

2-20-2007

## Supplementary Data for “Sequence and annotation of the 369-kb NY-2A and the 345-kb AR158 viruses that infect *Chlorella* NC64A”: Appendix C: Gene Names c001R – c814L

Lisa A. Fitzgerald

*University of Nebraska-Lincoln*, [lisa.fitzgerald@nrl.navy.mil](mailto:lisa.fitzgerald@nrl.navy.mil)

Michael V. Graves

*University of Massachusetts-Lowell*, [Michael\\_Graves@uml.edu](mailto:Michael_Graves@uml.edu)

Xiao Li

*University of Massachusetts-Lowell*

Tamara Feldblyum

*The Institute for Genomic Research, Rockville, MD*

William C. Nierman

*The Institute for Genomic Research, Rockville, MD*, [wnierman@tigr.org](mailto:wnierman@tigr.org)

*See next page for additional authors*

Follow this and additional works at: <http://digitalcommons.unl.edu/virologypub>



Part of the [Virology Commons](#)

---

Fitzgerald, Lisa A.; Graves, Michael V.; Li, Xiao; Feldblyum, Tamara; Nierman, William C.; and Van Etten, James L., "Supplementary Data for “Sequence and annotation of the 369-kb NY-2A and the 345-kb AR158 viruses that infect *Chlorella* NC64A”: Appendix C: Gene Names c001R – c814L" (2007). *Virology Papers*. 9.  
<http://digitalcommons.unl.edu/virologypub/9>

This Article is brought to you for free and open access by the Virology, Nebraska Center for at DigitalCommons@University of Nebraska - Lincoln. It has been accepted for inclusion in Virology Papers by an authorized administrator of DigitalCommons@University of Nebraska - Lincoln.

---

**Authors**

Lisa A. Fitzgerald, Michael V. Graves, Xiao Li, Tamara Feldblyum, William C. Nierman, and James L. Van Etten

## SUPPLEMENTARY DATA FOR

# Sequence and annotation of the 369-kb NY-2A and the 345-kb AR158 viruses that infect *Chlorella* NC64A

Lisa A. Fitzgerald<sup>a</sup>, Michael V. Graves<sup>b</sup>, Xiao Li<sup>b</sup>, Tamara Feldblyum<sup>c</sup>, William C. Nierman<sup>c, d</sup>, and James L. Van Etten<sup>e, \*</sup>

<sup>a</sup>Department of Chemistry, University of Nebraska-Lincoln, Lincoln, NE 68588-0304

<sup>b</sup>Department of Biological Sciences, University of Massachusetts-Lowell, Lowell, MA 01854

<sup>c</sup>The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, MD 20850

<sup>d</sup>The George Washington University School of Medicine, Department of Biochemistry and Molecular Biology, Washington, DC 20037

<sup>e</sup>Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE 68583-0722 and Nebraska Center for Virology, University of Nebraska-Lincoln, Lincoln, NE 68588-0666

\* Corresponding author. Email: [jvanetten@unlnotes.unl.edu](mailto:jvanetten@unlnotes.unl.edu)

**Abstract:** Viruses NY-2A and AR158, members of the family *Phycodnaviridae*, genus *Chlorovirus*, infect the fresh water, unicellular, eukaryotic, chlorella-like green alga, *Chlorella* NC64A. The 368,683-bp genome of NY-2A and the 344,690-bp genome of AR158 are the two largest chlorella virus genomes sequenced to date; NY-2A contains 404 putative protein-encoding and 7 tRNA-encoding genes and AR158 contains 360 putative protein-encoding and 6 tRNA-encoding genes. The protein-encoding genes are almost evenly distributed on both strands, and intergenic space is minimal. Two of the NY-2A genes encode inteins, the large subunit of ribonucleotide reductase and a superfamily II helicase. These are the first inteins to be detected in the chlorella viruses. Approximately 40% of the viral gene products resemble entries in the public databases, including some that are unexpected for a virus. These include GDP-d-mannose dehydratase, fucose synthase, aspartate transcarbamylase, Ca<sup>++</sup> transporting ATPase and ubiquitin. Comparison of NY-2A and AR158 protein-encoding genes with the prototype chlorella virus PBCV-1 indicates that 85% of the genes are present in all three viruses.

**Keywords:** Chlorella viruses, Phycodnaviridae, Virus NY-2A, Virus AR158, Genome sequence

Supplementary data associated with this article is archived in this repository as 4 separate files: Appendices A–D. Each document, in spreadsheet format, shows Gene Name, Genome Position, A.A. length, Peptide Mw, pI, CDD Hit Number, COGs, COG Definition, Bit Score, E-value, % Identity, % Positive, Query from-to, Hit from-to, BLASTp Hit Number, Hit Accession, BLASTp Definition, Bit Score, E-value, % Identity, % Positive, Query from-to, and Hit from-to.

