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(54) **Titre : SEQUENCES HCBI, MSBI, MSSI ET CMI UTILISABLES EN TANT QUE MARQUEURS PRECOCES DU FUTUR
DEVELOPPEMENT D'UN CANCER ET DE MALADIES DU SNC ET EN TANT QUE CIBLES POUR LE TRAITEMENT ET LA
PREVENTION DE CES MALADIES**
(54) **Title: HCBI, MSBI, MSSI AND CMI SEQUENCES AS AN EARLY MARKER FOR THE FUTURE DEVELOPMENT OF CANCER
AND DISEASES OF THE CNS AND AS A TARGET FOR THE TREATMENT AND PREVENTION OF THESE DISEASES**

(57) **Abrégé/Abstract:**

Described are HCBI (Healthy Cattle Blood Isolate), MSBI (Multiple Sclerosis Brain Isolate), MSSI (Multiple Sclerosis Serum Isolate) and CMI (Cow Milk Isolate) nucleotide sequences as well as probes and primers comprising part of said nucleotide sequences and antibodies against polypeptides encoded by said nucleotide sequences. Said compounds are useful as early markers for the future development of cancer and diseases of the CNS (Multiple sclerosis MS, Prion-linked diseases, amyotrophic lateral sclerosis, transmissible spongiforme encephalitis, Parkinson's disease, Alzheimer disease) and should represent targets for treatment and prevention.



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(57) Abstract: Described are HCBI (Healthy Cattle Blood Isolate), MSBI (Multiple Sclerosis Brain Isolate), MSSI (Multiple Scler-
osis Serum Isolate) and CMI (Cow Milk Isolate) nucleotide sequences as well as probes and primers comprising part of said nucle-
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HCBI, MSBI, MSSSI and CMI sequences as an early marker for the
future development of cancer and diseases of the CNS and as a
target for the treatment and prevention of these diseases

5

The present invention relates to HCBI (Healthy Cattle Blood Isolate), MSBI (Multiple Sclerosis Brain Isolate), MSSSI (Multiple Sclerosis Serum Isolate) and CMI (Cow Milk Isolate) nucleotide sequences as well as probes and primers comprising
10 part of said nucleotide sequences and antibodies against polypeptides encoded by said nucleotide sequences. Finally, the present invention relates to the use of said compounds as an early marker for the future development of diseases such as cancer and diseases of the CNS and as a target for treatment and
15 prevention of these diseases.

Background

Several epidemiological analyses conducted in recent decades
20 indicate that the long-term consumption of "red" meat processed by different ways (including smoked or air-dried meat and meat as component of sausages consumed rare, undercooked or grilled) can be regarded as a risk factor for colon cancer (World Cancer Report 2007, zur Hausen 2012). "Red" meat is regarded as
25 comprising beef, pork, mutton, lamb and goat meat, in contrast to "white" meat (poultry meat/fish).

Thus far, chemical carcinogenic substances being produced during roasting, grilling, barbecuing, smoking and air-drying
30 were blamed as risk factors for cancer. However, often the fact was disregarded that the same substances are also produced in comparable concentrations during analogous ways of preparation of poultry meat/fish. Accordingly, this does not support the assumption that these chemical substances play an exclusive
35 role as regards the development of colon cancer. Since, in

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addition, the current epidemiological analyses suggest that beef is the main risk factor it has been postulated that an additional species-specific - presumably infectious - factor contributes to the triggering of this type of cancer (zur Hausen, 2012). The results of the correlation of analyses of the global spreading of domesticated bovine species with the global incidence of colon cancer seem to suggest that the consumption of meat of bovine species stemming from European/Asian cattle (*Bos taurus*) but not from breedings of zebu, water buffalo or yak might be of importance as a main risk factor (zur Hausen, 2015)

Thus, the technical problem underlying the present invention is to identify specific nucleotide sequences that might be associated with diseases such as cancer or diseases of the CNS and, thus, to provide means for diagnosis and therapy.

Brief Description of the Present Invention

20

The solution to said technical problem is achieved by providing the embodiments characterized in the claims.

During the experiments resulting in the present invention sera of cattle were screened for infectious agents - starting from the assumption that the presence in sera is also indicative for the presence of these agents in "red" meat. Sera from healthy cows were screened and new viral nucleic acid components could be isolated. The DNA sequences and open reading frames of several of these components showed a recognizable relationship to two sequences which were already described for transmissible spongiform encephalopathies (TSE) for TSE-diseases of sheep, cattle and humans.

The TSE isolates have also been suspected to play a role in cancer induction (Manuelidis, 2011), thus, it is reasonable to assume that the viral sequences described might be associated with the development of diseases like cancer, specifically colon and breast cancers but also Hodgkin's disease and others, and diseases of the CNS (Multiple sclerosis MS, amyotrophic lateral sclerosis, transmissible spongiforme encephalopathies/ Prion-linked diseases, Parkinson's disease, Alzheimer disease).

Brief description of the drawings

Abbreviations for Figures 1-4: Rep = replication protein; CP = capsid protein

CMI: cattle milk isolate

HCBI: healthy cattle blood isolate

MSCI: MS brain isolate

MSSI: MS serum isolate

Sphinx: slow progressive hidden infection of variable (X) latency

Figure 1:

Group 1 - Isolates from bovine serum, bovine milk and multiple sclerosis (MS) brain samples (post mortem) - all related to Sphinx1.76

(a) HCBI6.252 (2522 bp) (Healthy Cattle Blood Isolate; identical to CMI1.252 (Cow Milk Isolate)).

(b) HCBI6.159 (1591 bp): A deletion in HCBI6.252 apparently resulted in HCBI6.159 - both were rescued independently from the bovine serum using back-to-back primer, i.e. circular DNA

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molecules and not an artefact. This could indicate that these infectious organisms have 2 forms - a large and small molecule related to or complementing each other

(c) MSBI1.176 (Multiple Sclerosis Brain Isolate) (1766 bp) - 98% similar to Sphinx1.76

(d) MSBI2.176 (1766 bp) - isolated from the same MS-brain sample as MSBI1.176

(e) CMI1.252 (2523 bp) (Cow Milk Isolate; identical to HCBI6.252)

(f) CMI2.214 (2148 bp)

(g) CMI3.168 (1687 bp)

(h) CMI4.158 (1583 bp)

The isolates were all generated by using back-to-back primers designed on the replication gene of Sphinx1.76.

Primers (several isolates were isolated twice by applying both primer pairs independently).

Nn (forward GGATTAATGCCAATGATCC), Xn (reverse CTTTGCCTGTTTCTCTCG), and/or No (forward GAGGACGAATTAATATTACAAGTC), Xo (reverse GTTCTCGTTTTCTTGGTAA)

Figure 2:

Group 2: Isolate HCBI7.228 (2280bp) (Healthy Cattle Blood Isolate) related to Sphinx2.36

This sample was generated by PCR from bovine serum using back-to-back primers

Primers: Nd (forward CAGATTGCAAAGCCTGTAATTCAT), Xd (reverse CTAAGGCAGATCAACACAGGGATA)

Figure 3:

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Group 3: Isolates from bovine serum and multiple sclerosis serum and MS brain samples (post mortem) - distantly related to known ssDNA viruses

5 Nucleotide sequences of (a) HCB18.215 (2152 bp) and (b) HCB19.212 (2121 bp) (Healthy Cattle Blood Isolate) as well as (c) MSS12.225 (2259 bp) (Multiple Sclerosis Serum Isolate). An identical sequence (MSBI3.224) to MSS12.225 was also isolated from an MS-brain sample.

These HCB1 isolates were generated as follows:

10 Serum samples were subjected to ultracentrifugation on Optiprep gradient centrifugation. The gradient was fractionated, DNA extracted from fractions and subjected to rolling circle amplification. Products were digested with BamHI or EcoRI enzymes. Products were cloned and sequenced. Complete genomes
15 were obtained by amplification of original DNA samples with back-to-back primers designed on the respective gradient clones. Complete genomes were sequenced in full.

The MSS1 isolate (as well as the clone MSBI3.224 from the MS-brain) was obtained after rolling circle amplification of the
20 extracted DNA from MS serum and MS brain, restriction enzyme digestion, cloning of the product and subsequent sequencing. The complete genome was obtained by amplification with back-to-back primers designed on the original clone. The complete genome was
25 sequenced in full.

Figure 4:

Group 4 - distantly related to *Psychrobacter* spp plasmid: Nucleotide sequence of MSS11.162 and putative open reading
30 frames

MS-serum isolate MSS11.162 (group 4) was generated by rolling circle amplification of a multiple MS-serum sample. The product

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 was digested with restriction enzyme HindIII, cloned and
 sequenced.

Figure 5:

5 Genome organisation of 4 groups of isolates

The isolates are grouped according to their sequence similarity to the Sphinx1.76 genome (group 1), Sphinx2.36 (group 2), myco-like Gemycircularviruses (group 3) and Psychrobacter spp. Plasmid (group 4).

10 (A) group 1

(B) groups 2,3 and 4

Figure 6:

15 Alignment of a replication gene/ iteron-like repeat region
 between 8 isolates and Sphinx1.76

Figure 7:

20 Schematic outline of latent infection of different types of
 brain cells with Herpes type genomes and BMF factor

Figure 8:

25 Spontaneous reactivation of Herpes DNA in a cell concomitantly
 infected by Herpes and BMF DNA

Amplification of BMF and inhibition of Herpes DNA replication.

Figure 9:

Schematic outline of the recognition of foreign antigens by the
 immune system, T cell response

30 Figure 10:

Mononuclear inflammatory cells surrounding a small vein in an
 early lesion

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 Lymphocytes, monocytes, plasma cells and occasional macrophages.

Figure 11:

Advancing age of the lesion (plaque) on the left with normal

5 white matter on the right

Macrophages are present in the lesion (arrows) and at the interphase.

Figure 12:

10 Schematic outline of the pathogenesis concept for multiple sclerosis

EBV is used as an example for the role of Herpes-type viruses.

Figure 13:

15 Tentative Scheme of MS pathogenesis

Detailed description of the present invention

20 In the present application a new concept for the pathogenesis of multiple sclerosis and cancer is presented: Interaction of an Amplifying Virus and the amplified DNA of a Bovine Milk (or serum) Factor (BMF)

25 Introduction

The incidence of multiple sclerosis (MS) increased in several parts of the world (reviewed in Kurtzke, 2000, Alcalde-Cabero et al., 2013). This increase has been mainly attributed to environmental factors. Migrants from high to lower risk areas
 30 retain the MS risk of their birth place only if they are at least age 15 at migration, frequently interpreted to be due to an infection acquired during early childhood (reviewed in

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Kurtzke, 2000). Clustering of cases and the geographic **PCT/EP2015/001399**
epidemiology has also been widely discussed: A rising incidence
of MS was noted in females linked to urbanization (*Kotzamani et*
al., 2012).

5

Demyelination is a characteristic feature of MS lesions. Four
fundamentally different patterns of demyelination were found,
defined on the basis of myelin protein loss, the location and
extension of plaques, the patterns of oligodendrocyte
10 destruction, and the immunopathological evidence of complement
activation (*Lucchinetti et al., 2000, Metz et al., 2014*). At a
given time point of the disease the patterns of demyelination
were heterogeneous between patients; but they were homogenous
within multiple active lesions from the same patient,
15 potentially pointing to different contributing factors.

Two of the risk factors seem to deserve special attention: the
relatively consistent results pointing to a possible role of
different, predominantly herpes-group viruses, and the
20 consumption of fresh cow milk, potentially including other
dairy products (see below). In addition, Vitamin D deficiency
plays a role as a risk factor.

- Viral Risk Factors

25 Apparently all Herpes virus types share two properties which
seem to be relevant for the subsequent discussion:

During their persistence in a latent stage, spontaneous
reactivation may occur, in part regulated by specific gene
functions, partly also by epigenetic mechanisms (*reviewed in*
30 *Nicoll et al., 2012, Grinde, 2013*). Reactivation may also be
triggered by interaction with extracellular cytokines, such as
transforming growth factor β .

Spontaneous induction of a lytic cycle has been observed for virtually every human pathogenic Herpes virus type. The high antibody titers against Epstein-Barr virus structural proteins in EBV-positive Burkitt's lymphomas and nasopharyngeal cancers (reviewed in Henle, W. and Henle, G., 1977) may serve here as one example. Reactivations of human Herpes virus type 6, Varicella-Zoster virus, Herpes simplex virus and others are not rare events and may affect a number of different cell types (Hu Knox et al., 2000).

10

A second remarkable property of herpes virus infection represents the amplification of various double- or single-stranded small DNA virus genomes upon infection of cells containing such DNAs in a latent state. This has been noted for human and monkey Polyoma viruses, JC and SV40, for human and bovine Papilloma viruses, as well as for single-stranded Adeno-associated (AAV) and Anello-/TT-viruses (Schlehofer and zur Hausen, 1990, Heilbronn et al., 1993, Borkosky et al., 2012). The Herpes-group viruses used in these studies were Herpes simplex virus, human cytomegalovirus and Epstein-Barr virus. The potential to induce amplification of latent small viral DNA genomes is also shared by Adeno- and Vaccinia viruses (Schlehofer and zur Hausen, 1990). The helper effect of Herpes- and adenovirus-induced amplification of parvoviruses has been intensively studied for adeno-associated viruses. The replication of the latter seems to depend on this helper effect but in turn leads to a reduction of Herpes- or adenovirus replication due to the preferential amplification of small viral DNA (Schlehofer et al., 1983, Matz et al., 1984, Bantel-Schaal and zur Hausen, 1988, Schmitt et al., 1989, Schlehofer and zur Hausen, 1990, Heilbronn et al., 1990a, Heilbronn et al., 1990b).

WO 2016/005054 Spontaneous induction of Herpes-group viruses and the **PCT/EP2015/001399** amplification of latent small viral DNA form the basis for the subsequent postulation of the mechanism underlying MS development.

5

- Bovine milk factor

Several reports noted a correlation between consumption of non-pasteurized cow milk and MS development (*Murray TJ. 1976, Sepčić et al., 1993, Malosse and Perron, 1993*), whereas others
10 stressed long-time consumption of cow milk as a risk factor, in particular when consumed in the early phase of life (*Agranoff and Goldberg, 1974, Christensen, 1975, Warren, 1984, Butcher, 1976, 1986, Winer et al., 2001, Munger et al., 2011a*).

15 If a specific factor in cow milk exists which increases the risk for MS development, one can anticipate a protective role of long-term breast-feeding. Long-term breast-feeding (for six months and more) has indeed repeatedly been reported as having a protective effect for MS development (*Christensen, 1975, Warren, 1984, Tarrats et al., 2002, Conradi et al., 2013*). The
20 existence of a cow milk factor would also not exclude a specific genetic predisposition for the development of MS. A monogenic predisposition for MS has been reported in a chromosomal localization close to BRCA1 (*Holzmann et al.,*
25 *2013*).

- Vitamin-D deficiency

A role of vitamin-D deficiency has repeatedly been implicated for the initiation of MS (*reviewed in Ascherio et al. 2012,*
30 *2013*).

A convincing relationship between vitamin D deficiency and Epstein Barr Virus reactivation originates from early studies

on EBV reactivation by transforming growth factor beta (TGF- β).

A serum factor, purified and labeled as Epstein-Barr virus-inducing factor (EIF) (*Bauer et al., 1982*) proved to be identical to the subsequently described TGF- β molecule (*Frolik et al., 1983, Bauer et al., 1991*). TGF- β in turn is negatively regulated by activated vitamin D receptors (*Isik et al., 2012, Ito et al., 2013, Zerr et al., 2014*). This could very well explain the season-related preferential onset of MS and of exacerbations.

10 The relationship between low vitamin D and EBV reactivation is further supported by studies describing a correlation between low vitamin D and elevated immunoreactivity against Epstein-Barr virus prior to the clinical manifestation of multiple sclerosis (*Munger et al., 2011b, Décard et al., 2012*) and a
15 higher rate of EBV excretion of EBV-positive MS patients in comparison to EBV-positive healthy controls (*Yea et al., 2013*).

Thus, at least two factors have been implicated as potential etiological contributors for both diseases of the CNS (e.g. MS)
20 and cancer (e.g. colon and breast cancer): vitamin D deficiency and the reactivation of various herpes group viruses, mainly Epstein-Barr virus (EBV), human herpes virus type 6, and varicella-zoster virus. According to the present invention the identification of several novel types of small circular single-
25 stranded DNAs, presumably of viral origin, from cattle sera of the present invention and commercially available dairy products, show a unifying concept. The inventors have demonstrated in the present invention that co-infection of cells with herpes-group viruses and small single-stranded or
30 double-stranded DNA viruses results in an substantial amplification of small viral DNA with partial inhibition of the herpes virus. Some of the molecules identified in dairy cattle sera and milk are distantly related to DNA reported in prion-

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linked brain lesions and have been found in two autopsy lesions of patients with multiple sclerosis. The amplification of these single-stranded DNA molecules by reactivation of a co-latently persisting herpes virus genome could result in their
5 amplification and evoking a local immune response resulting in destruction of the affected brain cells. This model could in part explain the North-South incidence gradient of multiple sclerosis, which is thought to be linked to vitamin-D deficiency and herpes virus reactivation (c.f. Fig. 12 and 13).

10

In addition, the full-length genomes of the isolates from MS brains and sera were isolated and re-circularized before transfection into the human cell line 293TT. Transfected cells were harvested on day 3 and total RNA extracted using the miRNA
15 Easy Kit (Qiagen). Samples were further purified (DNase digestion, ribosome removal) and subjected to high throughput RNA sequencing. RNA transcripts have been obtained for MSBI1,176, MSBI2,176 (Group 1), MSSI2.225 (Group 3) and MSSI1.162 (Group 4). The RNA transcripts clearly show that the
20 isolates replicate in human cells.

The inventors consider Vitamin D deficiency and herpes virus reactivations as risk factors also for breast and colon cancers. Reactivation of dual latent infections within the same
25 cell, outlined above for multiple sclerosis pathogenesis, could therefore also play a particular important role in the aetiology of these cancers.

Thus, it is considered by the inventors that multiple sclerosis
30 (MS) and also the other below mentioned diseases result from

- Latent infections of the same cell with two different infectious agents, one of them most likely a herpes-type virus (in particular EBV, HHV-6, VZV, but also HSV, HHV-7),

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the other one acquired by bovine milk consumption (bovine milk factor - BMF) as the first event. Each of them latently infects individual cells, but occasionally genomes of both agents occur within the same cell.

- 5 • Reactivation of the herpes-type virus most frequently, but not only, Epstein Barr virus (EBV) to a lytic cycle as a second precondition. For EBV this is probably linked to increased levels of transforming growth factor β (TGF β) which is negatively regulated by activated vitamin D
- 10 receptors;
- As third event, amplification of BMF, resulting in partial suppression of Herpes-type DNA synthesis and formation of BMF particles or spreading of its nucleic acid to neighbouring cells via neuronal interconnections;
- 15 • This is followed by an infection of neighbouring cells with expression of BMF protein;
- Finally, T-cell response against BMF leads to the destruction of affected cells and in case of MS to plaque formation. This supports the clinical observation of the
- 20 focal appearance of lesions, commonly starting from a central vein and the intensive localized immune response in early lesions.

Transmissions of agents present in milk or dairy products may

25 lead to latent infections in human brain cells followed by amplification of these agents in case of co-latency and spontaneous induction of a Herpes virus DNA or Herpes virus - like DNA. Potential BMF candidate agents are described in Examples 2-5 and the accompanying figures.

30

The presence of presumably circular single stranded DNA related to Sphinx-sequences, Anello-, Circo-, and Gemycircularvirus

families, as well as *Psychrobacter* species in cattle sera (see Examples 2-5), in commercially available milk samples, as well as in florid MS lesions and MS serum permits the development of a concept for MS pathogenesis. It integrates observations of involvement of Herpes-type viruses, most prominently of EBV, of their property to amplify small double- and single-stranded DNA viruses, of viral cow milk factors, of vitamin-D deficiency, the EBV inducing property of TGF β , and the partial season dependence of MS onset and of exacerbation in the course of disease. This concept is schematically outlined in Figures 7-13.

An initial dual latent infection of the same or closely flanking cells by a herpes virus genome and the postulated BMF, followed by a trigger for Herpes virus reactivation and the subsequent preferential amplification of single-stranded DNA are defined as the primary event. In the case of latent EBV infection, vitamin D deficiency with the subsequent up-regulation of TNF- β as an EBV-inducing factor could be the important trigger for up-regulation. Probably abortive infection of neighbouring cells with viral antigen expression results in an active T-cell response and the destruction of the affected cells. The frequently described seasonality of MS onset and of new rounds of MS exacerbations, the repeatedly reported North-South gradient of MS incidence should reflect the degree of sun-light exposure, negatively correlating vitamin D levels with TGF β concentration and EBV reactivation.

Thus, the inventors anticipate the presence of different BMF sequences also in susceptible normal human brain cells in a latent form. The remarkable heterogeneity of the BMF isolates may also find its reflection in variations for pathologic characteristics of MS in humans (*Lucchinetti et al., 2000, Metz*

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et al., 2014). It would not be too surprising if eventually
"high" and "low" risk types will be identified, in a certain
analogy to human papillomavirus pathogenicity (zur Hausen,
1985). The majority of those carriers will not develop MS,
5 since the latter should require latent co-infection of a BMF-
positive cell with a Herpes-type virus and spontaneous
induction of the latter. This should be a rare event,
increasing, however, under conditions resulting in frequent
Herpes virus reactivations.

10

As a final point, it should be of interest to also apply this
concept to other presumably autoimmune diseases and certain
cancers occurring at increased frequency under conditions of
vitamin D deficiency. As far as cancers are concerned, this
15 specifically accounts for colon- and breast cancer, and
possibly for ovarian, prostate, pancreatic cancer and lung
cancers.

The risk for insulin-dependent diabetes mellitus has been
20 repeatedly linked to cow milk consumption and vitamin D
deficiency (reviewed in Scott, 1990, in Grant, 2006, in
Hyppönen et al, 2010). The latter system seems to come
particularly close to the MS situation.

25 Accordingly, the present invention relates to an HCBI, MSBI,
MSSI or CMI polynucleic acid comprising:

- (a) a nucleotide sequence depicted in any one of Figures 1
to 4;
- (b) a nucleotide sequence having at least 90% identity to a
30 nucleotide sequence of (a);
- (c) a fragment of a nucleotide sequence of (a) or (b);
- (d) a nucleotide sequence being complementary to a
nucleotide sequence of (a), (b) or (c); or

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(e) a nucleotide sequence which is redundant as a result of the degeneracy of the genetic code compared to any of the above-given nucleotide sequences.

5 The term "polynucleic acid" refers to a single-stranded or double-stranded nucleic acid sequence. A polynucleic acid may consist of deoxyribonucleotides or ribonucleotides, nucleotide analogues or modified nucleotides or may have been adapted for diagnostic or therapeutic purposes. A polynucleic acid may also
10 comprise a double stranded cDNA clone which can be used, for example, for cloning purposes.

The HCBI, MSBI, MSSSI or CMI polynucleic acids of the invention can be prepared according to well-known routine methods, for
15 example, by (a) isolating the entire DNA or RNA from a sample, (b) detecting the HCBI, MSBI, MSSSI or CMI sequence by hybridization or PCR and (c) cloning of the HCBI, MSBI, MSSSI or CMI sequence into a vector.

20 Also included within the present invention are sequence variants of the polynucleic acid of the invention containing either deletions and/or insertions of one or more nucleotides, especially insertions or deletions of one or more codons, mainly at the extremities of oligonucleotides (either 3' or 5') and
25 which show at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to said polynucleic acid sequences of the invention. Polynucleic acid sequences according to the present invention which are similar to the sequences as shown in Figures 1 to 4 can be characterized and isolated according to any of the
30 techniques known in the art, such as amplification by means of sequence-specific primers, hybridization with sequence-specific probes under more or less stringent conditions, sequence

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determination of the genetic information of HCBI, MSBI, MSSSI or
CMI etc.

The present invention also provides fragments of the nucleotide
5 sequences of the present invention described above that harbour
a replication gene which codes for a replication protein. An
autonomous replicating nucleotide sequence comprises a
nucleotide sequence of the replication gene or a fragment
thereof which is capable of inducing autonomous replication.
10 Replication protein represents an endonuclease which binds
single-stranded DNA inducing a single-stranded cut at or near
the origin of replication (Wolds, 1997). The skilled person can
derive at such fragments capable of inducing autonomous
replication without undue experimentation. Such fragments may
15 have a length of at least 45, at least 55, or at least 65 nt.

The person skilled in the art can easily determine which nucleic
acid sequences are related to a nucleotide sequence of Figures 1
to 4 or which fragments are still capable of replicating
20 autonomously by using standard assays.

The present invention also provides polynucleic acid sequences
which are redundant as a result of the degeneracy of the genetic
code compared to any of the above-given nucleotide sequences.
25 These variant polynucleic acid sequences will thus encode the
same amino acid sequence as the polynucleic acids they are
derived from.

The HCBI, MSBI, MSSSI or CMI polynucleic acids of the invention
30 might be present as an extrachromosomal episome, might be
integrated into the host's genome and/or might be linked to a
host cell DNA.

The present invention also relates to an oligonucleotide primer
35 comprising or consisting of part of a polynucleic acid as

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defined above, with said primer being able to act as primer for specifically sequencing or specifically amplifying HCBI, MSBI, MSSI or CMI polynucleic acid of the invention.

5 The term "primer" refers to a single stranded DNA oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. The length and the sequence of the primer must be such that they
10 allow priming the synthesis of the extension products. Preferably the primer is about 5-50 nucleotides. Specific length and sequence will depend on the complexity of the required DNA or RNA targets, as well as on the conditions of primer use such as temperature and ionic strength.

15

The fact that amplification primers do not have to match exactly with a corresponding template sequence to warrant proper amplification is amply documented in the Literature. The amplification method used can be, for example, polymerase chain
20 reaction (PCR), ligase chain reaction (LCR), nucleic acid sequence-based amplification (NASBA), transcription-based amplification system (TAS), strand displacement amplification (SDA) or amplification by means of Qb replicase or any other suitable method to amplify nucleic acid molecules using primer
25 extension. During amplification, the amplified products can be labelled either using labelled primers or by incorporating labelled nucleotides.

Labels may be isotopic (^{32}P , ^{35}S , etc.) or non-isotopic (biotin, digoxigenin, etc.). The amplification reaction is repeated
30 between 20 and 70 times, advantageously between 25 and 45 times.

Any of a variety of sequencing reactions known in the art can be used to directly sequence the viral genetic information and
35 determine the ORF by translating the sequence of the sample into

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the corresponding amino acid sequence. Exemplary sequencing reactions include those based on techniques developed by Sanger or Maxam and Gilbert. It is also contemplated that a variety of automated sequencing procedures may be utilized when performing the subject assays including sequencing by mass spectrometry (see, for example: PCT publication WO 94/16101). It will be evident to one skilled in the art that, for example the occurrence of only two or three nucleic bases needs to be determined in the sequencing reaction.

10

Preferably, these primers are about 5 to 50 nucleotides long, more preferably from about 10 to 25 nucleotides. Most preferred are primers having a length of at least 13 bases.

15 The present invention also relates to an oligonucleotide probe comprising or consisting of part of an HCBI, MSBI, MSSSI or CMI polynucleic acid as defined above, with said probe being able to act as a hybridization probe for specific detection of a HCBI, MSBI or CMI polynucleic acid according to the invention.

20

The probe can be labelled or attached to a solid support.

The term "probe" refers to single stranded sequence-specific oligonucleotides which have a sequence which is complementary to the target sequence of an HCBI, MSBI, MSSSI or CMI polynucleic acid to be detected.

25

Preferably, these probes are about 5 to 50 nucleotides long, more preferably from about 10 to 25 nucleotides. Most preferred are probes having a length of at least 13 bases.

30

The term "solid support" can refer to any substrate to which an oligonucleotide probe can be coupled, provided that it retains its hybridization characteristics and provided that the background level of hybridization remains low. Usually the solid

35

substrate will be a microtiter plate, a membrane (e.g. nylon or nitrocellulose) or a microsphere (bead). Prior to application to the membrane or fixation it may be convenient to modify the nucleic acid probe in order to facilitate fixation or improve the hybridization efficiency. Such modifications may encompass homopolymer tailing, coupling with different reactive groups such as aliphatic groups, NH₂ groups, SH groups, carboxylic groups, or coupling with biotin or haptens.

10 The oligonucleotides according to the present invention, used as primers or probes may also contain or consist of nucleotide analogues such as phosphorothioates, alkylphosphorates or peptide nucleic acids or may contain intercalating agents. These modifications will necessitate adaptations with respect to the conditions under which the oligonucleotide should be used to obtain the required specificity and sensitivity. However, the eventual results will be essentially the same as those obtained with the unmodified oligonucleotides.

20 The introduction of these modifications may be advantageous in order to positively influence characteristics such as hybridization kinetics, reversibility of the hybrid-formation, biological stability of the oligonucleotide molecules, etc.

25 The polynucleic acids of the invention may be comprised in a composition of any kind. Said composition may be for diagnostic, therapeutic or prophylactic use.

The present invention also relates to a recombinant expression vector comprising an HCBI, MSBI, MSSI or CMI polynucleic acid of the invention as defined above operably linked to prokaryotic, eukaryotic or viral transcription and translation control elements as well as host cells containing such vector.

35 The term "vector" may comprise a plasmid, a cosmid, an

artificial chromosome, a phage, or a virus or a transgenic non-human animal. Particularly useful for vaccine development may be HCBI, MSBI, MSSI or CMI recombinant molecules, BCG or adenoviral vectors, as well as avipox recombinant viruses.

5

The term "recombinant expression" used within the context of the present invention refers to the fact that the polypeptides of the present invention are produced by recombinant expression methods be it in prokaryotes, or lower or higher eukaryotes as
10 discussed in detail below.

The term "host cell" refers to cells which can be or have been, used as recipients for a recombinant vector or other transfer polynucleotide, and include the progeny of the original cell
15 which has been transfected.

It is understood that the progeny of a single parental cell may not necessarily be completely identical in morphology or in genomic or total DNA complement as the original parent, due to
20 natural, accidental, or deliberate mutation or recombination.

The term "lower eukaryote" refers to host cells such as yeast, fungi and the like. Lower eukaryotes are generally (but not necessarily) unicellular. Preferred lower eukaryotes are yeasts,
25 particularly species within Saccharomyces, Schizosaccharomyces, Kluiveromyces, Pichia (e. g. Pichia pastoris), Hansenula (e. g. Hansenula polymorph), Schwaniomyces, Schizosaccharomyces, Yarowia, Zygosaccharomyces and the like. Saccharomyces cerevisiae, S. carlsbergensis and K. lactis are the most
30 commonly used yeast hosts, and are convenient fungal hosts.

The term "higher eukaryote" refers to host cells derived from higher animals, such as mammals, reptiles, insects, and the like. Presently preferred higher eukaryote host cells are
35 derived from Chinese hamster (e. g. CHO), monkey (e. g. COS and

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Vero cells), baby hamster kidney (BHK), pig kidney (PK15), rabbit kidney 13 cells (RK13), the human osteosarcoma cell line 143 B, the human cell line HeLa and human hepatoma cell lines like Hep G2, the 293TT cell line (Buck et al., 2004) and
5 insectcell lines (e.g. *Spodoptera frugiperda*). The host cells may be provided in suspension or flask cultures, tissue cultures, organ cultures and the like. Alternatively the host cells may also be transgenic non-human animals.

10 The term "prokaryotes" refers to hosts such as *E. coli*, *Lactobacillus*, *Lactococcus*, *Salmonella*, *Streptococcus*, *Bacillus subtilis* or *Streptomyces*. Also these hosts are contemplated within the present invention.

15 The segment of the HCBI, MSBI, MSSI or CMI DNA encoding the desired sequence inserted into the vector sequence may be attached to a signal sequence. Said signal sequence may be that from a non-HCBI, MSBI, MSSI or CMI source, but particularly preferred constructs according to the present invention contain
20 signal sequences appearing in the HCBI, MSBI, MSSI or CMI genome before the respective start points of the proteins.

Higher eukaryotes may be transformed with vectors, or may be infected with a recombinant virus, for example a recombinant
25 vaccinia virus. Techniques and vectors for the insertion of foreign DNA into vaccinia virus are well known in the art, and utilize, for example homologous recombination. A wide variety of viral promoter sequences, possibly terminator sequences and poly(A)-addition sequences, possibly enhancer sequences and
30 possibly amplification sequences, all required for the mammalian expression, are available in the art. Vaccinia is particularly preferred since vaccinia halts the expression of host cell proteins. For vaccination of humans the avipox and Ankara Modified Virus (AMV) are particularly useful vectors.

Also known are insect expression transfer vectors derived from baculovirus Autographa californica nuclear polyhedrosis virus (AcNPV), which is a helper-independent viral expression vector.

5 Expression vectors derived from this system usually use the strong viral polyhedrin gene promoter to drive the expression of heterologous genes. Different vectors as well as methods for the introduction of heterologous DNA into the desired site of baculovirus are available to the person skilled in the art for

10 baculovirus expression. Also different signals for posttranslational modification recognized by insect cells are known in the art.

The present invention also relates to a polypeptide having an amino acid sequence encoded by an HCBI, MSBI, MSSI or CMI polynucleic acid as defined above, or a part or an analogue thereof being substantially similar and biologically equivalent.

15

The term "polypeptide" refers to a polymer of amino acids and does not refer to a specific length of the product. Thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. This term also does not refer to or exclude post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the

20

25 like. Included within the definition are, for example, polypeptides containing one or more analogues of an amino acid (including, for example, unnatural amino acids, peptide nucleic acid (PNA), etc.), polypeptides with substituted linkages, as well as other modifications known in the art, both naturally

30 occurring and non-naturally occurring.

The polypeptides according to the present invention contain preferably at least 3, preferably 4 or 5 contiguous HCBI, MSBI, MSSI or CMI amino acids, 6 or 7 preferably however at least 8

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contiguous HCBI, MSBI, MSSSI or CMI amino acids, at least 10 or
at least 15.

The polypeptides of the invention, and particularly the
5 fragments, can be prepared by classical chemical synthesis. The
synthesis can be carried out in homogeneous solution or in solid
phase. The polypeptides according to this invention can also be
prepared by means of recombinant DNA techniques.
The present invention also relates to a method for production of
10 a recombinant polypeptide as defined above, comprising: (a)
transformation of an appropriate cellular host with a
recombinant vector, in which a polynucleic acid or a part
thereof as defined above has been inserted under the control of
the appropriate regulatory elements, (b) culturing said
15 transformed cellular host under conditions enabling the
expression of said insert, and (c) harvesting said polypeptide.

The present invention also relates to an antibody raised upon
immunization with at least one polypeptide as defined above,
20 with said antibody being specifically reactive with any of said
polypeptides, and with said antibody being preferably a
monoclonal antibody. The term „antibody“, preferably, relates to
antibodies which consist essentially of pooled monoclonal
antibodies with different epitopic specificities, as well as
25 distinct monoclonal antibody preparations. Monoclonal antibodies
are made from an antigen containing, e.g., a polypeptide encoded
by an HCBI, MSBI, MSSSI or CMI polynucleic acid of the invention
or a fragment thereof by methods well known to those skilled in
the art. As used herein, the term „antibody“ (Ab) or „monoclonal
30 antibody“ (Mab) is meant to include intact molecules as well as
antibody fragments (such as, for example, Fab and F(ab')₂
fragments) which are capable of specifically binding to protein.
Fab and F(ab')₂ fragments lack the Fc fragment of intact
antibody, clear more rapidly from the circulation, and may have
35 less non-specific tissue binding than an intact antibody. Thus,

WO 2016/005054 these fragments are preferred, as well as the products of a FAB **PCT/EP2015/001399** or other immunoglobulin expression library. Moreover, antibodies useful for the purposes of the present invention include chimerical, single chain, and humanized antibodies.

5 The present invention also relates to diagnostic and therapeutic approaches using cell-mediated immune responses.

10 Preferably, the antibody or antigen binding fragment thereof carries a detectable label. The antibody/fragment can be directly or indirectly detectably labeled, for example, with a radioisotope, a fluorescent compound, a bioluminescent compound, a chemiluminescent compound, a metal chelator or an enzyme. Those of ordinary skill in the art will know of other suitable
15 labels for binding to the antibody, or will be able to ascertain such, using routine experimentation.

The present invention also relates to a diagnostic kit for use in determining the presence of an HCBI, MSBI or CMI polynucleic
20 acid or polypeptide of the invention, said kit comprising a primer, a probe, and/or an antibody of the invention. Said kit may have any format well known to the person skilled in the art, e.g. can be an ELISA-based kit.

25 The present invention also relates to a method for the detection of an HCBI, MSBI, MSSI or CMI polynucleic acid according to the invention present in a biological sample, comprising: (a) optionally extracting sample polynucleic acid, (b) amplifying the polynucleic acid as described above with at least one primer
30 as defined above, optionally a labelled primer, and (c) detecting the amplified polynucleic acids.

The term "polynucleic acid" can also be referred to as analyte strand and corresponds to a single- or double-stranded
35 polynucleic acid molecule.

The term "labelled" refers to the use of labelled nucleic acids. This may include the use of labelled nucleotides incorporated during the polymerase step of the amplification or labelled
5 primers, or by any other method known to the person skilled in the art.

The present invention also relates to a method for the detection of an HCBI, MSBI, MSSI or CMI polynucleic acid according to the
10 invention present in a biological sample, comprising: (a) optionally extracting sample polynucleic acid, (b) hybridizing the polynucleic acid as described above with at least one probe as defined above, and (c) detecting the hybridized polynucleic acids.

15 The hybridization and washing conditions are to be understood as stringent and are generally known in the art. However, according to the hybridization solution (SSC, SSPE, etc.), these probes should be hybridized at their appropriate temperature in order
20 to attain sufficient specificity.

According to the hybridization solution (SSC, SSPE, etc.), these probes should be stringently hybridized at their appropriate temperature in order to attain sufficient specificity. However,
25 by slightly modifying the DNA probes, either by adding or deleting one or a few nucleotides at their extremities (either 3' or 5'), or substituting some non-essential nucleotides (i. e. nucleotides not essential to discriminate between types) by others (including modified nucleotides or inosine) these probes
30 or variants thereof can be caused to hybridize specifically at the same hybridization conditions (i.e. the same temperature and the same hybridization solution). Also changing the amount (concentration) of probe used may be beneficial to obtain more specific hybridization results. It should be noted in this
35 context, that probes of the same length, regardless of their GC

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content, will hybridize specifically at approximately the same temperature in TMACI solutions.

Suitable assay methods for purposes of the present invention to
5 detect hybrids formed between the oligonucleotide probes and the
HCBI, MSBI, MSSI or CMI polynucleic acid sequences in a sample
may comprise any of the assay formats known in the art, such as
the conventional dot-blot format, sandwich hybridization or
reverse hybridization. For example, the detection can be
10 accomplished using a dot blot format, the unlabelled amplified
sample being bound to a membrane, the membrane being
incorporated with at least one labelled probe under suitable
hybridization and wash conditions, and the presence of bound
probe being monitored.

15

An alternative and preferred method is a "reverse" dot-blot
format, in which the amplified sequence contains a label. In
this format, the unlabelled oligonucleotide probes are bound to
a solid support and exposed to the labelled sample under
20 appropriate stringent hybridization and subsequent washing
conditions. It is to be understood that also any other assay
method which relies on the formation of a hybrid between the
polynucleic acids of the sample and the oligonucleotide probes
according to the present invention may be used.

25

The present invention also relates to a method for detecting a
polypeptide encoded by an HCBI, MSBI, MSSI or CMI polynucleic
acid of the present invention or an antibody against said
polypeptide present in a biological sample, comprising: (a)
30 contacting the biological sample for the presence of such
polypeptide or antibody as defined above, and (b) detecting the
immunological complex formed between said antibody and said
polypeptide.

35 The immunoassay methods according to the present invention may

utilize antigens from different domains of the new and unique polypeptide sequences of the present invention. It is within the scope of the invention to use for instance single or specific oligomeric antigens, dimeric antigens, as well as combinations
5 of single or specific oligomeric antigens. The HCBI, MSBI, MSSI or CMI antigens of the present invention may be employed in virtually any assay format that employs a known antigen to detect antibodies or cell-mediated immune responses. Thus, the present invention also encompasses the detection of cell-
10 mediated immune responses against HCBI, MSBI, MSSI or CMI antigens and the application of therapeutic interferences based on cell-mediated immune responses against HCBI, MSBI, MSSI or CMI antigens.

15 Of course, an assay format that denatures the HCBI, MSBI, MSSI or CMI conformational epitope should be avoided or adapted. A common feature of all of these assays is that the antigen is contacted with the body component suspected of containing HCBI, MSBI, MSSI or CMI antibodies under conditions that permit the
20 antigen to bind to any such antibody present in the component. Such conditions will typically be physiologic temperature, pH and ionic strength using an excess of antigen. The incubation of the antigen with the specimen is followed by detection of immune complexes comprised of the antigen.

25 Design of the immunoassays is subject to a great deal of variation, and many formats are known in the art. Protocols may, for example, use solid supports, or immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the
30 labels may be, for example, enzymatic, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the immune complex are also known; examples of which are assays which utilize biotin and avidin or streptavidin, and enzyme-labeled and mediated immunoassays, such
35 as ELISA assays.

The immunoassay may be in a heterogeneous or in a homogeneous format, and of a standard or competitive type. In a heterogeneous format, the polypeptide is typically bound to a solid matrix or support to facilitate separation of the sample from the polypeptide after incubation. Examples of solid supports that can be used are nitrocellulose (e. g., in membrane or microtiter well form), polyvinyl chloride (e. g., in sheets or microtiter wells), polystyrene latex (e. g., in beads or microtiter plates, polyvinylidene fluoride (known as Immulon), diazotized paper, nylon membranes, activated beads, and Protein A beads. The solid support containing the antigenic polypeptides is typically washed after separating it from the test sample, and prior to detection of bound antibodies. Both standard and competitive formats are known in the art.

In a homogeneous format, the test sample is incubated with the combination of antigens in solution. For example, it may be under conditions that will precipitate any antigen-antibody complexes which are formed. Both standard and competitive formats for these assays are known in the art.

In a standard format, the amount of HCBI, MSBI, MSSSI or CMI antibodies in the antibody-antigen complexes is directly monitored. This may be accomplished by determining whether (labelled) anti-xenogeneic (e. g. anti-human) antibodies which recognize an epitope on anti-HCBI, -MSBI, -MSSSI or -CMI antibodies will bind due to complex formation. In a competitive format, the amount of HCBI, MSBI, MSSSI or CMI antibodies in the sample is deduced by monitoring the competitive effect on the binding of a known amount of labelled antibody (or other competing ligand) in the complex.

Complexes formed comprising anti-HCBI, -MSBI, -MSSSI or -CMI antibody (or in the case of competitive assays, the amount of

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competing antibody) are detected by any of a number of known techniques, depending on the format. For example, unlabeled HCBI, MSBI, MSSSI or CMI antibodies in the complex may be detected using a conjugate of anti-xenogeneic Ig complexed with
5 a label (e. g. an enzyme label).

In an immunoprecipitation or agglutination assay format the reaction between the HCBI, MSBI, MSSSI or CMI antigens and the antibody forms a network that precipitates from the solution or
10 suspension and forms a visible layer or film of precipitate. If no anti-HCBI, -MSBI, -MSSSI or -CMI antibody is present in the test specimen, no visible precipitate is formed.

There currently exist three specific types of particle
15 agglutination (PA) assays. These assays are used for the detection of antibodies to various antigens when coated to a support. One type of this assay is the hemagglutination assay using red blood cells (RBCs) that are sensitized by passively adsorbing antigen (or antibody) to the RBC. The addition of
20 specific antigen/antibodies present in the body component, if any, causes the RBCs coated with the purified antigen to agglutinate.

To eliminate potential non-specific reactions in the
25 hemagglutination assay, two artificial carriers may be used instead of RBC in the PA. The most common of these are latex particles.

The solid phase selected can include polymeric or glass beads,
30 nitrocellulose, microparticles, microwells of a reaction tray, test tubes and magnetic beads. The signal generating compound can include an enzyme, a luminescent compound, a chromogen, a radioactive element and a chemiluminescent compound. Examples of enzymes include alkaline phosphatase, horseradish peroxidase and
35 beta-galactosidase. Examples of enhancer compounds include

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biotin, anti-biotin and avidin. Examples of enhancer compounds
binding members include biotin, anti-biotin and avidin.

The above methods are useful for evaluating the risk of
developing diseases like cancer or an autoimmune disease due to
the deleterious effects of the presence of a subgenomic HCBI,
MSBI, MSSSI or CMI polynucleotide sequence by itself or linked to
a particular host gene or gene fragment within the patient's
cells and allow taking appropriate counter measures.

Thus, the present invention also relates to an antisense
oligonucleotide or iRNA specific for the HCBI, MSBI, MSSSI or CMI
virus polynucleic acid of the invention.

The generation of suitable antisense oligonucleotides or iRNAs
includes determination of a site or sites within the HCBI, MSBI,
MSSSI or CMI polynucleic acid for the antisense interaction to
occur such that the desired effect, e.g., inhibition of
expression of the polypeptide, will result. A preferred
intragenic site is (a) the region encompassing the translation
initiation or termination codon of the open reading frame (ORF)
of the gene or (b) a region of the mRNA which is a "loop" or
"bulge", i.e., not part of a secondary structure. Once one or
more target sites have been identified, oligonucleotides are
chosen which are sufficiently complementary to the target, i.e.,
hybridize sufficiently well and with sufficient specificity, to
give the desired effect. In the context of this invention,
"hybridization" means hydrogen bonding, which may be Watson-
Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between
complementary nucleoside or nucleotide bases. "Complementary" as
used herein, refers to the capacity for precise pairing between
two nucleotides. For example, if a nucleotide at a certain
position of an oligonucleotide is capable of hydrogen bonding
with a nucleotide at the same position of a DNA or RNA molecule,
then the oligonucleotide and the DNA or RNA are considered to be

WO 2016/005054 complementary to each other at that **PCT/EP2015/001399** position. The oligonucleotide and the DNA or RNA are complementary to each other when a sufficient number of corresponding positions in each molecule are occupied by nucleotides which can hydrogen
5 bond with each other. Thus, "specifically hybridizable" and "complementary" are terms which are used to indicate a sufficient degree of complementarity or precise pairing such that stable and specific binding occurs between the oligonucleotide and the DNA or RNA target. It is understood in
10 the art that the sequence of an antisense compound does not need to be 100% complementary to that of its target nucleic acid to be specifically hybridizable. An antisense compound is specifically hybridizable when binding of the compound to the target DNA or RNA molecule interferes with the normal function
15 of the target DNA or RNA to cause a loss of utility, and there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target sequences under conditions in which specific binding is desired, i.e., in the case of therapeutic treatment.

20

"Oligonucleotide" (in particular in the context of antisense compounds) refers to an oligomer or polymer of ribonucleic acid (RNA) or deoxyribonucleic acid (DNA) or mimetics thereof. This term includes oligonucleotides composed of naturally-occurring
25 nucleobases, sugars and covalent internucleoside (backbone) linkages as well as oligonucleotides having non-naturally-occurring portions which function similarly. Such modified or substituted oligonucleotides are often preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for nucleic acid
30 target and increased stability in the presence of nucleases. While antisense oligonucleotides are a preferred form of the antisense compound, the present invention comprehends other oligomeric antisense compounds, including but not limited to
35 oligonucleotide mimetics such as are described below. The

antisense compounds in accordance with this invention comprise from about 8 to about 50 nucleobases (i.e. from about 8 to about 50 linked nucleosides). Particularly preferred antisense compounds are antisense oligonucleotides, even more preferably those comprising from about 15 to about 25 nucleobases. Antisense compounds include ribozymes, external guide sequences (EGS), oligonucleotides (oligozymes), and other short catalytic RNAs or catalytic oligonucleotides which hybridize to the target nucleic acid and inhibit its expression. The antisense compounds also include an iRNA comprising a sense sequence and an antisense sequence, wherein the sense and antisense sequences form an RNA duplex and wherein the antisense sequence comprises a nucleotide sequence sufficiently complementary to the nucleotide sequence of an HCBI, MSBI, MSSSI or CMI polynucleic acid of the present invention.

Alternatively, the invention provides a vector allowing to transcribe an antisense oligonucleotide of the invention, e.g., in a mammalian host. Preferably, such a vector is a vector useful for gene therapy. Preferred vectors useful for gene therapy are viral vectors, e.g. adenovirus, adeno-associated virus, herpes simplex virus, vaccinia, or, an RNA virus such as a retrovirus. Preferably, the retroviral vector is a derivative of a murine or avian retrovirus. Examples of such retroviral vectors which can be used in the present invention are: Moloney murine leukemia virus (MoMuLV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV) and Rous sarcoma virus (RSV). Most preferably, a non-human primate retroviral vector is employed, such as the gibbon ape leukemia virus (GaLV), providing a broader host range compared to murine vectors. Since recombinant retroviruses are defective, assistance is required in order to produce infectious particles. Such assistance can be provided, e.g., by using helper cell lines that contain plasmids encoding all of the structural genes of the retrovirus under the control of regulatory sequences

within the LTR. Suitable helper cell lines are well known to those skilled in the art. Said vectors can additionally contain a gene encoding a selectable marker so that the transduced cells can be identified. Moreover, the retroviral vectors can be modified in such a way that they become target specific. This can be achieved, e.g., by inserting a polynucleotide encoding a sugar, a glycolipid, or a protein, preferably an antibody. Those skilled in the art know additional methods for generating target specific vectors. Further suitable vectors and methods for in vitro- or in vivo-gene therapy are described in the literature and are known to the persons skilled in the art; see, e.g., WO 94/29469 or WO 97/00957. The HCBI, MSBI, MSSI or CMI polynucleotide sequences of the invention may also serve as a suitable vector itself, either composed solely of rearranged HCBI, MSBI, MSSI or CMI sequences or of chimeric HCBI, MSBI, MSSI or CMI host cell DNA sequences. In addition, the nucleotide sequences of the invention may be used for the construction of artificial chromosomes.

In order to achieve expression only in the target organ, the DNA sequences for transcription of the antisense oligonucleotides can be linked to a tissue specific promoter and used for gene therapy. Such promoters are well known to those skilled in the art.

Within an oligonucleotide structure, the phosphate groups are commonly referred to as forming the internucleoside backbone of the oligonucleotide. The normal linkage or backbone of RNA and DNA is a 3' to 5' phosphodiester linkage. Specific examples of preferred antisense compounds useful in the present invention include oligonucleotides containing modified backbones or non-natural internucleoside linkages. Oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. Modified oligonucleotide backbones which can

result in increased stability are known to the person skilled in the art, preferably such modification is a phosphorothioate linkage.

5 A preferred oligonucleotide mimetic is an oligonucleotide mimetic that has been shown to have excellent hybridization properties, and is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an
10 aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone.

Modified oligonucleotides may also contain one or more
15 substituted or modified sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C₁ to C₁₀ alkyl or
20 C₂ to C₁₀ alkenyl and alkynyl. A particularly preferred modified sugar moiety is a 2'-O-methoxyethyl sugar moiety.

Antisense-oligonucleotides of the invention may also include nucleobase modifications or substitutions. Modified nucleobases
25 include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine
30 and 2-thiocytosine etc., with 5-methylcytosine substitutions being preferred since these modifications have been shown to increase nucleic acid duplex stability.

Another modification of the oligonucleotides of the invention
35 involves chemically linking to the oligonucleotide one or more

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moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. Such moieties include lipid moieties such as a cholesterol moiety, cholic acid, a thioether, a thiocholesterol, an aliphatic chain, e.g., dodecandiol or undecyl residues, a phospholipid, a polyamine or a polyethylene glycol chain, or adamantane acetic acid, a palmityl moiety, or an octadecylamine or hexylamino-carbonyl-oxysterol moiety.

10 The present invention also includes antisense compounds which are chimeric compounds. "Chimeric" antisense compounds or "chimeras," in the context of this invention, are antisense compounds, particularly oligonucleotides, which contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide in the case of an oligonucleotide compound. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide inhibition of gene expression. Consequently, comparable results can often be obtained with shorter oligonucleotides when chimeric oligonucleotides are used, compared to phosphorothioate deoxyoligonucleotides hybridizing to the same target region. Chimeric antisense compounds of the invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above. Such compounds have also been referred to in the art as hybrids or gapmers.

The present invention also relates to a pharmaceutical composition comprising an antibody or antisense oligonucleotide of the invention and a suitable excipient, diluent or carrier.

5 Preferably, in a pharmaceutical composition, such compound as described above is combined with a pharmaceutically acceptable carrier. "Pharmaceutically acceptable" is meant to encompass any carrier, which does not interfere with the effectiveness of the biological activity of the active ingredient and that is not

10 toxic to the host to which it is administered. Examples of suitable pharmaceutical carriers are well known in the art and include phosphate buffered saline solutions, water, emulsions, such as oil/water emulsions, various types of wetting agents, sterile solutions etc. Such carriers can be formulated by

15 conventional methods and the active compound can be administered to the subject at an effective dose.

An "effective dose" refers to an amount of the active ingredient that is sufficient to prevent the disease or to affect the

20 course and the severity of the disease, leading to the reduction or remission of such pathology. An "effective dose" useful for treating and/or preventing these diseases or disorders may be determined using methods known to one skilled in the art.

25 Administration of the suitable compositions may be effected by different ways, e.g. by intravenous, intraperitoneal, oral, subcutaneous, intramuscular, topical or intradermal administration. The route of administration, of course, depends on the kind of therapy and the kind of compound contained in the

30 pharmaceutical composition. The dosage regimen will be determined by the attending physician and other clinical factors. As is well known in the medical arts, dosages for any one patient depends on many factors, including the patient's size, body surface area, age, sex, the particular compound to be

35 administered, time and route of administration, the kind of

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therapy, general health and other drugs being administered
concurrently.

In a preferred embodiment of the present invention, the disease
5 that can be prevented/treated is cancer, preferably breast
cancer, ovarian cancer, lung cancer, prostate cancer, pancreatic
cancer, Hodgkin's disease, colorectal cancer or colon cancer or
a disease of the CNS, preferably Alzheimer's disease or multiple
sclerosis (MS), amyotrophic lateral sclerosis, Parkinson's
10 disease, or transmissible spongiforme encephalopathies/Prion-
linked diseases. In addition, due to a similarity of risk
factors between MS and diabetes mellitus, the latter condition
is also included. The terms "cancer" and "disease of the CNS"
also comprise early stages of said diseases.

15

The present invention also relates to a vaccine for immunizing a
mammal against an HCBI, MSBI, MSSSI or CMI infection, comprising
at least one polypeptide or HCBI, MSBI, MSSSI or CMI polynucleic
acid as defined above or corresponding VLP (virus-like particle)
20 or peptide/protein/DNA complexes, in a pharmaceutically
acceptable carrier. It also involves molecular and immunological
tests in animals (in particular cattle) and within their
products (e.g. milk and dairy products).

25 It may also include small chemicals for targeted therapy derived
from the analysis of structural components of these agents.

A "vaccine" is an immunogenic composition capable of eliciting
protection against HCBI, MSBI, MSSSI or CMI, whether partial or
30 complete. A vaccine may also be useful for treatment of an
already infected individual, in which case it is called a
therapeutic vaccine.

The term "therapeutic" refers to a composition capable of
35 treating HCBI, MSBI, MSSSI or CMI infection or diseases linked to

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this infection. The term "effective amount" refers to an amount of epitope-bearing polypeptide sufficient to induce an immunogenic response in the individual to which it is administered, or to otherwise detectably immunoreact in its intended system (e. g., immunoassay). Preferably, the effective amount is sufficient to effect treatment, as defined above. The exact amount necessary will vary according to the application. For vaccine applications or for the generation of polyclonal antiserum/antibodies, for example, the effective amount may vary depending on the species, age, and general condition of the individual, the severity of the condition being treated, the particular polypeptide selected and its mode of administration, etc. Effective amounts will be found within a relatively large, non-critical range. An appropriate effective amount can be readily determined using routine experimentation. Preferred ranges of proteins for prophylaxis of HCBI, MSBI, MSSSI or CMI caused diseases are 0.01 to 100 µg/dose, preferably 0.1 to 50 µg/dose. Several doses may be needed per individual in order to achieve a sufficient immune response and subsequent protection against an HCBI, MSBI, MSSSI or CMI infection and an HCBI, MSBI or CMI linked disease, respectively.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the vaccine. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, and amino acid copolymers. Such carriers are well known to those of ordinary skill in the art.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: aluminium hydroxide (alum), N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP) as found in U.S. Patent No. 4,606,918, N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-

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isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl sn-glycero-3-
hydroxy-phosphoryloxy)-ethylamine (MTP-PE) and RIBI, which
contains three components extracted from bacteria,
monophosphoryl lipid A, trehalose dimycolate, and cell wall
5 Skeleton (MPL +TDM + CWS) in a 2% squalene/Tween 80 emulsion.
Any of the 3 components . MPL, TDM or
CWS may also be used alone or combined 2 by 2. Additionally,
adjuvants such as Stimulon (Cambridge Bioscience, Worcester, MA)
or SAF-1 (Syntex) may be used. Further, Complete Freund's
10 Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA) may be
used for non-human applications and research purposes.

The immunogenic compositions typically will contain
pharmaceutically acceptable vehicles, such as water, saline,
15 glycerol, ethanol, etc. Additionally, auxiliary substances, such
as wetting or emulsifying agents, pH buffering substances,
preservatives, and the like, may be included in such vehicles.

Typically, the immunogenic compositions are prepared as
20 injectables, either as liquid solutions or suspensions. Solid
forms suitable for solution in, or suspension in, liquid
vehicles prior to injection may also be prepared. The
preparation also may be emulsified or encapsulated in liposomes
for enhanced adjuvant effect. The proteins may also be
25 incorporated into Immune Stimulating Complexes together with
saponins, for example Quil A (ISCOMS).

Immunogenic compositions used as vaccines comprise a "sufficient
amount" or "an immunologically effective amount" of the proteins
30 of the present invention, as well as any other of the above
mentioned components, as needed. "Immunologically effective
amount" means that the administration of that amount to an
individual, either in a single dose or as part of a series, is
effective for treatment, as defined above. This amount varies
35 depending upon the health and physical condition of the

WO 2016/005054 individual to be treated, the capacity of the individual's **PCT/EP2015/001399** immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors.
5 It is expected that the amount will fall in a relatively broad range that can be determined through routine trials. Usually the amount will vary from 0.01 to 1000 µg/dose, more particularly from 0.1 -100 µg/dose.

10

The following examples are intended to illustrate, but not to limit the invention. While such examples are typical of those that might be used, other methods known to those skilled in the art may alternatively be utilized.

15

Example 1

Material and Methods

20 (A) Fractionation of bovine sera on density-sedimentation gradients with subsequent cloning

Initially, pools of 5 sera from a total of 120 bovine sera were subjected to Optiprep-(iodixanol)-density gradient ultracentrifugation after prior benzonase treatment to remove
25 all free DNA and RNA (Buck et al., 2005). Protein-associated DNA was extracted from fractions (Qiagen PCR Purification Kit) and 1µl DNA/fraction subjected to RCA (rolling circle amplification) in a solution of 50µM Exo-resistant random primers (Thermo Scientific), 3.2µmol each dNTPs (Takara) and
30 10U phi29 polymerase (Biolabs). Restriction digested products (EcoR1 or BamH1) were separated by agarose gel electrophoresis, eluted and cloned into vector pUC19 prior to sequencing.

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(B) Rolling circle amplification of DNA extracted from sera, cow milk or brain tissue: DNA was extracted by phenol-chloroform from milk and post mortem brain tissue and sera from MS patients. DNA from all serum samples was extracted using the High Pure Viral Nucleic Acid Kit (Roche). RCA (rolling circle amplification) with random primers on DNA from protein-associated fractions, restriction digestion, cloning and sequencing of resulting fragments (refer above). Abutting primers used were designed either on the individual isolated DNA sequences, as well as on the replication genes of Sphinx1.76 or Sphinx2.36 and used in inverted PCR on RCA amplified DNA from single bovine sera and cow milk, as well as sera from multiple sclerosis patients and post mortem multiple sclerosis brain samples.

Example 2

Concept for the pathogenesis of multiple sclerosis:

Isolation of circular DNA molecules (bovine agents) from bovine serum, cow milk and multiple sclerosis brain (Group 1)

The epidemiology of colon cancer suggested the involvement of an infectious factor present in red meat derived from cattle of European/Asian descent (zur Hausen, 2012; zur Hausen, 2015) and cow milk consumption has been suspected to play a role in multiple sclerosis. In attempts to isolate these putative factors, sera from 120 healthy 5-year old cows were obtained from the Veterinary Faculty of the University of Leipzig and analyzed for the presence of circular episomal DNA. Since the first isolates HCBI6.252 (Healthy Cattle Blood Isolate) (2522bp) and HCBI6.159 (1591bp) revealed a distant relationship to DNA related to sequences found in brain

lesions of animals linked to prion-associated conditions (Manuelidis, 2011). The inventors concomitantly analysed 8 sera (from patients in relapse), 2 CSF and 1 PBMC from MS patients, as well as 12 biopsies from post mortem brain tissue for Sphinx-related sequences. Two circular DNA molecules related to Sphinx1.76 (1758bp acc. no. HQ444404) were isolated from one MS brain sample - MSBI1.176 (Multiple Sclerotic Brain Isolate) (1766bp) and MS2.176 (1766bp). Since there is an elevated MS risk after cow milk consumption, the inventors investigated commercially available pasteurized milk for the presence of related DNA. Indeed, they isolated episomal single-stranded DNA molecules from all 4 milk samples (CMI1.252 (Cow Milk Isolate), CMI2.214, CMI3.168 and CMI4.158) (HCBI6.252 and CMI1.252 are near identical). This was taken as an indication that milk excretion of these agents is indeed occurring.

The inventors used 2 primer pairs designed on Sphinx1.76 for inverted PCR on all human and bovine samples. These primer pairs were: forward 5'-GGATTAATGCCAATGATCC-3' (nt 721-739), reverse 5'-CGAGAGAAACAGGCAAAG-3' (nt703-720) and forward 5'-GAGGACGAATTAATATTACAAGTC-3' (nt868-891), reverse 5'-TTACCAAGAAAAGCGAGAAC-3' (nt848-867). The resulting sequences are all distantly similar (ranging from 79% - 98%) to the Sphinx1.76 isolate. HCBI6.159 apparently evolved from a deletion in HCBI6.252 (deletion of nt 1129-2060 in HCBI6.252) as their overlapping sequences are identical. HCBI6.159 was isolated independently from HCBI6.252 and it is therefore highly unlikely that it is an artifact. MSBI1.176 is 98% identical to Sphinx1.76, but the nature (patterns) of the single sequence differences are such that these can be regarded as two separate agents. As the Sphinx1.76 construct was not available in the inventor's laboratory, it could not have resulted from laboratory contamination. The inventors

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 isolated a second very distantly Sphinx1.76-related (but identical in size) circular DNA molecule MSBI2.176 from the same brain biopsy.

5 The large ORFs of the isolate of group 1 encode for replication protein (ProtSweep, del Val et al., 2007) sharing high similarity between them. Another common feature is the presence of iteron-like tandem repeats (3x22nt plus 17/18nt of the repeat in each isolate). Alignment of this repeat region
 10 indicates only single nucleotide variation in the core (Figure 6). These iteron-like repeats may constitute binding sites for Rep proteins (Chattoraj, 2000, Dziewit et al., 2013).

Nucleotide sequence accession number: The complete sequences
 15 of 8 isolates have been deposited in the EMBL Databank under the acc. no.:

CMI1.2522	Acc no. LK931487
CMI2.214	Acc no. LK931488
CMI3.168	Acc no. LK931489
20 CMI4.158	Acc no. LK931490
MSBI1.17	Acc no. LK931491
MSBI2.176	Acc no. LK931492
HCBI6.252	Acc no. LK931493
HCBI6.159	Acc no. LK931494

25

In this context, diseases of the CNS (e.g. Multiple sclerosis MS, amyotrophic lateral sclerosis, transmissible spongiforme encephalopathies/ Prion-linked diseases, Parkinson's disease, Alzheimer disease) are also highly interesting since the
 30 similar sequences described by Manuelidis are primarily found in the CNS.

Example 3**Isolation of a bovine factor from bovine serum (group 2)**

5 DNA from bovine serum was extracted followed by rolling circle amplification of the DNA. PCR amplification using abutting primers (forward (nt2313-2336) 5'CTAATGCAGATCAACACAGGGATA-3' and reverse (nt2312-2291) 5'-GAATTACAGGCTTTGCAATCTG-3') designed on the replication gene of Sphinx2.36 (2364bp, acc no. HQ444405)
10 (Manuelidis 2011) resulted in one circular DNA isolate HCBI7.228 (2280bp, acc no. LK931498) (group 2).

Example 4

15 **Isolation of sequences from bovine sera and multiple sclerosis serum distantly related to a novel group of single-stranded DNA viruses, the myco-like Gemycircularviruses (Group 3)**

A large number of circular ssDNA viruses have recently been
20 identified by metagenomic analyses (Rosario et al., 2012a). The group of Gemycircularviruses has been isolated from fungi, faeces of various animals and plants leaves (Rosario et al., 2012b; Sikorski et al. 2013). The inventors report the isolation of the genomes of 3 novel viruses distantly related to this
25 virus group.

Two sequences HCBI8.215 (2152bp) and HCBI9.2112 (2121bp) were isolated after density gradient fractionation of bovine serum pools. Fragments obtained after restriction digest (BamH1 and
30 EcoR1) were cloned into pUC19. Their full-length genomes were verified by inverted PCR using abutting primers. One multiple sclerosis serum isolate MSSI2.225 rescued using abutting primers and inverted PCR was related to the myco-like Gemycircularviruses isolated from cattle sera (HCBI8.215 and
35 HCBI9.212). The inventors subsequently isolated a sequence

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 MSBI3.224 from a post-mortem-MS affected brain tissue which
 proved to be identical to MSSI2.225.

The genome organization of all 3 isolates revealed a putative
 5 spliced replication protein coded for on the negative strand and
 the coat protein (CP) on the positive strand. The CP was
 arginine rich and a similarity to the TTV ORF1 protein was
 indicated in a DomainSweep analysis (del Val et al., 2007).
 Putative rolling circle motifs I, II and III and a Walker B
 10 motif of each were identified as follows: HCBI8.215 (LLTYA,
 HLHAFVD, YAIKD; VFDDI), for HCBI9.212 (LLKMP, HYHIYLG, YVGKD;
 VFDDI) and for MSSI2.225 (LLTYP, HLHAFVD, YAIKD; IFDDF). The GRS
 motifs were AVFDVGGFHPNISITK, TAFDYFGAHGNIKSIR and
 RAFDVEGCHPNVSPSR respectively. The nona-nucleotide motif for
 15 both HCBI8.215 and MSSI2.225 is (TAATGTTAT) and for HCBI9.212
 (TAATATTAT).

These 3 isolates probably constitute a novel group of viruses as
 their capsid proteins share similarities with the ORF1 of TT
 20 viruses from the family *Anelloviridae*, and not to that of the
 plant virus family *Geminiviridae* as in the Gemycircularviruses.
 The isolation of these 3 Gemycircularvirus-related genomes
 directly from animal and diseased human tissue links them to
 have some etiological relevance for diseases such as multiple
 25 sclerosis.

HCBI8.215	Acc no. LK931483
HCBI9.212	Acc no. LK931484
MSSI2.225	Acc no. LK931485

30

35

Example 5**Bacterial plasmid-related circular DNA from human serum (group 4)**

5 *Psychrobacter* species are frequently present as food
contaminants and have been isolated from human tissues including
brain, cerebrospinal fluid and blood. It is considered as an
opportunistic human pathogen (Caspar et al., 2013; Lloyd-Puryear
et al., 1991). The inventors report the isolation of a circular
10 DNA molecule, MSSI1.162, from serum taken from a multiple
sclerosis patient during relapse.

Rolling circle amplification and restriction digest were
performed on DNA extracted from sera from patients with multiple
15 sclerosis. The resulting fragment was cloned into vector pUC19.
The full-length genome was verified by inverted PCR
amplification using primers designed on the sequence identified
initially: forward primer 5'-GACTTCTGATTGATTGATGCCTG-3' and
reverse 5'-CCTGTTGAATACCGCTTAAATACT-3'. All products were
20 sequenced by primer walking. MSSI1.162 (multiple sclerosis serum
isolate) (1627bp) (Acc no. LK931486) shares 66% nucleotide
similarity by BlastN analysis to the pRWF102 plasmid of the
Psychrobacter species PRwf-1. The putative protein (321 amino
acids) encoded by the large ORF shows weak similarity to
25 replication protein family of *E. coli* as analysed by ProtSweep
(del Val et al., 2007).

This new isolate is only distantly related to known
Psychrobacter species and their plasmids. It may therefore
30 represent a yet unknown human pathogen.

Summary:

The presence of presumably infectious agents and their nucleic acids in the serum of healthy cows should imply that the same
5 particles are also present in red meat.

The inventors isolated 13 novel single-stranded DNA molecules from cattle serum and milk and MS brain tissue and sera. These isolates are grouped in 4 groups according to their sequence
10 similarity to the Sphinx1.76 genome (group 1), Sphinx2.36 genome (group 2), myco-like Gemycircularviruses (group 3) and *Psychrobacter* spp. plasmid (group 4). Their genome organizations are presented in Figure 5 A,B. The main feature of all the
15 sequences is the presence of a replication-associated protein encoding ORF.

All the isolates are presumably single-stranded DNA because of the bias of RCA towards amplification of single-stranded DNA (*del Solar et al., 1998*). A taxonomic classification of the
20 isolates is, at this stage, not possible. Only group 3 can be defined as clearly related to the myco-like Gemycircularviruses. This relatively novel group of viruses have been identified by metagenomics and isolated mainly from faeces of a very large variety of animals and insects, as well as plants and fungi.
25 They share some characteristics with the Geminiviruses of plants (*Sikorski et al., 2013*). Isolation from tissues of animals or humans has not yet been described. The putative replication-associated protein of all 3 isolates described in this application has an arginine-rich region with a similarity to
30 human single-stranded TT viruses.

Infection of human cells by such agents should evoke a strong immune reaction, quite distinct from human TT viruses, where reasonable evidence for vertical transmission has been obtained
35 (*reviewed in zur Hausen and de Villiers, 2014*). This could

explain the high susceptibility to environmental factors for MS development during the first 15 years of life: primary infection may initially lead to rounds of replication and spreading of BMF probably via blood cells, eventually resulting in latent brain cell infection. This initial infection should induce an immune response, probably neutralizing the agent in subsequent rounds of infection prior to entry of the brain. The isolates reported here seem to represent excellent candidates for the postulated bovine milk factor (BMF).

