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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”: Appendix A: Gene Names b002R – b797R

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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 A: Gene Names b002R – b797R

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	
b002R	1094-1315	74	8.633	7.51		No Hit Found									No Hit Found								
b005L	2238-1993	82	8.912	5.03		No Hit Found								1	NP_049046	identical to PBCV-1 terminal repeat ORF, corresponds to GenBank Accession Number M55319	97.06	1.64E-19	64%	75%	6-82	2-77	
b007R	2490-2783	98	11.941	6.93		No Hit Found									No Hit Found								
b009L	3809-3489	107	12.109	8.91		No Hit Found									No Hit Found								
b011R	4401-4643	81	9.618	10.10		No Hit Found									No Hit Found								
b012L	4938-4663	92	10.958	5.82		No Hit Found									No Hit Found								
b014R	5639-5839	67	8.180	7.70		No Hit Found									No Hit Found								
b015R	5727-5945	73	8.112	10.74		No Hit Found									No Hit Found								
b017R	6534-6788	85	9.952	8.18		No Hit Found									No Hit Found								
b019R	7503-7757	85	9.543	11.48		No Hit Found									No Hit Found								
b020R	7886-8089	68	8.041	9.50		No Hit Found									No Hit Found								
b021R	8099-8404	102	11.885	5.08		No Hit Found									No Hit Found								
b023L	10098-9820	93	10.453	10.95		No Hit Found									No Hit Found								
b025R	11545-11772	76	8.823	5.58		No Hit Found									No Hit Found								
b026R	11772-12020	83	9.549	6.77		No Hit Found									No Hit Found								
b028L	12034-11801	78	8.798	12.04		No Hit Found									No Hit Found								
b029R	11941-12279	113	10.711	5.51	1	pfam05642	Sporozoite_P67. Sporozoite P67 surface antigen. This family consists of several Theileria P67 surface antigens. A stage specific surface antigen of Theileria parva, p67, is the basis for the development of an anti-sporozoite vaccine for the control of East Coast fever (ECF) in cattle. The antigen has been shown to contain five distinct linear peptide sequences recognised by sporozoite-neutralising murine monoclonal antibodies.	42.86	5.94E-05	44%	50%	36-107	180-250		No Hit Found								
b030L	12532-12290	81	9.242	9.03		No Hit Found									No Hit Found								
b032L	13424-13227	66	7.378	12.02		No Hit Found									No Hit Found								
b035L	15050-14856	65	7.534	11.07		No Hit Found									No Hit Found								
b036R	16436-16714	93	10.260	4.54		No Hit Found									No Hit Found								
b037R	16808-17014	69	7.533	4.11		No Hit Found									No Hit Found								
b038R	17756-17971	72	8.118	4.88		No Hit Found									No Hit Found								
b041R	21050-21361	104	11.414	7.21		No Hit Found									No Hit Found								
b042R	22389-22667	93	11.857	12.12		No Hit Found									No Hit Found								
b043R	22421-22840	140	15.312	6.34		No Hit Found									No Hit Found								
b044R	23459-23809	117	12.727	4.77		No Hit Found									No Hit Found								
b045R	23930-24172	81	8.902	4.36		No Hit Found									No Hit Found								
b046R	24182-24586	135	14.731	4.23		No Hit Found									No Hit Found								
b048L	26325-26113	71	8.650	8.14		No Hit Found									No Hit Found								
b049R	26791-26985	65	8.149	12.09		No Hit Found									No Hit Found								
b050R	26811-27242	144	15.584	4.13		No Hit Found									No Hit Found								
b051R	27309-27836	176	18.677	4.12		No Hit Found									1	AAC39774	hepatitis A virus cellular receptor 1 long form	57.38	2.14E-07	28%	36%	2-152	164-320
															2	AAC39772	hepatitis A virus cellular receptor 1 short form	57.38	2.14E-07	28%	36%	2-152	159-315
															3	AAC39772	hepatitis A virus cellular receptor 1 long form	56.23	4.76E-07	27%	36%	2-152	164-316
															4	AAC39771	hepatitis A virus cellular receptor 1 short form	56.23	4.76E-07	27%	36%	2-152	159-311
															5	BAA21556	hepatitis A virus receptor	55.45	8.12E-07	29%	34%	2-152	171-302
															6	CAA68906	HAVcr-1 protein	54.68	1.38E-06	30%	35%	16-152	159-293
b052R	27861-28160	100	10.798	4.22		No Hit Found									No Hit Found								
b053R	28332-28574	81	8.934	4.36		No Hit Found									No Hit Found								
b054R	28584-28988	135	14.622	4.51		No Hit Found									No Hit Found								
b056R	29612-29983	124	13.368	3.94		No Hit Found									No Hit Found								
b057R	30320-30517	66	7.111	3.78		No Hit Found									No Hit Found								
b058R	31124-31525	134	15.086	6.88		No Hit Found									No Hit Found								
b060L	32920-32651	90	10.946	9.40		No Hit Found									No Hit Found								
b062L	33873-33604	90	10.316	10.95		No Hit Found									No Hit Found								
b063L	34102-33851	84	9.875	10.94		No Hit Found									No Hit Found								
b064L	34235-34002	78	8.999	9.54		No Hit Found									No Hit Found								
b065R	34224-34457	78	9.097	11.13		No Hit Found									No Hit Found								
b066L	34551-34315	79	8.906	11.19		No Hit Found									No Hit Found								
b067L	34994-34638	119	14.573	10.54		No Hit Found									No Hit Found								
