6-2012

Paramecium bursaria Chlorella Virus 1 Proteome Reveals Novel Architectural and Regulatory Features of a Giant Virus

David D. Dunigan
University of Nebraska-Lincoln, ddunigan2@unl.edu

Ronald Cerny
University of Nebraska-Lincoln, rcerny1@unl.edu

Andrew T. Bauman
Ocean Biologics

Jared C. Roach
Institute of Systems Biology, jroach@systemsbiology.org

Leslie C. Lane
University of Nebraska-Lincoln, llane1@unl.edu

See next page for additional authors

Dunigan, David D.; Cerny, Ronald; Bauman, Andrew T.; Roach, Jared C.; Lane, Leslie C.; Agarkova, Irina V.; Wulser, Kurt William; Yanai-Balser, Giane M.; Gurnon, James; Vitek, Jason C.; Kronschnabel, Bernard J.; Jeannard, Adrien; Blanc, Guillaume; Upton, Chris; Duncan, Garry A.; McClung, O. William; Ma, Fangrui; and Van Etten, James L., "*Paramecium bursaria* Chlorella Virus 1 Proteome Reveals Novel Architectural and Regulatory Features of a Giant Virus" (2012). *Virology Papers*. 233.
https://digitalcommons.unl.edu/virologypub/233

Authors

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J. Virol. doi:10.1128/JVI.00907-12

Title: *Paramecium bursaria* Chlorella Virus 1 Proteome Reveals Novel Architectural and Regulatory Features of a Giant Virus

David D. Dunigan[#] (1, 2), Ronald L. Cerny (3), Andrew T. Bauman (4), Jared C. Roach (5), Leslie C. Lane (1), Irina V. Agarkova (1, 2), Kurt Wulser (3), Giane M. Yanai-Balser (1), James R. Gurnon (1), Jason C.Vitek (1), Bernard J. Kronschnabel (1), Adrien Jeannard (6), Guillaume Blanc (6), Chris Upton (7), Garry A. Duncan (8), O. William McClung (8), Fangrui Ma (2), James L. Van Etten[#] (1, 2)

[1]Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE 68583-0900, USA;

[2]Nebraska Center for Virology, University of Nebraska-Lincoln, Lincoln, NE 68583-0900, USA;

[3]Department of Chemistry, University of Nebraska-Lincoln, Lincoln, NE 68588-0304, USA;

[4]Ocean Biologics, Seattle, WA 98133, USA

[5]Institute of Systems Biology, Seattle, WA 98103, USA;

[6]Structural and Genomic Information Laboratory, UMR7256 CNRS, Aix-Marseille University, Marseille, FR-13385, France

[7]Department of Biochemistry and Microbiology, University of Victoria, Victoria, British Columbia, Canada;

[8]Department of Biology, Nebraska Wesleyan University, Lincoln, NE 68504-2794, USA

Running title: PBCV-1 virion proteome

Key words: Chlorella, Phycodnaviridae, large dsDNA virus, protein mass-spectrometry

Abstract: 174 words

Text: 7,017 words

#Corresponding authors: David Dunigan, email: ddunigan2@unl.edu and James L. Van Etten, email: jvanetten1@unl.edu

ABSTRACT

The 331 kilobase pairs chlorovirus PBCV-1 genome was re-sequenced and annotated to correct errors in the original 15 year old sequence; forty codons was considered the minimum protein size of an open reading frame. PBCV-1 encodes 416 predicted protein encoding sequences and 11 tRNAs. A proteome analysis was also conducted on highly purified PBCV-1 virions using two mass-spectrometry based protocols. The mass spectrometry-derived data were compared to PBCV-1 and its host *Chlorella variabilis* NC64A predicted proteomes. Combined, these analyses revealed 148 unique virus-encoded proteins associated with the virion (about 35% of the coding capacity of the virus) and one host protein. Some of these proteins appear to be structural/architectural, whereas others have enzymatic, chromatin modification and signal transduction functions. Most (106) of these proteins have no known function or homologs in the existing gene databases except as orthologs with other chloroviruses, phycodnaviruses and nuclear-cytoplasmic large DNA viruses. The genes encoding these proteins are dispersed throughout the virus genome and most are transcribed late or early-late in the infection cycle, which is consistent with virion morphogenesis.

INTRODUCTION

Complex cellular and viral processes are modular and accomplished by the concerted action of functional modules. One of the important functional modules of a virus is the virion particle, which ranges in complexity from a single type protein and small nucleic acid (e.g., tomato bushy stunt virus) to having dozens of types of proteins and lipids, along with a large nucleic acid genome (e. g., poxviruses). Regardless, whether "simple" or complex in composition, all virions carry the legacy of their progenitors through encapsidation, release and stabilization. Virions facilitate propagation of progeny through a series of tightly regulated biochemical steps, called the immediate-early phase of infection, which includes attachment, penetration, uncoating of the viral genome, intracellular trafficking of the viral genome to its replication center, and augmentation of cellular functions to "accept" the exotic nucleic acid/replicon. The architectural elements of virions tend to be prominent, but studies on the supergroup nucleocytoplasmic large DNA viruses (NCLDV) (7, 37, 43) indicate that in addition to structural components, these virions perform multiple enzymatic and regulatory functions that are partitioned among several proteins. The purpose of this study was to determine the virion proteome of *Paramecium bursaria* chlorella virus 1 (PBCV-1), a member of the NCLDV (11, 54).

PBCV-1 is the type member of the genus *Chlorovirus* (family *Phycodnaviridae*) that infects certain chlorella-like green algae from fresh water sources; these viruses are found throughout the world (54, 56). The chlorovirus host algae are normally symbionts of aquatic protists, and in this state are resistant to virus infection. Nevertheless, virus titers from natural sources have been measured as high as 10^5 plaque forming units (pfu) per ml; however, titers fluctuate with the season (58, 61). Very little is known about the role chloroviruses play in freshwater ecology (41), but susceptible hosts lyse within 6-16 hours in the laboratory and burst sizes typically exceed 10^2 pfu per cell (54, 56). Thus, chloroviruses have the potential to alter microbial communities both quantitatively and qualitatively, as well as act as a driving force for microbial evolution (11). Fortunately, some of the host algae can be grown in the laboratory independent of their co-symbiotic protists.

The 331 kilobase pair (kbp) PBCV-1 dsDNA genome was sequenced and annotated about 15 years ago (26) and reported to have 689 open reading frames (ORF) of at least 65 codons. Of these 689 ORFs, 377 were predicted to encode proteins (CDS); PBCV-1 also encoded 11 tRNAs (reviewed in 21, 55, 57). The size of PBCV-1 extends beyond its coding capacity; the virion is a T = 169d quasi-icosahedral particle with a diameter of 190 nm across the 5-fold axis (63, 64) and has an estimated molecular mass of greater than 1×10^9 Da (53). The virion is ~64% protein consisting of at least 40 polypeptides, as seen on one dimensional SDS-PAGE (42). The particle contains 5-10% lipid, which is associated with a bi-layered membrane underneath an outer glycoprotein shell (5, 42, 64).

The capsid structure consists of the major capsid protein (MCP, Vp54), which is glycosylated at 6 sites (31) and is myristylated at least at one site (36). Vp54 complexes with itself, and perhaps other proteins, to form homotrimeric capsomers that are responsible for the planar features of the capsid. Initially it was assumed that, except for the 12 vertices, Vp54 was the only protein contributing to the external capsid and 5040 copies of Vp54 were predicted per virion (64). However, recent studies indicate that the

PBCV-1 virion is more complex than previously thought. i) PBCV-1 contains a unique vertex with a 560-Å-long spike structure, which protrudes 340 Å from the surface of the virus. The part of the spike structure that is outside of the capsid has an external diameter of 35 Å at the tip, expanding to 70 Å at the base. The spike structure widens to 160 Å inside the capsid and forms a closed cavity inside a large pocket between the capsid and membrane enclosing the virus DNA (5, 66). The related chlorovirus CVK1 has a virion-associated protein Vp130 (homolog of PBCV-1 A140/145R) that binds to algal cell walls and is located at a unique vertex (34, 35), suggesting this protein is associated with the spike structure. ii) Regularly spaced appendages occurring on the surface of the virion are present at approximately 1 per trisymmetron (66). These appendages probably assist in attaching the virion to its host cell (56). iii) The volume of the capsomers at the common vertices and those surrounding the spike structure at the unique vertex differ significantly, suggesting they consist of different proteins (5, 66). iv) At least one vertex region may have a retractable appendage, such that when probed with a scanning atomic force stylet the structure retracts, but then resets much like a plunger with a spring (23). It is not known if this plunger is at the unique spike structure vertex or one of the other 11 vertices. v) Six minor capsid proteins of varying stochiometries support the particle architecture and appear to interact with the internal membrane in both the tri- and pentasymmetron structures, as observed with an 8.5 Å resolution map of the virion (66). Of these, a "long protein" (~32 kDa) with similarity to the PRD1 bacteriophage long glue proteins forms an hexagonal network over the internal surface of the trisymmetrons, and a "membrane protein" dimer (~28 kDa) is located at the edge of the trisymmetrons and is connected to the internal membrane (1, 8). vi) PBCV-1 DNA binding proteins were evaluated with proteomic methods from isolated viral DNA of virions (59). Six proteins were identified that have high isoelectric points that are well suited for binding and neutralization of DNA. Thus, PBCV-1 structure has both symmetric and asymmetric elements, adding to the complexity of the virus morphology.

vii) In addition to these structural features, PBCV-1 contains several functions that initiate infection. PBCV-1 attaches specifically to its host *Chlorella variabilis* NC64A. Thus, we predict one or more surface proteins of the virus mediate attachment; it is probably the spike structure (66). Immediately upon PBCV-1 attachment, the cell wall is degraded at the site of attachment. viii) Virions contain cell wall degrading activity (28, 62). ix) Within the first minutes of infection the cell membrane depolarizes (12, 32), leaving the cell with significantly altered secondary transporter functions (2). This activity is hypothesized to be partially due to a PBCV-1-encoded K^+ channel, Kcv (A250R) (27); however, no direct evidence supports the presence of Kcv in the virion. x) In the first five min of infection host DNA begins to degrade and this is likely due to the two virus-encoded DNA restriction endonucleases [R.CviAI (A579L), R.CviAII (A252R)] packaged in PBCV-1 virions (3). Host chromatin degradation begins before viral transcripts appear. PBCV-1 DNA is resistant to the restriction enzymes because it is methylated. xi) The next major intracellular event is the synthesis of early viral transcripts, observed 5-10 min p.i. (67; Blanc et al., unpublished data), which apparently occurs by pirating the cellular transcriptional machinery, because the virus does not encode a recognizable RNA polymerase gene and no polymerase activity was detected in virion-derived extracts (Jon Rohozinski and James Van Etten, unpublished results).

The purpose of the current study is to evaluate the total viral complement of proteins associated with the PBCV-1 virion using proteomic technologies and to re-examine the structural/architectural features of this virus, as well as the initial events of infection in the context of the protein complement. This evaluation led to the re-sequencing of the PBCV-1 genome after preliminary proteomic analyses suggested there were errors in the PBCV-1 genome sequence (26). This report presents the newly revised PBCV-1 genome and annotations, and proteomic analyzes of the infectious particles.

MATERIALS AND METHODS

Virus, cells, and culture conditions. Procedures for growing virus PBCV-1 in the alga *C. variabilis* have been described (3, 52, 53).

Virus purification scheme. The virus was purified essentially as described (52) with the following modifications. Prior to sucrose density gradient separation, the virus-cell lysate (2 liters) was clarified by incubating with 1% (v/v) NP-40 detergent at room temperature for 1 - 2 h with constant agitation followed by centrifugation in a Beckman Type19 rotor at 53,000 ×g, 50 min, 4^{o}C. The pellet fraction was solubilized in virus storage buffer (VSB) (50 mM Tris-HCl, pH 7.8) and layered onto a 10 - 40% (w/v) linear sucrose density gradient made up in VSB, centrifuged in a Beckman SW28 rotor for 20 min at 72,000 ×g at 4^{o}C. The virus band was identified by light scattering, removed from the gradient and concentrated by centrifugation. Resuspended virus was incubated with 50 µg/ml proteinase K in VSB for 4 h at 25^{o}C to disassociate and degrade contaminating proteins (this treatment has no effect on virus infectivity). The proteinase K treated virus was layered onto a 20 - 40% linear iodixanol (OptiPrep™, Axis-Shield, Oslo, Norway) gradient in VSB and centrifuged at 72,000 ×g in a Beckman SW28 rotor for 4 h at 25^{o}C for isopynic separation. The gradient produced a single major light-scattering band at

~32% iodixanol corresponding to a density of 1.171 g/ml. The virus band was removed by side-puncture of the centrifugation tube, diluted approximately 10 fold with VSB, then concentrated by centrifugation in a Beckman Ti50.2 rotor at 80,000 ×g for 3 h at 4°C. The pellet fraction was re-suspended in VSB, then filter sterilized with a 0.45 µm cutoff membrane, and stored at 4°C. The virus was quantified by UV/visible scanning spectroscopy using an extinction coefficient of $A_{260/0.1\%} = 10.7$ (52) and plaque assayed to determine the number of infectious particles. These preparations typically yielded several milliliters of stock virus at 1 - 10 x 10^{11} pfu/ml. The infectious to total particle ratio is normally 0.25 - 0.5 for such preparations (53).

These preparations were used both for re-sequencing the PBCV-1 genome and the determination of the proteome; the proteome was determined by two independent methods using mass spectrometry of trypsin digested proteins.

Re-sequencing and annotation of the PBCV-1 genome. Preliminary proteomic analyzes using the existing PBCV-1 gene annotations (NCBI Refseq: NC_000852) revealed possible errors in the genome sequence, which prompted us to re-sequence the PBCV-1 genome. PBCV-1 DNA was purified from virions treated with DNase I, sequenced using Roche 454 Life Sciences GS FLX Titanium chemistry, and assembled as described in the Supplemental Information section (SI). PBCV-1 contigs were identified and annotated as described in the SI.

Proteomics method 1. SDS-PAGE/Trypsin/HPLC/Ion Spray/MS-MS.

Particle disruption and protein extraction. The PBCV-1 virion proteome was evaluated with two independent methodologies, see Figure 1. In the first method virion proteins were solubilized essentially as described (25) with reduction of the proteins by adjusting 50 µg of virions in 50 µl. An equal volume of cracking buffer [50 mM Tris pH 8.5, 5 mM of the reducing agent dithiothreitol (freshly reduced with tributylphosphine; in some experiments beta-mercaptoethanol was substituted for dithiothreitol), 1% SDS, 0.1% crystal violet and 1% Ficoll 400] was added. The sample was heated to 100°C for 3 min. The reduced proteins were subsequently alkylated by adjusting the solution to 12.5 mM iodoacetamide with a 0.25 M stock, then heating to 100°C for 1 min. These samples were immediately subjected to SDS-PAGE. Alternatively, the proteins were alkylated without previous reduction by the same procedure.

Alternatively, phenolic extractions were used to isolate virion proteins. Reduced and alkylated proteins were adjusted to 40% sucrose to increase the density of the solution. These preparations were then extracted with an equal volume of water-saturated phenol or water-saturated phenol with toluene added to increase the hydrophobicity of the phenol. The protein-containing phenolic phase was removed, and protein was precipitated with 10 volumes of methanol then dissolved and heated in cracking buffer.

One-dimensional SDS-PAGE. Proteins were separated on thirty-two cm linear gradient (4-20%) polyacrylamide gels with 0.1% SDS and 375 mM Tris, pH 8.7 tank buffer of 25 mM Tris/190 mM glycine. The samples were electrophoresed at room temperature till the crystal violet tracking dye reached the bottom of the gel.

The gel was fixed and stained with Sypro-Ruby according to the manufacturer's recommendation (Life Technologies Corporation). The stained gel was imaged using a blue box transluminator. Once imaged, the gel was cut into 32 one cm size pieces being careful to clean the scalpel between samples. These gel pieces were then processed for trypsin-digestion and mass spectrometry analyses.

MS-based microsequencing. Excised gel pieces were digested for peptide sequencing using a slightly modified version of a method described by (40). Briefly, the samples were washed with 100 mM ammonium bicarbonate, reduced with 10 mM DTT, alkylated with 55 mM iodoacetamide, washed twice with 100 mM ammonium bicarbonate, and digested *in situ* with 10 ng/µl trypsin. Peptides were extracted with two 60 µl aliquots of 1:1 acetonitrile:water containing 1% formic acid. The extracts were reduced in volume to approximately 25 µl using a vacuum centrifugation.

Ten µl of the extract solution was injected onto a trapping column (300 µm x 1 mm) in line with a 75 µm x 15 cm C18 reversed phase LC column (LC- Packings). Peptides were eluted from the column using a water + 0.1% formic acid (A)/95% acetonitrile:5% water + 0.1% formic acid (B) gradient with a flow rate of 270 µl/min. The gradient was developed with the following time profile: 0 min 5% B, 5 min 5% B, 35 min 35% B, 40 min 45% B, 42 min 60% B, 45 min 90% B, 48 min 90% B, 50 min 5% B.

The eluting peptides were analyzed using a Q-TOF Ultima tandem mass spectrometer (Micromass/Waters, Milford, MA) with electrospray ionization. Analyses were performed using data-dependent acquisition (DDA) with the following parameters: 1 sec survey scan (380-1900 Da) followed by up to three 2.4 sec MS/MS acquisitions (60-1900 Da). The instrument was operated at a mass resolution of 8,000. The instrument was calibrated using fragment ion masses of doubly protonated Glu-fibrinopeptide.

Mass ion analyses. The MS/MS data were processed using Masslynx software (Micromass) to produce peak lists for database searching. MASCOT (Matrix Science, Boston, MA) was used as the search engine. Data were searched against the NCBI non-redundant database. The following search parameters were used: mass accuracy 0.1 Da, enzyme specificity trypsin, fixed modification CAM, variable modification oxidized methionine. Protein identifications were based on random probability scores with a minimum value of 25. Although this number varied from experiment to experiment, typically it was 25 or less for $p < 0.05$ confidence.

Relative abundances. Approximate, relative quantitation of the proteins was determined using the exponentially modified protein abundance index (emPAI) (18). This method uses the number of observed peptides compared to the number of observable peptides giving a ratio that is directly proportional to relative abundance of the protein in the mixture when adjusted exponentially (emPAI= 10^{PAI}-1; where PAI = number of observed peptides per protein/number of observable peptides per protein).

Proteomics method 2. PPS/Trypsin/HPLC/MS-MS

Protein extraction and trypsin digest. One hundred µg of PBCV-1 was mixed 1:1 with 100 mM ammonium bicarbonate buffer pH 8.3 containing 0.2% PPS (Protein Discovery Labs, San Diego, CA) [final concentration 50 mM ammonium bicarbonate, 0.1% PPS], boiled for 5 min, cooled to room temperature, reduced and alkylated with 5 mM dithiothreitol and 15 mM iodoacetamide, then digested with sequencing grade trypsin at a 1:50 trypsin:protein ratio, for 4 h at 37°C, with shaking. The digested samples were acidified with HCl (200 mM), incubated at 37°C, and centrifuged at 4°C, to remove PPS prior to LC-MS application.

LC Methods. Buffer solutions were made with LC-MS grade water, acetonitrile, and formic acid and consisted of 5% acetonitrile/0.1% formic acid in water (Buffer A) and 100% acetonitrile/0.1% formic acid (Buffer B). Two or 4 µg total protein from each sample was loaded onto a reverse phase (RP) trap (5 µm, 200 Å, Magic; Michrom Bioresources, Auburn, CA) with 100% buffer A and washed for 10 min prior to separation on a microcapillary column. The microcapillary column was constructed by slurry packing 18 cm of C18 material (2.7 µm, 100 Å, HALO, Michrom Bioresources) into a 75 µm ID fused silica capillary, which was previously pulled to a tip diameter of 5 µm using a Sutter Instruments laser puller (Sutter Manufacturing, Novato, CA). Separations were performed on an Eksigent 1D+ nano-LC (Eksigent, Dublin, CA) LCQ-Deca XP Plus: 0-30% B over 240 min, 30-70% B over 10 min at 300µl/min; LTQ-Velos: 0-30% B over 80 min, 35-70% B over 10 minutes at 300µl/min.

Mass Spectrometry Methods. Data-dependent tandem mass spectrometry (MS/MS) analysis was performed using an LTQ-Velos or LCQ Deca XP Plus mass spectrometer (ThermoFisher, San Jose, CA). Full MS spectra were acquired in centroid mode, with a mass range of 400–2000 Da. To prevent repetitive analysis, dynamic exclusion was enabled with a LTQ-Velos: repeat count of 1, a repeat duration of 30 sec, an exclusion list size of 500, and an exclusion-duration of 90 sec. Tandem mass spectra were collected using a normalized collision energy of 35% and an isolation window of 3 Da.

For the LTQ one full scan was followed by 6 MS-MS scans of the 6 most intense precursor ions not on the dynamic exclusion list. LCQ-Deca XP Plus: repeat count of 1, a repeat duration of 30 sec, an exclusion list size of 100, and an exclusion-duration of 20 sec. Tandem mass spectra were collected using a normalized collision energy of 35% and an isolation window of 4 Da.

For the LCQ one full scan was followed by 3 MS-MS scans of the 3 most intense precursor ions not on the dynamic exclusion list.

Mass ion analyses. Processing and searching of MS/MS spectra and analyzing peptide and protein identification data were performed using SPIRE (Systematic Protein Investigative Research Environment, www.proteinspire.org) system with default parameters. Searches were conducted using the X!Tandem search engine (9) within a 2.5-Da mass error, a variable modification for methionine oxidation (16@M), and a fixed modification for iodoacetamide (57@C) along with the default search parameters. The sequence file for the searches of the modules contained PBCV-1 appended to a decoy database of *Ostreococcus tauri*. In addition, a randomly reshuffled version of each database was appended for error estimation. The search results were processed with the LIPS (logistic identification of peptide sequences) model (16) to generate peptide spectra scores. Peptide identification probabilities and FDRs were calculated based on the reshuffled matches using an isotonic regression model (17). A 90% certainty was used as the basis for spectra identifications. A recently introduced approach was used to estimate the protein identification FDR from individual peptide identification probabilities (17).

RESULTS AND DISCUSSION

Re-sequenced and re-annotated PBCV-1 genome. The original sequence and annotation of PBCV-1 was completed over 15 years ago using primitive procedures when compared to current technology. During the past 15 years we have corrected the sequence of individual genes as mistakes were detected. Those mistakes and preliminary results from the current proteomic analyses that indicated sequencing errors, prompted us to re-sequence PBCV-1. The revised PBCV-1 genome contains 330,805 nucleotide pairs compared to 330,743 nucleotide pairs from the earlier sequencing effort. The two genome versions differed by 458 indel positions (mostly single nucleotide indels) and 188 substitutions. This genome sequence and annotation are deposited at the National Center for Biotechnology Information (NCBI) as reference sequence NC_000852.5; the genome annotation is listed in SI Table S1. The re-sequenced genome submitted to NCBI includes the 2,222 base pair terminal inverted repeat ends, but not the incompletely base-paired covalently closed hairpin 35-nucleotide loops at each end of the genome. Thus, the genome is a linear double-stranded DNA of 330,805 base pairs with two 35-nucleotide partially paired terminal loops. Sequencing reads were obtained through the hairpin loops (data not shown). When compared to the published results from Zhang et al. (1994), the terminal repeats and hairpin loops are identical. Nucleotide 1 refers to the first paired nucleotide following the hairpin loop.

One significant change in the new annotation is that ORFs of 40 codons or more were classified as potential CDSs; the previous annotation used 65 codons as the minimum size. This resulted in 802 ORFs, of which 416 ORFs were classified as “major” CDSs (designated with an upper case “A”) based on the following supporting evidence: these ORFs did not have larger overlapping ORFs and/or were expressed transcriptionally (65) and/or the protein was identified in the proteomic analyses. The major ORFs cover 92.8% of the genome sequence and have an average protein product size of 249 amino acids. In addition, 11 tRNA genes were identified as reported previously. The remaining 386 ORFs were labeled “minor” ORFs (designated with a lower case “a”) and most of them are probably not CDSs. They encode putative proteins with an average size of 86 amino acids. The gene annotations, along with functional assignments, are listed in SI Table S1.

To avoid confusion in the literature, we kept the same gene numbering system as used previously, i.e., a gene labeled as *a250r* is still labeled *a250r*. When two adjacent ORFs were found to be a single ORF, e.g., A189R and A192R, we named it A189/192R. Finally, where smaller ORFs were identified that were not considered previously, we labeled them with a lower case letter, e.g., A254aR. These new gene annotations were used for the proteomic analyses of the virion proteins.

PBCV-1 virion proteome. Highly purified virions were used for the proteome analyses, including a "protease treatment" step where the particles were incubated with proteinase K to degrade proteins non-specifically associated with the particle surface. Proteinase K treatment does not affect PBCV-1 infectivity (3). Using a combination of sample treatment, separation and mass spectrometry methods, 148 virus-encoded proteins were detected in the PBCV-1 virion (Fig. 2B). For abundant proteins, any method was sufficient to detect mass ions allowing identification with high confidence. However, some of the low abundance and small proteins were only identified by one of the two methods, primarily due to differential separation where the protein of interest was separated from an abundant, and consequently masking, protein. The dynamic range of these analyses was ~10^4 with the MCP present at approximately 10^3 copies per virion relative to a hypothetical protein present at one copy per virion. Thus, the sample treatment and separation method selected were important elements in the proteome determination. The proteins were identified by two independent methods, 62% of the proteins were detected by both methods. Twenty six percent were uniquely identified with the SDS-PAGE method (Method 1) and 11% were uniquely identified with the PPS solubilization method (Method 2). It is important to note some proteins are not readily detected using mass spectrometric methods, e. g., small proteins associated with membranes (39). Thus, the proteome reported here may increase with additional data in the future. However, the results presented are the compilation of many experiments using varying conditions for protein extraction and isolation giving us high confidence in the compiled list of proteins including several proteins with predicted transmembrane domains, as well as many small proteins; i. e., less than 10 kDa (Table 1).

Method 1. SDS-PAGE/Trypsin/HPLC/Ion Spray/MS-MS. Method 1 identified 137 virus-encoded proteins in the virion. Virion proteins were either: i) extracted directly into gel sample buffer, ii) first extracted into a phenolic phase to remove nucleic acids, or iii) extracted into a hypo-polarized phenolic phase supplemented with toluene to further extract highly polar proteins such as glycosylated proteins. The extracted proteins were either alkylated with iodoacetamide and then reduced, or left alkylated. While these methods helped extract certain proteins, others were excluded and no additional proteins were detected beyond the standard method of extracting into the gel sample buffer.

Protein separation using one-dimensional gel electrophoresis resolved ~30 distinct SYPRO-Ruby stained bands. The dynamic range of observed polypeptides is large. For example, the MCP migrates at approximately 54 kDa and is the most abundant protein in the virion, migrating near the mid-point of the gel (Fig. 2A, gel position 13). The MCP has a nominal mass of 48 kDa and is post-translationally modified with sugars at 6 positions (31) and with at least one myristyl group (36), as well as having the amino terminal methionine removed (13). This very abundant protein contrasts to proteins detected in regions of the gel where little or no staining was observed, e. g., gel positions #1, 8, 9, 31, 32 in Fig. 2A. Although very little staining was observed in these regions, several proteins were detected by the mass spectrometry analyses. Indeed, proteins were detected in all regions of the gel.

Qualitative changes in protein mobility were observed with different sample treatments (SI Fig. S1). Samples that were alkylated with iodoacetamide, gave nearly the same number of bands as those that were reduced with dithiothreitol (or beta-mercaptoethanol) and alkylated. However, the mobility of a few proteins was altered by this differential treatment, as visualized by SYPRO-Ruby staining. For example, a protein band(s) migrating at gel position #5 in the alkylated sample is absent in the sample that was both reduced and alkylated. Conversely, proteins observed at gel positions 7 and 8 for the reduced and alkylated sample are not visible in samples only alkylated. Several other differentials occurred between these two treatments; nevertheless, the protein profiles determined for these treatments were similar for the prominent proteins. The use of multiple treatment and separation methods was most useful for low abundant polypeptides as indicated by MASCOT score.

Method 2. Trypsin/HPLC/MS-MS. The trypsin/HPLC/MS-MS method identified 126 virus-encoded proteins, 16 of which were unique to this method. All tryptic or semi-tryptic peptide matches were analyzed using the SPIRE analysis suite (14-17) against PBCV-1 and *C. variabilis* genome databases. Restricting the matches to tryptic only peptides did not decrease the false positive rate, so full semi-tryptic searching was employed. The false positive rate was estimated from searches of a decoy database of the *Ostreococcus tauri* proteome. The false positive rate was computed to be 0.42%, so one of the 126 proteins identified in this group of experiments might be a false positive. All the proteins identified had a confidence level of 'high' or 'very high' in at least one of the ten analyses in this group and were considered to be in the virion.

Of the ten analyses performed with this method, 6 proteins were detected in only one analysis. One of the proteins was found in 2 analyses, one in 3 analyses, 4 in four analyses, 21 in 5 analyses, 2 in 6 analyses, 2 in 9 analyses, and 89 in all 10 analyses. The number of analyses in which a protein is observed, can be influenced by either variability inherent in mass spectrometry based proteomics experiments, variability in expression, stability of the proteins or false positive results.

Proteome is lower (L) strand and right hand side (R) biased. The genes predicted to encode proteins in the PBCV-1 genome are biased to the right side (262 of 416) relative to the mid-point of the genome; this is also reflected in the number of gene products in the proteome (81 CDSs from right side, 67 CDSs from left side) (Fig. 3). In addition, there is a bias to the reverse strand (L) for the right half of the genome in both the total predicted proteins (159 of the 416, Fig. 3A) and the virion proteome (48 of 148, Fig. 3B). This bias is consistent with certain viable PBCV-1 spontaneous large deletion mutants where up to 40 kbp of the left side of the genome can be deleted (24, 54), and these are recapitulated in the chlorovirus CVK2 (6). The right side L strand virion-coding genes have a mean G+C content of 22%; whereas, the overall G+C content of the genome is 40% and mean G+C content of all the coding genes is 31%. These observations suggest the left side of the genome has less selection pressure relative to the right side for the essential functions of virion assembly and maturation, The right side L strand is relatively dense with virion-associated genes (38% of the total) with atypical nucleotide composition; whereas, the corresponding left side of the genome is relatively sparse (14%) with regards to virion proteins.

Proteome is skewed to small basic proteins. The PBCV-1 proteome has proteins ranging in molecular weights from 4.9 to 143 kDa and in isoelectric points from 3.6 to 13.0, assuming no post-translational modifications (Fig. 4). Quantitatively, the proteome is dominated by the MCP, centrally located in these distributions. Qualitatively, the proteome is skewed to basic (~75%) and relatively small proteins, approximately 50% are less than 20 kDa, and 63% of the proteins have molecular weights less than 50 kDa and pI values greater than 7.0. This skewing to the more basic side is interesting because the electrostatic charge of the 6 x 10^5 phosphate moieties in the virus genome are probably neutralized by basic proteins (59). However, this prediction must be evaluated further because the stoichiometry of the virion proteins is uncertain. Additionally, how these relate to the chlorovirus CVK2 proteins with DNA binding and protein kinase activities needs to be clarified (60).

Two-dimensional gel analyses using isoelectric focusing versus mass separations support the skewing to basic and small proteins, suggesting that the majority of these proteins are not post-translationally modified in such a way that causes significant deviations of the predicted charge-mass migration (results not shown). However, we never obtained good resolution of the proteins using 2-D gels, even though many protocols were tried, because the MCP dominated the gel.

Membrane proteins. The virion proteins were evaluated for potential transmembrane domains with three independent methods (20, 30, 50); these results suggest that at least 26% of the proteome may be associated with a membrane structure (Table 1), presumably the internal membrane of the virion. Two-thirds of the CDSs with predicted transmembrane domains (3 out of 3 programs used) were detected by both proteomic methods. The remaining 1/3 of the CDSs were detected equally with Method 1 biased to somewhat larger (mean MW = 23.8 kDa) and more basic proteins (mean pI = 9.2), whereas Method 2 was biased to smaller (mean MW = 10.3 kDa) and less basic proteins (mean pI = 7.8).

The origin of the PBCV-1 internal membrane is unknown. If all, or at least most, of the PBCV-1 internal membrane contains virus-encoded proteins and no host-encoded proteins, it would suggest extensive modification of the host membrane to form the virus membrane.

PBCV-basic adaptor domain containing proteins. Eight PBCV-1 CDSs have at least one copy of a small, highly positively charged C-terminal domain, referred to as the PBCV-basic adaptor domain (19): A092/093L, A176L, A205R, A278L, A282L, A436L, A571R and A676R. All of these CDS were detected in the virion (Table 1). These proteins range in size from 6.9 - 69 kDa, but their pI values are very basic, 10.6 - 13.0. Five of these proteins contain a single copy of the basic adaptor domain; however A092/093L and A278L have 2 copies, and A282L has 3 copies. A278L and A282L are S/T protein kinases (51). The A676R protein contains both the PBCV-basic adaptor domain and a 2-cysteine domain (Pfam 08793), which is a virus-specific domain fused to OUT/A20-like peptidases and S/T protein kinases and is suggested to function as a targeting device for specific substrates (19). The PBCV-basic adaptor domain is only found in the chloroviruses, and A176L is only found in PBCV-1. The function of the

PBCV-basic adaptor domain is unknown.