10

A high variability in size was noted in group 1. The circular isolate HCBI6.159 seem to have evolved from HCBI6.252 through deletion of 931 nucleotides from the latter. The isolates all possess a replication gene and have an iteron-like repeat region in common (*Dziewit et al., 2013*). Alignment of this region between 8 isolates and Sphinx1.76 reveals a central identical core (Figure 6). Group 2 and 4 isolates do not have repeat regions.

20 The "Sphinx" sequences (*Manuelidis, 2011*) show high homologies to plasmid sequences of the bacterium *Acinetobacter* (*Vallenet et al., 2008; Longkumer et al., 2013*). The sequences obtained in the present invention also exhibit striking homologies to the corresponding plasmid sequences. Although a large number of
25 plasmids have been isolated and sequenced from *Acinetobacter*, thus far none of them corresponded exactly to the bovine and human sequences reported in this invention. Interestingly, a group of scientists in the UK published serological data over a period of years pointing to an increased selective formation of
30 antibodies against *Acinetobacter* proteins but not against other bacterial antigens obtained from patients suffering from multiple sclerosis (see review article: *Ebringer et al., 2012*). These results could not be confirmed by the group of Chapman (*Chapman et al., 2005*). However, it has to be stressed that the
35 group of Chapman used a different strain of *Acinetobacter*

(*Acinetobacter calcoaceticus*). Unequivocal results were obtained by the group of Ebringer for three strains of *Acinetobacter* (*Acinetobacter lwoffii*, *A. radioesistens* and a specific isolate, *A. 11171*). However, the results obtained for *A. junii* 17908 were less impressive and significant reactivity was hardly detectable (Hughes et al., 2001). These results suggest that we are dealing with strain-specific reactivities wherein this sero-reactivity is due to strain-specific plasmids exhibiting homologies to the DNA sequences obtained in the present invention.

10

The isolate MSS11.162 (group 4) has similarity to a plasmid of the *Psychrobacter* spp. *Psychrobacter* species have been considered as an opportunistic human pathogen (Caspar et al., 2013) and has been isolated from a case of meningitis (Lloyd-Puryear et al., 1991). These bacteria have repeatedly been reported as contaminants during and after cold-storage of meat (de Filippis et al., 2013) and were frequently isolated from milk and a variety of cheeses (Coton et al., 2012).

15

20 It is of interest to note that Manuelidis reported two "Sphinx-structures", labeled as "large" (2.36) and "small" (1.76) Sphinx. Although most of the present sequences substantially differed from her isolates, the inventors also obtained large and small Sphinx-like sequences from the same probes. Circular
25 HCBI6.159 seems to have evolved from HCBI6.252 through a deletion of 931 nucleotides from the latter. It cannot be excluded that the other larger isolates may have smaller counterparts which were not isolated. It remains, however, to be determined whether the two structures found here persist within
30 the same protein coat or complement each other.

The isolation of DNA of similar, in part even identical single-stranded circular nucleic acids from cattle sera, commercially available cow milk and florid MS tissues argues in favour of the
35 concept outlined above.

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iterons: no longer paradoxical. Mol. Microbiol. 37: 467-476.
25

zur Hausen H. 2001. Proliferation-inducing viruses in non-
permissive systems as possible causes of human cancers. Lancet
357: 381-384.

30 Whitley C, Gunst K, Müller H, Funk M, zur Hausen H, de Villiers
E-M., Novel replication-competent circular DNA molecules from
healthy cattle serum, milk and multiple sclerosis-affected
human brain tissue, Genome Announcements 2(4): e00849-14, 2014.

WO 2016/005054
Lamberto I, Gunst K, Müller H, zur Hausen H, de Villiers E-M. **PCT/EP2015/001399**
Mycovirus-like DNA virus sequences from cattle serum, human
brain and serum from multiple sclerosis patients, Genome
Announcements 2(4): e00848-14, 2014

5

Gunst K, zur Hausen H, de Villiers E-M., Isolation of bacterial
plasmid-related replication-associated circular DNA from serum
sample of a multiple sclerosis patient, Genome announcement
2(4), e00847-14, 2014

10

Claims

1. An HCBI, MSBI, MSSSI or CMI polynucleic acid comprising:
- 5 (a) a nucleotide sequence depicted in any one of Figures 1 to 4;
- (b) a nucleotide sequence having at least 90% identity to a nucleotide sequence of (a);
- (c) a fragment of a nucleotide sequence of (a) or (b);
- 10 (d) a nucleotide sequence being complementary to a nucleotide sequence of (a), (b) or (c); or
- (e) a nucleotide sequence which is redundant as a result of the degeneracy of the genetic code compared to any of the above-given nucleotide sequences.
- 15
2. An oligonucleotide primer comprising part of an HCBI, MSBI, MSSSI or CMI polynucleic acid of claim 1, said primer being capable of acting as primer for specifically sequencing or specifically amplifying the nucleic acid of a certain HCBI,
- 20 MSBI, MSSSI or CMI isolate containing a nucleotide sequence in claim 1.
3. An oligonucleotide probe comprising part of an HCBI, MSBI, MSSSI or CMI polynucleic acid of claim 1, said probe being
- 25 capable of acting as a hybridization probe for specific detection of the nucleic acid of a certain HCBI, MSBI, MSSSI or CMI isolate containing a nucleotide sequence of claim 1.
4. An expression vector comprising an HCBI, MSBI, MSSSI or CMI
- 30 polynucleic acid of any one of claims 1 to 3 operably linked to prokaryotic, eukaryotic or viral transcription and translation control elements.
5. A host cell transformed or modified with an expression vector
- 35 according to claim 4.

6. A polypeptide being encoded by an HCBI, MSBI, MSSSI or CMI polynucleic acid of claim 1.

5 7. An antibody or antigen binding fragment thereof specifically binding to a polypeptide of claim 6.

8. Use of a primer according to claim 2, a probe according to claim 3, a polypeptide of claim 6, or an antibody or fragment
10 thereof according to claim 7 for the preparation of a diagnostic composition for the diagnosis of a predisposition or an early stage of cancer, a disease of the CNS or diabetes.

9. Use according to claim 8, wherein the cancer is breast
15 cancer, ovarian cancer, lung cancer, prostate cancer, colorectal cancer or colon cancer, and the disease of the CNS is Multiple sclerosis MS, amyotrophic lateral sclerosis, transmissible spongiforme encephalopathies/Prion-linked diseases, Parkinson's disease or Alzheimer disease.

20

10. A method for the detection of an HCBI, MSBI, MSSSI or CMI polynucleic acid according to claim 1 in a biological sample, comprising: (a) optionally extracting sample polynucleic acid, (b) amplifying the polynucleic acid as described above with at
25 least one primer according to claim 2, optionally a labelled primer, and (c) detecting the amplified polynucleic acid.

11. A method for the detection of an HCBI, MSBI, MSSSI or CMI polynucleic acid according to claim 1 in a biological sample, comprising: (a) optionally extracting sample polynucleic acid, (b) hybridizing the polynucleic acid as described above with at
30 least one probe according to claim 3, optionally a labelled probe, and (c) detecting the hybridized polynucleic acid.

12. A method for detecting a polypeptide of claim 6 or an antibody of claim 7 present in a biological sample, comprising: (a) contacting the biological sample for the presence and/or concentration of such polypeptide or antibody as defined above, and (b) detecting the immunological complex formed between said antibody and/or said polypeptide.

13. An antisense oligonucleotide reducing or inhibiting the expression of an HCBI, MSBI, MSSSI or CMI polynucleic acid of claim 1 or a vector containing said antisense oligonucleotide.

14. A pharmaceutical composition comprising the antibody or antigen binding fragment thereof of claim 7 or the antisense oligonucleotide of claim 16 and a suitable pharmaceutical carrier.

15. A vaccine comprising an HCBI, MSBI, MSSSI or CMI polynucleic acid of claim 1 or a polypeptide according to claim 6.

16. The vaccine of claim 15, which comprises a VLP or protein/DNA or polypeptide/DNA complex or specific proteins or attenuated infectious agents.

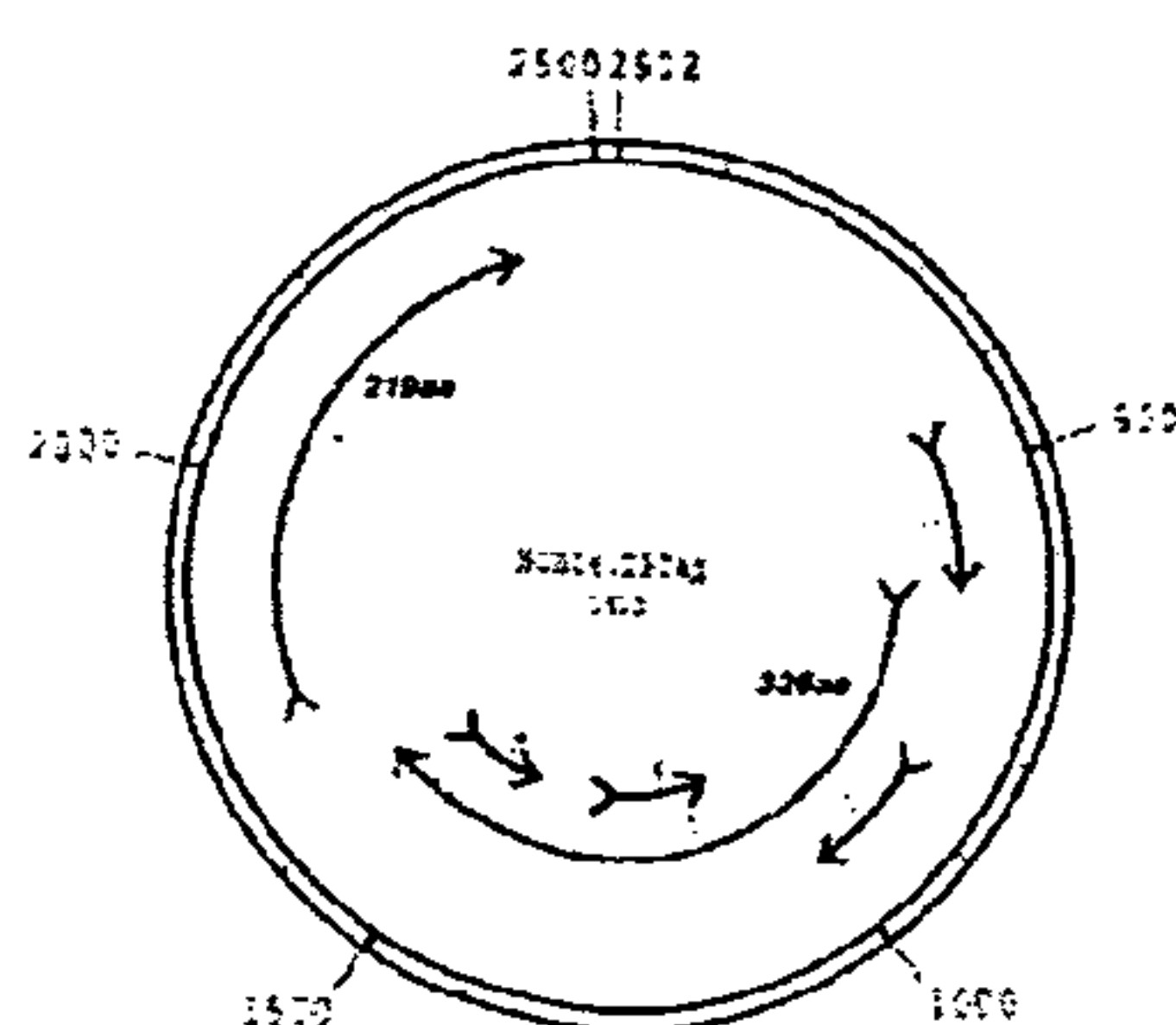
17. Use of an HCBI, MSBI, MSSSI or CMI polynucleic acid of claim 1 as a lead component for the development of a medicament for prevention or treatment of cancer, a disease of the CNS or diabetes.

18. Use according to claim 17, wherein the cancer is breast cancer, ovarian cancer, lung cancer, prostate cancer, colorectal cancer or colon cancer and the disease of the CNS is Multiple sclerosis MS, amyotrophic lateral sclerosis, transmissible spongiforme encephalopathies/Prion-linked diseases, Parkinson's disease or Alzheimer disease.

*HCBI6.252 (2522bp)**(identical to CMI1.252)**(ri55.NnXn.2300.7)*

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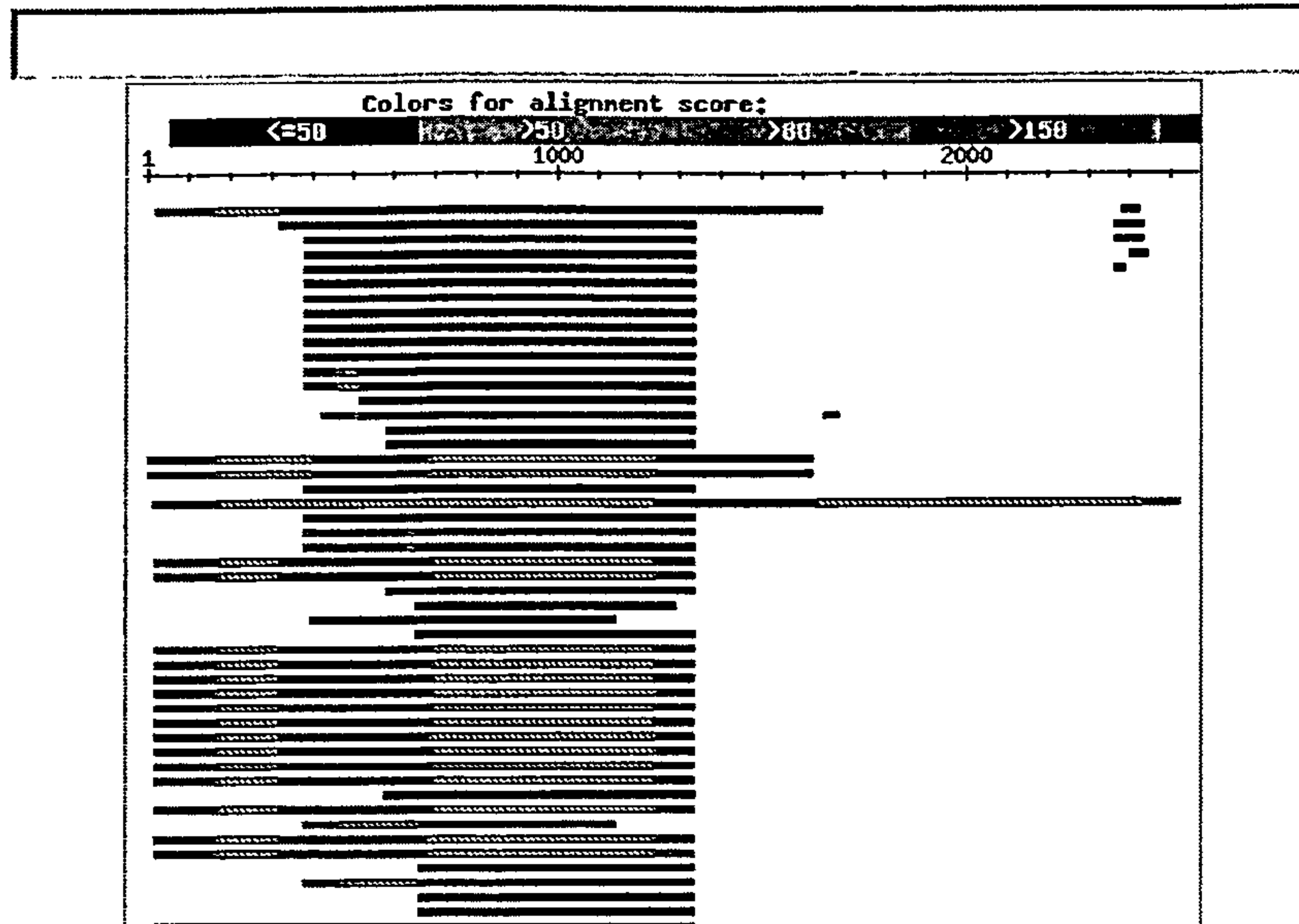
ATACCCCTACGTTTACCGATCA - repeat 3x + 17nt



86% nucleotide similarity to TSE-associated circular DNA isolate *Sphinx 1.76*

ORFs: 326aa – 85% similarity to Replicase 3-like protein of *Sphinx1.76*

Figure 1(a)

*219aa – regulation of transcription**Blastn – Geall:*

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>>>nrnuc:GI_462476960 Gi|462476960|gb|APGK01000458.1| Dendro... 731 0.0
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Sphinx 1.76, complete sequence. 0/0
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Score = 1552 bits (1720), Expect = 0.0
Identities = 1152/1334 (86%), Gaps = 13/1334 (0%)
Strand=Plus/Plus
```

```
Query 320 TTTTAAACCTTTGAACTTTTCCTT-TAATTTGCAGAAATTGCCCTCGACTAAGCTTGCT 378
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Query 379 TAGTCAAAAAAGTTTGTAGCAAAGCGAAAACATAGGGCAATTTTCATGATGAAAATGGGCT 438
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 334 TAGTCAAAAAAGTTTGTAGCAAAGCGAAAACATAGGGCAATTTTCATGAAGAAATTGGGCT 393

Query 439 TTTAAAGTTTTTAAATGCTTTTAAATGCTTTTAGACATGTTGAAATGCAAGCCTAGCAAG 498
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 394 TTTAAAGTTTTTAAATG-TTTTAAATGCTTTTAGACATGCTAAGAAGCCACACAGCAAG 452

Query 499 GCATACAGAGGACATACCCCTACGTTTACCGATCAATACCCCTACGTTTACCGATCAATA 558
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 453 GCATACAGAGGACATTCTCCTACGTTTACCGATCAATACCCC--CGTTTACCGATCAATA 510

Query 559 CCCCTACGTTTACCGATCAATACCCCTACGTTTACCTTGCATATCACTACAAACAATATT 618
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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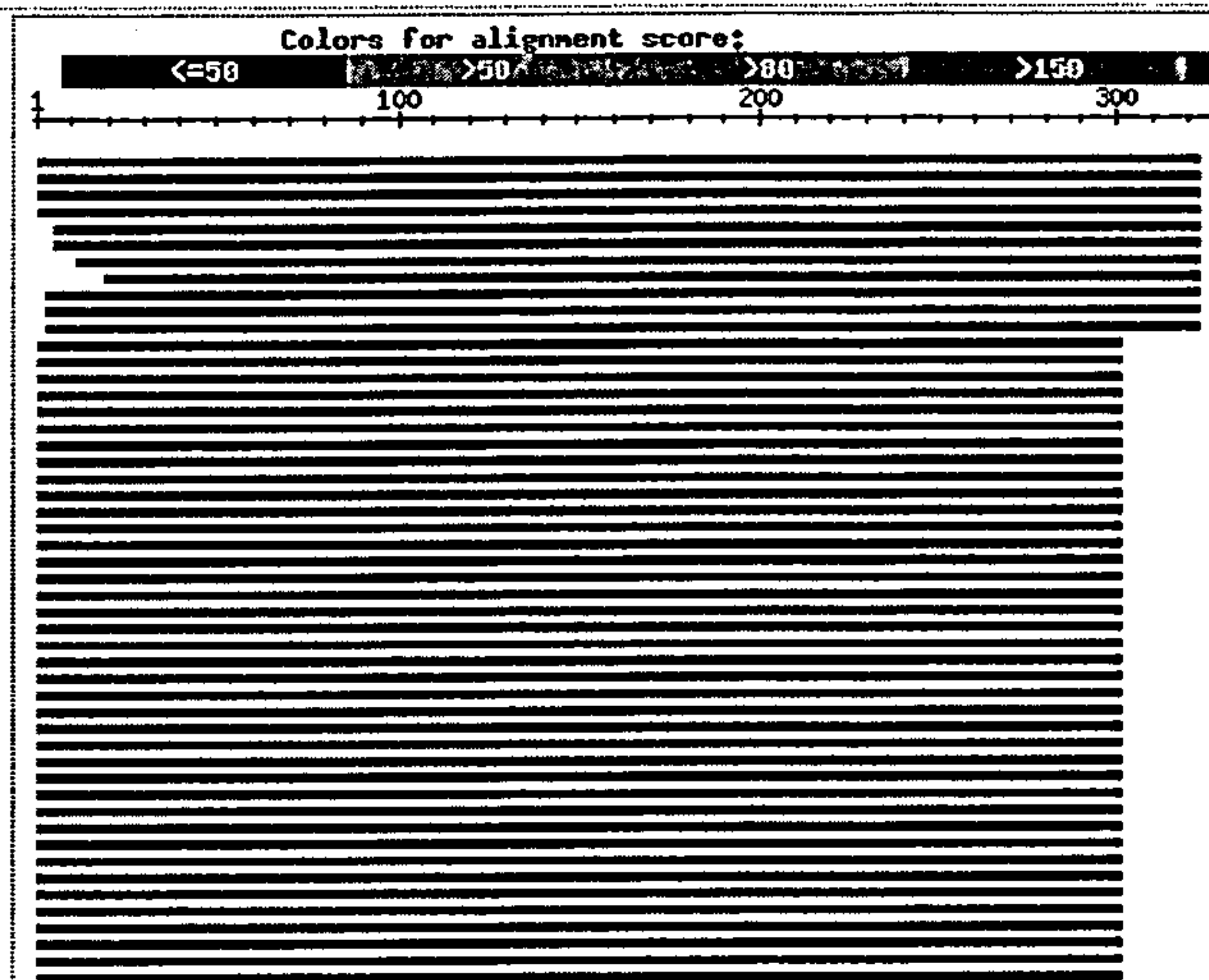
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| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 571 AGTGTAGTA-TAACTTCAAAAGAATAATTGTAGGTTATGAGCGATTTAATAGTAAAAGAT 629

Query 679 AACGCCCTAATGAACGCTAGTTACAACCTAGCTTTGGTTGAACAGCGTTTAATCCTTTTA 738
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Query 799 CATGCAAGTAGCTATATCAATCAATTTAACGTGGAAAGACATACGGCATATCAAGCATT 858
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```


BlastP – Uniprot:
ORF 326aa:



>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-li... 581 1e-163
>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterize... 558 9e-157

>>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-like protein *Sphinx1.76*; 5/2013
Length=324

Score = 581 bits (1498), Expect = 1e-163, Method: Compositional matrix adjust.
Identities = 278/324 (85%), Positives = 294/324 (90%), Gaps = 0/324 (0%)

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Sbjct	1	MSDLIVKDNALMNASYNLALVEQRLILLAILLEARETGKGINANDPLTVHAGSYINQFNVQ	60
Query	61	RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEIIFAPAVVP	120
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Sbjct	121	LITRLEEQFTQYDIEQISGLSSAYAVRMYELLCWRSTGKTPIIELDEFKRRIGVLDTEY	180
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		TRTDNLKM+VIEL LKQINEHTDITASIEQHKKGR ITGFSF FK KK+ + P + S	
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		SP I K SQIP NI KQPENAK DL HRAS++TG IM N L+DRFK+GDES IDMMKRI	
Sbjct	241	SPRIVKHSQIPTNIVKQPENAKMSDLEHRASRVTEIMRNRLSDRFKQGDSEIDMMKRI	300
Query	301	KEEITTDTTADQWENKLEEFQVIF 324	
		+ EI TD ADQWE+KLEEFQV+F	
Sbjct	301	QSEIITDAIADQWESKLEEFQVVF 324	

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Length=324

Score = 558 bits (1439), Expect = 9e-157, Method: Compositional matrix adjust.
Identities = 267/324 (82%), Positives = 290/324 (89%), Gaps = 0/324 (0%)

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		MS+LIVKDNALMNASYNL LVEQRLILLAILLEARE+GKGINANDPLTVHASSYINQF V	
Sbjct	1	MSELIVKDNALMNASYNLALVEQRLILLAILLEARESGKGINANDPLTVHASSYINQFGVH	60
Query	61	RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEIIFAPAVVP	120
		R TAYQALKDACKDLFARQFSYQEKREGR NITSRWVSQI Y+D+TATVEIIFAPAVVP	
Sbjct	61	RTTAYQALKDACKDLFARQFSYQEKREGRANITSRWVSQIAYIDETATVEIIFAPAVVP	120
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General Description References Copyright Links Sequence**General Information about the Entry**

Entry name	SPTREMBL:E5LG72_9ZZZZ
Prim. accession #	E5LG72
Created	8-FEB-2011
Last sequence update	version 1 8-FEB-2011
Last annotation update	version 8 1-MAY-2013

Description and Origin of the Protein

Keywords	
Description	subname: full=replicase 3-like protein;
Gene name(s)	
Organism source	TSE-associated circular DNA.
Organism classification	unclassified sequences.
NCBI Taxonomy ID	932710;

References

1.	Manuelidis, L.; Nuclease resistant circular DNAs copurify with infectivity in scrapie and CJD. J. Neurovirol. 0:0 (2010)
Position	nucleotide sequence.
Comment	strain=sphinx 1.76;

Copyright

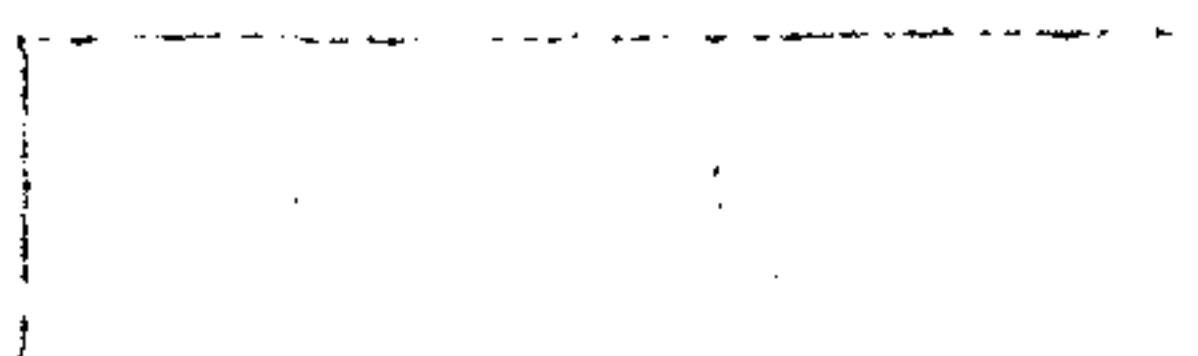
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Database Cross-references

EMBL	HQ444404; ADR65123.1; -; Genomic_DNA.
GO	GO:0005727; C:extrachromosomal circular DNA; IEA:InterPro. GO:0003887; F:DNA-directed DNA polymerase activity; IEA:InterPro. GO:0006270; P:DNA replication initiation; IEA:InterPro.
Gene3D	1.10.10.10; -; 2.
InterPro	IPR000525; Initiator_Rep_prot. IPR011991; WTH_DNA-bd_dom.
Pfam	PF01051; Rep_3; 1.

Sequence information

Characteristics	Length: 324 aa, molecular weight: 37186 Da, CRC64 check sum: 3F0A0F966DD3DCAF
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QSEIITDAIA DQWESKLEEF GVVF
324
//

ProtSweep

A Protein Identification Tool

Results for /home/vir088/rindneu/tsekompl/CMT1.252p.316.pep - identical to HCBI6.252
326.papin the first 300aa



Number of residues: 316	Molecular weight: 35.91 kD
Charge: 8	Isoelectric point: 10.04

more...

Prediction of protein localization:

cyto	13 %
extr	10 %
cyto_nucl	10 %

Identified Protein & Transcript:

Protein:

id: sptrembl:E5LG72 9ZZZZ

valuation: homologous

scientific organism: Dasypus novemcinctus

common organism: Nine-banded armadillo

abstract: E5lg72 SubName: Full=Replicase 3-like protein; 5/2013Length=324

isoform:



GO information:

accession	group	name	evidence
GO:0005727	cellular component	extrachromosomal circular DNA	IEA:InterPro
GO:0003887	molecular function	DNA-directed DNA polymerase activity	IEA:InterPro
GO:0006270	biological process	DNA replication initiation	IEA:InterPro

Interpro information:

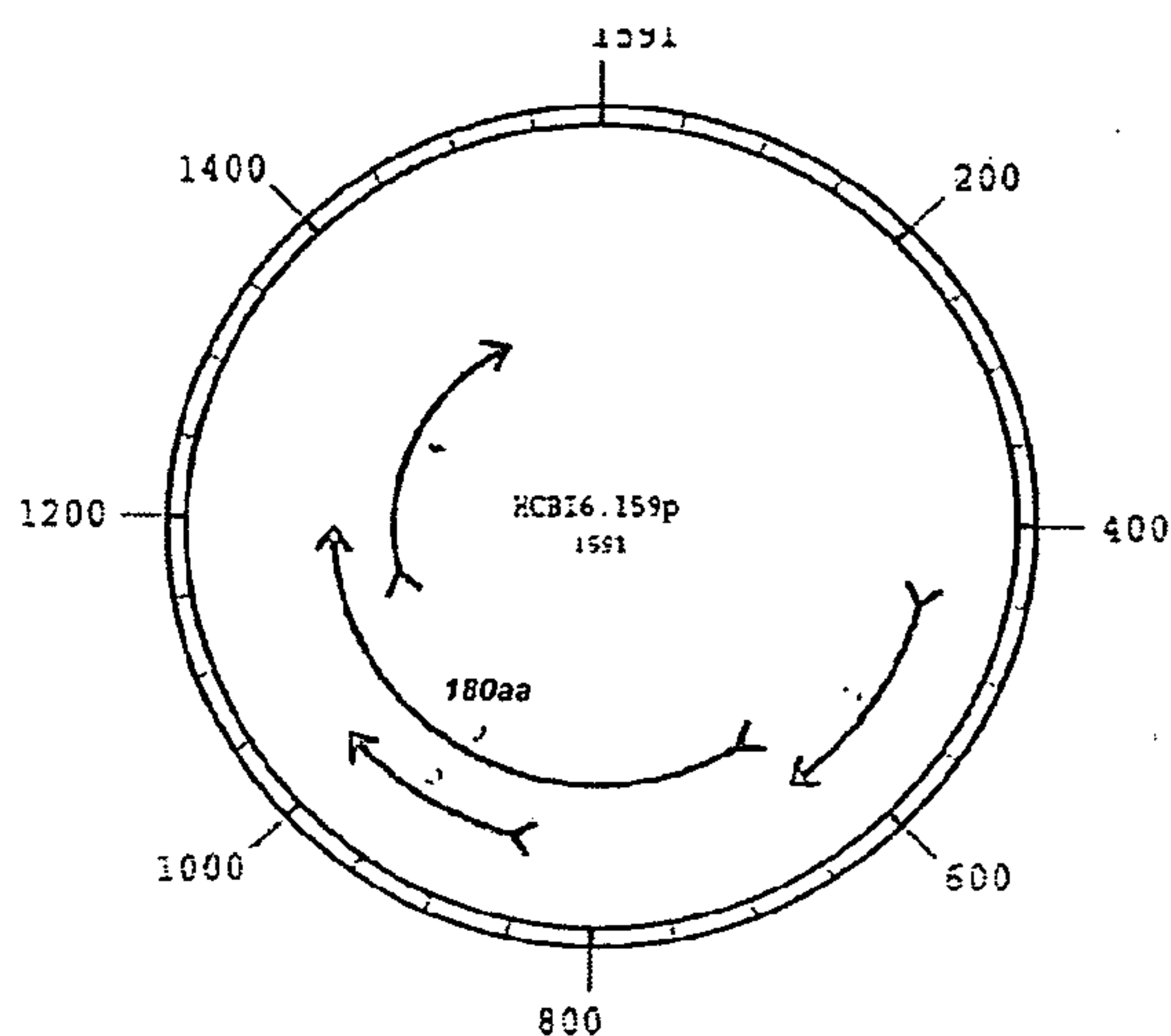
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IPR011991	WHTH_DNA-bd_dom

HCBI6.159 (1591bp)**(ri55.NnXn.1600.5)**

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 GTTTTAGTGTGTCACGTAGCAATCACTTAGAAGTTCCTTTGTATTACTTGTCTAGCAATGGTTTTAA
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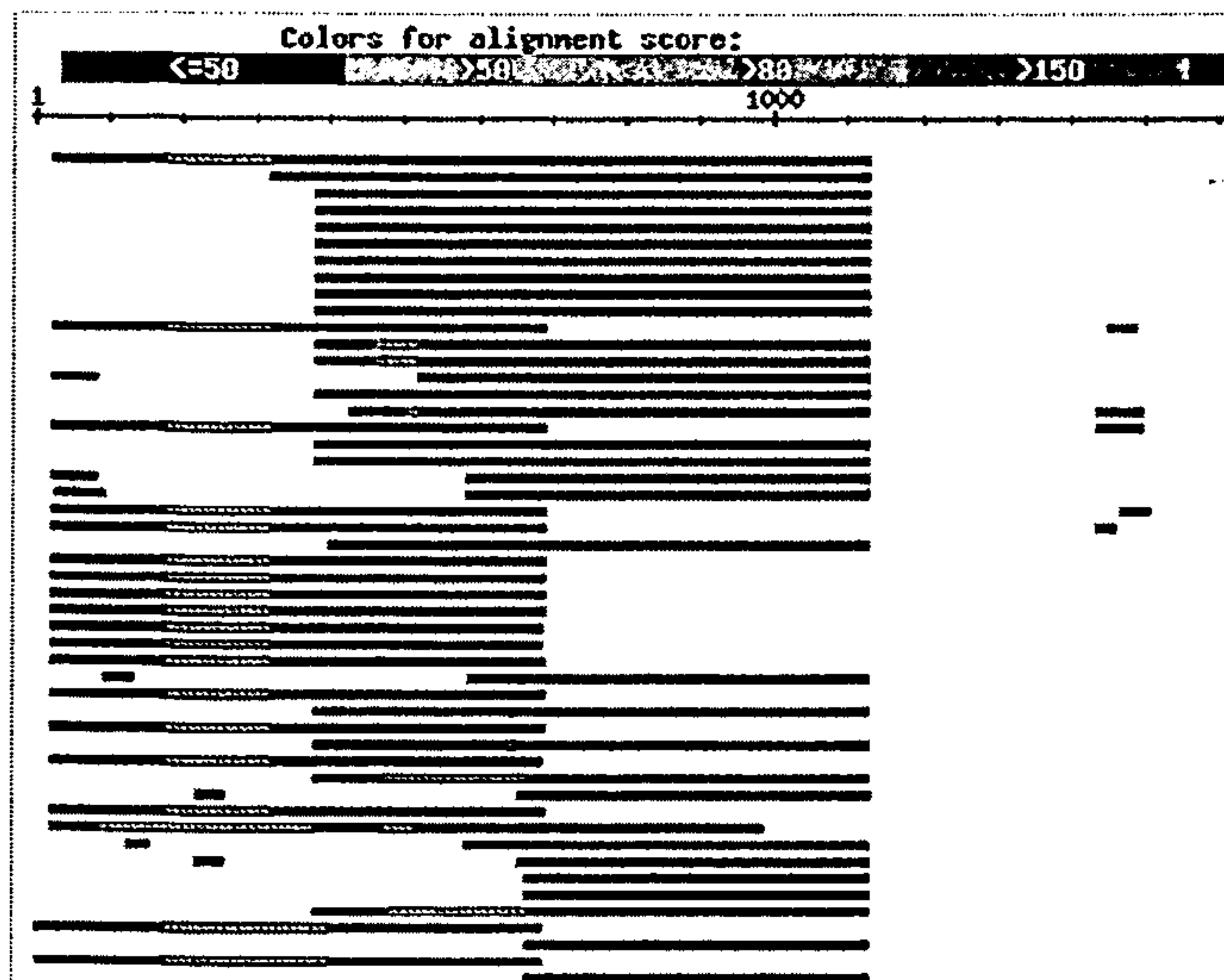
" - sequence of HCBI6.159 is same as HCBI6.252 except that nt 1132-2163 has been deleted. Both sequences were generated by the same back-to-back primers.



89% nucleotide similarity to TSE-associated circular DNA isolate Sphinx 1.76

ORF 180aa - 96% similarity to Replicase 3-like protein of Sphinx1.76

Figure 1(b)

Blastn-Geall:

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>>>>nrnuc:GI_313507477 Gi|313507477|gb|HQ444404.1| TSE-associated circular DNA isolate
Sphinx 1.76, complete sequence. 0/0
Length=1758

Score = 1070 bits (1186), Expect = 0.0
Identities = 728/812 (89%), Gaps = 8/812 (0%)
Strand=Plus/Plus

Query	320	TTTTAAACCTTTGAACTTTTCCTT-TAATTTGCAGAAATTGCCCTCGACTAAGCTTGCT	378
Sbjct	277	TTCTAAACCTTTGACTTCTTCCCCATTGTTTGCAGAAATTGCCCTCGA---AGCTTGCT	333
Query	379	TAGTCAAAAAGTTTGTAGCAAAGCGAAAACATAGGGCAATTTTCATGATGAAAATGGGCT	438
Sbjct	334	TAGTCAAAAAGTTTGTAGCAAAGCGAAAACATAGGGCAATTTTCATGAAGAAATTGGGCT	393
Query	439	TTTAAAGTTTTTAAATGCTTTTAAATGCTTTTAGACATGTTGAAATGCAAGCCTAGCAAG	498
Sbjct	394	TTTAAAGTTTTTAAATG-TTTTAAATGCTTTTAGACATGCTAAGAAGCCCACACAGCAAG	452
Query	499	GCACACAGAGGACATACCCCTGCGTTTACCGATCAATACCCCTACGTTTACCGATCAATA	558
Sbjct	453	GCATACAGAGGACATTCTCCTACGTTTACCGATCAATACCCC--CGTTTACCGATCAATA	510
Query	559	CCCCTACGTTTACCGATCAATACCCCTACGTTTACCTTGCATATCACTACAAACAATATT	618
Sbjct	511	CCCCTACGTTTACCGATCAATACCCCTACGTTTACCTTGCATATACTACAAAGAATACT	570
Query	619	AATGTAGTAATAACTTCAAAATAATAATGTAGGTTATGAGCGATTTAATAGTAAAAGAT	678
Sbjct	571	AGTGTAGTA-TAAGTTCAAAAGAATAATTGTAGGTTATGAGCGATTTAATAGTAAAAGAT	629
Query	679	AACGCCCTAATGAACGCTAGTTACAACCTTAGCTTTGGTTGAACAGCGTTAATCCTTTTA	738
Sbjct	630	AACGCCCTAATGAATGCTAGTTATAACTTAGCTTTGGTTGAACAGAGGTTAATTCTATTA	689
Query	739	GCTATATTGGAAGCGAGAGAAACAGGCAAAGGGATTAATGCCAATGATCCCTTAACAGTT	798
Sbjct	690	GCAATCATAGAAGCGAGAGAAACAGGCAAAGGGATTAATGCCAATGATCCTCTTACGGTT	749
Query	799	CATGCAAGTAGCTATATCAATCAATTTAACGTGGAAAGACATACGGCATATCAAGCATTA	858
Sbjct	750	CATGCAGGTAGCTATATCAATCAATTTAACGTACAAAGGCATACGGCATATCAAGCCCTC	809
Query	859	AAAGATGCTTGCAAAGACTTGTTTGCACGTCAATTTAGTTACCAAGAAAAGCGAGAACGT	918

```
|||||
Sbjct 810 AAAGATGCTTGTAAGACTTGTTGCCCGTCAATTCAGTTACCAAGAAAAGCGAGAACGA 869
Query 919 GGACGAATTAATATTACAAGTCGATGGGTTTCACAAATTGGTTATATGGACGATACAGCA 978
|||||
Sbjct 870 GGACGAATTAATATTACAAGTCGATGGGTTTCGCAAATTGGCTATATGGACGATACAGCA 929
Query 979 ACCGTTGAAATTATTTTGGCCCTGCGGTTGTTCTTTGATTACACGTTTAGAGGAACAA 1038
|||||
Sbjct 930 ACCGTTGAGATPATTTTGGCCCTGCGGTTGTTCTCTGATTACACGGCTAGAGGAACAG 989
Query 1039 TTCACTCAATACGATATTGAACAAATTAGCGAGTTATCGAGTGCTTATGCTGTCCGCCTA 1098
|||||
Sbjct 990 TTCACCCAGTACGATATTGAGCAAATTAGCGGTTTATCGAGTGCATATGCTGTTTCGTATG 1049
Query 1099 TATGAGTTACTAATTGTTGGCGTAGCACAGG 1130
|||||
Sbjct 1050 TACGAAGTCTGATTTGTTGGCGTAGCACAGG 1081
```

Score = 223 bits (246), Expect = 6e-54
Identities = 142/153 (92%), Gaps = 1/153 (0%)
Strand=Plus/Plus

```
Query 22 ATTGGCGAGTGTCTACGAGCGACACAATGAAAGTTCGATTATCCCTCCTCTAAAAAACC 81
|||||
Sbjct 22 ATTAGCGAGTGTCTACGAGCGACTCAATGAAAGTTCGATTATCCC-CCTCTGGAAAACC 80
Query 82 GCTTTTAAAAATATTGGTTGCTAGATGGTTTTAACTATCGTGAGCTTTTGCTTTTAAAAA 141
|||||
Sbjct 81 GCTTTTAAAAATATTGGCTGCTAGATGGTTTTTACTATAGTGAGGTTTGTCTTTTAAAAA 140
Query 142 TACACGAGCAAAGCGAGTTCATAGTCGCTTTTG 174
|||||
Sbjct 141 AACACGAGCAAAGCGAGTTCATAGTTGCTTTTG 173
```

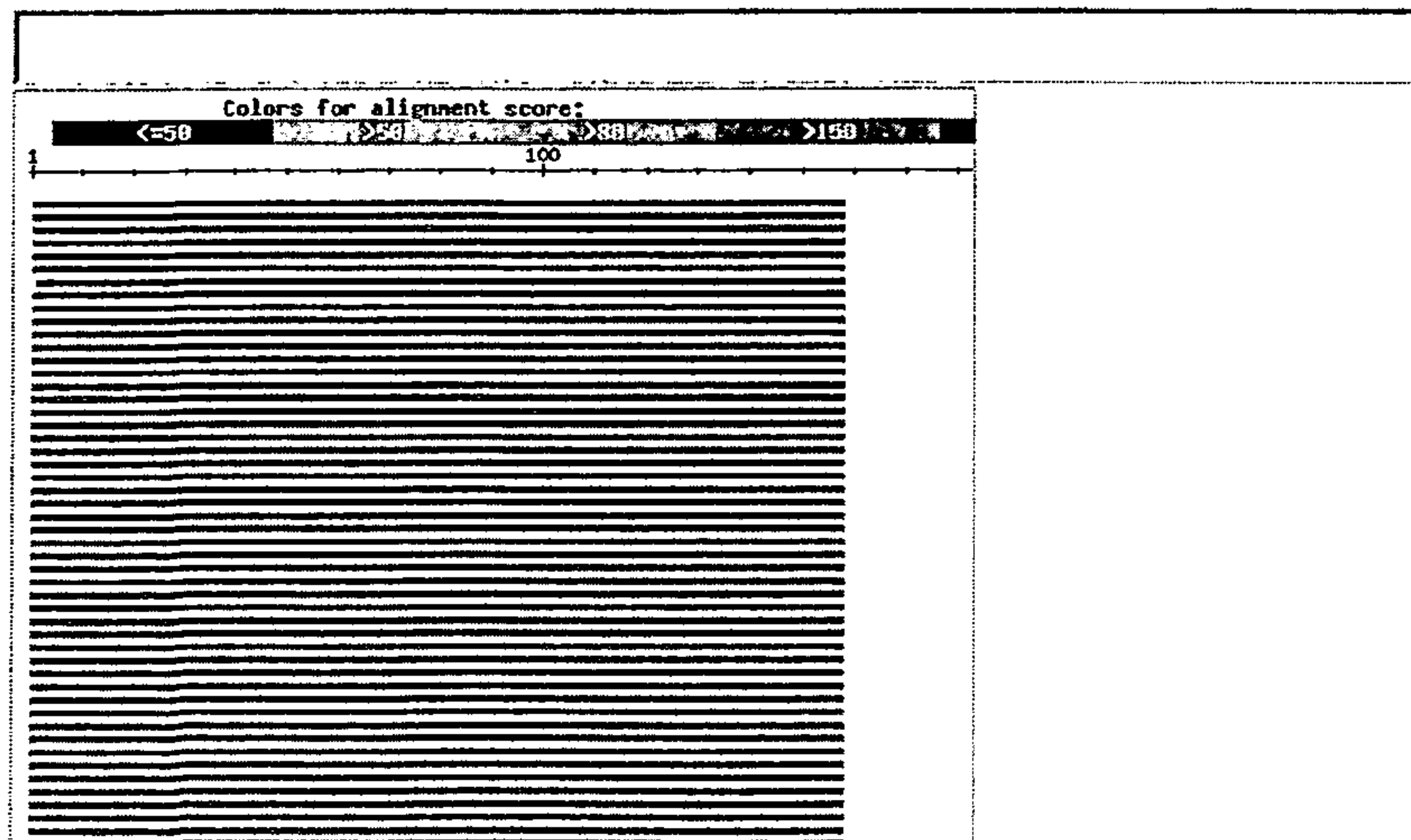
>>>>nrnuc:GI_462476960 Gi|462476960|gb|APGK01000458.1| Dendroctonus ponderosae Seq01000458,
whole genome shotgun sequence. 0/0
Length=1455

Score = 560 bits (620), Expect = 2e-155
Identities = 628/826 (76%), Gaps = 23/826 (2%)
Strand=Plus/Minus

```
Query 318 CTTTTTAAACCTTTGAACTTTTCCTTAATTTGCAGAAATTGCCCTCGACTAAGCTT-G 376
|||||
Sbjct 1380 CTTTTTAAACCTTTTCGACTTTCCCTATCCTTTGCATAAATTGCCCT-GACGTAGCAAAG 1322
```

Blastp – Uniprot:

ORF 180aa:



>>>sptrembl:E5LG72 9ZZZZ E5lg72 SubName: Full=Replicase 3-li... 324 7e-87

>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterize... 302 5e-80
>>>sptrembl:N9JLM2_ACIBA N9jlm2 SubName: Full=Uncharacterize... 286 2e-75

>>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-like protein;. 5/2013
Length=324
Score = 324 bits (831), Expect = 7e-87, Method: Compositional matrix adjust.
Identities = 154/159 (96%), Positives = 157/159 (98%), Gaps = 0/159 (0%)

Query 1 MSDLIVKDNALMNASYNLALVEQRLILLAILEARETGKGINANDPLTVHASSYINQFNVE 60
MSDLIVKDNALMNASYNLALVEQRLILLAI+EARETGKGINANDPLTVHA SYINQFNV+
Sbjct 1 MSDLIVKDNALMNASYNLALVEQRLILLAIEARETGKGINANDPLTVHAGSYINQFNVQ 60

Query 61 RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDDTATVEIIFAPAVVP 120
RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDDTATVEIIFAPAVVP
Sbjct 61 RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDDTATVEIIFAPAVVP 120

Query 121 LITRLEEQFTQYDIEQISELSSAYAVRLYELLCWRSTG 159
LITRLEEQFTQYDIEQIS LSSAYAVR+YELLCWRSTG
Sbjct 121 LITRLEEQFTQYDIEQISGLSSAYAVRMYELLCWRSTG 159

>>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterized protein;. 12/2013
Length=324
Score = 302 bits (773), Expect = 5e-80, Method: Compositional matrix adjust.
Identities = 144/159 (90%), Positives = 151/159 (94%), Gaps = 0/159 (0%)

Query 1 MSDLIVKDNALMNASYNLALVEQRLILLAILEARETGKGINANDPLTVHASSYINQFNVE 60
MS+LIVKDNALMNASYNL LVEQRLILLAI+EARE+GKGINANDPLTVHA SYINQF V
Sbjct 1 MSELIVKDNALMNASYNLDLVEQRLILLAIVEARESGKGINANDPLTVHAESYINQFGVH 60

Query 61 RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDDTATVEIIFAPAVVP 120
R TAYQALKDACKDLFARQFSYQEKREGR NITSRWVSI Y+D+TATVEIIFAPAVVP
Sbjct 61 RTTAYQALKDACKDLFARQFSYQEKREGRANITSRWVSIAYIDETATVEIIFAPAVVP 120

Query 121 LITRLEEQFTQYDIEQISELSSAYAVRLYELLCWRSTG 159
LITRLE+QFTQYDIEQIS LSSAYAVR+YELLCWRSTG
Sbjct 121 LITRLEKQFTQYDIEQISGLSSAYAVRMYELLCWRSTG 159

>>>>sptrembl:N9JLM2_ACIBA N9jlm2 SubName: Full=Uncharacterized protein;. 12/2013
Length=325
Score = 286 bits (733), Expect = 2e-75, Method: Compositional matrix adjust.
Identities = 134/160 (83%), Positives = 150/160 (93%), Gaps = 1/160 (0%)

Query 1 MSDLIVKDNALMNASYNLALVEQRLILLAILEARETGKGINANDPLTVHASSYINQFNVE 60
MS+LIVKDNALMNASYNLALVEQRLILLAI+EARE+G+GINANDPLTVHA SYINQF VE
Sbjct 1 MSELIVKDNALMNASYNLALVEQRLILLAIEARESGRGINANDPLTVHAESYINQFKVE 60

Query 61 RHTAYQALKDACKDLFARQFSYQEKREGR-INITSRWVSQIGYMDDTATVEIIFAPAVV 119
+HTAYQALKDACKDLFARQFSYQ++ +G N+TSRW+SQIGY ++ ATV+++FAPAVV
Sbjct 61 KHTAYQALKDACKDLFARQFSYQORSAGNTTNMTSRWISQIGYTENEATVQLVFAPAVV 120

Query 120 PLITRLEEQFTQYDIEQISELSSAYAVRLYELLCWRSTG 159
PLITRLEEQFT+YDIEQIS LSSAYAVRLYELLCWRSTG
Sbjct 121 PLITRLEEQFTKYDIEQISLSSAYAVRLYELLCWRSTG 160

MSBI1.176 (1766bp)**(MSBI = Multiple Sclerosis Brain Isolate)****(ms36.NnXn.1800.6)**

AAGCTTGCTTAGTCAAAAAAGTTTGAGCAAAGCGAAACATAGGGCAATTTTCATGAAGAAATTGGGCTTTTAAAGTTTTTAA
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ACCCCTACGTTTACCGATCAATACCCCTACGTTTACCGATCAATACCCCTACGTTTACGTTGCGTATAACTACAAAGAATACT
 AGTGTAGTAATAACTTCAAAAAGAATAATTGTAGGTTATGAGCGATTTAATAGTAAAAGATAACGCCCTAATGAATGCTAGTTA
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 TGTAAAGACTTGTGTCGCGTCAATTCAAGTACCAAGAAAAGCGAGAACGAGGACGAATTAATATTACAAGTCGATGGGTTC
 GCAAATTGGCTATATGGACGATACAGCAACCGTTGAGATTATTTTGGCCCTGCGGTTGTTCTCTGATTACACGGCTAGAGG
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 GTGGGGGTAAACCCCTCAACCCCAAAAGCAAAAACACTGTAATCAGGGAAAAACATTTTGTATTTGATCCTTGTTTGTAC
 TCGTAGACACTCGTTTTGTTTTGCTCTTTCTAGAATTACAAAAAAGATATTAGCGAGTGTCTACGAGCGACTCAATGAAAGT
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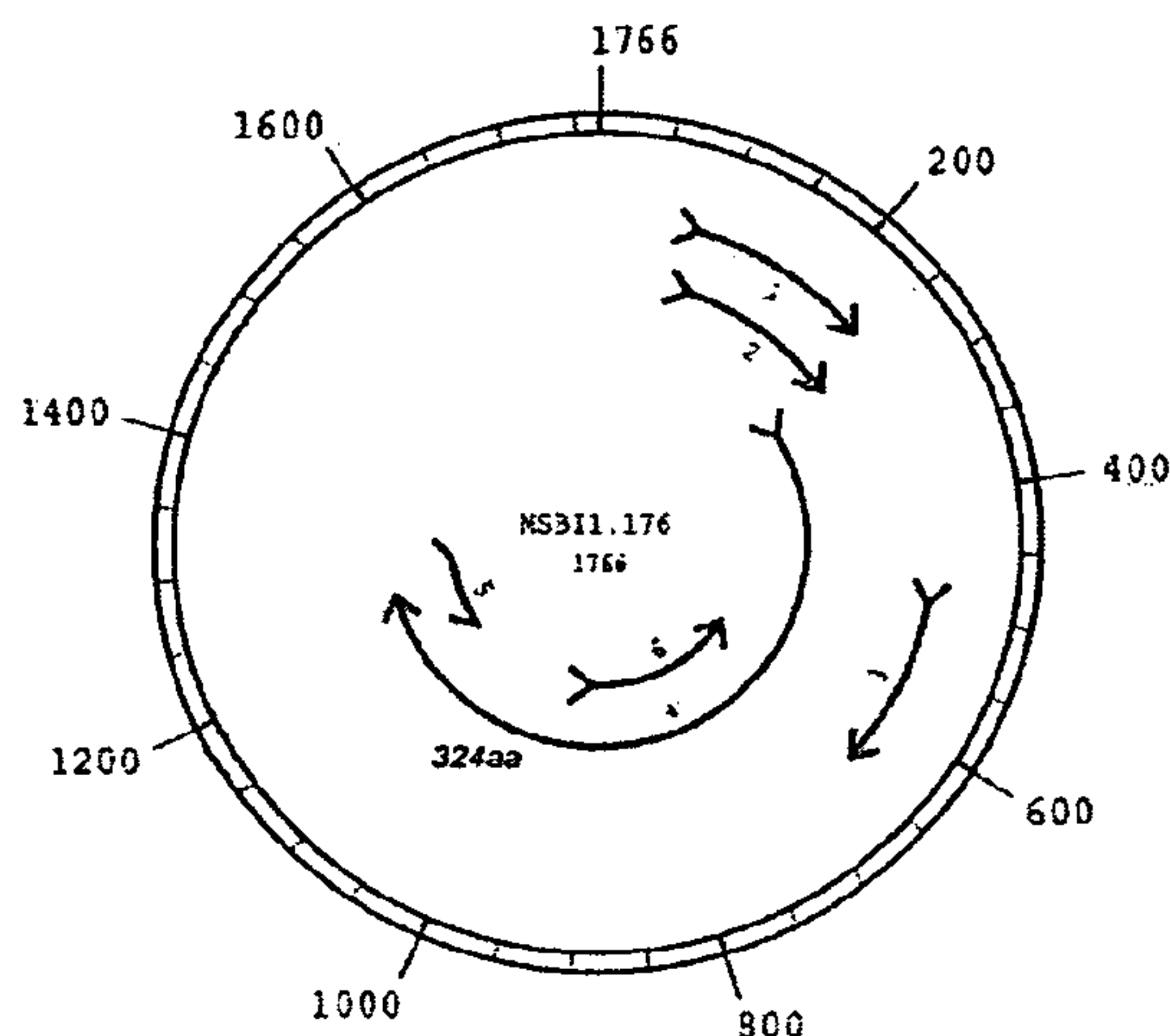
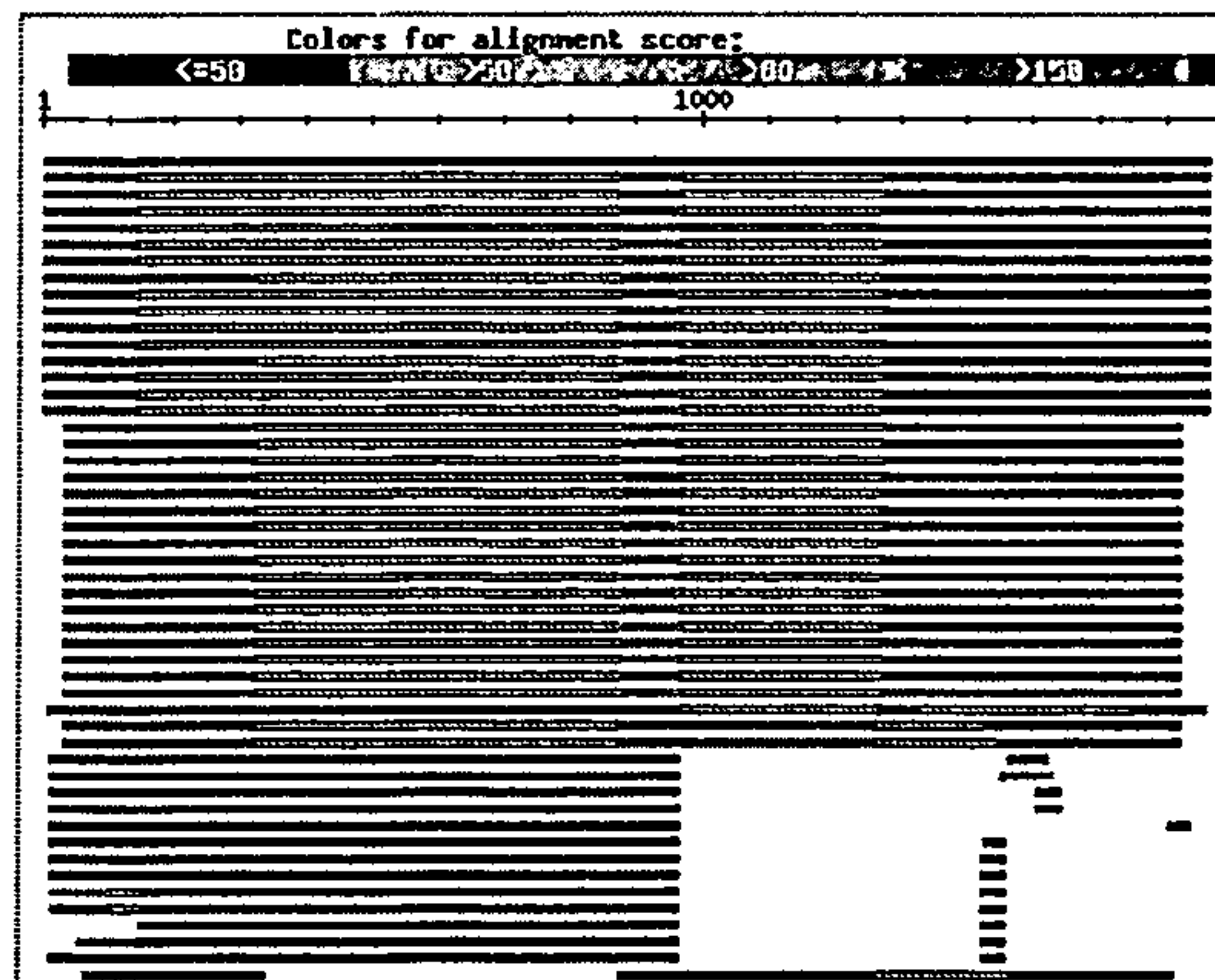
Repeat – 3x 22nt + 17nt**98% nucleotide similarity to TSE-associated circular DNA isolate Sphinx 1.76****ORF: 324aa – 97% similarity to replication protein of Sphinx 1.76**

Figure 1(c)

Blastn – Geall:

>>>nrnuc:GI_313507477 Gi|313507477|gb|HQ444404.1| TSE-associ... 2491 0.0
>>>nrnuc:GI_347602273 Gi|347602273|gb|JN541306.1| Uncultured... 886 0.0

>>>>nrnuc:GI_313507477 Gi|313507477|gb|HQ444404.1| TSE-associated circular DNA isolate
Sphinx 1.76, complete sequence. 0/0
Length=1758

Score = 2491 bits (2762), Expect = 0.0
Identities = 1419/1439 (98%), Gaps = 5/1439 (0%)
Strand=Plus/Plus

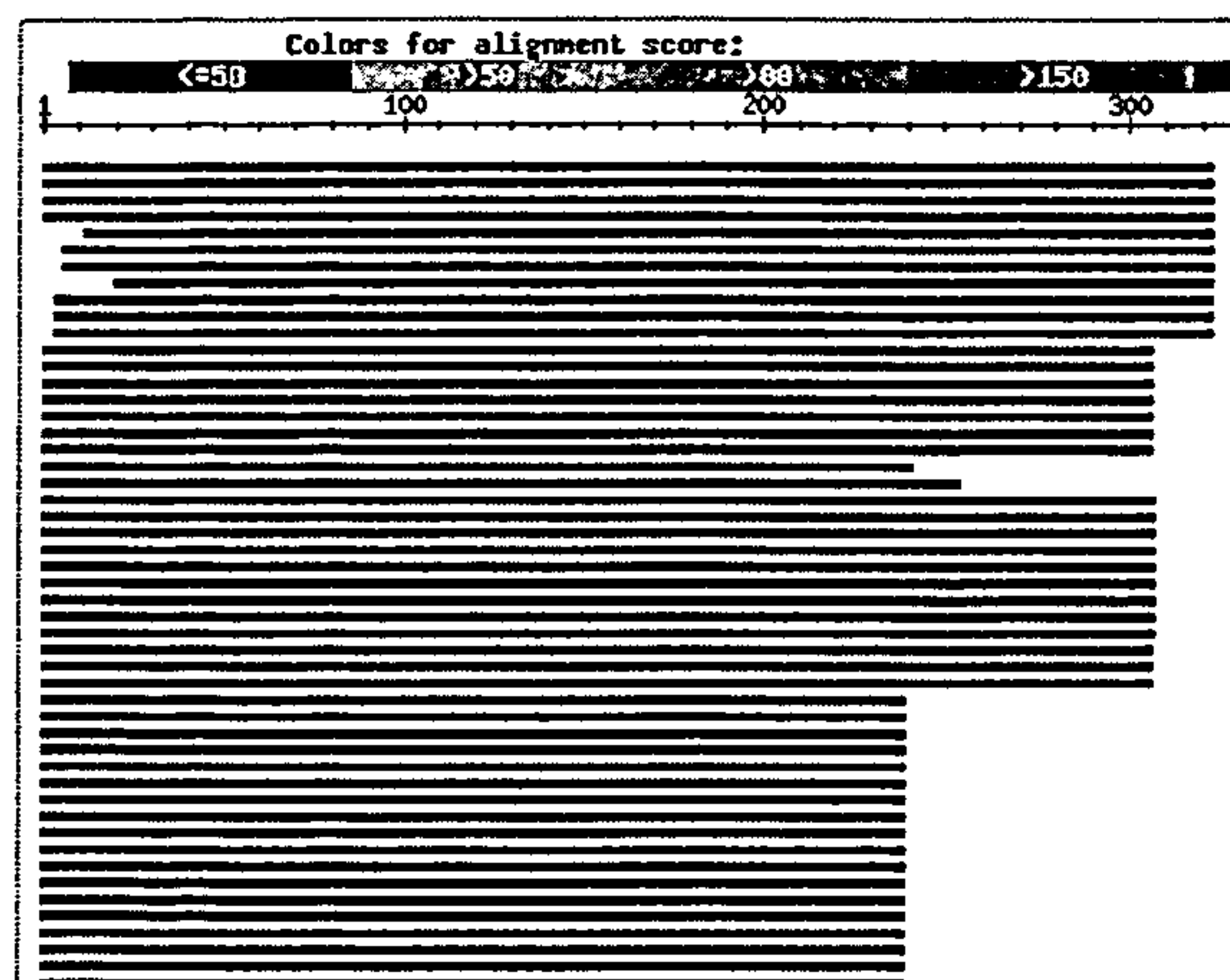
Query	1	AAGCTTGCTTAGTCAAAAAAGTTTGAGCAAAGCGAAAACATAGGGCAATTTTCATGAAGA	60
Sbjct	325	AAGCTTGCTTAGTCAAAAAAGTTTGAGCAAAGCGAAAACATAGGGCAATTTTCATGAAGA	384
Query	61	AATTGGGCTTTTAAAGTTTAAATGCTTTTAAATGCTTTTAGACATGCTAAGAAGCCCA	120
Sbjct	385	AATTGGGCTTTTAAAGTTTAAATG-TTTTAAATGCTTTTAGACATGCTAAGAAGCCCA	443
Query	121	CACAGCAAGGCATACAGAGGACATTCTCCTACGTTTACCGATCAATACCCCTACGTTTAC	180
Sbjct	444	CACAGCAAGGCATACAGAGGACATTCTCCTACGTTTACCGATCAATACCCC--CGTTTAC	501
Query	181	CGATCAATACCCCTACGTTTACCGATCAATACCCCTACGTTTACCTTGCGTATAACTACA	240
Sbjct	502	CGATCAATACCCCTACGTTTACCGATCAATACCCCTACGTTTACCTTGCGTATAACTACA	561
Query	241	AAGAATACTAGTGTAGTAATAACTTCAAAAGAATAATTGTAGGTTATGAGCGATTTAATA	300
Sbjct	562	AAGAATACTAGTGTAGTA-TAACTTCAAAAGAATAATTGTAGGTTATGAGCGATTTAATA	620
Query	301	GTAAAAGATAACGCCCTAATGAATGCTAGTTATAACTTAGCTTTGGTTGAACAGAGGTTA	360
Sbjct	621	GTAAAAGATAACGCCCTAATGAATGCTAGTTATAACTTAGCTTTGGTTGAACAGAGGTTA	680
Query	361	ATTCTATTAGCAATCATAGAAGCGAGAGAAACAGGCAAAGGGATTAATGCCAATGATCCT	420
Sbjct	681	ATTCTATTAGCAATCATAGAAGCGAGAGAAACAGGCAAAGGGATTAATGCCAATGATCCT	740
Query	421	TTAACAGTTCATGCAAGTAGCTATATCAATCAATTTAACGTAGAAAGGCATACGGCATAT	480
Sbjct	741	CTTACGGTTCATGCAGGTAGCTATATCAATCAATTTAACGTACAAAGGCATACGGCATAT	800
Query	481	CAAGCCCTCAAAGATGCTTGTAAGACTTGTTTGCCCGTCAATTCAGTTACCAAGAAAAG	540
Sbjct	801	CAAGCCCTCAAAGATGCTTGTAAGACTTGTTTGCCCGTCAATTCAGTTACCAAGAAAAG	860
Query	541	CGAGAACGAGGACGAATTAATATTACAAGTCGATGGGTTTCGCAAATTGGCTATATGGAC	600
Sbjct	861	CGAGAACGAGGACGAATTAATATTACAAGTCGATGGGTTTCGCAAATTGGCTATATGGAC	920
Query	601	GATACAGCAACCGTTGAGATTATTTTGCCCGTGCAGTTGTTCTCTGATTACACGGCTA	660
Sbjct	921	GATACAGCAACCGTTGAGATTATTTTGCCCGTGCAGTTGTTCTCTGATTACACGGCTA	980

Query	661	GAGGAACAGTTCACCCAGTACGATATTGAGCAAATTAGCGGTTTATCGAGTGCATATGCT	720
Sbjct	981	GAGGAACAGTTCACCCAGTACGATATTGAGCAAATTAGCGGTTTATCGAGTGCATATGCT	1040
Query	721	GTTCGTATGTACGAACTGCTGATTTGTTGGCGTAGCACAGGCAAAACACCAATTATTGAG	780
Sbjct	1041	GTTCGTATGTACGAACTGCTGATTTGTTGGCGTAGCACAGGCAAAACACCAATTATTGAG	1100
Query	781	CTAGACGAGTTTAGAAAGCGAATAGGTGTTTTAGATACTGAATACACTAGAACAGATAAT	840
Sbjct	1101	CTAGACGAGTTTAGAAAGCGAATAGGTGTTTTAGATACTGAATACACTAGAACAGATAAT	1160
Query	841	TTAAAGATGCGAGTTATTGAATTAGCCCTAAAACAAATCAACGAACATACAGACATCACA	900
Sbjct	1161	TTAAAGATGCAAGTTATTGAATTAGCCCTAAAACAAATCAACGAACATACTGACATCACA	1220
Query	901	GCAAGCTATGAACAACACAAAAAGGGCGAGTGATTACAGGATTCTCATTCAAGTTTAAG	960
Sbjct	1221	GCAAGCTATGAACAACACAAAAAGGGCGAGTGATTACCGGATTCTCATTCAAGTTTAAG	1280
Query	961	CACAAGAAACAAAACAGCGATAAAACGCCAAAAAATAGCGATTCTAGCCACGTATCGTA	1020
Sbjct	1281	CACAAGAAACAAAACAGCGATAAAACGCCCTGATACTAACGCTTCTAGCCACGTATCGTA	1340
Query	1021	AAACATAGTCAAATCCCTACCAACATTGTAAAACAGCCTGAAAACGCCAAAATGAGCGAT	1080
Sbjct	1341	AAACATAGTCAAATCCCTACCAACATTGTAAAACAGCCTGAAAACGCCAAAATGAGCGAT	1400
Query	1081	TTAGAACATAGAGCGAGCCGTGTTACAGGGGAAATAATGCGAAATCGTCTGTCAGATCGG	1140
Sbjct	1401	TTAGAACATAGAGCGAGCCGTGTTACAGGGGAAATAATGCGAAATCGTCTGTCAGATCGG	1460
Query	1141	TTTAAACAAGGCGATGAATCAGCAATCGACATGATGAAACGTATTCAAAGTGAAATAATA	1200
Sbjct	1461	TTTAAACAAGGCGATGAATCAGCAATCGACATGATGAAACGTATTCAAAGTGAAATAATA	1520
Query	1201	ACCGATGCAATAGCAGACCAAGTGGGAAAGCAAACCTGGAGGAGTTTGGCGTGGTTTTTTAG	1260
Sbjct	1521	ACCGATGCAATAGCAGACCAAGTGGGAAAGCAAACCTGGAGGAGTTTGGCGTGGTTTTTTAG	1580
Query	1261	TCATGACGATTTCCCGAAGGGCGCACTTAGCCATTGAGAAAAATCTTCGATTTTTTCAAT	1320
Sbjct	1581	TCATGACGATTTCCCGAAGGGCGCACTTAGCCATTGAGAAAAATCTTCGATTTTTTCAAT	1640
Query	1321	GGAAGTCCGTGGGGGTAAACCCCTCAACCCCAAAGCAAAAACACTGTAATCAGGGAAAA	1380
Sbjct	1641	GGAAGTCCGTGGGGGTAAACCCCTCAACCCCAAAGCAAAAACACTGTAATCAGGGAAAA	1700
Query	1381	AACATTTTTGATTTTGATCCTTGTTTGTCACCTCGTAGACACTCGTTTTGTTTTGCTCTT	1439
Sbjct	1701	AACATTTTTGATTTTGATCCTTGTTTG-CACTCGTAGACACTCGTTTTGTTTTGCTCTT	1758

Score = 587 bits (650), Expect = 2e-163
 Identities = 325/325 (100%), Gaps = 0/325 (0%)
 Strand=Plus/Plus

Query	1440	TCTAGAATTCACAAAAAGATATTAGCGAGTGTCTACGAGCGACTCAATGAAAGTTCGAT	1499
Sbjct	1	TCTAGAATTCACAAAAAGATATTAGCGAGTGTCTACGAGCGACTCAATGAAAGTTCGAT	60
Query	1500	TATTCCCCCTCTGGAAAACCGCTTTTAAAAATATTGGCTGCTAGATGGTTTTTACTATAG	1559
Sbjct	61	TATTCCCCCTCTGGAAAACCGCTTTTAAAAATATTGGCTGCTAGATGGTTTTTACTATAG	120
Query	1560	TGAGGTTTTGCTTTTaaaaaaCACGAGCAAAGCGAGTTCATAGTTGCTTTTGCTTGTTT	1619
Sbjct	121	TGAGGTTTTGCTTTTAAAAAACACGAGCAAAGCGAGTTCATAGTTGCTTTTGCTTGTTT	180
Query	1620	TCGGGTCTTAGGGGAAATCCCCTAACAAAGTCCTCGAATATCAAAATGTGGCTACATTTTG	1679
Sbjct	181	TCGGGTCTTAGGGGAAATCCCCTAACAAAGTCCTCGAATATCAAAATGTGGCTACATTTTG	240
Query	1680	TATATACGGGTAGGCTTGCTTATTTGAttttttcttCTAAACCTTTGACTTCTTCCCC	1739
Sbjct	241	TATATACGGGTAGGCTTGCTTATTTGATTTTTTTCTTCTAAACCTTTGACTTCTTCCCC	300
Query	1740	ATTGTTGCAGAAATTGCCCTCGA	1764

Sbjct 301 |||||
ATTGTTTGCAGAAATTGCCCTCGA 325

BlastP –Uniprot:**ORF 324aa:**

>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-li... 658 0.0
>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterize... 569 5e-160

>>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-like protein;. 5/2013
Length=324
Score = 658 bits (1698), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 316/324 (97%), Positives = 319/324 (98%), Gaps = 0/324 (0%)

Query	1	MSDLIVKDNALMNASYNLALVEQRLILLAIIEARETGKGINANDPLTVHASSYINQFNVE	60
		MSDLIVKDNALMNASYNLALVEQRLILLAIIEARETGKGINANDPLTVHA SYINQFNV+	
Sbjct	1	MSDLIVKDNALMNASYNLALVEQRLILLAIIEARETGKGINANDPLTVHAGSYINQFNVQ	60
Query	61	RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEIIFAPAVVP	120
		RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEIIFAPAVVP	
Sbjct	61	RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEIIFAPAVVP	120
Query	121	LITRLEEQFTQYDIEQISGLSSAYAVRMYELLCWRSTGKTPIELDEFKRIGVLDTEY	180
		LITRLEEQFTQYDIEQISGLSSAYAVRMYELLCWRSTGKTPIELDEFKRIGVLDTEY	
Sbjct	121	LITRLEEQFTQYDIEQISGLSSAYAVRMYELLCWRSTGKTPIELDEFKRIGVLDTEY	180
Query	181	TRTDNLKMRVIELALKQINEHTDITASIEQHKKGRVITGFSFKHKKQNSDKTPKNSDS	240
		TRTDNLKM+VIELALKQINEHTDITASIEQHKKGRVITGFSF FKHKKQNSDKTP + S	
Sbjct	181	TRTDNLKMVIELALKQINEHTDITASIEQHKKGRVITGFSFMFKHKKQNSDKTPDTNAS	240
Query	241	SPRIVKHSQIPTNIVKQPENAKMSDLEHRASRVTEIMRNRLSDRFKQGDESAIDMMKRI	300
		SPRIVKHSQIPTNIVKQPENAKMSDLEHRASRVTEIMRNRLSDRFKQGDESAIDMMKRI	
Sbjct	241	SPRIVKHSQIPTNIVKQPENAKMSDLEHRASRVTEIMRNRLSDRFKQGDESAIDMMKRI	300
Query	301	QSEIITDAIADQWESKLEEFVVF 324	
		QSEIITDAIADQWESKLEEFVVF	
Sbjct	301	QSEIITDAIADQWESKLEEFVVF 324	

>>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterized protein;. 12/2013
Length=324

Score = 569 bits (1467), Expect = 5e-160, Method: Compositional matrix adjust.
Identities = 272/324 (83%), Positives = 294/324 (90%), Gaps = 0/324 (0%)

Query	1	MSDLIVKDNALMNASYNLALVEQRLILLAIIEARETGKGINANDPLTVHASSYINQFNVE	60
		MS+LIVKDNALMNASYNL LVEQRLILLAI+EARE+GKGINANDPLTVHA SYINQF V	
Sbjct	1	MSELIVKDNALMNASYNLDLVEQRLILLAIIVEARESGKGINANDPLTVHAESYINQFGVH	60
Query	61	RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEIIFAPAVVP	120
		R TAYQALKDACKDLFARQFSYQEKREGR NITSRWVSI Y+D+TATVEIIFAPAVVP	
Sbjct	61	RTTAYQALKDACKDLFARQFSYQEKREGRANITSRWVSIAYIDETATVEIIFAPAVVP	120
Query	121	LITRLEEQFTQYDIEQISGLSSAYAVRMYELLCWRSTGKTPIELDEFKRIGVLDTEY	180
		LITRLE+QFTQYDIEQISGLSSAYAVRMYELLCWRSTGKTP+IEL EFRKRIGVLDTEY	

Sbjct 121 LITRLEKQFTQYDIEQISGLSSAYAVRMYELICWRSTGKTPVIELGEFRKRIGVLDTEY 180

Query 181 TRTDNLKMRVIELALKQINEHTDITASIEQHKKGRVITGFSFKFKHKKQNSDKTPKNSDS 240
RTDNLKMRVIELALKQIN+HTDITA+YEQHKKGR ITGFSFKFK K++ +TPKNSDS

Sbjct 181 IRTDNLKMRVIELALKQINDHTDITATYEQHKKGRITITGFSFKFKQKRKTELETPKNSDS 240

Query 241 SPRIVKHSQIPTNIVKQPENAKMSDLEHRASRVTGEIMRNRLSDRFKQGDESAIDMMKRI 300
K +IPTN+VKQPENA MSDL+HRAS++TG IM NRLSDRFKQ DES + MM RI

Sbjct 241 DVPKQKSVEIPTNLVKQPENANMSDLQHRASKITGLIMSNRLSDRFKQSDESIMQMMARI 300

Query 301 QSEIITDAIADQWESKLEEFQVVF 324
QSEI +AIA+QWE+KLEEFQV+F

Sbjct 301 QSEITDEAIANQWENKLEEFQVIF 324

ProtSweep

A Protein Identification Tool

Results for /home/vir088/rindneu/tsekompl/MSBI1.176.324.pep

Number of residues: 324	Molecular weight: 37.29 kD
Charge: 1	Isoelectric point: 8.14

more...