Appendix A: Gene Names b002R – b797R

Appendix B: Gene Names B001L – B886R

Appendix C: Gene Names c001R – c814L

Appendix D: Gene Names C006R – C815L

---

## Appendix C: Gene Names c001R – c814L

Gene Name	Genome Position	A.A. length	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to
c001R	858-1208	117	13,216	10.00		No Hit Found									No Hit Found							
c002L	1117-914	68	7,355	4.11		No Hit Found									No Hit Found							
c003L	1407-1162	82	9,208	5.03		No Hit Found									No Hit Found							
c004R	1345-1566	74	8,633	7.51		No Hit Found									No Hit Found							
c005L	2768-2553	72	7,560	6.39		No Hit Found									No Hit Found							
c007L	2853-2656	66	8,324	8.67		No Hit Found									No Hit Found							
c009R	4107-4307	67	8,180	7.70		No Hit Found									No Hit Found							
c010R	4195-4416	74	8,305	10.98		No Hit Found									No Hit Found							
c012R	4739-5137	133	14,851	10.74		No Hit Found									No Hit Found							
c013L	5249-4968	94	10,864	12.36		No Hit Found									No Hit Found							
c014L	6059-5835	75	9,020	11.14		No Hit Found									No Hit Found							
c016R	5923-6135	71	8,679	11.14		No Hit Found									No Hit Found							
c017R	6653-6874	74	8,908	7.95		No Hit Found									No Hit Found							
c019L	8506-8288	73	8,018	10.84		No Hit Found									No Hit Found							
c020L	8636-8364	91	10,668	4.74		No Hit Found									No Hit Found							
c022R	9629-9838	70	7,637	7.03		No Hit Found									No Hit Found							
c023R	10013-10267	85	9,780	7.03		No Hit Found									No Hit Found							
c025L	10493-10260	78	8,776	12.21		No Hit Found									No Hit Found							
c026R	10400-10885	162	15,129	6.51		No Hit Found									No Hit Found							
c027R	10482-10724	81	7,004	7.01		No Hit Found									No Hit Found							
c028L	11138-10896	81	9,300	9.03		No Hit Found									No Hit Found							
c030L	12030-11833	66	7,378	12.02		No Hit Found									No Hit Found							
c032L	12699-12505	65	7,548	11.07		No Hit Found									No Hit Found							
c033R	14085-14363	93	10,260	4.54		No Hit Found									No Hit Found							
c034R	14457-14663	69	7,533	4.11		No Hit Found									No Hit Found							
c035R	15405-15620	72	8,118	4.88		No Hit Found									No Hit Found							
c038L	20114-19836	93	10,815	11.75		No Hit Found									No Hit Found							
c039R	20154-20471	106	13,496	11.94		No Hit Found									No Hit Found							
c040R	20225-20644	140	15,363	6.44		No Hit Found									No Hit Found							
c041R	21263-21613	117	12,757	4.77		No Hit Found									No Hit Found							
c042R	21734-21976	81	8,902	4.36		No Hit Found									No Hit Found							
c043R	21986-22390	135	14,717	4.36		No Hit Found									No Hit Found							
c045R	23050-23385	112	12,025	3.86		No Hit Found									No Hit Found							
c046R	23722-23919	66	7,153	3.83		No Hit Found									No Hit Found							
c047R	24526-24927	134	15,178	5.19		No Hit Found									No Hit Found							
c049L	26322-26053	90	10,915	10.53		No Hit Found									No Hit Found							
c050L	27023-26817	69	8,732	10.36		No Hit Found									No Hit Found							
c053R	29160-29459	100	11,626	8.45		No Hit Found									No Hit Found							
c054R	30036-30260	75	8,463	6.50		No Hit Found									No Hit Found							
c058L	32400-32086	105	11,811	11.09		No Hit Found									No Hit Found							
c059R	32134-32358	75	9,266	8.65		No Hit Found								1	NP_048391	a43R	160.23	1.61E-38	92%	94%	1-75	1-75
c060L	32599-32345	85	9,926	7.79		No Hit Found								1	NP_048520	a172L	90.12	2.06E-17	49%	71%	4-85	4-86
c067R	36462-36772	107	12,931	8.17		No Hit Found								1	NP_048400	a52R	72.79	3.37E-12	88%	91%	39-74	1-36
c070L	37569-37273	99	11,285	8.46		No Hit Found									No Hit Found							
c071R	37404-37646	81	9,390	12.33		No Hit Found									No Hit Found							
c076R	40834-41088	85	9,619	10.52		No Hit Found									No Hit Found							
c077R	41317-41559	81	8,642	11.27		No Hit Found								1	NP_048874	a518R	82.42	4.19E-15	61%	66%	1-74	1-75
c079R	41856-42158	101	11,879	4.80		No Hit Found									No Hit Found							
c080R	42043-42243	67	7,428	11.66		No Hit Found									No Hit Found							
c082L	42700-42482	73	8,199	10.86		No Hit Found									No Hit Found							
c083L	42949-42734	72	7,961	11.22		No Hit Found									No Hit Found							
c084L	43118-42810	103	12,209	5.28		No Hit Found									No Hit Found							
c085R	42826-43095	90	10,283	12.37		No Hit Found									No Hit Found							
c087L	43830-43534	99	11,655	10.86		No Hit Found									No Hit Found							
c088L	44198-43725	158	18,278	6.91		No Hit Found								1	NP_048417	contains Gly-rich Gx motif LGGGLG (5X); contains type I hydrophobic tra	106.30	2.89E-22	60%	78%	77-158	1-82
c091R	45414-45683	90	10,722	12.10		No Hit Found									No Hit Found							
c092L	45973-45743	77	8,822	4.37		No Hit Found								1	NP_048503	a155R	88.20	7.74E-17	67%	81%	11-75	22-86
c094L	46408-46280	73	9,099	11.44		No Hit Found									No Hit Found							

