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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

Lisa A. Fitzgerald^a, Michael V. Graves^b, Xiao Li^b, Tamara Feldblyum^c, William C. Nierman^{c, d}, and James L. Van Etten^{e, *}

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⁺⁺ 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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Gene Name	Genome Position	A.A. lenath	Peptide Mw	pl	CDD Hit Number	COGs	COG Definition	Bit Score E-value		% % entity Positiv	Quei e from-	ry Hit to from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value Id	% entity P	% Query	Hit from-to
b002R	10941315	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 id	dentical to PBCV-1 terminal repeat ORF, corresponds to GenBank Accession Number M55319	97.06	1.64E-19	64%	75% 682	277
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 b015R	5639-5839	67	8,180 8,112	7.70 10.74		No Hit Found								No Hit Found						
b015R	5727-5945 6534-6788	73 85	9,952	8.18		No Hit Found								No Hit Found No Hit Found						
b019R	7503-7757	85	9,543	11.48		No Hit Found								No Hit Found						
b020R	78868089	68	8,041	9.50		No Hit Found								No Hit Found						
b021R	80998404	102	11,885	5.08		No Hit Found								No Hit Found						
b023L	100989820	93	10,453	10.95		No Hit Found								No Hit Found						
b025R	1154511772	76	8,823	5.58		No Hit Found								No Hit Found						
b026R	1177212020	83	9,549	6.77		No Hit Found								No Hit Found						
b028L	1203411801	78	8,798	12.04		No Hit Found								No Hit Found						
b029R	1194112279	113	10,711	5.51	1		Sporozoite, P67. Sporozoite P67 surface antigen. This family consists of several Theleria P67 surface antigens. A stage specific surface antigen of Theleria para, 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 the distinct linear petide sequences recognised by sporozoite-neutralising murine monoclonal antibodies.	42.86 5.94E-0	15	44% 509	% 36-	-107 180250		No Hit Found						
b030L	1253212290	81	9,242	9.03		No Hit Found								No Hit Found						
b032L	1342413227	66	7,378	12.02		No Hit Found								No Hit Found						
b035L	1505014856	65	7,534	11.07		No Hit Found								No Hit Found						
b036R	1643616714	93	10,260	4.54		No Hit Found								No Hit Found						
b037R	1680817014	69	7,533	4.11		No Hit Found								No Hit Found						
b038R b041R	1775617971 2105021361	72 104	8,118 11,414	4.88 7.21		No Hit Found								No Hit Found No Hit Found						
b041R	2238922667	93	11,857	12.12		No Hit Found								No Hit Found						
b043R	2242122840	140	15,312	6.34		No Hit Found								No Hit Found						
b044R	2345923809	117	12,727	4.77		No Hit Found								No Hit Found						
b045R	2393024172	81	8,902	4.36		No Hit Found								No Hit Found						
b046R	2418224586	135	14,731	4.23		No Hit Found								No Hit Found						
b048L	2632526113	71	8,650	8.14		No Hit Found								No Hit Found						
b049R	2679126985	65	8,149	12.09		No Hit Found								No Hit Found						
b050R	2681127242	144	15,584	4.13		No Hit Found								No Hit Found						
b051R	2730927836	176	18,677	4.12		No Hit Found							1 2 3 4 5	AAC39773 h AAC39772 h AAC39771 h BAA21556 h	sepatitis A virus cellular receptor 1 long form sepatitis A virus cellular receptor 1 short form sepatitis A virus receptor 1 short form se	57.38 57.38 56.23 56.23 55.45 54.68	2.14E-07 2.14E-07 4.76E-07 4.76E-07 8.12E-07 1.38E-06	28% 28% 27% 27% 29% 30%	36% 2-152 36% 2-152 36% 2-152 34% 2-152	164320 159315 164316 159311 171302 159293
b052R	2786128160	100	10,798	4.22		No Hit Found								No Hit Found						
b053R	2833228574	81	8,934	4.36		No Hit Found								No Hit Found						
b054R	2858428988	135	14,622	4.51		No Hit Found								No Hit Found						
b056R	2961229983	124	13,368	3.94		No Hit Found								No Hit Found						
b057R b058R	3032030517 3112431525	66 134	7,111 15,086	3.78 6.88		No Hit Found								No Hit Found No Hit Found						
b060L	3292032651	90	10,946	9.40		No Hit Found								No Hit Found						
b062L	3387333604	90	10,316			No Hit Found								No Hit Found						
b063L	3410233851	84	9.875	10.94		No Hit Found								No Hit Found						
b064L	3423534002	78	8,999	9.54		No Hit Found								No Hit Found						
b065R	3422434457	78	9,097	11.13		No Hit Found								No Hit Found						
b066L	3455134315	79	8,906	11.19		No Hit Found								No Hit Found						
b067L	3499434638	119	14,573	10.54		No Hit Found							1	NP_048385 A	A37L	177.95	7.36E-44	77%	92% 18119	4105
b069L	3589335486	136	12,300	4.42		No Hit Found							1	NP_048388 D	contains Gly-rich motifs GAGLGTGF (5X); similar to Arabidopsis Gly-rich protein. corresponds to Swiss-Prot Accession Number P27843	55.07	7.19E-07	75%	83% 102136	77112
b071R	3620636430	75	9,127	8.06		No Hit Found							1	NP_048391 a	s43R	161.38	7.24E-39	93%	96% 175	175
b072L	3667136417	85	9,942	8.06		No Hit Found							1	NP_048520 a	1172L	88.58	5.98E-17	50%	71% 485	486
b079R	4052440886	121	14,746	8.63		No Hit Found							1	NP 048400 a	152R	138.66	4.91E-32	74%	77% 39121	183
b081R	4105841315	86	9,916	10.96		No Hit Found								No Hit Found						
b082L	4151841318	67	8,187	11.43		No Hit Found								No Hit Found						

Gene Name	Genome Position	A.A. lenath	Peptide Mw	pl	CDD Hit CO	Gs COG Definition	Bit Score E-va	alue Ide	% % entity Posit		Query Hit rom-to from-to	BLASTp Hit Number	Hit Accession	BLASTp Definition	Bit Score	E-value I	% dentitv F	% Positive	Query from-to fr	Hit rom-to
b084R	4239542673	93	10,237	11.20	No I	lit Found							No Hit Found							
b085R	4264342984	114	13,326	7.05	No I	lit Found							No Hit Found							
b089R	4513345387	85	9,619	10.52	No I	lit Found							No Hit Found							