Prediction of protein localization:

cyto	13 %
cyto nucl	10.5 %
extr	10 %

Identified Protein & Transcript:

Protein:

id: sptrembl:E5LG72 9ZZZZ

valuation: homologous

scientific organism: Tupaia belangeri

common organism: Common tree shrew

abstract: E5lg72 SubName: Full=Replicase 3-like protein;. 5/2013Length=324

isoform:

GO information:

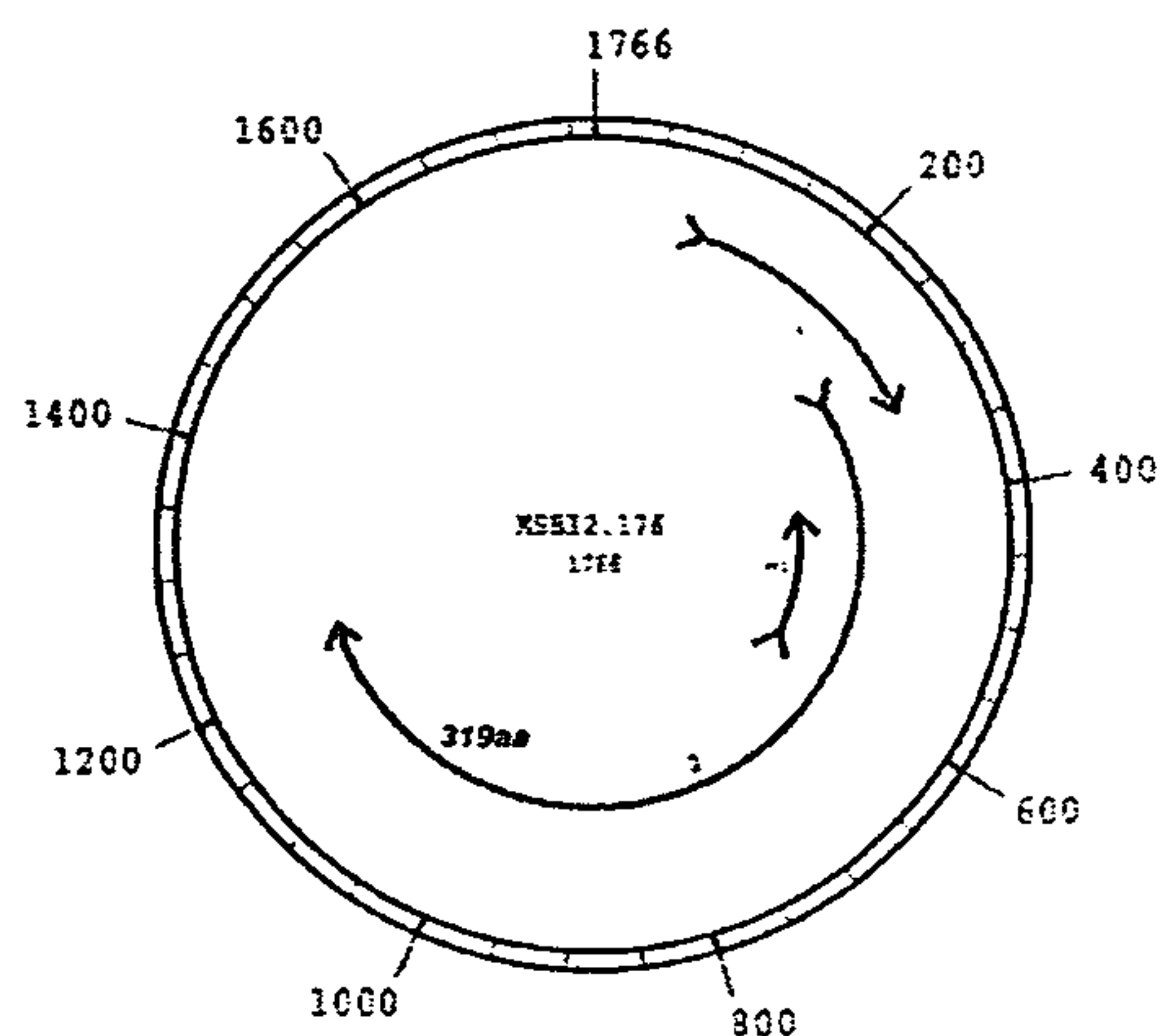
accession	group	name	evidence
GO:0005727	cellular component	extrachromosomal circular DNA	IEA:InterPro
GO:0003887	molecular function	DNA-directed DNA polymerase activity	IEA:InterPro
GO:0006270	biological process	DNA replication initiation	IEA:InterPro

Interpro information:

id	short name
IPR000525	Initiator_Rep_prot
IPR011991	WHTH_DNA-bd_dom

MSBI2.176 (1766bp)**(ms36.NnXn.1800.6)**

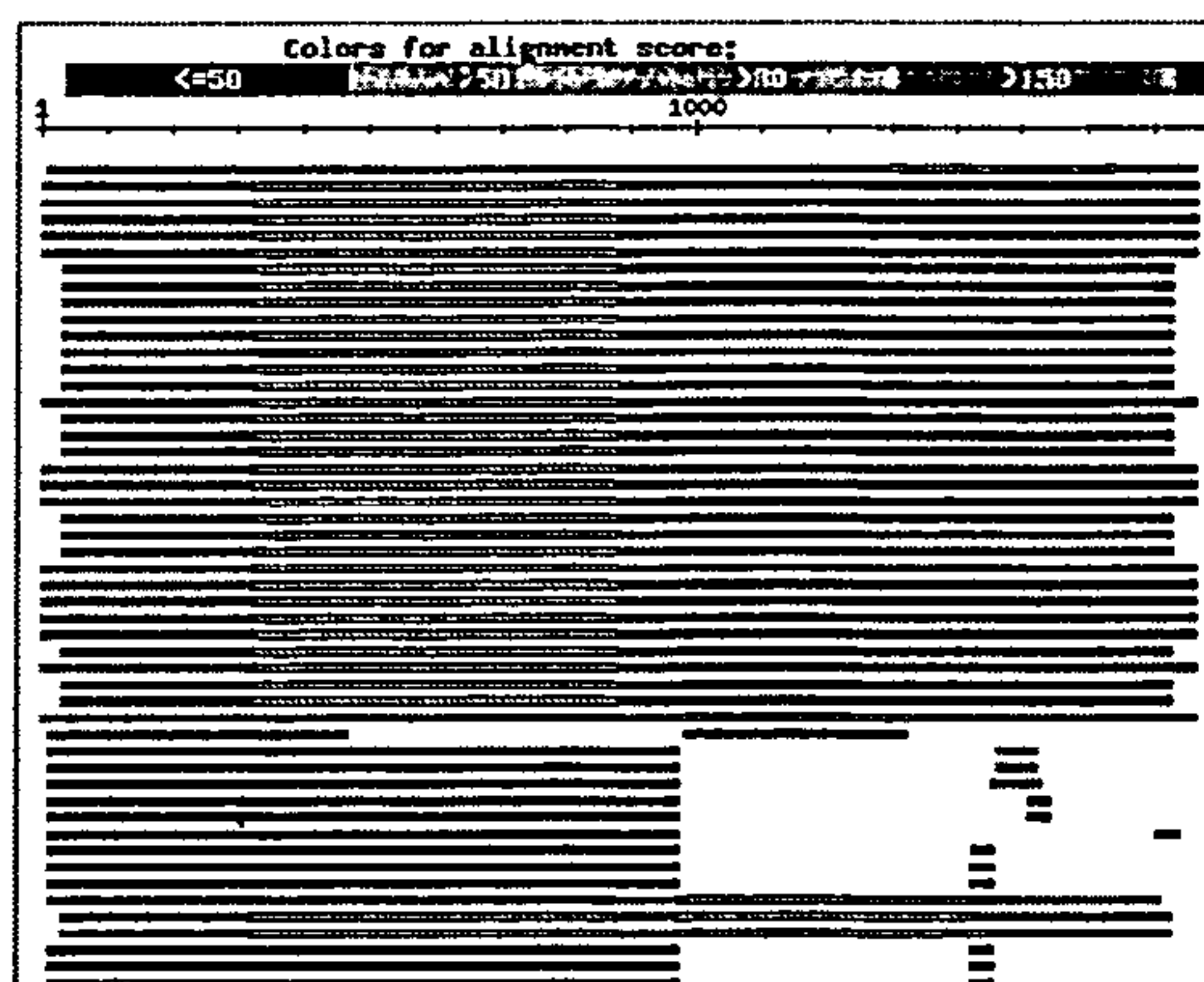
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 ATGCTTTTAAATGCTTTTAGACATGCTGAAACGCTTATATAGCAATGCATACAGAGGACATATGTCCACGTTTACCTATCAAT
ATGTCCACGTTTACCTATCAATATGTCCACGTTTACCTATCAATATGTCCACGTTTACCTTGCGTATTACACACATTTAAAT
 AGTATGGATATATCCAATGAAATTATAATGTGTACTTATGAGCAAATTAGTAGTGAAAGACAATGCCCTAATGAACGCTAGTT
 ACAACTTGATCTCGTTGAACAGCGTTTAATTCTATTGGCAATCATCGAAGCAAGAGAATCAGGCAAAGGAATTAATGCAAAT
 GACCCGCTTACGGTTCATGCAGAGAGTTATATCAATCAATTTGGTGTTCATCGAGTAAGTGCATATCAAGCTCTCAAAGATGC
 TTGTGATAACTTGTGTTGCACGTCAATTCAGCTACCAATCCAAAAGTGAAAAAGGGAACATACAAAATCATCGTTCACGTTGGG
 TTAGTGAAATTATTTACATTGATACAGAAGCAACAGTAAAAATAATTTGCACCTGCTATTGTCCCACTGATTACAAGGCTA
 GAAGAACAGTTCACCAAGTATGATATTGAGCAAATTAGTGATTTATCGAGTGCTTATGCAATTCGCTTATACGAGTTATTGAT
 TTGCTGGCGTAGCACAGGGAAAACACCAATTATTGGGCTAGGCGAATTTAGAAATCGGGTTGGTGTGTAGATAGTGAATATC
 ATCGAATTGCACACTTGAAAGAACGAGTTATTGAACATTCAATTAAACAGATTAACGAGCATACCGACATCACAGCCACCTAC
 GAACAGCACAAAAAGGGCGGACAATCACAGGATTTTCATTCAAGTTTAAGCAGAAGAAGCCCAAACAAGCCGAAATTGCTAC
 AGAAACGCCAAAAACAGCCACGAATGACCCAGACACGACAAAACCCCTTACAGAGCCTCAGATCGCAAATAACAGCATGATTC
 TGTGCAAACCTAGGCAGTATTTTCACTTGAAGTAAGTCCAGACTATCCAGCTTTTGCAAATTGGATTGGGAACATTTTGAGG
 AACCTTGAAAAAGCAGATGAACAAATAGCAAAACGGATTTTCACAGCATTGAAAACAGAAACCGACTACAGCAAGAAAACTA
 ATTTTTAGTTGTGATGGGTTTTCCCGAAATAACATGAAGGGCGCACTTACGCAAATTTTTGCTACGCCAAATTTTGCAAGTA
 CGGTCAGGGAAACCCCGACACCCCAAAGCAAAAACACTGTAATCAGGGAAAAACATTTTTGATTTTGATCCTTGTTTGTC
 CTCGTAGACACTCGTTTTGTTTTGCTCTTTCTAGAATTCACAAAAAGATATTAGCGAGTGTCTACGAGCGACTCAATGAAAG
 TTCGATTATTTCCCTCTGGAAAACCGCTTTTAAAAATATTGGCTGCTAGATGGTTTTTACTATAGTGAGGTTTTGCTTTTAA
 AAAACACGAGCAAAGCGAGTTCATAGTTGCTTTTGCTTGTGTTTTCGGGTCTTAGGGGAAATCCCCTAACAAGTCCTCGAATAT
 CAAAATGTGGCTACATTTTGTATATACGGGTAGGCTTGCTTATTTGATTTTTTTTCTTCTAAACCTTTGACTTCTTCCCCATT
 GTTTGCAGAAATGCCCCCGACC

Repeat – 3x 22nt + 18nt

78% nucleotide similarity in 984nt and 95-99% to 431nt of TSE-associated circular DNA isolate Sphinx 1.76

ORF: 319aa – initiation replication-B protein 65% amino acid similarity to Acinetobacter radioresistens

Figure 1(d)

Blastn - Geall:

```
>>>nrnuc:GI_462476960 Gi|462476960|gb|APGK01000458.1| Dendro... 1943 0.0
>>>nrnuc:GI_347602255 Gi|347602255|gb|JN541288.1| Uncultured... 1449 0.0
>>>>nrnuc:GI_462476960 Gi|462476960|gb|APGK01000458.1| Dendroctonus ponderosae Seq01000458,
whole genome shotgun sequence. 0/0
Length=1455
Score = 1943 bits (2154), Expect = 0.0
Identities = 1202/1284 (93%), Gaps = 1/1284 (0%)
Strand=Plus/Minus
```

```
Query 11 AGTCAAAAAGTTTGTAGCAAAGCGAAAACATAGGGCAATTTTCGTGATGAAAATGGGCTT 70
|||||
Sbjct 1318 AGTCAAAAAGTTTGTAGAGAAGCGAAAACATAGGGCAATTT-CATGGTGAGAATGGGCTT 1260

Query 71 TTAATGTTTTTAAATGCTTTTAAATGCTTTTAGACATGCTGAAACGCTTATATAGCAATG 130
|||||
Sbjct 1259 TTAAGGTTTTTAAAGCTTTTAAATGCTTTTAGACATGCTGAAACGACCACACAGCAAGG 1200

Query 131 CATACAGAGGACATATGTCCACGTTTACCTATCAATATGTCCACGTTTACCTATCAATAT 190
|||||
Sbjct 1199 CATACAGAGGGCATATGTCCACGTTTACCTATCAATATGTCCACGTTTACCTATCAATAT 1140

Query 191 GTCCACGTTTACCTATCAATATGTCCACGTTTACCTTGCGTATTTACACACATTTAAATA 250
|||||
Sbjct 1139 GTCCACGTTTACCTATCAATATGTCCACGTTTACCTTGCGTATTTACACACATTTAAATA 1080

Query 251 GTATGGATATATCCAATGAAATTATAATGTGTACTTATGAGCAAATTAGTAGTGAAAGAC 310
|||||
Sbjct 1079 ATATGGATATATCCAATAAAATTATAATGTGTACTTATGAGTAGGTTAGTAGTGAAAGAC 1020

Query 311 AATGCCCTAATGAACGCTAGTTACAACCTGGATCTCGTTGAACAGCGTTTAAATCTATTG 370
|||||
Sbjct 1019 AATGCCCTAATGAACGCTAGTTATAAATCTGGATCTCGTTGAACAGCGTTTAAATCCTATTG 960

Query 371 GCAATCATCGAAGCAAGAGAATCAGGCAAAGGAATTAATGCAAATGACCCGCTTACGGTT 430
|||||
Sbjct 959 GCAATCATCGAAGCGAGGAGTCAGGCAAAGGAATTAACGCCAATGACCCCTCAACAATC 900

Query 431 CATGCAGAGAGTTATATCAATCAATTTGGTGTTTCATCGAGTAACTGCATATCAAGCTCTC 490
|||||
Sbjct 899 CATGCAGAGAGCTACATCAATCAATTTGGTGTTTCATCGAGTAACTGCATATCAAGCTCTC 840

Query 491 AAAGATGCTTGTGATAAATGTTTGCACGTCAATTCAGCTACCAATCCAAAAGTGAAAAA 550
|||||
Sbjct 839 AAAGATGCTTGTGATAAATGTTTGCACGTCAATTCAGCTATCAGTCCAAAAGTGAAAAA 780

Query 551 GGGAACATACAAAATCATCGTTCACGTTGGGTTAGTGAAATTATTTACATTGATACAGAA 610
|||||
Sbjct 779 GGGAACATACAAAATCATCGTTCACGTTGGGTTAGTGAAATTATTTACATCGACACAGAA 720

Query 611 GCAACAGTAAAAATAATATTTGCACCTGCTATTGTCCACTGATTACAAGGCTAGAAGAA 670
|||||
Sbjct 719 GCAACAGTAAAAATAATCTTTGCACCTGCTATCGTCCACTGATTACAAGATTAGAAGAA 660
```

```
Query 671 CAGTTCACCAAGTATGATATTGAGCAAATTAGTGATTTATCGAGTGCTTATGCAATTCGC 730
          |||
Sbjct 659 CAGTTCACCAAGTATGATATTCAGCAAATTAGTGATTTATCGAGTGCTTATGCAATCCGC 600

Query 731 TTATACGAGTTATTGATTTGCTGGCGTAGCACAGGGAAAACACCAATTATTGGGCTAGGC 790
          |||
Sbjct 599 TTATACGAATTATTGATTTGTTGGCGTAGCACAGGGAAAACGCCAATTATTGAATTAGCT 540

Query 791 GAATTTAGAAATCGGGTTGGTGTGTTAGATAGTGAATATCATCGAATTGCACACTTGAAA 850
          |||
Sbjct 539 GAATTTAGGAATCGGGTTGGTGTGTTAGATACTGAATATCATCGAATTGCCCCACTTGAAA 480

Query 851 GAACGAGTTATTGAACATTCAATTAAACAGATTAACGAGCATACCGACATCACAGCCACC 910
          |||
Sbjct 479 GAGCGAGTTATTGAACATTCAATTAAACAAATTAACGAACATACCGACATCACAGCGACC 420

Query 911 TACGAACAGCACAAAAAGGGCGGACAATCACAGGATTTTCATTCAAGTTTAAGCAGAAG 970
          |||
Sbjct 419 TACGAACAGCATAAAAAGGGCGAGTGATTACAGGGTTCTCATTCAAATTTAAGCAGAAG 360

Query 971 AAGCCCAAAACAAGCCGAAATTGCTACAGAAACGCCAAAAACAGCCACGAATGACCCAGAC 1030
          |||
Sbjct 359 AAGCCCAAAACAAGCCGAGATTGCCACAGAAACGCCAAAAACAGCCACGAATGACCTAGAT 300

Query 1031 ACGACAAAACCCCTTACAGAGCCTCAGATCGCAAAATACAGCATGATTCTGTGCAAACTA 1090
          |||
Sbjct 299 ACGATAAAACCCCTTACAGAGCCACAGATCGCAAAATACAGCATGATTCTGTGCAAACTA 240

Query 1091 GGCAGTATTTTCAGACTTGAGTAACTTCCCAGACTATCCAGCTTTTGCAAATTGGATTGGG 1150
          |||
Sbjct 239 GGCAGTATTTTCAGACTTGAGTAACTTCCCAGACTATCCAGCTTTTGCAAATTGGATTGGG 180

Query 1151 AACATTTTGAGGAACCCCTGAAAAAGCAGATGAACAAATAGCAAAACGGATTTTCACAGCA 1210
          |||
Sbjct 179 AACATTTTGAGGAACCCCTGAAAAAGCAGATGAACAAATAGCAAAACGGATTTTCACAGCA 120

Query 1211 TTGAAAACAGAAACCGACTACAGCAAGAAAACTAATTTTGTAGTTGTGATGGGTTTCCC 1270
          |||
Sbjct 119 TTGAAAACAGAAACCGACTACAGCAAGAAAACTAATTTTGTAGTTGTGATGGGTTTCCC 60

Query 1271 GAAATAACATGAAGGGCGCACTTA 1294
          |||
Sbjct 59 GAAATAACATGAAGGGCGCACTTA 36
```

Score = 134 bits (148), Expect = 3e-27
Identities = 108/127 (85%), Gaps = 4/127 (3%)
Strand=Plus/Minus

```
Query 1641 CCTAACAAGTCCTCGAATATCAAAATGTGGCTACATTTTGTATATACGGGTAGGCTTGCT 1700
          |||
Sbjct 1455 CCTAACAAGTCCCCGAATATCAAAATGTGGCTACATTTTGTATATACGGGTAGGCTTGCT 1396

Query 1701 TATTTGAttttttttC-TTCTAAACCTTT-GACTTCTTCCCCATTGTTGCAGAAATGCC 1758
          |||
Sbjct 1395 TATTGAATCTAATTCTTTTAAACCTTTTCGACT--TTCCCTATCCTTTGCATAAATTGC 1338

Query 1759 CCCCAGAC 1765
          |||
Sbjct 1337 CCCTGAC 1331
```

>>>>nrnuc:GI_347602255 Gi|347602255|gb|JN541288.1| Uncultured bacterium plasmid clone
S6GIO-17 genomic sequence. 0/0
Length=1215
Score = 1449 bits (1606), Expect = 0.0
Identities = 858/893 (96%), Gaps = 11/893 (1%)
Strand=Plus/Plus

```
Query 881 ATTAACGAGCATACCGACATCACAGCCACCTACGAACAGCACAAAAAGGGCGGACAATC 940
          |||
Sbjct 1 ATCAACGAGCACACCGACATCACAGCCACCTACGAACAGCACAAAAAGGGCGGACAATC 60

Query 941 ACAGGATTTTCATTCAAGTTTAAGCAGAAGAAGCCCAACAAGCCGAAATTGCTACAGAA 1000
          |||
Sbjct 61 ACAGGATTTTCATTCAAGTTTAAGCAGAAGAAGCCCAACAAGCCGAAATTGCTACAGAA 120

Query 1001 ACGCCAAAAACAGCCACGAATGACCCAGACACGACAAAACCCCTTACAGAGCCTCAGATC 1060
```

```

Sbjct 121      |||||
ACGCCAAAACAGCCACGAATGACCCAGACACGACAAAACCCCTTACAGAGCCTCAGATC 180

Query 1061     GCAAAATACAGCATGATTCTGTGCAAACTAGGCAGTATTTTCAGACTTGAGTAACTTCCCA 1120
|||||

Sbjct 181      GCAAAATACAGCATGATTCTGTGCAAACTAGGCAGTATTTTCAGACTTGAGTAACTTCCCA 240
|||||

Query 1121     GACTATCCAGCTTTTGCAAATTGGATTGGGAACATTTTGAGGAACCCTGAAAAAGCAGAT 1180
|||||

Sbjct 241      GACTATCCAGCTTTTGCAAATTGGATTGGGAACATTTTGAGGAACCCTGAAAAAGEAGAT 300
|||||

Query 1181     GAACAAATAGCAAAACGGATTTTCACAGCATTGAAAACAGAAACCGACTACAGCAAGAAA 1240
|||||

Sbjct 301      GAACAAATAGCAAAACGGATTTTCACAGCATTGAAAACAGAAACCGACTACAGCAAGAAA 360
|||||

Query 1241     AACTAATTTTGTGATGGGTTTCCCGAAATAACATGAAGGGCGCACTTACGCA-- 1298
|||||

Sbjct 361      AACTAATTTTGTGATGGGTTTCCCGAAATAACATGAAGGGCGCACTTAGCCATT 420
|||||

Query 1299     -----AAATTTTGCTACGCCAAATTTTGCAAGTACGGTCAGGGAAACCCCGACACCCCA 1353
|||||

Sbjct 421      GAGAAAAATCTTCGATTTTTTCAAT---GGAAGTCCGTGGGGGTAAACCCCTCAACCCCA 477
|||||

Query 1354     AAAGCAAAAACACTGTAATCAGGGAAAAAACATTTTGTATTTGATCCTTGTTGTCACT 1413
|||||

Sbjct 478      AAAGCAAAAACACTGTAATCAGGGAAAAAACATTTTGTATTTGATCCTTGTTGTCACT 537
|||||

Query 1414     CGTAGACACTCGTTTGTGTTTGCTCTTTCTAGAATTCACAAAAAAGATATTAGCGAGTGT 1473
|||||

Sbjct 538      CGTAGACACTCGTTTGTGTTTGCTCTTTCTAGAATTCACAAAAAAGATATTAGCGAGTGT 597
|||||

Query 1474     CTACGAGCGACTCAATGAAAGTTCGATTATTCCCCCTCTGGAAAACCGCTTTTAAAAATA 1533
|||||

Sbjct 598      CTACGAGCGACTCAATGAAAGTTCGATTATTCCCCCTCTGGAAAACCGCTTTTAAAAATA 657
|||||

Query 1534     TTGGCTGCTAGATGGTTTTTACTATAGTGAGGTTTGTCTTTTaaaaaaCACGAGCAAAG 1593
|||||

Sbjct 658      TTGGCTGCTAGATGGTTTTTACTATAGTGAGGTTTGTCTTTTAAAAAACACGAGCAAAG 717
|||||

Query 1594     CGAGTTCATAGTTGCTTTTGCTTGTGTTTCGGGTCTTAGGGGAAATCCCCTAACAGTCCT 1653
|||||

Sbjct 718      CGAGTTCATAGTTGCTTTTGCTTGTGTTTCGGGTCTTAGGGGAAATCCCCTAACAGTCCT 777
|||||

Query 1654     CGAATATCAAAATGTGGCTACATTTTGTATATACGGGTAGGCTTGCTTATTTGAtttttt 1713
|||||

Sbjct 778      CGAATATCAAAATGTGGCTACATTTTGTATATACGGGTAGGCTTGCTTATTTGATTTTTT 837
|||||

Query 1714     ttCTTCTAAACCTTTGACTTCTTCCCCATTGTTTGCAGAAA-TGCCCCCGAC 1765
|||||

Sbjct 838      TTCTTCTAAACCTTTGACTTCTTCCCCATTGTTTGCAGAAATTGCCCTCGAC 890
|||||

Score = 576 bits (638), Expect = 3e-160
Identities = 322/324 (99%), Gaps = 0/324 (0%)
Strand=Plus/Plus
Query 1      AAGCTTGCTTAGTCAAAAAAGTTTGAGCAAAGCGAAAACATAGGGCAATTTTCGTGATGA 60
|||||
Sbjct 892     AAGCTTGCTTAGTCAAAAAAGTTTGAGCAAAGCGAAAACATAGGGCAATTTTCGTGATGA 951
|||||

Query 61      AAATGGGCTTTTAATGTTTTTAAATGCTTTTAAATGCTTTTAGACATGCTGAAACGCTTA 120
|||||
Sbjct 952     AAATGGGCTTTTAATGTTTTTAAATGCTTTTAAATGCTTTTAGACATGCTGAAACGCTTA 1011
|||||

Query 121     TATAGCAATGCATACAGAGGACATATGTCCACGTTTACCTATCAATATGTCCACGTTTAC 180
|||||
Sbjct 1012    TATAGCAATGCATACAGAGGACATATGTCCACGTTTACCTATCAATATGTCCACGTTTAC 1071
|||||

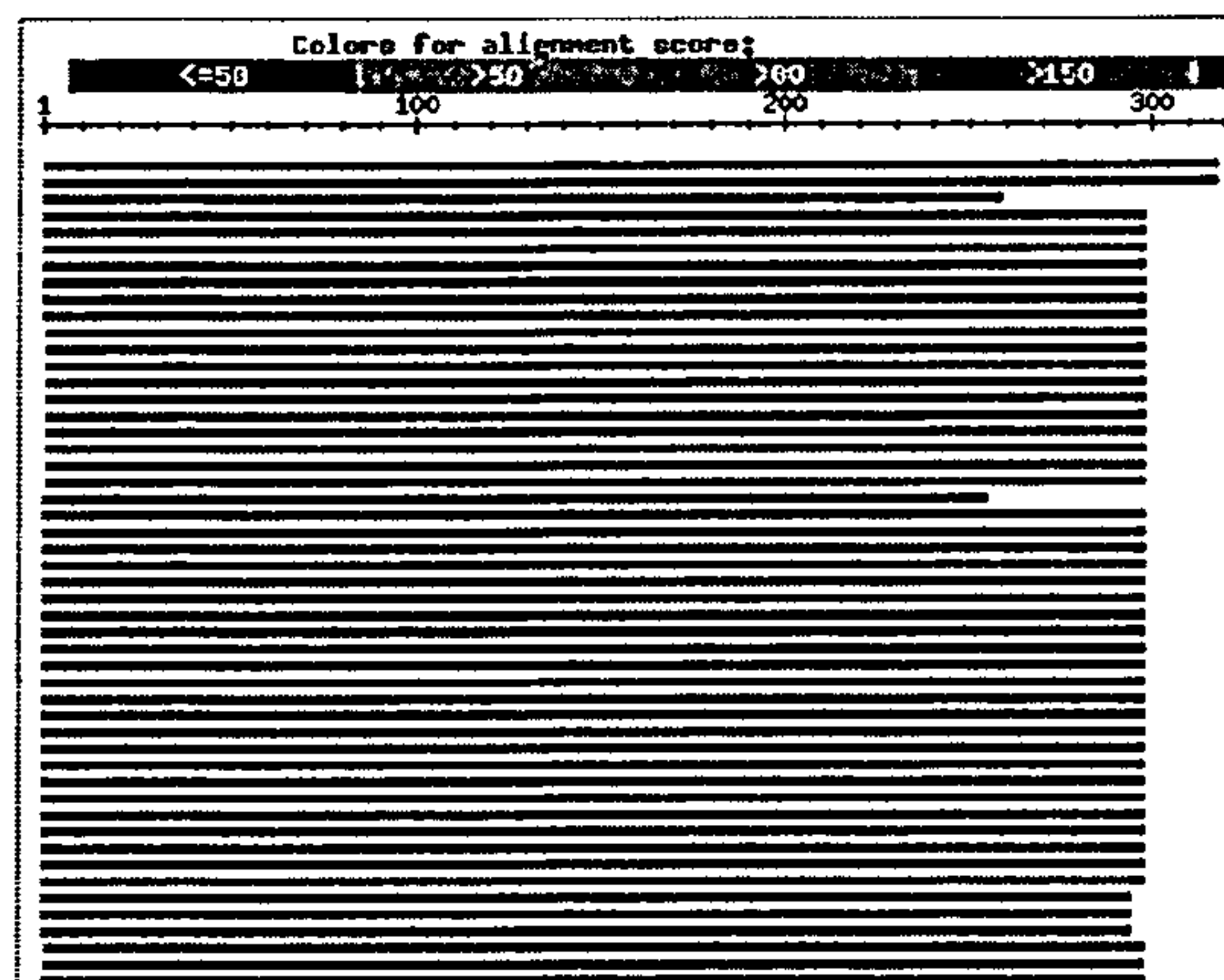
Query 181     CTATCAATATGTCCACGTTTACCTATCAATATGTCCACGTTTACCTTGCGTATTTACACA 240
|||||
Sbjct 1072    CTATCAATATGTCCACGTTTACCTATCAATATGTCCACGTTTACCTTGCGTATTTACACA 1131
|||||

Query 241     CATTTAAATAGTATGGATATATCCAATGAAATTATAATGTGTACTTATGAGCAAATTAGT 300
|||||
Sbjct 1132    CATTTAAATAGTATGGATATATCCAATGAGATTATAATGTGTACTTATGAGCAAATTAGT 1191
|||||

Query 301     AGTGAAAGACAATGCCCTAATGAA 324
|||||
Sbjct 1192    AGTGAAAGACAATGCCCTAATCAA 1215
|||||

```

BlastP – Uniprot:
ORF 319aa:



>>>sptrembl:D0T8X0 ACIRA D0t8x0 SubName: Full=Initiator RepB... 435 1e-119
>>>sptrembl:C6RK77 ACIRA C6rk77 SubName: Full=Initiator RepB... 435 1e-119

>>>>sptrembl:D0T8X0_ACIRA D0t8x0 SubName: Full=Initiator RepB protein;. 9/2013
Length=313
Score = 435 bits (1118), Expect = 1e-119, Method: Compositional matrix adjust.
Identities = 208/319 (65%), Positives = 252/319 (78%), Gaps = 7/319 (2%)

Query	1	MSKLVVKDNALMNASYNLDLVEQRLILLAIIEARESGKGINANDPLTVHAESYINQFGVH	60
		M +LVVKDNAL+NASYNLDLVEQRLILLAI+EARESGKGINANDPL VHAESYINQF VH	
Sbjct	1	MRELVVKDNALINASYNLDLVEQRLILLAIIVEARESGKGINANDPLVVHAESYINQFNVH	60
Query	61	RVTAYQALKDACDNLFARQFSYQSKSEKGNIQNHRSRWVSEIIYIDTEATVKIIFAPAIV	120
		R TAYQALKDAC +LF RQFSYQ +++GN++++RSRWVSEI Y+D EA VK+IFAPAIV	
Sbjct	61	RNTAYQALKDACHDLFVRQFSYQKVNDRGVNEHYRSRWVSEIGYVDNEAIVKLIFAPAIV	120
Query	121	PLITRLEEQFTKYDIEQISDLSSAYAIRLYELLICWRSTGKTPIIIGLGEFRNRVGVLDSE	180
		PLITRLEEQFTKY+++Q+S L+SAYA+RLYELLI WRSTGKTP+I L +FR R+G+L++E	
Sbjct	121	PLITRLEEQFTKYELQQVSQVLSAYAVRLYELLIAWRSTGKTPVIELADFRKRIGILETE	180
Query	181	YHRIAHLKERVIEHSIKQINEHTDITATYEQHKKGRITITGFSFKFKQKKPKQAEIATETP	240
		Y R+ K V+E +I QINEHTDI YEQHKKGR+I GFSF F QK+ K+ E	
Sbjct	181	YKRMERFKTSVLELAINQINEHTDINVAYEQHKKGRSIVGFSFNFSQKEKKK---ILEKA	237
Query	241	KTATNDPDTTKPLTEPQIAKYSMILCKLGSISDLSNFPDYPAFANWIGNILRNPEKADEQ	300
		+ + + K LTE QI KYS +L KL +SDLS F DY +F+ WIGNILR PE +	
Sbjct	238	QVS---EGFKKLTEAQITKYSTVLSKLHELSDLSTFQDYQSFSIWIGNILREPESVRFE	293
Query	301	IAKRIFTALKTETDYSKKN 319	
		A+RIF++L TD++ N	
Sbjct	294	TAERIFSSLFKRTDFASPN 312	

>>>>sptrembl:C6RK77_ACIRA C6rk77 SubName: Full=Initiator RepB protein;. 9/2013
Length=313
Score = 435 bits (1118), Expect = 1e-119, Method: Compositional matrix adjust.
Identities = 208/319 (65%), Positives = 252/319 (78%), Gaps = 7/319 (2%)

Query	1	MSKLVVKDNALMNASYNLDLVEQRLILLAIIEARESGKGINANDPLTVHAESYINQFGVH	60
		M +LVVKDNAL+NASYNLDLVEQRLILLAI+EARESGKGINANDPL VHAESYINQF VH	
Sbjct	1	MRELVVKDNALINASYNLDLVEQRLILLAIIVEARESGKGINANDPLVVHAESYINQFNVH	60
Query	61	RVTAYQALKDACDNLFARQFSYQSKSEKGNIQNHRSRWVSEIIYIDTEATVKIIFAPAIV	120
		R TAYQALKDAC +LF RQFSYQ +++GN++++RSRWVSEI Y+D EA VK+IFAPAIV	
Sbjct	61	RNTAYQALKDACHDLFVRQFSYQKVNDRGVNEHYRSRWVSEIGYVDNEAIVKLIFAPAIV	120
Query	121	PLITRLEEQFTKYDIEQISDLSSAYAIRLYELLICWRSTGKTPIIIGLGEFRNRVGVLDSE	180
		PLITRLEEQFTKY+++Q+S L+SAYA+RLYELLI WRSTGKTP+I L +FR R+G+L++E	
Sbjct	121	PLITRLEEQFTKYELQQVSQVLSAYAVRLYELLIAWRSTGKTPVIELADFRKRIGILETE	180
Query	181	YHRIAHLKERVIEHSIKQINEHTDITATYEQHKKGRITITGFSFKFKQKKPKQAEIATETP	240

Sbjct 181 Y R+ K V+E +I QINEHTDI YEQHKKGRI GFSF F QK+ K+ E 237
YKRMERFKTSVLELAINQINEHTDINVAYEQHKKGSI VGFNF S QKEKKK---ILEKA
Query 241 KTATNDPDTTKPLTEPQIAKYSMILCKLGSISDLSNFPDYPAFANWIGNILRNPEKADEQ 300
+ + + K LTE QI KYS +L KL +SDLS F DY +F+ WIGNILR PE +
Sbjct 238 QVS-----EGFKKLTEAQITKYSTVLSKLHELSDLSTFQDYQSFSIWIGNILREPESVRFE 293
Query 301 IAKRIFTALKTETDYSKKN 319
A+RIF++L TD++ N
Sbjct 294 TAERIFSSLFKRTDFASPN 312

ProtSweep

A Protein Identification Tool

Results for /home/vir088/rindneu/tsekompl/MSBI2.176.319.pep



Number of residues: 319	Molecular weight: 36.37 kD
Charge: 4	Isoelectric point: 9.07

more...

Prediction of protein localization:

cyto	18 %
extr	5 %
nucl	5 %



Identified Protein & Transcript:

Protein:
id: sptrembl:C6RK77 ACIRA
valuation: similar
scientific organism: Acinetobacter radioresistens
abstract: C6rk77 SubName: Full=Initiator RepB protein;. 9/2013Length=313
isoform:



GO information:

accession	group	name	evidence
GO:0005727	cellular component	extrachromosomal circular DNA	IEA:InterPro
GO:0003887	molecular function	DNA-directed DNA polymerase activity	IEA:InterPro
GO:0006270	biological process	DNA replication initiation	IEA:InterPro

Interpro information:

id	short name
IPR000525	Initiator_Rep_prot
IPR011991	WTH_DNA-bd_dom

CM11.252 (2523bp)**(CMI = Cow milk isolate)****(mil.NoXo.2500.7)****IDENTICAL TO HCBI6.252**

TTAAAAATATTGGTTGCTAGATGGTTTTAACTATCGTGGAGCTTTTGCTTTTAAAAATACACGAAGCAAAGCGAGTTCATAGT
 CGCTTTTGTATCTGCTCTTACTAACAGCTCATTTTTAAATGGGCCGTTAGTAAGAGATGCTTTTGGGGTTTCGGGGCTTGCCCTG
 AACAAAGGTCACAAAGTGGGAATTTATCACGGTAGTGAAAAAGTACCCCTTTGTGTATCCTTGCTTTTATGCTTTTAAACCTTTG
 GACTTTTCCCTTAATTTGCAGAAATTGCCCTCGACTAAGCAAGCTTAGTCAAAAAGTTTGAGCAAAGCGAAAACATAGGGC
 AATTTTCATGATGAAAATGGGCTTTTAAAGTTTTTAAATGCTTTTAAATGCTTTTAGACATGTTGAAATGCAAGCCTAGCAAG
 GCATACAGAGGACATACCCCTACGTTTACCGATCAATACCCCTACGTTTACCGATCAATACCCCTACGTTTACCGATCAATAC
 CCCTACGTTTACGTTGCATATCACTACAAACAATATTAATGTAGTAATAACTTCAAAATAATAAATGTAGGTTATGAGCGATT
 TAATAGTAAGGATAACGCCCTAATGAACGCTAGTTACAACCTAGCTTTGGTTGAACAGCGTTTAAATCCTTTTAGCTATATTG
 GAAGCGAGAGAAACAGGAAAAGGGATTAATGCCAATGACCCCTTAACAGTTTCATGCAAGTAGCTATATCAATCAATTTAACGT
 GGAAAGACATACGGCATATCAAGCATTAAAAGATGCTTGCAAAGACTTGTTTGACGTCATTTAGTTACCAAGAAAAGCGAG
 AACGAGGACGAATTAATATTACAAGTCGATGGGTTTACAAATTGGTTATATGGACGATACAGCAACCGTTGAAATTATTTTT
 GCCCTGCGGTTGTTTCTTTGATTACAGCTTTAGAGGAACAATTCACCTCAATACGATATTGAACAAATTAGCGAGTTATCGAG
 TGCTTATGCTGTCCGCCTATATGAGTTACTAATTTGTTGGCGTAGCACAGGAAAAACCCCAATTATGATCTAACAGAGTTTA
 GAAAGCGTCTAGGCGTTTATAGATACCGAATACACTAGGACAGATAACTTGAAGATGCGAGTGATTGAGCTAGGACTTAAACAA
 ATCAACGAGCATACGGACATTACAGCAAGCTACGAACAGCACAAAAAGGGCGGACAATCACAGGATTCTCATTCAAGTTTAA
 GCAGAAGAAGAAAACAGGGGCGGAAATGCCAAAAAATAGCGATTCTAGCCACATATCGAAAAACCTAGTCAAATCCCTGCCA
 ACATCGCAAAACAGCCTGAAAATGCCAAAAAAGATGATTTAGGGCACAGAGCAAGCAAGATTACAGGGTTAATTATGTGCAAT
 GGTTTAGCAGATCGGTTTAAACGTGGTGATGAGTCAGTAATAGACATGATGAAACGCATCNGAGGAAATTACAACCTGATACA
 ACAGCAGACCAATGGGAAAACAAGCTAGAAGAATTTGGCGTGATTTTTTCAGTCATGATCAATTTCCCGAAGGACATATAAAAA
 ATAATGTAGTTAAATATAGTAGTTATAATATTGACTACAATATTTAACTACTATATTGTAGTCTTAAATCAACTTACATAGAA
 TTTAAATTATGTCTCTTCGCCAAATTTTAGAACAATCTCTCTTTGATCAAACCTGATGAAAGCTCTACTGTGCCACTATCAATT
 AGACTTCCAAACAACCTGAATAATGAGCTTGAAGAAGTGAATAACACTAGATAAATCCAAGAGTTTCTACTCCTAGAGTT
 CATTAAGGCTGGAATTAGTGAGACTAGCAATATGTTAGAAGACAAAGCGAAGAACCCTATACTTGAAAGTCCAAGAGATTCTA
 GTGACTTTACAACCTCATAAGAAGTTTATGTTGAACACTAATTTCAATAACAATAAAGCATCACACATGACTATGTTGGAGAAT
 CAAGAAGCTGCTGCATTTTCGTAAAGGTTGGAAAGAATATATCTGTAATTTAGAAGAAGGCGATAAGGTTTACCTTTATCAAAG
 TGGCGTTGGTTTGTAGCATCTGGTATTGTCACTGGTGACTTAATCAAAAGTGAGTATCGTGGACAACCAGAAGAAAAATATT
 CTAAAAAATTAAAGGATTTTAAATAGGATTTAAAGCAATTTCTGCAAAAGAGTTTAAAGACCTTAACTGGCGGTGGTGCTAGC
 TTTCGTACAACAATGAGCGAGCTAAAGCCTGAACAATGTAGAAAATTAGATATGGAAATAGAAAAACGGATGAAGTCAGTAAG
 TTAATAATATGAGTTGTTGTTTTAGTGTGTACGTAGCAATCACTTAGAAGTTCCCTTTGTATTACTTGTCTAGCAATGGTTT
 TAAAAAGCGTCACTACTGATAGTGACGCTTTTTTTTGTTTTTTCAAAGGAAGTAATTAGCGAGTGTCTACGAGCGACACAATGAA
 AGTTGATTATTCCTCCTCTAAAAAACCGCTT

Repeat – 3x22nt + 17nt

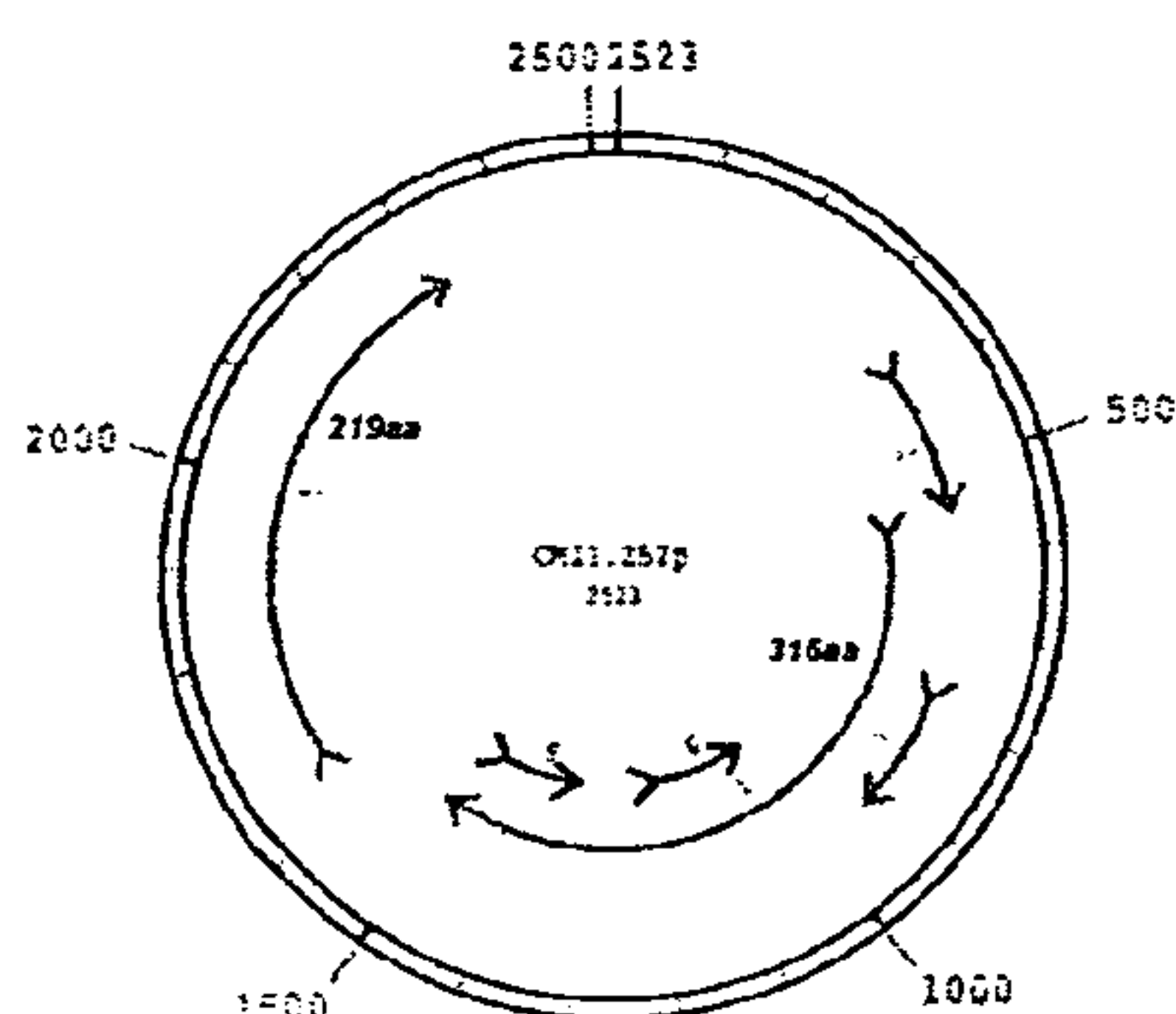
**85-90% nucleotide similarity to TSE-associated circular DNA isolate Sphinx 1.76****ORFs: 316aa – replication protein 85% similarity to Sphinx1.76**

Figure 1(e)

Colors for alignment score:

<=50 1000 2000 >150

1
2
3
4
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18

Score = 1519 bits (1684), Expect = 0.0				
Identities = 1144/1334 (85%), Gaps = 14/1334 (1%)				
Strand=Plus/Plus				
Query	237	TTTTAAACCTTTGGACTTTT--CCCTTAATTTGCAGAAATTGCCCCCTCGACTAAGCAAGC	294	
Sbjct	277	TTCTAAACCTTTG-ACTTCTTCCCCATTGTTTGCAGAAATTGCCCCCTCGA---AGCTTGC	332	
Query	295	TTAGTCAAAAAAGTTTGTAGCAAAGCGAAAACATAGGGCAATTTTCATGATGAAAATGGGC	354	
Sbjct	333	TTAGTCAAAAAAGTTTGTAGCAAAGCGAAAACATAGGGCAATTTTCATGAAGAAATTGGGC	392	
Query	355	TTTTAAAGTTTTTAAATGCTTTTAAATGCTTTTAGACATGTTGAAATGCAAGCCTAGCAA	414	
Sbjct	393	TTTTAAAGTTTTTAAATG-TTTTAAATGCTTTTAGACATGCTAAGAAGCCCACACAGCAA	451	
Query	415	GGCATAAGAGGACATACCCCTACGTTTACCGATCAATACCCCTACGTTTACCGATCAAT	474	
Sbjct	452	GGCATAAGAGGACATTCTCCTACGTTTACCGATCAATACCC--CGTTTACCGATCAAT	509	
Query	475	ACCCCTACGTTTACCGATCAATACCCCTACGTTTACCTTGCATATCACTACAAACAATAT	534	
Sbjct	510	ACCCCTACGTTTACCGATCAATACCCCTACGTTTACCTTGCATATACTACAAAGAATAC	569	
Query	535	TAATGTAGTAATAAATTCAAATAATAAATGTAGGTTATGAGCGATTTAATAGTAAAGGA	594	
Sbjct	570	TAGTGTAGTA-TAATTCAAAGAATAATTGTAGGTTATGAGCGATTTAATAGTAAAGA	628	
Query	595	TAACGCCCTAATGAACGCTAGTTACAACCTAGCTTTGGTTGAACAGCGTTAATCCTTTT	654	
Sbjct	629	TAACGCCCTAATGAATGCTAGTTATAACTAGCTTTGGTTGAACAGAGGTTAATCTATT	688	
Query	655	AGCTATATTGGAAGCGAGAGAAACAGGAAAAGGGATTAATGCCAATGACCCCTTAACAGT	714	
Sbjct	689	AGCAATCATAGAAGCGAGAGAAACAGGCAAAGGGATTAATGCCAATGATCCTCTTACGGT	748	
Query	715	TCATGCAAGTAGCTATATCAATCAATTTAACGTGGAAGACATACGGCATATCAAGCATT	774	
Sbjct	749	TCATGCAGGTAGCTATATCAATCAATTTAACGTACAAAGGCATACGGCATATCAAGCCCT	808	
Query	775	AAAAGATGCTTGCAAAGACTTGTTTGCACGTCAATTTAGTTACCAAGAAAAGCGAGAACG	834	
Sbjct	809	CAAAGATGCTTGTAAGACTTGTTTGCCCGTCAATTCAGTTACCAAGAAAAGCGAGAACG	868	

Query 835 AGGACGAATTAATATTACAAGTCGATGGGTTTCACAAATTGGTTATATGGACGATACAGC 894
|||||
Sbjct 869 AGGACGAATTAATATTACAAGTCGATGGGTTTCGCAAATTGGCTATATGGACGATACAGC 928
Query 895 AACCGTTGAAATTATTTTGGCCCTGCGGTTGTTCCCTTGATTACACGTTTAGAGGAACA 954
|||||
Sbjct 929 AACCGTTGAGATTATTTTGGCCCTGCGGTTGTTCCCTGATTACACGGCTAGAGGAACA 988
Query 955 ATTCACTCAATACGATATTGAACAAATTAGCGAGTTATCGAGTGCTTATGCTGTCCGCT 1014
|||||
Sbjct 989 GTTCACCCAGTACGATATTGAGCAAATTAGCGGTTTATCGAGTGCATATGCTGTTCTGAT 1048
Query 1015 ATATGAGTTACTAATTTGTTGGCGTAGCACAGGAAAAACCCCAATTATTGATCTAACAGA 1074
|||
Sbjct 1049 GTACGAAGTGTGATTTGTTGGCGTAGCACAGGCAAAACACCAATTATTGAGCTAGACGA 1108
Query 1075 GTTTAGAAAGCGTCTAGGCGTTTATAGATACCGAATACACTAGGACAGATAAATTGAAGAT 1134
|||||
Sbjct 1109 GTTTAGAAAGCGAATAGGTGTTTATAGATACTGAATACACTAGAACAGATAATTTAAAGAT 1168
Query 1135 GCGAGTGATTGAGCTAGGACTTAAACAAATCAACGAGCATACGGACATTACAGCAAGCTA 1194
|||
Sbjct 1169 GCAAGTTATTGAATTAGCCCTAAACAAATCAACGAACATACTGACATCACAGCAAGCTA 1228
Query 1195 CGAACAGCACAAAAAGGGCGGACAATCACAGGATTCTCATTCAAGTTTAAGCAGAAG-A 1253
|||||
Sbjct 1229 TGAACAACACAAAAAGGGCGAGTGATTACCGGATTCTCATTGTTTAAGCACAAGAA 1288
Query 1254 AGAAAACAGGGGCGGAAATGCCAAAAATAGCGATTCTAGCCACATATCGAAAAACCTA 1313
|
Sbjct 1289 ACAAAACA-GCGATAAACGCCTGATACTAACGCTTCTAGCCACGTATCGTAAACATA 1347
Query 1314 GTCAAATCCCTGCCAACATCGCAAAACAGCCTGAAAATGCCAAAAAGATGATTTAGGGC 1373
|||||
Sbjct 1348 GTCAAATCCCTACCAACATTGTAACAGCCTGAAAACGCCAAAATGAGCGATTTAGAAC 1407
Query 1374 ACAGAGCAAGCAAGATTACAGGGTTAATTATGTGCAATGGTTTAGCAGATCGGTTTAAAC 1433
|
Sbjct 1408 ATAGAGCGAGCCGTGTTACAGGGGAAATAATGCGAAATCGTCTGTCAGATCGGTTTAAAC 1467
Query 1434 GTGGTGATGAGTCAGTAATAGACATGATGAAACGCATCNGAG-GAAATTACAACGATA 1492
|||
Sbjct 1468 AAGGCGATGAATCAGCAATCGACATGATGAAACGTATTCAAAGTGAAATAATAACCGATG 1527
Query 1493 CAACAGCAGACCAATGGGAAAACAAGCTAGAAGAATTTGGCGTGATTTTTCAGTCATGAT 1552
|||
Sbjct 1528 CAATAGCAGACCAGTGGGAAAGCAAAGTGGAGGAGTTTGGCGTGTTTTCAGTCATGA- 1586
Query 1553 CAATTTCCCGAAGG 1566
|
Sbjct 1587 CGATTTCCCGAAGG 1600

Score = 122 bits (134), Expect = 2e-23
Identities = 83/91 (91%), Gaps = 2/91 (2%)
Strand=Plus/Plus

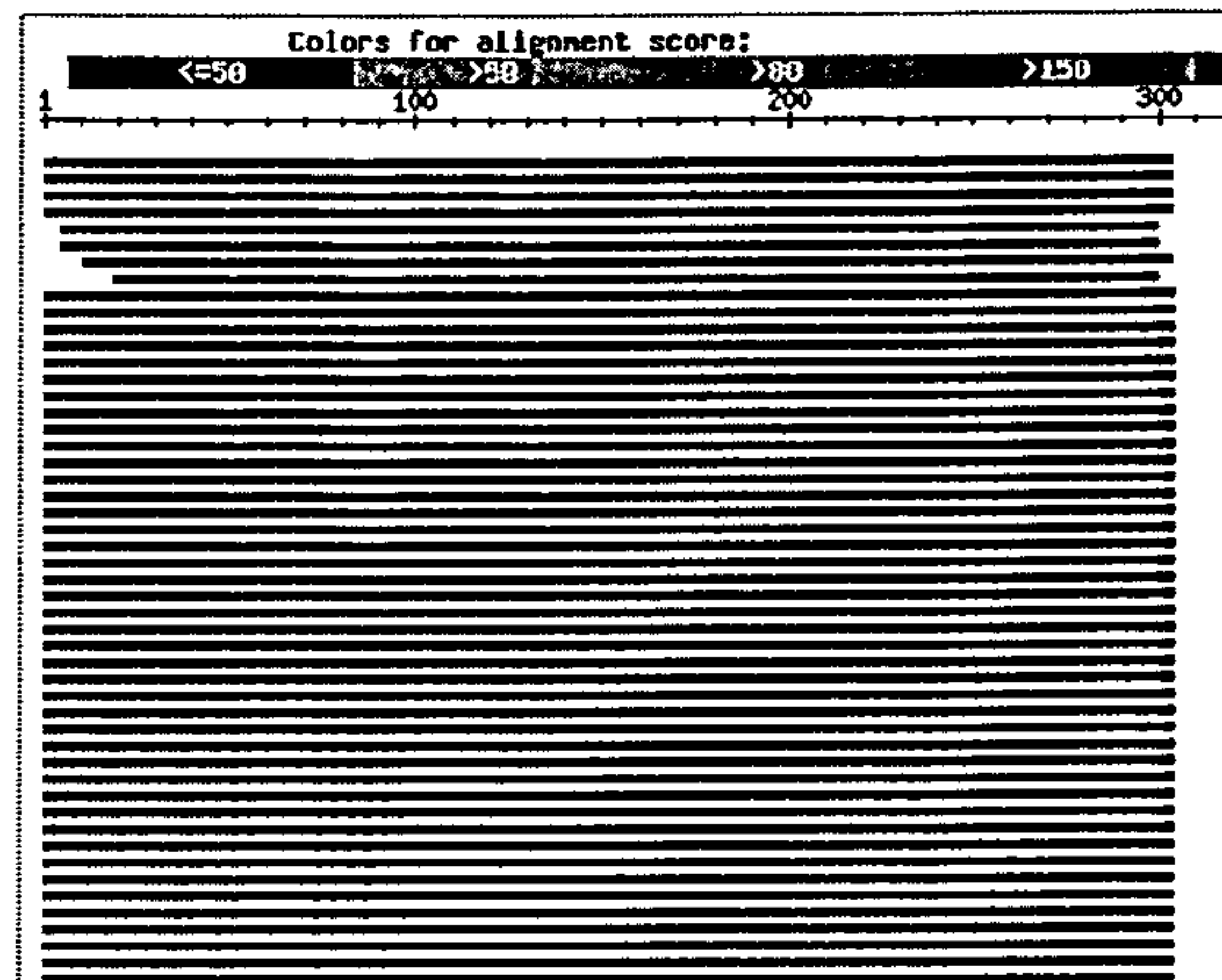
Query 1 TTAAAAATATTGGTTGCTAGATGGTTTTAACTATCGTGGAGCTTTTGCTTTTAAAAATAC 60
|||||
Sbjct 85 TTAAAAATATTGGCTGCTAGATGGTTTTACTATAGT-GAGGTTTGCTTTTAAAAAAC 143
Query 61 ACGAAGCAAAGCGAGTTCATAGTCGCTTTTG 91
|||
Sbjct 144 ACG-AGCAAAGCGAGTTCATAGTTGCTTTTG 173

Score = 95.1 bits (104), Expect = 3e-15
Identities = 60/64 (93%), Gaps = 1/64 (1%)
Strand=Plus/Plus

Query 2460 ATTAGCGAGTGTCTACGAGCGACACAATGAAAGTTTCGATTATTCCCTCCTCTAAAAAAC 2519
|||||
Sbjct 22 ATTAGCGAGTGTCTACGAGCGACTCAATGAAAGTTTCGATTATTCCC-CCTCTGGAAAC 80
Query 2520 GCTT 2523
|||
Sbjct 81 GCTT 84

>>>>nrnuc:GI_462476960 Gi|462476960|gb|APGK01000458.1| Dendroctonus ponderosae Seq01000458,

whole genome shotgun sequence. 0/0
Length=1455
Score = 733 bits (812), Expect = 0.0
Identities = 790/1033 (76%), Gaps = 21/1033 (2%)
Strand=Plus/Minus

ORF 316aa:**BlastP – Uniprot:**

>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-li... 545 1e-152
>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterize... 523 4e-146

>>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-like protein;. 5/2013
Length=324
Score = 545 bits (1403), Expect = 1e-152, Method: Compositional matrix adjust.
Identities = 261/304 (85%), Positives = 276/304 (90%), Gaps = 0/304 (0%)

Query	1	MSDLIVKDNALMNASYNLALVEQRLILLAILAEARETGKGINANDPLTVHASSYINQFNVE	60
Sbjct	1	MSDLIVKDNALMNASYNLALVEQRLILLAILAEARETGKGINANDPLTVHASSYINQFNVE	60
Query	61	RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEIIFAPAVVP	120
Sbjct	61	RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEIIFAPAVVP	120
Query	121	LITRLEEQFTQYDIEQISELSSAYAVRLYELLICWRSTGKTPIIDLTEFRKRLGVLDTEY	180
Sbjct	121	LITRLEEQFTQYDIEQISLSSAYAVRMYELLICWRSTGKTPIIELDEFKRKRGVLDTEY	180
Query	181	TRTDNLKMRVIELGLKQINEHTDITASIEQHKKGRITGFSFKFKQKKKTGAEMPKNSDS	240
Sbjct	181	TRTDNLKMQVIELALKQINEHTDITASIEQHKKGRVITGFSFMFKHKKQNSDKTPTNAS	240
Query	241	SPHIEKPSQIPANIAKQPENAKKDDLHRASKITGLIMSNGLADRFKRGDESVIDMMKRI	300
Sbjct	241	SPRIVKHSQIPTNIVKQPENAKMSDLEHRASRVTEIMRNRLSDRFKQGDSEIDMMKRI	300
Query	301	XRKL	304
Sbjct	301	QSEI	304

>>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterized protein;. 12/2013
Length=324
Score = 523 bits (1347), Expect = 4e-146, Method: Compositional matrix adjust.
Identities = 250/304 (82%), Positives = 272/304 (89%), Gaps = 0/304 (0%)

Query	1	MSDLIVKDNALMNASYNLALVEQRLILLAILAEARETGKGINANDPLTVHASSYINQFNVE	60
Sbjct	1	MS+LIVKDNALMNASYNL LVEQRLILLAILAEARE+GKGINANDPLTVHASSYINQF V	60
Query	61	RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEIIFAPAVVP	120
Sbjct	61	R TAYQALKDACKDLFARQFSYQEKREGR NITSRWVSI Y+D+TATVEIIFAPAVVP	120

Query 121 LITRLEEQFTQYDIEQISELSSAYAVRLYELLICWRSTGKTPIIDLTEFRKRLGVLDTEY 180
LITRLE+QFTQYDIEQIS LSSAYAVR+YELLICWRSTGKTP+I+L EFRKR+GVLDTEY
Sbjct 121 LITRLEKQFTQYDIEQISGLSSAYAVRMYELLICWRSTGKTPVIELGEFRKRIGVLDTEY 180

Query 181 TRTDNLKMRVIELGLKQINEHTDITASIEQHKKGRTITGFSFKFKQKKKTGAEMPKNSDS 240
RTDNLKMRVIEL LKQIN+HTDITA+YEQHKKGRTITGFSFKFKQK+KT E PKNSDS
Sbjct 181 IRTDNLKMRVIELALKQINDHTDITATYEQHKKGRTITGFSFKFKQKRKTELETPKNSDS 240

Query 241 SPHIEKPSQIPANIAKQPENAKKDDLGHASKITGLIMSNGLADRFKRGDESVIDMMKRI 300
+K +IP·N+ KQPENA DL HRASKITGLIMSN L+DRFK+ DES++ MM RI
Sbjct 241 DVPKQKSVEIPTNLVKQPENANMSDLQHRASKITGLIMSNRLSDRFKQSDSIMQMMARI 300

Query 301 XRKL 304
++
Sbjct 301 QSEI 304

>>>>sptrembl:N9JLM2_ACIBA N9jlm2 SubName: Full=Uncharacterized protein;. 12/2013
Length=325

Score = 481 bits (1239), Expect = 1e-133, Method: Compositional matrix adjust.
Identities = 239/305 (78%), Positives = 270/305 (88%), Gaps = 1/305 (0%)

