIVIQVGRPGELKQVWKRGSTKVVCRNHFLY AGW27457.1 SLVDSNVRIDKIKRRFPLSHRLRGIVQISVRPDRTFG-VTTCGIVKHKICKKTLLKQ AGJ83662.1 KVVLVRMPGYVFGNDELLTKLLN AGJ83612.1 RVLLLKFSGHVFGNDEMLTKLLN AGJ83612.1 RVLLLKFSGHVFGNDEMLTKLLN ABB71694.1 DIVLLKFSGHVFGNDEMLTKLLN AKV60674.1 QILLLKFSGHVFGNDEMLTKLLN ABB71700.1 KVILVRMPGYVFGNDELLMTKLLN AGW27481.1 DIVLLKFSGHVFGNDEMLTKLLN AGW27481.1 DIVLLKFSGHVFGNDEMLTKLLN AGS3563.1 DVVLFKFSGYVFGNDEMLTKLLN AGJ83472.1 KVVLVKMPGYVFGNDELLMTKLLN AGJ83512.1 KVVLVKMPGYVFGNDELLTKLLN AGJ83512.1 KVVLVKMPGYVFGNDELLTKLLN AGJ83512.1 KVVLVKVKGYVFGNDELLTKLLN AGJ83512.1 KVVLVKKGYVFGNDELLTKLLN AGJ83512.1 KVVLVKKGYVFGNDELLTKLLN AKV60616.1 DVILLQTPGYVFGNDELLTKLLN AGJ83462.1 QILLLKFSGHVFGNDEMLTKLLN AGJ83592.1 KVVLIKVKGYVFGNDELLTKLLN AGJ83592.1 KVVLIKVKGYVFGNDELLTKLLN AKV60677.1 KVVLIKFAGLVYGNYELLTKLAN AGJ83592.1 KVVLIKVKGYVFGNDEMLTKLLN AGJ83592.1 KVVLIKVKGYVFGNDEMLTKLLN AGJ83592.1 KVVLIKVKGYVFGNDEMLTKLLN AGJ83592.1 KVVLIKVKGYVFGNDEMLTKLLN AKV60678.1 QVALLKVKGYVFGNDEMLTKLLN	AGJ83592.1	GKGSASDCVRRVT	RKLRYIQHHIRGSVVISILSDGSIN-TYSEGIAKATLCDKSVLKYSY	
ACJ3231DKLETGISQUWRAMD7980.1DWPLSVRRERILSRPLSSNHVKGTALTSVØDRØVS-VETEGIVTHRLCKKNLLKYAGJ83582.1DVVPATVRKERILSRPLSSNHVKGTALTSVØDRØVS-VETEGIVTHRLCKKNLLKYAKV60675.1DQVQPQVQCETALRRPPVTREYLHDVIVIQVGRPGELKQWKRGSTKVKVCRNFLEKYAGJ83602.1KTILIRMPGHVFGNDELMTKLLNABB71704.1RVALLKVKGYVFGNDEMLTKLLNAGJ83612.1RVLLKKSGHVFGNDEMLTKLLNAGJ83612.1RVLLLKFSGHVFGNDEMLTKLLNAGJ83612.1RVLLLKFSGHVFGNDEMLTKLLNABB71694.1DIVLLKFGNDEMLTKLLNABB71694.1DIVLLKFGNDEMLTKLLNAGW27481.1DIVLLKFSGHVFGNDEMLTKLLNAGW27481.1DIVLLKFSGHVFGNDEMLTKLLNAGW27481.1DIVLLKFSGHVFGNDEMLTKLLNAG38350.1KVULVRMPGYVFGNDELMTKLLNAGW27481.1DIVLLKFSGHVFGNDEMLTKLLNAGW27481.1DIVLLKFSGHVFGNDEMLTKLLNAGW27481.1DIVLLKFSGHVFGNDELMTKLLNAGS3563.1DVVLFKFSGYVFGNDELMTKLLNAGS3563.1DVVLFKFSGYVFGNDELMTKLLNAGJ83472.1KVVLVKMPGYVFGNDELMTKLLNAGJ83512.1KVVLVKKGYVFGNDELLTKLNAGS3552.1VVLTKFAGLVYGNYELLTKLANAKV60616.1DVILLQTPGYVFGNDELLTKLLNAKV60677.1KVVLTKFAGLVYGNYELTKLANAGJ83592.1KVVLIKVKGYVFGNDEMLTKLLNAKV60678.1QVALLKVKGYVFGNDEMLTKLLNAKV60678.1QVALLKVKGYVFGNDEMLTKLLNAKV60678.1QVALLKVKGYVFGNDEMLTKLLN	AKV60678.1			
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AGJ83472.1KVVLVKVKGYVFGHDEMLTKLLNAGJ83512.1KVVLVKMPGYVFGNDELMTKLLNAEP22601.1DVILIQTPGYVFGNDELLTKLLNCAE51109.1KVILTKFAGLVYGNYELLTKLANAKV60616.1DVILLQTPGYVFGNDELLTKLLNAKV60677.1KVVLTKFAGLVYGNYELITKLANAGJ83462.1QILLLKFSGHVFGNDEMLTKLLNAGJ83592.1KVVLIKVKGHVFGHDEMLTKLLNAKV60678.1QVALLKVKGYVFGNDEMLIKLLNALI51285.1KVVLVRMPGHVFGNDELMTKLLN	AGC83563	.1	DVVLFKFSGYVFGNDEMLTKLLNV	
AGJ83512.1KVVLVKMPGYVFGNDELMTKLLNAEP22601.1DVILIQTPGYVFGNDELLTKLLNCAE51109.1KVILTKFAGLVYGNYELLTKLANAKV60616.1DVILLQTPGYVFGNDELLTKLLNAKV60677.1KVVLTKFAGLVYGNYELITKLANAGJ83462.1QILLLKFSGHVFGNDEMLTKLLNAGJ83592.1KVVLIKVKGHVFGHDEMLTKLLNAKV60678.1QVALLKVKGYVFGNDEMLIKLLNALI51285.1KVVLVRMPGHVFGNDELMTKLLN	AGJ83472	.1	KVVLVKVKGYVFGHDEMLTKLLNV	