b090R	4561645858	81	8,612	11.27	No I	lit Found						1	NP 048874 a5	18R	81.65	7.14E-15	61%	65%	174	175
b092R	4615546457	101	11,907	4.80	No I	lit Found							No Hit Found							
b093R	4634246542	67	7,428	11.66	No I	lit Found							No Hit Found							
b095L	4699946781	73	8,199	10.86	No I	lit Found							No Hit Found							
b096L	4724847033	72	7,961	11.22	No I	lit Found							No Hit Found							
b097L	4741747109	103	12,209	5.28	No I	lit Found							No Hit Found							
b098R	4712547394	90	10,283	12.37	No I	lit Found							No Hit Found							
b100L	4793347526	136	15,468	5.10	No I	lit Found							No Hit Found							
b101L	4812947833	99	11,743	10.52	No I	lit Found							No Hit Found							
b102L	4849748024	158	18,278	6.91	No I	iit Found						1	NP_048417 tra Ari	ntains Gly-rich Gx motif LGGGLG (5X); contains type I hydrophobic nsmembrane sequence; contains protein splicing signature; similar to abidopsis Gly-rich protein, corresponds to Swiss-Prot Accession umber P27483	106.30	2.89E-22	60%	78%	77158	182
b105L	5027249586	229	26,576	6.29	No I	lit Found						1	NP_048503 a1	55R	88.97	1.20E-16	58%	76%	683	1494
b106R	4971649982	89	10,581	12.10	No I	lit Found							No Hit Found							
b107L	5132750464	288	34,170	6.02	1 p	Exostosin. Exostosin family. The EXT family is a family of turno suppressor genes. Mutations of EXT1 on 8924.1 EXT2 on 11911.13 and EXT3 on 199 have been associated with the attoornal dominal disorder known as herefalliny multiple exostoses (HME). This is the mos common known skeletal dysplasia. The chromosomal locations of the EXT2 prese suggest association with other forms of neoplasia. EVI and EXT2 have both been shown to encode a heparan sulphate polymeras with both D-glucurony (IGAA) and N-acetyl-D-glucosaminoglyca (IGCNAC) transferase activites. The nature of the defect in hepara sulphate histoevarhosis in HME's incidanr.	35.80 8.0	04E-03	19% 4	46%	164229 206279	5 1	NP_048423 A7	'SL	520.39	2.45E-146	87%	96%	9288	1–280
b111R	5146251686	75	9,216	7.34	No I	lit Found							No Hit Found							
b112R	5164751868	74	8,973	11.96	No I	lit Found							No Hit Found							
b114L	5213051936	65	7,804	11.98	No I	lit Found						1	NP_048424 a7	6L	63.16	2.67E-09	63%	75%	2865	55103
b119L	5507354867	69	7,758	7.69	No I	lit Found							No Hit Found							
b121L	5579755411	129	15,078	9.57	No I	lit Found						1	NP 048428 a8	OL nilar to PBCV-1 ORF a80L, encoded by GenBank Accession Number 7055		2.45E-15	56%	73%	478	
												2	NP_048808 U1	7055	52.37	4.64E-06	55%	77%	145	56100
b123R	5635856660	101	11,832	4.77		lit Found							No Hit Found							
b125R	5698457238	85	9,982	10.33		lit Found							No Hit Found							
b127L	5792357681	81	9,810	10.44		lit Found							No Hit Found							
b128L	5810457910	65	7,040	11.12		lit Found						1	NP_048434 a8	6L	107.46	1.23E-22	83%	86%	164	166
b129L	5833958139	67	8,131	12.07		lit Found							No Hit Found							
b131R	5836558580	72	8,257	12.41		lit Found							No Hit Found							
b132L	5897458741	78	8,912	11.90		lit Found							No Hit Found							
b134L	5911458806	103	12,582	7.81		lit Found							No Hit Found							
b135L	5921459017	66	7,496	6.31		lit Found							No Hit Found							
b138R b140L	6169461936 6290462710	81	9,887 6,945	12.34		lit Found lit Found							No Hit Found No Hit Found							
b140L	6331362990	65	12,676	7.21																
b141L	6432363958	108 122	14,435	6.88		lit Found lit Found							No Hit Found No Hit Found							
b144L	6452564286	80	9,314	11.01		lit Found						1	NP_048449 a1	041	80.49	1.60E-14	65%	87%	155	33_87
b145L	6509264772		13,059	7.97		lit Found							No Hit Found	oit.	00.40	1.002 14	00%	0770		00 07
b146L	6566865348	107	12,914	10.36		lit Found							No Hit Found							
b147L	6632265981	114	12,774	9.71		lit Found						1	NP_048450 a1	021	145.98	3.16E-34	64%	72%	1114	1114
b149L	6669266306	129	15.406	6.16		it Found						1	NP 048452 a1		87.81	9.96E-17	43%	65%		196
b151R	6720167521	107	12.414	6.23		lit Found						1	NP_048454 a1		97.06	1.67E-19	48%	67%	1107	
b152R	6739267622	77	9,392	9.18	No I	lit Found							No Hit Found							
b153R	6766267856	65	8,103	10.69		lit Found							No Hit Found							
b155R	6832768539	71	8,476	8.22		lit Found						1	NP_048456 a1	08R	62.39	4.46E-09	42%	67%	171	171
b156R	6871768917	67	8,208	4.17		lit Found							No Hit Found							
b158R	6900969377	123	14,530	7.98		lit Found							No Hit Found							
b160L	7041370195	73	8,003	8.94		lit Found						1	NP_048460 a1	12L	142.12	4.58E-33	97%	97%	173	173
b161R	7074371039	99	11,535	8.53		lit Found						1	NP_048464 a1		114.01	1.31E-24	74%	79%		181
b162L	7162971201	143	16,697	6.14	No I	lit Found						1	NP 048465 a1	17L	177.95	7.38E-44	63%	80%	7136	1-130
b164L	7286972432	146	17,221	7.77	No I	lit Found							No Hit Found							
b166L	7385473651	68	7,204	7.15	No I	lit Found							No Hit Found							
b167R	7381874012	65	7,455	11.31	No I	lit Found							No Hit Found							

Gene Name b169L	Genome Position 7478174560	A.A. lenath	Peptide Mw 8,638	pl 7.34		COGs No Hit Found	COG Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	BLASTp Hit Number	Acc	Hit BLASTp Definition	Bit Score	E-value	% Identity	% Positive	Query from-to	Hit o from-to
b171L	7762077417	68	7,444	4.32	N	No Hit Found								No	No Hit Found						
b172L	7836778167	67	7,415	4.37	N	No Hit Found								No	No Hit Found						
b174L	8097680674	101	11,613	11.09	N	No Hit Found							1	N	NP_048473 a124L	127.87	8.72E-29	73%	78%	18101	184
b176R	8126081481	74	8,758	12.52		No Hit Found									No Hit Found						
b178L	8190281696	69	7,421	4.35		No Hit Found							1		NP_048476 a128L	111.69	6.46E-24	81%	85%	169	169