CM12.214 (2148bp)**(mi2.NnXn.2000.8)**

TTGTACTGAATTAATGAACGAGTGTCTACGAGTGGCATAAAGAAAGTTCGCTTATTGCCCTCTGAAAAACCGCTTTTCTAT
 ATCTAATTTTCATGAAAATTTTAACTACTGTGAGCTTTTGCTTTTGAAAAGACACGAGCGAAGCGAGTGCCATTTTGTCTCTT
 GCTTTTGGGGTTTGGGGCTTGCCCCAACAGGGCACAGAGTAGGAATTTTACACGGTAGTGAAAAAGTCCCCTCTGTGTGTCCT
 TGCCCTATGCTTTTAAACCTTTGAATTTTCCCTGTAATTTGAAGAAATTGCCCTCGACTAAGCTTGCTTAGTCAAAAAAG
 TTTGAGCAAAGCGAAAACATAGGGCAATTTTCATAATAAAAAATGGGCTTTTAAAGTTTAAATGCTTTTAAATGCTTTTGA
 CATGCTGAAATGCCTACACAGCAAGGCATACAGAGGACTACTCCTAGGTTTACCCACCAATACTCCTAGGTTTACCTACCAA
TACTCCTAGGTT TACCTACCAATACTCCTAGGTTTACCTTGCGTAATCCTAAAAGATATAATACAAAGGAAGTACTAGGTTT
 AATATTAATAAGTAAAATGAGCGATTTAATAGTAAAAGATAATGCCTTAATGAACGCTAGTTATAACCTAGACTTAGTTGAGC
 AGCGTTTAATCTCTTGGCTATCCTTGAGGCGAGAGAAACAGGCAAAGGGATTAATGCCAATGATCCTCTAACCGTTCATGCT
 GAAAGCTATATCAATCAATTTGGTGTAGCTAGACAGACTGCATATCAAGCATTAAGAGATGCTTGTAAGGACTTATTGACAG
 CCAATTTAGTTACCAAGAAAAACGTGAGCGTGGGCGAGCTAATATTACAAGTCGTTGGGTATCGCAAATTGCTTACATTGATG
 AAACGGCAACAGTTGAGGTTATTTTTGCCCTGCCGTTGTTCCACTGATTACACGATTAGAGGAACAATTCACCCAATACGAT
 ATTGAACAAATTAGCGGTTTATCGAGTGCCTATGCCGTCCGTCTATATGAATTATTGATTTGTTGGCGTAGTACAGGGAAAAC
 ACCTGTTATTGAACTAGCAGAGTTTAGAAAGCGTTTAGGTGTTTAAATGATGAATATACTAGATCGGATAATTTCAAAAAT
 GGATTATTGAAAACCTATTAAACAAATAAACGAGCATAACGACATCACAGCAAGCTACGAACAGCACAAAAAGGGCGGACA
 ATCACAGGGTTTTTCATTCAAGTTTAAGCAGAAGAAAAAACAGAACCTGAAACGCCAAAAACAGCGATTCTAGCCAACGTAT
 CGAAAAGCCTAGTCAAATCCCTGCCAACATCGTAAACAACCTGAAAACGCAAATTTGAGCGATTTACAGCATCGAGCAAGCA
 AGATTACAGGGTTAATCATGTCTAACCGTCTATCAGATCGGTTTAAACAAGGTGATGAATCAATCATGCAGATGATGGCACGT
 ATTCAAAGTGAGATTACAACCGATTCAATAGCCGACCAATGGCAATCAAATTAGAAGAATTTGGCGTAGTTTTTTAGTCTGT
 CACGTAGCAATCACGTAGAAAATTATGCTTGAAAGGCTTGCTGTTATTACATTTCAAAAAGCGTCACTACTGATAGTGACGCT
 TTTCTTAGTTTGCCTGTTGAATTAAACAGTGAGTGATAGACCTCTTTTGGTTAGGACTTCATTAACCTTTTCATGCCATTCTT
 TAATTATTTTTGTGCTTCTGCATTTTCACTAGAACAAATACTAATGTTTTTCTTGGCTGAGGTAGTGTTTTCCCCAAATG
 TCCCAATCCAATACGAATAGGGCGTCTGAAAACAATCCAATCGGTTTCACTTTCATCACCATTGACTTCATAAGCTCCACC
 AATTACCTGAACTAATGCAATTAATTTGCCACCATTTTTAATAGCAACAATATCATTCACTTTCATTCTGTAAAAAGTCCT
 CTTTTTCAACCTGTCTCCAGCCATTTTCCTAAACCTATAATTTTTTTGTTCTCTAAAATTGAATGTAAACTTCCGAAAAG
 CTTTGATCATCAGGGTGCATCTGCATATGCCAATATTGAGTCATGTTTTTTTTCCATAGGTAATTATGTTTGT

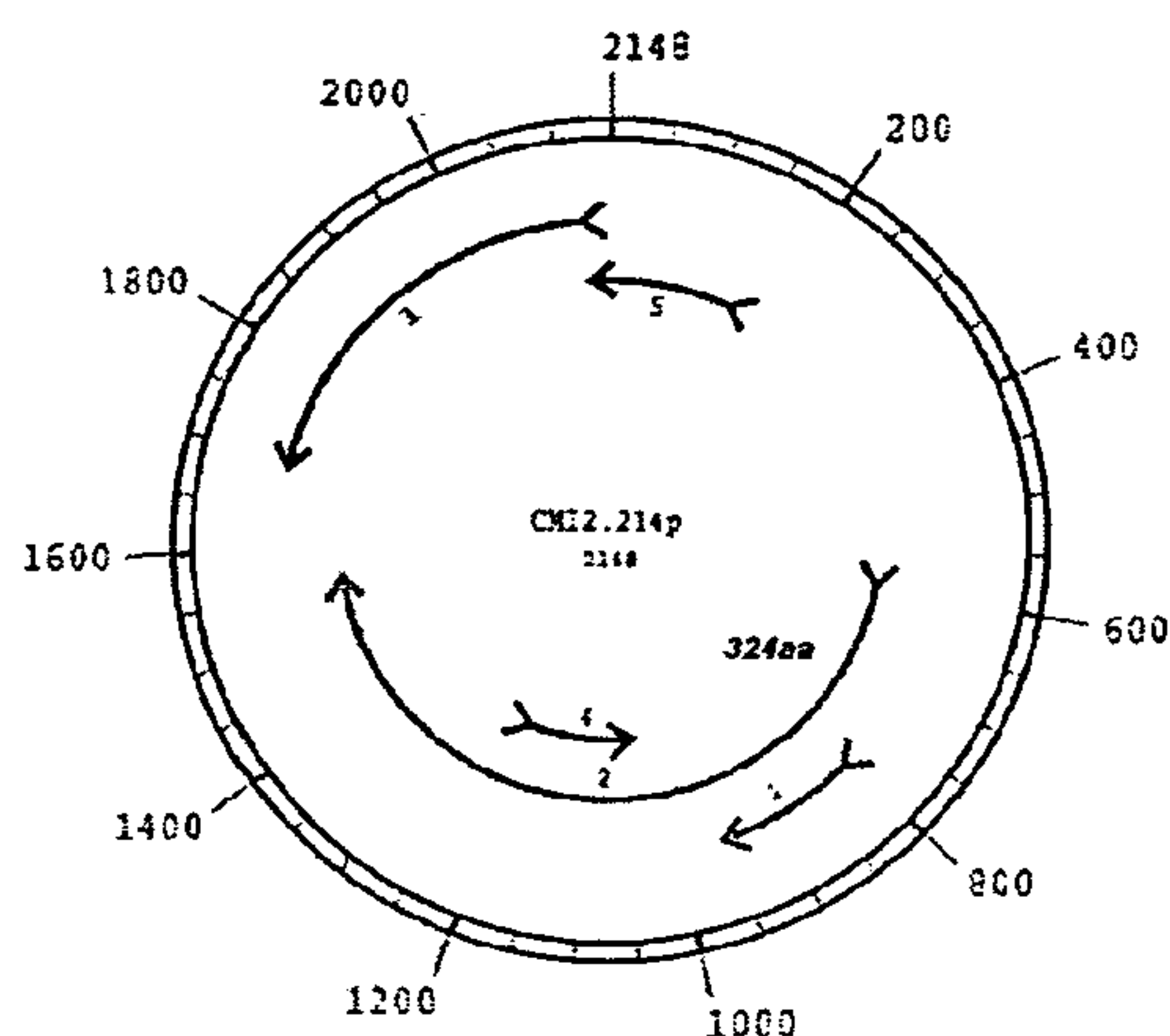
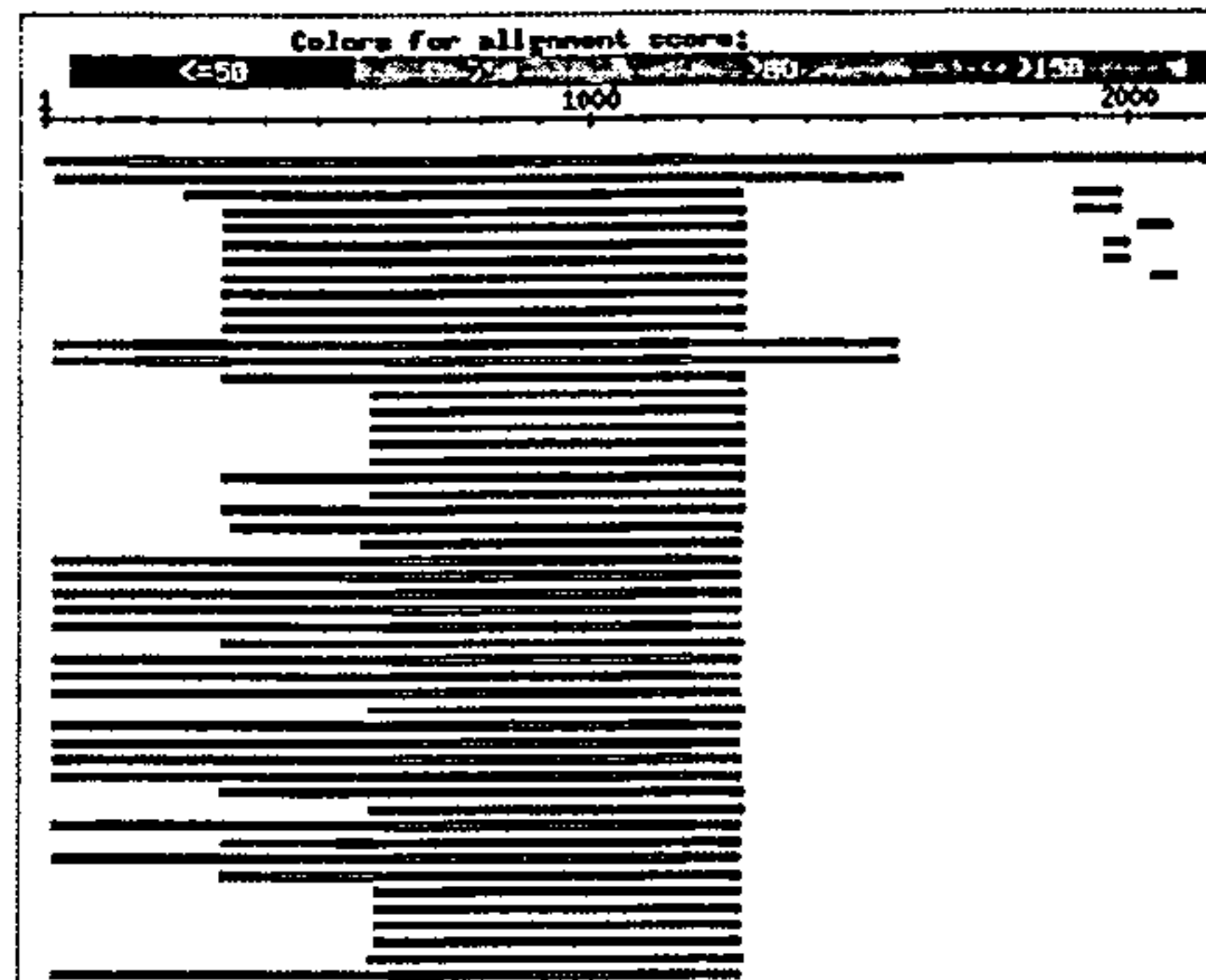
Repeat – 3x22nt + 17nt**79% nucleotide similarity to TSE-associated circular DNA isolate Sphinx 1.76****ORF: 324aa – replication protein 86% similarity to Sphinx1.76**

Figure 1(f)

Blastn – Geall:



>>>nrnuc:GI_347602261	Gi 347602261 gb JN541294.1	Uncultured...	1671	0.0
>>>nrnuc:GI_313507477	Gi 313507477 gb HQ444404.1	TSE-associ...	1301	0.0
>>>nrnuc:GI_462476960	Gi 462476960 gb APGK01000458.1	Dendro...	711	0.0
>>>nrnuc:GI_586961986	Gi 586961986 gb CP006964.1	Acinetobac...	416	7e-112

```
>>>>nrnuc:GI_347602261 Gi|347602261|gb|JN541294.1| Uncultured bacterium plasmid clone
S6GIO-25 genomic sequence. 0/0
```

Length=1257

Score = 1671 bits (1852), Expect = 0.0

Identities = 948/961 (98%), Gaps = 1/961 (0%)

Strand=Plus/Plus

Query	1188	ATAAACGAGCATACCGACATCACAGCAAGCTACGAACAGCACAAAAAAGGGCGGACAATC 	1247
Sbjct	1	ATAAACGAGTACACCGACATCATAGCAAGCTACGAACAGCACAAAAAAGGGCGGACAATC	60
Query	1248	ACAGGGTTTTTCATTCAAGTTTAAGCAGAAAGaaaaaaCAGAACCTGAAACGCCAAAAAAC 	1307
Sbjct	61	ACAGGGTTTTTCATTCAAGTTTAAGCAGAAAGAAAAAACAGAACCTGAAACGCCAAAAAAT	120
Query	1308	AGCGATTCTAGCCAACGTATCGAAAAGCCTAGTCAAATCCCTGCCAACATCGTAAACAA 	1367
Sbjct	121	AGCGATTCTAGCCAACGTATCGAAAAGCCTAGTCAAATCCCTGCCAACATCGTAAACAA	180
Query	1368	CCTGAAAACGCAAATTTGAGCGATTTACAGCATCGAGCAAGCAAGATTACAGGGTTAATC 	1427
Sbjct	181	CCTGAAAACGCAAATTTGAGCGATTTACAGCATCGAGCAAGCAAGATTACAGGGTTAATC	240
Query	1428	ATGTCTAACCGTCTATCAGATCGGTTTAAACAAGGTGATGAATCAATCATGCAGATGATG 	1487
Sbjct	241	ATGTCTAACCGTCTATCAGATCGGTTTAAACAAGGTGATGAATCAATCATGCAGATGATG	300
Query	1488	GCACGTATTCAAAGTGAGATTACAACCGATTCAATAGCCGACCAATGGCAATCAAAATTA 	1547
Sbjct	301	GCACGTATTCAAAGTGAGATTACAACCGATTCAATAGCCGACCAATGGCAATCAAAATTA	360
Query	1548	GAAGAATTTGGCGTAGTTTTTTAGTCTGTCACGTAGCAATCACGTAGAAAATTATGCTTG 	1607
Sbjct	361	GAAGAATTTGGCGTAGTTTTTTAGTCTGTCACGTGGCAATCACGTAGAAAATTATGTTTG	420
Query	1608	AAAGGCTTGCTGTTATTACATTTCAAAAAGCGTCACTACTGATAGTGACGCTTTTCTTAG 	1667
Sbjct	421	AAAGGCTTGCTGTTATTACATTTCAAAAAGCGTCACTACTGATAGTGACGCTTTTCTTAG	480
Query	1668	TTTGCCTGTTGAATTAAACAGTGAGTGATAGACCTCTTTTGGTTAGGACTTCATTAACCT 	1727
Sbjct	481	TTTGCCTGTTGAATTAAACAGTGAGTGATAGACCTCTTTTGGTTAGGACTTCATTAACCT	540
Query	1728	TTTCATGCCATTCTTTAATTATTTTTGTCGTTTCTGCATTTTCACTAGAACAAATAACTA 	1787
Sbjct	541	TTTCATGCCATTCTTTAATTATTTTTGTCGTTTCTGCATTTTCACTAGAACAAATAACTA	600
Query	1788	ATGTTTTTCTTGCGTGAGGTAGTGTTCCTCCCAATGTCCCAATCCAATACACGAATAG 	1847
Sbjct	601	ATGTTTTTCTTGCGTGAGGTAGTGTTCCTCCCAATGTCCCAATCCAATATACGAATAG	660

Query 1848 GCGTCTGAAAACAATCCAATCGGTTTCACCTTCATCACCATTGACTTCATAAGCTCCAC 1907
 |||||
 Sbjct 661 GCGTCTGAAAACAATCCAATCGGTTTCACCTTCATCATTGACTTCATAAGCTCCAC 720
 Query 1908 CAATTACCTGAACATAATGCAATTAATTTGCCACCATTTTAAATAGCAACAATATCATTCA 1967
 |||||
 Sbjct 721 CAATTACCTGAACATAATGCAATTAATTTGCCACCATTTTAAATAGCAACAATATCATTCA 780
 Query 1968 CTTTCATTCTGTTAAAAAAGTCCTCTTTTCAACCTGTCCTCCAGCCCATTTTCCTAAAC 2027
 |||||
 Sbjct 781 CTTTCATTCTGTTAGAAAAGTCCTCTTTTCAACCTGTCCTCCAGCCCATTTTCCTAAAC 840
 Query 2028 CTATAAAttttttGTTCTCTAAATTTGAATGTAAACTTCCGAAAAGCTTTGATCATCAG 2087
 |||||
 Sbjct 841 CTATAAAttttttGTTCTCTAAATTTGAATGTAAACTTCTGAAAAGTTTGTATCATCAG 900
 Query 2088 GGTGCATCTGCATATGCCAATATTGAGTCATGtttttttCCATAGGTAATTATGTTTGT 2147
 |||||
 Sbjct 901 GGTGCATCTGCATATGCCAATATTGAGTCATG-TTTTTTCCATAGGTAATTATGTTTGT 959

Query 2148 T 2148
 |
 Sbjct 960 T 960
 Score = 165 bits (182), Expect = 2e-36
 Identities = 128/151 (84%), Gaps = 1/151 (0%)
 Strand=Plus/Plus

Query 1 TTGTACTGAATTAATGAACGAGTGTCTACGAGTGGCATAAAGAAAGTTCGCTTATTGCCC 60
 |||||
 Sbjct 961 TTGTACTGAATTAATGAACGAGTGTCTACGAGTGGCATAAAGAAAGTTCGCTCATTGCCC 1020
 Query 61 -CTCTGAAAACCGCTTTTTCTATATCTAATTTTCATGAAAATTTTAACTACTGTGAGCTT 119
 || |||||
 Sbjct 1021 TCTTTGAAAACCGCTTTTAAAAATACTGGCTGCTCGATAATTTTACTATCGAGTGCTT 1080

Query 120 TTGCTTTTGAAAAGACACGAGCGAAGCGAGT 150
 |||||
 Sbjct 1081 TTGCTTTTGAAAATAACGAGCGAAGCGAGT 1111
 Score = 69.8 bits (76), Expect = 1e-07
 Identities = 44/48 (91%), Gaps = 0/48 (0%)
 Strand=Plus/Minus
 Query 1188 ATAAACGAGCATACCGACATCACAGCAAGCTACGAACAGCACAAAAAA 1235
 |||||
 Sbjct 1257 ATAAACGAGTACACCGACATCACAGCCACCTACGAACAGCACAAAAAA 1210

>>>>nrruc:GI_313507477 Gi|313507477|gb|HQ444404.1| TSE-associated circular DNA isolate
 Sphinx 1.76, complete sequence. 0/0
 Length=1758
 Score = 1301 bits (1442), Expect = 0.0
 Identities = 1248/1577 (79%), Gaps = 43/1577 (2%)
 Strand=Plus/Plus

Query 19 CGAGTGTCTACGAGTGGCATAAAGAAAGTTCGCTTATTGCCCCCTCTGAAAACCGCTTTT 78
 |||||
 Sbjct 27 CGAGTGTCTACGAGCGACTCAATGAAAGTTCGATTATCCCCCTCTGGAAAACCGCTTTT 86
 Query 79 TCTA-TATCTAATTTTCATGAAAATTTTAACTACTGTGAGCTTTTGCTTTTGAAAAGACAC 137
 | ||| | | || |||||
 Sbjct 87 AAAAATAT-TGGCTGCTAGATGGTTTTTACTATAGTGAGGTTTGTCTTTTAAAAAACAC 145
 Query 138 GAGCGAAGCGAGTGCATTTTGTCTCTTGCTT---TTGGGGTTT---GGGGCTTGCCCC 191
 |||||
 Sbjct 146 GAGCAAAGCGAGTTCA--TAGTTGCTTTTGCTTGTTCGGGTCTTAGGGGAAATCCCCCT 203
 Query 192 AACAGGGCACAGAGTAGGAATTT-----TACACGGTAGTGAAAAGTCCCCCTCTGTGTGT 246
 |||||
 Sbjct 204 AACAGTCCCTCGAATATCAAATGTGGCTACATTTT-GTATATACGGGTAGGCT-TGCTT 261
 Query 247 CCTTGCCCTATGCTTTT-TAAACCTTTGAATTTTCCCTGTAATTTGAAGAAATTGCCCC 305
 |||||
 Sbjct 262 ATTTGATTTTTTTTCTTCTAAACCTTTGACTTCTTCCCCATTGTTTGCAGAAATTGCCCC 321
 Query 306 TCGACTAAGCTTGCTTAGTCAAAAAAGTTTGAGCAAAGCGAAAACATAGGGCAAttttca 365
 |||||
 Sbjct 322 TCGA---AGCTTGCTTAGTCAAAAAAGTTTGAGCAAAGCGAAAACATAGGGCAATTTTCA 378
 Query 366 taataaaaaatgggcttttaaatgttttaaatgcttttaaatgcttttaGACATGCTGAAA 425

Sbjct	379	TGAAGAAATTGGGCTTTTAAAGTTTTTAATG-TTTTAAATGCTTTTAGACATGCTAAGA	437
Query	426	TGCCTACACAGCAAGGCATACAGAGGACATACTCCTAGGTTTACCCACCAATACTCCTAG	485
Sbjct	438	AGCCCACACAGCAAGGCATACAGAGGACATTCTCCTACGTTTACCCHATCAATACCCCC--	495
Query	486	GTTTACCTACCAATACTCCTAGGTTTACCTACCAATACTCCTAGGTTTACCTTGCGTAAT	545
Sbjct	496	GTTTACCGATCAATACCCCTACGTTTACCCHATCAATACCCCTACGTTTACCTTGCGTATA	555
Query	546	CCTAAAAGATATAATAACAAGGAAGTACTAGGTTTAAATATTAATAAGTAAA----ATGAG	601
Sbjct	556	ACTACAA---AGAATACTAGTGTAGTA-TAAGTTCAAAG-AATAATTGTAGGTTATGAG	610
Query	602	CGATTTAATAGTAAAAGATAATGCCTTAATGAACGCTAGTTATAACCTAGACTTAGTTGA	661
Sbjct	611	CGATTTAATAGTAAAAGATAACGCCCTAATGAATGCTAGTTATAACTTAGCTTTGGTTGA	670
Query	662	GCAGCGTTTAATTCTCTTGCGTATCCTTGAGGCGAGAGAAACAGGCCAAAGGGATTAATGC	721
Sbjct	671	ACAGAGGTTAATTCTATTAGCAATCATAGAAGCGAGAGAAACAGGCCAAAGGGATTAATGC	730
Query	722	CAATGATCCTCTAACCGTTCATGCTGAAAGCTATATCAATCAATTTGGTGTAGCTAGACA	781
Sbjct	731	CAATGATCCTCTTACGGTTCATGCAGGTAGCTATATCAATCAATTTAACGTACAAAGGCA	790
Query	782	GACTGCATATCAAGCATTAAAAGATGCTTGTAAGGACTTATTTGCACGCCAATTTAGTTA	841
Sbjct	791	TACGGCATATCAAGCCCTCAAAGATGCTTGTAAGAGACTTGTTTGCCCGTCAATTCAGTTA	850
Query	842	CCAAGAAAAACGTGAGCGTGGGCGAGCTAATATTACAAGTCGTTGGGTATCGCAAATTGC	901
Sbjct	851	CCAAGAAAAGCGAGAACGAGGACGAATTAATATTACAAGTCGATGGGTTCGCAAATTGG	910
Query	902	TTACATTGATGAAACGGCAACAGTTGAGGTTATTTTGCCCTGCGGTTGTTCCACTGAT	961
Sbjct	911	CTATATGGACGATACAGCAACCGTTGAGATTATTTTGCCCTGCGGTTGTTCCCTCTGAT	970
Query	962	TACACGATTAGAGGAACAATTCACCCAATACGATATTGAACAAATTAGCGGTTTATCGAG	1021
Sbjct	971	TACACGGCTAGAGGAACAGTTCACCCAGTACGATATTGAGCAAATTAGCGGTTTATCGAG	1030
Query	1022	TGCCTATGCCGTCCGTCTATATGAATTATTGATTTGTTGGCGTAGTACAGGGAAAACACC	1081
Sbjct	1031	TGCATATGCTGTTTCGTATGTACGAAGTCTGATTTGTTGGCGTAGCACAGGCCAAAACACC	1090
Query	1082	TGTTATTGAACTAGCAGAGTTTAGAAAGCGTTTAGGTGTTTTAAATGATGAATATACTAG	1141
Sbjct	1091	AATTATTGAGCTAGACGAGTTTAGAAAGCGAATAGGTGTTTTAGATACTGAATACACTAG	1150
Query	1142	ATCGGATAATTTCAAAAAATGGA--TTATTGAA--AACCTATTAAACAAATAAACGAGC	1197
Sbjct	1151	AACAGATAATTT--AAAGATGCAAGTTATTGAATTAGCCCTA--AAACAAATCAACGAAC	1206
Query	1198	ATACCGACATCACAGCAAGCTACGAACAGCACAAAAAAGGGCGGACAATCACAGGGTTTT	1257
Sbjct	1207	ATACTGACATCACAGCAAGCTATGAACAACAAAAAAGGGCGAGTGATTACCGGATTCT	1266
Query	1258	CATTCAAGTTTAAGCAGAAAGaaa-aaaaCAGAACCTGAAACGCCAAAAAACAGCGATTCT	1316
Sbjct	1267	CATTCTGTTTAAGCACAAGAAACAAACAG-CGATAAACGCCTGATACTAACGCTTCT	1325
Query	1317	AGCCAACGTATCGAAAAGCCTAGTCAAATCCCTGCCAACATCGTAAAACAACCTGAAAAC	1376
Sbjct	1326	AGCCCACGTATCGTAAAACATAGTCAAATCCCTACCAACATTGTAAAACAGCCTGAAAAC	1385
Query	1377	GCAAATTTGAGCGATTTACAGCATCGAGCAAGCAAGATTACAGGGTTAATCATGTCTAAC	1436
Sbjct	1386	GCCAAAATGAGCGATTTAGAACATAGAGCGAGCCGTGTTACAGGGGAAATAATGCGAAAT	1445
Query	1437	CGTCTATCAGATCGGTTTAAACAAGGTGATGAATCAATCATGCAGATGATGGCACGTATT	1496
Sbjct	1446	CGTCTGTCAGATCGGTTTAAACAAGGCGATGAATCAGCAATCGACATGATGAAACGTATT	1505
Query	1497	CAAAGTGAGATTACAACCGATTCAATAGCCGACCAATGGCAATCAAATTAGAAGAATTT	1556
Sbjct	1506	CAAAGTGAAATAATAACCGATGCAATAGCAGACCAGTGGGAAAGCAAACCTGGAGGAGTTT	1565

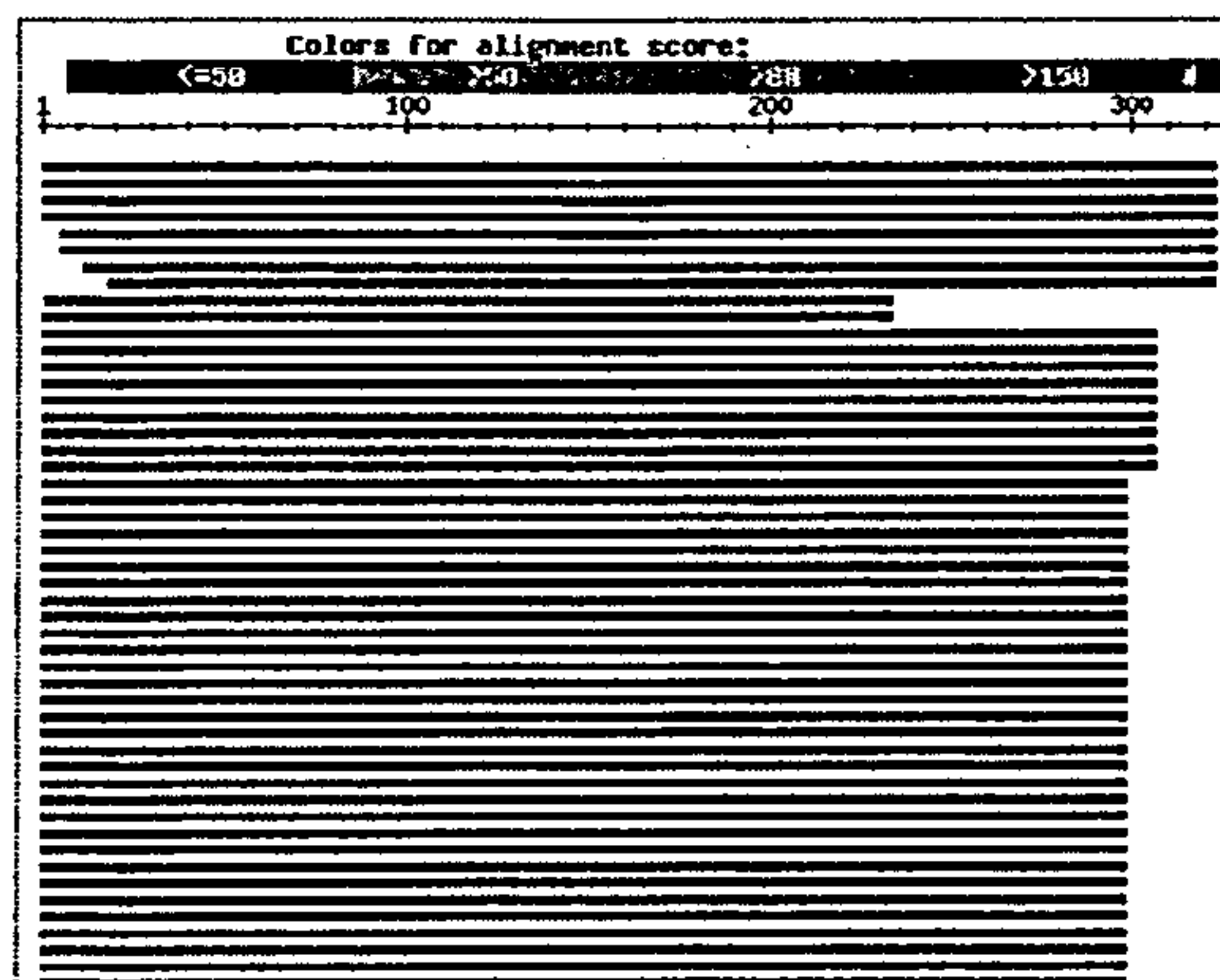
Query 1557 GCGGTAGTTTTTTAGTC 1573
||||| |||||
Sbjct 1566 GCGGTGGTTTTTTAGTC 1582

>>>>nrnuc:GI_462476960 Gi|462476960|gb|APGK01000458.1| Dendroctonus ponderosae Seq01000458,
whole genome shotgun sequence. 0/0
Length=1455

Score = 711 bits (788), Expect = 0.0
Identities = 782/1032 (75%), Gaps = 20/1032 (1%)

ORF 324aa:

BlastP – Uniprot:



>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterize... 589 6e-166
>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-li... 562 7e-158
>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterized protein;. 12/2013
Length=324
Score = 589 bits (1518), Expect = 6e-166, Method: Compositional matrix adjust.
Identities = 280/324 (86%), Positives = 304/324 (93%), Gaps = 0/324 (0%)

Query 1 MSDLIVKDNALMNASYNLDLVEQRLILLAILEARETGKGINANDPLTVHAESYINQFGVA 60
MS+LIVKDNALMNASYNLDLVEQRLILLAI+EARE+GKGINANDPLTVHAESYINQFGV
Sbjct 1 MSELIVKDNALMNASYNLDLVEQRLILLAIVEARES+GKGINANDPLTVHAESYINQFGVH 60

Query 61 RQTAYQALKDACKDLFARQFSYQEKREGRANITSRWVSQIAYIDETATVEVIFAPAVVP 120
R TAYQALKDACKDLFARQFSYQEKREGRANITSRWVSQIAYIDETATVE+IFAPAVVP
Sbjct 61 RTTAYQALKDACKDLFARQFSYQEKREGRANITSRWVSQIAYIDETATVEIIFAPAVVP 120

Query 121 LITRLEEQFTQYDIEQISGLSSAYAVRLYELLICWRSTGKTPVIELAEFRKRLGVLNDEY 180
LITRLE+QFTQYDIEQISGLSSAYAVR+YELLICWRSTGKTPVIEL EFRKR+GVL+ EY
Sbjct 121 LITRLEKQFTQYDIEQISGLSSAYAVRMYELLICWRSTGKTPVIELGEFRKRIGVLDTEY 180

Query 181 TRSDNFKKWIENPIKQINEHTDITASIEQHKKGRITITGFSFKFKQKKTEPETPKNSDS 240
R+DN K +IE +KQIN+HTDITA+YEQHKKGRITITGFSFKFKQK+KTE ETPKNSDS
Sbjct 181 IRTDNLKMRVIELALKQINDHTDITATYEQHKKGRITITGFSFKFKQKRKTELETPKNSDS 240

Query 241 SQRIEKPSQIPANIVKQPENANLSDLQHRASKITGLIMSNRLSDRFKQGDDESIMQMMARI 300
+K +IP N+VKQPENAN+SDLQHRASKITGLIMSNRLSDRFKQ DESIMQMMARI
Sbjct 241 DVPKQKSVEIPTNLVKQPENANMSDLQHRASKITGLIMSNRLSDRFKQSDDESIMQMMARI 300

Query 301 QSEITTDSDIADQWQSKLEEFQGVVF 324
QSEIT ++IA+QW++KLEEFQGV+F
Sbjct 301 QSEITDEAIAQWENKLEEFQGVIF 324

>>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-like protein;. 5/2013
Length=324
Score = 562 bits (1449), Expect = 7e-158, Method: Compositional matrix adjust.
Identities = 269/324 (83%), Positives = 290/324 (89%), Gaps = 0/324 (0%)

Query 1 MSDLIVKDNALMNASYNLDLVEQRLILLAILEARETGKGINANDPLTVHAESYINQFGVA 60
MSDLIVKDNALMNASYNL LVEQRLILLAI+EARETGKGINANDPLTVHA SYINQF V
Sbjct 1 MSDLIVKDNALMNASYNLALVEQRLILLAIEARETGKGINANDPLTVHAGSYINQFNVQ 60

Query 61 RQTAYQALKDACKDLFARQFSYQEKREGRANITSRWVSQIAYIDETATVEVIFAPAVVP 120

Sbjct 61 R TAYQALKDACKDLFARQFSYQEKREGR NITSRWVSI Y+D+TATVE+IFAPAVVP 120
RHTAYQALKDACKDLFARQFSYQEKREGRNITSRWVSIQGYMDDTATVEIIFAPAVVP 120
Query 121 LITRLEEQFTQYDIEQISGLSSAYAVRLYELLICWRSTGKTPVIELAEFRKRLGVLNDEY 180
LITRLEEQFTQYDIEQISGLSSAYAVR+YELLICWRSTGKTP+IEL EFRKR+GVL+ EY 180
Sbjct 121 LITRLEEQFTQYDIEQISGLSSAYAVRMYELLICWRSTGKTPIELDEFKRIGVLDTEY 180
Query 181 TRSDNFKKWIENPIKQINEHTDITASIEQHKKGRITGFSFKFKQKKKTEPETPKNSDS 240
TR+DN K +IE +KQINEHTDITASIEQHKKGR ITGFSF FK KK+ +TP + S 240
Sbjct 181 TRTDNLKMQVIELALKQINEHTDITASIEQHKKGRVITGFSFMFKHKKQNSDKTPDTNAS 240
Query 241 SQRIEKPSQIPANIVKQPENANLSDLQHRASKITGLIMSNRLSDRFKQGDESIMQMARI 300
S RI K SQIP NIVKQENA +SDL+HRAS++TG IM NRLSDRFKQGDES + MM RI 300
Sbjct 241 SPRIVKHSQIPTNIVKQPENAKMSDLEHRASRVTGEIMRNRLSDRFKQGDESAIDMMKRI 300
Query 301 QSEITTDSDIADQWQSKLEEFQGVVF 324
QSEI TD+IADQW+SKLEEFQGVVF 324
Sbjct 301 QSEIITDAIADQWESKLEEFQGVVF 324

>>>>sptrembl:N9JLM2_ACIBA N9jlm2 SubName: Full=Uncharacterized protein;. 12/2013
Length=325

Score = 517 bits (1332), Expect = 3e-144, Method: Compositional matrix adjust.
Identities = 257/325 (79%), Positives = 291/325 (89%), Gaps = 1/325 (0%)

ProtSweep

A Protein Identification Tool

Results for /home/vir088/rindneu/tsekompl/CMI2.214p.324.pep

Number of residues: 324 Molecular weight: 37.11 kD

Isoelectric point: 7.51

more...

Prediction of protein localization:

cyto	17 %
cyto_nucl	12.5 %
extr	6 %
nucl	6 %

Identified Protein & Transcript:

Protein:

id: sptrembl:N9LWE7 9GAMM

valuation: homologous

scientific organism: Monodelphis domestica

common organism: Short-tailed gray opossum

abstract: N9lwe7 SubName: Full=Uncharacterized protein;. 12/2013Length=324

isoform:

GO information:

accession	group	name	evidence
GO:0005727	cellular component	extrachromosomal circular DNA	IEA:InterPro
GO:0003887	molecular function	DNA-directed DNA polymerase activity	IEA:InterPro
GO:0006270	biological process	DNA replication initiation	IEA:InterPro

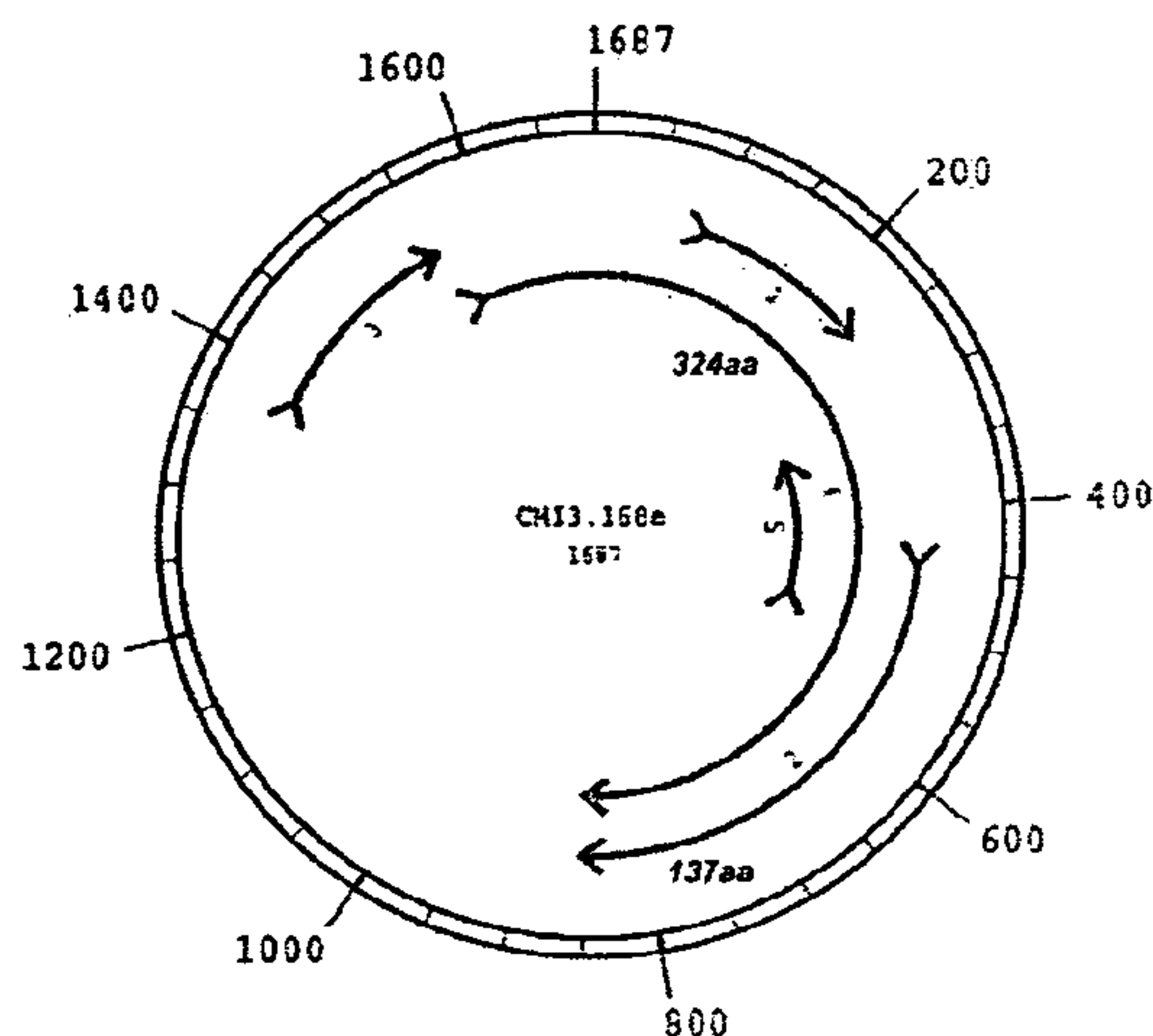
Interpro information:

id	short name
----	------------

CM13.168 (1687bp)***(mi3.NnXn.1600.5)***

GGATTAATGCCAATGATCCCTTAACAGTTCATGCAAGTAGCTATATCAATCAATTTAACGTTGAAAGACATACGGCATATCAA
GCATTAAAAGATGCTTGTAAGGACTTATTTGCACGCCAATTTAGTTACCAAGAAAAACGTGAGCGTGGGCGAGCTAATATTAC
AAGTCGTTGGGTATCGCAAATTGCTTACATTGATGAAACGGCAACAGTTGAGGTTATTTTGGCCCTGCCGTTGTTCCACTGA
TTACACGATTAGAGGAACAATTCACCCAATACGATATTGAACAAATTAGCGGTTTATCGAGTGCCTATGCAGTTCGCTTATAT
GAGTTATTGATCTGCTGGAGAACAACAGGAAAGACACCAGTTCCTTGACTTAACAGAGTTTAGAAAGCGTCTAGGTGTTTTAGA
TACCGAATACACTAGAACAGATAACTTGAAGATGCGAGTGATTGAGCAGTCACTCAAGCAAATAAACAAGCATACCGACATCA
CAGCGAGCTACGAACAGCACAAAAAGGGCGGACAATCACAGGATTCTCATTCAAGTTTAAGCAGAAGAAGAAAACAGAGCCA
GAAACGCCAAAAACAACGATTCTGGCGTTTCTAAGCCGAAAACAGTAGAAATCCCTGCCGAAGTCGTAAAACAGCCTAAAAA
CACCAATTTGAGCGATTTAGAGAAACGAGTAAGGATGATCACAGGGGCAATTGCTAAAAATAACCTGGCAAGTCGTTTTCAAC
ATGGGAATGAATCACCCTGGATATGATGAAACGTATTCAAAGTGAAATCACATCAGACGAAACTGCCGATCTATGGCAAAC
AACTTGAATCAATGGGTGTGGTTTTTTAGTCATGACGAATTTCCCGAAGGGCGCACTTTCCCAAATATCGTTTGAGTGCGT
TTTTCTATCGAAAAAGTAAAAAGACAAAGAAAATTTTCTTTGTCTTTTTTTCTGTTTTTCAAAAAAGGGATTAGCGAGTGTC
TACGAGCGACACAATGAAAGTTCGATTATTTCCCCCTCTGAAAAACCGCTTTTTTGTATCTGATTTCAAGAAAATTTTAATA
TCGTGCGCTTTTGTCTTTTGAGAAGACACGAGCGAAGCGAGTGCCATTTTTGCTTTTGTCTTTTGGGGTTTGGGGCTT
GCCCCAACAAGGCACAGAGTAGGAATTTTACACGGTAGTGGAAGTCCCCTCTGTGTGCTTGCTCTAATCTTTTTTAAAC
CTTTGATTCTTCACCGTAATTTGCTAAAAATTGCCCGACTGAGTGAAGCGAAGTCAAAAAAGTTTGAGCAAAGCGAAAACAT
AGGGCAATTTTCGTGATGAAAATGGGCTTTTAAAGTTTTTAAATGCTTTTAAATGCTTTTAGACACGCTGAAACGCAAGCCTA
GCAAGGTATACAGAGGGCATTTACCTACGTTTACCGATCAATACCCCTACGTTTACCGATCAATACCCCTACGTTTACCGATC
AATACCCCTACGTTTACCTTGCATATACTACAAAATATAATAATGTAGTAATAACTTCAAAATAATAAACGTAGGTATGAG
CGATTTAATAGTAAAAGATAACGCCCTAATGAACGCTAGTTACAACCTAGCTTTGGTTGAACAGCGTTTAATTCTATTGGCTA
TCCTAGAGGCGAGAGAAACAGGCAAAG

Repeat - ATACCCCTACGTTTACCGATCA - 3x22nt + 12nt



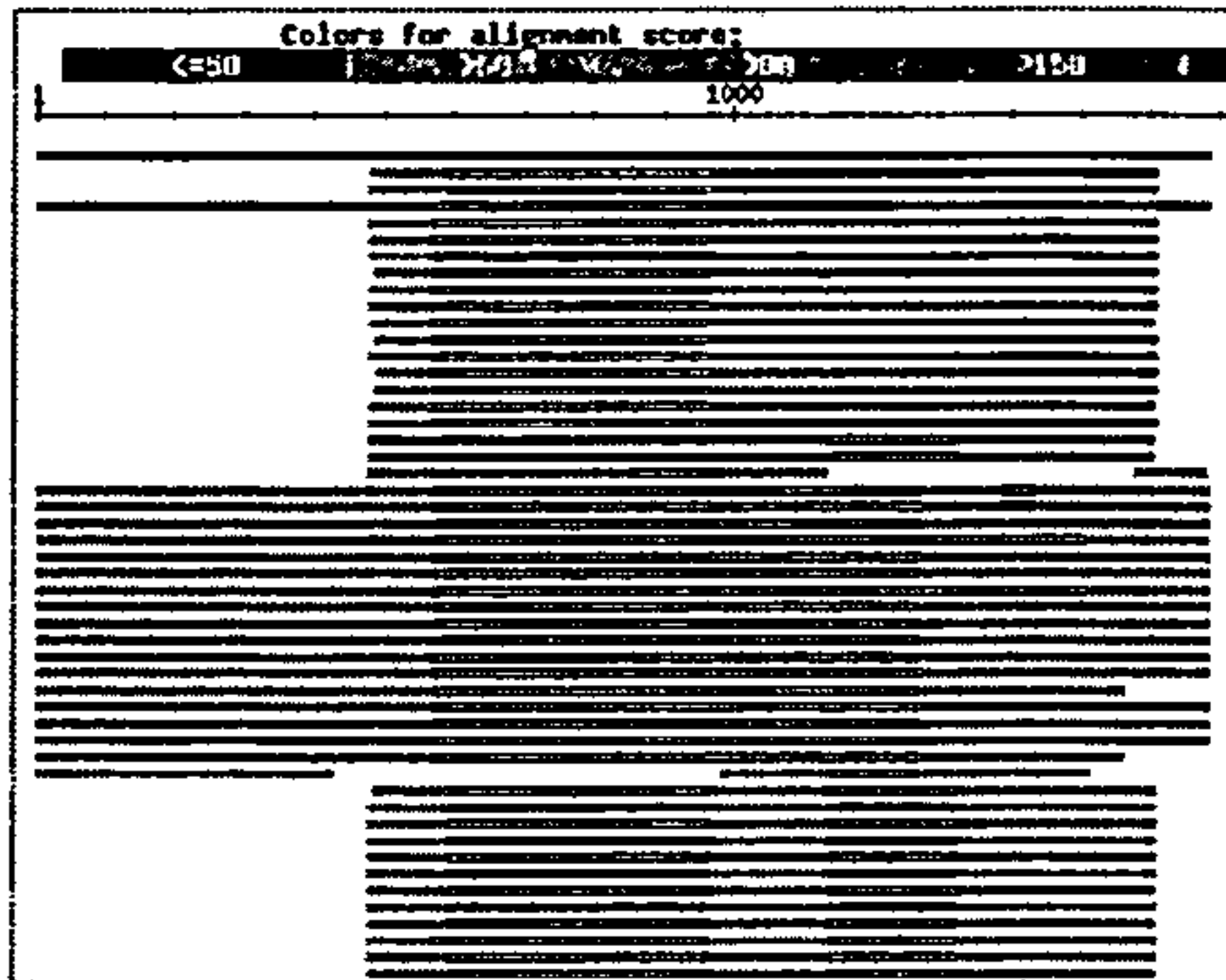
79% nucleotide similarity to TSE-associated circular DNA isolate Sphinx 1.76

ORF: 324aa – replication protein 80% similarity to Spinx1.76

137aa – replication protein 59% similarity to Spinx1.76

Figure 1(g)

Blastn – Geall:



```
>>>nrrnuc:GI_313507477|Gi|313507477|gb|HQ444404.1|TSE-associ...7470.0
>>>nrrnuc:GI_347602268|Gi|347602268|gb|JN541301.1|Uncultured...3942e-105
```

```
>>>>nrnuc:GI_313507477 Gi|313507477|gb|HQ444404.1| TSE-associated circular DNA isolate
Sphinx 1.76, complete sequence. 0/0
Length=1758
```

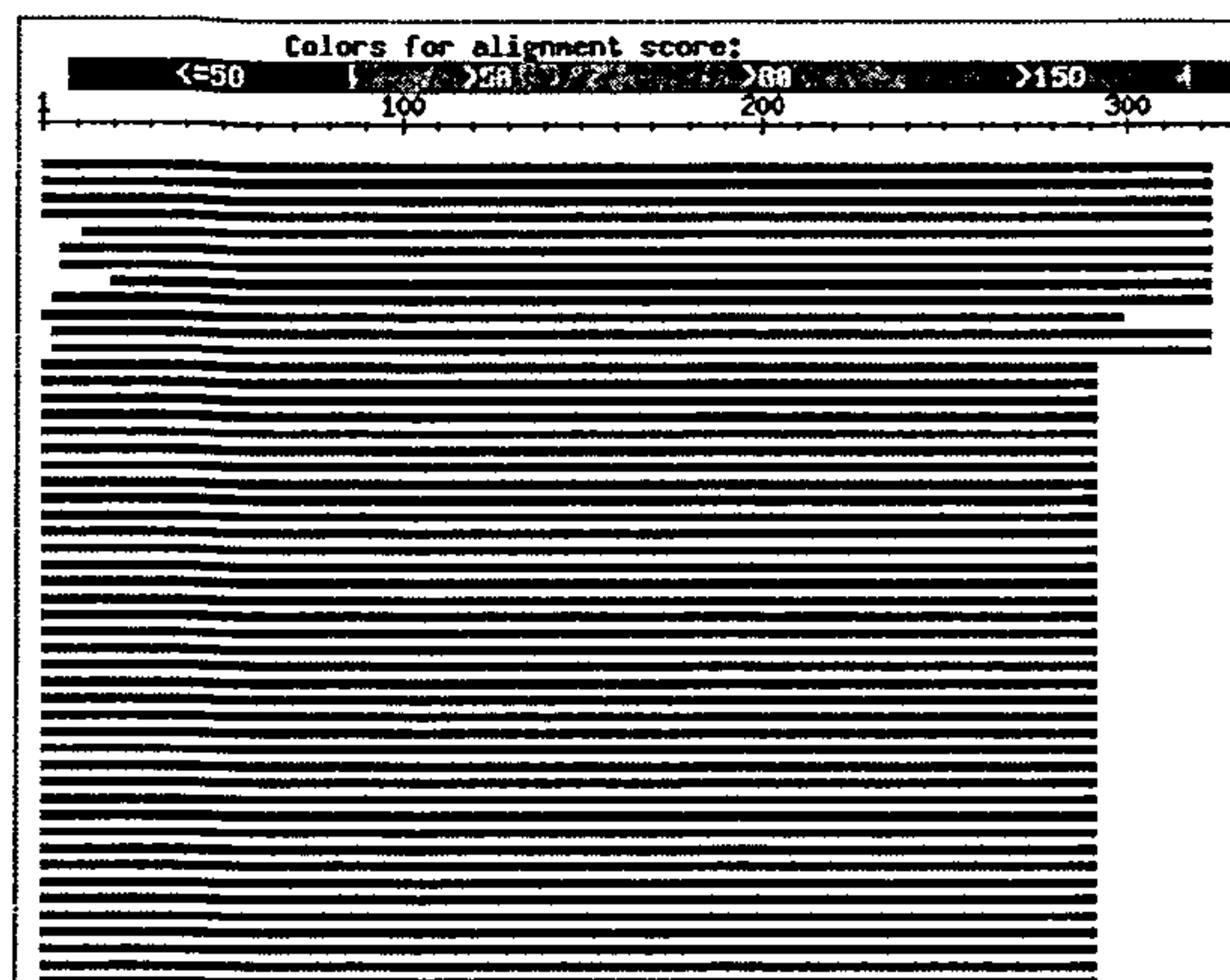
Score = 747 bits (828), Expect = 0.0
Identities = 708/894 (79%), Gaps = 11/894 (1%)
Strand=Plus/Plus

Query	1	GGATTAATGCCAATGATCCCTTAACAGTTCATGCAAGTAGCTATATCAATCAATTTTAACG	60
Sbjct	721	GGATTAATGCCAATGATCCTCTTACGGTTCATGCAGGTAGCTATATCAATCAATTTTAACG	780
Query	61	TTGAAAGACATACGGCATATCAAGCATTAAAAGATGCTTGTAAGGACTTATTTGCACGCC	120
Sbjct	781	TACAAAGGCATACGGCATATCAAGCCCTCAAAGATGCTTGTAAGGACTTGTTTGCCCGTC	840
Query	121	AATTTAGTTACCAAGAAAAACGTGAGCGTGGGCGAGCTAATATTACAAGTCGTTGGGTAT	180
Sbjct	841	AATTCAGTTACCAAGAAAGCGAGAACGAGGACGAATTAATATTACAAGTCGATGGGTTT	900
Query	181	CGCAAATTGCTTACATTGATGAAACGGCAACAGTTGAGGTATTTTTGCCCCTGCCGTTG	240
Sbjct	901	CGCAAATTGGCTATATGGACGATACAGCAACCGTTGAGATTATTTTTGCCCCTGCCGTTG	960
Query	241	TTCCACTGATTACACGATTAGAGGAACAATTCACCCAATACGATATTGAACAAATTAGCG	300
Sbjct	961	TTCTCTGATTACACGGCTAGAGGAACAGTTCACCCAGTACGATATTGAGCAAATTAGCG	1020
Query	301	GTTTATCGAGTGCCTATGCAGTTCGCTTATATGAGTTATTGATCTGCTGGAGAACAACAG	360
Sbjct	1021	GTTTATCGAGTGCATATGCTGTTCGTATGTACGAACTGCTGATTTGTTGGCGTAGCACAG	1080
Query	361	GAAAGACACCAAGTTCTTGACTTAACAGAGTTTAGAAAGCGTCTAGGTGTTTTAGATACCG	420
Sbjct	1081	GCAAAACACCAATTATTGAGCTAGACGAGTTTAGAAAGCGAATAGGTGTTTTAGATACTG	1140
Query	421	AATACACTAGAACAGATAACTTGAAGATGCGAGTGATTGAGCAGTCACTCAAGCAAATAA	480
Sbjct	1141	AATACACTAGAACAGATAATTTAAAGATGCAAGTTATTGAATTAGCCCTAAAACAAATCA	1200
Query	481	ACAAGCATACCGACATCACAGCGAGCTACGAACAGCACAAAAAAGGGCGGACAATCACAG	540
Sbjct	1201	ACGAACATACTGACATCACAGCAAGCTATGAACAACACAAAAAAGGGCGAGTGATTACCG	1260
Query	541	GATTCTCATTCAAGTTTAAGCAGAAG-AAGAAAACAGAGCCAGAAACGCCAAAAAAACAAC	599

Sbjct	1261	GATTCTCATTCATGTTTAAGCACAAGAAAACAAAAACAGCGATA-AAACGCCTGATACTAAC	1319
Query	600	GATTCTGGCGTTTTCTAAGCCGAAAACAGTAG--AAATCCCTGCCGAAGTCGTAAAACAGC	657
Sbjct	1320	GCTTCTAGC-CCACGTATCGTAAACA-TAGTCAAATCCCTACCAACATTGTAAAACAGC	1377
Query	658	CTAAAAACACCAATTTGAGCGATTTAGAGAAACGAGTAAGGATGATCACAGGGGCAAT--	715
Sbjct	1378	CTGAAAACGCCAAAATGAGCGATTTAGAACATAGAGCGAGCCGTGTTACAGGGGAAATAA	1437
Query	716	TGCTAAAAATAACCTGGCAAGTCGTTTTCAACATGGGAATGAATCACC ACTGGATATGAT	775
Sbjct	1438	TGC--GAAATCGTCTGT CAGATCGGTTTAAACAAGGC GATGAATCAGCAATCGACATGAT	1495
Query	776	GAAACGTATTCAAAGTGAAATCACATCAGACGAAACTGCCGATCTATGGCAAAACAACT	835
Sbjct	1496	GAAACGTATTCAAAGTGAAATAATAACCGATGCAATAGCAGACCAGTGGGAAAGCAA CT	1555
Query	836	TGAATCAATGGGTGTGGTTTTTTTAGTCATGACGAATTTCCC GAAGGGCGCACTT	889
Sbjct	1556	GGAGGAGTTTGGCGTGGTTTTTTTAGTCATGACG-ATTTCCC GAAGGGCGCACTT	1608

Score = 627 bits (694), Expect = 2e-175
Identities = 585/726 (80%), Gaps = 22/726 (3%)
Strand=Plus/Plus

[illegible]

ORF 324aa:**BlastP – Uniprot:**

```
>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterize... 550 5e-154
>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-li... 540 3e-151
>>>sptrembl:N9JLM2_ACIBA N9jlm2 SubName: Full=Uncharacterize... 523 5e-146
```

```
>>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterized protein;. 12/2013
Length=324
Score = 550 bits (1416), Expect = 5e-154, Method: Compositional matrix adjust.
Identities = 261/324 (80%), Positives = 288/324 (88%), Gaps = 0/324 (0%)
```

```
Query 1 MSDLIVKDNALMNASYNLALVEQRLILLAILEARETGKGINANDPLTVHASSYINQFNVE 60
      MS+LIVKDNALMNASYNL LVEQRLILLAI+EARE+GKGINANDPLTVHA SYINQF V
Sbjct 1 MSELIVKDNALMNASYNLDLVEQRLILLAIVEARES+GKGINANDPLTVHAESYINQFGVH 60

Query 61 RHTAYQALKDACKDLFARQFSYQEKREGRANITSRWVSIAYIDETATVEVIFAPAVVP 120
      R TAYQALKDACKDLFARQFSYQEKREGRANITSRWVSIAYIDETATVE+IFAPAVVP
Sbjct 61 RTTAYQALKDACKDLFARQFSYQEKREGRANITSRWVSIAYIDETATVEIIFAPAVVP 120

Query 121 LITRLEEQFTQYDIEQISGLSSAYAVRLYELLICWRTTGKTPVLDLTFRKRRLGVLDTEY 180
      LITRLE+QFTQYDIEQISGLSSAYAVR+YELLICWR+TGKTPV++L EFRKR+GVLDTEY
Sbjct 121 LITRLEKQFTQYDIEQISGLSSAYAVRMYELLICWRSTGKTPVIELGEFRKRIGVLDTEY 180

Query 181 TRTDNLKMRVIEQSLKQINKHTDITASIEQHKKGRTITGFSFKFKQKKTEPETPKNNDS 240
      RTDNLKMRVIE +LKQIN HTDITA+YEQHKKGRTITGFSFKFKQK+KTE ETPKN+DS
Sbjct 181 IRTDNLKMRVIELALKQINDHTDITATYEQHKKGRTITGFSFKFKQKRKTELETPKNDS 240

Query 241 GVSKPKTVEIPAENVKQPKNTNLSLEKRVRMITGAIKNNLASRFQHGNEPLDMMKRI 300
      V K K+VEIP +VKQP+N N+SDL+ R ITG I N L+ RF+ +ES + MM RI
Sbjct 241 DVPKQKSVEIPTNLVKQPENANMSDLQHRASKITGLIMSNRLSDRFKQSDSIMQMMARI 300

Query 301 QSEITSDETADLWQNKLESMGVVF 324
      QSEIT + A+ W+NKLE GV+F
Sbjct 301 QSEITDEAIAQWENKLEEFVIF 324
```

```
>>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-like protein (Sphinx);. 5/2013
Length=324
Score = 540 bits (1391), Expect = 3e-151, Method: Compositional matrix adjust.
Identities = 254/324 (78%), Positives = 283/324 (87%), Gaps = 0/324 (0%)
```

```
Query 1 MSDLIVKDNALMNASYNLALVEQRLILLAILEARETGKGINANDPLTVHASSYINQFNVE 60
      MSDLIVKDNALMNASYNLALVEQRLILLAI+EARETGKGINANDPLTVHA SYINQFN+
Sbjct 1 MSDLIVKDNALMNASYNLALVEQRLILLAIIEARETGKGINANDPLTVHAGSYINQFNQ 60

Query 61 RHTAYQALKDACKDLFARQFSYQEKREGRANITSRWVSIAYIDETATVEVIFAPAVVP 120
      RHTAYQALKDACKDLFARQFSYQEKREGR NITSRWVSI Y+D+TATVE+IFAPAVVP
Sbjct 61 RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSIQGYMDDTATVEIIFAPAVVP 120
```

Query 121 LITRLEEQFTQYDIEQISGLSSAYAVRLYELICWRTTGKTPVLDLTEFRKRLGVLDTEY 180
LITRLEEQFTQYDIEQISGLSSAYAVR+YELICWR+TGKTP+++L EFRKR+GVLDTEY
Sbjct 121 LITRLEEQFTQYDIEQISGLSSAYAVRMYELICWRSTGKTPIIELDEFKRRIGVLDTEY 180

Query 181 TRTDNLKMRVIEQSLKQINKHTDITASYEQHKKGRTITGFSFKFKQKKKTEPETPKNNDS 240
TRTDNLKM+VIE +LKQIN+HTDITASYEQHKKGR ITGFSF FK KK+ +TP N S
Sbjct 181 TRTDNLKMQVIELALKQINEHTDITASYEQHKKGRVITGFSFMFKHKKQNSDKTPDTNAS 240

Query 241 GVSKPKTVEIPAENVKQPKNTNLSLEKRVRMITGAIKNNLASRFQHGNEsplDMMKRI 300
K +IP +VKQP+N +SDLE R +TG I +N L+ RF+ G+ES +DMMKRI
Sbjct 241 SPRIVKHSQIPTNIVKQPENAKMSDLEHRASRVTEIMRNRLSDRFKQGDSESAIDMMKRI 300

Query 301 QSEITSDETADLWQNKLESMGVVF 324
QSEI +D AD W++KLE GVVVF
Sbjct 301 QSEIITDAIADQWESKLEEFVVVF 324

ProtSweep**A Protein Identification Tool**

Results for /home/vir088/rindneu/tsekompl/CM13.168.324.pep

Number of residues: 324 Molecular weight: 36.97 kD
Charge: 5 Isoelectric point: 9.63

more...