b069L	35893-35486	136	12.300	4.42		No Hit Found									1	NP_048385	A37L	177.95	7.36E-44	77%	92%	18-119	4-105
b071R	36206-36430	75	9.127	8.06		No Hit Found									1	NP_048391	a43R	161.38	7.24E-39	93%	96%	1-75	1-75
b072L	36671-36417	85	9.942	8.06		No Hit Found									1	NP_048520	a172L	88.58	5.98E-17	50%	71%	4-85	4-86
b079R	40524-40886	121	14.746	8.63		No Hit Found									1	NP_048400	a52R	138.66	4.91E-32	74%	77%	39-121	1-83
b081R	41058-41315	86	9.916	10.96		No Hit Found									No Hit Found								
b082L	41518-41318	67	8.187	11.43		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
b084R	42395-42673	93	10,237	11.20		No Hit Found									No Hit Found							
b085R	42643-42984	114	13,326	7.05		No Hit Found									No Hit Found							
b089R	45133-45387	85	9,619	10.52		No Hit Found									No Hit Found							
b090R	45616-45858	81	8,612	11.27		No Hit Found								1	NP_048874 a518R		81.65	7.14E-15	61%	65%	1-74	1-75
b092R	46155-46457	101	11,907	4.80		No Hit Found									No Hit Found							
b093R	46342-46542	67	7,428	11.66		No Hit Found									No Hit Found							
b095L	46999-46781	73	8,199	10.86		No Hit Found									No Hit Found							
b096L	47248-47033	72	7,961	11.22		No Hit Found									No Hit Found							
b097L	47417-47109	103	12,209	5.28		No Hit Found									No Hit Found							
b098R	47125-47394	90	10,283	12.37		No Hit Found									No Hit Found							
b100L	47933-47526	136	15,468	5.10		No Hit Found									No Hit Found							
b101L	48129-47833	99	11,743	10.52		No Hit Found									No Hit Found							
b102L	48497-48024	158	18,278	6.91		No Hit Found								1	NP_048417	contains Gly-rich Gx motif LGGGLG (GX); contains type I hydrophobic transmembrane sequence; contains protein splicing signature; similar to Arabidopsis Gly-rich protein, corresponds to Swiss-Prot Accession Number P27483	106.30	2.89E-22	60%	78%	77-158	1-82
b105L	50272-49586	229	26,576	6.29		No Hit Found								1	NP_048503 a155R		88.97	1.20E-16	58%	76%	6-83	14-94
b106R	49716-49982	89	10,581	12.10		No Hit Found									No Hit Found							
b107L	51327-50464	288	34,170	6.02	1	pfam03016	Exostosin, Exostosin family. The EXT family is a family of tumour suppressor genes. Mutations of EXT1 on 8q24.1, EXT2 on 11p11-13, and EXT3 on 15q have been associated with the autosomal dominant disorder known as hereditary multiple exostoses (HME). This is the most common known skeletal dysplasia. The chromosomal locations of other EXT genes suggest association with other forms of neoplasia. EXT1 and EXT2 have both been shown to encode a heparan sulphate polymerase with both D-glucuronyl (GlcA) and N-acetyl-D-glucosaminoglycan (GlcNAc) transferase activities. The nature of the defect in heparan sulphate biosynthesis in HMF is unclear	35.80	8.04E-03	19%	46%	164-229	206-275	1	NP_048423 A75L		520.39	2.45E-146	87%	96%	9-288	1-280
b111R	51462-51686	75	9,216	7.34		No Hit Found									No Hit Found							
b112R	51647-51868	74	8,973	11.96		No Hit Found									No Hit Found							
b114L	52130-51936	65	7,804	11.98		No Hit Found								1	NP_048424 a76L		63.16	2.67E-09	63%	75%	28-65	55-103
b119L	55073-54867	69	7,758	7.69		No Hit Found									No Hit Found							
b121L	55797-55411	129	15,078	9.57		No Hit Found								1	NP_048428 a80L		83.19	2.45E-15	56%	73%	4-78	59-133
														2	NP_048808	similar to PBCV-1 ORF a80L, encoded by GenBank Accession Number U17055	52.37	4.64E-06	55%	77%	1-45	56-100
b123R	56388-56660	101	11,832	4.77		No Hit Found									No Hit Found							
b125R	56984-57238	85	9,982	10.33		No Hit Found									No Hit Found							
b127L	57923-57681	81	9,810	10.44		No Hit Found									No Hit Found							
b128L	58104-57910	65	7,040	11.12		No Hit Found								1	NP_048434 a86L		107.46	1.23E-22	83%	86%	1-64	1-66
b129L	58339-58139	67	8,131	12.07		No Hit Found									No Hit Found							
b131R	58365-58580	72	8,257	12.41		No Hit Found									No Hit Found							
b132L	58974-58741	78	8,912	11.90		No Hit Found									No Hit Found							
b134L	59114-58806	103	12,582	7.81		No Hit Found									No Hit Found							
b135L	59214-59017	66	7,496	6.31		No Hit Found									No Hit Found							
b138R	61694-61936	81	9,887	12.34		No Hit Found									No Hit Found							
b140L	62904-62710	65	6,945	11.08		No Hit Found									No Hit Found							
b141L	63313-62990	108	12,676	7.21		No Hit Found									No Hit Found							
b142L	64323-63958	122	14,435	6.88		No Hit Found									No Hit Found							
b144L	64525-64286	80	9,314	11.01		No Hit Found								1	NP_048449 a101L		80.49	1.60E-14	65%	87%	1-55	33-87
b145L	65092-64772	107	13,059	7.97		No Hit Found									No Hit Found							
b146L	65688-65348	107	12,914	10.36		No Hit Found									No Hit Found							
b147L	66322-65981	114	12,774	9.71		No Hit Found								1	NP_048450 a102L		145.98	3.16E-34	64%	72%	1-114	1-114
b149L	66692-66306	129	15,406	6.16		No Hit Found								1	NP_048452 a104L		87.81	9.96E-17	43%	65%	1-96	1-96
b151R	67201-67521	107	12,414	6.23		No Hit Found								1	NP_048454 a106R		97.06	1.67E-19	48%	67%	1-107	15-121