b180L b182R	8306382866 8341983661	66 81	7,786	11.48		No Hit Found									No Hit Found NP 048480 a132R	70.48	1.65E-11	44%	64%	178	381
			9,356	6.79									1		NP_048481 similar to Synechoccystis 3-pyrophosphohydrolase, corresponds						
b184R	8433885078	247	28,196	10.16	N	No Hit Found							1 2 3 4 5 6 7 8	X ZP_	NP_56540 Transactions for American Vision 1	110.92 110.92 109.77 109.38 109.00 107.84 93.97 85.89	3.42E-23 3.42E-23 7.63E-23 9.96E-23 1.30E-22 2.90E-22 4.33E-18 1.18E-15	95% 31% 31% 28% 30% 28% 30% 32% 27%		42243 42245 49245 49245 50243 51243	5 57–269 5 57–263 7 58–266 5 57–263 8 66–268 3 6–216 7 6–221
14000	05004 05000		0.404	40.04									10		ABA24174 conserved hypothetical protein	85.89	1.18E-15	27%	50%	51245	5 6-219
b186R b189L	8508185329 8641186196	83 72	9,101 8.495	10.81		No Hit Found									No Hit Found No Hit Found						
b191L	8698286740	81	9,786	9.63		No Hit Found									No Hit Found						
b193L	8826687616	217	25,488	8.10		No Hit Found							1		NP_048492 a144L	67.01	4.40E-10	43%	64%	176	412487
													2		T17632 hypothetical protein a141L - Chlorella virus PBCV-1	67.01	4.40E-10	43%	64%		179254
b194L	8938588375	337	40,259	8.28	N	No Hit Found							1		NP_048492 a144L T17632 hypothetical protein a141L - Chlorella virus PBCV-1	275.40 94.36	1.78E-72 5.62E-18	44% 44%	56%	208336	3 18–374 3 14–141
b195L	8978489557	76	9,346	8.73	N	No Hit Found							3 1 2	N	NP_048495 Phe-, Gly-rich protein: RCGF 3X, GCGF 11X, RSGF 5X, GSGF 2X NP_048495 Phe-, Gly-rich protein: RCGF 3X, GCGF 11X, RSGF 5X, GSGF 2X NP_048492 a144L	77.80 112.46 60.85	5.44E-13 3.84E-24 1.33E-08	45% 70% 53%	81% 65%	476	112224 3 187260 5 92155
b196L	9017689838	113	10,996	8.83	N	No Hit Found								No	No Hit Found						
b198R	9013790361	75	8,439	8.43	N	No Hit Found								No	No Hit Found						
b200L	9167991437	81	10,052	7.95		No Hit Found									No Hit Found						
b202L	9300492609	132	14,802	11.06		No Hit Found							1		NP 048500 contains prokaryotic membrane lipoprotein lipid attachment site	85.50	5.05E-16	70%	75%	68131	972
b204L b205R	9350993300 9373993954	70 72	8,333 8,763	9.47		No Hit Found									No Hit Found						
b210R	9612996323	65	7,842	9.24		No Hit Found									No Hit Found						
b213R	9679097029	80	8,836	4.83		No Hit Found									No Hit Found						
b216L	9869198431	87	10,545	10.78	N	No Hit Found								No	No Hit Found						
b217R	9855098768	73	8,448	12.09	N	No Hit Found								No	No Hit Found						
b219L	9921098755	152	17,793	9.44	N	No Hit Found								No	No Hit Found						
b220L	9964399197	149	18,182	10.31		No Hit Found									No Hit Found						
b221L	9944499232	71	8,522	10.99		No Hit Found									No Hit Found						
	100651100370	94	11,356	6.86		No Hit Found									No Hit Found	50.54	0.045.00	44%	500/		
	101320101604 102443102192	95 84	11,388 10,095	11.86		No Hit Found							1		NP_048391 a43R No Hit Found	58.54	6.64E-08	44%	52%	175	175
	102495102710	72	7.509	5.54		No Hit Found									No Hit Found						
b229L	102791102513	93	11,601	11.64	N	No Hit Found								No	No Hit Found						
b231R	103109103453	115	13,639	8.18	N	No Hit Found								No	No Hit Found						
b232R	103233103436	68	7,750	12.25	N	No Hit Found								No	No Hit Found						
b233R	103730103939	70	8,368	8.40	N	No Hit Found								No	No Hit Found						
	103983104261	93	10,894	7.81		No Hit Found									No Hit Found						
	104784105032	83 68	10,159	10.93		No Hit Found									No Hit Found						
	104938105141 105932105717	72	7,817 8,792	6.24		No Hit Found							1		NP_048601 a251aL No Hit Found	72.40	4.36E-12	67%	76%	156	83141
	106345105953	131	13,927	10.62		No Hit Found									No Hit Found						
b242L	106218106024	65	7,762	11.24		No Hit Found									No Hit Found						
b243R	107021107254	78	9,691	11.50	N	No Hit Found								No	No Hit Found						
b244L	107501107232	90	10,701	7.36	N	No Hit Found								No	No Hit Found						
	107728107528	67	7,078	5.33		No Hit Found									No Hit Found						
	108376108164	71	8,635	12.09		No Hit Found									No Hit Found						
	109088108885	68	7,362	11.50		No Hit Found									No Hit Found						
	109008109310 110856110620	101 79	11,568 9,282	6.51		No Hit Found									No Hit Found No Hit Found						
	111274111071	68	7,244	12.22		No Hit Found							1		NP_048535_a188L	105 15	6.06E-22	83%	86%	168	572
	111590111303	96	11,556	8.52		No Hit Found									No Hit Found	100.10		5576	00 /0	. 30	
			****											-							

Gene Name b257R	Genome Position 112119112529	A.A. lenath	Peptide Mw 16,216	pl CDD H Number		COG Definition	Bit Score E-value	% % Identity Positive	Query from-to fro	Hit BLASTp Hit m-to Number	Hit Accession No Hit Found	BLASTp Definition	Bit Score	E-value I	% dentitv P	% Que	ery Hit n-to from-to
b259L	113388113164	75	8,878	10.94	No Hit Found						No Hit Found						
b260R	113323113523	67	8,127	11.41	No Hit Found						No Hit Found						
b262R	117035117439	135	16,277	6.23	No Hit Found						No Hit Found						
b263R	117285117485	67	7,828	10.53	No Hit Found					1	NP_048541 a194R		117.09	1.55E-25	80%	83% 1-	67 167
b265R	117803118018	72	8,315	7.94	No Hit Found					1	NP_048545 a198R		78.95	4.59E-14	47%	72% 1-	72 172
b266R	117834118028	65	7,213	6.52	No Hit Found					1	NP_048544 a197R		93.59	1.84E-18	77%	83% 1-	62 3192
b269R	118429118767	113	13,193	9.76	No Hit Found						No Hit Found						
b270L	119236118970	89	10,827	10.28	No Hit Found						No Hit Found						
	120539120330	70	7,143	9.46	No Hit Found					1	NP_048551 a204L		124.02	1.25E-27	91%	92% 1-	70 170
b276L	121069120797	91	10,102	4.78	No Hit Found						No Hit Found						
	121992121729	88	10,438	5.13	No Hit Found						No Hit Found						
b280L	122077121781	99	12,015	10.24	No Hit Found						No Hit Found						