Gene Name	Genome Position	A.A. length	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to
c095R	46384-46647	88	10,427	6.51		No Hit Found									No Hit Found							
c096R	46559-46783	75	8,714	11.72		No Hit Found									No Hit Found							
c099R	47348-47569	74	8,973	11.96		No Hit Found									No Hit Found							
c101L	47831-47637	65	7,735	11.80		No Hit Found								1	NP_048424	a76L	81.26	9.47E-15	59%	72%	7-65	29-103
c103R	48127-48393	89	10,619	9.04		No Hit Found									No Hit Found							
c105L	48553-48332	74	8,787	6.23		No Hit Found									No Hit Found							
c106R	48477-48920	148	16,988	12.25		No Hit Found									No Hit Found							
c107R	48667-49050	128	15,872	12.73		No Hit Found									No Hit Found							
c108L	49030-48701	110	12,147	4.53		No Hit Found									No Hit Found							
c109R	48951-49169	73	8,248	4.44		No Hit Found									No Hit Found							
c111L	50241-50035	69	7,818	7.69		No Hit Found									No Hit Found							
c113L	50991-50605	129	14,954	8.53		No Hit Found								1	NP_048428	a80L	83.19	2.45E-15	56%	73%	4-78	59-133
c113L														2	NP_048808	similar to PBCV-1 ORF a80L, encoded by GenBank Accession Number U	52.37	4.64E-06	55%	77%	1-45	56-100
c115R	51552-51854	101	11,969	5.03		No Hit Found									No Hit Found							
c117R	52181-52435	85	10,012	10.33		No Hit Found									No Hit Found							
c119L	53120-52878	81	9,832	10.44		No Hit Found									No Hit Found							
c120L	53301-53107	65	6,979	10.84		No Hit Found								1	NP_048434	a86L	115.16	5.92E-25	88%	91%	1-65	1-67
c122L	53809-53456	118	14,006	8.74		No Hit Found									No Hit Found							
c125R	54576-54854	93	10,295	6.27		No Hit Found									No Hit Found							
c127R	56008-56250	81	9,887	12.34		No Hit Found									No Hit Found							
c129L	57218-57024	65	6,945	11.08		No Hit Found									No Hit Found							
c130L	57627-57304	108	12,676	7.21		No Hit Found									No Hit Found							
c131L	58671-58321	117	13,915	7.33		No Hit Found									No Hit Found							
c133L	58873-58634	80	9,314	11.01		No Hit Found								1	NP_048449	a101L	80.49	1.60E-14	65%	87%	1-55	33-87
c135R	60778-60999	74	8,490	5.70		No Hit Found									No Hit Found							
c136L	62005-61682	108	12,746	11.14		No Hit Found									No Hit Found							
c138L	62271-62071	67	7,631	11.05		No Hit Found								1	NP_048450	a102L	74.71	8.81E-13	67%	70%	1-55	1-55
c139R	62218-62478	87	10,553	8.38		No Hit Found									No Hit Found							
c141R	63522-63800	93	10,443	9.04		No Hit Found									No Hit Found							
c144R	64162-64443	94	11,576	10.77		No Hit Found									No Hit Found							
c145R	64563-64808	82	10,093	8.66		No Hit Found									No Hit Found							
c147R	64964-65188	75	8,899	9.58		No Hit Found									No Hit Found							
c148L	65584-65348	79	9,420	9.90		No Hit Found									No Hit Found							
c149L	65751-65419	111	13,009	11.06		No Hit Found								1	NP_048458	a110L	178.72	4.30E-44	85%	89%	10-111	1-102
c151L	66402-66112	97	10,606	9.77		No Hit Found								1	NP_048460	a112L	191.05	8.51E-48	96%	96%	1-97	1-97
c152L	66829-66602	76	8,774	9.66		No Hit Found								1	NP_048463	a115L	97.44	1.28E-19	61%	68%	1-76	1-76
c153R	66732-66965	78	9,066	7.94		No Hit Found								1	NP_048464	a116R	105.15	6.10E-22	70%	75%	1-78	1-78
c154L	67618-67190	143	16,723	6.22		No Hit Found								1	NP_048465	a117L	177.56	9.63E-44	63%	80%	7-136	1-130
c156L	68903-68421	161	19,134	8.25		No Hit Found									No Hit Found							
c158L	69548-69270	93	10,616	7.09		No Hit Found									No Hit Found							
c159L	70317-69982	112	13,401	9.58		No Hit Found									No Hit Found							
c161L	70671-70441	77	8,834	6.50		No Hit Found									No Hit Found							
c163L	72962-71135	606	66,489	4.07		No Hit Found								1	XP_499823	hypothetical protein	53.53	2.42E-05	23%	36%	231-670	135-438
c164L	73444-73241	68	7,426	4.32		No Hit Found									No Hit Found							
c165L	74207-73557	217	25,658	10.46		No Hit Found									No Hit Found							
c166L	73876-73613	88	9,636	6.62		No Hit Found									No Hit Found							
c168L	75179-74985	65	7,619	11.13		No Hit Found								1	NP_048473	a124L	59.31	3.85E-08	58%	66%	18-65	1-48
c170L	76055-75735	107	12,611	10.91		No Hit Found									No Hit Found							
c172R	76271-76723	151	17,718	9.90		No Hit Found								1	NP_048480	a132R	59.31	3.81E-08	47%	67%	61-120	19-79
c173L	77323-76730	198	23,198	4.95		No Hit Found								1	AAK23092	hypothetical protein	67.40	2.78E-10	29%	52%	40-177	69-210
c173L														2	ZP_00811430	Methyltransferase FkbM	64.70	1.80E-09	30%	51%	43-180	114-248
c173L														3	ABA05654	methyltransferase FkbM	63.54	4.01E-09	34%	52%	59-180	116-235
c178R	78081-78329	83	9,177	10.51		No Hit Found									No Hit Found							
c178R	79120-79335	72	8,465	7.77		No Hit Found									No Hit Found							
c181L	79875-79660	72	7,514	5.54		No Hit Found									No Hit Found							
c183L	81681-80872	270	28,002	5.53		No Hit Found								1	NP_048490	a142L	172.17	1.47E-41	78%	78%	103-213	21-131
c183L														2	NP_048491	a143L	55.84	1.54E-06	89%	89%	20-47	23-50
c184L	82264-80882	461	53,389	8.44		No Hit Found								1	NP_048492	a144L	526.17	8.95E-148	57%	67%	5-461	18-473
c184L														2	T17832	hypothetical protein a141L - Chlorella virus PBCV-1	279.26	1.91E-73	60%	70%	235-461	14-240
c184L														3	NP_048495	Phe-, Gly-rich protein: RCGF 3X, GCGF 11X, RSGF 5X, GSGF 2X	60.08	1.82E-07	37%	47%	40-116	132-224
c185L	82663-82436	76	9,380	8.73		No Hit Found								1	NP_048495	Phe-, Gly-rich protein: RCGF 3X, GCGF 11X, RSGF 5X, GSGF 2X	114.78	7.74E-25	71%	82%	4-76	187-260