Prediction of protein localization:

cyto	12 %
cyto_nucl	10 %
extr	6 %
nucl	6 %
mito	6 %

Identified Protein & Transcript:**Protein:**id: sptrembl:N9LWE7 9GAMM

valuation: similar

scientific organism: Acinetobacter sp

abstract: N9lwe7 SubName: Full=Uncharacterized protein; 12/2013Length=324

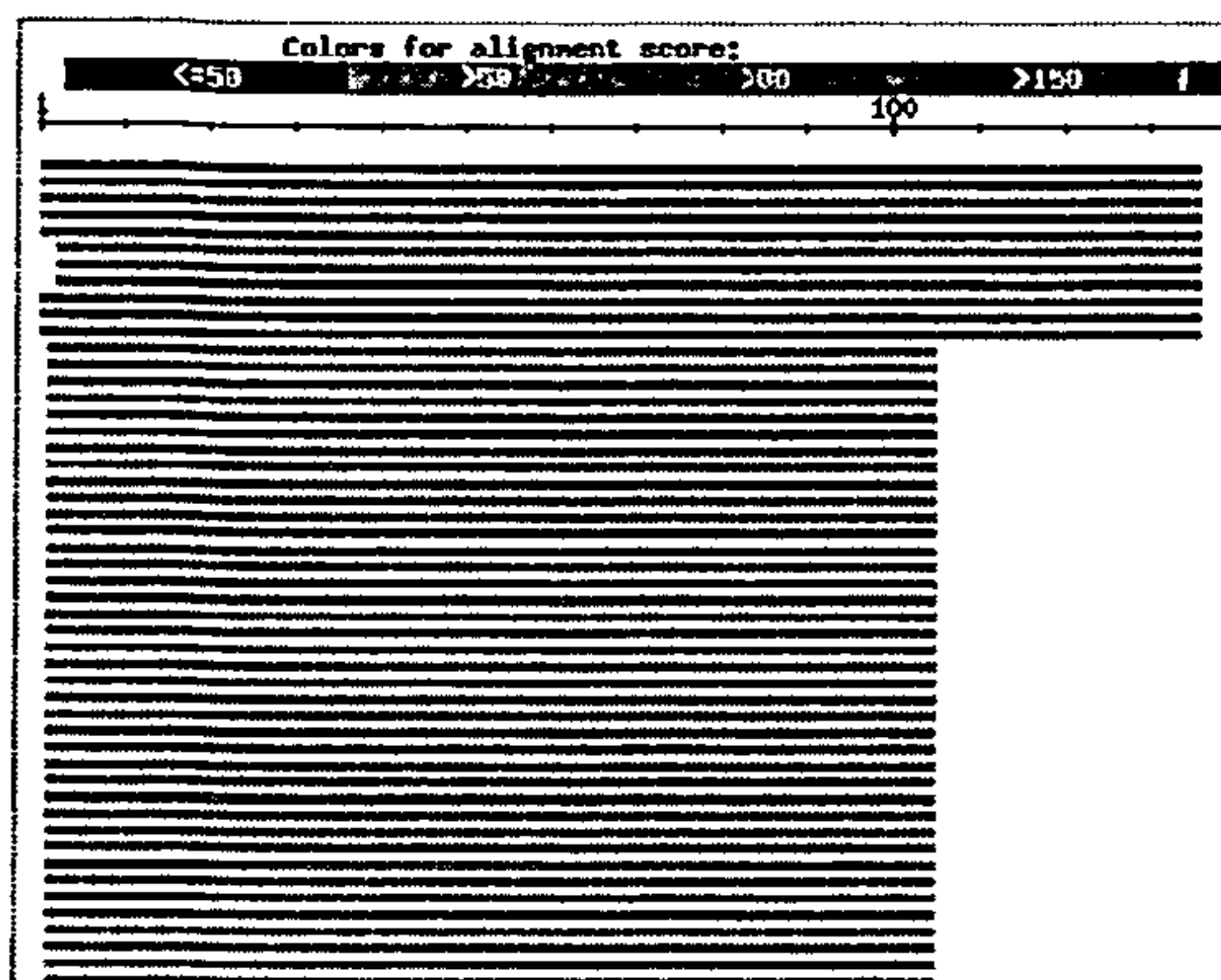
isoform:

GO information:

accession	group	name	evidence
GO:0005727	cellular component	extrachromosomal circular DNA	IEA:InterPro
GO:0003887	molecular function	DNA-directed DNA polymerase activity	IEA:InterPro
GO:0006270	biological process	DNA replication initiation	IEA:InterPro

Interpro information:

id	short name
IPR000525	Initiator_Rep_prot
IPR011991	WHTH_DNA-bd_dom

ORF 137aa:**BlastP – Uniprot:**

```
>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterize... 191 1e-46
>>>sptrembl:N9JLM2_ACIBA N9jlm2 SubName: Full=Uncharacterize... 190 2e-46
>>>sptrembl:N8ZNY0_9GAMM N8zny0 SubName: Full=Uncharacterize... 190 2e-46
>>>sptrembl:S7WS39_9GAMM S7ws39 SubName: Full=DNA replicatio... 190 2e-46
>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-li... 171 9e-41
```

```
>>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterized protein;. 12/2013
Length=324
```

```
Score = 191 bits (484), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 91/137 (66%), Positives = 108/137 (78%), Gaps = 0/137 (0%)
```

```
Query 1 MRVIEQSLKQINKHTDITASIEQHKKGRITITGFSFKFKQKKKTEPETPKNNDSGVSKPKT 60
MRVIE +LKQIN HTDITA+YEQHKKGRITITGFSFKFKQK+KTE ETPKN+DS V K K+
Sbjct 188 MRVIELALKQINDHTDITATYEQHKKGRITITGFSFKFKQKRKTELETPKNSDSVDPKQKS 247

Query 61 VEIPAEVVKQPKNTNLSLEKRVRMITGAIKNNLASRFQHGNEPLDMMKRIQSEITSD 120
VEIP +VKQP+N N+SDL+ R ITG I N L+ RF+ +ES + MM RIQSEIT +
Sbjct 248 VEIPTNLVKQPENANMSDLQHRASKITGLIMSNRLSDRFKQSDSIMQMMARIQSEITDE 307

Query 121 ETADLWQNKLESMGVVF 137
A+ W+NKLE GV+F
Sbjct 308 AIANQWENKLEEFVGF 324
```

```
>>>>sptrembl:N9JLM2_ACIBA N9jlm2 SubName: Full=Uncharacterized protein;. 12/2013
Length=325
```

```
Score = 190 bits (483), Expect = 2e-46, Method: Compositional matrix adjust.
Identities = 103/137 (75%), Positives = 113/137 (82%), Gaps = 0/137 (0%)
```

```
Query 1 MRVIEQSLKQINKHTDITASIEQHKKGRITITGFSFKFKQKKKTEPETPKNNDSGVSKPKT 60
MRVIE +LKQIN +TDITASIEQHKKGR ITGFSFKFKQKKKTE ETPKN+DSGVSK K
Sbjct 189 MRVIELALKQINDYTDITASIEQHKKGRVITGFSFKFKQKKKTEAETPKNSDSGVSKQKP 248

Query 61 VEIPAEVVKQPKNTNLSLEKRVRMITGAIKNNLASRFQHGNEPLDMMKRIQSEITSD 120
+EIP EVVKQPKN NLSLE R ITG I +N L RF+ +ESPL+MMKRIQSEIT+D
Sbjct 249 IEIPTEVVKQPKNANLSLEHRASRITGEIMRNRLTDRFKQADESPLEMMKRIQSEITD 308

Query 121 ETADLWQNKLESMGVVF 137
AD W+NKLE GVVVF
Sbjct 309 TIADQWENKLEEFVGF 325
```

```
>>>>sptrembl:N8ZNY0_9GAMM N8zny0 SubName: Full=Uncharacterized protein;. 12/2013
Length=325
```

```
Score = 190 bits (483), Expect = 2e-46, Method: Compositional matrix adjust.
Identities = 103/137 (75%), Positives = 113/137 (82%), Gaps = 0/137 (0%)
```

Query 1 MRVIEQSLKQINKHTDITASYEQHKKGRTITGFSFKFKQKKKTEPETPKNNDSGVSKPKT 60
MRVIE +LKQIN +TDITASYEQHKKGR ITGFSFKFKQKKKTE ETPKN+DSGVSK K
Sbjct 189 MRVIELALKQINDYTDITASYEQHKKGRVITGFSFKFKQKKKTEAETPKNSDSGVSKQKP 248

Query 61 VEIPAEVVKQPKNTNLSLEKRVRMITGAIKNNLASRFQHGNEsplDMMKRIQSEITSD 120
+EIP EVVKQPKN NLSLE R ITG I +N L RF+ +ESPL+MMKRIQSEIT+D
Sbjct 249 IEIPTEVVKQPKNANLSLEHRASRITGEIMRNRLTDRFKQADESPLEMMKRIQSEITTD 308

Query 121 ETADLWQNKLESMGVVF 137
AD W+NKLE GVVF
Sbjct 309 TIADQWENKLEEFGVVF 325

>>>>sptrembl:S7WS39_9GAMM S7ws39 SubName: Full=DNA replication protein;. 12/2013
Length=314

Score = 190 bits (483), Expect = 2e-46, Method: Compositional matrix adjust.
Identities = 103/137 (75%), Positives = 113/137 (82%), Gaps = 0/137 (0%)

Query 1 MRVIEQSLKQINKHTDITASYEQHKKGRTITGFSFKFKQKKKTEPETPKNNDSGVSKPKT 60
MRVIE +LKQIN +TDITASYEQHKKGR ITGFSFKFKQKKKTE ETPKN+DSGVSK K
Sbjct 178 MRVIELALKQINDYTDITASYEQHKKGRVITGFSFKFKQKKKTEAETPKNSDSGVSKQKP 237

Query 61 VEIPAEVVKQPKNTNLSLEKRVRMITGAIKNNLASRFQHGNEsplDMMKRIQSEITSD 120
+EIP EVVKQPKN NLSLE R ITG I +N L RF+ +ESPL+MMKRIQSEIT+D
Sbjct 238 IEIPTEVVKQPKNANLSLEHRASRITGEIMRNRLTDRFKQADESPLEMMKRIQSEITTD 297

Query 121 ETADLWQNKLESMGVVF 137
AD W+NKLE GVVF
Sbjct 298 TIADQWENKLEEFGVVF 314

>>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-like protein;. 5/2013
Length=324

Score = 171 bits (434), Expect = 9e-41, Method: Compositional matrix adjust.
Identities = 82/137 (59%), Positives = 100/137 (72%), Gaps = 0/137 (0%)

Query 1 MRVIEQSLKQINKHTDITASYEQHKKGRTITGFSFKFKQKKKTEPETPKNNDSGVSKPKT 60
M+VIE +LKQIN+HTDITASYEQHKKGR ITGFSF FK KK+ +TP N S K
Sbjct 188 MQVIELALKQINEHTDITASYEQHKKGRVITGFSFMFKHKKQNSDKTPDTNASSPRIVKH 247

Query 61 VEIPAEVVKQPKNTNLSLEKRVRMITGAIKNNLASRFQHGNEsplDMMKRIQSEITSD 120
+IP +VKQP+N +SDLE R +TG I +N L+ RF+ G+ES +DMMKRIQSEI +D
Sbjct 248 SQIPTNIVKQPENAKMSDLEHRASRVTEIMRNRLSDRFKQGDESAIDMMKRIQSEIITD 307

Query 121 ETADLWQNKLESMGVVF 137
AD W++KLE GVVF
Sbjct 308 AIADQWESKLEEFGVVF 324

CMI4.158 (1583bp)***(mil.NoXo.1500.5)***

GAGGACGAATTAATATTACAAGTCGTTGGGTTTCACAAATTGGTTATATGGACGATACAGCAACCGTTGAGGTTATTTTGGCC
 CCTGCGGTTGTTCCATTGATTACAAGACTGGAGGAACAATTCACCCAGTACGATATTGAGCAAATTAGCGGTTTATCTAGTGC
 TTATGCCGTCCGTCTGTATGAATTATTGATCTGTTGGCGTAGCACAGGAAAAACGCCCGTCATAGAACTAGCAGAGTTTAGAA
 AACGAATAGGTGTTTTAGATACTGAATACAGGAAACAGATAACTTAAAGATGCGAGTTATTGAGCTAGCACTCAAGCAGATC
 AACGAACATACAGACATCACAGCAAGCTATGAACAGCACAAAAAAGGGCGGACAATCACTGGGTTCTCATTCAAGTTTAAAGCA
 GAAGAAGAAAACAGAGCTAGAAACGCCAAAAAACAGCGATTCTAGCCCACATATCGAAAAACCTAGTCAAATCCCTACCAACA
 TCGTAAAACAGCCTGAAAACGCCAAAAAAGACGATTTAGGGCATAGAGCAAGTAAGATTACAGGTTTAAATCATGTCCAATGGT
 TTAGCAGATCGGTTTAAACGTGGTGATGAGTCCGTCATGAATATGATGAAACGCATCAAAGAAGAAATTACAACCGATGCAAC
 AGCCGATCTATGGCAAAACAACTTGAATCAATGGTGTGGTTTTTTAGTCATGACTAAATTGGCTATGCAATGTCTCCGCTCT
 TTTTCTAAGAACCGTTTTTGTCTTTTCAAAATCGCGGCTCGCGGGTGTCTTTACTGGTATATGCGCTTTTTCGTGCTGCTTTT
 CAAAAATGTGGCGATAGCCAACATTCTCGATTTTGATCTTGATTTTGGGGTTTTAGGGTCTCCCTAACCAAGACATAGAGACA
 CAACTCGCTAGAGGGGTCTCTATGTGTCTTGCCTTAATTAATAAACTAAATAAATTTTACCCGTTTTTGCTTTAAAAAAG
 GCAGGTTTTTCTTTGTCCTTACTTTTGACTTTGATTTTCTCCTGTTTTTTTGGAGTTACCCACAAGAATTTTCATGTGGTTTTG
 GGCTTTTAAGGTTTTTAAATGCTTTTAAATGCTTTTAAACATGCTGAAACGTAAGCATAGCAAGGTATACAGAGTTCATTCTC
 CTACGTTTACCGATCAATACCCCTACGTTTACCGATCAATACCCCTACGTTTACCGATCAATACCCCTACGTTTACCGATCA
TACCCCTACGTTTACGTTGCATATAACTACAAAAACAATAATGTAGTAATAACTTCAAAATAATAAGAGTAGGTTATGAGCG
ATTTAATAGTAAAGATAACGCCCTAATGAACGCTAGTTACAACCTAGCTTTGGTTGAACAGCGTTTAATCTTTTAGCTATA
 TTGGAAGCGAGAGAAACAGGAAAAGGGATTAATGCCAATGATCCCTAACAGTTCATGCAAATAGCTATATCAATCAATTTAA
 CGTGGAAGACATACGGCATATCAAGCATTAAAAGATGCCTGCAAAGACTTGTTTGCACGTCAATTCAGTTACCAAGAAAAGC
 GAGAAC

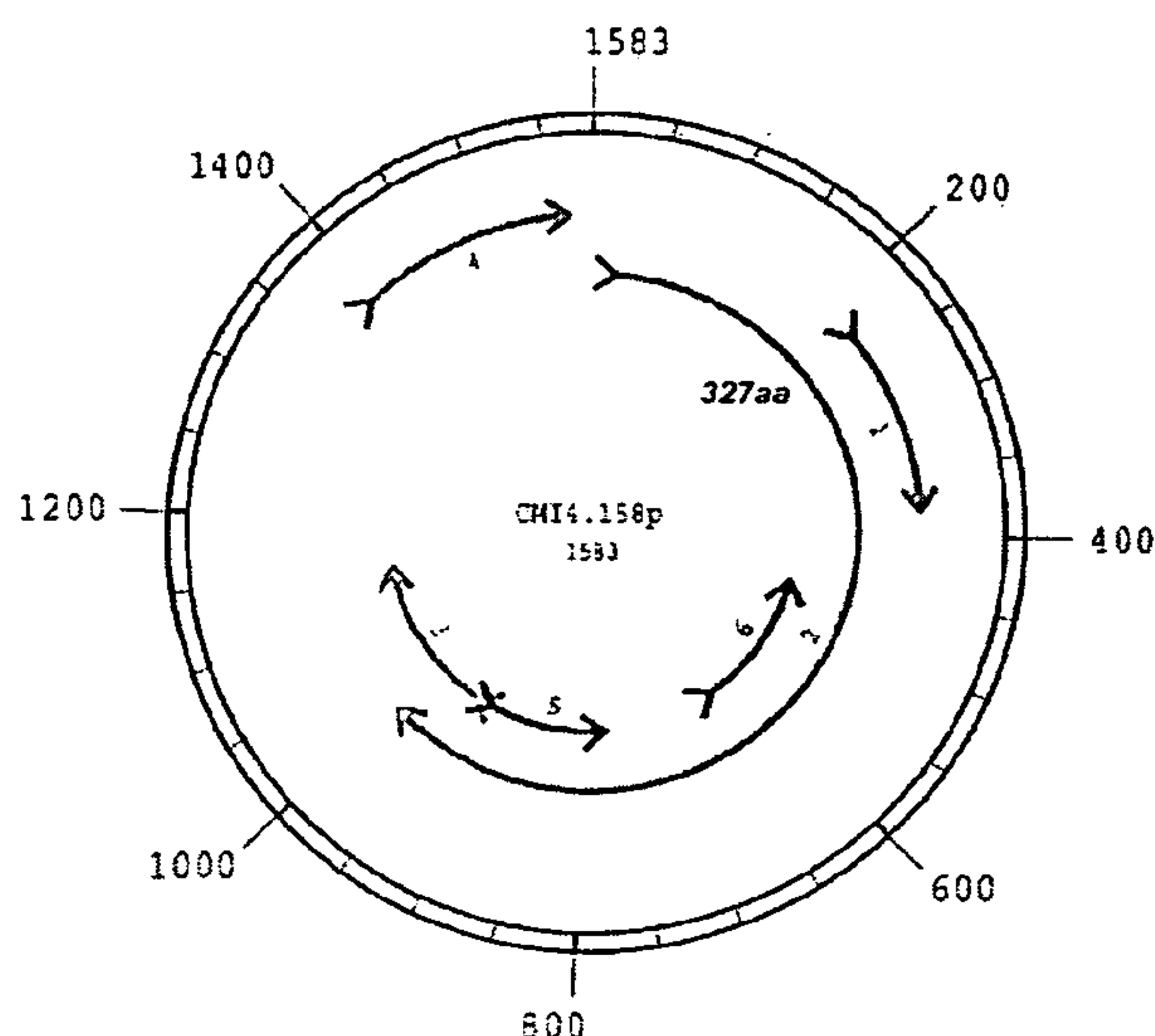
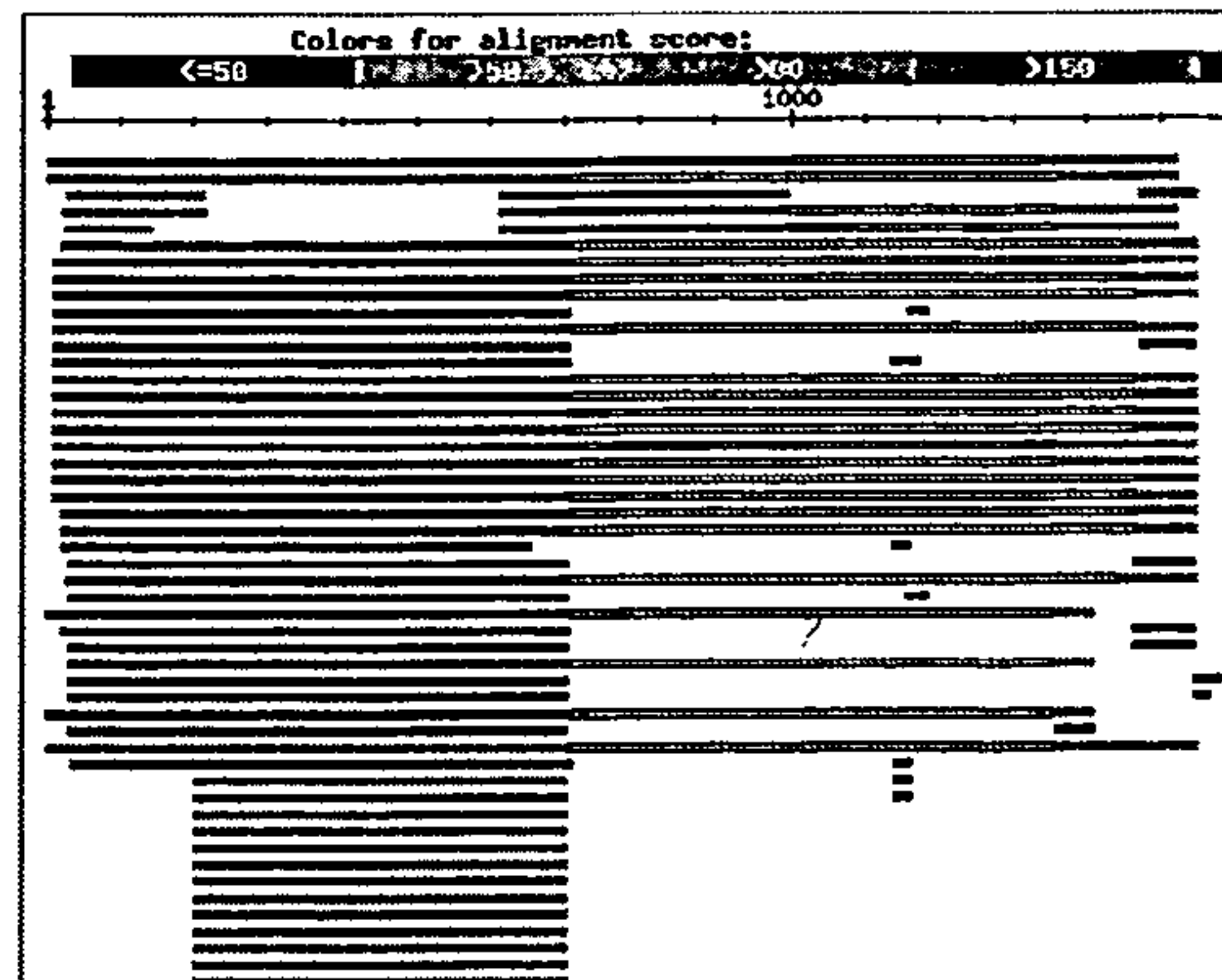
Repeat – 3x22nt + 17nt***85% nucleotide similarity to TSE-associated circular DNA isolate Sphinx 1.76******ORF 327aa replication protein 80% similarity to Sphinx 1.76***

Figure 1(h)

Blastn – Geall:



```
>>>nrnuc:GI 313507477  Gi|313507477|gb|HQ444404.1| TSE-associ... 1128 0.0
>>>nrnuc:GI 462476960  Gi|462476960|gb|APGK01000458.1| Dendro... 477 2e-130
```

```
>>>>nrnuc:GI_313507477 Gi|313507477|gb|HQ444404.1| TSE-associated circular DNA isolate
Sphinx 1.76, complete sequence. 0/0
Length=1758
```

Score = 1128 bits (1250), Expect = 0.0
Identities = 857/1005 (85%), Gaps = 5/1005 (0%)
Strand=Plus/Plus

Query	1	TCAAAATAATAAGAGTAGGTTATGAGCGATTTAATAGTAAAAGATAACGCCCTAATGAAC	60
Sbjct	585	TCAAAAGAATAATTGTAGGTTATGAGCGATTTAATAGTAAAAGATAACGCCCTAATGAAT	644
Query	61	GCTAGTTACAACCTTAGCTTTGGTTGAACAGCGTTTAAATTCTTTAGCTATATTGGAAGCG	120
Sbjct	645	GCTAGTTATAACTTAGCTTTGGTTGAACAGAGGTTAATTCTATTAGCAATCATAGAAGCG	704
Query	121	AGAGAAACAGGAAAAGGGATTAATGCCAATGATCCCTTAACAGTTCATGCAAATAGCTAT	180
Sbjct	705	AGAGAAACAGGCCAAAGGGATTAATGCCAATGATCCTCTTACGGTTCATGCAGGTAGCTAT	764
Query	181	ATCAATCAATTTAACGTGGAAAGACATACGGCATATCAAGCATTTAAAAGATGCCTGCAAA	240
Sbjct	765	ATCAATCAATTTAACGTACAAAGGCATACGGCATATCAAGCCCTCAAAGATGCTTGTA	824
Query	241	GACTTGTTTGCACGTCAATTCAGTTACCAAGAAAAGCGAGAACGAGGACGAATTAATATT	300
Sbjct	825	GACTTGTTTGGCCGTCAATTCAGTTACCAAGAAAAGCGAGAACGAGGACGAATTAATATT	884
Query	301	ACAAGTCGTTGGGTTTCACAAATTGGTTATATGGACGATACAGCAACCGTTGAGGTTATT	360
Sbjct	885	ACAAGTCGATGGGTTTCGCAAATTGGCTATATGGACGATACAGCAACCGTTGAGATTATT	944
Query	361	TTTGCCCTGCGGTTGTTCCATTGATTACAAGACTGGAGGAACAATTCACCCAGTACGAT	420
Sbjct	945	TTTGCCCTGCGGTTGTTCTCTGATTACACGGCTAGAGGAACAGTTCACCCAGTACGAT	1004
Query	421	ATTGAGCAAATTAGCGGTTTATCTAGTGCTTATGCCGTCCGTCTGTATGAATTATTGATC	480
Sbjct	1005	ATTGAGCAAATTAGCGGTTTATCGAGTGCATATGCTGTTTCGTATGTACGAACTGCTGATT	1064
Query	481	TGTTGGCGTAGCACAGGAAAAACGCCCGTCATAGAACTAGCAGAGTTTAGAAAACGAATA	540
Sbjct	1065	TGTTGGCGTAGCACAGGCAAAACACCAATTATTGAGCTAGACGAGTTTAGAAAGCGAATA	1124
Query	541	GGTGTTTTAGATACTGAATACACGAGAACAGATAACTTAAAGATGCGAGTTATTGAGCTA	600

>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterize... 563 3e-158

>>>>sptrembl:E5LG72_9ZZZZ E5lg72 SubName: Full=Replicase 3-like protein;. 5/2013
Length=324

Score = 574 bits (1479), Expect = 2e-161, Method: Compositional matrix adjust.
Identities = 276/324 (85%), Positives = 294/324 (90%), Gaps = 0/324 (0%)

```
Query 1  MSDLIVKDNALMNASYNLALVEQRLILLAILEARETGKGINANDPLTVHANSYINQFNVE 60
Sbjct 1  MSDLIVKDNALMNASYNLALVEQRLILLAIEARETGKGINANDPLTVHAGSYINQFNQV 60

Query 61 RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEVIFAPAVVP 120
Sbjct 61 RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEIIFAPAVVP 120

Query 121 LITRLEEQFTQYDIEQISGLSSAYAVRLYELLICWRSTGKTPVIELAEFRKRIGVLDTEY 180
Sbjct 121 LITRLEEQFTQYDIEQISGLSSAYAVRMYELLICWRSTGKTPIELDEFKRKRIGVLDTEY 180

Query 181 TRTDNLKMRVIELALKQINEHTDITASIEQHKKGRITITGFSFKFKQKKKTELETPKNSDS 240
Sbjct 181 TRTDNLKMQVIELALKQINEHTDITASIEQHKKGRVITGFSFMFKHKKQNSDKTPDTNAS 240

Query 241 SPHIEKPSQIPTNIVKQPENAKKDDLHRASKITGLIMSNGLADRFRKRGDESVMNMMKRI 300
Sbjct 241 SPRIVKHSQIPTNIVKQPENAKMSDLEHRASRVTGEIMRNRLSDRFKQGDSEIDMMKRI 300

Query 301 KEEITTDATADLWQNKLESMVWFF 324
+ EI TDA AD W++KLE F
Sbjct 301 QSEIITDAIADQWESKLEEFVVF 324
```

>>>>sptrembl:N9LWE7_9GAMM N9lwe7 SubName: Full=Uncharacterized protein;. 12/2013
Length=324

Score = 563 bits (1452), Expect = 3e-158, Method: Compositional matrix adjust.
Identities = 271/324 (83%), Positives = 292/324 (90%), Gaps = 0/324 (0%)

```
Query 1  MSDLIVKDNALMNASYNLALVEQRLILLAILEARETGKGINANDPLTVHANSYINQFNVE 60
Sbjct 1  MS+LIVKDNALMNASYNL LVEQRLILLAI+EARE+GKGINANDPLTVHA SYINQF V 60

Query 61 RHTAYQALKDACKDLFARQFSYQEKREGRINITSRWVSQIGYMDTATVEVIFAPAVVP 120
Sbjct 61 R TAYQALKDACKDLFARQFSYQEKREGR NITSRWVSI Y+D+TATVE+IFAPAVVP 120

Query 121 LITRLEEQFTQYDIEQISGLSSAYAVRLYELLICWRSTGKTPVIELAEFRKRIGVLDTEY 180
Sbjct 121 LITRLE+QFTQYDIEQISGLSSAYAVR+YELLICWRSTGKTPVIEL EFRKRIGVLDTEY 180

Query 181 TRTDNLKMRVIELALKQINEHTDITASIEQHKKGRITITGFSFKFKQKKKTELETPKNSDS 240
Sbjct 181 RTDNLKMRVIELALKQIN+HTDITA+YEQHKKGRITITGFSFKFKQK+KTELETPKNSDS 240

Query 241 SPHIEKPSQIPTNIVKQPENAKKDDLHRASKITGLIMSNGLADRFRKRGDESVMNMMKRI 300
+K +IPTN+VKQPEN A DL HRASKITGLIMSN L+DRFK+ DES+M MM RI
Sbjct 241 DVPKQKSVEIPTNLVKQPENANMSDLQHRASKITGLIMSNRLSDRFKQSDSIMQMMARI 300

Query 301 KEEITTDATADLWQNKLESMVWFF 324
+ EIT +A A+ W+NKLE F
Sbjct 301 QSEITDEAIANQWENKLEEFVIF 324
```

>>>>sptrembl:N9JLM2_ACIBA N9jlm2 SubName: Full=Uncharacterized protein;. 12/2013
Length=325

Score = 517 bits (1331), Expect = 3e-144, Method: Compositional matrix adjust.
Identities = 260/325 (80%), Positives = 287/325 (88%), Gaps = 1/325 (0%)

ProtSweep

A Protein Identification Tool

Results for /home/vir088/rindneu/tsekompl/CMI4.158.327.pep

Number of residues: 327	Molecular weight: 37.51 kD
Charge: 2	Isoelectric point: 8.59

more...

Prediction of protein localization:

cyto_nucl	9.5 %
cyto	9 %
nucl	8 %

Identified Protein & Transcript:

Protein:

id: sptrembl:E5LG72-92222

valuation: homologous

scientific organism: Vicugna pacos

common organism: Alpaca

abstract: E5lg72 SubName: Full=Replicase 3-like protein;. 5/2013Length=324

isoform:

GO information:

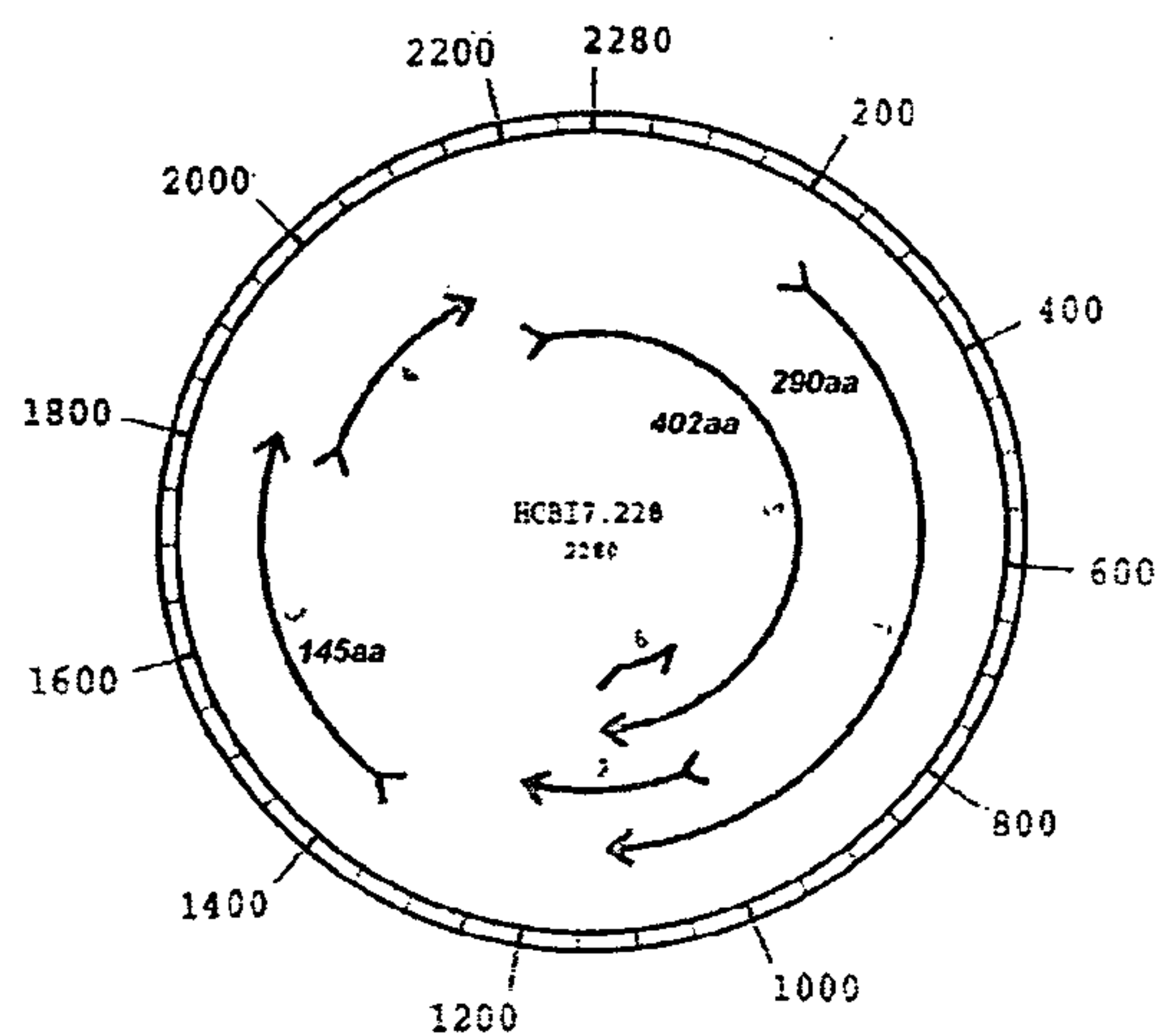
accession	group	name	evidence
GO:0005727	cellular component	extrachromosomal circular DNA	IEA:InterPro
GO:0003887	molecular function	DNA-directed DNA polymerase activity	IEA:InterPro
GO:0006270	biological process	DNA replication initiation	IEA:InterPro

Interpro information:

id	short name
IPR000525	Initiator_Rep_prot
IPR011991	WTH_DNA-bd_dom

HCBI7.228 (2280bp)**(ri71.NdXd.2500.4G)**

CTAAGGCAGATCAACACAGGGATAGAATAACACGTTTTGGGATTTTGAAACATAGAGCGAAGCTACAAGAACAATATTTGTGG
 ACGCAGGTTGATTTCAAATCTGAAGGCGAAGACGATCTATCCAATAAGGCTCTTAAGGCTGCAACAAAATTTAAAGGTTGTGG
 CCAGTTTCTTATATTAGAAATTACTACACTATCGACCAAGTTAAGCTCGAAAAATTCCACGTATGTGGACAGCATTGTCTAT
 GCCAATGTGTGCAGGTATTCGCGCTGCTCGCTCAATGAAACGCTATTTAGATCGTATCCATGAATTAATGCGTCAGAATCCG
 CGTTTAAAGCCTGTTTTGATCACTTTAACGGTCAAGAACGGGGAAGACTTAGAAGAACGCTATAATCACCTTACAAGCTCATT
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 TTTGACCCATTTGATATTGAGAGAGAAGAATACGACTTCTACCCTTAAGGGGTTGACCCCTTAAACCCCAAAGGGCGCACTT
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 AAACCTTCTCTCCCTGATTACAAGCTCCCTTTTGCCTTTCTCCGGAAGTTTTAGCCATCCCAAACGGGTGGCGACGCATTGA
 CAATTATAATTTAATCTGCAATATTCATCGGACATTCATAAATAATCTGATTGGAATATTAAATATGCTTTTTTAAATCTCTAG
 GCGTTGCAATCGCTACAAATAATGCTTCTAATCTGACGAAGACTTGAAACCAATTACTATCCGTTTAGCTGATAGTGAAATT
 CAGGCGTATGACACTGTTGCAAAATCAATGGGTCTAATCTGTCAGATTTTCTATCACACGTTATTCGTTCCAACCTCCGACA
 GGCTTTAAAGAGTTTGTAGTGGGTATACAAGTTCAAATCCTTCTACACCCTTATCTGTTTTGTTTAAATCAAATACGGACA
 ATGACGAAGTTAAGCTCAAACCTTTCCAACCTTCTCTCATCTATTTCTCAAGAATTAATGGACGAAGAAGAAAAAGAAATTCAT
 GAAGCAATCGAAAACCATATGAATACTTCCATATGCATATGCAACTCGTCCAAAAGGCATCTTTGTTGAGAAGGATGATTCAAA
 ATGATTAAGCTTGAAGGGATCGTTTTTAAACGTATTTACCCAGCAAGGTGGTAAAGATAAAAAACAGGTGATCAATTTGCTGA
 CCGTGACAAGGTGCAAATTTTAGGTGCTATGGATCTGCCTAACGGTGACGTTAAAAATGAGTTATTTACGTTATCTGTAGAAA
 ACTATCGGGACTTTAAAGACTTCTTAAATCAGAAAATCTGTATTGCTGTTGGTGCAATGGCAAGTGGTCGCAATGTTATTTT
 TACGTTGCTAAAGGCGCAAAGCCTGTTTTAGCAGAAATGATGTGAAACACGAAAAAAACAGTGGGTAGCCTTGGCTTCTCG
 CTGTTTTTCTTCTCTTGATACTATTAATAAGTGGGGATGAAATTGACTAAAAAAGACAATAAAAAAGCCATAATTCTG
 AACTTTGGCGGGTGATGAATTACAGGCTTTGCAATCTG



78% nucleotide similarity to TSE-associated circular DNA isolate Sphinx 2.36

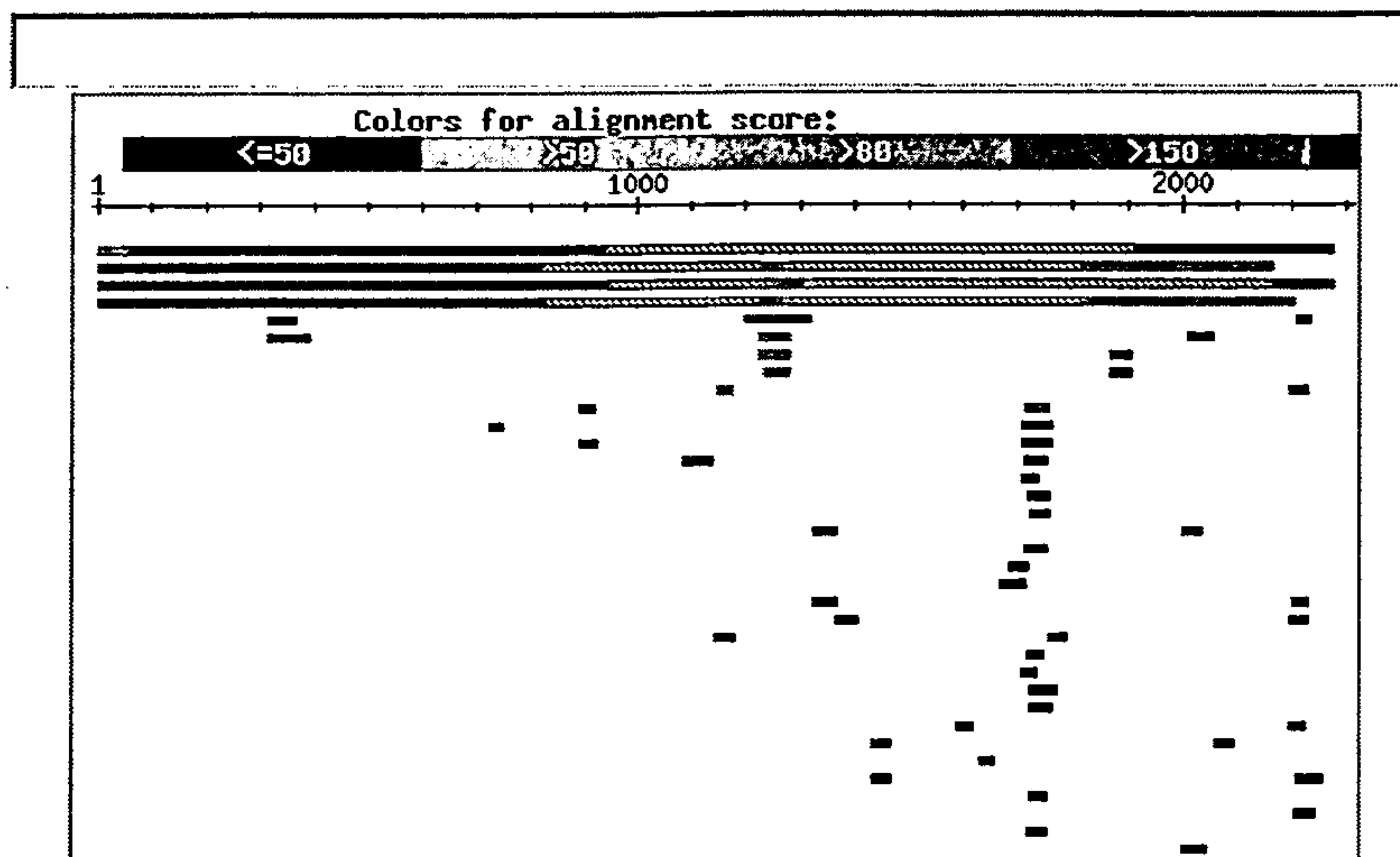
ORFs:

402aa – 81% in 232aa of the replication protein of Sphinx 2.36

290aa – 89% in 168aa of the replication protein of Sphinx 2.36

145aa – vague similarity to capsid protein of narcissus mosaic virus (nmv)

Figure 2

Blastn – Geall:

>>>nrnuc:GI_313507479 Gi|313507479|gb|HQ444405.1| TSE-associ... 719 0.0
>>>nrnuc:GI_169147044 Gi|169147044|emb|CU459139.1| Acinetoba... 358 2e-94
>>>nrnuc:GI_377552564 Gi|377552564|gb|JN872565.1| Acinetobac... 347 3e-91

>>>>nrnuc:GI_313507479 Gi|313507479|gb|HQ444405.1| TSE-associated circular DNA isolate
Sphinx 2.36, complete sequence. 0/0
Length=2364

Score = 719 bits (796), Expect = 0.0
Identities = 691/878 (78%), Gaps = 11/878 (1%)
Strand=Plus/Plus

Query	66	CAAGAACAATATTTGTGGACGCAGGTTGATTTCAAATCTGAAGGCGAAGACGATCTATCC	125
Sbjct	15	CAAGAACAATATTTGTGGACTCAGGTTGATTTCAAGGTTGGAAGTGAA-AC-ATCTATCA	72
Query	126	AATAAGGCTCTTAAGGCTGCAACAAATTAAGGTTGTGGCCAGTTTCTTATATTCAGA	185
Sbjct	73	AA----GCTCTTAAGGCTGCAACCAATTAAGGGATGCGGTCAATTTCTGCTTTTTCGT	128
Query	186	AATTACTACACTATCGACCAAGTTAAGCTCGAAAAATTCCACGTATGTGGACAGCATTG	245
Sbjct	129	AATTACTACACCATAGATCAAATCAAGCTCGAAAAATTCCACGTATGCGGACAGCATTG	188
Query	246	CTATGCCCAATGTGTGCAGGTATTCGCGCTGCTCGCTCAATGAAACGCTATTTAGATCGT	305
Sbjct	189	CTATGTCCAATGTGTGCTGGTATTCGTGCTGCCCGTTCAATGAATCGGTATATTCAACGC	248
Query	306	ATCCATGAATTAATGCGTCAGAATCCGCGTTTAAAGCCTGTTTGATCACTTTAACGGTC	365
Sbjct	249	ATCGAAGAAATAATGCGTCAGAATCGCAAGCTAAAGCCCGTATTGATCACTTTGACCGTT	308
Query	366	AAGAACGGGGAAGACTTAGAAGAACGCTATAATCACCTTACAAGCTCATTTAGAAAGCTT	425
Sbjct	309	AAGAACGGTGAAGACCTACAGGAACGCTTGAACACCTCACAGGCTCATTTAAGACGCTT	368
Query	426	CTATCGCGTTATAGGGATTACAAGAAAAGGGTTGGGGGTTTAACCAATTCTGTAAAATT	485
Sbjct	369	TTACAGCGTTACCGTGATTTTAAGAAAAGGGTCGAGGGTTAATCAATTTTGCAAATT	428
Query	486	GATGGTGCTTTCTATACCACTGAATACACCTACAACGAAAAGACAAAACAATGGCATCCG	545
Sbjct	429	GATGGCGGTTTTTATACGACCGAATACACCTACAACGAAACAACCAACAATGGCATCCG	488
Query	546	CATATTCATATTTTCGCTTTACTCAATGAATGGATAGACCAGGAAGAATTATCTGAGACC	605
Sbjct	489	CATATTCATATTTTTCGCTTAGTGACTGACCGGATTGACCAGGAGGAAGTAGCAGAACT	548
Query	606	TGGCATGACATTACCCTGGATTCTTATATCATCGATATTCGTAGAGTTaaaaaaCCAAA	665
Sbjct	549	TGGCACGATATAACGCTTGATTCATACATTGTGGACATCCGCAGGGTCAAAAAAACTAAA	608
Query	666	GAACACGGCTATAGCAAAA-GCTGTTGCTGAGGTATGTAAATACGCTCTTAAGTTTGGCGA	724

47/88

Sbjct	609	GAACACGGATAT-GCAAAGGCTGTTGCCGAAGTCTGCAAATACGCTCTTAAGTTTAGCGA	667
Query	725	TCTATCAGTTGAAAACACTTGGGATGCA-TTTTTAACGCTTAAGGGTAAACGCTTACAG	783
Sbjct	668	TCTATCCACTGAGAAAACCTTTCAAGCATTTTTTGACCCTTAAGGGCAAAAGGCTTACAG	727
Query	784	GCTCTTTTCGGTTCTATGCATGGAGTTAAAATTCCAGATAAGGCCACGGATGATATGCCAC	843
Sbjct	728	GTTCATTTCGGCTCTATGCATGGTGTAAAAATTCTGAAAGCGGACCCGATGAAATGCCTA	787
Query	844	TGGAGGAGCTGCCGTACTTAGAAATGTTCTATCGTTTCGTGTTTGATAAAAAATCCTACT	903
Sbjct	788	AAGAGGAACCTCCATATCTTGAGCTGCTCTATCGTTTCGTTTTTGGTGAAAGGTCTTATT	847
Query	904	ACAACCTAGAAATAACAAAAGACGTAACGCC--ACAAA 939	
Sbjct	848	ACAACCTAGAGTTAACTAAGGACGTAAAGCCGAACAAA 885	

Score = 315 bits (348), Expect = 2e-81
Identities = 294/371 (79%), Gaps = 2/371 (0%)
Strand=Plus/Plus

Query	1911	CGTGACAAGGTGCAAATTTTAGGTGCTATGGATCTGCCTAACGGTGACGTTAAAAATGAG	1970
Sbjct	1943	CGTGACAAGGTGCAAATCTTGGTTCGCTGGAGTTGCCAACGGTGAGATCAAACATGAG	2002
Query	1971	-TTATTTACGTTATCTGTAGAAACTATCGGGACTTTAAAGACTTCTTAAATCAGAAAAT	2029
Sbjct	2003	CTTGTTGAC-TTAACGGTTGAAGATGCTCGCATCTTTGAGCCATTCAAACACAAGGTAAT	2061
Query	2030	CTGTATTGCTGTTGGTGCAATGGCAAGTGGTCGCAATGTTATTTTTTACGTTGCTAAAGG	2089
Sbjct	2062	TAGCATTTCATGCGGTGCTATGGCTATCGGTCGAAATGTTGTTTTTTATGTTCGAAAAGG	2121
Query	2090	CGCAAAGCCTGTTTTAGCAGAAATGATGTGAAACACGaaaaaaaaCAGTGGGTTAGCCTT	2149
Sbjct	2122	TGCAAAGCCTGTTTTAGCAGATGTAATGTAATTCATGAAAAAAACAGTGAGTTAGGCTT	2181
Query	2150	GGCTTCTCGCTGTTTTTTCTTTCTCTTGATACTATTAATAAGTGGGGATGAAATTGAC	2209
Sbjct	2182	GCCGACTCGCTGTTTTTTCTTTTACTTGATACTATTAATAAGTGGGGACAAAATTGAC	2241
Query	2210	TAAAAAAGACAATAAAAAAGCCCATAAATCTGACACTTTGGCGGGTGATGAATTACAGGC	2269
Sbjct	2242	TAAAAAAGACAATAAAAAAGCCCATAAATCTGATGCTTTGGCGGGCGACGAATTACAGGC	2301
Query	2270	TTTGCAATCTG	2280
Sbjct	2302	TTTGCAATCTG	2312

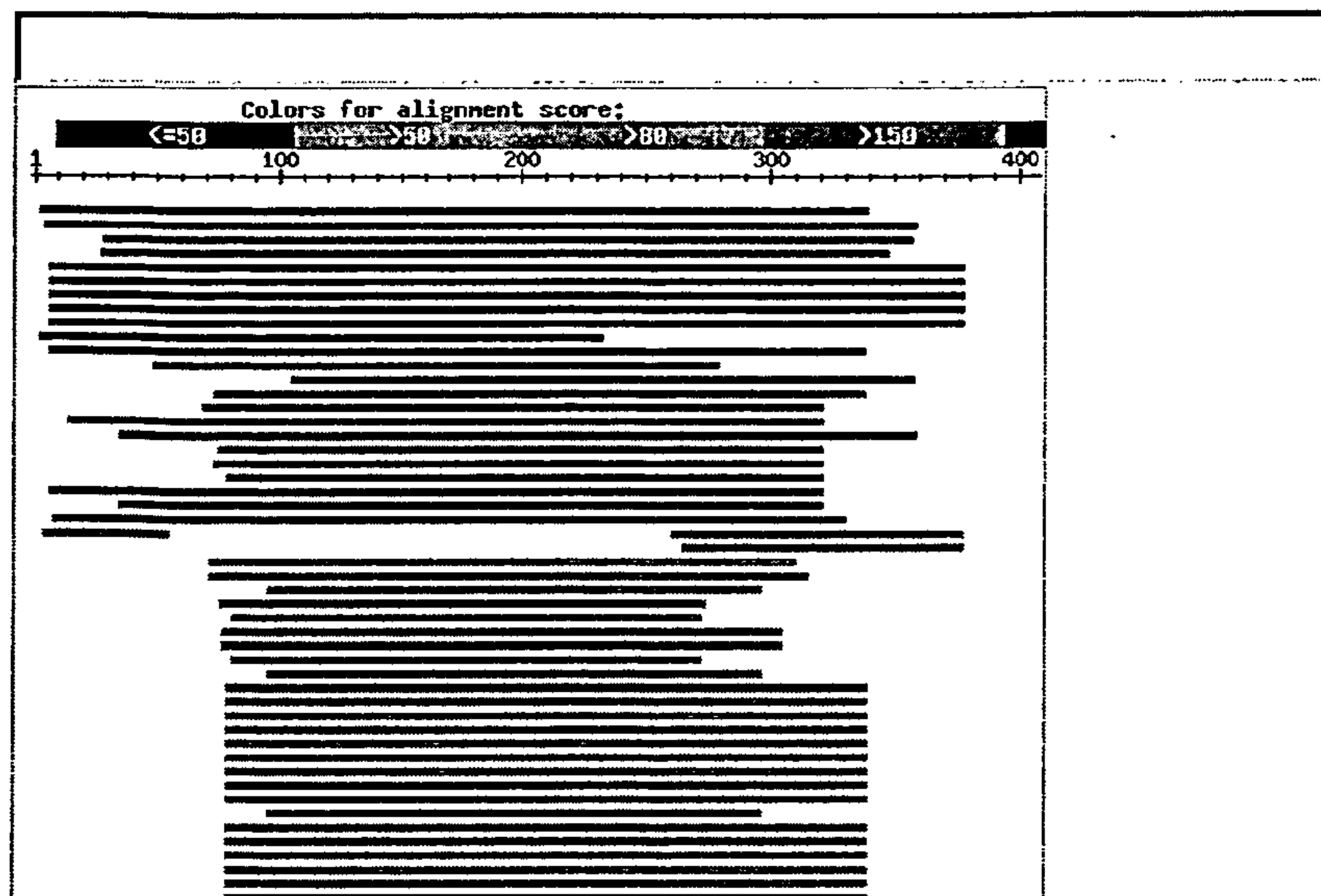
Score = 77.0 bits (84), Expect = 8e-10
Identities = 48/52 (92%), Gaps = 0/52 (0%)
Strand=Plus/Plus

Query	1	CTAAGGCAGATCAACACAGGGATAGAATAACACGTTTTGGGATTTGAAACA	52
Sbjct	2313	CTAATGCAGATCAACACAGGGATAGAATATCACGTTTTGGACTTTGAAACA	2364

```
>>>>nrnuc:GI_169147044 Gi|169147044|emb|CU459139.1| Acinetobacter baumannii str. AYE  
plasmid p4ABAYE, complete genome. 0/0  
Length=2726
```

Score = 358 bits (396), Expect = 2e-94
Identities = 580/832 (69%), Gaps = 17/832 (2%)
Strand=Plus/Plus

Query	3	AAGGCAGATCAACACAGGGATAGAATAACACGTTTTGGGATTTTGAACATAGAGCGAAG	62
Sbjct	115	AAGG-AGATCAACATAGGGATAGAATAACACGTTTTGGCATTTTGAACATAGATCGAAG	173
Query	63	CTACAAGAACAATATTTGTGGACGCAGGTTGATTTCAA-----TCTGAAGGCGAAG--	114
Sbjct	174	CAACAAGAAAACATTTATTTTCGTTAGCTAAGATTAAAGAAAATTATCATGCCGATGTA	233

*BlastP – Uniprot:**ORF 402aa:*

>>>sptrembl:H6VTN7_ACIBA H6vtn7 SubName: Full=Replication pr... 476 8e-132
>>>sptrembl:K5PFB3_ACIBA K5pfb3 SubName: Full=Replication pr... 459 1e-126

>>>>sptrembl:H6VTN7_ACIBA H6vtn7 SubName: Full=Replication protein;. 11/2013
Length=378

Score = 476 bits (1225), Expect = 8e-132, Method: Compositional matrix adjust.
Identities = 222/342 (64%), Positives = 270/342 (78%), Gaps = 4/342 (1%)

Query 3 LTKKDNKKAHNSDTLAGDELQALQSAKADQHRDRITRFGILKHKRAKLQEYLTQVDFKS 62
+ KKDNNKAH S+ LAG E+QALQSA ADQHRDRITR LKHKRAK QE YL+T FK
Sbjct 1 MLKKDNKKAHISEALAGGEIQALQSANADQHRDRITRFATLKHRAKNQENYLFITLAKFKE 60

Query 63 EGEDDLN----KALKAATKLKGCQFLIFRNYTIDQVKLEKHFVCGQHLLCPMCAGIR 118
E D+ N KALK+A KL CG +L+F+N+YTI +VKL K CGQHLLCP CA IR
Sbjct 61 NYEKDVKNESIKALKSAQKLNCEGNYLLFKNFYTIGEVKLSKLRTCGQHLLCPFCAAIR 120

Query 119 AARSMKRYLDRIHELMRQNPRLKPVLTITLVKNGEDLEERYNHLTSSFRKLLSRDYK 178
A+R++++Y++RI +++++N +LKPVLITITLVKNG DL ER HL SFR LL R RDY+K
Sbjct 121 ASRAIQKYVERIDQVLQENRKLKPVLTITLVKNGSDLAERSEHLMKSFRITLLERRRDYK 180

Query 179 KGWGFNQFCKIDGAFYTTEYTYNEKTKQWPHIHIFALLNEWIDQEELSETWHDITLDSY 238
KG GFN+FCK+ GA Y+ E T+NEKT +WHPHIH+FAL+++WIDQ+E SE WH +T DS
Sbjct 181 KGRGFNEFCKVQGAMYSYENTFNEKTGEWHPHIHMFALVDQWIDQEFSEYWHSLTGDSM 240

Query 239 IIDIRRVKKTKEHGYSKAVAECVYALKFGDLSVENTWDAFLTGLKGRLTGSFGSMHGVK 298
++D+RR +K K +GYSKA AEVCKYALKFGDLSVE TW+AF LKGRLTGSFG + GVK
Sbjct 241 VVDVRRARKEKGYGYSKAAAEVCKYALKFGDLSVEKTWEAFKVLKGRLTGSFGLLWGVK 300

Query 299 IPDKATDDMPLEELPYLEMFYRFVFDKKSYYNLEITKDVTPQ 340
IPD TDDMP E+LPYLEM Y+F + KKSYY+L IT+ V PQ
Sbjct 301 IPDSMTDDMPSEDLPYLEMFLYKFAYSKKSYYDLITRHVEPQ 342

>>>>sptrembl:K5PFB3_ACIBA K5pfb3 SubName: Full=Replication protein;. 11/2013
Length=421

Score = 459 bits (1181), Expect = 1e-126, Method: Compositional matrix adjust.
Identities = 221/360 (61%), Positives = 274/360 (76%), Gaps = 5/360 (1%)

Query 5 KKDNNKAHNSDTLAGDELQALQSAKADQHRDRITRFGILKHKRAKLQEYLTQVDFKSEG 64
+KD KK S TL G + + S +ADQHRDRITRFGILKHKRAK QE YLWT +K
Sbjct 2 QKDIKKPLLSSTLVGGDNKGSNSVEADQHRDRITRFGILKHKRSKQENYLTAKYKENY 61

Query 65 EDDLNS----KALKAATKLKGCQFLIFRNYTIDQVKLEKHFVCGQHLLCPMCAGIRAA 120
++D N +A K+A KL GCG FL+F+N+YTIDQVKL KHFVC QHLLCP CAGIRA+
Sbjct 62 QNDQPNEESVRATKSAQKLLGCGNFFLKNFYTIDQVKLSKFHVCNQHLLCPFCAGIRAS 121

```
Query 121 RSMKRYLDRIHELMRQNPRCLKPVLITLTVKNGEDLEERYNHLSFRKLLSRDYKKKG 180
+++++Y +R+ E++ + LKPVLIT TVKNG DL ER +HL SFR L+ R RDY KKG
Sbjct 122 KAIQKYTERVDEVLSKKRTLKPVLITFTVKNGLDGLSSHLMKSFRTLMERRRDYLKKG 181

Query 181 WGFNQFCKIDGAFYTTTEYTYNEKTKQWHPHIHIFALLNEWIDQEELSETWHDITLDSYII 240
GFN+FCKI+GA Y+ E TYNE+TK+WHPH+H+FALL++WIDQEELS+ WH IT DS I+
Sbjct 182 RGFNEFCKINGAMYSYENTYNEQTKEWHPHLHMFALLDDWIDQEELSQYWHSITGDSMIV 241

Query 241 DIRRVKKTKEHGYSKAVAECVCKYALKFGDLSVENTWDAFLTLKGKRLTGSFGSMHGVKIP 300
DIR+VKK K GYSKA AEVCKYALKFGDLSVENTW+AF LKGKRL+G+FGS++GVKIP
Sbjct 242 DIRKVKKEKGLGYSKAAAEVCKYALKFGDLSVENTWEAFKILKGKRLSGAFGSLYGVKIP 301

Query 301 DKATDDMPLE-ELPYLEMFYRFVFDKKSYYNLEITKDVTPTQNSRQSEEAAPTDTTGEN 359
+ D+MP E +LPYLEM Y+FVF KKSYY+L +T+ V P+ + E T GE+
Sbjct 302 ENLADEMPDENDLPYLEMLYKFVFGKKSYYDLTMRHVEPRAQDDRPMEKELRRPTEGES 361
```

>>>>sptrembl:E5LG73_9ZZZZ E5lg73 SubName: Full=Replicase 1-like protein (Sphinx2.36);. 4/2011
Length=232

Score = 382 bits (980), Expect = 2e-103, Method: Compositional matrix adjust.
Identities = 189/232 (81%), Positives = 207/232 (89%), Gaps = 2/232 (0%)

```
Query 49 LQEQLWTQVDFKSEGEDDLSENKALKAAATKLKGCQFLIFRNYTIDQVKLEKHFVCGQH 108
+QEQLWTQVDFK E + KALKAAATKLKGCQFL+FRNYTIDQ+KLEKHFVCGQH
Sbjct 1 MQEQLWTQVDFKVGSETSI--KALKAAATKLKGCQFLIFRNYTIDQIKLEKHFVCGQH 58

Query 109 LLCPMCAGIRAARSMKRYLDRIHELMRQNPRCLKPVLITLTVKNGEDLEERYNHLSFRK 168
LLCPMCAGIRAARSM RY+ RI E+MRQN +LKPVLITLTVKNGEDL+ER+ HLT SF+
Sbjct 59 LLCPMCAGIRAARSMNRYIQRIEIMRQNRLKPVLITLTVKNGEDLQERFEHLTGSFKT 118

Query 169 LLSRYRDYKKKGWGFNQFCKIDGAFYTTTEYTYNEKTKQWHPHIHIFALLNEWIDQEELSE 228
LL RYRD+KKKG GFNQFCKIDG FYTTEYTYNE T+QWHPHIHIFAL+ + IDQEEL+E
Sbjct 119 LLQRYRDFKKKGRGFNQFCKIDGGFYTTEYTYNETTQWHPHIHIFALVTDRIDQEELAE 178

Query 229 TWHDTLDSYIIDIRRVKKTKEHGYSKAVAECVCKYALKFGDLSVENTWDAFL 280
TWHDTLDSYI+DIRRVKKTKEHGY+KAVAECVCKYALKF DLS E T+ AF
Sbjct 179 TWHDTLDSYIVDIRRVKKTKEHGYAKAVAECVCKYALKFSDLSTEKTFQAFF 230
```

ProtSweep
A Protein Identification Tool

Results for /home/vir088/rindneu/tsekompl/HCB17.228.402.pep

General Information:

Number of residues: 402

Molecular weight: 47.20 kD

Charge: 2

Isoelectric point: 8.03

[more...](#)

Prediction of protein localization:

cyto	20.5 %
cyto_nucl	12 %
pero	4 %

Identified Protein & Transcript:

Protein:

id: [sptrembl:H6VTN7](#) ACIBA

valuation: similar

scientific organism: Acinetobacter baumannii

abstract: H6vtn7 SubName: Full=Replication protein;. 11/2013Length=378

isoform:

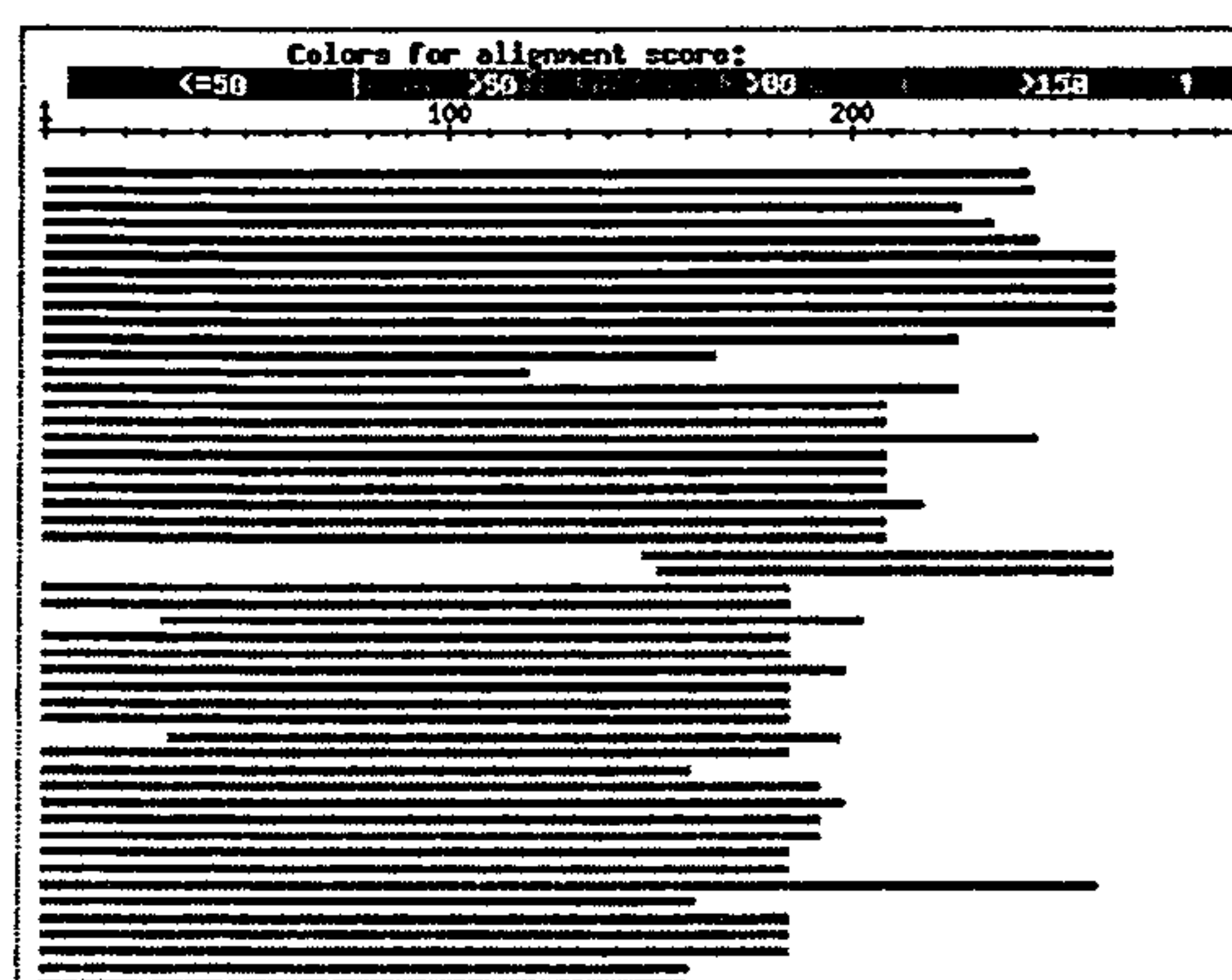
Features & Functions:

GO INFORMATION:

ACCESSION	GROUP	NAME	EVIDENCE
GO:0005727	cellular component	extrachromosomal circular DNA	IEA:InterPro
GO:0003677	molecular function	DNA binding	IEA:InterPro
GO:0006260	biological process	DNA replication	IEA:InterPro

Del Val C., Ernst P., Falkenhahn M., Fladerer., Glatting K.H., Suhai S., Hotz-Wagenblatt A.: ProtSweep, 2DSweep and DomainSweep: protein analysis suite at DKFZ. Nucleic Acids Research, 2007, 1-7

ORF 290aa:



```
>>>sptrembl:N9TLP0_9GAMM N9tlp0 SubName: Full=Uncharacterize... 343 5e-92
>>>sptrembl:C6RQ49_ACIRA C6rq49 SubName: Full=Putative Repli... 336 7e-90
>>>sptrembl:H6VTN7_ACIBA H6vtn7 SubName: Full=Replication pr... 333 7e-89
```

```
>>>>sptrembl:N9TLP0_9GAMM N9tlp0 SubName: Full=Uncharacterized protein; Flags: Fragment;.
12/2013
Length=399
```

Score = 343 bits (880), Expect = 5e-92, Method: Compositional matrix adjust.
Identities = 159/247 (64%), Positives = 198/247 (80%), Gaps = 2/247 (0%)

```
Query 1 MCAGIRAARSMKRYLDRIHELMRQNPRCLKPVLITLTVKNGEDLEERYNHLTSSFRKLLSR 60
      CAGIRA++S+++Y DR+ E++ +N +LKPVLIT TVKNG DL ER +HL SFR LL R
Sbjct 89 FCAGIRASKSIQKYTDREVLSKNRKLKPVLTFTVKNGLDLGERSHLLIKSFRTLLER 148

Query 61 YRDYKKKGWGFNQFCKIDGAFYTTEYTYNEKTKQWHPHIHIFALLNEWIDQEELSETWHD 120
      RDY KKG GFN+FCKIDGA Y+ E T+NE TK+WHPH+H+FALL+EWIDQE+LSE WHD
Sbjct 149 RRDYLLKKGRGFNEFCKIDGAMYSYENTFNESTKEWHPHLHLFALLDEWIDQEQLSELWHD 208

Query 121 ITLDSYIIDIRRVKKTKEHGYSKAVAEVCKYALKFGDLSVENTWDAFLTLKGKRLTGSFG 180
      IT DSYI+D+R+VKK+K+ GY+KA AEVCKYALKFGDL+VENTW+AF LKGKRL+G+FG
Sbjct 209 ITGDSYIIVDRVKVKS KDTGYAKAAAEVCKYALKFGDLTVENTWEAFKILKGKRLSGAFG 268

Query 181 SMHGVKIPDKATDDMPLEELPYLEM FYRFVFDKKSYYNLEITKDVTPTQT--NSRQSEEEA 238
      S++GVKIPD DD+ +LPYLEM Y+FVF KKSYY+L +T+ V PQ N E+
Sbjct 269 SLYGVKIPDNPADDIDDS DLPYLEM VYKFVFGKKSYYDLTMTRHVEPQQDNDNDNEEKEG 328

Query 239 PTTDTTG 245
      T+D G
Sbjct 329 ATSDRGG 335
```

```
>>>>sptrembl:C6RQ49_ACIRA C6rq49 SubName: Full=Putative Replication protein; Flags: Fragment;.
9/2013
Length=303
```

Score = 336 bits (861), Expect = 7e-90, Method: Compositional matrix adjust.
Identities = 155/245 (63%), Positives = 192/245 (78%), Gaps = 0/245 (0%)

Query 2 CAGIRAARSMKRYLDRIHELMRQNPRCLKPVLITLTVKNGEDLEERYNHLTSSFRKLLSRY 61
CA IRA+R++++Y++RI +++++N +LKPVLITLTVKNG DL ER HL SFRKLL R
Sbjct 9 CAAIRASRAIQKYVERIDQVLQENRKLKPVLTITLTVKNGSDLAERSEHLMKSFRKLLDRR 68

Query 62 RDYKKKGWGFNQFCKIDGAFYTTEYTYNEKTKQWHPHIHIFALLNEWIDQEELSETWHD 121
RDY+KKG GFN+FCK+ GA Y+ E T+NEKT +WHPHIH+FAL+++WIDQ+E SE WH +
Sbjct 69 RDYEKKGRGFNEFCKVQGAMYSYENTFNEKTGEWHPHIHMFALVDQWIDQQEFSEYWHSL 128

Query 122 TLDSYIIDIRRVKKTKEHGYSKAVAEVCKYALKFGDLSVENTWDAFLTLKGKRLTGSFGS 181
T DS ++D+RR KK K HGYSKA AEVCKYALKFGDLSVE TW+AF LKGKRLTGSFG
Sbjct 129 TGDSMVVDVRRAKKEKGHGYSKAAAEVCKYALKFGDLSVEKTWEAFKVLKGKRLTGSFGL 188

Query 182 MHGVKIPDKATDDMPLEELPYLEM FYRFVFDKKSYYNLEITKDVTPTQNSRQSEEAAPT 241
+ GVKIPD TDDMP E+LPYLEM Y+F + KKSYY+L IT+ V P+ E+ P
Sbjct 189 LWGVKIPDTMTDDMPEDLPYLEMLYKFAYGKKSYYDLLITRHVEPKAKDDNDEKEEPRQ 248

Query 242 DTTGE 246
GE
Sbjct 249 RRGGE 253

>>>>sptrembl:H6VTN7_ACIBA H6vtn7 SubName: Full=Replication protein;. 11/2013
Length=378

Score = 333 bits (853), Expect = 7e-89, Method: Compositional matrix adjust.
Identities = 149/228 (65%), Positives = 186/228 (81%), Gaps = 0/228 (0%)

Query 1 MCAGIRAARSMKRYLDRIHELMRQNPRCLKPVLITLTVKNGEDLEERYNHLTSSFRKLLSR 60
CA IRA+R++++Y++RI +++++N +LKPVLITLTVKNG DL ER HL SFR LL R
Sbjct 115 FCAAIRASRAIQKYVERIDQVLQENRKLKPVLTITLTVKNGSDLAERSEHLMKSFRLLER 174

Query 61 YRDYKKKGWGFNQFCKIDGAFYTTEYTYNEKTKQWHPHIHIFALLNEWIDQEELSETWHD 120
RDY+KKG GFN+FCK+ GA Y+ E T+NEKT +WHPHIH+FAL+++WIDQ+E SE WH
Sbjct 175 RRDYEKKGRGFNEFCKVQGAMYSYENTFNEKTGEWHPHIHMFALVDQWIDQQEFSEYWH 234

Query 121 ITLDSYIIDIRRVKKTKEHGYSKAVAEVCKYALKFGDLSVENTWDAFLTLKGKRLTGSFG 180
+T DS ++D+RR +K K +GYSKA AEVCKYALKFGDLSVE TW+AF LKGKRLTGSFG
Sbjct 235 LTGDSMVVDVRRARKEKGYGYSKAAAEVCKYALKFGDLSVEKTWEAFKVLKGKRLTGSFG 294

Query 181 SMHGVKIPDKATDDMPLEELPYLEM FYRFVFDKKSYYNLEITKDVTPTQ 228
+ GVKIPD TDDMP E+LPYLEM Y+F + KKSYY+L IT+ V PQ
Sbjct 295 LLWGVKIPDSMTDDMPSEDLPYLEMLYKFAYS KKSYYDLLITRHVEPQ 342

>>>>sptrembl:E5LG73_9ZZZZ E5lg73 SubName: Full=Replicase 1-like protein (*Sphinx2.36*);.
4/2011
Length=232

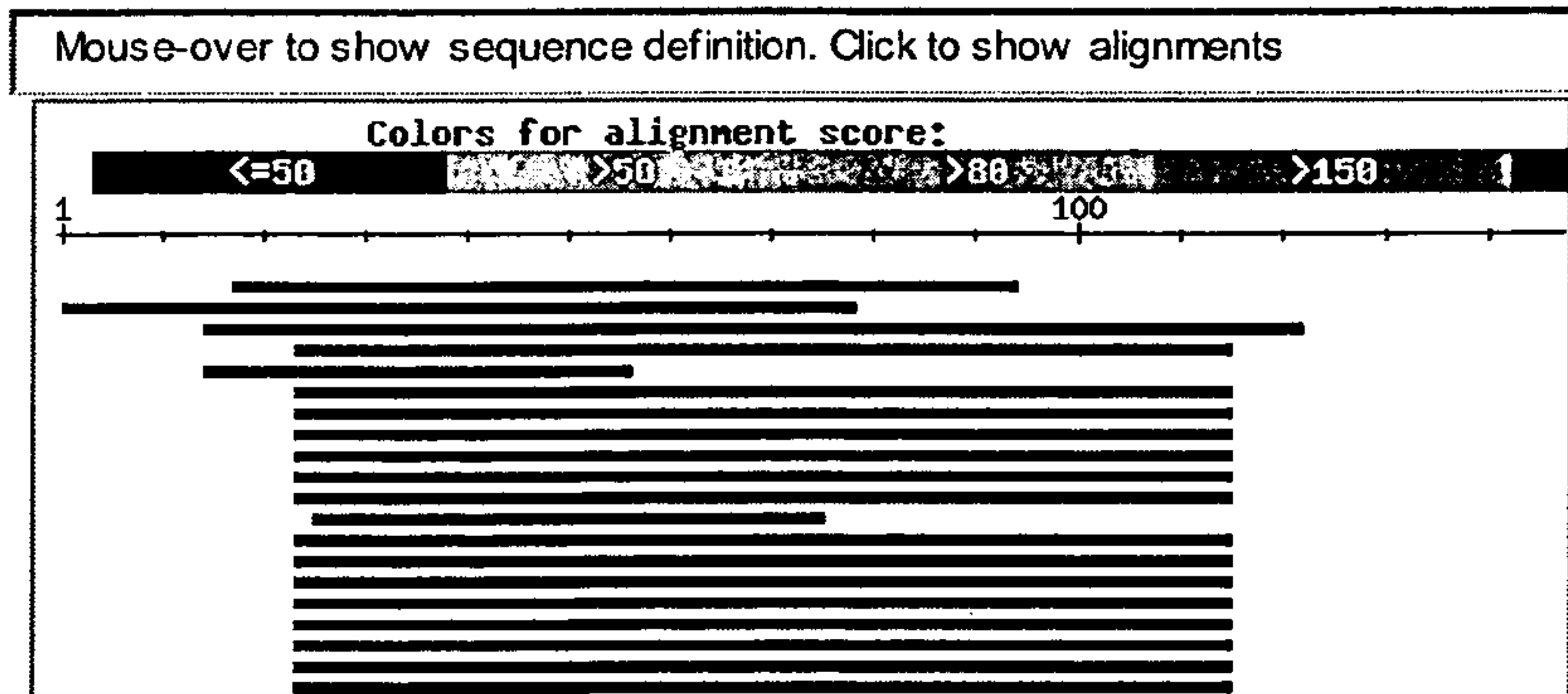
Score = 271 bits (694), Expect = 2e-70, Method: Compositional matrix adjust.
Identities = 136/168 (80%), Positives = 150/168 (89%), Gaps = 0/168 (0%)