b152R	67392-67622	77	9,392	9.18		No Hit Found									No Hit Found							
b153R	67662-67856	65	8,103	10.69		No Hit Found									No Hit Found							
b155R	68327-68539	71	8,476	8.22		No Hit Found								1	NP_048456 a108R		62.39	4.46E-09	42%	67%	1-71	1-71
b156R	68717-68917	67	8,208	4.17		No Hit Found									No Hit Found							
b158R	69009-69377	123	14,530	7.98		No Hit Found									No Hit Found							
b160L	70413-70195	73	8,003	8.94		No Hit Found								1	NP_048460 a112L		142.12	4.58E-33	97%	97%	1-73	1-73
b161R	70743-71039	99	11,535	8.53		No Hit Found								1	NP_048464 a116R		114.01	1.31E-24	74%	79%	1-81	1-81
b162L	71629-71201	143	16,697	6.14		No Hit Found								1	NP_048465 a117L		177.95	7.38E-44	63%	80%	7-136	1-130
b164L	72869-72432	146	17,221	7.77		No Hit Found									No Hit Found							
b166L	73854-73651	68	7,204	7.15		No Hit Found									No Hit Found							
b167R	73818-74012	65	7,455	11.31		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
b257R	112119-112529	137	16.216	11.53		No Hit Found																
b259L	113388-113164	75	8.878	10.94		No Hit Found																
b260R	113323-113523	67	8.127	11.41		No Hit Found																
b262R	117035-117439	135	16.277	6.23		No Hit Found																
b263R	117285-117485	67	7.828	10.53		No Hit Found																
b265R	117803-118018	72	8.315	7.94		No Hit Found								1	NP_048541 a194R		117.09	1.55E-25	80%	83%	1-67	1-67
b266R	117834-118028	65	7.213	6.52		No Hit Found								1	NP_048545 a198R		78.95	4.59E-14	47%	72%	1-72	1-72
b266R	117834-118028	65	7.213	6.52		No Hit Found								1	NP_048544 a197R		93.59	1.84E-18	77%	83%	1-62	31-92
b269R	118429-118767	113	13.193	9.76		No Hit Found																
b270L	119236-118970	89	10.827	10.28		No Hit Found																
b275L	120539-120330	70	7.143	9.46		No Hit Found								1	NP_048551 a204L		124.02	1.25E-27	91%	92%	1-70	1-70
b276L	121069-120797	91	10.102	4.78		No Hit Found																
b279L	121992-121729	88	10.438	5.13		No Hit Found																
b280L	122077-121781	99	12.015	10.24		No Hit Found																
b281L	122298-122041	86	9.877	5.90		No Hit Found																
b282L	122941-122702	80	8.645	9.12		No Hit Found																
b287L	124767-124498	90	10.697	11.24		No Hit Found																
b290R	127120-127383	88	10.012	9.40		No Hit Found																
b293R	128201-128839	213	24.250	9.78		No Hit Found								1	NP_048578 A230R		310.07	2.85E-83	79%	91%	19-211	3-196
b294R	128500-128799	100	11.742	8.53		No Hit Found																
b295L	128706-128512	65	7.395	9.43		No Hit Found																
b299R	130109-130351	81	9.106	6.50		No Hit Found																
b300R	130765-130971	69	8.280	10.25		No Hit Found								1	NP_048580 a232R		73.17	2.55E-12	58%	73%	6-65	6-65
b301L	131445-131212	78	9.722	10.37		No Hit Found																
b304R	131655-131891	79	9.397	5.59		No Hit Found								1	NP_048583 a235R		70.09	2.17E-11	46%	64%	1-75	1-75
b306L	132505-132089	139	16.463	6.10		No Hit Found																
b307R	132274-132567	98	11.648	11.76		No Hit Found																
b308L	132988-132749	80	9.422	9.59		No Hit Found																
b309L	133471-133082	130	16.215	8.42		No Hit Found																
b311L	134132-133839	98	11.592	8.01		No Hit Found																
b312L	134378-134160	73	8.907	10.68		No Hit Found																
b313L	134482-134234	83	9.384	4.25		No Hit Found								1	NP_048503 a155R		81.26	9.27E-15	52%	77%	11-82	22-93
b315R	134867-135145	93	11.173	8.70		No Hit Found																
b317L	136156-135806	117	13.667	5.15		No Hit Found								1	NP_048590 a242L		174.48	8.20E-43	74%	79%	1-117	1-117
b318L	136446-136159	96	10.473	10.81		No Hit Found																
b319L	136869-136612	86	9.936	8.09		No Hit Found																
b320L	136906-136649	86	9.952	9.45		No Hit Found																
b321L	137268-136969	100	11.250	10.05		No Hit Found																
b325R	139886-140236	117	13.791	6.49		No Hit Found																
b326R	140005-140223	73	8.789	10.24		No Hit Found																
b327L	140436-140149	96	11.149	11.95		No Hit Found																
b328R	140472-140714	81	8.953	8.07		No Hit Found																
b329R	140783-141151	123	14.325	10.43		No Hit Found																
b330R	140919-141173	85	9.507	6.49		No Hit Found																
b332L	142200-141823	126	15.612	10.02		No Hit Found																
b333L	142088-141870	73	8.030	11.07		No Hit Found																
b335R	142847-143104	86	10.131	10.16		No Hit Found																
b337L	144046-143831	72	7.897	8.66		No Hit Found																
b338R	143894-144286	131	15.935	11.93		No Hit Found																
b340R	144567-144782	72	8.568	8.19		No Hit Found								1	NP_049004 a648L		55.84	4.16E-07	45%	55%	1-69	1-66
b343L	145670-145419	84	10.506	9.57		No Hit Found								1	NP_048603 a252aL		90.51	1.58E-17	66%	80%	25-84	25-84
b345R	146532-146744	71	8.555	7.43		No Hit Found																
b347R	147171-147377	69	7.951	9.15		No Hit Found																
b351R	148536-148856	107	11.855	8.82		No Hit Found																