MCP paralogs. The initial understanding of the architectural makeup of the PBCV-1 virion was a simple quasi-icosahedral particle consisting of a single MCP (Vp54) (64). This picture has evolved to the present 8.5 Å resolution complex particle with several surface features, including a unique vertex with a spike structure and fiber-like structures associated with some capsomers in the trisymmetrons (5, 66). Genome sequencing revealed genes encoding 6 additional capsid-like proteins (26). Previously these paralogs were not considered relevant because at least two of them (genes *a010r* and *a011l*) could be deleted from the genome without loss of virion formation (24). However, the proteome presented here indicates that all of the capsid-like proteins are present in the virion (Table 1) and they fall into 5 paralog classes (Fig. 5A). Each of these proteins contain 2 conserved domains [D1 (green) and D2 (red)] (Fig. 5B) consistent with the Vp54 structure (Fig. 5C). The relative abundance of the proteins, as estimated by their emPAI value, ranged from 1 (A384dL and A383R) to 13 (A430L and A011L). These abundance ratios support the hypothesis that the architecture of-the PBCV-1 virion is composed of a complex mixture of capsids and that the capsomers are composed of heteromeric proteins with a conserved structure. Additionally, the 2 minor capsid-like proteins, A383R and A384dL, contain an additional domain that is similar to the chitin binding peritrophin-A domain (Pfam 01607.17) (SI Table S1) and may contribute to the attachment of the virion to the algal cell surface. The relative abundance of these proteins is consistent with the frequency of fiber structures found in each trisymmetron, but the composition of these structures is unknown.

The estimated relative abundances of virion proteins were determined using the emPAI method (18) for the Method 1 data set. The distribution of the capsid proteins suggests a more complex assembly of PBCV-1 capsids than was previously assumed for a single MCP (Vp54) responsible for the particle architecture. We assume the MCP (A430L) is present in 1440 copies per virion for these calculations and other protein abundances were estimated from this value (Fig. 5B). The data indicate there are two capsid proteins of relatively high abundance (A430L and A011L), two capsid proteins were present at approximately one-half the abundance of these (A010R and A558L), one capsid protein present at one-third abundance (A622L), and two capsid proteins were present in relatively low abundance (A383R and A384dL). Assuming these ratios, icosahedral symmetry, and the fact that the virion is composed of 1680 capsids (64), each of the triangular facets of the icosahedron would contain seven proteins in ratios of 72:72:36:36:24:1:1. Recent structural analysis of PBCV-1 at 8.5 Å resolution indicates the capsomer volumes are more varied than previously thought (66), but how these capsids are arranged is not known. The trimeric capsomers may be homomeric (as previously thought), or possibly heteromeric utilizing the conserved beta-barrel domains as binding surfaces. This higher complexity of virion structure is consistent with several other large DNA viruses where multiple capsid proteins have been detected; herpes viruses have 4 to 7 capsid proteins (22, 33) and mimivirus has at least 5 capsid proteins (37). The emPAI method was used to estimate abundances of intracellular mature virion proteins of vaccinia virus (7) indicating a dynamic range of 1 to 1000 with certain core proteins being most abundant (i. e., A4L, A10L, F17R and A3L), as well as one with low abundance (i. e., E11L).

PBCV-1 proteome functionalities. The 148 virion proteins were grouped into 11 functional/structural categories (SI Fig. S3A) and compared to the distribution of CDSs of the overall genome (SI Fig. S3B). The majority (72%) of virion proteins are in the unknown function category. However, several functions are inferred by sequence similarity analyses and 13 of the 148 proteins have demonstrated functions that include DNA binding, cell signaling via phosphorylation, DNA degradation, virus structure, cell attachment, and polyamine biosynthesis such as homospermidine synthase. Among the identified CDSs are the restriction endonucleases R.CviAII (A252R) and R.CviAI (A579L) thought to be responsible for host DNA degradation early in the infection cycle (3).

Virion morphogenesis is one of the last events in the PBCV-1 replication cycle and it is reasonable that virion proteins are synthesized during the late phase. Most of the proteome (87%) is from genes expressed either late or early-late (65); however, the time of expression has not been determined for 23 new CDSs discovered with the resequence and annotation (SI Fig. S2). Eleven proteins are from genes transcribed in the early phase of replication: 7 of these proteins were detected by a single proteomic method with a relatively low number of unique peptides detected. Therefore, these 7 proteins require further verification. Three of these early proteins, A171R, A440L and A443R have unknown functions. The A456L protein has two conserved domains, a D5 N superfamily domain found in certain viral DNA primases (PfamA: PF08706.4) and a phage/plasmid primase P4 family C-terminal domain with predicted ATPase activity. The A548L protein has two conserved P-loop NTPase domains that are associated with DEXDc-, DEAD- and DEAH-box proteins, including the hepatitis C virus NS3 helicases (PfamA:

PF00176.16). Thus, these proteins might contribute to early transcriptional events that occur within minutes of infection.

PBCV-1 packaged host protein. The PBCV-1 proteome contains one protein (101 amino acids) derived from the host (GenBank: EFN53917.1; 4); the protein was detected by both proteomic methods. This protein is most similar to a fungal 93 amino acid *Naumovozyma dairenensis* CBS 421 nucleosome binding protein (NCBI reference sequence: XP_003667927.1) and similar to the HMGB-UBF_HMG-box, class II and III members of the HMG-box superfamily of DNA-binding proteins. It has no similarity to any PBCV-1 encoded protein. HMG-box containing proteins bind non-B-type DNA conformations with high affinity (45) and they are involved in regulation of DNA-dependent processes such as transcription, replication and DNA repair, all of which require changing the conformation of chromatin (49). Thus, this host protein may be important in initiating PBCV-1 gene expression, which occurs within minutes of infection (65). At least two other large DNA viruses contain chromosomal proteins in the virion. An HMG-box protein (HMG1) and a histone H2B.q protein occur in the Western Reserve strain of vaccinia virus (38) and murine cytomegalovirus virions have a histone H2A protein (22), suggesting large DNA viruses utilize host-derived proteins for DNA binding functions.

Presumed virion proteins that were not detected. A few proteins were expected to be packaged in PBCV-1 that were absent in the proteome analysis. As noted previously, PBCV-1 packages one or more enzymes involved in digesting the host cell wall during infection (29). Annotation of the PBCV-1 genome identified 5 enzymes that might be involved in this process - two chitinases, a chitosanase, a β 1-3 glucanase and a β & α 1,4 glucuoronic lyase (SI Table S1). Recombinant proteins indicated that all of these enzymes are functional (46, 47) and western blots suggested that one of the chitinases and the chitosanase were in the virion (47). However, none of these five proteins were detected in the proteome analysis. Consequently, the enzyme(s) involved in digesting the host cell wall is unknown.

Circumstantial evidence suggests that PBCV-1 and other chloroviruses package a small virus-encoded K^+ channel protein, named Kcv (12). It has been hypothesized that Kcv is involved in depolarizing the host membrane, which occurs immediately after virus infection. However, Kcv was not detected in this proteome study. On the other hand, at least one putative protein (A201L) with predicted physical/chemical transmembrane properties similar to Kcv was detected in the PBCV-1 virion with proteomic method 1. Thus, this methodology can detect small proteins with transmembrane domains, as in Kcv.

CONCLUSIONS

Re-sequencing and annotation of the 331 kbp chlorovirus PBCV-1 genome revealed that the virus encodes 416 predicted CDSs, using a minimum ORF size of 40 codons, and 11 tRNAs. Proteome analysis of highly purified PBCV-1 virions identified 148 virus-encoded proteins (about 35% of the coding capacity of the virus) and one host protein. Some of these proteins appear to be structural/architectural, whereas others have enzymatic, chromatin modification and signal transduction functions. However, 106 of these proteins have no known function or homologs in the existing gene databases except as orthologs with other chloroviruses, phycodnaviruses and NCLDVs. The genes encoding these proteins are dispersed throughout the virus genome and 84% are transcribed late or early-late in the infection cycle, which is consistent with virion morphogenesis.

Probably the biggest surprise is that so many virus-encoded proteins were detected in the virion and only one host encoded protein. However, except for the MCP Vp54, we cannot definitively assign a protein(s) to any of the other structural features of the virus, including the additional 6 major capsid-like proteins, the long spike structure, the surface fibers on the trisymmetrons, or the long glue protein homologs of PRD1 and the membrane protein dimer located at the edge of the trisymmetrons and internal membrane (66). These await further structural analyses. Obviously one question is: Are all of these virion-associated proteins essential for creating an infectious virus or are some of them the result of 'sloppy packaging', i. e., fortuitously associated with the particle. This is a difficult question to answer - but it is clear that PBCV-1 morphogenesis is selective in terms of what it incorporates; e.g., the virus packages 2 virus-encoded restriction endonucleases, but not their corresponding DNA methyltransferases. In addition, only one host protein was detected in the virion; no host membrane proteins were detected.

The PBCV-1 capsid protein composition may be somewhat flexible because the genes encoding 2 of the capsid proteins (A010R and A011L) can be deleted (6, 24), yet these deletion mutants are viable. This finding suggests some type of compensation in capsid protein utility. Among large DNA viruses, the number of capsid proteins ranges from 4 to 7 and these homologs are virion-associated (e. g., 22, 33, 37), thus the discovery of 7 putative capsid proteins in the PBCV-1 virion is consistent with this theme yet little is known how these proteins contribute to virion structure or function.

These data are essential for understanding the immediate-early events of infection such as binding, entrisome, macromolecular synthetic shutoff, DNA degradation, viral transcription, etc. (48). PBCV-1 is emblematic of the giant viruses in that they are large, complex, and highly diverse (11). When characterizing these viruses, the traditional meaning of the term “structural protein” (i. e., virion-associated) has lost its meaning. Giant virus virions incorporate both structural/architectural proteins as well as many other proteins with a wide range of functionalities likely directed at the immediate-early events of infection before viral transcription *de novo* is initiated. Why giant viruses have so many genes continues to intrigue virologists, but as more giant viruses are discovered there will be more opportunities to explore this question.

ACKNOWLEDGEMENTS

The UNL mass spectrometry facility is supported in part by NIH Grant P20 RR15635 from the COBRE Program of the National Center for Research Resources, NCI Cancer Center Support Grant P30 CA36727, and the Nebraska Research Initiative. Additional support was from NIH COBRE Grant P20RR015635 (DDD), NIH R0l GM32441 (JLVE), NSF-EPSCoR EPS-1004094 (JLVE), DOE DE-EE0003142 (JLVE), Discovery grant from NSERC (Canada) (CU), National Center for Research Resources 5P20RR016469 and NIGMS 8P20GM103427 (GD).

We thank Jaehyoung Kim and Joe Nietfeldt at the UNL Core for Applied Genomics and Ecology for the PBCV-1 sequencing.

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Figure legends

Figure 1. Proteomic methodologies for PBCV-1 virions.

Figure 2. SDS-PAGE protein separation and virion proteome mapped onto the PBCV-1 genome. The PBCV-1 genome was re-sequenced, assembled and annotated to correct existing sequence errors. The 416 predicted CDSs are represented as grey arrows running both clockwise and counter-clockwise along the genome (panel B). Note: the diagram is circular, but there is a break at the 12 o'clock position because the viral genome is a linear molecule with terminal inverted repeats and closed hairpin ends. The terminal sequences (inverted repeats and hairpin ends) were found to be identical to those reported previously (68). The polycistronic gene encoding 11 tRNAs is presented in red (see 6 o'clock). The 148 proteins of the virion proteome were determined using two independent mass spectrometry-based methods (see Materials and Methods). The results of each method are shown, proteins determined uniquely by method 1 are presented in magenta, proteins determined uniquely by method 2 are presented in blue, proteins determined by both methods 1 and 2 are presented in brown. The map was developed from the CGView software (44). Panel A shows the distribution of virion proteins with SDS polyacrylamide gel separation. The numbers to the left indicate the gel fragment that was analyzed.

Figure 3. Expression stage distribution of PBCV-1 CDSs, a quartile analysis. The number of all coding CDSs (panel A) expressed either during the early (blue), early-late (red), late (green), or not determined (nd, purple) is shown as a function of the genome map position. The genome map is divided into four regions, both the direct ("R" genes)

and reverse ("L" genes) on each half of the genome (left half gene numbers: 001 – 327; right half gene numbers: 328 – 692). Panel B shows the distribution of virion-associated CDSs with respect to expression stage and genome position.

Figure 4. Mass versus pI distribution of PBCV-1 virion CDSs identified by two independent proteomic methods. The virion proteins are displayed as a function of their intrinsic molecular weight and isoelectric point. The results of each method are shown, proteins determined uniquely using method 1 are presented in magenta, proteins determined uniquely using method 2 are presented in blue, proteins determined using both methods 1 and 2 are presented in brown. Note that Method 2 was especially useful for discovering a set of low molecular weight proteins that were not detected with Method 1.

Figure 5. Capsid protein paralog classes and relative abundances in PBCV-1. The seven capsid-like proteins detected in the PBCV-1 virion were evaluated against a dataset of chloroviruses, including PBCV-1 (RefSeq NC_000852.5), NY-2A (RefSeq NC_009898.1), AR158 (RefSeq NC_009899.1), MT325 (GenBank DQ491001.1), FR483 (RefSeq NC_008603.1), and ATCV-1 (RefSeq NC_008724.1). These 7 proteins had homologs in each of the viruses that separate into 5 distinct paralog classes (I – V) as shown in the neighbor joining tree (panel A) (see SI Table S3 for CDS accession numbers). The sequence for PBCV-1 A384dL, a member of paralog class V which is distantly related, was used as the out-group to root the phylogenetic analysis using the website www.phylogeny.fr (10). Muscle was used to align the sequences. Bootstrap analysis was used to construct the tree. Similar tree topologies were produced by

maximum likelihood and maximum parsimony analyses. The values on the branches are the percentage of bootstrap support (200 replicates). Only bootstrap values >50% are shown. The distance bar represents 0.2 amino acid substitution per site. Panel B presents the PBCV-1 capsid proteins grouped into 5 paralog classes within their two conserved domains. The D1 domain (green, column A) and the D2 (red, column D) NCLDV superfamily capsid domain were previously determined by structure analysis of the Vp54 MCP (31) (panel C). The relative abundances as determined with the emPAI method for the Method 1 data are listed to the right of the table, as well as the hypothetical estimated copies per virion of each capsid protein. Note, the two proteins of relatively lower abundance contain chitin binding peritrophin-A conserved domains (columns C and E).

Table 1. PBCV-1 virion proteome

Protein (CDS)	Da	pI	Expression stage	Function or putative function	Proteomic method	TM prediction[a]		
						T	H	P
A010R	44998	5.2	Late	Capsid protein; PfamA: PF4451.5 [1.9e-50]	1&2	0	0	0
A011L	45076	5.4	Late	Capsid protein; PfamA: PF4451.5 [2.9e-61]	1&2	0	0	0
A014R	141382	6.3	Late	Unknown protein	1&2	0	0	0
A018L	137639	4.9	Late	Unknown protein; PfamA: PF06598.4 [Chlorovirus glycoprotein repeat] [1.2e-11]	1	0	0	0
A025/027/029L	140095	4.4	Late	Unknown protein	1&2	0	0	0
A034R	35163	10.4	Late	Protein kinase; PfamA: PF00069.18 [Protein kinase domain] [1.4e-07]	1&2	0	1	0
A035L	65606	8.9	Late	Unknown protein	1&2	0	1	0
A041R	44315	10.8	Late	Unknown protein	1&2	0	1	0
A051L	22804	8.6	Late	Unknown protein	1&2	1	2	1
A085R	27812	7.8	Late	Prolyl 4-hydroxylase; PfamA: PF03171.13 [2OG-Fe(II) oxygenase superfamily] [3.5e-11]	1&2	1	1	1
A092/093L	49577	10.7	Early-Late	Unknown protein; PfamA: PF08789.3 [PBCV-specific basic adaptor domain] [1.2e-15]	1&2	0	0	0
A121R	12486	10.8	Early-Late	Unknown protein	1&2	0	0	0
A122/123cL	4912	10.1	N/A	Unknown protein	1	0	0	0
A122/123R	137880	5.0	Late	COG5295 [Autotransporter adhesin] [4e-12]; PfamA: PF06598.4 [Chlorovirus glycoprotein repeat] [3.6e-11] / PF11962.1 [Domain of unknown function (DUF3476)] [8.2e-66]	1	0	31	0
A127R	27126	10.1	Late	Unknown protein	1&2	0	0	0
A136R	16367	11.5	N/A	Unknown protein	1&2	0	0	0
A137R	8777	10.9	Early	Unknown protein	1	0	0	0

A139L	17701	8.4	Late	Unknown protein	1&2	2	2	2
A140/145R	120898	11.0	Early-Late	Unknown protein	1&2	0	1	0
A157L	12328	3.9	Early-Late	Unknown protein	2	1	1	1
A164aR	7094	5.8	N/A	Unknown protein	2	1	0	0
A165aL	19024	10.1	N/A	Unknown protein	1&2	0	0	0
A168R	18317	4.6	Late	Unknown protein	1&2	1	1	1
A171R	42413	10.2	Early	Unknown protein	1&2	0	0	0
A172aL	6053	9.8	N/A	Unknown protein	1	1	1	0
A173L	31933	8.2	Early	COG1752 [Predicted esterase of the alpha-beta hydrolase superfamily] [2e-06]; PfamA: PF01734.15 [Patatin-like phospholipase] [4.2e-27]	1	0	2	0
A174L	7453	12.2	N/A	Unknown protein	2	0	0	0
A176L	9167	11.3	N/A	Unknown protein; PfamA: PF08789.3 [PBCV-specific basic adaptor domain] [9e-12]	1&2	0	0	0
A188aR	17326	10.0	N/A	COG0417 [DNA polymerase elongation subunit (family B)] [3e-07]; PfamA: PF00136.14 [DNA polymerase family B] [6.5e-17]	1	0	0	0
A189/192R	143575	11.4	Late	Unknown protein	1&2	0	0	0
A196L	17456	8.4	Late	Unknown protein	2	3	3	1
A201aL	6787	8.8	N/A	Unknown protein	1	0	0	0
A201L	10005	10.7	Early-Late	Unknown protein	1	2	2	2
A202L	12232	5.0	Early-Late	Unknown protein	2	0	0	0
A203R	24011	6.0	Late	Unknown protein	1&2	1	2	0
A205R	22452	12.1	Late	Unknown protein; PfamA: PF08789.3 [PBCV-specific basic adaptor domain] [4.2e-16]	1&2	0	0	0
A213L	16483	4.5	Early-Late	Unknown protein	1&2	1	1	1
A217L	45248	9.9	Early-Late	Unknown protein	1&2	0	0	1
A219/222/226R	77797	7.0	Early	COG1215 [Glycosyltransferases probably involved in cell wall biogenesis] [4e-06]; Swissprot: P58932 [RecName: FullCellulose synthase catalytic subunit (UDP-forming)]	1	9	8	10

				[6e-07]				
A227L	15689	10.0	Late	Unknown protein	1&2	0	0	0
A230R	22055	8.4	Late	Unknown protein	1&2	4	4	4
A231L	43644	9.9	Early-Late	Unknown protein	1&2	1	0	0
A237R	58565	9.5	Late	Homospermidine synthase	1&2	0	0	0
A245R	19748	9.3	Late	Cu/Zn superoxide dismutase	1&2	1	1	0
A246R	12017	11.5	Late	Unknown protein	1&2	0	0	0
A252R	39856	10.3	Early	R.CviAII restriction endonuclease	1&2	0	0	0
A255R	17300	5.1	N/A	Unknown protein	1	0	0	0
A256/257L	96729	7.2	Early-Late	Unknown protein	1	0	0	0
A260aR	7742	11.9	N/A	Unknown protein	1	0	0	0
A262/263L	29470	9.6	N/A	Unknown protein	1&2	2	3	2
A271L	31114	7.1	Early-Late	COG2267 [Lysophospholipase] [1e-07]	1	0	3	0
A273L	15713	9.9	Late	PF03713.6 [Domain of unknown function (DUF305)] [6.8e-13]	1	3	3	3
A278L	69231	10.8	Late	Protein kinase; PfamA: PF00069.18 [Protein kinase domain] [1.2e-07] / PF08789.3 [PBCV-specific basic adaptor domain] [7.5e-10]	1&2	0	1	0
A282L	63371	10.8	Late	Protein kinase; PfamA: PF00069.18 [Protein kinase domain] [1.2e-07] / PF08789.3 [PBCV-specific basic adaptor domain] [1.3e-17]	1&2	0	1	0
A284L	30766	9.2	Early-Late	Amindase	1&2	0	0	0
A286R	43042	9.6	Late	Unknown protein	1&2	0	0	0
A287R	31349	9.4	Early-Late	PfamA: PF01541.17 [GIY-YIG catalytic domain] [4.2e-11] / PF07453.6 [NUMOD1 domain] [8.6e-11]	1	0	0	0
A295L	35626	7.9	Early-Late	Fucose synthetase; Swissprot: Q9LMU0 [RecName: FullPutative GDP-L-fucose synthase 2 AltName: FullGDP-4-keto-6-deoxy-D-mannose-3 5-epimerase-4-reductase 2 ShortAtGER2] [1e-100]	1	0	0	0

A296R	17393	12.2	Late	Unknown protein	1&2	0	1	1
A304R	9490	5.8	Late	Unknown protein	1	0	0	0
A305L	22910	10.7	Late	Protein phosphatase; Swissprot: Q9BY84 [RecName: FullDual specificity protein phosphatase 16 AltName: FullMitogen-activated protein kinase phosphatase 7 ShortMAP kinase phosphatase 7 ShortMKP-7] [7e-12]	1&2	0	0	0
A310L	18268	8.5	Late	Unknown protein	1&2	0	0	0
A314R	9114	6.7	Late	Unknown protein	1&2	1	1	1
A316R	48779	10.7	Late	Unknown protein	1&2	0	1	0
A320R	15685	10.5	Late	Unknown protein	1&2	1	1	1
A321R	12830	8.8	Late	Unknown protein	1	2	2	2
A322L	20039	5.0	Late	Unknown protein	1&2	1	1	1
A339L	7372	11.1	Early-Late	Unknown protein	1	0	0	0
A342L	63813	9.2	Early-Late	Unknown protein	1&2	1	1	1
A349L	21077	10.0	Early-Late	Unknown protein	1&2	0	1	0
A350R	14676	9.7	N/A	PfamA: PF12239.1 [Protein of unknown function (DUF3605)] [4.4e-23]	2	0	0	0
A352L	23310	3.6	Late	Swissprot: Q5UQF7 [RecName: FullUncharacterized protein R489 Flags: Precursor] [1e-05]	1&2	0	1	1
A356R	12512	10.5	N/A	Unknown protein	1	0	0	0
A363R	128448	10.9	Early	Swissprot: P0C9B2 [RecName: FullPutative ATP-dependent RNA helicase Q706L] [2e-06]	1&2	0	2	0
A375R	19085	9.4	Early-Late	Unknown protein	1&2	2	2	2
A378L	29219	9.4	Late	Unknown protein	1&2	1	1	0
A383R	52511	5.2	Late	Capsid protein; Pfam: PF04451.5 [Large eukaryotic DNA virus major capsid protein] [1.6e-25]	1&2	0	0	0
A384bL	6809	9.0	N/A	Unknown protein	2	1	1	1
A384dL	69009	8.0	Early-Late	Capsid protein; PfamA: PF01607.17 [Chitin binding Peritrophin-A domain] [2.4e-07] / PF04451.5 [Large eukaryotic DNA virus	1&2	1	2	1

				major capsid protein] [2e-11]				
A398L	12987	9.9	Late	Unknown protein	1&2	2	3	3
A400R	13634	9.5	Early-Late	Unknown protein	2	0	0	0
A405R	53502	10.3	Late	Unknown protein	1&2	1	2	1
A407L	23382	8.9	Late	Unknown protein	1&2	1	2	2
A413L	26998	9.5	Late	Unknown protein	1&2	2	2	2
A414R	10612	10.8	Late	Unknown protein	1&2	2	2	2
A420L	7918	6.4	Late	Unknown protein	2	1	1	1
A421R	11056	10.1	Late	Unknown protein	1&2	1	1	1
A423R	18458	6.5	Late	Unknown protein	2	0	1	0
A430L	48165	7.5	Late	Major capsid protein	1&2	0	0	0
A436L	6932	13.0	N/A	Unknown protein; Pfam: PF08789.3 [PBCV-specific basic adaptor domain] [1.5e-16]	1	0	0	0
A437L	10876	11.0	Late	PfamA: PF05854.4 [Non-histone chromosomal protein MC1] [5.9e-07]	1&2	0	1	0
A438L	8988	10.7	Early-Late	Glutaredoxin	2	0	0	0
A440L	10112	11.1	Early	Unknown protein	1&2	0	0	0
A443R	34961	5.3	Early	Unknown protein	1	0	0	0
A448L	12369	10.4	Late	Protein disulphide isomerase with heme binding site	1&2	0	0	0
A454L	31194	4.7	Early-Late	Unknown protein	1&2	1	1	0
A456L	75235	5.5	Early	COG3378 [Predicted ATPase] [3e-06]; PfamA: PF08706.4 [D5 N terminal like] [3.9e-09]	1	0	0	0
A465R	13528	10.2	Early-Late	COG5054 [Mitochondrial sulfhydryl oxidase involved in the biogenesis of cytosolic Fe/S proteins] [4e-06]; PfamA: PF04777.6 [Erv1 / Alr family] [3.5e-22]	1&2	0	0	0
A476R	37393	4.4	Early-Late	Swissprot: Q6Y657 [RecName: FullPutative ribonucleoside-diphosphate reductase small chain B AltName: FullRibonucleotide reductase small subunit B AltName: FullRibonucleoside-diphosphate reductase	1	0	0	1

				R2B subunit] [1e-113]				
A480L	9838	10.0	Late	Unknown protein	1&2	2	2	2
A484L	18604	9.6	Early-Late	Unknown protein	1&2	0	0	0
A488R	34631	5.0	Late	Swissprot: Q5UQL4 [RecName: FullUncharacterized protein L417] [2e-09]	1&2	0	3	0
A497R	15378	10.4	Late	Unknown protein	1&2	2	2	1
A500L	38463	5.0	N/A	Unknown protein	1&2	1	2	1
A502L	11069	9.4	Late	Unknown protein	2	1	1	1
A520L	11674	10.7	Late	Unknown protein	2	0	0	0
A521aL	22578	6.3	N/A	Swissprot: O55742 [RecName: FullUncharacterized protein 136R] [2e-07]	1&2	0	0	0
A521L	23738	11.4	Early-Late	Unknown protein	1&2	0	0	0
A523R	19096	9.6	Late	Unknown protein	1&2	0	0	0
A526R	16434	9.3	Late	Unknown protein	1&2	0	1	0
A527R	11605	10.7	Late	Unknown protein	1&2	0	0	0
A531L	7670	7.5	Late	Unknown protein	2	1	1	1
A532aL	5479	4.5	N/A	Unknown protein	2	1	1	1
A532L	8698	9.7	Late	Unknown protein	1&2	1	1	1
A533R	40132	3.8	Early-Late	Unknown protein	1&2	0	0	0
A534R	11783	9.7	N/A	Unknown protein	1&2	0	0	0
A535L	8210	4.7	Early-Late	Unknown protein	1&2	0	0	0
A536L	8485	10.0	Early-Late	Unknown protein	1&2	1	1	0
A540L	127197	6.2	Late	Unknown protein	1	0	0	0
A548L	57432	9.5	Early	PfamA: PF00176.16 [SNF2 family N-terminal domain] [6.7e-34] / PF00271.24 [Helicase conserved C-terminal domain] [1.5e-10]	1	0	0	0
A558L	45547	5.1	Early-Late	Capsid protein; PfamA: PF04451.5 [Large eukaryotic DNA virus major capsid protein] [6.6e-60]	1&2	0	0	0
A559L	24034	10.2	Late	Unknown protein	1&2	1	1	0

A561L	71004	9.9	Late	Unknown protein	1&2	1	2	1
A565R	73169	7.3	Early-Late	Unknown protein	1&2	1	1	1
A567L	17418	10.1	Early-Late	Unknown protein	1	0	0	0
A571R	12972	12.0	Late	Pfam hit: PF08789.3 [PBCV-specific basic adaptor domain] [5.7e-17]; Refseq best hit: YP_001426112 [hypothetical protein FR483_N480R (Paramecium bursaria Chlorella virus FR483)] [3e-39]	1	0	0	0
A572R	20606	7.1	Late	Unknown protein	1&2	0	0	0
A577L	15442	11.0	Late	Unknown protein	1&2	0	0	0
A579L	27445	10.1	Late	R.CviAI restriction endonuclease	1&2	0	0	0
A586R	8567	11.8	N/A	Unknown protein	1	0	0	0
A598L	41558	6.9	Early-Late	COG0076 [Glutamate decarboxylase and related PLP-dependent proteins] [5e-06]; PfamA: PF00282.12 [Pyridoxal-dependent decarboxylase conserved domain] [1.1e-17]	1	0	0	0
A605L	17769	10.9	Early-Late	Unknown protein	1&2	1	1	1
A612L	13587	8.7	Late	Histone H3K27 methylase	2	0	0	0
A614L	64733	11.2	Late	Protein kinase; PfamA: PF00069.18 [Protein kinase domain] [5.6e-11]	1&2	0	0	0
A617R	37586	9.9	Early-Late	Swissprot: Q5UQJ6 [RecName: FullPutative serine/threonine-protein kinase R400] [7e-12]	1	0	0	0
A621L	12935	9.5	Late	Unknown protein	1	2	2	2
A622L	58097	5.7	Late	Capsid protein; PfamA: PF04451.5 [Large eukaryotic DNA virus major capsid protein] [1.7e-66]	1&2	0	0	0
A624R	13570	9.3	Late	Unknown protein; PfamA: PF09945.2 [Predicted membrane protein (DUF2177)] [3.4e-26]	1	3	4	3
A625R	49945	10.7	Late	COG0675 [Transposase and inactivated derivatives] [1e-06]; PfamA: PF12323.1 [Helix-turn-helix domain] [1.4e-06] / PF07282.4 [Putative transposase DNA-binding domain] [6.7e-18]	1	0	0	0
A627R	49629	11.1	Late	Unknown protein	1&2	1	3	0

A629R	86292	7.5	Early-Late	PfamA: PF03477.9 [ATP cone domain] [8.5e-15] / PF00317.14 [Ribonucleotide reductase all-alpha domain] [7.9e-19] / PF02867.8 [Ribonucleotide reductase barrel domain] [2e-194]	1	0	0	0
A631L	10392	9.9	N/A	Unknown protein	1	0	0	0
A643R	53097	11.3	Late	Unknown protein	1&2	0	0	0
A644R	19207	6.0	Late	Unknown protein	1&2	0	0	0
A655L	12002	11.4	N/A	Unknown protein	1	0	1	0
A676R	42432	10.6	Late	Unknown protein; PfamA: PF08789.3 [PBCV-specific basic adaptor domain] [1.9e-17] / PF08793.3 [2-cysteine adaptor domain] [1.8e-15]	1&2	0	0	0
A678R	41287	10.3	Late	Unknown protein	1&2	0	3	0
A686L	18316	6.9	Early	Unknown protein	1	0	1	0

a – Transmembrane regions of the protein were predicted by TMHMM [T] (30), HMMTOP [H] (50), and Phobius [P] (20) methods. For all the method default parameters were used for the prediction. The number shown in the table is the number of helixes predicted by the method.