Gene Name	Genome Position	A.A. length	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	Hit	BLASTp Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to	
c185L															2	NP_048492	a144L		59.31	3.86E-08	51%	64%	4-65	92-155
c186L	83049-82717	111	10,598	9.60		No Hit Found										No Hit Found								
c188R	83010-83234	75	8,439	8.43		No Hit Found										No Hit Found								
c190L	84315-83878	146	16,674	10.89		No Hit Found									1	NP_048500	contains prokaryotic membrane lipoprotein lipid attachment site	75.87	3.90E-13	53%	61%	67-143	9-85	
c192L	84820-84611	70	8,351	10.54		No Hit Found										No Hit Found								
c196R	86464-86658	65	7,842	9.24		No Hit Found										No Hit Found								
c199R	87125-87364	80	8,733	4.43		No Hit Found										No Hit Found								
c201L	87976-87776	67	7,962	6.91		No Hit Found									1	NP_048515	a167L	61.23	1.01E-08	48%	62%	1-66	1-66	
c205L	90963-90712	94	11,356	6.86		No Hit Found										No Hit Found								
c207R	91662-91946	95	11,440	11.54		No Hit Found									1	NP_048391	a43R	80.88	1.25E-14	54%	65%	1-75	1-75	
c209L	92782-92531	84	10,068	10.74		No Hit Found										No Hit Found								
c210R	92834-93049	72	7,509	5.54		No Hit Found										No Hit Found								
c211L	93130-92852	93	11,611	11.43		No Hit Found										No Hit Found								
c213R	93448-93792	115	13,719	8.19		No Hit Found										No Hit Found								
c214R	94069-94278	70	8,428	8.40		No Hit Found										No Hit Found								
c215R	94322-94600	93	10,894	7.81		No Hit Found										No Hit Found								
c218R	95123-95371	83	10,219	11.05		No Hit Found										No Hit Found								
c219R	95277-95480	68	7,747	6.80		No Hit Found									1	NP_048601	a251aL	73.94	1.50E-12	67%	76%	1-56	83-141	
c221L	96277-96062	72	8,732	12.02		No Hit Found										No Hit Found								
c222L	96690-96298	131	13,927	10.62		No Hit Found										No Hit Found								
c223L	96563-96369	65	7,794	11.02		No Hit Found										No Hit Found								
c224R	97366-97599	78	9,691	11.50		No Hit Found										No Hit Found								
c225L	97846-97577	90	10,690	5.48		No Hit Found										No Hit Found								
c226L	98073-97873	67	7,104	5.33		No Hit Found										No Hit Found								
c229L	99585-99382	68	7,374	11.50		No Hit Found										No Hit Found								
c231L	99829-99557	91	11,323	11.81		No Hit Found										No Hit Found								
c232L	100234-100004	77	9,087	8.20		No Hit Found									1	NP_048534	a187L	51.60	8.02E-06	59%	87%	1-32	216-247	
c233L	101771-101568	68	7,244	12.23		No Hit Found									1	NP_048535	a188L	105.15	6.06E-22	83%	86%	1-68	5-72	
c235L	102087-101800	96	11,556	8.52		No Hit Found										No Hit Found								
c237L	102706-102467	80	9,028	4.91		No Hit Found										No Hit Found								
c238R	102616-103026	137	16,220	11.53		No Hit Found										No Hit Found								
c240L	107496-107272	75	8,593	10.37		No Hit Found										No Hit Found								
c243R	108582-108794	71	8,346	8.35		No Hit Found										No Hit Found								
c247L	110412-110158	85	10,356	9.47		No Hit Found										No Hit Found								
c248L	110609-110232	126	13,951	10.58		No Hit Found									1	NP_048548	A201L	135.96	3.23E-31	66%	79%	24-116	1-93	
c249R	110539-110739	67	7,624	10.92		No Hit Found										No Hit Found								
c251L	110992-110705	96	11,788	10.16		No Hit Found										No Hit Found								
c253L	111325-111116	70	7,097	9.46		No Hit Found									1	NP_048551	a204L	125.56	4.31E-28	92%	94%	1-70	1-70	
c254L	112026-111583	148	16,166	5.80		No Hit Found										No Hit Found								
c257L	112858-112664	65	7,957	9.66		No Hit Found										No Hit Found								
c258L	113487-113155	111	13,135	8.09		No Hit Found										No Hit Found								
c262R	115076-115321	82	9,540	10.65		No Hit Found										No Hit Found								
c266L	118141-117878	88	10,558	9.46		No Hit Found										No Hit Found								
c267L	118131-117883	83	9,410	11.05		No Hit Found									1	T17711	hypothetical protein a221L - Chlorella virus PBCV-1	70.09	2.14E-11	75%	88%	1-44	1-44	
c268R	118076-118285	70	7,704	9.74		No Hit Found									1	NP_048570	a223R	102.06	5.10E-21	71%	78%	1-70	1-70	
c269L	118757-118551	69	8,032	9.41		No Hit Found									1	NP_048572	a224L	78.57	6.06E-14	90%	92%	1-40	49-88	
c273R	120301-120582	94	10,998	7.83		No Hit Found										No Hit Found								
c274L	120507-120313	65	7,395	9.43		No Hit Found										No Hit Found								
c276R	120772-120999	76	8,512	10.38		No Hit Found										No Hit Found								
c277R	121048-121383	112	12,845	7.74		No Hit Found										No Hit Found								
c278R	121413-121619	69	8,266	10.25		No Hit Found									1	NP_048580	a232R	72.79	3.32E-12	56%	73%	6-65	6-65	
c279L	122093-121860	78	9,730	10.37		No Hit Found										No Hit Found								
c282L	123270-123076	65	7,071	10.86		No Hit Found										No Hit Found								
c283L	123376-123122	85	10,277	8.92		No Hit Found										No Hit Found								
c284R	123303-123560	86	10,147	11.32		No Hit Found										No Hit Found								
c287L	124418-124002	139	16,327	7.51		No Hit Found										No Hit Found								
c288R	124187-124480	98	11,601	11.21		No Hit Found										No Hit Found								
c289L	124901-124662	80	9,384	9.63		No Hit Found										No Hit Found								

Gene Name	Genome Position	A.A. length	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identitiv	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identitiv	% Positive	Query from-to	Hit from-to
c291R	125565-125843	93	11,173	8.70		No Hit Found																
c293L	126861-126511	117	13,667	5.15		No Hit Found								1	NP_048590	a242L	174.48	8.20E-43	74%	79%	1-117	1-117
c294L	127151-126864	96	10,473	10.81		No Hit Found																
c295L	127574-127317	86	9,989	9.40		No Hit Found																
c296L	127611-127354	86	9,966	9.45		No Hit Found																
c297L	127973-127674	100	11,308	10.05		No Hit Found																
c301L	131397-131020	126	15,612	10.02		No Hit Found																
c302L	131285-131067	73	8,030	11.07		No Hit Found																
c304R	132044-132301	86	10,130	10.16		No Hit Found																
c305R	132980-133429	150	17,984	10.04		No Hit Found																
c308L	134760-134509	84	10,506	9.57		No Hit Found								1	NP_048603	a252aL	90.51	1.58E-17	66%	80%	25-84	25-84
c310R	135238-135864	209	23,434	7.79		No Hit Found																
c312R	135952-136152	67	7,723	9.56		No Hit Found								1	NP_048618	a264R	100.91	1.15E-20	67%	85%	1-61	1-61
c314R	136332-136652	107	11,951	10.71		No Hit Found																
c316R	136926-137177	84	9,454	10.79		No Hit Found								1	NP_048624	a270R	82.03	5.62E-15	63%	67%	1-68	1-68
c317R	137108-137710	201	23,972	6.45		No Hit Found								1	NP_048626	a272R	71.63	1.50E-11	52%	74%	28-90	5-67
c320R	139175-139543	123	13,615	8.82		No Hit Found								1	NP_048635	a281R	174.48	8.29E-43	83%	85%	8-113	70-176
c322R	139561-139776	72	8,843	9.57		No Hit Found								1	NP_048633	a279R	158.69	4.56E-38	95%	95%	1-72	1-72
c323R	140657-140935	93	10,245	3.62		No Hit Found								1	NP_048634	a280R	174.10	1.05E-42	93%	93%	1-93	1-93
c325L	141664-141464	67	7,712	11.12		No Hit Found								1	NP_048637	a283L	138.27	6.49E-32	94%	97%	1-67	1-67
c326R	142606-142806	67	8,415	10.20		No Hit Found																
c328L	143060-142797	88	10,735	12.19		No Hit Found																
c330R	144222-144461	80	9,135	10.73		No Hit Found																
c331L	144656-144390	89	11,112	12.13		No Hit Found																
c332R	144409-144618	70	8,349	11.47		No Hit Found																
c333R	144618-144854	79	9,404	11.24		No Hit Found																
c335L	145962-145684	93	10,511	8.11		No Hit Found																
c336L	146098-145880	73	8,842	11.23		No Hit Found																
c338R	146527-146901	125	15,299	8.38		No Hit Found																
c340L	147527-147114	138	16,602	10.27		No Hit Found								1	BAA20344	ORF245	137.50	1.09E-31	60%	74%	1-115	125-243
c341L	147342-147124	73	8,987	10.31		No Hit Found																
c343R	148034-148369	112	12,380	10.29		No Hit Found								1	NP_048647	a293R	149.83	2.13E-35	73%	79%	1-102	67-168
c345R	148727-148927	67	7,924	6.08		No Hit Found																
c347L	150220-149966	85	9,964	7.48		No Hit Found																
c350R	151847-152107	87	10,253	8.53		No Hit Found																
c352L	152482-152276	69	8,208	9.95		No Hit Found																
c353L	152664-152470	65	7,404	10.57		No Hit Found																
c355R	152725-152958	78	8,970	11.50		No Hit Found																
c356L	153512-152814	233	27,426	7.38		No Hit Found								1	NP_048503	a155R	92.43	1.13E-17	66%	86%	16-83	27-94
c357L	153343-153101	81	9,010	9.52		No Hit Found																
c359R	153860-154096	76	9,221	10.65		No Hit Found																
c360R	154116-154376	87	9,662	8.83		No Hit Found																
c361R	154629-154838	70	7,340	10.81		No Hit Found																
c362L	155116-154841	92	10,661	11.19		No Hit Found																
c364L	155750-155502	83	9,737	9.91		No Hit Found																
c366R	157011-157211	67	7,781	8.41		No Hit Found								1	CAB92310 2 AAF74028	DNA methyltransferase M.Hpy188I	64.70 64.70	9.11E-10 9.11E-10	51% 51%	67% 67%	1-66 1-66	348-415 348-415
c368L	157552-157358	65	7,724	8.65		No Hit Found																
c370L	158288-157893	132	16,358	11.06		No Hit Found																
c371R	158093-158320	76	8,992	5.88		No Hit Found																
c373R	158541-158852	104	12,534	7.89		No Hit Found																
c375L	160225-159938	96	10,814	12.55		No Hit Found																
c376L	160494-160288	69	7,990	9.44		No Hit Found																
c383R	163604-163978	125	14,390	8.56		No Hit Found																
c385R	164062-164265	68	8,318	9.37		No Hit Found																
c388L	165204-164764	147	13,781	4.87	1	pfam05277	DUF726, Protein of unknown function (DUF726). This family consists of s	38.34	1.41E-03	45%	57%	32-120	85-161									
c390R	164874-165239	122	14,249	11.34		No Hit Found																
c391L	165795-165550	82	8,693	9.57		No Hit Found								1	NP_048675	a319L	148.29	6.19E-35	87%	90%	1-82	1-82
c393L	166974-166720	85	10,251	10.65		No Hit Found																