b352R	148738-148965	76	8.919	8.38		No Hit Found								1	NP_048620 a266R		56.23	3.27E-07	47%	60%	1-69	15-83
b353R	148965-149192	76	8.794	7.69		No Hit Found																
b355R	149131-149382	84	9.507	11.57		No Hit Found								1	NP_048624 a270R		85.11	6.64E-16	64%	69%	1-68	1-68
b356R	149313-149915	201	23.988	6.34		No Hit Found								1	NP_048626 a272R		71.63	1.50E-11	52%	74%	28-90	5-67
b360L	151701-151483	73	7.955	7.90		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
b362L	152549-152340	70	7.769	7.30		No Hit Found									No Hit Found							
b363L	153719-153282	146	15.325	3.75		No Hit Found									No Hit Found							
b364R	153945-154202	86	9.586	7.34		No Hit Found								1	NP_048635 a281R		130.18	1.79E-29	78%	83%	7-86	6-85
b366R	154349-154564	72	8.863	10.19		No Hit Found								1	NP_048633 a279R		161.77	5.39E-39	97%	97%	1-72	1-72
b367R	155445-155723	93	10.257	3.62		No Hit Found								1	NP_048634 a280R		176.02	2.77E-43	94%	94%	1-93	1-93
b369L	156439-156239	67	7.696	11.51		No Hit Found								1	NP_048637 a283L		134.81	7.17E-31	92%	95%	1-67	1-67
b372R	158851-159141	97	10.279	8.07		No Hit Found									No Hit Found							
b373R	159166-159447	94	10.984	10.49		No Hit Found								1	NP_048639 a285R		110.92	1.09E-23	91%	93%	1-58	1-58
b374L	159688-159353	112	12.759	9.83	1	cd00204	ANK, ankyrin repeats; ankyrin repeats mediate protein-protein interactions in very diverse families of proteins. The number of ANK repeats in a protein can range from 2 to over 20 (ankyrins, for example). ANK repeats may occur in combinations with other types of domains. The structural repeat unit contains two antiparallel helices and a beta-hairpin, repeats are stacked in a superhelical arrangement; this alignment contains 4 consecutive repeats	66.64	3.55E-12	41%	60%	2-93	21-112	1	1NOR_A	Chain A. 4ank: A Designed Ankyrin Repeat Protein With Four Identical Consensus Repeats	71.63	7.37E-12	39%	63%	1-93	15-107
					2	COG0666	Arp, FOG: Ankyrin repeat [General function prediction only].	45.65	8.05E-06	34%	50%	2-99	87-192	2	AA033811	ankyrin repeat protein mbp3 5	68.94	4.78E-11	39%	65%	5-83	31-119
														3	EAL87814	NAZHT domain protein, putative	67.78	1.06E-10	38%	58%	2-92	100-1190
														4	AAH73370	MGCC80792 protein	66.63	2.37E-10	39%	60%	3-91	512-600
														5	AAO37830	mind bomb	65.08	6.90E-10	38%	60%	3-91	512-600
														6	NP_065825	mindbomb homolog 1	64.31	1.18E-09	38%	59%	3-91	512-600
														7	XP_512056	PREDICTED: similar to mind bomb	64.31	1.18E-09	38%	59%	3-91	481-549
														8	XP_613236	PREDICTED: similar to mindbomb homolog 1	64.31	1.18E-09	38%	59%	3-91	582-670
														9	XP_419157	PREDICTED: similar to mindbomb homolog 1; ubiquitin ligase mind bomb; DAPK-interacting protein 1	64.31	1.18E-09	38%	59%	3-91	601-689
														10	AAN18023	MINDBOMB: ubiquitin E3 ligase	64.31	1.18E-09	38%	59%	3-91	503-591
b375L	160259-159723	179	21.715	7.26		No Hit Found									No Hit Found							
b376L	160212-159946	89	11.086	12.01		No Hit Found									No Hit Found							
b379R	160441-160698	86	9.916	10.96		No Hit Found									No Hit Found							
b380L	160901-160701	67	8.187	11.43		No Hit Found									No Hit Found							
b382R	161778-162056	93	10.237	11.20		No Hit Found									No Hit Found							
b383R	162026-162367	114	13.310	7.05		No Hit Found									No Hit Found							
b384L	163226-162792	145	15.888	4.78		No Hit Found									No Hit Found							
b386L	163670-163392	93	10.511	8.11		No Hit Found									No Hit Found							
b387L	163806-163588	73	8.842	11.23		No Hit Found									No Hit Found							
b390L	165197-164808	130	15.523	7.74		No Hit Found								1	BAA20344	ORF245	105.92	3.52E-22	53%	65%	9-107	145-243
b391L	165036-164818	73	8.906	8.85		No Hit Found									No Hit Found							
b392L	165564-165283	94	11.411	8.02		No Hit Found									No Hit Found							
b394R	165839-166252	138	15.507	11.36		No Hit Found								1	NP_048647	a293R	170.24	1.52E-41	69%	77%	1-123	46-188
b396R	166583-166783	67	7.924	6.08		No Hit Found									No Hit Found							
b398R	168014-168238	75	9.124	5.75		No Hit Found									No Hit Found							
b400L	169541-169287	85	9.924	7.48		No Hit Found									No Hit Found							
b405L	172778-172572	69	8.130	8.95		No Hit Found									No Hit Found							
b406L	173638-172895	248	29.949	12.18		No Hit Found									No Hit Found							
b407R	172923-173879	319	36.489	11.43		No Hit Found								1	NP_048504	a156L	62.39	2.16E-08	45%	53%	34-140	1-103
b409R	173722-174117	132	15.852	12.21		No Hit Found									No Hit Found							
b410L	174082-173795	96	10.948	5.68		No Hit Found								1	NP_048503	a155R	113.62	1.73E-24	62%	79%	1-96	1-94
b412R	174400-174627	76	9.154	10.06		No Hit Found									No Hit Found							
b413R	174847-174907	87	9.675	10.35		No Hit Found									No Hit Found							
b414R	175160-175369	70	7.340	10.81		No Hit Found									No Hit Found							
b415L	175647-175372	92	10.661	11.19		No Hit Found									No Hit Found							
b417L	176281-176033	83	9.737	9.91		No Hit Found									No Hit Found							