Virus purification:
Differential centrifugation
Protease-wash
Rate-zonal gradient centrifugation Isopycnic gradient centrifugation

Method 1
SDS-PAGE/Trypsin/HPLC/Ion Spray/ MS-MS

Virus solubilzation:
+/- alkylation
Reduction
+/- phenol or phenol-toluene extraction
SDS/crystal violet/Ficoll
100 ^{o}C

Protein separation and fragmentation:
One-dimensional SDS-PAGE
Sypro-Ruby staining
Gel slices
Imbibe with trypsin
Eluted tryptic fragments

Peptide separation:
Tryptic fragments injected onto C-18 reverse phase LC

Mass spectrometry:
Electrospray ionization injection
Q-TOF Ultima
MS/MS acquisitions – 60 to 1900 daltons

Mass ion analyses:
Masslynx produce peak lists
MASCOT to NCBI (nr database)
Mass accuracy at 0.1 daltons
Protein identification: $p < 0.5$

Relative abundance:
emPAI

Method 2
PPS/Trypsin/HPLC/MS-MS

Virus solubilization:
PPS
100 ^{o}C
Reduction
Alkylation

Protein fragmentation:
Trypsin
Acid to hydrolyse PPS

Peptide separation:
Tryptic fragments injected onto C-18 reverse phase LC

Mass spectrometry:
LTQ-Velos or LCQ Deca XP Plus
MS/MS acquisitions – exclusion list 100 daltons

Mass ion analyses:
Xcalibur produced peak lists
X!Tandem and SPIRE to custom DB
Mass Accuracy at 2.5 Da
Protein identification <= 1% FDR

Figure 1

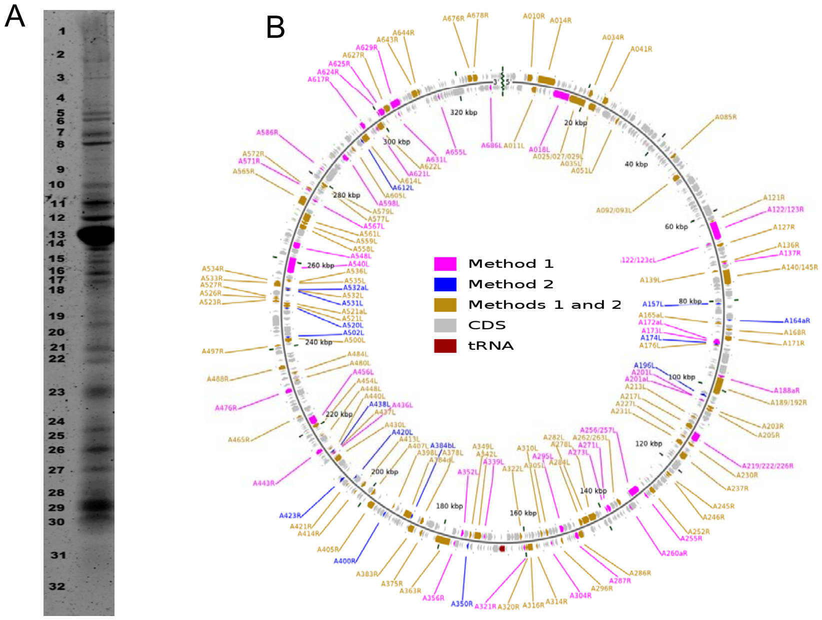
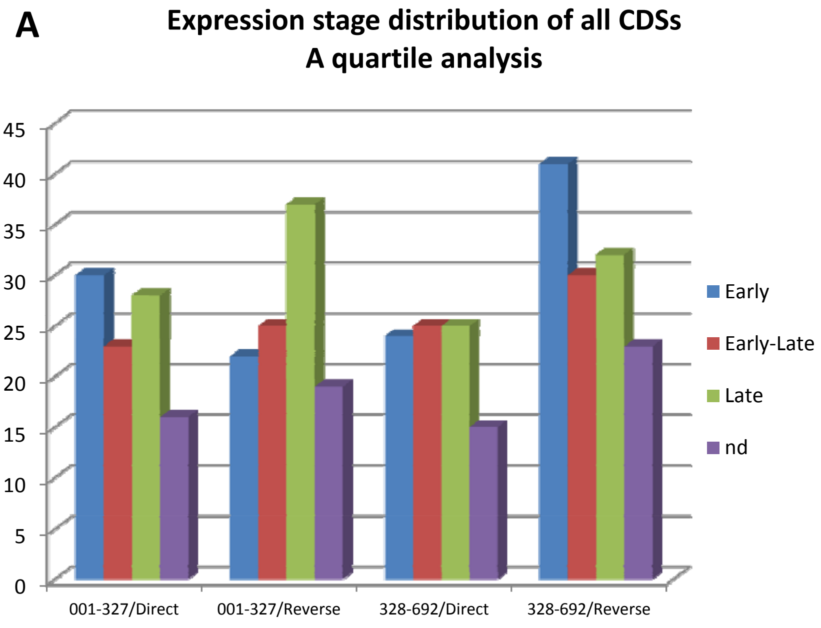

A
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
B
Method 1
Method 2
Methods 1 and 2
CDS
tRNA
20 kbp
40 kbp
60 kbp
80 kbp
100 kbp
120 kbp
140 kbp
160 kbp
180 kbp
200 kbp
220 kbp
240 kbp
260 kbp
280 kbp
300 kbp
320 kbp
A010R
A014R
A034R
A041R
A085R
A092/093L
A121R
A122/123R
A127R
A136R
A137R
A140/145R
122/123cL
A139L
A157L
A164aR
A165aL
A172aL
A173L
A174L
A176L
A168R
A171R
A196L
A201L
A201aL
A213L
A217L
A227L
A231L
A188aR
A189/192R
A203R
A205R
A219/222/226R
A230R
A237R
A245R
A246R
A252R
A255R
A260aR
A256/257L
A262/263L
A271L
A273L
A278L
A282L
A284L
A295L
A305L
A310L
A322L
A339L
A342L
A349L
A352L
A286R
A287R
A296R
A304R
A314R
A316R
A320R
A321R
A350R
A356R
A363R
A375R
A383R
A400R
A405R
A414R
A421R
A423R
A443R
A384bL
A384dL
A378L
A398L
A407L
A413L
A420L
A430L
A436L
A437L
A438L
A440L
A448L
A454L
A456L
A480L
A484L
A465R
A476R
A488R
A497R
A500L
A502L
A520L
A521L
A521aL
A531L
A532L
A532aL
A535L
A536L
A540L
A523R
A526R
A527R
A533R
A534R
A548L
A558L
A559L
A561L
A567L
A577L
A579L
A565R
A571R
A572R
A586R
A598L
A605L
A612L
A614L
A621L
A622L
A631L
A655L
A686L
A011L
A018L
A025/027/029L
A035L
A051L
A617R
A624R
A625R
A627R
A629R
A643R
A644R
A676R
A678R

Figure 2.


A
Expression stage distribution of all CDSs
A quartile analysis
45
40
35
30
25
20
15
10
5
0
001-327/Direct
001-327/Reverse
328-692/Direct
328-692/Reverse
Early
Early-Late
Late
nd

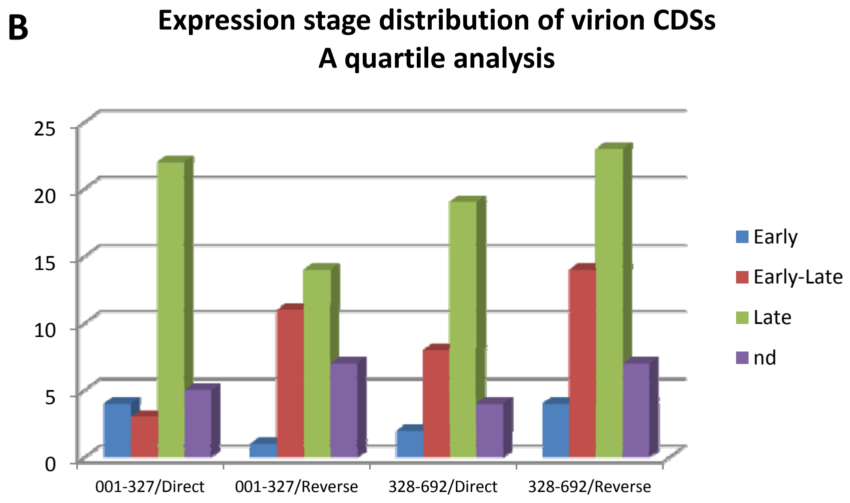

B
Expression stage distribution of virion CDSs
A quartile analysis
25
20
15
10
5
0
001-327/Direct
001-327/Reverse
328-692/Direct
328-692/Reverse
Early
Early-Late
Late
nd

Figure 3

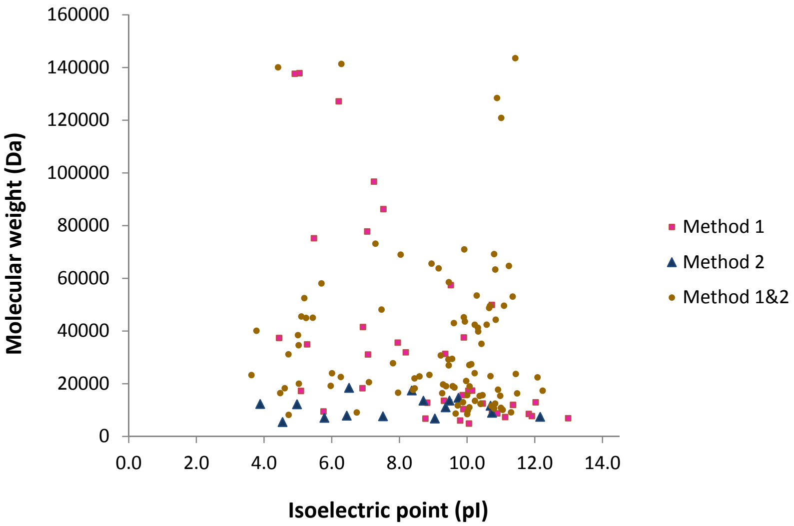
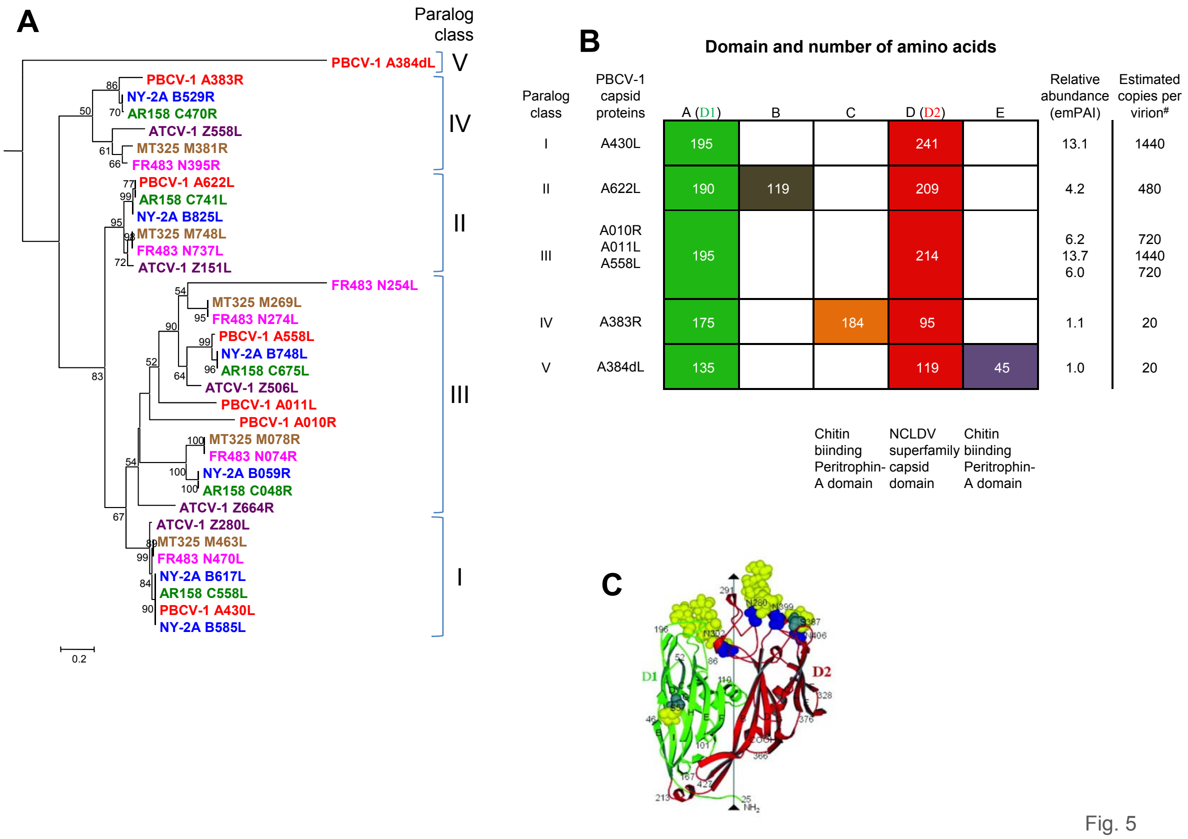

160000
140000
120000
100000
80000
60000
40000
20000
0
Molecular weight (Da)
0.0
2.0
4.0
6.0
8.0
10.0
12.0
14.0
Isoelectric point (pI)
Method 1
Method 2
Method 1&2

Figure 4



Domain and number of amino acids

Paralog class	PBCV-1 capsid proteins	A (D1)	B	C	D (D2)	E	Relative abundance (emPAI)	Estimated copies per virion#
I	A430L	195			241		13.1	1440
II	A622L	190	119		209		4.2	480
III	A010R A011L A558L	195			214		6.2 13.7 6.0	720 1440 720
IV	A383R	175		184	95		1.1	20
V	A384dL	135			119	45	1.0	20
				Chitin biinding Peritrophin-A domain	NCLDV superfamily capsid domain	Chitin biinding Peritrophin-A domain		

Fig. 5

Supplemental Information

Paramecium bursaria Chlorella Virus 1 Proteome Reveals Novel Architectural and Regulatory Features of a Giant Virus

David D. Dunigan, Ronald L. Cerny, Andrew T. Bauman, Jared C. Roach, Leslie C. Lane, Irina V. Agarkova, Kurt Wulser, Giane M. Yanai-Balser, James R. Gurnon, Jason C.Vitek, Bernard J. Kronschnabel, Adrien Jeannard, Guillaume Blanc, Chris Upton, Garry A. Duncan, O. William McClung, Fangrui Ma, James L. Van Etten

Genome re-sequencing with Roche 454 Life Sciences GS FLX Titanium

Preliminary proteomic analyzes using the existing PBCV-1 gene annotations (NCBI Refseq: NC_000852) revealed possible errors in the genome sequence, which prompted re-sequencing of the PBCV-1 genome. PBCV-1 DNA was purified from virions that had been treated with 10 units DNase I per ml in 50 mM Tris-HCl pH 7.8/1 mM $CaCl_2$/10 mM $MnCl_2$ at 37°C for 1 hr, then prepared as described above, using the UltraClean®Blood DNA Isolation Kit (MO BIO Laboratories, Carlsbad, CA). The DNA was evaluated for quantity and quality by measuring absorbance at 260 and 280 nm with a Thermo Scientific NanoDrop 2000 spectrophotometer, and by measuring fluorescence of dye-augmented DNA using the PicoGreen and a Qubit fluorometer (Invitrogen, Carlsbad, California). Using the Roche Rapid Library Preparation method for GS FLX Titanium chemistry (Roche 454 Life Sciences, Branford, Connecticut), sample DNA was fragmented by nebulization. DNA fragments were end repaired with polynucleotide kinase and T4 DNA polymerase, then purified by size exclusion chromatography.

Selected DNA fragments were ligated to a Rapid Library Multiplex Identifier (MID) adaptor designed for GS FLX Titanium chemistry. The MID adaptors were designed with a unique decamer sequence to facilitate multiplex sequencing with the 454 technology, such that the resulting library reads can be reliably sorted after sequencing using SFF software tools. MID adaptor ligated DNA fragments were again size selected by chromatography, quantified with a TBS-380 mini-fluorometer (Promega, Madison, Wisconsin). The Rapid Library quality was assessed with an Agilent Bioanalyzer High Sensitivity DNA chip (Agilent Technologies, Santa Clara, California). The average fragment length was between 600 bp and 900 bp, with the lower size cut-off at less than 10% below 350 bp. Pooled DNAs were titrated to obtain the optimal copies per bead (cpb). After titration, 3 cpb was chosen as the best DNA and bead ratio and corresponding amounts of DNA were added to the subsequent emPCR reactions. EmPCR was performed with the 454/Roche Lib-L (LV) kits following manufacturer's protocol for the Roche 454 GS FLX Titanium.

Deep pyrosequencing and data processing

The emPCR products were sequenced using Roche-454 GS FLX Titanium chemistry. PBCV-1 DNA was sequenced twice giving a total of 98,258 quality-filtered reads. Raw reads were filtered according to length and quality criteria. Filter-pass reads were parsed into sample-barcoded bins and ported to a local database

The raw data from the 454 pyrosequencing machine were first processed through a quality filter that removed sequence reads that did not meet the following criteria: i) A complete forward primer and barcode. ii) ≤ 2 “N” in a sequence read, where N is equivalent to an interrupted and resumed signals from sequential flows. iii) 200 nt ≤ sequence length ≤ 500 nt. iv) Average quality score ≥ 20. After filtering, each read was trimmed to remove 3' adapter and primer sequences and was parsed by a MID adaptor barcode. The corresponding QUAL file also was updated to remove quality scores from reads not passing quality filters. The files are associated with sample information in a hierarchical manner in MySQL tables. The processed data and the MySQL database tables were stored on a database server and shared within the assembly/annotation team.

Genome assembly

Genome assembly was achieved using both automated pipeline and hand-curation methods. Initially, the sff files were processed with the 454 Life Sciences GS De novo Assembler software (program version 2.3). The sample was passed through the program using default settings. Adjustments to those default settings gave no significant improvement in the assembled sequence. The sample assembled into 12 contigs. Additionally, 454 Life Science GS Mapper software was used with the original PBCV-1 genome used as the reference sequence; this too resulted in multiple contigs (>12) assigned to PBCV-1.

The average sequence depth of coverage was >40X over the entire PBCV-1 genome from duplicate sequencing runs; however, some regions had approximately100X coverage while there was no coverage in other regions (i. e., 11 contig gaps). As part of this sequencing project, 10 PBCV-1 antigenic mutants were also sequenced (samples prepared and processed as described above). The mutants were also passed through the GS De Novo Assembler and Mapper software programs. Both methods yielded multiple contigs for each viral genome. One persistent major gap region observed in all of the PBCV-1 isolates involved the *a122/123r* gene region, which contains highly repetitive sequences, perhaps explaining why the gsMapper and gsAssembler programs were unable to assign sequencing reads to this region. This region was re-sequenced with Sanger-based methods and the revised *a122/123r* gene sequence was used to fill in the gap between these two adjacent contigs. Sequencing the PBCV-1 antigenic mutants also proved helpful, because we obtained at least one read from at least one antigenic mutant for each of the remaining gaps. The final sequencing problem occurred at the 5' and 3' ends of the sequence, which are reverse complementary repeats of one another (5). One of the PBCV-1 antigenic mutants had reads that extended to near one end of the genome. This region was reverse complemented and used to fill in the gap at the other end of the genome.

Identification of the PBCV-1 contigs

The PBCV-1 contigs were identified by BLAST searches (1) against the NCBI non-redundant/nucleotide database limited to Chlorovirus (tax id: 181083). The contigs were assumed to match viruses that infect *C. variabilis* (PBCV-1, NY-2A or AR158). Each contig was assigned to a virus based on the best BLAST hit. Most of the reads (99.28%) fit PBCV-1, seven relatively small contigs were ambiguous as to their BLAST search and discarded.

Genome annotation

The genome annotation was conducted using a semi-automatic in-house annotation pipeline. The majority of protein-coding genes were annotated with the

Genome Annotation Transfer Utility (GATU) tool using the PBCV-1 genome and gene calls (Refseq: NC 000852.4) as the reference genome (7). The GATU tool was used iteratively, initially to accept ORFs that were substantially unchanged (100% identity, Unassigned ORFs >95% identity), creating a list of 613 ORFs. The second pass identified ORFs that had substantially changed, e.g., a few cases two adjacent ORFs were found to be a single ORF due to a single nucleotide polymorphism (SNP) resulting in a stop-codon. The third pass selected all New Annotations and all Unassigned-ORFs with percent identity values above zero. Where two ORFs had identical starts or stops, the larger ORF was selected and the smaller one was not considered further. In the fourth iteration, GATU was used where the "third iteration" with all ORFs (both assigned and unassigned) was the reference sequence and the newly 454 sequenced and assembled PBCV-1 was annotated. The result was a list of New Annotations of the ORFs, with no Unassigned-ORFs. These were evaluated by eye to determine if there were overlapping and in-frame ORFs; there were none. The list contained 802 ORFs. These gene calls were then examined for predicted function.

Functional annotations (gene and protein properties) of the called genes were assigned to give both qualitative and qualitative data for the determined ORFs. Transfer RNAs were predicted using the tRNAscan-SE software (3). Gene calls were checked using the following 5-step process: i) putative homologs were identified by searching the protein sequences against the Swiss-Prot (8) and RefSeq (9) protein databases using the BLASTp (1) program (e-value < 1e-5). Because of very strong similarities between *C. variabilis* NC64A infecting viruses, hits from PBCV-1, NY2A and AR158 viruses were discarded in RefSeq while only previously existing entries from PBCV-1 were ignored in the Swiss-Prot alignments. Only the best hit from the two databases was kept and assigned as possible homologs of the predicted ORFs. ii) KEGG terms were assigned by submitting the entire predicted proteome to the KEGG Automatic Annotation Server [KAAS] (4), using the Bidirectionnal Best Hit method with an extended "Representative for GENE" reference dataset, combining 30 complete genomes ranging from eukaryotes to prokaryotes. iii) Genes were also assigned to a functional cluster using the BLASTp program against the Clusters of Orthologous Groups [COG] (6) dataset and assigning the best-hit's cluster to the query protein (e-value < 1e-5). iv) Protein domain/family predictions were made using PfamScan software (e-value < 1e-5), keeping only matches from the manually curated portion of the Pfam database (2). v) And finally, annotations were manually added to genes when experimental evidence from the literature supported the existence of a protein or characterized its function.

Table S1. PBCV-1 genes and gene annotations

Gene	Start	End	%AT	nt	aa	Da	pI	Stage	Virionic	COG	PfamA	BLASTp	Swissprot	Product	TM prediction[1]		
															T	H	P
a001L	280	549	68	270	89	10191	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A002L	512	1063	66	552	183	21545	9.4	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a002aR	1022	1177	66	156	51	5820	9.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A002bL	1174	1335	56	162	53	6037	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A002cR	1367	1513	14	147	48	5331	11.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a002dR	1408	1539	12	132	43	4606	12.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A003R	1792	2217	70	426	141	15974	8.5	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	1	1
a004L	1891	2127	58	237	78	8746	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a004aL	2221	2361	52	141	46	5788	10.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A005R	2288	3094	66	807	268	28726	6.1	Early	N/A	COG0666 [FOG: Ankyrin repeat] [1e-05]	PF00023.23 [Ankyrin repeat] [6.3e-11]	YP_001426468 [hypothetical protein FR483_N836L (Paramecium bursaria Chlorella virus FR483)] [2e-44]	Q54KA7 [RecName: FullAnkyrin repeat PH and SEC7 domain containing protein secG] [1e-29]	Unknown protein	0	0	0
a006L	2393	2611	60	219	72	8415	8.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A007/008L	3292	4701	84	1410	469	51172	9.2	Early	N/A	COG0666 [FOG: Ankyrin repeat] [6e-06]	PF00023.23 [Ankyrin repeat] [1.1e-07]	XP_749852 [Pfs NACHT and Ankyrin domain protein (Aspergillus fumigatus Af293)] [2e-55]	Q502K3 [RecName: FullSerine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C ShortSerine/threonine-protein phosphatase 6 regulatory subunit ARS-C ShortPP6-ARS-C] [2e-48]	Unknown protein	0	0	0
A009R	4998	5735	84	738	245	27634	8.1	Early	N/A	N/A	PF07150.4 [Protein of unknown function (DUF1390)] [7.8e-89]	YP_001426165 [hypothetical protein FR483_N533L (Paramecium bursaria Chlorella virus FR483)] [2e-80]	N/A	Unknown protein	0	0	0
A010R	5768	6973	88	1206	401	44998	5.2	Late	Yes	N/A	PF04451.5 [Large eukaryotic DNA virus major capsid protein] [1.9e-50]	YP_001426987 [hypothetical protein ATCV1_Z506L (Acanthocystis turfacea Chlorella virus 1)] [1e-89]	A7U6E9 [RecName: FullMajor capsid protein ShortMCP] [8e-45]	Capsid protein	0	0	0
a010aR	6837	7022	60	186	61	7342	11.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A011L	6970	8181	84	1212	403	45076	5.4	Late	Yes	N/A	PF04451.5 [Large eukaryotic	YP_001426987 [hypothetical protein	A7U6E9 [RecName: FullMajor capsid	Capsid protein	0	0	0

											DNA virus major capsid protein] [2.9e-61]	ATCV1_Z506L (Acanthocystis turfacea Chlorella virus 1)] [1e-106]	protein ShortMCP] [2e-43]				
a012R	7897	8190	64	294	97	11450	8.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a013L	8230	8571	58	342	113	12408	9.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A014R	8255	12364	40	4110	1369	141382	6.3	Late	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a015L	8863	9411	48	549	182	20131	4.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	3	0
a016L	9808	10500	64	693	230	25288	4.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	3	4	3
a017L	11371	11571	54	201	66	7325	4.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A018L	12367	16374	80	4008	1335	####	4.9	Late	Yes	N/A	PF06598.4 [Chlorovirus glycoprotein repeat] [1.2e-11]	N/A	N/A	Unknown protein	0	0	0
a019R	12869	13519	60	651	216	23794	5.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	3	0
a020R	13889	14143	62	255	84	9524	10.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	1
a021R	14165	14632	68	468	155	17744	3.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
a022R	14702	15031	58	330	109	12127	4.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
a023R	15482	15706	70	225	74	8102	6.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	2
a024R	15770	16132	64	363	120	13384	3.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	1
A025/027/029L	16432	20511	78	4080	1359	####	4.4	Late	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a026R	16916	17512	72	597	198	21885	5.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	5	5	5
a030R	18185	18721	72	537	178	20284	4.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	3	2
a031R	18755	19030	54	276	91	10478	4.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	1
a032R	19232	19810	68	579	192	21498	5.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	5	3
a033R	20189	20428	66	240	79	8651	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A034R	20572	21498	18	927	308	35163	10.4	Late	Yes	N/A	PF00069.18 [Protein kinase domain] [1.4e-07]	N/A	N/A	Protein kinase	0	1	0
A035L	21500	23260	88	1761	586	65606	8.9	Late	Yes	N/A	N/A	YP_001426757 [hypothetical protein ATCV1_Z276L (Acanthocystis turfacea Chlorella virus 1)] [1e-10]	N/A	Unknown protein	0	1	0

a036R	22696	23037	56	342	113	12942	8.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A037L	23288	23605	68	318	105	12822	9.8	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a038R	23584	23823	68	240	79	9448	10.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A039L	23623	24078	80	456	151	17102	4.1	Early	N/A	COG5201 [SCF ubiquitin ligase SKP1 component] [6e-16]	PF03931.8 [Skp1 family tetramerisation domain] [5.5e-19] / PF01466.12 [Skp1 family dimerisation domain] [6.8e-31]	XP_001753031 [predicted protein (Physcomitrella patens subsp. patens)] [2e-27]	Q9LNT9 [RecName: FullSKP1-like protein 4 ShortAtSK4] [9e-26]	Unknown protein	0	1	0
a040L	24087	24476	56	390	129	12234	3.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	0
A041R	24148	25386	34	1239	412	44315	10.8	Late	Yes	N/A	N/A	YP_001426427 [hypothetical protein FR483_N795L (Paramecium bursaria Chlorella virus FR483)] [1e-116]	N/A	Unknown protein	0	1	0
a042L	24238	24504	32	267	88	11031	12.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a043R	24798	25025	64	228	75	9172	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a044aL	25328	25492	66	165	54	6518	12.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A044L	25383	27182	84	1800	599	67849	6.4	Early	N/A	COG0464 [ATPases of the AAA+ class] [8e-06]	PF00004.22 [ATPase family associated with various cellular activities (AAA)] [1.7e-10]	XP_810119 [hypothetical protein (Trypanosoma cruzi strain CL Brener)] [6e-21]	Q5UR45 [RecName: FullPutative AAA family ATPase L572] [6e-17]	Unknown protein	0	0	0
a045R	26328	26540	52	213	70	8446	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a046R	26720	27220	68	501	166	19641	11.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a047L	26830	27033	64	204	67	7734	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a047aL	27217	27387	58	171	56	6491	4.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A048R	27248	27619	18	372	123	14017	7.6	Early-Late	N/A	N/A	N/A	YP_001425805 [hypothetical protein FR483_N173R (Paramecium bursaria Chlorella virus FR483)] [2e-19]	N/A	Unknown protein	0	0	0
A049L	27610	28269	70	660	219	25062	8.0	Early-Late	N/A	COG0584 [Glycerophosphoryl diester phosphodiesterase] [5e-06]	PF03009.10 [Glycerophosphoryl diester phosphodiesterase family] [3.8e-43]	YP_001426558 [hypothetical protein ATCV1_Z077L (Acanthocystis turfacea Chlorella virus 1)] [5e-48]	O07592 [RecName: FullPutative glycerophosphoryl diester phosphodiesterase yhdW ShortGlycerophosphodiester phosphodiesterase] [3e-23]	Unknown protein	0	0	0

A050L	28286	28711	84	426	141	16481	9.9	Early	N/A	N/A	PF03013.7 [Pyrimidine dimer DNA glycosylase] [9.7e-45]	YP_001426261 [hypothetical protein FR483_N629L (Paramecium bursaria Chlorella virus FR483)] [2e-49]	P04418 [RecName: FullEndonuclease V] [2e-21]	Pyrimidine dimer-specific glycosylase	0	0	0
A050aL	28821	28961	84	141	46	5443	8.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A051L	28984	29595	72	612	203	22804	8.6	Late	Yes	N/A	N/A	YP_001427069 [hypothetical protein ATCV1_Z588L (Acanthocystis turfacea Chlorella virus 1)] [2e-49]	N/A	Unknown protein	1	2	1
a052R	29167	29418	62	252	83	10100	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A053R	29684	30775	62	1092	363	40175	6.4	Early	N/A	COG1052 [Lactate dehydrogenase and related dehydrogenases] [1e-05]	PF00389.23 [D-isomer specific 2-hydroxyacid dehydrogenase catalytic domain] [1.4e-34] / PF02826.12 [D-isomer specific 2-hydroxyacid dehydrogenase NAD binding domain] [3.5e-56]	YP_001426776 [hypothetical protein ATCV1_Z295L (Acanthocystis turfacea Chlorella virus 1)] [1e-124]	P52643 [RecName: FullD-lactate dehydrogenase ShortD-LDH AltName: FullFermentative lactate dehydrogenase] [7e-67]	Unknown protein	0	0	0
a054L	29800	30123	56	324	107	11750	10.2	N/A	N/A	N/A	N/A	YP_001426779 [hypothetical protein ATCV1_z298R (Acanthocystis turfacea Chlorella virus 1)] [9e-06]	N/A	Hypothetical protein	0	0	0
a055L	30008	30403	62	396	131	15734	8.3	N/A	N/A	N/A	N/A	YP_001426778 [hypothetical protein ATCV1_z297R (Acanthocystis turfacea Chlorella virus 1)] [6e-18]	N/A	Hypothetical protein	0	0	0
a056L	30289	30603	58	315	104	11511	11.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A058L	30976	31623	58	648	215	24718	4.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
a057R	31034	31447	74	414	137	14937	11.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A057aR	31650	32666	38	1017	338	37918	4.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a059L	31779	32003	52	225	74	8442	8.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A060L	32796	33500	86	705	234	27189	4.9	Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A061L	33529	34158	74	630	209	24425	4.7	Late	N/A	N/A	PF05711.4 [Macrocin-O-methyltransferase (TylF)] [8.9e-20]	YP_003300173 [macrocin-O-methyltransferase domain-containing protein (Thermomonospora curvata DSM 43183)] [9e-31]	N/A	Unknown protein	0	0	0

a062R	33808	34179	60	372	123	14812	9.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
a062aR	34016	34198	54	183	60	6727	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A063L	34191	34889	96	699	232	27050	6.0	Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A064R	34956	36872	24	1917	638	74913	4.9	Early-Late	N/A	N/A	PF05637.5 [galactosyl transferase GMA12/MNN10 family] [1.2e-10]	ZP_04834875 [conserved hypothetical protein (Prevotella melaninogenica ATCC 25845)] [6e-15]	N/A	UDP-Glucose glycosyltransferase	0	0	0
a065L	35265	35510	60	246	81	9861	7.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a066L	36607	36945	70	339	112	13228	10.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	0	1
a066aL	36851	36976	58	126	41	4846	8.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A067R	37043	37972	62	930	309	33211	3.6	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	1	0
a068L	37375	37677	66	303	100	9518	3.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a069L	37433	37873	56	441	146	15049	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	0
a070L	37798	38064	66	267	88	10265	9.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A071R	38003	39067	80	1065	354	41967	7.4	Early	N/A	N/A	N/A	ZP_06054798 [TPR repeat-containing protein (alpha proteobacterium HIMB114)] [8e-16]	N/A	Unknown protein	0	0	0
a072L	38164	38436	64	273	90	10264	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
a073L	38417	38626	56	210	69	8105	7.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a074L	38660	38863	74	204	67	8104	6.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A075L	39078	39920	80	843	280	33254	5.4	Early-Late	N/A	N/A	PF03016.8 [Exostosin family] [5.5e-09]	YP_001425644 [hypothetical protein FR483_N012L (Paramecium bursaria Chlorella virus FR483)] [3e-58]	N/A	Unknown protein	0	0	0
a075aR	39784	39933	60	150	49	5568	9.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A075bL	39950	40138	80	189	62	7489	4.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A075cR	40014	40172	70	159	52	5931	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A076L	40190	40501	50	312	103	12094	11.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A077L	40470	40745	76	276	91	10180	5.0	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	1	1	1
A078R	40863	41759	74	897	298	33179	5.7	Early	N/A	COG0388 [Predicted amidohydrolase]	PF00795.15 [Carbon-nitrogen hydrolase] [5.5e-	YP_001425727 [hypothetical protein FR483_N095L	Q3HVN1 [RecName: FullN-carbamoylputrescine	N-carbamoylputrescine amidohydrolase	0	2	0