b281L b282L	122298122041 122941122702	86 80	9,877 8,645	5.90 9.12	No Hit Found No Hit Found						No Hit Found No Hit Found						
b287L	124767124498	90	10,697	11.24	No Hit Found						No Hit Found						
	127120127383	88	10.012	9.40	No Hit Found						No Hit Found						
b293R	128201128839	213	24.250	9.78	No Hit Found					1	NP_048578 A230R		310.07	2.85E-83	79%	91% 19	211 3196
b294R	128500128799	100	11.742	8.53	No Hit Found						No Hit Found		310.07	2.002-00	1070	0170 10	211 3-180
b295L	128706128512	65	7,395	9.43	No Hit Found						No Hit Found						
b299R	130109130351	81	9,106	6.50	No Hit Found						No Hit Found						
b300R	130765130971	69	8,280	10.25	No Hit Found					1	NP_048580 a232R		73.17	2.55E-12	58%	73% 6-	65 665
	131445131212	78	9,722	10.37	No Hit Found						No Hit Found		70.17	2.002 12	00%	7070 0	00 0 00
b304R	131655131891	79	9,397	5.59	No Hit Found					1	NP_048583 a235R		70.09	2.17E-11	46%	64% 1-	75 175
b306L	132505132089	139	16,463	6.10	No Hit Found						No Hit Found						
b307R	132274132567	98	11,648	11.76	No Hit Found						No Hit Found						
b308L	132988132749	80	9,422	9.59	No Hit Found						No Hit Found						
b309L	133471133082	130	16,215	8.42	No Hit Found						No Hit Found						
	134132133839	98	11,592	8.01	No Hit Found						No Hit Found						
b312L	134378134160	73	8,907	10.68	No Hit Found						No Hit Found						
b313L	134482134234	83	9,384	4.25	No Hit Found					1	NP_048503 a155R		81.26	9.27E-15	52%	77% 11-	-82 2293
b315R	134867135145	93	11,173	8.70	No Hit Found						No Hit Found						
b317L	136156135806	117	13,667	5.15	No Hit Found					1	NP 048590 a242L		174.48	8.20E-43	74%	79% 1	117 1-117
b318L	136446136159	96	10,473	10.81	No Hit Found						No Hit Found						
b319L	136869136612	86	9,936	8.09	No Hit Found						No Hit Found						
b320L	136906136649	86	9,952	9.45	No Hit Found						No Hit Found						
b321L	137268136969	100	11,250	10.05	No Hit Found						No Hit Found						
b325R	139886140236	117	13,791	6.49	No Hit Found						No Hit Found						
b326R	140005140223	73	8,789	10.24	No Hit Found						No Hit Found						
b327L	140436140149	96	11,149	11.95	No Hit Found						No Hit Found						
b328R	140472140714	81	8,953	8.07	No Hit Found						No Hit Found						
b329R	140783141151	123	14,325	10.43	No Hit Found						No Hit Found						
b330R	140919141173	85	9,507	6.49	No Hit Found						No Hit Found						
b332L	142200141823	126	15,612	10.02	No Hit Found						No Hit Found						
b333L	142088141870	73	8,030	11.07	No Hit Found						No Hit Found						
	142847143104	86	10,131	10.16	No Hit Found						No Hit Found						
	144046143831	72	7,897	8.66	No Hit Found						No Hit Found						
	143894144286	131	15,935	11.93	No Hit Found						No Hit Found						
	144567144782	72	8,568	8.19	No Hit Found					1	NP_049004 a648L			4.16E-07	45%		69 166
	145670145419	84	10,506	9.57	No Hit Found					1	NP_048603 a252aL		90.51	1.58E-17	66%	80% 25-	84 2584
b345R	146532146744	71	8,555	7.43	No Hit Found						No Hit Found						
	147171147377	69	7,951	9.15	No Hit Found						No Hit Found						
b351R	148536148856	107	11,855	8.82	No Hit Found No Hit Found						No Hit Found NP_048620_a266R		E0 22	3.27E-07	47%	60% 4	69 1583
	148738148965 148965149192	76	8,919	8.38	No Hit Found No Hit Found					1			56.23	3.21E-U1	4/%	60% 1-	ua 1383
	148965149192	76 84	8,794 9,507	7.69 11.57	No Hit Found No Hit Found						No Hit Found NP_048624 a270R		05.44	6.64E-16	64%	69% 1-	68 168
	149131149382	201	9,507	6.34	No Hit Found No Hit Found					1	NP_048624 a270R NP_048626 a272R		85.11 71.63	6.64E-16 1.50E-11	52%		68 168 90 567
										1			/1.63	1.00E-11	3Z%	/++70 28-	ou 56/
b360L	151701151483	73	7,955	7.90	No Hit Found						No Hit Found						

Gene Name b362L	Genome Position 152549152340	A.A. lenath	Peptide Mw 7,769	pl 7.30	CDD Hit Number	COGs No Hit Found		Bit Score	E-value	% Identit	% v Positive	Query from-t	Hit o from-to	BLASTp Hit Number	Acc	Hit BLASTp Definition to Hit Found	Bit Score	E-value	% Identitv l	% (Positive f	Query rom-to fr	Hit om-to
b363L	153719153282	146	15,325	3.75		No Hit Found									No	lo Hit Found						
b364R	153945154202	86	9,586	7.34		No Hit Found								1	1 N	NP_048635 a281R	130.18	1.79E-29	78%	83%	786	685
b366R	154349154564	72	8,863	10.19		No Hit Found								1	1 N	NP_048633 a279R	161.77	5.39E-39	97%	97%	172	172
b367R	155445155723	93	10,257	3.62		No Hit Found								1	1 N	NP_048634 a280R	176.02	2.77E-43	94%	94%	193	193
b369L	156439156239	67	7,696	11.51		No Hit Found								1	1 N	NP_048637 a283L	134.81	7.17E-31	92%	95%	167	167
b372R	158851159141	97	10,279	8.07		No Hit Found										lo Hit Found						
b373R	159166159447	94	10,984	10.49		No Hit Found								1	1 N	NP 048639 a285R	110.92	1.09E-23	91%	93%	158	158
b374L	159688159353	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	66.64	3.55E-12	41	% 60%	2-	93 21112	1	1	1NOR_A Chain A, 4ank: A Designed Ankyrin Repeat Protein With Four Identical Consensus Repeats	71.63	7.37E-12	39%	63%	193 1	15–107
					2	COG0666	contains 4 consecutive repeats 6 Arp, FOG: Ankyrin repeat [General function prediction only].	45.65	8.05E-06	34	% 50%	2-	99 87192	2		AAQ93811 ankyrin repeat protein mbp3 5	68.94 67.78	4.78E-11 1.06E-10	39% 38%	65% 56%	593 3 292 100	
														4	4 A	EAL87814 NACHT domain protein, putative AAH73370 MGC80792 protein AAO37830 mind bomb	66.63 65.08	2.37E-10 6.90E-10	39% 38%	60% 60%	391 51 391 51	12600
														6	6 NI	XP_065825 mindbomb homolog 1 XP_512056 PREDICTED: similar to mind bomb	64.31 64.31	1.18E-09 1.18E-09	38% 38%	59% 59%	391 51 391 46	12600
														8	R X	XP_613236 PREDICTED: similar to mindbomb homolog 1 VP_410167 PREDICTED: similar to mindbomb homolog 1; ubiquitin ligase mind	64.31 64.31	1.18E-09 1.18E-09	38%	59% 59%	391 58 391 60	32670