b420L	178083-177889	65	7.724	8.65		No Hit Found									No Hit Found							
b422L	178819-178424	132	16.358	11.06		No Hit Found									No Hit Found							
b423R	178624-178851	76	8.992	5.88		No Hit Found									No Hit Found							
b425R	179072-179383	104	12.436	7.29		No Hit Found									No Hit Found							
b427L	180756-180469	96	10.796	12.55		No Hit Found									No Hit Found							
b428L	181027-180821	69	7.976	10.47		No Hit Found								1	NP_048657	a303L	52.37	4.65E-06	44%	55%	1-69	1-66
b436R	185022-185396	125	14.356	8.56		No Hit Found									No Hit Found							
b439R	185526-185840	105	12.536	10.27		No Hit Found								1	NP_048670	A314R	120.17	1.86E-26	71%	80%	24-105	1-80
b442L	187558-187112	149	13.787	4.87		No Hit Found									No Hit Found							
b444R	187222-187593	124	14.391	11.07		No Hit Found									No Hit Found							
b447R	188648-188845	66	7.615	11.29		No Hit Found									No Hit Found							
b448L	189490-189179	104	12.356	6.13		No Hit Found									No Hit Found							
b449L	189953-189657	99	11.408	6.76		No Hit Found									No Hit Found							
b452R	190383-190751	123	15.640	10.35		No Hit Found									No Hit Found							
b454R	190762-190980	73	7.772	10.81		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
b456R	191807-192172	122	14.530	11.17		No Hit Found																
b459R	193084-193281	66	7.742	6.23		No Hit Found																
b464L	196239-196009	77	8.847	4.55		No Hit Found																
b466L	196973-196767	69	7.669	11.30		No Hit Found																
b467L	197178-196843	112	13.300	7.99		No Hit Found																
b470R	198020-198229	70	7.691	10.25		No Hit Found																
b471R	198286-198519	78	9.537	10.82		No Hit Found																
b473L	199573-199373	67	7.293	10.23		No Hit Found																
b474L	199871-199656	72	8.469	4.76		No Hit Found																
b475L	199876-199670	69	7.834	9.63		No Hit Found																
b476R	200290-200508	73	8.106	8.19		No Hit Found																
b478L	201560-201330	77	8.676	11.20		No Hit Found																
b479L	201818-201618	67	7.608	10.07		No Hit Found								1	NP_048687 a331L		134.04	1.22E-30	98%	98%	1-67	1-67
b481L	202819-202559	87	10.765	12.42		No Hit Found								1	NP_048689 PLPRNLLL (4X), SPPPSKP (3X)		57.38	1.47E-07	100%	100%	63-87	275-299
b482R	202586-202927	114	13.269	10.71		No Hit Found																
b483L	203374-203162	71	8.016	4.77		No Hit Found																
b484L	203801-203206	132	15.909	11.80		No Hit Found																
b486R	203549-203761	71	8.603	10.24		No Hit Found																
b489R	205122-205565	148	16.753	11.47		No Hit Found								1	NP_048701 a344R		128.26	6.77E-29	55%	71%	34-148	1-115
b490L	205678-205439	80	9.336	11.87		No Hit Found								1	NP_048702 a345L		80.11	2.09E-14	64%	75%	12-79	28-95
b491R	206097-206432	112	13.489	11.01		No Hit Found																
b493L	206785-206546	80	9.138	4.26		No Hit Found								1	NP_048435 A87R		71.63	7.42E-12	58%	77%	11-72	22-81
b495L	207124-206915	70	8.187	5.47		No Hit Found								1	NP_048704 a347L		84.34	1.10E-15	52%	70%	1-70	1-70
b500R	209963-210292	110	12.244	10.57		No Hit Found																
b501R	210076-210408	111	13.069	11.06		No Hit Found																
b502R	210590-210799	70	7.944	8.52		No Hit Found																
b504L	211098-210889	70	7.708	12.35		No Hit Found																
b505R	210940-211143	68	8.921	12.71		No Hit Found																
b507R	211564-212289	242	26.364	4.58		No Hit Found																
b509L	212669-212454	72	8.113	9.03		No Hit Found																
b510L	212878-212681	66	8.485	8.38		No Hit Found																
b511L	213222-212938	95	10.839	6.91		No Hit Found																
b512L	214583-214365	73	8.307	8.36		No Hit Found																
b513L	214842-214642	67	7.790	7.74		No Hit Found																
b514L	215348-214983	122	13.590	8.20		No Hit Found																
b515L	215996-215754	81	8.912	4.70		No Hit Found																
b516L	216333-215839	165	19.662	10.11		No Hit Found																
b517L	216826-216593	78	9.128	7.98		No Hit Found																
b518L	217097-216813	95	10.029	3.14		No Hit Found																
b520R	217366-217635	90	10.868	10.95		No Hit Found																
b521R	217670-217951	94	10.557	7.87		No Hit Found																
b523R	218670-218969	100	11.265	12.65		No Hit Found								1	NP_048734 a377R		84.34	1.11E-15	54%	62%	14-100	6-91
b526R	219582-220112	177	20.545	10.99		No Hit Found								1	NP_048737 a380R		144.05	1.77E-33	71%	82%	49-149	1-101
b527R	219832-220035	68	7.734	11.11		No Hit Found								1	NP_048738 a381R		127.49	1.14E-28	89%	91%	1-68	9-76
b528L	220152-219955	66	8.133	11.25		No Hit Found																
b530L	220800-220432	123	14.002	10.71		No Hit Found																
b531L	221479-221249	77	9.221	8.69		No Hit Found																
b534R	222934-223146	71	8.458	11.71		No Hit Found								1	NP_048745 a388R		48.14	8.71E-05	75%	75%	2-33	40-71
b535R	223332-223583	84	9.429	10.81		No Hit Found								1	NP_048748 a391R		85.11	6.64E-16	55%	60%	1-84	1-95