										[7e-06]	34]	(Paramecium bursaria Chlorella virus FR483)] [1e-113]	amidase] [2e-73]			
A078aL	41756	41878	92	123	40	4848	10.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A078bR	42007	42183	52	177	58	6943	10.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a078cL	42431	42565	62	135	44	5301	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	0
A079R	42467	43195	80	729	242	27092	9.3	Early	N/A	N/A	PF07150.4 [Protein of unknown function (DUF1390)] [5.4e-78]	YP_001425662 [hypothetical protein FR483_N030R (Paramecium bursaria Chlorella virus FR483)] [5e-29]	N/A	Unknown protein	0	0	0
a080L	42638	43045	58	408	135	16179	10.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
A081L	43192	43761	76	570	189	21916	9.0	Early	N/A	N/A	N/A	YP_001425639 [hypothetical protein FR483_N007L (Paramecium bursaria Chlorella virus FR483)] [5e-23]	N/A	Unknown protein	0	0	0
a082R	43760	43975	60	216	71	8434	6.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a083R	43791	44063	4	273	90	9976	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A084L	43811	44377	76	567	188	22309	7.0	Early	N/A	N/A	N/A	YP_001425642 [hypothetical protein FR483_N010L (Paramecium bursaria Chlorella virus FR483)] [7e-11]	N/A	Unknown protein	0	0	0
a084aL	44458	44580	46	123	40	4742	9.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A085R	44498	45226	66	729	242	27812	7.8	Late	Yes	N/A	PF03171.13 [2OG-Fe(II) oxygenase superfamily] [3.5e-11]	YP_001426050 [hypothetical protein FR483_N418R (Paramecium bursaria Chlorella virus FR483)] [7e-56]	Q5UP57 [RecName: FullPutative prolyl 4-hydroxylase Short4-PH AltName: FullProcollagen-proline2-oxoglutarate-4-dioxygenase] [2e-14]	Prolyl 4-hydroxylase	1	1	1
a086L	44953	45195	60	243	80	8487	10.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a086aL	45101	45229	54	129	42	5047	10.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A087R	45223	46623	32	1401	466	53644	8.5	Early	N/A	N/A	PF01844.16 [HNH endonuclease] [6.1e-13]	YP_001426447 [hypothetical protein FR483_N815L (Paramecium bursaria Chlorella virus FR483)] [4e-07]	N/A	Unknown protein	0	1	0
a086bL	46489	46632	72	144	47	5602	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a086cL	46508	46639	14	132	43	4980	4.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A088R	46755	47528	72	774	257	29442	5.0	Early	N/A	N/A	N/A	YP_001426459 [hypothetical protein	N/A	Unknown protein	0	0	0

												FR483_N827R (Paramecium bursaria Chlorella virus FR483)] [7e-07]					
A089R	47628	47834	78	207	68	7634	10.6	Early-Late	N/A	N/A	N/A	YP_001426713 [hypothetical protein ATCV1_Z232L (Acanthocystis turfacea Chlorella virus 1)] [2e-14]	N/A	Unknown protein	0	0	0
a089aL	47826	47972	76	147	48	5538	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A090R	47851	48315	70	465	154	18442	4.9	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A092/093L	48326	49627	72	1302	433	49577	10.7	Early-Late	Yes	N/A	PF08789.3 [PBCV-specific basic adaptor domain] [1.2e-15]	YP_001427042 [hypothetical protein ATCV1_Z561L (Acanthocystis turfacea Chlorella virus 1)] [2e-90]	N/A	Unknown protein	0	0	0
a092/093aL	48547	48732	68	186	61	7472	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A094L	49662	50756	74	1095	364	40734	4.3	Early	N/A	COG2273 [Beta-glucanase/Beta-glucan synthetase] [4e-06]	PF00722.14 [Glycosyl hydrolases family 16] [7.5e-13]	YP_001425751 [hypothetical protein FR483_N119L (Paramecium bursaria Chlorella virus FR483)] [1e-110]	P23903 [RecName: FullGlucan endo-13-beta-glucosidase A1 AltName: Full(1->3)-beta-glucan endohydrolase AltName: Full(1->3)-beta-glucanase A1 Flags: Precursor] [1e-22]	beta-1-3-glucanase	1	1	1
a095R	50014	50232	52	219	72	7701	10.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a096R	50346	50549	68	204	67	7873	12.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a097R	50678	50893	68	216	71	8581	9.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A098R	50886	52592	76	1707	568	65159	8.2	Early	N/A	COG1215 [Glycosyltransferases probably involved in cell wall biogenesis] [4e-06]	PF03142.8 [Chitin synthase] [4.4e-09]	YP_001425756 [hypothetical protein FR483_N124R (Paramecium bursaria Chlorella virus FR483)] [0.0]	B1WB39 [RecName: FullHyaluronan synthase 1 AltName: FullHyaluronate synthase 1 AltName: FullHyaluronic acid synthase 1 ShortHA synthase 1] [1e-56]	Hyaluronan synthase	7	8	7
a099L	52152	52394	62	243	80	8644	9.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a099aL	52539	52682	60	144	47	5250	6.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A100R	52691	54478	60	1788	595	65408	6.1	Early	N/A	COG0449 [Glucosamine 6-phosphate synthetase contains amidotransferase and phosphosugar isomerase domains] [8e-07]	PF00310.14 [Glutamine amidotransferases class-II] [5.6e-15] / PF01380.15 [SIS domain] [2.2e-26]	YP_001425667 [hypothetical protein FR483_N035R (Paramecium bursaria Chlorella virus FR483)] [0.0]	Q7WE36 [RecName: FullGlucosamine--fructose-6-phosphate aminotransferase (isomerizing)] [1e-153]	Glutamine:fructose-6-phosphate amidotransferase	0	0	0

a101L	52925	53188	54	264	87	10061	8.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a102L	54468	54974	56	507	168	19199	11.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	1
A103R	54622	55614	84	993	330	37832	8.4	Early	N/A	COG5226 [mRNA capping enzyme guanylyltransferase (alpha) subunit] [4e-13]	PF01331.12 [mRNA capping enzyme catalytic domain] [2.1e-50] / PF03919.8 [mRNA capping enzyme C-terminal domain] [7.8e-15]	YP_001427200 [hypothetical protein ATCV1_Z719L (Acanthocystis turfacea Chlorella virus 1)] [2e-90]	P78587 [RecName: FullmRNA-capping enzyme subunit alpha AltName: FullmRNA guanylyltransferase AltName: FullGTP--RNA guanylyltransferase ShortGTase] [7e-16]	mRNA guanylyltransferase	0	3	0
a104L	55054	55344	58	291	96	10912	7.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A105L	55626	56480	84	855	284	33063	6.8	Early	N/A	N/A	PF00443.22 [Ubiquitin carboxyl-terminal hydrolase] [5.7e-25]	YP_001425764 [hypothetical protein FR483_N132L (Paramecium bursaria Chlorella virus FR483)] [8e-70]	P40818 [RecName: FullUbiquitin carboxyl-terminal hydrolase 8 AltName: FullUbiquitin thioesterase 8 AltName: FullUbiquitin-specific-processing protease 8 AltName: FullDeubiquitinating enzyme 8 AltName: FullUbiquitin isopeptidase Y ShorthUBPy] [3e-09]	Unknown protein	0	0	0
a106R	55770	56168	56	399	132	15709	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A107L	56516	57388	80	873	290	32511	6.2	Early	N/A	N/A	PF00382.12 [Transcription factor TFIIB repeat] [4.6e-06]	YP_001425767 [hypothetical protein FR483_N135L (Paramecium bursaria Chlorella virus FR483)] [2e-57]	Q9SS44 [RecName: FullTranscription initiation factor IIB-2 AltName: FullGeneral transcription factor TFIIB-2 ShortAtTFIIB2] [4e-10]	Unknown protein	0	0	0
a108R	56933	57148	60	216	71	8190	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A108aR	57212	57400	52	189	62	7278	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A108bL	57471	57977	84	507	168	19692	7.1	N/A	N/A	N/A	PF01541.17 [GIY-YIG catalytic domain] [1.9e-06]	YP_001427194 [hypothetical protein ATCV1_Z713L (Acanthocystis turfacea Chlorella virus 1)] [1e-54]	N/A	Hypothetical protein	0	0	0
a110L	58082	58390	50	309	102	11775	10.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A111/114R	58098	60680	80	2583	860	98045	6.6	Early	N/A	N/A	PF00852.12 [Glycosyltransferase family 10 (fucosyltransferase)] [1.4e-06]	YP_001426104 [hypothetical protein FR483_N472R (Paramecium bursaria Chlorella virus FR483)] [0.0]	N/A	Unknown protein	0	0	0
a112L	58775	59068	42	294	97	10605	9.2	N/A	N/A	N/A	N/A	YP_001426602 [hypothetical protein ATCV1_z121L (Acanthocystis turfacea	N/A	Hypothetical protein	1	2	1

												Chlorella virus 1)] [3e-11]					
a113L	58809	59093	34	285	94	10720	7.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a115L	59265	59495	58	231	76	8591	8.7	N/A	N/A	N/A	N/A	YP_001426603 [hypothetical protein ATCV1_z122L (Acanthocystis turfacea Chlorella virus 1)] [8e-07]	N/A	Hypothetical protein	0	0	0
a116R	59398	59643	52	246	81	8980	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a117L	59874	60266	68	393	130	14929	8.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A118R	60726	61763	74	1038	345	38498	5.5	Early-Late	N/A	COG0451 [Nucleoside-diphosphate-sugar epimerases] [1e-05]	PF01370.14 [NAD dependent epimerase/dehydratase family] [2.2e-67]	YP_069550 [GDP-D-mannose dehydratase (Yersinia pseudotuberculosis IP 32953)] [1e-113]	Q56872 [RecName: FullProbable GDP-mannose 46-dehydratase AltName: FullGDP-D-mannose dehydratase AltName: FullORF13.7] [1e-112]	GDP-D-mannose dehydratase	0	0	0
a119L	61628	62029	70	402	133	14860	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	1
a120L	61675	61947	50	273	90	10840	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
A121R	61780	62094	72	315	104	12486	10.8	Early-Late	Yes	N/A	N/A	YP_001425784 [hypothetical protein FR483_N152R (Paramecium bursaria Chlorella virus FR483)] [4e-31]	N/A	Unknown protein	0	0	0
A122/123R	62145	66176	88	4032	1343	####	5.0	Late	Yes	COG5295 [Autotransporter adhesin] [4e-12]	PF06598.4 [Chlorovirus glycoprotein repeat] [3.6e-11] / PF11962.1 [Domain of unknown function (DUF3476)] [8.2e-66]	YP_001426596 [hypothetical protein ATCV1_Z115L (Acanthocystis turfacea Chlorella virus 1)] [1e-140]	Q37893 [RecName: FullPre-neck appendage protein AltName: FullLate protein GP12] [3e-11]	Unknown protein	0	31	0
A122/123aR	66133	66258	68	126	41	5076	8.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a122/123bL	66203	66346	62	144	47	5426	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A122/123cL	66407	66541	64	135	44	4912	10.1	N/A	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a124L	66517	66771	60	255	84	9614	10.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A125L	66178	67120	84	943	180	21071	9.6	Early	N/A	COG1594 [DNA-directed RNA polymerase subunit M/Transcription elongation factor TFIIS] [9e-06]	PF07500.7 [Transcription factor S-II (TFIIS) central domain] [2.4e-12] / PF01096.11 [Transcription factor S-II (TFIIS)] [2.3e-19]	YP_001425797 [hypothetical protein FR483_N165L (Paramecium bursaria Chlorella virus FR483)] [1e-73]	P20232 [RecName: FullTranscription elongation factor S-II AltName: FullRNA polymerase II elongation factor DMS-II AltName: FullTFIIS] [1e-13]	Unknown protein	0	0	0

a126R	66620	66820	24	201	66	7964	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	2
A127R	67154	67891	14	738	245	27126	10.1	Late	Yes	N/A	N/A	YP_001425800 [hypothetical protein FR483_N168R (Paramecium bursaria Chlorella virus FR483)] [1e-76]	N/A	Unknown protein	0	0	0
a128L	67510	67770	56	261	86	9678	4.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A129R	67952	69028	82	1077	358	40533	8.4	Early-Late	N/A	N/A	N/A	YP_001425778 [hypothetical protein FR483_N146R (Paramecium bursaria Chlorella virus FR483)] [8e-69]	N/A	Unknown protein	0	0	0
A130R	69049	69366	84	318	105	11644	10.0	Early-Late	N/A	N/A	N/A	YP_001426755 [hypothetical protein ATCV1_Z274R (Acanthocystis turfacea Chlorella virus 1)] [3e-24]	N/A	Unknown protein	4	3	3
A130aR	69261	69404	62	144	47	5585	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a130bR	69344	69475	58	132	43	5215	10.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A131L	69359	69769	68	411	136	16124	4.6	Early	N/A	N/A	N/A	YP_001426009 [hypothetical protein FR483_N377L (Paramecium bursaria Chlorella virus FR483)] [4e-06]	N/A	Unknown protein	0	0	0
a132R	69533	69805	54	273	90	10395	5.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A133R	69960	70583	86	624	207	23480	9.6	Early	N/A	N/A	PF11264.1 [Thylakoid formation protein] [4.8e-52]	XP_001693657 [inositol phosphatase-like protein (Chlamydomonas reinhardtii)] [1e-24]	Q84PB7 [RecName: FullProtein THYLAKOID FORMATION1 chloroplastic Flags: Precursor] [5e-23]	Unknown protein	0	1	0
A134L	70558	71055	92	498	165	19545	9.9	Early-Late	N/A	N/A	PF01541.17 [GIY-YIG catalytic domain] [1.8e-11]	YP_001425818 [hypothetical protein FR483_N186L (Paramecium bursaria Chlorella virus FR483)] [2e-23]	N/A	Unknown protein	0	0	0
A135L	71055	71603	74	549	182	20728	8.4	Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	5	5	5
A136R	71134	71574	30	441	146	16367	11.5	N/A	Yes	N/A	N/A	YP_001425749 [hypothetical protein FR483_N117R (Paramecium bursaria Chlorella virus FR483)] [6e-07]	N/A	Unknown protein	0	0	0
A137R	71625	71843	44	219	72	8777	10.9	Early	N/A	N/A	N/A	YP_001427214 [hypothetical protein ATCV1_z733L (Acanthocystis turfacea Chlorella virus 1)] [2e-07]	N/A	Unknown protein	0	0	0
A138R	71880	72701	84	822	273	31471	4.4	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0

a138aR	72604	72747	72	144	47	5766	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A139L	72698	73153	60	456	151	17701	8.4	Late	Yes	N/A	N/A	YP_001425821 [hypothetical protein FR483_N189L (Paramecium bursaria Chlorella virus FR483)] [6e-24]	N/A	Unknown protein	2	2	2
A140/145R	73107	76490	90	3384	1127	####	11.0	Early-Late	Yes	N/A	N/A	YP_001425827 [hypothetical protein FR483_N195R (Paramecium bursaria Chlorella virus FR483)] [0.0]	N/A	Unknown protein	0	1	0
a144L	74244	75740	64	1497	498	57630	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	4	4
a142L	74474	74875	48	402	133	13511	8.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	4	4	4
a146L	75752	76006	68	255	84	8946	3.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
a147L	75882	76655	56	774	257	29267	8.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	5	1
A148R	76540	76872	82	333	110	11990	9.8	Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a149L	76642	77052	62	411	136	16083	11.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A150L	76856	77314	74	459	152	17089	4.1	Early	N/A	N/A	N/A	YP_001425837 [hypothetical protein FR483_N205L (Paramecium bursaria Chlorella virus FR483)] [4e-11]	N/A	Unknown protein	0	0	0
A151R	77397	77804	52	408	135	15099	8.3	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a152L	77822	78094	58	273	90	10135	11.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A153R	77880	79259	80	1380	459	51301	9.2	Early-Late	N/A	COG1061 [DNA or RNA helicases of superfamily II] [2e-06]	PF04851.8 [Type III restriction enzyme res subunit] [5.5e-15]	YP_001425838 [hypothetical protein FR483_N206R (Paramecium bursaria Chlorella virus FR483)] [1e-176]	Q5UQ46 [RecName: FullPutative ATP-dependent RNA helicase L396] [1e-46]	Unknown protein	0	0	0
A154L	79256	80299	70	1044	347	38950	8.4	Early-Late	N/A	N/A	N/A	YP_001425778 [hypothetical protein FR483_N146R (Paramecium bursaria Chlorella virus FR483)] [5e-65]	N/A	Unknown protein	0	0	0
a155R	79412	79696	52	285	94	11209	10.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a156L	79885	80217	52	333	110	12610	11.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A157L	80393	80725	80	333	110	12328	3.9	Early-Late	Yes	N/A	N/A	YP_001425841 [hypothetical protein FR483_N209L (Paramecium bursaria Chlorella virus FR483)] [2e-16]	N/A	Unknown protein	1	1	1

A158L	80770	81084	68	315	104	12162	3.3	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A159R	81104	81436	36	333	110	12869	8.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
a160L	81257	81751	68	495	164	17774	10.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	4	4	4
A161R	81345	81716	58	372	123	13383	11.0	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A162L	81717	82952	78	1236	411	46696	4.4	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	3	3	3
a162aR	82831	82959	68	129	42	4676	7.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A163R	82995	84296	12	1302	433	48956	7.0	Early-Late	N/A	N/A	PF00060.19 [Ligand-gated ion channel] [1.8e-09]	N/A	N/A	Unknown protein	3	3	3
a164L	83873	84277	80	405	134	15629	9.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	3	1
A164aR	84314	84493	14	180	59	7094	5.8	N/A	Yes	N/A	N/A	N/A	N/A	Unknown protein	1	0	0
A165L	84486	84935	60	450	149	17251	6.8	Early-Late	N/A	N/A	N/A	YP_001425846 [hypothetical protein FR483_N214L (Paramecium bursaria Chlorella virus FR483)] [7e-12]	N/A	Unknown protein	0	0	1
A165aL	84835	85326	70	492	163	19024	10.1	N/A	Yes	N/A	N/A	YP_001425848 [hypothetical protein FR483_N216L (Paramecium bursaria Chlorella virus FR483)] [3e-18]	N/A	Unknown protein	0	0	0
A166R	85431	86237	80	807	268	31183	4.7	Early-Late	N/A	N/A	PF09588.3 [YqaJ-like viral recombinase domain] [7.9e-24]	YP_001425850 [hypothetical protein FR483_N218R (Paramecium bursaria Chlorella virus FR483)] [1e-81]	Q5UQV1 [RecName: FullUncharacterized protein R354] [5e-12]	Unknown protein	0	0	0
a167L	85677	85880	64	204	67	8077	8.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a167aR	86128	86283	68	156	51	6043	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A168R	86276	86776	86	501	166	18317	4.6	Late	Yes	N/A	N/A	YP_001427100 [hypothetical protein ATCV1_Z619L (Acanthocystis turfacea Chlorella virus 1)] [3e-19]	N/A	Unknown protein	1	1	1
A169R	86904	87875	74	972	323	36836	5.8	Early-Late	N/A	COG0078 [Ornithine carbamoyltransferase] [5e-07]	PF02729.14 [Aspartate/ornithine carbamoyltransferase carbamoyl-P binding domain] [2.4e-44] / PF00185.17 [Aspartate/ornithine carbamoyltransferase Asp/Orn	NP_001148757 [LOC100282373 (Zea mays)] [7e-78]	Q43087 [RecName: FullAspartate carbamoyltransferase 2 chloroplastic AltName: FullAspartate transcarbamylase 2 ShortATCase 2 Flags: Precursor] [5e-79]	Aspartate transcarbamylase	0	0	0

											binding domain] [1.6e-35]						
a170L	86990	87259	46	270	89	9855	4.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A171R	87904	89067	84	1164	387	42413	10.2	Early	Yes	N/A	N/A	YP_001426427 [hypothetical protein FR483_N795L (Paramecium bursaria Chlorella virus FR483)] [1e-110]	N/A	Unknown protein	0	0	0
a172L	88627	88947	52	321	106	12288	8.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A172aL	88944	89111	60	168	55	6053	9.8	N/A	Yes	N/A	N/A	N/A	N/A	Unknown protein	1	1	0
A173L	89068	89934	68	867	288	31933	8.2	Early	Yes	COG1752 [Predicted esterase of the alpha-beta hydrolase superfamily] [2e-06]	PF01734.15 [Patatin-like phospholipase] [4.2e-27]	YP_001425854 [hypothetical protein FR483_N222L (Paramecium bursaria Chlorella virus FR483)] [2e-83]	Q91F63 [RecName: FullProbable lipid hydrolase 463L] [2e-13]	Unknown protein	0	2	0
A174L	89941	90138	76	198	65	7453	12.2	N/A	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A175R	89974	90183	22	210	69	8092	11.4	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	1	2	1
A176L	90180	90413	62	234	77	9167	11.3	N/A	Yes	N/A	PF08789.3 [PBCV-specific basic adaptor domain] [9e-12]	N/A	N/A	Unknown protein	0	0	0
A176aL	90415	90537	64	123	40	5159	11.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A177R	90639	91379	84	741	246	27565	9.0	Early-Late	N/A	N/A	PF07150.4 [Protein of unknown function (DUF1390)] [1.1e-72]	YP_001425662 [hypothetical protein FR483_N030R (Paramecium bursaria Chlorella virus FR483)] [4e-27]	N/A	Unknown protein	0	0	0
a178L	90915	91160	66	246	81	9937	12.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
a179L	91201	91530	62	330	109	12906	10.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A180R	91466	91792	78	327	108	12101	8.9	Early	N/A	COG1293 [Predicted RNA-binding protein homologous to eukaryotic snRNP] [2e-06]	PF05670.6 [Domain of unknown function (DUF814)] [3.5e-23]	YP_001426409 [hypothetical protein FR483_N777L (Paramecium bursaria Chlorella virus FR483)] [2e-23]	O34693 [RecName: FullUncharacterized protein yloA] [3e-08]	Unknown protein	0	0	0
A181/182R	91810	94302	80	2493	830	90858	8.0	Late	N/A	N/A	PF00553.12 [Cellulose binding domain] [9.8e-11]	YP_001426411 [hypothetical protein FR483_N779R (Paramecium bursaria Chlorella virus FR483)] [0.0]	P13656 [RecName: FullProbable bifunctional chitinase/lysozyme Includes: RecName: FullChitinase Includes: RecName: FullLysozyme Flags: Precursor] [1e-30]	Chitinase	0	0	0
a183L	93624	93854	60	231	76	8237	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
a184L	94120	94470	76	351	116	13534	7.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0

A185R	94548	97390	40	2843	913	####	8.3	Early	N/A	COG0417 [DNA polymerase elongation subunit (family B)] [1e-07]	PF03104.12 [DNA polymerase family B exonuclease domain] [1.3e-70] / PF00136.14 [DNA polymerase family B] [1.8e-118]	YP_001425655 [hypothetical protein FR483_N023L (Paramecium bursaria Chlorella virus FR483)] [0.0]	P30320 [RecName: FullDNA polymerase] [0.0]	Unknown protein	0	0	0
a186L	94966	95220	46	255	84	9946	5.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a187L	95295	96038	58	744	247	28922	10.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a188L	96724	96957	56	234	77	8398	11.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A188aR	96944	97390	58	447	148	17326	10.0	N/A	Yes	COG0417 [DNA polymerase elongation subunit (family B)] [3e-07]	PF00136.14 [DNA polymerase family B] [6.5e-17]	YP_001427279 [hypothetical protein ATCV1_Z798L (Acanthocystis turfacea Chlorella virus 1)] [8e-60]	P30320 [RecName: FullDNA polymerase] [2e-72]	Unknown protein	0	0	0
a188bR	97258	97398	72	141	46	5774	11.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A189/192R	97433	1E+05	28	3900	1299	143575	11.4	Late	Yes	N/A	N/A	YP_001427275 [hypothetical protein ATCV1_Z794L (Acanthocystis turfacea Chlorella virus 1)] [1e-157]	N/A	Unknown protein	0	0	0
a190L	97525	97743	52	219	72	7634	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A193L	1E+05	1E+05	72	789	262	29627	4.7	Early-Late	N/A	COG0592 [DNA polymerase sliding clamp subunit (PCNA homolog)] [7e-06]	PF00705.11 [Proliferating cell nuclear antigen N-terminal domain] [6.4e-26] / PF02747.8 [Proliferating cell nuclear antigen C-terminal domain] [1.2e-21]	YP_001425651 [hypothetical protein FR483_N019R (Paramecium bursaria Chlorella virus FR483)] [1e-103]	O82134 [RecName: FullProliferating cell nuclear antigen] [7e-36]	Unknown protein	0	0	0
a194R	1E+05	1E+05	56	249	82	9602	10.7	N/A	N/A	N/A	N/A	YP_001425650 [hypothetical protein FR483_n018L (Paramecium bursaria Chlorella virus FR483)] [1e-12]	N/A	Hypothetical protein	0	0	0
a195R	1E+05	1E+05	66	249	82	9700	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A196L	1E+05	1E+05	90	459	152	17456	8.4	Late	Yes	N/A	N/A	YP_001425648 [hypothetical protein FR483_N016R (Paramecium bursaria Chlorella virus FR483)] [2e-44]	N/A	Unknown protein	3	3	1
a197R	1E+05	1E+05	62	288	95	11090	8.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a198R	1E+05	1E+05	62	225	74	8873	10.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A199R	1E+05	1E+05	6	306	101	10904	10.1	Late	N/A	N/A	N/A	YP_001427266 [hypothetical protein	N/A	Unknown protein	2	3	2

												ATCV1_Z785L (Acanthocystis turfacea Chlorella virus 1)] [1e-12]				
A200R	1E+05	1E+05	76	357	118	13165	9.3	Early	N/A	N/A	PF00383.15 [Cytidine and deoxycytidylate deaminase zinc-binding region] [8.4e-13]	YP_001425646 [hypothetical protein FR483_N014L (Paramecium bursaria Chlorella virus FR483)] [4e-39]	N/A	Unknown protein	0	0	0
a200aR	1E+05	1E+05	52	165	54	6424	8.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A201L	1E+05	1E+05	74	285	94	10005	10.7	Early-Late	Yes	N/A	N/A	YP_001425713 [hypothetical protein FR483_N081L (Paramecium bursaria Chlorella virus FR483)] [3e-22]	N/A	Unknown protein	2	2	2
A201aL	1E+05	1E+05	18	177	58	6787	8.8	N/A	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A202L	1E+05	1E+05	90	342	113	12232	5.0	Early-Late	Yes	N/A	N/A	YP_001425949 [hypothetical protein FR483_N317R (Paramecium bursaria Chlorella virus FR483)] [2e-25]	N/A	Unknown protein	0	0	0
A203R	1E+05	1E+05	26	651	216	24011	6.0	Late	Yes	N/A	N/A	YP_001425947 [hypothetical protein FR483_N315L (Paramecium bursaria Chlorella virus FR483)] [2e-57]	N/A	Unknown protein	1	2	0
a204L	1E+05	1E+05	62	240	79	8029	10.5	N/A	N/A	N/A	N/A	YP_001425948 [hypothetical protein FR483_n316R (Paramecium bursaria Chlorella virus FR483)] [9e-15]	N/A	Hypothetical protein	0	0	0
a204aL	1E+05	1E+05	58	162	53	6061	4.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A205R	1E+05	1E+05	80	621	206	22452	12.1	Late	Yes	N/A	PF08789.3 [PBCV-specific basic adaptor domain] [4.2e-16]	YP_001425945 [hypothetical protein FR483_N313L (Paramecium bursaria Chlorella virus FR483)] [6e-29]	N/A	Unknown protein	0	0	0
a206L	1E+05	1E+05	64	258	85	10043	11.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A207R	1E+05	1E+05	86	1119	372	41969	4.7	Early-Late	N/A	COG1166 [Arginine decarboxylase (spermidine biosynthesis)] [1e-06]	PF02784.9 [Pyridoxal-dependent decarboxylase pyridoxal binding domain] [3.3e-61] / PF00278.15 [Pyridoxal-dependent decarboxylase C-terminal sheet domain] [5.5e-23]	YP_001425944 [hypothetical protein FR483_N312L (Paramecium bursaria Chlorella virus FR483)] [1e-139]	P27117 [RecName: FullOrnithine decarboxylase ShortODC] [2e-74]	Arginine/Ornithine decarboxylase	0	0	0
A208R	1E+05	1E+05	76	936	311	35364	4.2	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0

a210L	1E+05	1E+05	64	492	163	16631	5.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
a211R	1E+05	1E+05	56	324	107	12159	12.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	2
A212R	1E+05	1E+05	78	168	55	6345	12.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A213L	1E+05	1E+05	84	447	148	16483	4.5	Early-Late	Yes	N/A	N/A	YP_001425936 [hypothetical protein FR483_N304R (Paramecium bursaria Chlorella virus FR483)] [1e-30]	N/A	Unknown protein	1	1	1
a213aL	1E+05	1E+05	56	147	48	5567	12.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A214L	1E+05	1E+05	76	408	135	15424	7.1	Early	N/A	N/A	N/A	YP_001425935 [hypothetical protein FR483_N303R (Paramecium bursaria Chlorella virus FR483)] [9e-21]	N/A	Unknown protein	0	0	0
a214aL	1E+05	1E+05	46	144	47	5815	10.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	0	1
A215L	1E+05	1E+05	82	966	321	35707	10.1	Late	N/A	N/A	N/A	YP_001425925 [hypothetical protein FR483_N293R (Paramecium bursaria Chlorella virus FR483)] [1e-115]	N/A	Alkaline alginate lyas / 1-4 polyglucuronic acid lysase / polysaccharide lyase family 14 / vAL-1	0	0	0
a216R	1E+05	1E+05	62	324	107	11708	6.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	2
A217L	1E+05	1E+05	70	1185	394	45248	9.9	Early-Late	Yes	N/A	N/A	YP_001425921 [hypothetical protein FR483_N289R (Paramecium bursaria Chlorella virus FR483)] [1e-164]	N/A	Unknown protein	0	0	1
a218L	1E+05	1E+05	18	366	121	14878	10.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A219/222/226R	1E+05	1E+05	58	2034	677	77797	7.0	Early	Yes	COG1215 [Glycosyltransferases probably involved in cell wall biogenesis] [4e-06]	N/A	YP_001426347 [hypothetical protein FR483_N715L (Paramecium bursaria Chlorella virus FR483)] [0.0]	P58932 [RecName: FullCellulose synthase catalytic subunit (UDP-forming)] [6e-07]	Unknown protein	9	8	10
a220L	1E+05	1E+05	50	390	129	15951	8.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	0	1
a223R	1E+05	1E+05	60	213	70	7560	11.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a223aL	1E+05	1E+05	64	279	92	10021	8.5	N/A	N/A	N/A	N/A	YP_001426907 [hypothetical protein ATCV1_z426L (Acanthocystis turfacea Chlorella virus 1)] [4e-12]	N/A	Hypothetical protein	0	0	0
a224L	1E+05	1E+05	54	267	88	9977	10.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a225L	1E+05	1E+05	66	273	90	11049	6.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0