Query 1 MCAGIRAARSMKRYLDRIHELMRQNPRCLKPVLITLTVKNGEDLEERYNHLTSSFRKLLSR 60
MCAGIRAARSM RY+ RI E+MRQN +LKPVLITLTVKNGEDL+ER+ HLT SF+ LL R
Sbjct 63 MCAGIRAARSMNRYIQRIEIMRQNRLKPVLTITLTVKNGEDLQERFEHLTGSFKTLQR 122

Query 61 YRDYKKKGWGFNQFCKIDGAFYTTEYTYNEKTKQWHPHIHIFALLNEWIDQEELSETWHD 120
YRD+KKKG GFNQFCKIDG FYTTEYTYNE T+QWHPHIHIFAL+ + IDQEEL+ETWHD
Sbjct 123 YRDFKKKGRGFNQFCKIDGGFYTTEYTYNETTQWHPHIHIFALVTDRIQDEELAETWHD 182

Query 121 ITLDSYIIDIRRVKKTKEHGYSKAVAEVCKYALKFGDLSVENTWDAFL 168
ITLDSYI+DIRRVKKTKEHGY+KAVAEVCKYALKF DLS E T+ AF
Sbjct 183 ITLDSYIVDIRRVKKTKEHGYAKAVAEVCKYALKFSDLSTEKTFQAFF

ORF 145aa:



>>>swissprot:CAPSD_NMV P15100 narcissus mosaic virus (nmv). ... 38.9 0.85
>>>sptrembl:G0L9E1_ZOBGA G019e1 SubName: Full=Uncharacterize... 38.9 0.94
>>>>swissprot:CAPSD_NMV P15100 narcissus mosaic virus (nmv). rename: full=coat protein;
altname: full=capsid protein; short=cp;. 10/2013
Length=240

Score = 38.9 bits (89), Expect = 0.85, Method: Compositional matrix adjust.
Identities = 28/78 (35%), Positives = 40/78 (51%), Gaps = 8/78 (10%)

Query 18 SDEDLKPITIRLADSEIQAYDTVAKSMGLTRQDFLSHVIRSNFRQALKEFVVGYSNP 77
+D ++P + R EIQA+ T AK L RQ + + ++F LK VG S P
Sbjct 167 ADGLIRPPSQR----EIQAHS-AKYGALARQRYR---METSFPPLKSLTVGSAVSTPC 218

Query 78 TPLSVLFNSNTDNDEVKL 95
TPL L N N + ++KL
Sbjct 219 TPLKHLQNCNRNTSKLKL 236

>>>>sptrembl:G0L9E1_ZOBGA G019e1 SubName: Full=Uncharacterized protein;. 5/2013
Length=291

Score = 38.9 bits (89), Expect = 0.94, Method: Compositional matrix adjust.
Identities = 28/84 (33%), Positives = 42/84 (50%), Gaps = 5/84 (5%)

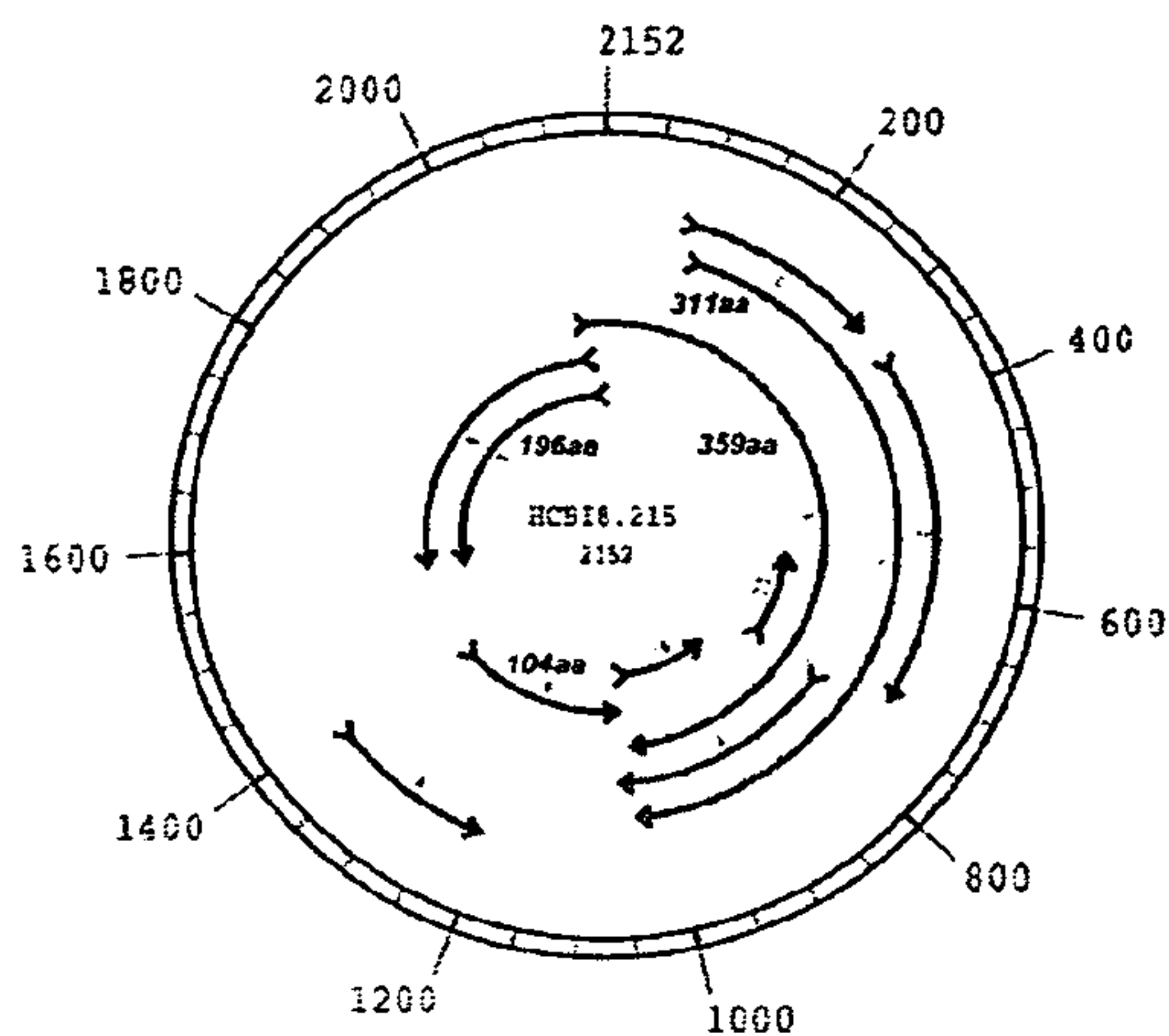
Query 1 MLFKSLGVAIATNNASNSDEDLKPITIRLADSEIQAYDTVA-KSMGLTRQD----FLSHV 55
LF+S+ V I TNN ++ L +++ L S I Y TV K M L R+D F +
Sbjct 83 FLFRSIAVLITNNWDMTEIFLFSVLLISCIVYYTVPDKEMILNRRDGLVSFPAPT 142

Query 56 IRSNFRQALKEFVVGYSNPSTP 79

HCB18.215 (2152bp)

(HCBI = Healthy Cattle Blood Isolate)

(ril.10E.1.5)

[illegible]

70% nucleotide similarity to Gemycircularvirus 3 isolate P24c

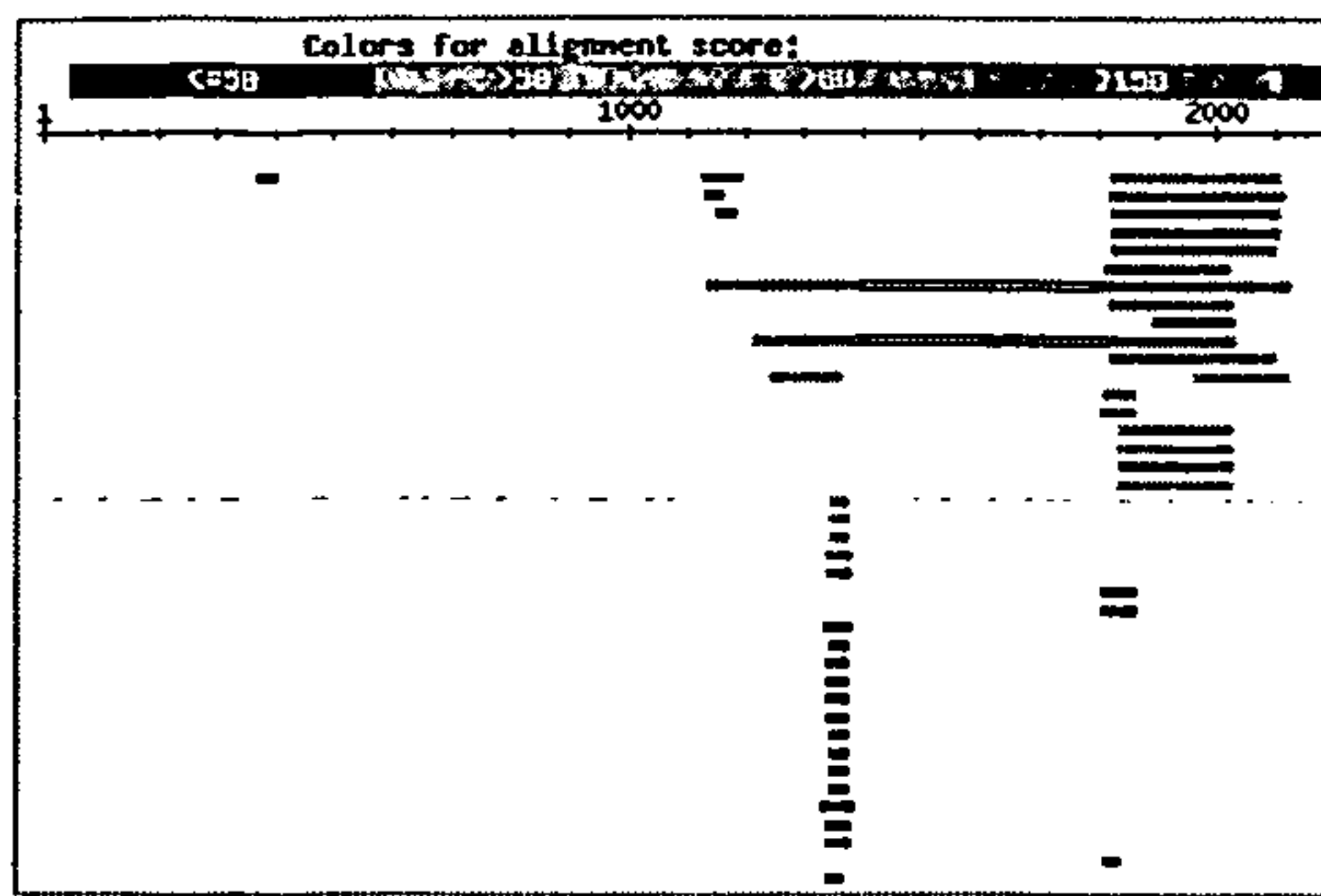
ORFs: 359aa – coat protein 32% similarity to Dragonfly-associated virus 1

311aa – coat protein 32% similarity to Dragonfly-associated virus 1

196aa – replication associated protein 54% similarity to Gemycircularvirus 4

104aa – replication-associated protein 63% similarity to Gemycircularvirus 8

Figure 3(a)

Blastn - Geall:

```
>>>nrnuc:GI_537367996 Gi|537367996|gb|KF371639.1| Gemycircul... 120 7e-23
>>>nrnuc:GI_537367993 Gi|537367993|gb|KF371638.1| Gemycircul... 116 9e-22
>>>nrnuc:GI_537368005 Gi|537368005|gb|KF371642.1| Gemycircul... 114 3e-21
```

```
>>>>nrnuc:GI_537367996 Gi|537367996|gb|KF371639.1| Gemycircularvirus 3 isolate P24c,
complete genome. 0/0
```

```
Length=2199
```

```
Score = 120 bits (132), Expect = 7e-23
```

```
Identities = 205/290 (70%), Gaps = 8/290 (2%)
```

```
Strand=Plus/Plus
```

```
Query 1823 CCTCCAGCGACAACATCACCATCCTTGATCGCGTAATCATAATGGACTTGAGGGTCGCGC 1882
          ||||| ||||| || || ||||| ||||| || || ||| || || || || ||
Sbjct 1857 CCTCCAGCGACCACGTCTCCATCTTTGATCGCATAGTCGTAACCGCCTTCCGGCTTTCCG 1916

Query 1883 TTAGTAATTGAG--ATGTTAGGGTGGAAACCTCCAACATCAAAGACAGCAGCACGTCTTG 1940
          || || || || || || ||||| ||||| ||||| || || ||||| ||
Sbjct 1917 TAAG--ATGGAACAAGGTTTCGGGTGGCGGCCTCCAACATCAAAGACATCGGATCGTCGGG 1974

Query 1941 ATTGAAATCGTCGTCCAAAATCCACA-AAAGCGTGCAGATGAGTTCCGCCATCAGAGTGG 1999
          || ||||| || || ||||| ||||| || ||||| || ||||| || ||
Sbjct 1975 ATCGAAATCGGCGGGAGAAAT-CACAGAAAGCATGGAGATGAGTACCTCCATCAGCGTGC 2033

Query 2000 GCTTCTCTTCCAATGATGCATTCTCCTCCAAGG-TCACCAATGTGTGAAACAATAGTGAA 2058
          ||||| ||||| || || ||||| || ||||| || || || || || ||
Sbjct 2034 AACTCTCGTCCAATGATACACTCAGCTCCAAGGAACGCCAA-ATGGTCATTAACGGTCCA 2092

Query 2059 TGGGTCGAGGCCGCCGCATTGAGCGTAGGTGAGAAGCGCATATCGGGCAT 2108
          || || || || ||||| || ||||| ||||| ||||| ||||| ||||
Sbjct 2093 TGCATCAAGAGTGCCGCACTGTGCGTACGTGAGAAGAAAGTATCGGCCAT 2142
```

```
>>>>nrnuc:GI_537367993 Gi|537367993|gb|KF371638.1| Gemycircularvirus 4 isolate as50,
complete genome. 0/0
```

```
Length=2224
```

```
Score = 116 bits (128), Expect = 9e-22
```

```
Identities = 208/301 (69%), Gaps = 2/301 (0%)
```

```
Strand=Plus/Plus
```

```
Query 1820 AGTCCTCCAGCGACAACATCACCATCCTTGATCGCGTAATCATAATGGACTTGAGGGTCG 1879
          || ||||| ||||| || || ||||| ||||| || ||||| || || || ||
Sbjct 1893 AGCCCTCCAGCGACCACGTCTCCATCTTTGATCGCATAGTCATAACCGCCTTCCGGCCTT 1952

Query 1880 CGCTTAG-TAATTGAGATGTTAGGGTGGAAACCTCCAACATCAAAGACAGCAGCACGTCT 1938
          | || || || || ||||| ||||| ||||| ||||| || || || || ||
Sbjct 1953 CCTCGAGATGCTTCA-ATGTTAGGGTGGAAAGCCTCCAACATCAAACACATCGGGTCTTCG 2011

Query 1939 TGATTGAAATCGTCGTCCAAAATCCACAAAAGCGTGCAGATGAGTTCCGCCATCAGAGTG 1998
          || ||||| || || ||||| ||||| || ||||| || ||||| || ||
Sbjct 2012 GGATCGAAACTTTCGGGAGAAATCGCAGAAAGCATGGAGATGAGTACCCCATCAGCGTG 2071

Query 1999 GGCTTCTCTTCCAATGATGCATTCTCCTCCAAGGTCACCAATGTGTGAAACAATAGTGAA 2058
          ||||| ||||| || || || ||||| || || || || || || || || ||
Sbjct 2072 ATGCTCTCGTCCAATGATACACTCACCGCCAAGGAATGCCAGATGGTCATTAACGGCCCA 2131

Query 2059 TGGGTCGAGGCCGCCGCATTGAGCGTAGGTGAGAAGCGCATATCGGGCATAGAAGCGAAA 2118
          || || || || ||||| || ||||| || || ||||| || || || || || ||
Sbjct 2132 TGCATCAAGGTCGCCGCACTGTGCGTAGGTAAGGAGGACATAGCGTGCTTGGAATTGAAA 2191

Query 2119 T 2119
          |
Sbjct 2192 T 2192
```

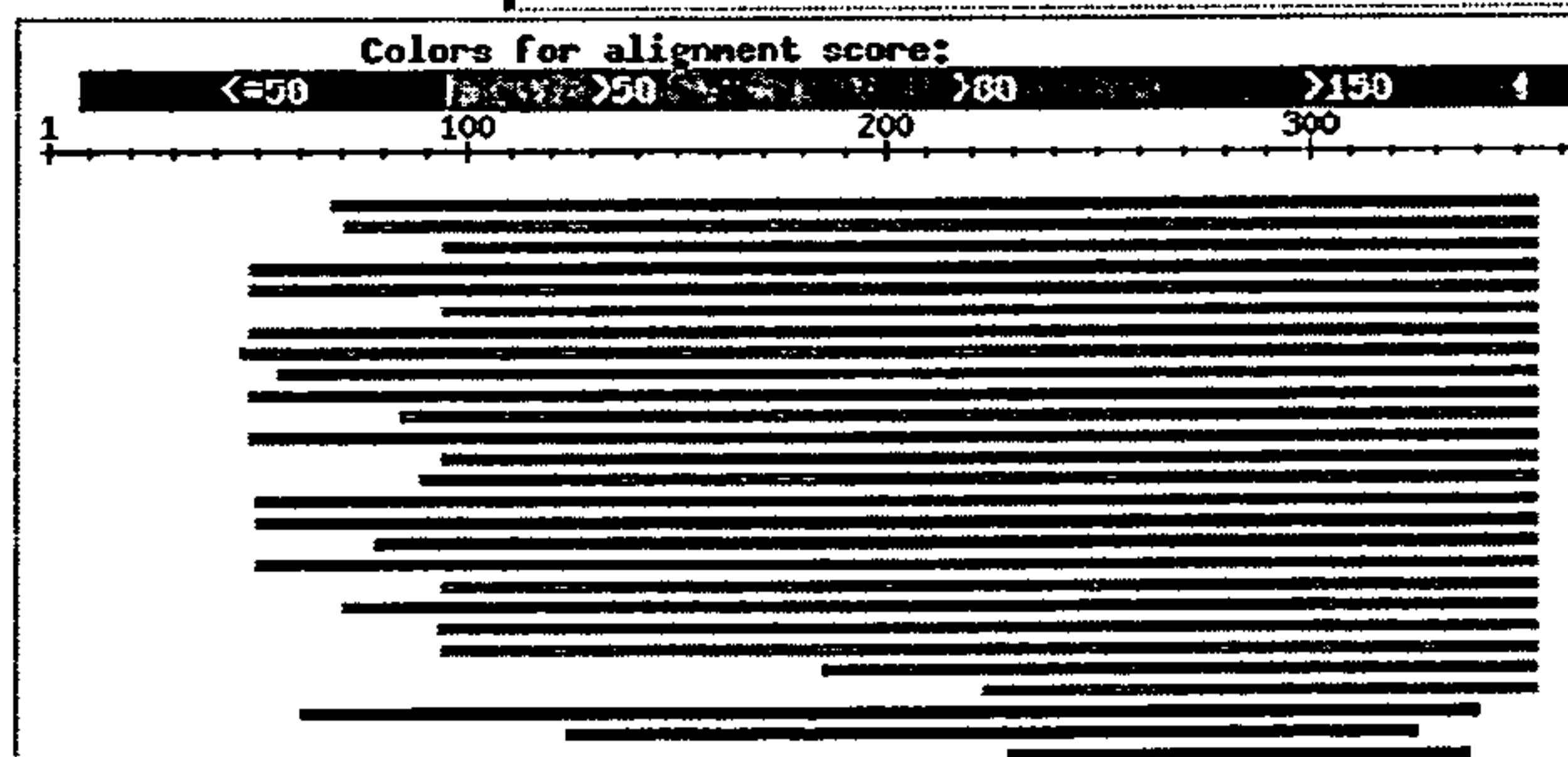
```
>>>>nrnuc:GI_537368005 Gi|537368005|gb|KF371642.1| Gemycircularvirus 1b isolate P22,
complete genome. 0/0
Length=2160
```

Score = 114 bits (126), Expect = 3e-21
Identities = 197/284 (69%), Gaps = 4/284 (1%)
Strand=Plus/Plus

Query	1823	CCTCCAGCGACAACATCACCATCCTTGATCGCGTAATCATAAATGGACTTGAGGGTCGCGC 	1882
Sbjct	1825	CCTCCAGCGACCACGTCTCCATCTTTGATCGCATAGTCATAACCGCCTTCCGGGCTTCCG	1884
Query	1883	TTAGTAATTGAG--ATGTTAGGGTGGAAACCTCCAACATCAAAGACAGCAGCACGTCTTG 	1940
Sbjct	1885	TAAG--ATGGAACAAGGTTCCGGATGGCGGCCTCCAACATCAAAGACATCGGATCTTCTGG	1942
Query	1941	ATTGAAAATCGTCGTCCAAAATCCACAAAAGCGTGCAGATGAGTTCCGCCATCAGAGTGGG 	2000
Sbjct	1943	ATCGAAACTTCCGGGAGAAATCGACGAAAGCATGGAGATGAGTACCTCCATCAGCATGCA	2002
Query	2001	CTTCTCTTCCAATGATGCATTCTCTCCAAGGTCACCAATGTGTGAAACAATAGTGAATG 	2060
Sbjct	2003	ATTCTCGTCCAATGATACACTCACCGCCAAGAAATGCCATATGGTCATTAACGGCCCATG	2062
Query	2061	GGTCGAGGCCCGCCGCATTGAGCGTAGGTGAGAAGCGCATATCGG 2104 	
Sbjct	2063	CATCAAGGTCGCCGCACTGTGCGTAGGTAAGGAGGGCATAACGG 2106	

BlastP – Uniprot:

ORF 359aa:



```
>>>sptrembl:K0A2I9 9VIRU K0a2i9 SubName: Full=Putative coat ... 129 3e-27
>>>sptrembl:S5RC76 9VIRU S5rc76 SubName: Full=Putative coat ... 124 9e-26
>>>sptrembl:K0A169 9VIRU K0a169 SubName: Full=Putative coat ... 123 1e-25
```

```
>>>>sptrembl:K0A2I9_9VIRU K0a2i9 SubName: Full=Putative coat protein (Dragonfly-associated virus 1);. 5/2013
Length=290
```

Score = 129 bits (323), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 94/289 (32%), Positives = 141/289 (48%), Gaps = 18/289 (6%)

Query	69	STFRRRSF--RNGRSRTTRRYSRPRTNVRRVRNLASRKRCDNMICTPIDDTGTPQTGPV	126
		S+ +RRS+ R SR T + RT+ RR+ N++S+K R+N + G PG	
Sbjct	17	SSKKRRSYVGRRLSSRRTTKTVMKRTSRRRILNISSQKKRNNAPVNFNYLGESPIPGSK	76
Query	127	SMDASSVYGFI FSP TARTAGTQLESGERVNAPSSAQRRKSKCYVRGYGETVEIQTD DASP	186
		M + ++ PTA T T + S SA R + Y RG E E+ T +	
Sbjct	77	VMGSDRTTYLLWRPTALTDDTDIYS-----SASRGAQQIYWRGIKERA EVGTSSGAA	128
Query	187	WVWRRIVFSTIGLASQFDPGLLYNNDETGRGWGRSLFNIRSGTQQASILEGVVFRYLFQGT	246
		W WRRIVF L GL+ N + + G+ R++ + SG A+ L + +LFQG+	
Sbjct	129	WRWRRIVFEAKSLNIN---GLISNVETSAGFN RAMVEL-SGDPPAN-LRNSLESFLFQGS	183
Query	247	EGVDWANVMTATTAPRHVRVYSDRRRVIQSPNSEGGTIRLSKHYDGINRSIIYDDVEIGA	306
		GVDW V A R+ SD+ R +QS N G + + +N++++Y+D E+G	
Sbjct	184	VGVDWNTVFENAKVDNNRCRLLSDKVRHLQSGNDRGRFYTF-RQWIPLNKTMYNDDEVG-	241

Query 307 GAKATNAIASGTPYGNMGDLFVLDFSSASDDETSFGASFPHGKFWHE 355
K +N AS G MGD++V D F + D + +F P YWHE
Sbjct 242 DDKQSNTFASPGRKG-MGDVYVYDMFQCLTSDAINTLNFPQATLYWHE 289

>>>>sptrembl:S5RC76_9VIRU S5rc76 SubName: Full=Putative coat protein;. 12/2013
Length=304

Score = 124 bits (310), Expect = 9e-26, Method: Compositional matrix adjust.
Identities = 93/295 (31%), Positives = 136/295 (46%), Gaps = 29/295 (9%)

Query 72 RRRSFRNGRSRTTRRYSRPRTNVRVRNLASRKCRDNM-----ICTPIDDTGTPQTPG 124
RRRS+ R RRY R +T +R+ N++S K RDNM + PI+ G G
Sbjct 27 RRRSYPTTR----RRYPR-KTLAKRILNISSTKKRDNMMSYTNVTVANPIN--GQTYAAG 79

Query 125 PVSM DASSVYGFIFSP TARTAGTQLESGERVNAPS-SAQRKSKCYVRGYGETVEIQTD 183
P + Y F + PTAR + + N P A R + CY+RG E + ++T+
Sbjct 80 PAVLRGDQTYIFAWIPTARDL---IRADGEPNTPVWLAGRTRQTCYMRGLKEAMNVRTNS 136

Query 184 ASPWVWRRIVFSTIG--LASQFDPGLLYNNDETRGRSLFNIRSGTQQASILEGVVFRY 241
S W WRR I F+ G L G + + G R++ N+ + L +
Sbjct 137 GSSWQWRRICFTMKGPNLIGYATTGSNLWQETSNGMVRTMNNVNT-----KPLGNEILAQ 191

Query 242 LFQGT EGV DWANVMTATTAPRHVRVYSDRRRVIQSPNSEGGTIRLSKHYDGINRSIIYDD 301
LF+G + DW NV A T + DR I S N E G +R KH+ +N++++Y+D
Sbjct 192 LFRGAQNQDWLNVFNAQTDTTKFTIKYDRTISIASGN-EQGLVRTYKHWYPMNKNLVYND 250

Query 302 VEIGAGAKATNAIASGTPYGNMGDLFVLDFSSASD-DETSFGASFPHGKFWHE 355
E G + +G P MGD +V+DFF A D + + P YWHE
Sbjct 251 DENADGVLTSYTSTNGKP--GMGDYVVDFFQPADGADASDTLALLPEATLYWHE 303

>>>>sptrembl:K0A169_9VIRU K0a169 SubName: Full=Putative coat protein;. 5/2013
Length=289

Score = 123 bits (309), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 89/267 (33%), Positives = 131/267 (49%), Gaps = 27/267 (10%)

Query 95 RRVNRLASRKCRDNMICTPIDDTG-TPQTPGPVSM DASSVYGFIFSP TARTAGTQLESGE 153
RR+ N++S+K RDNMI TG P G ++ A+ ++ TAR +
Sbjct 43 RRILNVSSKKKRDNMINVSFSP TGINPAVRGFIATGAAPTM-LVWCATAR-----D 92

Query 154 RV----NAPSSAQRKSKCYVRGYGETVEIQTD DASPWVWRRIVFSTIGLASQFDPGLLY 209
RV N + + R CY+RG E + I T++ + W+WRR I F+ GL S G
Sbjct 93 RVSNASNPTADSVRESQTCYMRGLKEHIRINTNNTPSWLWRRICFTAKGLFSGL--GTSA 150

Query 210 NNDET-RGWGRSLFNIRSGTQQASILEGVVFRYLFQGT EGV DWANVMTATTAPRHVRVYS 268
++ ET GW R+L + ++GT + L + LF GT GVDW + TA T +V++
Sbjct 151 DSVETSNGWVRALMD-QTGTSGTSLTNL----LFAGTNGVDWNTFTANTDSTNVKIMY 205

Query 269 DRRRVIQSPNSEGGTIRLSKHYDGINRSIIYDDVEIGAGAKATNAIASGTPYGNMGDLFV 328
D+ I S S G IR K + G+N++I+Y + E G G G P MGD +V
Sbjct 206 DKTFTINSGVS--GVIRDYKMWHGMMKNIVYGEDENGEINNRYSTIGRP--GMGDYV 261

Query 329 LDFSSASDDETSFGASFPHGKFWHE 355
+D +S S +F YWHE
Sbjct 262 VDILLASNSSAAADTLTFSTEATLYWHE 288

Results for /home/vir088/rindneu/gemi/HCB18.215.359.pep



Number of residues: 359	Molecular weight: 40.45 kD
Charge: 25	Isoelectric point: 11.19

more...

Prediction of protein localization:

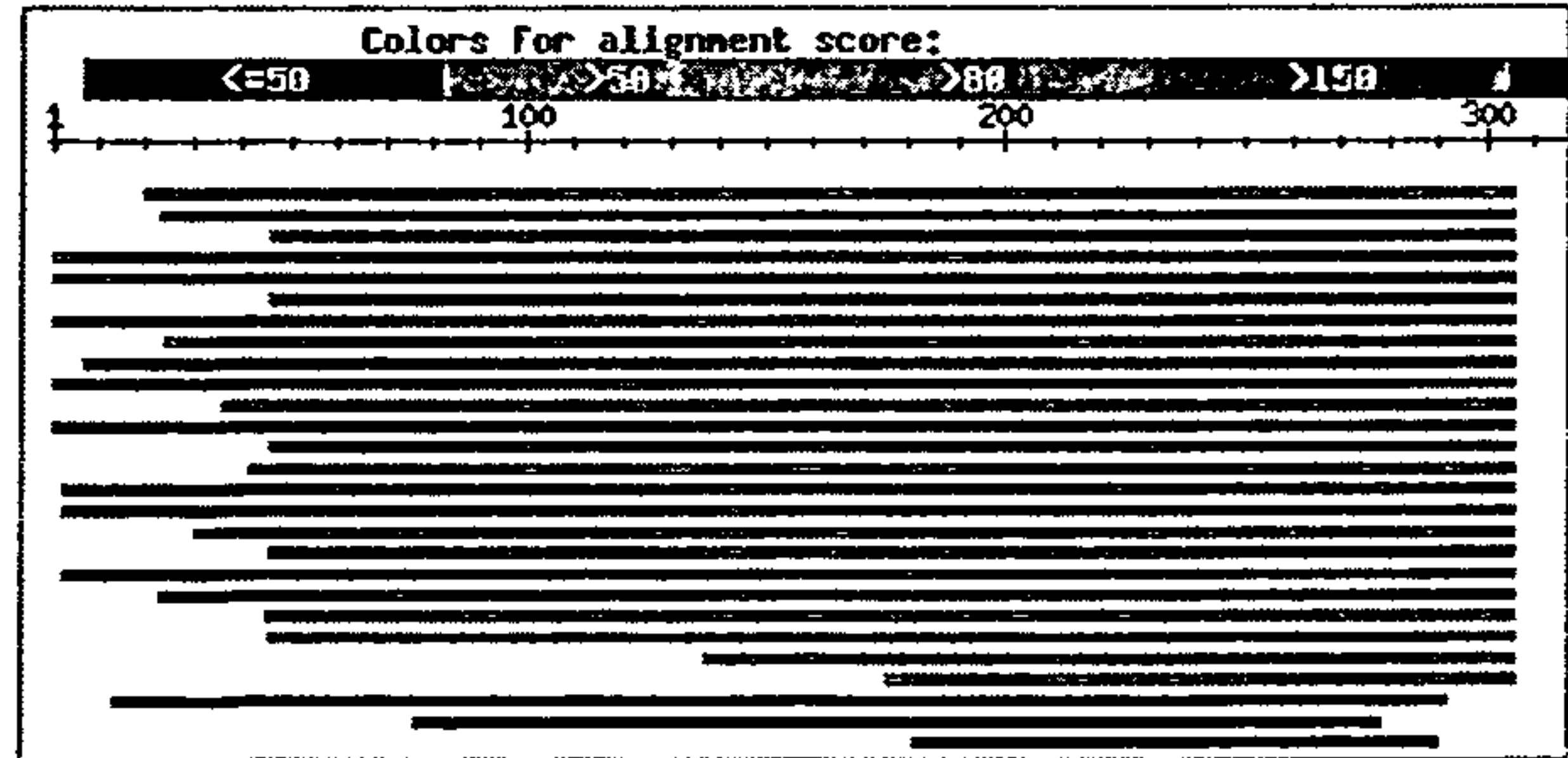
extr	19%
E.R.	6%
plas	3%
E.R. mito	3%



Identified Protein & Transcript:

Protein:
id: <u>sptrembl:TIYSG7_9VIRU</u>
valuation: putative
scientific organism: Gemycircularvirus 1c
abstract: Tlysg7 SubName: Full=Capsid protein; 2/2014Length=307
isoform:

ORF 311aa:



>>>sptrembl:K0A2I9_9VIRU	K0a2i9 SubName: Full=Putative coat ...	128	3e-27
>>>sptrembl:S5RC76_9VIRU	S5rc76 SubName: Full=Putative coat ...	124	7e-26
>>>sptrembl:K0A169_9VIRU	K0a169 SubName: Full=Putative coat ...	123	1e-25
>>>>sptrembl:K0A2I9_9VIRU K0a2i9 SubName: Full=Putative coat protein (Dragonfly-associated circular virus 1);. 5/2013			
Length=290			
Score = 128 bits (322), Expect = 3e-27, Method: Compositional matrix adjust.			
Identities = 94/289 (32%), Positives = 141/289 (48%), Gaps = 18/289 (6%)			
Query 21	STFRRRSF--RNGRSRTTTRYSRPRTNVRRVRNLSARKCRDNMICTPIDDTGTPQTPGPV	78	
	S+ +RRS+ R SR T + RT+ RR+ N++S+K R+N + G PG		
Sbjct 17	SSKKRRSYVGRRLSSRRTTKTVMKRTSRRRILNISSQKKRNNAPVNFNYLGESPIPGSK	76	
Query 79	SMDASSVYGFIPTARTAGTQLESGERVNAPSSAQRRKSKCYVRGYGETVEIQTDASP	138	
	M + ++ PTA T T + S SA R + Y RG E E+ T +		
Sbjct 77	VMGSDRTTYLLWRPTALTDDTDIYS-----SASGAQQIYWRGIKERAEGVTSSGAA	128	
Query 139	WVWRRIVFSTIGLASQFDPGLLYNNDETRGGWGRSLFNIRSGTQQASILEGVVFRYLFQGT	198	
	W WRRIVF L GL+ N + + G+ R++ + SG A+ L + +LFQG+		
Sbjct 129	WRWRRIVFEAKSLNIN---GLISNVETSAGFNAMVEL-SGDPPAN-LRNSLESFLFQGS	183	

Query 199 EGV DWANVMTATTAPRHVRVYSDRRRVIQSPNSEGGTIRLSKHYDGINRSIIYDDVEIGA 258
 GVDW V A R+ SD+ R +QS N G + + +N++++Y+D E+G
 Sbjct 184 VGV DWNTVFNAKVDNNRCRLLSDKVRHLQSGNDRGRFYTF-RQWIPLNKTMVYNDDEVG- 241

Query 259 GAKATNAIASGTPYGNMGDLFVLDFSSASDDETS GASFQPHGKFYWHE 307
 K +N AS G MGD++V D F + D + +F P YWHE
 Sbjct 242 DDKQSNTFASPGRKG-MGDVYVYDMFQCLTSDAINTLNFN PQATLYWHE 289

>>>>sptrembl:S5RC76_9VIRU S5rc76 SubName: Full=Putative coat protein;. 12/2013
 Length=304

Score = 124 bits (310), Expect = 7e-26, Method: Compositional matrix adjust.
 Identities = 94/295 (31%), Positives = 136/295 (46%), Gaps = 29/295 (9%)

Query 24 RRRSFRNGRSRTT RRYSRPRTNVRVRNLASRKCRDNM-----ICTPIDDTGTFQTPG 76
 RRRS+ R RRY R +T +R+ N++S K RDNM + PI+ G G
 Sbjct 27 RRRSYPTTR-----RRYPR-KTLAKRILNISSTKKRDNMMSYTNVTVANPIN--GQTYAAG 79

Query 77 PVSM DASSVYGFIFSP TARTAGTQLESGERVNAPS-SAQRKSKCYVRGYGETVEIQTDD 135
 P + Y F + PTAR + + N P A R + CY+RG E + ++T+
 Sbjct 80 PAVLRGDQTYIFAWIPTARDL---IRADGEPNTPVWLAGRTRQTCYMRGLKEAMNVRTNS 136

Query 136 ASPWVWRRIVFSTIG--LASQFDPGLLYNND ETRGWGRSLFNIRSGTQQASILEGVVFRY 193
 S W WRR I F+ G L G + + G R++ N+ + IL
 Sbjct 137 GSSWQWRRICFTMKGP NLIGYATTGSNLWQETSNGMVRTMNNVNTKPLGNEILAQ----- 191

Query 194 LFQGT EGV DWANVMTATTAPRHVRVYSDRRRVIQSPNSEGGTIRLSKHYDGINRSIIYDD 253
 LF+G + DW NV A T + DR I S N E G +R KH+ +N++++Y+D
 Sbjct 192 LFRGAQNQDWLNVFNAQTDTTKFTIKYDRTISIASGN-EQGLVRTYKHWYPMNKNLVYND 250

Query 254 VEIGAGAKATNAIASGTPYGNMGDLFVLDFSSASD-DETS GASFQPHGKFYWHE 307
 E G + +G P MGD +V+DFF A D + + P YWHE
 Sbjct 251 DENADGVLTSYTSTNGKP--GMGDYVVDFFQPADGADASDTLALLPEATLYWHE 303

>>>>sptrembl:K0A169_9VIRU K0a169 SubName: Full=Putative coat protein;. 5/2013
 Length=289

Score = 123 bits (309), Expect = 1e-25, Method: Compositional matrix adjust.
 Identities = 89/267 (33%), Positives = 131/267 (49%), Gaps = 27/267 (10%)

Query 47 RRVRLASRKCRDNMICTPIDDTG-TPQTPGPVSM DASSVYGFIFSP TARTAGTQLESGE 105
 RR+ N++S+K RDNMI TG P G ++ A+ ++ TAR +
 Sbjct 43 RRILNVSSKKKRDNM INVSFSP TGINPAVRGFIATGAAPT M-LVWCATAR-----D 92

Query 106 RV----NAPSSAQRKSKCYVRGYGETVEIQTDDASPWVWRRIVFSTIGLASQFDPGLLY 161
 RV N + + R CY+RG E + I T++ + W+WRR I F+ GL S G
 Sbjct 93 RVSNASNPTADSVRESQTCYMRGLKEHIRINTNNTSWLWRRICFTAKGLFSGL--GTSA 150

Query 162 NNDET-RGWGRSLFNIRSGTQQASILEGVVFRYLFQGT EGV DWANVMTATTAPRHVRVYS 220
 ++ ET GW R+L + ++GT + L + LF GT GVDW + TA T +V++
 Sbjct 151 DSVETSNGWVRALMD-QTGTSFGTSLTNL----LFA GTNGVDWNDTFTANTDSTNVKIMY 205

Query 221 DRRRVIQSPNSEGGTIRLSKHYDGINRSIIYDDVEIGAGAKATNAIASGTPYGNMGDLFV 280
 D+ I S S G IR K + G+N++I+Y + E G G G P MGD +V
 Sbjct 206 DKTFTINS GVS--GVIRDYKMW HGMNKNIVYGEDENGEINNRYSTIGRP--GMGDYV 261

Query 281 LDFSSASDDETS GASFQPHGKFYWHE 307
 +D +S S +F YWHE
 Sbjct 262 VD LLASNSSAAADTLTFSTEATLYWHE 288

Results for /home/vir088/rindneu/gemi/HCB18.215.311.pep

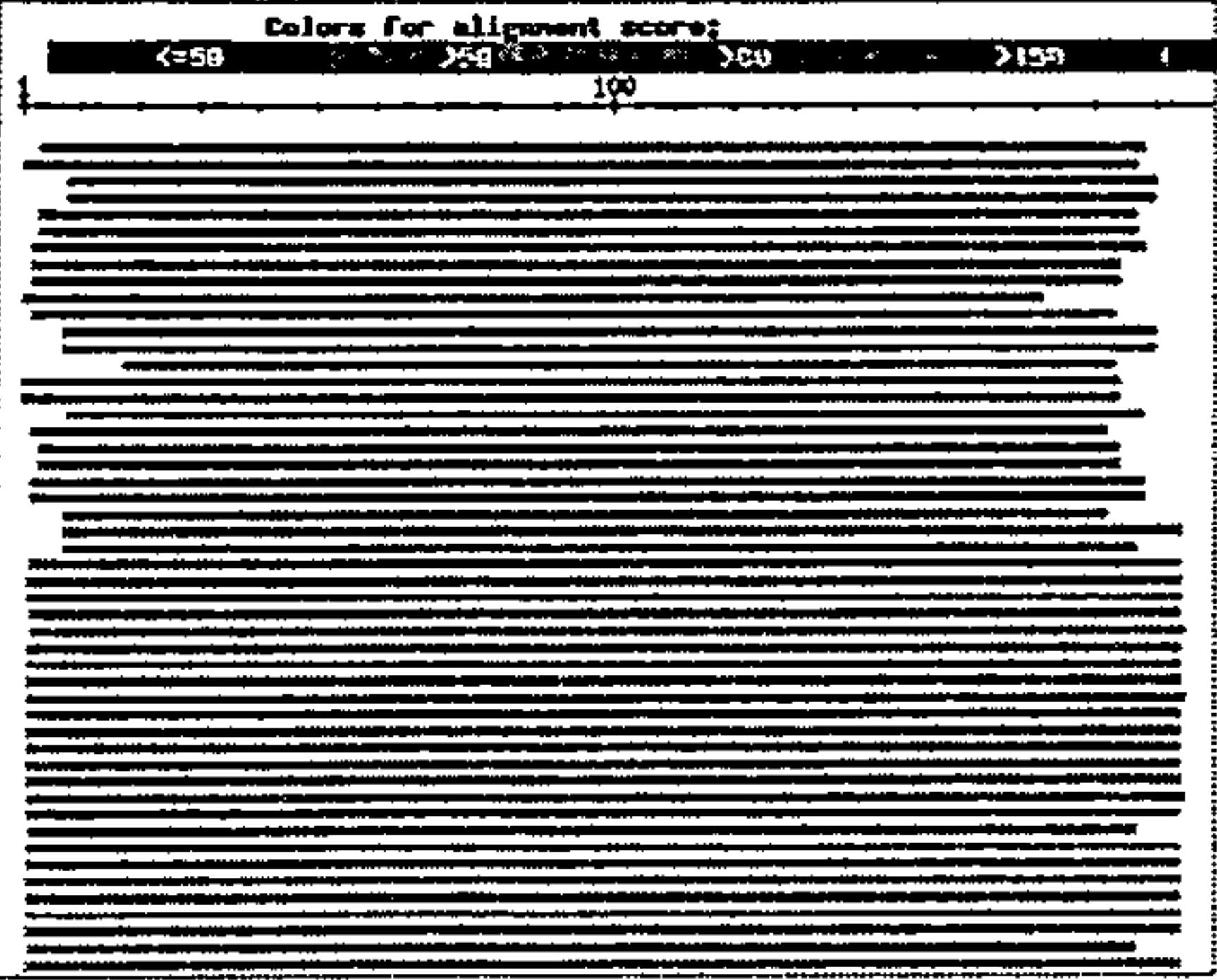
Protein Information

Number of residues: 311	Molecular weight: 35.07 kD
Charge: 20	Isoelectric point: 11.40
more...	
Prediction of protein localization:	
nucl	28 %
mito	3 %

Identified Protein & Transcript

Protein:
id: sptrembl:F6KIE3_9VIRU
valuation: putative
scientific organism: Mosquito VEM
abstract: F6kie3 SubName: Full=Coat protein; 5/2013Length=327
isoform:

ORF 196aa:



>>>sptrembl:Tlysg3_9VIRU	Tlysg3	SubName: Full=Replication as...	199	5e-49
>>>sptrembl:Tlysf1_9VIRU	Tlysf1	SubName: Full=Replication as...	189	5e-46
>>>sptrembl:Tlyqu3_9VIRU	Tlyqu3	SubName: Full=Replication as...	189	6e-46
>>>>sptrembl:Tlysg3_9VIRU Tlysg3 SubName: Full=Replication associated protein Gemycirucularvirus 4);. 2/2014 Length=338 Score = 199 bits (506), Expect = 5e-49, Method: Compositional matrix adjust. Identities = 101/186 (54%), Positives = 120/186 (64%), Gaps = 0/186 (0%)				
Query	4	FRFYARYALLTYAQCGGLDPFTIVSHIGDLGGECIIGREAHSDGGTHLHAFVDFGRRFQS	63	
		F+F ARY LLTYAQCG LD + + H+ LGGECIIGRE H+DGGTHLHAF DF R+F+S		
Sbjct	6	FQFQARYVLLTYAQCGDLDAWAVNDHLAFLGGECIIGREHHADGGTHLHAFCDFSRKFRS	65	
Query	64	RRAAVFDVGGFHPNISITKRDPQVHYDYAIKDGDVAVAGGLERPAADASAGVENKHHQIVL	123	
		RR VFDVGGFHPNI ++ P+ YDYAIKDGDVAVAGGL RP + IV		
Sbjct	66	RRPDVFDVGGFHPNIEASRGRPEGGYDYAIKDGDVAVAGGLSRPGRGVYEDVSSWSIIVS	125	
Query	124	APTRAEFFAVRDLDPRLLLTSEFPSLEKYADWHYRVDPPYRHDPEYEFDTSQFPELNQW	183	
		+ +F+E V LDPR L T++ SL YA+W YR P Y H EF+ PEL W		
Sbjct	126	QESEGDWFECVARLDPRSLCTNYSNLSLAYANWKYRPTPVQYVHPAGVEFELGMVPELAVW	185	
Query	184	AEDYIG	189	
		E +G		
Sbjct	186	REIALG	191	

>>>>sptrembl:TlYSF1_9VIRU TlYSf1 SubName: Full=Replication associated protein;. 4/2014
Length=325

Score = 189 bits (480), Expect = 5e-46, Method: Compositional matrix adjust.
Identities = 100/191 (52%), Positives = 118/191 (61%), Gaps = 3/191 (1%)

Query 1 MSTFRFYARYALLTYAQCGGLDPFTIVSHIGDLGGECEIIGREAHSDGGTHLHAFVDFGRR 60
MS+FRF ARYALLTYAQCG LDPF + H+ L ECIIGRE H+D G HLHAFVDFG +
Sbjct 1 MSSFRFQARYALLTYAQCGDLDPFAVSDHLSGLRAECIIGRETHADEGIHLHAFVDFGVK 60
Query 61 FQSRRAAVFDVGGFHPNISITKRDPQVHYDYAIKGDGVVAGGLERPAADASAGVEN---K 117
F +R VFDV G HPN+ ++ P YDYAIKGDGVVAGGL+RPA D GV K
Sbjct 61 FSTRNVRVFDVQGHHPNVEPSRGRPAGGYDYAIKGDGVVAGGLDRPADDGGVGVSKTTQK 120
Query 118 HHQIVLAPTRAEFFEAVRDLDPRLLLTSPFPSLEKYADWHYRVDPPYRHDPEYEFDTSQF 177
IV A TR EF+ + +LDP ++ SF YAD +R P+ Y DT
Sbjct 121 WATIVGAQTRDEFWALLAELDFGAMVRSFTQCRAADHRFRESPEYVTPESIIIDTGHV 180
Query 178 PELNQWAEDYI 188
LN+WA I
Sbjct 181 DGLNEWALSNI 191

>>>>sptrembl:TlYQU3_9VIRU Tlyqu3 SubName: Full=Replication associated protein;. 2/2014
Length=340

Score = 189 bits (479), Expect = 6e-46, Method: Compositional matrix adjust.
Identities = 97/183 (53%), Positives = 119/183 (65%), Gaps = 0/183 (0%)

Query 9 RYALLTYAQCGGLDPFTIVSHIGDLGGECEIIGREAHSDGGTHLHAFVDFGRRFQSRRAAV 68
RYALLTYAQCG LD + + H+ LGGECEIIGRE H+DGGTHLHAFVDF R+F+SRR+ V
Sbjct 13 RYALLTYAQCGDLDAWAVNDHMAFLGGCEIIGRELHADGGTHLHAFVDFSRKFRSRRSDV 72
Query 69 FDVGGFHPNISITKRDPQVHYDYAIKGDGVVAGGLERPAADASAGVENKHHQIVLAPTRA 128
FDVGG HPN+ + P+ YDYAIKGDGVVAGGL RP+ + IV +
Sbjct 73 FDVGGRHPNLVPSYGSPEGGYDYAIKGDGVVAGGLSRPSGRGVYEDVSSWSIIIVSQESEG 132
Query 129 EFFEAVRDLDPRLLLTSPFPSLEKYADWHYRVDPPYRHDPEYEFDTSQFPELNQWAEDYI 188
+F+E V LDPR L T++ SL YA+W Y+ P Y H +F+ PEL W E +
Sbjct 133 DFWECDVARLDPRSLCTNYSNLRAYANWKYQPLPVRYEHPAGVKFELGMVPELAVWREVAL 192
Query 189 GWD 191
G D
Sbjct 193 GVD 195

ProtSweep
A Protein Identification Tool

Results for /home/vir088/rindneu/gemi/HCB18.215.196r.pep

Number of residues: 196	Molecular weight: 22.17 kD
Charge: -11	Isoelectric point: 5.31
more...	
Prediction of protein localization:	
mito	15 %
cyto nucl	9.5 %
cyto	9 %

Identified Protein & Transcript:

Protein:

id: sptrembl:Q06FD4_9GEMI

valuation: putative

scientific organism: Tomato mosaic

abstract: Q06fd4 SubName: Full=Replication protein; Flags: Fragment;. 4/2014Length=220

ORF 104aa:

>>>sptrembl:TLRW0_9VIRU Tlyrw0 SubName: Full=Replication as... 139 4e-31
>>>sptrembl:K0A1L7_9VIRU K0a1l7 SubName: Full=Spliced replic... 137 2e-30
>>>sptrembl:TLYSF1_9VIRU Tlysf1 SubName: Full=Replication as... 127 2e-27

>>>>sptrembl:TLRW0_9VIRU Tlyrw0 SubName: Full=Replication associated protein
(*Gemycircularvirus 8*);. 2/2014
Length=320

Score = 139 bits (351), Expect = 4e-31, Method: Composition-based stats.
Identities = 65/103 (63%), Positives = 77/103 (74%), Gaps = 1/103 (0%)

Query 1 MWARSLAKHAYFGGLFSLEESLEDVKYAVFDDIAGGLKFFPQYKSWLGNQLDFYSTDKYK 60
+WARSL HAYFGGLFSLEE LE V YA+FDD+ GGLKFF YK WLG Q F++TDKY+
Sbjct 212 LWARSLGNHAYFGGLFSLEEELEGVDYAFDDMQGGLKFFHSYKFWLGAQSQFWATDKYR 271

Query 61 KKKAIKWGKPCIWISNEYPIIT-EGVDQDWMKNCIFVEVTTPL 102
KK I WG+P I+I N+ P+ EGVD DW+ NC FVE+T L
Sbjct 272 GKKLHWGRPSIYICNQNPLCDEGVDHDLIGNCDFVEITESL 314

>>>>sptrembl:K0A1L7_9VIRU K0a1l7 SubName: Full=Spliced replication-associated protein;. 4/2014
Length=318

Score = 137 bits (345), Expect = 2e-30, Method: Composition-based stats.
Identities = 61/104 (58%), Positives = 78/104 (75%), Gaps = 1/104 (0%)

Query 1 MWARSLAKHAYFGGLFSLEESLEDVKYAVFDDIAGGLKFFPQYKSWLGNQLDFYSTDKYK 60
+WARSL +HAYFGGLF L+ESLEDV YAVFDD+ GGL+FF YK WLG Q FY+TDKY+
Sbjct 210 LWARSLGRHAYFGGLFCLDESLEDVDYAVFDDMQGGLFFHAYKFWLGAQKQFYATDKYR 269

Query 61 KKKAIKWGKPCIWISNEYPIIT-GVDQDWMKNCIFVEVTTPLY 103
K+ + WG+P I+ISN P+ + G D DW+ NC+ V V P++
Sbjct 270 GKQLVNWGRPSIYISNTNPLADKGADVVDWLMGNCVIVHVDRPIF 313

>>>>sptrembl:TLYSF1_9VIRU Tlysf1 SubName: Full=Replication associated protein;. 4/2014
Length=325

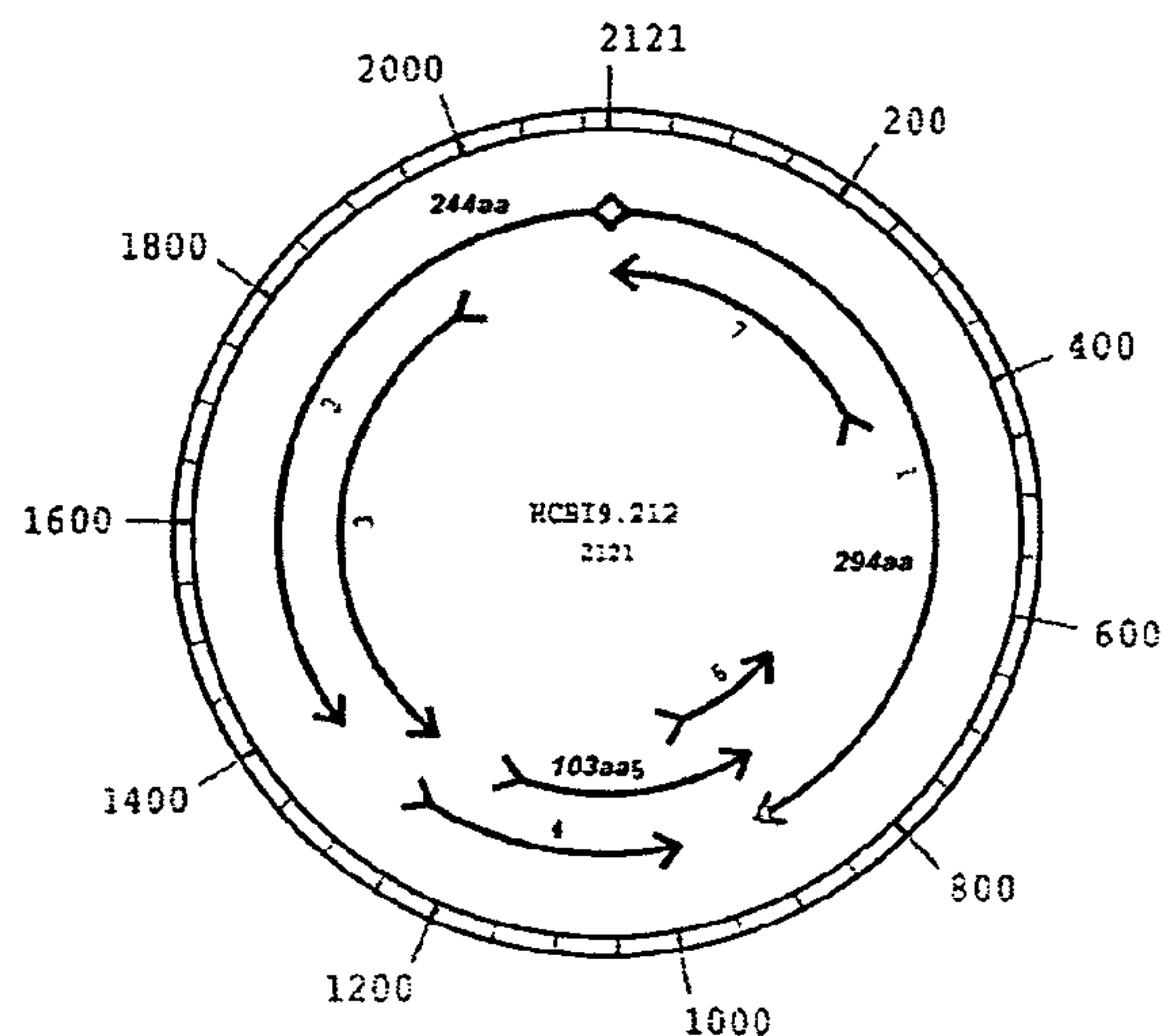
Score = 127 bits (319), Expect = 2e-27, Method: Composition-based stats.
Identities = 59/106 (55%), Positives = 76/106 (71%), Gaps = 5/106 (4%)

Query 1 MWARSLAKHAYFGGLFSLEESLEDVKYAVFDDIAGGLKFFPQYKSWLGNQLDFYSTDKYK 60
+WARSL HAYFGGLFS++E + YAVFDD GGLKF P YK W+G+Q FY TDKYK
Sbjct 215 VWARSLGDHAYFGGLFSMEDISSATYAVFDDF-GGLKFLPSYKFWMGHQKQFYVTDKYK 273

Query 61 KKKAIKWGKPCIWISNEYPIIT-GVDQD---WMDKNCIFVEVTTPL 102
KK ++WG+P IWI+NE P E GV D W+++NCIF+ + + +
Sbjct 274 GKKLVEWGRPSIWINNEDPREEHGVRCDIEWLEQNCIFIRLDSTI 319

HCBI9.212 (2121bp)
(rkg.S1.8B.1.2)

ATTTTTCGACCAGTAAAAAATGGCTTACGGATTCCGCCGCCGCTTTGGTCGCTCCCGTCGCTCGTACCGACGAAG
 GCCCGTTCCGCCGCTATTCCCGAAGGGGTAGAAGCGGGTATGGTCGTGGCGGTTACAACCGTCGGCGTTATCGTCG
 TCGTCGCCGCTCTTGGATTAGTCCTTACAACAAAAGCATGACGTGATTAAGGGGGCGCATGATTCGAATGATAA
 TTCGTTCCGCCCTATAGGTGCCCCCAACACCTTTTTTGGGTTCTGCCCAACCTACATGCCCAACGCCGTTGCTGG
 GGATACTGGTCACAATCCTCAAAAGGTTTCGGACCAGTAAGAATGTTGGGTTTCAGTGGATATCAGGAACGTGTTCA
 TATTGCTACGGCTGAATCTTTGATTTGGCGTCGCATGGTTATTTGGTCATATAACCGGCTTGAGAATACGGCCGG
 TCCGACGAAGACGGATGATCAGGGTACTTCGTACACGACACGTCAGCTTACCCCGCTCCAATTAAACGAAGGGGT
 CCGTGCGTTTTTTGTTCCGAGGTACTCAGGGTATCGATTACACTGAGAACACCTTGCATGAGGCTCCGCTGAATTC
 CGATCACTTTACCGTTGCGTATGATCGTACACGTGTGTTACAGCCTCGTCGTCTACTGGTGACGAATACGGTCA
 TATTTTTTAATATGAAGTTCTGGAACCCTGGTGAAGGATTATTTACTCGGATGATGAGGATGGTTTACAGAAGGG
 TCCTCTTGTGAACGGATGGTCTTCTCTTGGACGTGTGTCTAAGGGAAACATGTATATTTTTTGATGTCTTTTCTAC
 GGGGTATTCTTTGAGTAGTAATACTCCTTCTATTGCTAGATTTGCTCCGACTGGGACTCGTTACTGGACGGAGGG
 TTAGATACAATACAAATTGGATCCACCACATTGATTATGTGACAGTTGTTTCATAAGCCAATCGTAGTCCACCCCT
 TTAGCGAAGTGTGGGTCCTCGTTCATGCACATGATTGAGGGTTTGCCCCAGTAGATCGTTTCGCTTCTTTTCGGTAC
 TTGTCCGTGATGACGAATTGTTTTTGTGCGCCTAGCCACCCCTTGATGAGTGGAAGTATTCGAATCCTCCCTGG
 ATGTCGTCGAAGACGGCGTATTGACAATCGTCGGAGAATTCGTCCATGTTGAATTGTAGGTTGAAGTACGCATGG
 TGTCCCAACGATCTGGCGTATAGCGTCTTCCGGTTCTTGTGGTCCCCATAAAATGAGTGATTTAACTCTGCCC
 AAGTAAAGATCAGTAATGGGGTTCGGGGCGAAGCCCTGAAGCGGACAAGATTTGATCGTGCGAGGACGCTACGTC
 GGCCGCAGCGCCAGCAGACTTACCTCTCGGGTCTACAGTCCCAATGGCTGCCTGATTCTCCCACTCGGAGATCT
 CAGGATAGCGTTCTCTCTCCACAATGATGGGCGGCGCCTCGTATTCCGGTTTCTCGTCGGGGTAATAAAAATTGG
 CGTATTCGATGATGCGCTGATTGGTAGCAACCAATCTCTTGGAGCTTGTTGACGGACAGCCGACAGAAATGATTC
 TTTAGTGTCGCAGCTGATGATATCAGCCCACTTATTTGAATTATCCCCGTCACATGAGCGAGCATCTGCTGGGGG
 CTCGCCGTGCTCAAGTCGGATGTCTCCATCCTTGCCGACATAATCGAAGACCTTGTGTGGAGTTCGACGAATCGA
 TTTAATATTGCCGTGAGCTCCAAAGTAGTCGAACGCAGTTGCCGAGTTGACAGTGACAATCTTGTCGAAGCCAAG
 ATATATGTGGTAATGAATTCCTCCATCCGAATGGCGCTCTCGTCCGAGTCGACAGCATAAAGGATTTCCAAAATT
 CGCTGTGACACGTTCAAGGAAAGGAGTTCTGCGTCGAATTCATGTTGGAGGTGTTTCGGGGACTTGTGGAAACGT
 AATGATAAGATTTCTTGCTCTGACTTGAATCGTCGAGGCATTTTAAGGAGTCGTTACGTGACGTGTGCAAATA
 GAGAGAGACTTGGCTAATATTATCTCTCTATTTGCAGTTTGCACATTGCACATGGCTGCCTATAAATACCCCT
 CATCCCCCTGCGGTGAGTC



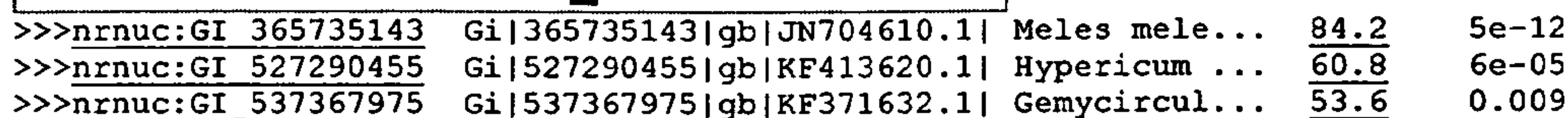
71% nucleotide similarity to Meles meles fecal virus

ORFs: 294aa – capsid protein 26% similarity to Gemycircularvirus 8

244aa – replication protein 34% similarity to Meles meles fecal virus

103aa – replication-associated protein 59% similarity to Dragonfly-associated virus 1

Figure 3(b)



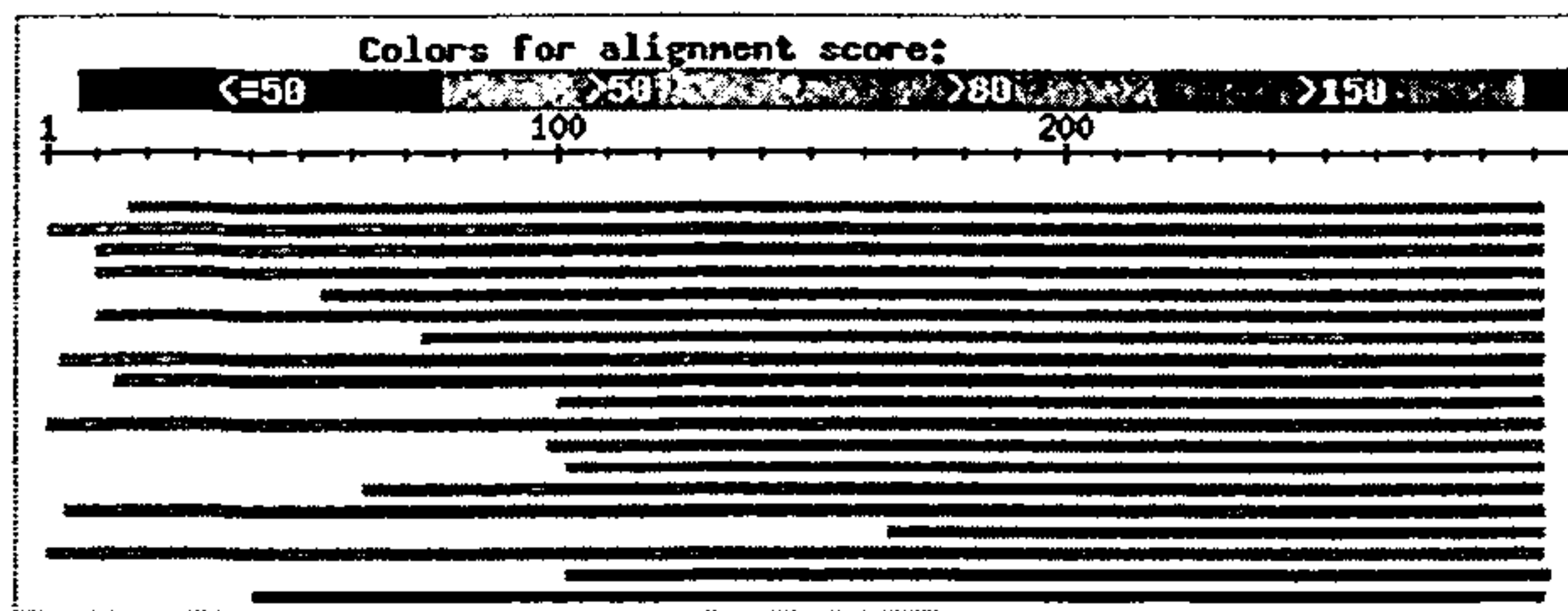
Score = 84.2 bits (92), Expect = 5e-12
Identities = 105/146 (71%), Gaps = 0/146 (0%)
Strand=Plus/Plus

Score = 60.8 bits (66), Expect = 6e-05
Identities = 56/71 (78%), Gaps = 0/71 (0%)
Strand=Plus/Plus

Score = 53.6 bits (58), Expect = 0.009
Identities = 75/103 (72%), Gaps = 2/103 (1%)
Strand=Plus/Plus

Query	1044	TCGGTACTTGTTCCGTGA-TGACGAATTGTTTTTGTGCGCCTAGCCACCCCTTGATGAGT	1102
Sbjct	1280	TCTGTACTTGTTCCGTAAGTGTAACTTGGACT-GCGCCCCCAACCACCCCTTGATGACG	1338
Query	1103	GGAAGTATTCGAATCCTCCCTGGATGTCGTCGAAGACGGCGTA	1145
Sbjct	1339	GGAAATACTTGAATCCGCCCTGCATATCATCAAATACTGCATA	1381

BlastP – Uniprot:
ORF 294aa:



>>>sptrembl:K0A2I9_9VIRU K0a2i9 SubName: Full=Putative coat ... 80.5 8e-13
 >>>sptrembl:T1YTB1_9VIRU Tlytbl SubName: Full=Capsid protein... 75.1 3e-11
 >>>sptrembl:C7FFR0_9VIRU C7ffr0 SubName: Full=Coat protein;... 67.8 5e-09

>>>>sptrembl:K0A2I9_9VIRU K0a2i9 SubName: Full=Putative coat protein (*Dragonfly-associated virus 1*);. 5/2013

Length=290

Score = 80.5 bits (197), Expect = 8e-13, Method: Compositional matrix adjust.
 Identities = 75/301 (24%), Positives = 131/301 (43%), Gaps = 39/301 (12%)

```

Query 18  RRPVRRYSRRGRSGYG---RGGYNRRRYRRRRRSWISPYNKKHDKVIGAHDSNDNSFAPI 74
          RR  R  RRGR+G  R  RR  RR  +  +  ++  +  N+  P+
Sbjct 3   RRKYTRTIRRGGRAGSSKKRRSYVGRRLSSRRTTKTVMKRTSRRRILNISSQKKRNNAQPV 62

Query 75  GAPNTFFGFCP-----TYM---PNAVAGDTGHNPKVRTSKNVGFSGYQERVH 119
          + G  P          TY+  P A+  DT          R ++ + + G +ER
Sbjct 63  NF--NYLGESPIPGSKVMGSDRTTYLLWRPTALTDDTDIYSSASRGAQQIYWRGIKERA 120

Query 120 IATAESLIWR-RMVIWSYNRLENTAGPTKTDDQGTSTYTRQLT-----PLQLNEGVRAFL 173
          + T+  WR R +++  L N G  +  +  +  P  L  + +FL
Sbjct 121 VGTSSGAARWRRIWFVFEAKSL-NINGLISNVETSAGFNAMVELSGDPPANLRNSLESFL 179

Query 174 FRGTQGIDYTENTLHEAPLNSDHFTVAYDRTRVLQPRRPTGDEYGHIFNMKFWNPGGR-I 232
          F+G+ G+D+ NT+  A ++++  +  D+ R LQ  +G++ G  +  + W P  + +
Sbjct 180 FQGSVGVDW--NTVFNAKVDNRCRLLSDKVRHLQ----SGNDRGRFYTFRQWIPLNKTM 233

Query 233 IYSDDDEDGLQKGPLVNGWSSLGRVSKGNMYIFDVSTGYSLSSTNTPSIARFAPTGTTRYWT 292
          +Y+DDE G  K  N ++S GR  G++Y++D+F  L+S+  +  F P  T YW
Sbjct 234 VYNDDEVGDDKQS--NTFASPGRKGMDVYVYDMFQC---LTSDAINTLNFPQATLYWH 288

Query 293  E  293
          E
Sbjct 289  E  289
  