b538L	224818-224621	66	8.079	6.08		No Hit Found																
b544R	227430-227627	66	7.352	5.69		No Hit Found																
b545R	227716-227919	68	8.180	8.38		No Hit Found																
b551L	230873-230565	103	11.190	4.98		No Hit Found																
b555L	233373-233167	69	7.186	4.54		No Hit Found																
b557R	234738-234974	79	9.001	10.44		No Hit Found																
b558L	235011-234769	81	9.631	10.72		No Hit Found																
b561R	235907-236272	122	13.676	10.97		No Hit Found								1	NP_048766 a409R		72.79	3.30E-12	80%	86%	1-46	37-82
b563L	236923-236720	68	7.929	11.79		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
b565R	236938-237180	81	9.563	11.58		No Hit Found																
b569L	240525-240130	132	15.171	10.25		No Hit Found								1	NP_048772 a415L		110.54	1.47E-23	80%	86%	34-100	3-69
b572R	241059-241328	90	10.143	11.78		No Hit Found																
b574R	241925-242155	77	9.241	10.31		No Hit Found																
b577L	243362-242958	135	16.597	7.62		No Hit Found																
b578L	243175-242978	66	7.868	7.86		No Hit Found																
b584L	246026-245799	76	9.524	9.59		No Hit Found																
b586R	247244-247477	78	9.952	11.38		No Hit Found																
b588L	247502-247308	65	7.553	4.26		No Hit Found																
b589R	247529-247726	66	7.965	11.91		No Hit Found																
b594R	248630-248881	84	10.180	7.72		No Hit Found																
b599R	251031-251231	67	7.603	10.41		No Hit Found																
b600L	251379-251143	79	8.994	11.47		No Hit Found																
b601R	251179-251382	68	8.238	7.95		No Hit Found																
b603L	252727-252494	78	8.991	8.19		No Hit Found																
b604L	252864-252643	74	9.185	12.38		No Hit Found																
b605R	253105-253410	102	11.578	10.84		No Hit Found																
b607R	253570-253773	68	7.452	9.49		No Hit Found								1	NP_048803 a446R		92.82	3.11E-18	88%	90%	17-68	1-52
b608R	253773-253970	66	7.868	8.84		No Hit Found																
b609R	254050-254244	65	7.222	11.63		No Hit Found								1	NP_048804 a447R		126.72	1.97E-28	95%	98%	1-65	35-99
b610R	254993-254817	75	8.874	10.15		No Hit Found																
b613L	255578-255324	85	9.529	9.01		No Hit Found																
b615L	256808-256602	69	8.333	8.68		No Hit Found																
b616L	257115-256912	68	8.304	8.25		No Hit Found																
b620R	259287-259511	75	8.506	5.50		No Hit Found								1	NP_048810 a453R		88.20	7.79E-17	64%	66%	1-75	15-89
b621R	259760-260128	123	13.096	7.03		No Hit Found								1	NP_048812 a455R		168.70	4.55E-41	70%	79%	2-123	20-143
b622L	260375-260136	80	9.626	11.37		No Hit Found																
b624R	260319-260525	69	7.794	11.15		No Hit Found								1	NP_048814 a457R		75.87	3.93E-13	100%	100%	32-69	1-38
b625R	260550-260744	65	7.054	12.09		No Hit Found																
b626R	260597-260923	109	13.173	5.19		No Hit Found																
b627L	260838-260632	69	8.277	10.97		No Hit Found								1	NP_048815 a458L		92.82	3.10E-18	60%	76%	1-69	1-69
b632R	265053-265292	80	9.469	5.58		No Hit Found																
b634L	267000-266803	66	7.022	10.53		No Hit Found								1	NP_048825 a469L		53.53	2.11E-06	46%	53%	1-66	12-76
b635L	267178-266948	77	9.378	10.64		No Hit Found																
b637R	267598-267801	68	8.113	12.45		No Hit Found																
b639L	268357-268103	85	9.811	8.83		No Hit Found								1	NP_048828 a472L		89.35	3.51E-17	60%	67%	5-85	10-90
b640L	268734-268318	139	16.229	8.27		No Hit Found								1	NP_048833 contains prokaryotic membrane lipoprotein lipid attachment site: similar to vaccinia virus F-ORF-C 11.6 kD protein, corresponds to Swiss-Prot Accession Number P20561 vsv189		59.31	3.76E-08	60%	82%	1-40	33-72
														2	NP_477711		51.99	6.01E-06	38%	60%	23-90	23-89
b642L	269022-268774	83	9.645	5.15		No Hit Found																
b643R	268842-269081	80	9.555	12.51		No Hit Found																
b646R	270265-270516	84	10.271	9.90		No Hit Found																
b648L	271204-270695	170	20.338	4.26		No Hit Found																
b649R	271189-271398	70	8.321	9.57		No Hit Found																
b653L	273025-272702	108	12.230	11.09		No Hit Found																
b654L	273393-273157	79	8.996	10.54		No Hit Found																
b658L	274835-274641	65	7.893	9.49		No Hit Found																
b660R	274930-275157	76	8.839	10.84		No Hit Found																
b661L	275246-275007	80	9.264	5.74		No Hit Found																
b664L	276274-276032	81	9.315	7.18		No Hit Found																
b665L	277079-276648	144	16.446	12.18		No Hit Found								1	NP_048854 Pro-rich, IPPPNMMLPLLS (3x)		63.93	1.55E-09	85%	85%	2-36	8-42
b668R	277504-277908	135	12.578	7.86		No Hit Found																
b669L	277873-277565	103	12.637	12.85		No Hit Found																
b673R	279838-280050	71	8.679	7.83		No Hit Found								1	NP_048863 a507R		83.96	1.43E-15	55%	72%	1-70	1-70
b674R	280183-280389	69	8.384	10.36		No Hit Found								1	NP_048863 a507R		70.86	1.26E-11	57%	71%	1-67	116-184