A227L	1E+05	1E+05	80	414	137	15689	10.0	Late	Yes	N/A	N/A	YP_001425876 [hypothetical protein FR483_N244R (Paramecium bursaria Chlorella virus FR483)] [6e-41]	N/A	Unknown protein	0	0	0
a228R	1E+05	1E+05	60	231	76	8736	9.7	N/A	N/A	N/A	N/A	YP_001425877 [hypothetical protein FR483_n245L (Paramecium bursaria Chlorella virus FR483)] [4e-11]	N/A	Hypothetical protein	0	1	0
a228aR	1E+05	1E+05	64	135	44	5254	10.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A229L	1E+05	1E+05	82	234	77	8329	8.5	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	2	2	2
A230R	1E+05	1E+05	36	591	196	22055	8.4	Late	Yes	N/A	N/A	YP_001425874 [hypothetical protein FR483_N242L (Paramecium bursaria Chlorella virus FR483)] [8e-34]	N/A	Unknown protein	4	4	4
A231L	1E+05	1E+05	80	1152	383	43644	9.9	Early-Late	Yes	N/A	N/A	YP_001426097 [hypothetical protein FR483_N465R (Paramecium bursaria Chlorella virus FR483)] [1e-137]	N/A	Unknown protein	1	0	0
a232R	1E+05	1E+05	60	264	87	10420	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a232aR	1E+05	1E+05	52	135	44	5103	10.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A233R	1E+05	1E+05	42	339	112	13599	9.3	Late	N/A	N/A	N/A	YP_001425872 [hypothetical protein FR483_N240L (Paramecium bursaria Chlorella virus FR483)] [1e-14]	N/A	Unknown protein	0	0	0
A234L	1E+05	1E+05	72	327	108	12388	10.4	Early-Late	N/A	N/A	N/A	YP_001425871 [hypothetical protein FR483_N239R (Paramecium bursaria Chlorella virus FR483)] [6e-21]	N/A	Unknown protein	0	0	0
a235R	1E+05	1E+05	54	252	83	9647	7.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a236L	1E+05	1E+05	68	264	87	10307	8.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	1	2
A237R	1E+05	1E+05	22	1557	518	58565	9.5	Late	Yes	COG5310 [Homospermidine synthase] [4e-23]	PF03435.11 [Saccharopine dehydrogenase] [1.2e-96]	YP_001425864 [hypothetical protein FR483_N232L (Paramecium bursaria Chlorella virus FR483)] [0.0]	Q98H64 [RecName: FullHomospermidine synthase ShortHSS] [2e-54]	Homospermidine synthase	0	0	0
a238L	1E+05	1E+05	46	345	114	12804	9.4	N/A	N/A	N/A	N/A	YP_001425865 [hypothetical protein FR483_n233R (Paramecium bursaria Chlorella virus FR483)] [3e-17]	N/A	Hypothetical protein	0	0	0
A239L	1E+05	1E+05	72	447	148	17052	5.0	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0

a240L	1E+05	1E+05	48	198	65	7734	12.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A240aL	1E+05	1E+05	72	186	61	7125	10.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	0
a240bR	1E+05	1E+05	68	141	46	5363	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
a240cL	1E+05	1E+05	52	165	54	6440	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a240dL	1E+05	1E+05	60	147	48	5633	6.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A241R	1E+05	1E+05	78	2178	725	82753	6.6	Early	N/A	COG1201 [Lhr-like helicases] [5e-06]	PF00270.22 [DEAD/DEAH box helicase] [7.3e-19] / PF08148.5 [DSHCT (NUC185) domain] [1.4e-15]	YP_001425859 [hypothetical protein FR483_N227L (Paramecium bursaria Chlorella virus FR483)] [0.0]	Q15477 [RecName: FullHelicase SKI2W AltName: FullHelicase-like protein ShortHLP] [7e-87]	Unknown protein	0	0	0
a242L	1E+05	1E+05	62	354	117	13745	6.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	3	0
A243R	1E+05	1E+05	92	909	302	36101	10.3	Early-Late	N/A	N/A	N/A	YP_001425731 [hypothetical protein FR483_N099R (Paramecium bursaria Chlorella virus FR483)] [1e-134]	N/A	Unknown protein	0	0	0
a244L	1E+05	1E+05	44	234	77	8398	9.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A245R	1E+05	1E+05	80	564	187	19748	9.3	Late	Yes	COG2032 [Cu/Zn superoxide dismutase] [9e-07]	PF00080.13 [Copper/zinc superoxide dismutase (SODC)] [3.1e-49]	YP_001426671 [hypothetical protein ATCV1_Z190L (Acanthocystis turfacea Chlorella virus 1)] [1e-68]	Q751L8 [RecName: FullSuperoxide dismutase (Cu-Zn)] [8e-41]	Cu/Zn superoxide dismutase	1	1	0
A246R	1E+05	1E+05	82	342	113	12017	11.5	Late	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A246aR	1E+05	1E+05	56	459	152	16618	8.0	N/A	N/A	N/A	PF00967.10 [Barwin family] [3e-47]	NP_187123 [PR4 (PATHOGENESIS-RELATED 4) chitin binding (Arabidopsis thaliana)] [8e-10]	P43082 [RecName: FullHevein-like protein Flags: Precursor] [6e-11]	Hypothetical protein	0	0	0
A247R	1E+05	1E+05	84	1152	383	44592	6.1	Early-Late	N/A	COG0666 [FOG: Ankyrin repeat] [1e-09]	PF00023.23 [Ankyrin repeat] [8.6e-06]	YP_001958455 [hypothetical protein Aasi_1435 (Candidatus Amoebophilus asiaticus 5a2)] [9e-26]	Q4UMH6 [RecName: FullPutative ankyrin repeat protein RF_0381] [2e-20]	Unknown protein	0	0	0
A248R	1E+05	1E+05	70	927	308	35564	8.0	Early	N/A	COG0515 [Serine/threonine protein kinase] [1e-05]	PF00069.18 [Protein kinase domain] [2.4e-52]	YP_001426416 [hypothetical protein FR483_N784R (Paramecium bursaria Chlorella virus FR483)] [3e-61]	Q1ZXH2 [RecName: FullProbable serine/threonine-protein kinase fhkB AltName: FullForkhead-associated kinase protein B] [4e-24]	Protein kinase	0	0	0
a249L	1E+05	1E+05	70	309	102	11134	10.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A250R	1E+05	1E+05	82	285	94	10620	8.8	Early-Late	N/A	N/A	PF07885.9 [Ion channel] [3.2e-11]	YP_001427066 [hypothetical protein ATCV1_Z585R (Acanthocystis turfacea Chlorella virus 1)] [4e-	N/A	Potassium ioin channel protein (Kcv)	2	2	2

												10]				
a250aR	1E+05	1E+05	54	156	51	6310	10.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A251R	1E+05	1E+05	82	981	326	37421	7.8	Early	N/A	COG3392 [Adenine-specific DNA methylase] [1e-13]	PF02086.8 [D12 class N6 adenine-specific DNA methyltransferase] [5.8e-61]	ZP_01049738 [Site-specific DNA-methyltransferase (adenine-specific) (Dokdonia donghaensis MED134)] [2e-50]	P24582 [RecName: FullModification methylase NlaIII ShortM.NlaIII AltName: FullAdenine-specific methyltransferase NlaIII] [2e-48]	M.CviAII adenine methylase	0	0	0
a251aL	1E+05	1E+05	56	426	141	15825	10.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
a251bL	1E+05	1E+05	80	156	51	6088	10.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A252R	1E+05	1E+05	74	1029	342	39856	10.3	Early	Yes	N/A	N/A	N/A	N/A	R.CviAII restriction endonuclease	0	0	0
a252bL	1E+05	1E+05	70	153	50	5808	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a252aL	1E+05	1E+05	56	255	84	10478	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	0
A253R	1E+05	1E+05	62	453	150	17547	8.8	Early	N/A	N/A	N/A	YP_001426645 [hypothetical protein ATCV1_Z164L (Acanthocystis turfacea Chlorella virus 1)] [3e-17]	N/A	Unknown protein	0	0	0
a253aR	1E+05	1E+05	56	135	44	5288	10.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A254R	1E+05	1E+05	72	477	158	19092	5.3	Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A255R	1E+05	1E+05	86	447	148	17300	5.1	N/A	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A256/257L	1E+05	1E+05	68	2514	837	96729	7.2	Early-Late	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a258R	1E+05	1E+05	60	252	83	9071	3.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A259L	1E+05	1E+05	78	525	174	20050	8.1	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a259aR	1E+05	1E+05	68	243	80	9552	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
a259bR	1E+05	1E+05	26	201	66	7789	9.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A260R	1E+05	1E+05	78	1518	505	56188	9.0	Late	N/A	COG3325 [Chitinase] [4e-09]	PF00704.21 [Glycosyl hydrolases family 18] [2.1e-73]	YP_001427261 [hypothetical protein ATCV1_Z780L (Acanthocystis turfacea Chlorella virus 1)] [1e-171]	P32470 [RecName: FullChitinase 1 Flags: Precursor] [4e-47]	Chitinase	0	0	0
A260aR	1E+05	1E+05	60	198	65	7742	11.9	N/A	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a260bR	1E+05	1E+05	54	270	89	10396	13.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0

A261R	1E+05	1E+05	88	618	205	25196	8.7	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A262/263L	1E+05	1E+05	64	771	256	29470	9.6	N/A	Yes	N/A	N/A	YP_001425738 [hypothetical protein FR483_N106L (Paramecium bursaria Chlorella virus FR483)] [4e-46]	N/A	Unknown protein	2	3	2
a264R	1E+05	1E+05	84	204	67	7641	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	1
A265L	1E+05	1E+05	90	750	249	27947	9.3	Early-Late	N/A	N/A	PF04848.6 [Poxvirus A22 protein] [8.6e-11]	YP_001426640 [hypothetical protein ATCV1_Z159R (Acanthocystis turfacea Chlorella virus 1)] [5e-73]	N/A	Unknown protein	0	0	0
a266R	1E+05	1E+05	68	252	83	9838	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a266aR	1E+05	1E+05	58	126	41	4771	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A267L	1E+05	1E+05	80	945	314	36686	8.2	Early	N/A	N/A	N/A	YP_142777 [hypothetical protein MIMI_R423 (Acanthamoeba polyphaga mimivirus)] [2e-15]	Q5UQL9 [Uncharacterized protein R423] [2e-16]	Unknown protein	0	0	0
a268R	1E+05	1E+05	50	216	71	8208	9.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a269R	1E+05	1E+05	62	207	68	8054	8.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A271L	1E+05	1E+05	74	825	274	31114	7.1	Early-Late	Yes	COG2267 [Lysophospholipase] [1e-07]	PF12146.1 [Putative lysophospholipase] [1.9e-10]	YP_001426877 [hypothetical protein ATCV1_Z396R (Acanthocystis turfacea Chlorella virus 1)] [5e-51]	Q55EQ3 [RecName: FullUncharacterized abhydrolase domain-containing protein DDB_G0269086] [6e-08]	Unknown protein	0	3	0
a270R	1E+05	1E+05	80	282	93	10237	10.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	2
a272R	1E+05	1E+05	54	204	67	8074	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a272aR	1E+05	1E+05	58	240	79	9104	6.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A273L	1E+05	1E+05	88	417	138	15713	9.9	Late	Yes	N/A	PF03713.6 [Domain of unknown function (DUF305)] [6.8e-13]	YP_142507 [hypothetical protein MIMI_L153 (Acanthamoeba polyphaga mimivirus)] [4e-16]	Q5UPL7 [RecName: FullUncharacterized protein L153] [2e-17]	Unknown protein	3	3	3
A274R	1E+05	1E+05	16	792	263	31386	4.4	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A275R	1E+05	1E+05	80	759	252	28394	9.1	Early	N/A	N/A	PF07150.4 [Protein of unknown function (DUF1390)] [8.6e-79]	YP_001425662 [hypothetical protein FR483_N030R (Paramecium bursaria Chlorella virus FR483)] [2e-26]	N/A	Unknown protein	0	0	0
a276L	1E+05	1E+05	60	285	94	11687	10.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	2

A277L	1E+05	1E+05	70	912	303	34378	8.5	Late	N/A	COG0515 [Serine/threonine protein kinase] [1e-05]	PF00069.18 [Protein kinase domain] [2.2e-42]	YP_001426416 [hypothetical protein FR483_N784R (Paramecium bursaria Chlorella virus FR483)] [2e-28]	Q1ZXC8 [RecName: FullProbable serine/threonine-protein kinase pXi] [7e-23]	Protein kinase	0	0	0
A278L	1E+05	1E+05	80	1833	610	69231	10.8	Late	Yes	N/A	PF00069.18 [Protein kinase domain] [1.2e-07] / PF08789.3 [PBCV-specific basic adaptor domain] [7.5e-10]	YP_001427189 [hypothetical protein ATCV1_Z708L (Acanthocystis turfacea Chlorella virus 1)] [1e-130]	Q99078 [RecName: FullDual specificity protein kinase FUZ7] [5e-07]	Protein kinase	0	1	0
a279R	1E+05	1E+05	68	219	72	8802	10.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	1
a280R	1E+05	1E+05	56	282	93	10103	3.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a281R	1E+05	1E+05	52	720	239	25998	4.6	N/A	N/A	N/A	N/A	YP_001426034 [hypothetical protein FR483_n402R (Paramecium bursaria Chlorella virus FR483)] [5e-25]	N/A	Hypothetical protein	0	6	0
A282L	1E+05	1E+05	60	1710	569	63371	10.8	Late	Yes	N/A	PF00069.18 [Protein kinase domain] [4.8e-10] / PF08789.3 [PBCV-specific basic adaptor domain] [1.3e-17]	YP_001427189 [hypothetical protein ATCV1_Z708L (Acanthocystis turfacea Chlorella virus 1)] [1e-129]	N/A	Protein kinase	0	1	0
a283L	1E+05	1E+05	52	297	98	11412	12.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A284L	1E+05	1E+05	82	840	279	30766	9.2	Early-Late	Yes	COG3049 [Penicillin V acylase and related amidases] [1e-06]	PF02275.11 [Linear amide C-N hydrolases choloylglycine hydrolase family] [1e-49]	YP_001425725 [hypothetical protein FR483_N093R (Paramecium bursaria Chlorella virus FR483)] [4e-91]	P54948 [RecName: FullUncharacterized protein yxeI] [1e-29]	Amindase	0	0	0
a285R	1E+05	1E+05	64	216	71	7946	12.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A286R	1E+05	1E+05	30	1137	378	43042	9.6	Late	Yes	N/A	N/A	YP_001425721 [hypothetical protein FR483_N089L (Paramecium bursaria Chlorella virus FR483)] [2e-92]	N/A	Unknown protein	0	0	0
a286aR	1E+05	1E+05	76	174	57	6925	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
a286bL	1E+05	1E+05	52	174	57	6719	9.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A287R	1E+05	1E+05	74	807	268	31349	9.4	Early-Late	Yes	N/A	PF01541.17 [GIY-YIG catalytic domain] [4.2e-11] / PF07453.6 [NUMOD1 domain] [8.6e-11]	YP_001426191 [hypothetical protein FR483_N559R (Paramecium bursaria Chlorella virus FR483)] [6e-50]	N/A	Unknown protein	0	0	0
a288L	1E+05	1E+05	62	267	88	9946	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A289L	1E+05	1E+05	74	852	283	32038	7.3	Early-Late	N/A	COG0515 [Serine/threonine protein kinase] [9e-06]	PF00069.18 [Protein kinase domain] [5.5e-50]	YP_001426180 [hypothetical protein FR483_N548R (Paramecium bursaria	Q54DF2 [RecName: FullProbable serine/threonine-protein kinase MARK-	Protein kinase	0	0	0

												Chlorella virus FR483)] [2e-31]	A] [1e-23]				
a290R	1E+05	1E+05	48	408	135	15384	7.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	3	2
a291R	1E+05	1E+05	68	270	89	10691	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	1
A292L	1E+05	2E+05	80	987	328	36771	9.3	Late	N/A	N/A	PF01374.11 [Glycosyl hydrolase family 46] [6.1e-97]	YP_001426685 [hypothetical protein ATCV1_Z204R (Acanthocystis turfacea Chlorella virus 1)] [1e-114]	O07921 [RecName: FullChitosanase Flags: Precursor] [9e-17]	Chitosanase	0	0	0
a293R	1E+05	1E+05	56	507	168	18889	11.7	N/A	N/A	N/A	N/A	YP_001426689 [hypothetical protein ATCV1_z208L (Acanthocystis turfacea Chlorella virus 1)] [4e-14]	N/A	Hypothetical protein	1	1	1
a294R	1E+05	2E+05	54	225	74	7580	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A295L	2E+05	2E+05	84	954	317	35626	7.9	Early-Late	Yes	COG1088 [dTDP-D-glucose 46-dehydratase] [8e-06]	PF01370.14 [NAD dependent epimerase/dehydratase family] [1.6e-68]	YP_001426763 [hypothetical protein ATCV1_Z282L (Acanthocystis turfacea Chlorella virus 1)] [1e-119]	Q9LMU0 [RecName: FullPutative GDP-L-fucose synthase 2 AltName: FullGDP-4-keto-6-deoxy-D-mannose-3 5-epimerase-4-reductase 2 ShortAtGER2] [1e-100]	Fucose synthetase	0	0	0
A296R	2E+05	2E+05	14	474	157	17393	12.2	Late	Yes	N/A	N/A	YP_001426690 [hypothetical protein ATCV1_Z209R (Acanthocystis turfacea Chlorella virus 1)] [3e-16]	N/A	Unknown protein	0	1	1
A297L	2E+05	2E+05	88	534	177	20931	9.5	Late	N/A	N/A	N/A	YP_001425724 [hypothetical protein FR483_N092L (Paramecium bursaria Chlorella virus FR483)] [5e-47]	N/A	Unknown protein	0	0	0
a297aL	2E+05	2E+05	40	129	42	5180	11.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A298L	2E+05	2E+05	72	678	225	25489	5.1	Early	N/A	N/A	N/A	YP_001425716 [hypothetical protein FR483_N084R (Paramecium bursaria Chlorella virus FR483)] [4e-36]	N/A	Unknown protein	0	0	0
a299R	2E+05	2E+05	48	519	172	18677	11.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	3	2
a300R	2E+05	2E+05	58	231	76	9009	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A301L	2E+05	2E+05	80	726	241	27394	4.5	Early	N/A	N/A	N/A	YP_001425714 [hypothetical protein FR483_N082R (Paramecium bursaria Chlorella virus FR483)] [8e-11]	N/A	Unknown protein	0	0	0
a302R	2E+05	2E+05	50	423	140	16434	7.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	1

a303L	2E+05	2E+05	68	339	112	13416	11.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A304R	2E+05	2E+05	8	237	78	9490	5.8	Late	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A305L	2E+05	2E+05	66	615	204	22910	10.7	Late	Yes	N/A	PF00782.13 [Dual specificity phosphatase catalytic domain] [3.6e-33]	YP_001425950 [hypothetical protein FR483_N318L (Paramecium bursaria Chlorella virus FR483)] [9e-64]	Q9BY84 [RecName: FullDual specificity protein phosphatase 16 AltName: FullMitogen-activated protein kinase phosphatase 7 ShortMAP kinase phosphatase 7 ShortMKP-7] [7e-12]	Protein phosphatase	0	0	0
A306L	2E+05	2E+05	82	261	86	10359	4.0	Early-Late	N/A	N/A	N/A	YP_001426702 [hypothetical protein ATCV1_Z221L (Acanthocystis turfacea Chlorella virus 1)] [9e-23]	N/A	Unknown protein	0	0	0
a307R	2E+05	2E+05	30	237	78	9139	9.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
a307aR	2E+05	2E+05	68	243	80	9482	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A308L	2E+05	2E+05	72	360	119	13562	4.0	Early	N/A	N/A	N/A	YP_001425955 [hypothetical protein FR483_N323L (Paramecium bursaria Chlorella virus FR483)] [6e-10]	N/A	Unknown protein	0	0	0
a309R	2E+05	2E+05	64	129	42	4922	7.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A310L	2E+05	2E+05	88	513	170	18268	8.5	Late	Yes	N/A	N/A	YP_001426703 [hypothetical protein ATCV1_Z222L (Acanthocystis turfacea Chlorella virus 1)] [3e-52]	N/A	Unknown protein	0	0	0
a311R	2E+05	2E+05	54	252	83	8714	6.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A312L	2E+05	2E+05	66	717	238	26612	5.0	Early-Late	N/A	N/A	N/A	YP_001425959 [hypothetical protein FR483_N327L (Paramecium bursaria Chlorella virus FR483)] [4e-94]	N/A	Unknown protein	0	0	0
a312aR	2E+05	2E+05	42	159	52	6074	4.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A313L	2E+05	2E+05	78	216	71	7838	9.8	Late	N/A	N/A	N/A	YP_001425961 [hypothetical protein FR483_N329L (Paramecium bursaria Chlorella virus FR483)] [9e-06]	N/A	Unknown protein	1	1	1
a313aR	2E+05	2E+05	64	162	53	6275	9.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A314R	2E+05	2E+05	68	243	80	9114	6.7	Late	Yes	N/A	N/A	YP_001425962 [hypothetical protein FR483_N330R (Paramecium bursaria Chlorella virus FR483)]	N/A	Unknown protein	1	1	1

												[2e-25]					
A315L	2E+05	2E+05	80	741	246	27853	9.0	Early-Late	N/A	N/A	PF01541.17 [GIY-YIG catalytic domain] [1.3e-08] / PF07453.6 [NUMOD1 domain] [9.1e-09]	YP_001427114 [hypothetical protein ATCV1_Z633L (Acanthocystis turfacea Chlorella virus 1)] [3e-62]	N/A	Unknown protein	0	0	0
A316R	2E+05	2E+05	18	1317	438	48779	10.7	Late	Yes	N/A	N/A	YP_001426452 [hypothetical protein FR483_N820R (Paramecium bursaria Chlorella virus FR483)] [1e-102]	N/A	Unknown protein	0	1	0
a317L	2E+05	2E+05	50	456	151	18346	12.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a319L	2E+05	2E+05	60	255	84	9165	9.9	N/A	N/A	N/A	N/A	YP_001426455 [hypothetical protein FR483_n823L (Paramecium bursaria Chlorella virus FR483)] [6e-09]	N/A	Hypothetical protein	0	1	0
a318L	2E+05	2E+05	70	174	57	6536	5.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A320R	2E+05	2E+05	68	420	139	15685	10.5	Late	Yes	N/A	N/A	YP_001425965 [hypothetical protein FR483_N333R (Paramecium bursaria Chlorella virus FR483)] [2e-07]	N/A	Unknown protein	1	1	1
A321R	2E+05	2E+05	90	360	119	12830	8.8	Late	Yes	N/A	N/A	YP_001425967 [hypothetical protein FR483_N335R (Paramecium bursaria Chlorella virus FR483)] [8e-16]	N/A	Unknown protein	2	2	2
a321aR	2E+05	2E+05	56	138	45	5447	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A322L	2E+05	2E+05	90	531	176	20039	5.0	Late	Yes	N/A	N/A	YP_001425968 [hypothetical protein FR483_N336L (Paramecium bursaria Chlorella virus FR483)] [3e-16]	N/A	Unknown protein	1	1	1
a323R	2E+05	2E+05	52	399	132	14343	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	3	1
A324L	2E+05	2E+05	68	1362	453	50352	4.9	Late	N/A	N/A	N/A	YP_001425971 [hypothetical protein FR483_N339L (Paramecium bursaria Chlorella virus FR483)] [1e-90]	Q5UQN9 [Uncharacterized protein R449] [2e-08]	Unknown protein	0	0	0
a325R	2E+05	2E+05	44	225	74	9361	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	2
A326L	2E+05	2E+05	66	630	209	24179	9.5	Late	N/A	N/A	N/A	YP_001425974 [hypothetical protein FR483_N342L (Paramecium bursaria Chlorella virus FR483)] [3e-63]	N/A	Unknown protein	0	0	0
a327R	2E+05	2E+05	60	327	108	13081	9.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0

A328L	2E+05	2E+05	88	1068	355	42024	9.2	N/A	N/A	N/A	N/A	YP_001425978 [hypothetical protein FR483_N346L (Paramecium bursaria Chlorella virus FR483)] [3e-69]	N/A	Hypothetical protein	0	0	0
A329R	2E+05	2E+05	64	291	96	10756	4.8	Late	N/A	N/A	N/A	YP_001426735 [hypothetical protein ATCV1_Z254R (Acanthocystis turfacea Chlorella virus 1)] [3e-13]	N/A	Unknown protein	0	0	0
a329aL	2E+05	2E+05	36	135	44	4997	8.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A329bR	2E+05	2E+05	80	186	61	6905	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	1	1
a329cR	2E+05	2E+05	74	186	61	6892	9.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	1
A330R	2E+05	2E+05	84	1299	432	49958	7.5	Early-Late	N/A	COG0666 [FOG: Ankyrin repeat] [9e-06]	PF00023.23 [Ankyrin repeat] [1.3e-07]	XP_001321901 [ankyrin repeat protein (Trichomonas vaginalis G3)] [7e-31]	Q12955 [RecName: FullAnkyrin-3 ShortANK-3 AltName: FullAnkyrin-G] [1e-26]	Unknown protein	0	0	0
a331L	2E+05	2E+05	62	204	67	7616	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	1
A333L	2E+05	2E+05	92	1173	390	43025	8.1	Early-Late	N/A	N/A	PF03067.8 [Chitin binding domain] [2.1e-24] / PF01607.17 [Chitin binding Peritrophin-A domain] [1.7e-07]	YP_001426322 [hypothetical protein FR483_N690R (Paramecium bursaria Chlorella virus FR483)] [2e-85]	N/A	Unknown protein	1	2	1
a334L	2E+05	2E+05	54	270	89	10302	12.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a335R	2E+05	2E+05	58	225	74	7939	10.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a336R	2E+05	2E+05	60	258	85	9750	8.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A337L	2E+05	2E+05	76	609	202	23000	8.8	Early-Late	N/A	N/A	N/A	YP_001426717 [hypothetical protein ATCV1_Z236L (Acanthocystis turfacea Chlorella virus 1)] [5e-16]	N/A	Unknown protein	0	0	0
a340R	2E+05	2E+05	62	279	92	11149	8.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A339L	2E+05	2E+05	76	186	61	7372	11.1	Early-Late	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A341L	2E+05	2E+05	76	408	135	15341	4.0	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a341aR	2E+05	2E+05	52	198	65	7269	4.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a341bR	2E+05	2E+05	8	159	52	5765	8.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A342L	2E+05	2E+05	74	1731	576	63813	9.2	Early-Late	Yes	N/A	N/A	YP_001425991 [hypothetical protein FR483_N359L (Paramecium bursaria Chlorella virus FR483)] [0.0]	N/A	Unknown protein	1	1	1

a343R	2E+05	2E+05	56	261	86	10111	8.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a344R	2E+05	2E+05	44	348	115	13071	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a345L	2E+05	2E+05	54	291	96	11083	10.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a346L	2E+05	2E+05	48	228	75	8680	9.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	2
a347L	2E+05	2E+05	40	213	70	8435	7.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A348R	2E+05	2E+05	66	480	159	18321	8.9	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a348aR	2E+05	2E+05	52	156	51	5768	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A349L	2E+05	2E+05	66	549	182	21077	10.0	Early-Late	Yes	N/A	N/A	YP_001426595 [hypothetical protein ATCV1_Z114L (Acanthocystis turfacea Chlorella virus 1)] [2e-31]	N/A	Unknown protein	0	1	0
A350R	2E+05	2E+05	64	369	122	14676	9.7	N/A	Yes	N/A	PF12239.1 [Protein of unknown function (DUF3605)] [4.4e-23]	YP_001426000 [hypothetical protein FR483_n368R (Paramecium bursaria Chlorella virus FR483)] [6e-30]	N/A	Unknown protein	0	0	0
a350aR	2E+05	2E+05	52	135	44	5299	11.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A351L	2E+05	2E+05	80	1077	358	41335	9.6	Early	N/A	N/A	PF01541.17 [GIY-YIG catalytic domain] [3.6e-08]	YP_001426752 [hypothetical protein ATCV1_Z271R (Acanthocystis turfacea Chlorella virus 1)] [3e-84]	N/A	Unknown protein	0	1	0
a351aL	2E+05	2E+05	36	132	43	5148	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A352L	2E+05	2E+05	90	624	207	23310	3.6	Late	Yes	N/A	N/A	YP_001426751 [hypothetical protein ATCV1_Z270R (Acanthocystis turfacea Chlorella virus 1)] [2e-65]	Q5UQF7 [RecName: FullUncharacterized protein R489 Flags: Precursor] [1e-05]	Unknown protein	0	1	1
a353R	2E+05	2E+05	48	207	68	9017	12.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A354R	2E+05	2E+05	88	1038	345	40103	9.6	Early-Late	N/A	N/A	N/A	YP_001427263 [hypothetical protein ATCV1_Z782L (Acanthocystis turfacea Chlorella virus 1)] [4e-72]	N/A	Unknown protein	0	0	0
a355L	2E+05	2E+05	64	219	72	8354	7.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A356R	2E+05	2E+05	68	324	107	12512	10.5	N/A	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A357L	2E+05	2E+05	82	987	328	36796	4.0	Early-Late	N/A	N/A	N/A	YP_001426005 [hypothetical protein FR483_N373L (Paramecium bursaria Chlorella virus FR483)]	N/A	Unknown protein	0	0	0

												[4e-42]					
a358R	2E+05	2E+05	54	315	104	10600	3.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
a359L	2E+05	2E+05	72	168	55	6725	12.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A363R	2E+05	2E+05	48	3540	1179	####	10.9	Early	Yes	N/A	N/A	YP_001426015 [hypothetical protein FR483_N383R (Paramecium bursaria Chlorella virus FR483)] [0.0]	P0C9B2 [RecName: FullPutative ATP-dependent RNA helicase Q706L] [2e-06]	Unknown protein	0	2	0
a364L	2E+05	2E+05	56	204	67	7367	9.7	N/A	N/A	N/A	N/A	YP_001426743 [hypothetical protein ATCV1_z262R (Acanthocystis turfacea Chlorella virus 1)] [1e-06]	N/A	Hypothetical protein	0	0	0
a365L	2E+05	2E+05	76	291	96	11311	9.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A366L	2E+05	2E+05	72	768	255	28582	8.9	Early-Late	N/A	N/A	PF07150.4 [Protein of unknown function (DUF1390)] [6.5e-41]	YP_001426479 [hypothetical protein FR483_N847R (Paramecium bursaria Chlorella virus FR483)] [4e-35]	N/A	Unknown protein	0	0	0
a367R	2E+05	2E+05	68	276	91	10811	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
A368L	2E+05	2E+05	66	1512	503	59785	4.5	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a370R	2E+05	2E+05	72	249	82	10060	8.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	1
a371R	2E+05	2E+05	62	189	62	7317	10.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a372L	2E+05	2E+05	64	231	76	9518	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A373R	2E+05	2E+05	76	459	152	17599	9.8	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a374L	2E+05	2E+05	64	264	87	9593	7.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
A375R	2E+05	2E+05	88	522	173	19085	9.4	Early-Late	Yes	N/A	N/A	YP_001426196 [hypothetical protein FR483_N564R (Paramecium bursaria Chlorella virus FR483)] [1e-49]	N/A	Unknown protein	2	2	2
a376R	2E+05	2E+05	50	192	63	7566	7.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A378L	2E+05	2E+05	88	786	261	29219	9.4	Late	Yes	N/A	N/A	YP_001426886 [hypothetical protein ATCV1_Z405L (Acanthocystis turfacea Chlorella virus 1)] [3e-41]	N/A	Unknown protein	1	1	0
A379L	2E+05	2E+05	76	624	207	24256	10.3	Early	N/A	N/A	N/A	YP_001426021 [hypothetical protein FR483_N389L (Paramecium bursaria Chlorella virus FR483)]	N/A	Unknown protein	0	0	0