														10		bomb: DAPK-interacting protein 1 AAN18023 MINDBOMB; ubiquitin E3 ligase	64.31	1.18E-09	38%	59%	391 50	
b375L	160259159723	179	21,715	7.26		No Hit Found									No	lo Hit Found						
b376L	160212159946	89	11,086	12.01		No Hit Found									No	lo Hit Found						
b379R	160441160698	86	9,916	10.96		No Hit Found									No	lo Hit Found						
b380L	160901160701	67	8,187	11.43		No Hit Found									No	lo Hit Found						
b382R	161778162056	93	10,237	11.20		No Hit Found									No	lo Hit Found						
b383R	162026162367	114	13,310	7.05		No Hit Found									No	lo Hit Found						
b384L	163226162792	145	15,888	4.78		No Hit Found										lo Hit Found						
b386L	163670163392	93	10,511	8.11		No Hit Found										lo Hit Found						
	163806163588	73	8,842	11.23		No Hit Found										lo Hit Found		3.52E-22				
	165197164808 165036164818	130 73	15,523 8.906	7.74 8.85		No Hit Found								1		BAA20344 ORF245 Io Hit Found	105.92	3.52E-22	53%	65%	9107 14	15243
	165564165283	94	11.411	8.02		No Hit Found										lo Hit Found						
h394R	165839166252	138	15,507	11.36		No Hit Found								1		NP_048647 a293R	170.24	1.52E-41	69%	77%	1123 4	16168
b396R	166583166783	67	7,924	6.08		No Hit Found										lo Hit Found						
b398R	168014168238	75	9,124	5.75		No Hit Found									No	lo Hit Found						
b400L	169541169287	85	9,924	7.48		No Hit Found									No	lo Hit Found						
b405L	172778172572	69	8,130	8.95		No Hit Found									No	lo Hit Found						
b406L	173638172895	248	29,949	12.18		No Hit Found									No	lo Hit Found						
b407R	172923173879	319	36,489	11.43		No Hit Found								1	1 N	NP 048504 a156L	62.39	2.16E-08	45%	53%	34140	1103
	173722174117	132	15,852	12.21		No Hit Found										lo Hit Found						
b410L	174082173795	96	10,948	5.68		No Hit Found								1		NP_048503 a155R	113.62	1.73E-24	62%	79%	196	194
	174400174627	76	9,154	10.06		No Hit Found										lo Hit Found						
	174647174907 175160175369	87 70	9,675 7.340	10.35		No Hit Found										to Hit Found						
	175647175372	92	10,661	11.19		No Hit Found										Io Hit Found						
	176281176033	83	9,737	9.91		No Hit Found										lo Hit Found						
b420L	178083177889	65	7,724	8.65		No Hit Found									No	lo Hit Found						
b422L	178819178424	132	16,358	11.06		No Hit Found									No	lo Hit Found						
b423R	178624178851	76	8,992	5.88		No Hit Found									No	lo Hit Found						
b425R	179072179383	104	12,436	7.29		No Hit Found									No	lo Hit Found						
b427L	180756180469	96	10,796	12.55		No Hit Found									No	lo Hit Found						
b428L	181027180821	69	7,976	10.47		No Hit Found								1	1 N	NP_048657 a303L	52.37	4.65E-06	44%	55%	169	166
	185022185396	125	14,356	8.56		No Hit Found										lo Hit Found						
	185526185840	105	12,536	10.27		No Hit Found								1		NP 048670 A314R	120.17	1.86E-26	71%	80%	24105	180
	187558187112 187222187593	149 124	13,787	4.87		No Hit Found										lo Hit Found						
	187222187593 188648188845	124 66	14,391 7.615	11.07		No Hit Found										to Hit Found						
D447R b448L	189490189179	104	12,356	6.13		No Hit Found										to Hit Found						
	189953189657	99	11,408	6.76		No Hit Found										lo Hit Found						
	190383190751	123	15,640	10.35		No Hit Found										lo Hit Found						
b454R	190762190980	73	7,772	10.81		No Hit Found										lo Hit Found						

Gene Name b456R	Genome Position 191807192172	A.A. lenath	Peptide Mw 14,530	pl CDD Hit Number	COGs No Hit Found	COG Definition	Bit Score E-value	% % Identity Positive	Query Hit from-to from-t	BLASTp Hit o Number	Hit Accession No Hit Found	BLASTp Definition	Bit Score E-value Id	% % C entity Positive fr	Query Hit rom-to from-to
b459R	193084193281	66	7,742	6.23	No Hit Found						No Hit Found				
b464L	196239196009	77	8,847	4.55	No Hit Found						No Hit Found				
b466L	196973196767	69	7,669	11.30	No Hit Found						No Hit Found				
b467L	197178196843	112	13,300	7.99	No Hit Found						No Hit Found				
b470R	198020198229	70	7,691	10.25	No Hit Found						No Hit Found				
b471R	198286198519	78	9,537	10.82	No Hit Found						No Hit Found				
b473L	199573199373	67	7,293	10.23	No Hit Found						No Hit Found				
b474L	199871199656	72	8,469	4.76	No Hit Found						No Hit Found				
b475L	199876199670	69	7,834	9.63	No Hit Found						No Hit Found				
	200290200508 201560201330	73 77	8,106 8,676	8.19 11.20	No Hit Found						No Hit Found No Hit Found				
	201818201618	67	7,608	10.07	No Hit Found					1	NP_048687 a331L		134.04 1.22E-30	98% 98%	167 167
	202819202559	87	10,765	12.42	No Hit Found					1	NP 048689 PLPRNLLI	I (AY) SPPPSKP (3Y)	57.38 1.47E-07		6387 275299
	202586202927	114	13,269	10.71	No Hit Found						No Hit Found	E (M) O I I Gu (OV)	07.00	100%	00 07 270 200
	203374203162	71	8,016	4.77	No Hit Found						No Hit Found				
	203601203206	132	15,909	11.80	No Hit Found						No Hit Found				
b486R	203549203761	71	8,603	10.24	No Hit Found						No Hit Found				
b489R	205122205565	148	16,753	11.47	No Hit Found					1	NP_048701 a344R		128.26 6.77E-29	55% 71% :	34148 1115
b490L	205678205439	80	9,336	11.87	No Hit Found					1	NP 048702 a345L		80.11 2.09E-14	64% 75%	1279 2895
b491R	206097206432	112	13,489	11.01	No Hit Found						No Hit Found				
b493L	206785206546	80	9,138	4.26	No Hit Found					1	NP_048435 A87R		71.63 7.42E-12	58% 77%	1172 2281
b495L	207124206915	70	8,187	5.47	No Hit Found					1	NP 048704 a347L		84.34 1.10E-15	52% 70%	170 170
b500R	209963210292	110	12,244	10.57	No Hit Found						No Hit Found				
b501R	210076210408	111	13,069	11.06	No Hit Found						No Hit Found				