Gene Name	Genome Position	A.A. length	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to
c394R	166963--167274	104	12,249	12.09		No Hit Found									No Hit Found							
c395L	167296--167054	81	9,032	9.53		No Hit Found									No Hit Found							
c399R	168424--168642	73	7,772	10.81		No Hit Found									No Hit Found							
c401R	169138--169344	69	7,754	9.38		No Hit Found									No Hit Found							
c402R	169430--169825	132	15,519	10.69		No Hit Found									No Hit Found							
c403L	170154--169894	87	10,415	9.01		No Hit Found									No Hit Found							
c405R	170653--170910	86	10,333	10.62		No Hit Found								1	NP_048683	a327R	79.72	2.77E-14	64%	75%	25--86	24--85
c407L	171282--171010	91	11,145	10.73		No Hit Found									No Hit Found							
c408L	171736--171488	83	9,597	8.64		No Hit Found									No Hit Found							
c409R	172546--172800	85	9,366	10.41		No Hit Found									No Hit Found							
c410R	172862--173068	69	8,172	6.46		No Hit Found									No Hit Found							
c411L	173150--172947	68	7,941	8.81		No Hit Found									No Hit Found							
c412L	173465--173232	78	9,004	4.36		No Hit Found									No Hit Found							
c416R	175246--175455	70	7,673	10.25		No Hit Found									No Hit Found							
c417R	175512--175745	78	9,550	11.08		No Hit Found									No Hit Found							
c419L	176799--176599	67	7,351	9.43		No Hit Found									No Hit Found							
c420L	177097--176882	72	8,469	4.76		No Hit Found									No Hit Found							
c421L	177102--176896	69	7,865	9.63		No Hit Found									No Hit Found							
c422R	177516--177734	73	8,106	8.19		No Hit Found									No Hit Found							
c424L	178650--178339	104	12,773	12.59		No Hit Found									No Hit Found							
c425R	178438--178758	107	12,519	7.07		No Hit Found									No Hit Found							
c426L	179432--179037	132	16,002	11.55		No Hit Found									No Hit Found							
c428R	179380--179592	71	8,587	10.24		No Hit Found									No Hit Found							
c431R	180919--181362	148	16,592	8.66		No Hit Found								1	NP_048701	a344R	143.28	2.03E-33	60%	77%	34--148	1--115
c432R	181894--182229	112	13,285	11.17		No Hit Found									No Hit Found							
c433R	182240--182512	91	10,959	11.10		No Hit Found									No Hit Found							
c436L	183172--182717	152	18,139	6.83		No Hit Found								1	NP_048704	a347L	92.05	5.29E-18	57%	72%	83--152	1--70
c441R	185762--186091	110	12,244	10.57		No Hit Found									No Hit Found							
c442R	185875--186207	111	13,069	11.06		No Hit Found									No Hit Found							
c443R	186389--186598	70	7,646	4.83		No Hit Found									No Hit Found							
c445L	186897--186688	70	7,690	12.35		No Hit Found									No Hit Found							
c446R	186739--186942	68	8,981	12.71		No Hit Found									No Hit Found							
c448R	187744--188016	91	9,560	4.77		No Hit Found									No Hit Found							
c450L	188399--188181	73	8,160	8.21		No Hit Found									No Hit Found							
c451L	188608--188411	66	8,354	8.68		No Hit Found									No Hit Found							
c452L	188952--188668	95	10,699	7.95		No Hit Found									No Hit Found							
c453L	189466--189254	71	8,352	10.01		No Hit Found									No Hit Found							
c454L	189905--189540	122	13,554	8.20		No Hit Found									No Hit Found							
c455L	190553--190311	81	8,974	4.64		No Hit Found									No Hit Found							
c456L	190890--190396	165	19,722	9.86		No Hit Found									No Hit Found							
c457L	191383--191150	78	9,128	7.98		No Hit Found									No Hit Found							
c458L	191654--191370	95	10,029	3.14		No Hit Found									No Hit Found							
c460R	191923--192192	90	10,868	10.95		No Hit Found									No Hit Found							
c461R	192227--192478	84	9,864	8.22		No Hit Found									No Hit Found							
c463R	192330--192695	122	15,030	10.78		No Hit Found								1	NP_048724	a367R	69.32	3.64E-11	41%	49%	1--91	1--91
c464R	192682--192903	74	8,075	3.54		No Hit Found									No Hit Found							
c465R	193494--193793	100	11,295	12.65		No Hit Found									No Hit Found							
c468R	194418--194948	177	20,563	11.10		No Hit Found									No Hit Found							
c469R	194668--194871	68	7,734	11.11		No Hit Found								1	NP_048737	a380R	144.05	1.77E-33	71%	82%	49--149	1--101
c471L	195563--195276	96	10,916	8.81		No Hit Found								1	NP_048738	a381R	127.49	1.14E-28	89%	91%	1--68	9--76
c472L	195962--195699	88	9,947	12.15		No Hit Found									No Hit Found							
c473L	196443--196084	120	14,174	8.04		No Hit Found									No Hit Found							
c474L	197139--196792	116	12,847	10.36		No Hit Found								1	NP_048742	a385L	59.31	3.86E-08	85%	85%	35--69	1--35
c476R	196916--197356	147	17,664	12.63		No Hit Found								1	NP_048743	Gly-rich, AGLG (9x); similar to herpesvirus hypothetical protein 5, herpes	61.62	7.82E-09	80%	80%	61--96	57--92
c477R	197986--198198	71	8,501	11.94		No Hit Found								1	NP_048745	a388R	50.83	1.34E-05	78%	78%	2--33	40--71
c478R	198384--198680	99	11,302	10.98		No Hit Found								1	NP_048748	a391R	146.36	2.39E-34	76%	77%	1--99	1--95
c480L	199076--198861	72	8,047	6.73		No Hit Found									No Hit Found							
c481R	199524--199727	68	7,583	6.49		No Hit Found									No Hit Found							