b675R	280283-280759	159	17.661	10.62		No Hit Found								1	NP_048864 a508R		109.00	4.57E-23	80%	82%	84-153	1-70
b676R	280793-281068	92	10.820	11.07		No Hit Found								1	NP_048866 a510R		90.89	1.18E-17	87%	90%	13-67	2-56
b678L	281578-281279	100	11.484	11.13		No Hit Found																
b679L	281763-281494	90	10.291	11.06		No Hit Found								1	NP_048875 A519L		133.65	1.59E-30	80%	83%	9-89	1-81

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
b682R	282509-282754	82	10,102	9.25		No Hit Found									No Hit Found							
b683R	283064-283300	79	8,852	7.18		No Hit Found									No Hit Found							
b686R	284131-284334	68	8,388	8.68		No Hit Found									No Hit Found							
b689R	285314-285586	91	10,217	4.48		No Hit Found								1	NP_048503 a155R		83.57	1.88E-15	61%	79%	16-82	27-93
b690R	285433-285651	73	8,924	12.36		No Hit Found									No Hit Found							
b691R	285722-286018	99	12,307	11.85		No Hit Found									No Hit Found							
b693R	286618-286869	84	9,950	6.00		No Hit Found									No Hit Found							
b695L	287587-287015	191	20,832	8.61		No Hit Found								1	NP_048874 a518R		115.16	1.05E-24	62%	71%	30-125	4-100
														2	NP_048885 a529L		102.83	5.41E-21	80%	83%	59-124	1-67
														3	NP_049041 a685R		52.76	6.42E-06	50%	56%	61-124	8-66
b698L	288061-287840	74	8,350	7.46		No Hit Found									No Hit Found							
b703R	290057-290284	76	9,000	8.21		No Hit Found									No Hit Found							
b706L	292254-292054	67	7,436	11.01		No Hit Found									No Hit Found							
b707R	292215-292505	97	11,405	11.85		No Hit Found									No Hit Found							
b708R	292258-292650	131	15,251	10.26		No Hit Found									No Hit Found							
b709L	292505-292275	77	8,527	7.25		No Hit Found									No Hit Found							
b713L	293503-293303	67	8,187	11.43		No Hit Found									No Hit Found							
b716R	294379-294657	93	10,237	11.20		No Hit Found									No Hit Found							
b717R	294627-294968	114	13,310	7.05		No Hit Found									No Hit Found							
b721R	296554-296793	80	8,610	11.46		No Hit Found									No Hit Found							
b722R	297145-297351	69	8,054	10.67		No Hit Found									No Hit Found							
b726R	298958-299224	89	10,443	11.53		No Hit Found									No Hit Found							
b727R	299509-299772	88	9,960	9.37		No Hit Found									No Hit Found							
b728R	300382-300609	76	8,530	4.88		No Hit Found									No Hit Found							
b729L	300654-300427	76	9,356	8.93		No Hit Found									No Hit Found							
b730R	300703-300972	90	9,784	4.27		No Hit Found									No Hit Found							
b731L	301192-300995	66	7,724	11.79		No Hit Found									No Hit Found							
b732L	301942-301715	76	9,239	11.76		No Hit Found									No Hit Found							
b733R	302090-302287	66	7,668	6.75		No Hit Found									No Hit Found							
b735L	303135-302809	109	13,000	9.64		No Hit Found									No Hit Found							
b737R	304424-304690	89	10,170	4.38		No Hit Found									No Hit Found							
b739R	304868-305146	93	10,973	6.62		No Hit Found								1	NP_048905 a549R		72.79	3.30E-12	41%	62%	1-79	1-79
b740R	305522-305755	78	9,198	7.09		No Hit Found								1	NP_048906 a550R		77.80	1.04E-13	44%	73%	1-78	55-132
b742L	306626-306414	71	8,897	9.48		No Hit Found									No Hit Found							
b745R	307583-307795	71	7,778	11.33		No Hit Found									No Hit Found							
b746R	308440-308664	75	8,597	9.41		No Hit Found									No Hit Found							
b749L	310397-310173	75	8,706	10.82		No Hit Found									No Hit Found							
b750R	310396-310731	112	14,021	10.89		No Hit Found									No Hit Found							
b752R	311491-311916	142	15,792	8.34		No Hit Found								1	NP_048916 a560R		72.79	3.36E-12	65%	75%	3-62	45-104
b754R	311928-312416	163	18,551	10.29		No Hit Found									No Hit Found							
b755R	312549-312839	97	10,795	7.25		No Hit Found									No Hit Found							
b757R	313468-313770	101	12,258	9.53		No Hit Found									No Hit Found							
b758L	314268-314020	83	9,614	12.35		No Hit Found									No Hit Found							
b760L	316659-316252	136	15,665	7.64		No Hit Found								1	NP_048922 a566L		164.08	1.10E-39	87%	87%	1-89	1-90
b764L	319044-318475	190	21,975	10.58		No Hit Found									No Hit Found							
b768R	319808-320029	74	8,008	6.65		No Hit Found									No Hit Found							
b770L	320661-320425	79	8,679	10.91		No Hit Found								1	NP_048874 a518R		64.31	1.19E-09	53%	66%	17-78	1-62
b773R	321985-322182	66	7,959	8.96		No Hit Found									No Hit Found							
b775R	322472-322714	81	10,045	12.26		No Hit Found									No Hit Found							
b776R	323143-323376	78	9,173	11.50		No Hit Found									No Hit Found							
b778R	323613-323951	113	12,462	10.12		No Hit Found									No Hit Found							
b779L	324315-323848	156	18,062	11.00		No Hit Found									No Hit Found							
b780R	323873-324247	125	14,864	8.73		No Hit Found									No Hit Found							
b782R	324577-324658	94	11,087	11.00		No Hit Found									No Hit Found							
b783R	324644-324937	98	11,189	11.60		No Hit Found								1	NP_048940 contains prenyl group binding site (CAAX) box		179.10	3.33E-44	91%	93%	1-98	1-98