b502R	210590210799	70	7,944	8.52	No Hit Found						No Hit Found				
b504L	211098210889	70	7,708	12.35	No Hit Found						No Hit Found				
	210940211143	68	8,921	12.71	No Hit Found						No Hit Found				
	211564212289	242	26,364	4.58	No Hit Found						No Hit Found				
	212669212454	72	8,113	9.03	No Hit Found						No Hit Found				
	212878212681 213222212938	66	8,485 10.839	8.38 6.91	No Hit Found						No Hit Found No Hit Found				
	213222212938	95 73		8.36	No Hit Found										
	214842214642	67	8,307 7,790	7.74	No Hit Found						No Hit Found No Hit Found				
	215348214983	122	13,590	8.20	No Hit Found						No Hit Found				
		81	8,912	4.70	No Hit Found						No Hit Found				
	216333215839	165	19,662	10.11	No Hit Found						No Hit Found				
	216826216593	78	9,128	7.98	No Hit Found						No Hit Found				
b518L	217097216813	95	10,029	3.14	No Hit Found						No Hit Found				
b520R	217366217635	90	10,868	10.95	No Hit Found						No Hit Found				
b521R	217670217951	94	10,557	7.87	No Hit Found						No Hit Found				
b523R	218670218969	100	11,265	12.65	No Hit Found					1	NP 048734 a377R		84.34 1.11E-15	54% 62%	14100 691
b526R	219582220112	177	20,545	10.99	No Hit Found					1	NP_048737 a380R		144.05 1.77E-33	71% 82%	49149 1101
b527R	219832220035	68	7,734	11.11	No Hit Found					1	NP_048738 a381R		127.49 1.14E-28	89% 91%	168 976
b528L	220152219955	66	8,133	11.25	No Hit Found						No Hit Found				
	220800220432	123	14,002	10.71	No Hit Found						No Hit Found				
	221479221249	77	9,221	8.69	No Hit Found						No Hit Found				
	222934223146	71	8,458	11.71	No Hit Found					1			48.14 8.71E-05		233 4071
	223332223583	84	9,429	10.81	No Hit Found					1	NP_048748 a391R		85.11 6.64E-16	55% 60%	184 195
	224818224621 227430227627	66	8,079	6.08	No Hit Found						No Hit Found				
		66	7,352	5.69	No Hit Found						No Hit Found				
	227716227919 230873230565	68 103	8,180 11,190	8.38 4.98	No Hit Found No Hit Found						No Hit Found No Hit Found				
	230873230565	69	7,186	4.54	No Hit Found						No Hit Found				
	234738234974	79	9,001	10.44	No Hit Found						No Hit Found				
	235011234769	81	9,631	10.72	No Hit Found						No Hit Found				
	235907236272	122	13,676	10.97	No Hit Found					1			72.79 3.30E-12	80% 86%	146 3782
	236923236720	68	7,929	11.79	No Hit Found						No Hit Found				
											-				

Gene Name b565R	Genome Position 236938237180	A.A. lenath 81	Peptide Mw 9,563	pl CDD Hit Number	COGs No Hit Found	COG Definition	Bit Score E-value	% % Identity Positive	Query H from-to from	lit BLASTp Hit n-to Number	Hit Accession No Hit Found	BLASTp Definition	Bit Score	E-value Id	% entity Pos	% Qu sitive fro	uery Hit m-to from-to	
b569L	240525240130	132	15,171	10.25	No Hit Found					1	NP_048772 a415L		110.54	1.47E-23	80%	86% 34	I100 369	
b572R	241059241328	90	10,143	11.78	No Hit Found						No Hit Found							
b574R	241925242155	77	9,241	10.31	No Hit Found						No Hit Found							
b577L	243362242958	135	16,597	7.62	No Hit Found						No Hit Found							
b578L	243175242978	66	7,868	7.86	No Hit Found						No Hit Found							
b584L	246026245799	76	9,524	9.59	No Hit Found						No Hit Found							
b586R	247244247477	78	9,952	11.38	No Hit Found						No Hit Found							
b588L	247502247308	65	7,553	4.26	No Hit Found						No Hit Found							
b589R	247529247726	66	7,965	11.91	No Hit Found						No Hit Found							
b594R	248630248881	84	10,180	7.72	No Hit Found						No Hit Found							
b599R	251031251231	67	7,603	10.41	No Hit Found						No Hit Found							
b600L	251379251143	79	8,994	11.47	No Hit Found						No Hit Found							
b601R	251179251382	68	8,238	7.95	No Hit Found						No Hit Found							
b603L	252727252494	78	8,991	8.19	No Hit Found						No Hit Found							
b604L	252864252643	74	9,185	12.38	No Hit Found						No Hit Found							
b605R	253105253410	102	11,578	10.84	No Hit Found						No Hit Found							
b607R	253570253773	68	7,452	9.49	No Hit Found					1	NP_048803 a446R		92.82	3.11E-18	88%	90% 1	1768 152	
b608R	253773253970	66	7,868	8.84	No Hit Found						No Hit Found							
b609R	254050254244	65	7,222	11.63	No Hit Found					1	NP 048804 a447R		126.72	1.97E-28	95%	98%	165 3599	
b610R	254593254817	75	8,874	10.15	No Hit Found						No Hit Found							
b613L	255578255324	85	9,529	9.01	No Hit Found						No Hit Found							
b615L	256808256602	69	8,333	8.68	No Hit Found						No Hit Found							
b616L	257115256912	68	8,304	8.25	No Hit Found						No Hit Found							
b620R	259287259511	75	8,506	5.50	No Hit Found					1	NP_048810 a453R		88.20	7.79E-17	64%	66%	175 1589	
b621R	259760260128	123	13,096	7.03	No Hit Found					1	NP_048812 a455R		168.70	4.55E-41	70%	79% 2	2-123 20-143	
b622L	260375260136	80	9,626	11.37	No Hit Found						No Hit Found							
b624R	260319260525	69	7,794	11.15	No Hit Found					1	NP_048814 a457R		75.87	3.93E-13	100%	100% 3	3269 138	
b625R	260550260744	65	7,054	12.09	No Hit Found						No Hit Found							
b626R	260597260923	109	13,173	5.19	No Hit Found						No Hit Found							
b627L	260838260632	69	8,277	10.97	No Hit Found					1	NP_048815 a458L		92.82	3.10E-18	60%	76%	169 169	
b632R	265053265292	80	9,469	5.58	No Hit Found						No Hit Found							
b634L	267000266803	66	7,022	10.53	No Hit Found					1	NP 048825 a469L		53.53	2.11E-06	46%	53%	166 1276	
b635L	267178266948	77	9,378	10.64	No Hit Found						No Hit Found							
b637R	267598267801	68	8,113	12.45	No Hit Found						No Hit Found							
b639L	268357268103	85	9,811	8.83	No Hit Found					1	NP 048828 a472L		89.35	3.51E-17	60%	67%	585 1090	
b640L	268734268318	139	16,229	8.27	No Hit Found					1	NP_048833 vaccinia virus F-ORF	embrane lipoprotein lipid attachment site; similar to -C 11.6 kD protein, corresponds to Swiss-Prot 0561	59.31	3.76E-08	60%		140 3372	
