

February 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

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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.  
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## SUPPLEMENTARY DATA FOR

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

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**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

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## 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	44108-43725	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
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	% 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
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								