												[3e-36]					
a380R	2E+05	2E+05	42	306	101	11357	5.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a381R	2E+05	2E+05	66	258	85	9747	10.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A383R	2E+05	2E+05	94	1383	460	52511	5.2	Late	Yes	N/A	PF04451.5 [Large eukaryotic DNA virus major capsid protein] [1.6e-25]	YP_001426027 [hypothetical protein FR483_N395R (Paramecium bursaria Chlorella virus FR483)] [1e-117]	A7U6E9 [RecName: FullMajor capsid protein ShortMCP] [1e-33]	Capsid protein	0	0	0
a384R	2E+05	2E+05	70	213	70	8080	12.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A384aL	2E+05	2E+05	68	189	62	7365	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A384bL	2E+05	2E+05	76	183	60	6809	9.0	N/A	Yes	N/A	N/A	N/A	N/A	Unknown protein	1	1	1
a384cR	2E+05	2E+05	42	147	48	5750	7.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A384dL	2E+05	2E+05	92	1929	642	69009	8.0	Early-Late	Yes	N/A	PF01607.17 [Chitin binding Peritrophin-A domain] [2.4e-07] / PF04451.5 [Large eukaryotic DNA virus major capsid protein] [2e-11]	YP_001426225 [hypothetical protein FR483_N593R (Paramecium bursaria Chlorella virus FR483)] [1e-83]	N/A	Capsid protein	1	2	1
a385L	2E+05	2E+05	50	231	76	8760	10.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a388R	2E+05	2E+05	62	330	109	13151	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a391R	2E+05	2E+05	74	288	95	10732	10.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
A392R	2E+05	2E+05	26	780	259	29705	9.4	Late	N/A	N/A	PF04665.5 [Poxvirus A32 protein] [5.2e-06]	YP_001426221 [hypothetical protein FR483_N589L (Paramecium bursaria Chlorella virus FR483)] [1e-110]	Q196X2 [RecName: FullUncharacterized protein 088R] [6e-30]	Unknown protein	0	1	0
a393L	2E+05	2E+05	74	198	65	7393	6.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a393aL	2E+05	2E+05	2	135	44	5745	9.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A394R	2E+05	2E+05	62	366	121	13915	3.8	Early-Late	N/A	N/A	N/A	YP_001426218 [hypothetical protein FR483_N586L (Paramecium bursaria Chlorella virus FR483)] [2e-14]	N/A	Unknown protein	0	0	0
A395R	2E+05	2E+05	76	249	82	9254	9.9	Early-Late	N/A	N/A	N/A	YP_001426214 [hypothetical protein FR483_N582L (Paramecium bursaria Chlorella virus FR483)] [1e-23]	N/A	Unknown protein	0	0	0
A395aL	2E+05	2E+05	72	123	40	4466	9.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1

a395bL	2E+05	2E+05	64	138	45	5372	9.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A396L	2E+05	2E+05	82	459	152	18281	7.9	Early-Late	N/A	N/A	N/A	YP_001426451 [hypothetical protein FR483_N819R (Paramecium bursaria Chlorella virus FR483)] [3e-13]	N/A	Unknown protein	1	1	1
A397R	2E+05	2E+05	86	459	152	18036	4.4	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A398L	2E+05	2E+05	60	357	118	12987	9.9	Late	Yes	N/A	N/A	YP_001426210 [hypothetical protein FR483_N578R (Paramecium bursaria Chlorella virus FR483)] [1e-35]	N/A	Unknown protein	2	3	3
a398aR	2E+05	2E+05	54	180	59	6906	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A399R	2E+05	2E+05	64	585	194	21832	8.9	Early	N/A	N/A	PF00075.17 [RNase H] [6.7e-19]	YP_001426207 [hypothetical protein FR483_N575L (Paramecium bursaria Chlorella virus FR483)] [9e-37]	N/A	Unknown protein	0	0	0
A400R	2E+05	2E+05	78	357	118	13634	9.5	Early-Late	Yes	N/A	N/A	YP_001426835 [hypothetical protein ATCV1_z354L (Acanthocystis turfacea Chlorella virus 1)] [3e-20]	N/A	Unknown protein	0	0	0
A401R	2E+05	2E+05	78	834	277	31433	6.8	Early-Late	N/A	N/A	N/A	YP_001426204 [hypothetical protein FR483_N572L (Paramecium bursaria Chlorella virus FR483)] [2e-95]	N/A	Unknown protein	0	1	1
A402R	2E+05	2E+05	78	684	227	25380	7.5	Late	N/A	N/A	N/A	YP_001426843 [hypothetical protein ATCV1_Z362R (Acanthocystis turfacea Chlorella virus 1)] [6e-67]	N/A	Unknown protein	0	0	0
A403R	2E+05	2E+05	78	282	93	10830	10.0	Early-Late	N/A	N/A	N/A	YP_001426844 [hypothetical protein ATCV1_Z363R (Acanthocystis turfacea Chlorella virus 1)] [7e-20]	N/A	Unknown protein	0	0	0
A404R	2E+05	2E+05	88	576	191	22111	2.9	Late	N/A	N/A	N/A	YP_001426199 [hypothetical protein FR483_N567L (Paramecium bursaria Chlorella virus FR483)] [2e-13]	N/A	Unknown protein	1	1	1
A404aL	2E+05	2E+05	84	159	52	5910	4.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A405R	2E+05	2E+05	6	1491	496	53502	10.3	Late	Yes	N/A	N/A	YP_001426197 [hypothetical protein FR483_N565L (Paramecium bursaria Chlorella virus FR483)] [1e-42]	N/A	Unknown protein	1	2	1

a406L	2E+05	2E+05	70	201	66	7386	9.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A407L	2E+05	2E+05	80	633	210	23382	8.9	Late	Yes	N/A	N/A	YP_001426955 [hypothetical protein ATCV1_Z474R (Acanthocystis turfacea Chlorella virus 1)] [2e-70]	N/A	Unknown protein	1	2	2
A408L	2E+05	2E+05	56	834	277	30772	4.5	Early-Late	N/A	N/A	N/A	YP_001426126 [hypothetical protein FR483_N494R (Paramecium bursaria Chlorella virus FR483)] [8e-48]	N/A	Unknown protein	0	0	0
a409R	2E+05	2E+05	44	249	82	9006	5.4	N/A	N/A	N/A	N/A	YP_001426951 [hypothetical protein ATCV1_z470L (Acanthocystis turfacea Chlorella virus 1)] [3e-06]	N/A	Hypothetical protein	1	2	1
A410L	2E+05	2E+05	72	333	110	13015	4.4	Early	N/A	N/A	N/A	YP_001426942 [hypothetical protein ATCV1_Z461L (Acanthocystis turfacea Chlorella virus 1)] [1e-26]	N/A	Unknown protein	0	0	0
A411R	2E+05	2E+05	78	513	170	19584	4.6	Late	N/A	N/A	N/A	YP_001426120 [hypothetical protein FR483_N488R (Paramecium bursaria Chlorella virus FR483)] [3e-09]	N/A	Unknown protein	0	0	0
A412R	2E+05	2E+05	74	540	179	20539	7.4	Early	N/A	N/A	N/A	YP_001426947 [hypothetical protein ATCV1_Z466R (Acanthocystis turfacea Chlorella virus 1)] [3e-47]	N/A	Unknown protein	0	0	0
A413L	2E+05	2E+05	80	735	244	26998	9.5	Late	Yes	N/A	N/A	YP_001426125 [hypothetical protein FR483_N493L (Paramecium bursaria Chlorella virus FR483)] [1e-29]	N/A	Unknown protein	2	2	2
A414R	2E+05	2E+05	48	282	93	10612	10.8	Late	Yes	N/A	N/A	YP_001426117 [hypothetical protein FR483_N485R (Paramecium bursaria Chlorella virus FR483)] [5e-11]	N/A	Unknown protein	2	2	2
a415L	2E+05	2E+05	66	210	69	7685	10.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A416R	2E+05	2E+05	82	567	188	22361	6.5	Late	N/A	COG1428 [Deoxynucleoside kinases] [8e-07]	PF01712.12 [Deoxynucleoside kinase] [1.1e-36]	YP_001426070 [hypothetical protein FR483_N438R (Paramecium bursaria Chlorella virus FR483)] [6e-48]	Q197D1 [RecName: FullPutative kinase protein 029R] [4e-21]	Unknown protein	0	1	0
A417L	2E+05	2E+05	82	1290	429	48932	7.5	Late	N/A	N/A	N/A	YP_001426073 [hypothetical protein FR483_N441L (Paramecium bursaria Chlorella virus FR483)] [4e-52]	A6UWR5 [RecName: FullReplication factor C large subunit ShortRFC large subunit AltName: FullClamp loader large subunit] [1e-06]	Unknown protein	0	0	0

a418R	2E+05	2E+05	62	240	79	9726	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
a419R	2E+05	2E+05	74	213	70	7892	5.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A420L	2E+05	2E+05	82	213	70	7918	6.4	Late	Yes	N/A	N/A	YP_001426933 [hypothetical protein ATCV1_Z452R (Acanthocystis turfacea Chlorella virus 1)] [5e-21]	N/A	Unknown protein	1	1	1
A421R	2E+05	2E+05	10	297	98	11056	10.1	Late	Yes	N/A	N/A	YP_001426078 [hypothetical protein FR483_N446R (Paramecium bursaria Chlorella virus FR483)] [2e-16]	N/A	Unknown protein	1	1	1
A422R	2E+05	2E+05	82	993	330	37736	9.6	Early-Late	N/A	N/A	PF07463.4 [NUMOD4 motif] [5.7e-13] / PF01844.16 [HNH endonuclease] [1.4e-06]	YP_001426831 [hypothetical protein ATCV1_Z350L (Acanthocystis turfacea Chlorella virus 1)] [6e-15]	Q5UPT4 [RecName: FullUncharacterized HNH endonuclease L247] [1e-12]	Unknown protein	0	0	0
A422aR	2E+05	2E+05	74	192	63	7880	9.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	0
A423R	2E+05	2E+05	72	474	157	18458	6.5	Late	Yes	N/A	N/A	YP_001426081 [hypothetical protein FR483_N449R (Paramecium bursaria Chlorella virus FR483)] [3e-12]	N/A	Unknown protein	0	1	0
A424R	2E+05	2E+05	86	330	109	12637	11.3	Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a425L	2E+05	2E+05	58	189	62	7087	4.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A426R	2E+05	2E+05	52	345	114	13391	5.0	Late	N/A	N/A	N/A	YP_001426084 [hypothetical protein FR483_N452R (Paramecium bursaria Chlorella virus FR483)] [2e-17]	N/A	Unknown protein	0	0	0
A427L	2E+05	2E+05	76	360	119	13765	6.5	Early	N/A	N/A	PF00085.13 [Thioredoxin] [8.6e-12]	YP_001426085 [hypothetical protein FR483_N453L (Paramecium bursaria Chlorella virus FR483)] [5e-14]	N/A	Unknown protein	0	0	0
A428L	2E+05	2E+05	80	438	145	15912	3.8	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A429L	2E+05	2E+05	70	1431	476	55474	4.7	Early	N/A	N/A	N/A	YP_001426092 [hypothetical protein FR483_N460L (Paramecium bursaria Chlorella virus FR483)] [6e-50]	N/A	Unknown protein	0	0	0
A430L	2E+05	2E+05	76	1314	437	48165	7.5	Late	Yes	N/A	PF04451.5 [Large eukaryotic DNA virus major capsid protein] [2.6e-80]	YP_001426761 [hypothetical protein ATCV1_Z280L (Acanthocystis turfacea Chlorella virus 1)] [0.0]	A7U6E9 [RecName: FullMajor capsid protein ShortMCP] [5e-90]	Major capsid protein	0	0	0
A431L	2E+05	2E+05	64	201	66	7999	10.3	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0

A432R	2E+05	2E+05	14	474	157	17358	10.1	Late	N/A	N/A	N/A	YP_001426109 [hypothetical protein FR483_N477R (Paramecium bursaria Chlorella virus FR483)] [9e-27]	N/A	Unknown protein	0	0	0
a433R	2E+05	2E+05	56	342	113	13111	9.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a433aR	2E+05	2E+05	46	135	44	5413	10.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a434L	2E+05	2E+05	58	171	56	5966	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a434aR	2E+05	2E+05	62	189	62	6769	9.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A436L	2E+05	2E+05	60	192	63	6932	13.0	N/A	Yes	N/A	PF08789.3 [PBCV-specific basic adaptor domain] [1.5e-16]	YP_001426679 [hypothetical protein ATCV1_Z198L (Acanthocystis turfacea Chlorella virus 1)] [3e-06]	N/A	Unknown protein	0	0	0
A435R	2E+05	2E+05	30	192	63	6795	11.2	Early	N/A	N/A	N/A	YP_001426611 [hypothetical protein ATCV1_z130R (Acanthocystis turfacea Chlorella virus 1)] [1e-05]	N/A	Unknown protein	0	1	0
A437L	2E+05	2E+05	76	312	103	10876	11.0	Late	Yes	N/A	PF05854.4 [Non-histone chromosomal protein MC1] [5.9e-07]	YP_001426116 [hypothetical protein FR483_N484L (Paramecium bursaria Chlorella virus FR483)] [3e-30]	N/A	Unknown protein	0	1	0
A437aR	2E+05	2E+05	40	153	50	5255	10.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A438L	2E+05	2E+05	86	237	78	8988	10.7	Early-Late	Yes	COG0695 [Glutaredoxin and related proteins] [3e-06]	PF00462.17 [Glutaredoxin] [3e-10]	YP_001426068 [hypothetical protein FR483_N436R (Paramecium bursaria Chlorella virus FR483)] [8e-18]	Q1RHJ0 [RecName: FullGlutaredoxin-1] [3e-06]	Glutaredoxin	0	0	0
A439R	2E+05	2E+05	34	339	112	12855	8.3	N/A	N/A	N/A	N/A	YP_001426616 [hypothetical protein ATCV1_Z135R (Acanthocystis turfacea Chlorella virus 1)] [8e-28]	N/A	Hypothetical protein	3	3	2
A439aR	2E+05	2E+05	70	171	56	6279	6.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A440L	2E+05	2E+05	70	267	88	10112	11.1	Early	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A441L	2E+05	2E+05	72	414	137	15531	4.4	Early	N/A	N/A	N/A	YP_001426062 [hypothetical protein FR483_N430L (Paramecium bursaria Chlorella virus FR483)] [1e-27]	N/A	Unknown protein	0	0	0
a442R	2E+05	2E+05	10	396	131	15348	8.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A443R	2E+05	2E+05	74	927	308	34961	5.3	Early	Yes	N/A	N/A	YP_001426065 [hypothetical protein FR483_N433R	N/A	Unknown protein	0	0	0

												(Paramecium bursaria Chlorella virus FR483)] [2e-50]					
A444L	2E+05	2E+05	84	315	104	11654	5.2	Late	N/A	N/A	N/A	YP_001426058 [hypothetical protein FR483_N426R (Paramecium bursaria Chlorella virus FR483)] [2e-06]	N/A	Unknown protein	0	0	0
A445L	2E+05	2E+05	86	1389	462	52542	8.5	Early	N/A	COG0661 [Predicted unusual protein kinase] [5e-06]	PF03109.9 [ABC1 family] [1.3e-29]	YP_001426053 [hypothetical protein FR483_N421R (Paramecium bursaria Chlorella virus FR483)] [1e-168]	Q55884 [RecName: FullUncharacterized protein sll0095] [1e-21]	Unknown protein	0	0	0
a446R	2E+05	2E+05	44	306	101	11199	9.4	N/A	N/A	N/A	N/A	YP_001426569 [hypothetical protein ATCV1_z088L (Acanthocystis turfacea Chlorella virus 1)] [5e-12]	N/A	Hypothetical protein	1	2	2
a447R	2E+05	2E+05	46	300	99	10962	12.1	N/A	N/A	N/A	N/A	YP_001426568 [hypothetical protein ATCV1_z087L (Acanthocystis turfacea Chlorella virus 1)] [4e-11]	N/A	Hypothetical protein	0	2	0
A447aR	2E+05	2E+05	8	138	45	5187	4.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A448L	2E+05	2E+05	76	321	106	12369	10.4	Late	Yes	N/A	PF00085.13 [Thioredoxin] [6.7e-16]	YP_001426562 [hypothetical protein ATCV1_Z081L (Acanthocystis turfacea Chlorella virus 1)] [1e-31]	Q9XI01 [RecName: FullProbable protein disulfide-isomerase 1 ShortPDI 1 Flags: Precursor] [1e-07]	Protein disulphide isomerase with heme binding site	0	0	0
a448aL	2E+05	2E+05	40	144	47	5352	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A449R	2E+05	2E+05	70	582	193	22451	8.9	Early	N/A	N/A	PF02940.8 [mRNA capping enzyme beta chain] [3.1e-18]	YP_001426048 [hypothetical protein FR483_N416L (Paramecium bursaria Chlorella virus FR483)] [5e-47]	N/A	Unknown protein	0	0	0
A450R	2E+05	2E+05	86	750	249	28143	9.4	Early	N/A	N/A	PF07150.4 [Protein of unknown function (DUF1390)] [2.5e-82]	YP_001426424 [hypothetical protein FR483_N792R (Paramecium bursaria Chlorella virus FR483)] [2e-29]	N/A	Unknown protein	0	0	0
a451L	2E+05	2E+05	54	306	101	12174	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
A452L	2E+05	2E+05	82	240	79	9447	4.2	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a453R	2E+05	2E+05	10	270	89	10218	7.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A454L	2E+05	2E+05	82	870	289	31194	4.7	Early-Late	Yes	N/A	N/A	YP_001426311 [hypothetical protein FR483_N679R (Paramecium bursaria Chlorella virus FR483)] [1e-102]	N/A	Unknown protein	1	1	0
a455R	2E+05	2E+05	42	444	147	15433	7.9	N/A	N/A	N/A	N/A	YP_001426312 [hypothetical protein	N/A	Hypothetical protein	2	2	2

												FR483_n680L (Paramecium bursaria Chlorella virus FR483)] [5e-12]					
A456L	2E+05	2E+05	74	1965	654	75235	5.5	Early	Yes	COG3378 [Predicted ATPase] [3e-06]	PF08706.4 [D5 N terminal like] [3.9e-09]	YP_001426306 [hypothetical protein FR483_N674R (Paramecium bursaria Chlorella virus FR483)] [0.0]	N/A	Unknown protein	0	0	0
a457R	2E+05	2E+05	44	231	76	8771	12.0	N/A	N/A	N/A	N/A	YP_001426309 [hypothetical protein FR483_n677L (Paramecium bursaria Chlorella virus FR483)] [2e-06]	N/A	Hypothetical protein	0	0	0
a458L	2E+05	2E+05	60	252	83	9651	12.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a459R	2E+05	2E+05	52	303	100	11291	10.5	N/A	N/A	N/A	N/A	YP_001426309 [hypothetical protein FR483_n677L (Paramecium bursaria Chlorella virus FR483)] [2e-22]	N/A	Hypothetical protein	0	0	0
a460R	2E+05	2E+05	56	237	78	9235	11.2	N/A	N/A	N/A	N/A	YP_001426548 [hypothetical protein ATCV1_z067L (Acanthocystis turfacea Chlorella virus 1)] [5e-11]	N/A	Hypothetical protein	0	0	0
A461R	2E+05	2E+05	54	234	77	8987	10.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A462R	2E+05	2E+05	36	216	71	8338	9.7	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a463L	2E+05	2E+05	54	576	191	22590	10.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A464R	2E+05	2E+05	50	828	275	31170	6.7	Early	N/A	COG0571 [dsRNA-specific ribonuclease] [1e-07]	PF00636.19 [RNase3 domain] [8.7e-21] / PF00035.18 [Double-stranded RNA binding motif] [1.2e-11]	YP_001426302 [hypothetical protein FR483_N670L (Paramecium bursaria Chlorella virus FR483)] [9e-98]	Q8KAN7 [RecName: FullRibonuclease 3 AltName: FullRibonuclease III ShortRNase III] [5e-32]	Rnase III	0	0	0
A464aR	2E+05	2E+05	58	126	41	5049	11.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A465R	2E+05	2E+05	74	357	118	13528	10.2	Early-Late	Yes	COG5054 [Mitochondrial sulfhydryl oxidase involved in the biogenesis of cytosolic Fe/S proteins] [4e-06]	PF04777.6 [Erv1 / Alr family] [3.5e-22]	YP_001426300 [hypothetical protein FR483_N668R (Paramecium bursaria Chlorella virus FR483)] [8e-42]	Q5UQV6 [RecName: FullProbable FAD-linked sulfhydryl oxidase R368] [3e-12]	Unknown protein	0	0	0
a466L	2E+05	2E+05	68	276	91	10518	8.9	N/A	N/A	N/A	N/A	YP_001426543 [hypothetical protein ATCV1_z062L (Acanthocystis turfacea Chlorella virus 1)] [5e-15]	N/A	Hypothetical protein	0	0	0
A467L	2E+05	2E+05	78	939	312	36694	7.5	Early-Late	N/A	N/A	N/A	YP_001426297 [hypothetical protein FR483_N665R (Paramecium bursaria Chlorella virus FR483)]	N/A	Unknown protein	0	0	0

												[1e-106]				
A468R	2E+05	2E+05	72	1332	443	50331	8.8	Early-Late	N/A	N/A	PF01896.12 [Eukaryotic and archaeal DNA primase small subunit] [8.5e-12] / PF03121.8 [Herpesviridae UL52/UL70 DNA primase] [2.4e-09]	YP_001426294 [hypothetical protein FR483_N662L (Paramecium bursaria Chlorella virus FR483)] [1e-109]	N/A	Unknown protein	0	0	0
a469L	2E+05	2E+05	60	231	76	8105	5.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A470R	2E+05	2E+05	80	612	203	22924	4.5	Early-Late	N/A	N/A	N/A	YP_001426290 [hypothetical protein FR483_N658L (Paramecium bursaria Chlorella virus FR483)] [7e-66]	N/A	Unknown protein	0	1	0
a470aL	2E+05	2E+05	66	162	53	6435	12.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A471R	2E+05	2E+05	70	522	173	20628	9.4	Late	N/A	N/A	N/A	YP_001426287 [hypothetical protein FR483_N655L (Paramecium bursaria Chlorella virus FR483)] [6e-52]	Q5UQ75 [RecName: FullUncharacterized protein L507] [5e-25]	Unknown protein	0	0	0
a472L	2E+05	2E+05	70	273	90	10292	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A473L	2E+05	2E+05	70	1554	517	59295	8.0	Early	N/A	COG1215 [Glycosyltransferases probably involved in cell wall biogenesis] [6e-07]	PF00535.19 [Glycosyl transferase family 2] [9.6e-23] / PF03552.7 [Cellulose synthase] [1.1e-06]	YP_001425823 [hypothetical protein FR483_N191R (Paramecium bursaria Chlorella virus FR483)] [0.0]	P58931 [RecName: FullCellulose synthase catalytic subunit (UDP-forming)] [7e-40]	Unknown protein	6	6	6
a474R	2E+05	2E+05	46	318	105	12405	10.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
a475R	2E+05	2E+05	50	273	90	10347	4.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A476R	2E+05	2E+05	80	975	324	37393	4.4	Early-Late	Yes	COG0208 [Ribonucleotide reductase beta subunit] [9e-07]	PF00268.14 [Ribonucleotide reductase small chain] [1.3e-100]	YP_001426283 [hypothetical protein FR483_N651L (Paramecium bursaria Chlorella virus FR483)] [1e-151]	Q6Y657 [RecName: FullPutative ribonucleoside-diphosphate reductase small chain B AltName: FullRibonucleotide reductase small subunit B AltName: FullRibonucleoside-diphosphate reductase R2B subunit] [1e-113]	Unknown protein	0	0	1
a477L	2E+05	2E+05	52	222	73	8634	10.7	N/A	N/A	N/A	N/A	N/A	P20561 [RecName: FullUncharacterized 11.6 kDa protein] [3e-06]	Hypothetical protein	0	0	0
A478L	2E+05	2E+05	74	933	310	36612	8.9	Early-Late	N/A	N/A	N/A	YP_001426114 [hypothetical protein FR483_N482R (Paramecium bursaria	Q5UQL9 [Uncharacterized protein R423] [2e-33]	Unknown protein	0	0	0

												Chlorella virus FR483)] [7e-44]					
a478aL	2E+05	2E+05	56	507	168	20088	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	3	3	5
a479L	2E+05	2E+05	52	240	79	9529	11.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A480L	2E+05	2E+05	82	282	93	9838	10.0	Late	Yes	N/A	N/A	YP_001426775 [hypothetical protein ATCV1_Z294L (Acanthocystis turfacea Chlorella virus 1)] [3e-13]	N/A	Unknown protein	2	2	2
A481L	2E+05	2E+05	78	675	224	26058	4.7	Early	N/A	N/A	N/A	YP_001426265 [hypothetical protein FR483_N633L (Paramecium bursaria Chlorella virus FR483)] [2e-51]	N/A	Unknown protein	0	0	0
a481aL	2E+05	2E+05	64	123	40	4542	9.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A482R	2E+05	2E+05	86	648	215	24682	9.5	N/A	N/A	N/A	PF06467.7 [MYM-type Zinc finger with FCS sequence motif] [3.7e-12]	YP_001426272 [hypothetical protein FR483_N640R (Paramecium bursaria Chlorella virus FR483)] [9e-52]	N/A	Hypothetical protein	0	0	0
a483L	2E+05	2E+05	68	216	71	8039	10.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A484L	2E+05	2E+05	82	468	155	18604	9.6	Early-Late	Yes	N/A	N/A	YP_001426769 [hypothetical protein ATCV1_Z288R (Acanthocystis turfacea Chlorella virus 1)] [2e-51]	N/A	Unknown protein	0	0	0
A485R	2E+05	2E+05	54	447	148	17234	10.7	Late	N/A	N/A	N/A	YP_001426260 [hypothetical protein FR483_N628L (Paramecium bursaria Chlorella virus FR483)] [5e-45]	N/A	Unknown protein	0	0	0
A486L	2E+05	2E+05	80	459	152	17807	4.0	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a487R	2E+05	2E+05	60	198	65	7897	10.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A488R	2E+05	2E+05	82	954	317	34631	5.0	Late	Yes	N/A	N/A	YP_001426256 [hypothetical protein FR483_N624L (Paramecium bursaria Chlorella virus FR483)] [1e-101]	Q5UQL4 [RecName: FullUncharacterized protein L417] [2e-09]	Unknown protein	0	3	0
a489R	2E+05	2E+05	56	369	122	14606	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A490L	2E+05	2E+05	82	933	310	36640	8.5	Early-Late	N/A	N/A	N/A	YP_001426114 [hypothetical protein FR483_N482R (Paramecium bursaria Chlorella virus FR483)] [5e-39]	Q5UQL9 [Uncharacterized protein R423] [3e-29]	Unknown protein	0	0	0
A491R	2E+05	2E+05	78	231	76	8259	4.5	Late	N/A	N/A	N/A	YP_001426253 [hypothetical protein FR483_N621L (Paramecium bursaria	N/A	Unknown protein	2	2	2

												Chlorella virus FR483)] [7e-13]					
a491aL	2E+05	2E+05	52	150	49	5610	10.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A492L	2E+05	2E+05	70	570	189	22611	8.0	Early	N/A	N/A	N/A	YP_001426803 [hypothetical protein ATCV1_Z322L (Acanthocystis turfacea Chlorella virus 1)] [6e-22]	N/A	Unknown protein	0	0	0
A493L	2E+05	2E+05	92	576	191	22651	9.8	Early	N/A	N/A	N/A	YP_001426245 [hypothetical protein FR483_N613L (Paramecium bursaria Chlorella virus FR483)] [3e-16]	N/A	Unknown protein	0	0	0
A494R	2E+05	2E+05	14	1083	360	42027	8.6	Early-Late	N/A	N/A	PF08792.3 [A2L zinc ribbon domain] [5.9e-12] / PF04947.7 [Poxvirus Late Transcription Factor VLTF3 like] [4.2e-57]	YP_001426246 [hypothetical protein FR483_N614R (Paramecium bursaria Chlorella virus FR483)] [1e-102]	A7IXI8 [RecName: FullUncharacterized protein B663R] [1e-151]	Unknown protein	0	0	0
A495R	2E+05	2E+05	76	666	221	25277	10.6	Early-Late	N/A	N/A	PF01541.17 [GIY-YIG catalytic domain] [1.3e-08]	YP_001426023 [hypothetical protein FR483_N391R (Paramecium bursaria Chlorella virus FR483)] [2e-28]	N/A	Unknown protein	0	0	0
a496L	2E+05	2E+05	60	213	70	8230	7.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A497R	2E+05	2E+05	88	441	146	15378	10.4	Late	Yes	N/A	N/A	N/A	N/A	Unknown protein	2	2	1
a498L	2E+05	2E+05	60	375	124	13544	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a499L	2E+05	2E+05	66	234	77	9531	8.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A500L	2E+05	2E+05	86	1059	352	38463	5.0	N/A	Yes	N/A	N/A	YP_001426251 [hypothetical protein FR483_N619L (Paramecium bursaria Chlorella virus FR483)] [2e-31]	N/A	Unknown protein	1	2	1
A502L	2E+05	2E+05	92	288	95	11069	9.4	Late	Yes	N/A	N/A	YP_001426337 [hypothetical protein FR483_N705R (Paramecium bursaria Chlorella virus FR483)] [2e-21]	N/A	Unknown protein	1	1	1
A503L	2E+05	2E+05	72	915	304	35101	9.6	Early	N/A	N/A	N/A	YP_001426335 [hypothetical protein FR483_N703R (Paramecium bursaria Chlorella virus FR483)] [6e-47]	N/A	Unknown protein	0	0	0
a504R	2E+05	2E+05	66	291	96	11689	7.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
a504aL	2E+05	2E+05	52	129	42	5014	9.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0

A505L	2E+05	2E+05	64	1455	484	54765	5.4	Early	N/A	N/A	N/A	YP_001426328 [hypothetical protein FR483_N696R (Paramecium bursaria Chlorella virus FR483)] [1e-127]	N/A	Unknown protein	0	0	0
a506R	2E+05	2E+05	50	213	70	7759	10.4	N/A	N/A	N/A	N/A	YP_001426333 [hypothetical protein FR483_n701L (Paramecium bursaria Chlorella virus FR483)] [9e-14]	N/A	Hypothetical protein	0	0	0
a507R	2E+05	2E+05	48	561	186	21950	10.5	N/A	N/A	N/A	N/A	YP_001426327 [hypothetical protein FR483_n695L (Paramecium bursaria Chlorella virus FR483)] [2e-10]	N/A	Hypothetical protein	0	0	0
a508R	2E+05	2E+05	54	234	77	8501	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
a509R	2E+05	2E+05	52	306	101	12606	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a510R	2E+05	2E+05	50	204	67	7609	10.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a511L	2E+05	2E+05	50	222	73	8589	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A512R	2E+05	2E+05	56	2415	804	89893	5.5	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a513R	2E+05	2E+05	56	363	120	13489	12.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	3	3
a514L	2E+05	2E+05	62	435	144	15673	12.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	1
a515L	2E+05	2E+05	44	612	203	22683	10.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a516R	2E+05	2E+05	44	207	68	7990	12.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A517L	2E+05	2E+05	86	1035	344	39045	8.8	Early	N/A	COG0270 [Site-specific DNA methylase] [9e-06]	PF00145.10 [C-5 cytosine-specific DNA methylase] [5.4e-40]	YP_001426001 [hypothetical protein FR483_N369L (Paramecium bursaria Chlorella virus FR483)] [1e-126]	P36216 [RecName: FullModification methylase CviJI ShortM.CviJI AltName: FullCytosine-specific methyltransferase CviJI] [9e-76]	Unknown protein	0	1	0
a518R	2E+05	2E+05	62	303	100	10825	9.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A519L	2E+05	2E+05	74	249	82	9332	9.8	Late	N/A	N/A	N/A	YP_001425920 [hypothetical protein FR483_N288R (Paramecium bursaria Chlorella virus FR483)] [9e-16]	N/A	Unknown protein	2	2	2
A520L	2E+05	2E+05	74	303	100	11674	10.7	Late	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A521L	2E+05	2E+05	70	630	209	23738	11.4	Early-Late	Yes	N/A	N/A	YP_001426325 [hypothetical protein FR483_N693R (Paramecium bursaria Chlorella virus FR483)]	N/A	Unknown protein	0	0	0

												[1e-47]					
A521aL	2E+05	3E+05	96	609	202	22578	6.3	N/A	Yes	N/A	N/A	YP_001426138 [hypothetical protein FR483_N506L (Paramecium bursaria Chlorella virus FR483)] [6e-76]	O55742 [RecName: FullUncharacterized protein 136R] [2e-07]	Unknown protein	0	0	0
a522R	2E+05	3E+05	62	273	90	9820	4.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	2
A523R	3E+05	3E+05	2	516	171	19096	9.6	Late	Yes	N/A	N/A	YP_001426959 [hypothetical protein ATCV1_Z478R (Acanthocystis turfacea Chlorella virus 1)] [2e-64]	N/A	Unknown protein	0	0	0
a524L	3E+05	3E+05	48	324	107	11954	8.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	2
a525R	3E+05	3E+05	48	201	66	7360	8.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A526R	3E+05	3E+05	90	441	146	16434	9.3	Late	Yes	N/A	N/A	YP_001426144 [hypothetical protein FR483_N512R (Paramecium bursaria Chlorella virus FR483)] [1e-27]	N/A	Unknown protein	0	1	0
A527R	3E+05	3E+05	58	300	99	11605	10.7	Late	Yes	N/A	N/A	YP_001426961 [hypothetical protein ATCV1_Z480R (Acanthocystis turfacea Chlorella virus 1)] [1e-23]	N/A	Unknown protein	0	0	0
A527aL	3E+05	3E+05	78	177	58	6776	13.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a528R	3E+05	3E+05	74	285	94	10046	12.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
a529L	3E+05	3E+05	38	219	72	7782	10.8	N/A	N/A	N/A	N/A	YP_001426520 [hypothetical protein ATCV1_z039L (Acanthocystis turfacea Chlorella virus 1)] [7e-06]	N/A	Hypothetical protein	0	1	0
A530R	3E+05	3E+05	2	1041	346	39178	8.7	Late	N/A	COG0270 [Site-specific DNA methylase] [2e-06]	PF00145.10 [C-5 cytosine-specific DNA methylase] [6.6e-41]	YP_001426001 [hypothetical protein FR483_N369L (Paramecium bursaria Chlorella virus FR483)] [1e-138]	P36216 [RecName: FullModification methylase CviJI ShortM.CviJI AltName: FullCytosine-specific methyltransferase CviJI] [2e-80]	Unknown protein	0	0	0
A531L	3E+05	3E+05	64	204	67	7670	7.5	Late	Yes	N/A	N/A	N/A	N/A	Unknown protein	1	1	1
A532L	3E+05	3E+05	78	240	79	8698	9.7	Late	Yes	N/A	N/A	YP_001426963 [hypothetical protein ATCV1_z482L (Acanthocystis turfacea Chlorella virus 1)] [1e-15]	N/A	Unknown protein	1	1	1
A532aL	3E+05	3E+05	84	153	50	5479	4.5	N/A	Yes	N/A	N/A	N/A	N/A	Unknown protein	1	1	1