AEP22601.1DVILIQTPGYVFGNDELLTKLLNCAE51109.1KVILTKFAGLVYGNYELLTKLANAKV60616.1DVILLQTPGYVFGNDELLTKLLNAKV60677.1KVVLTKFAGLVYGNYELITKLANAGJ83462.1QILLLKFSGHVFGNDEMLTKLLNAGJ83592.1KVVLIKVKGHVFGHDEMLTKLLNAKV60678.1QVALLKVKGYVFGNDEMLIKLLNALI51285.1KVVLVRMPGHVFGNDELMTKLLN	AGJ83512	.1	KVVLVKMPGYVFGNDELMTKLLNV	
CAE51109.1 KVILTKFAGLVYGNYELLTKLAN AKV60616.1 DVILLQTPGYVFGNDELLTKLLN AKV60677.1 KVVLTKFAGLVYGNYELITKLAN AGJ83462.1 QILLLKFSGHVFGNDEMLTKLLN AGJ83592.1 KVVLIKVKGHVFGHDEMLTKLLN AKV60678.1 QVALLKVKGYVFGNDEMLIKLLN ALI51285.1 KVVLVRMPGHVFGNDELMTKLLN	AEP22601	.1	DVILIQTPGYVFGNDELLTKLLNI	
AKV60616.1DVILLQTPGYVFGNDELLTKLLNAKV60677.1KVVLTKFAGLVYGNYELITKLANAGJ83462.1QILLLKFSGHVFGNDEMLTKLLNAGJ83592.1KVVLIKVKGHVFGHDEMLTKLLNAKV60678.1QVALLKVKGYVFGNDEMLIKLLNALI51285.1KVVLVRMPGHVFGNDELMTKLLN	CAE51109	.1	KVILTKFAGLVYGNYELLTKLANL	
AKV60677.1KVVLTKFAGLVYGNYELITKLANAGJ83462.1QILLLKFSGHVFGNDEMLTKLLNAGJ83592.1KVVLIKVKGHVFGHDEMLTKLLNAKV60678.1QVALLKVKGYVFGNDEMLIKLLNALI51285.1KVVLVRMPGHVFGNDELMTKLLN	AKV60616	.1	DVILLQTPGYVFGNDELLTKLLNI	
AGJ83462.1QILLLKFSGHVFGNDEMLTKLLNAGJ83592.1KVVLIKVKGHVFGHDEMLTKLLNAKV60678.1QVALLKVKGYVFGNDEMLIKLLNALI51285.1KVVLVRMPGHVFGNDELMTKLLN	AKV60677	.1	KVVLTKFAGLVYGNYELITKLANL	
AGJ83592.1 KVVLIKVKGHVFGHDEMLTKLLN AKV60678.1 QVALLKVKGYVFGNDEMLIKLLN ALI51285.1 KVVLVRMPGHVFGNDELMTKLLN	AGJ83462	.1	QILLLKFSGHVFGNDEMLTKLLNV	
AKV60678.1 QVALLKVKGYVFGNDEMLIKLLN ALI51285.1 KVVLVRMPGHVFGNDELMTKLLN	AGJ83592	.1	KVVLIKVKGHVFGHDEMLTKLLNV	
ALI51285.1 KVVLVRMPGHVFGNDELMTKLLN	AKV60678	.1	QVALLKVKGYVFGNDEMLIKLLNV	
	AL151285	.1	<b>KVVLVRMPGHVFGNDELMTKLLNV</b>	
AMD77980.1 DVILFKFSGHVFGNDEMLTKLLN	AMD77980	.1	DVILFKFSGHVFGNDEMLTKLLNV	
	AG183582	.1	DVILEKESGYVEGNDEMLTKLLNV	
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#### **RESULTS**

AKV60675.1

AGW27457.1

Sequence alignment produced by CLUSTAL X program of above Protein sequences is a key denoting: conserved sequences (\*), Conservative mutation (:), semi-conserved mutation (.), and non conservative mutation (().).

**KVILSRLCGLVYGNYELMTKLTNI** 

DVILIQIPGYVFGNDELLTKLLNI \* : \* \*:\*: \*:: \*\* \*: Following are the Screen shots of mulitiple sequence alingnment of 24 serotypes of VP2 Bluetongue virus.

### Tree Construction in CLUSTAL Omega

Phylogenetic Tree construction was carried out in clustal omega.



### Phylogenetic tree in CLUSTAL Omega

**Discussion:**The study in CLUSTAL X for multiple sequence alignment, of 24 serotypes of viral Protien 2 of Bluetongue virus, and CLUSTAL Omega for phylogenetic tree construction to review the Relation between different serotypes(1 to 24) of Bluetongue virus having same Protein (Viral protein 2), and from result of multiple sequence alignment, it is shown the conserved sequence, semiconservative mutation, conservative mutation and non conservative mutations among 24 different sequences.

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