Gene Name	Genome Position	A.A. length	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to
c482L	199906-199709	66	8,079	6.08		No Hit Found									No Hit Found							
c488R	202540-202737	66	7,352	5.69		No Hit Found									No Hit Found							
c489R	202826-203029	68	8,180	8.38		No Hit Found									No Hit Found							
c495L	205972-205670	101	10,913	4.64		No Hit Found									No Hit Found							
c499L	207957-207397	187	19,795	13.59		No Hit Found									No Hit Found							
c500L	208594-208388	69	7,216	4.54		No Hit Found									No Hit Found							
c501L	208895-209098	68	9,523	11.30		No Hit Found									No Hit Found							
c502R	209135-208896	80	7,695	10.89		No Hit Found									No Hit Found							
c505R	210028-210228	67	7,716	8.19		No Hit Found								1	NP_048712	a355L	69.71	2.83E-11	59%	62%	2-65	14-70
c508R	210244-210450	69	8,191	7.34		No Hit Found									No Hit Found							
c508R	211235-211603	123	13,737	10.64		No Hit Found								1	NP_048766	a409R	73.94	1.52E-12	82%	86%	1-46	37-82
c511L	212597-212268	110	12,766	10.20		No Hit Found									No Hit Found							
c514R	213721-213972	84	9,652	8.82		No Hit Found									No Hit Found							
c516R	214835-215071	79	8,394	10.76		No Hit Found									No Hit Found							
c517R	215109-215402	98	9,869	6.50		No Hit Found									No Hit Found							
c520R	216571-216768	66	8,038	7.12		No Hit Found									No Hit Found							
c524L	218761-218330	144	17,685	6.94		No Hit Found									No Hit Found							
c525L	218547-218350	66	7,822	7.78		No Hit Found									No Hit Found							
c526R	218409-218711	101	11,774	10.92		No Hit Found									No Hit Found							
c530R	219598-219834	79	10,083	12.42		No Hit Found									No Hit Found							
c533R	222712-222963	84	10,680	11.63		No Hit Found									No Hit Found							
c534L	222970-222776	65	7,619	4.64		No Hit Found									No Hit Found							
c536R	223213-223422	70	7,946	11.50		No Hit Found									No Hit Found							
c541R	224827-225084	86	10,233	11.09		No Hit Found									No Hit Found							
c544R	225889-226092	68	8,318	10.15		No Hit Found								1	NP_048799	a442R	74.33	1.15E-12	47%	70%	1-65	2-66
c548L	228137-227904	78	8,991	8.19		No Hit Found									No Hit Found							
c549L	228274-228053	74	9,185	12.38		No Hit Found									No Hit Found							
c550R	228515-228820	102	11,578	10.84		No Hit Found									No Hit Found							
c552R	228980-229195	72	7,853	9.49		No Hit Found								1	NP_048803	a446R	102.45	3.88E-21	89%	91%	17-72	1-56
c553R	229460-229654	65	7,222	11.63		No Hit Found								1	NP_048804	a447R	126.72	1.97E-28	95%	98%	1-65	35-99
c555L	230640-230437	68	8,309	9.20		No Hit Found									No Hit Found							
c557L	231355-231155	67	7,965	8.72		No Hit Found									No Hit Found							
c561R	233698-233922	75	8,478	5.50		No Hit Found								1	NP_048810	a453R	88.58	5.96E-17	64%	66%	1-75	15-89
c563R	234730-235155	142	15,769	11.78		No Hit Found								1	NP_048814	a457R	115.16	5.90E-25	78%	80%	32-107	1-76
c564L	235249-235001	83	10,029	11.39		No Hit Found								1	NP_048815	a458L	107.07	1.58E-22	60%	74%	1-83	1-83
c565R	235008-235334	109	13,234	6.23		No Hit Found									No Hit Found							
c568R	235497-235772	92	10,922	10.74		No Hit Found									No Hit Found							
c567R	235840-236046	69	7,712	11.10		No Hit Found									No Hit Found							
c572R	239382-239621	80	9,499	5.58		No Hit Found									No Hit Found							
c574L	241380-241135	82	8,847	9.44		No Hit Found								1	NP_048825	a469L	54.30	1.22E-06	42%	52%	8-82	3-76
c576R	242004-242207	68	8,156	12.37		No Hit Found									No Hit Found							
c578L	243006-242806	67	7,615	7.28		No Hit Found									No Hit Found							
c581R	244422-244925	168	20,013	9.69		No Hit Found								1	NP_048835	Phe-rich	63.16	3.42E-09	34%	36%	1-107	1-107
c582L	244885-244649	79	9,482	12.03		No Hit Found									No Hit Found							
c585R	245549-245776	76	8,634	8.17		No Hit Found									No Hit Found							
c589L	247798-247472	109	12,914	6.61		No Hit Found									No Hit Found							
c591L	248180-247986	65	7,590	8.15		No Hit Found									No Hit Found							
c592L	248677-248378	100	11,404	10.13		No Hit Found									No Hit Found							
c594L	248861-248628	78	9,004	8.82		No Hit Found									No Hit Found							
c598R	250572-250826	85	9,909	9.04		No Hit Found									No Hit Found							
c599L	251481-251077	135	14,606	10.36		No Hit Found								1	NP_048854	Pro-rich, IPPPNMSLPLS (3x)	108.61	5.50E-23	52%	52%	1-120	1-120
c601L	251366-251136	77	9,761	8.11		No Hit Found								1	NP_048855	a499L	56.23	3.26E-07	88%	92%	1-27	1-27
c603R	251958-252380	141	12,711	9.35		No Hit Found									No Hit Found							
c606R	253462-253725	88	10,755	8.05		No Hit Found								1	NP_048860	a504R	176.79	1.65E-43	90%	95%	1-87	1-87
c607L	253954-253745	70	8,193	10.53		No Hit Found									No Hit Found							
c609R	254024-254254	77	9,572	8.82		No Hit Found									No Hit Found							
c610R	254295-254501	69	8,436	11.12		No Hit Found								1	NP_048863	a507R	87.43	1.30E-16	60%	78%	1-65	3-67
c611R	254634-254846	71	8,705	11.52		No Hit Found								1	NP_048863	a507R	77.80	1.03E-13	57%	71%	1-71	116-186