A533R	3E+05	3E+05	82	1125	374	40132	3.8	Early-Late	Yes	N/A	N/A	YP_001426965 [hypothetical protein ATCV1_Z484R (Acanthocystis turfacea Chlorella virus 1)] [1e-117]	N/A	Unknown protein	0	0	0
A534R	3E+05	3E+05	56	318	105	11783	9.7	N/A	Yes	N/A	N/A	YP_001426148 [hypothetical protein FR483_N516R (Paramecium bursaria Chlorella virus FR483)] [3e-37]	N/A	Unknown protein	0	0	0
A535L	3E+05	3E+05	82	216	71	8210	4.7	Early-Late	Yes	N/A	N/A	YP_001426150 [hypothetical protein FR483_N518L (Paramecium bursaria Chlorella virus FR483)] [7e-11]	N/A	Unknown protein	0	0	0
A536L	3E+05	3E+05	80	222	73	8485	10.0	Early-Late	Yes	N/A	N/A	YP_001426152 [hypothetical protein FR483_N520L (Paramecium bursaria Chlorella virus FR483)] [6e-09]	N/A	Unknown protein	1	1	0
a536aL	3E+05	3E+05	48	177	58	6753	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	0
A537L	3E+05	3E+05	78	798	265	31237	6.6	Early	N/A	N/A	N/A	YP_001426153 [hypothetical protein FR483_N521L (Paramecium bursaria Chlorella virus FR483)] [1e-18]	N/A	Unknown protein	0	0	0
a538L	3E+05	3E+05	68	198	65	7367	9.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A539R	3E+05	3E+05	80	522	173	19839	10.1	Early	N/A	N/A	PF01541.17 [GIY-YIG catalytic domain] [1.1e-06]	YP_001426156 [hypothetical protein FR483_N524R (Paramecium bursaria Chlorella virus FR483)] [2e-46]	N/A	Unknown protein	0	0	0
a539aR	3E+05	3E+05	64	165	54	6339	9.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A540L	3E+05	3E+05	82	3771	1256	127197	6.2	Late	Yes	N/A	N/A	YP_001426157 [hypothetical protein FR483_N525L (Paramecium bursaria Chlorella virus FR483)] [1e-173]	N/A	Unknown protein	0	0	0
a541R	3E+05	3E+05	52	291	96	10536	4.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a542R	3E+05	3E+05	48	219	72	9007	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A543L	3E+05	3E+05	58	168	55	5802	6.5	Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	2	1
A544R	3E+05	3E+05	52	897	298	34250	8.2	Late	N/A	COG1793 [ATP-dependent DNA ligase] [5e-11]	PF01068.14 [ATP dependent DNA ligase domain] [1.3e-22]	YP_001426668 [hypothetical protein ATCV1_Z187L (Acanthocystis turfacea Chlorella virus 1)] [1e-86]	P44121 [RecName: FullDNA ligase AltName: FullPolydeoxyribonucleotide synthase (ATP)] [5e-10]	ATP-dependent DNA ligase	0	0	0
a545L	3E+05	3E+05	72	222	73	8111	10.0	N/A	N/A	N/A	N/A	YP_001426667 [hypothetical protein ATCV1_z186R	N/A	Hypothetical protein	0	1	0

												(Acanthocystis turfacea Chlorella virus 1)] [2e-08]					
A546L	3E+05	3E+05	78	1191	396	44504	6.1	Early-Late	N/A	N/A	PF00534.13 [Glycosyl transferases group 1] [2.7e-08]	YP_001427148 [hypothetical protein ATCV1_Z667L (Acanthocystis turfacea Chlorella virus 1)] [4e-25]	N/A	Unknown protein	0	0	0
a547R	3E+05	3E+05	58	234	77	8397	10.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A548L	3E+05	3E+05	72	1488	495	57432	9.5	Early	Yes	COG0553 [Superfamily II DNA/RNA helicases SNF2 family] [9e-07]	PF00176.16 [SNF2 family N-terminal domain] [6.7e-34] / PF00271.24 [Helicase conserved C-terminal domain] [1.5e-10]	YP_001425909 [hypothetical protein FR483_N277L (Paramecium bursaria Chlorella virus FR483)] [1e-124]	Q9US25 [RecName: FullChromodomain helicase hrp1 AltName: FullATP-dependent helicase hrp1] [2e-31]	Unknown protein	0	0	0
a549R	3E+05	3E+05	56	246	81	9249	7.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	1
a550R	3E+05	3E+05	66	411	136	15566	9.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a550aR	3E+05	3E+05	54	159	52	6043	6.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	1
a550bL	3E+05	3E+05	68	189	62	7695	10.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A551L	3E+05	3E+05	70	426	141	14879	4.9	Early	N/A	COG0756 [dUTPase] [1e-09]	PF00692.12 [dUTPase] [7.3e-40]	YP_001425901 [hypothetical protein FR483_N269L (Paramecium bursaria Chlorella virus FR483)] [4e-46]	Q54BW5 [RecName: FullDeoxyuridine 5-triphosphate nucleotidohydrolase ShortdUTPase AltName: FulldUTP pyrophosphatase] [6e-35]	dUTP pyrophosphatase	0	0	0
a551aR	3E+05	3E+05	44	129	42	4642	4.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A551bL	3E+05	3E+05	62	168	55	6774	8.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	0
A552R	3E+05	3E+05	86	954	317	35974	9.3	Early	N/A	N/A	PF00352.14 [Transcription factor TFIID (or TATA-binding protein TBP)] [3.1e-07]	YP_001425903 [hypothetical protein FR483_N271R (Paramecium bursaria Chlorella virus FR483)] [8e-42]	N/A	Unknown protein	0	0	0
a553L	3E+05	3E+05	50	216	71	8044	11.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A554/556/557L	3E+05	3E+05	70	1497	498	58730	7.2	Early	N/A	COG0037 [Predicted ATPase of the PP-loop superfamily implicated in cell cycle control] [2e-06]	PF01171.13 [PP-loop family] [1e-27]	YP_001427209 [hypothetical protein ATCV1_Z728L (Acanthocystis turfacea Chlorella virus 1)] [0.0]	Q82VP4 [RecName: FulltRNA(Ile)-lysidine synthase AltName: FulltRNA(Ile)-lysidine synthetase AltName: FulltRNA(Ile)-2-lysyl-cytidine synthase] [7e-19]	Unknown protein	0	0	0
a555R	3E+05	3E+05	54	342	113	12901	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	0
A555aR	3E+05	3E+05	58	138	45	5180	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0

A558L	3E+05	3E+05	82	1203	400	45547	5.1	Early-Late	Yes	N/A	PF04451.5 [Large eukaryotic DNA virus major capsid protein] [6.6e-60]	YP_001426987 [hypothetical protein ATCV1_Z506L (Acanthocystis turfacea Chlorella virus 1)] [1e-156]	A7U6E9 [RecName: FullMajor capsid protein ShortMCP] [3e-47]	Capsid protein	0	0	0
a558aL	3E+05	3E+05	36	141	46	5526	5.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A559L	3E+05	3E+05	78	642	213	24034	10.2	Late	Yes	N/A	N/A	YP_001425898 [hypothetical protein FR483_N266R (Paramecium bursaria Chlorella virus FR483)] [1e-16]	N/A	Unknown protein	1	1	0
a560R	3E+05	3E+05	68	315	104	11524	8.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A561L	3E+05	3E+05	90	1950	649	71004	9.9	Late	Yes	N/A	N/A	YP_001426992 [hypothetical protein ATCV1_Z511L (Acanthocystis turfacea Chlorella virus 1)] [4e-60]	N/A	Unknown protein	1	2	1
a562R	3E+05	3E+05	42	198	65	7690	11.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a563R	3E+05	3E+05	68	180	59	6418	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A564L	3E+05	3E+05	70	1056	351	39884	8.4	Early-Late	N/A	N/A	N/A	YP_001425778 [hypothetical protein FR483_N146R (Paramecium bursaria Chlorella virus FR483)] [5e-66]	N/A	Unknown protein	0	0	0
A565R	3E+05	3E+05	70	2013	670	73169	7.3	Early-Late	Yes	N/A	N/A	YP_001425891 [hypothetical protein FR483_N259L (Paramecium bursaria Chlorella virus FR483)] [2e-69]	N/A	Unknown protein	1	1	1
a566L	3E+05	3E+05	60	273	90	10337	7.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A567L	3E+05	3E+05	76	459	152	17418	10.1	Early-Late	Yes	N/A	N/A	YP_001425887 [hypothetical protein FR483_N255R (Paramecium bursaria Chlorella virus FR483)] [1e-12]	N/A	Unknown protein	0	0	0
A568L	3E+05	3E+05	72	540	179	20899	7.5	Early	N/A	N/A	N/A	YP_001426314 [hypothetical protein FR483_N682L (Paramecium bursaria Chlorella virus FR483)] [3e-10]	N/A	Unknown protein	1	1	2
a569R	3E+05	3E+05	66	255	84	9639	9.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	1
A570L	3E+05	3E+05	86	387	128	14556	4.8	Late	N/A	N/A	N/A	YP_001426316 [hypothetical protein FR483_N684L (Paramecium bursaria Chlorella virus FR483)] [9e-38]	N/A	Unknown protein	0	0	0
A571R	3E+05	3E+05	14	351	116	12972	12.0	Late	Yes	N/A	PF08789.3 [PBCV-specific basic adaptor	YP_001426112 [hypothetical protein FR483_N480R	N/A	Unknown protein	0	0	0

											domain] [5.7e-17]	(Paramecium bursaria Chlorella virus FR483)] [3e-39]					
A572R	3E+05	3E+05	74	546	181	20606	7.1	Late	Yes	N/A	N/A	YP_001426317 [hypothetical protein FR483_N685R (Paramecium bursaria Chlorella virus FR483)] [6e-63]	N/A	Unknown protein	0	0	0
a573L	3E+05	3E+05	60	210	69	8088	11.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A574L	3E+05	3E+05	64	795	264	29862	4.2	Early	N/A	COG0592 [DNA polymerase sliding clamp subunit (PCNA homolog)] [1e-06]	PF00705.11 [Proliferating cell nuclear antigen N-terminal domain] [1e-21] / PF02747.8 [Proliferating cell nuclear antigen C-terminal domain] [2.4e-14]	YP_001426319 [hypothetical protein FR483_N687L (Paramecium bursaria Chlorella virus FR483)] [4e-59]	Q43266 [RecName: FullProliferating cell nuclear antigen ShortPCNA] [1e-30]	Unknown protein	0	0	0
A574aL	3E+05	3E+05	64	186	61	7021	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A575L	3E+05	3E+05	78	507	168	19015	8.2	Early	N/A	N/A	N/A	YP_001426321 [hypothetical protein FR483_N689L (Paramecium bursaria Chlorella virus FR483)] [2e-28]	N/A	Unknown protein	0	0	0
a576R	3E+05	3E+05	60	222	73	8044	9.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A577L	3E+05	3E+05	84	402	133	15442	11.0	Late	Yes	N/A	N/A	YP_001426193 [hypothetical protein FR483_N561R (Paramecium bursaria Chlorella virus FR483)] [4e-25]	N/A	Unknown protein	0	0	0
A579L	3E+05	3E+05	82	717	238	27445	10.1	Late	Yes	N/A	N/A	YP_003406771 [hypothetical protein MAR_ORF016 (Marseillevirus)] [8e-30]	N/A	R.CviAI restriction endonuclease	0	0	0
a578L	3E+05	3E+05	62	132	43	5225	9.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a580R	3E+05	3E+05	64	222	73	8765	6.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A581R	3E+05	3E+05	52	798	265	30522	7.6	Early	N/A	COG0338 [Site-specific DNA methylase] [7e-06]	PF02086.8 [D12 class N6 adenine-specific DNA methyltransferase] [3.3e-65]	YP_003406772 [Dam-like adenine-specific DNA methylase (Marseillevirus)] [4e-46]	Q58015 [RecName: FullModification methylase MjaIII ShortM.MjaIII AltName: FullAdenine-specific methyltransferase MjaIII] [4e-37]	6mA DNA methylase M.CviAI	0	2	0
a582L	3E+05	3E+05	64	237	78	9519	11.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a582aL	3E+05	3E+05	54	168	55	6615	9.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a582bL	3E+05	3E+05	58	159	52	5954	12.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A583L	3E+05	3E+05	82	3186	1061	120193	8.4	Early	N/A	COG0187 [Type IIA	PF00204.18 [DNA gyrase B]	YP_001426181 [hypothetical protein	P08096 [RecName: FullDNA	DNA topoisomerase II	0	0	0

										topoisomerase (DNA gyrase/topo II topoisomerase IV) B subunit] [2e-08]	[1.4e-22] / PF00521.13 [DNA gyrase/topoisomerase IV subunit A] [6.5e-124]	FR483_N549R (Paramecium bursaria Chlorella virus FR483)] [0.0]	topoisomerase 2 AltName: FullDNA topoisomerase II] [0.0]				
a584R	3E+05	3E+05	56	297	98	11326	11.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a585R	3E+05	3E+05	62	240	79	9304	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A586R	3E+05	3E+05	62	228	75	8567	11.8	N/A	Yes	N/A	N/A	YP_001426187 [hypothetical protein FR483_n555L (Paramecium bursaria Chlorella virus FR483)] [1e-11]	N/A	Unknown protein	0	0	0
a587R	3E+05	3E+05	60	345	114	12877	8.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a588R	3E+05	3E+05	42	351	116	13729	11.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a589L	3E+05	3E+05	56	231	76	8638	12.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A589aL	3E+05	3E+05	80	153	50	5921	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A590L	3E+05	3E+05	84	1047	348	42036	4.6	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A590aL	3E+05	3E+05	44	126	41	4735	12.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
a591L	3E+05	3E+05	68	168	55	6171	10.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A592R	3E+05	3E+05	82	210	69	7861	4.7	Early-Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A593R	3E+05	3E+05	74	900	299	32019	7.1	N/A	N/A	N/A	N/A	YP_001426230 [hypothetical protein FR483_N598R (Paramecium bursaria Chlorella virus FR483)] [3e-35]	N/A	Hypothetical protein	0	0	0
a594R	3E+05	3E+05	42	351	116	14065	12.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a595L	3E+05	3E+05	56	255	84	9195	7.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A596R	3E+05	3E+05	78	429	142	15892	6.5	Early-Late	N/A	COG2131 [Deoxycytidylate deaminase] [9e-07]	PF00383.15 [Cytidine and deoxycytidylate deaminase zinc-binding region] [1.1e-26]	YP_001427097 [hypothetical protein ATCV1_Z616L (Acanthocystis turfacea Chlorella virus 1)] [2e-56]	P33968 [RecName: FullUncharacterized deaminase in luxG 3region] [1e-19]	Unknown protein	0	0	0
a597L	3E+05	3E+05	54	297	98	10825	6.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A598L	3E+05	3E+05	84	1092	363	41558	6.9	Early-Late	Yes	COG0076 [Glutamate decarboxylase and related PLP-dependent proteins] [5e-06]	PF00282.12 [Pyridoxal-dependent decarboxylase conserved domain] [1.1e-17]	YP_001426232 [hypothetical protein FR483_N600L (Paramecium bursaria Chlorella virus FR483)] [1e-132]	P54772 [RecName: FullHistidine decarboxylase ShortHDC AltName: FullTOM92] [3e-53]	Unknown protein	0	0	0

a599R	3E+05	3E+05	62	540	179	21558	8.7	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a600R	3E+05	3E+05	52	249	82	9151	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
a600aR	3E+05	3E+05	58	141	46	5877	8.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A601R	3E+05	3E+05	52	306	101	11592	10.6	Early-Late	N/A	N/A	N/A	YP_001426767 [hypothetical protein ATCV1_Z286L (Acanthocystis turfacea Chlorella virus 1)] [5e-19]	N/A	Unknown protein	0	2	2
A602L	3E+05	3E+05	60	606	201	23569	5.1	Early	N/A	N/A	N/A	YP_001426587 [hypothetical protein ATCV1_z106R (Acanthocystis turfacea Chlorella virus 1)] [3e-14]	N/A	Unknown protein	0	0	0
a603R	3E+05	3E+05	78	318	105	12141	4.6	N/A	N/A	N/A	N/A	YP_001426236 [hypothetical protein FR483_N604R (Paramecium bursaria Chlorella virus FR483)] [6e-20]	N/A	Hypothetical protein	0	0	0
A603aL	3E+05	3E+05	72	186	61	6697	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
a603bR	3E+05	3E+05	72	147	48	5317	4.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	0
A604L	3E+05	3E+05	80	405	134	15162	9.9	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	3	0
A605L	3E+05	3E+05	80	477	158	17769	10.9	Early-Late	Yes	N/A	N/A	N/A	N/A	Unknown protein	1	1	1
a606L	3E+05	3E+05	50	345	114	13257	10.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A607R	3E+05	3E+05	12	1176	391	46171	7.2	Early-Late	N/A	N/A	N/A	YP_001426342 [hypothetical protein FR483_N710R (Paramecium bursaria Chlorella virus FR483)] [9e-77]	Q02357 [RecName: FullAnkyrin-1 ShortANK-1 AltName: FullErythrocyte ankyrin] [3e-06]	Unknown protein	0	0	0
A609L	3E+05	3E+05	82	1170	389	43459	4.7	Early	N/A	COG0677 [UDP-N-acetyl-D-mannosaminuronate dehydrogenase] [2e-06]	PF03721.7 [UDP-glucose/GDP-mannose dehydrogenase family NAD binding domain] [8.7e-41] / PF00984.12 [UDP-glucose/GDP-mannose dehydrogenase family central domain] [5.8e-23] / PF03720.8 [UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain] [5e-08]	YP_001426344 [hypothetical protein FR483_N712L (Paramecium bursaria Chlorella virus FR483)] [1e-133]	O33952 [RecName: FullUDP-glucose 6-dehydrogenase ShortUDP-Glc dehydrogenase ShortUDP-GlcDH ShortUDPGDH] [1e-119]	UDP-glucose dehydrogenase	0	0	0

a610R	3E+05	3E+05	66	276	91	10725	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a611R	3E+05	3E+05	62	225	74	8698	8.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A612L	3E+05	3E+05	78	360	119	13587	8.7	Late	Yes	COG2940 [Proteins containing SET domain] [1e-06]	PF00856.21 [SET domain] [1.2e-12]	YP_001426351 [hypothetical protein FR483_N719L (Paramecium bursaria Chlorella virus FR483)] [3e-33]	Q0U3A4 [RecName: FullHistone-lysine N-methyltransferase SET9 AltName: FullSET domain protein 9] [4e-07]	Histone H3K27 methylase	0	0	0
a613R	3E+05	3E+05	54	264	87	10383	10.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A614L	3E+05	3E+05	86	1734	577	64733	11.2	Late	Yes	N/A	PF00069.18 [Protein kinase domain] [5.6e-11]	YP_001426352 [hypothetical protein FR483_N720L (Paramecium bursaria Chlorella virus FR483)] [1e-100]	N/A	Protein kinase	0	0	0
a615R	3E+05	3E+05	66	201	66	7112	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a616R	3E+05	3E+05	60	282	93	9978	7.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A617R	3E+05	3E+05	34	966	321	37586	9.9	Early-Late	Yes	N/A	N/A	YP_001426356 [hypothetical protein FR483_N724R (Paramecium bursaria Chlorella virus FR483)] [3e-82]	Q5UQJ6 [RecName: FullPutative serine/threonine-protein kinase R400] [7e-12]	Unknown protein	0	0	0
A618L	3E+05	3E+05	70	396	131	15223	3.8	Late	N/A	N/A	N/A	YP_001426357 [hypothetical protein FR483_N725L (Paramecium bursaria Chlorella virus FR483)] [3e-14]	N/A	Unknown protein	0	0	0
A619L	3E+05	3E+05	84	714	237	26943	4.5	Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A620L	3E+05	3E+05	86	252	83	9739	9.6	Late	N/A	N/A	N/A	YP_001426363 [hypothetical protein FR483_N731L (Paramecium bursaria Chlorella virus FR483)] [1e-16]	N/A	Unknown protein	2	2	2
a620aR	3E+05	3E+05	56	174	57	6932	9.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A621L	3E+05	3E+05	84	354	117	12935	9.5	Late	Yes	N/A	N/A	YP_001427169 [hypothetical protein ATCV1_z688R (Acanthocystis turfacea Chlorella virus 1)] [4e-35]	N/A	Unknown protein	2	2	2
a621aR	3E+05	3E+05	76	168	55	6081	4.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
a621bL	3E+05	3E+05	56	141	46	5224	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A622L	3E+05	3E+05	80	1563	520	58097	5.7	Late	Yes	N/A	PF04451.5 [Large eukaryotic DNA virus major capsid protein] [1.7e-66]	YP_001426369 [hypothetical protein FR483_N737L (Paramecium bursaria Chlorella virus FR483)] [0.0]	A7U6E9 [RecName: FullMajor capsid protein ShortMCP] [9e-57]	Capsid protein	0	0	0

A623L	3E+05	3E+05	72	204	67	7703	9.2	Early	N/A	N/A	PF01428.9 [AN1-like Zinc finger] [1.7e-12]	XP_002466323 [hypothetical protein SORBIDRAFT_01g005640 (Sorghum bicolor)] [2e-07]	Q852K6 [RecName: FullZinc finger A20 and AN1 domain-containing stress-associated protein 7 ShortOsSAP7] [2e-08]	Unknown protein	0	0	0
A623aL	3E+05	3E+05	56	180	59	6781	4.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A624R	3E+05	3E+05	32	366	121	13570	9.3	Late	Yes	N/A	PF09945.2 [Predicted membrane protein (DUF2177)] [3.4e-26]	YP_001426373 [hypothetical protein FR483_N741R (Paramecium bursaria Chlorella virus FR483)] [2e-21]	N/A	Unknown protein	3	4	3
A625R	3E+05	3E+05	72	1299	432	49945	10.7	Late	Yes	COG0675 [Transposase and inactivated derivatives] [1e-06]	PF12323.1 [Helix-turn-helix domain] [1.4e-06] / PF07282.4 [Putative transposase DNA-binding domain] [6.7e-18]	ZP_03272524 [transposase IS605 OrfB family (Arthrospira maxima CS-328)] [2e-20]	Q5UPI0 [RecName: FullPutative transposase R104] [8e-19]	Unknown protein	0	0	0
a626L	3E+05	3E+05	48	225	74	8395	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a626aR	3E+05	3E+05	60	159	52	6068	11.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A627R	3E+05	3E+05	68	1338	445	49629	11.1	Late	Yes	N/A	N/A	YP_001426405 [hypothetical protein FR483_N773L (Paramecium bursaria Chlorella virus FR483)] [1e-135]	N/A	Unknown protein	1	3	0
a627aR	3E+05	3E+05	54	138	45	5526	12.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A628L	3E+05	3E+05	82	294	97	10499	4.5	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A629R	3E+05	3E+05	74	2316	771	86292	7.5	Early-Late	Yes	COG0209 [Ribonucleotide reductase alpha subunit] [4e-11]	PF03477.9 [ATP cone domain] [8.5e-15] / PF00317.14 [Ribonucleotide reductase all-alpha domain] [7.9e-19] / PF02867.8 [Ribonucleotide reductase barrel domain] [2e-194]	YP_001426398 [hypothetical protein FR483_N766L (Paramecium bursaria Chlorella virus FR483)] [0.0]	Q03604 [RecName: FullRibonucleoside-diphosphate reductase large subunit AltName: FullRibonucleotide reductase large subunit] [0.0]	Unknown protein	0	0	0
a630R	3E+05	3E+05	50	240	79	9246	12.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A631L	3E+05	3E+05	42	270	89	10392	9.9	N/A	Yes	N/A	N/A	YP_001426402 [hypothetical protein FR483_n770R (Paramecium bursaria Chlorella virus FR483)] [3e-08]	N/A	Unknown protein	0	0	0
a632L	3E+05	3E+05	64	219	72	7985	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	2
A633R	3E+05	3E+05	76	363	120	13184	9.2	Late	N/A	N/A	N/A	YP_001426396 [hypothetical protein FR483_N764L	N/A	Unknown protein	3	3	3

												(Paramecium bursaria Chlorella virus FR483)] [2e-37]				
A634L	3E+05	3E+05	72	405	134	15555	8.9	Early	N/A	N/A	N/A	YP_001426391 [hypothetical protein FR483_N759R (Paramecium bursaria Chlorella virus FR483)] [8e-40]	N/A	Unknown protein	0	0	0
a634aL	3E+05	3E+05	46	129	42	4798	11.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A635R	3E+05	3E+05	14	258	85	9862	9.4	Late	N/A	N/A	N/A	YP_001427170 [hypothetical protein ATCV1_Z689R (Acanthocystis turfacea Chlorella virus 1)] [5e-10]	N/A	Unknown protein	2	2	2
a635aR	3E+05	3E+05	64	195	64	8208	10.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	2	1
A636R	3E+05	3E+05	84	291	96	11214	5.8	Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
A637R	3E+05	3E+05	84	426	141	16457	8.2	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	1	0
a637aL	3E+05	3E+05	62	174	57	7150	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A638R	3E+05	3E+05	80	1080	359	40840	5.8	Early	N/A	COG2957 [Peptidylarginine deiminase and related enzymes] [2e-31]	PF04371.8 [Porphyromonas-type peptidyl-arginine deiminase] [1.2e-126]	YP_001427287 [hypothetical protein ATCV1_Z806R (Acanthocystis turfacea Chlorella virus 1)] [1e-148]	Q8YAS5 [RecName: FullPutative agmatine deiminase 1 AltName: FullAgmatine iminohydrolase 1] [1e-107]	Agmatine iminohydrolase	0	0	0
a639L	3E+05	3E+05	48	399	132	14863	9.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	2	1
a640R	3E+05	3E+05	52	240	79	8869	12.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a641L	3E+05	3E+05	42	258	85	9654	10.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A643R	3E+05	3E+05	68	1398	465	53097	11.3	Late	Yes	N/A	N/A	YP_001426388 [hypothetical protein FR483_N756L (Paramecium bursaria Chlorella virus FR483)] [1e-123]	N/A	Unknown protein	0	0	0
A644R	3E+05	3E+05	84	522	173	19207	6.0	Late	Yes	N/A	N/A	YP_001426387 [hypothetical protein FR483_N755L (Paramecium bursaria Chlorella virus FR483)] [3e-62]	N/A	Unknown protein	0	0	0
a644aR	3E+05	3E+05	48	171	56	6313	10.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A645R	3E+05	3E+05	84	372	123	14385	7.9	Early	N/A	N/A	N/A	YP_001425763 [hypothetical protein FR483_N131L (Paramecium bursaria Chlorella virus FR483)] [2e-17]	N/A	Unknown protein	0	0	0
A646L	3E+05	3E+05	78	552	183	21717	7.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0

A646aL	3E+05	3E+05	84	126	41	5031	10.0	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A647R	3E+05	3E+05	26	570	189	22158	8.3	Early	N/A	N/A	PF07150.4 [Protein of unknown function (DUF1390)] [5.7e-46]	YP_001426682 [hypothetical protein ATCV1_Z201L (Acanthocystis turfacea Chlorella virus 1)] [1e-25]	N/A	Unknown protein	0	0	0
a648L	3E+05	3E+05	54	210	69	8097	8.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A649R	3E+05	3E+05	68	780	259	28689	9.0	Early	N/A	N/A	PF07150.4 [Protein of unknown function (DUF1390)] [9.1e-85]	YP_001426165 [hypothetical protein FR483_N533L (Paramecium bursaria Chlorella virus FR483)] [6e-29]	N/A	Unknown protein	0	0	0
a650L	3E+05	3E+05	72	264	87	10200	12.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a650aL	3E+05	3E+05	10	123	40	4447	7.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
a650bL	3E+05	3E+05	72	177	58	6871	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a650cR	3E+05	3E+05	40	183	60	7437	9.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A651L	3E+05	3E+05	80	693	230	26344	9.6	Early-Late	N/A	N/A	PF01541.17 [GIY-YIG catalytic domain] [2.1e-06] / PF07453.6 [NUMOD1 domain] [1.3e-11]	YP_001426012 [hypothetical protein FR483_N380R (Paramecium bursaria Chlorella virus FR483)] [5e-51]	N/A	Unknown protein	0	0	0
a652R	3E+05	3E+05	38	228	75	8583	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	0
a653R	3E+05	3E+05	26	198	65	7565	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A654L	3E+05	3E+05	78	594	197	22397	6.1	Early	N/A	N/A	PF00583.17 [Acetyltransferase (GNAT) family] [6.8e-06]	YP_001426628 [hypothetical protein ATCV1_Z147L (Acanthocystis turfacea Chlorella virus 1)] [4e-53]	N/A	Unknown protein	0	0	0
A655L	3E+05	3E+05	66	321	106	12002	11.4	N/A	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	1	0
A656L	3E+05	3E+05	82	723	240	26607	5.0	Early	N/A	N/A	PF01391.11 [Collagen triple helix repeat (20 copies)] [9.1e-11]	YP_001426629 [hypothetical protein ATCV1_Z148L (Acanthocystis turfacea Chlorella virus 1)] [2e-11]	N/A	Unknown protein	2	2	2
A658R	3E+05	3E+05	54	288	95	11136	8.1	Late	N/A	N/A	N/A	N/A	N/A	Unknown protein	1	2	1
A659L	3E+05	3E+05	86	579	192	21545	3.4	Late	N/A	N/A	N/A	YP_001427157 [hypothetical protein ATCV1_Z676R (Acanthocystis turfacea Chlorella virus 1)] [2e-12]	N/A	Unknown protein	1	1	1
a660R	3E+05	3E+05	58	333	110	13462	11.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0

a661R	3E+05	3E+05	58	309	102	11735	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
A662L	3E+05	3E+05	74	516	171	19589	10.8	Early-Late	N/A	N/A	PF04117.5 [Mpv17 / PMP22 family] [2.1e-10]	YP_001425817 [hypothetical protein FR483_N185L (Paramecium bursaria Chlorella virus FR483)] [1e-54]	Q54FR4 [RecName: FullPXMP2/4 family protein 4] [8e-08]	Unknown protein	2	4	2
a663R	3E+05	3E+05	52	240	79	9660	11.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A664L	3E+05	3E+05	80	465	154	17176	5.6	Early	N/A	N/A	N/A	YP_001425783 [hypothetical protein FR483_N151R (Paramecium bursaria Chlorella virus FR483)] [1e-42]	N/A	Unknown protein	0	0	0
A665L	3E+05	3E+05	50	516	171	19498	9.8	Early	N/A	N/A	N/A	YP_001425783 [hypothetical protein FR483_N151R (Paramecium bursaria Chlorella virus FR483)] [1e-26]	N/A	Unknown protein	0	0	0
A666L	3E+05	3E+05	74	2757	918	####	6.2	Early	N/A	COG1126 [ABC-type polar amino acid transport system ATPase component] [1e-05]	PF00005.20 [ABC transporter] [2.7e-15]	YP_001426365 [hypothetical protein FR483_N733R (Paramecium bursaria Chlorella virus FR483)] [0.0]	Q75EV6 [RecName: FullElongation factor 3 ShortEF-3] [0.0]	Unknown protein	0	0	0
a667R	3E+05	3E+05	52	291	96	10975	8.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	1	0
a668R	3E+05	3E+05	50	198	65	7392	6.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a669R	3E+05	3E+05	50	252	83	9142	10.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a670R	3E+05	3E+05	46	369	122	13755	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a671L	3E+05	3E+05	78	294	97	11430	9.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
A672R	3E+05	3E+05	80	636	211	23295	5.2	Early	N/A	COG0666 [FOG: Ankyrin repeat] [2e-06]	PF00023.23 [Ankyrin repeat] [2.1e-09]	YP_002840971 [Ankyrin (Sulfolobus islandicus Y.N.15.51)] [2e-26]	Q4UMH6 [RecName: FullPutative ankyrin repeat protein RF_0381] [2e-17]	Unknown protein	0	0	0
a673L	3E+05	3E+05	46	207	68	7488	4.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A674R	3E+05	3E+05	84	651	216	24902	8.1	Early	N/A	COG1351 [Predicted alternative thymidylate synthase] [5e-07]	PF02511.8 [Thymidylate synthase complementing protein] [6.2e-55]	YP_001427299 [hypothetical protein ATCV1_Z818L (Acanthocystis turfacea Chlorella virus 1)] [3e-78]	P73053 [RecName: FullThymidylate synthase thyX ShortTS ShortTSase] [9e-57]	Thymidylate synthase X	0	0	0
a675L	3E+05	3E+05	54	369	122	14417	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	2	2	2
A676R	3E+05	3E+05	70	1125	374	42432	10.6	Late	Yes	N/A	PF08789.3 [PBCV-specific basic adaptor domain] [1.9e-17] / PF08793.3 [2-cysteine adaptor domain] [1.8e-15]	YP_001425796 [hypothetical protein FR483_N164R (Paramecium bursaria Chlorella virus FR483)] [6e-55]	N/A	Unknown protein	0	0	0

a677L	3E+05	3E+05	70	231	76	8171	4.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A678R	3E+05	3E+05	90	1158	385	41287	10.3	Late	Yes	N/A	N/A	YP_001426663 [hypothetical protein ATCV1_Z182R (Acanthocystis turfacea Chlorella virus 1)] [7e-75]	N/A	Unknown protein	0	3	0
a679L	3E+05	3E+05	64	285	94	10193	11.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a680R	3E+05	3E+05	56	264	87	10337	3.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a681R	3E+05	3E+05	28	225	74	9708	13.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A681aL	3E+05	3E+05	54	177	58	7012	10.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A682L	3E+05	3E+05	82	1107	368	39915	5.8	Early	N/A	COG0666 [FOG: Ankyrin repeat] [8e-06]	PF00023.23 [Ankyrin repeat] [4.3e-10]	XP_001649474 [ankyrin 23/unc44 (Aedes aegypti)] [2e-51]	Q54KA7 [RecName: FullAnkyrin repeat PH and SEC7 domain containing protein secG] [3e-46]	Unknown protein	0	0	0
a682aL	3E+05	3E+05	52	138	45	5452	10.9	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
a682bR	3E+05	3E+05	38	144	47	5490	9.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A683L	3E+05	3E+05	74	1104	367	41847	7.9	Early-Late	N/A	COG0270 [Site-specific DNA methylase] [1e-06]	PF00145.10 [C-5 cytosine-specific DNA methylase] [5.6e-66]	YP_001426001 [hypothetical protein FR483_N369L (Paramecium bursaria Chlorella virus FR483)] [4e-73]	P36216 [RecName: FullModification methylase CviJI ShortM.CviJI AltName: FullCytosine-specific methyltransferase CviJI] [0.0]	Unknown protein	0	0	0
a684R	3E+05	3E+05	54	321	106	12535	8.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a685R	3E+05	3E+05	50	243	80	8650	6.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A686L	3E+05	3E+05	68	489	162	18316	6.9	Early	Yes	N/A	N/A	N/A	N/A	Unknown protein	0	1	0
a686aL	3E+05	3E+05	78	189	62	7504	8.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A685bR	3E+05	3E+05	78	171	56	6326	9.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a685cL	3E+05	3E+05	62	135	44	4817	9.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A687R	3E+05	3E+05	66	228	75	8976	4.4	Early	N/A	N/A	N/A	N/A	N/A	Unknown protein	0	0	0
a688L	3E+05	3E+05	62	216	71	7957	12.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	0
A689L	3E+05	3E+05	70	426	141	15974	8.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	1	1
a690R	3E+05	3E+05	36	237	78	8746	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a690aL	3E+05	3E+05	78	126	41	4982	10.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1

A690bL	3E+05	3E+05	78	144	47	5751	7.6	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	1	1	1
a690cR	3E+05	3E+05	36	126	41	5159	10.5	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a690dR	3E+05	3E+05	40	132	43	4606	12.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A690eR	3E+05	3E+05	44	147	48	5331	11.2	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A690fR	3E+05	3E+05	0	162	53	6037	11.8	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a690gR	3E+05	3E+05	64	156	51	5820	9.3	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
A691R	3E+05	3E+05	66	552	183	21545	9.4	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0
a692R	3E+05	3E+05	68	270	89	10191	9.1	N/A	N/A	N/A	N/A	N/A	N/A	Hypothetical protein	0	0	0

1 – Transmembrane regions of the protein were predicted by TMHMM (T), HMMTOP (H), and Phobius (P) methods. For all the method default parameters were used for the prediction. The number shown in the table is the number of helices predicted by the methods.