```

>>>>sptrembl:T1YTB1_9VIRU Tlytbl SubName: Full=Capsid protein (*Gemycircularvirus 8*);. 2/2014

Length=302

Score = 75.1 bits (183), Expect = 3e-11, Method: Compositional matrix adjust.
 Identities = 86/321 (26%), Positives = 154/321 (47%), Gaps = 48/321 (14%)

```

Query 1   MAYGFRRRFRGRSRRSYRRRPVRRYSRRGRSGYGRGGYNRRRYRRRRRSWISPYN----- 55
          MAY  RRRF  SR  R+P+RR  R  G+  RR  R+R  S  +  NK
Sbjct 1   MAYA-RRRFTSSRA---RKPIRR----SRRPAGKRRSYRRSTRKRGMSRTRLLNKTSQKK 52

Query 56  KHDVIKGAHDSNDNSFA-----PIGA--PNTF-FGFCPTYMPNAVAGDTGHNPK 100
          + +++  ++  + ++ F+          P+GA  P  F  +  +  T  P+ ++  TG
Sbjct 53  RDNMLSFSNTTAEDPFSTDYTIGPAVMRRPVGADLPAEFYVWNATGRPHELS--TGFRG 110

Query 101 QKV----RTSKNVGFSGYQERVHIAATAESLIWR-RMVIWSYNRLENTAGPTKTD--DQGT 153
          K+  RT+  +  G +ER+ + T  S  WR R  + ++  A P ++D  + +
Sbjct 111 SKIDTSLRTNTTIFAVGLKERIKLETNNSAPWRWRRICFTSKNDYGEADPDESDFRRTS 170

Query 154 SYTTRQLTPLQLNEGVRAFLFRGTQGIDYTENTLHEAPLNSDHFTVAYDRTRVLQPRRPT 213
          +  R L  E  +  +F G  + +D+  AP+N  H  +V YDRTR +Q  +
Sbjct 171 NGMVRLRLRAQSQAEEINDDVFDGQRNVDWLSAIT--APINRRHVSVDYDRTRTIQ----S 224

Query 214 GDEYGHIFNMKFWNPGGR-IIYSDDDEDGLQKGPLVNGWSSLGRVSKGNMYIFDVSTGYS 272
          G++ G  + W+P  + ++Y+D++ G  +G  + +G S  G+V  GN Y+ D+F T  +
Sbjct 225 GNQSGVTRTYRQWHPMRKNVYADEQAG--EGMVDSGVSVTGKVMGNYYVMDIF-TKHG 281

Query 273  LSSNTPSIARFAPTGTTRYWTE 293
          L+  +  +++  + P  T +W E
Sbjct 282  LNDDQSTLS-YEPESTFFWHE 301
  
```

>>>>sptrembl:C7FFR0_9VIRU C7ffr0 SubName: Full=Coat protein;. 5/2013
Length=312

Score = 67.8 bits (164), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 86/319 (26%), Positives = 145/319 (45%), Gaps = 50/319 (15%)

Query 11 RSRRSYRRRPVRRYSRRGRSGYGRGGYN--RRRYRRR----RRSWISPYNKK--HDVIKG 62
RS R RRP++ R G S R Y+ +R YR++ +RS ++ ++K + ++
Sbjct 7 RSSRFRARRPIKTSRRGGVSKPRRRSYSAKKRTYRKASMSKRSILNTTSRKKRNGMLTF 66

Query 63 AHDSNDN-SFAPIGAP---NTFFG----FCPTYMPNAVAGDTGHNPKVRTSKNVGFSGY 114
++ +N S AP AP N G +CPT M N VA N T+ G
Sbjct 67 SNTTNSGASTAPAAAPVYVNAVLGGTFIWCPTAM-NLVAQSLISN-MSSHTATTTCYMRGL 124

Query 115 QERVHIATAESLIW-RRMVIWSYNRL-----ENTAGPTKTDDQGTSY--TTRQLTPLQLN 166
E + I T+ + W R V +++ L T PT +D Y ++ + L N
Sbjct 125 SEHIRIQTSSGIPWFHRRVCFTWKGLGPFNVMATESPT-SDFPWLPHYQDSSNGVQRLFFN 183

Query 167 EGV-----RAFLFRGTQGIDYTENTLHEAPLNSDHFTVAYDRTRVLQPRRPTGDE 216
E V R LF+G + +D+T+ + APL++ TV +D+T +Q +G+
Sbjct 184 ENVNMPQTINRQRNLFKGAENVWDTPII--APLDTGRITVKFDKTWTMQ----SGNT 237

Query 217 YGHIFNMKFWNPGGR-IIYSDDDEDG-LQKGPLVNGWSSLGRVSKGNMYIFDVSTGYSLS 274
G + K W+P ++Y DDE G ++ G + +S+ + G+ Y+ D+ G +
Sbjct 238 NGIVRERKLWHPMHNHNVYDDDEYGDIESG---SWFSTDSKAGMGDYYVMDIIQGGQGGT 294

Query 275 SNTPSIARFAPTGTTRYWTE 293
++ + R T YW E
Sbjct 295 AS--DLLRMTANSTMYWHE 311

ProtSweep
A Protein Identification Tool

Results for /home/vir088/rindneu/gemi/HCB19.212.294.pep



Number of residues: 294	Molecular weight: 33.86 kD
Charge: 25	Isoelectric point: 11.38

[more...](#)

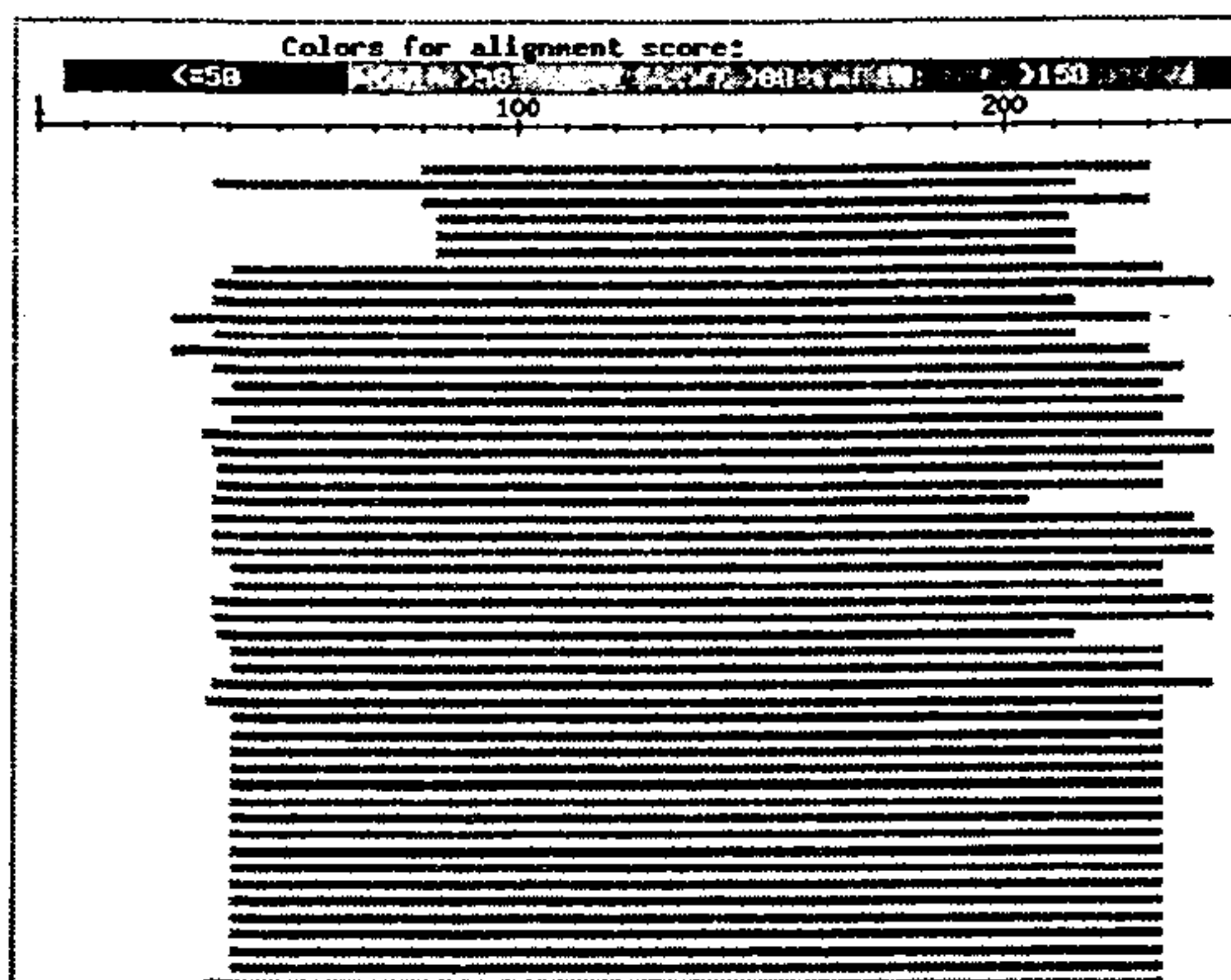
Prediction of protein localization:

nucl	30%
------	-----



Protein:
id: sptrembl:TIYTBI_9VIRU
valuation: putative
scientific organism: Gemycircularvirus 8
abstract: Tlytbi SubName: Full=Capsid protein;. 2/2014Length=302
isoform:

ORF 244aa:



```
>>>sptrembl:G9ITS8_9VIRU G9its8 SubName: Full=Replication-as... 90.5 6e-16
>>>sptrembl:T1YRX6_9VIRU Tlyrx6 SubName: Full=Replication as... 89.4 1e-15
>>>sptrembl:T1YQS5_9VIRU Tlyqs5 SubName: Full=Replication as... 85.5 2e-14
```

```
>>>>sptrembl:G9ITS8_9VIRU G9its8 SubName: Full=Replication-associated protein (Meles meles
fecal virus);. 4/2014
```

Length=237

Score = 90.5 bits (223), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 52/152 (34%), Positives = 76/152 (50%), Gaps = 3/152 (1%)

```
Query 81 PLCCRLGRERHSDGGIHYHIYLGFDKIVTVNSATAFDYFGAHGNIKSIRRTPHKVFDYVG 140
          P C +GRE H+DGGIH H ++ F K V + FD G H NI RTP K+ DY
Sbjct 36 PAECIIGRENHADGGIHLHAFVDFGKRVDIRDNRFRDVEGFHPNIAPCGRTPQKMLDYAI 95

Query 141 KDGDIRLEHGEPPADARSCDGDNSNKWADIISCDTKESFLSAVRQQAPRDWLLSNQRIIE 200
          KDGD+ P D D + + W I + + + F + R+ APR L ++Q +
Sbjct 96 KDGDVVAGGLNPILDLP--DAETDSIWHRIANAPSVDEFWAITRELAPRALLCNHQLRA 153

Query 201 YANFYYPDEKPEYEAP-PIIVERERYPEISEW 231
          YA ++Y YE P + + + P++ EW
Sbjct 154 YAEWHYRPVATRYEHPHGLSLRTDHVPQLDEW 185
```

```
>>>>sptrembl:T1YRX6_9VIRU Tlyrx6 SubName: Full=Replication associated protein
(Gemycircularvirus 7);. 4/2014
```

Length=332

Score = 89.4 bits (220), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 59/190 (31%), Positives = 91/190 (47%), Gaps = 17/190 (8%)

```
Query 38 MPRRFQVR-ARNLIITFPQVPEHLQHEFDAGTPFL---ERV TANFGNPLCCRLGRERHSD 93
          M R+F ++ A+ ++T+PQ+PE +EF L ERV AN+ +GRE H+D
Sbjct 1 MSRQFCLKDAKYCLLTYPQIPETEAYEFPELASELFSSSERVDANY-----VIGRELHAD 54

Query 94 GGIHYHIYLGFDKIVTVNSATAFDYFGAHGNIKSIRRTPHKVFDYVGKDGDIRLEHGE-- 151
          GG H +L F + + FD G H NI+ + RTP ++Y KD D+ GE
Sbjct 55 GGYTSHCFLDGFRKFSSRDTRIFDIQGHHPNIERVGRTPRTAYNYTIKNDVVARSGEYS 114

Query 152 -PPAD---ARSCDGDNSNKWADIISCDTKESFLSAVRQQAPRDWLLSNQRIIEYANFYY 206
          PP + R D S+ WA I+ ++++ F + PR S + YA++ Y
Sbjct 115 GPPENNNRERQSGNDTSSDWATILCAESRDEFFDLCKSLQPRSLACSLTRYADWRY 174

Query 207 PDEKPEYEAP 216
          Y+ P
Sbjct 175 RPVPTPYQHP 184
```

```
>>>>sptrembl:T1YQS5_9VIRU Tlyqs5 SubName: Full=Replication associated protein
(Gemycircularvirus 10);. 4/2014
```

Length=324

Score = 85.5 bits (210), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 50/153 (32%), Positives = 75/153 (49%), Gaps = 2/153 (1%)

```
Query 81 PLCCRLGRERHSDGGIHYHIYLGFDKIVTVNSATAFDYFGAHGNIKSIRRTPHKVFDYVG 140
          P C +GRE H+DGG H H + F + FD G H N++ RTP+K +DY
Sbjct 35 PAECIIGREAHADGGTHLHAFCDGFERFYTADPRRFDVDGYHPNVQPFGRTPYKGWDYAI 94
```

Query 141 KDGDIRLEHGEPADARSCDGDNS-NKWADIISCDTKESFLSAVRQQAPRDWLLSNQRII 199
KDGD+ E P D + ++W I+ +T + F +R+ APR L + +
Sbjct 95 KDGDVVCGLERPGTGPGLTGVSGAGSQWDRIVGAETPDEFWRLIRELAPRTLLTNFNSVR 154

Query 200 EYANFYYPDEKPEYEAPP-IIVERERYPEISEW 231
YA+++Y YE+PP I + E+ EW
Sbjct 155 AYADWHYRPVVAPYESPPEIEFDLSGVEELREW 187

ProtSweep
A Protein Identification Tool

Results for /home/vir088/rindneu/gemi/HCB19.212.244r.pep



Number of residues: 244	Molecular weight: 28.34 kD
Charge: -2	Isoelectric point: 6.97

[more...](#)

Prediction of protein localization:

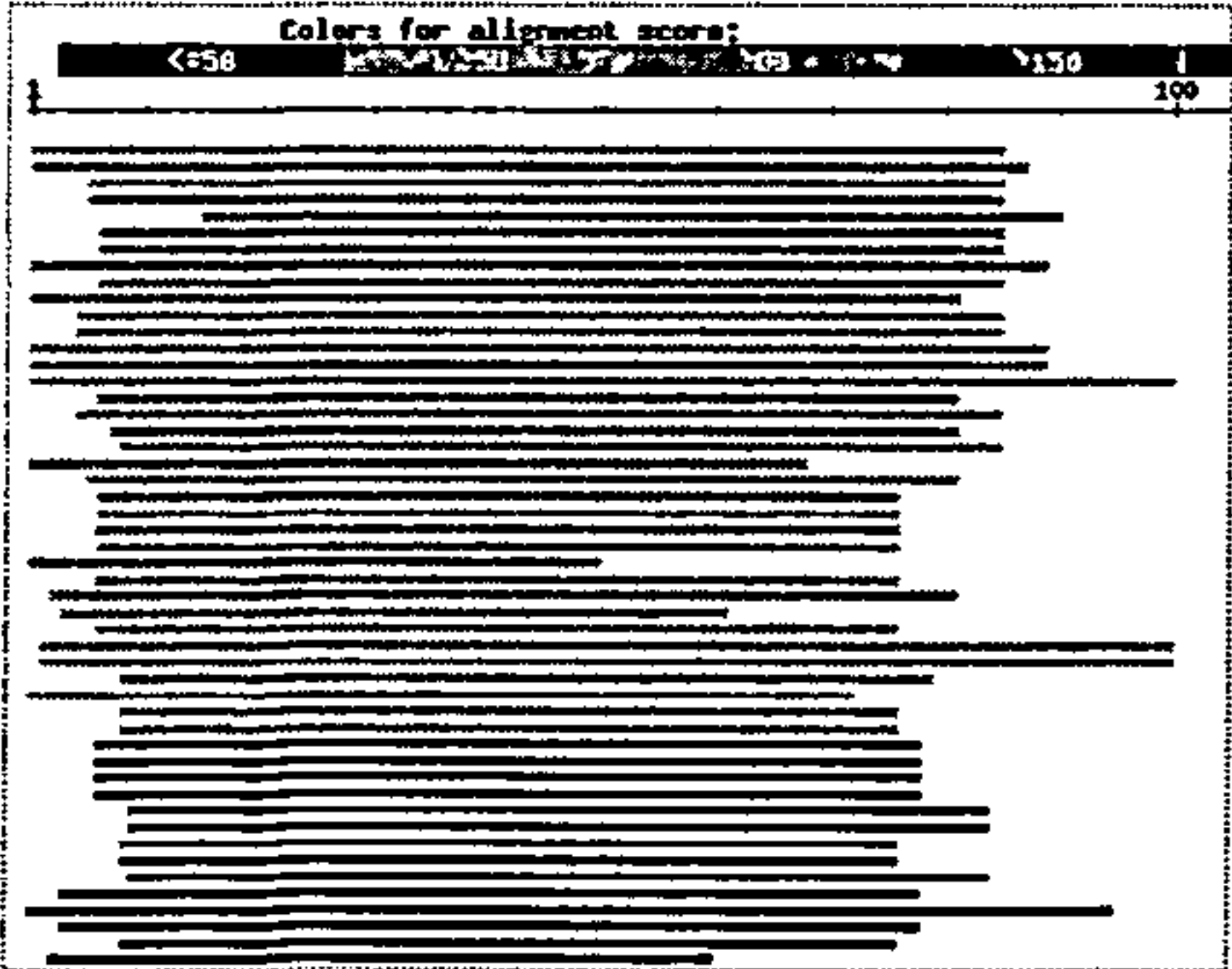
cyto_nucl	12.5 %
mito	10 %
cyto	9 %



Identified Protein & Transcript:

Protein:
id: sptrembl:O8OPT6_9GEMI
valuation: putative
scientific organism: Tomato mottle
abstract: Q8opt6 SubName: Full=Replication-associated protein; Flags: Fragment; 4/2014Length=232
isoform:

ORF 103aa:



>>>sptrembl:K0A1L7_9VIRU K0a1l7 SubName: Full=Spliced replic... 115 7e-24
>>>sptrembl:T1YRW0_9VIRU T1yrw0 SubName: Full=Replication as... 106 4e-21
>>>sptrembl:J0YHY6_9PSED J0yhy6 SubName: Full=Uncharacterize... 106 5e-21

>>>>sptrembl:K0A1L7_9VIRU K0a1l7 SubName: Full=Spliced replication-associated protein
(*Dragonfly-associated virus 1*);.
4/2014
Length=318
Score = 115 bits (288), Expect = 7e-24, Method: Composition-based stats.
Identities = 51/86 (59%), Positives = 62/86 (72%), Gaps = 0/86 (0%)

Query 1 MDEFSDDCQYAVFDDIQQGGFEYFHSYKGWLGAQKQFVITDKYRKKRTIYWGKPSIMCMNE 60
+DE +D YAVFDD+QGG E+FH+YK WLGAQKQF TDKYR K+ + WG+PSI N
Sbjct 227 LDESLEDVDYAVFDDMQGGLEFFHAYKFWLGAQKQFYATDKYRGKQLVNWGRPSIYISNT 286

Query 61 DPHFAKGVDYDWLMNNCHIINVVDPI 86
+P KG D DWLM NC I++V PI
Sbjct 287 NPLADKGADVVDWLMGNCVIVHVD RPI 312

>>>>sptrembl:T1YRW0_9VIRU T1yrw0 SubName: Full=Replication associated protein
(*Gemycircularvirus 8*);. 2/2014
Length=320

Score = 106 bits (264), Expect = 4e-21, Method: Composition-based stats.
Identities = 43/88 (48%), Positives = 63/88 (71%), Gaps = 0/88 (0%)

Query 1 MDEFSDDCQYAVFDDIQGGFEYFHSYKGWLGAQKQFVITDKYRKKRTIYWGKPSIMCMNE 60
++E + YA+FDD+QGG ++FHSYK WLGAQ QF TDKYR K+ I+WG+PSI N+
Sbjct 229 LEEELGVVDYAIFFDDMQGGLKFFHSYKFWLGAQSQFWATDKYRGKKLIHWGRPSIYICNQ 288

Query 61 DPHFAKGVVDYDWMNNCHIINVVDPICI 88
+P +GVD+DWL+ NC + + + + +
Sbjct 289 NPLCDEGVVDHDLIGNCDFVEITESLLV 316

>>>>sptrembl:JOYHY6_9PSED JOyhy6 SubName: Full=Uncharacterized protein;. 4/2013
Length=103

Score = 106 bits (264), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 46/81 (56%), Positives = 58/81 (71%), Gaps = 0/81 (0%)

Query 6 DDCQYAVFDDIQGGFEYFHSYKGWLGAQKQFVITDKYRKKRTIYWGKPSIMCMNEDPHFA 65
DD QYAV DDIQG F++F +YKGWLGAQ+ F +TDKYR K TI WG+P+I MNEDP
Sbjct 21 DDAQYAVLDDIQGNFQFFPAYKGWLGAQESFTVTDKYRGKTTITWGRPTIWLNMNEDPEEV 80

Query 66 KGVVDYDWMNNCHIINVVDPI 86
VD +WL NC I+++ +
Sbjct 81 GHVDLNWLRGNCTIVHLTQSL 101

ProtSweep
A Protein Identification Tool

Results for /home/vir088/rindneu/gemi/HCB19.212.103r.pep

Number of residues: 103

Molecular weight: 12.03 kD

Charge: -6

Isoelectric point: 4.65

[more...](#)

Prediction of protein localization:

cyto	18.5%
cyto_nucl	11%
extr	10%

Identified Protein & Transcript:

Protein:

id: sptrembl:H6WAT6_9GEMI

valuation: putative

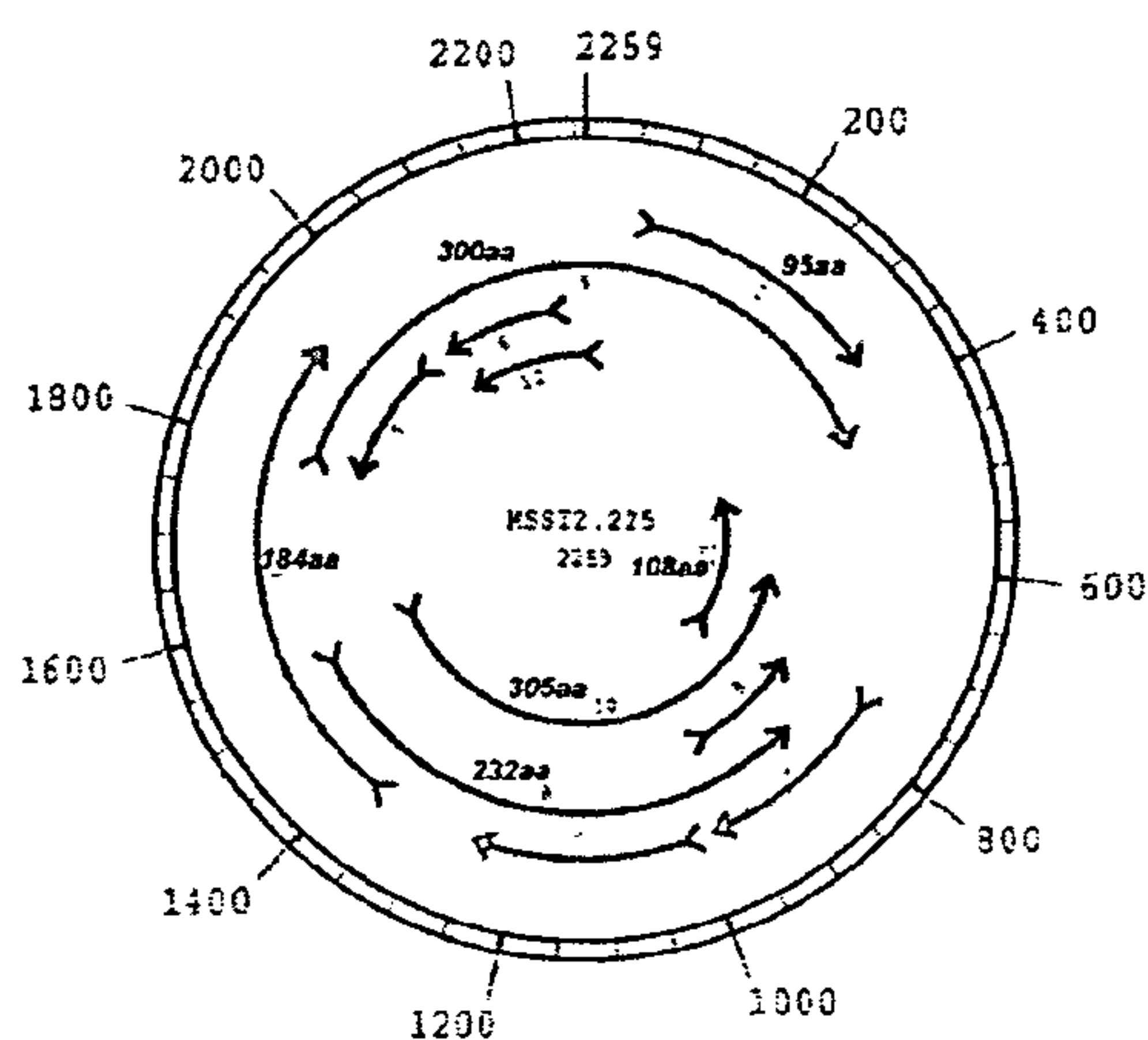
scientific organism: Papaya leaf

abstract: H6wat6 SubName: Full=Replication-associated protein; Flags: Fragment;. 6/2012Length=123

isoform:

MSSI2.225 (2259bp)***(MSSI = Multiple sclerosis serum isolate)******(ms24.RCA.1700.3)***

TTCCTAATCAGCTGTTTCGATCAGACCACCGAAGGTGGATGTCGACGCGTCATCGGCCCACTTCTCGGGGTCACTA
 ATGCCCCGAGATGAGCTGCAATCTTACGTCTTCCGGGGTCAGGAAGATTCTGATTGGGCAGATCAGTTTACTGCCC
 CCCTTGATACTCGTCGCATTACGGTTAAGTCCGACAACTCCGCGTCATCCGCCCCGGTAATGAAACAGGTGCTT
 CGCGCTTGTTTAAGTTTTGGTACCCCATTCGTCGTACCATCTCTTACGAAGATGACCTTGAGTCCGACGTTGTCG
 GTGATCGGCCCTTTTCTACCGCAGGTTTACGAGGTGTTGGGGATATGTACGTCATGGATATAATGGGTATTACGA
 ATTTGGTGAATGATGCACCTCCAACGTCCTACAGGTTCCGGTCCTGAGGGCAGCTTTTATTGGCATGAGCGGTAAA
 TTAGGAGACTATGGGGCTATCTAGGTACACGAAATCGCAGTTGGCATTAAAGCCACTCGGTGTCAACACCAAGCTC
 GTCACGTGGGTTCGGAGTTAGATAGCCAAATTGAGGGCCGAGCCCAGTGTACCAACTTTTTCCCCTTGTAATTATC
 CGTGACGTAGAACTGCTTTTGATGACCTAACCAAGATTTGTAGCTGGGAAGGAATTTAATTCCCTCCGAAGTCGTC
 AAAGATGGCGTACTCAACCCCATCAAGGTTTTCGTCCAAGCTAAAGAGGCCTCCGAAGTAAGCATGGTTTCCCAG
 GCTTCTAGCCCAAATGGTTTTTCCCATTCTGGAAGGCCCGTATACCACAAGTGATTTTCTTCGTTCTGTATATCG
 AAGTCAGCATCCAGATTTGTTGATGCGCACTCGAGCGAGGCGCTGCGCGAGGCCCGCCGAGCATGGAGGCGCG
 CGTAGCCGCGGACTGCAGCCGCTGCGACGTGCATGATAACTTACCTCCAGTTTCACCTCGTCCAAGATTTTGTTG
 TACCCATTGATTGAGTTCAGCCACCCAAGACGTATCGATGTTAACTCCCTCCGGTGTCTCATACGGGACTCTGAT
 TGGTGGGAATTTCCAGGCTGCGTATGCCCTGAGCTGGGTGAAGGAGGTGACCAATGAGCGTGGAGCCAGGCGTTT
 GCATAGGTCCCAAACTCTTGCTCACTCTCAGCATTGATGATTTTACGCCACACCCCACTAGTTGCATCCACTCT
 GCCTGCAACAGGTGCTCGAGTCCCCCAGCAACAACATCTCCATCTTTGATTGCATAATCAAACCCCTCTTCTGG
 TGTTCGCGGAGAAGGCGATACATTTGGGTGGCATCCTTCAACATCGAATGCACGCGCGTTCCGGGTCTATATTT
 GACTCCGAAGTCGACAAAAGCGTGCAGATGAAGACCCCATCTGCGTGATTCTCTCGGCCGATGATGCATTCAGC
 TCCAAGTCCCGCAAGATGATTGACCACTGCAAAAGGGTTCGAGGTCTCCACATTGTGGATAGGTGAGCAAGGCGTA
 CCGTGCTTGAAATCGAAAAGAGGACATAGTTCGTTGTTGCACATTTTCCTTGGGTCCAAGTCTGGGCAGTTAATG
 TTATATGCCAGACGGACCCAGACCCGGGTCCCTTCGAACATAAATACCCCTCGCTCGTCCCCAACCTCCTCGTT
 TTTTGTATGCGCGATTTATCATGTCTGCCTTGATCCACCCCGTTGCCTGCAATCGGACTTGCCAAGACTACGTC
 AACCACGCTAGACACGAATGTTGTTTAGTGTGTAACCCTCCGCCACCCCTTCATCTCCTACTGTCGCACATTGT
 TCAGAATGTCGGTCGCCCCGTCGATCTGGTTCGAAGAACTCGCAAAGCTTTCCGCCGCGGTGGTAGAGCTACAAGAT
 CTCGTGGCCGAAGTACACGCCGCTCTTCTAGGCGAAGAGTCAGACGGCGAAGTATGACTACCCGACGTGTCCTCA
 ACATAACCACTCGTAAGAAGGTGGATAACATGTTGCCTGTTGTTGTTGCCGAGGATAACACGACTACTGTGGGGC
 CTTACACGTCCGTGTCACCCCTCCTTTCCCTTTTCGTTCCCAATGCCCGCACGACCCGAACCCCTGTTACCAATC
 CTGCCGTCCGAAATTCCTCGGATATTTTCGCGGTCCGATATAGGGAGCGCGTCCGCATTGATCTTATGGGTGGTG
 GAACTTTTATGTGGCGCCGCATCGTCTTCATGTTGAAGGGATCCGATTTGAGAGTTGCTATGAATTCCAGTGATT
 CAGGCAACA



75% nucleotide similarity to Gemycircularvirus 9 isolate P22.

ORFs:

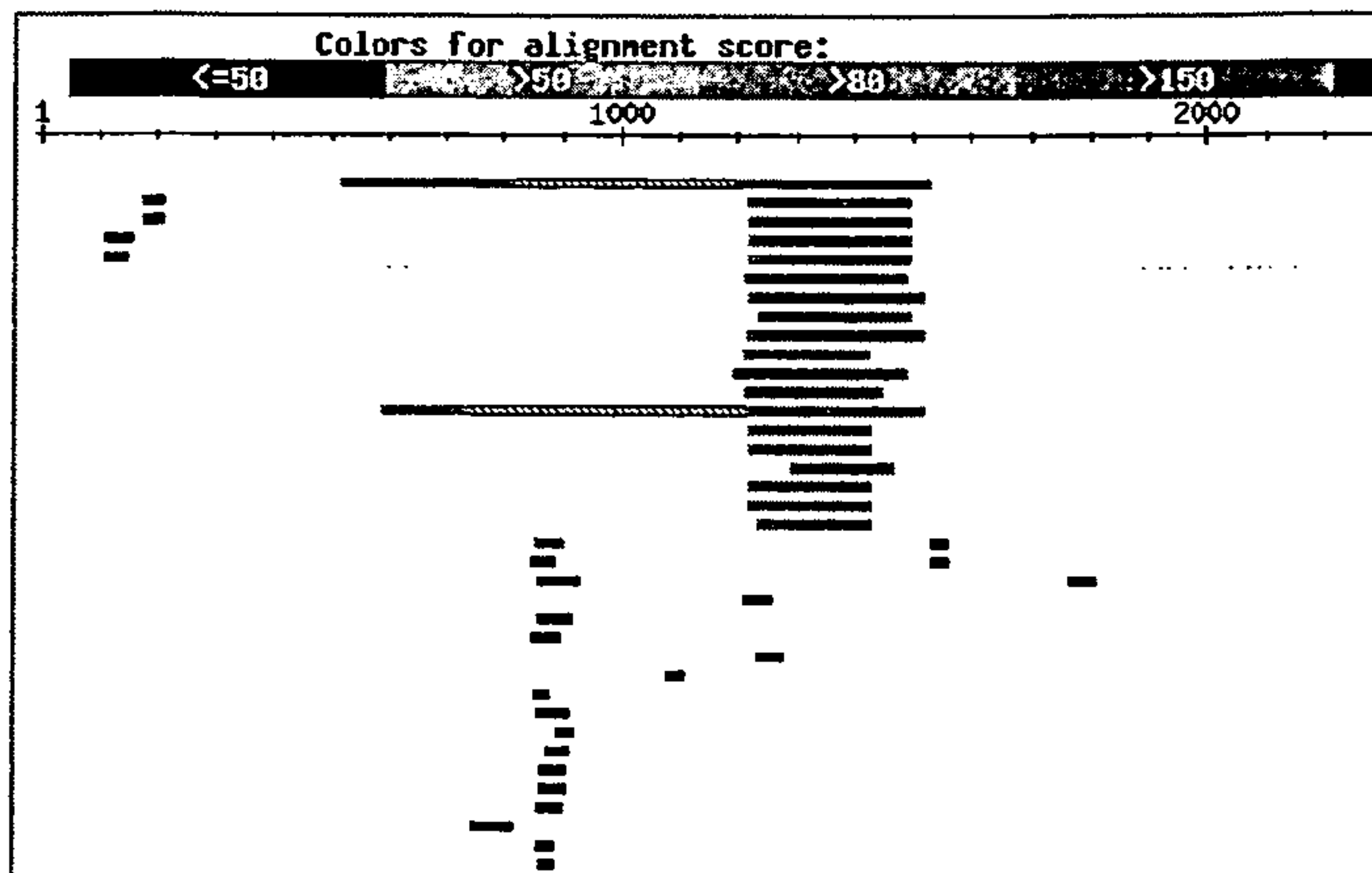
300aa – coat protein 33-36% similarity to Gemycircularvirus 8 and Meles meles fecal virus

232aa – replication-associated protein 61% similarity to Gemycircularvirus

108aa – replication-associated protein 71% similarity to Gemycircularvirus

Figure 3(c)

Blastn – Geall:



>>>nrnuc:GI_537367978	Gi 537367978 gb KF371633.1	Gemycircul...	<u>230</u>	6e-56
>>>nrnuc:GI_537367981	Gi 537367981 gb KF371634.1	Gemycircul...	<u>141</u>	2e-29
>>>nrnuc:GI_520689312	Gi 520689312 gb KF268026.1	Sclerotini...	<u>123</u>	6e-24

>>>>nrnuc:GI_537367978 Gi|537367978|gb|KF371633.1| Gemycircularvirus 9 isolate P22, complete genome. 0/0

Length=2130

Score = 230 bits (254), Expect = 6e-56

Identities = 254/338 (75%), Gaps = 3/338 (0%)

Strand=Plus/Plus

Query	1194	CCACTCTGCCTGCAACAG---GTCGCTCGAGTCCCCCAGCAACAACATCTCCATCTTTGA 	1250
Sbjct	1768	CCACTCCGCCATCATCAGCGGGTCTGTCCAGTCCTCCAGCAACAACATCCCCATCTTTGA	1827
Query	1251	TTGCATAATCAAACCCCTCTTCTGGTGTTCCGCGAGAAGGCGATACATTGGGGTGGCATC 	1310
Sbjct	1828	TTGCATAGTCGTATCCGCCAGCTGGGCGTCCCCGAGATGGTTCAACATTCGGGTGGTGTC	1887
Query	1311	CTTCAACATCGAATGCACGCGCGTTCCGGGTCTTATATTTGACTCCGAAGTCGACAAAAG 	1370
Sbjct	1888	CTTGACATCGAAGACGCGTACGTTCCGCGTACTAAATTTGACTCCGAAGTCGACGAAAG	1947
Query	1371	CGTGCAGATGAAGACCCCATCTGCGTGATTCTCTCGGCCGATGATGCATTAGCTCCAA 	1430
Sbjct	1948	CATGGAGATGAATTCTTCATCAGCGTGAGTCTCTCGTCCAATGATGCACTCTGCTCTAA	2007
Query	1431	GTCCCGCAAGATGATTGACCACTGCAAAGGGTCGAGGTCTCCACATTGTGGATAGGTGA 	1490
Sbjct	2008	GGCCTGATAGGTGGTCAGACACAGCAAACGGGTCGAGGTCTCCACACTGGGCGTAAGTGA	2067
Query	1491	GCAAGGCGTACCGTGCTTGAAATCGAAAAGAGGACATA 1528 	
Sbjct	2068	GTAAGGCATATCTGGCCTGGAATCTGAATGATGACATA 2105	

Score = 138 bits (152), Expect = 3e-28

Identities = 219/309 (70%), Gaps = 4/309 (1%)

Strand=Plus/Plus

Query	515	ACACCAAGCTCGTCACGTGGGTCGGAGTTAGATAGCCAAATTGAGGGCCGAGCCCAGTGT	574
Sbjct	1092	ACCCCATGCTCCTCGCGTGGGTCCTCATTGTTGATCCATATTGATGGTCTGCCCCATTCA	1151
Query	575	ACCAACTTTTTCCCCTTGTA CTTATCCGTGACGTAGAACTGCTTTTGATGACCTAACCAG	634
Sbjct	1152	ACCAACTTTTTCCCCTTGTA CTTGTCTGTGACGTAAACTGCTTCTGGTGTCCCATCCAA	1211
Query	635	AATTTGT-AGCTGGGAAGGAATTTAATTCCTCCGAAGTCGTCAAAGATGGCGTACTCAAC	693
Sbjct	1212	AATTTGTAAGATGGG-AGGAATTTTAAACCTCCAAAATCATCAAACACCGCATA-TGTGG	1269
Query	694	CCCATC-AAGGTTTTTCGTCCAAGCTAAAGAGGCCTCCGAAGTAAGCATGGTTTCCCAGGC	752
Sbjct	1270	CCGAGCTTATGTCTCTCGTCCATTGAGAAAAGCCCTCCGAAATAGGCATGGTCTCCTAGTG	1329

71/88

```

Query    753      TTCTAGCCCAATGGTTTTTCCCATTCCTGGAAGGCCCGTATACCACAAGTGATTTTCTTC      812
          || ||||| | || ||| ||| || || ||||| || ||||| | ||
Sbjct    1330      ACCTGGCCACACAGTCTTACCCGTTTCGGGTGGACCATATAGCACTAGTGATTTCCTC      1389

Query    813      GTTCTGTAT      821
          | |||
Sbjct    1390      TTACTATAT      1398

```

```
>>>nrnuc:GI_537367981 Gi|537367981|gb|KF371634.1| Gemycircularvirus 8 isolate P21,
complete genome. 0/0
Length=2174
```

Score = 141 bits (156), Expect = 2e-29
Identities = 200/279 (71%), Gaps = 4/279 (1%)
Strand=Plus/Plus

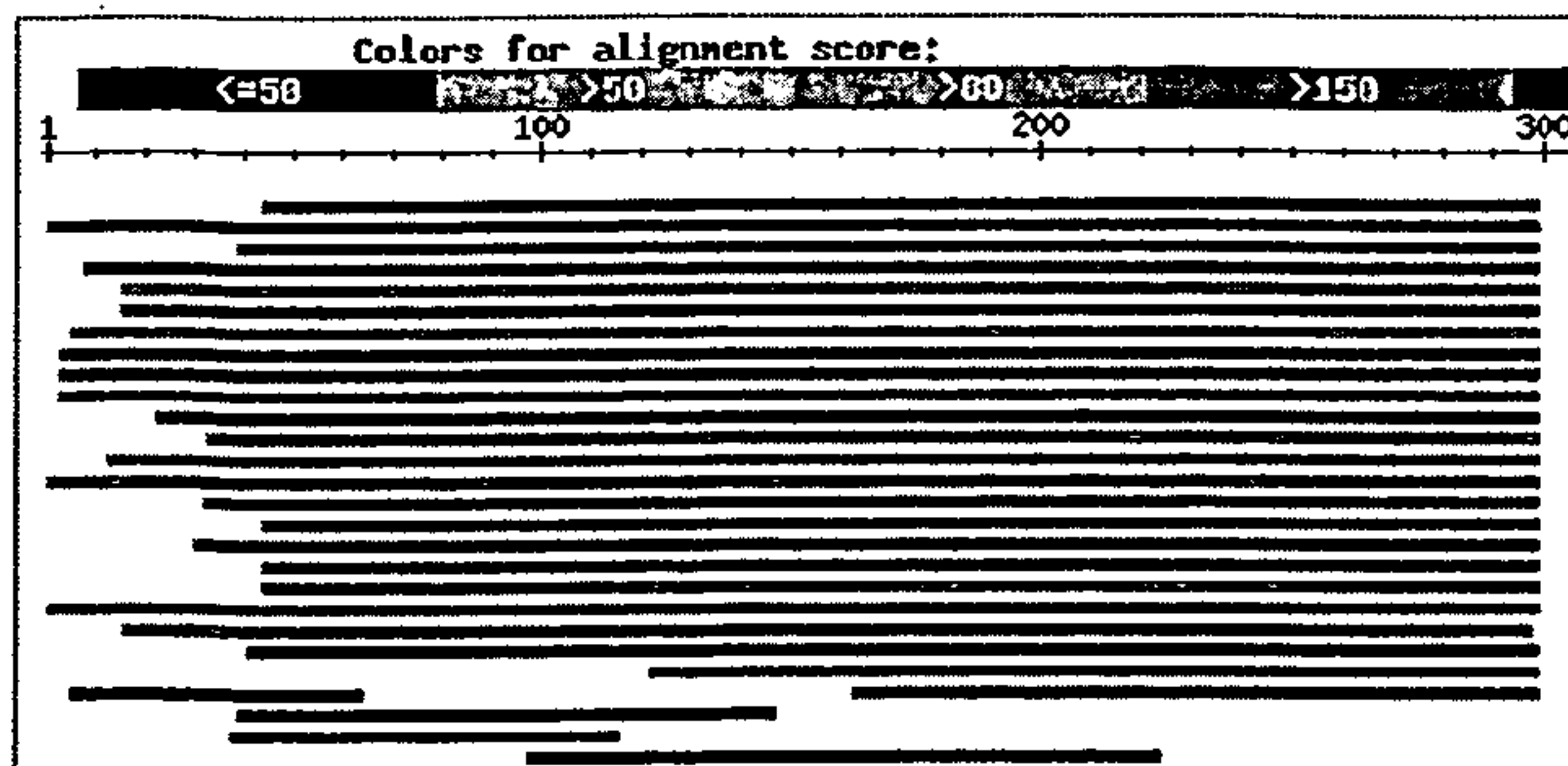
Query	1217	TCGAGTCCCCCAGCAACAACATCTCCATCTTTGATTGCATAATCAAACCCCTCTTCTGGT	1276
Sbjct	1828	TCGAGTCCTCCAGCAACAACATCTCCGTCCTTGATCGCATAAGTTGCACCCTTTTCCGGT	1887
Query	1277	GTTCCGCGAGAAGGCGAT--ACATTTGGGTGGCATCCTTCAACATCGAATGCACGCGCGT	1334
Sbjct	1888	GTT--GAGTAACCGCGTACGACATTTGGGTGGCGTCCGTCCACATCGAATACGCGGACAT	1945
Query	1335	TCCGGGTCTTATATTTGACTCCGAAGTCGACAAAAGCGTGCAGATGAAGACCCCCATCTG	1394
Sbjct	1946	TTCTTGACTCAAACCTCCGTTCGAACATGAAGAAAGCGTGCAGGTGAAGTCCTCCATCAG	2005
Query	1395	CGTGATTCTCTCGGCCGATGATGCATTAGCTCCAAGTCCCAGCAAGATGATTGACCACTG	1454
Sbjct	2006	CGTGCTCTTCTCGGCCAATGATGCACTCAGCTCCCAGGCGTCCAAGATGGTCGTTAACTT	2065
Query	1455	CAAAAGGGTTCGAGGTCTCCACATTGTGGATAGGTGAGCA	1493
Sbjct	2066	CCCAGGGGTTCAGGTCTCCGGACTGGGGGAACGTGAGCA	2104

```
>>>>nrnuc:GI_520689312 Gi|520689312|gb|KF268026.1| Sclerotinia sclerotiorum hypovirulence
associated DNA virus 1 isolate SsSHADV-1_NZ_SR1_2012, complete
genome. 0/0
Length=2166
```

Score = 123 bits (136), Expect = 6e-24
Identities = 193/276 (69%), Gaps = 0/276 (0%)
Strand=Plus/Plus

Query	1220	AGTCCCCCAGCAACAACATCTCCATCTTTGATTGCATAATCAAACCCCTCTTCTGGTGTT	1279
Sbjct	1824	AGGCCCCCACAAATGACATCTCCATCTTTGATCGCGTAGTCATACCCCTTCTCCGAGATC	1883
Query	1280	CCGCGAGAAGGCGATACATTTGGGTGGCATCCTTCAACATCGAATGCACGCGGTTCCGG	1339
Sbjct	1884	CCTCGAGACTTTGTAATGTTTGGGTGGTGACCATCGACATCGAATACATCAGCCTTTCTA	1943
Query	1340	GTCCTATATTTGACTCCGAAGTCGACAAAAGCGTGCAGATGAAGACCCCATCTGCGTGA	1399
Sbjct	1944	CTGCGAAACTTCCGTCCGAACCTTGCAAAGCAGTGTAGGTGAATGCCTCCATCCTCGTGA	2003
Query	1400	TTCTCTCGGCCGATGATGCATTGAGCTCCAAGTCCCGCAAGATGATTGACCACTGCAAAA	1459
Sbjct	2004	TGCTCTCTTCCAATGATGCACTCAGCTCCAGAAGTGAAAGTTTATCCATAACTCGGAAA	2063
Query	1460	GGGTGCGAGGTCTCCACATTGTGGATAGGTGAGCAAG	1495
Sbjct	2064	GCATCGAGCTCTCCACATTGTGCGTATGTGAGCAAG	2099

ORF300aa:



```
>>>sptrembl:G9ITS7_9VIRU G9its7 SubName: Full=Coat protein;.... 159 2e-36
>>>sptrembl:TlytB1_9VIRU Tlytb1 SubName: Full=Capsid protein... 151 4e-34
>>>sptrembl:I0AY94_9VIRU I0ay94 SubName: Full=Capsid protein... 137 8e-30

>>>>sptrembl:G9ITS7_9VIRU G9its7 SubName: Full=Coat protein (Meles meles);. 5/2013
Length=310
Score = 159 bits (401), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 100/271 (36%), Positives = 141/271 (52%), Gaps = 21/271 (7%)
```

```
Query 45 RRVLNITTRKKVDNMLPVVVAEDNTT-TVGPYTSVSPLLSLFVFNARTTRTPVTN--PAV 101
          RR+LN+ + KK DNML +V D T+GP T + SL++P+AR P + +
Sbjct 46 RRILNVASIKKRDNMLSMVQTSQAPPTIGPITVGTGFASLYMPSARPL-GPANDVGEST 104

Query 102 RNSSDIFAVGYRERVRIDLMGGGTFMWRRI VFMLKGSDLRVAMNSSDSGNIPNQLFDQTT 161
          R D F+VGY+ERV++D+ GGG + WRR+VF KG L N + Q F+
Sbjct 105 RQRRDTFSVGYKERVQVDIHGGGVWVWRRRVFTXKGDQL---YNKGEFIGDWTQPFESKA 161

Query 162 EGGCRRVIGPLLGV-----TNARDELQSYVFRGQEDSDWADQFTAPLDTRRITVK 211
          PL GV T + ++ ++ G E DW +FTA + T RITV
Sbjct 162 VKPSPXDPNPL-GVDMVRLIGQPTTEQHNAIRDLIWDGHEGIDWTSEFTAKVSTTRITVL 220

Query 212 SDKLRVIRPGNETGASRLFKFWYPIRRTISYEDDLESDDVVGDR--PFSTAGLRGVGDMYV 269
          SDK PGNE+G SR F+ WYP R+ + Y+DD V R P S +G+GD+ +
Sbjct 221 SDKTYHFNPGNESGMSRTFRLWYPTKRRLIYDDDERGGAVFSRGSPVSVTSRQGMGDLXI 280

Query 270 MDIMGITNLVNDAPPTS YRFGPEG SFYWHER 300
          DI + + P S + PEG++YWHER
Sbjct 281 YDI-AYAVVPSAGNPGSMTWAPEGTYYWHER 310
```

```
>>>>sptrembl:TlytB1_9VIRU Tlytb1 SubName: Full=Capsid protein (Gemycircularvirus 8);. 2/2014
Length=302
Score = 151 bits (381), Expect = 4e-34, Method: Compositional matrix adjust.
Identities = 107/321 (33%), Positives = 161/321 (50%), Gaps = 40/321 (12%)
```

```
Query 1 MSVARR--SGRRTRKAFRRGGRATRSRGRSTRSSRRRVRRRTMTTRRVLNITTRKKVDN 58
          M+ ARR + R RK RR R RRS RR R+R M+TR +LN T++KK DN
Sbjct 1 MAYARRRFTSSRARKPIRRSRRPA-----GKRRSYRRSTRKRGMSRTLLNKTSQKKRDN 55

Query 59 MLPV--VVAED---NTTTVGPYTSVSP----LLSLFV-----PNARTT--RTPVTNP 99
          ML AED T+GP P L + F+ P+ +T R +
Sbjct 56 MLSFSNTTAEDPFSTDYTIGPAVMRRPVGADLPAEFYVWNATGRPHELSTGFRGSKIDT 115

Query 100 AVRNSSDIFAVGYRERVRIDLMGGGTFMWRRI VFMLKGSDLRVAMNSSDSGNIPNQLFDQ 159
          ++R ++ IFAVG +ER++++ + WRRI F K + SD F +
Sbjct 116 SLRTNTTIFAVGLKERIKLETNNSAPWRWRRICFTSKNDYGEADPDESD-----YFRR 168

Query 160 TTEGGCRRVIGPLLGV TNARDELQSYVFRGQEDSDWADQFTAPLDTRRITVKSDKLRVIR 219
          T+ G R LL + +E+ VF GQ + DW TAP++ R ++V D+ R I+
Sbjct 169 TSNGMVR-----LLRAQSQAEEINDDVFDGQRNVDWLSAITAPINRRHVSVHYDRTRTIQ 223

Query 220 PGNETGASRLFKFWYPIRRTISYEDDLESDDVVGDRPFSTAGLRGVGDMYVMDIMGITNLV 279
          GN++G +R ++ W+P+R+ + Y D+ + + D S G G+G+ YVMDI L
Sbjct 224 SGNQSGVTRTYRQWHPMRKNVVYADEQAGEGMVDSGVSVTGKVGMGNYVMDIFTKHGLN 283

Query 280 NDAPPTS YRFGPEG SFYWHER 300
          +D SY PE +F+WHE+
Sbjct 284 DDQSTLSYE--PESTFFWHEK 302
```

>>>>sptrembl:I0AY94_9VIRU I0ay94 SubName: Full=Capsid protein (Cassava associated ssDNA virus);. 7/2012
Length=315
Score = 137 bits (344), Expect = 8e-30, Method: Compositional matrix adjust.
Identities = 94/288 (32%), Positives = 133/288 (46%), Gaps = 37/288 (12%)

Query 40 RTMTTRRVLNITTRKKVDNMLPVVVAEDNTTTVGPTYTSVSPLLS-----LFVP 87
R M+ RR+LNIT+ KK D M + T G S P + L+
Sbjct 38 RKMSKRRILNITSTKKKDTMTGYTNSTPANQTGGTVYSTDPAIVTGGLNANQCNAFLWCA 97

Query 88 NARTTRTPVTNP-----AVRNSSDIFAVGYRERVRLDLMGGGTFMWRRIVFM 134
ART + V NP A R S+ + VG E++ I G + WRRI +
Sbjct 98 TARTNQ--VINPTQNTLVPGNKFYTACRTDSNPYMGVLSEKIEIQNSGMPWQWRRICWT 155

Query 135 LKGSDLRVAMNSSDSGNIPNQLFDQTTEGGCRRVIGPLLGVTNARDE--LQSYVFRGQED 192
KG A ++S + L Q G RV+ + G D+ L ++FRGQ
Sbjct 156 QKGGQGLPANSTSFN-----LSQQNAITGWNRMNVQVAGNPGTGDQYNLFHHIFRGQVG 209

Query 193 SDWADQFTAPLDTRRITVKSDKLRVIRPGNETGASRLFKFWYPIRRTISYEDDLES DVVG 252
SDW D TAPLD + ITVK DK+ + GNE G R ++ W+P+++T+SY D+ +V
Sbjct 210 SDWVDVMTAPLDPQHITVKYDKVVTLASGNEEGFIRAYRRWHPMKKTLSYADEEYGNVEN 269

Query 253 DRPFSTAGLRGVGDMYVMDIMGITNLVNDAPPTS YRFGPEGSFYWHER 300
FS G +G+GD YV+D+ S R P + YWHE+
Sbjct 270 ADAFSQVGKKGMGDYYVLDLFRARQGAQTNDSISIR--PCATLYWHEK 315

ProtSweep
A Protein Identification Tool

Results for /home/vir088/rindneu/gemi/MSSI2.225.300.pep



Number of residues: 300	Molecular weight: 34.10 kD
Charge: 23	Isoelectric point: 11.80

[more...](#)

Prediction of protein localization:

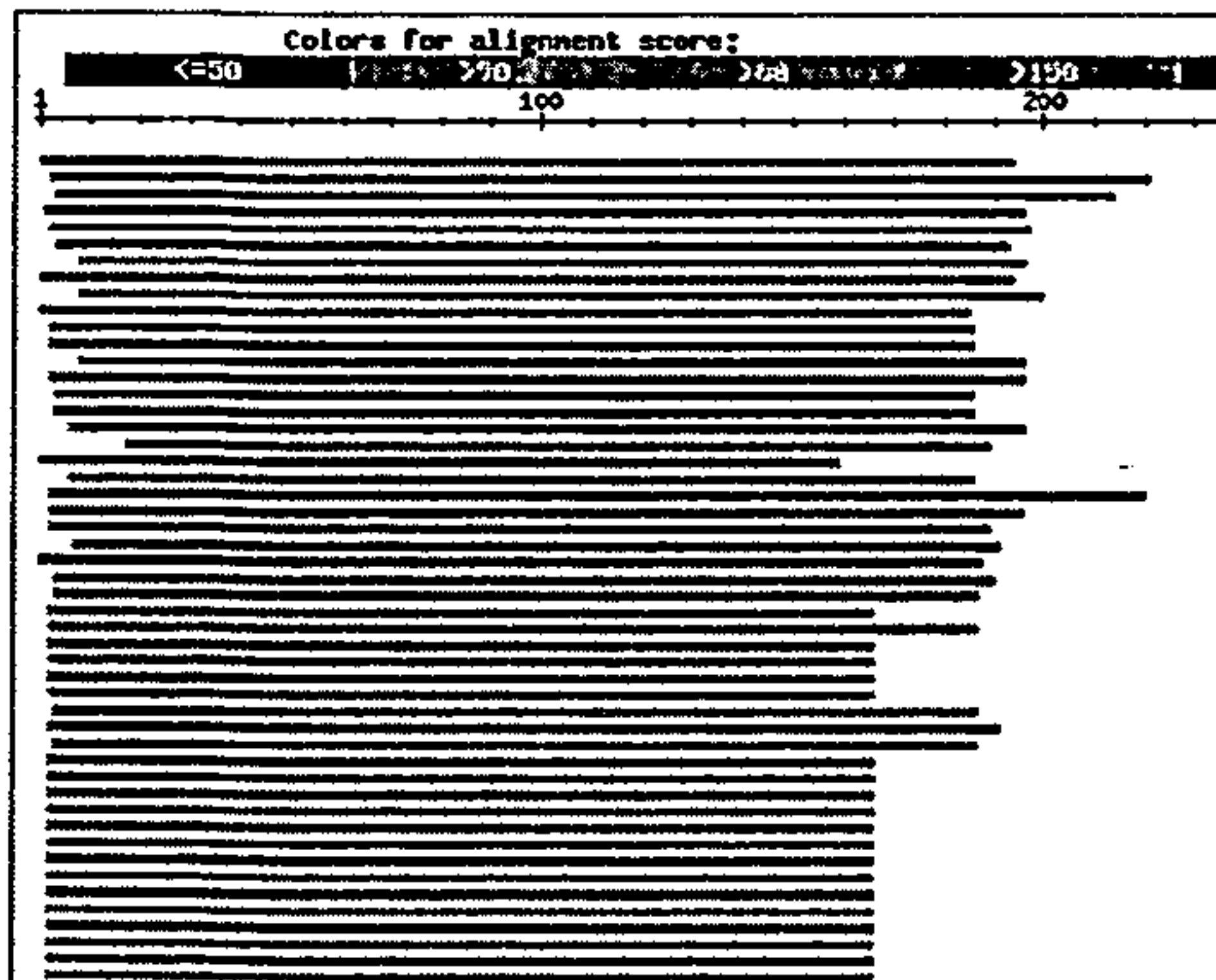
nucl	24 %
mito	7 %



Identified Protein & Transcript:

Protein:
id: sptrembl:T1YTBI_9VIRU
valuation: putative
scientific organism: Gemycircularvirus 8
abstract: T1ytb1 SubName: Full=Capsid protein; 2/2014Length=302
isoform:

ORF 232aa:



>>>sptrembl:Tlysfl_9VIRU Tlysfl SubName: Full=Replication as... 240 3e-61
>>>sptrembl:G9ITS8_9VIRU G9its8 SubName: Full=Replication-as... 225 9e-57
>>>sptrembl:K0A109_9VIRU K0a109 SubName: Full=Replication-as... 218 2e-54

>>>>sptrembl:Tlysfl_9VIRU Tlysfl SubName: Full=Replication associated protein;. 4/2014
Length=325

Score = 240 bits (613), Expect = 3e-61, Method: Compositional matrix adjust.
Identities = 122/198 (61%), Positives = 139/198 (70%), Gaps = 3/198 (1%)

Query 1 MSSFRFQARYALLTYPQCGDLDPFAVVNHLAAGLGAECIIGRENHADGGLHLHAFVDFGVK 60
Sbjct 1 MSSFRFQARYALLTY QCGDLDPFAV +HL+GL AECIIGRE HAD G+HLHAFVDFGVK 60

Query 61 YRTRNARAFDVEGCHPNVSPSRGTPEEGFDYAIKDGDDVAGGLERPVG---RVDATSGV 117
Sbjct 61 FSTRNVRVFDVQGHHPNVEPSRGRPAGGYDYAIKDGDDVAGGLDRPADGGVGVSKTQK 120

Query 118 WAEIINAESEQEFWDLCKRLAPRSLVTSFTQLRAYAAWKFPPIRVVPYETPEGVNIDTSWV 177
Sbjct 121 WATIVGAQTRDEFWALLAELDPGAMVRSFTQCRAYADHRFRESPEYVTPESIIIDTGHV 180

Query 178 AELNQWVQQLGRGETGG 195
LN+W N+ GG
Sbjct 181 DGLNEWALSNIIVGHRRGG 198

>>>>sptrembl:G9ITS8_9VIRU G9its8 SubName: Full=Replication-associated protein;. 4/2014
Length=237

Score = 225 bits (574), Expect = 9e-57, Method: Compositional matrix adjust.
Identities = 118/223 (52%), Positives = 148/223 (66%), Gaps = 10/223 (4%)

Query 3 SFRFQARYALLTYPQCGDLDPFAVVNHLAAGLGAECIIGRENHADGGLHLHAFVDFGVKYR 62
Sbjct 5 TFRSQRYVLLTYAQCGLDLPVHNHVVAFPAECIIGRENHADGGIHLHAFVDFGKRV 64

Query 63 TRNARAFDVEGCHPNVSPSRGTPEEGFDYAIKDGDDVAGGLERPVGGRVDA-TSGVWAEI 121
Sbjct 65 IRDNRRFDVEGFHPNIAPCGRTPQKMLDYAIKDGDDVAGGLN-PILDLPDAETDSIWHRI 123

Query 122 INAESEQEFWDLCKRLAPRSLVTSFTQLRAYAAWKFPPIRVVPYETPEGVNIDTSWVAELN 181
Sbjct 124 ANAPSVDEFWAIITRELAPRALLCNHQSRLRAYAEWHYRPVATRYEHPHGLSLRTHVPQLD 183

Query 182 QWVQQLGRGETGGKLSCTSQRQLQSAATRSMGGG--LAQRL 222
+WV+ NL +G S T R SA+ RAS+ GG L Q L
Sbjct 184 EWVRDNL----SGSSKSYTYTR--SASGRASLPSGGPSLVQSL 220

>>>>sptrembl:K0A109_9VIRU K0a109 SubName: Full=Replication-associated protein;. 4/2014
Length=249

Score = 218 bits (554), Expect = 2e-54, Method: Compositional matrix adjust.
Identities = 114/213 (53%), Positives = 139/213 (65%), Gaps = 2/213 (0%)

Query 4 FRFQARYALLTYPQCGDLDPFAVVNHLAAGLGAECIIGRENHADGGLHLHAFVDFGVKYRT 63
Sbjct 3 FRFAAKYGLLTYPQCGDLDPWAVNDMLGRLGAECVIGRENHQAGGVHLHAFVDFGVK 62

Query 64 RNARAFDVEGCHPNVSPSRGTPEEGFDYAIKDGDDVAGGLERPVA-GRVDATSGVWAEI 122

Sbjct 63 RN R FDV+G HPN+ TPE+G+ YA KDGDVVAG LE P V +S WA I
RNVRVFDVDGHPNIVRGYSTPEDGWAYATKDGDVVAGALECPRPRTEVSESSSKWARAI 122

Query 123 NAESEQEFWDLCKRLAPRSLVTSFTQLRAYAAWKFPPIRVPYETPEGVNIDTSWVAELNQ 182
AE+ +EF+ + L PR+L SF LRAYA WK+ P R PY TPEG++ DTS + EL+

Sbjct 123 LAETREEFFAIVAELDPRALCVSFGSLRAYADWKYRPARDPYITPEGISFDTSELPELDL 182

Query 183 WVQQNLGRGETGGKLSCTSQRQLQSAATRASMLG 215
WVQQ L G + GK S L+ + S G

Sbjct 183 WVQQTLS-GLSTGKQPPPSAPLRGVPEQISARG 214

ProtSweep
A Protein Identification Tool

Results for /home/vir088/rindneu/gemi/MSSI2.225.232r.pep



Number of residues: 232	Molecular weight: 25.37 kD
Isoelectric point: 7.34	

[more...](#)

Prediction of protein localization:

cyto_nucl	12.1667 %
cyto	11 %
nucl	9 %



Identified Protein & Transcript:

Protein:
id: sptrembl:G9ITS8_9VIRU
valuation: weakly similar
scientific organism: Meles meles
abstract: G9its8 SubName: Full=Replication-associated protein; 4/2014Length=237
Isoform:

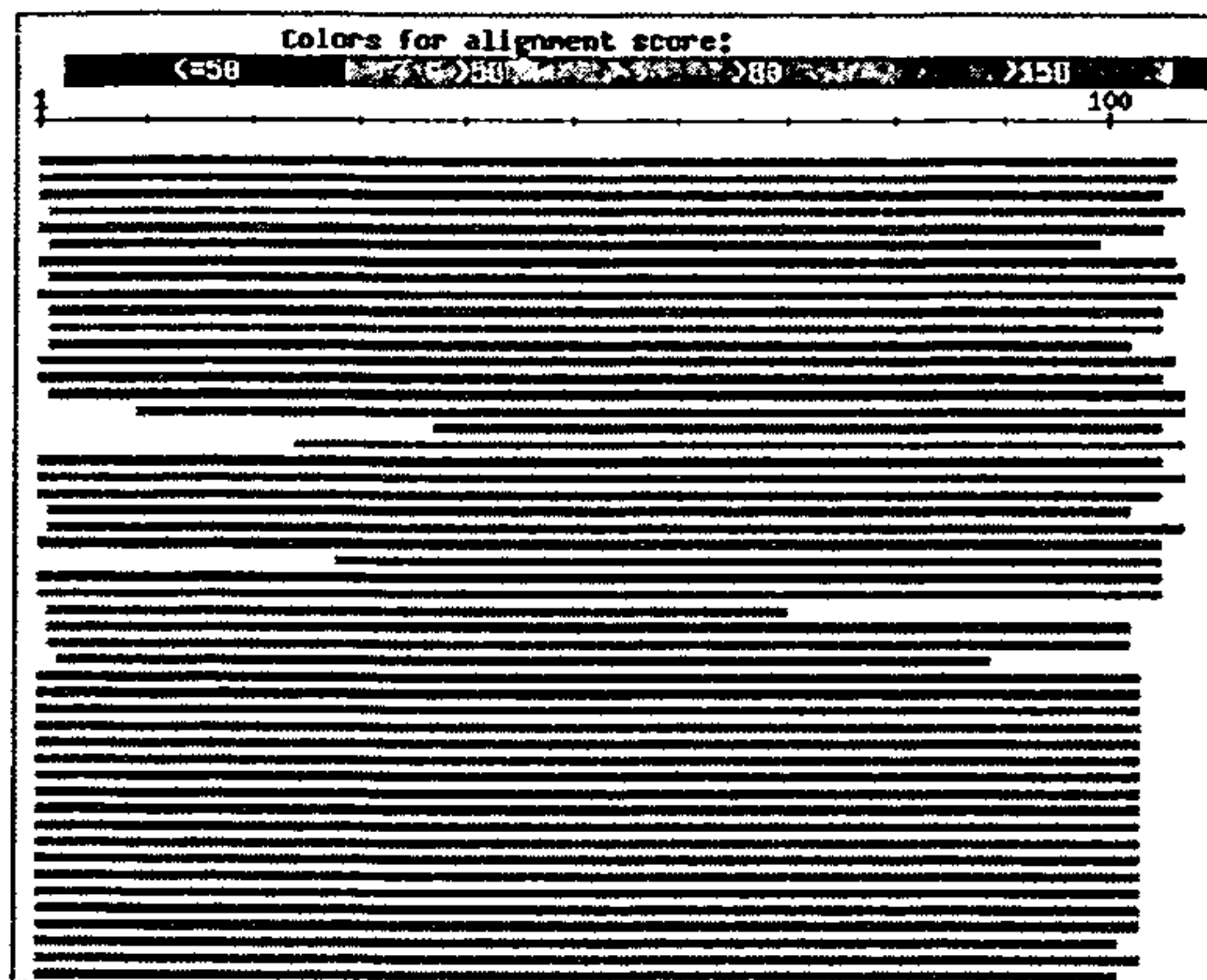


GO INFORMATION:

ACCESSION	GROUP	NAME	EVIDENCE
GO:0016888	molecular function	endodeoxyribonuclease activity, producing 5'-phosphomonoesters	IEA:InterPro
GO:0006260	biological process	DNA replication	IEA:InterPro

INTERPRO INFORMATION:

ID	SHORT NAME
IPR022690	Gemini_ALI_REP_cat-dom
IPR022692	Gemini_ALI_REP_central

ORF 108aa:

```
>>>sptrembl:T1YSF1_9VIRU Tlysfl SubName: Full=Replication as... 174 1e-41
>>>sptrembl:T1YRW0_9VIRU Tlyrw0 SubName: Full=Replication as... 151 1e-34
>>>sptrembl:K0A1L7_9VIRU K0a1l7 SubName: Full=Spliced replic... 149 5e-34
```

```
>>>>sptrembl:T1YSF1_9VIRU Tlysfl SubName: Full=Replication associated protein
(Gemycircularvirus 9);. 4/2014
Length=325
Score = 174 bits (441), Expect = 1e-41, Method: Compositional matrix adjust.
Identities = 79/110 (71%), Positives = 92/110 (83%), Gaps = 3/110 (2%)
```

```
Query 1 MGKTIWARS LGNHAYFGGLFSLDENLDGVEY AIFDDF GGIKFLPSYKFWLGHQKQFYVTD 60
      GKT+WARS LG+HAYFGGLFS+DE++ YA+FDDF GGIKFLPSYKFW+GHQKQFYVTD
Sbjct 211 TGKTVWARS LGDHAYFGGLFSMDEDISSATYAVFDDF GGLKFLPSYKFWMGHGHQKQFYVTD 270

Query 61 KYKGKKLVHWARPSIWLSNSDPRDELGV---DTEWLNANCDFVYLDSPIV 107
      KYKGKKLV W RPSIW++N DPR+E GV +EWL NC F+ LDS IV
Sbjct 271 KYKGKKLVEWGRPSIWINNEDPREEHGVRCD EIEWLEQNCIFIRLDSTIV 320
```

```
>>>>sptrembl:T1YRW0_9VIRU Tlyrw0 SubName: Full=Replication associated protein;. 2/2014
Length=320
```

```
Score = 151 bits (381), Expect = 1e-34, Method: Compositional matrix adjust.
Identities = 70/108 (64%), Positives = 87/108 (80%), Gaps = 1/108 (0%)
```

```
Query 1 MGKTIWARS LGNHAYFGGLFSLDENLDGVEY AIFDDF-GGIKFLPSYKFWLGHQKQFYVT 59
      +GKT+WARS LGNHAYFGGLFSL+E L+GV+YAIFDD GG+KF SYKFWLG Q QF+ T
Sbjct 208 LGKTLWARS LGNHAYFGGLFSL EEELEGVDY AIFDDMQGGLKFFHSYKFWLGAQSQFWAT 267

Query 60 DKYKGKKLVHWARPSIWLSNSDPRDELGV DTEWLNANCDFVYLDSPIV 107
      DKY+GKKL+HW RPSI++ N +P +GVD +WL NCDFV + ++
Sbjct 268 DKYRGKKLIHWGRPSIYICNQNP L CDEGVDHDLIGNCDFVEITESLL 315
```

```
>>>>sptrembl:K0A1L7_9VIRU K0a1l7 SubName: Full=Spliced replication-associated protein;.
4/2014
Length=318
```

```
Score = 149 bits (376), Expect = 5e-34, Method: Compositional matrix adjust.
Identities = 67/107 (62%), Positives = 87/107 (81%), Gaps = 1/107 (0%)
```

```
Query 1 MGKTIWARS LGNHAYFGGLFSLDENLDGVEY AIFDDF-GGIKFLPSYKFWLGHQKQFYVT 59
      +GKT+WARS LG HAYFGGLF LDE+L+ V+YA+FDD GG++F +YKFWLG QKQFY T
Sbjct 206 LGKTLWARS LGRHAYFGGLFCLDESLEDVDYAVFDDMQGGL EFFFHAYKFWLGAQKQFYAT 265

Query 60 DKYKGKKLVHWARPSIWLSNSDPRDELGV DTEWLNANCDFVYLDSP I 106
      DKY+GK+LV+W RPSI++SN++P +G D +WL NC V++D P I
Sbjct 266 DKYRGKQLVNWGRPSIYISNTNPLADKGADVDWLMGNCVIVHVD RPI 312
```

ProtSweep

A Protein Identification Tool

Results for /home/vir088/rindneu/gemi/MSSI2.225.108r.pep

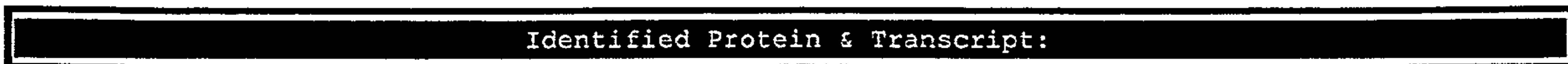


Number of residues: 108	Molecular weight: 12.46 kD
Charge: -3	Isoelectric point: 5.63

[more...](#)

Prediction of protein localization:

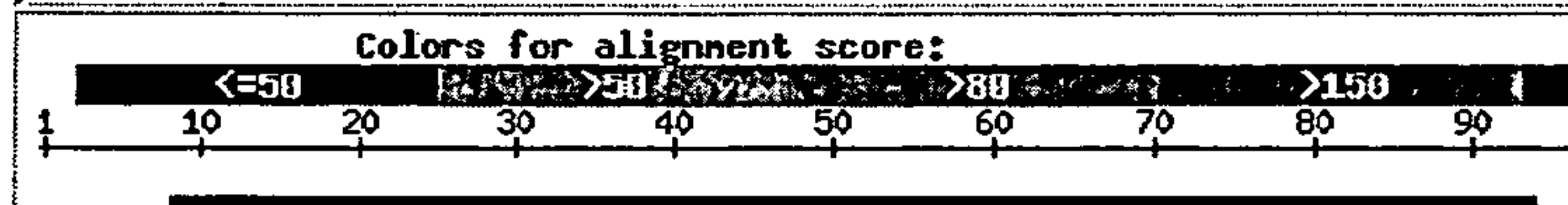
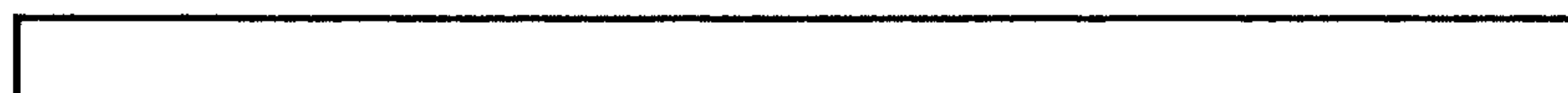
mito	11 %
cyto	10.5 %
cyto_nucl	10 %



Identified Protein & Transcript:

Protein:
id: sptrembl:S6DDT1 9GEMI
valuation: putative.
scientific organism: Euphorbia caput-medusae
abstract: S6ddt1 SubName: Full-Replication associated protein;. 12/2013Length=130
isoform:

ORF 95aa:



>>>sptrembl:V8NBT2 OPHHA V8nbt2 SubName: Full=Putative E3 ub... 35.4 8.8

>>>>sptrembl:V8NBT2_OPHHA V8nbt2 SubName: Full=Putative E3 ubiquitin-protein ligase HERC6;
Flags: Fragment;. 4/2014
Length=735Score = 35.4 bits (80), Expect = 8.8, Method: Composition-based stats.
Identities = 31/95 (32%), Positives = 47/95 (49%), Gaps = 12/95 (12%)

```
Query 9 TSSGVRKILIGQISLLPPLILVALRLSPTNSASSAPVMKQVLRACLSFGTPFVPSL--- 65
      TSSGV+ +L SLL L L R SP A + + V C++ G +PSL
Sbjct 302 TSSGVKIVLTIDSSLLDHLFLALPRSSPHQEALA--IFLLVPECCVALGA-CRIPSLALR 358

Query 66 -----TKMTLSPTLSVIGPFLPQVYEVLGICTSWI 95
      T ++ + +++GPFL Q+ ++L C S I
Sbjct 359 FAEAVTGLSKGSS-NILGPFLEQIVQMLKTCVSAI 392
```

MSSI1.162 (1627bp)***(MSSI = Multiple sclerosis serum isolate)******(ms24.RCA.1700.3)***

GACTTCTGATTGATTGATGCCTGCCGACTTTTGATAATTTTTTGATAGATGATTTTTCTTGACTGAAATAAAAAACCCCTTA
 TTGTTGTAAGTGCTTGGTTCACAACTTAATAAGAGGTTTTAATTATGATGTCACATGATGGCACACCTGTCAATTTTTGTCC
 GATATTCAACCCAGTGAGAAAAGCTGGGACACTCACCGAGCCGAAGCCGAAAGCGTCCGATTGCTTTACAGTCTTTCGACTGA
 GTTCACCAAATACGCTAGCCGTATTTATGACTGTTCCCAAATCCTAAAATTTGCCCTACCCCTGATAAGCTGGTACTTAAAC
 ACGCCTTTTTCTGTCGTGTTAGGTATTGCCCTGTTTGCCAGTGGCGTAGGTCGTTATTATGGCGGGCGGTGATGTTTCAGCAG
 TTACCAGCAATCAAAGAGAAGTACCCTAGTTATCGTTGGGTGTTTCTTACCCTTACTGTCAAAAATCCCCCAGTTACTGAATT
 AAGGGACACCTTAAAGGCTATGAATTCAGCTTGGCAACGCCTAGCACAACTAAACGCTTTAAAGGGGTCGTTAAAGGCTTTA
 TTCGCACAACCGAAGTTACAAGGGGTAAAGATGGCGACATGATGGCTCACCCCATTTCCATGCGCTGTTATTAGTTCAAAGT
 AATTATTTCACTACAAATTATATTAAACAAAATGATTGGGTGAAATGTGGCAAAGGCGTTAAGGGTCGATTATGCCCCATC
 GGTCAACGTAAAAGCCGTAAACCCCTAAAAAGGGTGAAAAGGATAATCTCGATAAGGCGATATGTGAAACGCTCAAATATA
 GCGTTAAACCGTCTGATATTGCCAAAGATGACGATGGGGGCGAATGGTTGCATGAAATGACCAGACAAACCCTAAATATGCGT
 TTTATTGCCACTGGTGGCATTTTGAAGGGTGTACTTAAACCCGATGAGCAAGTAACACAACAAGAAATGCTTACCCCACTGG
 TGAAGATGAAGCACCAACCGAACAACGATTTGGATTTAGATTTTACCCCATCATGGGCGTTATGTTTTTCGCCAGCTA
 TACGAATTTTTGACTTGCTGTTTTTGCAAGTCGTAAGTTCGCCCTTATAGCAAATGTGTTGTGCCTGTAAGTGCTGTAAGGCA
 TATCCAGCGTTAGCAATAAACGGCTTTATCGTTTATTGCGTTAGCGTCTTTATATCCCCAACCTTTCCCCCTTTGAAGTCCCA
 GCTTTTTTTTTGTGGCTGTTCTATTGTTGCTCTTTATTGACCTTACGCCACATAAAAAAAGTGGGTACATATCGGTGAATTT
 GGGTTGCAATAGTCTAGGGACATTCAAAAATAATCCTTCTTGGTAGTATTACGAAATCTCATGTAATCCGCATTGGTGGCGGT
 TTACCCAAAAACAACCAAGAAAAATTCGTCTTGCGAATTTTTATTGCTTTTTGCTTTTTGGGGTATAAAAACCTATAGAAA
 AACTATAAAAAACCTATAGAATTATAGGTGCTTACTGGGGGTTGCCTTGATTTATTATTAAGGGATAACTCTGATTTTATT
 TTATATGATTTTTTATACTGGCAAACCTGTTGAATACCGCTTAAATACT .