										2	NP_477711 wsv189		51.99	6.01E-06	38%	60% 2	2390 2389	
b642L	269022268774	83	9,645	5.15	No Hit Found						No Hit Found							
b643R	268842269081	80	9,555	12.51	No Hit Found						No Hit Found							
b646R	270265270516	84	10,271	9.90	No Hit Found						No Hit Found							
b648L	271204270695	170	20,338	4.26	No Hit Found						No Hit Found							
	271189271398	70	8,321	9.57	No Hit Found						No Hit Found							
b653L		108	12,230	11.09	No Hit Found						No Hit Found							
	273393273157	79	8,996	10.54	No Hit Found						No Hit Found							
b658L		65	7,893	9.49	No Hit Found						No Hit Found							
b660R	274930275157	76	8,839	10.84	No Hit Found						No Hit Found							
	275246275007	80	9,264	5.74	No Hit Found						No Hit Found							
	276274276032	81	9,315	7.18	No Hit Found						No Hit Found							
	277079276648	144	16,446	12.18	No Hit Found					1	NP_048854 Pro-rich, IPPPNMSLP	LS (3x)	63.93	1.55E-09	85%	85%	236 842	
	277504277908	135	12,578	7.86	No Hit Found						No Hit Found							
b669L	277873277565	103	12,637	12.85	No Hit Found						No Hit Found							
	279838280050	71	8,679	7.83	No Hit Found					1	NP 048863 a507R		83.96	1.43E-15	55%		170 170	
	280183280389	69	8,384	10.36	No Hit Found					1	NP_048863 a507R		70.86	1.26E-11	57%		167 116184	
	280283280759	159	17,661	10.62	No Hit Found					1	NP_048864 a508R		109.00	4.57E-23	80%		I153 170	
	280793281068	92	10,820	11.07	No Hit Found					1	NP 048866 a510R		90.89	1.18E-17	87%	90% 1	1367 256	
	281578281279	100	11,484	11.13	No Hit Found						No Hit Found							
b679L	281763281494	90	10,291	11.06	No Hit Found					1	NP_048875 A519L		133.65	1.59E-30	80%	83%	989 181	

Gene Name	Genome Position	A.A. lenath	Peptide Mw		CDD Hit COGs	COG Definition	Bit Score E-value	% % Identity Positive	Query from-to fr	Hit BLASTp Hit	Hit Accession	BLASTp Definition	Bit Score	E-value	% dentity Po	% Quer	y Hit to from-to
b682R	282509282754	82	10,102	9.25	No Hit Found						No Hit Found						
b683R	283064283300	79	8,852	7.18	No Hit Found						No Hit Found						
b686R	284131284334	68	8,388	8.68	No Hit Found						No Hit Found						
b689R	285314285586	91	10,217	4.48	No Hit Found					1	NP 048503 a155R		83.57	1.88E-15	61%	79% 168	32 2793
b690R	285433285651	73	8,924	12.36	No Hit Found						No Hit Found						
b691R	285722286018	99	12,307	11.85	No Hit Found						No Hit Found						
b693R	286618286869	84	9,950	6.00	No Hit Found						No Hit Found						
b695L	287587287015	191	20,832	8.61	No Hit Found					1	NP_048874 a518R		115.16	1.05E-24	62%	71% 3012	25 4100
										2	NP_048885 a529L NP_049041 a685R		102.83 52.76	5.41E-21 6.42E-06	80% 50%	83% 5912 56% 6112	24 167 24 866
b698L	288061287840	74	8,350	7.46	No Hit Found						No Hit Found						
b703R	290057290284	76	9,000	8.21	No Hit Found						No Hit Found						
b706L	292254292054	67	7,436	11.01	No Hit Found						No Hit Found						
b707R	292215292505	97	11,405	11.85	No Hit Found						No Hit Found						
b708R	292258292650	131	15,251	10.26	No Hit Found						No Hit Found						
b709L	292505292275	77	8,527	7.25	No Hit Found						No Hit Found						
b713L	293503293303	67	8,187	11.43	No Hit Found						No Hit Found						
b716R	294379294657	93	10,237	11.20	No Hit Found						No Hit Found						
b717R	294627294968	114	13,310	7.05	No Hit Found						No Hit Found						
b721R	296554296793	80	8,610	11.46	No Hit Found						No Hit Found						
b722R	297145297351	69	8,054	10.67	No Hit Found						No Hit Found						
b726R	298958299224	89	10,443	11.53	No Hit Found						No Hit Found						
b727R	299509299772	88	9,960	9.37	No Hit Found						No Hit Found						
b728R	300382300609	76	8,530	4.88	No Hit Found						No Hit Found						
b729L	300654300427	76	9,356	8.93	No Hit Found						No Hit Found						
b730R	300703300972	90	9,784	4.27	No Hit Found						No Hit Found						
b731L	301192300995	66	7,724	11.79	No Hit Found						No Hit Found						
b732L	301942301715	76	9,239	11.76	No Hit Found						No Hit Found						
b733R	302090302287	66	7,668	6.75	No Hit Found						No Hit Found						
b735L	303135302809	109	13,000	9.64	No Hit Found						No Hit Found						
b737R	304424304690	89	10,170	4.38	No Hit Found						No Hit Found						
b739R	304868305146	93	10,973	6.62	No Hit Found					1	NP_048905 a549R		72.79	3.30E-12	41%	62% 17	79 179
b740R	305522305755	78	9,198	7.09	No Hit Found					1	NP 048906 a550R		77.80	1.04E-13	44%	73% 17	78 55-132
b742L	306626306414	71	8,897	9.48	No Hit Found						No Hit Found						
b745R	307583307795	71	7,778	11.33	No Hit Found						No Hit Found						
b746R	308440308664	75	8,597	9.41	No Hit Found						No Hit Found						
b749L	310397310173	75	8,706	10.82	No Hit Found						No Hit Found						
	310396310731	112	14,021	10.89	No Hit Found						No Hit Found						
b752R		142	15,792	8.34	No Hit Found					1	NP_048916 a560R		72.79	3.36E-12	65%	75% 36	32 45104
	311928312416	163	18,551	10.29	No Hit Found						No Hit Found						
b755R		97	10,795	7.25	No Hit Found						No Hit Found						
	313468313770	101	12,258	9.53	No Hit Found						No Hit Found						
	314268314020	83	9.614	12.35	No Hit Found						No Hit Found						
	316659316252	136	15.665	7.64	No Hit Found					1	NP_048922 a566L		164.08	1.10E-39	87%	87% 18	39 190
b764L	319044318475	190	21.975	10.58	No Hit Found						No Hit Found						
b768R	319808320029	74	8,008	6.65	No Hit Found						No Hit Found						
	320661320425	79	8,679	10.91	No Hit Found					1	NP_048874 a518R		64.31	1.19E-09	53%	66% 17-7	78 162
b773R	321985322182	66	7,959	8.96	No Hit Found						No Hit Found						
	322472322714	81	10,045	12.26	No Hit Found						No Hit Found						