Table S2. PBCV-1 virionic proteome and mass spectral data from each method

		Proteomic Methods and Parameters						
		Method 1				**Method 2**		
Protein	**Method number**	**Mascot score**	**Queries matched**	**Unique peptides**	**emPAI***	**Unique peptides**	**Coverage fraction**	**Number spectra**
A010R	1&2	3408	53	25	6.21	19	0.5736	238
A011L	1&2	8196	113	29	13.68	22	0.7047	463
A014R	1&2	160	4	3	0.07	3	0.0226	20
A025/027/029L	1&2	161	3	2	0.07	3	0.028	49
A034R	1&2	839	43	13	2.2	17	0.4838	232
A035L	1&2	5397	100	23	2.48	30	0.6058	1175
A041R	1&2	1479	32	13	1.72	15	0.4515	281
A051L	1&2	690	12	8	1.6	9	0.601	78
A085R	1&2	1597	24	12	3.8	11	0.5868	131
A092/093L	1&2	1016	25	16	1.62	11	0.3118	223
A121R	1&2	41	4	3	0.28	6	0.4327	70
A127R	1&2	511	17	8	0.77	9	0.3469	66
A136R	1&2	109	11	6	0.46	4	0.2877	126
A139L	1&2	354	11	4	1	8	0.4503	294
A140|145R	1&2	11632	241	46	3	58	0.5209	3522
A165aL	1&2	491	13	8	2.14	6	0.5337	134
A168R	1&2	1439	25	7	1.76	7	0.494	569
A171R	1&2	405	12	7	0.25	4	0.1809	13
A176L	1&2	298	5	2	0.9	4	0.3636	166
A189|192R	1&2	1870	58	29	0.5	30	0.3087	511
A203R	1&2	1811	37	10	4.46	7	0.5463	192
A205R	1&2	664	27	8	2.05	8	0.2427	302
A213L	1&2	767	12	8	4.4	5	0.5541	147
A217L	1&2	844	26	13	0.88	16	0.5025	174
A227L	1&2	519	17	5	1.19	4	0.365	128
A230R	1&2	228	6	4	0.76	5	0.2806	20
A231L	1&2	313	11	8	0.43	16	0.5561	139
A237R	1&2	3551	79	38	5.72	31	0.7297	724
A245R	1&2	151	5	4	0.59	4	0.369	19
A246aR	1&2	60	2	1	0.2	7	0.6842	57
A252R	1&2	462	17	14	1.39	13	0.4064	107
A262/263L	1&2	169	8	6	0.7	14	0.543	632
A278L	1&2	3106	89	35	3.6	25	0.4213	822
A282L	1&2	5342	128	34	4.83	25	0.4499	1228
A284L	1&2	1996	38	11	2.41	13	0.7312	311

A286R	1&2	1284	28	16	1.42	15	0.5661	206
A296R	1&2	334	10	3	0.7	2	0.1911	101
A305L	1&2	873	22	12	3.44	14	0.6373	200
A310L	1&2	976	10	3	1.33	5	0.4824	180
A314R	1&2	43	3	1	0.38	3	0.4875	51
A316R	1&2	224	4	2	0.14	11	0.3014	95
A320R	1&2	486	10	4	0.79	3	0.2446	102
A322L	1&2	420	9	6	1.53	11	0.5341	229
A342L	1&2	2337	52	22	1.87	23	0.7188	1093
A349L	1&2	2517	51	13	11.17	10	0.5	759
A352L	1&2	1496	31	10	3.38	8	0.4589	1536
A363R	1&2	4467	120	46	2.01	55	0.5589	1112
A375R	1&2	419	14	7	1.24	6	0.3584	117
A378L	1&2	868	64	11	1.57	8	0.2375	306
A383R	1&2	946	17	12	1.06	13	0.4609	157
A384dL	1&2	2041	37	15	0.98	21	0.4548	659
A398L	1&2	330	5	4	1.53	6	0.4237	184
A405R	1&2	219	9	7	0.35	16	0.3387	252
A407L	1&2	584	12	7	0.94	10	0.6714	335
A413L	1&2	144	7	4	0.42	3	0.1475	41
A414R	1&2	144	7	4	0.75	2	0.5054	54
A421R	1&2	63	1	1	0.31	6	0.5306	230
A430L	1&2	34014	531	33	13.06	23	0.5995	2982
A437L	1&2	1500	29	9	19.75	11	0.7864	722
A440L	1&2	22	4	2	nd	2	0.2386	12
A448L	1&2	221	5	4	1.06	7	0.6132	160
A454L	1&2	3358	79	14	3.54	12	0.7474	1027
A465R	1&2	94	4	2	0.56	7	0.4576	119
A480L	1&2	47	3	1	0.35	2	0.2473	56
A484L	1&2	34	2	2	0.18	9	0.5548	43
A488R	1&2	2030	46	19	4.68	12	0.4732	365
A497R	1&2	291	8	2	1.69	7	0.3973	93
A500L	1&2	705	15	8	0.77	13	0.3722	764
A521aL	1&2	972	19	10	3.53	7	0.4257	118
A521L	1&2	605	9	5	0.93	6	0.4306	66
A523R	1&2	2560	49	18	24.79	11	0.8304	762
A526R	1&2	431	13	8	1.55	9	0.8014	328
A527R	1&2	223	7	6	2.69	6	0.4242	73
A532L	1&2	82	4	2	0.4	4	0.519	430
A533R	1&2	200	3	3	0.35	3	0.0722	4
A534R	1&2	66	1	1	0.31	3	0.4857	30
A535L	1&2	260	3	1	0.42	2	0.4085	60
A536L	1&2	234	3	1	0.42	5	0.5342	331

A558L	1&2	2749	47	24	6.04	13	0.5025	133
A559L	1&2	599	14	7	1.84	9	0.3474	178
A561L	1&2	2045	69	24	1.44	19	0.4206	331
A565R	1&2	4321	70	26	2.49	33	0.6045	709
A572R	1&2	233	9	6	1.11	11	0.7293	125
A577L	1&2	54	2	2	0.22	3	0.2105	13
A579L	1&2	663	17	6	0.77	9	0.4706	101
A605L	1&2	72	6	3	0.42	8	0.5633	220
A614L	1&2	1895	51	26	2.59	25	0.5338	571
A622L	1&2	3903	71	29	4.19	18	0.5115	261
A627R	1&2	1547	28	15	1.77	19	0.5483	384
A643R	1&2	1337	50	26	3.22	12	0.2774	409
A644R	1&2	2024	40	16	17.33	10	0.5723	370
A676R	1&2	913	31	21	3.1	20	0.5561	302
A678R	1&2	768	16	10	1.51	13	0.4494	232
A157L	2					3	0.2273	25
A164aR	2					4	0.5424	38
A174L	2					2	0.1385	43
A196L	2					4	0.3289	57
A202L	2					4	0.4513	44
A350R	2					2	0.2459	13
A384bL	2					2	0.5	300
A400R	2					2	0.2288	5
A420L	2					2	0.3714	7
A423R	2					2	0.1465	7
A438L	2					2	0.3077	32
A502L	2					7	0.4105	215
A520L	2					4	0.5	30
A531L	2					2	0.5821	176
A532aL	2					3	0.32	35
A612L	2					2	0.2437	6
A018L	1	193	2	1	0.05			
A122/123cLz	1	123	16	2	0.02			
A122/123R	1	14	3	1	nd			
A137R	1	24	1	1	nd			
A172aL	1	18	6	1	nd			
A173L	1	16	3	1	0.1			
A188aR	1	17	7	4	0.19			
A201aL	1	18	8	1	nd			
A201L	1	53	1	1	0.35			
A219|222|226R	1	14	5	2	0.04			
A255R	1	35	7	2	0.2			
A256/257L	1	26	14	6	0.03			

A260aR	1	16	4	2	0.44
A271L	1	13	3	1	nd
A273L	1	133	3	2	0.22
A287R	1	13	9	5	0.11
A295L	1	14	2	1	nd
A304R	1	14	2	2	nd
A321R	1	38	1	1	0.26
A339L	1	17	5	1	0.48
A356R	1	19	3	1	nd
A436L	1	322	8	2	1.3
A443R	1	250	133	3	0.09
A456L	1	31	5	4	0.04
A476R	1	33	4	1	nd
A540L	1	199	3	3	0.17
A548L	1	20	14	5	0.06
A567L	1	18	1	1	0.19
A571R	1	28	7	3	0.26
A586R	1	15	1	1	nd
A598L	1	13	4	3	0.08
A617R	1	23	5	3	nd
A621L	1	165	3	1	0.26
A624R	1	103	1	1	0.25
A625R	1	15	5	3	0.07
A629R	1	14	10	4	0.04
A631L	1	17	3	1	nd
A655L	1	23	11	3	0.28
A686L	1	17	31	1	0.18

*emPAI: exponentially-modified protein abundance index

Table S3. Chlorovirus accession numbers and capsid protein paralog classes

Chlorovirus	**CDS**	**NCBI Accession Number**	**Capsid protein paralog class**
AR158	C048R	YP_001498130.1	III
AR158	C470R	YP_001498551.1	IV
AR158	C558L	YP_001498639.1	I
AR158	C675L	YP_001498756.1	III
AR158	C741L	YP_001498822.1	II
ATCV-1	Z151L	YP_001426632.1	II
ATCV-1	Z280L	YP_001426761.1	I
ATCV-1	Z506L	YP_001426987.1	III
ATCV-1	Z558L	YP_001427039.1	IV
ATCV-1	Z664R	YP_001427145.1	III
FR483	N074R	YP_001425706.1	III
FR483	N254L	YP_001425886.1	III
FR483	N274L	YP_001425906.1	III
FR483	N395R	YP_001426027.1	IV
FR483	N470L	YP_001426102.1	I
FR483	N737L	YP_001426369.1	II
MT325	M078R	ABT13632	III
MT325	M269L	ABT13823	III
MT325	M381R	ABT13935	IV
MT325	M463L	ABT14017	I

MT325	M748L	ABT14302	II
NY-2A	B059R	YP_001497255.1	III
NY-2A	B529R	YP_001497725.1	IV
NY-2A	B585L	YP_001497781.1	I
NY-2A	B617L	YP_001497813.1	I
NY-2A	B748L	YP_001497944.1	III
NY-2A	B825L	YP_001498021.1	II
PBCV-1	A010R	NP_048358.2	III
PBCV-1	A011L	NP_048359.1	III
PBCV-1	A383R	NP_048739.2	IV
PBCV-1	A384dL	NP_048747.2	V
PBCV-1	A430L	NP_048787.1	I
PBCV-1	A558L	NP_048914.1	III
PBCV-1	A622L	NP_048978.1	II

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Sample Treatment				
Iodoacetamide	+	+	+	+
B-mercaptoethanol		+	+	+
Phenol extracted			+	
Phenol-toluene extracted				+

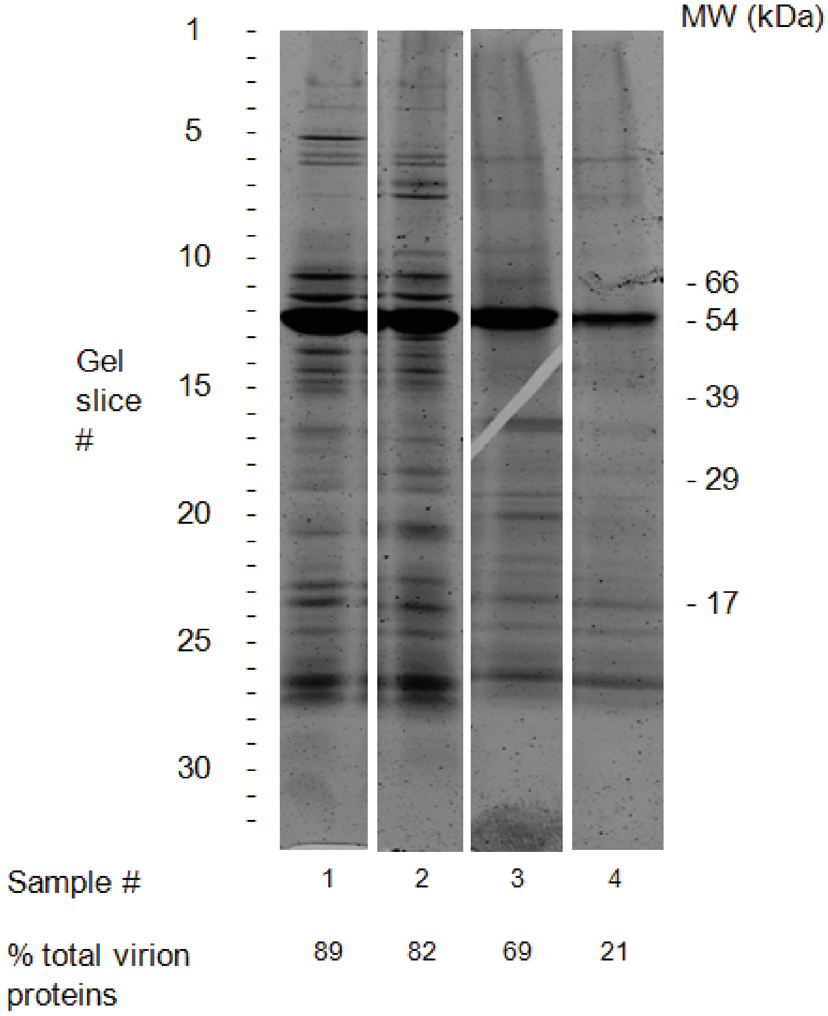
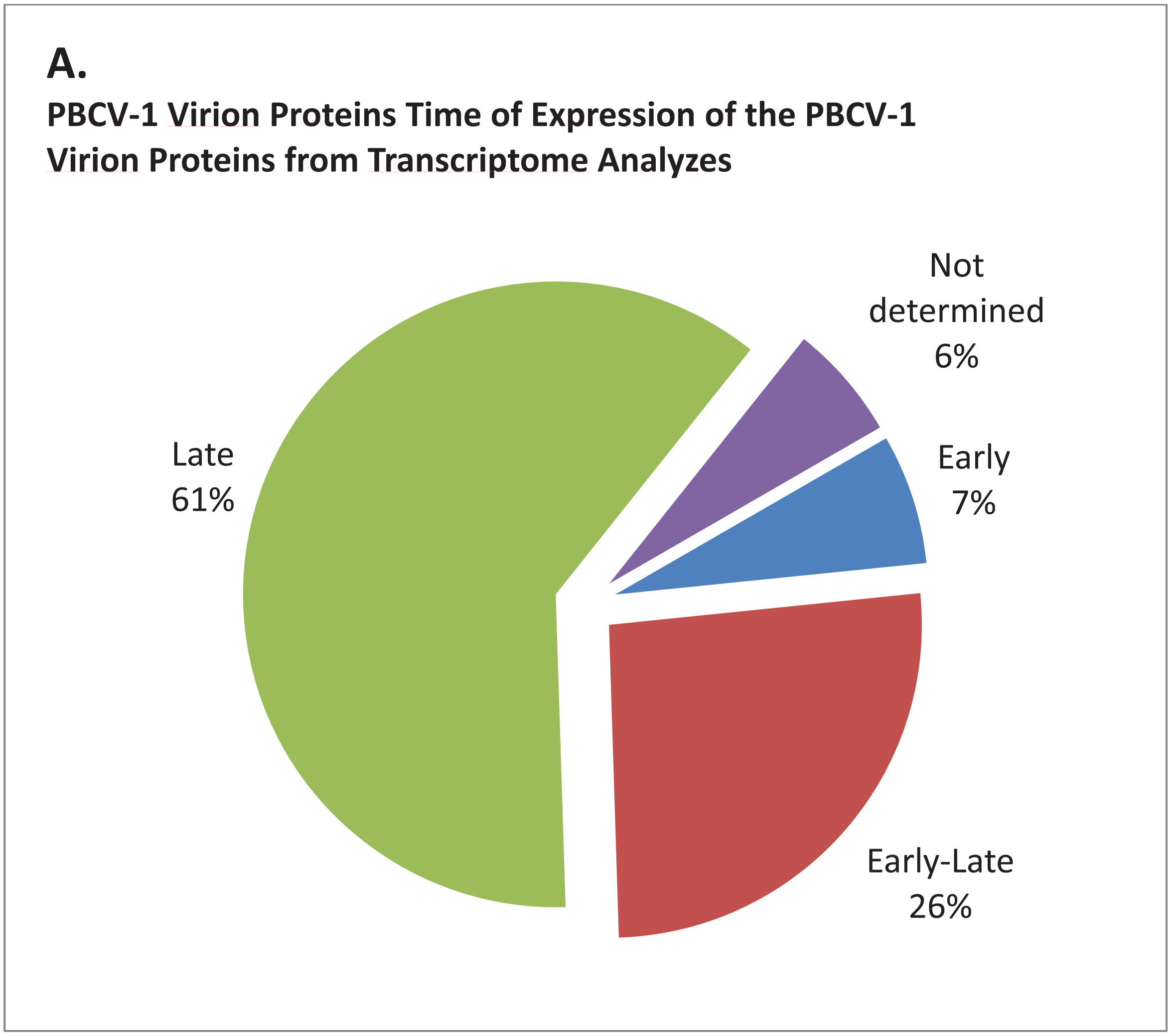


Figure S1. Protein extraction and separation of PBCV-1 virions using SDS-PAGE. Gradient purified virions were solubilized and treated with various reagents, then separated on SDS-PAGE. The gels were cut into 32 pieces and each gel piece was analyzed for tryptic peptide fragments by Method 1. All the samples were treated with iodoacetamide; sample 2 was treated with beta-mercaptoethanol or dithiothreitol; sample 3 was treated as # 2 with phenol extraction; sample 4 was treated as #2 with phenol-toluene extraction. The percent of the total virion proteins detected with each method is at the bottom of the figure.



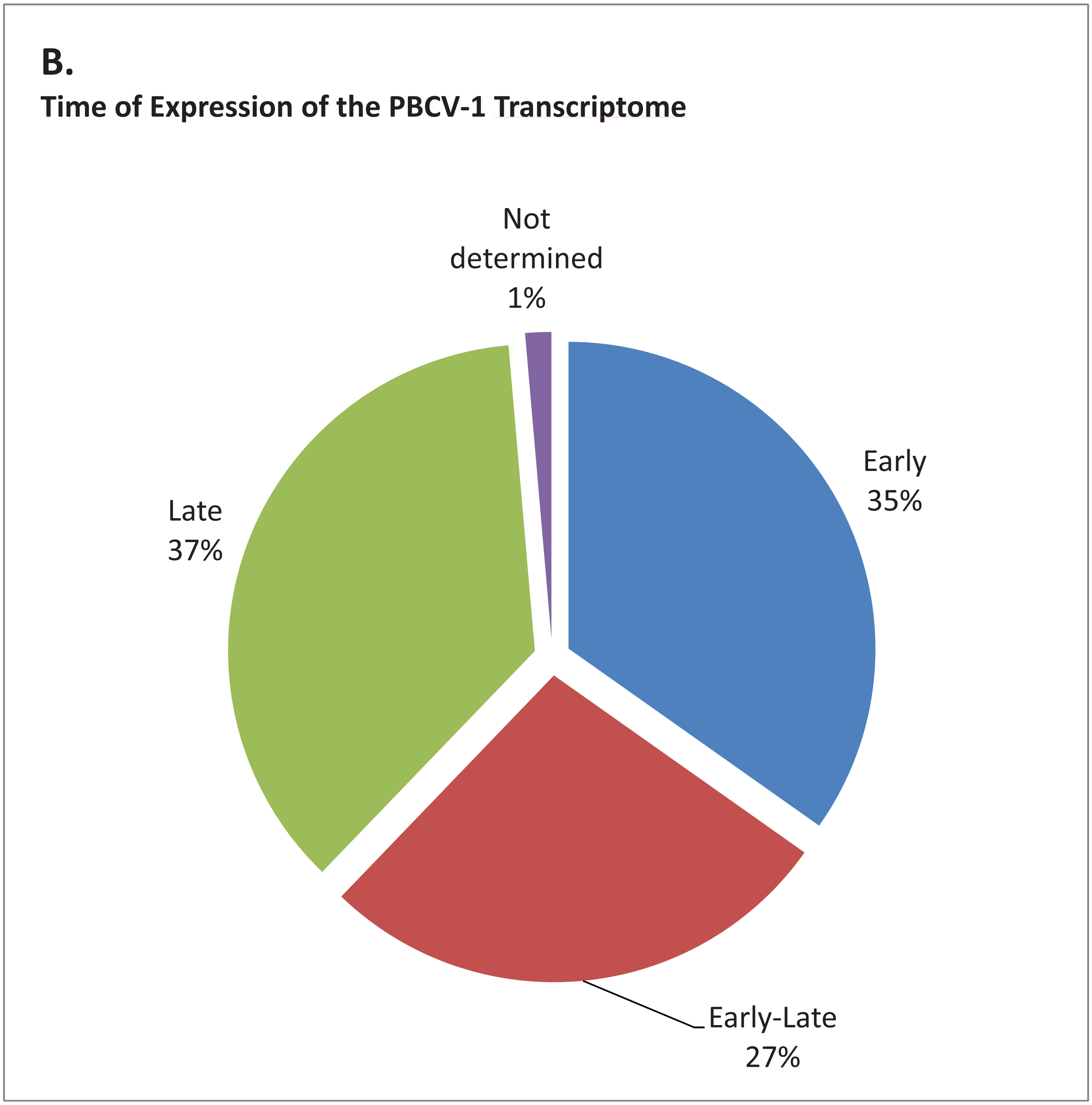
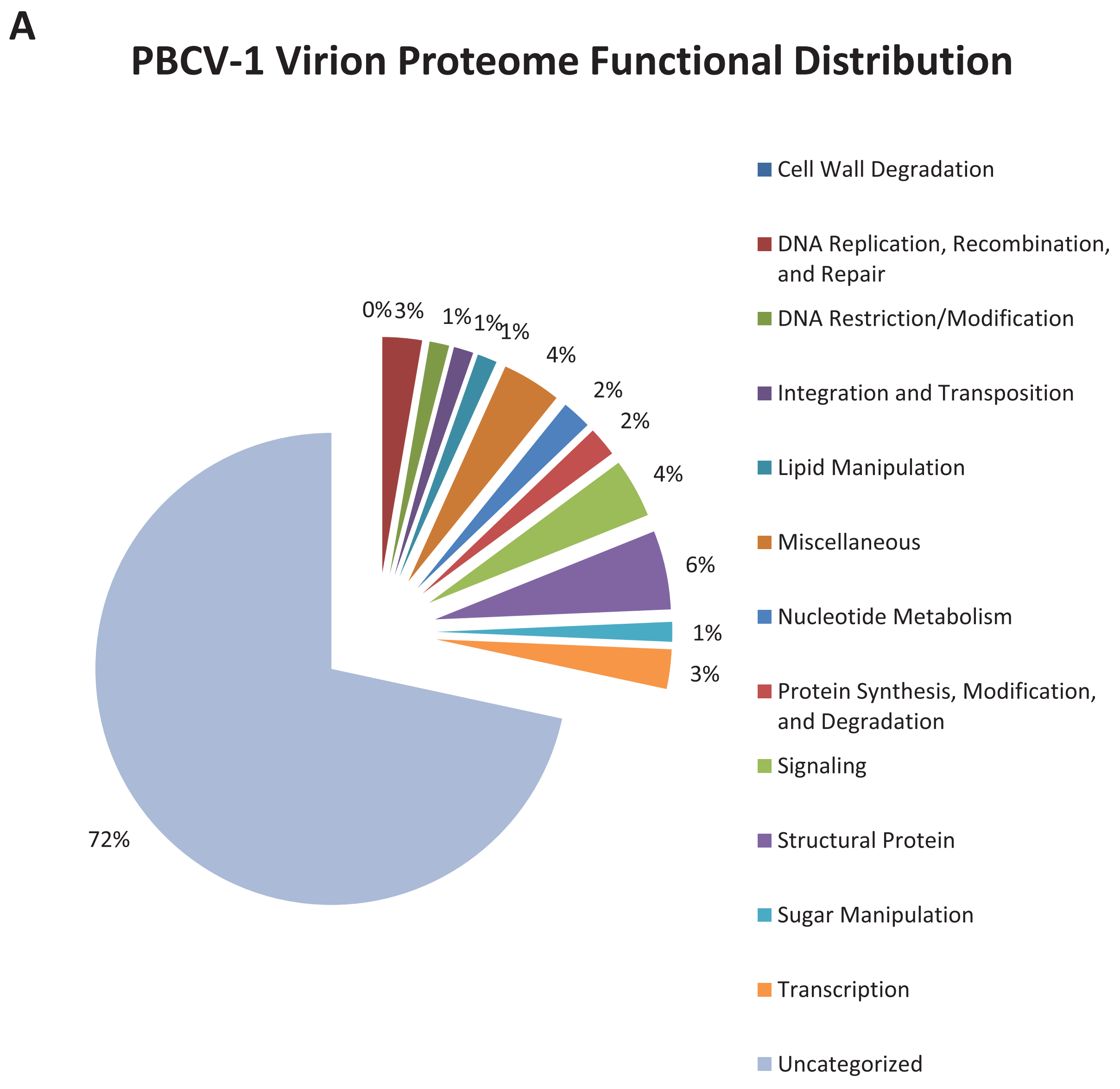
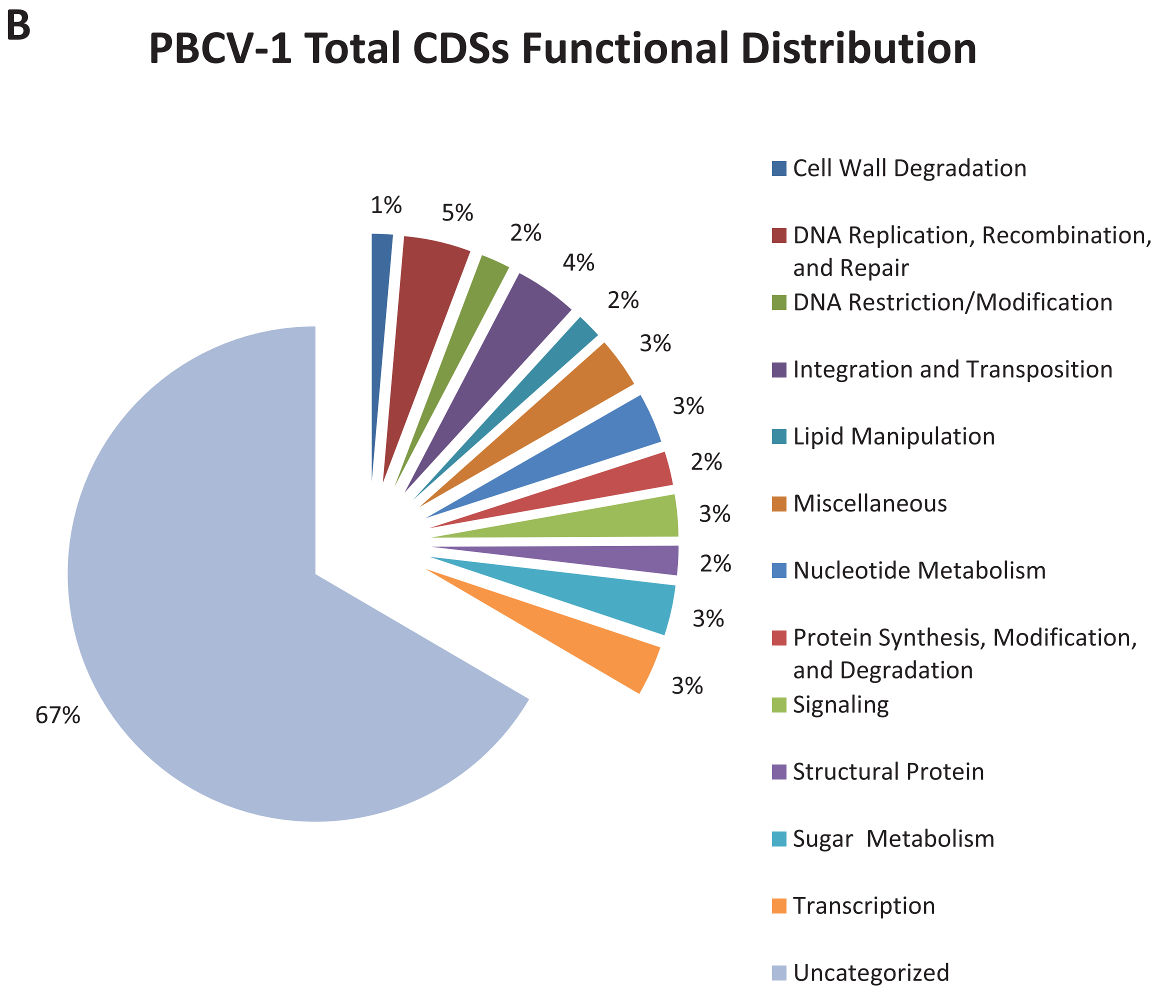


Figure S2. **(A)** Distribution of PBCV-1 genes as measured during the time course of replication. (A) The expression stages and relative abundances of the total CDSs as measured by microarray sequence hybridizations (10). **(B)** The expression stages of the genes associated with the virion proteome. Note, the fractions labeled “not determined” are genes that were not included in the microarray analyses.


A
PBCV-1 Virion Proteome Functional Distribution
0%
3%
1%
1%
1%
4%
2%
2%
4%
6%
1%
3%
72%
Cell Wall Degradation
DNA Replication, Recombination, and Repair
DNA Restriction/Modification
Integration and Transposition
Lipid Manipulation
Miscellaneous
Nucleotide Metabolism
Protein Synthesis, Modification, and Degradation
Signaling
Structural Protein
Sugar Manipulation
Transcription
Uncategorized


B

PBCV-1 Total CDSs Functional Distribution

Figure S3. Functional distribution of PBCV-1 transcriptome and virion-associated proteome. (**A**) The functional distribution of the virion-associated proteins into 13 functional categories. The functional categories were determined from either sequence similarity analyses against the GenBank non-redundant database, or the proteins had activities determined biochemically. Note, there were no proteins detected with cell wall degradation associated with the virion proteins. (**B**) The 416 PBCV-1 coding CDSs are distributed into 13 functional categories.

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