No repeat

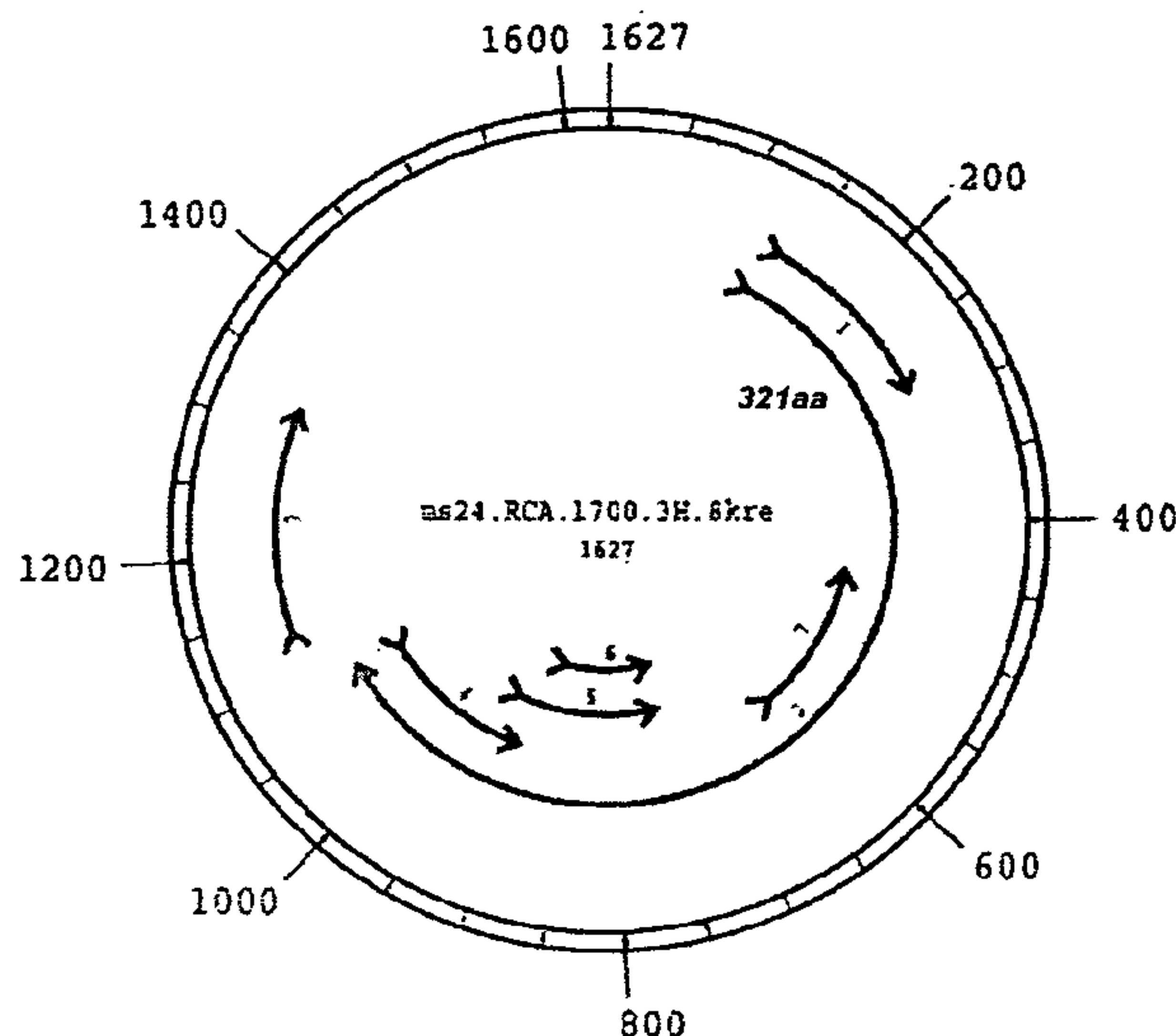
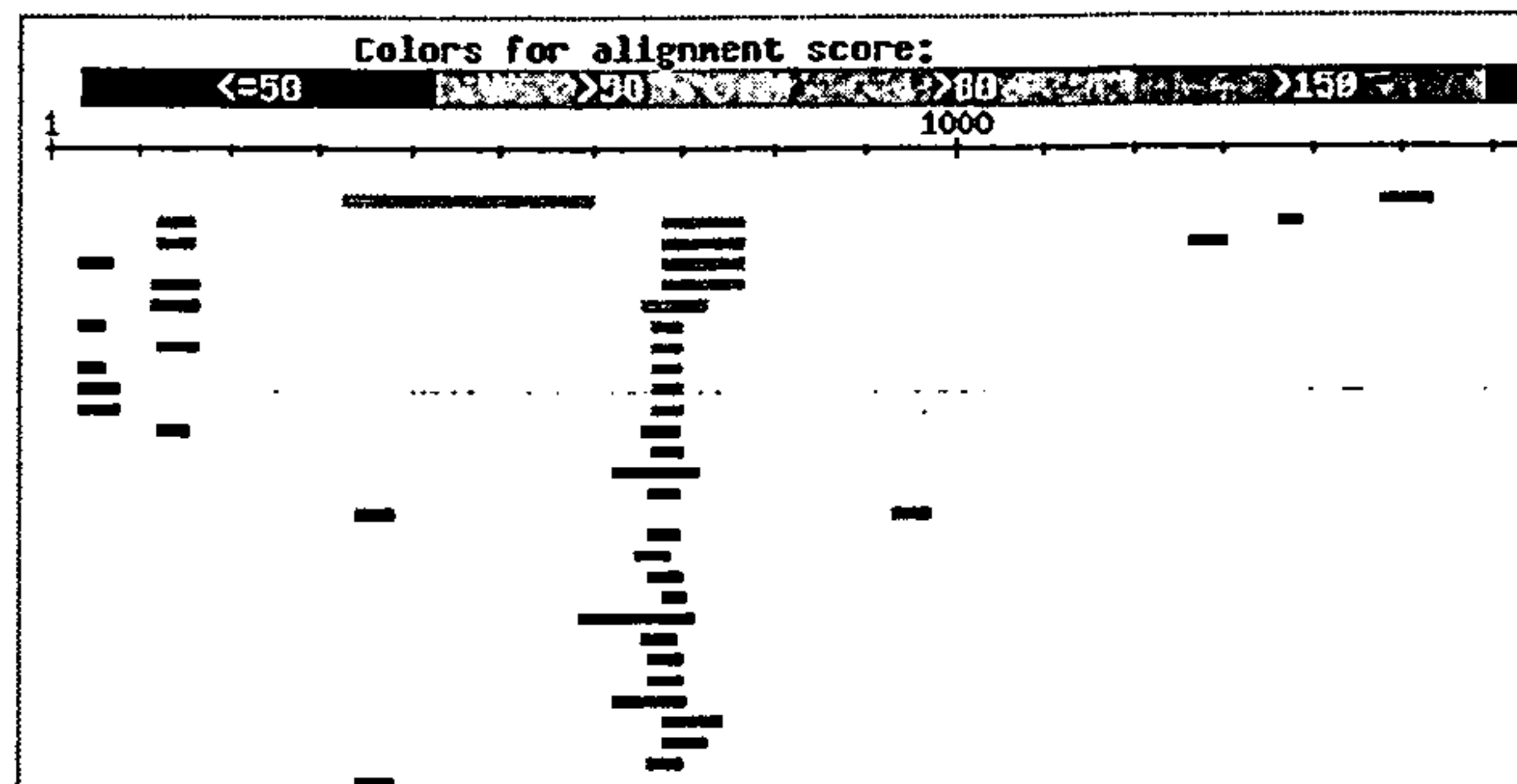
***66% nucleotide similarity to Psychrobacter sp. PRwf-1 plasmid pRWF102,******ORF – 321aa – replication protein 62% similarity to Acetivibacter generi MTCC9824.******This isolate was generated by restriction enzyme EcoRI digestion of the DNA sample after rolling circle amplification.***

Figure 4

Blastn – Geall:

>>>nrnuc:GI_148573295 Gi|148573295|gb|CP000715.1| Psychrobac... 77.0 6e-10
>>>nrnuc:GI_27462698 Gi|27462698|gb|AF459640.1| Lactobacillu... 60.8 5e-05

>>>>nrnuc:GI_148573295 Gi|148573295|gb|CP000715.1| Psychrobacter sp. PRwf-1 plasmid
pRWF102, complete sequence. 0/0
Length=2117

Score = 77.0 bits (84), Expect = 6e-10
Identities = 183/274 (66%), Gaps = 2/274 (0%)
Strand=Plus/Minus

```
Query 329 AAACACGCCCTTTTCTGTCGTGTTAGGTATTGCCCTGTTGCCAGTGGCGTAGGTCGTTA 388
      ||||| ||||| || ||||| | || ||| | ||||| ||||| ||||| |||||
Sbjct 1356 AAACAAGCCTTTTTCGCCGTGTTCTGTTACTGCGGTATGTGCCAATGGCGTAGGTCATTA 1297

Query 389 TTATGGCGGGCGGTCATGTTTCAGCAGTTACCA-GCAATCAAAGAGAAGTACCCTAGTTA 447
      | ||| || || |||| | | ||| | ||| | ||| ||| ||| |
Sbjct 1296 CTCTGGAAGCCTTGATGTAT-AAAACATACGATGAAATTATGCAGACACACCCGACACA 1238

Query 448 TCGTTGGGTGTTTCTTACCCTTACTGTCAAAAATCCCCAGTTACTGAATTAAGGGACAC 507
      ||| | ||||| || ||||| || ||||| || || ||| || || || ||
Sbjct 1237 TCGCTTTGTGTTTTTAACCCTGACGCTTAAAAATCCGCCTATCGGTGACTTGCGCGAAAC 1178

Query 508 CTTAAAGGCTATGAATTCAGCTTGGCAACGCCCTAGCACAACTAAACGCTTTAAAGGGGT 567
      ||| || ||||| || || ||||| || || || ||| ||||| || ||
Sbjct 1177 CTTGCAGCACATGAATAAATCATGGCAACGCTTAAAGATCGTAAAGAATTTATAGCAGG 1118

Query 568 CGTTAAAGGCTTTATTCGCACAACCGAAGTTACA 601
      |||| |||| | || ||||| ||||| |||
Sbjct 1117 CGTTGAAGGTTGGGTACGCACAACGGAAGTCACA 1084
```

>>>>nrnuc:GI_27462698 Gi|27462698|gb|AF459640.1| Lactobacillus paraplantarum plasmid
pC7, complete sequence. 0/0
Length=2134

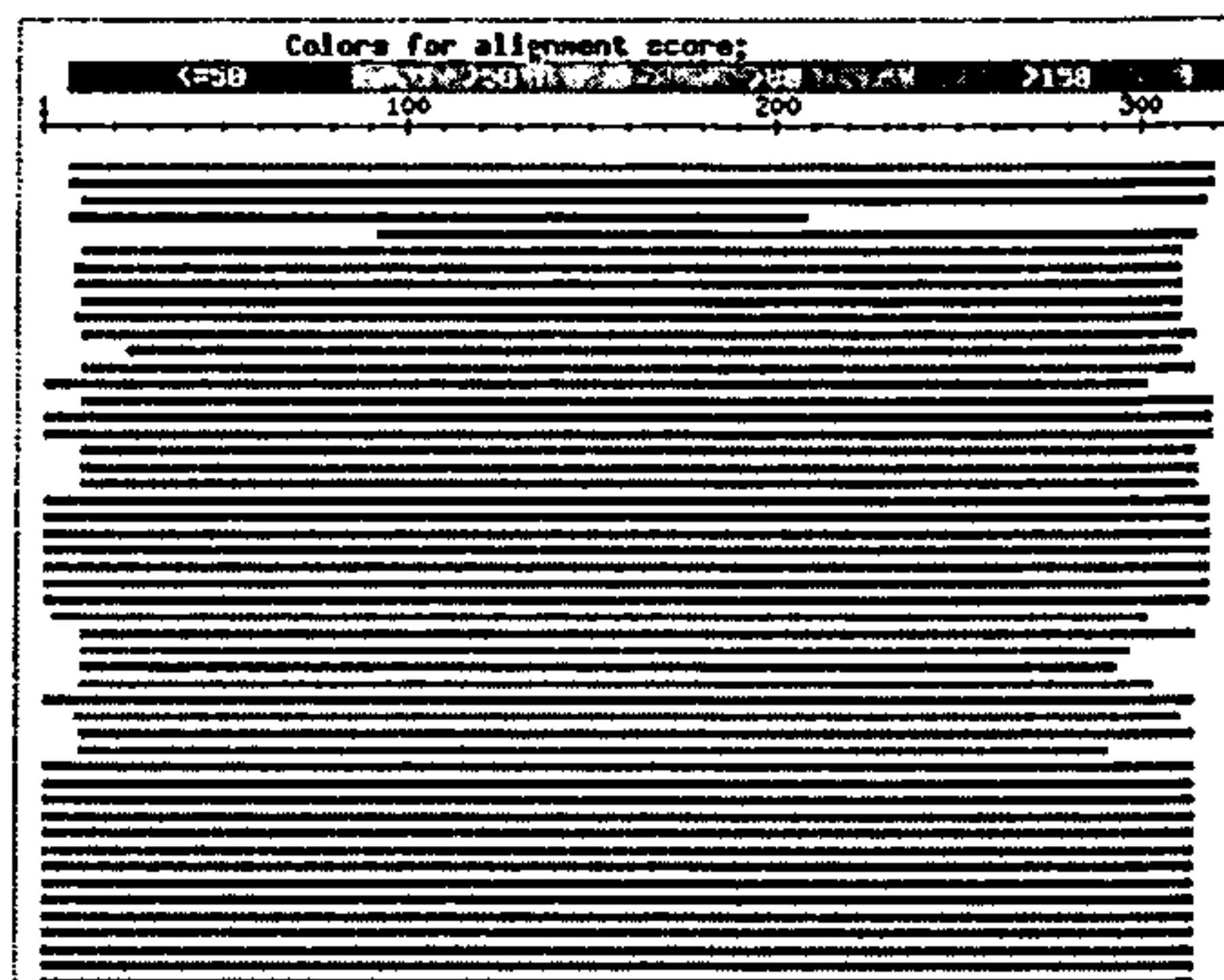
Score = 60.8 bits (66), Expect = 5e-05
Identities = 69/90 (76%), Gaps = 2/90 (2%)
Strand=Plus/Plus

```
Query 680 AATTATATTAAACAAAATGATTGGGTCGA-AATGTGGCAAAGGCGTTAAGGGTCGATTA 738
      ||||| ||||| ||| || || || || || ||||| ||||| ||||| |||||
Sbjct 1248 AATTATATTAATCAAGAAGAAT-GGACGAGACTGTGGCGAAAGGCGTTAAAAGTCGATTA 1306

Query 739 TGCCCCATCGGTCAACGTAAAAGCCGTTAA 768
      || ||| ||| || || || |||||
Sbjct 1307 TGAGCCAGTGGTGCATGTGCAAGTCGTTAA 1336
```

ORF 321aa

BlastP – Uniprot:



>>>sptrembl:S7XX00_9GAMM S7xx00 SubName: Full=Replication pr... 425 1e-116
>>>sptrembl:N9KWE3_ACIBA N9kwe3 SubName: Full=Uncharacterize... 425 1e-116

>>>>sptrembl:S7XX00_9GAMM S7xx00 SubName: Full=Replication protein;. 12/2013
Length=328

Score = 425 bits (1093), Expect = 1e-116, Method: Compositional matrix adjust.
Identities = 197/316 (62%), Positives = 246/316 (77%), Gaps = 4/316 (1%)

Query 9 VNFLSDIQPSEKSWDTHRAEAEVRLLYSLSTEF TKYASRIYDCSQILKFAPTPD--KLV 66
+NFL++I P E SWD HR++AESV++LY+ S E KYA RI CS ILKF +P+ KLV
Sbjct 12 INFLTEISPHEVSWDEHRSDAESVKILYNYSVELAKYADRINGCSGILKFGVSPNQGLV 71

Query 67 LKHAFRCRVRYCPVCQWRRSLLWRAVMFQQLPAIKEKYPSYRWVFLTTLTVKNPPVTEL RD 126
LK AFFCRVR+CPVCQWRRSLLWRAVMFQQLP I++ YP++RWVFLT+TV+NPP+ ELRD
Sbjct 72 LKQAFFCRVRHCPVCQWRRSLLWRAVMFQQLPKIQKLYPTHRWWVFLTMTVRNPPIELRD 131

Query 127 TLKAMNSAWQRLAQTKRFGVVGKFIRTTTEVTRGKDGDMMAHPHFHALLLVQSNYFTTNY 186
TLK MN +WQRL QTK FK V GFIRTTTEVTRGKD +MM+HPH+HALLLV+ YF+ Y
Sbjct 132 TLKHMNESWQRLIQTKAFKSGVAGFIRTTTEVTRGKDAEMMSHPHYHALLLVKPGYFSKYY 191

Query 187 IKQNDWVEMWQKALRVDYAPSVNVKAVKPP--KKGEKDNLDKAICETLKYSVKPSDIKDD 245
I Q++WVEMW KALR DY PSNVKA++ + K L+K ICETLKYSVKPSD+A +
Sbjct 192 INQSEWVEMWAKALRADYLPVNVKAIRAGNNEKSKKALEKQICETLKYSVKPSDLAVER 251

Query 246 DGGEWLHEMTRQTLNMRFIATGGILKGVLKPDEQVTQQEMLTPTGEDEAPTEQKRIGFRF 305
D G WLHEMT+Q MRF+ATGG+LKG+LKP++++T +EM++ + E E E R+ F+F
Sbjct 252 DKGAWLHEMTKQVHKMRFVATGGVLKGILKPDEITNEEMISSSEETEDVGE-GRVAFQF 310

Query 306 YPHHGRYVFSPAHTNF 321
+ RYV++P +
Sbjct 311 NSEYRRYVYAPKFNEY 326

>>>>sptrembl:N9KWE3_ACIBA N9kwe3 SubName: Full=Uncharacterized protein;. 12/2013
Length=328

Score = 425 bits (1093), Expect = 1e-116, Method: Compositional matrix adjust.
Identities = 197/316 (62%), Positives = 246/316 (77%), Gaps = 4/316 (1%)

Query 9 VNFLSDIQPSEKSWDTHRAEAEVRLLYSLSTEF TKYASRIYDCSQILKFAPTPD--KLV 66
+NFL++I P E SWD HR++AESV++LY+ S E KYA RI CS ILKF +P+ KLV
Sbjct 12 INFLTEISPHEVSWDEHRSDAESVKILYNYSVELAKYADRINGCSGILKFGVSPNQGLV 71

Query 67 LKHAFRCRVRYCPVCQWRRSLLWRAVMFQQLPAIKEKYPSYRWVFLTTLTVKNPPVTEL RD 126
LK AFFCRVR+CPVCQWRRSLLWRAVMFQQLP I++ YP++RWVFLT+TV+NPP+ ELRD
Sbjct 72 LKQAFFCRVRHCPVCQWRRSLLWRAVMFQQLPKIQKLYPTHRWWVFLTMTVRNPPIELRD 131

Query 127 TLKAMNSAWQRLAQTKRFGVVGKFIRTTTEVTRGKDGDMMAHPHFHALLLVQSNYFTTNY 186
TLK MN +WQRL QTK FK V GFIRTTTEVTRGKD +MM+HPH+HALLLV+ YF+ Y
Sbjct 132 TLKHMNESWQRLIQTKAFKSGVAGFIRTTTEVTRGKDAEMMSHPHYHALLLVKPGYFSKYY 191

Query 187 IKQNDWVEMWQKALRVDYAPSVNVKAVKPP--KKGEKDNLDKAICETLKYSVKPSDIKDD 245
I Q++WVEMW KALR DY PSNVKA++ + K L+K ICETLKYSVKPSD+A +
Sbjct 192 INQSEWVEMWAKALRADYLPVNVKAIRAGNNEKSKKALEKQICETLKYSVKPSDLAVER 251

Query 246 DGGEWLHEMTRQTLNMRFIATGGILKGVLKPDEQVTQQEMLTPTGEDEAPTEQKRIGFRF 305
D G WLHEMT+Q MRF+ATGG+LKG+LKP++++T +EM++ + E E E R+ F+F
Sbjct 252 DKGAWLHEMTKQVHKMRFVATGGVLKGILKPDEITNEEMISSSEETEDVGE-GRVAFQF 310

Sbjct 252 DKGAWLHEMTKQVHKMRFVATGGVLKGILKPDDEITNEEMISSSEETEDVGE-GRVAFQF 310
Query 306 YPHHGRYVFSPAHTNF 321
+ RYV++P +
Sbjct 311 NSEYRRYVYAPKFNEY 326

>>>>sptrembl:A5WI54_PSYWF A5wi54 SubName: Full=Uncharacterized protein;. 3/2014
Length=377

Score = 311 bits (796), Expect = 3e-82, Method: Compositional matrix adjust.
Identities = 151/331 (45%), Positives = 216/331 (65%), Gaps = 23/331 (6%)

ProtSweep

A Protein Identification Tool

Results for /home/vir088/rindneu/tsekompl/MSSI1.162.321.pep

Number of residues: 321 Molecular weight: 37.27 kD
Charge: 12 Isoelectric point: 10.10
more...

Prediction of protein localization:

cyto	24 %
cyto_nucl	16.5 %
nucl	5 %

Identified Protein & Transcript:

Protein:

id: sptrembl:H4VAM4 ECOLX

valuation: weakly similar

scientific organism: Escherichia coli

abstract: H4vam4 SubName: Full=Replication family protein;. 4/2013Length=322

isoform:

GO information:

accession	group	name	evidence
GO:0005727	cellular component	extrachromosomal circular DNA	IEA:InterPro
GO:0003677	molecular function	DNA binding	IEA:InterPro
GO:0006260	biological process	DNA replication	IEA:InterPro

Interpro information:

id	short name
IPR000989	Rep

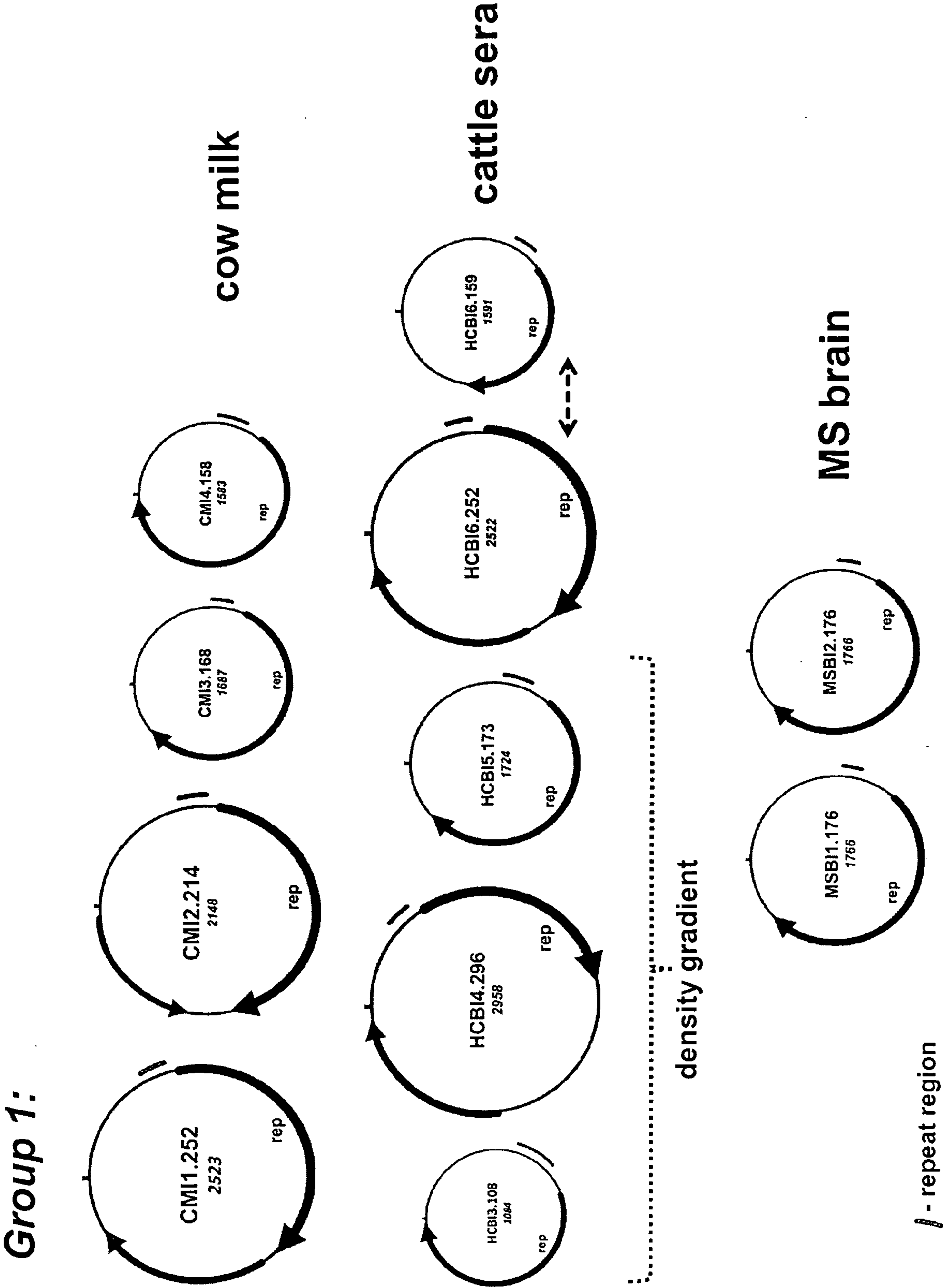
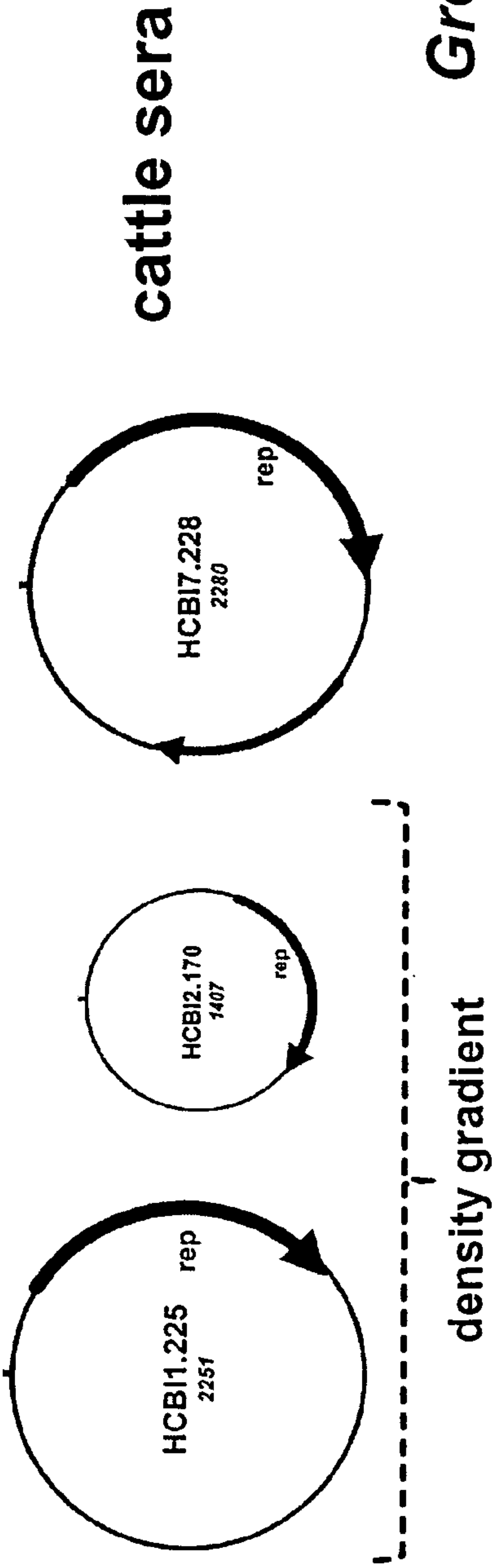
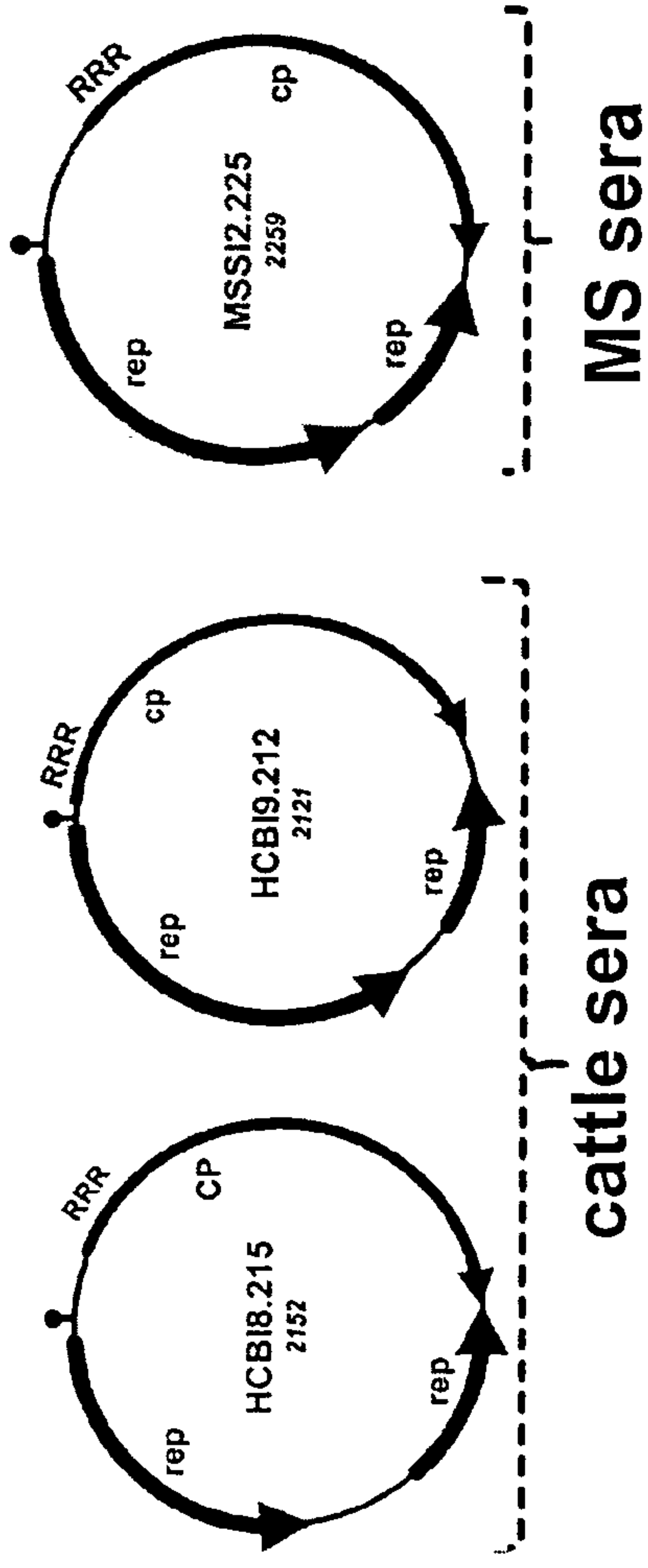


Figure 5

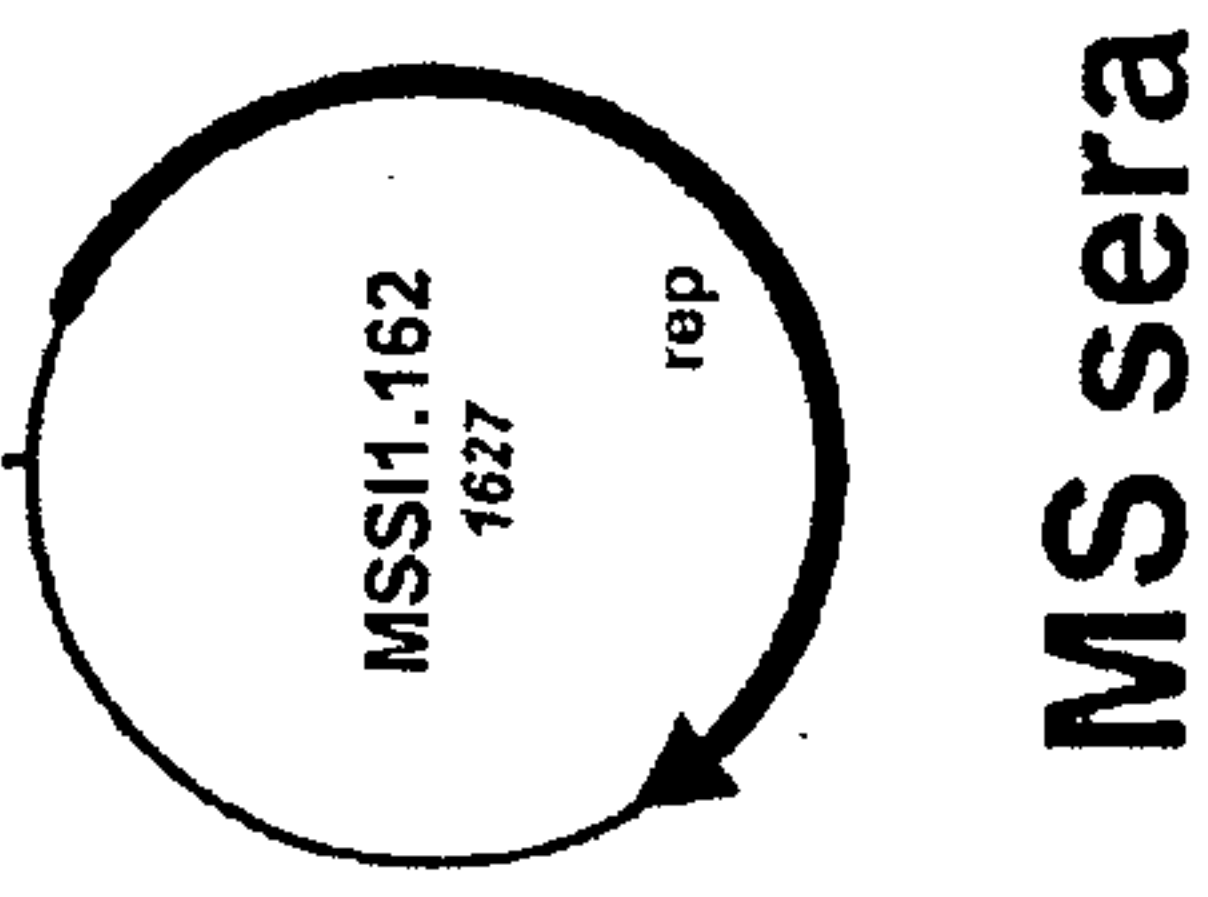
Group 2:



Group 3:



Group 4:



MS sera

- * - identical nucleotides
- ° - one or more nucleotide differences

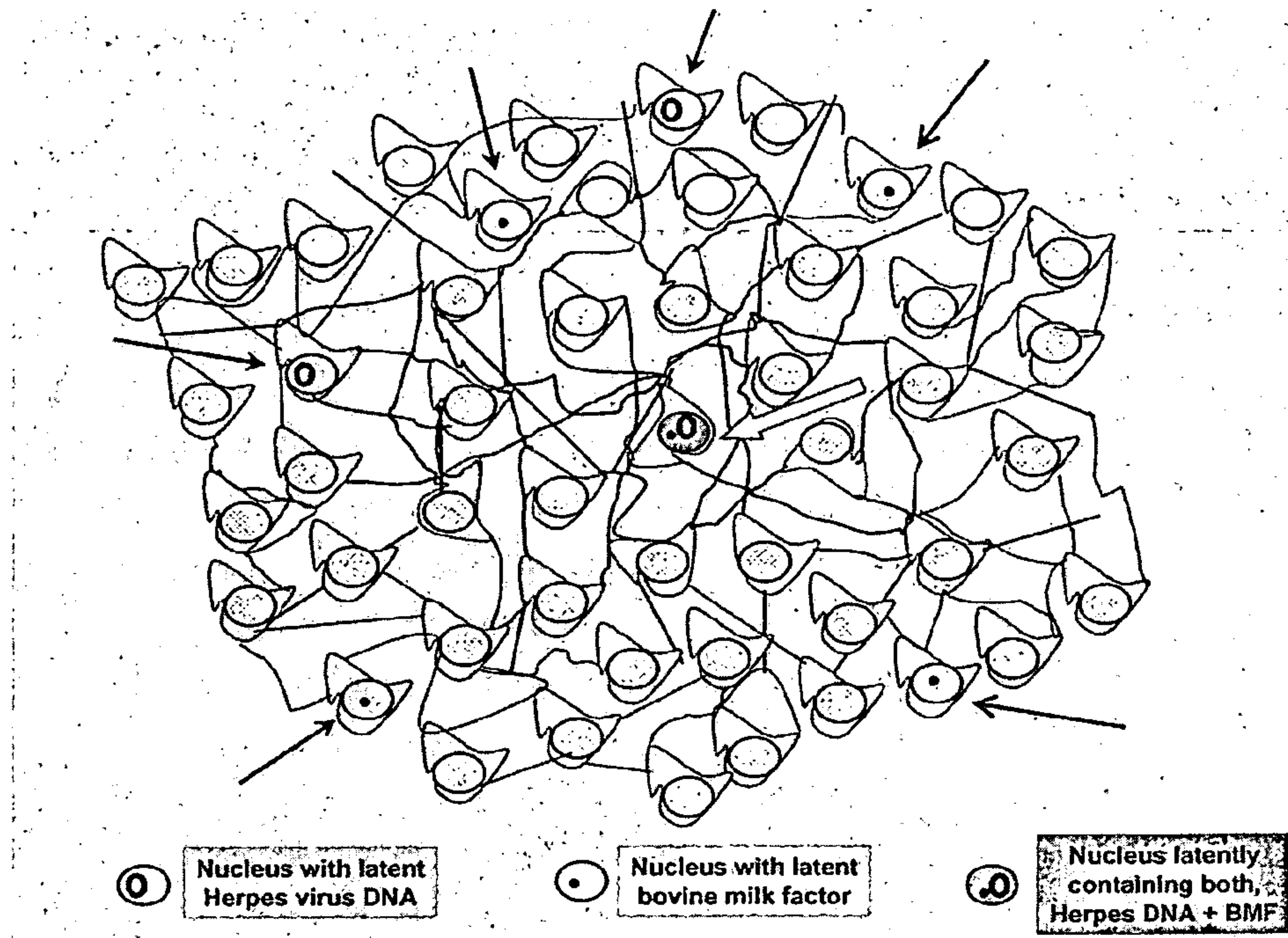


Figure 7

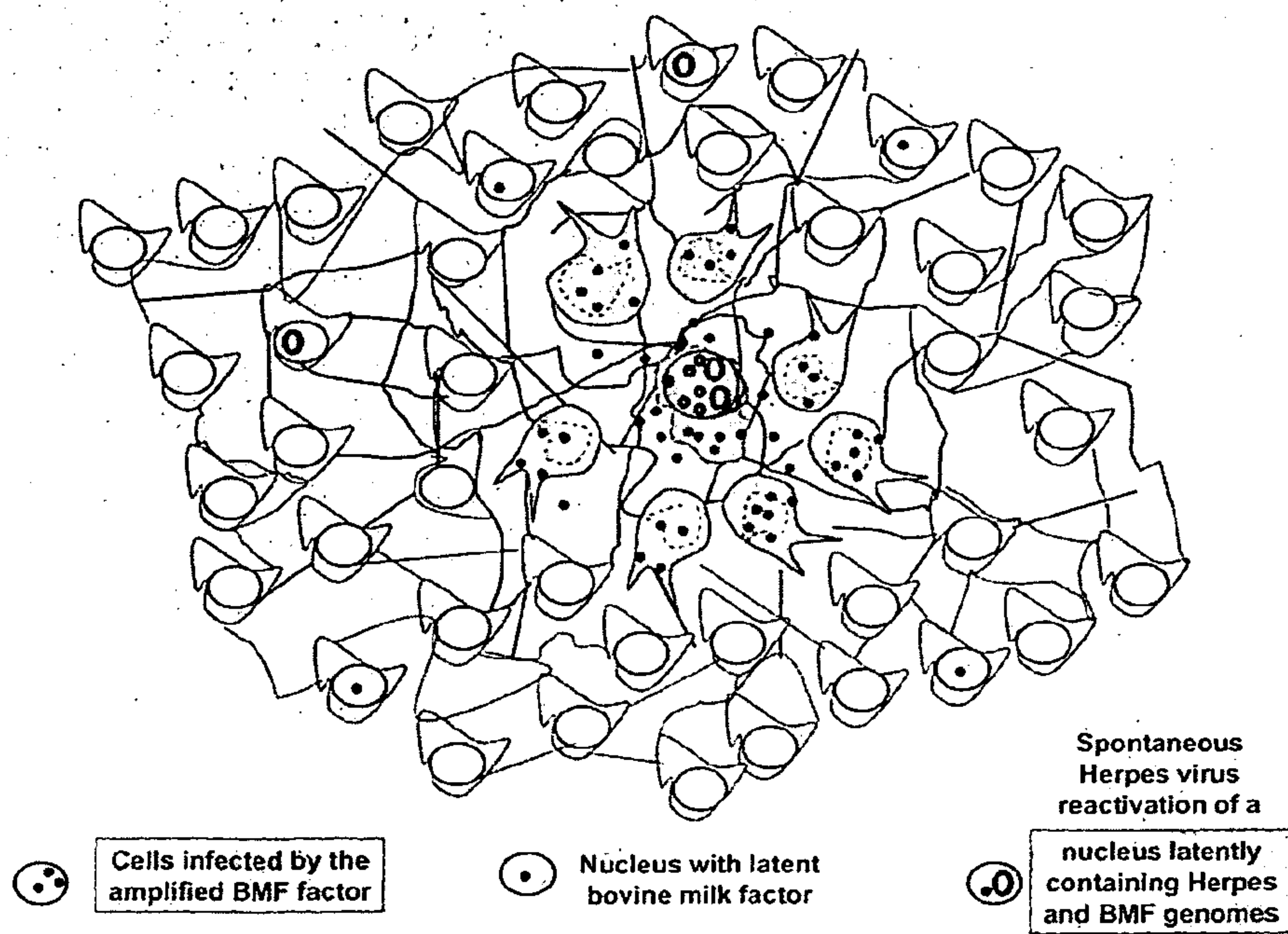


Figure 8

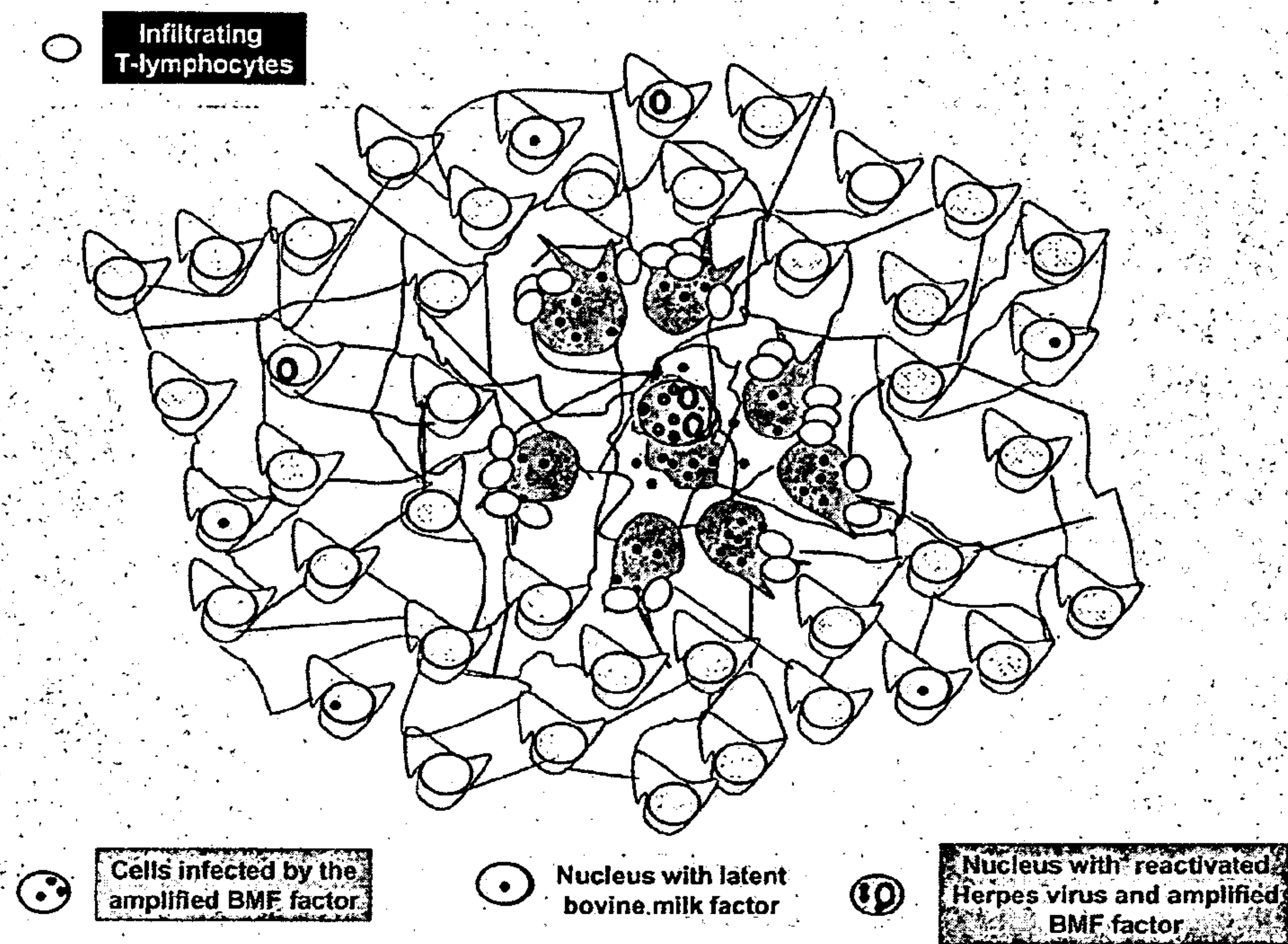


Figure 9

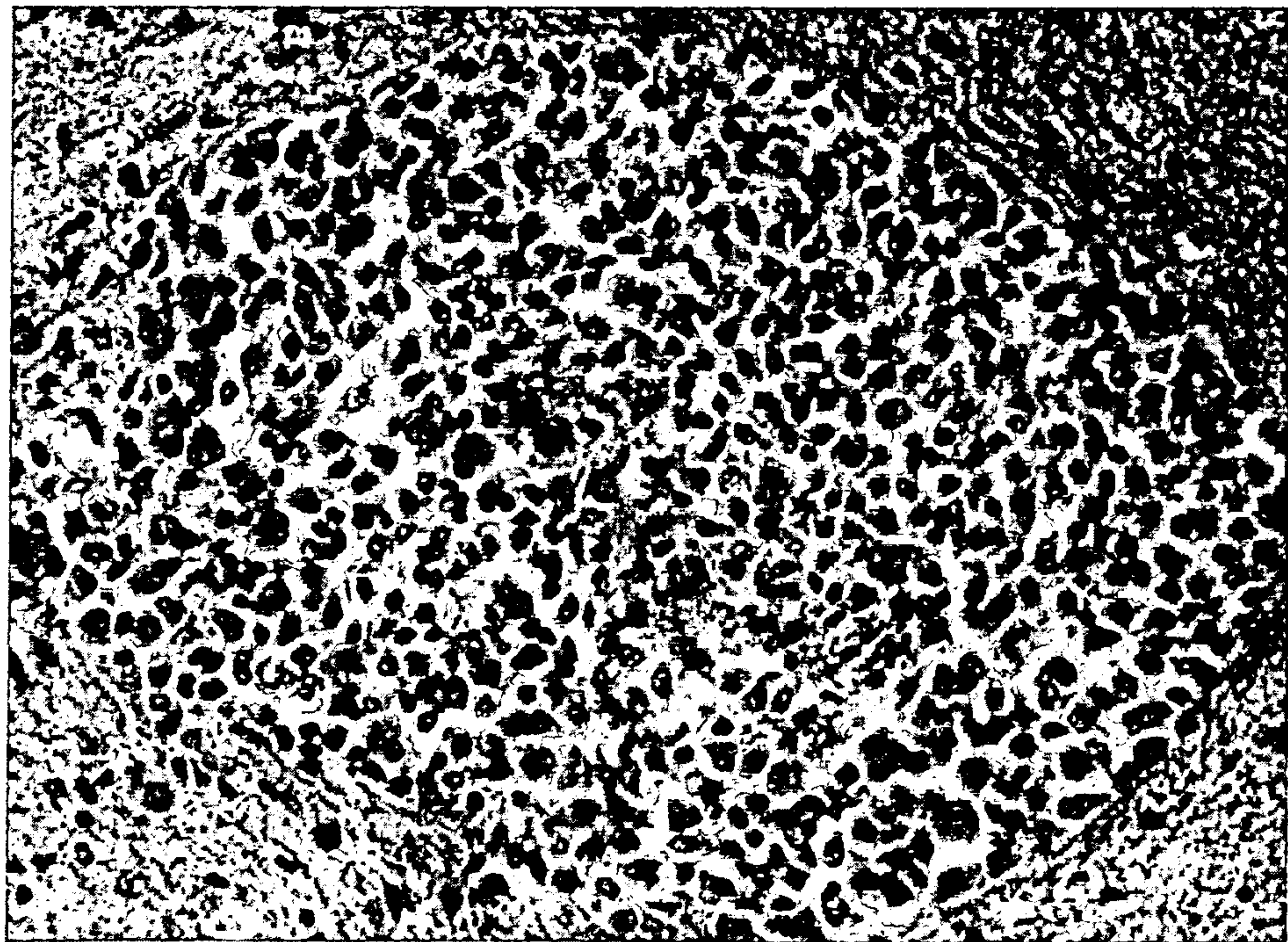


Figure 10

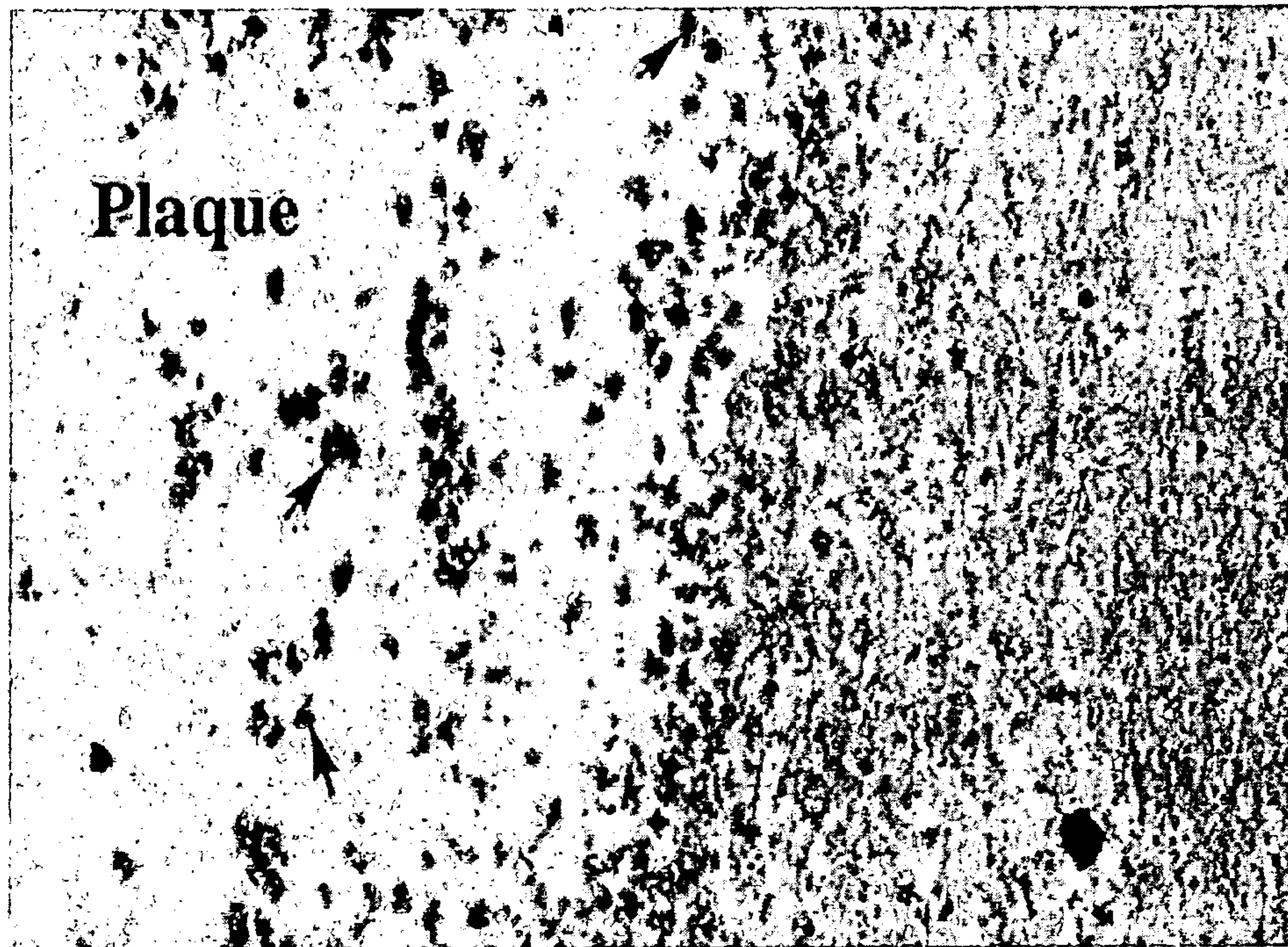
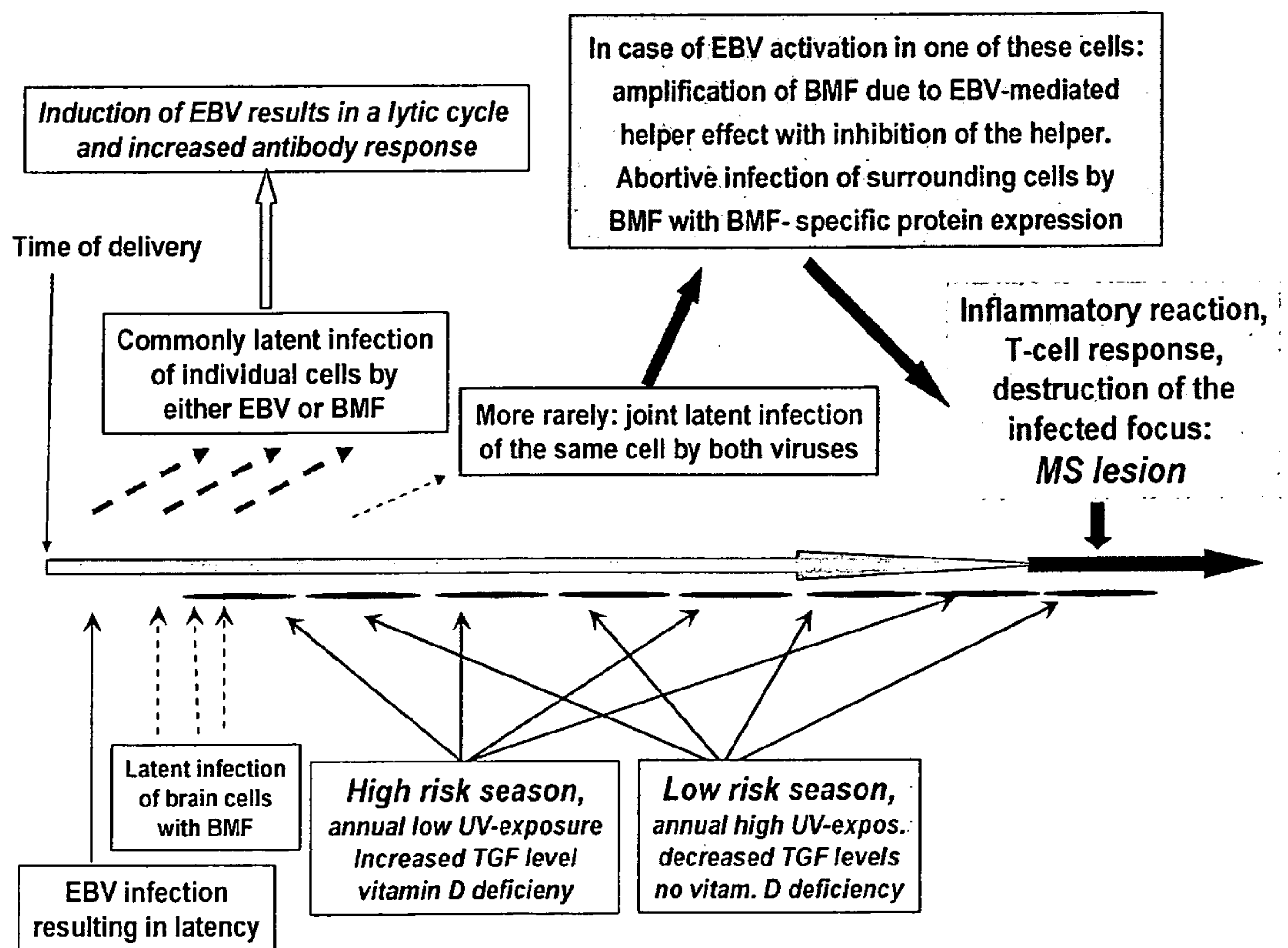


Figure 11



Vitamin D deficiency results in TGF β increase and higher rates of spontaneous EBV induction, seasonably pronounced in early spring (reduced UV-exposure)

Figure 12

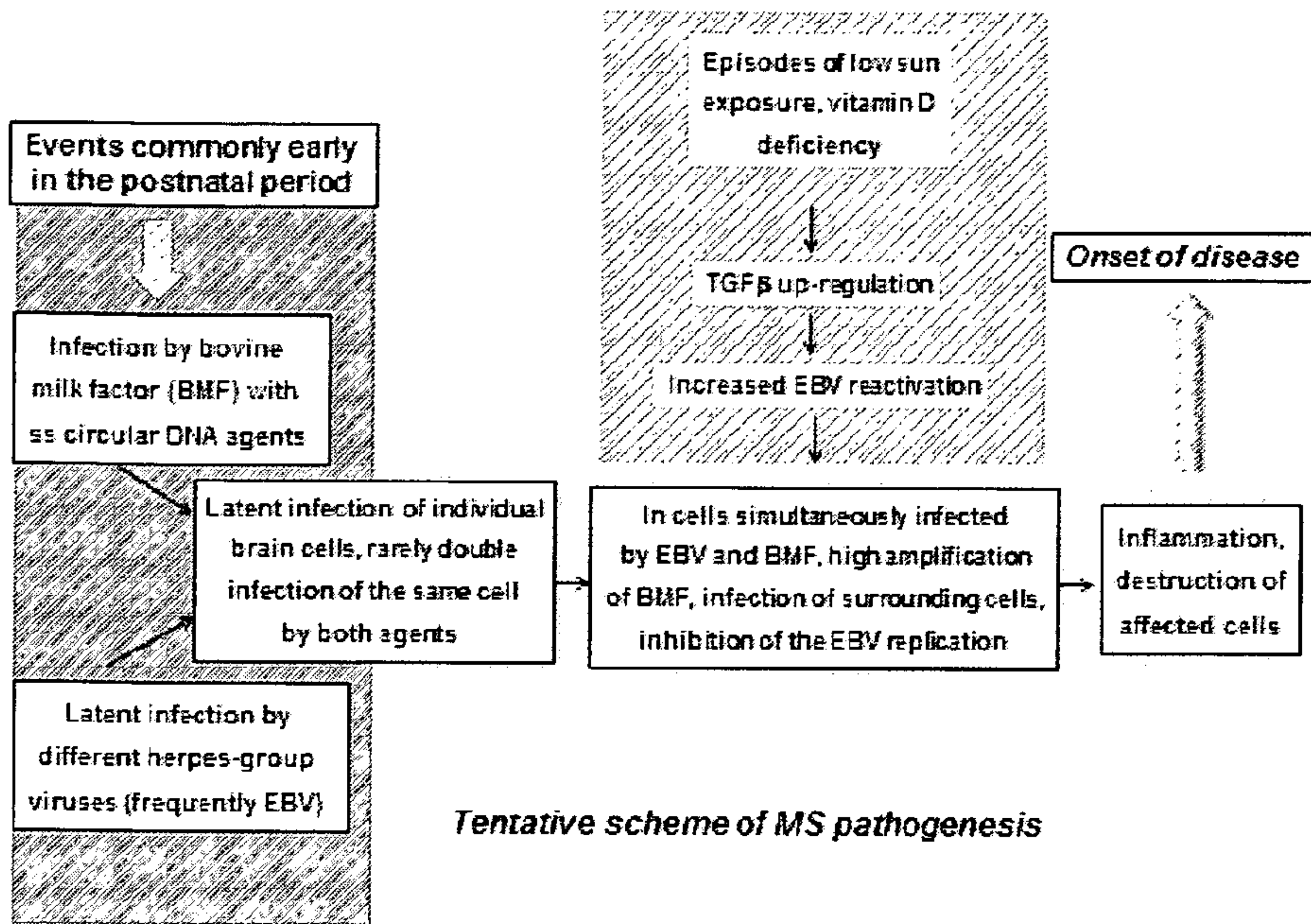


Fig. 13