Gene Name	Genome Position	A.A. length	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identitiv	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identitiv	% Positive	Query from-to	Hit from-to
c612R	255250-255477	76	8,867	10.98		No Hit Found								1	NP_048866	a510R	93.50	1.85E-18	89%	92%	13-67	2-56
c614L	256042-255743	100	11,629	11.36		No Hit Found									No Hit Found							
c617R	256457-256780	108	13,055	3.84		No Hit Found									No Hit Found							
c623R	260350-260727	126	14,999	10.45		No Hit Found									No Hit Found							
c625R	260645-260917	91	10,217	4.48		No Hit Found								1	NP_048503	a155R	83.57	1.88E-15	61%	79%	16-82	27-93
c626R	261053-261349	99	12,307	11.85		No Hit Found									No Hit Found							
c628R	261049-262200	84	9,930	6.00		No Hit Found									No Hit Found							
c631L	262842-262534	103	11,102	6.48		No Hit Found								1	NP_048874	a518R	123.64	1.63E-27	64%	72%	1-98	3-100
c631L														2	NP_048885	a529L	112.85	2.88E-24	86%	88%	31-97	1-67
c631L														3	NP_049041	a685R	52.37	4.62E-06	53%	59%	46-97	15-66
c633L	263400-263116	95	10,738	7.34		No Hit Found									No Hit Found							
c637R	265541-265768	76	9,000	8.21		No Hit Found									No Hit Found							
c639L	267680-267480	67	7,432	11.01		No Hit Found									No Hit Found							
c640R	267684-267893	70	7,788	8.08		No Hit Found									No Hit Found							
c642R	268730-268954	75	9,167	10.45		No Hit Found									No Hit Found							
c646R	269556-269795	80	8,610	11.46		No Hit Found									No Hit Found							
c647R	270148-270354	69	8,068	10.67		No Hit Found									No Hit Found							
c649R	270408-270824	139	15,586	10.08		No Hit Found									No Hit Found							
c650R	270560-270859	100	12,308	8.19		No Hit Found									No Hit Found							
c653R	272131-272412	94	10,313	4.45		No Hit Found									No Hit Found							
c654R	272479-272742	88	9,942	7.69		No Hit Found									No Hit Found							
c655R	273079-273276	66	7,138	4.14		No Hit Found								1	NP_048897	a541R	59.69	2.94E-08	51%	62%	3-66	34-96
c656R	274303-274548	82	8,845	4.71		No Hit Found									No Hit Found							
c657L	275164-274937	76	9,244	11.55		No Hit Found									No Hit Found							
c659L	276357-275908	150	17,931	8.50		No Hit Found									No Hit Found							
c660L	276176-275958	73	8,154	10.82		No Hit Found								1	NP_048901	a545L	132.11	4.74E-30	87%	91%	1-73	1-73
c662R	277646-277912	89	10,287	5.06		No Hit Found									No Hit Found							
c664R	278090-278368	93	10,919	6.62		No Hit Found								1	NP_048905	a549R	74.33	1.14E-12	41%	62%	1-80	1-80
c665R	278744-278977	78	9,229	6.35		No Hit Found								1	NP_048906	a550R	77.80	1.04E-13	44%	74%	1-78	55-132
c666R	279068-279433	122	14,344	6.84		No Hit Found									No Hit Found							
c668L	280152-279628	175	21,526	9.79		No Hit Found									No Hit Found							
c671R	280659-281009	117	13,112	10.68		No Hit Found									No Hit Found							
c672R	280985-281263	93	10,824	8.37		No Hit Found								1	NP_048911	a555R	168.32	5.78E-41	89%	91%	1-93	1-93
c673R	281654-281881	76	8,378	8.06		No Hit Found									No Hit Found							
c674L	282272-282066	69	7,971	10.96		No Hit Found									No Hit Found							
c677R	283694-284077	128	14,105	6.98		No Hit Found								1	NP_048916	a560R	72.79	3.33E-12	65%	75%	3-62	45-104
c679R	284289-284639	117	13,356	4.85		No Hit Found									No Hit Found							
c680R	284566-284850	95	10,558	7.72		No Hit Found									No Hit Found							
c682R	285472-285705	78	9,588	11.24		No Hit Found									No Hit Found							
c683R	285888-286115	76	8,753	7.57		No Hit Found								1	NP_048922	a566L	95.13	6.35E-19	95%	95%	35-76	49-90
c684L	286278-286030	83	9,586	12.35		No Hit Found									No Hit Found							
c686L	288667-288263	135	15,524	7.64		No Hit Found								1	NP_048922	a566L	168.70	4.48E-41	88%	88%	1-88	1-90
c689R	290040-290249	70	8,717	8.45		No Hit Found									No Hit Found							
c692L	291082-290816	89	10,577	8.63		No Hit Found									No Hit Found							
c695R	291831-292052	74	8,008	6.65		No Hit Found									No Hit Found							
c697L	292684-292448	79	8,679	10.91		No Hit Found								1	NP_048874	a518R	64.31	1.19E-09	53%	66%	17-78	1-62
c700R	294008-294205	66	7,959	8.96		No Hit Found									No Hit Found							
c702R	294495-294737	81	10,045	12.26		No Hit Found									No Hit Found							
c703L	295008-294775	78	9,649	11.87		No Hit Found								1	NP_048938	a582L	122.87	2.82E-27	78%	85%	1-78	1-78
c704R	295166-295399	78	9,098	11.65		No Hit Found									No Hit Found							
c706R	295636-295863	76	8,209	9.61		No Hit Found									No Hit Found							
c708R	296776-297015	80	9,519	4.84		No Hit Found									No Hit Found							
c709R	297878-298177	100	11,570	11.19		No Hit Found									No Hit Found							
c710R	298147-298341	65	7,526	7.53		No Hit Found								1	NP_048943	a587R	112.08	5.01E-24	80%	89%	1-65	1-65
c711R	298310-298549	80	8,692	12.12		No Hit Found									No Hit Found							
c712R	298822-299517	232	26,620	5.51		No Hit Found								1	NP_048944	a588R	109.38	8.85E-23	50%	68%	1-116	1-116
c713R	299039-299362	108	12,116	10.65		No Hit Found									No Hit Found							
c716L	301023-300682	114	11,519	7.30		No Hit Found								1	NP_048951	a595L	65.86	4.16E-10	62%	68%	1-59	19-82
c717R	300930-301148	73	8,461	11.74		No Hit Found									No Hit Found							