	323143323376	78	9,173	11.50	No Hit Found						No Hit Found						
	323613323951	113	12,462	10.12	No Hit Found						No Hit Found						
	324315323848	156	18,062	11.00	No Hit Found						No Hit Found						
	323873324247	125	14,864	8.73	No Hit Found						No Hit Found						
	324577324858	94	11,087	11.00	No Hit Found						No Hit Found						
	324644324937	98	11,087	11.60	No Hit Found					1		erenyl group binding site (CAAX) box	470.40	3.33E-44	91%	93% 19	98 1 98
	324877325542	222	25,862	7.86	No Hit Found					1	NP_048940 contains pi	Control of the contro		2.70F-34	82%	93% 1	
	325757326056	100	11,570	11.19	No Hit Found					1	NP_048941_a585R No Hit Found		147.52	2.702-34	0470	oz.n 2310	. 1-19
													***	2.045.24	042	909/	ne 4.05
		65	7,512	7.53	No Hit Found					1	NP 048943 a587R		112.46	3.84E-24	81%	89% 16	35 165
b787R	326189326428	80	8,692	12.12	No Hit Found						No Hit Found						

Gene Name	Genome Position	A.A. length	Peptide Mw	pl	CDD Hit Number	COGs	COG Definition	Bit Score	E-value	% % Identity Positive	Query from-to	Hit BLASTp H		Hit Accession	BLASTp Definition	Bit Score	E-value	% Identity F	%	Query	
b788R	326701327336	212	24,494	6.10		No Hit Found							1	NP 048944 a588R		109.38	7.31E-23	50%	68%	1116	1116
b789R	326918327241	108	12,116	10.65		No Hit Found							١	No Hit Found							
b790L	327290327063	76	8,810	11.20		No Hit Found							1	NP_048945 a589L		67.78	1.09E-10	52%	57%	176	176
b793L	328864328547	106	10,790	7.30		No Hit Found							1	NP 048951 a595L		65.86	4.14E-10	62%	68%	159	1982
b794R	328771328989	73	8,487	11.74		No Hit Found							١	No Hit Found							
b797R	329840330391	184	21,832	5.31		No Hit Found							١	No Hit Found							
b799R	331312331542	77	8,587	10.80		No Hit Found							١	No Hit Found							
b804L	333525333319	69	8,639	9.60		No Hit Found							١	No Hit Found							
b806L	333814333374	147	17,496	6.47		No Hit Found							١	No Hit Found							
b807R	333596333799	68	7,964	10.78		No Hit Found							١	No Hit Found							
b808L	334041333769	91	10,550	5.17		No Hit Found							١	No Hit Found							
b809L	334305334063	81	9,347	7.85		No Hit Found							١	No Hit Found							
b810L	335041334361	227	25,362	10.85		No Hit Found							1 2	NP_048961 A605L NP 048962 a606L		244.20 83.19	2.19E-63 6.47E-15	77% 63%	84% 71%	70227 174	1158 174
b814L	336462336259	68	8.087	10.04		No Hit Found								No Hit Found							
b815R	336299336529	77	9,427	10.54		No Hit Found							1	NP 048969 a613R		92.82	3.14E-18	52%	77%	174	982
b817R	337681337953	91	9,911	8.36		No Hit Found							1	NP 048972 a616R		119.78	2.37E-26	63%	68%	291	493
b821R	339599339850	84	10,006	9.75		No Hit Found							١	No Hit Found							
b822R	339622339861	80	9,858	11.23		No Hit Found							١	No Hit Found							
b827R	342463342705	81	9,985	11.15		No Hit Found							١	No Hit Found							
b830L	343739343518	74	8,396	10.19		No Hit Found							1	NP_048982 a626L		164.85	6.57E-40	100%	100%	174	174
b833R	346107346328	74	8,495	11.36		No Hit Found							1	NP_048986 a630R		95.13	6.39E-19	67%	67%	174	174
b834R	346425346676	84	9,368	10.23		No Hit Found							١	No Hit Found							
b835L	346759346532	76	8,645	9.54		No Hit Found							١	No Hit Found							
b836R	347103347369	89	10,548	11.40		No Hit Found							١	No Hit Found							
b837L	348868348416	151	17,573	4.91		No Hit Found							١	No Hit Found							
b838R	348898349290	131	15,301	8.35		No Hit Found							١	No Hit Found							
b845R	351293351529	79	8,874	12.12		No Hit Found							1	NP_048996 a640R		153.68	1.49E-36	96%	97%	179	179
b846L	351821351600	74	8,317	10.74		No Hit Found							1	NP_048997 a641L		144.82	7.04E-34	95%	98%	174	1285
b848L	352899352660	80	9,155	11.33		No Hit Found							١	No Hit Found							
b851R	355248355451	68	8,215	10.22		No Hit Found								No Hit Found							
b854R	355888356205		12,117	7.92		No Hit Found								No Hit Found							
b855L	356272356060	71	8,137	10.71		No Hit Found								NP 049011 a655L		62.39	4.46E-09	54%	65%	170	170
b856R	356289356531	81	9,958	10.96		No Hit Found								No Hit Found							
b861L	358591358397	65	7,677	8.67		No Hit Found								No Hit Found							
b863R	358777358998	74	8,275	6.35		No Hit Found								No Hit Found							
b864R b866R	358998359285 360033360350	96 106	11,535 12,385	8.06 11.46		No Hit Found								No Hit Found No Hit Found							
	360109360750	214	25,351	8.65		No Hit Found								ND 040400 -001		131.34	1.84E-29	49%	600/	47175	4 420
DOOOR	360109360750	214	25,351	0.00		No Hit Found							2	NP_048808 similar to PBCV-1 ORF U17055	a80L, encoded by GenBank Accession Number	101.29	2.04E-20	53%		50146	
													3	NP_048630 similar to PBCV-1 O Number U17055	RF a80L, corresponds to GenBank Accession	97.06	3.84E-19	57%	71%	50140	494
b870L	361566361168	133	14,344	5.96		No Hit Found								NP_049033 a677L		111.31	8.56E-24	77%	82%	169	175
b872L	363026362796	77	9,058	10.26		No Hit Found							١	No Hit Found							
b873R	362956363204	83	9,941	7.92		No Hit Found							١	No Hit Found							
b875R	363278363748	157	17,695	6.56		No Hit Found							1	NP 048354 a6L		63.93	1.60E-09	47%	66%	74143	171
b876R	363453363680	76	8,273	11.42		No Hit Found							١	No Hit Found							
b877R	364224364448	75	8,723	4.38		No Hit Found							١	No Hit Found							
b879R	364671365129	153	18,134	9.66		No Hit Found							١	No Hit Found							
b881R	365789366214	142	15,912	5.88		No Hit Found							1	NP_048354 a6L		51.99	6.13E-06	48%	68%	66112	147
b882R	366333366578	82	8,912	5.03		No Hit Found							1	NP_049046 identical to PBCV-1 t Accession Number M5	erminal repeat ORF, corresponds to GenBank	99.37	3.30E-20	67%	75%	682	277
b885L	367548367327	74	8,633	7.51		No Hit Found							1	No Hit Found							