b784R	324877-325542	222	25,862	7.86		No Hit Found								1	NP_048941 a585R		147.52	2.70E-34	82%	92%	23-101	1-79
b785R	325757-326056	100	11,570	11.19		No Hit Found									No Hit Found							
b786R	326026-326220	65	7,512	7.53		No Hit Found								1	NP_048943 a587R		112.46	3.84E-24	81%	89%	1-65	1-65
b787R	326189-326428	80	8,692	12.12		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
b788R	326701-327336	212	24,494	6.10		No Hit Found								1	NP_048944 a588R		109.38	7.31E-23	50%	68%	1-116	1-116
b789R	326918-327241	108	12,116	10.65		No Hit Found									No Hit Found							
b790L	327290-327063	76	8,810	11.20		No Hit Found								1	NP_048945 a589L		67.78	1.09E-10	52%	57%	1-76	1-76
b793L	328864-328547	106	10,790	7.30		No Hit Found								1	NP_048951 a595L		65.86	4.14E-10	62%	68%	1-59	19-82
b794R	328771-328989	73	8,487	11.74		No Hit Found									No Hit Found							
b797R	329840-330391	184	21,832	5.31		No Hit Found									No Hit Found							
b799R	331312-331542	77	8,587	10.80		No Hit Found									No Hit Found							
b804L	333525-333319	69	8,639	9.60		No Hit Found									No Hit Found							
b806L	333814-333374	147	17,496	6.47		No Hit Found									No Hit Found							
b807R	333596-333799	68	7,964	10.78		No Hit Found									No Hit Found							
b808L	334041-333769	91	10,550	5.17		No Hit Found									No Hit Found							
b809L	334305-334063	81	9,347	7.85		No Hit Found									No Hit Found							
b810L	335041-334361	227	25,362	10.85		No Hit Found								1	NP_048961 a605L		244.20	2.19E-63	77%	84%	70-227	1-158
														2	NP_048962 a609L		83.19	6.47E-15	63%	71%	1-74	1-74
b814L	336462-336259	68	8,087	10.04		No Hit Found									No Hit Found							
b815R	336290-336529	77	9,427	10.54		No Hit Found								1	NP_048969 a613R		92.82	3.14E-18	52%	77%	1-74	9-82
b817R	337681-337953	91	9,911	8.36		No Hit Found								1	NP_048972 a616R		119.78	2.37E-26	63%	68%	2-91	4-93
b821R	339599-339850	84	10,006	9.75		No Hit Found									No Hit Found							
b822R	339622-339861	80	9,858	11.23		No Hit Found									No Hit Found							
b827R	342463-342705	81	9,985	11.15		No Hit Found									No Hit Found							
b830L	343739-343518	74	8,396	10.19		No Hit Found								1	NP_048982 a626L		164.85	6.57E-40	100%	100%	1-74	1-74
b833R	346107-346328	74	8,495	11.36		No Hit Found								1	NP_048986 a630R		95.13	6.39E-19	67%	67%	1-74	1-74
b834R	346425-346676	84	9,368	10.23		No Hit Found									No Hit Found							
b835L	346759-346532	76	8,645	9.54		No Hit Found									No Hit Found							
b836R	347103-347369	89	10,548	11.40		No Hit Found									No Hit Found							
b837L	348868-348416	151	17,573	4.91		No Hit Found									No Hit Found							
b838R	348998-349290	131	15,301	8.35		No Hit Found									No Hit Found							
b845R	351293-351529	79	8,874	12.12		No Hit Found								1	NP_048996 a640R		153.68	1.49E-36	96%	97%	1-79	1-79
b846L	351821-351600	74	8,317	10.74		No Hit Found								1	NP_048997 a641L		144.82	7.04E-34	95%	98%	1-74	12-85
b848L	352899-352660	80	9,155	11.33		No Hit Found									No Hit Found							
b851R	355248-355451	68	8,215	10.22		No Hit Found									No Hit Found							
b854R	355888-356205	106	12,117	7.92		No Hit Found									No Hit Found							
b855L	356272-356060	71	8,137	10.71		No Hit Found								1	NP_049011 a655L		62.30	4.46E-09	54%	65%	1-70	1-70
b856R	356289-356531	81	9,958	10.96		No Hit Found									No Hit Found							
b861L	358591-358397	65	7,677	8.67		No Hit Found									No Hit Found							
b863R	358777-358998	74	8,275	6.35		No Hit Found									No Hit Found							
b864R	359998-359285	96	11,535	8.06		No Hit Found									No Hit Found							
b866R	360033-360350	106	12,385	11.46		No Hit Found									No Hit Found							
b868R	360109-360750	214	25,351	8.65		No Hit Found								1	NP_048428 a80L		131.34	1.84E-29	49%	69%	47-175	1-129
														2	NP_048808 similar to PBCV-1 ORF a80L, encoded by GenBank Accession Number U17055		101.29	2.04E-20	53%	71%	50-146	4-100
														3	NP_048630 similar to PBCV-1 ORF a80L, corresponds to GenBank Accession Number U17055		97.06	3.84E-19	57%	71%	50-140	4-94
b870L	361566-361168	133	14,344	5.96		No Hit Found								1	NP_049033 a677L		111.31	8.56E-24	77%	82%	1-69	1-75
b872L	363026-362796	77	9,058	10.26		No Hit Found									No Hit Found							
b873R	362956-363204	83	9,941	7.92		No Hit Found									No Hit Found							
b875R	363278-363748	157	17,695	6.56		No Hit Found								1	NP_048354 a6L		63.93	1.60E-09	47%	66%	74-143	1-71
b876R	363453-363680	76	8,273	11.42		No Hit Found									No Hit Found							
b877R	364224-364448	75	8,723	4.38		No Hit Found									No Hit Found							
b879R	364671-365129	153	18,134	9.66		No Hit Found									No Hit Found							
b881R	365789-366214	142	15,912	5.88		No Hit Found								1	NP_048354 a6L		51.99	6.13E-06	48%	68%	66-112	1-47
b882R	366333-366578	82	8,912	5.03		No Hit Found								1	NP_049046 identical to PBCV-1 terminal repeat ORF, corresponds to GenBank Accession Number M55319		99.37	3.30E-20	67%	75%	6-82	2-77
b885L	367548-367327	74	8,633	7.51		No Hit Found									No Hit Found							