Gene Name	Genome Position	A.A. length	Peptide Mw	pI	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit from-to	
c720R	301999-302544	182	21,575	6.23		No Hit Found									No Hit Found								
c721R	302351-302581	77	8,832	10.50		No Hit Found								1	NP_048956	a600R	95.52	4.85E-19	67%	75%	3-76	11-81	
c724L	303571-303308	88	10,598	5.09		No Hit Found									No Hit Found								
c730R	306186-306458	91	10,984	9.52		No Hit Found								1	NP_048966	a610R	173.71	1.38E-42	89%	89%	1-91	1-91	
c732R	307630-307887	86	9,951	6.95		No Hit Found									No Hit Found								
c734R	308977-309249	91	9,847	9.69		No Hit Found								1	NP_048972	a616R	116.32	2.62E-25	62%	67%	2-91	4-93	
c738R	310936-311184	83	9,070	5.59		No Hit Found									No Hit Found								
c743R	313791-314033	81	10,084	11.26		No Hit Found									No Hit Found								
c746L	315067-314846	74	8,396	10.19		No Hit Found									1	NP_048982	a626L	164.85	6.57E-40	100%	100%	1-74	1-74
c749R	317565-317786	74	8,495	11.36		No Hit Found									1	NP_048986	a630R	95.13	6.39E-19	67%	67%	1-74	1-74
c750R	317883-318134	84	9,368	10.23		No Hit Found									No Hit Found								
c751L	318217-317990	76	8,645	9.54		No Hit Found									No Hit Found								
c752R	319348-319650	101	11,949	9.40		No Hit Found									No Hit Found								
c758L	321419-321105	105	12,528	4.79		No Hit Found									No Hit Found								
c760L	321983-321588	132	14,744	9.00		No Hit Found								1	NP_048995	a639L	250.37	1.19E-65	95%	96%	1-132	1-132	
c761R	321812-322048	79	8,848	11.89		No Hit Found								1	NP_048996	a640R	152.14	4.33E-36	94%	97%	1-79	1-79	
c762L	322373-322119	85	9,710	11.11		No Hit Found								1	NP_048997	a641L	168.32	5.94E-41	96%	97%	1-85	1-85	
c764L	323418-323110	103	11,914	11.57		No Hit Found									No Hit Found								
c768R	325179-325496	106	12,145	7.92		No Hit Found									No Hit Found								
c769L	325587-325351	79	9,349	11.86		No Hit Found								1	NP_049011	a655L	73.17	2.56E-12	57%	70%	9-78	1-70	
c770R	325499-325759	87	11,038	11.44		No Hit Found									No Hit Found								
c775R	327489-327767	93	43,880	8.00		No Hit Found									No Hit Found								
c776R	327685-327906	74	8,238	4.18		No Hit Found								1	NP_048503	a155R	84.34	1.13E-15	66%	76%	5-73	18-84	
c777L	328022-327756	89	9,671	10.81		No Hit Found									No Hit Found								
c778R	327854-328186	111	12,186	8.25		No Hit Found									No Hit Found								
c779L	328307-328026	94	11,341	12.45		No Hit Found								1	NP_048504	a156L	56.61	2.44E-07	39%	59%	6-93	19-107	
c780L	328556-328332	75	8,562	12.23		No Hit Found									No Hit Found								
c782L	329124-328930	65	7,536	7.92		No Hit Found									No Hit Found								
c784R	329322-329543	74	8,289	8.07		No Hit Found									No Hit Found								
c786R	330130-330351	74	8,035	10.78		No Hit Found									No Hit Found								
c787R	330745-331128	128	14,130	7.85		No Hit Found									No Hit Found								
c789R	332984-333271	96	11,065	7.85		No Hit Found								1	NP_049023	similar to Chlorella virus CVK2 unknown ORF, corresponds to GenBank #	189.12	3.24E-47	91%	97%	1-96	1-96	
c790R	333374-333568	65	7,433	7.72		No Hit Found								1	NP_049024	similar to Chlorella virus CVK2 unknown ORF, corresponds to GenBank #	125.18	5.72E-28	87%	93%	1-65	1-65	
c791R	333483-333698	72	8,040	11.46		No Hit Found								1	NP_049025	similar to Chlorella virus CVK2 unknown ORF, corresponds to GenBank #	149.83	2.12E-35	100%	100%	1-72	12-83	
c792R	334913-335278	122	14,173	9.90		No Hit Found								1	NP_049026	similar to Chlorella virus CVK2 unknown ORF, corresponds to GenBank #	223.79	1.16E-57	87%	92%	1-122	1-122	
c794L	336130-335867	88	10,592	4.66		No Hit Found									No Hit Found								
c795R	336125-336397	91	10,499	11.12		No Hit Found									No Hit Found								
c797R	336198-336527	110	13,279	10.96		No Hit Found									1	NP_048630	similar to PBCV-1 ORF a80L, corresponds to GenBank Accession Numbe	59.31	3.82E-08	48%	66%	49-110	3-64
c799L	337668-337270	133	14,418	6.65		No Hit Found									1	NP_049033	a677L	115.16	5.93E-25	76%	82%	1-69	1-75
c801R	339024-339272	83	9,941	7.92		No Hit Found									No Hit Found								
c803R	339346-339963	206	23,724	7.94		No Hit Found								1	NP_048354	a6L	67.40	3.02E-10	47%	67%	74-143	1-71	
c804R	339521-339748	76	8,121	9.74		No Hit Found									No Hit Found								
c805R	340292-340516	75	8,658	4.17		No Hit Found									No Hit Found								
c807R	340362-340592	77	8,449	10.19		No Hit Found									No Hit Found								
c808R	340919-341197	93	10,890	10.90		No Hit Found									No Hit Found								
c810R	341935-342282	116	13,092	5.54		No Hit Found								1	NP_048354	a6L	57.38	1.47E-07	51%	72%	40-86	1-47	
c811L	342680-342471	70	8,233	5.13		No Hit Found									No Hit Found								
c812R	342546-342746	67	7,515	7.18		No Hit Found									1	NP_049046	identical to PBCV-1 terminal repeat ORF, corresponds to GenBank Acces	58.54	6.53E-08	50%	68%	1-60	12-66
c813L	343070-342846	75	8,636	6.66		No Hit Found									No Hit Found								
c814L	343967-343539	143	16,443	10.82		No Hit Found									No Hit Found								